Table S1. All specimens'information, including individual factors, clinical diagnosis, comorbidity-GI problem, comorbidity sleep complaints, immune-related diseases, and infection

Sample ID	Interindividual factors					Clinical dignosis				Comorbidity - GI problem									Comorbidity - Sleep complaints
	Group	Age	Age categories	Gender	District	Total ASD score	Repetitive behavior	Social retardation	Language retardation	Any GI problem	otal GI problem scor	Esophageal reflux	Peptic ulcer	Dyspepsia	Abdominal distension	Abdominal pain	Constipation	Abnormal stool consistency	Any sleep complaint
S010267417	ASD-current cohort	3	3-4	female	Hunan	7	light	severe	severe	1	2	0	0	1	0	0	1	0	1
S028149270	ASD-current cohort	3	3-4	male	Neimeng	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	1
S017880137	ASD-current cohort	3.5	3-4	male	Anhui	7	light	severe	severe	1	1	0	0	1	0	0	0	0	1
S052209877	ASD-current cohort	5	5-6	male	Beijing	4	secondary	light	light	0	0	0	0	0	0	0	0	0	1
S047332083	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S029726634	ASD-current cohort	4.6	4-5	male	Hunan	7	secondary	severe	secondary	1	1	0	0	0	0	0	1	0	0
S066011047	ASD-current cohort	4.7	4-5	male	Zhejiang	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	1
S062191615	ASD-current cohort	3	3-4	male	Hunan	3	light	light	light	1	3	1	0	1	0	0	1	0	1
S079220702	ASD-current cohort	2.7	2-3	male	Chongqing	6	light	secondary	severe	1	2	0	0	0	0	0	1	1	0
S042076907	ASD-current cohort	2.3	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S068401956	ASD-current cohort	2.9	2-3	male	Hunan	3	light	light	light	1	1	0	0	1	0	0	0	0	0
S052149606	ASD-current cohort	3.4	3-4	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0
S079824184	ASD-current cohort	2.2	2-3	male	Hunan	3	light	light	light	1	2	0	0	1	0	0	0	1	0
S052769051	ASD-current cohort	2.5	2-3	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S057524001	ASD-current cohort	4	4-5	male	Hunan	8	secondary	severe	severe	1	2	1	0	1	0	0	0	0	1
S030914369	ASD-current cohort	3.8	3-4	male	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	1
S071415007	ASD-current cohort	3	3-4	male	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S075299371	ASD-current cohort	5	5-6	male	Jiangxi	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1
S091029468	ASD-current cohort	5	5-6	male	Jiangxi	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0
S006513895	ASD-current cohort	3.6	3-4	male	Hunan	8	severe	secondary	severe	1	2	0	0	1	0	0	1	0	1
S045951214	ASD-current cohort	3	3-4	female	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S029882492	ASD-current cohort	6	5-6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	0	1	0
S009731184	ASD-current cohort	4	4-5	female	Guanxi	3	light	light	light	1	2	0	0	0	0	0	1	1	1
S015431498	ASD-current cohort	2	2-3	male	Hunan	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1
S002421481	ASD-current cohort	3.5	3-4	male	Hubei	4	secondary	light	light	0	0	0	0	0	0	0	0	0	1
S046570220	ASD-current cohort	3.1	3-4	male	Hubei	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	0
S088641125	ASD-current cohort	5	5-6	male	Guandong	6	light	secondary	severe	1	2	0	0	1	0	0	1	0	0
S014873118	ASD-current cohort	9	6	female	Hunan	7	secondary	severe	secondary	1	1	0	0	0	0	0	1	0	1
S059314691	ASD-current cohort	5	5-6	male	Beijing	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0
S063709960	ASD-current cohort	3.1	3-4	female	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0
S023158806	ASD-current cohort	2.6	2-3	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S081074504	ASD-current cohort	3.8	3-4	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	1
S024005657	ASD-current cohort	3	3-4	female	Liaoning	4	secondary	light	light	1	1	0	0	0	0	0	1	0	0
S058857453	ASD-current cohort	2.5	2-3	male	Guanxi	4	light	secondary	light	1	1	0	0	0	1	0	0	0	0
S068664629	ASD-current cohort	9	6	female	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	1
S053236573	ASD-current cohort	2	2-3	male	Sichuan	3	light	light	light	1	2	0	0	0	0	1	1	0	0
S072022190	ASD-current cohort	4	4-5	male	Hunan	5	light	severe	light	1	1	0	0	0	0	0	1	0	0
S062202200	ASD-current cohort	3.8	3-4	male	Hubei	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S034382127	ASD-current cohort	4.1	4-5	male	Hubei	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S066259065	ASD-current cohort	2.5	2-3	male	Hunan	3	light	light	light	1	2	0	0	1	1	0	0	0	0
S043523344	ASD-current cohort	2.1	2-3	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S013971050	ASD-current cohort	2.1	2-3	male	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S005597599	ASD-current cohort	9	6	male	Guandong	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0
S057895423	ASD-current cohort	7	6	male	Sichuan	6	light	secondary	severe	1	5	0	0	1	1	1	1	1	1
S099270985	ASD-current cohort	3	3-4	male	Sichuan	8	severe	secondary	severe	1	1	0	0	0	0	0	1	0	0
S034936868	ASD-current cohort	4	4-5	male	Beijing	5	light	light	severe	1	1	0	0	0	0	0	1	0	0
S099197996	ASD-current cohort	4	4-5	male	Chongqing	7	light	severe	severe	1	2	0	1	1	0	0	0	0	0
S053217533	ASD-current cohort	3	3-4	male	Hunan	5	light	light	severe	1	1	0	0	0	0	0	1	0	0
S085063070	ASD-current cohort	2.11	2-3	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S002211627	ASD-current cohort	5.1	5-6	male	Hubei	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1
S014132811	ASD-current cohort	2	2-3	female	Chongqing	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1
S050497716	ASD-current cohort	2	2-3	female	Chongqing	2	light	light	no	1	3	0	0	1	1	0	1	0	1
S021546620	ASD-current cohort	3.3	3-4	female	Jiangsu	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S059302885	ASD-current cohort	11	6	male	Anhui	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S035140008	ASD-current cohort	2.1	2-3	female	Beijing	4	light	light	secondary	0	0	0	0	0	0	0	0	0	1
S070858712	ASD-current cohort	3	3-4	male	Shanghai	3	no	light	secondary	0	0	0	0	0	0	0	0	0	0
S063360395	ASD-current cohort	2.3	2-3	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	1
S048433160	ASD-current cohort	3.9	3-4	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S020681155	ASD-current cohort	4.3	4-5	male	Guandong	7	light	severe	severe	1	3	1	0	1	0	0	1	0	0
S020301068	ASD-current cohort	2	2-3	male	Guandong	5	secondary	secondary	light	1	1	0	0	0	0	0	1	0	1
S098869964	ASD-current cohort	1.8	1.5-2	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S019487834	ASD-current cohort	14	6	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S061801651	ASD-current cohort	5	5-6	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S004067924	ASD-current cohort	2.4	2-3	male	Hunan	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0
S047662697	ASD-current cohort	9.5	6	male	Shanxi	7	secondary	secondary	severe	1	1	0	0	0	0	0	1	0	0
S042773471	ASD-current cohort	5	5-6	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S012877108	ASD-current cohort	5	5-6	male	Hunan	5	light	light	severe	0	0	0	0	0	0	0	0	0	0
S048463887	ASD-current cohort	6.1	6	male	Beijing	5	light	severe	light	1	1	0	0	0	0	0	1	0	1
S022229670	ASD-current cohort	5.5	5-6	male	Hubei	6	severe	secondary	light	1	1	0	0	0	0	0	1	0	1
S087067002	ASD-current cohort	5.5	5-6	male	Beijing	5	light	secondary	secondary	1	3	0	0	0	1	0	1	1	0
S084617351	ASD-current cohort	10	6	female	Shanghai	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0
S096977815	ASD-current cohort	3	3-4	female	Hunan	5	light	secondary	secondary	1	1	1	0	0	0	0	0	0	1
S000276670	ASD-current cohort	5	5-6	male	Guandong	4	light	light	secondary	1	3	1	0	1	0	0	1	0	0
S098952913	ASD-current cohort	2.3	2-3	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S005182383	ASD-current cohort	4.8	4-5	male	Hubei	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S080206726	ASD-current cohort	3.7	3-4	male	Hunan	5	light	light	severe	0	0	0	0	0	0	0	0	0	0
S083663388	ASD-current cohort	1.6	1-1.5	male	Jiangsu	5	secondary	light	secondary	1	3	0	0	1	1	0	0	1	1
S076990470	ASD-current cohort	4.8	4-5	female	Guandong	7	light	severe	severe	1	1	0	0	0	0	0	1	0	0
S077133964	ASD-current cohort	3.3	3-4	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S054302828	ASD-current cohort	8	6	female	Sichuan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S053327428	ASD-current cohort	2.8	2-3	male	Jiangsu	4	light	light	secondary	1	1	0	0	0	0	0	1	0	0
S023730656	ASD-current cohort	3.4	3-4	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	0	1	0
S085204715	ASD-current cohort	5	5-6	male	Shanghai	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0
S079144888	ASD-current cohort	9	6	male	Hunan	6	light	severe	secondary	1	1	0	0	1	0	0	0	0	0
S009471117	ASD-current cohort	3	3-4	female	Hunan	7	light	severe	severe	1	1	0	0	1	0	0	0	0	1
S069086747	ASD-current cohort	3	3-4	male	Beijing	6	light	secondary	severe	1	1	0	0	0	0	0	0	1	0
S061373309	ASD-current cohort	5	5-6	female	Guandong	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0
S001828848	ASD-current cohort	6	5-6	male	Beijing	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S014007621	ASD-current cohort	7	6	male	Beijing	2	no	light	light	1	1	0	0	0	0	0	1	0	1
S096543417	ASD-current cohort	3	3-4	male	Shandong	7	severe	severe	light	0	0	0	0	0	0	0	0	0	0
S063577478	ASD-current cohort	2.11	2-3	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S008560385	ASD-current cohort	5	5-6	male	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S007579015	ASD-current cohort	4.5	4-5	female	Chongqing	5	light	severe	light	1	1	0	0	0	0	0	1	0	1
S075081714	ASD-current cohort	4.2	4-5	female	Chongqing	4	no	secondary	secondary	1	2	0	0	1	0	0	0	1	0
S098555214	ASD-current cohort	2.8	2-3	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S011313064	ASD-current cohort	3.1	3-4	male	Shanxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S046955999	ASD-current cohort	5.5	5-6	male	Hubei	4	light	light	secondary	1	1	0	0	0	0	0	1	0	1
S040274488	ASD-current cohort	6	5-6	male	Shanghai	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S087258705	ASD-current cohort	2.6	2-3	male	Fujian	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S017709506	ASD-current cohort	3.8	3-4	female	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S001908720	ASD-current cohort	3.5	3-4	male	Jiangxi	8	secondary	severe	severe	1	1	0	0	1	0	0	0	0	0
S042224956	ASD-current cohort	5.7	5-6	male	Hubei	2	no	light	light	0	0	0	0	0	0	0	0	0	0
S088860709	ASD-current cohort	1.7	1.5-2	male	Hunan	7	light	severe	severe	1	6	1	0	1	1	1	1	1	1
S044419278	ASD-current cohort	2.1	2-3	male	Hunan	4	light	secondary	light	1	5	1	0	1	1	0	1	1	1
S093988708	ASD-current cohort	6.5	6	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S005328514	ASD-current cohort	8.9	6	male	Shanghai	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S049933245	ASD-current cohort	5	5-6	female	Guizhou	6	secondary	secondary	secondary	1	3	0	0	1	0	0	1	1	0
S018676161	ASD-current cohort	5.1	5-6	female	Henan	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1
S010611464	ASD-current cohort	2	2-3	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S051274682	ASD-current cohort	2.3	2-3	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	1
S010415363	ASD-current cohort	1.6	1-1.5	female	Hunan	3	light	light	light	1	3	1	0	1	1	0	0	0	0
S091597196	ASD-current cohort	8	6	male	Guandong	7	secondary	severe	secondary	1	4	0	0	0	1	1	1	1	0
S081674347	ASD-current cohort	4.6	4-5	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S001320733	ASD-current cohort	5.3	5-6	male	Hunan	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	1
S023330207	ASD-current cohort	5.7	5-6	male	Hunan	9	severe	severe	severe	1	3	1	0	1	0	0	0	1	1
S079915611	ASD-current cohort	2.11	2-3	female	Hunan	3	light	light	light	1	2	0	0	1	0	0	1	0	0
S058385865	ASD-current cohort	4.8	4-5	male	Tianjin	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S059965092	ASD-current cohort	9.6	6	male	Hunan	7	light	severe	severe	1	1	1	0	0	0	0	0	0	1
S049846695	ASD-current cohort	5.9	5-6	male	Jiangxi	4	light	secondary	light	1	2	0	0	1	0	0	1	0	1
S039963949.2	ASD-current cohort	3.4	3-4	male	Hunan	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S095995882	ASD-current cohort	6.9	6	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	0
S036828742	ASD-current cohort	3	3-4	male	Gansu	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1
S004432885	ASD-current cohort	3	3-4	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	1
S046555664	ASD-current cohort	3	3-4	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S072092727	ASD-current cohort	10	6	male	Guandong	5	secondary	light	secondary	1	1	0	0	0	0	0	1	0	1
S066570971	ASD-current cohort	6	5-6	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S021581713	ASD-current cohort	10	6	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S016861097	ASD-current cohort	5	5-6	male	Hunan	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	0
S077378480	ASD-current cohort	7	6	female	Hunan	6	light	secondary	severe	1	3	1	0	1	1	0	0	0	1
S092534368	ASD-current cohort	6	5-6	male	Sichuan	5	light	severe	light	0	0	0	0	0	0	0	0	0	1
S076470868	ASD-current cohort	11	6	male	Sichuan	5	light	severe	light	0	0	0	0	0	0	0	0	0	1
S079452384	ASD-current cohort	6	5-6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	0	1	1
S020577597	ASD-current cohort	2.6	2-3	male	Guandong	4	light	light	secondary	1	4	0	0	1	1	0	1	1	0
S076140518	ASD-current cohort	6.6	6	male	Hunan	4	light	light	secondary	1	1	0	0	1	0	0	0	0	1
S063659078	ASD-current cohort	6.6	6	male	Xinjiang	7	severe	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S002053989	ASD-current cohort	6.5	6	male	Xinjiang	6	light	severe	secondary	1	4	1	0	1	1	0	1	0	0
S032692741	ASD-current cohort	5.4	5-6	male	Hunan	8	secondary	severe	severe	1	1	0	0	0	0	0	1	0	1
S085747164	ASD-current cohort	4	4-5	male	Gansu	7	light	severe	severe	1	1	0	0	0	0	0	1	0	1
S058328649	ASD-current cohort	4	4-5	male	Gansu	7	secondary	secondary	severe	1	2	0	0	1	0	0	1	0	1
S067288193	ASD-current cohort	4	4-5	male	Zhejiang	6	secondary	severe	light	0	0	0	0	0	0	0	0	0	0
S087581413	ASD-current cohort	2.6	2-3	female	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S029083948	ASD-current cohort	3.6	3-4	male	Shanxi	7	light	severe	severe	1	4	1	0	1	1	0	1	0	1
S027849771	ASD-current cohort	3	3-4	male	Hebei	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S065936597	ASD-current cohort	3.2	3-4	male	Hebei	8	secondary	severe	severe	1	5	0	0	1	1	1	1	1	1
S069265075	ASD-current cohort	3	3-4	male	Shandong	4	no	secondary	secondary	1	3	0	0	1	1	0	0	1	1
S063355259	ASD-current cohort	3	3-4	male	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1
S078473882	ASD-current cohort	5	5-6	male	Guandong	6	light	severe	secondary	1	2	0	0	0	0	0	1	1	0
S084025488	ASD-current cohort	5.1	5-6	male	Sichuan	3	no	light	secondary	0	0	0	0	0	0	0	0	0	0
S028086940	ASD-current cohort	4.1	4-5	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	0
S069630133	ASD-current cohort	4.5	4-5	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S072704995	ASD-current cohort	4.11	4-5	male	Shanxi	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0
S059652972	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	1	2	0	0	1	0	0	1	0	1
S066629531	ASD-current cohort	3.11	3-4	male	Hunan	4	light	secondary	light	1	1	0	0	1	0	0	0	0	0
S087343596	ASD-current cohort	4	4-5	male	Shanghai	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S093346335	ASD-current cohort	9.4	6	male	Beijing	4	light	light	secondary	1	1	0	0	1	0	0	0	0	1
S094983537	ASD-current cohort	3.2	3-4	male	Zhejiang	5	light	secondary	secondary	1	1	0	0	1	0	0	0	0	1
S046850700	ASD-current cohort	3.8	3-4	male	Zhejiang	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S098177018	ASD-current cohort	3.1	3-4	male	Hubei	3	light	light	light	1	2	0	0	1	1	0	0	0	1
S015913346	ASD-current cohort	8.7	6	female	Zhejiang	5	secondary	light	secondary	1	2	0	0	0	0	1	1	0	1
S038844724	ASD-current cohort	3	3-4	male	Beijing	5	light	secondary	secondary	1	3	0	0	1	1	0	1	0	0
S073457294	ASD-current cohort	7	6	male	Zhejiang	6	secondary	secondary	secondary	1	5	1	1	1	1	1	0	0	1
S079769924	ASD-current cohort	2.6	2-3	female	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S062812981	ASD-current cohort	2.1	2-3	female	Hunan	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0
S013894893	ASD-current cohort	3	3-4	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S005035486	ASD-current cohort	4	4-5	male	Hunan	8	secondary	severe	severe	1	3	0	0	1	0	0	1	1	1
S074572074	ASD-current cohort	4.4	4-5	male	Hunan	6	secondary	secondary	secondary	1	2	0	0	1	0	0	1	0	0
S029435804	ASD-current cohort	7	6	male	Hubei	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S086486751	ASD-current cohort	13	6	male	Hunan	2	light	light	no	1	1	0	0	0	0	0	1	0	1
S055175567	ASD-current cohort	2.5	2-3	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1
S015241457	ASD-current cohort	4.9	4-5	male	Beijing	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S054675596	ASD-current cohort	1.4	1-1.5	female	Hunan	9	severe	severe	severe	1	4	0	0	1	1	0	1	1	1
S000562768	ASD-current cohort	12	6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S011064567	ASD-current cohort	12	6	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S025617581	ASD-current cohort	3.3	3-4	male	Liaoning	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1
S087718915	ASD-current cohort	5	5-6	male	Sichuan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S063904986	ASD-current cohort	8	6	male	Hunan	5	light	secondary	secondary	1	1	0	0	1	0	0	0	0	1
S050234356	ASD-current cohort	9	6	male	Hunan	4	light	light	secondary	1	1	0	0	1	0	0	0	0	1
S061631863	ASD-current cohort	3.1	3-4	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S042460945	ASD-current cohort	4	4-5	male	Xinjiang	7	severe	secondary	secondary	1	4	1	0	1	1	1	0	0	1
S068181854	ASD-current cohort	2.1	2-3	male	Beijing	6	severe	secondary	light	1	1	0	0	0	0	0	1	0	1
S036715009	ASD-current cohort	3	3-4	male	Guandong	3	no	light	secondary	1	3	0	0	0	1	0	1	1	0
S056676277	ASD-current cohort	7	6	male	Hunan	9	severe	severe	severe	1	1	0	0	0	0	0	1	0	0
S029051097	ASD-current cohort	3.11	3-4	male	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	1
S092103864	ASD-current cohort	3.1	3-4	male	Guandong	5	secondary	light	secondary	1	2	0	0	1	0	0	1	0	0
S035352387	ASD-current cohort	1.4	1-1.5	male	Hunan	9	severe	severe	severe	1	5	0	0	1	1	1	1	1	1
S043678642	ASD-current cohort	3.5	3-4	male	Hunan	6	severe	secondary	light	1	3	0	0	1	0	0	1	1	1
S067424125	ASD-current cohort	3.7	3-4	male	Hebei	7	secondary	severe	secondary	1	4	0	0	1	1	1	0	1	1
S048284345	ASD-current cohort	2.11	2-3	female	Sichuan	4	secondary	light	light	1	3	0	0	1	0	0	1	1	1
S078709830	ASD-current cohort	2.4	2-3	male	Hunan	3	light	secondary	no	0	0	0	0	0	0	0	0	0	1
S060599906	ASD-current cohort	7	6	male	Shanghai	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S033494219	ASD-current cohort	2.8	2-3	female	Shandong	7	light	severe	severe	1	2	0	0	0	1	0	1	0	1
S085510566	ASD-current cohort	6	5-6	male	Neimeng	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S007086362	ASD-current cohort	6.4	6	male	Shandong	3	light	light	light	1	1	0	0	0	1	0	0	0	0
S060500323	ASD-current cohort	3.5	3-4	male	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S033672671	ASD-current cohort	5	5-6	female	Hunan	5	light	secondary	secondary	1	2	0	0	0	1	0	1	0	0
S040996793	ASD-current cohort	4.6	4-5	female	Hunan	5	secondary	secondary	light	1	1	0	0	1	0	0	0	0	0
S063637597	ASD-current cohort	3.4	3-4	male	Hunan	8	secondary	severe	severe	1	2	0	0	1	0	0	1	0	1
S082906960	ASD-current cohort	6.8	6	male	Hunan	7	secondary	severe	secondary	1	1	0	0	1	0	0	0	0	1
S021715901	ASD-current cohort	7.8	6	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S056165605	ASD-current cohort	6.1	6	male	Guandong	7	light	severe	severe	1	2	0	0	1	0	0	0	1	0
S029986363	ASD-current cohort	4	4-5	male	Chongqing	3	light	light	light	1	2	0	0	1	0	0	0	1	1
S032001033	ASD-current cohort	2	2-3	male	Shandong	3	light	light	light	1	2	0	0	1	0	0	1	0	0
S043010385	ASD-current cohort	2	2-3	male	Hunan	7	secondary	secondary	severe	1	4	0	0	1	1	0	1	1	1
S092071370	ASD-current cohort	3.7	3-4	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S071935193	ASD-current cohort	5	5-6	male	Beijing	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1
S003541520	ASD-current cohort	6	5-6	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1
S064084034	ASD-current cohort	7.1	6	female	Jiangsu	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S063706036	ASD-current cohort	2.4	2-3	male	Hainan	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S083840744	ASD-current cohort	7	6	male	Beijing	8	secondary	severe	severe	1	4	1	0	1	1	1	0	0	1
S021696107	ASD-current cohort	2.8	2-3	male	Hunan	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S078887382	ASD-current cohort	3	3-4	male	Hunan	5	light	severe	light	0	0	0	0	0	0	0	0	0	0
S000607410	ASD-current cohort	2.1	2-3	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1
S036871611	ASD-current cohort	3	3-4	male	Hunan	8	secondary	severe	severe	1	2	0	0	1	1	0	0	0	1
S023289671	ASD-current cohort	3	3-4	male	Hebei	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S030433161	ASD-current cohort	5.7	5-6	male	Hainan	4	light	light	secondary	1	1	0	0	0	0	0	1	0	0
S068031538	ASD-current cohort	1.4	1-1.5	male	Guanxi	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1
S092899001	ASD-current cohort	1.7	1.5-2	male	Guanxi	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0
S090668313	ASD-current cohort	5	5-6	male	Guandong	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1
S077745846	ASD-current cohort	4	4-5	male	Guandong	7	secondary	secondary	severe	1	3	0	0	1	0	1	0	1	1
S036766727	ASD-current cohort	1.4	1-1.5	male	Jiangxi	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0
S043874901	ASD-current cohort	5	5-6	male	Zhejiang	5	secondary	secondary	light	1	1	0	0	0	0	0	1	0	0
S058082440	ASD-current cohort	4	4-5	male	Fujian	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S042522580	ASD-current cohort	10	6	male	Hainan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S059113922	ASD-current cohort	7	6	male	Hunan	3	no	light	secondary	0	0	0	0	0	0	0	0	0	0
S084424503	ASD-current cohort	3.4	3-4	male	Shandong	7	secondary	severe	secondary	1	5	1	0	1	1	1	1	0	1
S076441039	ASD-current cohort	6	5-6	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0
S099177289	ASD-current cohort	5.6	5-6	male	Hebei	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S089610227	ASD-current cohort	5.9	5-6	male	Hebei	3	light	secondary	no	1	1	0	0	0	0	0	1	0	0
S054829376	ASD-current cohort	3	3-4	male	Hubei	5	secondary	secondary	light	1	1	0	0	0	0	0	1	0	0
S039388824	ASD-current cohort	5.5	5-6	male	Shandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	0	1	0
S079044310	ASD-current cohort	11	6	male	Sichuan	7	secondary	secondary	severe	1	1	0	0	0	0	0	1	0	1
S095478366	ASD-current cohort	1.5	1-1.5	female	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S097730537	ASD-current cohort	12	6	male	Beijing	2	light	light	no	0	0	0	0	0	0	0	0	0	0
S001129570	ASD-current cohort	4.8	4-5	male	Sichuan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S077315646	ASD-current cohort	4.5	4-5	male	Beijing	5	light	secondary	secondary	1	2	0	0	0	1	0	1	0	0
S079362228	ASD-current cohort	5	5-6	male	Beijing	5	light	secondary	secondary	1	3	0	0	0	1	0	1	1	0
S024586216	ASD-current cohort	3	3-4	male	Beijing	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S079826129	ASD-current cohort	8	6	male	Xinjiang	5	light	secondary	secondary	1	5	0	0	1	1	1	1	1	1
S021653713	ASD-current cohort	2.3	2-3	male	Tianjin	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S032056551	ASD-current cohort	5	5-6	male	Fujian	3	light	light	light	1	1	0	0	0	0	0	1	0	1
S005136066	ASD-current cohort	2.8	2-3	male	Hunan	5	light	light	severe	0	0	0	0	0	0	0	0	0	0
S028297290	ASD-current cohort	2.3	2-3	female	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	0
S057034674	ASD-current cohort	2.6	2-3	female	Hunan	4	no	light	severe	0	0	0	0	0	0	0	0	0	0
S071954091	ASD-current cohort	7	6	male	Guandong	8	secondary	severe	severe	1	1	0	0	1	0	0	0	0	1
S036637115	ASD-current cohort	3.4	3-4	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S016640409	ASD-current cohort	4.2	4-5	male	Jiangxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S030569933	ASD-current cohort	3.1	3-4	male	Hubei	7	light	severe	severe	1	2	0	0	1	0	0	1	0	0
S024661856	ASD-current cohort	3.3	3-4	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1
S049700886	ASD-current cohort	3.11	3-4	male	Shandong	4	light	light	secondary	0	0	0	0	0	0	0	0	0	1
S037895617	ASD-current cohort	3	3-4	female	Sichuan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0
S054635235	ASD-current cohort	3	3-4	male	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0
S095096450	ASD-current cohort	3	3-4	male	Sichuan	6	secondary	secondary	secondary	1	5	0	0	1	1	1	1	1	1
S027137763	ASD-current cohort	4.6	4-5	male	Hainan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0
S016103763	ASD-current cohort	5	5-6	male	Hunan	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	0
S089048800	ASD-current cohort	2.2	2-3	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	1
S012439451	ASD-current cohort	2.2	2-3	male	Hunan	7	secondary	secondary	severe	1	5	1	0	1	1	0	1	1	0
S073317673	ASD-current cohort	3	3-4	male	Hunan	8	secondary	severe	severe	1	2	0	0	0	1	0	1	0	0
S004168813	ASD-current cohort	4	4-5	male	Sichuan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0
S058947991	ASD-current cohort	11	6	female	Shanxi	3	light	secondary	no	1	1	0	0	0	0	0	1	0	0

S052347644	ASD-current cohort	8	6	female	Hunan	3	light	light	light	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S042488240	ASD-current cohort	4	4-5	male	Hunan	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		34	40	Cesarean section	3	2	0	0	0	0	0	35	Yes
S055471018	ASD-current cohort	4	4-5	male	Guandong	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	1	0	0	0	0		0	0	0	0		26	39	Cesarean section	1	1	0	0	0	0	0	26	Yes
S068728515	ASD-current cohort	2	2-3	female	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	1	2	1	2	0	1	0	1	0	0	0	0		0	0	0	0		35	37	Cesarean section	4	1	0	0	0	0	0	37	Yes
S033175635	ASD-current cohort	4.5	4-5	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	2	1	2	0	1	0	1	0	0	1	0		0	1	0	0		29	39+1	Cesarean section	3	2	0	0	0	0	0	32	Yes
S042780854	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	3	1	3	1	1	0	1	0	0	0	0		0	0	0	0		29	39+1	Cesarean section	3	2	0	0	0	0	0	32	Yes
S044796684	ASD-current cohort	5.3	5-6	male	Jiangsu	6	no	severe	severe	1	3	0	0	1	1	0	0	1	1	2	1	2	0	1	0	1	1	0	0	0		0	0	0	0		26	34+	Vaginally delivery	1	1	1	0	0	0	0	27	Yes
S011909923	ASD-current cohort	3.3	3-4	male	Hunan	4	no	secondary	secondary	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	1	0	0		0	1	0	0		32	40+4	Cesarean section	1	1	1	0	1	0	0	32	Yes
S046065218	ASD-current cohort	7	6	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	1	2	1	2	1	0	0	1	1	1	1	0		0	0	0	0		27	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S090423397	ASD-current cohort	3.2	3-4	male	Jiangsu	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	1	0	0	0	0		0	0	0	0		26	40	Cesarean section	3	2	0	0	0	0	0	26	Yes
S015397436	ASD-current cohort	3.1	3-4	male	Shandong	4	light	secondary	light	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	1	1	0	1	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S016699451	ASD-current cohort	2	2-3	male	Shandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	1	1	0	0	0		0	0	0	0		32	39+5	Cesarean section	1	1	0	0	0	0	0	33	Yes
S085537502	ASD-current cohort	3	3-4	male	Shandong	7	light	severe	severe	1	3	0	0	1	1	0	0	1	1	2	1	2	1	1	0	0	1	0	1	0		0	1	0	0		32	39+5	Cesarean section	1	1	0	0	0	0	0	33	Yes
S094459692	ASD-current cohort	1.8	1.5-2	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	2	2	0	0	1	0	0	30	Yes
S018789918	ASD-current cohort	1.6	1-1.5	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	39	Vaginally delivery	2	2	0	0	0	0	0	31	Yes
S044264474	ASD-current cohort	3	3-4	male	Hebei	6	secondary	secondary	secondary	1	2	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		32	39	Cesarean section	2	2	1	0	0	0	0	33	Yes
S087607695	ASD-current cohort	3	3-4	male	Jiangsu	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	0	1	0	1	0	0	0		0	0	0	0		33	39	Cesarean section	2	2	0	0	0	0	0	36	Yes
S025259034	ASD-current cohort	3	3-4	male	Jiangsu	5	light	secondary	secondary	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	39	Cesarean section	2	2	0	0	0	0	0	36	Yes
S076156851	ASD-current cohort	4.7	4-5	male	Guandong	7	secondary	severe	secondary	1	4	0	0	1	1	0	1	1	1	1	1	1	0	0	1	0	0	0	0	0		0	0	1	0		29	38+2	Vaginally delivery	1	1	1	0	0	0	0	28	Yes
S002427806	ASD-current cohort	7	6	male	Hunan	8	secondary	severe	severe	1	2	0	0	1	0	0	1	0	1	3	1	3	1	1	1	0	0	0	0	0		0	0	0	0		38	40	Vaginally delivery	3	2	0	0	0	0	0	38	Yes
S076175320	ASD-current cohort	3.1	3-4	male	Shanxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		31	39	Vaginally delivery	1	1	0	0	0	0	0	34	Yes
S061184614	ASD-current cohort	3.5	3-4	male	Shanxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	1	1	0	0	0	0	0	34	Yes
S075097141	ASD-current cohort	6	5-6	male	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	2	2	0	0	0	0	0	37	Yes
S061327562	ASD-current cohort	6.5	6	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	2	2	0	0	0	0	0	37	Yes
S077881396	ASD-current cohort	6	5-6	male	Guandong	4	no	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		27	41	Cesarean section	1	1	0	0	0	0	0	32	Yes
S007268307	ASD-current cohort	5	5-6	male	Hebei	6	secondary	secondary	secondary	1	1	0	0	0	1	0	0	0	1	2	1	2	1	0	1	0	1	0	0	0		0	0	0	0		27	38	Cesarean section	1	1	0	0	1	0	0	29	Yes
S046356382	ASD-current cohort	4.1	4-5	male	Hebei	3	light	light	light	1	1	0	0	0	0	0	1	0	1	2	1	2	1	1	0	0	1	0	0	0		0	0	0	0		27	38+3	Cesarean section	1	1	0	0	0	0	0	29	Yes
S071053119	ASD-current cohort	4	4-5	male	Hunan	9	severe	severe	severe	1	2	0	0	0	1	0	0	1	1	1	1	1	0	0	1	0	1	0	0	0		0	0	0	0		28	39	Cesarean section	1	1	0	0	0	0	0	28	Yes
S069993055	ASD-current cohort	4	4-5	male	Hunan	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		28	40	Cesarean section	1	1	1	0	0	0	0	28	Yes
S009098815	ASD-current cohort	9	6	male	Sichuan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	37	Cesarean section	3	2	0	0	0	0	0	34	Yes
S057957606	ASD-current cohort	4.8	4-5	female	Shanxi	7	light	severe	severe	1	1	0	0	1	0	0	0	0	1	1	1	1	0	0	1	0	1	1	1	0		0	0	0	0		30	36+6	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S010406156	ASD-current cohort	6	5-6	female	Shandong	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		40	40	Vaginally delivery	5	2	0	0	0	0	0	40	Yes
S029346708	ASD-current cohort	6	5-6	female	Shandong	5	light	light	severe	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		40	40	Vaginally delivery	2	2	0	0	0	0	0	40	Yes
S067434907	ASD-current cohort	9	6	female	Hunan	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	1	2	1	2	1	1	0	0	1	0	0	0		0	0	0	0		26	39+4	Vaginally delivery	3	2	0	0	0	0	0	27	Yes
S016323446	ASD-current cohort	6.5	6	female	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	1	2	1	2	1	1	0	0	1	0	0	0		0	0	0	0		27	40+2	Cesarean section	2	1	0	0	0	0	0	28	Yes
S021274737	ASD-current cohort	6	5-6	female	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	37	Cesarean section	4	2	0	0	0	0	0	45	Yes
S067121792	ASD-current cohort	6.5	6	male	Hunan	4	light	secondary	light	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		39	38	Cesarean section	4	2	0	0	0	0	0	45	Yes
S027914411	ASD-current cohort	7.6	6	male	Guandong	8	secondary	severe	severe	1	5	1	1	1	0	0	1	1	1	2	1	2	0	1	0	0	1	0	0	1	Cytomegalovirus	0	0	0	1	Amniotic fluid choking	31	39	Cesarean section	1	1	1	0	0	0	0	31	Yes
S066914998	ASD-current cohort	14	6	male	Hunan	2	light	light	no	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	1	1	0	0		0	0	0	0		27	40	Cesarean section	2	1	0	0	0	0	0	26	Yes
S037280938	ASD-current cohort	3.9	3-4	male	Beijing	4	light	secondary	light	1	3	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	1	1	1	0		0	1	0	0		30	42	Vaginally delivery	1	1	1	0	0	0	0	34	Yes
S058677003	ASD-current cohort	3.6	3-4	male	Beijing	6	light	severe	secondary	1	1	0	0	1	0	0	0	0	1	2	1	2	0	1	0	1	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	1	1	0	0	0	0	0	35	Yes
S086007084	ASD-current cohort	3.1	3-4	male	Hunan	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		35	40	Cesarean section	4	2	0	0	0	0	0	41	Yes
S070213977	ASD-current cohort	5	5-6	male	Henan	5	light	secondary	secondary	1	2	0	0	1	1	0	0	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		28	42	Cesarean section	2	1	0	0	0	0	0	32	Yes
S046320325	ASD-current cohort	2.1	2-3	male	Shandong	6	light	severe	secondary	1	4	0	0	1	1	0	1	1	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		28	39	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S035031679	ASD-current cohort	6	5-6	male	Beijing	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	39	Cesarean section	1	1	0	0	0	0	0	27	Yes
S059632902	ASD-current cohort	5	5-6	male	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	1	0		40	40	Vaginally delivery	2	2	0	0	1	0	0	46	Yes
S034338117	ASD-current cohort	8	6	male	Shandong	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	1	1	1	1	1	0	0	0	1	0	0	0		0	0	0	0		26	40	Cesarean section	1	1	0	0	0	0	0	29	Yes
S026133809	ASD-current cohort	2	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	38	Cesarean section	3	2	0	0	0	0	0	27	Yes
S041740920	ASD-current cohort	4	4-5	female	Beijing	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		28	37	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S016098792	ASD-current cohort	1.10	1.5-2	female	Hunan	4	light	light	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	1	0		30	39+3	Cesarean section	4	3	0	0	0	0	0	35	Yes
S071282920	ASD-current cohort	5	5-6	male	Jiangsu	3	light	light	light	1	1	0	0	0	0	0	1	0	1	2	1	2	1	1	0	0	0	0	0	0		0	0	0	0		24	38	Cesarean section	2	2	0	0	1	0	0	32	Yes
S073114907	ASD-current cohort	2.2	2-3	male	Beijing	5	light	secondary	secondary	1	5	0	0	1	1	1	1	1	1	3	1	3	1	1	0	1	1	1	1	0		0	1	0	0		35	36	Vaginally delivery	1	1	1	0	0	0	0	35	Yes
S010188350	ASD-current cohort	2	2-3	male	Beijing	3	light	light	light	1	1	0	0	1	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		35	40	Vaginally delivery	1	1	1	0	0	0	0	35	Yes
S036341843	ASD-current cohort	9	6	male	Beijing	6	secondary	secondary	secondary	1	1	0	0	0	1	0	0	0	1	2	1	2	0	1	0	1	0	0	0	0		0	0	0	0		31	40	Cesarean section	1	1	0	0	0	0	0	27	Yes
S082318931	ASD-current cohort	2.3	2-3	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		31	39+5	Cesarean section	3	1	0	0	0	0	0	36	Yes
S099323003	ASD-current cohort	2.6	2-3	male	Hunan	4	light	light	secondary	1	4	1	0	1	1	0	1	0	1	3	1	3	1	1	1	0	0	0	0	0		0	1	0	0		30	39+5	Cesarean section	3	1	0	0	0	0	0	36	Yes
S002446745	ASD-current cohort	3	3-4	male	Jiangsu	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	1	0	1	0		0	0	0	0		32	40	Cesarean section	2	2	0	0	0	0	0	33	Yes
S086637781	ASD-current cohort	4.8	4-5	male	Jiangxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		36	41	Vaginally delivery	2	2	0	0	0	0	0	38	Yes
S006358720	ASD-current cohort	5	5-6	male	Jiangxi	4	light	secondary	light	1	2	0	0	1	0	0	0	1	1	1	1	1	1	0	0	0	1	1	1	0		0	1	0	0		36	41	Vaginally delivery	2	2	0	0	0	0	0	39	Yes
S051700604	ASD-current cohort	3	3-4	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		25	34	Vaginally delivery	1	1	1	0	1	0	0	32	Yes
S035050739	ASD-current cohort	3.6	3-4	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	1	0		34	37	Vaginally delivery	4	2	0	0	0	0	0	36	Yes
S056014528	ASD-current cohort	4	4-5	male	Hunan	8	secondary	severe	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		34	37	Vaginally delivery	4	2	0	0	0	0	0	37	Yes
S062424159	ASD-current cohort	2.4	2-3	male	Jiangsu	5	secondary	secondary	light	1	1	0	0	1	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		32	40	Cesarean section	2	2	0	0	0	0	0	-	Yes
S006906781	ASD-current cohort	2.6	2-3	male	Hunan	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	1	4	1	4	1	1	0	1	1	0	0	0		0	0	0	1	Hypoxia	33	38	Vaginally delivery	1	1	0	0	0	0	0	34	Yes
S045381844	ASD-current cohort	7	6	male	Sichuan	7	secondary	severe	secondary	1	2	0	0	1	0	0	1	0	0	1	0	1	0	0	0	0	1	1	0	0		0	0	0	1	Hypoxia	29	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S009433789	ASD-current cohort	3	3-4	male	Guandong	7	light	severe	severe	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	1	1	0	0	0		0	0	0	0		26	41	Cesarean section	3	1	0	0	0	0	0	26	Yes
S009676754	ASD-current cohort	3.5	3-4	male	Hunan	8	secondary	severe	severe	1	2	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		28	39	Cesarean section	1	1	0	0	0	0	0	30	Yes
S058044513	ASD-current cohort	3	3-4	male	Hunan	4	light	secondary	light	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	1	1	0	0	0	0	0	30	Yes
S006064766	ASD-current cohort	2.6	2-3	male	Shandong	4	light	light	secondary	1	2	1	0	1	0	0	1	0	1	1	1	1	1	0	0	0	1	0	0	0		0	0	0	0		40	39	Cesarean section	7	2	0	0	0	0	0	41	Yes
S058129833	ASD-current cohort	4.1	4-5	female	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	3	2	0	0	0	0	0	27	Yes
S042310953	ASD-current cohort	5.1	5-6	male	Hunan	2	no	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	38	Cesarean section	5	2	0	0	0	0	0	34	Yes
S062658943	ASD-current cohort	2.11	2-3	female	Hunan	4	no	light	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		28	39	Vaginally delivery	2	2	0	0	0	0	0	33	Yes
S066398372	ASD-current cohort	5.8	5-6	male	Hunan	6	no	severe	severe	1	4	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	38	Cesarean section	1	1	0	0	0	0	0	28	Yes
S064912538	ASD-current cohort	1.8	1.5-2	male	Hunan	5	light	secondary	secondary	1	4	0	0	1	1	0	1	1	1	4	1	4	1	1	1	0	0	0	0	0		0	1	0	1	Hypoxia	38	38	Cesarean section	2	2	1	0	0	0	0	36	Yes
S047794318	ASD-current cohort	6	5-6	male	Shanghai	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	1	1	0	0	0		0	0	1	0		25	39	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S088044721	ASD-current cohort	6.4	6	male	Shanghai	7	light	severe	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		25	39	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S020509008	ASD-current cohort	2	2-3	female	Henan	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S006711647	ASD-current cohort	4.5	4-5	female	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		33	40	Cesarean section	3	1	1	0	1	0	0	34	Yes
S026298087	ASD-current cohort	4.6	4-5	male	Shandong	1	no	light	no	1	4	1	0	0	1	1	1	0	1	1	1	1	1	0	0	0	1	1	1	0		0	0	1	0		31	36	Cesarean section	2	2	1	0	0	0	0	31	Yes
S000492720	ASD-current cohort	5	5-6	male	Shandong	3	light	light	light	1	4	1	0	1	1	0	1	0	1	1	1	1	0	1	0	0	1	1	0	0		0	0	0	0		31	36	Cesarean section	3	2	0	0	0	0	0	31	Yes
S099986045	ASD-current cohort	3	3-4	male	Shanxi	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		37	38+5	Cesarean section	3	2	0	0	0	0	0	37	Yes
S022973618	ASD-current cohort	7	6	male	Guandong	7	secondary	severe	secondary	1	2	1	0	1	0	0	0	0	1	1	1	1	1	0	0	0	1	0	0	0		0	0	1	0		25	39	Vaginally delivery	2	2	1	0	0	0	0	26	Yes
S094589877	ASD-current cohort	3.5	3-4	male	Jiangsu	7	light	severe	severe	1	2	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		36	40	Cesarean section	4	2	0	0	0	0	0	36	Yes
S051507365	ASD-current cohort	8	6	male	Shanghai	4	light	secondary	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		29	40	Cesarean section	2	1	0	0	0	0	0	32	Yes
S096610584	ASD-current cohort	6.3	6	female	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		37	38	Cesarean section	2	2	0	0	0	0	0	40	Yes
S040038430	ASD-current cohort	2	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	2	1	2	1	1	0	0	1	0	0	0		0	0	0	0		45	38	Cesarean section	3	2	0	0	0	0	0	44	Yes
S083681612	ASD-current cohort	2.3	2-3	male	Hunan	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		45	38	Cesarean section	3	2	0	0	0	0	0	44	Yes
S059149935	ASD-current cohort	2.4	2-3	male	Hunan	4	secondary	light	light	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	1	0	0		0	0	0	0		45	38+	Cesarean section	3	2	0	0	0	0	0	44	Yes
S053381856	ASD-current cohort	5	5-6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	38	Cesarean section	1	1	0	0	0	0	0	33	Yes
S073970992	ASD-current cohort	6	5-6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	0	0		31	36	Cesarean section	1	1	0	0	0	0	0	33	Yes
S072820295	ASD-current cohort	12	6	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		22	38	Vaginally delivery	3	1	0	0	0	0	0	26	Yes
S040526821	ASD-current cohort	6	5-6	male	Guandong	7	severe	secondary	secondary	1	4	0	0	1	1	0	1	1	1	4	1	4	1	1	1	1	1	1	0	0		0	0	0	0		25	39	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S065166954	ASD-current cohort	7	6	male	Hunan	4	no	secondary	secondary	1	4	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	37	Cesarean section	4	2	0	0	0	0	0	36	Yes
S039159211	ASD-current cohort	5	5-6	female	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		37	38	Vaginally delivery	2	2	1	0	0	0	0	48	Yes
S025325216	ASD-current cohort	5.4	5-6	female	Hunan	5	light	secondary	secondary	1	6	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		36	38	Vaginally delivery	3	2	0	0	0	0	0	47	Yes
S017829765	ASD-current cohort	2.11	2-3	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	37	Vaginally delivery	2	2	0	0	0	0	0	31	Yes
S085035862	ASD-current cohort	4	4-5	male	Beijing	6	secondary	severe	light	1	2	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	1	1	0	0		0	0	0	0		38	39	Cesarean section	2	2	0	0	0	0	0	42	Yes
S054090548	ASD-current cohort	3.4	3-4	male	Sichuan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		28	39+2	Cesarean section	2	2	0	0	0	0	0	30	Yes
S058302840	ASD-current cohort	2.2	2-3	male	Anhui	4	light	light	secondary	0	0	0	0	0	0	0	0	0	1	2	1	2	0	1	1	0	1	0	0	0		0	0	0	0		26	40	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S015817201	ASD-current cohort	3.4	3-4	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	1	0	1	0	1	0	0	1	0	0	0		0	0	0	0		30	39	Vaginally delivery	2	1	0	0	0	0	0	27	Yes
S050697833	ASD-current cohort	8	6	female	Jiangxi	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	1	0	0	0	0		0	0	0	0		24	38	Cesarean section	3	1	0	0	0	0	0	24	Yes
S055028682	ASD-current cohort	4.1	4-5	female	Sichuan	4	light	light	secondary	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	1	0	0	0	0		0	0	0	0		32	38	Cesarean section	2	2	0	0	0	0	0	45	Yes
S032650772	ASD-current cohort	7	6	male	Guandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S035294472	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		28	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S054102093	ASD-current cohort	2.6	2-3	male	Anhui	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		26	41	Vaginally delivery	2	2	0	0	0	0	0	28	Yes
S057345116	ASD-current cohort	4	4-5	male	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	40	Vaginally delivery	2	1	0	0	0	0	0	30	Yes
S047828999	ASD-current cohort	7	6	male	Hubei	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		28	38	Cesarean section	2	2	0	0	1	0	0	30	Yes
S004810373	ASD-current cohort	2.8	2-3	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		29	42	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S064587730	ASD-current cohort	3	3-4	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		29	42	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S098533695	ASD-current cohort	6.7	6	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	1	0	0	0	0	1	1	0		0	0	0	0		31	37+1	Vaginally delivery	3	1	0	0	0	0	0	37	Yes
S097765270	ASD-current cohort	7	6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	0	1	1	2	1	2	1	1	0	0	0	0	1	0		0	0	0	0		30	37	Vaginally delivery	3	3	0	0	0	0	0	36	Yes
S095050861	ASD-current cohort	4	4-5	female	Hubei	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		25	38	Cesarean section	1	1	0	0	0	0	0	26	Yes
S046857630	ASD-current cohort	3	3-4	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S017938886	ASD-current cohort	1.10	1.5-2	male	Hunan	7	light	severe	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S097224234	ASD-current cohort	8	6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	41	Cesarean section	1	1	0	0	0	0	0	30	Yes
S065708483	ASD-current cohort	3.2	3-4	male	Chongqing	5	light	secondary	secondary	1	3	0	0	1	1	1	0	0	1	1	1	1	1	0	0	0	1	0	0	0		0	1	0	0		28	35+4	Cesarean section	1	1	1	0	0	0	0	29	Yes
S093651148	ASD-current cohort	4	4-5	male	Sichuan	3	no	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		23	38	Cesarean section	1	1	0	0	0	0	0	26	Yes
S068085771	ASD-current cohort	8.1	6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	37	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S037408446	ASD-current cohort	3.2	3-4	male	Jiangsu	3	light	light	light	1	1	0	0	0	0	0	1	0	1	3	1	3	1	1	0	1	1	0	0	0		0	0	0	0		33	42	Cesarean section	3	1	0	0	0	0	0	37	Yes
S028244767	ASD-current cohort	3.8	3-4	male	Jiangsu	4	light	secondary	light	1	2	0	0	1	1	0	0	0	1	2	1	2	1	0	0	1	1	0	0	0		0	0	0	0		34	42	Cesarean section	4	1	0	0	0	0	0	38	Yes
S099329759	ASD-current cohort	2.7	2-3	male	Shanxi	6	secondary	secondary	secondary	1	2	0	0	1	0	0	1	0	1	3	1	3	0	1	1	1	1	0	0	0		0	0	0	0		26	41	Cesarean section	1	1	0	0	1	0	0	28	Yes
S093159376	ASD-current cohort	8	6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	1	1	0	0	1	Virus	0	0	0	0		30	42	Cesarean section	3	2	0	0	0	0	0	32	Yes
S021418197	ASD-current cohort	1.6	1-1.5	male	Jiangxi	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	1	Mycoplasma	0	0	0	0		29	40	Cesarean section	2	2	0	0	0	0	0	29	Yes
S087758455	ASD-current cohort	2.1	2-3	male	Hubei	7	secondary	secondary	severe	1	6	1	0	1	1	1	1	1	1	2	1	2	1	0	0	1	1	1	0	0		0	0	0	0		28	38+5	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S037810180	ASD-current cohort	5.2	5-6	male	Shanxi	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		37	40	Vaginally delivery	4	2	0	0	0	0	0	39	Yes
S058849172	ASD-current cohort	2.8	2-3	male	Shandong	5	light	secondary	secondary	1	4	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		27	38	Cesarean section	4	2	0	0	0	0	0	26	Yes
S029937634	ASD-current cohort	6	5-6	male	Shanghai	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		40	36	Cesarean section	2	1	0	0	0	0	0	46	Yes
S086565756	ASD-current cohort	6.4	6	male	Shanghai	7	secondary	severe	secondary	1	3	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	1	1	0		0	0	0	0		40	36	Cesarean section	2	1	0	0	0	0	0	46	Yes
S081580245	ASD-current cohort	4	4-5	male	Gansu	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	3	1	3	1	1	0	1	1	0	0	0		0	1	0	0		33	39	Vaginally delivery	2	2	0	0	0	0	0	33	Yes
S015639415	ASD-current cohort	5	5-6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		29	42	Cesarean section	1	1	0	0	0	0	0	32	Yes
S091183547	ASD-current cohort	8	6	male	Henan	3	light	light	light	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	2	1	0	0	0	0	0	33	Yes
S086193482	ASD-current cohort	8	6	male	Henan	5	light	severe	light	1	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	1	0	1	1	0		0	1	0	0		31	40	Vaginally delivery	2	1	0	0	0	0	0	33	Yes
S082081587	ASD-current cohort	2.4	2-3	female	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		28	39+3	Cesarean section	1	1	0	0	0	0	0	28	Yes
S011796790	ASD-current cohort	4	4-5	male	Chongqing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	1	0	0	1	1	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S050093844	ASD-current cohort	2.2	2-3	male	Guandong	3	no	light	secondary	0	0	0	0	0	0	0	0	0	1	4	1	4	1	1	1	1	1	1	1	0		0	0	0	0		27	40	Cesarean section	1	1	0	0	0	0	0	37	Yes
S071268840	ASD-current cohort	3	3-4	male	Guandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		37	38	Cesarean section	1	1	1	0	0	0	0	39	Yes
S040560609	ASD-current cohort	4.9	4-5	male	Jiangsu	4	no	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0		0	0	0	0		33	38 + 3	Cesarean section	4	2	0	0	0	0	0	34	Yes
S039372875	ASD-current cohort	2.4	2-3	male	Hunan	7	severe	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Cesarean section	2	2	0	0	0	0	0	27	Yes
S049990446	ASD-current cohort	3	3-4	male	Hubei	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		29	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S085834035	ASD-current cohort	3.3	3-4	male	Hubei	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		29	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S036858549	ASD-current cohort	3	3-4	female	Xinjiang	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		34	34	Cesarean section	1	1	0	0	0	0	0	36	Yes
S081811079	ASD-current cohort	3.4	3-4	female	Xinjiang	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		32	34	Cesarean section	1	1	0	0	0	0	0	36	Yes
S053290592	ASD-current cohort	2.5	2-3	female	Beijing	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S056003579	ASD-current cohort	4	4-5	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		34	38	Cesarean section	1	1	0	0	0	0	0	37	Yes
S078911371	ASD-current cohort	2	2-3	female	Beijing	5	light	secondary	secondary	1	6	1	1	1	1	1	1	0	1	1	1	1	0	1	0	0	1	1	1	0		0	0	0	0		32	38	Cesarean section	1	1	0	0	0	0	0	34	Yes
S047673389	ASD-current cohort	5	5-6	female	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	1	1	0	0	0		0	0	0	0		30	39	Cesarean section	1	1	0	0	1	0	0	35	Yes
S088192659	ASD-current cohort	2.9	2-3	male	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	1	0	0	0	0		0	0	0	1	Amniotic fluid choking	27	39	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S070873487	ASD-current cohort	6.6	6	male	Tianjin	6	light	severe	secondary	1	5	0	0	1	1	1	1	1	0	2	0	2	0	0	0	1	0	0	0	0		0	0	0	1	Amniotic fluid choking	27	38+	Cesarean section	1	1	0	0	1	0	0	32	Yes
S099727433	ASD-current cohort	2.4	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		38	39	Cesarean section	6	2	0	0	0	0	0	38	Yes
S060827077	ASD-current cohort	4.11	4-5	male	Neimeng	3	light	light	light	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		32	35	Cesarean section	2	2	0	0	0	0	0	30	Yes
S068891145	ASD-current cohort	4.6	4-5	male	Guandong	5	secondary	secondary	light	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		29	38+5	Vaginally delivery	3	2	0	0	0	0	0	34	Yes
S036292266	ASD-current cohort	8	6	male	Hubei	3	light	light	light	1	5	1	0	1	1	1	1	0	1	1	1	1	0	1	0	0	1	1	1	0		0	0	0	0		34	39	Cesarean section	1	1	0	0	0	0	0	37	Yes
S070298888	ASD-current cohort	18	6	male	Guandong	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	0	1	0	0	0		0	0	0	1	Umbilical cord around neck	27	38	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S091700989	ASD-current cohort	7.3	6	male	Xinjiang	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		28	38	Cesarean section	2	1	0	0	0	0	0	33	Yes
S056870921	ASD-current cohort	4	4-5	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		24	37+2	Cesarean section	3	2	0	0	0	0	0	28	Yes
S064287285	ASD-current cohort	2.7	2-3	male	Sichuan	4	no	secondary	secondary	1	3	0	0	1	0	0	1	1	1	1	1	1	0	1	0	0	1	1	0	0		0	0	0	0		25	39	Cesarean section	1	1	0	0	0	0	0	31	Yes
S077058381	ASD-current cohort	2.11	2-3	male	Sichuan	3	no	secondary	light	1	3	0	0	1	0	0	1	1	1	2	1	2	0	1	0	1	1	1	0	0		0	0	0	0		25	39	Cesarean section	1	1	0	0	0	0	0	31	Yes
S020109930	ASD-current cohort	7	6	male	Shanxi	5	light	secondary	secondary	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		35	38	Vaginally delivery	3	2	0	0	0	0	0	35	Yes
S075928150	ASD-current cohort	4.7	4-5	male	Sichuan	5	light	secondary	secondary	1	3	0	0	1	0	0	1	1	1	1	1	1	1	0	0	0	1	0	0	0		0	0	0	0		28	40	Cesarean section	1	1	0	0	0	0	0	31	Yes
S094905813	ASD-current cohort	8	6	male	Anhui	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	1	0	0	0	0	0	34	Yes
S073552783	ASD-current cohort	3.5	3-4	female	Beijing	6	secondary	secondary	secondary	1	4	1	0	1	1	0	0	1	1	4	1	4	1	1	1	1	1	1	1	0		0	0	0	0		35	40	Vaginally delivery	2	2	0	0	0	0	0	35	Yes
S060211458	ASD-current cohort	3	3-4	female	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	40	Vaginally delivery	2	2	0	0	0	0	0	35	Yes
S015668764	ASD-current cohort	2.1	2-3	female	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		29	39+5	Vaginally delivery	3	2	0	0	1	0	0	28	Yes
S076157093	ASD-current cohort	6.9	6	male	Guandong	6	light	severe	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		37	35	Vaginally delivery	3	2	0	0	0	0	0	40	Yes
S061328606	ASD-current cohort	3	3-4	female	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0		0	0	0	1	Hypoxia	28	37	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S094581242	ASD-current cohort	5.9	5-6	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		37	39	Cesarean section	2	1	0	0	0	0	0	40	Yes
S098101836	ASD-current cohort	6	5-6	male	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		38	39	Cesarean section	2	1	0	0	0	0	0	40	Yes
S081800131	ASD-current cohort	5.1	5-6	male	Hunan	1	no	light	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	39	Cesarean section	3	2	0	0	0	0	0	40	Yes
S013908689	ASD-current cohort	1.8	1.5-2	female	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		38	39	Cesarean section	3	1	0	0	0	0	0	51	Yes
S088238139	ASD-current cohort	3.2	3-4	female	Hunan	7	light	severe	severe	1	2	0	0	1	0	0	1	0	1	3	1	3	1	0	1	0	0	0	0	0		0	0	0	1	Placental abruption and Hypoxia	29	34	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S048037844	ASD-current cohort	4	4-5	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	0	0	0	0	0		0	0	0	1	Asphyxia	32	40	Cesarean section	2	1	0	0	1	0	0	32	Yes
S018532737	ASD-current cohort	3.6	3-4	male	Shandong	3	light	light	light	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	1	0	0	0		0	0	0	0		21.5	40	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S061174015	ASD-current cohort	3	3-4	male	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	38	Vaginally delivery	4	1	0	0	0	0	0	40	Yes
S065815694	ASD-current cohort	6.7	6	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	36	Cesarean section	5	2	0	0	0	0	0	30	Yes
S015723685	ASD-current cohort	9.6	6	male	Jiangsu	3	light	light	light	1	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0		0	0	1	1	Hypoxia	27	40	Cesarean section	2	1	1	0	0	0	0	29	Yes
S032401420	ASD-current cohort	6	5-6	male	Guandong	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	2	1	0	0	0	0	0	29	Yes
S013157309	ASD-current cohort	6	5-6	male	Guandong	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	2	1	0	0	0	0	0	29	Yes
S071619712	ASD-current cohort	3.7	3-4	female	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		42	39	Cesarean section	5	2	0	0	0	0	0	43	Yes
S059560939	ASD-current cohort	5	5-6	male	Sichuan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	1	1	0	0		0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	0	28	Yes
S084221460	ASD-current cohort	3	3-4	male	Hebei	6	secondary	severe	light	1	3	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	40	Vaginally delivery	2	2	0	0	0	0	0	34	Yes
S008341716	ASD-current cohort	6.6	6	male	Sichuan	4	light	light	secondary	1	4	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		30	39	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S066680294	ASD-current cohort	4	4-5	male	Guandong	5	light	secondary	secondary	1	2	0	0	0	0	0	1	1	1	2	1	2	1	0	1	0	1	0	0	0		0	0	0	0		40	36	Cesarean section	4	3	0	0	0	0	0	45	Yes
S033816210	ASD-current cohort	4	4-5	male	Guizhou	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	1	1	0	0	0	0	0	35	Yes
S038474544	ASD-current cohort	5	5-6	male	Guandong	5	light	secondary	secondary	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	40	Cesarean section	4	2	0	0	0	0	0	32	Yes
S043799295	ASD-current cohort	4	4-5	male	Hunan	4	light	light	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	39	Vaginally delivery	5	2	0	0	0	0	0	44	Yes
S056439081	ASD-current cohort	4.4	4-5	male	Hunan	3	no	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	39	Vaginally delivery	5	2	0	0	0	0	0	42	Yes
S076819435	ASD-current cohort	2.5	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	39	Cesarean section	3	2	0	0	0	0	0	33	Yes
S053915139	ASD-current cohort	5	5-6	male	Guandong	6	secondary	secondary	secondary	1	1	1	0	0	0	0	0	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		27	39	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S033555890	ASD-current cohort	3.3	3-4	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		35	39	Cesarean section	5	2	0	0	0	0	0	35	Yes
S086128846	ASD-current cohort	5	5-6	male	Henan	4	light	light	secondary	1	3	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	39	Cesarean section	5	3	0	0	0	0	0	39	Yes
S015984625	ASD-current cohort	3.5	3-4	male	Shanghai	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		37	38	Cesarean section	4	2	0	0	0	0	0	43	Yes
S082771296	ASD-current cohort	4	4-5	male	Guandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		38	40	Cesarean section	4	1	0	0	0	0	0	42	Yes
S064059638	ASD-current cohort	2.3	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	38	Cesarean section	6	2	1	0	0	0	0	39	Yes
S069601030	ASD-current cohort	4.1	4-5	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	42	Cesarean section	6	2	0	0	0	0	0	35	Yes
S082598833	ASD-current cohort	6.5	6	male	Shandong	5	light	secondary	secondary	1	2	1	0	0	0	0	1	0	1	1	1	1	0	0	1	0	0	0	0	0		0	0	0	0		38	38	Cesarean section	1	1	0	0	0	0	0	37	Yes
S054436239	ASD-current cohort	7	6	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		30	37	Cesarean section	2	1	0	0	0	0	0	30	Yes
S055070573	ASD-current cohort	1.8	1.5-2	male	Hunan	6	secondary	secondary	secondary	1	5	0	0	1	1	1	1	1	1	3	1	3	1	1	0	1	1	1	0	0		0	0	0	0		25	38	Cesarean section	2	2	0	0	0	0	0	29	Yes
S050431364	ASD-current cohort	5.6	5-6	male	Hunan	3	light	secondary	no	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		21	38	Cesarean section	1	1	0	0	0	0	0	25	Yes
S008045783	ASD-current cohort	8.9	6	male	Hubei	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		31	39	Cesarean section	3	1	0	0	0	0	0	32	Yes
S030553656	ASD-current cohort	9.3	6	male	Hubei	3	light	light	light	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		31	39	Cesarean section	3	1	0	0	0	0	0	32	Yes
S000374601	ASD-current cohort	9	6	male	Sichuan	4	no	secondary	secondary	1	5	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S004458161	ASD-current cohort	7	6	male	Shanghai	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	1	2	1	2	1	0	1	0	0	0	0	0		0	0	0	0		30	39	Cesarean section	1	1	0	0	0	0	0	31	Yes
S018863698	ASD-current cohort	5.1	5-6	male	Beijing	5	secondary	secondary	light	1	1	0	0	0	1	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	2	1	0	0	0	0	0	31	Yes
S043949105	ASD-current cohort	9	6	male	Beijing	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	2	1	2	1	0	1	0	1	0	0	0		0	1	0	0		33	36	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S005097542	ASD-current cohort	9	6	male	Beijing	7	secondary	severe	secondary	1	3	0	0	0	0	0	1	1	1	5	1	5	1	1	1	1	1	0	0	1	Cytomegalovirus	0	0	0	1	Hypoxia	33	38	Vaginally delivery	2	1	1	0	1	0	0	32	Yes
S000525184	ASD-current cohort	2.5	2-3	male	Guandong	7	light	severe	severe	1	4	0	0	1	1	1	0	1	1	1	1	1	1	0	0	0	1	1	1	0		0	0	0	0		40	36	Vaginally delivery	4	2	0	0	0	0	0	48	Yes
S044533893	ASD-current cohort	4.9	4-5	male	Beijing	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	38	Cesarean section	1	1	0	0	0	0	0	32	Yes
S046772737	ASD-current cohort	4.6	4-5	male	Shanxi	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	40	Cesarean section	1	1	0	0	0	0	0	33	Yes
S009798333	ASD-current cohort	3	3-4	male	Hunan	1	no	light	no	1	5	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	1	1	0	0		0	1	0	0		38	32+1	Vaginally delivery	6	2	0	0	1	0	0	40	Yes
S014581530	ASD-current cohort	2.5	2-3	male	Guandong	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	39	Vaginally delivery	2	1	0	0	0	0	0	31	Yes
S004808835	ASD-current cohort	2.8	2-3	male	Guandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		31	39	Vaginally delivery	2	1	0	0	0	0	0	31	Yes
S055369015	ASD-current cohort	4.3	4-5	male	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S023095308	ASD-current cohort	5	5-6	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	2	1	2	1	1	0	0	1	0	0	0		0	0	1	0		26	40	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S002977051	ASD-current cohort	10	6	male	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	1	3	1	3	1	1	0	0	0	0	0	0		0	0	0	1	Umbilical cord around neck	28	36+1	Cesarean section	1	1	0	0	0	1	0	31	Yes
S089447180	ASD-current cohort	10.4	6	male	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	1	2	1	2	1	1	0	0	0	0	0	0		0	0	0	0		29	35	Cesarean section	1	1	0	0	0	0	0	31	Yes
S063803819	ASD-current cohort	2.2	2-3	male	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		26	39+2	Vaginally delivery	4	2	0	0	0	0	0	30	Yes
S004172671	ASD-current cohort	1.8	1.5-2	female	Hunan	4	light	light	secondary	1	3	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		38	37	Cesarean section	2	2	0	0	0	0	1	37	Yes
S018986140	ASD-current cohort	5.4	5-6	male	Shanghai	6	light	severe	secondary	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0		0	1	0	0		32	40	Vaginally delivery	2	2	0	0	1	0	0	33	Yes
S054863117	ASD-current cohort	5	5-6	male	Shanghai	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S097646390	ASD-current cohort	4	4-5	male	Shanghai	7	secondary	secondary	severe	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		36	40	Vaginally delivery	4	1	0	0	0	0	0	39	Yes
S031300289	ASD-current cohort	5.1	5-6	male	Xinjiang	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		30	40	Cesarean section	1	1	0	0	1	0	0	31	Yes
S030063741	ASD-current cohort	4	4-5	male	Shanxi	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S031145505	ASD-current cohort	2.4	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		22	37	Vaginally delivery	5	3	0	0	1	0	0	25	Yes
S076183221	ASD-current cohort	10.2	6	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	37	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S020398302	ASD-current cohort	4	4-5	male	Shanghai	7	light	severe	severe	1	1	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0		0	0	0	1	Pneumothorax	36	38+3	Cesarean section	1	1	1	0	0	0	0	37	Yes
S031304695	ASD-current cohort	4	4-5	male	Hunan	7	secondary	severe	secondary	1	3	0	0	1	0	1	1	0	1	4	1	4	1	1	1	1	0	0	0	0		0	0	0	0		20	42	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S073548117	ASD-current cohort	5	5-6	male	Beijing	5	light	secondary	secondary	1	2	0	0	1	1	0	0	0	1	1	1	1	1	0	0	0	1	0	1	0		0	0	0	0		30	37	Cesarean section	1	1	1	0	0	0	0	32	Yes
S039871836	ASD-current cohort	5.4	5-6	male	Beijing	4	light	secondary	light	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	0	0		31	37	Cesarean section	1	1	1	0	0	0	0	32	Yes
S082103209	ASD-current cohort	2	2-3	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	1	Cytomegalovirus	0	0	0	0		40	40	Cesarean section	4	1	1	0	0	0	0	37	Yes
S048105139	ASD-current cohort	2.3	2-3	male	Beijing	8	secondary	severe	severe	1	6	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		26	40	Vaginally delivery	2	2	0	0	0	0	0	26	Yes
S048932658	ASD-current cohort	4.6	4-5	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	40	Cesarean section	4	2	0	0	0	0	0	39	Yes
S018713702	ASD-current cohort	3	3-4	female	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		29	36	Cesarean section	3	2	0	0	0	0	0	32	Yes
S008680604	ASD-current cohort	3.4	3-4	female	Hunan	5	light	light	severe	1	3	0	0	1	1	0	0	1	1	3	1	3	0	1	1	1	0	0	0	0		0	0	0	0		29	37	Cesarean section	3	2	0	0	0	0	0	32	Yes
S046112045	ASD-current cohort	2	2-3	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	38+2	Cesarean section	1	1	1	0	0	0	0	32	Yes
S002815335	ASD-current cohort	6	5-6	female	Hunan	6	light	severe	secondary	1	3	0	0	1	0	1	1	0	1	2	1	2	0	1	0	1	1	1	0	0		0	0	0	0		27	39	Cesarean section	1	1	0	0	0	0	0	29	Yes
S071817012	ASD-current cohort	5.8	5-6	female	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	2	1	2	0	1	0	1	0	0	0	0		0	0	0	0		27	40	Cesarean section	1	1	0	0	0	0	0	30	Yes
S085840923	ASD-current cohort	1.6	1-1.5	female	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		32	39	Cesarean section	5	2	0	0	0	0	0	32	Yes
S024432562	ASD-current cohort	4	4-5	male	Beijing	4	light	secondary	light	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	1	0		29	29	Vaginally delivery	1	1	1	0	0	0	0	25	Yes
S097892633	ASD-current cohort	7	6	male	Guandong	5	secondary	secondary	light	1	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		32	40	Vaginally delivery	1	1	1	0	0	0	0	32	Yes
S012521091	ASD-current cohort	2.9	2-3	male	Hunan	3	no	light	secondary	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	Virus	0	0	0	0		28	38	Cesarean section	6	2	0	0	0	0	0	31	Yes
S041130785	ASD-current cohort	2.9	2-3	male	Hunan	6	light	secondary	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		36	36	Cesarean section	4	2	0	0	0	0	0	45	Yes
S004978827	ASD-current cohort	2.5	2-3	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	Mycoplasma	0	0	0	0		36	40	Cesarean section	6	2	0	0	0	0	0	45	Yes
S064065028	ASD-current cohort	4	4-5	female	Beijing	5	no	secondary	severe	1	1	0	0	0	0	0	1	0	1	1	1	1	0	0	1	0	1	1	0	0		0	0	0	0		33	37	Cesarean section	3	2	0	0	1	0	0	32	Yes
S050440950	ASD-current cohort	2.6	2-3	male	Hunan	4	light	light	secondary	1	2	0	0	0	0	0	1	1	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		39	38	Cesarean section	2	2	0	0	0	0	0	37	Yes
S038515496	ASD-current cohort	2.9	2-3	male	Hunan	5	light	secondary	secondary	1	5	1	0	1	1	1	1	0	1	3	1	3	1	1	0	1	1	0	1	0		0	0	0	0		38	38	Cesarean section	2	2	0	0	0	0	0	36	Yes
S001680900	ASD-current cohort	5.4	5-6	male	Hunan	3	light	light	light	1	2	0	0	0	0	1	1	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	3	2	1	0	0	0	0	25	Yes
S060929136	ASD-current cohort	6.5	6	male	Hunan	7	light	severe	severe	1	2	0	0	0	1	0	1	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		25	38	Cesarean section	2	1	0	0	0	0	0	26	Yes
S067634646	ASD-current cohort	3	3-4	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0		0	0	0	0		29	39	Cesarean section	4	2	0	0	0	0	0	30	Yes
S053655907	ASD-current cohort	5.6	5-6	male	Shandong	3	light	light	light	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	1	1	1	0	0		0	0	0	0		27	40	Cesarean section	1	1	1	0	0	0	0	26	Yes
S037373938	ASD-current cohort	3	3-4	male	Beijing	3	light	light	light	1	1	0	0	0	0	0	1	0	1	2	1	2	1	1	0	0	0	0	0	0		0	0	0	0		36	40	Vaginally delivery	4	2	0	0	0	0	0	36	Yes
S075163781	ASD-current cohort	3.5	3-4	male	Beijing	6	secondary	secondary	secondary	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Cesarean section	1	1	1	0	0	0	0	34	Yes
S084490041	ASD-current cohort	5	5-6	male	Tianjin	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		26	38	Cesarean section	2	1	0	0	0	0	0	32	Yes
S087609883	ASD-current cohort	7.1	6	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	1	1	1	1	0	0	1	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	36	Yes
S008965756	ASD-current cohort	6.5	6	male	Hunan	4	light	secondary	light	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		27	41	Cesarean section	1	1	0	0	0	0	0	36	Yes
S028070540	ASD-current cohort	6.6	6	male	Hubei	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		35	37	Cesarean section	2	2	0	0	0	0	0	34	Yes
S083897228	ASD-current cohort	2.4	2-3	female	Hunan	2	light	light	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		30	38+2	Cesarean section	1	1	0	0	0	0	0	30	Yes
S036641643	ASD-current cohort	2	2-3	female	Hunan	4	light	secondary	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Cesarean section	1	1	0	0	0	0	0	30	Yes
S000597148	ASD-current cohort	5	5-6	male	Tianjin	4	light	light	secondary	1	3	0	0	1	1	0	1	0	1	2	1	2	1	1	0	0	1	1	1	0		0	0	0	0		33	38	Cesarean section	1	1	0	0	0	0	0	35	Yes
S000566368	ASD-current cohort	5.1	5-6	male	Shandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	4	1	4	1	1	1	0	0	0	0	0		0	0	1	1	Hypoxia	30	40	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S082274273	ASD-current cohort	4.7	4-5	male	Hunan	8	secondary	severe	severe	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		32	39	Vaginally delivery	3	1	0	0	0	0	0	32	Yes
S020688205	ASD-current cohort	8.6	6	male	Jilin	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	40	Cesarean section	2	2	0	0	0	0	0	45	Yes
S004398997	ASD-current cohort	8	6	male	Jilin	7	light	severe	severe	1	2	0	0	1	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		38	40	Cesarean section	2	2	0	0	0	0	0	45	Yes
S091692366	ASD-current cohort	9.6	6	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	1	0	0	0	27	Yes
S022302444	ASD-current cohort	6.6	6	male	Hunan	5	no	secondary	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	38	Cesarean section	2	2	0	0	0	0	0	40	Yes

S091572287	ASD-current cohort	3.3	3-4	male	Guandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S051121042	ASD-current cohort	4	4-5	female	Jiangxi	5	no	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		33	30	Vaginally delivery	4	2	0	0	0	0	0	34	Yes
S007421821	ASD-current cohort	7.5	6	male	Hunan	5	secondary	secondary	light	1	1	0	0	0	0	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		23	36	Vaginally delivery	3	2	0	0	0	0	0	24	Yes
S067957634	ASD-current cohort	3.1	3-4	male	Hubei	7	light	severe	severe	1	4	0	0	1	1	1	0	1	1	1	1	1	1	0	0	0	1	0	1	1	Rubella virus	0	0	0	0		35	41+4	Cesarean section	2	1	1	0	0	0	0	42	Yes
S011006414	ASD-current cohort	8	6	male	Henan	8	secondary	severe	severe	1	3	0	0	1	1	0	1	0	1	0	1	4	1	1	1	1	0	0	0	0		0	0	0	0		24	39	Cesarean section	4	2	0	0	0	0	0	25	Yes
S062443725	ASD-current cohort	10	6	male	Guandong	2	light	light	no	1	1	0	0	0	0	0	1	0	1	0	1	2	1	0	1	0	1	0	0	0		0	0	1	0		33	39	Cesarean section	3	2	0	0	0	0	0	37	Yes
S091796963	ASD-current cohort	5.5	5-6	female	Xinjiang	3	light	light	light	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	0	0	1	0	0	0		0	0	0	0		29	42	Cesarean section	1	1	0	0	0	0	0	25	Yes
S023049183	ASD-current cohort	7	6	male	Hunan	2	light	light	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	41	Vaginally delivery	2	2	1	0	0	0	0	30	Yes
S062120932	ASD-current cohort	3.3	3-4	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		0	1	0	1	Asphyxia	28	37	Vaginally delivery	3	1	0	0	0	0	0	26	Yes
S006867610	ASD-current cohort	3.3	3-4	male	Beijing	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	39	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S011929779	ASD-current cohort	4	4-5	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	38	Cesarean section	1	1	0	0	0	0	0	30	Yes
S036551486	ASD-current cohort	3.6	3-4	male	Guandong	7	light	severe	severe	1	4	0	0	1	1	1	0	1	1	1	1	2	1	0	0	1	1	0	0	0		0	0	0	0		32	40	Cesarean section	3	1	1	0	0	0	0	38	Yes
S084986086	ASD-current cohort	9	6	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	37	Cesarean section	2	1	0	0	0	0	0	41	Yes
S061942107	ASD-current cohort	10	6	male	Guandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	0		0	0	0	0		38	37	Cesarean section	2	1	0	0	0	0	0	41	Yes
S025648377	ASD-current cohort	5	5-6	male	Guandong	3	light	light	light	1	1	1	0	0	0	0	0	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		29	40	Cesarean section	2	2	0	0	0	0	0	38	Yes
S055874538	ASD-current cohort	5	5-6	male	Guandong	5	light	secondary	secondary	1	3	0	0	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0	1	0		0	0	0	0		29	37	Cesarean section	2	2	0	0	0	0	0	37	Yes
S044518277	ASD-current cohort	2.7	2-3	male	Hebei	5	light	secondary	secondary	1	3	1	0	1	0	0	1	0	1	0	1	5	1	1	1	1	1	0	0	0		0	1	1	1	Hypoxia and Asphyxia	30	40	Vaginally delivery	4	2	0	0	1	0	0	32	Yes
S088051863	ASD-current cohort	3.6	3-4	male	Guandong	7	light	severe	severe	1	1	0	0	0	0	0	1	0	1	0	1	1	0	1	0	0	1	0	0	0		0	0	0	0		32	35+5	Cesarean section	3	1	1	0	0	0	0	38	Yes
S079437294	ASD-current cohort	3.6	3-4	male	Shanghai	4	light	light	secondary	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		35	37+2	Vaginally delivery	3	2	0	0	0	0	0	36	Yes
S012452774	ASD-current cohort	3	3-4	female	Hunan	4	no	light	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		36	40	Cesarean section	4	2	0	0	0	0	0	40	Yes
S005497155	ASD-current cohort	4.7	4-5	male	Hubei	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		24	40	Cesarean section	1	1	0	0	0	0	0	24	Yes
S043770618	ASD-current cohort	11.5	6	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	1	1	0	0	0	0	0	30	Yes
S076778601	ASD-current cohort	9	6	male	Zhejiang	4	no	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	38	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S023191214	ASD-current cohort	3	3-4	male	Beijing	9	severe	severe	severe	1	2	0	0	1	0	0	0	1	1	1	1	2	0	1	0	1	1	1	1	0		0	0	0	0		29	40	Vaginally delivery	2	1	0	0	0	0	0	30	Yes
S078367056	ASD-current cohort	6.9	6	male	Beijing	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	1	0		33	40	Vaginally delivery	3	3	0	0	0	0	0	33	Yes
S028132692	ASD-current cohort	2	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	38+6	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S020640641	ASD-current cohort	3	3-4	female	Guandong	2	light	light	no	1	4	0	0	1	1	1	0	1	0	1	0	0	0	0	0	0	1	1	0	0		0	0	0	0		27	39	Cesarean section	1	1	1	0	0	0	0	29	Yes
S089983820	ASD-current cohort	3	3-4	male	Tianjin	6	secondary	secondary	secondary	1	3	1	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		38	39	Cesarean section	4	2	0	0	1	0	0	39	Yes
S080812672	ASD-current cohort	2.3	2-3	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		34	40	Vaginally delivery	2	2	0	0	0	0	0	35	Yes
S049097605	ASD-current cohort	4.1	4-5	male	Tianjin	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	40+1	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S048760280	ASD-current cohort	5	5-6	male	Tianjin	7	light	severe	severe	1	5	1	0	1	1	0	1	1	1	1	1	1	0	1	0	0	1	0	0	0		0	0	1	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S078026186	ASD-current cohort	4.1	4-5	male	Shanghai	2	light	light	no	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	0	0	0	0	1	0		0	0	0	0		26	39	Cesarean section	1	1	0	0	0	0	0	23	Yes
S006612985	ASD-current cohort	11.6	6	female	Sichuan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	0	1	2	0	1	0	0	1	0	0	0		0	0	0	1	Hypoxia	27	36	Cesarean section	5	1	0	0	0	0	1	33	Yes
S047126932	ASD-current cohort	4	4-5	male	Zhejiang	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	0	1	2	0	1	0	1	1	0	0	0		0	0	0	0		25	41	Cesarean section	3	1	0	0	0	0	0	25	Yes
S038355317	ASD-current cohort	4.6	4-5	female	Shandong	7	light	severe	severe	1	2	1	0	1	0	0	0	0	1	0	1	2	1	0	1	0	1	0	0	0		0	0	0	0		34	40	Vaginally delivery	5	2	0	0	0	0	0	35	Yes
S034700516	ASD-current cohort	6	5-6	male	Hunan	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		26	39	Cesarean section	1	1	0	0	0	0	0	28	Yes
S057669009	ASD-current cohort	7	6	female	Hunan	6	secondary	severe	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		31	39	Cesarean section	3	2	0	0	0	0	0	31	Yes
S095022685	ASD-current cohort	10	6	male	Guizhou	8	secondary	severe	severe	1	1	0	0	0	0	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		25	40	Cesarean section	3	1	0	0	0	0	0	26	Yes
S077519451	ASD-current cohort	6	5-6	male	Beijing	3	no	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	40	Cesarean section	1	1	0	0	0	0	0	45	Yes
S045746862	ASD-current cohort	5.4	5-6	male	Hunan	8	secondary	severe	severe	1	3	1	0	1	0	0	1	0	1	0	1	2	1	0	1	0	0	0	0	0		0	1	0	0		37	42+5	Cesarean section	1	1	0	0	0	0	0	38	Yes
S033106062	ASD-current cohort	5	5-6	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		37	40	Cesarean section	1	1	0	0	0	0	0	38	Yes
S073861199	ASD-current cohort	2.6	2-3	male	Anhui	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	1	0	1	1	0	1	0	0	1	0	0	0		0	0	0	0		32	40	Vaginally delivery	1	1	0	0	0	0	0	34	Yes
S047572058	ASD-current cohort	2.5	2-3	male	Guandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	1	4	1	1	0	1	1	1	0	0		0	0	0	1	Asphyxia	31	39	Cesarean section	3	2	0	0	0	0	0	34	Yes
S074274696	ASD-current cohort	3	3-4	male	Shandong	6	light	secondary	severe	1	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		31	42	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S029537078	ASD-current cohort	8	6	male	Guandong	7	severe	secondary	secondary	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	0	0		30	39	Cesarean section	1	1	0	0	0	0	0	33	Yes
S006875046	ASD-current cohort	3	3-4	female	Liaoning	5	light	secondary	secondary	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		37	40	Cesarean section	2	1	0	0	0	0	0	38	Yes
S033698579	ASD-current cohort	7	6	male	Hunan	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	40	Cesarean section	2	1	0	0	0	0	0	29	Yes
S063469084	ASD-current cohort	3.1	3-4	male	Hunan	5	light	secondary	secondary	1	3	0	0	1	1	0	1	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	2	1	0	0	0	0	29	Yes
S078802809	ASD-current cohort	4	4-5	male	Hunan	8	secondary	severe	severe	1	4	0	0	1	1	0	1	1	1	1	1	1	0	1	0	0	1	0	0	0		0	0	0	0		33	40	Vaginally delivery	2	2	0	0	0	0	0	34	Yes
S027126360	ASD-current cohort	2.1	2-3	male	Anhui	3	light	light	light	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S032702131	ASD-current cohort	3.2	3-4	male	Anhui	3	light	light	light	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	1	0	0		26	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S099949601	ASD-current cohort	5.6	5-6	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	40	Cesarean section	2	2	0	0	0	0	0	40	Yes
S054872475	ASD-current cohort	5.9	5-6	male	Hunan	7	secondary	secondary	severe	1	2	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	36	Cesarean section	2	2	0	0	0	0	0	40	Yes
S062437139	ASD-current cohort	6.6	6	female	Zhejiang	5	light	light	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S046117843	ASD-current cohort	4	4-5	male	Shandong	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	41	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S098024496	ASD-current cohort	19	6	male	Hunan	3	light	secondary	no	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	0		0	0	0	0		28	36	Cesarean section	3	1	1	0	0	0	0	27	Yes
S059665135	ASD-current cohort	5.4	5-6	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		34	40	Cesarean section	2	1	0	0	0	0	0	37	Yes
S085862246	ASD-current cohort	4	4-5	male	Guandong	5	light	secondary	secondary	1	1	0	0	0	0	0	0	1	1	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	1	0	0	0	0	30	Yes
S021109156	ASD-current cohort	5	5-6	male	Jiangxi	3	light	light	light	1	2	0	0	0	1	1	0	0	1	0	1	2	1	0	0	1	0	0	0	0		0	0	0	0		24	40	Cesarean section	1	1	0	0	0	0	0	26	Yes
S081654561	ASD-current cohort	5.9	5-6	male	Jiangxi	3	light	light	light	1	2	0	0	0	0	1	0	1	1	1	1	1	0	1	0	0	1	0	0	1	Cytomegalovirus	0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	1	26	Yes
S025836282	ASD-current cohort	2.1	2-3	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	39	Cesarean section	2	2	0	0	0	0	0	30	Yes
S057691995	ASD-current cohort	5	5-6	male	Jiangxi	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S060210302	ASD-current cohort	2.8	2-3	male	Beijing	5	light	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S028021013	ASD-current cohort	4.4	4-5	male	Guandong	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	1	4	1	1	1	1	1	1	1	0		0	0	0	0		29	38	Cesarean section	1	1	1	0	1	0	0	33	Yes
S074738997	ASD-current cohort	5.8	5-6	female	Guandong	8	secondary	severe	severe	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	0	0		27	36+6	Cesarean section	1	1	0	0	0	0	0	26	Yes
S085951531	ASD-current cohort	5.5	5-6	female	Guandong	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	1	0	1	4	1	1	1	1	0	0	0	0		0	0	0	0		26	40	Cesarean section	1	1	0	0	0	0	0	26	Yes
S057101136	ASD-current cohort	1.4	1-1.5	male	Hunan	3	light	light	light	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		30	40	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S370593256	ASD-current cohort	3.1	3-4	male	Hunan	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	40	Cesarean section	2	2	0	0	0	0	0	33	Yes
S014414167	ASD-current cohort	5	5-6	male	Guandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	39	Cesarean section	2	2	0	0	0	0	0	32	Yes
S003879260	ASD-current cohort	4.9	4-5	male	Hunan	4	no	secondary	secondary	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		26	42	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S034533475	ASD-current cohort	6	5-6	female	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	40	Vaginally delivery	3	2	0	0	0	0	0	39	Yes
S029816849	ASD-current cohort	3.1	3-4	male	Hunan	5	light	secondary	secondary	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	35	Cesarean section	1	1	0	0	0	0	0	29	Yes
S004018515	ASD-current cohort	5	5-6	male	Sichuan	6	light	severe	secondary	1	3	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		28	39+5	Cesarean section	1	1	0	0	1	0	0	29	Yes
S009897088	ASD-current cohort	5	5-6	male	Hunan	7	light	severe	severe	1	2	0	0	1	0	0	0	1	1	1	1	1	0	0	1	0	0	0	1	0		0	0	0	0		29	39	Cesarean section	4	1	0	0	1	0	0	32	Yes
S031642792	ASD-current cohort	3	3-4	male	Zhejiang	9	severe	severe	severe	1	2	0	0	1	0	0	0	1	1	1	1	4	1	1	1	1	0	0	0	0		0	0	0	0		24	36+2	Vaginally delivery	2	1	1	0	0	0	0	48	Yes
S022745587	ASD-current cohort	2	2-3	female	Shanghai	8	secondary	severe	severe	1	7	1	1	1	1	1	1	1	1	1	1	2	1	0	1	0	1	1	1	0		0	0	0	0		34	42	Cesarean section	2	2	0	0	0	0	0	40	Yes
S058681353	ASD-current cohort	3.11	3-4	male	Henan	9	severe	severe	severe	1	5	1	0	1	1	0	1	1	1	1	1	2	0	1	1	0	1	1	1	1	Respiratory infections	0	0	0	0		23	39	Vaginally delivery	1	1	0	0	0	0	0	23	Yes
S070789075	ASD-current cohort	3.3	3-4	female	Hunan	6	secondary	light	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	40	Cesarean section	2	2	0	0	0	0	0	45	Yes
S066193904	ASD-current cohort	2.9	2-3	male	Hunan	6	light	secondary	severe	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	1	0	0	27	Yes
S065667265	ASD-current cohort	7	6	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		22	40	Cesarean section	3	1	0	0	0	0	0	23	Yes
S013759453	ASD-current cohort	3.6	3-4	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	39.5	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S001459304	ASD-current cohort	6	5-6	female	Sichuan	7	secondary	secondary	severe	1	3	0	0	1	0	0	1	0	1	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		29	39	Cesarean section	3	3	0	0	0	0	0	29	Yes
S004849889	ASD-current cohort	5	5-6	male	Sichuan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	0	1	4	1	1	1	1	1	1	0	0		0	0	1	0		28	39	Cesarean section	1	1	0	0	0	0	0	28	Yes
S053505152	ASD-current cohort	6.1	6	male	Guandong	6	secondary	secondary	secondary	1	2	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		38	40+1	Vaginally delivery	2	2	0	0	0	0	0	40	Yes
S025808292	ASD-current cohort	7	6	female	Hunan	4	no	secondary	secondary	1	0	0	0	0	0	0	0	0	1	0	1	2	0	1	0	1	0	0	1	0		0	0	0	0		28	37	Cesarean section	1	1	0	0	0	0	0	29	Yes
S098672952	ASD-current cohort	8	6	male	Jiangsu	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	39	Cesarean section	1	1	0	0	0	0	0	24	Yes
S011101340	ASD-current cohort	4.7	4-5	male	Guandong	8	secondary	severe	severe	1	2	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		38	38+5	Vaginally delivery	5	2	0	0	0	0	0	38	Yes
S073750230	ASD-current cohort	5	5-6	male	Guandong	6	severe	secondary	light	1	5	0	0	1	1	1	1	1	1	1	1	3	1	1	1	0	1	0	0	0		0	0	0	0		23	38+4	Cesarean section	3	1	0	0	0	0	0	27	Yes
S095418441	ASD-current cohort	3	3-4	female	Jiangsu	4	light	light	secondary	1	4	0	0	1	1	1	1	0	1	0	1	1	0	0	0	0	1	1	0	0		0	0	0	0		30	38	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S057974805	ASD-current cohort	6.2	6	male	Hunan	9	severe	severe	severe	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	39	Cesarean section	1	1	0	0	0	0	0	35	Yes
S007963411	ASD-current cohort	4	4-5	male	Hunan	8	severe	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	37+4	Cesarean section	1	1	1	0	0	0	0	27	Yes
S093809713	ASD-current cohort	5	5-6	male	Jiangxi	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		23	37	Vaginally delivery	1	1	1	0	0	0	0	26	Yes
S002938594	ASD-current cohort	4.9	4-5	male	Guandong	8	secondary	severe	severe	1	5	0	0	1	1	1	1	1	1	1	1	4	1	1	1	1	1	1	0	0		0	0	0	0		23	40	Cesarean section	2	2	1	0	0	0	0	35	Yes
S013977459	ASD-current cohort	4	4-5	male	Liaoning	6	light	secondary	severe	1	6	1	0	1	1	1	1	1	1	1	1	4	1	1	1	1	1	1	0	0		0	0	0	0		30	40	Vaginally delivery	2	1	0	0	0	0	0	33	Yes
S041725340	ASD-current cohort	3	3-4	male	Hunan	6	light	severe	secondary	1	1	0	0	1	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		27	38	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S051300789	ASD-current cohort	3.9	3-4	male	Hubei	7	light	severe	severe	1	2	0	0	1	0	0	0	1	1	1	1	2	0	0	1	1	0	0	1	0		0	0	0	0		35	38	Cesarean section	2	1	1	0	0	0	0	43	Yes
S046644624	ASD-current cohort	3.11	3-4	male	Hunan	7	light	severe	severe	1	1	0	0	0	0	0	1	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		27	39	Vaginally delivery	2	2	0	0	0	0	0	28	Yes
S026275115	ASD-current cohort	3.6	3-4	male	Shandong	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0		0	0	0	0		29	38	Cesarean section	4	2	0	0	0	0	0	30	Yes
S028156471	ASD-current cohort	4.4	4-5	female	Shandong	7	light	severe	severe	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		26	37+2	Cesarean section	1	1	0	0	0	0	0	24	Yes
S052906373	ASD-current cohort	7	6	male	Hunan	8	secondary	severe	severe	1	2	0	0	1	1	0	0	0	1	0	1	1	1	0	0	0	1	1	0	0		0	0	0	0		37	40	Cesarean section	4	2	0	0	0	0	0	35	Yes
S031958036	ASD-current cohort	4.2	4-5	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S066559184	ASD-current cohort	2.11	2-3	male	Hunan	3	secondary	light	no	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	38+5	Cesarean section	2	1	1	0	0	0	0	36	Yes
S042190794	ASD-current cohort	2.6	2-3	male	Hubei	7	secondary	severe	secondary	1	2	0	0	1	0	0	1	0	1	0	1	3	0	1	1	1	1	1	0	0		0	0	0	0		32	38	Cesarean section	2	2	0	0	0	0	0	34	Yes
S096079565	ASD-current cohort	2.9	2-3	male	Henan	6	secondary	secondary	secondary	1	5	0	0	1	1	1	1	1	1	1	1	4	1	1	1	1	1	0	0	0		0	0	1	0		30	39+5	Vaginally delivery	2	1	1	0	0	0	0	38	Yes
S026091217	ASD-current cohort	2.6	2-3	female	Hunan	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	3	1	1	0	1	0	0	0	0		0	0	0	0		31	40	Cesarean section	1	1	0	0	0	0	0	46	Yes
S062330955	ASD-current cohort	5.6	5-6	male	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	39	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S025879130	ASD-current cohort	5.5	5-6	male	Shanxi	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0		0	0	0	0		36	40	Cesarean section	5	2	0	0	0	0	0	42	Yes
S066755219	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	1	0		27	42	Vaginally delivery	3	2	0	0	0	0	0	30	Yes
S099934309	ASD-current cohort	4.4	4-5	male	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	2	0	1	1	0	0	0	0	0		0	0	0	0		24	37	Cesarean section	1	1	0	0	0	0	0	25	Yes
S099612799	ASD-current cohort	8.8	6	male	Hunan	6	secondary	secondary	secondary	1	5	0	0	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0		0	0	0	0		32	40	Cesarean section	3	1	0	0	0	0	0	47	Yes
S065314165	ASD-current cohort	4.5	4-5	male	Guandong	8	secondary	severe	severe	1	2	0	0	0	1	0	1	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		35	29	Vaginally delivery	3	2	0	0	1	0	0	40	Yes
S004183884	ASD-current cohort	4	4-5	male	Guandong	8	secondary	severe	severe	1	3	0	0	1	0	1	0	1	1	1	1	2	1	1	0	0	1	1	1	0		0	0	0	0		28	39	Vaginally delivery	5	1	0	0	1	0	0	40	Yes
S006937930	ASD-current cohort	5	5-6	male	Hunan	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	0		0	0	0	0		25	37	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S064402994	ASD-current cohort	6.4	6	male	Hunan	6	secondary	severe	light	0	0	0	0	0	0	0	0	0	1	0	1	2	1	1	0	0	0	0	0	0		0	0	0	0		25	32+6	Cesarean section	2	2	0	0	0	0	1	25	Yes
S074040053	ASD-current cohort	5	5-6	male	Shanghai	7	secondary	severe	severe	1	2	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0		0	1	0	0		41	39	Cesarean section	1	1	0	0	0	0	0	39	Yes
S046824167	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		42	40	Cesarean section	2	2	0	0	0	0	0	44	Yes
S077254988	ASD-current cohort	3.6	3-4	male	Hunan	5	light	secondary	secondary	1	2	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	37	Cesarean section	1	1	0	0	0	0	0	28	Yes
S001220802	ASD-current cohort	2	2-3	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	1	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		30	38	Vaginally delivery	1	1	1	0	0	0	0	29	Yes
S070826666	ASD-current cohort	3	3-4	female	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	39+6	Cesarean section	6	2	0	0	0	0	0	35	Yes
S065770717	ASD-current cohort	1.9	1.5-2	male	Shandong	5	light	secondary	secondary	1	3	0	0	1	1	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		25	39	Cesarean section	1	1	0	0	0	0	0	25	Yes
S098601130	ASD-current cohort	2.5	2-3	male	Shandong	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		26	40	Vaginally delivery	3	2	0	0	0	0	0	31	Yes
S014643625	ASD-current cohort	7	6	male	Sichuan	4	light	light	secondary	1	1	0	0	0	0	0	1	0	1	0	1	3	0	1	1	1	0	0	0	0		0	0	0	0		27	38	Cesarean section	2	2	0	0	0	0	0	27	Yes
S082659941	ASD-current cohort	3.7	3-4	male	Guandong	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S072635536	ASD-current cohort	4	4-5	male	Hunan	6	secondary	secondary	secondary	1	3	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		33	32+1	Cesarean section	3	1	0	0	0	0	0	33	Yes
S033032062	ASD-current cohort	4	4-5	male	Beijing	6	secondary	secondary	secondary	1	2	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	37+1	Cesarean section	1	1	0	0	0	0	0	31	Yes
S025221062	ASD-current cohort	7	6	male	Chongqing	7	secondary	severe	secondary	1	2	0	0	1	0	0	1	0	1	0	1	2	1	0	0	1	1	0	1	0		0	0	0	0		23	40	Cesarean section	1	1	1	0	0	0	0	28	Yes
S026513184	ASD-current cohort	3.2	3-4	male	Sichuan	8	secondary	severe	severe	1	5	0	0	1	1	1	1	1	1	1	1	2	1	0	0	1	0	0	0	0		0	0	0	0		37	40+5	Cesarean section	3	1	0	0	0	0	0	36	Yes
S094205393	ASD-current cohort	3	3-4	male	Zhejiang	7	light	severe	severe	1	4	0	0	1	1	0	1	1	1	1	1	2	1	0	0	1	1	0	0	0		0	0	0	0		30	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S071239872	ASD-current cohort	2.1	2-3	female	Hunan	7	light	severe	severe	1	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	38+5	Vaginally delivery	4	2	0	0	0	0	0	30	Yes
S029320535	ASD-current cohort	6	5-6	male	Beijing	3	light	light	light	1	4	0	1	1	1	0	0	1	0	1	0	0	0	0	0	0	1	1	1	0		0	0	0	0		26	40+3	Vaginally delivery	1	1	1	0	0	0	0	26	Yes
S073601674	ASD-current cohort	3.9	3-4	female	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	1	0	1	3	0	1	1	1	1	0	0	0		0	0	0	0		23	40	Vaginally delivery	1	1	1	0	0	0	0	29	Yes
S002922807	ASD-current cohort	9	6	male	Guanxi	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	39	Vaginally delivery	3	1	1	0	0	0	0	30	Yes
S087608885	ASD-current cohort	5	5-6	male	Shanghai	3	light	light	light	1	3	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		29	39	Cesarean section	2	1	1	0	0	0	0	29	Yes
S072260822	ASD-current cohort	3.8	3-4	female	Shandong	7	secondary	secondary	severe	1	4	0	0	1	1	0	1	0	1	1	1	5	1	1	1	1	1	1	0	0		0	0	0	1	Umbilical cord around neck	28	40	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S072238306	ASD-current cohort	5.6	5-6	male	Shandong	3	light	secondary	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	38	Vaginally delivery	4	1	1	0	0	0	0	36	Yes
S010498512	ASD-current cohort	3.4	3-4	male	Hunan	4	light	light	secondary	1	2	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	1	1	0	0		0	0	0	0		34	40	Vaginally delivery	2	2	0	0	0	0	0	31	Yes
S047529861	ASD-current cohort	3.6	3-4	male	Sichuan	8	secondary	severe	severe	1	3	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	37+	Cesarean section	2	2	0	0	0	0	0	42	Yes
S092984682	ASD-current cohort	3	3-4	male	Zhejiang	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		29	37	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S039397001	ASD-current cohort	2.3	2-3	male	Hunan	5	light	secondary	secondary	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		0	0	0	1	Amniotic fluid choking	25	42	Vaginally delivery	3	2	0	0	0	0	0	22	Yes
S006307584	ASD-current cohort	1.8	1.5-2	male	Hunan	6	light	secondary	severe	1	2	0	0	1	0	0	1	0	1	0	1	1	0	1	0	0	1	0	0	0		0	0	0	0		20	40	Vaginally delivery	2	1	0	0	0	0	0	24	Yes
S045091762	ASD-current cohort	3.4	3-4	female	Shandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		23	37	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S058521449	ASD-current cohort	3.1	3-4	male	Jiangxi	6	light	secondary	severe	1	1	0	0	1	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		35	41	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S007103006	ASD-current cohort	5	5-6	male	Hunan	6	light	secondary	severe	1	3	0	0	1	0	0	1	1	1	1	1	2	0	1	0	1	1	1	0	0		0	0	0	0		31	41	Cesarean section	1	1	0	0	1	1	0	31	Yes
S086599150	ASD-current cohort	5	5-6	male	Zhejiang	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		24	36+	Vaginally delivery	2	1	0	0	0	0	0	48	Yes
S059898881	ASD-current cohort	4.2	4-5	male	Shandong	6	light	secondary	severe	1	2	0	0	1	1	0	0	0	1	0	1	2	1	1	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	2	0	0	0	0	0	36	Yes
S090498597	ASD-current cohort	5	5-6	male	Fujian	6	secondary	secondary	secondary	1	2	0	0	1	0	0	0	1	1	1	1	4	1	1	1	1	1	0	0	0		0	0	0	0		38	39	Cesarean section	4	2	0	0	0	0	0	43	Yes
S089132346	ASD-current cohort	3.6	3-4	female	Shandong	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	36+	Cesarean section	2	2	0	0	0	0	0	26	Yes
S064137399	ASD-current cohort	5	5-6	male	Jiangxi	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	1	1	1	1	0		0	0	0	0		35	41	Vaginally delivery	2	2	0	0	0	0	0	35	Yes
S025752514	ASD-current cohort	4.6	4-5	male	Zhejiang	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	1	1	0	0		0	0	0	0		35	39	Cesarean section	1	1	1	0	0	0	0	37	Yes
S018363154	ASD-current cohort	6.8	6	female	Shandong	7	light	severe	severe	0	0	0	0	0	0	0	0	0	1	0	1	2	1	0	0	0	1	1	1	0		0	0	0	1	Hypoxia	29	41	Cesarean section	2	1	0	0	0	0	0	28	Yes
S011413613	ASD-current cohort	4.3	4-5	male	Hunan	5	light	light	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	2	2	0	0	0	0	0	28	Yes
S087886356	ASD-current cohort	6	5-6	male	Guandong	3	light	light	light	1	1	0	0	1	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		30	39	Cesarean section	2	1	0	0	0	0	0	30	Yes
S036815835	ASD-current cohort	2.7	2-3	female	Guandong	7	light	severe	severe	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S025370756	ASD-current cohort	5.5	5-6	male	Hunan	4	light	secondary	light	1	1	0	0	0	1	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		32	36	Cesarean section	1	1	0	0	0	0	1	32	Yes
S026659772	ASD-current cohort	2.6	2-3	male	Anhui	6	light	light	severe	1	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		35	37	Cesarean section	4	2	0	0	0	0	0	35	Yes
S016428734	ASD-current cohort	6.5	6	female	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	10	Vaginally delivery	2	1	0	0	0	0	0	26	Yes
S089443026	ASD-current cohort	3	3-4	female	Shandong	6	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	3	1	0	0	0	0	0	28	Yes
S017583004	ASD-current cohort	3.5	3-4	male	Shanghai	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	1	0	1	2	1	0	1	0	0	1	0	0		0	0	0	0		33	37+4	Cesarean section	1	1	0	0	0	0	0	23	Yes
S002914152	ASD-current cohort	6	5-6	male	Shandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Vaginally delivery	2	1	1	0	0	0	0	32	Yes
S099266032	ASD-current cohort	8	6	male	Hunan	2	no	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	3	1	0	0	0	0	0	29	Yes
S043475258	ASD-current cohort	7.6	6	male	Xinjiang	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	1	0	1	4	1	1	1	1	1	1	1	0		0	0	0	0		30	35+4	Vaginally delivery	3	1	0	0	0	1	0	37	Yes
S074345339	ASD-current cohort	4	4-5	male	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		25	40	Cesarean section	1	1	0	0	0	0	0	29	Yes
S073805417	ASD-current cohort	2	2-3	female	Shandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	2	1	1	0	0	1	0	0	0		0	0	0	0		27	40	Cesarean section	3	1	0	0	0	0	0	28	Yes
S039071971	ASD-current cohort	3	3-4	female	Guandong	4	no	secondary	secondary	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		24	39	Vaginally delivery	1	1	1	0	0	0	0	27	Yes
S012516698	ASD-current cohort	3.1	3-4	male	Shandong	4	light	light	secondary	1	1	0	0	1	0	0	0	0	1	0	1	3	1	1	0	1	1	1	0	0		0	0	0	0		26	40+3	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S001965710	ASD-current cohort	13	6	male	Zhejiang	8	secondary	severe	severe	1	4	1	1	1	1	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		40	38	Vaginally delivery	3	2	0	0	0	0	0	43	Yes
S018736257	ASD-current cohort	3.6	3-4	male	Tianjin	6	secondary	severe	secondary	1	2	0	0	1	1	0	0	0	1	0	1	3	1	0	0	1	1	1	0	0		0	0	0	1	Amniotic fluid choking	29	41	Cesarean section	1	1	0	0	0	0	0	33	Yes
S048942713	ASD-current cohort	7	6	male	Guandong	4	no	light	severe	1	2	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	1	0	0		0	0	0	0		39	39	Cesarean section	2	2	0	0	1	0	0	33	Yes
S044789394	ASD-current cohort	5.1	5-6	female	Hunan	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	39	Cesarean section	3	2	0	0	1	0	0	29	Yes
S096698135	ASD-current cohort	7	6	male	Hunan	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		29	39	Vaginally delivery	1	1	0	0	0	0	0	38	Yes
S080755039	ASD-current cohort	2.1	2-3	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		48	37	Vaginally delivery	3	2	1	0	0	0	0	52	Yes
S060647864	ASD-current cohort	11	6	male	Hunan	2	light	light	no	1	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S053123083	ASD-current cohort	6.4	6	male	Hunan	6	secondary	secondary	secondary	1	5	1	0	1	0	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	0	0	0	0	0		33	39+1	Cesarean section	5	1	0	0	1	0	0	35	Yes
S000065974	ASD-current cohort	5	5-6	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		25	39+5	Cesarean section	1	1	0	0	0	0	0	28	Yes
S074049040	ASD-current cohort	9.6	6	male	Sichuan	5	secondary	secondary	light	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	1	0		26	40	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S035088083	ASD-current cohort	5.9	5-6	male	Shandong	8	severe	severe	secondary	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	1	0		0	1	0	0		32	39+5	Vaginally delivery	2	1	0	0	0	0	0	32	Yes
S030996126	ASD-current cohort	5.7	5-6	female	Sichuan	3	light	light	light	1	3	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0	0	1	1	0		0	0	0	0		38	39	Cesarean section	3	2	0	0	0	0	0	38	Yes
S084432635	ASD-current cohort	3.5	3-4	male	Shandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	1	0		31	40	Cesarean section	1	1	0	0	0	0	0	27	Yes
S038870636	ASD-current cohort	4	4-5	male	Shandong	5	light	secondary	secondary	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	40	Vaginally delivery	2	2	0	0	0	0	0	32	Yes
S049948659	ASD-current cohort	3.6	3-4	male	Shandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	38+5	Cesarean section	2	1	0	0	0	0	0	27	Yes
S041441177	ASD-current cohort	3.6	3-4	male	Guandong	4	light	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	Oral herpes	0	0	0	0		33	41	Vaginally delivery	1	1	0	0	1	0	0	35	Yes
S068870405	ASD-current cohort	1.9	1.5-2	female	Hunan	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	37	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S053689114	ASD-current cohort	4	4-5	male	Hunan	7	light	severe	severe	1	2	0	0	1	0	0	1	0	1	0	1	1	1	0	0	0	0	1	0	0		0	0	0	0		23	39	Vaginally delivery	3	2	0	0	0	0	0	25	Yes
S061669023	ASD-current cohort	4.1	4-5	male	Shandong	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		26	39+1	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S094443284	ASD-current cohort	4.6	4-5	male	Chongqing	7	secondary	secondary	severe	1	4	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		22	40	Cesarean section	2	1	0	0	0	0	0	23	Yes
S037401340	ASD-current cohort	1.11	1.5-2	male	Hebei	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	0		0	0	0	0		29	40	Cesarean section	2	2	0	0	1	0	0	26	Yes
S082107988	ASD-current cohort	3	3-4	male	Shandong	8	secondary	severe	severe	1	1	1	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	1	0	0		31	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S086769941	ASD-current cohort	5.6	5-6	male	Shandong	6	no	severe	severe	1	3	0	0	0	0	1	1	0	1	0	1	2	1	0	1	0	1	0	0	0		0	0	0	0		35	36+4	Cesarean section	3	2	1	0	0	0	0	39	Yes
S030458199	ASD-current cohort	4	4-5	male	Hunan	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	39	Vaginally delivery	3	2	0	0	0	0	0	36	Yes
S029442609	ASD-current cohort	4.1	4-5	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S082549886	ASD-current cohort	5	5-6	female	Jiangsu	7	secondary	severe	secondary	1	2	0	0	1	1	0	0	0	1	0	1	2	1	0	1	0	1	1	0	0		0	0	0	0		30	37	Vaginally delivery	1	1	1	0	0	0	0	35	Yes
S037885612	ASD-current cohort	5.4	5-6	male	Hunan	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		31	37	Vaginally delivery	3	2	0	0	0	0	0	31	Yes
S051135498	ASD-current cohort	4	4-5	male	Hunan	8	severe	secondary	severe	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		26	40	Vaginally delivery	6	2	0	0	0	0	0	31	Yes
S050974300	ASD-current cohort	3	3-4	male	Sichuan	6	light	severe	secondary	1	5	0	0	1	1	1	1	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	40+5	Vaginally delivery	1	1	0	0	0	0	0	34	Yes
S031233999	ASD-current cohort	3.1	3-4	male	Shandong	8	secondary	severe	severe	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	2	2	0	0	0	0	0	15	Yes
S037223336	ASD-current cohort	8	6	female	Shandong	4	light	secondary	light	1	2	0	0	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0		0	0	0	0		32	40	Vaginally delivery	2	1	1	0	0	0	0	36	Yes
S062865844	ASD-current cohort	2	2-3	male	Hunan	5	secondary	secondary	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	35+2	Vaginally delivery	1	1	1	0	0	0	0	32	Yes
S058918697	ASD-current cohort	3.5	3-4	female	Jiangsu	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	2	0	1	0	1	1	0	0	0		0	0	0	0		27	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S066815916	ASD-current cohort	5.5	5-6	male	Shandong	9	severe	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	42	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S070923703	ASD-current cohort	3	3-4	male	Zhejiang	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	39+3	Vaginally delivery	3	2	0	0	0	0	0	29	Yes
S095989479	ASD-current cohort	2.3	2-3	male	Hunan	6	light	secondary	severe	1	3	0	0	1	0	0	1	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		27	37	Vaginally delivery	2	1	0	0	0	0	0	30	Yes
S048470945	ASD-current cohort	5	5-6	male	Tianjin	1	no	light	no	1	3	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	1	0	0		0	0	0	0		31	38	Vaginally delivery	1	1	0	0	0	0	0	41	Yes
S015682936	ASD-current cohort	3.6	3-4	male	Hunan	6	secondary	secondary	secondary	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S085497971	ASD-current cohort	2.6	2-3	male	Shandong	7	light	severe	severe	1	2	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	37+6	Cesarean section	2	2	0	0	0	0	0	29	Yes
S050150441	ASD-current cohort	4.6	4-5	male	Hunan	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		29	39	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S035186503	ASD-current cohort	5.6	5-6	female	Shandong	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	1	0	1	4	1	1	1	0	0	1	0	0		0	0	0	1	Umbilical cord around neck	27	40	Cesarean section	2	1	0	0	0	0	0	28	Yes
S014182761	ASD-current cohort	2.1	2-3	male	Hubei	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		0	0	0	1	Premature birth and hypoxia	28	32+5	Cesarean section	3	1	1	0	0	0	0	30	Yes
S024456461	ASD-current cohort	4	4-5	male	Hunan	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		25	30	Vaginally delivery	5	2	0	0	0	0	0	26	Yes
S096048511	ASD-current cohort	4	4-5	male	Sichuan	3	light	secondary	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	39	Cesarean section	2	1	0	0	0	0	0	30	Yes
S049814008	ASD-current cohort	4.6	4-5	female	Hunan	5	light	light	severe	1	2	0	0	1	0	0	1	0	1	0	1	3	0	1	1	0	1	0	0	0		0	1	0	1	Amniotic fluid choking	33	38	Vaginally delivery	2	2	1	0	0	0	0	33	Yes
S027800836	ASD-current cohort	2.11	2-3	male	Hunan	8	secondary	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	0	25	Yes
S036154620	ASD-current cohort	6	5-6	male	Hubei	6	secondary	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		20	40	Cesarean section	2	2	0	0	0	0	0	25	Yes
S059753787	ASD-current cohort	8	6	female	Jiangxi	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		0	0	0	1	Hypoxia	30	38	Cesarean section	2	2	0	0	0	0	0	32	Yes
S074662364	ASD-current cohort	5	5-6	male	Hebei	6	secondary	secondary	secondary	1	3	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	1	0	1	0		0	0	1	0		35	40	Vaginally delivery	6	2	0	0	0	0	0	36	Yes
S047507632	ASD-current cohort	5	5-6	male	Shandong	6	secondary	light	severe	1	5	0	0	1	1	1	1	1	1	1	1	4	1	1	1	1	0	0	0	0		0	0	0	0		26	46+1	Cesarean section	3	3	0	0	0	0	0	27	Yes
S008462841	ASD-current cohort	5.8	5-6	male	Hunan	7	light	severe	severe	1	2	1	0	1	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		27	38	Cesarean section	1	1	0	0	0	0	0	32	Yes
S089552974	ASD-current cohort	8	6	male	Guandong	7	light	severe	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		23	38	Cesarean section	1	1	0	0	0	0	0	24	Yes
S000729969	ASD-current cohort	4	4-5	male	Shandong	8	severe	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S018851442	ASD-current cohort	3	3-4	male	Shandong	4	light	light	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		41	39	Cesarean section	3	2	0	0	0	0	0	42	Yes
S097474539	ASD-current cohort	4.4	4-5	male	Shandong	4	no	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		25	40	Cesarean section	3	2	0	0	0	0	0	25	Yes
S059119936	ASD-current cohort	5.11	5-6	male	Guandong	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		27	39+1	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S016606188	ASD-current cohort	3.8	3-4	female	Shanghai	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		28	39	Cesarean section	3	1	0	1	0	0	0	40	Yes
S083954462	ASD-current cohort	4.5	4-5	male	Shandong	8	secondary	severe	severe	1	4	0	1	1	0	1	0	1	1	1	1	1	1	0	0	0	1	1	1	0		0	0	1	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S091222045	ASD-current cohort	2	2-3	male	Hunan	7	secondary	secondary	severe	1	2	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		23	39+3	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S012876647	NT-current cohort	7	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Cesarean section	2	1	0	0	0	0	0	25	Yes
S015255601	NT-current cohort	12	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	37	Cesarean section	1	1	0	0	0	0	0	33	Yes
S059985569	NT-current cohort	4	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	36	Cesarean section	1	1	0	0	0	0	0	28	Yes
S011019765	NT-current cohort	2.5	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S062124284	NT-current cohort	5	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	39	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S061860942	NT-current cohort	9	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S011913717	NT-current cohort	2.5	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	38	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S027643692	NT-current cohort	4	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Vaginally delivery	3	1	0	0	0	0	0	23	Yes
S068558934	NT-current cohort	2	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	41	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S003019078	NT-current cohort	4	4-5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S002753197	NT-current cohort	5	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	43	Vaginally delivery	3	2	0	0	0	0	0	21	Yes
S089688621	NT-current cohort	4	4-5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S051180279	NT-current cohort	3	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	37	Vaginally delivery	1	1	0	0	0	0	0	32	Yes
S029026834	NT-current cohort	3.5	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	37	Vaginally delivery	NA	NA	0	0	0	0	0	-	Yes
S008394324	NT-current cohort	5.5	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	38	Vaginally delivery	1	1	0	0	0	0	0	21	Yes
S045664016	NT-current cohort	9	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Cesarean section	1	1	0	0	0	0	0	33	Yes
S018561460	NT-current cohort	5	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	40	Cesarean section	3	2	0	0	0	0	0	37	Yes
S077705440	NT-current cohort	4.5	4-5	male	Hunan	0	no	no	no	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	42	Cesarean section	1	1	0	0	0	0	0	24	Yes
S025488028	NT-current cohort	1.8	1.5-2	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Cesarean section	1	1	0	0	0	0	0	36	Yes
S003457098	NT-current cohort	3.2	3-4	female	Guizhou	0	no	no	no	1	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	35+4	Cesarean section	1	1	1	0	0	0	0	29	Yes
S052666607	NT-current cohort	1.5	1-1.5	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		39	41	Vaginally delivery	4	2	0	0	0	0	0	42	Yes
S003647360	NT-current cohort	4	4-5	male	Hunan	0	no	no	no	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S091424325	NT-current cohort	5	5-6	male	Hunan	0	no	no	no	1	4	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0		29	38+2	Cesarean section	1	1	0	0	1	0	0	34	Yes
S033928693	NT-current cohort	3.1	3-4	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		32	39+1	Cesarean section	2	2	0	0	0	0	0	32	Yes
S033394097	NT-current cohort	6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	36	Cesarean section	1	1	0	0	0	0	0	30	Yes
S051532676	NT-current cohort	1.3	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		32	39	Cesarean section	2	2	0	0	0	0	0	34	Yes
S096154208	NT-current cohort	10	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		29	37	Vaginally delivery	4	2	0	0	0	0	0	30	Yes
S044391226	NT-current cohort	3	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		36	37	Vaginally delivery	6	3	0	0	0	0	1	37	Yes
S038412775	NT-current cohort	2.6	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S015596991	NT-current cohort	3.5	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	36	Cesarean section	4	2	0	0	0	0	0	32	Yes
S083438507	NT-current cohort	5.1	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S019824350	NT-current cohort	10.1	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	4	2	0	0	0	0	0	28	Yes
S064278604	NT-current cohort	3.1	3-4	female	Hunan	0	no	no	no	1	1	1	0	0	0	0	0	0	1	0	1	1	0	0	0	1	0	0	0	0		0	0	0	0		37	38	Cesarean section	6	3	0	0	0	0	0	36	Yes
S061055659	NT-current cohort	3.7	3-4	female	Hunan	0	no	no	no	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Cesarean section	2	1	0	0	0	0	0	25	Yes
S072438337	NT-current cohort	9.7	6	female	Hunan	0	no	no	no	1	1	0	1	0	0	0	0	0	1	0	1	1	0	1	0	0	0	1	0	0		0	0	0	0		21	39	Vaginally delivery	1	1	0	0	0	0	0	-	Yes
S062114770	NT-current cohort	5.6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0	1	0	0		0	0	0	0		25	39	Vaginally delivery	2	2	0	0	0	0	0	31	Yes
S003192544	NT-current cohort	5.11	5-6	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		24	38	Vaginally delivery	2	2	0	0	0	0	0	28	Yes
S076234393	NT-current cohort	3.6	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S028283361	NT-current cohort	10	6	female	Beijing	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		27	40	Cesarean section	1	1	0	0	0	0	0	26	Yes
S091955555	NT-current cohort	5.4	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		34	40	Vaginally delivery	2	2	0	0	0	0	0	43	Yes

S004952626	NT-current cohort	5.3	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		24	40+3	Vaginally delivery	2	2	0	0	0	0	0	25	Yes
S026198892	NT-current cohort	3.9	3-4	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		32	42+	Cesarean section	2	2	0	0	0	0	0	33	Yes
S051426986	NT-current cohort	6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	38	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S011167657	NT-current cohort	4.2	4-5	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		24	41	Cesarean section	1	1	0	0	0	0	0	24	Yes
S097518390	NT-current cohort	6.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	40	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S051003630	NT-current cohort	6	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	Forgotten	Cesarean section	2	2	0	0	0	0	0	30	Yes
S066111379	NT-current cohort	4.3	4-5	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	38+2	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S036387349	NT-current cohort	4	4-5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40+1	Cesarean section	1	1	0	0	0	0	0	31	Yes
S017627932	NT-current cohort	3.1	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	38	Cesarean section	1	1	0	0	0	0	0	37	Yes
S072113251	NT-current cohort	1.3	1-1.5	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	35	Cesarean section	2	2	0	0	0	0	0	37	Yes
S034773681	NT-current cohort	7.6	6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		20	39+4	Vaginally delivery	2	2	0	0	0	0	0	24	Yes
S049246325	NT-current cohort	6.1	6	female	Hunan	0	no	no	no	1	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	39	Vaginally delivery	3	2	0	0	0	0	0	28	Yes
S087158924	NT-current cohort	6.11	6	female	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	2	2	0	0	0	0	0	25	Yes
S075200458	NT-current cohort	7.3	6	female	Hainan	0	no	no	no	1	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	2	2	0	0	0	0	0	25	Yes
S066000068	NT-current cohort	7.5	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	39+6	Vaginally delivery	2	2	0	0	0	0	0	-	Yes
S021447089	NT-current cohort	7.5	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	36	Cesarean section	NA	NA	0	0	0	0	0	22	Yes
S040515990	NT-current cohort	7.3	6	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	37	Cesarean section	1	1	0	0	0	0	0	27	Yes
S033457703	NT-current cohort	6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	0	Cesarean section	NA	NA	0	0	0	0	0	26	Yes
S088097027	NT-current cohort	6.8	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	0	Vaginally delivery	NA	NA	0	0	0	0	0	42	Yes
S059804671	NT-current cohort	7.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	39.5	Cesarean section	3	2	0	0	0	0	0	38	Yes
S079234079	NT-current cohort	7.4	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	38	Vaginally delivery	2	2	0	0	0	0	0	26	Yes
S086029189	NT-current cohort	7.1	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Cesarean section	2	2	0	0	0	0	0	29	Yes
S028744084	NT-current cohort	7.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	42	Cesarean section	3	2	0	0	0	0	0	28	Yes
S013103338	NT-current cohort	8.11	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	3	0	1	1	1	0	0	0	0		0	0	0	0		0	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S086988313	NT-current cohort	7.5	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	39	Vaginally delivery	2	2	0	0	0	0	0	22	Yes
S009264253	NT-current cohort	7.2	6	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	0	Cesarean section	1	1	0	0	0	0	0	24	Yes
S003536857	NT-current cohort	7	6	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		20	0	Cesarean section	1	1	0	0	0	0	0	22	Yes
S081439620	NT-current cohort	7.6	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	40	Cesarean section	1	1	0	0	0	0	0	30	Yes
S080330056	NT-current cohort	6.1	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	31	Cesarean section	NA	NA	0	0	0	0	0	32	Yes
S019728208	NT-current cohort	6.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Vaginally delivery	NA	NA	0	0	0	0	0	31	Yes
S048269745	NT-current cohort	7.5	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39	Cesarean section	3	2	0	0	0	0	0	29	Yes
S008150038	NT-current cohort	6.11	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	38	Cesarean section	1	1	0	0	0	0	0	25	Yes
S080884017	NT-current cohort	7.5	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Vaginally delivery	2	1	0	0	0	0	0	25	Yes
S043091711	NT-current cohort	6.11	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	38	Cesarean section	2	1	1	0	0	0	0	33	Yes
S046877117	NT-current cohort	6.1	6	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		28	37	Vaginally delivery	3	2	0	0	0	0	0	34	Yes
S047388171	NT-current cohort	6.11	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		25	40	Vaginally delivery	NA	NA	0	0	0	0	0	32	Yes
S025901820	NT-current cohort	7.6	6	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Cesarean section	1	1	0	0	0	0	0	27	Yes
S026229461	NT-current cohort	8.8	6	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	40	Vaginally delivery	2	1	0	0	0	0	0	22	Yes
S055450099	NT-current cohort	8.3	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Cesarean section	1	1	0	0	0	0	0	22	Yes
S099224479	NT-current cohort	8	6	female	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	0	26	Yes
S026490943	NT-current cohort	8.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	38	Vaginally delivery	1	1	0	0	0	0	0	22	Yes
S067277664	NT-current cohort	9.6	6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		18	38	Cesarean section	2	2	0	0	0	0	0	24	Yes
S059980013	NT-current cohort	7.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39	Cesarean section	1	1	0	0	0	0	0	24	Yes
S049912907	NT-current cohort	8	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	1	1	0	0	0	0	0	24	Yes
S075023591	NT-current cohort	8.6	6	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39+3	Cesarean section	1	1	0	0	0	0	0	23	Yes
S024371330	NT-current cohort	7.8	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Vaginally delivery	2	2	0	0	0	0	0	24	Yes
S034983989	NT-current cohort	2.9	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40+1	Cesarean section	1	1	0	0	0	0	0	25	Yes
S050295087	NT-current cohort	6.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		29	38+2	Cesarean section	1	1	0	0	0	0	0	34	Yes
S084844176	NT-current cohort	5.1	5-6	male	Hunan	0	no	no	no	1	3	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		31	40+3	Cesarean section	1	1	0	0	0	0	0	32	Yes
S097918514	NT-current cohort	5.1	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	37	Cesarean section	1	1	1	0	0	0	0	31	Yes
S019541272	NT-current cohort	5.1	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	37	Cesarean section	1	1	1	0	0	0	0	31	Yes
S035314238	NT-current cohort	3.9	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	3	2	0	0	0	0	0	30	Yes
S045809469	NT-current cohort	2	2-3	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39	Cesarean section	3	3	0	0	0	0	0	30	Yes
S074970729	NT-current cohort	0.11	1-1.5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	39+1	Cesarean section	2	2	0	0	0	0	0	32	Yes
S097184998	NT-current cohort	3.5	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40+	Cesarean section	1	1	0	0	0	0	0	26	Yes
S077510130	NT-current cohort	3	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		37	39	Cesarean section	4	2	0	0	0	0	0	40	Yes
S074914518	NT-current cohort	2.2	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	37	Cesarean section	2	2	0	0	0	0	0	45	Yes
S061343400	NT-current cohort	2.2	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		29	40	Cesarean section	1	1	0	0	0	0	0	28	Yes
S046500814	NT-current cohort	5.7	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		24	39	Cesarean section	1	1	0	0	0	0	0	30	Yes
S027595735	NT-current cohort	3.8	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	39	Cesarean section	1	1	0	0	0	0	0	26	Yes
S015477362	NT-current cohort	1.2	1-1.5	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	1	1	0	0	0	1	0	0	0	0		0	0	0	0		29	37+5	Cesarean section	2	2	0	0	0	0	0	27	Yes
S009299451	NT-current cohort	5.8	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	0	0	0	0	21	Yes
S059360421	NT-current cohort	6.2	6	male	Hunan	0	no	no	no	1	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	3	2	0	0	0	0	0	31	Yes
S005135760	NT-current cohort	6.3	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Cesarean section	1	1	0	0	0	0	0	22	Yes
S042496861	NT-current cohort	4.11	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		21	39	Cesarean section	2	2	0	0	0	0	0	27	Yes
S004313657	NT-current cohort	6.5	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		30	39	Cesarean section	2	2	0	0	0	0	0	32	Yes
S047946262	NT-current cohort	5.1	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S072858593	NT-current cohort	6.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	39	Vaginally delivery	2	2	0	0	0	0	0	36	Yes
S021762070	NT-current cohort	6.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	39+	Cesarean section	2	2	0	0	0	0	0	27	Yes
S096550440	NT-current cohort	6.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		23	40	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S048435737	NT-current cohort	6.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	36	Yes
S055577539	NT-current cohort	6	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	0	0	0	0	22	Yes
S072670769	NT-current cohort	3.5	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	36	Cesarean section	2	2	0	0	0	0	0	49	Yes
S055918907	NT-current cohort	6.5	6	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		22	39	Cesarean section	2	2	0	0	0	0	0	24	Yes
S018801510	NT-current cohort	2.4	2-3	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		27	40+5	Cesarean section	1	1	0	0	0	0	0	30	Yes
S034302204	NT-current cohort	3.11	3-4	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		20	40	Cesarean section	2	1	0	0	0	0	0	20	Yes
S025054684	NT-current cohort	5.1	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Cesarean section	2	2	0	0	0	0	0	35	Yes
S048829494	NT-current cohort	6.1	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	40	Vaginally delivery	2	2	0	0	0	0	0	37	Yes
S041462795	NT-current cohort	6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Cesarean section	2	1	0	0	0	0	0	22	Yes
S074961978	NT-current cohort	6.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	43	Cesarean section	1	1	0	0	0	0	0	26	Yes
S070455573	NT-current cohort	6.6	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	38	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S049805234	NT-current cohort	4.8	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	39	Cesarean section	1	1	0	0	0	0	0	25	Yes
S002431553	NT-current cohort	5.6	5-6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S090411417	NT-current cohort	5.4	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	2	0	1	0	1	0	0	0	0		0	0	0	0		36	40	Cesarean section	2	2	1	0	0	0	0	38	Yes
S031833195	NT-current cohort	4.5	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	38+5	Vaginally delivery	1	1	0	0	0	0	0	22	Yes
S096352119	NT-current cohort	5.1	5-6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	39+1	Vaginally delivery	2	2	0	0	0	0	0	30	Yes
S002189490	NT-current cohort	2.11	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	39+	Cesarean section	4	2	0	0	0	0	0	29	Yes
S012669221	NT-current cohort	4	4-5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	0	28	Yes
S014375524	NT-current cohort	4.6	4-5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	36	Cesarean section	1	1	0	0	0	0	0	27	Yes
S001887626	NT-current cohort	5	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	34+6	Vaginally delivery	1	1	0	0	0	0	0	20	Yes
S016131675	NT-current cohort	3.4	3-4	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	39	Cesarean section	1	1	0	0	0	0	0	26	Yes
S020949701	NT-current cohort	3.9	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	38	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S053872221	NT-current cohort	3.11	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		19	35	Cesarean section	3	2	0	0	0	0	0	25	Yes
S071109432	NT-current cohort	6.1	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	39+2	Cesarean section	1	1	0	0	0	0	1	29	Yes
S012970695	NT-current cohort	4.6	4-5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	40	Cesarean section	1	1	0	0	0	0	0	26	Yes
S038498323	NT-current cohort	3.7	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0		0	0	0	0		31	39	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S013723309	NT-current cohort	2.3	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		37	40+	Vaginally delivery	2	2	0	0	0	0	0	38	Yes
S061757032	NT-current cohort	2.1	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	36+3	Cesarean section	5	2	0	0	0	0	0	-	Yes
S048745504	NT-current cohort	2.9	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39+4	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S072687488	NT-current cohort	3.5	3-4	male	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		30	38	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S088452008	NT-current cohort	1.6	1-1.5	female	Hunan	0	no	no	no	1	1	0	0	1	0	0	0	0	1	1	0	0	1	0	0	0	0	0		0	0	0	0		31.5	39	Vaginally delivery	2	2	0	0	0	0	0	32.5	Yes
S043650673	NT-current cohort	8.5	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		0	0	Vaginally delivery	NA	NA	0	0	0	0	0	-	Yes
S043226785	NT-current cohort	9.1	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	36	Vaginally delivery	2	2	0	0	0	0	0	36	Yes
S025242765	NT-current cohort	8.3	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	0	Cesarean section	2	NA	0	0	0	0	0	36	Yes
S037545265	NT-current cohort	8.3	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	36	Cesarean section	1	1	0	0	0	0	0	23	Yes
S022327341	NT-current cohort	8.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	36	Vaginally delivery	4	2	0	0	0	0	0	25	Yes
S000531667	NT-current cohort	9.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	39	Cesarean section	2	1	0	0	0	0	0	30	Yes
S005681792	NT-current cohort	8.2	6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		35	40	Vaginally delivery	2	2	0	0	0	0	0	40	Yes
S028593544	NT-current cohort	8	6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	37	Cesarean section	2	2	0	0	0	0	0	35	Yes
S083798242	NT-current cohort	8.6	6	female	Hunan	0	no	no	no	1	3	0	0	0	0	1	1	0	1	1	0	0	0	1	0	0	0	0		0	0	0	0		26	40	Cesarean section	1	1	0	0	0	0	0	33	Yes
S095977947	NT-current cohort	8.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		20	39	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S005947097	NT-current cohort	8.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		21	40	Vaginally delivery	2	2	0	0	0	0	0	21	Yes
S087372996	NT-current cohort	9.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	34	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S079185934	NT-current cohort	8.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	36	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S094080213	NT-current cohort	9	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		23	39	Cesarean section	1	1	0	1	0	0	0	24	Yes
S061883347	NT-current cohort	6.4	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Cesarean section	1	1	0	0	0	0	0	28	Yes
S096405432	NT-current cohort	4.4	4-5	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	39	Cesarean section	2	2	0	0	0	0	0	28	Yes
S041878419	NT-current cohort	6.7	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		33	40	Vaginally delivery	2	2	0	0	0	0	0	41	Yes
S065592688	NT-current cohort	6.6	6	male	Hunan	0	no	no	no	1	3	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		35	40	Vaginally delivery	3	2	0	0	0	0	0	40	Yes
S004843722	NT-current cohort	6.6	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S092940966	NT-current cohort	6.3	6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		26	40+2	Vaginally delivery	1	1	0	0	0	0	0	33	Yes
S099099486	NT-current cohort	5.6	5-6	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		39	40	Vaginally delivery	2	2	0	0	0	0	0	-	Yes
S097025688	NT-current cohort	2.7	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	41	Cesarean section	3	1	0	0	0	0	0	26	Yes
S071142136	NT-current cohort	1.1	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	38+1	Cesarean section	1	1	0	0	0	0	0	30	Yes
S056743265	NT-current cohort	3.8	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S072077651	NT-current cohort	3.4	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Cesarean section	1	1	0	0	0	0	0	31	Yes
S070491067	NT-current cohort	2.1	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S092477162	NT-current cohort	3.3	3-4	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		30	40	Vaginally delivery	2	2	0	0	0	0	0	36	Yes
S005559234	NT-current cohort	2.7	2-3	female	Hunan	0	no	no	no	1	2	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		28	40+3	Vaginally delivery	2	2	0	0	0	0	0	29	Yes
S074728881	NT-current cohort	2.9	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		0	0	0	1	Hypoxia	23	38+6	Cesarean section	1	1	0	0	0	0	0	25	Yes
S040423418	NT-current cohort	2.3	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		36	39	Cesarean section	2	1	1	0	0	0	0	40	Yes
S052399823	NT-current cohort	1.5	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	39	Cesarean section	3	2	0	0	0	0	0	33	Yes
S096969205	NT-current cohort	3.7	3-4	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		35	39	Vaginally delivery	4	2	0	0	0	0	0	38	Yes
S067772489	NT-current cohort	3.5	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		42	37	Cesarean section	4	2	1	0	0	0	0	50	Yes
S005270467	NT-current cohort	1.7	1.5-2	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	40	Cesarean section	3	1	0	0	0	0	0	-	Yes
S046751169	NT-current cohort	3	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0		0	1	0	0		28	39+2	Cesarean section	2	2	0	0	0	0	0	32	Yes
S066857064	NT-current cohort	3.2	3-4	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	39	Cesarean section	1	1	0	0	0	0	0	32	Yes
S051714892	NT-current cohort	2.11	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		38	40	Vaginally delivery	3	2	0	0	0	0	0	38	Yes
S063475923	NT-current cohort	1.1	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	41	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S042299860	NT-current cohort	3.1	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	39	Cesarean section	1	1	0	0	0	0	0	26	Yes
S011221885	NT-current cohort	2.9	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	39	Cesarean section	2	2	0	0	0	0	0	30	Yes
S066924215	NT-current cohort	3.1	3-4	female	Hunan	0	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	42	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S091943702	NT-current cohort	3.9	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	0	Vaginally delivery	2	2	0	0	0	0	0	-	Yes
S056987173	NT-current cohort	1.2	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		33	41	Vaginally delivery	3	1	0	0	0	0	0	32	Yes
S031223958	NT-current cohort	1.8	1.5-2	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S083936624	NT-current cohort	2.1	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		42	38+5	Cesarean section	4	2	0	0	0	0	0	48	Yes
S043303867	NT-current cohort	3.7	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		31	33+5	Vaginally delivery	1	1	0	0	0	0	0	31	Yes
S005083436	NT-current cohort	2.9	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	38	Cesarean section	1	1	0	0	0	0	0	31	Yes
S084188681	NT-current cohort	2.9	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	37	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S012228908	NT-current cohort	3.7	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		39	38	Cesarean section	3	2	0	0	0	0	0	42	Yes
S015928302	NT-current cohort	1.1	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	39	Cesarean section	1	1	0	0	0	0	0	30	Yes
S093222599	NT-current cohort	3.2	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		24	40	Cesarean section	1	1	0	0	0	0	0	25	Yes
S015138149	NT-current cohort	2.8	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	2	1	0	0	0	0	0	30	Yes
S037130629	NT-current cohort	2.8	2-3	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		24	39+2	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S088215363	NT-current cohort	1.3	1-1.5	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	39	Vaginally delivery	1	1	0	0	0	0	0	27	Yes
S075436975	NT-current cohort	3.6	3-4	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	40+1	Cesarean section	2	2	0	0	0	0	0	36	Yes
S009620142	NT-current cohort	3.3	3-4	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		36	39	Cesarean section	2	2	0	0	0	0	0	36	Yes
S029414609	NT-current cohort	2.8	2-3	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		29	38+1	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S091518266	NT-current cohort	1.3	1-1.5	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	2	2	0	0	0	0	0	31	Yes
S018585773	ASD-current cohort	11	6	male	Guandong	2	light	light	no	1	1	0	0	0	0	0	1	0	1	1	0	1	0	0	1	0	0	0		0	0	0	0		33	38	Cesarean section	3	1	0	0	0	0	0	37	Yes
S097724212	ASD-current cohort	3.4	3-4	female	Hunan	9	severe	severe	severe	1	2	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		28	40	Cesarean section	2	1	0	0	0	0	0	30	Yes
S034703269	ASD-current cohort	3	3-4	male	Guandong	6	light	secondary	severe	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0		0	0	0	0		26	38	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S082822397	ASD-current cohort	3	3-4	male	Hunan	6	light	severe	secondary	1	3	0	0	1	0	0	1	1	0	0	0	0	0	0	1	1	0	0		0	0	0	0		27	40	Vaginally delivery	3	2	1	0	0	0	0	32	Yes
S083211397	ASD-current cohort	3	3-4	male	Beijing	5	secondary	secondary	light	1	3	0	0	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		30	39	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S017610360	ASD-current cohort	8	6	female	Hunan	3	light	light	light	1	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		34	38	Cesarean section	2	2	0	0	0	0	0	35	Yes
S034903911	ASD-current cohort	14	6	male	Hunan	7	secondary	secondary	severe	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		29	36	Vaginally delivery	1	1	0	0	0	0	0	30	Yes
S092946865	ASD-current cohort	7.7	6	male	Xinjiang	4	light	secondary	light	1	1	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		30	40	Cesarean section	3	1	0	0	0	0	0	34	Yes
S068725163	ASD-current cohort	2.7	2-3	male	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		33	39	Vaginally delivery	2	2	0	0	1	0	0	36	Yes
S088546066	ASD-current cohort	17	6	male	Hunan	6	light	severe	secondary	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0		0	0	0	0		26	38	Cesarean section	2	1	0	0	0	0	0	30	Yes
S093264613	NT-current cohort	5	5-6	female	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		0	37	Vaginally delivery	1	1	0	0	0	0	0	25	Yes
S029907899	ASD-current cohort	5	5-6	male	Shandong	8	severe	secondary	severe	1	4	1	0	1	0	0	1	1	1	2	1	0	0	1	1	1	1	0		0	0	0	0		36	39	Cesarean section	1	1	1	0	0	0	0	36	Yes
S010781138	NT-current cohort	8	6	female	Jiangsu	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0		0	0	0	0		30	40	Cesarean section	2	2	0	0	0	0	0	30	Yes
S002082053	ASD-current cohort	6	5-6	male	Hunan	5	secondary	light	secondary	0	0	0	0	0	0	0	0	0	0	2	0	1	0	1	0	0	0	0		0	0	0	0		25	38	Cesarean section	1	1	1	0	0	0	0	24	Yes
S034225824	ASD-current cohort	5	5-6	male	Neimeng	6	secondary	secondary	secondary	1	1	0	0	1	0	0	0	0	0	1	0	0	0	1	1	0	0	0		0	0	0	0		32	35	Cesarean section	2	2	0	0	0	0	1	30	Yes
S053996337	ASD-current cohort	4	4-5	male	Zhejiang	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		28	40	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S065147629	NT-current cohort	5.5	5-6	female	Hunan	0	no	no	no	1	3	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	39	Vaginally delivery	2	2	0	0	0	0	0	27	Yes
S045446412	ASD-current cohort	4.6	4-5	female	Guandong	3	light	light	light	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	0	0	0		0	1	0	0		34	39	Vaginally delivery	3	2	0	0	0	0	0	42	Yes
S029879579	ASD-current cohort	2.9	2-3	male	Guandong	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	1	0	0	0		0	0	0	0		29	40+4	Vaginally delivery	2	1	0	0	0	0	0	29	Yes
S056202627	ASD-current cohort	3.1	3-4	male	Tianjin	3	light	light	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Cesarean section	1	1	0	0	0	0	0	29	Yes
S051010549	ASD-current cohort	6.5	6	male	Shandong	4	light	secondary	light	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0		0	1	0	0		28	36	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S011620320	NT-current cohort	6	5-6	male	Hunan	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	40	Vaginally delivery	NA	NA	0	0	0	0	0	33	Yes
S066640463	NT-current cohort	5.9	5-6	male	Hunan	0	no	no	no	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	39	Vaginally delivery	1	1	0	0	0	0	0	23	Yes
S085671404	ASD-current cohort	4	4-5	male	Gansu	8	secondary	severe	severe	1	1	0	0	1	0	0	0	0	1	3	1	1	1	0	1	1	1	0		0	0	1	0		33	39	Vaginally delivery	4	2	0	0	0	0	0	33	Yes
S041350940	ASD-current cohort	4.4	4-5	male	Hunan	6	light	severe	secondary	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0		0	0	0	0		34	34	Vaginally delivery	2	2	0	0	0	0	0	35	Yes
S059167074	ASD-current cohort	4	4-5	male	Beijing	7	secondary	severe	secondary	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0		0	0	0	0		31	40	Cesarean section	3	1	1	0	0	0	0	35	Yes
S024364430	ASD-current cohort	4	4-5	male	Guandong	7	light	severe	severe	1	1	0	0	0	0	0	1	0	1	1	1	0	0	0	0	0	0	0		0	0	0	0		35	40	Cesarean section	2	2	0	0	0	0	0	35	Yes
S012350013	ASD-current cohort	4	4-5	male	Gansu	6	secondary	secondary	secondary	1	1	0	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0		0	0	0	0		33	40	Vaginally delivery	2	2	0	0	0	0	0	33	Yes
S097075151	ASD-current cohort	3.6	3-4	male	Hunan	5	light	secondary	secondary	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		29	38	Cesarean section	2	1	0	0	0	0	0	29	Yes
S041060323	ASD-current cohort	3.2	3-4	female	Hunan	3	light	light	light	0	0	0	0	0	0	0	0	0	1	2	1	0	0	1	1	0	0	0		0	1	0	0		36	39	Cesarean section	4	2	0	0	0	0	0	37	Yes
S027103892	NT-current cohort	1	1-1.5	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		22	40	Vaginally delivery	1	1	0	0	0	0	0	24	Yes
S055519308	NT-current cohort	1	1-1.5	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S360886669	NT-current cohort	1	1-1.5	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S010851674	NT-current cohort	2	2-3	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S055683828	NT-current cohort	2	2-3	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S029475264	NT-current cohort	2	2-3	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S073665246	NT-current cohort	2	2-3	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015674034	NT-current cohort	2	2-3	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S022135387	NT-current cohort	2	2-3	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S033568605	NT-current cohort	2	2-3	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S058932620	NT-current cohort	2	2-3	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S086910663	NT-current cohort	2	2-3	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S213080736	NT-current cohort	2	2-3	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S356165855	NT-current cohort	2	2-3	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S066790385	NT-current cohort	2	2-3	male	Guandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S087369825	NT-current cohort	2	2-3	female	Guandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013997240	NT-current cohort	2	2-3	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S050200953	NT-current cohort	3	3-4	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S052794229	NT-current cohort	3	3-4	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S003535143	NT-current cohort	3	3-4	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S025934558	NT-current cohort	3	3-4	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S037409382	NT-current cohort	3	3-4	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S040409279	NT-current cohort	3	3-4	female	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S080862660	NT-current cohort	3	3-4	female	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013245787	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013537165	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013579589	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013625836	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013948618	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014157937	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014225597	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014482972	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014580657	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014613719	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015137919	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015545066	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015549955	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015622448	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019668978	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019872539	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019952600	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S020259387	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S020288529	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S022718019	NT-current cohort	3	3-4	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S022970891	NT-current cohort	3	3-4	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S020004104	NT-current cohort	3	3-4	female	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S058701229	NT-current cohort	3	3-4	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S072546306	NT-current cohort	3	3-4	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S375599185	NT-current cohort	3	3-4	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S092908823	NT-current cohort	3	3-4	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019920574	NT-current cohort	4	4-5	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S091643306	NT-current cohort	4	4-5	female	Shanghai	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S095059383	NT-current cohort	4	4-5	male	Zhejiang	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S021957050	NT-current cohort	4	4-5	male	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S083009793	NT-current cohort	4	4-5	female	Hubei	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S008747305	NT-current cohort	4	4-5	female	USA	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013354379	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013839784	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013871852	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S013901482	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014073994	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014102262	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014135970	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014302951	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014429510	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014547144	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014705872	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S014842833	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015286364	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015382694	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015550250	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015650077	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S015767009	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019678347	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes
S019777759	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		NA	NA	Vaginally delivery	1	1	0	0	0	0	0	NA	Yes

S020153536	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S020316655	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S020537489	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S020912033	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S021277101	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S021302008	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S021385792	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S022354294	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S022415317	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S022477670	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S022703907	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S022835665	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S023922211	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S044123933	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S044180736	NT-current cohort	4	4-5	female	Shandong	0	no	no	no	0	0
S044524605	NT-current cohort	4	4-5	male	Shandong	0	no	no	no	0	0
S184038211	NT-current cohort	4	4-5	male	Zhejiang	0	no	no	no	0	0
S039692960	NT-current cohort	4	4-5	female	Zhejiang	0	no	no	no	0	0
S048725289	NT-current cohort	4	4-5	male	Zhejiang	0	no	no	no	0	0
S079393149	NT-current cohort	4	4-5	male	Zhejiang	0	no	no	no	0	0
S082690726	NT-current cohort	4	4-5	female	Zhejiang	0	no	no	no	0	0
S087455632	NT-current cohort	4	4-5	male	Beijing	0	no	no	no	0	0
S045452669	NT-current cohort	5	5-6	female	Shanghai	0	no	no	no	0	0
S046012869	NT-current cohort	5	5-6	female	Shanghai	0	no	no	no	0	0
S292265254	NT-current cohort	5	5-6	male	Shanghai	0	no	no	no	0	0
S096386072	NT-current cohort	5	5-6	female	Shanghai	0	no	no	no	0	0
S089349572	NT-current cohort	5	5-6	male	Zhejiang	0	no	no	no	0	0
S006973519	NT-current cohort	5	5-6	male	Hubei	0	no	no	no	0	0
S024417857	NT-current cohort	5	5-6	male	Hubei	0	no	no	no	0	0
S063825083	NT-current cohort	5	5-6	male	Hubei	0	no	no	no	0	0
S013467689	NT-current cohort	5	5-6	female	Shandong	0	no	no	no	0	0
S014038518	NT-current cohort	5	5-6	female	Shandong	0	no	no	no	0	0
S014256734	NT-current cohort	5	5-6	female	Shandong	0	no	no	no	0	0
S014265530	NT-current cohort	5	5-6	male	Shandong	0	no	no	no	0	0
S014280611	NT-current cohort	5	5-6	male	Shandong	0	no	no	no	0	0

S087266621	NT-validation cohort 1	5Y7M	5-6Y	male	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	1	0	0		26	38+3	Vaginally delivery	1	1	0	0	0	0	0	29	Yes
S038235650	NT-validation cohort 1	6Y	6-7Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		32	40	Cesarean section	1	1	0	0	0	0	0	40	Yes
S013863345	NT-validation cohort 1	6Y	6-7Y	male	Hunan	no	no	no	no	1	4	0	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	41	Vaginally delivery	3	2	0	0	0	0	0	31	Yes
S032447687	NT-validation cohort 1	6Y3M	6-7Y	male	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		27	40	Vaginally delivery	2	1	0	0	0	0	0	28	Yes
S066418984	NT-validation cohort 1	6Y7M	6-7Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		28	37+4	Cesarean section	1	1	0	0	0	0	0	29	Yes
S043325014	NT-validation cohort 1	7Y11M	7-8Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		0	0	0	0		22	40	Vaginally delivery	2	2	0	0	0	0	0	24	Yes
S082366127	NT-validation cohort 1	7Y1M	7-8Y	male	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		26	41	Vaginally delivery	1	1	0	0	0	0	0	28	Yes
S014372436	NT-validation cohort 1	7Y3M	7-8Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	40	Vaginally delivery	1	1	0	0	0	0	0	26	Yes
S043038532	NT-validation cohort 1	8Y6M	8-9Y	male	Hunan	no	no	no	no	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0		0	0	0	0		21	40	Vaginally delivery	1	1	0	0	0	0	0	23	Yes
S011931893	NT-validation cohort 1	8Y8M	8-9Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		25	38	Cesarean section	2	2	0	0	0	0	0	27	Yes
S073193247	NT-validation cohort 1	8Y9M	8-9Y	female	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0		29	40	Vaginally delivery	1	1	0	0	0	0	0	36	Yes
S078776205	NT-validation cohort 1	9Y2M	8-9Y	male	Hunan	no	no	no	no	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0		0	0	0	0		21	40	Vaginally delivery	1	1	0	0	0	0	0	23	Yes

Table 2 Summary of subject's distributions according to age categories

	age brackets (y)	**ASD**	**NT**
Current cohort	1-1.5	11	16
	1.5-2	14	3
	2-3	128	40
	3-4	179	70
	4-5	134	63
	5-6	152	75
	6-7Y	34	65
	7-8Y	40	33
	8-9Y	29	29
	9-12Y	39	28
	12-15Y	9	8
	adult	3	20
	total	772	450
Validation cohort 1	age brackets	**ASD**	**NT**
	11-23 mo	8	4
	24-35mo	9	3
	36-47mo	8	3
	4-5Y	9	6
	5-6Y	8	5
	6-7Y	8	4
	7-8Y	8	3
	8-9Y	7	4
	9Y~	8	none
	total	73	32

Table 3 Identification of severity levels for autism spectrum disorder based on DSM-IV and DSM-V

	Social communication	Restricted, repetitive behaviors	Language development delay
Mild	Requiring support. Without supports in place, deficits in social communication cause noticeable impairments. Difficulty initiating social interactions, and clear examples of atypical or unsuccessful response to social overtures of others. May appear to have decreased interest in social interactions.	Requiring support. Inflexibility of behavior causes significant interference with functioning in one or more contexts. Difficulty switching between activities. Problems of organization and planning hamper independence.	Difficulty in putting words together into a sentence or leaving words out of a sentence.
Moderate	Requiring substantial support. Marked deficits in verbal and nonverbal social communication skills; social impairments apparent even with supports in place; limited initiation of social interactions; and reduced or abnormal responses to social overtures from others.	Requiring substantial support. Inflexibility of behavior, difficulty coping with change, or other restricted/repetitive behaviors appear frequently enough to be obvious to the casual observer and interfere with functioning in a variety of contexts. Distress and/or difficulty changing focus or action.	Imitation, just babbling or inability to speak in short sentences.
Severe	Requiring very substantial support. Severe deficits in verbal and nonverbal social communication skills cause severe impairments in functioning, very limited initiation of social interactions, and minimal response to social overtures from others.	Requiring very substantial support. Inflexibility of behavior, extreme difficulty coping with change, or other restricted/repetitive behaviors markedly interfere with functioning in all spheres. Great distress/difficulty changing focus or action.	Language only for needs or not talking.

Table 4 Summary of **subject's distributions** according to district categories

	Region	**ASD**	**NT**
Current cohort	Hunan	285	198
	Guandong	104	2
	Shandong	65	120
	Beijing	56	10
	Sichuan	36	1
	Hubei	28	33
	Shanghai	25	25
	Zhejiang	24	57
	Jiangsu	20	3
	Jiangxi	18	0
	Shanxi	15	0
	Hebei	13	0
	Chongqing	11	0
	Tianjin	11	0
	Xinjiang	11	0
	Anhui	9	0
	Henan	9	0
	Gansu	6	0
	Guanxi	5	0
	Fujian	4	0
	Hainan	4	1
	Liaoning	4	0
	Neimeng	4	0
	Guizhou	3	1
	Jilin	2	0
Validation cohort 1	**Region**	**ASD**	**NT**
	Hunan	31	32
	Shandong	20	0
	Guandong	6	0
	Zhejiang	6	0
	Chongqing	2	0
	Hubei	2	0
	Jiangsu	2	0
	Gansu	1	0
	Jiangxi	1	0
	Shanghai	1	0
	SIchuan	1	0

Table5 **Alpha diversity under different under different parameters**

shannon	20 adults	5.73 ± 0.756	p value	Adults vs. NT	Adults vs. ASD	NT vs. ASD
	NT	5.4206 ± 1.14		0.4691	0.0007	<0.0001
	ASD	4.77 ± 1.16				
simpson	20 adults	0.94 ± 0.04	p value	Adults vs. NT	Adults vs. ASD	NT vs. ASD
	NT	0.91 ± 0. 09		0.3992	0.0141	<0.0001
	ASD	0.87 ± 0.12				
chao1	20 adults	2355.07 ± 1274.39	p value	Adults vs. NT	Adults vs. ASD	NT vs. ASD
	NT	2977.13 ± 1583.84		0.1283	0.9587	<0.0001
	ASD	2267.15 ± 1294.37				
ace	20 adults	2394.17 ± 1329.29	p value	Adults vs. NT	Adults vs. ASD	NT vs. ASD
	NT	3052.70 ± 1630.33		0.1118	0.9717	<0.0001
	ASD	2319.87 ±1319.99				
goods_coverage	20 adults	99.51% ± 0.33%	p value	NA		
	NT	99.35% ± 0.39%				
	ASD	99.55% ± 0.29%				

Shannon index

	NT		ASD	
	mean	sd	mean	sd
0-16mo	4.759399451	1.359547967	3.836082927	0.964003457
16-18mo	3.764213312	1.025357825	2.849265085	1.619845272
18-20mo	4.196894667	0.606140885	3.616706239	1.347681161
20-22mo	4.926090339	0.752870905	3.775844587	1.573532974
22-24mo	5.542285549	1.01700189	3.841787444	1.387423655
24-26mo	5.463804669	1.194155942	4.701179309	0.926512271
26-28mo	5.022808685	1.136191124	4.458895719	0.733147925
28-30mo	4.353316031	0.753168643	4.586324527	1.110997305
30-32mo	4.745291597	0.912644623	4.570967246	1.179000381
32-34mo	4.642527458	0.76418573	5.26308442	0.960932
34-36mo	5.21101315	0.84406933	4.647607285	1.099560467
3-4y	4.543924885	1.135308193	4.568936906	1.000936654
4-5y	5.59501416	0.995748552	4.928618373	1.122853308
5-6y	5.47851421	1.041302464	4.858354881	1.109141125
6-7y	5.743279675	1.157214041	4.97313772	1.213777533
7-8y	5.60510922	1.060199335	4.984953987	1.299020924
8-9y	6.011443948	1.199575446	5.329017922	1.058225814
9-16y	5.781164334	1.030728251	5.299373648	1.081186082
adults	5.7284785	0.757131446	5.230236748	0.22090182

Table 6 Host multifactorial effects on composition of gut microbiota calculated by EnvFit

EnvFit				
Factors	≤3y		>3y	
	r-square	p value	r-square	p value
ASD diagnosis	0.0170	0.038	0.0173	0.001
District	0.0544	0.981	0.0295	0.196
Age	0.0384	0.001	0.0283	0.001
Gender	0.0059	0.292	0.0010	0.379
Any GI problem	0.0033	0.49	0.0050	0.01
Esophageal reflux	0.0033	0.505	0.0019	0.165
Peptic ulcer	0.0019	0.687	0.0030	0.041
Dyspepsia	0.0019	0.69	0.0022	0.106
Abdominal distension	0.0166	0.033	0.0003	0.753
Abdominal pain	0.0168	0.021	0.0016	0.198
Constipation	0.0064	0.266	0.0049	0.009
Abnormal stool consistency	0.0137	0.055	0.0006	0.569
Any Sleep complaints	0.0153	0.045	0.0011	0.334
Difficulty falling asleep	0.0089	0.149	0.0001	0.92
Sleep fragmentation	0.0155	0.042	0.0024	0.089
Short sleep duration	0.0021	0.638	0.0006	0.565
Shallow sleep	0.0131	0.057	0.0001	0.914
Food allergy or intolerance	0.0070	0.233	0.0103	0.001
Skin allergy	0.0015	0.724	0.0004	0.707
Respiratory hypersensitivity	0.0113	0.084	0.0027	0.072
Antibiotic usage with in 3 mo	0.0149	0.047	0.0113	0.001
Infection within 1 mo	0.0025	0.605	0.0002	0.791
Age of mother during pregnancy	0.0000	1.000	0.0000	1.000
Age of father during pregnancy	0.0000	1.000	0.0000	1.000
Assisted reproduction	0.0111	0.09	0.0028	0.069
Smoking	0.0000	1.000	0.0001	0.965
Drinking	0.0056	0.329	0.0002	0.825
Infection during pregnancy	0.0023	0.603	0.0007	0.489
Eclampsia/Pre-eclampsia	0.0052	0.37	0.0011	0.355
Gestational age	0.0000	1.000	0.0000	1.000
Mode of delivery	0.0037	0.454	0.0024	0.081
Neonatal asphyxia	0.0001	0.971	0.0028	0.062
Family history of mental disorders	0.0129	0.054	0.0030	0.049
…				

Table 7 Summary of **demographic and clinical characteristics** of healthy children (NT) and kids with ASD

				ASD	**NT (healthy adults included)**
Current cohort	Diagnosis	Total ASD score	mean ± SEM	4.18 ± 0.15	/
		Repetitive behavior	mean ± SEM	1.38 ± 0.05	/
		Social retardation	mean ± SEM	2.00 ± 0.07	/
		Language retardation	mean ± SEM	2.04 ± 0.07	/
	Demographic	Gender	Female (Male)	127 (645)	217 (233)
	Comorbidity	Any GI problems	Yes/all	494/772 (63.9%)	48/450 (10.7%)
		Mean value of total GI problem score of each subject	mean ± SEM	1.05 ± 1.33	0.18 ± 0.56
		Esophageal reflux	Yes/all	54/772 (6.9%)	2/450 (0.4%)
		Peptic ulcer	Yes/all	10/772 (1.3%)	1/450 (0.2%)
		Dyspepsia	Yes/all	238/772 (30.8%)	15/450 (3.3%)
		Abdominal distension	Yes/all	129/772 (16.7%)	1/450 (0.2%)
		Abdominal pain	Yes/all	61/772 (7.9%)	9/450 (2%)
		Constipation	Yes/all	346/772 (44.8%)	19/450 (4.2%)
		Abnormal stool consistency	Yes/all	127/772 (16.4%)	7/450 (1.6%)
		Any sleep complaints	Yes/all	354/772 (45.8%)	21/450 (4.7%)
		Mean value of sleep complaints score	mean ± SEM	0.71 ± 1.02	0.07 ± 0.25
		Difficulty falling asleep	Yes/all	193/772 (25.0%)	2/450 (0.4%)
		Sleep fragmentation	Yes/all	216/772 (27.9%)	9/450 (2.1%)
		Short sleep duration	Yes/all	84/772 (10.9%)	7/450 (1.6%)
		Shallow sleep	Yes/all	119/772 (15.4%)	7/450 (1.6%)
		Total Allergy score	mean ± SEM	0.67 ± 0.03	0.13 ± 0.02
		Food allergy or intolerance	Yes/all	353/772 (45.7%)	15/450 (3.3%)
		Skin allergy	Yes/all	157/772 (20.3%)	15/450 (3.3%)
		Respiratory hypersensitivity	Yes/all	109/772 (14.1%)	5/450 (1.1%)
	Clinical	Antibiotic usage within 3 mo	Yes/all	67/772 (8.7%)	3/450 (0.6%)
		Any infection within 1 mo	Yes/all	21/772 (2.7%)	2/450 (0.4%)
	Perinatal	Any neonatal asphyxia	Yes/all	51/772 (6.6%)	1/450 (0.02%)
		Age of mother during pregnancy	mean ± SEM	29.28 ± 0.20	26.58 ± 0.34
		Age of father during pregnancy	mean ± SEM	31.83 ± 0.21	29.88 ± 0.26
		Premature delivery	Yes/all/NA or Forgotten	83/772 (10.7%) /0	18/197 (9.1%) /253
		Mode of delivery	Cesarean section/Vaginally delivery	446/327	106/343
		Assisted reproduction	Yes/all	97/772 (12.5%)	7/450 (1.6%)
		Eclampsia/Pre-eclampsia	Yes/all	9/772 (1.2%)	2/450 (0.4%)
		Infection during pregnancy	Yes/all	55/772 (7.1%)	1/450 (0.2%)
	Family history	Family history of mental disorders	Yes/all	42/772 (5.4%)	0/450 (0%)
Validation cohort 1				**ASD**	**NT**
	Diagnosis	Total ASD score	mean ± SEM	6.21 ± 0.18	/
		Repetitive behavior	mean ± SEM	1.62 ± 0.08	/
		Social retardation	mean ± SEM	2.34 ± 0.07	/
		Language retardation	mean ± SEM	2.27 ± 0.09	/
	Demographic	Gender	Female (Male)	15 (73)	14 (32)
	Comorbidity	Any GI problems	Yes/all	45/73 (61.6%)	5/32 (15.6%)
		Mean value of total GI problem score of each subject	mean ± SEM	1.33 ± 0.17	0.31 ± 0.15
		Esophageal reflux	Yes/all	8/73 (10.9%)	0/32 (0%)
		Peptic ulcer	Yes/all	3/73 (4.1%)	0/32 (0%)
		Dyspepsia	Yes/all	32/73 (43.8%)	3/32 (9.4%)
		Abdominal distension	Yes/all	19/73 (26.0%)	0/32 (0%)
		Abdominal pain	Yes/all	8/73 (10.9%)	1/32 (3.1%)
		Constipation	Yes/all	23/73 (31.5%)	4/32 (12.5%)
		Abnormal stool consistency	Yes/all	1/73 (1.44%)	2/32 (6.3%)
		Any sleep complaints	Yes/all	37/73 (50.7%)	2/32 (6.3%)
		Mean value of sleep complaints score	mean ± SEM	0.78 ± 0.13	0.09 ± 0.07
		Difficulty falling asleep	Yes/all	24/73 (32.9%)	0/32 (0%)

		Sleep fragmentation	Yes/all	13/73 (17.8%)	2/32 (6.3%)
		Short sleep duration	Yes/all	11/73 (15.1%)	0/32 (0%)
		Shallow sleep	Yes/all	9/73 (12.3%)	1/32 (3.1%)
		Total Allergy score	mean ± SEM	0.64 ± 0.10	0.28 ± 0.09
		Food allergy or intolerance	Yes/all	26/73 (35.6%)	3/32 (9.4%)
		Skin allergy	Yes/all	14/73 (19.2%)	5/32 (15.6%)
		Respiratory hypersensitivity	Yes/all	7/73 (9.6%)	1/32 (3.1%)
	Clinical	Antibiotic usage within 3 mo	Yes/all	7/73 (9.6%)	2/32 (6.3%)
		Any infection within 1 mo	Yes/all	2/73 (2.7%)	0/32 (0%)
	Perinatal	Any neonatal asphyxia	Yes/all	6/73 (8.2%)	1/32 (3.1%)
		Age of mother during pregnancy	mean ± SEM	28.83 ± 0.41	28.67 ± 0.27
		Age of father during pregnancy	mean ± SEM	30.00 ± 0.43	28.33 ± 0.80
		Premature delivery	Yes/all/NA or Forgotten	4/72 (5.5%) /1	1/32 (3.1%) /0
		Mode of delivery	Cesarean section/Vaginally delivery	31/42	12/20
		Assisted reproduction	Yes/all	11/73 (15.1%)	1/32 (3.1%)
		Eclampsia/Pre-eclampsia	Yes/all	1/73 (1.44%)	0/32 (0%)
		Infection during pregnancy	Yes/all	8/73 (10.9%)	0/32 (0%)
	Family history	Family history of mental disorders	Yes/all	3/72 (4.2%)	0/32 (0%)

Table 8 Predicted microbiota age and Physiological age.

Group	**Physiological age**	**Predicted microbiota age**
ASD	1.1	1.063991283
ASD	1.1	1.781075827
ASD	1.11	3.15698653
ASD	1.4	0.565391134
ASD	1.4	0.70140548
ASD	1.4	2.292544432
ASD	1.4	4.436245802
ASD	1.4	0.377813951
ASD	1.5	1.282486519
ASD	1.6	0.36967383
ASD	1.6	0.529338239
ASD	1.6	2.217356637
ASD	1.6	2.241657771
ASD	1.6	3.203106806
ASD	1.7	0.840901886
ASD	1.7	1.937369565
ASD	1.8	0.318060694
ASD	1.8	0.803481103
ASD	1.8	0.882089074
ASD	1.8	1.754950471
ASD	1.8	1.960165915
ASD	1.8	2.237232407
ASD	1.8	3.204896043
ASD	1.9	2.18280643
ASD	1.9	3.550967351
ASD	2	0.467091715
ASD	2	1.176347592
ASD	2	1.259873981
ASD	2	1.741770705
ASD	2	1.770958338
ASD	2	1.91951554
ASD	2	1.926712148
ASD	2	1.93072657
ASD	2	1.943004082
ASD	2	1.945972593
ASD	2	2.108131684
ASD	2	2.187255621
ASD	2	2.29659678
ASD	2	2.520844315
ASD	2	2.935516641
ASD	2	3.050283375
ASD	2	3.161383723
ASD	2	3.516339334
ASD	2	3.709160877
ASD	2	4.515946781
ASD	2	5.023961999
ASD	2	29.64666025
ASD	2	44.64305183
ASD	2	54.19206455
ASD	2.1	1.245212627
ASD	2.1	1.2649716
ASD	2.1	1.559959012
ASD	2.1	1.766049805
ASD	2.1	1.77713922
ASD	2.1	1.96702221
ASD	2.1	2.124653667
ASD	2.1	2.251197644
ASD	2.1	2.252430715
ASD	2.1	2.527564928
ASD	2.1	2.900313087
ASD	2.1	3.562744701
ASD	2.1	3.674741159
ASD	2.1	3.822704226
ASD	2.1	3.318712701
ASD	2.11	1.760552255
ASD	2.11	1.932818675
ASD	2.11	2.595862962
ASD	2.11	3.365695231

Mean value of Physiological age - Predicted microbiota age of each subject, mean ± SEM, p value were calculated by one-way ANOVA respectly.

	NT		**ASD**	
	mean	SEM	mean	SEM
0-16mo	-7.388849941	6.164149533	-0.867568166	0.615385255
16-18mo	-0.698748974	0.742024791	-0.385390627	0.539326174
18-20mo	-0.547379962	0.228995236	-0.080775177	0.362014509
20-22mo	-0.980615501	0.265384868	-0.109104888	0.538079514
22-24mo	-2.569078497	0.184055844	-5.626443526	2.997902786
24-26mo	-2.180152462	0.793446388	-1.061452151	0.2511445
26-28mo	-1.294482887	0.658205823	-1.170565375	0.483696901
28-30mo	-0.634614481	0.416162351	0.017160573	0.142037715
30-32mo	-0.661850718	0.369507484	-0.904633062	0.286685052
32-34mo	-0.515342378	0.713771612	-0.802546909	0.31722984
34-36mo	-2.395941997	0.411907781	-3.125436405	1.530681936
3-4y	-2.89390495	1.938138562	-1.476573692	0.885561967
4-5y	-5.079561805	1.481656833	-2.768736079	1.069005948
5-6y	-8.958558559	2.389885103	-2.195826422	1.160442858
6-7y	-10.03102089	2.415255895	-1.895388965	1.378608687
7-8y	-8.594485612	3.648938311	-7.303945452	3.21544231
8-9y	-11.1081029	3.833408235	0.063331717	1.765338513
9-16y	-3.629092634	2.295032983	-8.023251275	3.075474676
adults	-2.663537246	3.010763383	-18.17773156	14.77089379

Microbiota-for-age Z score (MAZ) of each subject.
The value of MAZ of each subject was calculated as: (microbiota age - median microbiota age of healthy children of same physiological age) / (standard deviation of microbiota age of healthy children of the same physiological age).

ASD	
Physiological age	MAZ
1.1	-0.039034064
1.1	-0.00024896
1.11	0.074170215
1.4	-0.066001956
1.4	-0.05864532
1.4	0.027414951
1.4	0.143361783
1.4	-0.076147483
1.5	-0.720506371
1.6	-1.46481042
1.6	-1.334620658
1.6	0.041783222
1.6	0.061598276
1.6	0.845560218
1.7	-3.011405719
1.7	-0.186517188
1.8	-1.506895578
1.8	-1.111085594
1.8	-1.046988949
1.8	-0.335261034
1.8	-0.167929129
1.8	0.05798985
1.8	0.847019155
1.9	-0.468395672
1.9	1.935357817
2	-3.48277444
2	-2.236666425
2	-2.089916985
2	-1.243261513
2	-4.796785208
2	-4.430704934
2	-4.412970781
2	-4.40307829
2	-4.372823582
2	-4.365508465
2	-3.965909901
2	-3.770929706
2	-3.501487087
2	-2.948887834
2	-1.927036615
2	-1.64422409
2	-1.370446412
2	-0.495751377
2	-0.020593243
2	1.96751908
2	3.219389384
2	excluded
2	excluded
2	excluded
2.1	-1.044695913
2.1	-1.03346807
2.1	-0.865844365
2.1	-0.748735291
2.1	-0.74243384
2.1	-0.634534692
2.1	-0.544962161
2.1	-0.473054787
2.1	-0.472354107
2.1	-0.316011787
2.1	-0.104201299
2.1	0.272218973
2.1	0.335859863
2.1	0.419938425
2.1	0.133550181

ASD	2.11	3.590261744
ASD	2.11	4.105028244
ASD	2.11	4.652653031
ASD	2.11	7.336691931
ASD	2.11	8.579041071
ASD	2.2	0.383731536
ASD	2.2	1.133225705
ASD	2.2	1.909490027
ASD	2.2	3.842345749
ASD	2.2	3.848045799
ASD	2.2	3.92455407
ASD	2.2	4.01154422
ASD	2.3	1.753805439
ASD	2.3	1.76626794
ASD	2.3	1.768342674
ASD	2.3	1.775403517
ASD	2.3	1.934150894
ASD	2.3	1.951543423
ASD	2.3	1.969422452
ASD	2.3	1.975056921
ASD	2.3	2.32311893
ASD	2.3	2.840479095
ASD	2.3	2.916988897
ASD	2.3	3.070233725
ASD	2.3	3.506979659
ASD	2.4	1.182039351
ASD	2.4	1.433945643
ASD	2.4	1.769037947
ASD	2.4	1.770056576
ASD	2.4	1.777827079
ASD	2.4	1.799120598
ASD	2.4	2.436815482
ASD	2.4	2.49150978
ASD	2.4	3.041442528
ASD	2.4	1.589790419
ASD	2.5	0.888687275
ASD	2.5	1.696395082
ASD	2.5	1.924532332
ASD	2.5	1.933812387
ASD	2.5	1.934680137
ASD	2.5	2.234722289
ASD	2.5	2.462285846
ASD	2.5	2.565051084
ASD	2.5	2.826727351
ASD	2.5	3.132576088
ASD	2.5	3.706315006
ASD	2.6	1.542560885
ASD	2.6	1.595070732
ASD	2.6	1.753531106
ASD	2.6	1.780306071
ASD	2.6	1.805664947
ASD	2.6	1.894824741
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ASD	2.6	1.955851225
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ASD	2.6	3.173000092
ASD	2.6	3.229318281
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ASD	2.6	3.891048426
ASD	2.7	1.730023456
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ASD	2.7	1.907207444
ASD	2.7	2.988800014
ASD	2.7	4.382687517
ASD	2.8	1.944459197
ASD	2.8	2.286573842
ASD	2.8	2.662176127
ASD	2.8	2.818519699
ASD	2.8	3.087934721

2.11	-0.75185922
2.11	-0.653970516
2.11	-0.277202098
2.11	0.160247543
2.11	0.287855263
2.11	0.580366281
2.11	0.891548699
2.11	3.863399312
2.11	5.139408564
2.2	-3.277944053
2.2	-2.508143147
2.2	-1.71084678
2.2	0.274377586
2.2	0.280232072
2.2	0.358813252
2.2	0.448160307
2.3	-1.870749474
2.3	-1.857949314
2.3	-1.855818368
2.3	-1.848566219
2.3	-1.685517752
2.3	-1.667653992
2.3	-1.64929055
2.3	-1.643503421
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2.3	-0.518653982
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2.4	-1.771870471
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2.4	-1.757547028
2.4	-1.722845476
2.4	-0.683608975
2.4	-0.59447495
2.4	0.301737642
2.4	-2.063985994
2.5	-3.206557459
2.5	-1.890254857
2.5	-1.518464894
2.5	-1.503341403
2.5	-1.501927253
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2.5	-0.642100515
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2.5	-0.048178683
2.5	0.450255882
2.5	1.385264835
2.6	-2.140954864
2.6	-2.05538079
2.6	-1.797141609
2.6	-1.753507072
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2.6	0.729036139
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3.5	-0.068760311
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3.5	0.042836774
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NT-adult	23	25.69227237
NT-adult	24	22.92748238
NT-adult	24	35.18252164

Table 9 Detection rate in NT and ASD cohort

taxa	Detection rate in NT	Detection rate in ASD	pvalue	qvalue	Difference	Type
d__Bacteria;p__Firmic	0.997772829	1	0.367430442	0.393410372	0.002227171	Increasing
d__Bacteria;p__Prote	0.997772829	0.998706339	1	1	0.00093351	Increasing
d__Bacteria;p__Bacte	0.997772829	0.997412678	1	1	-0.000360151	Decreasing
d__Bacteria;p__Firmic	0.997772829	0.996119017	1	1	-0.001653812	Decreasing
d__Bacteria;p__Firmic	0.997772829	0.984476067	0.038972124	0.045900502	-0.013296761	Decreasing
d__Bacteria;p__Actin	0.995545657	0.985769728	0.149452142	0.166757127	-0.009775929	Decreasing
d__Bacteria;p__Firmic	0.997772829	0.981888745	0.013942934	0.016987942	-0.015884083	Decreasing
d__Bacteria;p__Firmic	0.995545657	0.980595084	0.040093391	0.046702191	-0.014950573	Decreasing
d__Bacteria;p__Firmic	0.986636971	0.96377749	0.018832868	0.022685046	-0.022859481	Decreasing
d__Bacteria;p__Actin	0.975501114	0.966364812	0.488817317	0.513016194	-0.009136301	Decreasing
d__Bacteria;p__Firmic	0.975501114	0.943078913	0.009395497	0.011716737	-0.0324222	Decreasing
d__Bacteria;p__Firmic	0.964365256	0.943078913	0.10130244	0.115462996	-0.021286343	Decreasing
d__Bacteria;p__Firmic	0.971046771	0.927554981	0.001205835	0.001578006	-0.04349179	Decreasing
d__Bacteria;p__Bacte	0.959910913	0.928848642	0.032666675	0.038906377	-0.031062271	Decreasing
d__Bacteria;p__Firmic	0.935412027	0.940491591	0.712592404	0.733347522	0.005079564	Decreasing
d__Bacteria;p__Firmic	0.968819599	0.915912031	0.000245859	0.000338455	-0.052907568	Decreasing
d__Bacteria;p__Firmic	0.9844098	0.905562743	5.92E-09	1.06E-08	-0.078847057	Decreasing
d__Bacteria;p__Firmic	0.968819599	0.908150065	3.47E-05	5.04E-05	-0.060669534	Decreasing
d__Bacteria;p__Firmic	0.953229399	0.913324709	0.011159374	0.013754577	-0.03990469	Decreasing
d__Bacteria;p__Firmic	0.942093541	0.919793014	0.168495819	0.186047467	-0.022300527	Decreasing
d__Bacteria;p__Firmic	0.93986637	0.919793014	0.210302441	0.229815039	-0.020073355	Decreasing
d__Bacteria;p__Prote	0.95545657	0.909443726	0.002971231	0.003794584	-0.046012844	Decreasing
d__Bacteria;p__Firmic	0.95545657	0.891332471	7.20E-05	0.000101813	-0.064124099	Decreasing
d__Bacteria;p__Firmic	0.968819599	0.880983182	2.42E-08	4.14E-08	-0.087836417	Decreasing
d__Bacteria;p__Firmic	0.926503341	0.899094437	0.121507975	0.137019631	-0.027408903	Decreasing
d__Bacteria;p__Bacte	0.966592428	0.870633894	5.90E-09	1.06E-08	-0.095958534	Decreasing
d__Bacteria;p__Firmic	0.953229399	0.877102199	6.61E-06	9.73E-06	-0.076127199	Decreasing
d__Bacteria;p__Firmic	0.957683742	0.861578266	2.69E-08	4.53E-08	-0.096105475	Decreasing
d__Bacteria;p__Firmic	0.93986637	0.839586028	1.18E-07	1.85E-07	-0.100280341	Decreasing
d__Bacteria;p__Firmic	0.879732739	0.861578266	0.381648535	0.404547447	-0.018154473	Decreasing
d__Bacteria;p__Firmic	0.942093541	0.81759379	1.53E-10	2.95E-10	-0.124499751	Decreasing
d__Bacteria;p__Firmic	0.93986637	0.816300129	3.24E-10	6.14E-10	-0.12356624	Decreasing
d__Bacteria;p__Firmic	0.926503341	0.813712807	2.95E-08	4.89E-08	-0.112790534	Decreasing
d__Bacteria;p__Prote	0.902004454	0.81759379	6.48E-05	9.29E-05	-0.084410664	Decreasing
d__Bacteria;p__Firmic	0.915367483	0.800776197	5.49E-08	8.82E-08	-0.114591287	Decreasing
d__Bacteria;p__Firmic	0.846325167	0.831824062	0.521518481	0.541970186	-0.014501105	Decreasing
d__Bacteria;p__Firmic	0.937639198	0.777490298	1.53E-14	3.97E-14	-0.160148901	Decreasing
d__Bacteria;p__Firmic	0.899777283	0.794307891	1.07E-06	1.60E-06	-0.105469392	Decreasing
d__Bacteria;p__Firmic	0.93986637	0.767141009	1.87E-16	6.19E-16	-0.172725361	Decreasing
d__Bacteria;p__Bacte	0.935412027	0.752910737	3.12E-17	1.14E-16	-0.182501289	Decreasing
d__Bacteria;p__Firmic	0.888641425	0.778783959	1.03E-06	1.55E-06	-0.109857467	Decreasing
d__Bacteria;p__Firmic	0.917594655	0.74385511	1.09E-14	2.89E-14	-0.173739545	Decreasing
d__Bacteria;p__Firmic	0.890868597	0.724450194	1.48E-12	3.21E-12	-0.166418403	Decreasing
d__Bacteria;p__Firmic	0.897550111	0.698576973	9.22E-17	3.15E-16	-0.198973139	Decreasing
d__Bacteria;p__Firmic	0.890868597	0.701164295	3.63E-15	1.04E-14	-0.189704302	Decreasing
d__Bacteria;p__Fusob	0.848552339	0.690815006	3.82E-10	7.10E-10	-0.157737332	Decreasing
d__Bacteria;p__Firmic	0.917594655	0.650711514	4.61E-28	5.42E-27	-0.266883141	Decreasing
d__Bacteria;p__Firmic	0.881959911	0.668822768	1.02E-17	3.99E-17	-0.213137142	Decreasing
d__Bacteria;p__Firmic	0.853006682	0.675291074	3.32E-12	6.76E-12	-0.177715608	Decreasing
d__Bacteria;p__Firmic	0.795100223	0.706338939	0.000715978	0.00094867	-0.088761284	Decreasing
d__Bacteria;p__Firmic	0.861915367	0.663648124	5.47E-15	1.53E-14	-0.198267243	Decreasing
d__Bacteria;p__Firmic	0.86636971	0.64683053	1.07E-17	4.07E-17	-0.21953918	Decreasing
d__Bacteria;p__Desul	0.848552339	0.64683053	9.39E-15	2.55E-14	-0.201721808	Decreasing
d__Bacteria;p__Firmic	0.832962138	0.630012937	1.73E-14	4.38E-14	-0.202949201	Decreasing
d__Bacteria;p__Firmic	0.841870824	0.608020699	1.59E-18	7.34E-18	-0.233850125	Decreasing
d__Bacteria;p__Firmic	0.752783964	0.655886158	0.000406791	0.000552819	-0.096897807	Decreasing
d__Bacteria;p__Firmic	0.861915367	0.591203105	1.57E-24	1.11E-23	-0.270712263	Decreasing
d__Bacteria;p__Firmic	0.812917595	0.619663648	7.43E-13	1.64E-12	-0.193253947	Decreasing
d__Bacteria;p__Firmic	0.772828508	0.627425614	1.17E-07	1.85E-07	-0.145402893	Decreasing
d__Bacteria;p__Actin	0.795100223	0.593790427	3.05E-13	7.36E-13	-0.201309796	Decreasing
d__Bacteria;p__Prote	0.844097996	0.564036223	5.08E-25	3.85E-24	-0.280061773	Decreasing
d__Bacteria;p__Firmic	0.839643653	0.553686934	1.25E-25	1.02E-24	-0.285956719	Decreasing
d__Bacteria;p__Firmic	0.815144766	0.562742561	6.02E-20	3.04E-19	-0.252402205	Decreasing
d__Bacteria;p__Verru	0.779510022	0.576972833	3.80E-13	8.57E-13	-0.202537189	Decreasing
d__Bacteria;p__Firmic	0.857461024	0.522639069	1.78E-34	3.78E-33	-0.334821956	Decreasing
d__Bacteria;p__Firmic	0.797327394	0.53686934	1.34E-20	7.49E-20	-0.260458054	Decreasing
d__Bacteria;p__Firmic	0.812917595	0.517464424	5.24E-26	5.55E-25	-0.29545317	Decreasing
d__Bacteria;p__Firmic	0.788418708	0.473479948	4.38E-28	5.42E-27	-0.31493876	Decreasing
d__Bacteria;p__Firmic	0.706013363	0.504527814	4.17E-12	8.35E-12	-0.201485549	Decreasing
d__Bacteria;p__Bacte	0.766146993	0.433376455	1.66E-30	2.94E-29	-0.332770538	Decreasing
d__Bacteria;p__Firmic	0.710467706	0.459249677	9.25E-18	3.77E-17	-0.251218029	Decreasing
d__Bacteria;p__Firmic	0.694877506	0.437257439	2.33E-18	1.03E-17	-0.257620067	Decreasing
d__Bacteria;p__Firmic	0.65701559	0.455368693	1.02E-11	2.00E-11	-0.201646897	Decreasing
d__Bacteria;p__Firmic	0.563474388	0.460543338	0.00057499	0.000771506	-0.10293105	Decreasing
d__Bacteria;p__Firmic	0.708240535	0.375161708	9.10E-30	1.38E-28	-0.333078827	Decreasing
d__Bacteria;p__Firmic	0.632516704	0.385510996	6.56E-17	2.32E-16	-0.247005708	Decreasing
d__Bacteria;p__Firmic	0.599109131	0.39068564	1.95E-12	4.13E-12	-0.208423491	Decreasing
d__Bacteria;p__Firmic	0.605790646	0.363518758	2.33E-16	7.48E-16	-0.242271888	Decreasing
d__Bacteria;p__Bacte	0.576837416	0.342820181	1.86E-15	5.48E-15	-0.234017235	Decreasing
d__Bacteria;p__Bacte	0.603563474	0.323415265	2.08E-21	1.30E-20	-0.280148209	Decreasing
d__Bacteria;p__Bacte	0.659242762	0.253557568	2.95E-44	3.13E-42	-0.405685194	Decreasing
d__Bacteria;p__Desul	0.527839644	0.315653299	3.79E-13	8.57E-13	-0.212186345	Decreasing
d__Bacteria;p__Firmic	0.621380846	0.227684347	1.50E-42	7.95E-41	-0.3936965	Decreasing
d__Bacteria;p__Firmic	0.523385301	0.26778784	5.59E-19	2.69E-18	-0.255597461	Decreasing
d__Bacteria;p__Bacte	0.592427617	0.226390686	2.07E-37	7.33E-36	-0.366036931	Decreasing
d__Bacteria;p__Firmic	0.46325167	0.263906856	2.42E-12	5.02E-12	-0.199344814	Decreasing
d__Bacteria;p__Firmic	0.556792873	0.204398448	6.92E-36	1.83E-34	-0.352394425	Decreasing
d__Bacteria;p__Firmic	0.5077951	0.228978008	4.81E-23	3.18E-22	-0.278817092	Decreasing
d__Bacteria;p__Firmic	0.481069042	0.221216041	1.51E-20	8.02E-20	-0.259853001	Decreasing
d__Bacteria;p__Firmic	0.467706013	0.226390686	5.45E-18	2.31E-17	-0.241315328	Decreasing
d__Bacteria;p__Firmic	0.483296214	0.192755498	5.76E-26	5.56E-25	-0.290540716	Decreasing
d__Bacteria;p__Syner	0.354120267	0.250970246	0.000145438	0.000202847	-0.103150021	Decreasing
d__Bacteria;p__Bacte	0.454342984	0.172056921	1.04E-25	9.21E-25	-0.282286063	Decreasing
d__Bacteria;p__Firmic	0.432071269	0.179818887	5.49E-21	3.23E-20	-0.252252382	Decreasing
d__Bacteria;p__Firmic	0.389755011	0.179818887	1.67E-15	5.07E-15	-0.209936124	Decreasing
d__Bacteria;p__Firmic	0.378619154	0.179818887	3.38E-14	8.32E-14	-0.198800266	Decreasing
d__Bacteria;p__Prote	0.369710468	0.160413972	4.37E-16	1.36E-15	-0.209296496	Decreasing
d__Bacteria;p__Firmic	0.265033408	0.135834411	4.02E-08	6.55E-08	-0.129198996	Decreasing
d__Bacteria;p__Verru	0.229398664	0.078913325	3.34E-13	7.87E-13	-0.150485339	Decreasing
d__Bacteria;p__Firmic	0.131403118	0.094437257	0.055536841	0.063988099	-0.036965861	Decreasing
d__Bacteria;p__Actin	0.08908686	0.068564036	0.218265806	0.236083422	-0.020522823	Decreasing
d__Bacteria;p__Bacte	0.042316258	0.091849935	0.00135048	0.001745742	0.049533677	Decreasing
d__Bacteria;p__Cyan	0.113585746	0.029754204	7.75E-09	1.37E-08	-0.083831542	Decreasing
d__Bacteria;p__Bacte	0.111358575	0.029754204	2.41E-08	4.14E-08	-0.08160437	Decreasing
d__Bacteria;p__Firmic	0.026726058	0.06080207	0.008040858	0.010146797	0.034076012	Decreasing
d__Bacteria;p__Desul	0.08908686	0.021992238	1.75E-07	2.68E-07	-0.067094622	Decreasing

Table 10 Detection rate by age

taxa	NT0_2	ASD0_2	NT2_3	ASD2_3	NT3_4	ASD3_4	NT4_5	ASD4_5	NT5_6	ASD5_6	NT6	ASD6
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	1	1	1	1	0.988505747	1	1	1	1	1	1	1
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia-Shigella	1	1	1	1	0.988505747	0.994285714	1	1	1	1	1	1
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	1	1	1	0.994382022	0.988505747	0.994285714	1	1	1	1	1	1
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Veillonellaceae;g__Veillonella	1	0.979591837	1	1	0.988505747	0.994285714	1	1	1	1	1	0.993506494
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnoclostridium	1	0.979591837	1	0.966292135	0.988505747	0.994285714	1	0.984848485	1	0.988235294	1	0.993506494
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	1	1	1	0.97752809	0.977011494	0.977142857	1	0.992424242	1	0.988235294	1	0.993506494
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia	1	0.979591837	1	0.966292135	0.988505747	0.994285714	1	0.977272727	1	0.964705882	1	1
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium	0.971428571	0.93877551	1	0.971910112	0.988505747	0.977142857	1	0.992424242	1	1	1	0.987012987
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Incertae_Sedis	0.914285714	0.87755102	0.983606557	0.949438202	0.988505747	0.971428571	0.982758621	0.96969697	1	0.976470588	1	0.987012987
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	0.914285714	0.93877551	1	0.960674157	0.977011494	0.977142857	0.965517241	0.96969697	0.984126984	0.976470588	0.979310345	0.961038961
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Flavonifractor	0.971428571	0.87755102	0.983606557	0.949438202	0.954022989	0.96	1	0.939393939	0.968253968	0.952941176	0.979310345	0.935064935
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerostipes	0.914285714	0.857142857	0.983606557	0.95505618	0.931034483	0.948571429	0.965517241	0.916666667	1	0.941176471	0.972413793	0.974025974
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-004	0.914285714	0.795918367	0.950819672	0.938202247	0.965517241	0.925714286	0.982758621	0.916666667	1	0.941176471	0.979310345	0.961038961
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella	0.942857143	1	0.983606557	0.921348315	0.965517241	0.92	0.965517241	0.924242424	0.936507937	0.894117647	0.95862069	0.948051948
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Roseburia	0.885714286	0.816326531	0.950819672	0.882022472	0.942528736	0.908571429	0.982758621	0.946969697	0.984126984	0.941176471	1	0.954545455
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_torques_group	0.914285714	0.775510204	1	0.887640449	0.965517241	0.925714286	0.982758621	0.901515152	1	0.917647059	1	0.941558442
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Butyricicoccaceae;g__Butyricicoccus	0.8	0.734693878	0.950819672	0.876404494	0.954022989	0.897142857	1	0.96969697	1	0.929411765	1	0.948051948
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_gnavus_group	1	0.959183673	1	0.938202247	0.965517241	0.942857143	0.982758621	0.886363636	0.920634921	0.941176471	0.917241379	0.844155844
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Romboutsia	0.914285714	0.857142857	0.885245902	0.876404494	0.965517241	0.92	0.913793103	0.954545455	0.904761905	0.917647059	0.986206897	0.961038961
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Hungatella	0.942857143	0.959183673	0.967213115	0.943820225	0.965517241	0.931428571	0.965517241	0.939393939	0.968253968	0.870588235	0.889655172	0.876623377
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus	0.942857143	0.836734694	0.967213115	0.91011236	0.965517241	0.925714286	1	0.909090909	0.984126984	0.929411765	0.917241379	0.902597403
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospira	0.857142857	0.795918367	0.967213115	0.853932584	0.942528736	0.874285714	0.965517241	0.931818182	0.984126984	0.905882353	0.965517241	0.941558442
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__uncultured	0.885714286	0.755102041	0.983606557	0.876404494	0.965517241	0.828571429	0.965517241	0.893939394	1	0.905882353	0.972413793	0.961038961
d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium_sensu_stricto_1	0.942857143	0.87755102	0.93442623	0.898876404	0.908045977	0.902857143	0.948275862	0.916666667	0.873015873	0.870588235	0.944827586	0.902597403
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides	0.8	0.734693878	0.93442623	0.803370787	0.965517241	0.862857143	1	0.856060606	1	0.952941176	0.993103448	0.967532468
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_NK4A136_group	0.828571429	0.775510204	0.901639344	0.853932584	0.942528736	0.845714286	0.982758621	0.893939394	0.984126984	0.917647059	0.986206897	0.935064935
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Agathobacter	0.857142857	0.714285714	0.93442623	0.820224719	0.91954023	0.857142857	0.982758621	0.878787879	0.984126984	0.882352941	0.993103448	0.935064935
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Veillonellaceae;g__Dialister	0.942857143	0.795918367	0.918032787	0.775280899	0.931034483	0.845714286	0.965517241	0.909090909	0.920634921	0.870588235	0.951724138	0.844155844
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcaceae;g__Intestinibacter	0.8	0.653061224	0.885245902	0.853932584	0.862068966	0.885714286	0.965517241	0.893939394	0.857142857	0.882352941	0.882758621	0.87012987
d__Bacteria;p__Firmicutes;c__Clostridia;o__Monoglobales;f__Monoglobaceae;g__Monoglobus	0.8	0.693877551	0.983606557	0.803370787	0.942528736	0.822857143	0.948275862	0.810606061	0.936507937	0.870588235	0.95862069	0.844155844
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Subdoligranulum	0.685714286	0.632653061	0.918032787	0.735955056	0.931034483	0.805714286	0.931034483	0.856060606	0.984126984	0.858823529	1	0.922077922
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_eligens_group	0.828571429	0.755102041	0.885245902	0.780898876	0.885057471	0.845714286	0.931034483	0.772727273	1	0.894117647	0.95862069	0.824675325
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Parasutterella	0.685714286	0.632653061	0.868852459	0.724719101	0.885057471	0.805714286	0.982758621	0.901515152	0.952380952	0.905882353	0.924137931	0.876623377
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Colidextribacter	0.657142857	0.510204082	0.885245902	0.730337079	0.91954023	0.811428571	0.965517241	0.833333333	0.920634921	0.882352941	0.965517241	0.88961039
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Fusicatenibacter	0.8	0.530612245	0.901639344	0.758426966	0.91954023	0.76	0.982758621	0.78030303	0.968253968	0.858823529	0.965517241	0.850649351
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__UBA1819	0.8	0.693877551	0.918032787	0.786516854	0.873563218	0.817142857	0.931034483	0.787878788	0.904761905	0.764705882	0.917241379	0.831168831
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus	0.857142857	0.551020408	0.93442623	0.764044944	0.91954023	0.748571429	0.948275862	0.795454545	0.968253968	0.847058824	0.95862069	0.792207792
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes	0.685714286	0.510204082	0.868852459	0.651685393	0.954022989	0.737142857	1	0.818181818	0.968253968	0.823529412	0.972413793	0.87012987
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Tyzzerella	0.942857143	0.775510204	0.885245902	0.814606742	0.908045977	0.84	0.913793103	0.727272727	0.888888889	0.752941176	0.855172414	0.727272727
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Dorea	0.714285714	0.571428571	0.885245902	0.646067416	0.91954023	0.748571429	0.948275862	0.765151515	0.968253968	0.823529412	0.944827586	0.844155844
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Oscillibacter	0.6	0.469387755	0.836065574	0.668539326	0.91954023	0.714285714	0.913793103	0.712121212	0.936507937	0.835294118	0.937931034	0.831168831
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Acidaminococcales;f__Acidaminococcaceae;g__Phascolarctobacterium	0.828571429	0.632653061	0.770491803	0.646067416	0.873563218	0.64	0.896551724	0.704545455	0.936507937	0.776470588	0.965517241	0.798701299
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__UCG-002	0.6	0.510204082	0.803278689	0.629213483	0.908045977	0.662857143	0.913793103	0.71969697	0.952380952	0.823529412	0.951724138	0.805194805
d__Bacteria;p__Fusobacteriota;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	0.771428571	0.734693878	0.868852459	0.679775281	0.816091954	0.72	0.913793103	0.666666667	0.888888889	0.658823529	0.834482759	0.694805195
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__[Eubacterium]_coprostanoligenes_group;g__[Eubacterium]_cop	0.685714286	0.551020408	0.93442623	0.668539326	0.931034483	0.594285714	0.948275862	0.689393939	0.888888889	0.635294118	0.95862069	0.701298701
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__uncultured	0.714285714	0.285714286	0.836065574	0.629213483	0.873563218	0.674285714	0.879310345	0.742424242	0.920634921	0.741176471	0.931034483	0.727272727
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_ND3007_group	0.628571429	0.448979592	0.786885246	0.612359551	0.827586207	0.662857143	0.862068966	0.71969697	0.904761905	0.717647059	0.924137931	0.772727273
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__CAG-352	0.771428571	0.571428571	0.901639344	0.657303371	0.827586207	0.651428571	0.844827586	0.674242424	0.873015873	0.764705882	0.889655172	0.649350649
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_ventriosum_group	0.657142857	0.346938776	0.803278689	0.584269663	0.83908046	0.6	0.862068966	0.689393939	0.920634921	0.729411765	0.937931034	0.785714286
d__Bacteria;p__Desulfobacterota;c__Desulfovibrionia;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Bilophila	0.571428571	0.408163265	0.770491803	0.52247191	0.781609195	0.605714286	0.879310345	0.689393939	0.920634921	0.741176471	0.944827586	0.824675325
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__uncultured	0.428571429	0.265306122	0.704918033	0.56741573	0.804597701	0.565714286	0.948275862	0.696969697	0.920634921	0.764705882	0.917241379	0.75974026
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Coprococcus	0.542857143	0.408163265	0.721311475	0.47752809	0.793103448	0.605714286	0.896551724	0.666666667	0.968253968	0.694117647	0.917241379	0.727272727
d__Bacteria;p__Firmicutes;c__Clostridia;o__Christensenellales;f__Christensenellaceae;g__Christensenellaceae_R-7_group	0.571428571	0.224489796	0.836065574	0.483146067	0.862068966	0.571428571	0.844827586	0.651515152	0.888888889	0.741176471	0.937931034	0.720779221
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_hallii_group	0.6	0.428571429	0.754098361	0.56741573	0.770114943	0.594285714	0.827586207	0.666666667	0.936507937	0.647058824	0.855172414	0.714285714
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella	0.571428571	0.346938776	0.721311475	0.443820225	0.827586207	0.605714286	0.793103448	0.674242424	0.873015873	0.623529412	0.827586207	0.746753247
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Sutterellaceae;g__Sutterella	0.742857143	0.530612245	0.786885246	0.494382022	0.827586207	0.554285714	0.879310345	0.583333333	0.904761905	0.529411765	0.862068966	0.668831169
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__UCG-003	0.571428571	0.265306122	0.721311475	0.488764045	0.804597701	0.514285714	0.862068966	0.583333333	0.920634921	0.670588235	0.931034483	0.675324675
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelatoclostridiaceae;g__Erysipelotrichaceae_UCG-003	0.542857143	0.346938776	0.68852459	0.449438202	0.804597701	0.577142857	0.775862069	0.545454545	0.857142857	0.658823529	0.937931034	0.707792208
d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia	0.685714286	0.469387755	0.786885246	0.578651685	0.793103448	0.537142857	0.844827586	0.575757576	0.80952381	0.588235294	0.751724138	0.649350649
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Selenomonadaceae;g__Megamonas	0.771428571	0.489795918	0.852459016	0.539325843	0.816091954	0.514285714	0.931034483	0.537878788	0.888888889	0.423529412	0.862068966	0.564935065
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-010	0.6	0.244897959	0.672131148	0.438202247	0.75862069	0.468571429	0.844827586	0.568181818	0.904761905	0.647058824	0.855172414	0.733766234
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__UCG-005	0.542857143	0.326530612	0.737704918	0.449438202	0.747126437	0.457142857	0.862068966	0.613636364	0.857142857	0.611764706	0.910344828	0.590909091
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella	0.942857143	1	1	0.926966292	0.977011494	0.948571429	0.948275862	0.924242424	0.920634921	0.976470588		
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelatoclostridiaceae;g__Erysipelatoclostridium	0.942857143	0.959183673	0.950819672	0.904494382	0.850574713	0.834285714	0.931034483	0.825757576	0.857142857	0.776470588		
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Eisenbergiella	0.628571429	0.489795918	0.737704918	0.617977528	0.804597701	0.674285714	0.793103448	0.674242424	0.841269841	0.658823529		
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter			0.62295082	0.280898876	0.701149425	0.337142857	0.844827586	0.484848485	0.873015873	0.576470588	0.875862069	0.681818182
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_FCS020_group			0.540983607	0.337078652	0.643678161	0.377142857	0.793103448	0.53030303	0.80952381	0.552941176	0.84137931	0.662337662
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__NK4A214_group			0.540983607	0.387640449	0.655172414	0.325714286	0.724137931	0.53030303	0.698412698	0.494117647	0.827586207	0.597402597
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-008			0.557377049	0.353932584	0.494252874	0.405714286	0.706896552	0.522727273	0.761904762	0.564705882	0.779310345	0.584415584
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__CAG-56			0.655737705	0.292134831	0.666666667	0.325714286	0.810344828	0.409090909	0.825396825	0.458823529	0.724137931	0.519480519
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-001			0.573770492	0.314606742	0.482758621	0.371428571	0.637931034	0.409090909	0.682539683	0.541176471	0.689655172	0.474025974
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Ruminococcus]_gauvreauii_group			0.655737705	0.353932584	0.482758621	0.348571429	0.603448276	0.363636364	0.746031746	0.305882353	0.620689655	0.487012987
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Butyricimonas			0.491803279	0.219101124	0.505747126	0.205714286	0.689655172	0.356060606	0.698412698	0.435294118	0.689655172	0.525974026
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Barnesiellaceae;g__Barnesiella			0.590163934	0.213483146	0.586206897	0.205714286	0.75862069	0.265151515	0.73015873	0.341176471	0.724137931	0.344155844
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Moryella			0.31147541	0.179775281	0.367816092	0.182857143	0.534482759	0.348484848	0.555555556	0.317647059	0.613793103	0.422077922
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__[Eubacterium]_siraeum_group			0.508196721	0.202247191	0.586206897	0.142857143	0.603448276	0.25	0.603174603	0.305882353	0.537931034	0.207792208
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_xylanophilum_group			0.409836066	0.162921348	0.528735632	0.205714286	0.568965517	0.265151515	0.412698413	0.270588235	0.531034483	0.272727273
d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__uncultured;g__uncultured			0.344262295	0.129213483	0.402298851	0.142857143	0.379310345	0.159090909	0.46031746	0.188235294	0.351724138	0.214285714
d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridia_UCG-014;f__Clostridia_UCG-014;g__Clostridia_UCG-014	0.8	0.387755102	0.754098361	0.426966292					0.841269841	0.505882353	0.779310345	0.564935065
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Sellimonas			0.606557377	0.505617978	0.67816092	0.428571429	0.637931034	0.537878788	0.571428571	0.458823529		
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalitalea			0.655737705	0.247191011	0.597701149	0.165714286	0.775862069	0.21969697	0.650793651	0.258823529		
d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridia_vadinBB60_group;f__Clostridia_vadinBB60_group;g__Clostridia_vadinBB60_group			0.409836066	0.196629213	0.436781609	0.194285714	0.551724138	0.287878788			0.6	0.279220779
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcales-Tissierellales;g__Anaerococcus			0.409836066	0.129213483	0.448275862	0.165714286	0.327586207	0.242424242			0.406896552	0.272727273
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptococcales;f__Peptococcaceae;g__Peptococcus			0.213114754	0.134831461	0.298850575	0.148571429	0.413793103	0.227272727			0.537931034	0.233766234
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter					0.643678161	0.577142857	0.844827586	0.757575758	0.698412698	0.729411765	0.848275862	0.75974026
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__GCA-900066575					0.563218391	0.337142857	0.672413793	0.462121212	0.746031746	0.470588235	0.731034483	0.512987013
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Paraprevotella					0.655172414	0.234285714	0.775862069	0.196969697	0.714285714	0.176470588	0.496551724	0.337662338
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	0.742857143	0.897959184			0.850574713	0.731428571			0.714285714	0.752941176		
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculaceae	0.485714286	0.224489796					0.620689655	0.325757576			0.537931034	0.422077922
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas			0.606557377	0.382022472	0.609195402	0.342857143					0.662068966	0.564935065
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcales-Tissierellales;g__Peptoniphilus			0.508196721	0.191011236	0.563218391	0.257142857					0.537931034	0.415584416
d__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;g__TM7x					0.873563218	0.794285714	0.793103448	0.734848485	0.80952381	0.682352941		
d__Bacteria;p__Desulfobacterota;c__Desulfovibrionia;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio					0.540229885	0.337142857			0.523809524	0.305882353	0.627586207	0.409090909
d__Bacteria;p__Synergistota;c__Synergistia;o__Synergistales;f__Synergistaceae;g__Pyramidobacter					0.379310345	0.268571429	0.379310345	0.310606061			0.379310345	0.279220779
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Frisingicoccus					0.137931034	0.097142857			0.174603175	0.152941176	0.172413793	0.103896104
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Anaerovoracaceae;g__Family_XIII_AD3011_group							0.75862069	0.613636364	0.80952381	0.6	0.834482759	0.623376623
d__Bacteria;p__Firmicutes;c__Bacilli;o__RF39;f__RF39;g__RF39							0.431034483	0.28030303	0.507936508	0.2	0.517241379	0.253246753
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Barnesiellaceae;g__Coprobacter							0.534482759	0.227272727	0.317460317	0.258823529	0.572413793	0.233766234
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcales-Tissierellales;g__Murdochiella			0.327868852	0.084269663	0.390804598	0.085714286						
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__UCG-010;g__UCG-010							0.448275862	0.234848485			0.544827586	0.233766234
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Negativibacillus									0.412698413	0.188235294	0.55862069	0.292207792
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Eggerthella	0.857142857	0.816326531										
d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Rothia	0.8	0.714285714										
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Veillonellaceae;g__Megasphaera	0.8	0.714285714										
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Anaerotruncus	0.657142857	0.408163265										
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemania	0.4	0.367346939										
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter	0.457142857	0.326530612										
d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Morganellaceae;g__Morganella	0.457142857	0.244897959										
d__Bacteria;p__Firmicutes;c__Clostridia;o__Christensenellales;f__Christensenellaceae;g__uncultured			0.327868852	0.241573034								
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Selenomonadaceae;g__uncultured			0.180327869	0.073033708								
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Intestinimonas					0.632183908	0.354285714						
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Lachnospiraceae_UCG-003					0.390804598	0.125714286						
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus											0.779310345	0.701298701
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcales-Tissierellales;g__Fenollaria											0.634482759	0.396103896
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__[Eubacterium]_ruminantium_group											0.496551724	0.194805195
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostreptococcales-Tissierellales;f__Peptostreptococcales-Tissierellales;g__Ezakiella											0.517241379	0.285714286
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Butyricicoccaceae;g__UCG-009											0.462068966	0.266233766
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillonellales-Selenomonadales;f__Veillonellaceae;g__Allisonella											0.351724138	0.201298701
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Acidaminococcales;f__Acidaminococcaceae;g__Acidaminococcus											0.2	0.142857143
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Anaerosporobacter											0.227586207	0.116883117
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Angelakisella											0.351724138	0.181818182
d__Bacteria;p__Verrucomicrobiota;c__Lentisphaeria;o__Victivallales;f__Victivallaceae;g__Victivallis											0.289655172	0.155844156
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Tuzzerella											0.220689655	0.090909091
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Holdemanella											0.172413793	0.090909091
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Senegalimassilia											0.103448276	0.11038961
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__uncultured											0.15862069	0.071428571

NT0_2: taxa detection rate in NT cohort under 2(included) years old
ASD0_2: taxa detection rate in ASD cohort under 2(included) years old
NT2_3: taxa detection rate in NT cohort between 2 and 3(included) years old
ASD2_3: taxa detection rate in ASD cohort between 2 and 3(included) years old
NT3_4: taxa detection rate in NT cohort between 3 and 4(included) years old
ASD3_4: taxa detection rate in ASD cohort between 3 and 4(included) years old
NT4_5: taxa detection rate in NT cohort between 4 and 5(included) years old
ASD4_5: taxa detection rate in ASD cohort between 4 and 5(included) years old
NT5_6: taxa detection rate in NT cohort under between 5 and 6(included) years old
ASD5_6: taxa detection rate in ASD cohort between 5 and 6(included) years old
NT6: taxa detection rate in NT cohort after 6 years old
ASD6: taxa detection rate in NT cohort after 6 years old

Table 11 The detection rate of children under and after 3years

taxa	NT0	ASD0	NT1	ASD1	NT0_ASD0_differen	NT1_ASD1_difference
d__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridia			0.033994334	0.06959707		0.035602735
d__Bacteri	0.979166667	0.942731278	0.923512748	0.93956044	-0.036435389	0.016047692
d__Bacteri	1	1	0.997167139	1	0	0.002832861
d__Bacteri	1	1	0.997167139	0.998168498	0	0.001001359
d__Bacteri	1	0.995594714	0.997167139	0.998168498	-0.004405286	0.001001359
d__Bacteri	1	0.995594714	0.997167139	0.996336996	-0.004405286	-0.000830142
d__Bacteria;p__Actinobacteriota;c__Coriobacteriia;o_			0.076487252	0.075091575		-0.001395677
d__Bacteri	0.854166667	0.810572687	0.886685552	0.882783883	-0.043593979	-0.00390167
d__Bacteri	1	0.969162996	0.997167139	0.990842491	-0.030837004	-0.006324648
d__Bacteri	0.96875	0.955947137	0.97733711	0.970695971	-0.012802863	-0.00664114
d__Bacteri	1	0.982378855	0.994334278	0.987179487	-0.017621145	-0.00715479
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospi			0.042492918	0.034798535		-0.007694383
d__Bacteri	0.989583333	0.964757709	0.997167139	0.987179487	-0.024825624	-0.009987652
d__Bacteri	1	0.969162996	0.997167139	0.987179487	-0.030837004	-0.009987652
d__Bacteri	0.895833333	0.872246696	0.954674221	0.93956044	-0.023586637	-0.015113781
d__Bacteri	0.958333333	0.933920705	0.994334278	0.976190476	-0.024412628	-0.018143801
d__Bacteri	0.958333333	0.933920705	0.966005666	0.946886447	-0.024412628	-0.019119219
d__Bacteri	0.947916667	0.916299559	0.818696884	0.796703297	-0.031617107	-0.021993587
d__Bacteri	0.9375	0.894273128	0.923512748	0.901098901	-0.043226872	-0.022413847
d__Bacteri	0.958333333	0.947136564	0.934844193	0.908424908	-0.011196769	-0.026419284
d__Bacteri	0.979166667	0.933920705	0.974504249	0.946886447	-0.045245962	-0.027617802
d__Bacteri	0.96875	0.938325991	0.957507082	0.924908425	-0.030424009	-0.032598657
d__Bacteri	0.958333333	0.894273128	0.954674221	0.915750916	-0.064060206	-0.038923305
d__Bacteri	1	0.942731278	0.940509915	0.901098901	-0.057268722	-0.039411014
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnosp			0.150141643	0.10989011		-0.040251533
d__Bacteri	0.9375	0.907488987	0.980169972	0.935897436	-0.030011013	-0.044272536
d__Bacteri	0.927083333	0.86784141	0.980169972	0.935897436	-0.059241924	-0.044272536
d__Bacteri	0.927083333	0.841409692	0.963172805	0.912087912	-0.085673642	-0.051084892
d__Bacteri	0.895833333	0.845814978	0.988668555	0.934065934	-0.050018355	-0.054602621
d__Bacteri	0.802083333	0.704845815	0.92917847	0.864468864	-0.097237518	-0.064709606
d__Bacteri	0.96875	0.863436123	0.988668555	0.923076923	-0.105313877	-0.065591632
d__Bacteria;p__Desulfobacterota;c__Desulfovibrionia			0.099150142	0.027472527		-0.071677614
d__Bacteria;p__Firmicutes;c__Bacilli;o__Erysipelotrich			0.770538244	0.695970696		-0.074567548
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacte			0.113314448	0.034798535		-0.078515913
d__Bacteri	0.927083333	0.779735683	0.943342776	0.864468864	-0.147347651	-0.078873912
d__Bacteri	0.875	0.837004405	0.974504249	0.893772894	-0.037995595	-0.080731356
d__Bacteri	0.947916667	0.850220264	0.974504249	0.893772894	-0.097696402	-0.080731356
d__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillale			0.801699717	0.71978022		-0.081919497
d__Bacteri	0.90625	0.797356828	0.971671388	0.888278388	-0.108893172	-0.083393
d__Bacteri	0.885416667	0.788546256	0.988668555	0.904761905	-0.096870411	-0.08390665
d__Bacteria;p__Synergistota;c__Synergistia;o__Syner			0.376770538	0.282051282		-0.094719256
d__Bacteri	0.802083333	0.682819383	0.946175637	0.84981685	-0.11926395	-0.096358788
d__Bacteria;p__Cyanobacteria;c__Vampirivibrionia;o			0.130311615	0.031135531		-0.099176084
d__Bacteri	0.875	0.766519824	0.906515581	0.805860806	-0.108480176	-0.100654775
d__Bacteri	0.833333333	0.713656388	0.968838527	0.858974359	-0.119676946	-0.109864168
d__Bacteri	0.864583333	0.775330396	0.943342776	0.82967033	-0.089252937	-0.113672447
d__Bacteri	0.541666667	0.475770925	0.569405099	0.454212454	-0.065895742	-0.115192645
d__Bacteri	0.916666667	0.779735683	0.949008499	0.833333333	-0.136930984	-0.115675165
d__Bacteri	0.90625	0.806167401	0.883852691	0.767399267	-0.100082599	-0.116453424
d__Bacteria;p__Firmicutes;c__Negativicutes;o__Veillc			0.280453258	0.148351648		-0.132101609
d__Bacteri	0.697916667	0.59030837	0.793201133	0.642857143	-0.107608297	-0.15034399
d__Bacteri	0.864583333	0.709251101	0.957507082	0.805860806	-0.155332232	-0.151646276
d__Bacteri	0.822916667	0.629955947	0.943342776	0.791208791	-0.19296072	-0.152133985
d__Bacteri	0.90625	0.718061674	0.949008499	0.787545788	-0.188188326	-0.161462711
d__Bacteri	0.833333333	0.691629956	0.852691218	0.69047619	-0.141703377	-0.162215028
d__Bacteri	0.75	0.625550661	0.92917847	0.765567766	-0.124449339	-0.163610705
d__Bacteri	0.802083333	0.621145374	0.971671388	0.807692308	-0.180937959	-0.16397908
d__Bacteria;p__Verrucomicrobiota;c__Lentisphaeria;			0.263456091	0.098901099		-0.164554992
d__Bacteri	0.666666667	0.422907489	0.830028329	0.664835165	-0.243759178	-0.165193164
d__Bacteri	0.729166667	0.577092511	0.886685552	0.716117216	-0.152074156	-0.170568336
d__Bacteri	0.697916667	0.497797357	0.889518414	0.708791209	-0.20011931	-0.180727205
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnosp			0.694050992	0.509157509		-0.184893482
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostre			0.399433428	0.210622711		-0.188810717
d__Bacteri	0.854166667	0.63876652	0.864022663	0.673992674	-0.215400147	-0.190029989
d__Bacteri	0.697916667	0.537444934	0.844192635	0.653846154	-0.160471733	-0.190346481
d__Bacteri	0.791666667	0.555066079	0.906515581	0.716117216	-0.236600587	-0.190398365
d__Bacteri	0.489583333	0.281938326	0.628895184	0.435897436	-0.207645007	-0.192997748
d__Bacteri	0.729166667	0.603524229	0.934844193	0.741758242	-0.125642438	-0.193085951
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostre			0.767705382	0.567765568		-0.199939815
d__Bacteri	0.75	0.555066079	0.787535411	0.586080586	-0.194933921	-0.201454825
d__Bacteri	0.75	0.533039648	0.898016997	0.694139194	-0.216960352	-0.203877803
d__Bacteri	0.791666667	0.643171806	0.926345609	0.721611722	-0.14849486	-0.204733887
d__Bacteri	0.604166667	0.502202643	0.895184136	0.683150183	-0.101964023	-0.212033953
d__Bacteri	0.302083333	0.127753304	0.388101983	0.173992674	-0.174330029	-0.214109309
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnosp			0.529745042	0.311355311		-0.218389731
d__Bacteria;p__Desulfobacterota;c__Desulfovibrionia			0.560906516	0.340659341		-0.220247175
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnosp			0.606232295	0.384615385		-0.22161691
d__Bacteri	0.65625	0.462555066	0.892351275	0.668498168	-0.193694934	-0.223853106
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostre			0.526912181	0.296703297		-0.230208885
d__Bacteri	0.177083333	0.13215859	0.433427762	0.1996337	-0.044924743	-0.233794062
d__Bacteri	0.739583333	0.427312775	0.895184136	0.659340659	-0.312270558	-0.235843477
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospi			0.436260623	0.197802198		-0.238458425
d__Bacteri	0.645833333	0.396475771	0.838526912	0.595238095	-0.249357562	-0.243288817
d__Bacteri	0.635416667	0.427312775	0.864022663	0.619047619	-0.208103891	-0.244975044
d__Bacteri	0.447916667	0.259911894	0.682719547	0.437728938	-0.188004772	-0.244990609
d__Bacteria;p__Firmicutes;c__Bacilli;o__RF39;f__RF39;			0.487252125	0.238095238		-0.249156887
d__Bacteri	0.46875	0.325991189	0.606232295	0.34981685	-0.142758811	-0.256415445
d__Bacteri	0.458333333	0.308370044	0.779036827	0.521978022	-0.149963289	-0.257058805
d__Bacteria;p__Firmicutes;c__Clostridia;o__Peptostre			0.495750708	0.232600733		-0.263149976
d__Bacteri	0.354166667	0.154185022	0.515580737	0.249084249	-0.199981645	-0.266496487
d__Bacteria;p__Firmicutes;c__Clostridia;o__Oscillospi			0.470254958	0.203296703		-0.266958254
d__Bacteri	0.510416667	0.339207048	0.745042493	0.478021978	-0.171209618	-0.267020515
d__Bacteri	0.770833333	0.502202643	0.864022663	0.58974359	-0.26863069	-0.274279073
d__Bacteri	0.447916667	0.215859031	0.645892351	0.368131868	-0.232057636	-0.277760483
d__Bacteri	0.84375	0.643171806	0.937677054	0.653846154	-0.200578194	-0.2838309
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacte			0.487252125	0.203296703		-0.283955421
d__Bacteri	0.666666667	0.440528634	0.886685552	0.600732601	-0.226138032	-0.285952952
d__Bacteri	0.666666667	0.422907489	0.852691218	0.556776557	-0.243759178	-0.295914661
d__Bacteri	0.770833333	0.418502203	0.793201133	0.496336996	-0.352331131	-0.296864137
d__Bacteri	0.34375	0.18061674	0.552407932	0.249084249	-0.16313326	-0.303323683
d__Bacteria;p__Firmicutes;c__Clostridia;o__Lachnosp			0.515580737	0.206959707		-0.30862103
d__Bacteri	0.541666667	0.255506608	0.827195467	0.507326007	-0.286160059	-0.31986946
d__Bacteri	0.583333333	0.264317181	0.742209632	0.421245421	-0.319016153	-0.32096421
d__Bacteri	0.822916667	0.528634361	0.866855524	0.52014652	-0.294282305	-0.346709004
d__Bacteri	0.5	0.185022026	0.57223796	0.212454212	-0.314977974	-0.359783748
d__Bacteri	0.489583333	0.18061674	0.620396601	0.245421245	-0.308966593	-0.374975355
d__Bacteri	0.541666667	0.215859031	0.64305949	0.232600733	-0.325807636	-0.410458757
d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacte			0.696883853	0.28021978		-0.416664072

NT0: taxa detection rate in NT cohort under 3(included) years old
ASD0: taxa detection rate in ASD cohort under 3(included) years old
NT1: taxa detection rate in NT cohort after 3 years old
ASD1: taxa detection rate in ASD cohort after 3 years old
NT0_ASD0_difference: ASD0-NT0
NT1_ASD1_difference: ASD1-NT1

Table 12 Enlarging microbial relationship alternation with increasing ASD scor

index	Taxon1	Taxon2	Group 1	Group 2	Group 3	Group 4	R-square	coefficient	Taxon1 detecti	Taxon2 detection rate
1	d Bacteria;p	d Bacteria;p	0	0.030402191	0.177473584	0.414827419	0.98194699	0.192212614	0.449593496	0.258536585
2	d Bacteria;p	d Bacteria;p	0.023748621	0	0.110463288	0.395550352	0.913334129	0.185900866	0.639837398	0.258536585
3	d Bacteria;p	d Bacteria;p	0.023835102	0	0.108514535	0.38325046	0.914739418	0.179707679	0.473170732	0.309756098
4	d Bacteria;p	d Bacteria;p	0	0.052013578	0.347375405	0.408958343	0.874902924	0.178472382	0.334146341	0.25203252
5	d Bacteria;p	d Bacteria;p	0.099926855	0	0.101828421	0.456326731	0.754001498	0.178199938	0.494308943	0.258536585
6	d Bacteria;p	d Bacteria;p	0.086644323	0.121380717	0	0.431995102	0.824598097	0.17267539	0.565853659	0.318699187
7	d Bacteria;p	d Bacteria;p	0	0.01102781	0.014173968	0.328526328	0.757431166	0.158749259	0.369918699	0.28699187
8	d__Bacteria;p_	d__Bacteria;p_	0.012065936	0.18235507	0	0.327553328	0.997896068	0.157743696	0.369918699	0.258536585
9	d__Bacteria;p_	d__Bacteria;p_	0.02006529	0.02715604	0.327051117	0	0.767314024	0.153492914	0.42601626	0.31300813
10	d Bacteria;p	d Bacteria;p	0	0.065714026	0.113487186	0.364164351	0.866499156	0.149225162	0.331707317	0.257723577
11	d Bacteria;p	d Bacteria;p	0	0.001069837	0.06821461	0.282069571	0.916705326	0.140499867	0.742276423	0.309756098
12	d Bacteria;p	d Bacteria;p	0.057002013	0.06881672	0.329716111	0	0.782428395	0.136357049	0.403252033	0.369918699
13	d Bacteria;p	d Bacteria;p	0	0.060738219	0.126146912	0.329131261	0.91947012	0.134196521	0.363414634	0.292682927
14	d Bacteria;p	d Bacteria;p	0.00084512	0	0.056072492	0.25995212	0.901132794	0.1295535	0.449593496	0.423577236
15	d Bacteria;p	d Bacteria;p	0.012213275	0.117099432	0	0.270772682	0.988271454	0.129279704	0.663414634	0.25203252
16	d Bacteria;p	d Bacteria;p	0.051784664	0.168763272	0.306393477	0	0.997811796	0.127304406	0.574796748	0.468292683
17	d__Bacteria;p_	d__Bacteria;p_	0	0.008278091	0.150762693	0.256752623	0.992860592	0.124237266	0.28699187	0.271544715
18	d__Bacteria;p_	d__Bacteria;p_	0.115123806	0.119556459	0.407929303	0.432233013	0.835636456	0.123970046	0.369918699	0.31300813
19	d Bacteria;p	d Bacteria;p	0.092391017	0.114711334	0	0.339014151	0.817271958	0.123311567	0.501626016	0.331707317
20	d Bacteria;p	d Bacteria;p	0.011881272	0.076745968	0.253252791	0.351257541	0.97164616	0.119463563	0.4	0.369918699
21	d Bacteria;p	d Bacteria;p	0.004325414	0.06394526	0.235094524	0	0.927766146	0.115384555	0.411382114	0.332520325
22	d Bacteria;p	d Bacteria;p	0.0053728	0	0.065154918	0.233226345	0.929981524	0.113926772	0.404878049	0.371544715
23	d Bacteria;p	d Bacteria;p	0	0.05196818	0.087604647	0.278473112	0.864631674	0.113252466	0.318699187	0.258536585
24	d Bacteria;p	d Bacteria;p	0.027066119	0.104629283	0	0.245828533	0.972567831	0.109381207	0.899186992	0.25203252
25	d Bacteria;p	d Bacteria;p	0	0.116599337	0.268246561	0.330462256	0.944921176	0.10693146	0.359349593	0.309756098
26	d Bacteria;p	d Bacteria;p	0.002354059	0	0.073293788	0.215095836	0.964335824	0.106370888	0.336585366	0.309756098
27	d__Bacteria;p_	d__Bacteria;p_	0.032505371	0.046971201	0	0.240278073	0.801946854	0.103886351	0.722764228	0.565853659
28	d__Bacteria;p_	d__Bacteria;p_	0.117006024	0	0.147996596	0.319150603	0.861876097	0.101072289	0.359349593	0.334146341
29	d Bacteria;p	d Bacteria;p	0.015447881	0.130907556	0.215845452	0	0.992326945	0.100198785	0.576422764	0.251219512
30	d Bacteria;p	d Bacteria;p	0.003376937	0.079387598	0	0.202788849	0.981521756	0.099705956	0.276422764	0.257723577
31	d Bacteria;p	d Bacteria;p	0.081460367	0.12470783	0.279834188	0	0.904139076	0.09918691	0.814634146	0.252845528
32	d Bacteria;p	d Bacteria;p	0.041914965	0	0.099050416	0.239401589	0.944121829	0.098743312	0.825203252	0.269105691
33	d Bacteria;p	d Bacteria;p	0	0.058389053	0.08340845	0.253551838	0.844369203	0.097581392	0.358536585	0.25203252
34	d Bacteria;p	d Bacteria;p	0	0.111752145	0.295358974	0.306649989	0.793295496	0.097448922	0.336585366	0.251219512
35	d Bacteria;p	d Bacteria;p	0.029409561	0	0.087155548	0.223218557	0.948379144	0.096904498	0.722764228	0.258536585
36	d__Bacteria;p_	d__Bacteria;p_	0	0.048883358	0.17326723	0.239705352	0.970179351	0.095410997	0.359349593	0.252845528
37	d__Bacteria;p_	d__Bacteria;p_	0.02268124	0.094254489	0.211206385	0	0.981053202	0.094262572	0.42601626	0.252845528
38	d Bacteria;p	d Bacteria;p	0	0.14254242	0.205135171	0.330065365	0.964473046	0.093761472	0.460162602	0.369918699
39	d Bacteria;p	d Bacteria;p	0	0.038125728	0.06607506	0.214382938	0.865477583	0.088128605	0.288617886	0.278861789
40	d Bacteria;p	d Bacteria;p	0.076582864	0	0.158717037	0.251335956	0.998801539	0.087376546	0.62195122	0.258536585
41	d Bacteria;p	d Bacteria;p	0.074137919	0	0.105454162	0.248811134	0.879395819	0.087336608	0.62195122	0.309756098
42	d Bacteria;p	d Bacteria;p	0.056668778	0	0.109921633	0.230653646	0.952252858	0.086992434	0.641463415	0.297560976
43	d Bacteria;p	d Bacteria;p	0.039755924	0.14422583	0.206873837	0.307395873	0.991491458	0.086556785	0.473170732	0.269105691
44	d Bacteria;p	d Bacteria;p	0.032874903	0.041753922	0	0.20110612	0.78946793	0.084115609	0.508943089	0.4
45	d__Bacteria;p_	d__Bacteria;p_	0.126021265	0.186395793	0.266986772	0.371496405	0.985599159	0.08170164	0.370731707	0.369918699
46	d__Bacteria;p_	d__Bacteria;p_	0.044619261	0	0.066441916	0.207194647	0.848620797	0.081287693	0.38699187	0.255284553
47	d Bacteria;p	d Bacteria;p	0.042536155	0	0.185733871	0.204514319	0.835655744	0.080989082	0.460162602	0.332520325
48	d Bacteria;p	d Bacteria;p	0.032411456	0.074644448	0.107523267	0.273287022	0.855344902	0.075550552	0.9	0.392682927
49	d Bacteria;p	d Bacteria;p	0.015889585	0.034772553	0.038108974	0.245495837	0.679573089	0.069215518	0.473170732	0.334146341
50	d Bacteria;p	d Bacteria;p	0.093511349	0.184044756	0	0.224981329	0.954709739	0.06573499	0.403252033	0.25203252
51	d Bacteria;p	d Bacteria;p	0.106764786	0.122792022	0	0.229529293	0.846031977	0.061382254	0.517073171	0.297560976
52	d Bacteria;p	d Bacteria;p	0.135826107	0	0.220416102	0.24961324	0.926788298	0.056893566	0.52601626	0.371544715
53	d Bacteria;p	d Bacteria;p	0.184601111	0	0.256590113	0.291608441	0.961733295	0.053503665	0.54796748	0.334146341
54	d__Bacteria;p_	d__Bacteria;p_	0.145877766	0.171130851	0.179044719	0.311646317	0.766421797	0.050521952	0.369918699	0.334146341

Taxon1: relationship node
Taxon2: relationship node
Group 1: PM score of ASD cohort with ASD score 1 to 3 compared to NT
Group 2: PM score of ASD cohort with ASD score 4 to 5 compared to NT
Group 3: PM score of ASD cohort with ASD score 7 compared to NT
Group 4: PM score of ASD cohort with ASD score 7 to 9 compared to NT
R-square: the linear regression R-square
coefficient: the linear regression coefficient
Taxon1 detection rate: detection rate of taxon1
Taxon2 detection rate: detection rate of taxon2

Table13 Summary of the statistical results of the 20 significant changed microbial taxa across age

	1			2			3			4			5			6			7			8			9		
Row.names	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean ASD	mean NT	p-value
g__Lachnospiraceae_UCG-004							0.44%	0.77%	0.025199	0.45%	0.95%	0.020612															
g__Escherichia-Shigella																5.40%	7.38%	0.001517				6.77%	2.27%	0.025688			
g__Butyricicoccus																									0.46%	0.24%	0.01217
g__Faecalibacterium	11.98%	4.12%	0.03829				17.55%	13.00%	0.013482																		
g__Parabacteroides																						1.75%	2.48%	0.011476			
f__Enterobacteriaceae|__										2.75%	6.82%	0.014322				4.99%	5.13%	0.004266	7.21%	3.53%	1.13724E-05				1.69%	1.70%	0.019414
g__Lachnospiraceae_NK4A136_group																									1.46%	0.59%	0.006228
g__Bifidobacterium										2.70%	5.00%	0.007976															
g__Haemophilus							0.29%	0.83%	0.047153																0.25%	0.50%	0.039359
g__Veillonella	10.25%	19.99%	0.032053	1.69%	10.47%	5.7118E-05	3.60%	8.03%	0.003709	0.80%	5.48%	8.03E-05	0.76%	6.52%	0.001105	0.66%	3.87%	0.030332							0.47%	2.76%	0.047391
f__Ruminococcaceae|__	0.03%	0.14%	0.030366				0.16%	0.09%	0.015762																		
g__Anaerostipes										0.23%	0.43%	0.00098															
g__Lachnospira							1.87%	3.58%	0.014366							1.56%	3.01%	0.024705	1.65%	2.58%	0.028512499						
g__Blautia													1.43%	0.71%	0.002988												
g__Granulicatella													0.08%	0.08%	0.01799				0.01%	0.06%	0.003949691	0.01%	0.05%	0.020742			
g__Romboutsia										0.15%	0.17%	0.014176	0.11%	0.33%	0.032767												
g__Actinomyces													0.05%	0.32%	0.007578										0.04%	0.12%	0.011881
g__Roseburia																3.08%	3.30%	0.022073									
g__Incertae_Sedis													0.22%	0.21%	0.025056												
g__Hungatella				0.13%	0.80%	0.000636712																			0.07%	0.35%	0.017442

Total proportion of the 20 microbial taxa in different age brackets

age bracket	1	2	3	4	5	6	7	8	9
NT	65.91%	40.10%	50.53%	40.04%	37.16%	38.59%	40.97%	33.41%	35.09%
ASD	62.42%	55.85%	50.09%	45.66%	46.73%	46.45%	39.02%	37.09%	35.70%

Table 14 Summary of the statistical results of the 39 significant changed GBM across age

		1			2			3			4			5			6			7			8			9		
No.	Row name	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value
1	MGB004 Kynurenine synthesis	1092.797	297.3598	0.021074				1160.483	423.7885	0.014966																		
2	MGB025 Nitric oxide synthesis I (NO synthase)	48.63158	3.12	0.00303				196.8714	2.631285	3.06E-07													3	2.586207	0.007224			
3	MGB045 Acetate synthesis III				78271.83	94693.84	0.039124	92155.87	86980.81	0.02902							76626.3	83367.28	0.018106									
4	MGB047 Acetate degradation				34185.86	33968.58	0.035049																					
5	MGB050 Glutamate degradation I				5282.641	14521.4	5.68E-05							4234.183	11689.16	0.028959												
6	MGB028 Nitric oxide degradation II (NO reductase)				1300.1	6200.144	0.142984	1576.387	4628.157	0.023838				715.2168	4315.926	0.012537												
7	MGB009 Histamine synthesis				6216.852	5725.541	0.171932																					
8	MGB031 17-beta-Estradiol degradation							56799.02	52701.34	0.044281							46593.32	49709.97	0.039599									
9	MGB055 Propionate synthesis III							35100.37	47227.68	0.015738							33119.66	40996.46	0.022824							34050.77	53703.55	0.000129
10	MGB044 Acetate synthesis II							69193.54	44421.63	0.033508																		
11	MGB034 Isovaleric acid synthesis I (KADH pathway)							21377.53	29567.96	0.001956							17763.45	26259.03	0.012571							19892.22	33138.89	0.01256
12	MGB024 DOPAC synthesis							19395.03	16628.75	0.001334																		
13	MGB051 Glutamate degradation II							6278.562	3765.424	0.021857	5264.89	4397.712	0.008437				4380.876	3094.99	0.000249	6386.679	3447.318	0.037749						
14	MGB015 p-Cresol synthesis																									83274.66	118679.3	0.000268
15	MGB056 Propionate degradation I										2259.034	247.979	5.97E-06	1231.779	2904.984	0.042978	1478.688	88.24674	5.86E-06	1161.887	870.508	0.001545				1859.713	1104.982	0.000152
16	MGB023 Dopamine degradation																			2386.973	1767.557	0.048214				397.3296	506.3824	0.012873
17	MGB021 GABA synthesis II																			5050.97	3532.61	0.011751	5159.807	2860.345	0.000162	4398.596	5065.86	0.00462
18	MGB020 GABA synthesis I																2979.323	3440.453	0.002932	2770.88	1635.698	0.005035	2434.388	2124.651	0.036131			
19	MGB016 p-Cresol degradation										1687.501	1012.833	0.033167	398.9685	2864.111	0.041861	1099.75	629.1248	0.003041	828.4491	368.7868	0.00438				320.7989	78.82941	0.003953
20	MGB048 Propionate synthesis I																1478.989	1721.478	0.001436	2286.921	1605.805	0.004333						
21	MGB010 Histamine degradation																1096.704	1232.576	0.030099	1481.074	651.145	0.000279						
22	MGB026 Nitric oxide synthesis II (nitrite reductase)										696.2562	653.8108	0.043096													555.3852	805.9735	0.031165
23	MGB052 Butyrate synthesis I																									23393.96	30034.2	0.003496
24	MGB007 Glutamate synthesis II																98660.29	105796.9	0.002209							101169.1	122042.4	0.006389
25	MGB038 Inositol degradation													7386.579	7494.644	0.035399												
26	MGB006 Glutamate synthesis I																99085.17	100277.3	0.040773							100197.7	118560.9	0.004365
27	MGB033 Quinolinic acid degradation																79722.27	85805.27	0.005075							84853.1	98243.76	0.046034
28	MGB035 Isovaleric acid synthesis II (KADC pathway)																54185.15	59998.62	0.001644									
29	MGB036 S-Adenosylmethionine (SAM) synthesis													90423.15	105440.7	0.035302	89667.01	97680.31	0.001664									
30	MGB049 Tryptophan degradation													10332.87	9637.566	0.025768												
31	MGB037 Inositol synthesis										33992.74	39414.31	0.014555													35428.22	45181.6	0.002122
32	MGB027 Nitric oxide degradation I (NO dioxygenase)													4375.189	10843.07	0.00012												
33	MGB019 GABA degradation																						11257.43	6400.679	0.041149			
34	MGB005 Tryptophan synthesis																57626.33	65420.19	0.008114							56928.03	77007.84	0.000511
35	MGB040 Menaquinone synthesis (vitamin K2) I													23046.35	35277.73	0.014219										25949.26	37159.62	0.001383
36	MGB029 ClpB (ATP-dependent chaperone protein)																82244.97	86773.31	0.009216									
37	MGB032 Quinolinic acid synthesis																70137.28	72081.29	0.036633							69053.07	82871.76	0.018522
38	MGB039 g-Hydroxybutyric acid (GHB) degradation																						3822.884	6090.431	0.003407	4356.258	4179.57	0.012649
39	MGB043 Acetate synthesis I													78948.7	93955.13	0.013526	80907.01	86281.85	0.006756									

Table 15 Summary of the statistical results of the 286 significant changed METACYC across age

			1			2			3			4			5			6			7			8			9		
No.	Row name	Higher level functional annotation	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean NT	mean ASD	p-value	mean ASD	mean NT	p-value
1	PWY-6467 Kdo transfer to lipid IVA III_Chlamydia	Cell-Structure-Biosynthesis	46011.33368	57669.7756	0.045533164				34540.91571	43375.01363	0.018662527				28033.37853	43427.22983	0.01593963										31694.50929	43554.0598	0.009342289
2	PWY-7328 superpathway of UDP-glucose-derived O-antigen building blocks biosynth	Carbohydrates-metabolism	24785.94839	26974.26765	0.043282018																								
3	GLCMANNANAUT-PWY superpathway of N-acetylglucosamine N-acetylmannosamine	AMINE-metabolism	46600.82136	26265.91592	0.042517728				41688.25006	36155.5547	0.007292866																		
4	HEXITOLDEGSUPER-PWY superpathway of hexitol degradation_bacteria	SECONDARY-METABOLITE-metabolism	28863.04556	14558.9774	0.044264065				15398.24158	14266.40674	0.013865097										21402.11043	15109.77867	0.022930643						
5	PWY-5304 superpathway of sulfur oxidation_Acidianus ambivalens	Noncarbon-Nutrients	13232.49474	3048.4472	0.039564677																								
6	PWY-6263 superpathway of menaquinol-8 biosynthesis II	Cofactor-Biosynthesis	8598.603763	953.3151	0.006283996				6464.238364	4027.000816	0.006041979				6410.836737	5197.06559	0.031917665	9420.796474	9511.482333	0.003057083									
7	PWY-7371 1_4-dihydroxy-6-naphthoate biosynthesis II	Cofactor-Biosynthesis	6438.593468	425.125368	0.005346376				4059.22195	3703.098392	0.011398935				6778.919474	3290.317683	0.016649036	5705.273564	7253.294698	0.009765784									
8	PWY-5088 L-glutamate degradation VIII_to propanoate	Amino-Acid-metabolism	4162.207195	204.579396	0.003799906				2439.56412	602.5388112	3.1071E-07				1097.392894	452.7595521	0.004243678	2409.82525	604.3751879	0.003903393				5470.174254	1434.999445	0.040271174			
9	PWY-7374 1_4-dihydroxy-6-naphthoate biosynthesis I	Cofactor-Biosynthesis	389.6973263	42.717488	0.000775331										1074.786421	732.3204306	0.022728005				2059.732333	960.39717	0.031413954						
10	METHYLGALLATE-DEGRADATION-PWY methylgallate degradation	AROMATIC-COMPOUNDS-metabolism	719.5115263	18.90496	0.04102115										23.30229265	116.680043	3.07046E-09												
11	GALLATE-DEGRADATION-I-PWY gallate degradation II	AROMATIC-COMPOUNDS-metabolism	584.5447632	15.143492	0.045515981										18.64854559	94.78714876	6.23905E-09												
12	GALLATE-DEGRADATION-II-PWY gallate degradation I	AROMATIC-COMPOUNDS-metabolism	7.032068421	15.012668	0.004400837																								
13	PWY-7527 L-methionine salvage cycle III	Amino-Acid-metabolism	25.02793684	11.285224	0.004991771	441.82331	7.680916406	0.025849186	183.93645	5.98765419	1.04497E-07				9.198991176	6.406295868	0.023284652	10.77305972	5.206589394	0.001405754	599.3185333	5.7962475	5.15288E-05	7.957864286	6.183141379	0.018857989	80.78314286	1.70527451	0.005270313
14	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	Amino-Acid-metabolism	15.07476842	6.782268	0.005036054	312.0413	4.612629688	0.016250679	122.7082429	3.594768715	4.81722E-08							6.478415278	3.133857576	0.002429678	592.9125212	3.4821425	0.000146451	4.778371429	3.718917241	0.014901942	49.50753571	1.023292157	0.00652384
15	GLYCOLYSIS-E-D superpathway of glycolysis and Entner-Doudoroff	GLYCOLYSIS-metabolism				35236.19625	46854.33951	0.043814775				29274.0364	40912.91932	0.024816377	27252.43858	40625.42705	0.003034421	32179.01193	38638.91635	0.007852712									
16	PWY490-3 nitrate reduction VI_assimilatory	Noncarbon-Nutrients				29283.3368	38806.25393	0.023411489																					
17	SULFATE-CYS-PWY superpathway of sulfate assimilation and cysteine biosynthesis	Noncarbon-Nutrients				39033.4344	38763.53567	0.015761693				41826.28901	36407.7603	0.015202789	35667.54745	39737.10094	0.023889057							40643.38571	36430.085	0.029796927			
18	PWY-7254 TCA cycle VII_acetate-producers	TCA-pathway				22922.34835	32467.96947	0.025496386				17072.64287	25475.83156	0.043519083				20221.934	28430.9653	0.029394284									
19	PWY-7377 cobIlyrinate a_c-diamide biosynthesis I_early cobalt insertion	Cofactor-Biosynthesis				15152.89166	30347.48872	0.002566916																					
20	SO4ASSIM-PWY sulfate reduction I_assimilatory	Noncarbon-Nutrients				24745.03782	24348.05425	0.012151101				26240.82217	22303.39302	0.013735987	21408.22711	25114.17903	0.0109677							25657.93869	21991.60069	0.021188852			
21	PWY0-1241 ADP-L-glycero-b-D-manno-heptose biosynthesis	Carbohydrates-metabolism				12080.54372	23220.37275	0.011564544	16544.64956	20632.71786	0.039896173	10164.71427	17961.45495	0.024661408															
22	PWY-5005 biotin biosynthesis II	Cofactor-Biosynthesis				7773.738855	15322.24462	0.000941234																					
23	PWY-5022 4-aminobutanoate degradation V	AMINE-metabolism				6316.302615	9817.890252	0.016304064																					
24	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-	AROMATIC-COMPOUNDS-metabolism				3495.470235	3358.371579	0.046952759	1239.792397	2980.433499	0.00694999	2890.392933	1816.778939	0.001350845	694.9028132	6198.372321	0.0013136	1969.2361	1021.625871	0.000210551	1554.045658	854.0680975	0.000252494				687.5720589	191.4666255	0.000259204
25	PWY-7094 fatty acid salvage	Lipid-Biosynthesis				3105.970268	1953.611165	0.002162558	544.4362571	1758.952977	0.000787875	3481.786751	572.8985224	2.45229E-07	1012.077368	4647.28576	0.002149862	2378.345778	107.1017833	0.002055444				1537.5915	1155.169255	0.038395215	1111.714638	64.91551961	0.00251016
26	PWY-5747 2-methylcitrate cycle II	CARBOXYLATES-DEG				2000.215198	1603.603878	0.038732318	1995.080799	1430.511551	0.003519756	2415.69434	325.5825112	1.85977E-07	1291.65	2955.469277	0.005467699	1575.903146	116.9647985	2.63936E-07	1290.159788	948.2591575	0.004041135				1926.48683	1128.011635	2.35345E-05
27	LEU-DEG2-PWY L-leucine degradation I	Amino-Acid-metabolism				1969.324995	1260.073678	0.009096858				1050.365349	289.9929545	4.09683E-05	323.8595603	3425.43754	0.000725367										282.9912911	9.904211765	0.010093346
28	PWY-6562 norspermidine biosynthesis	others				1111.108025	1180.981642	0.010251764	1100.763723	1618.725246	0.037756919	774.8088889	1219.100031	0.010484583	746.4763265	1539.395613	0.018142902	1176.813911	1110.124397	0.013679461	1136.932112	572.02401	0.000814525				198.6536357	169.6047	0.040460976
29	PWY-6071 superpathway of phenylethylamine degradation	AMINE-metabolism				1300.794635	1173.339063	0.034239338	1092.79371	1079.461694	0.039821948	826.200646	1336.303172	0.013952917	543.5819338	646.9908008	0.027067816	937.1829903	1018.614729	0.005936035	1192.189964	526.1358325	0.000103761				165.1434304	147.8983608	0.045640813
30	PWY0-321 phenylacetate degradation I_aerobic	AROMATIC-COMPOUNDS-metabolism				1224.9438	1113.756348	0.036285569	1051.699036	1017.273318	0.035406018	993.9877444	1283.499042	0.012196954	545.0144176	624.0023612	0.020514855	999.0972667	981.6301015	0.004041028	1149.832052	505.364935	6.75457E-05				170.4341964	148.7019745	0.017953223
31	TYRFUMCAT-PWY L-tyrosine degradation I	Amino-Acid-metabolism				1507.921395	968.9262586	0.00011005				1416.128943	285.9657082	4.41479E-07	272.7201029	2687.243537	0.000570446	657.1039722	9.240216667	0.020453864	404.8633636	11.5058575	0.017523814				268.3408768	7.643803922	0.001067186
32	PWY-5415 catechol degradation I_meta-cleavage pathway	AROMATIC-COMPOUNDS-metabolism				418.1389425	38.58009922	0.003345648	202.4937243	42.10337207	0.006365506	101.5414905	171.330697	4.78101E-05				59.16923056	34.35555152	0.010402027	204.3722879	26.5642475	0.000771027				125.669625	40.78697647	0.001939638
33	PWY-5178 toluene degradation IV_aerobic_via catechol	AROMATIC-COMPOUNDS-metabolism				83.2327725	26.95920234	0.002609306	62.91488	39.23898659	0.000851762	77.30545079	52.53387239	1.59215E-06	49.32262794	43.64406694	0.045645247	49.60872083	39.06673333	0.003655419	86.80778788	11.7779575	3.38574E-05				38.74591607	35.10712157	0.000153614
34	PWY-7220 adenosine deoxyribonucleotides de novo biosynthesis II	Nucleic-Acid-metabolism							127958.8427	125146.8563	0.04590882				104476.2261	126552.6589	0.041331657	104765.0923	110027.0856	0.036313067									
35	PWY-7222 guanosine deoxyribonucleotides de novo biosynthesis II	Nucleic-Acid-metabolism							127958.8427	125146.8563	0.04590882				104476.2261	126552.6589	0.041331657	104765.0923	110027.0856	0.036313067									
36	GLYCOGENSYNTH-PWY glycogen biosynthesis I_from ADP-D-Glucose	Carbohydrates-metabolism							99529.27178	93364.84871	0.048213582							95088.79294	96910.29149	0.02773655									
37	PWY-6609 adenine and adenosine salvage III	Nucleic-Acid-metabolism							99504.4861	92551.33919	0.011668026							89331.93419	92980.85093	0.014696648									
38	PWY-6317 galactose degradation I_Leloir pathway	Carbohydrates-metabolism							90876.83976	84571.55058	0.007748135							80531.88917	84395.28647	0.016118079									
39	PWY-621 sucrose degradation III_sucrose invertase	Carbohydrates-metabolism							85218.09012	75750.47402	0.000765131																		
40	PWY0-1296 purine ribonucleosides degradation	Nucleic-Acid-metabolism							83850.10151	75046.17887	0.000816337							69807.93634	75836.32052	0.00744296									
41	PWY-6700 queuosine biosynthesis	Nucleic-Acid-metabolism							59295.69946	70239.34317	0.032628473				53822.3702	72802.32219	0.039914382	57588.25667	66027.84892	0.00512517							57075.53172	80277.89864	0.001306885
42	PWY-6151 S-adenosyl-L-methionine cycle I	Cofactor-Biosynthesis							75700.21294	70206.52192	0.00377755							69406.15967	72114.08303	0.01323819									
43	PWY0-1298 superpathway of pyrimidine deoxyribonucleosides degradation	Nucleic-Acid-metabolism							74061.85899	68612.07143	0.005115974							57990.79147	67272.97319	0.00300963									
44	PWY-7199 pyrimidine deoxyribonucleosides salvage	Nucleic-Acid-metabolism							67274.27802	63020.70715	0.037978834																63118.57255	71060.65432	0.039853507
45	THISYN-PWY superpathway of thiamin diphosphate biosynthesis I	Cofactor-Biosynthesis							52243.86143	62947.36763	0.007311907																53131.27185	72217.10585	0.001102939
46	P161-PWY acetylene degradation	CARBOXYLATES-DEG							72988.0242	62564.77682	0.000139104							55702.12486	62503.79512	0.024909676							61109.8422	61010.08885	0.041611951
47	PWY0-1297 superpathway of purine deoxyribonucleosides degradation	Nucleic-Acid-metabolism							71696.51985	61590.52402	0.000116332							55473.3178	61159.35797	0.005756486									
48	PWY-6703 preQ0 biosynthesis	SECONDARY-METABOLITE-metabolism							50639.47908	61293.68365	0.009945489							49413.78327	58437.22857	0.004087672							49027.68797	72031.35115	0.000589996
49	PWY-1269 CMP-3-deoxy-D-manno-octulosonate biosynthesis I	Carbohydrates-metabolism							42052.10016	50039.68887	0.033302671																39617.35708	61023.43698	0.001163409
50	NAGLIPASYN-PWY lipid IVA biosynthesis	Cell-Structure-Biosynthesis							40275.5998	49443.00324	0.026115623				33589.65338	50309.67515	0.025546921										38353.64274	54848.95954	0.005435124
51	PWY-6471 peptidoglycan biosynthesis IV_Enterococcus faecium	Cell-Structure-Biosynthesis							48326.04545	44209.59183	0.010416085																		
52	PWY-5384 sucrose degradation IV_sucrose phosphorylase	Carbohydrates-metabolism							50190.30966	42353.24538	0.000247476																		
53	PWY0-1061 superpathway of L-alanine biosynthesis	Amino-Acid-metabolism							34761.36599	32000.67862	0.008754016																27785.75466	28101.24117	0.029805701
54	HEMESYN2-PWY heme biosynthesis II_anaerobic	Cofactor-Biosynthesis							17008.93139	26111.70054	0.021847609				10569.97348	26911.29496	0.00140159												
55	PWY-7392 taxadiene biosynthesis_engineered	SECONDARY-METABOLITE-metabolism							25608.76877	21308.86986	0.001220107	22031.66229	20924.53963	0.023407787							28976.82938	19175.06974	0.00652318						
56	FUC-RHAMCAT-PWY superpathway of fucose and rhamnose degradation	others							20620.67216	17116.80016	0.019789923	20528.29123	16972.43817	0.02822479															
57	FUCCAT-PWY fucose degradation	Carbohydrates-metabolism							17316.76326	14279.38718	0.023044239	14807.58353	12604.73779	0.037988416	15097.1651	12780.26364	0.012804763												
58	P105-PWY TCA cycle IV_2-oxoglutarate decarboxylase	TCA-pathway							12586.7186	13356.35164	0.004642538	13274.07099	11899.15527	0.00167189				14261.19153	12161.26476	3.32486E-05	17148.13426	8909.252738	0.000103016	17326.97093	12329.91184	0.02396939			
59	REDCITCYC TCA cycle VIII_helicobacter	TCA-pathway							12403.3652	12168.35779	0.020710342				8300.35765	13982.49938	0.001475673	11847.87213	11109.8836	0.038457558	14217.82998	8522.7275	0.009960554				11592.74829	10269.72339	0.00018835
60	P461-PWY hexitol fermentation to lactate formate ethanol and acetate	CARBOXYLATES-DEG							12842.45872	11668.10155	0.006473443																		
61	PWY-6629 superpathway of L-tryptophan biosynthesis	Amino-Acid-metabolism							12695.70598	11641.01618	0.004851462	10864.52161	11523.73312	0.004149261				13460.05617	12194.28638	5.11125E-05									
62	GLYCOLYSIS-TCA-GLYOX-BYPASS superpathway of glycolysis pyruvate dehydrogenase	GLYCOLYSIS-metabolism							10548.19622	11355.30715	0.009826924	10376.7733	10462.44775	0.003137388				11637.54138	10613.02995	3.89194E-05	13695.42983	7738.124323	0.000183865	14209.86374	9427.581121	0.025051953			
63	PWY-5850 superpathway of menaquinol-6 biosynthesis I	Cofactor-Biosynthesis							9516.660821	9239.112024	0.019496221	7878.097568	8227.43988	0.006430035				8426.153215	8508.216979	0.000107239	9587.795145	7205.651935	0.00175449	9641.079439	7591.3511	0.026901735			
64	PWY-5896 superpathway of menaquinol-10 biosynthesis	Cofactor-Biosynthesis							9516.660821	9239.112024	0.019496221	7878.097568	8227.43988	0.006430035				8426.153215	8508.216979	0.000107239	9587.795145	7205.651935	0.00175449	9641.079439	7591.3511	0.026901735			
65	PWY-5845 superpathway of menaquinol-9 biosynthesis	Cofactor-Biosynthesis							9516.660821	9239.112024	0.019496221	7878.097568	8227.43988	0.006430035				8426.153215	8508.216979	0.000107239	9587.795145	7205.651935	0.00175449	9641.079439	7591.3511	0.026901735			
66	FAO-PWY fatty acid b-oxidation I	others							10464.4713	8267.557108	0.017981303	9268.133802	7004.777299	0.003455599	5863.249778	10475.44098	0.00619823	9803.493568	7985.669464	8.33156E-05	9628.746806	6024.213108	0.002032986	10768.4963	6518.571321	0.006203867	8515.242243	7195.279347	0.032245427
67	ENTBACSYN-PWY enterobactin biosynthesis	SECONDARY-METABOLITE-metabolism							8764.474957	8129.591923	0.013714818	6064.805643	7736.492487	0.0247221				7596.904017	7681.018352	0.00037265	8910.386467	5548.18555	0.000539465	10122.81154	6725.185893	0.022660347			
68	ALL-CHORISMATE-PWY superpathway of chorismate metabolism	others							8822.097047	7914.275861	0.007439981	7601.809722	7318.472988	0.005751336				8219.511179	7750.579971	2.56509E-05	9071.519215	5920.311303	0.000510852	9536.498889	6725.776862	0.019482051			
69	PPGPPMET-PWY ppGpp biosynthesis	others							8662.653436	7681.290216	0.01348234	7949.500957	8162.282561	0.000769468				8692.028671	7504.015441	0.03374394	8336.923609	5214.335588	0.011656546						
70	TCA-GLYOX-BYPASS superpathway of glyoxylate bypass and TCA	TCA-pathway							7134.666557	7651.909274	0.010056717	7503.688694	6909.078067	0.002710025				8050.471958	7385.042912	3.05106E-05	9531.099948	5210.606623	0.000134383	9615.136818	6080.153997	0.021295948			
71	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	Cofactor-Biosynthesis							8231.577889	7461.629468	0.016094978	6291.551175	6628.236111	0.007667417				6864.761688	7108.556188	0.000105585	7772.381076	5751.716583	0.001567144	7851.103521	5771.212969	0.022679806			
72	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	Cofactor-Biosynthesis							8231.577889	7461.629468	0.016094978	6291.551175	6628.236111	0.007667417				6864.761688	7108.556188	0.000105585	7772.381076	5751.716583	0.001567144	7851.103521	5771.212969	0.022679806			
73	GLYOXYLATE-BYPASS glyoxylate cycle	others							6137.285864	6846.502483	0.020875238	6494.959951	6103.824747	0.004835096				7488.008754	6832.191856	2.73898E-05	8681.642855	5010.385185	0.001146975	9351.000718	5283.062786	0.005763514			
74	NAD-BIOSYNTHESIS-II NAD salvage pathway II	Cofactor-Biosynthesis							7875.305921	6565.286561	0.030844965	6599.565081	5479.376448	0.001740056				7311.927538	6443.537626	0.003545513	7233.07933	4766.827643	0.016954811						
75	PWY-5857 ubiquinol-10 biosynthesis_prokaryotic	Cofactor-Biosynthesis							6987.389804	5507.006969	0.03031528	6101.556154	4581.507533	0.025134119	4060.227432	6954.946857	0.012324126	6388.006176	4850.851445	3.10628E-06	6086.92007	4100.481278	0.0332924	6601.846582	4150.443852	0.01237773			
76	PWY-5855 ubiquinol-7 biosynthesis_prokaryotic	Cofactor-Biosynthesis							6987.389804	5507.006969	0.03031528	6101.556154	4581.507533	0.025134119	4060.227432	6954.946857	0.012324126	6388.006176	4850.851445	3.10628E-06	6086.92007	4100.481278	0.0332924	6601.846582	4150.443852	0.01237773			
77	PWY-6708 ubiquinol-8 biosynthesis_prokaryotic	Cofactor-Biosynthesis							6987.389804	5507.006969	0.03031528	6101.556154	4581.507533	0.025134119	4060.227432	6954.946857	0.012324126	6388.006176	4850.851445	3.10628E-06	6086.92007	4100.481278	0.0332924	6601.846582	4150.443852	0.01237773			
78	PWY-5856 ubiquinol-9 biosynthesis_prokaryotic	Cofactor-Biosynthesis							6987.389804	5507.006969	0.03031528	6101.556154	4581.507533	0.025134119	4060.227432	6954.946857	0.012324126	6388.006176	4850.851445	3.10628E-06	6086.92007	4100.481278	0.0332924	6601.846582	4150.443852	0.01237773			
79	UBISYN-PWY superpathway of ubiquinol-8 biosynthesis_prokaryotic	Cofactor-Biosynthesis							6731.57866	5094.239577	0.029153524	6027.098549	4529.662226	0.023234776	4028.348731	5052.882371	0.011355569	6287.20369	4814.496326	3.28607E-06	5975.09663	4052.432115	0.035776336	6437.957511	4119.057341	0.012823839			
80	PWY0-1533 methylphosphonate degradation I	Noncarbon-Nutrients							5338.889599	4842.622712	0.025140934							5688.652613	5962.459005	0.000887174	6884.169927	5093.060525	0.017070773				5386.172221	5694.903184	0.004983903
81	P162-PWY L-glutamate degradation V_via hydroxyglutarate	Amino-Acid-metabolism							5090.237799	4527.543404	0.01313862																		
82	GLYCOL-GLYOXDEG-PWY superpathway of glycol metabolism and degradation	others							4124.421824	4018.923793	0.006952677	4077.627578	3507.193325	0.002073947				4476.272215	4914.004238	6.26618E-05	6184.269255	3715.496223	0.006026796	5925.784336	3535.690648	0.007486913			
83	AST-PWY L-arginine degradation II_AST pathway	Amino-Acid-metabolism							3457.544274	4016.523605	0.035765506	3069.21921	3345.308674	0.009325321				3570.707953	3737.700529	0.000150307	4183.908676	2622.978555	0.000393821	3625.328207	2593.586831	0.011864507			
84	ECASYN-PWY enterobacterial common antigen biosynthesis	Cell-Structure-Biosynthesis							5672.08258	3880.527163	0.004130596	3830.67356	3650.22535	0.005486661				4734.725592	4561.482418	8.84598E-05	5266.629567	3461.672163	0.000837789	5435.907229	3315.209228	0.015338286			
85	ORNDEG-PWY superpathway of ornithine degradation	AMINE-metabolism							3997.315191	3813.716053	0.03805899	3476.722954	3583.477075	0.010376241				4145.12224	4244.843283	0.000100754	4670.236306	2973.41961	0.00047204	5477.815082	2843.851555	0.00969332			
86	ARGDEG-PWY superpathway of L-arginine putrescine and 4-aminobutanoate degrada	Amino-Acid-metabolism							3539.264461	3203.474239	0.014590944	2828.010349	3451.258614	0.014025449				3889.642029	4378.20333	0.00011775	4358.379203	2568.76038	0.000777252	3914.951261	3086.974062	0.033202464			
87	ORNARGDEG-PWY superpathway of L-arginine and L-ornithine degradation	Amino-Acid-metabolism							3539.264461	3203.474239	0.014590944	2828.010349	3451.258614	0.014025449				3889.642029	4378.20333	0.00011775	4358.379203	2568.76038	0.000777252	3914.951261	3086.974062	0.033202464			
88	PWY0-1338 polymyxin resistance	Cell-Structure-Biosynthesis							4485.23244	2641.496755	0.003740628	3060.293875	2562.195104	0.003258713				3652.741851	3243.247426	3.20933E-05	3668.344564	2411.844365	0.000314079	3835.664868	2148.93381	0.015241182			
89	METHGLYUT-PWY superpathway of methylglyoxal degradation	others							2671.269713	2583.439526	0.014987201	2370.004997	2387.096077	0.002954646				3036.389278	3703.4678	9.69981E-05	3148.979445	2157.955493	0.001465523	3249.598393	2121.797531	0.040291868			
90	P562-PWY myo-inositol degradation I	SECONDARY-METABOLITE-metabolism							2786.303457	2511.290719	0.015046818																		
91	PWY-6470 peptidoglycan biosynthesis V_b-lactam resistance	Cell-Structure-Biosynthesis							2883.144964	2257.600463	0.018737337	2808.413444	1637.383978	0.001946123															
92	PWY-5705 allantoin degradation to glyoxylate III	AMINE-metabolism							2418.018711	1964.196417	0.015222686							2030.669807	1740.192336	0.002030462									
93	PWY-5417 catechol degradation III_ortho-cleavage pathway	AROMATIC-COMPOUNDS-metabolism							766.27094	1803.039149	0.046878425	1069.753651	993.6305993	0.01292859	439.6170147	3662.336597	0.004799563	1171.976364	680.013347	0.000816	824.4077364	362.1109425	0.000138749				309.2198446	85.09009216	0.002158548
94	PWY-5431 aromatic compounds degradation via b-ketoadipate	AROMATIC-COMPOUNDS-metabolism							766.27094	1803.039149	0.046878425	1069.753651	993.6305993	0.01292859	439.6170147	3662.336597	0.004799563	1171.976364	680.013347	0.000816	824.4077364	362.1109425	0.000138749				309.2198446	85.09009216	0.002158548
95	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	AROMATIC-COMPOUNDS-metabolism							697.7207529	1626.216334	0.047681648	1007.524114	904.5252933	0.012252906	402.8953279	3281.73525	0.004547398	1121.594564	623.2323576	0.000842171	755.539497	331.330105	0.000158282				310.4210464	77.15234902	0.002011208
96	PWY-5181 toluene degradation III_aerobic_via p-cresol	AROMATIC-COMPOUNDS-metabolism							921.9867314	944.7770006	0.035267526	1098.137138	1248.105418	0.006192526	479.4620059	549.1854215	0.008219338	1256.248588	831.5828212	0.002466748	1029.516682	478.8306825	0.000104645				194.1793	107.081449	0.001076824
97	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY 4-hydroxyphenylacetate degradati	AROMATIC-COMPOUNDS-metabolism							936.3893571	906.2514017	0.0221868	591.5318032	1149.692672	0.007712663	359.0135015	626.6881174	0.028041066	1068.627364	870.4884939	0.003476365	1051.459873	457.96253	0.000115423				361.3228875	129.4854745	0.034729718
98	PWY-5180 toluene degradation I_aerobic_via o-cresol	AROMATIC-COMPOUNDS-metabolism							1584.470331	895.3127715	0.039052054	1462.207954	431.7984843	5.07816E-05															
99	PWY-5182 toluene degradation II_aerobic_via 4-methylcatechol	AROMATIC-COMPOUNDS-metabolism							1584.470331	895.3127715	0.039052054	1462.207954	431.7984843	5.07816E-05															
100	KETOGLUCONMET-PWY ketogluconate metabolism	CARBOXYLATES-DEG							1066.4724	829.9111765	0.002436783	1313.260021	534.2232358	0.001591033				975.6331653	336.4336985	4.09935E-05							1724.550596	1797.041088	0.003002206
101	PWY-6182 superpathway of salicylate degradation	AROMATIC-COMPOUNDS-metabolism							745.4747686	804.8515413	0.029470638	892.6616063	959.3326485	0.012379421	396.0495794	540.6714587	0.004157852	1075.876351	672.2319561	0.002308195	810.6981152	358.0673475	0.000149337				155.3500018	81.77690196	0.002432146
102	PWY-6185 4-methylcatechol degradation_ortho cleavage	AROMATIC-COMPOUNDS-metabolism							766.3011643	774.8363374	0.042398108	881.7389127	991.9389045	0.011593679	407.4270015	451.1274347	0.009884084	1083.327958	693.3099712	0.00258512	835.0798788	366.25335	0.000127895				142.9857179	82.85903725	0.002044225
103	P281-PWY 3-phenylpropanoate degradation	AROMATIC-COMPOUNDS-metabolism							768.3598257	767.0761799	0.017196198	486.0923587	940.7769425	0.013263894	322.2364853	683.9037835	0.008192239	955.1257556	754.32145	0.00033584	839.1632606	378.52576	0.000326536				325.3597179	147.8254725	0.024502203
104	LPSSYN-PWY superpathway of lipopolysaccharide biosynthesis	Lipid-Biosynthesis							2765.830553	640.5385123	1.11731E-07	1508.712902	959.385894	0.00526655	1591.524228	964.3729438	0.01191325	3448.581965	1636.030579	0.015995584	3278.438858	618.1244175	0.022340276						
105	PWY0-42 2-methylcitrate cycle I	CARBOXYLATES-DEG							1969.89106	604.6429011	0.000162151	1789.342602	266.9338358	1.4748E-06	1024.359032	513.9207116	0.003875583	1247.951481	106.4926833	7.24138E-06	1256.079791	924.6454	0.00063418				1874.693921	1117.031098	3.17344E-05
106	PWY-5028 L-histidine degradation II	Amino-Acid-metabolism							217.8378843	572.6601296	0.035876495				432.1704206	462.5318372	0.029818005												
107	PWY0-1277 3-phenylpropanoate and 3-3-hydroxyphenylpropanoate degradation	AROMATIC-COMPOUNDS-metabolism							691.3817686	529.3482352	0.037820269	1022.812779	74.73257313	4.67574E-05	136.8484603	530.5814917	0.003375194	410.1442819	57.3496697	0.013547938	1696.023997	1060.342088	0.002455074				1342.010838	1398.261743	0.000854103
108	PWY-7431 aromatic biogenic amine degradation_bacteria	AMINE-metabolism							851.9006971	526.9949173	0.024805351																399.5920339	545.9133157	0.022536918
109	PWY-5532 adenosine nucleotides degradation IV	Nucleic-Acid-metabolism							624.6838857	382.1585966	0.002275753							594.8205319	223.4745667	0.010722533									
110	PWY-7446 sulfoglycolysis	SECONDARY-METABOLITE-metabolism							583.8760214	379.2237592	0.005389328	732.8608381	76.18239776	0.001490787				358.1200903	105.41595	0.000339788							967.4666375	1130.900386	0.006633824
111	PWY-5507 adenosylcobalamin biosynthesis I_early cobalt insertion	Cofactor-Biosynthesis							274.4114914	311.629938	0.000786869	918.5380746	234.0500567	1.35023E-09	415.8619544	377.115862	0.000337342							165.1196321	630.3853241	0.000433518	261.3309286	32.26925882	0.000394959
112	PWY0-41 allantoin degradation IV_anaerobic	AMINE-metabolism							543.9564386	267.3037922	0.041736139							289.8901903	167.6902864	0.007370574									
113	PWY-7376 cobIlyrinate a_c-diamide biosynthesis II_late cobalt incorporation	Cofactor-Biosynthesis							100.2575186	87.38274134	3.71588E-07	1150.188357	313.3779187	2.2422E-07	638.3593015	208.7270504	5.15917E-05	250.9401264	4.137822727	0.008874042				274.4271857	533.2108724	0.008167544	48.88697857	9.777782353	0.042938169
114	P381-PWY adenosylcobalamin biosynthesis II_late cobalt incorporation	Cofactor-Biosynthesis							160.7545757	67.50976425	8.56077E-08	740.2814222	236.6227918	6.40804E-08	449.2092382	181.1538645	7.38276E-05	241.76415	6.930915152	0.006970396	71.03022424	45.705275	0.049571604	108.3635571	531.8716586	0.001425817	81.49342857	16.31981961	0.026907391
115	VALDEG-PWY L-valine degradation I	Amino-Acid-metabolism							147.3555357	39.45574022	0.00106365	206.7530159	12.76651642	1.68896E-10	110.4078632	11.88322727	0.002309547	322.9031278	47.99304848	2.49691E-05							169.8529179	30.54976471	0.001590175
116	PWY-4722 creatinine degradation II	AMINE-metabolism							17.74049	7.029121788	0.004999643																8.343528571	3.577827451	0.018742942
117	PWYG-321 mycolate biosynthesis	Lipid-Biosynthesis										51280.09241	47579.84371	0.01312652															
118	PWY-7664 oleate biosynthesis IV_anaerobic	Lipid-Biosynthesis										50279.07302	47337.21752	0.013410062															
119	PWY0-862 5Z-dodec-5-enoate biosynthesis	Lipid-Biosynthesis										46227.27015	46238.66394	0.017774069															
120	PWY-5989 stearate biosynthesis II_bacteria and plants	Lipid-Biosynthesis										47055.54099	44119.80983	0.017314265															
121	PWY-6282 palmitoleate biosynthesis I_from 5Z-dodec-5-enoate	Lipid-Biosynthesis										46855.98813	43673.06585	0.014406584															
122	BIOTIN-BIOSYNTHESIS-PWY biotin biosynthesis I	Cofactor-Biosynthesis										43428.18043	39935.73821	0.008944805															
123	PWY-6519 8-amino-7-oxononanoate biosynthesis I	others										44652.44735	39573.74255	0.007122603															
124	FASYN-INITIAL-PWY superpathway of fatty acid biosynthesis initiation_E. coli	Lipid-Biosynthesis										40742.11748	37486.033	0.01649322															
125	KDO-NAGLIPASYN-PWY superpathway of_Kdo2-lipid A biosynthesis	Cell-Structure-Biosynthesis										10178.4387	9806.123649	0.002767228							10924.99947	8109.71075	0.013038936						
126	PWY-6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	Fermentation										8993.787114	8001.382827	0.005271816	7074.873575	7378.146279	0.004306403	9099.429521	7266.066627		10340.71135	6494.288485	0.046118275	10161.75347	7875.127983	0.04356208			
127	CENTFERM-PWY pyruvate fermentation to butanoate	Fermentation										7315.161213	6464.020637	0.005033192	5710.223343	5957.534855	0.004241475	7400.9466	5897.32585		8438.362745	5235.27041	0.04500706	8363.280057	6389.965641	0.04417975			
128	PWY-5177 glutaryl-CoA degradation	CARBOXYLATES-DEG										5732.996502	6278.359794	0.025324964	4878.488816	8821.003145	0.0145917	7107.047411	5653.837303		7194.475791	4750.033048	0.025484024	9982.400339	4926.139141	0.000929446			
129	PWY-2941 L-lysine biosynthesis II	Amino-Acid-metabolism										5702.686595	6110.003821	0.042257274				7029.493403	4729.336205										
130	ARGORNPROST-PWY arginine ornithine and proline interconversion	others										5179.787335	3867.733634	0.049343821				5314.105117	3115.331858								5490.812461	4200.9625	0.003900845
131	METH-ACETATE-PWY methanogenesis from acetate	others										5724.724511	3817.406232	0.019781594															
132	PWY-3781 aerobic respiration I_cytochrome c	others										6830.033979	3262.033456	0.000306648	3050.753943	2679.574245	0.00735531	4436.57999	923.1132182								4655.200323	2645.926004	0.012429087
133	THREOCAT-PWY superpathway of L-threonine metabolism	Amino-Acid-metabolism										2820.365106	1797.122416	0.008588623	830.2038	2440.332609	0.022631208	1948.270022	2295.875018		3705.374355	2411.906468	0.001412656						
134	GOLPDLCAT-PWY superpathway of glycerol degradation to 1_3-propanediol	others										3202.247438	1313.755857	0.000525014	1394.817931	1820.586025	0.002588672												

135	PWY-5910 superpathway of geranylgeranyldiphosphate biosynthesis I_via mevalonate	Polyprenyl-Biosynthesis										991.069254	551.9204485	0.011024187															
136	PWY-922 mevalonate pathway I	SECONDARY-METABOLITE-metabolism										706.602173	390.0153142	0.011168286															
137	PWY-5265 peptidoglycan biosynthesis II_staphylococci	Cell-Structure-Biosynthesis										416.1252619	272.4024396	0.005422949															
138	PWY-6165 chorismate biosynthesis II_archaea	AROMATIC-COMPOUNDS-metabolism										268.5767619	247.5817187	0.031108171															
139	PWY-5420 catechol degradation II_meta-cleavage pathway	AROMATIC-COMPOUNDS-metabolism										40.19063492	115.2750187	7.33247E-09															
140	PWY-5419 catechol degradation to 2-oxopent-4-enoate II	AROMATIC-COMPOUNDS-metabolism										29.37922381	105.6636687	3.15161E-07															
141	PWY-181 photorespiration	Amino-Acid-metabolism										426.979573	69.6964097	0.001850093	295.7941294	136.6113116	0.025438415							192.5252179	480.1104828	0.002028104			
142	HCAMHPDEG-PWY 3-phenylpropanoate and 3-3-hydroxyphenylpropanoate degradat	AROMATIC-COMPOUNDS-metabolism										709.5766095	42.23259552	8.43952E-05	71.59693824	438.3761496	0.005401598	292.4419375	31.12768485		1177.086364	891.019095	0.004145015				1012.386529	1164.847696	0.00094779
143	PWY-6690 cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate	AROMATIC-COMPOUNDS-metabolism										709.5766095	42.23259552	8.43952E-05	71.59693824	438.3761496	0.005401598	292.4419375	31.12768485		1177.086364	891.019095	0.004145015				1012.386529	1164.847696	
144	PWY-5823 superpathway of CDP-glucose-derived O-antigen building blocks biosynth	Carbohydrates-metabolism										448.8907206	36.95406269	1.73734E-06	163.3614721	114.0250058	1.0852E-05	67.47883333	2.76								168.8414036	15.97731373	
145	PWY-7209 superpathway of pyrimidine ribonucleosides degradation	Nucleic-Acid-metabolism										15.87620952	10.20294552	1.34024E-05	86.56206618	2.932263636	0.03344527	23.39453889	36.77948182										
146	PWY-1622 formaldehyde assimilation I_serine pathway	C1-COMPOUNDS										170.114827	2.647890299	0.000159514															
147	PWY-7323 superpathway of GDP-mannose-derived O-antigen building blocks biosynt	Carbohydrates-metabolism																									46765.40792	60091.63821	0.005049979
148	PWY-6737 starch degradation V	Carbohydrates-metabolism																116953.6181	118780.2718										
149	ARGSYNBSUB-PWY L-arginine biosynthesis II_acetyl cycle	Amino-Acid-metabolism																62634.50563	73610.83946										
150	PRPP-PWY superpathway of histidine purine and pyrimidine biosynthesis	others																39540.19675	41111.46936										
151	PWY-5667 CDP-diacylglycerol biosynthesis I	Lipid-Biosynthesis																102395.2799	112146.3237										
152	P441-PWY superpathway of N-acetylneuraminate degradation	CARBOXYLATES-DEG													35061.09031	47367.12604	0.036287867												
153	PWY-7237 myo- chiro- and scillo-inositol degradation	SECONDARY-METABOLITE-metabolism													11249.23515	9574.74719	0.018425525										7942.239464	14940.45314	0.023784637
154	PWY-5103 L-isoleucine biosynthesis III	Amino-Acid-metabolism																96633.81335	106218.1345										
155	PWY-6612 superpathway of tetrahydrofolate biosynthesis	Cofactor-Biosynthesis																									55332.89674	69819.65945	0.001586587
156	UDPNAGSYN-PWY UDP-N-acetyl-D-glucosamine biosynthesis I	Carbohydrates-metabolism																59522.01699	67477.46072										
157	PWY-5121 superpathway of geranylgeranyl diphosphate biosynthesis II_via MEP	Polyprenyl-Biosynthesis																86631.45292	96042.12773								90839.07598	110157.5364	0.033982051
158	PWY-5101 L-isoleucine biosynthesis II	Amino-Acid-metabolism																110321.8676	121248.3167										
159	PWY-5973 cis-vaccenate biosynthesis	Lipid-Biosynthesis																103267.5365	111824.8689								105779.3058	129700.6457	0.040568723
160	PWY-6123 inosine-5-phosphate biosynthesis I	Nucleic-Acid-metabolism																91444.02366	100227.7676								95454.03083	116287.9839	0.026323805
161	PWY-6269 adenosylcobalamin salvage from cobinamide II	Cofactor-Biosynthesis																78018.78226	84385.12766										
162	DAPLYSINESYN-PWY L-lysine biosynthesis I	Amino-Acid-metabolism																67481.72288	74768.39593										
163	PWY-5100 pyruvate fermentation to acetate and lactate II	CARBOXYLATES-DEG													85855.04694	101532.2456	0.028509079	86507.17089	94440.72817										
164	RUMP-PWY formaldehyde oxidation I	C1-COMPOUNDS																4583.879183	2769.383155										
165	PWY-7221 guanosine ribonucleotides de novo biosynthesis	Nucleic-Acid-metabolism																91337.3346	99212.90906										
166	BRANCHED-CHAIN-AA-SYN-PWY superpathway of branched amino acid biosynthesis	Amino-Acid-metabolism																97235.38681	107252.3794										
167	GLUCARDEG-PWY D-glucarate degradation I	CARBOXYLATES-DEG																6313.785674	6549.250133										
168	PWY-7539 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III_Chlamydia	Cofactor-Biosynthesis																									54504.77468	76178.21179	0.000202439
169	VALSYN-PWY L-valine biosynthesis	Amino-Acid-metabolism																102878.5728	113696.4343										
170	PWY-6628 superpathway of L-phenylalanine biosynthesis	Amino-Acid-metabolism													46472.89994	69465.93273	0.011679892	50582.12153	63811.29717								55245.05755	80512.84396	0.027618407
171	PWY-5659 GDP-mannose biosynthesis	Carbohydrates-metabolism																									61729.75156	80392.22294	0.003353148
172	PWY-7373 superpathway of demethylmenaquinol-6 biosynthesis II	Cofactor-Biosynthesis																132.8602597	5.046960606		46.08247879	24.051655	0.035071843	177.5661571	107.4438172	0.029311636	250.4947446	11.3968098	0.023933011
173	PWY-7560 methylerythritol phosphate pathway II	SECONDARY-METABOLITE-metabolism																90082.36824	100367.946								94370.47783	115659.1963	0.033981653
174	PWY-6277 superpathway of 5-aminoimidazole ribonucleotide biosynthesis	Nucleic-Acid-metabolism																92424.37588	100685.3471								96334.9483	116761.8659	0.032597321
175	DHGLUCONATE-PYR-CAT-PWY glucose degradation_oxidative	Carbohydrates-metabolism													155.8346515	43.21561736	9.69716E-07	326.6000556	6.650072727								213.4575214	0.595756863	7.95124E-05
176	PWY-5695 urate biosynthesis_inosine 5-phosphate degradation	Nucleic-Acid-metabolism																									78553.1801	100672.3293	0.009792306
177	CALVIN-PWY Calvin-Benson-Bassham cycle	Carbohydrates-metabolism																103572.717	111318.5347								105778.8109	130572.7471	0.03354098
178	PWY-5505 L-glutamate and L-glutamine biosynthesis	Amino-Acid-metabolism													58352.05609	75911.1471	0.030434029	58165.38339	67010.68859										
179	COMPLETE-ARO-PWY superpathway of aromatic amino acid biosynthesis	Amino-Acid-metabolism																94913.42667	104708.8851										
180	PWY-7031 protein N-glycosylation_bacterial	Carbohydrates-metabolism																93.30333194	1.978525758										
181	GLUCOSE1PMETAB-PWY glucose and glucose-1-phosphate degradation	Carbohydrates-metabolism																			7812.029785	6361.54026	0.006364668						
182	P42-PWY incomplete reductive TCA cycle	C1-COMPOUNDS																									75910.98467	102062.3182	0.006042317
183	TRPSYN-PWY L-tryptophan biosynthesis	Amino-Acid-metabolism																67594.6385	75555.51523					70307.82277	68048.91143	0.020998121	66298.0756	90201.18272	0.001822905
184	PWY0-1319 CDP-diacylglycerol biosynthesis II	Lipid-Biosynthesis																102395.2799	112146.3237										
185	ILEUSYN-PWY L-isoleucine biosynthesis I_from threonine	Amino-Acid-metabolism																102878.5728	113696.4343										
186	PWY-6386 UDP-N-acetylmuramoyl-pentapeptide biosynthesis II_lysine-containing	Cell-Structure-Biosynthesis																89939.91749	98816.41159										
187	PWY-7229 superpathway of adenosine nucleotides de novo biosynthesis I	Nucleic-Acid-metabolism																104206.7794	112568.6963										
188	PWY-5676 acetyl-CoA fermentation to butanoate II	Fermentation																20607.70935	17570.96065								25907.83512	26913.36136	0.017829049
189	PWY-7208 superpathway of pyrimidine nucleobases salvage	Nucleic-Acid-metabolism																103113.853	114312.2633										
190	PANTOSYN-PWY pantothenate and coenzyme A biosynthesis I	Cofactor-Biosynthesis																66088.70772	71949.10049								66913.20705	85127.93677	0.005213644
191	PHOSLIPSYN-PWY superpathway of phospholipid biosynthesis I_bacteria	Lipid-Biosynthesis																92102.65386	100129.3123										
192	PWY0-1479 tRNA processing	Nucleic-Acid-metabolism													12090.73922	20781.18588	0.015140609	13616.62748	17176.06476										
193	PWY-7315 dTDP-N-acetylthomosamine biosynthesis	Carbohydrates-metabolism																11239.62857	9801.206594										
194	PYRIDNUCSYN-PWY NAD biosynthesis I_from aspartate	Cofactor-Biosynthesis																									64427.90322	78857.95237	0.008102334
195	PWY-7196 superpathway of pyrimidine ribonucleosides salvage	Nucleic-Acid-metabolism																65471.59525	69883.50816								66467.17701	89128.58992	0.006084692
196	PWY-7200 superpathway of pyrimidine deoxyribonucleoside salvage	Nucleic-Acid-metabolism																									48161.49687	58438.05594	0.031246937
197	AEROBACTINSYN-PWY aerobactin biosynthesis	SECONDARY-METABOLITE-metabolism													1.089308824	4.378803306	0.004753846												
198	P341-PWY glycolysis V_Pyrococcus	GLYCOLYSIS-metabolism													631.2033147	798.985805	0.026237927	811.7880528	378.5204394										
199	P108-PWY pyruvate fermentation to propanoate I	Fermentation																									52264.1032	74496.77597	0.002050291
200	PWY-5484 glycolysis II_from fructose 6-phosphate	GLYCOLYSIS-metabolism																71668.80947	77877.14533										
201	PWY-5097 L-lysine biosynthesis VI	Amino-Acid-metabolism																97868.80647	106583.9309										
202	COBALSYN-PWY adenosylcobalamin salvage from cobinamide I	Cofactor-Biosynthesis																81373.92399	88889.5076										
203	MET-SAM-PWY superpathway of S-adenosyl-L-methionine biosynthesis	others																42888.25566	50914.50922										
204	PWY-6630 superpathway of L-tyrosine biosynthesis	Amino-Acid-metabolism													45915.74747	67587.37874	0.011950414	49634.43365	62942.95003								54594.35405	78914.26473	0.037438829
205	PWY-7663 gondoate biosynthesis_anaerobic	Lipid-Biosynthesis																110368.2079	119837.2085								112760.3634	140657.9064	0.01676893
206	PWY0-166 superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis_E.	Nucleic-Acid-metabolism																50532.19885	54678.97052								53439.3529	66688.21622	0.031940633
207	P4-PWY superpathway of L-lysine L-threonine and L-methionine biosynthesis I	Amino-Acid-metabolism																40084.57076	45329.68015										
208	GLYCOLYSIS glycolysis I_from glucose 6-phosphate	GLYCOLYSIS-metabolism																83787.55501	90360.43413										
209	PWY-6895 superpathway of thiamin diphosphate biosynthesis II	Cofactor-Biosynthesis																									32058.7494	45752.62503	0.02851834
210	PWY0-781 aspartate superpathway	others																34705.51806	39871.49844										
211	TRNA-CHARGING-PWY tRNA charging	others																89400.49025	98124.94085										
212	PWY-6892 thiazole biosynthesis I_E. coli	Cofactor-Biosynthesis																62381.72558	68528.11504								62093.23442	85765.20262	0.000820869
213	PWY-7003 glycerol degradation to butanol	Fermentation																8240.879028	5019.608455		10313.70267	8675.275525	0.010190453						
214	PWY-5154 L-arginine biosynthesis III_via N-acetyl-L-citrulline	Amino-Acid-metabolism																									45842.13151	58204.94029	0.049969902
215	PWY0-1415 superpathway of heme biosynthesis from uroporphyrinogen-III	Cofactor-Biosynthesis													4777.967385	9633.309875	0.038168795							7026.767707	9760.881521	0.03159816			
216	PWY-2942 L-lysine biosynthesis III	Amino-Acid-metabolism																99342.40013	109025.0731										
217	PWY-5347 superpathway of L-methionine biosynthesis_transsulfuration	Amino-Acid-metabolism																50671.21757	58949.24628										
218	PYRIDNUCSAL-PWY NAD salvage pathway I	Cofactor-Biosynthesis																71404.27289	75229.42885								72357.12036	85947.36554	0.012558958
219	PWY-6122 5-aminoimidazole ribonucleotide biosynthesis II	Nucleic-Acid-metabolism																92424.37588	100685.3471								96334.9483	116761.8659	0.032597321
220	PWY-5345 superpathway of L-methionine biosynthesis_by sulfhydrylation	Amino-Acid-metabolism																			18765.94338	13710.46826	0.007868194				16696.62421	17212.6805	0.045896457
221	TCA TCA cycle I_prokaryotic	TCA-pathway																									56316.43248	71807.98281	0.024960027
222	PWY-5677 succinate fermentation to butanoate	Fermentation																						5569.003489	7916.443517	0.034046173			
223	PWY0-162 superpathway of pyrimidine ribonucleotides de novo biosynthesis	Nucleic-Acid-metabolism																70618.59288	76519.002								72105.94782	95603.97797	0.007064922
224	RIBOSYN2-PWY flavin biosynthesis I_bacteria and plants	Cofactor-Biosynthesis													65914.33814	83191.14611	0.044088615	68686.4727	75540.10196								69393.57794	90582.53587	0.004027941
225	FOLSYN-PWY superpathway of tetrahydrofolate biosynthesis and salvage	Cofactor-Biosynthesis																									64132.52924	79852.38632	0.002563842
226	PWY-7111 pyruvate fermentation to isobutanol_engineered	Fermentation																117423.7004	126501.0328										
227	HISTSYN-PWY L-histidine biosynthesis	Amino-Acid-metabolism																82708.99424	90799.7859								88020.37513	106177.117	0.044611783
228	PWY-6749 CMP-legionaminate biosynthesis I	Carbohydrates-metabolism																30764.99043	32416.30048										
229	PEPTIDOGLYCANSYN-PWY peptidoglycan biosynthesis I_meso-diaminopimelate conta	Cell-Structure-Biosynthesis																88758.013	97463.42696										
230	PWY-5918 superpathay of heme biosynthesis from glutamate	Cofactor-Biosynthesis													7567.307825	18659.94523	0.044889464												
231	1CMET2-PWY N10-formyl-tetrahydrofolate biosynthesis	Cofactor-Biosynthesis													73775.30253	89619.4641	0.042301847	76301.09557	81343.07208								78219.39103	94730.09021	0.019403157
232	PWY-6876 isopropanol biosynthesis	others																						496.1444607	250.6059	0.04513692			
233	HOMOSER-METSYN-PWY L-methionine biosynthesis I	Amino-Acid-metabolism																32687.50586	39911.84919										
234	THRESYN-PWY superpathway of L-threonine biosynthesis	Amino-Acid-metabolism																92302.98839	100540.9474								96275.66439	118043.7851	0.021126122
235	PWY-6125 superpathway of guanosine nucleotides de novo biosynthesis II	Nucleic-Acid-metabolism																61880.26591	66928.86671								63549.28343	84139.79207	0.006836881
236	PWY-6897 thiamin salvage II	Cofactor-Biosynthesis													60233.3634	78508.97994	0.014629912	60611.86968	71990.47528								63091.90222	83214.42631	0.003811421
237	PWY-3001 superpathway of L-isoleucine biosynthesis I	Amino-Acid-metabolism																95239.48331	104273.2102								99315.04476	120828.4583	0.031616436
238	PWY-6126 superpathway of adenosine nucleotides de novo biosynthesis II	Nucleic-Acid-metabolism																99630.71863	107291.5384										
239	PWY-7187 pyrimidine deoxyribonucleotides de novo biosynthesis II	Nucleic-Acid-metabolism																50941.12093	56073.42881								53888.38241	67795.07488	0.02989533
240	PWY-6507 4-deoxy-L-threo-hex-4-enopyranuronate degradation	SECONDARY-METABOLITE-metabolism																									62910.48375	79345.1297	0.015475513
241	PWY-5686 UMP biosynthesis	Nucleic-Acid-metabolism																99537.57067	108595.1773										
242	GLUCONEO-PWY gluconeogenesis I	Carbohydrates-metabolism																83421.76768	89131.39534								86219.07931	103751.4103	0.020630702
243	FASYN-ELONG-PWY fatty acid elongation - saturated	Lipid-Biosynthesis																									70298.29266	90351.22591	0.03251258
244	COA-PWY coenzyme A biosynthesis I	Cofactor-Biosynthesis																82602.21826	89929.67726								84438.20767	102783.0666	0.023506691
245	PWY-6147 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	Cofactor-Biosynthesis																52754.6362	60727.69791								52320.88567	74391.49713	0.000157459
246	ARO-PWY chorismate biosynthesis I	AROMATIC-COMPOUNDS-metabolism																90642.91733	99760.28618										
247	PWY-7013 L-1_2-propanediol degradation	others													3864.464615	7129.300255	0.012030049												
248	SER-GLYSYN-PWY superpathway of L-serine and glycine biosynthesis I	Amino-Acid-metabolism																91639.92546	96921.89221										
249	PWY-6387 UDP-N-acetylmuramoyl-pentapeptide biosynthesis I_meso-diaminopimela	Cell-Structure-Biosynthesis																89768.64399	98643.0142										
250	POLYISOPRENSYN-PWY polyisoprenoid biosynthesis_E. coli	Polyprenyl-Biosynthesis													52234.42271	69383.17194	0.04672336	57846.65513	60648.56597								57793.70423	73067.23022	0.006290923
251	PWY-6969 TCA cycle V_2-oxoglutarate:ferredoxin oxidoreductase	TCA-pathway																									68484.30282	86254.39173	0.012808275
252	PWY-6385 peptidoglycan biosynthesis III_mycobacteria	Cell-Structure-Biosynthesis																88346.72264	97054.89718										
253	COLANSYN-PWY colanic acid building blocks biosynthesis	Carbohydrates-metabolism																									46284.89271	55700.20845	0.027213815
254	ASPASN-PWY superpathway of L-aspartate and L-asparagine biosynthesis	Amino-Acid-metabolism													77729.01753	100897.4372	0.021124917	79040.09806	87792.25845								82058.66372	107009.4357	0.016148231
255	PWY-7197 pyrimidine deoxyribonucleotide phosphorylation	Nucleic-Acid-metabolism																									45166.26971	63431.71461	0.008031059
256	PWY-841 superpathway of purine nucleotides de novo biosynthesis I	Nucleic-Acid-metabolism																70174.04936	75920.91								72305.49001	93625.34145	0.008405066
257	ANAEROFRUCAT-PWY homolactic fermentation	Fermentation																74590.32757	81144.9334										
258	PWY-7219 adenosine ribonucleotides de novo biosynthesis	Nucleic-Acid-metabolism																103058.9613	112913.5318										
259	PWY-5509 adenosylcobalamin biosynthesis from cobyrinate a_c-diamide I	Cofactor-Biosynthesis																77536.27038	83909.82463										
260	PWY-6588 pyruvate fermentation to acetone	Fermentation																									18220.01778	18528.58079	0.017401531
261	PWY-7400 L-arginine biosynthesis IV_archaebacteria	Amino-Acid-metabolism																63680.11959	74947.75914										
262	GALACTUROCAT-PWY D-galacturonate degradation I	CARBOXYLATES-DEG													45156.88751	57195.54321	0.042543385												
263	DENOVOPURINE2-PWY superpathway of purine nucleotides de novo biosynthesis II	Nucleic-Acid-metabolism																71552.83094	77576.17899								73939.79314	95386.44281	0.008822137
264	PANTO-PWY phosphopantothenate biosynthesis I	Cofactor-Biosynthesis																60830.77638	66027.67957					64179.76164	66016.29629	0.026602399	61359.41451	79283.88689	0.005144387
265	PWY-5104 L-isoleucine biosynthesis IV	Amino-Acid-metabolism													101257.2342	117478.2367	0.044944312	99926.06424	109868.6571										
266	PWY-7228 superpathway of guanosine nucleotides de novo biosynthesis I	Nucleic-Acid-metabolism																57745.94849	62498.68379								58876.40558	79441.31966	0.0058365
267	PWY1G-0 mycothiol biosynthesis	Cofactor-Biosynthesis																									9.870321429	6.561776471	0.011110496
268	NONOXIPENT-PWY pentose phosphate pathway_non-oxidative branch	others																129972.3864	141324.9144										
269	PWY-6121 5-aminoimidazole ribonucleotide biosynthesis I	Nucleic-Acid-metabolism																94299.25652	102431.2555								98136.90001	118739.5075	0.034072848
270	PWY-1861 formaldehyde assimilation II_RuMP Cycle	C1-COMPOUNDS																6734.329382	3930.444374										
271	DTDPRHAMSYN-PWY dTDP-L-rhamnose biosynthesis I	Carbohydrates-metabolism																90664.31011	95601.83441										
272	RHAMCAT-PWY L-rhamnose degradation I	Carbohydrates-metabolism																									37026.58486	48913.2717	0.002010242
273	TEICHOICACID-PWY teichoic acid_poly-glycerol biosynthesis	Cell-Structure-Biosynthesis																5875.184786	4365.467367										

274	**ARGSYN-PWY L-arginine biosynthesis I_via L-ornithine**	Amino-Acid-metabolism																63627.33773	74945.62203										
275	**NONMEVIPP-PWY methylerythritol phosphate pathway I**	SECONDARY-METABOLITE-metabolism																90082.36824	100367.946								94370.47783	115659.1963	0.033981653
276	**PWY-5920 superpathway of heme biosynthesis from glycine**	Cofactor-Biosynthesis																2501.730653	2330.042082		2922.208624	1860.21609	0.00462001						
277	**PWY-6163 chorismate biosynthesis from 3-dehydroquinate**	AROMATIC-COMPOUNDS-metabolism																89048.71359	98281.16296										
278	**PWY-7184 pyrimidine deoxyribonucleotides de novo biosynthesis I**	Nucleic-Acid-metabolism																43802.85656	47512.68089								45487.40396	58922.26163	0.017006294
279	**GLUTORN-PWY L-ornithine biosynthesis**	Amino-Acid-metabolism																57629.97092	66759.27001										
280	**PWY4FS-7 phosphatidylglycerol biosynthesis I_plastidic**	Lipid-Biosynthesis																84483.21838	90449.77685										
281	**PWY4FS-8 phosphatidylglycerol biosynthesis II_non-plastidic**	Lipid-Biosynthesis																84483.21838	90449.77685										
282	**OANTIGEN-PWY O-antigen building blocks biosynthesis_E. coli**	Carbohydrates-metabolism																67379.57713	73401.24867										
283	**PWY-7242 D-fructuronate degradation**	CARBOXYLATES-DEG																									68394.0724	86939.81083	0.016783634
284	**PWY-6383 mono-trans poly-cis decaprenyl phosphate biosynthesis**	Cofactor-Biosynthesis																									77.31607679	204.3712667	0.000668393
285	**ANAGLYCOLYSIS-PWY glycolysis III_from glucose**	GLYCOLYSIS-metabolism																102203.9995	109308.7959										
286	**CODH-PWY reductive acetyl coenzyme A pathway**	C1-COMPOUNDS													4557.304422	9828.429407	0.001788726							5377.620936	12751.77708	0.045161057			

Table 16 Summary of the statistical results of correlations between bacterial taxa and clinical phenotypes according to spearman's rank correlations analysis

age bracket 1 (11~23 mo)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value										NA																	
		RHO										NA																	
	g__Faecalibacterium	p-value		0.027687094	0.047986133		0.049834392	0.024854641				NA																	
		RHO		-0.335832478	-0.303355448		-0.301000538	-0.341846693				NA																	
	f__Ruminococcaceae|__	p-value										NA																	
		RHO										NA																	
age bracket 2 (24~35 mo)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value										NA																	
		RHO										NA																	
	g__Faecalibacterium	p-value		0.027687094	0.047986133		0.049834392	0.024854641				NA																	
		RHO		-0.335832478	-0.303355448		-0.301000538	-0.341846693				NA																	
	f__Ruminococcaceae|__	p-value										NA																	
		RHO	-0.152312485		-0.09632954		-0.136631658	-0.103938877				NA																	
	g__Veillonella	p-value	0.003272914		0.021369618		0.014962299	0.007493989				0.045380713																	0.017556272
		RHO	0.22631108		0.177999225		0.188023375	0.206244236				-0.155077107																	0.183585277
	g__Hungatella	p-value	0.005841154		0.032457505	0.041947252	0.02758148	0.025209096	0.039055395							0.018098351													
		RHO	0.212464438		0.16559932	0.157597685	0.170517981	0.173185736	0.159858651							0.18273062													
age bracket 3 (36~47 mo)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value	0.010334006	0.02728472	0.041519736		0.021226242	0.022478636				NA										0.00063882							0.012210828
		RHO	0.162579124	0.140186654	0.129540894		0.146251422	0.144885137				NA										0.215363724							0.158920956
	_Lachnospiraceae_UCG-(	p-value										NA																	
		RHO										NA																	
	g__Lachnospira	p-value										NA																	
		RHO										NA																	
	g__Haemophilus	p-value										NA															0.007781702		
		RHO										NA															-0.168638812		
	g__Faecalibacterium	p-value	0.000446609	0.009442127	0.001048164	0.007611341	0.000109407	0.004966951	0.014938248	0.020106626		NA	0.032822465						0.010690898			0.004970431							
		RHO	-0.22128943	-0.164528315	-0.206895779	-0.169103681	-0.243194392	-0.177856558	-0.154403184	-0.147533276		NA	-0.135583456						-0.161840639			-0.177842513							
	f__Ruminococcaceae|__	p-value	0.005326731		0.010324175		0.001350352	0.003227718				NA							0.01346329	0.027459866		0.00036586		0.010747771	0.011083517				0.023332738
		RHO	-0.176449022		-0.162599784		-0.202432864	-0.186319717				NA							-0.156746674	-0.140029305		-0.224524636		-0.161724978	0.161052983				-0.143990621
age bracket 4 (4~5 y)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value	0.000163002		0.004944235	0.000219451	0.00284851	0.042897784	0.001122821	0.021169315					0.019435946	0.000418737			0.020597194	0.001779889		0.022341355		0.019435975				0.004340748	0.004321608
		RHO	0.266141363		0.200007093	0.261042709	0.21204393	0.14478487	0.231021261	0.164567863					-0.16682853	0.249595127			0.165295715	0.221824157		0.163128375		0.166828491				0.202908145	0.203005956
	g__Romboutsia	p-value																	0.039652081	0.012567623		0.041451638				0.012801366			
		RHO									-0.020476962	0.027302803							-0.147094482	-0.177983606		-0.145795126				-0.177524362			
	_Lachnospiraceae_UCG-(	p-value										0.037116591				0.032987498							0.018655869						
		RHO									0.012618657					-0.152386622							-0.167903419						
	g__Bifidobacterium	p-value									0.03023592					0.043287744									0.031694157				
		RHO									0.154840394					0.144517348									0.153517375				
	f__Enterobacteriaceae|__	p-value	0.000635299		0.006097449	0.005391089	0.022739241	0.001200286					0.041747669		0.029272271				0.012953255	0.004065467	0.037871871								
		RHO	-0.241918449		-0.195252329	-0.198057322	-0.162654502	-0.229711521					-0.145585941		-0.155744858				-0.177229872	-0.204353918	-0.148429687								
age bracket 5 (5~6 y)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value	0.000172909		8.91E-06	0.000125347	8.80E-07	0.000241858	0.003043003	0.001522625	0.01358723		0.044645541	0.032735706		0.024576603			0.014354229	0.013500822						0.006859331		0.032905522	0.004455996
		RHO	0.270584456		0.317665289	0.276111204	0.349537541	0.26469007	0.215025466	0.229653847	0.179727531		0.146632315	0.155820194		0.163934331			0.178314608	0.179891058						0.196563667		0.155670575	0.206551493
	g__Romboutsia	p-value									0.006666014																		
		RHO									0.197239823																		
	g__Incertae_Sedis	p-value									0.030802427																		
		RHO									0.157571782																		
	g__Granulicatella	p-value		0.009174054		0.042586269																							0.002550278
		RHO		-0.189563685		0.148059877																							0.218845772
	g__Blautia	p-value	0.000266094		0.002849922	0.001689939	0.000613302	0.010568068	0.012466922	0.049469151											0.030492651								0.000244429
		RHO	-0.262987632		-0.216450631	-0.227508877	-0.247591896	-0.186073673	-0.181922426	-0.143492437											-0.157861093								-0.264502092
	g__Actinomyces	p-value									0.014142236																		
		RHO									0.178698389																		
age bracket 6 (6~7 y)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Roseburia	p-value												0.04601093											0.00416546				
		RHO												-0.170779703											-0.243342231				
	g__Lachnospira	p-value											0.034931834			0.042560584												0.04426377	0.031525986
		RHO											0.180368661			-0.173536596												0.172153301	-0.183834146
	g__Escherichia-Shigella	p-value	0.009867845		0.010172776	0.025957426	0.006634712	0.006544232							0.045236731				0.045702659	0.009284724	0.006064301			0.042132101					0.009844617
		RHO	-0.219772163		-0.21889758	-0.19025447	-0.23090058	-0.231276622							-0.171382908				-0.171018867	-0.221513119	-0.233352147			-0.173891874					0.219839754
	f__Enterobacteriaceae|__	p-value	0.000412011		0.000369018	0.000762577	0.001748632	0.000126086	0.000178272	0.000101272			0.000905766	0.019204929		0.008982851													
		RHO	-0.297639929		-0.29997336	-0.284228982	-0.265035356	-0.321752985	-0.314909697	-0.32600016			-0.280360078	-0.199858856		-0.222452625													
age bracket 7 (7~8 y)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Lachnospira	p-value							0.034124721	0.038782383				0.036416246															NA
		RHO							0.250073559	0.244112664				0.247061397															NA
	g__Granulicatella	p-value	0.034507439		0.036945393	0.016621811	0.03857284													0.008219021	0.033813583			0.039318235					NA
		RHO	0.24955896		0.246388401	0.281444407	0.244367666													0.309211669	0.250495483			0.243465735					NA
	f__Enterobacteriaceae|__	p-value	5.84E-05	0.000781838	0.000315612	0.001005487	0.000190234	0.001906104						0.013087828					0.022441162	0.004313786	0.037123197		0.032336246		0.02645667			0.039702088	NA
		RHO	-0.455389195	0.387099414	-0.412653602	-0.379634681	-0.426077158	-0.359826216						-0.291162186					-0.268765577	-0.332566169	-0.246164064		-0.252544331		-0.261569555			-0.2430068	NA
age bracket 8 (8~9 y)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Parabacteroides	p-value										NA									0.013942065	0.043959743							
		RHO										NA									0.326856947	-0.270258826							
	g__Granulicatella	p-value	0.024638631		0.03241908	0.021064291	0.039260266	0.040634065				NA																	
		RHO	0.300082041		0.28630686	0.307683193	0.276316328	0.274486408				NA																	
	g__Escherichia-Shigella	p-value			0.035998562	0.010877404						NA																	
		RHO			-0.280882629	-0.337854377						NA																	
age bracket 9 (9 y ~)	microbial taxa		Group	age	ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_3_months
	g__Veillonella	p-value																								0.036442666			
		RHO																								-0.20347036			
	chnospiraceae_NK4A136_	p-value	0.003784307		0.004069278	0.009636008	0.003171907	0.003942247	0.007657618	0.005558386															0.003656619				
		RHO	-0.278948138	0.151092285	-0.276832759	-0.250379882	-0.284025484	-0.277758794	-0.257688485	-0.267557781															-0.279942628				
	g__Hungatella	p-value													0.045716278										0.044290493	0.047770437	0.04365623		
		RHO													-0.194511837										0.195784193	0.192735445	0.196361175		
	g__Haemophilus	p-value																							0.007490661				
		RHO																							-0.258379184				
	g__Butyricicoccus	p-value	0.003263148	0.003326781	0.013588101	0.04204303	0.006269931	0.019516255	0.046622207	0.044864538			0.011111268																
		RHO	-0.28321601	0.282663417	-0.239058639	-0.197860776	-0.263889253	-0.226573758	-0.193720416	-0.195267884			-0.245746407																
	g__Actinomyces	p-value	1.95E-05		0.001128811	0.000823771	0.00069618	0.00522082																					
		RHO	0.401950883		0.312041878	0.320069028	0.324268488	0.269446558																					
	f__Enterobacteriaceae|__	p-value						0.017883777																					
		RHO						-0.229642099																					

≤ 3 y	microbial taxa		ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	_allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_1_m	biotic_within_3_months
	g__Veillonella	p-value	0.006725048		0.005147455	0.001534367																		0.043193553			0.003705801
		RHO	0.186488507		0.192398132	0.217298677																		0.139668815			0.19944363
	g__Hungatella	p-value	0.021875579	0.025931035	0.027023573	0.013916187						0.032255558	0.027618045														
		RHO	0.158146076	0.153697377	0.152601766	0.169497933						-0.147828421	0.152021481														

> 3 y	microbial taxa		ASD_score	Repetitive_behavi	Social_retardation	inguage_retardati	any_GI_problem	GI_problem_score	esophageal_reflu	peptic_ulcer	dyspepsia	dominal_distensi	abdominal_pain	constipation	rmal_stool_consis	within_1_months	y_sleep_complai	ep_complaints_sc	ficulty_falling_asle	leep_fragmentati	ort_sleep_duratic	Shallow_sleep	y_neonatal_asphy	allergy_or_intole	skin_allergy	ratory_hypersens	biotic_within_1_m	biotic_within_3_m	istory_of_mental	mother_during_pr	mber_of_pregnan	umber_of_parturiti	sisted_reproducti	king_during_preg	tion_during_preg	king_during_preg	ampsia/preeclam	fathe_during_pregnancy
	g__Veillonella	p-value	1.22E-08	1.11E-08	3.81E-10	1.03E-07	3.97E-05	0.000558253	0.034072854		0.020826647			0.022123163			0.00035648	0.000265439		0.000639044				0.001117835		0.000267152		6.09E-06			0.005190309		0.014937313					
		RHO	0.178288981	0.178803634	0.195648767	0.16672583	0.129115148	0.108567454	0.0667903		0.072823066			0.072104452			0.11229528	0.114686142		0.107421261				0.102558044		0.114634473		0.141997137			0.088015602		0.076680842					
	g__uncultured	p-value	1.15E-06	1.99E-06	3.88E-08	1.92E-06	5.62E-06	7.23E-05				0.006769435		0.009200652			0.027103413	0.01303635		0.014533224				3.24E-06		0.02530305		9.54E-07	0.037057309	0.030470145	0.0299083		0.047714533	0.042750858				
		RHO	-0.152576929	-0.149163075	-0.172122487	-0.149406295	-0.142524195	-0.124726429				-0.085286061		-0.082038496			-0.069645727	-0.078216132		-0.076992167				-0.146076245		-0.070485661		-0.153711739	-0.065718671	-0.077538402	-0.068428331		-0.062408697	0.063863096				
	g__Romboutsia	p-value																					0.005068036	0.003284609								0.029063149				0.031609898		
		RHO																					-0.088257079	-0.09255591								0.068784432				-0.06773681		
	_Lachnospiraceae_UCG-(	p-value																										0.007921016										0.045424469
		RHO																		0.003106686								-0.083636558										-0.071983385
	chnospiraceae_NK4A136_	p-value	0.000107058	4.74E-05	0.000133313	0.000117866	5.43E-05	0.000338031	0.016164358		0.008105313			0.006373761				0.016136704		0.01980861			0.001098903	0.000126775	0.030086509			7.12E-06			0.000612055							
		RHO	-0.121777121	-0.127831171	-0.120099675	-0.121044226	-0.126844414	-0.112729527	-0.075778874		-0.083392777			-0.085911368				-0.075798528					-0.102709639	-0.120486149	-0.068354348			-0.14096089			-0.107788382							
	g__Lachnospira	p-value	0.016037938	0.020955276	0.006077122		0.01816125	0.026979943			0.039994393				0.00225304											0.013178601					0.035888213							
		RHO	0.075868968	0.072750059	0.086403472		0.074431998	0.069701769			0.064733455				0.096157295											0.078094628					-0.066129381							
	g__Hungatella	p-value					0.011082208	0.049662483						0.00017637																0.000873386								0.001284819
		RHO					0.080016222	0.061872535						0.117927147																0.119020179								0.115590663
	g__Haemophilus	p-value												0.020086954									0.001879333															
		RHO												-0.073250682									-0.097848786															
	g__Granulicatella	p-value													0.006294614					0.031927786										0.024194705								0.021293225
		RHO													-0.086040619					0.067611173										0.080756508								0.082815669
	g__Flavonifractor	p-value																									0.044924614			0.031797279								
		RHO																		-0.002027903							0.063209552			0.076931971								
	g__Faecalibacterium	p-value	1.34E-07	1.29E-05	9.87E-08	6.12E-08	1.13E-05	0.000178396			0.010922468			0.006311781			0.000542952	0.001285583		0.004949218			0.049548781		0.012675317			0.004613098			1.03E-07	6.45E-05						0.006290662
		RHO	-0.165247377	-0.136996737	-0.166961942	-0.169618534	-0.137873377	-0.117837712			-0.080175535			-0.086012462			-0.10880178	-0.101309659		-0.088496825			-0.061903342		-0.078529849			-0.089204336			-0.166749145	-0.125577505						-0.098192923
	g__Escherichia-Shigella	p-value	0.00728248		0.048314371	0.001302463				0.016509815	0.021146646	0.016412771																0.037013264										
		RHO	-0.084522382		-0.062241669	-0.101192494				0.075535798	-0.07264216	-0.075603627																0.065733943										
	g__Blautia	p-value	1.52E-11	1.81E-11	1.35E-12	1.04E-10	3.07E-07	5.32E-06			0.01815424	0.012462311		0.000748485			0.005483487	0.000714095		0.019458019			0.018432278	0.005008505				0.000179984			2.59E-11	7.23E-06						
		RHO	-0.210449089	-0.209687798	-0.220893999	-0.201763306	-0.160470376	-0.142875422			-0.074436495	-0.078718663		-0.106066654			-0.087456873	-0.106471324		-0.073625202			-0.074259308	-0.088376556				-0.117768263			-0.208079557	-0.140859295						
	g__Anaerostipes	p-value																	0.02374042		0.037995187										0.048235114							
		RHO																	0.07125765		0.065397079										-0.062263638							
	g__Actinomyces	p-value										0.00208741												0.016672525	0.020143993	0.013771924												
		RHO										-0.096872577												-0.075422851	-0.073217224	-0.077600006												
	f__Ruminococcaceae|__	p-value	0.000402795	0.001173746	4.32E-06	0.003279321												0.000112136		5.71E-05				0.02551734				1.23E-05			0.007572474							
		RHO	-0.111291283	-0.102123806	-0.144232759	-0.092571558												-0.121424488		-0.126466927				-0.070383031				-0.137306589			-0.084111802							
	f__Enterobacteriaceae|__	p-value	7.93E-12	1.49E-09	1.41E-10	1.87E-13	0.021674246	0.002772309			0.000844889	0.010506188					0.010279318	0.000752318	0.037271146		0.002145261				0.004776802	0.000513482				0.0148642	0.005893803	0.001199014			0.002487602			
		RHO	-0.213317916	-0.189039255	-0.200345689	-0.229054899	-0.072349026	-0.094190639			-0.105017883	-0.080600632					-0.080838645	-0.106022619	-0.065644744		-0.096617025				-0.088854131	-0.109270943				-0.087240626	-0.086718499	-0.101933791			-0.095222569			

Table 17 Summary of the statistical results of correlations between GBMs and clinical phenotypes according to spearman's rank correlations analysis

			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 1 (11~23 mo)	MGB025 Nitric oxide synthesis I (NO synthase)	p-value										NA														0.0142611			
		RHO										NA														-0.371194			
	MGB004 Kynurenine synthesis	p-value	0.0398539						0.0148358	0.006618		NA	0.0128595			0.0180647	0.0396495		0.0131474	0.0058668		0.0161615							
		RHO	-0.314685						-0.36919	-0.407942		NA	-0.376386			-0.359018	-0.314993		-0.375282	-0.413362		-0.364807							
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 2 (24~35 mo)	MGB050 Glutamate degradation I	p-value	0.0006428			0.013211	0.0357678													0.043013				0.0243176					
		RHO	0.2614528			0.191417	0.1626071													0.1567974				0.1742441					
	MGB047 Acetate degradation	p-value								0.0452591		0.0062537				0.0288911							0.0127874						
		RHO								0.1551636		0.2107774				0.1691284							0.1922967						
	MGB045 Acetate synthesis III	p-value	0.004519			0.0234473											0.0409295			0.028861		0.0387396							
		RHO	0.2187003			0.1753099											0.1583781			0.1691597		0.160114							
	MGB028 Nitric oxide degradation II (NO reductase)	p-value	0.0399588																										0.0153316
		RHO	0.1591376																										0.1873524
	MGB009 Histamine synthesis	p-value																									0.0038128		
		RHO																									-0.22274		
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 3 (36~47 mo)	MGB055 Propionate synthesis III	p-value	0.0160898		0.0340283		0.0077929	0.0169971				NA																	
		RHO	0.1527106		0.13467		0.1686086	0.15145				NA																	
	MGB051 Glutamate degradation II	p-value	0.0291039			0.0356219		0.019125			0.0043015	NA											0.0394732				0.009201	0.0393983	
		RHO	-0.138593			-0.133504		-0.148709			-0.180721	NA											-0.130859				-0.165083	-0.130908	
	MGB045 Acetate synthesis III	p-value	0.0351219			0.0373082	0.0324105					NA											0.0162142						
		RHO	-0.133865			-0.132317	-0.135902					NA											-0.152534						
	MGB044 Acetate synthesis II	p-value	3.04E-06		1.79E-05	0.000479	2.52E-05	2.24E-06				NA			0.0088695				0.0360077										
		RHO	-0.291454		-0.268715	-0.220142	-0.264079	-0.295137				NA			-0.165868				-0.133228										
	MGB034 Isovaleric acid synthesis I (KADH pathway)	p-value	0.0129666		0.007482		0.0013108	0.0118023				NA	0.0030421							0.0400233				0.0252811					
		RHO	0.1575868		0.1694629		0.2029619	0.1596728				NA	0.1874557							0.1304991				0.1420513					
	MGB031 17-beta-Estradiol degradation	p-value										NA																	
		RHO										NA																	
	MGB028 Nitric oxide degradation II (NO reductase)	p-value	0.0267118				0.0267881					NA										0.0008424							0.0248289
		RHO	0.1407075				0.1406376					NA										0.2106728							0.1424896
	MGB025 Nitric oxide synthesis I (NO synthase)	p-value										NA	0.0384311											0.0445916					
		RHO										NA	-0.131552											-0.127662					
	MGB024 DOPAC synthesis	p-value	0.0001037		2.92E-05	0.002628	3.36E-06	0.0002247	0.0069832	0.0165879		NA	0.0060596																
		RHO	-0.243995		-0.26209	-0.190234	-0.290194	-0.232243	-0.170902	-0.152011		NA	-0.173828																
	MGB004 Kynurenine synthesis	p-value	9.80E-05		1.08E-05	3.18E-05	3.78E-06	0.0003633	0.0003167	0.0001859	0.0468141	NA	0.000364						0.0245503	0.0126512						0.0244402	0.0305092		
		RHO	-0.244819		-0.275446	-0.260886	-0.288743	-0.224637	-0.226835	-0.235181	-0.126369	NA	-0.224607						-0.142763	-0.158135						-0.142872	-0.137419		
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 4 (4~5 y)	MGB056 Propionate degradation I	p-value	0.0008348		0.0073273	0.0116206	0.0253713	0.0021939												0.0084768					0.0321418				
		RHO	-0.236756		-0.190997	-0.179925	-0.159688	-0.217526												-0.187561					-0.153122				
	MGB051 Glutamate degradation II	p-value	0.020523		0.0028524		0.0144195	0.0003241										0.024387											
		RHO	-0.165391		-0.212015		-0.174533	-0.254199										0.1607651											
	MGB037 Inositol synthesis	p-value			0.0179683		0.0118131	0.0279198																					
		RHO			0.1688836		0.1795192	0.1570581																					
	MGB026 Nitric oxide synthesis II (nitrite reductase)	p-value																									0.0100936		
		RHO																									-0.18337		
	MGB016 p-Cresol degradation	p-value	0.0004452		0.0021331	0.001352	0.0076852	0.0015232		0.0421038			0.0128944		0.0254399				0.0129613	0.0047389		0.0452481							
		RHO	-0.24848		-0.218109	-0.227356	-0.189879	-0.224973		-0.145336			-0.177344		-0.159615				-0.177214	-0.200957		-0.143202							
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 5 (5~6 y)	MGB050 Glutamate degradation I	p-value	0.0003137		0.0038058	0.0017376	0.0035005	0.0067443	0.0015087	0.0040276						0.0317619										0.019358			0.030689
		RHO	0.2600242		0.2100942	0.2269336	0.2119504	0.1969639	0.2298424	0.2088281						0.1566912										0.1704441			0.1576774
	MGB049 Tryptophan degradation	p-value																										0.0466748	
		RHO																										-0.145279	
	MGB043 Acetate synthesis I	p-value	0.0039431		0.0086393	0.0029393	0.030717	0.0075659	0.0090211	0.0066068				0.0064779	0	0.0271847			0.0010732	0.0001538	0.0001776	0.0111842				0.0023802			
		RHO	0.209303		0.1910282	0.2157801	0.1576513	0.1942288	0.1899747	0.1974506				0.1979149	0.1168593	0.1611179			0.2367118	0.2726157	0.2701232	0.1846594				0.220321			
	MGB040 Menaquinone synthesis (vitamin K2) I	p-value	0.0008716		0.02097		0.0028633	0.0275163								0.0083628			0.0290451							0.017702			
		RHO	0.2408143		0.1682863		0.2163495	0.1607766								0.1918175			0.1592472							0.1728297			
	MGB038 Inositol degradation	p-value																										0.0189793	
		RHO																										-0.170974	
	MGB036 S-Adenosylmethionine (SAM) synthesis	p-value	0.0182118		0.0176625	0.0037157		0.0157211	0.020017	0.0234249						0.0385268			0.0039261	0.0008989	0.0006982	0.014798				0.0074475			
		RHO	0.1720754		0.1728889	0.2106275		0.1759528	0.1695438	0.1652606						0.1510527			0.2093999	0.2402116	0.2451145	0.1775271				0.1946059			
	MGB028 Nitric oxide degradation II (NO reductase)	p-value	0.008945		0.003061	0.0088299	8.40E-05	0.0439939	0.0185271	0.0145586	0.044207			0.0117625					0.029729							0.0440145			0.0261462
		RHO	0.1901814		0.2148969	0.1904974	0.2828199	0.147078	0.171618	0.1779494	0.1469316			0.1833931					0.1585851							0.1470638			0.1622104
	MGB027 Nitric oxide degradation I (NO dioxygenase)	p-value	1.75E-07		2.74E-06	4.20E-08	3.47E-07	0.0001718	0.0229964	0.0310844	0.0311354								0.0013267	0.0023134	0.0286621	0.0320033				0.0058124			0.0368957
		RHO	0.3698582		0.3343265	0.3867426	0.3614174	0.2706954	0.1657683	0.1573106	0.1572636								0.2324577	0.2209272	0.1596237	0.1564732				0.2004521			0.1523306
	MGB016 p-Cresol degradation	p-value	0.0207853		0.0074035	0.0446755	0.0243883	0.0019968																					
		RHO	-0.168526		-0.194748	-0.146612	-0.164147	-0.224035																					
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 6 (6~7 y)	MGB056 Propionate degradation I	p-value	1.50E-05		2.40E-05	4.10E-05	7.05E-05	5.67E-06	0.0089011	0.0073955																			
		RHO	-0.360595		-0.352493	-0.342916	-0.332882	-0.376811	-0.222712	-0.227907																			
	MGB055 Propionate synthesis III	p-value	0.0493458	0.0401901		0.044003	0.045666						0.0326962																
		RHO	0.1682742	0.1755411		0.1723622	0.1710474						0.1826092																
	MGB051 Glutamate degradation II	p-value	0.0013628		0.0020339	0.005953	0.0026154	0.0003569						0.0456722						0.0436902				0.0398049					0.0475795
		RHO	-0.270947		-0.261386	-0.233854	-0.2552	-0.300675						-0.171043						-0.172614				-0.175876					0.169583
	MGB048 Propionate synthesis I	p-value	0.023917		0.0199592		0.0255234	0.0093117																					0.0078937
		RHO	-0.192905		-0.198653		-0.190803	-0.221431																					0.2260922
	MGB045 Acetate synthesis III	p-value																							0.005125				
		RHO																							-0.237877				
	MGB043 Acetate synthesis I	p-value																							0.0034131				
		RHO																							-0.248485				
	MGB036 S-Adenosylmethionine (SAM) synthesis	p-value	0.0294851					0.0195682																	0.0016909				
		RHO	0.186066					0.1992732																	-0.265839				
	MGB035 Isovaleric acid synthesis II (KADC pathway)	p-value	0.0422459					0.0496042																	0.0021843				
		RHO	0.1737972					0.168086																	-0.259646				
	MGB034 Isovaleric acid synthesis I (KADH pathway)	p-value	0.025597		0.0259396	0.0109852		0.017872												0.0459193									
		RHO	0.1907093		0.1902768	0.2166754		0.2020933												-0.170851									
	MGB033 Quinolinic acid degradation	p-value						0.0132316																	0.0011218				0.0081791
		RHO						0.2112067																	-0.275472				-0.225097
	MGB032 Quinolinic acid synthesis	p-value						0.0352352																	0.0013163				0.0030797
		RHO						0.1800741																	-0.27176				-0.251098
	MGB031 17-beta-Estradiol degradation	p-value		0.0456749																					0.0006124				0.0107377
		RHO		-0.171041																					-0.289082				-0.217337
	MGB029 ClpB (ATP-dependent chaperone protein)	p-value																							0.0011179				0.0122805
		RHO																							-0.275553				-0.213414
	MGB020 GABA synthesis I	p-value	0.0165376		0.0165125	0.0390935	0.0227423	0.0069953		0.0441976																			0.0119546
		RHO	-0.20448		-0.204527	-0.176502	-0.19452	-0.229446		-0.172206																			0.2142052
	MGB016 p-Cresol degradation	p-value	0.0001693		0.0001262	0.0002151	0.0007901	4.58E-05	0.0008321	0.0003071			0.0032617	0.0151466		0.0080974											0.0329357		
		RHO	-0.315935		-0.321738	-0.311125	-0.283437	-0.340893	-0.282274	-0.303816			-0.249642	-0.207153		-0.225379											-0.182363		
	MGB010 Histamine degradation	p-value	0.0021542		0.0019969	0.0020725	0.0076641	0.0008788	0.0002637	0.0001719			0.0029381	0.0201743		0.0149816											0.041253		
		RHO	-0.259985		-0.261832	-0.260929	-0.226915	-0.281043	-0.306969	-0.315638			-0.252286	-0.198317		-0.207484											-0.17463		
	MGB007 Glutamate synthesis II	p-value						0.040185																	0.0061421				0.0229648
		RHO						0.1755455																	-0.233006				-0.194209
	MGB006 Glutamate synthesis I	p-value																							0.0012189				0.0184485
		RHO																							-0.273552				-0.20111
	MGB005 Tryptophan synthesis	p-value	0.0072223		0.0082267	0.0190843	0.0091075	0.0049111																	0.023562				
		RHO	0.2285639		0.2249345	0.2000555	0.2220613	0.2390112																	-0.193385				
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 7 (7~8 y)	MGB056 Propionate degradation I	p-value	5.64E-05	0.0210248	0.0003076	0.0003005	0.000162	0.0043835	0.0182227	0.0375506	0.0329659			0.0458867		0.0173249			0.00073	0.0011044									NA
		RHO	-0.456197	0.2715667	-0.413346	-0.413975	-0.430223	-0.332007	-0.277619	-0.245628	-0.251662			-0.236077		-0.279727			-0.389105	-0.376804									NA
	MGB051 Glutamate degradation II	p-value	0.0394777													0.0482867													NA
		RHO	-0.243275													-0.233594													NA
	MGB048 Propionate synthesis I	p-value	0.0248946	0.0107709			0.0450956							0.0442019															NA
		RHO	-0.264251	0.2988539			-0.236918							-0.237884															NA
	MGB023 Dopamine degradation	p-value			0.0263628	0.0200953	0.0279382																				0.0013967		NA
		RHO			-0.261727	-0.273494	-0.259147																				-0.369611		NA
	MGB021 GABA synthesis II	p-value	0.0036683		0.0037576	0.0174583	0.0045049	0.0018186												0.0182653					0.0070292				NA
		RHO	-0.338169		-0.337344	-0.279408	-0.33105	-0.361324												-0.277521					-0.315043				NA
	MGB020 GABA synthesis I	p-value	0.0046833	0.0155844	0.0176629		0.0075862	0.0365469																					NA
		RHO	-0.329686	0.2840962	-0.278923		-0.312214	-0.246894																					NA
	MGB016 p-Cresol degradation	p-value	8.01E-05	0.0023198	0.0001667	0.0002192	6.64E-05	0.0018773						0.0487688					0.022002	0.0116687					0.0424672				NA
		RHO	-0.44779	0.3534851	-0.429484	-0.422371	-0.452316	-0.360313						-0.233108					-0.269618	-0.295717					-0.239805				NA
	MGB010 Histamine degradation	p-value	0.000351	0.0007433	0.0017091	0.0044759	0.0010125	0.0075508						0.0097787					0.0467228	0.0103358			0.0236767					0.0375798	NA
		RHO	-0.40976	0.3885802	-0.363293	-0.331277	-0.379427	-0.312388						-0.302597					-0.2352	-0.300457			-0.266442					-0.245592	NA
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 8 (8~9 y)	MGB039 g-Hydroxybutyric acid (GHB) degradation	p-value	0.0157712		0.027108	0.0228277	0.0472699	0.0174004				NA		0.0291609															
		RHO	0.3212503		0.2953572	0.3038075	0.2663041	0.3167071				NA		0.2916966															
	MGB025 Nitric oxide synthesis I (NO synthase)	p-value										NA																	
		RHO										NA																	
	MGB021 GABA synthesis II	p-value	0.0411169		0.0118035	0.0222556	0.0208933	0.0252964				NA	0.0311892																
		RHO	-0.273855		-0.334276	-0.305036	-0.308073	-0.298786				NA	-0.288286																
	MGB020 GABA synthesis I	p-value				0.0345076						NA																	
		RHO				-0.283085						NA																	
	MGB019 GABA degradation	p-value	0.0208418									NA														0.004155			
		RHO	-0.308191									NA														-0.377252			
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_m	any_sleep_c	sleep_comp	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months

age bracket 9 (9 y ~)	MGB056 Propionate degradation I	p-value						0.0285878																0.0342847					
		RHO						-0.212709																-0.205827					
	MGB055 Propionate synthesis III	p-value	0.0012107		0.0021443	0.0038295	0.0022078	0.002468																					
		RHO	0.3102259		0.2949693	0.2786032	0.2941676	0.2910878																					
	MGB052 Butyrate synthesis I	p-value	0.0222918		0.0381579	0.0385289	0.0460147	0.0371627											0.0350781										
		RHO	0.2218307		0.2016798	0.2013014	0.1942497	0.2027102											0.2049462										
	MGB040 Menaquinone synthesis (vitamin K2) I	p-value	0.0002021		0.0013998	0.0001658	0.0021849	0.0055296					0.0124895																
		RHO	0.3534312		0.3064292	0.3578569	0.2944541	0.2677149					0.2418814																
	MGB039 g-Hydroxybutyric acid (GHB) degradation	p-value			0.0165079		0.0151506	0.0188207																					
		RHO			-0.232422		-0.235369	-0.227853																					
	MGB037 Inositol synthesis	p-value	0.0043718		0.0098523	0.0058664	0.0132527	0.0140466															0.0113392		0.0145375				
		RHO	0.2747273		0.2496633	0.2659213	0.2398987	0.2379392															0.2450794		0.2367751				
	MGB034 Isovaleric acid synthesis I (KADH pathway)	p-value	0.0051714		0.0258857	0.026263	0.0145416														0.0084221								
		RHO	0.2697321		0.21639	0.215857	0.2367655														0.2546865								
	MGB033 Quinolinic acid degradation	p-value	0.0335945		0.0380757		0.045665	0.0194889																					
		RHO	0.2066064		0.2017641		0.194557	0.2266234																					
	MGB032 Quinolinic acid synthesis	p-value	0.0372486		0.025069	0.0333263	0.0306265	0.0184698																					
		RHO	0.2026204		0.2175669	0.2069132	0.2101227	0.2285139																					
	MGB026 Nitric oxide synthesis II (nitrite reductase)	p-value	0.0062133				0.0316323																						
		RHO	0.2641672				0.2089001																						
	MGB023 Dopamine degradation	p-value	0.0370238		0.0055579		0.005783	0.0008398																					
		RHO	-0.202856		-0.267561		-0.266357	-0.319583																					
	MGB016 p-Cresol degradation	p-value			0.0129846		0.0181212	0.0011097																					
		RHO			-0.240584		-0.229181	-0.312483																					
	MGB015 p-Cresol synthesis	p-value	0.0014291		0.0023147	0.0030929	0.0022685	0.0021775																					
		RHO	0.3058825		0.2928649	0.2847437	0.2934211	0.2945472																					
	MGB007 Glutamate synthesis II	p-value	0.0083965		0.0070271	0.0078922	0.0089347	0.0058162															0.0275232						
		RHO	0.2547829		0.2603711	0.2567403	0.2528052	0.2661826															0.2141225						
	MGB006 Glutamate synthesis I	p-value	0.0370431		0.0277758	0.0388325	0.0275286	0.0287284															0.0386978						
		RHO	0.2028357		0.2137829	0.200994	0.2141152	0.2125257															0.2011301						
	MGB005 Tryptophan synthesis	p-value	0.0003295		0.0004494	0.0009961	0.0004506	0.0004168	0.0240838	0.0229723																			
		RHO	0.3422487		0.3349187	0.3152557	0.3348577	0.3367106	0.2190311	0.2207456																			

			ASD_score	Repetitive_b	Social_retar	Language_r	any_GI_prob	GI_problem_	esophageal_	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_comp	difficulty_fal	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_w	Antibiotic_within_3_months
≤ 3 y	MGB056 Propionate degradation I	p-value		0.0298644							0.0462278							0.0155588									
		RHO		-0.149921							-0.137717							-0.166759									
	MGB050 Glutamate degradation I	p-value	0.0440334	0.0310382	0.0437378	0.0407304															0.043745						0.0222143
		RHO	0.1391174	0.1488766	0.1393105	0.1413396															0.1393058						0.1577485
	MGB028 Nitric oxide degradation II (NO reductase)	p-value																						0.0225935			0.003177
		RHO																						0.1573094			0.2026673
	MGB025 Nitric oxide synthesis I (NO synthase)	p-value											0.0188988							0.0410268			0.0089127				
		RHO											-0.161891							-0.141134			-0.180076				
	MGB004 Kynurenine synthesis	p-value	0.0390351		0.0055796								0.0324475			0.0073235					0.0285254				0.0283375	0.0294987	
		RHO	-0.14254		-0.190633								-0.147666			-0.184568					-0.151156				-0.151333	0.1502536	

			ASD_score	Repetitive_b	Social_retar	Language_r	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_comp	difficulty_fal	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_w	Antibiotic_w	family_histo	age_of_moth	number_of_	number_of_	assisted_rep	smoking_du	infection_du	drinking_du	eclampsia/p	age_of_fathe_during_pregnancy
> 3 y	MGB056 Propionate degradation I	p-value	1.92E-09	1.04E-08	1.82E-08	9.11E-11	0.0069955	0.0055738			0.0018918	0.0104972					0.0052602	0.0003116						0.0262756	0.0344843	0.0019543				0.0007645	0.008037		0.0162397		0.0187258			0.0195821
		RHO	-0.187772	-0.179157	-0.176186	-0.202369	-0.084943	-0.08729			-0.097788	-0.08061					-0.08788	-0.113393						-0.070026	-0.066638	-0.097486				-0.12033	-0.083483		-0.075725		-0.074075			-0.083945
	MGB055 Propionate synthesis III	p-value	7.99E-07	0.0001103	2.06E-07	3.53E-08	0.001517	0.0011809			0.0053965			0.0009628		0.0187127				0.0389712					0.0203087						0.0060274		0.0027517					
		RHO	0.1547888	0.12155	0.1627793	0.1726321	0.099814	0.1020695			0.0876197			0.1038763		0.074083				0.0650695					0.0731211						0.086488		0.094262					
	MGB051 Glutamate degradation II	p-value	8.57E-05	0.0027669	0.000425	5.41E-06																			0.0434285					0.028601								0.019179
		RHO	-0.123459	-0.094209	-0.110848	-0.14277																			-0.063656					-0.078432								-0.084224
	MGB049 Tryptophan degradation	p-value	0.0157599	0.0103844	0.0347681	0.0205884										0.0025669								0.0261637							0.0215235		0.0283277					
		RHO	-0.076069	-0.080728	-0.066534	-0.072959										0.0949246								-0.070078							-0.072432		0.0691016					
	MGB048 Propionate synthesis I	p-value																			0.0359709							0.0013243										
		RHO																			-0.0661							0.1010432										
	MGB043 Acetate synthesis I	p-value				0.0214245		0.0382407										0.0296949						0.0094075		0.0350486					0.0177777							
		RHO				0.072487		0.065314										0.0685174						0.081799		0.0664314					-0.07468							
	MGB041 alternative pathway: futalosine pathway	p-value	0.0269005	0.0305346	0.0090149	0.0272964	0.0042055	0.0122171		0.0019802							0.0488948	0.0350058		0.01995				0.0001514		0.0021753		0.0496472	0.0100365									
		RHO	-0.069738	-0.06817	-0.082258	-0.069559	-0.090128	-0.07894		-0.097364							-0.062082	-0.066447		-0.073331				-0.119117		-0.096487		-0.061877	-0.081099									
	MGB040 Menaquinone synthesis (vitamin K2) I	p-value	4.24E-05	0.0001003	6.83E-07	0.0001752	0.0195707	0.0316526								0.0492874	0.0272313	0.0431869		0.0142051								0.0004361			0.0426364		0.0452508					
		RHO	0.1286403	0.1222724	0.1557331	0.1179805	0.0735573	0.0677199								0.0619744	0.0695879	0.0637298		0.0772506								0.1106347			0.0638983		0.0631138					
	MGB037 Inositol synthesis	p-value	0.0072494	0.0247702	0.0029413	0.0009797																																
		RHO	0.0845701	0.0707442	0.0936232	0.1037238																																
	MGB036 S-Adenosylmethionine (SAM) synthesis	p-value	0.0204121	0.0173833		0.0029996	0.0182219	0.0205822													0.0493742					0.0334377								0.0262091				
		RHO	0.073061	0.0749405		0.093434	0.0743931	0.0729629													0.0619508					0.0670286								0.0700567				
	MGB027 Nitric oxide degradation I (NO dioxygenase)	p-value	9.79E-06	4.87E-07	3.56E-07	0.0001704	0.0006661	0.005862						0.019405			0.0005174	0.0012676		0.0031374				0.0024014				5.65E-05	0.0011777		0.0010409							
		RHO	0.1388368	0.1577496	0.1596061	0.1181983	0.1070669	0.0867741						0.0736572			0.1092065	0.101436		0.0930004				0.0955562				0.126547	0.1020939		0.1031898							
	MGB024 DOPAC synthesis	p-value	0.0011221	0.0177262	0.0027352	0.000738	0.0053489	0.0129392			0.0033535														0.0251725						3.97E-05	0.0378442						
		RHO	-0.102524	-0.074714	-0.09432	-0.106188	-0.08771	-0.0783			-0.092354														-0.070549						-0.129113	-0.065448						
	MGB023 Dopamine degradation	p-value	0.0017607	0.0088126	0.0107061	0.0014614																														0.0384646		
		RHO	-0.098451	-0.082501	-0.080395	-0.100153																														-0.065239		
	MGB020 GABA synthesis I	p-value	0.0178845			0.0018092					0.0122248	0.031034																0.0235576										
		RHO	-0.074611			-0.0982					-0.078933	-0.067967																0.0713508										
	MGB019 GABA degradation	p-value																												0.0050236	0.0028451							
		RHO																												-0.100425	0.0939425							
		p-value	0.0002116	0.0018441	0.0001701	4.09E-05		0.0299988			0.0277622																						0.0288481	0.0142145				
	MGB015 p-Cresol synthesis	RHO	0.1164926	0.0980239	0.1182095	0.1288935		0.0683907			0.0693504																						0.0688764	0.0772431				
	MGB007 Glutamate synthesis II	p-value	0.0403913	0.0486263		0.0100871																									0.0042135			0.0436278				
		RHO	0.0646051	0.0621555		0.081044																									-0.090109			0.0635961				
	MGB005 Tryptophan synthesis	p-value	6.97E-08	1.48E-06	9.30E-08	7.91E-09	0.0008602	0.0023081			0.0269473						0.0220778	0.0033437			0.0301515	0.0418449		0.0148699		0.0138226							0.0090156	0.0123714				
		RHO	0.1688988	0.1510063	0.1672976	0.1805673	0.1048617	0.09593			0.0697166						0.072129	0.0923827	0.0316358		0.0683275	0.0641438		0.0767323		0.0775586							0.0822568	0.0788001				
	MGB004 Kynurenine synthesis	p-value	9.38E-16	7.66E-13	5.64E-17	7.24E-15	1.71E-09	2.38E-09	0.0273358		7.14E-06	0.0050022	0.0156879	4.79E-05	0.0043046		3.63E-05	2.93E-05	0.0342427	0.0013199		0.002583		0.0010344	0.0032059	0.005891					0.0001192		0.0003673					
		RHO	-0.249491	-0.223273	-0.259627	-0.241828	-0.188349	-0.186687	-0.069541		-0.140946	-0.088389	-0.076122	-0.127753	-0.089896		-0.129747	-0.131287	-0.066727	-0.101073		-0.094865		-0.103245	-0.092791	-0.086723					-0.12096		-0.112051					

Table18 Summary of the statistical results of correlations between METACYC and clinical phenotypes according to spearman's rank correlations analysis

			Group	age	ASD_score	Repetitive_b	Social_retarc	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_co	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_h	Antibiotic_within_3_months
age bracket 1 (11~23 mo)	PWY-7527 L-methionine salvage cycle III	p-value										NA														0.0032462			
		RHO										NA														-0.438787			
	PWY-7374 1_4-dihydroxy-6-naphthoate biosynthesis I	p-value	0.009821		0.0239872	0.0097412	0.017576	0.0406287				NA																	
		RHO	-0.38955		-0.343803	-0.389941	-0.360453	-0.313528				NA																	
	PWY-7371 1_4-dihydroxy-6-naphthoate biosynthesis II	p-value	0.004871		0.0081523	0.0075572	0.0038728	0.0157839				NA																	
		RHO	-0.421562		-0.398352	-0.40187	-0.431404	-0.366023				NA																	
	PWY-7328 superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis	p-value									0.0459514	NA																0.0459514	
		RHO									0.3060344	NA																0.3060344	
	PWY-6467 Kdo transfer to lipid IVA III_Chlamydia	p-value									0.046261	NA																0.046261	
		RHO									0.3056207	NA																0.3056207	
	PWY-6263 superpathway of menaquinol-8 biosynthesis II	p-value	0.008779		0.0124979	0.0117655	0.0059209	0.0259455				NA																	
		RHO	-0.394879		-0.377804	-0.380785	-0.412952	-0.339466				NA																	
	PWY-5304 superpathway of sulfur oxidation_Acidianus ambivalens	p-value	0.0123796		0.0252682	0	0.0087669	0.026073				NA																	
		RHO	-0.378275		-0.340934	-0.289967	-0.394944	-0.339193				NA																	
	PWY-5088 L-glutamate degradation VIII_to propanoate	p-value	0.0022708		0.022912	0.008048	0.0247085	0.0094065				NA														0.012455			
		RHO	-0.453257		-0.346311	-0.398952	-0.342172	-0.391609				NA														-0.377974			
	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	p-value										NA														0.0032462			
		RHO										NA														-0.438787			
	METHYLGALLATE-DEGRADATION-PWY methylgallate degradation	p-value							0.0084109	0.0106912		NA	0.0313064																
		RHO							-0.396892	-0.385459		NA	-0.32885																
	HEXITOLDEGSUPER-PWY superpathway of hexitol degradation_bacteria	p-value	0.0004686		0.0019071	0.0017942	0.0026002	0.0016506				NA																	
		RHO	-0.510568		-0.460105	-0.462466	-0.447845	-0.465667				NA																	
	GLCMANNANAUT-PWY superpathway of N-acetylglucosamine N-acetylmannosamine and N-acetylneuraminate degradation	p-value	0.0114765				0.0368303					NA																	
		RHO	-0.382006				-0.319382					NA																	
	GALLATE-DEGRADATION-I-PWY gallate degradation II	p-value							0.0084109	0.0106912		NA	0.0313064																
		RHO							-0.396892	-0.385459		NA	-0.32885																
	GALLATE-DEGRADATION-II-PWY gallate degradation I	p-value							0.0460094			NA																	
		RHO							-0.305957			NA																	
			Group	age	ASD_score	Repetitive_b	Social_retarc	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_co	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_h	Antibiotic_within_3_months
age bracket 2 (24~35 mo)	TYRFUMCAT-PWY L-tyrosine degradation I	p-value	0.0191884																										
		RHO	-0.181077																										
	SULFATE-CYS-PWY superpathway of sulfate assimilation and cysteine biosynthesis	p-value																0.0079724											
		RHO																0.2046728											
	SO4ASSIM-PWY sulfate reduction I_assimilatory	p-value																0.010877											
		RHO																0.1966133											
	PWY-7527 L-methionine salvage cycle III	p-value							0.0432757	0.0190755													0.0253242			0.0152381	0.0379002		
		RHO							-0.156603	-0.181245													-0.173051			-0.187521	-0.160801		
	PWY-7377 cobllyrinate a_c-diamide biosynthesis I_early cobalt insertion	p-value	0.0009029					0.0188797				0.013945																	0.0139876
		RHO	0.254512					0.181537				-0.189949																	0.1898663
	PWY-7254 TCA cycle VII_acetate-producers	p-value	0.003486		0.0346839	0.039755	0.029961	0.0288741				0.0149518								0.0350794									0.0167187
		RHO	0.2248419		0.16356	0.1592991	0.1680324	0.169146				-0.188043								0.1632094									0.1849519
	PWY-7094 fatty acid salvage	p-value	0.0096542																								0.0316725	0.0405214	
		RHO	-0.199742																								-0.166347	-0.158696	
	PWY-6562 norspermidine biosynthesis	p-value											0.0128958										0.0329363						
		RHO											-0.192069										-0.165151						
	PWY-6071 superpathway of phenylethylamine degradation	p-value											0.0151419										0.0457322						
		RHO											-0.187695										-0.154828						
	PWY-5747 2-methylcitrate cycle II	p-value											0				0.0462147				0.0324055								
		RHO											-0.150234				-0.154489				-0.165648								
	PWY-5415 catechol degradation I_meta-cleavage pathway	p-value							0.0178533	0.0069713			0.0395345			0.0288957	0.0335015				0.0481883								
		RHO							-0.183114	-0.208066			-0.159475			-0.169124	-0.164629				-0.153132								
	PWY-5178 toluene degradation IV_aerobic_via catechol	p-value							0.0148148	0.0065455			0.0018002				0.0497911												
		RHO							-0.188295	-0.209643			-0.239805				-0.152063												
	PWY-5022 4-aminobutanoate degradation V	p-value	0.0048481																0.0154185	0.000453	0.0244876	0.0127322		0.0028587					
		RHO	0.2170089																0.1871966	0.2684062	0.1740397	0.1924132		0.2294323					
	PWY-5005 biotin biosynthesis II	p-value	0.0078683			0.0145683						0.0137715												0.0415681					
		RHO	0.2050074			0.1887553						-0.19029												0.1578865					
	PWY490-3 nitrate reduction VI_assimilatory	p-value												0.0313737															
		RHO												0.1666353															
	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	p-value							0.0432757	0.0190755						0.004406							0.0253242						
		RHO							-0.156603	-0.181245						-0.219307							-0.173051						
	PWY0-321 phenylacetate degradation I_aerobic	p-value											0.0113713										0.0376159						
		RHO											-0.195436										-0.161037						
	PWY0-1241 ADP-L-glycero-b-D-manno-heptose biosynthesis	p-value	0.0005344		0.0055322	0.015089	0.0026451	0.0072924				0.0074323										0.0341805		0.0242147					0.0124495
		RHO	0.2651463		0.2137988	0.1877915	0.231205	0.2069332				-0.206453										0.1640112		0.1743684					0.1930169
	LEU-DEG2-PWY L-leucine degradation I	p-value	0.0025731		0.0417867	0.038328	0.0073056												0.0432673									0.0204935	
		RHO	-0.231832		-0.15772	-0.160449	-0.206888												-0.156609									-0.179201	
	GLYCOLYSIS-E-D superpathway of glycolysis and Entner-Doudoroff	p-value	0.0018048		0.0065581	0.0009274	0.0078588	0.0323185	0.0406718										0.0117764	0.0071791		0.0436154		0.0318944					0.0392866
		RHO	0.2397485		0.2095953	0.2539575	0.205038	0.1657306	0.1585782										0.1945043	0.2073279		0.1563523		0.1661338					0.1596728
			Group	age	ASD_score	Repetitive_b	Social_retarc	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_co	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_h	Antibiotic_within_3_months
age bracket 3 (36~47 mo)	VALDEG-PWY L-valine degradation I	p-value	5.43E-05		0.0013449	0.0098586	0.0001883	0.0007737				NA														0.0029498		0.005162	
		RHO	-0.253383		-0.202505	-0.163599	-0.234984	-0.212127				NA														-0.188044		-0.177082	
	THISYN-PWY superpathway of thiamin diphosphate biosynthesis I	p-value	0.0071861		0.020765	0	0.0033309	0.0151624				NA																	
		RHO	0.1703057		0.1467722	0.0818901	0.1857137	0.154065				NA																	
	TCA-GLYOX-BYPASS superpathway of glyoxylate bypass and TCA	p-value									0.0189383	NA																	
		RHO									-0.148939	NA																	
	PWY-7446 sulfoglycolysis	p-value	0.0075346		0.0123728	0.0136798	0.0137631	0.0110566				NA															0.0164418	0.0417456	
		RHO	-0.169316		-0.158629	-0.156389	-0.156253	-0.161106				NA															-0.152214	-0.129399	
	PWY-7392 taxadiene biosynthesis_engineered	p-value			0	0	0	0				NA							0.0400214										
		RHO			-0.10992	-0.087011	-0.120927	-0.092621				NA							0.1305003										
	PWY-7371 1_4-dihydroxy-6-naphthoate biosynthesis II	p-value	7.21E-05		0.0005473	0.0033145	9.25E-05	0.0013052				NA			0.0129559					0.0394125				0.0460773					0.0013069
		RHO	-0.249324		-0.217942	-0.185809	-0.245669	-0.203038				NA			-0.157605					-0.130899				-0.126791					-0.203015
	PWY-7094 fatty acid salvage	p-value	7.99E-09	0.0310378	8.90E-08	4.90E-07	5.33E-09	6.82E-07	0.0006067	0.000165	0.0443467	NA	0.0001989	0.0052667	0.0048171				0.006956	0.0067695				0.0134802		0.0263199			
		RHO	-0.356031	-0.136989	-0.331604	-0.312935	-0.359939	-0.309176	-0.216228	-0.237004	-0.127807	NA	-0.234138	-0.176678	-0.17847				-0.170983	-0.171547				-0.156719		-0.141069			
	PWY-6703 preQ0 biosynthesis	p-value	0.004963		0.0282819	0	0.0070639	0.0139364				NA	0.0405062																
		RHO	0.1778724		0.1393021	0.0811524	0.170663	0.1559715				NA	0.1301866																
	PWY-6629 superpathway of L-tryptophan biosynthesis	p-value										NA															0.0066864		
		RHO										NA															-0.171802		
	PWY-6609 adenine and adenosine salvage III	p-value	0.010208		0.0495954	0.0071405	0.0113472					NA																	
		RHO	-0.162845		-0.124821	-0.170439	-0.160538					NA																	
	PWY-6471 peptidoglycan biosynthesis IV_Enterococcus faecium	p-value	0.0097003		0.0233577		0.0022475					NA										0.0161039							
		RHO	-0.163948		-0.143965		-0.193165					NA										-0.15269							
	PWY-6317 galactose degradation I_Leloir pathway	p-value	0.0132337			0.0374884	0.0121869					NA																	
		RHO	-0.157132			-0.132193	-0.158964					NA																	
	PWY-6263 superpathway of menaquinol-8 biosynthesis II	p-value	6.95E-05		0.0004582	0.0030183	8.55E-05	0.0011195				NA			0.0122848					0.0372897				0.04011					0.0017084
		RHO	-0.249846		-0.220871	-0.187605	-0.246827	-0.205745				NA			-0.158787					-0.13233				-0.130443					-0.198205
	PWY-621 sucrose degradation III_sucrose invertase	p-value	0.002622		0.0108885	0.0063506	0.001896					NA																	
		RHO	-0.190278		-0.161441	-0.172865	-0.196304					NA																	
	PWY-6151 S-adenosyl-L-methionine cycle I	p-value	0.0098362			0.0328871	0.0233581		0.0163115	0.0361223	0.0117526	NA				0.0113113													
		RHO	-0.163648			-0.135534	-0.143964		-0.152397	-0.133147	-0.159766	NA				-0.160607													
	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	p-value									0.0232026	NA															0.0414241		
		RHO									-0.144125	NA															-0.129601		
	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	p-value									0.0232026	NA															0.0414241		
		RHO									-0.144125	NA															-0.129601		
	PWY-5747 2-methylcitrate cycle II	p-value	0.0056955		0.0070344	0.0073345	0.0100278	0.0058052			0.0407289	NA																0.0023282	
		RHO	-0.175092		-0.17075	-0.169879	-0.163231	-0.174704			-0.130044	NA																-0.192507	
	PWY-5705 allantoin degradation to glyoxylate III	p-value										NA																	
		RHO										NA																	
	PWY-5532 adenosine nucleotides degradation IV	p-value	0.0001795		0.0002739	0.0019401	1.05E-05	0.0005943				NA		0.0170679			0.0208927											0.0026121	
		RHO	-0.235716		-0.229138	-0.195882	-0.275818	-0.216573				NA		-0.151354			-0.146627											-0.190349	
	PWY-5507 adenosylcobalamin biosynthesis I_early cobalt insertion	p-value	5.81E-08		6.71E-09	1.10E-07	1.47E-09	6.79E-07	2.04E-06	1.49E-06		NA	1.87E-05	0.0112165		0.0346349	0.0122185	0	0.0023854	0.0012397	0.0255996	0.0292324	0	0.0211843	0	0.0207177	0.0094796	0.0135783	
		RHO	-0.336083		-0.357734	-0.329373	-0.372039	-0.30922	-0.296312	-0.300027		NA	-0.268099	-0.160792		-0.134221	-0.158907	0.0146598	-0.192054	-0.203949	-0.141747	-0.138483	-0.075926	-0.146298	-0.078573	-0.146826	-0.164443	-0.156556	
	PWY-5415 catechol degradation I_meta-cleavage pathway	p-value	0.0001478		0.0005236	0.0011711	0.0019074	0.0001555			0.0415496	NA															0.0057051	0.0010044	
		RHO	-0.238679		-0.218675	-0.204953	-0.196194	-0.237913			-0.129522	NA															-0.175058	-0.207638	
	PWY-5384 sucrose degradation IV_sucrose phosphorylase	p-value	0.0004291		0.0034175	0.0091347	0.0005856	0.0083301				NA							0.0497774										
		RHO	-0.221942		-0.185218	-0.165238	-0.216818	-0.167202				NA							-0.124722										
	PWY-5178 toluene degradation IV_aerobic_via catechol	p-value	1.37E-06		4.73E-05	0.0005411	2.26E-05	1.10E-05				NA															0.0086061	0.0058079	0.0174796
		RHO	-0.301055		-0.255348	-0.218133	-0.265573	-0.275163				NA															-0.16651	-0.174694	0.1508033
	PWY-4722 creatinine degradation II	p-value	0.0105948		0.0366832	0.0133324	0.0202371					NA															0	0	0
		RHO	-0.162037		-0.132752	-0.156965	-0.147381					NA															-0.010889	-0.06205	-0.010107
	PWY0-42 2-methylcitrate cycle I	p-value	0.0034179		0.0022655	0.0021783	0.0046215	0.0024384				NA															0.0386124	0.0048967	0
		RHO	-0.185216		-0.193016	-0.193745	-0.179297	-0.191642				NA															-0.131431	-0.178142	0.0809305
	PWY0-1338 polymyxin resistance	p-value									0.0205906	NA															0.0461886	0	0
		RHO									-0.146972	NA															-0.126727	-0.093363	0.1024461
	PWY0-1298 superpathway of pyrimidine deoxyribonucleosides degradation	p-value	0.0174544		0	0.0369759	0.0191612					NA											0.0158062						
		RHO	-0.150837		-0.124487	-0.132548	-0.148665					NA											-0.153117						
	PWY0-1297 superpathway of purine deoxyribonucleosides degradation	p-value	0.0001227		0.0021782	0.0009151	0.0002082	0.0172543				NA																	
		RHO	-0.24148		-0.193746	-0.209251	-0.23343	-0.151103				NA																	
	PWY0-1296 purine ribonucleosides degradation	p-value	0.0017592		0.020873	0.0086583	0.0023417					NA																	
		RHO	-0.197671		-0.146649	-0.166381	-0.192399					NA																	
	PWY0-1061 superpathway of L-alanine biosynthesis	p-value			0.0404436			0.0395408				NA																	
		RHO			-0.130227			-0.130814				NA																	
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value	0.0014654		0.0006045	0.0107954	0.0005183	0.0004344			0.0338247	NA																0.042384	
		RHO	-0.200972		-0.216288	-0.161629	-0.218845	-0.22174			-0.134822	NA																-0.129001	
	PPGPPMET-PWY ppGpp biosynthesis	p-value									0.0141582	NA							0.0307051	0.0407259							0.0053674		0.020346
		RHO									-0.155616	NA							0.137259	0.1300455							-0.176295		0.1472541
	P562-PWY myo-inositol degradation I	p-value	0.0315588		0.0493436		0.0182402					NA																	
		RHO	-0.136572		-0.124958		-0.149815					NA																	
	P461-PWY hexitol fermentation to lactate formate ethanol and acetate	p-value	0.0499331									NA																	
		RHO	-0.124638									NA																	
	P281-PWY 3-phenylpropanoate degradation	p-value	0.0050053		0.0009123	0.0130999	0.0013066	0.0006691			0.0150706	NA															0.0336972	0.0307576	0.030509
		RHO	-0.177702		-0.209302	-0.157359	-0.203018	-0.214585			-0.154203	NA															-0.134918	-0.137216	0.1374191
	P162-PWY L-glutamate degradation V_via hydroxyglutarate	p-value										NA																	
		RHO										NA																	
	P161-PWY acetylene degradation	p-value	0.0001881		0.0023543	0.0019984	0.0002531	0.0144403				NA																	
		RHO	-0.234998		-0.192299	-0.195338	-0.230381	-0.155171				NA																	
	P105-PWY TCA cycle IV_2-oxoglutarate decarboxylase	p-value									0.0180171	NA																	
		RHO									-0.150101	NA																	
	ORNARGDEG-PWY superpathway of L-arginine and L-ornithine degradation	p-value									0.023106	NA																	
		RHO									-0.144225	NA																	
	METHGLYUT-PWY superpathway of methylglyoxal degradation	p-value									0.0155295	NA															0.049617		
		RHO									-0.15352	NA															-0.124809		
	KETOGLUCONMET-PWY ketogluconate metabolism	p-value	0.0027813		0.0093171	0.0433131	0.002354	0.0030842				NA															0.0189027		
		RHO	-0.189162		-0.164814	-0.12843	-0.192301	-0.187193				NA															-0.148983		
	HEXITOLDEGSUPER-PWY superpathway of hexitol degradation_bacteria	p-value					0.0249882					NA																	
		RHO					-0.142334					NA																	
	GLYCOLYSIS-TCA-GLYOX-BYPASS superpathway of glycolysis pyruvate dehydrogenase TCA and glyoxylate bypass	p-value									0.0198577	NA																	

		RHO									-0.147827	NA																	
	GLYCOL-GLYOXDEG-PWY superpathway of glycol metabolism and degradation	p-value									0.0305948	NA																	
		RHO									-0.137349	NA																	
	GLCMANNANAUT-PWY superpathway of N-acetylglucosamine N-acetylmannosamine and N-acetylneuraminate degradation	p-value	0.0242558				0.0086261					NA																	
		RHO	-0.143055				-0.16646					NA																	
	ENTBACSYN-PWY enterobactin biosynthesis	p-value									0.0223636	NA																	
		RHO									-0.145008	NA																	
	ECASYN-PWY enterobacterial common antigen biosynthesis	p-value									0.0242719	NA															0.0323579		
		RHO									-0.143039	NA															-0.135943		
	ARGDEG-PWY superpathway of L-arginine putrescine and 4-aminobutanoate degradation	p-value									0.023106	NA																	
		RHO									-0.144225	NA																	
	ALL-CHORISMATE-PWY superpathway of chorismate metabolism	p-value									0.0241521	NA																	
		RHO									-0.143159	NA																	
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 4 (4~5 y)	THREOCAT-PWY superpathway of L-threonine metabolism	p-value						0.0420416					0.0157669		0.0302287						0.032197								
		RHO						-0.14538					-0.172258		-0.154847						-0.153073								
	TCA-GLYOX-BYPASS superpathway of glyoxylate bypass and TCA	p-value						0.0148808			0.0324507		0.0189951		0.0414205														
		RHO						-0.173734			-0.152851		-0.167431		-0.145817														
	PWY-922 mevalonate pathway I	p-value						0																		0.024843			
		RHO						-0.138162																		-0.160262			
	PWY-7446 sulfoglycolysis	p-value						0							0.0281026														0.0117571
		RHO						-0.108389							-0.156877														-0.179636
	PWY-6629 superpathway of L-tryptophan biosynthesis	p-value						0.0440901																					
		RHO						-0.143973																					
	PWY-6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	p-value						0.0136837					0.0450474										0.0487395						
		RHO						-0.175855					-0.143335										-0.140974						
	PWY-6562 norspermidine biosynthesis	p-value	0.0024028		0.0077149	0.0041558		0.0019741		0.0406806			0.0239646						0.0245382	0.004426				0.0312081					
		RHO	-0.215631		-0.189788	-0.20387		-0.219705		-0.146346			-0.161239						-0.160597	-0.202477				-0.153952					
	PWY-6519 8-amino-7-oxononanoate biosynthesis I	p-value																		0.0440534									
		RHO																		-0.143998									
	PWY-6470 peptidoglycan biosynthesis V_b-lactam resistance	p-value	0.0016109					0.0197286																		0.0177981			
		RHO	-0.223847					-0.166435																		-0.169131			
	PWY-6185 4-methylcatechol degradation_ortho cleavage	p-value	0.0001887		0.0019289	0.0012107	0.0128157	0.000334		0.0381096			0.0247885		0.0419528				0.02184	0.0085149									
		RHO	-0.263646		-0.220181	-0.229542	-0.177497	-0.253662		-0.148248			-0.160321		-0.145442				-0.163736	-0.187454									
	PWY-6182 superpathway of salicylate degradation	p-value	0.0004694		0.0046608	0.0024582	0.022657	0.0011579					0.0273655		0.0377989				0.0386838	0.0153222									
		RHO	-0.247516		-0.201328	-0.215154	-0.162752	-0.230418					-0.157612		-0.148486				-0.147814	-0.17299									
	PWY-5910 superpathway of geranylgeranyldiphosphate biosynthesis I_via mevalonate	p-value	0.0098464					0																		0.024836			
		RHO	-0.18397					-0.138232																		-0.160269			
	PWY-5896 superpathway of menaquinol-10 biosynthesis	p-value						0.048853			0.0444043																		
		RHO						-0.140904			-0.143762																		
	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	p-value						0.0473383			0.0444462																		
		RHO						-0.141852			-0.143734																		
	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	p-value						0.0473383			0.0444462																		
		RHO						-0.141852			-0.143734																		
	PWY-5850 superpathway of menaquinol-6 biosynthesis I	p-value						0.048853			0.0444043																		
		RHO						-0.140904			-0.143762																		
	PWY-5845 superpathway of menaquinol-9 biosynthesis	p-value						0.048853			0.0444043																		
		RHO						-0.140904			-0.143762																		
	PWY-5431 aromatic compounds degradation via b-ketoadipate	p-value	0.0006647		0.0047245	0.0019437	0.0242059	0.0016301					0.0340771		0.0351178				0.0343143	0.0136923									
		RHO	-0.24107		-0.201025	-0.220024	-0.160967	-0.223607					-0.151463		-0.150604				-0.151265	-0.175839									
	PWY-5417 catechol degradation III_ortho-cleavage pathway	p-value	0.0006647		0.0047245	0.0019437	0.0242059	0.0016301					0.0340771		0.0351178				0.0343143	0.0136923									
		RHO	-0.24107		-0.201025	-0.220024	-0.160967	-0.223607					-0.151463		-0.150604				-0.151265	-0.175839									
	PWY-5265 peptidoglycan biosynthesis II_staphylococci	p-value	0.0304743																										
		RHO	-0.15462																										
	PWY-5181 toluene degradation III_aerobic_via p-cresol	p-value	0.0001193		0.0019131	0.0013054	0.010994	0.0003075		0.0322557			0.0205014		0.0390145				0.022334	0.008817									
		RHO	-0.271382		-0.22035	-0.228053	-0.181287	-0.25513		-0.153022			-0.165419		-0.147567				-0.163137	-0.186624									
	PWY-3781 aerobic respiration I_cytochrome c	p-value	4.85E-06		0.0006927	8.50E-05	0.0004775	0.0048171	0.0309315	0.0484469					0.0276252		0.0255893		1.37E-05	3.90E-05	0.0169096	0.0019082	0.033942				0.0458402		
		RHO	-0.319933		-0.240295	-0.276962	-0.247204	-0.200591	-0.154203	-0.141155					-0.157351		-0.159455		-0.305086	-0.289354	-0.170459	-0.220402	-0.151576				-0.142814		
	PWY-181 photorespiration	p-value	4.81E-12	0.0016939	8.69E-07	6.92E-07	2.70E-08	1.25E-06	1.24E-06	7.42E-06			0.0274341			3.28E-05	0.029187		0.0002007	0.0001193	0.0043716	0.0107497	0.0088362			0.0016997	0.0032007	0.0080416	
		RHO	-0.467682	-0.22283	-0.34286	-0.345766	-0.384224	-0.338157	-0.338237	-0.313966			-0.157543			-0.292046	-0.155826		-0.262585	-0.271387	-0.202751	-0.181837	-0.186572			-0.222761	-0.209553	-0.18881	
	PWY-1622 formaldehyde assimilation I_serine pathway	p-value	1.07E-11	0.0004405	2.60E-06	3.35E-06	4.99E-08	2.79E-06	4.07E-06	2.13E-05			0.0341779			8.09E-05	0.0381731		0.0005198	0.0003298	0.0076939	0.0160166	0.0128315			0.0013518	0.0014577	0.0115301	
		RHO	-0.460805	-0.248674	-0.328468	-0.325008	-0.37732	-0.327508	-0.322365	-0.298597			-0.151379			-0.277762	-0.1482		-0.245643	-0.253885	-0.189852	-0.171856	-0.177466			-0.22736	-0.225855	-0.180117	
	PWY0-321 phenylacetate degradation I_aerobic	p-value	0.0003682	0	0.0052535	0.0034292	0.0273645	0.0006002		0.0423943			0.0314621						0.0199369	0.0066297									
		RHO	-0.251916	-0.061165	-0.198642	-0.208066	-0.157613	-0.242978		-0.145133			-0.153724						-0.166158	-0.193325									
	PWY0-1338 polymyxin resistance	p-value						0.024364			0.0370025		0.0262166																
		RHO						-0.160791			-0.149101		-0.158792																
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value	0.0003186		0.0038766	0.0015133	0.0130197	0.00252					0.0333648		0.0212218				0.0189847	0.0075159									
		RHO	-0.254501		-0.205398	-0.225105	-0.177102	-0.214633					-0.152064		-0.164502				-0.167446	-0.190402									
	PPGPPMET-PWY ppGpp biosynthesis	p-value						0.0089355			0.0145546			0.0433399									0.0420268						
		RHO						-0.186305			-0.174297			-0.144482									-0.14539						
	P281-PWY 3-phenylpropanoate degradation	p-value	0.0003461		0.006512	0.0041875	0.0172106	0.0028454					0.0368869							0.0363617									0.0445129
		RHO	-0.253026		-0.193739	-0.203702	-0.170002	-0.212067					-0.149191							-0.149605									-0.14369
	P105-PWY TCA cycle IV_2-oxoglutarate decarboxylase	p-value						0.0168043			0.0362204		0.0175947		0.0416544														
		RHO						-0.17062			-0.149717		-0.16943		-0.145652														
	ORNDEG-PWY superpathway of ornithine degradation	p-value									0.0307439		0.033485																
		RHO									-0.154373		-0.151962																
	NAD-BIOSYNTHESIS-II NAD salvage pathway II	p-value						0.029993								0.0474257													
		RHO						-0.155066								0.1417963													
	METHGLYUT-PWY superpathway of methylglyoxal degradation	p-value			0.0356772			0.0057973			0.0415628		0.0209642																
		RHO			-0.150151			-0.196407			-0.145716		-0.164827																
	LPSSYN-PWY superpathway of lipopolysaccharide biosynthesis	p-value	9.01E-08	0.0177496	4.08E-05	3.60E-05	3.19E-05	7.91E-05	9.54E-05	0.0002951			0.0011259			0.0441389	0.0186088		0.0021103	0.0017305		0.0420661	0.0105251			0.0024634		0.0372717	0.016348
		RHO	-0.370521	-0.169202	-0.288633	-0.290572	-0.292438	-0.278126	-0.275077	-0.255861			-0.230968			-0.14394	-0.167969		-0.218331	-0.222397		-0.145362	-0.182352			-0.21511		-0.148892	-0.17133
	KETOGLUCONMET-PWY ketogluconate metabolism	p-value	0.0107814		0.0479487	0.0162314							0.0204767		0.0033039													0.0054681	0.003175
		RHO	-0.181765		-0.141467	-0.171514							-0.165451		-0.20887													-0.197736	-0.209726
	KDO-NAGLIPASYN-PWY superpathway of_Kdo2-lipid A biosynthesis	p-value						0.0308074			0.0222987				0.0373362														
		RHO						-0.154316			-0.16318				-0.148842														
	GOLPDLCAT-PWY superpathway of glycerol degradation to 1_3-propanediol	p-value	0.0003975		0.0336653		0.0401493	0.0037754																					
		RHO	-0.250538		-0.151809		-0.146731	-0.205976																					
	GLYOXYLATE-BYPASS glyoxylate cycle	p-value						0.020316			0.0290519		0.0203704																
		RHO						-0.16566			-0.155955		-0.165589																
	GLYCOLYSIS-TCA-GLYOX-BYPASS superpathway of glycolysis pyruvate dehydrogenase TCA and glyoxylate bypass	p-value						0.0157946			0.027753		0.0204552		0.0418873														
		RHO						-0.172213			-0.157224		-0.165479		-0.145488														
	GLYCOL-GLYOXDEG-PWY superpathway of glycol metabolism and degradation	p-value			0.0217322			0.0030093			0.0372735		0.0154483																
		RHO			-0.163868			-0.210874			-0.14889		-0.17278																
	FAO-PWY fatty acid b-oxidation I	p-value						0.0459317					0.0483778																
		RHO						-0.142755					-0.141198																
	ECASYN-PWY enterobacterial common antigen biosynthesis	p-value						0.0259295			0.0341169		0.0267499																
		RHO						-0.159093			-0.15143		-0.158239																
	CENTFERM-PWY pyruvate fermentation to butanoate	p-value						0.0137925					0.044324										0.0476657						
		RHO						-0.175655					-0.143816										-0.141645						
	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	p-value	0.0006279		0.0044991	0.0018116	0.0227115	0.0016494					0.0327496		0.0326594				0.0364516	0.0151742									
		RHO	-0.242139		-0.202113	-0.221465	-0.162687	-0.22337					-0.152592		-0.15267				-0.149533	-0.173237									
	AST-PWY L-arginine degradation II_AST pathway	p-value						0.0429665			0.0401537		0.0259373		0.0474792														
		RHO						-0.144738			-0.146727		-0.159085		-0.141762														
	ALL-CHORISMATE-PWY superpathway of chorismate metabolism	p-value						0.0392325			0.0360394		0.0439136																
		RHO						-0.147405			-0.149861		-0.144092																
	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY 4-hydroxyphenylacetate degradation	p-value	0.0003098		0.0052246	0.0034081	0.0281198	0.0005178		0.0469264			0.0457653						0.0231302	0.0079364									
		RHO	-0.254998		-0.198766	-0.2082	-0.156861	-0.245714		-0.142114			-0.142863						-0.162196	-0.189121									
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 5 (5~6 y)	VALDEG-PWY L-valine degradation I	p-value	0.0214736		0.0184403		0.0081505	0.0386073	0.0223835																				
		RHO	-0.167642		-0.171743		-0.192439	-0.150991	-0.166509																				
	TYRFUMCAT-PWY L-tyrosine degradation I	p-value	0.0002215	0.0023589	0.0061709	0.0140348	0.0129688	0.00087	0.0022754	0.0012729			0.0387442			0.003599								0.04073		0.0132884	0.0129641		
		RHO	-0.266247	-0.220513	-0.199055	-0.178895	-0.180919	-0.24085	-0.221279	-0.233294			-0.150886			-0.211336								-0.149397		-0.180297	-0.180928		
	SO4ASSIM-PWY sulfate reduction I_assimilatory	p-value																										0.0201489	
		RHO																										-0.169367	
	PWY-7371 1_4-dihydroxy-6-naphthoate biosynthesis II	p-value	0.0005412	0	0.0001687	0.0010758	0.0001174	0.0003292						0.0136348					0.0039699	0.0027038	0.0020938	0.0352482			0.0250524	0.0034724	0.0002614		0.003568
		RHO	-0.24996	-0.017725	-0.271015	-0.236665	-0.277223	-0.259154						-0.179638					-0.209152	-0.217589	-0.223037	-0.153671			-0.163402	-0.212128	-0.263309		-0.211528
	PWY-7237 myo- chiro- and scillo-inositol degradation	p-value															0.0492968												
		RHO															-0.1436												
	PWY-7094 fatty acid salvage	p-value	0.0001715	0.0001334	0.0012797	0.0044711	0.0027444	0.0001097	0.0349748	0.027068														0.019458		0.0276922	0.0396849	0.0167	
		RHO	-0.270727	-0.275049	-0.233187	-0.206475	-0.217267	-0.278362	-0.153898	-0.161239														-0.170306		-0.160597	-0.150173	-0.174369	
	PWY-7013 L-1_2-propanediol degradation	p-value																											
		RHO																											
	PWY-6897 thiamin salvage II	p-value	3.59E-05		0.0002317	0.0001453	0.0005703	0.0001536	0.0039521	0.0196719				0.0104941					0.0044923	0.0022633	0.0036717	0.0294024				0.0209711			
		RHO	0.2965473		0.2654503	0.2735832	0.2489709	0.2726296	0.2092524	0.170012				0.1862482					0.2063676	0.2213921	0.2108924	0.1588996				0.1682848			
	PWY-6630 superpathway of L-tyrosine biosynthesis	p-value	2.06E-08		1.30E-06	2.35E-08	3.32E-06	5.09E-06	0.000167	0.0002866			0.0197827	0.026786	0.0423158	0.0151766			0.0147664	0.0100852	0.0110643	0.0231308				0.0003794		0.0035732	0.0018446
		RHO	0.3948441		0.3443742	0.3933611	0.3317141	0.3256931	0.2711848	0.2616549			0.1698609	0.161533	0.1482517	0.1768713			0.1775824	0.1872339	0.1849291	0.1656082				0.2565613		0.2114954	0.2256922
	PWY-6628 superpathway of L-phenylalanine biosynthesis	p-value	2.41E-08		1.43E-06	2.19E-08	3.87E-06	5.67E-06	0.0001877	0.0003424			0.019097	0.031316	0.0467433	0.0177942			0.0168702	0.0116064	0.0134598	0.0221742				0.0005066		0.0040476	0.0020395
		RHO	0.3930575		0.3431712	0.394116	0.329549	0.3241657	0.269157	0.2584396			0.1708081	0.1570975	0.1452336	0.1726919			0.1741021	0.1837294	0.1799691	0.166766				0.2512012		0.2087176	0.2235903
	PWY-6562 norspermidine biosynthesis	p-value	0.0399178					0.0168392								0.0127423													
		RHO	-0.149999					-0.174151								-0.181367													
	PWY-6467 Kdo transfer to lipid IVA III_Chlamydia	p-value	3.51E-05		0.0020913	0.0035934	0.0001219	0.0056321	0.0426379							0.0037208			0.0126218	0.0290509	0.0499715					0.0358726			0.0321925
		RHO	0.2969093		0.2230627	0.2113707	0.2765902	0.201184	0.1480233							0.2105973			0.181609	0.1592415	0.1431803					0.1531566			0.1563033
	PWY-6185 4-methylcatechol degradation_ortho cleavage	p-value	0.0068022		0.0059395	0.0438956	0.0142062	0.0024646																					
		RHO	-0.196762		-0.199948	-0.147146	-0.178582	-0.219577																					
	PWY-6182 superpathway of salicylate degradation	p-value	0.0068816		0.005199	0.036669	0.0135941	0.0023541																					
		RHO	-0.196487		-0.203032	-0.152512	-0.179715	-0.220557																					
	PWY-5747 2-methylcitrate cycle II	p-value									0.0474768																		
		RHO									0.1447569																		
	PWY-5507 adenosylcobalamin biosynthesis I_early cobalt insertion	p-value	0.0006494	0.0197837	0.0055295	0.0327194	0.0030604	0.0011341	0.0014502	0.003969			0.0238336			0.0289394											0.037763		
		RHO	-0.246502	-0.16986	-0.20161	-0.155835	-0.214901	-0.235613	-0.230649	-0.209156			-0.164784			-0.159351											-0.151645		
	PWY-5431 aromatic compounds degradation via b-ketoadipate	p-value	0.0079385		0.0050259	0.0389669	0.0159813	0.0019366																					
		RHO	-0.193074		-0.20381	-0.150716	-0.175524	-0.224676																					
	PWY-5417 catechol degradation III_ortho-cleavage pathway	p-value	0.0079385		0.0050259	0.0389669	0.0159813	0.0019366																					
		RHO	-0.193074		-0.20381	-0.150716	-0.175524	-0.224676																					
	PWY-5181 toluene degradation III_aerobic_via p-cresol	p-value	0.0063534		0.0057264	0.0403768	0.0134944	0.0025453																					
		RHO	-0.198371		-0.200799	-0.149657	-0.179903	-0.218888																					
	PWY-5088 L-glutamate degradation VIII_to propanoate	p-value	1.31E-08		1.40E-05	0.0010653	1.52E-06	8.41E-06	0.0110245	0.0045143			0.015827	0.0059947	0	0.0186869		0.0399571	0.0059837	0.00223		0.0099554			0.0404891	1.17E-05	0.0002337		
		RHO	-0.399828		-0.310985	-0.236859	-0.34233	-0.318503	-0.185019	-0.206257			-0.175777	-0.199732	-0.035441	-0.171389		-0.149969	-0.199775	-0.221706		-0.187554			-0.149575	-0.313609	-0.265301		
	PWY-3781 aerobic respiration I_cytochrome c	p-value	0.0266413		0.0194211		0.0074505	0.0230004																					
		RHO	-0.161685		-0.170357		-0.194597	-0.165764																					
	PWY0-321 phenylacetate degradation I_aerobic	p-value	0.0071423		0.0082537		0.0157574	0.0035385																					
		RHO	-0.195604		-0.192135		-0.175893	-0.211711																					
	PWY0-1479 tRNA processing	p-value	1.33E-05		8.23E-05	1.34E-06	2.00E-05	0.0026594	0.0471936		0.0316186								3.60E-05	9.99E-05	0.003983	0.0015027				0.0242314			0.0133817
		RHO	0.311777		0.2831752	0.3440128	0.3056092	0.2179455	0.1449403		0.1568212								0.2964914	0.279938	0.2090778	0.2299236				0.1643261			0.180118
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value	0.0067795		0.0039076	0.0268535	0.0103184	0.0015624																					
		RHO	-0.196841		-0.209505	-0.161462	-0.186667	-0.229125																					
	P281-PWY 3-phenylpropanoate degradation	p-value						0.031705																					
		RHO						-0.156743																					
	LPSSYN-PWY superpathway of lipopolysaccharide biosynthesis	p-value	1.85E-06		0.0015541		0.0002075	0.0002638		0.0245495				0.0037894		0.0342816				0.0379023						0.0002132	0.0007273		
		RHO	-0.339661		-0.229234		-0.267402	-0.263143		-0.163965				-0.210191		-0.154482				-0.151537						-0.266917	-0.244327		
	LEU-DEG2-PWY L-leucine degradation I	p-value	0.0001266	0.0005631	0.0019534	0.0070239	0.0027169	0.0002453	0.0043577	0.0042444						0.0037846										0.0161432	0.0139439		

		RHO	-0.275948	-0.249212	-0.224495	-0.196001	-0.217484	-0.264437	-0.207056	-0.207651						-0.210219										-0.17526	-0.179062		
	HEMESYN2-PWY heme biosynthesis II_anaerobic	p-value	2.22E-06		5.44E-05	1.04E-05	2.47E-06	0.0035607	0.0024315	0.0026419	0.005478		0.0464533	0.032152					0.0010813	0.0020617	0.0370951	0.0240562				0.0082401			0.0066513
		RHO	0.33721		0.2899249	0.3154503	0.3357466	0.2115732	0.2198666	0.2180876	0.2018268		0.1454238	0.1563395					0.2365632	0.223363	0.1521718	0.1645268				0.192175			0.1972918
	GLYCOLYSIS-E-D superpathway of glycolysis and Entner-Doudoroff	p-value	1.07E-08		4.86E-06	1.22E-06	3.88E-06	1.41E-05	0.0061666	0.0052488				0.0195474		0.0109246			0.0015484	0.0019135	0.0099701	0.0071642				0.0013018	0.0446533	0.0480206	0.0023736
		RHO	0.402096		0.3263561	0.3452126	0.3295126	0.3109163	0.1990713	0.2028128				0.1701827		0.1852466			0.2293099	0.2249266	0.1875176	0.1955311				0.232841	0.1466271	0.1444075	0.2203807
	CODH-PWY reductive acetyl coenzyme A pathway	p-value	1.68E-06		2.27E-06	3.78E-07	4.09E-06	5.48E-05												0.0316316	0.0480811	0.0312047				0.0105598			
		RHO	0.3409567		0.3369426	0.3603585	0.3287892	0.2898151												0.1568094	0.1443688	0.1571997				0.186093			
	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	p-value	0.0082704		0.0049981	0.0380673	0.0159714	0.0019286																					
		RHO	-0.192086		-0.203937	-0.151408	-0.17554	-0.224762																					
	ASPASN-PWY superpathway of L-aspartate and L-asparagine biosynthesis	p-value	0.0004461		0.0074423	0.0020166	0.0061205	0.0124488											0.0097446	0.0037199	0.0075453	0.0102186				0.0189215			
		RHO	0.2535725		0.1946228	0.2238276	0.1992468	0.1819592											0.1880822	0.2106027	0.1942939	0.1869084				0.1710551			
	AEROBACTINSYN-PWY aerobactin biosynthesis	p-value	0.0333815			0.0153414			0.0339125	0.0233772	0.0323501					0.0201161	0.0374263		0.0057978	0.0177611		0.0377023	0.0324883			0.0198985			
		RHO	0.1552547			0.1765902			0.1547966	0.1653167	0.1561624					0.1694107	0.1519097		0.2005106	0.1727413		0.1516928	0.1560394			0.1697038			
age bracket 6 (6~7 y)			Group	age	ASD_score	Repetitive_b	Social_retarc	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_(	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_cc	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_h	Antibiotic_within_3_months
	VALSYN-PWY L-valine biosynthesis	p-value	0.0185328		0.0460818		0.0306259	0.0136871																	0.0032481				
		RHO	0.2009683		0.1707249		0.1848029	0.2101982																	-0.249748				
	TRNA-CHARGING-PWY tRNA charging	p-value	0.0261538					0.0161133																	0.0021214				0.0411815
		RHO	0.1900089					0.205274																	-0.26036				-0.174691
	THRESYN-PWY superpathway of L-threonine biosynthesis	p-value	0.0276481					0.0178																	0.0040649				
		RHO	0.1881902					0.2022182																	-0.243979				
	PWY-7560 methylerythritol phosphate pathway II	p-value	0.0073662		0.025189	0.0478265	0.0223362	0.0042571																	0.0024833				0.0255971
		RHO	0.2280175		0.1912309	0.1693976	0.1950947	0.2427743																	-0.256487				-0.190709
	PWY-7527 L-methionine salvage cycle III	p-value	0.0476584				0.0362318	0.0424907										0.0330998											
		RHO	-0.169524				-0.179121	-0.173594										0.1821953											
	PWY-7446 sulfoglycolysis	p-value	0.0065108		0.0045267	0.0038503	0.0122506	0.0038006						0.0396872												0.0286639	0.0159807		
		RHO	-0.231417		-0.241164	-0.245385	-0.213486	-0.245722						-0.175979												-0.187001	-0.205526		
	PWY-7400 L-arginine biosynthesis IV_archaebacteria	p-value	0.0046297		0.0067531	0.0280888	0.0064099	0.0020573																	0.0115336				
		RHO	0.2405717		0.2304154	0.1876699	0.2318437	0.2611077																	-0.215255				
	PWY-7219 adenosine ribonucleotides de novo biosynthesis	p-value	0.0207021					0.0114046																	0.0016172				0.0272474
		RHO	0.1975036					0.2155841																	-0.266902				-0.18867
	PWY-7208 superpathway of pyrimidine nucleobases salvage	p-value	0.013585		0.0334195		0.0315376	0.0068858																	0.0018454				0.030146
		RHO	0.2104217		0.1818705		0.1838218	0.2298804																	-0.263741				-0.185329
	PWY-6630 superpathway of L-tyrosine biosynthesis	p-value	0.001602		0.0008149	0.0002172	0.0021165	0.0018999																					
		RHO	0.2671276		0.2827446	0.3109302	0.2604168	0.2630379																					
	PWY-6628 superpathway of L-phenylalanine biosynthesis	p-value	0.0019944		0.0009558	0.000253	0.002583	0.0022481																					
		RHO	0.2618629		0.2791393	0.3078232	0.2555094	0.2589406																					
	PWY-6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	p-value	0.0186766		0.0082764	0.0159104	0.0301946	0.0064187	0.0278955	0.0311233										0.0481712					0.0497058		0.0441739		
		RHO	-0.200728		-0.224765	-0.20566	-0.185276	-0.231806	-0.187897	-0.184265										-0.16914					-0.168012		-0.172225		
	PWY-6387 UDP-N-acetylmuramoyl-pentapeptide biosynthesis I_meso-diaminopimelate containing	p-value	0.0244404					0.0121485																	0.0020411				0.029967
		RHO	0.1922069					0.2137325																	-0.261301				-0.185527
	PWY-6386 UDP-N-acetylmuramoyl-pentapeptide biosynthesis II_lysine-containing	p-value	0.023231					0.0132729																	0.0018993				0.0294698
		RHO	0.1938393					0.211114																	-0.263046				-0.186083
	PWY-6385 peptidoglycan biosynthesis III_mycobacteria	p-value	0.0230841					0.012651																	0.0019677				0.0311737
		RHO	0.1940425					0.2125371																	-0.26219				-0.18421
	PWY-6163 chorismate biosynthesis from 3-dehydroquinate	p-value	0.0269319					0.0131607																	0.0019191				0.0252046
		RHO	0.1890512					0.2113665																	-0.262795				-0.191211
	PWY-6123 inosine-5-phosphate biosynthesis I	p-value	0.0198779		0.048049			0.0102475																	0.0026349				0.0258831
		RHO	0.1987812		0.1692312			0.2186869																	-0.255014				-0.190348
	PWY-5920 superpathway of heme biosynthesis from glycine	p-value	0.0047056		0.003181	0.0095916	0.0070831	0.001892		0.0436228																	0.0308381		
		RHO	-0.240142		-0.250278	-0.220585	-0.229102	-0.263139		-0.172669																	-0.184572		
	PWY-5896 superpathway of menaquinol-10 biosynthesis	p-value	0.0238904		0.0168145	0.0446471	0.0239984	0.0090477																					0.0067048
		RHO	-0.19294		-0.203971	-0.171848	-0.192795	-0.222248																					0.2306126
	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	p-value	0.0262903		0.0191836	0.0497489	0.0261252	0.0101663																					0.006402
		RHO	-0.189839		-0.199893	-0.167981	-0.190045	-0.218916																					0.2318773
	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	p-value	0.0262903		0.0191836	0.0497489	0.0261252	0.0101663																					0.006402
		RHO	-0.189839		-0.199893	-0.167981	-0.190045	-0.218916																					0.2318773
	PWY-5850 superpathway of menaquinol-6 biosynthesis I	p-value	0.0238904		0.0168145	0.0446471	0.0239984	0.0090477																					0.0067048
		RHO	-0.19294		-0.203971	-0.171848	-0.192795	-0.222248																					0.2306126
	PWY-5845 superpathway of menaquinol-9 biosynthesis	p-value	0.0238904		0.0168145	0.0446471	0.0239984	0.0090477																					0.0067048
		RHO	-0.19294		-0.203971	-0.171848	-0.192795	-0.222248																					0.2306126
	PWY-5431 aromatic compounds degradation via b-ketoadipate	p-value	0.0001805		0.000139	0.0002172	0.0007792	5.60E-05	0.0006071	0.0002426			0.0043466	0.0214777		0.0065786											0.0266269		
		RHO	-0.314663		-0.31984	-0.31093	-0.283747	-0.337181	-0.289272	-0.308679			-0.24223	-0.196341		-0.231133											-0.189424		
	PWY-5417 catechol degradation III_ortho-cleavage pathway	p-value	0.0001805		0.000139	0.0002172	0.0007792	5.60E-05	0.0006071	0.0002426			0.0043466	0.0214777		0.0065786											0.0266269		
		RHO	-0.314663		-0.31984	-0.31093	-0.283747	-0.337181	-0.289272	-0.308679			-0.24223	-0.196341		-0.231133											-0.189424		
	PWY-5177 glutaryl-CoA degradation	p-value	0.0344897		0.0263199			0.0118015	0.0412342	0.04292																	0.0240918		0.0170304
		RHO	-0.180802		-0.189802			-0.214584	-0.174646	-0.173241																	-0.19267		0.2035798
	PWY-5121 superpathway of geranylgeranyl diphosphate biosynthesis II_via MEP	p-value	0.0104183		0.0329141		0.0300276	0.0060866																	0.0021995				0.0214712
		RHO	0.2182101		0.1823852		0.1854602	0.2332523																	-0.259476				-0.19635
	PWY-5104 L-isoleucine biosynthesis IV	p-value	0.0246488		0.0463128		0.0356042	0.0145219																	0.002393				
		RHO	0.1919326		0.1705468		0.1797185	0.2084236																	-0.257402				
	PWY-5103 L-isoleucine biosynthesis III	p-value	0.0199542		0.0454799		0.0297743	0.0139327																	0.0028297				
		RHO	0.198661		0.1711925		0.1857419	0.2096666																	-0.253231				
	PWY-5101 L-isoleucine biosynthesis II	p-value	0.0166299		0.0420996		0.0261858	0.0119396																	0.0033006				
		RHO	0.2043097		0.1739189		0.189969	0.214242																	-0.24934				
	PWY-3001 superpathway of L-isoleucine biosynthesis I	p-value	0.0213096		0.0431849		0.0339328	0.0138916																	0.0037517				
		RHO	0.1965895		0.1730243		0.1813544	0.2097549																	-0.246056				
	PWY-2942 L-lysine biosynthesis III	p-value	0.0199922					0.0143637																	0.0018637				0.0436537
		RHO	0.1986014					0.2087531																	-0.263503				-0.172644
	PWY0-1533 methylphosphonate degradation I	p-value																									0.0450556		0.0214464
		RHO																									-0.171525		0.1963867
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value	3.51E-05		2.83E-05	5.03E-05	0.0001981	1.24E-05	0.0008729	0.0003702			0.0045549	0.0150251		0.0059282											0.0189894		
		RHO	-0.345678		-0.349558	-0.339148	-0.312791	-0.363786	-0.281196	-0.299908			-0.241	-0.207397		-0.233967											-0.200211		
	PEPTIDOGLYCANSYN-PWY peptidoglycan biosynthesis I_meso-diaminopimelate containing	p-value	0.023479					0.0123459																	0.0019621				0.0310069
		RHO	0.1934987					0.2132579																	-0.262259				-0.18439
	P281-PWY 3-phenylpropanoate degradation	p-value	7.79E-05	0.0419616	4.46E-05	4.88E-05	0.000326	2.09E-05	3.01E-05	1.57E-05			0.0013648	0.0084751		0.0025072											0.0290333		
		RHO	-0.33101	-0.174034	-0.341352	-0.339725	-0.302578	-0.354864	-0.348473	-0.359792			-0.270912	-0.224098		-0.256249											-0.186578		
	ORNDEG-PWY superpathway of ornithine degradation	p-value	0.0145614		0.0140031	0.0345446	0.0167907	0.0071942																					0.0133426
		RHO	-0.208342		-0.209516	-0.180748	-0.204015	-0.228672																					0.2109582
	ORNARGDEG-PWY superpathway of L-arginine and L-ornithine degradation	p-value	0.0162453		0.0142354	0.0338306	0.0177449	0.0079067																					0.0139082
		RHO	-0.205025		-0.209022	-0.181457	-0.202314	-0.226046																					0.2097193
	NONMEVIPP-PWY methylerythritol phosphate pathway I	p-value	0.0073662		0.025189	0.0478265	0.0223362	0.0042571																	0.0024833				0.0255971
		RHO	0.2280175		0.1912309	0.1693976	0.1950947	0.2427743																	-0.256487				-0.190709
	ILEUSYN-PWY L-isoleucine biosynthesis I_from threonine	p-value	0.0185328		0.0460818		0.0306259	0.0136871																	0.0032481				
		RHO	0.2009683		0.1707249		0.1848029	0.2101982																	-0.249748				
	HISTSYN-PWY L-histidine biosynthesis	p-value	0.0120355		0.0207101		0.0177392	0.0043892																	0.0040733				
		RHO	0.2140072		0.1974913		0.2023238	0.2419745																	-0.243925				
	ENTBACSYN-PWY enterobactin biosynthesis	p-value	0.0222326		0.0175723	0.0420383	0.0233044	0.0102631																					0.011183
		RHO	-0.195243		-0.202616	-0.17397	-0.193738	-0.218643																					0.2161562
	DHGLUCONATE-PYR-CAT-PWY glucose degradation_oxidative	p-value	9.95E-05	0.0106775	1.06E-05	3.62E-05	2.08E-05	2.90E-05								0.0008388													
		RHO	-0.326338	-0.2175	-0.366415	-0.345137	-0.354955	-0.349145								-0.282093													
	COMPLETE-ARO-PWY superpathway of aromatic amino acid biosynthesis	p-value	0.0166736		0.0338608		0.0304001	0.0081861																	0.0017046				0.029932
		RHO	0.2042293		0.1814264		0.1850497	0.2250732																	-0.265646				-0.185566
	CENTFERM-PWY pyruvate fermentation to butanoate	p-value	0.0181337		0.0080391	0.0153573	0.0293127	0.0062474	0.0267896	0.0297368										0.0489858							0.0427568		
		RHO	-0.201643		-0.225581	-0.206735	-0.186261	-0.232544	-0.189225	-0.185784										-0.168538							-0.173375		
	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	p-value	0.0002239		0.0001359	0.0002229	0.0008305	6.17E-05	0.0005121	0.000186			0.0045142	0.0189345		0.0046982											0.0355644		
		RHO	-0.310313		-0.320281	-0.31041	-0.282317	-0.335371	-0.292976	-0.314056			-0.241237	-0.200301		-0.240184											-0.179757		
	BRANCHED-CHAIN-AA-SYN-PWY superpathway of branched amino acid biosynthesis	p-value	0.0166299		0.0399389		0.0261943	0.0115347																	0.002828				
		RHO	0.2043097		0.1757592		0.1899585	0.2152528																	-0.253246				
	AST-PWY L-arginine degradation II_AST pathway	p-value	0.0107178		0.0107327	0.0255367	0.0136821	0.0054997		0.0429255				0.049176															0.0125394
		RHO	-0.21739		-0.21735	-0.190786	-0.210209	-0.23599		-0.173236				-0.168398															0.2127989
	ARGSYN-PWY L-arginine biosynthesis I_via L-ornithine	p-value	0.0045419		0.0065489	0.0281206	0.0062129	0.001968																	0.0119071				
		RHO	0.2410759		0.2312571	0.1876326	0.2326946	0.2621865																	-0.214322				
	ARGDEG-PWY superpathway of L-arginine putrescine and 4-aminobutanoate degradation	p-value	0.0162453		0.0142354	0.0338306	0.0177449	0.0079067																					0.0139082
		RHO	-0.205025		-0.209022	-0.181457	-0.202314	-0.226046																					0.2097193
			Group	age	ASD_score	Repetitive_b	Social_retarc	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_(	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_cc	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_h	Antibiotic_within_3_months
	TYRFUMCAT-PWY L-tyrosine degradation I	p-value	8.97E-05		0.0086804		0.0050651	0.0018137	0.0083629	0.0396262									0.0357154										NA
		RHO	-0.445023		-0.307148		-0.326914	-0.36141	-0.308557	-0.243097									-0.247965										NA
	THREOCAT-PWY superpathway of L-threonine metabolism	p-value	0.0095692	0.004429	0.0396701		0.0298062												0.0402953	0.0090538									NA
		RHO	-0.303429	0.3316452	-0.243045		-0.256243												-0.242305	-0.305547									NA
	TCA-GLYOX-BYPASS superpathway of glyoxylate bypass and TCA	p-value	0.0011062	0.0088095	0.0068094	0.0320466	0.002844	0.0155448												0.0260363									NA
		RHO	-0.376755	0.3065879	-0.316215	-0.252955	-0.346769	-0.2842												-0.262278									NA
	REDCITCYC TCA cycle VIII_helicobacter	p-value		0.0218399	0.0304795	0.0406241	0.0208045																						NA
		RHO		0.2699358	-0.255234	-0.241919	-0.272017																						NA
	PWY-7392 taxadiene biosynthesis_engineered	p-value	0.0013094		0.0014215	0.0084964	0.0015003	0.0010627											0.0270774	0.0051712		0.0147153	0.029912		0.0359759				NA
		RHO	-0.371605		-0.369066	-0.307959	-0.367387	-0.37797											-0.260541	-0.326176		-0.286437	-0.256083		-0.247628				NA
	PWY-7003 glycerol degradation to butanol	p-value																									0.0011029		NA
		RHO																									-0.376846		NA
	PWY-6690 cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate	p-value	0.0015521	0.0052486	0.021947	0.0296264	0.0185986	0.0449716											0.0169093	0.0097219									NA
		RHO	-0.366326	0.3256471	-0.269725	-0.256516	-0.276763	-0.237051											-0.280735	-0.302821									NA
	PWY-6562 norspermidine biosynthesis	p-value	0.005059	0.0024651	0.0099936	0.0172447	0.0073368	0.0238253																	0.0181481				NA
		RHO	-0.326956	0.3514967	-0.301759	-0.27992	-0.313457	-0.26617																	-0.277791				NA
	PWY-6185 4-methylcatechol degradation_ortho cleavage	p-value	8.63E-06	0.0010416	5.35E-05	0.0002513	3.41E-05	0.0003139						0.0225923					0.0238721	0.0064995					0.0202741				NA
		RHO	-0.497785	0.3785722	-0.457459	-0.418761	-0.46785	-0.412797						-0.268476					-0.266085	-0.317924					-0.273117				NA
	PWY-6182 superpathway of salicylate degradation	p-value	1.98E-05	0.0005449	0.000186	0.0007103	0.0001047	0.0008419						0.023557					0.0310097	0.0143327					0.0289721				NA
		RHO	-0.480084	0.3975181	-0.426661	-0.3899	-0.441212	-0.384923						-0.266663					-0.254452	-0.287506					-0.25752				NA
	PWY-6071 superpathway of phenylethylamine degradation	p-value	0.0001497	0.0005964	0.0013797	0.0045284	0.0007578	0.0053406						0.008746					0.0432027	0.0087539			0.0265774	0	0			0.0472754	NA
		RHO	-0.432234	0.3949411	-0.369991	-0.330868	-0.388014	-0.325026						-0.306862					-0.238983	-0.306828			-0.261368	-0.116833	-0.227591			-0.234628	NA
	PWY-5920 superpathway of heme biosynthesis from glycine	p-value	0.0010301		0.00346	0.0078998	0.0012316	0.0137828											0.0114498	0.0067428									NA
		RHO	-0.378909		-0.340165	-0.3107	-0.373485	-0.289086											-0.296462	-0.316576									NA
	PWY-5896 superpathway of menaquinol-10 biosynthesis	p-value	0.0069541	0.0138701	0.0220292		0.0112911	0.0441043						0.0289781															NA
		RHO	-0.31544	0.2888313	-0.269564		-0.29701	-0.237991						-0.257511															NA
	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	p-value	0.00621	0.0146757	0.020082		0.0102428	0.0394456						0.0289781						0.0499586									NA
		RHO	-0.319587	0.2865468	-0.273522		-0.300807	-0.243313						-0.257511						-0.231924									NA
	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	p-value	0.00621	0.0146757	0.020082		0.0102428	0.0394456						0.0289781						0.0499586									NA
		RHO	-0.319587	0.2865468	-0.273522		-0.300807	-0.243313						-0.257511						-0.231924									NA
	PWY-5850 superpathway of menaquinol-6 biosynthesis I	p-value	0.0069541	0.0138701	0.0220292		0.0112911	0.0441043						0.0289781															NA
		RHO	-0.31544	0.2888313	-0.269564		-0.29701	-0.237991						-0.257511															NA
	PWY-5845 superpathway of menaquinol-9 biosynthesis	p-value	0.0069541	0.0138701	0.0220292		0.0112911	0.0441043						0.0289781															NA
		RHO	-0.31544	0.2888313	-0.269564		-0.29701	-0.237991						-0.257511															NA
	PWY-5747 2-methylcitrate cycle II	p-value	0.0004316	0.0271944	0.0018815	0.0020825	0.0011494	0.0147542						0.0282796		0.0437032				0.0036213									NA
		RHO	-0.404067	0.2603494	-0.360241	-0.356984	-0.375594	-0.28633						-0.258605		-0.23843			-0.352381	-0.338611									NA
	PWY-5431 aromatic compounds degradation via b-ketoadipate	p-value	1.79E-05	0.0004218	0.0001686	0.0006197	9.17E-05	0.0008266						0.0287258					0.0307859	0.015201					0.0459276				NA
		RHO	-0.482249	0.4047031	-0.429204	-0.393841	-0.444479	-0.385463						-0.257903					-0.254781	-0.285115					-0.236033				NA
	PWY-5417 catechol degradation III_ortho-cleavage pathway	p-value	1.79E-05	0.0004218	0.0001686	0.0006197	9.17E-05	0.0008266						0.0287258					0.0307859	0.015201					0.0459276				NA
		RHO	-0.482249	0.4047031	-0.429204	-0.393841	-0.444479	-0.385463						-0.257903					-0.254781	-0.285115					-0.236033				NA
	PWY-5415 catechol degradation I_meta-cleavage pathway	p-value	0.0008996	0.0220376	0.0185813	0.0427184	0.0157289	0.0215205						0.0323345					0.0104367	0.0118553									NA
		RHO	-0.38296	0.269548	-0.276802	-0.239523	-0.283718	-0.270569						-0.252547					-0.30008	-0.295092									NA
	PWY-5345 superpathway of L-methionine biosynthesis_by sulfhydrylation	p-value	0.0222129	0.0349631	0.0079392	0.0401668	0.0044383	0.0229239																					NA
		RHO	-0.269207	0.2489525	-0.310513	-0.242456	-0.331572	-0.267845																					NA
	PWY-5181 toluene degradation III_aerobic_via p-cresol	p-value	9.00E-06	0.0011331	6.22E-05	0.000298	3.52E-05	0.0003668						0.0211757					0.0236968	0.006667					0.0171484				NA
		RHO	-0.496909	0.3760269	-0.453888	-0.414208	-0.467175	-0.40856						-0.271261					-0.266405	-0.316991					-0.280152				NA
	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	p-value						0.0450517																0.048244					NA

age bracket 7 (7–8 y)	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	RHO						-0.236965																0.2336375					NA
	PWY0-42 2-methylcitrate cycle I	p-value	0.0010444	0.0237665	0.0067232	0.0133584	0.0045577	0.0247264						0.0495534					0.009862	0.0131496									NA
		RHO	-0.378493	0.2662775	-0.316683	-0.290343	-0.330641	-0.264548						-0.232325					-0.302271	-0.290974									NA
	PWY0-1533 methylphosphonate degradation I	p-value			0.0414123		0.0203475				0.04453																		NA
		RHO			-0.241006		-0.272963				-0.237528																		NA
	PWY0-1338 polymyxin resistance	p-value	0.0036118	0.0078754	0.0185752		0.008836	0.0353267																					NA
		RHO	-0.3387	0.3108153	-0.276816		-0.306474	-0.248473																					NA
	PWY0-1277 3-phenylpropanoate and 3-3-hydroxyphenylpropanoate degradation	p-value	0.0013873	0.0056286	0.0212284	0.0292577	0.0171302	0.0438703						0.047112					0.0145623	0.0100818									NA
		RHO	-0.369822	0.3231428	-0.271154	-0.25708	-0.280197	-0.238246						-0.234796					-0.286862	-0.30142									NA
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value	1.31E-05	0.0015014	4.35E-05	9.17E-05	1.89E-05	0.0005272						0.0210961					0.0128631	0.0055244					0.0324826				NA
		RHO	-0.488944	0.3673633	-0.462302	-0.444484	-0.48108	-0.398451						-0.271422					-0.291854	-0.323814					-0.252338				NA
	PPGPPMET-PWY ppGpp biosynthesis	p-value	0.0313157	0.0189829			0.0366936							0															NA
		RHO	-0.254006	0.2759023			-0.246708							-0.132814															NA
	P281-PWY 3-phenylpropanoate degradation	p-value	0.0001869	0.0007057	0.0018301	0.0060263	0.0007746	0.0057337						0.0161292					0.0202101	0.01041									NA
		RHO	-0.426541	0.3900915	-0.361125	-0.320677	-0.387373	-0.322477						-0.282685					-0.273251	-0.300179									NA
	P105-PWY TCA cycle IV_2-oxoglutarate decarboxylase	p-value	0.0010663	0.0081043	0.00854	0.0344258	0.0038181	0.0181002						0.0358279						0.0265631									NA
		RHO	-0.377867	0.3097405	-0.307766	-0.249668	-0.336795	-0.277901						-0.247819						-0.261392									NA
	ORNDEG-PWY superpathway of ornithine degradation	p-value	0.0037439	0.0090781	0.0181371		0.0093576	0.0346454						0.0398784						0.0480219									NA
		RHO	-0.33747	0.305445	-0.277816		-0.304286	-0.249375						-0.242797						-0.233863									NA
	ORNARGDEG-PWY superpathway of L-arginine and L-ornithine degradation	p-value	0.0046625	0.0174395	0.0207738		0.0102836	0.0405235						0.0404544															NA
		RHO	-0.329842	0.2794529	-0.27208		-0.300653	-0.242037						-0.242118															NA
	NAD-BIOSYNTHESIS-II NAD salvage pathway II	p-value					0.0425176																						NA
		RHO					-0.239749																						NA
	METHGLYUT-PWY superpathway of methylglyoxal degradation	p-value	0.0073577	0.0367716	0.0287588	0	0.0145941																						NA
		RHO	-0.313352	0.2466086	-0.257852	-0.200157	-0.286773																						NA
	KDO-NAGLIPASYN-PWY superpathway of_Kdo2-lipid A biosynthesis	p-value	0.0379583	0.0321531			0.0368921																		0.0331861				NA
		RHO	-0.245122	0.2528038			-0.246456																		-0.251356				NA
	HCAMHPDEG-PWY 3-phenylpropanoate and 3-3-hydroxyphenylpropanoate degradation to 2-oxopent-4-enoate	p-value	0.0015521	0.0052486	0.021947	0.0296264	0.0185986	0.0449716											0.0169093	0.0097219									NA
		RHO	-0.366326	0.3256471	-0.269725	-0.256516	-0.276763	-0.237051											-0.280735	-0.302821									NA
	GLYOXYLATE-BYPASS glyoxylate cycle	p-value	0.0029399	0.0257527	0.0110124	0.0332897	0.0047677	0.0292685						0.0280985						0.0252612									NA
		RHO	-0.345661	0.2627609	-0.297989	-0.251213	-0.329056	-0.257063						-0.258892						-0.263609									NA
	GLYCOLYSIS-TCA-GLYOX-BYPASS superpathway of glycolysis pyruvate dehydrogenase TCA and glyoxylate bypass	p-value	0.0012436	0.0086992	0.0075718	0.0346739	0.0032715	0.0169825						0.0284197						0.026716									NA
		RHO	-0.373189	0.3070659	-0.312284	-0.249337	-0.342066	-0.280556						-0.258383						-0.261137									NA
	GLYCOL-GLYOXDEG-PWY superpathway of glycol metabolism and degradation	p-value	0.0052912		0.0129966	0.0293053	0.0074523	0.0423191						0.0438087						0.0283085									NA
		RHO	-0.325358		-0.291442	-0.257006	-0.312877	-0.239972						-0.238314						-0.258559									NA
	GLUCOSE1PMETAB-PWY glucose and glucose-1-phosphate degradation	p-value		0.0360955	0.0456148		0.0293881						0.0402266																NA
		RHO		0.2474733	-0.236365		-0.256879						-0.242386																NA
	FAO-PWY fatty acid b-oxidation I	p-value	0.0038925	0.016319	0.0244251		0.0079681																						NA
		RHO	-0.33613	0.2822033	-0.265085		-0.310377																						NA
	ENTBACSYN-PWY enterobactin biosynthesis	p-value	0.0039589	0.0278648	0.0154522		0.0077727	0.0312992						0.047327															NA
		RHO	-0.335547	0.2592647	-0.284445		-0.311307	-0.25403						-0.234574															NA
	ECASYN-PWY enterobacterial common antigen biosynthesis	p-value	0.0042888	0.0176357	0.0178673		0.0096896	0.0359482						0.0464592															NA
		RHO	-0.332769	0.2789869	-0.278443		-0.302949	-0.247664						-0.235475															NA
	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	p-value	1.56E-05	0.0004115	0.0001413	0.0005498	7.70E-05	0.000701						0.0302527					0.0302185	0.0154455					0.047204				NA
		RHO	-0.485284	0.4053898	-0.433713	-0.397264	-0.448763	-0.390285						-0.255572					-0.255623	-0.284463					-0.234701				NA
	AST-PWY L-arginine degradation II_AST pathway	p-value	0.0025437	0.0069469	0.0118591	0.0472135	0.0058602	0.0260589						0.0300309						0.0476162									NA
		RHO	-0.350464	0.3154781	-0.295079	-0.234691	-0.321689	-0.262239						-0.255904						-0.234277									NA
	ARGDEG-PWY superpathway of L-arginine putrescine and 4-aminobutanoate degradation	p-value	0.0046625	0.0174395	0.0207738		0.0102836	0.0405235						0.0404544															NA
		RHO	-0.329842	0.2794529	-0.27208		-0.300653	-0.242037						-0.242118															NA
	ALL-CHORISMATE-PWY superpathway of chorismate metabolism	p-value	0.0031213	0.0149916	0.0145614		0.0060378	0.0328329																					NA
		RHO	-0.343652	0.2856803	-0.286864		-0.320608	-0.251847																					NA
	3-HYDROXYPHENYLACETATE-DEGRADATION-PWY 4-hydroxyphenylacetate degradation	p-value	0.0002198	0.0001954	0.0019762	0.0065669	0.001027	0.0069352						0.0131811					0.0488579	0.0124167			0.0373901						NA
		RHO	-0.422299	0.4253798	-0.35867	-0.317546	-0.379	-0.31554						-0.290878					-0.233018	-0.29326			-0.245829						NA
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_(	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
age bracket 8 (8–9 y)	UBISYN-PWY superpathway of ubiquinol-8 biosynthesis_prokaryotic	p-value										NA	0.0367902															
		RHO										NA	-0.279744															
	TRPSYN-PWY L-tryptophan biosynthesis	p-value										NA																	
		RHO										NA																	
	TCA-GLYOX-BYPASS superpathway of glyoxylate bypass and TCA	p-value	0.0413848		0.0113428	0.0058527	0.0277535	0.0254088				NA	0.0349169						0.0496135		0.0247097								
		RHO	-0.273508		-0.336025	-0.363771	-0.294182	-0.298567				NA	-0.282473						-0.263639		-0.299941								
	SULFATE-CYS-PWY superpathway of sulfate assimilation and cysteine biosynthesis	p-value			0.0228256	0.0383753	0.0428479	0.0359586				NA																	
		RHO			-0.303812	-0.277523	-0.271642	-0.280941				NA																	
	SO4ASSIM-PWY sulfate reduction I_assimilatory	p-value	0.0426072		0.0138007	0.0240413	0.0244357	0.022798				NA																	
		RHO	-0.271945		-0.327316	-0.301285	-0.300488	-0.303871				NA																	
	PWY-7527 L-methionine salvage cycle III	p-value										NA																	
		RHO										NA																	
	PWY-7376 cobllyrinate a_c-diamide biosynthesis II_late cobalt incorporation	p-value	0.0377401		0.0407264	0.0262197						NA																	
		RHO	-0.278404		-0.274365	-0.297014						NA																	
	PWY-7373 superpathway of demethylmenaquinol-6 biosynthesis II	p-value										NA																	
		RHO										NA																	
	PWY-7094 fatty acid salvage	p-value	0.0056512		0.021584	0.0304964	0.0166555	0.0268837				NA	0.0410094															
		RHO	-0.365175		-0.306513	-0.28943	-0.318737	-0.295771				NA	-0.273995															
	PWY-6876 isopropanol biosynthesis	p-value										NA														0.0139162		0.0496423	
		RHO										NA														-0.326941		-0.263607	
	PWY-6708 ubiquinol-8 biosynthesis_prokaryotic	p-value										NA	0.0334892															
		RHO										NA	-0.284635															
	PWY-6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	p-value										NA																	
		RHO										NA																	
	PWY-5896 superpathway of menaquinol-10 biosynthesis	p-value			0.0191146	0.0095332	0.0455065	0.0424115				NA	0.0497651								0.0236058								
		RHO			-0.312302	-0.343548	-0.268382	-0.272193				NA	-0.26347								-0.302177								
	PWY-5862 superpathway of demethylmenaquinol-9 biosynthesis	p-value			0.0198361	0.0098231	0.0464791	0.0429132				NA	0.0459804								0.0223866								
		RHO			-0.310548	-0.342264	-0.267228	-0.27156				NA	-0.267817								-0.304753								
	PWY-5860 superpathway of demethylmenaquinol-6 biosynthesis I	p-value			0.0198361	0.0098231	0.0464791	0.0429132				NA	0.0459804								0.0223866								
		RHO			-0.310548	-0.342264	-0.267228	-0.27156				NA	-0.267817								-0.304753								
	PWY-5857 ubiquinol-10 biosynthesis_prokaryotic	p-value										NA	0.0334892															
		RHO										NA	-0.284635															
	PWY-5856 ubiquinol-9 biosynthesis_prokaryotic	p-value										NA	0.0334892															
		RHO										NA	-0.284635															
	PWY-5855 ubiquinol-7 biosynthesis_prokaryotic	p-value										NA	0.0334892															
		RHO										NA	-0.284635															
	PWY-5850 superpathway of menaquinol-6 biosynthesis I	p-value			0.0191146	0.0095332	0.0455065	0.0424115				NA	0.0497651								0.0236058								
		RHO			-0.312302	-0.343548	-0.268382	-0.272193				NA	-0.26347								-0.302177								
	PWY-5845 superpathway of menaquinol-9 biosynthesis	p-value			0.0191146	0.0095332	0.0455065	0.0424115				NA	0.0497651								0.0236058								
		RHO			-0.312302	-0.343548	-0.268382	-0.272193				NA	-0.26347								-0.302177								
	PWY-5677 succinate fermentation to butanoate	p-value				0.0309131		0.0472419				NA	0.0216691	0.0099709															
		RHO				0.2887391		0.2663365				NA	0.3063241	0.3416216															
	PWY-5507 adenosylcobalamin biosynthesis I_early cobalt insertion	p-value										NA											0.024039						
		RHO										NA											0.3012892						
	PWY-5177 glutaryl-CoA degradation	p-value			0.0262509	0.0154792	0.0475347	0.0442342				NA																	
		RHO			-0.296955	-0.322107	-0.265998	-0.269922				NA																	
	PWY-5088 L-glutamate degradation VIII_to propanoate	p-value	0.002518		0.0080297	0.0168185	0.0087226	0.0099846				NA														0.0240122			
		RHO	-0.396007		-0.350808	-0.318286	-0.347327	-0.341563				NA														-0.301344			
	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	p-value										NA																	
		RHO										NA																	
	PWY-181 photorespiration	p-value										NA								0.0330292									
		RHO										NA								-0.285348									
	PWY0-1415 superpathway of heme biosynthesis from uroporphyrinogen-III	p-value									0.0317858	NA							0.0444445										
		RHO									-0.287318	NA							0.2696648										
	PWY0-1338 polymyxin resistance	p-value			0.0140203	0.0082726	0.0357215	0.0321046				NA									0.0212192								
		RHO			-0.326605	-0.349559	-0.281286	-0.286807				NA									-0.307332								
	PANTO-PWY phosphopantothenate biosynthesis I	p-value										NA												0.0293969					
		RHO										NA												0.2912898					
	P381-PWY adenosylcobalamin biosynthesis II_late cobalt incorporation	p-value	0.0399051		0.0434502	0.0274892						NA																	
		RHO	-0.275451		-0.270889	-0.29466						NA									-0.174324								
	P105-PWY TCA cycle IV_2-oxoglutarate decarboxylase	p-value	0.0457969		0.0115399	0.0073013	0.0275265	0.0252841				NA	0.020262						0.0444463		0.0247029								
		RHO	-0.268035		-0.335269	-0.354761	-0.294592	-0.29881				NA	-0.309538						-0.269663		-0.299954								
	ORNDEG-PWY superpathway of ornithine degradation	p-value			0.0130815	0.0064788	0.0335863	0.0308854				NA	0.0354043								0.0187066								
		RHO			-0.329716	-0.359661	-0.284486	-0.288785				NA	-0.281751								-0.313319								
	ORNARGDEG-PWY superpathway of L-arginine and L-ornithine degradation	p-value			0.0278879	0.0154239						NA									0.0262957								
		RHO			-0.29394	-0.322271						NA									-0.29687								
	METHGLYUT-PWY superpathway of methylglyoxal degradation	p-value			0.0297847	0.0152661						NA									0.0311754								
		RHO			-0.290627	-0.32274						NA									-0.288308								
	GLYOXYLATE-BYPASS glyoxylate cycle	p-value	0.0407969		0.0100911	0.0044066	0.0275195	0.0249188				NA	0.0304997								0.0304261								
		RHO	-0.274273		-0.341105	-0.374977	-0.294605	-0.299527				NA	-0.289424								-0.289547								
	GLYCOLYSIS-TCA-GLYOX-BYPASS superpathway of glycolysis pyruvate dehydrogenase TCA and glyoxylate bypass	p-value	0.0415747		0.011736	0.0059742	0.0286636	0.0259226				NA	0.037965								0.0260596								
		RHO	-0.273263		-0.334528	-0.362944	-0.292563	-0.297578				NA	-0.278091								-0.297317								
	GLYCOL-GLYOXDEG-PWY superpathway of glycol metabolism and degradation	p-value			0.0146411	0.007432	0.0382517	0.0346302				NA	0.0385653								0.0301225								
		RHO			-0.324644	-0.354027	-0.277694	-0.282901				NA	-0.277262								-0.290056								
	FAO-PWY fatty acid b-oxidation I	p-value			0.025722	0.0180877		0.0484942				NA																	
		RHO			-0.297962	-0.314898		-0.264899				NA																	
	ENTBACSYN-PWY enterobactin biosynthesis	p-value			0.0183657	0.0105976	0.0441453	0.0406				NA	0.0380828								0.0194675								
		RHO			-0.314183	-0.338987	-0.270031	-0.274531				NA	-0.277927								-0.311438								
	ECASYN-PWY enterobacterial common antigen biosynthesis	p-value			0.0156652	0.0084735	0.0388219	0.0346929				NA	0.033682								0.0146374								
		RHO			-0.32156	-0.34855	-0.276911	-0.282807				NA	-0.284339								-0.324655								
	CODH-PWY reductive acetyl coenzyme A pathway	p-value	0.0010389		0.0024766	0.0059975	0.0002332	0.0016722				NA							0.0220077	0.0403199									
		RHO	0.4267389		0.3966096	0.3627869	0.4728566	0.4105748				NA							0.305577	0.2749004									
	CENTFERM-PWY pyruvate fermentation to butanoate	p-value										NA																	
		RHO										NA																	
	AST-PWY L-arginine degradation II_AST pathway	p-value			0.0133049	0.0070947	0.0334455	0.0300273				NA	0.0398623						0.0450229		0.016073								
		RHO			-0.328959	-0.355944	-0.284703	-0.290216				NA	-0.275508						-0.268963		-0.320379								
	ARGDEG-PWY superpathway of L-arginine putrescine and 4-aminobutanoate degradation	p-value			0.0278879	0.0154239						NA									0.0262957								
		RHO			-0.29394	-0.322271						NA									-0.29687								
	ALL-CHORISMATE-PWY superpathway of chorismate metabolism	p-value			0.0218527	0.0113965	0.0471387	0.0463125				NA	0.0348662								0.0212681								
		RHO			-0.305918	-0.335818	-0.266456	-0.267424				NA	-0.282548								-0.307221								
			Group	age	ASD_score	Repetitive_b	Social_retar	Language_re	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_(	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_within_3_months
	VALDEG-PWY L-valine degradation I	p-value	0.0349357																							0.0059676			
		RHO	-0.205103																							-0.265401			
	TYRFUMCAT-PWY L-tyrosine degradation I	p-value	0.0018176	0.0036337	0.001226	0.0034355	0.0010335	0.0042489													0.0489749								
		RHO	-0.299465	0.2801241	-0.309901	-0.281741	-0.314313	-0.275566													-0.191723								
	TRPSYN-PWY L-tryptophan biosynthesis	p-value	0.0004259		0.0005289	0.0007867	0.0005286	0.0005965	0.0156452	0.0135711																			
		RHO	0.3362002		0.3310016	0.3212244	0.3310118	0.328074	0.2342692	0.2391009																			
	THISYN-PWY superpathway of thiamin diphosphate biosynthesis I	p-value	0.0002849	0.0423589	0.0006519	0.0003068	0.0008035	0.0019929													0.0282153		0.0376481						
		RHO	0.3456183	-0.197563	0.3258938	0.343906	0.3206949	0.2969693													0.2131984		0.2022048						
	RIBOSYN2-PWY flavin biosynthesis I_bacteria and plants	p-value	0.0009962		0.0010012	0.0017323	0.0014685	0.0006552	0.0498085	0.0413797													0.0417905						
		RHO	0.315254		0.3151258	0.3007603	0.305164	0.3257696	0.1910344	0.1984914													0.1980998						
	RHAMCAT-PWY L-rhamnose degradation I	p-value	0.0132806		0.0151764	0.0092191	0.0193071	0.0263113															0.0216938						
		RHO	0.239828		0.2353103	0.2518022	0.2269543	0.2157891															0.2228079						
	PWY-7539 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III_Chlamydia	p-value	0.0004097		0.0007068	0.0004438	0.0009758	0.0015849																					
		RHO	0.3371219		0.3238931	0.3352159	0.3157813	0.3031387																					
	PWY-7527 L-methionine salvage cycle III	p-value	0.0093586		0.0404662		0.0277693											0.0492887	0.0132897										
		RHO	-0.25132		-0.199374		-0.213792											0.1914627	-0.239805										
	PWY-7446 sulfoglycolysis	p-value														0.0415513										0.0315924			

age bracket 9 (9 y ~)		RHO														0.1983274										0.2089479			
	PWY-7323 superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis	p-value	0.0034371		0.006531	0.0026409	0.0069299	0.0138568										0.046449					0.0175902						
		RHO	0.2817278		0.2626358	0.2891996	0.2608032	0.2383986										0.1938707					0.2302193						
	PWY-7228 superpathway of guanosine nucleotides de novo biosynthesis I	p-value	0.0045636		0.0078677	0.0052122	0.0094809	0.0091748															0.03685						
		RHO	0.273459		0.2568381	0.2694963	0.2509025	0.2519565															0.2030389						
	PWY-7197 pyrimidine deoxyribonucleotide phosphorylation	p-value	0.0053355		0.0113429	0.0070193	0.0117189	0.0154048																					
		RHO	0.2687932		0.2450685	0.2604054	0.2439934	0.2347997																					
	PWY-7196 superpathway of pyrimidine ribonucleosides salvage	p-value	0.0044938		0.0075654	0.0055865	0.0086868	0.0093902															0.0459101						
		RHO	0.2739153		0.2580684	0.2674049	0.2537027	0.2512118															0.1943414						
	PWY-7094 fatty acid salvage	p-value	0.0005144	0.0102211	0.0015517	0.0013768	0.0014499	0.0085342																					
		RHO	-0.331674	0.2484724	-0.303703	-0.306865	-0.305501	-0.254267																					
	PWY-6897 thiamin salvage II	p-value	0.0009033		0.0008241	0.0013594	0.0013052	0.0005573	0.0129492	0.0105074			0.0498661																
		RHO	0.3177421		0.3200586	0.3071993	0.3082662	0.3297316	0.2406747	0.2475736			0.1909872																
	PWY-6892 thiazole biosynthesis I_E. coli	p-value	0.0004241		0.0002988	0.0001567	0.0005357	0.0004323	0.0410679	0.0338793																			
		RHO	0.3363021		0.3445185	0.3590945	0.3306886	0.3358472	0.1987907	0.206283																			
	PWY-6703 preQ0 biosynthesis	p-value	0.0002435	0.0371206	0.0004065	0.0003775	0.0005548	0.0005448															0.0432072						
		RHO	0.34922	-0.202754	0.3373098	0.3390596	0.3298417	0.3302809															0.1967739						
	PWY-6700 queuosine biosynthesis	p-value	0.0001761		0.0004739	0.0003865	0.0004987	0.0009538	0.0365811	0.0296995			0.0353604										0.0474223						
		RHO	0.3565092		0.3336489	0.3384999	0.3324214	0.3163632	0.2033232	0.21128			0.2046369										0.193032						
	PWY-6612 superpathway of tetrahydrofolate biosynthesis	p-value	0.0023262		0.003476	0.0015973	0.0050126	0.0062197																					
		RHO	0.2927281		0.281404	0.3029304	0.2706668	0.2641359																					
	PWY-6383 mono-trans poly-cis decaprenyl phosphate biosynthesis	p-value	1.52E-05		0.0003987	0.0007542	0.0002057	0.0016012	0.0382536	0.0401461																			
		RHO	0.4066932		0.3377644	0.3222779	0.3530413	0.3028667	0.2015819	0.1996868																			
	PWY-6185 4-methylcatechol degradation_ortho cleavage	p-value			0.0376728		0.0465275	0.0042562																					
		RHO			-0.202179		-0.193803	-0.275516																					
	PWY-6182 superpathway of salicylate degradation	p-value			0.0447951			0.0050136																					
		RHO			-0.19533			-0.27066																					
	PWY-6147 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	p-value	0.0003696	0	0.0005922	0.0003282	0.0009032	0.0013172																		0.0453091		
		RHO	0.339554	-0.181873	0.3282499	0.3423373	0.3177467	0.3080259																		0.1948718		
	PWY-6125 superpathway of guanosine nucleotides de novo biosynthesis II	p-value	0.0047319	0	0.0080549	0.0052532	0.0097987	0.0093513															0.0334928						
		RHO	0.2723848	-0.139153	0.2560968	0.2692607	0.2498396	0.2513451															0.2067225						
	PWY-5659 GDP-mannose biosynthesis	p-value	0.0024563	0	0.0037063	0.0014073	0.0036009	0.0075117															0.018705		0.0205625				
		RHO	0.2912197	-0.088012	0.2795522	0.306288	0.2803864	0.2582916															0.2280697		0.2247217				
	PWY-5507 adenosylcobalamin biosynthesis I_early cobalt insertion	p-value	0.0002926	0.0005817	0.0004224	0.002285	0.0002711	0.0020557																					
		RHO	-0.345006	0.3286846	-0.336399	-0.293221	-0.346765	-0.296123																					
	PWY-5431 aromatic compounds degradation via b-ketoadipate	p-value			0.0456549			0.0041127																					
		RHO			-0.194566			-0.276522																					
	PWY-5417 catechol degradation III_ortho-cleavage pathway	p-value			0.0456549			0.0041127																					
		RHO			-0.194566			-0.276522																					
	PWY-5415 catechol degradation I_meta-cleavage pathway	p-value	0.018668		0.0432073		0.0326379	0.0466465																					
		RHO	-0.228139		-0.196774		-0.20771	-0.193699																					
	PWY-5181 toluene degradation III_aerobic_via p-cresol	p-value			0.0250531		0.0320682	0.0026336																					
		RHO			-0.21759		-0.20838	-0.289277																					
	PWY-5178 toluene degradation IV_aerobic_via catechol	p-value	0.0351306		0.0276099		0.0222038	0.0154465																					
		RHO	-0.204888		-0.214006		-0.221973	-0.234707																					
	PWY-4361 S-methyl-5-thio-b-D-ribose 1-phosphate degradation	p-value	0.0093586		0.0404662		0.0277693											0.0492887	0.0132897										
		RHO	-0.25132		-0.199374		-0.213792											0.1914627	-0.239805										
	PWY-1269 CMP-3-deoxy-D-manno-octulosonate biosynthesis I	p-value	0.0001774		0.0011081	0.0003702	0.0011542	0.0030295													0.0263728								
		RHO	0.3563508		0.3125188	0.3395194	0.3114674	0.2853315													0.215703								
	PWY0-162 superpathway of pyrimidine ribonucleotides de novo biosynthesis	p-value	0.0052255		0.007627	0.005694	0.0084021	0.0086494															0.0405916						
		RHO	0.2694198		0.2578142	0.2668276	0.2547618	0.2538402															0.1992516						
	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY protocatechuate degradation II_ortho-cleavage pathway	p-value			0.0137827		0.0171804	0.0014106			0.0463783																	0.0491975	
		RHO			-0.238579		-0.231039	-0.306227			-0.193932																	-0.191538	
	POLYISOPRENSYN-PWY polyisoprenoid biosynthesis_E. coli	p-value	0.0036481		0.0113755	0.0026419	0.014106	0.0219623					0.0412865										0.0283373						
		RHO	0.28001		0.244974	0.2891887	0.2377963	0.2223662					0.1985806										0.2130375						
	PANTOSYN-PWY pantothenate and coenzyme A biosynthesis I	p-value	0.0058874		0.0057596	0.0055409	0.0075026	0.0038435															0.0488508						
		RHO	0.2658126		0.2664798	0.2676531	0.2583295	0.2784971															0.1918264						
	PANTO-PWY phosphopantothenate biosynthesis I	p-value	0.0052551		0.0043788	0.0039859	0.0060689	0.0030379															0.0487789						
		RHO	0.2692499		0.27468	0.2774372	0.2648866	0.2852527															0.1918864						
	P42-PWY incomplete reductive TCA cycle	p-value	0.0072322		0.0111713	0.0083257	0.012056	0.0138093															0.030222						
		RHO	0.2594756		0.2455695	0.2550512	0.2430549	0.2385145															0.210624						
	P108-PWY pyruvate fermentation to propanoate I	p-value	0.0064073		0.0117567	0.0193524	0.0102858	0.0122891																					
		RHO	0.2632237		0.243887	0.2268715	0.2482673	0.2424193																					
	NAGLIPASYN-PWY lipid IVA biosynthesis	p-value	0.0004214		0.0034638	0.0005939	0.0043845	0.0110748					0.0312602										0.0264155						
		RHO	0.3364508		0.2815049	0.3281803	0.2746422	0.2458543					0.2093485										0.2156433						
	KETOGLUCONMET-PWY ketogluconate metabolism	p-value						0.0455621				0.0409375																	
		RHO						-0.194648				-0.198916																	
	FOLSYN-PWY superpathway of tetrahydrofolate biosynthesis and salvage	p-value	0.0053361		0.0060097	0.0036155	0.0078445	0.0084677																					
		RHO	0.2687899		0.2651861	0.2802697	0.2569308	0.2545151																					
	CATECHOL-ORTHO-CLEAVAGE-PWY catechol degradation to b-ketoadipate	p-value			0.0438613			0.003863																					
		RHO			-0.196174			-0.27835																					
	ARGORNPROST-PWY arginine ornithine and proline interconversion	p-value	0.0039994		0.005179	0.0054336	0.0031978	0.0317186	0.0183003	0.0179054				0.0333754															
		RHO	-0.277339		-0.269688	-0.268244	-0.283794	-0.208797	-0.228837	-0.2296				-0.206857															
≤ 3 y	none																												

			ASD_score	Repetitive_b	Social_retar	Language_r	any_GI_prob	GI_problem_	esophageal_	peptic_ulcer	dyspepsia	abdominal_	abdominal_	constipation	abnormal_st	within_1_mo	any_sleep_c	sleep_compl	difficulty_fall	sleep_fragm	short_sleep_	Shallow_slee	any_neonata	food_allergy	skin_allergy	respiratory_	Antibiotic_w	Antibiotic_w	family_histo	age_of_mot	number_of_	number_of_	assisted_rep	smoking_du	infection_du	drinking_du	eclampsia/p	age_of_fathe	during_pregnancy
> 3 y	THRESYN-PWY superpathway of L-threonine biosynthesis	p-value	0.00035	0.0006144	0.0007583	2.23E-05	0.0063517	0.0081417										0.0323541															0.0433708	0.0116065	0.0495182				
		RHO	0.1124455	0.1077553	0.1059545	0.133196	0.0859473	0.0833452										0.0674443															0.0636739	0.0795073	0.0619116				
	TEICHOICACID-PWY teichoic acid_poly-glycerol biosynthesis	p-value	3.30E-06	8.64E-05	3.76E-07	1.88E-05																			0.0096089						0.0040809								
		RHO	-0.145975	-0.123394	-0.159284	-0.134386																			-0.08157						-0.090426								
	SULFATE-CYS-PWY superpathway of sulfate assimilation and cysteine biosynthesis	p-value	0.0006066	0.0021976	0.0035686	0.0007146	0.0016523	0.0081139										0.0442798		0.0466934						0.0055297				0.0040781	0.0010571	0.0087407						0.0003137	
		RHO	-0.107864	-0.096391	-0.091747	-0.106466	-0.099034	-0.083382										-0.063401		-0.062697						-0.087371				-0.102794	-0.103053	-0.082589						-0.12928	
	SO4ASSIM-PWY sulfate reduction I_assimilatory	p-value	0.0001363	0.0007635	0.0011293	0.0001016	0.0004857	0.0032051			0.048326			0.0464192				0.0351669						0.0492112		0.003504			0.0192709	0.002363	0.0018799	0.0108905						0.0002074	
		RHO	-0.11993	-0.105895	-0.102468	-0.122175	-0.109736	-0.092794			-0.062238			-0.062775				-0.066389						-0.061995		-0.091926			0.0737386	-0.108783	-0.097846	-0.080208						-0.133055	
	RIBOSYN2-PWY flavin biosynthesis I_bacteria and plants	p-value	9.12E-08	9.13E-07	1.16E-07	6.70E-09	0.0001576	0.0003215			0.001829						0.0035245	0.000635	0.0426167	0	0.0220441	0.0465948				0.0457248		0.0446884					0.0028592	0.0075861					
		RHO	0.1674061	0.1539774	0.1660453	0.1814255	0.1188049	0.113139			0.0981						0.0918689	0.1074749	0.0639043	0.0542133	0.0721472	0.0627253				0.0629757		0.0632793					0.093895	0.0840928					
	PWY-841 superpathway of purine nucleotides de novo biosynthesis I	p-value	7.59E-06	1.94E-05	3.85E-06	2.35E-06	0.0103052	0.0113453			0.0393552							0.0401588										0.0246987					0.0036162						
		RHO	0.140534	0.1341867	0.1449715	0.1481379	0.0808113	0.0797582			0.0649425							0.0646801										0.0707792					0.0916175						
	PWY-7539 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III_Chlamydia	p-value	5.45E-06	2.41E-05	4.64E-07	4.28E-06	0.0186803	0.0149701			0.0167936					0.0332609	0.0037391	0.0050843										0.0099665					0.0097881						
		RHO	0.1427194	0.132656	0.1580391	0.1442942	0.0741032	0.0766559			0.0753395					0.0670957	0.0912894	0.0882246										0.0811746					0.0813704						
	PWY-7431 aromatic biogenic amine degradation_bacteria	p-value	0.0035667	0.0095971	0.0029663	0.0019665																																	
		RHO	-0.091752	-0.081584	-0.093542	-0.097428																																	
	PWY-7400 L-arginine biosynthesis IV_archaebacteria	p-value	7.54E-07	8.08E-07	1.62E-06	1.08E-07	0.0001715	0.0010372						0.0066404			0.0163145	0.0031679						0.004531		0.0437593								0.0254315					
		RHO	0.1551375	0.1547186	0.1504474	0.1664661	0.1181447	0.1032213						0.0854864			0.0756727	0.0929069						0.0893842		0.0635565								0.0704241					
	PWY-7374 1_4-dihydroxy-6-naphthoate biosynthesis I	p-value	9.27E-15	2.22E-13	3.43E-15	8.53E-13	0.0001735	0.000284	0.0083753	0.0004461	0.0043294	0.0031087			0.0298333		1.03E-05	7.67E-06	0.0001401	0.0002434				4.61E-08	7.91E-05	3.01E-05		2.54E-05		0.0259483	0.0025152							0.015093	
		RHO	-0.240882	-0.22836	-0.244657	-0.222826	-0.118054	-0.114143	-0.083044	-0.110445	-0.089839	-0.093089			-0.06846		-0.138465	-0.140469	-0.119717	-0.115381				-0.171179	-0.124057	-0.131096		-0.132291		-0.079791	-0.095118							-0.08738	
	PWY-7332 superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis	p-value	5.81E-06	2.97E-06	3.23E-06	0.0001096	0.0099218																	0.0143615	0.0295621						5.67E-05	0.0128094							
		RHO	-0.142303	-0.146646	-0.146108	-0.121601	-0.081223																	-0.077127	-0.068573						-0.126521	-0.078412							
	PWY-7254 TCA cycle VII_acetate-producers	p-value	1.13E-06	2.12E-07	7.65E-07	1.10E-06	3.93E-05	0.0009538						0.0017478			0.010218	0.0037634		0.0014224				0.0350638		0.0114106		0.0026586			1.92E-08	0.0005204							
		RHO	0.1526577	0.1626069	0.1550502	0.1528295	0.129175	0.1039591						0.0985184			0.0809038	0.0912258		0.1003982				0.0664259		0.079695		0.0945908			0.1759001	0.1091592							
	PWY-7228 superpathway of guanosine nucleotides de novo biosynthesis I	p-value	2.90E-06	1.09E-05	6.48E-07	1.50E-06	0.0068778	0.009935						0.0337262			0.0370484	0.024296		0.0433764								0.0037631			0.0145737		0.0042479						
		RHO	0.1467829	0.138098	0.1560472	0.1509423	0.0851205	0.081209						0.0669199			0.0657218	0.0709782		0.0636722								0.0912266			0.0769607		0.0900279						
	PWY-7209 superpathway of pyrimidine ribonucleosides degradation	p-value	0.0006638	0.0019406	0.0001827	0.0002458					0.0494754							0.0445351										0.0288645											
		RHO	-0.107096	-0.097551	-0.117649	-0.115303					-0.061923							-0.063325										-0.068869											
	PWY-7197 pyrimidine deoxyribonucleotide phosphorylation	p-value	1.21E-06	4.54E-06	2.95E-07	8.44E-07	0.0054835	0.0092146						0.028739			0.0463107	0.0319636		0.0352764								0.0045677			0.00212		0.0055508						
		RHO	0.1522378	0.1439157	0.1607016	0.1544582	0.0874569	0.0820222						0.0689234			0.0628066	0.0675971		0.0663489								0.0893035			0.0967277		0.0873325						
	PWY-7187 pyrimidine deoxyribonucleotides de novo biosynthesis II	p-value	0.0003912	0.0001049	0.0001014	0.000185	0.0138066	0.0309333						0.0079052				0.0143187										0.002336			0.0161463	0.0430654							
		RHO	0.1115326	0.1219344	0.1221909	0.1175542	0.0775717	0.0680079						0.0836577				0.0771605										0.095817			0.0757917	0.0637668							
	PWY-7184 pyrimidine deoxyribonucleotides de novo biosynthesis I	p-value	6.79E-05	4.04E-05	9.98E-06	6.76E-05	0.020916	0.0421854						0.0169302			0.0141456	0.0095995		0.0316066								0.0002786			0.0104284		0.0499348						
		RHO	0.1251902	0.128993	0.1387104	0.1252204	0.0727723	0.0640377						0.0752459			0.0772981	0.081581		0.0677381								0.114298			0.0806817		0.061799						
	PWY-7090 UDP-2_3-diacetamido-2_3-dideoxy-b-D-mannuronate biosynthesis	p-value	3.08E-07	7.63E-08	5.15E-08	5.70E-05	0.000878	0.0024305						0.0294387			0.00265	0.0128597						0.0002849	2.97E-05						2.25E-07	0.0006095							
		RHO	-0.160445	-0.1684	-0.170576	-0.126477	-0.104683	-0.095442						-0.068625			-0.094621	-0.078369						-0.114116	-0.131183						-0.162276	-0.107824							
	PWY-7003 glycerol degradation to butanol	p-value	0.0031618	0.0147528	0.0025107	0.007666																																	
		RHO	-0.092925	-0.076822	-0.095135	-0.083982																																	
	PWY-6471 peptidoglycan biosynthesis IV_Enterococcus faecium	p-value	0.0012948	0.0141908	0.0004244	0.0011843	0.0078898	0.025203									0.0239399	0.0381312		0.0105263					0.0007984						8.62E-06	0.007754						0.0347285	
		RHO	-0.101246	-0.077262	-0.110859	-0.102044	-0.083678	-0.070534									-0.071157	-0.065351		-0.08058					-0.105509						-0.139692	-0.083862						-0.075959	
	PWY-6470 peptidoglycan biosynthesis V_b-lactam resistance	p-value	0.000139	0.0009949	0.000417	0.0002091									0.0005546	0.0230561							0.032725		0.0110339						0.0004033	0.004407							
		RHO	-0.119779	-0.103588	-0.111004	-0.116587									-0.108623	-0.07161							-0.067301		-0.080064						-0.111281	-0.089662							
	PWY-621 sucrose degradation III_sucrose invertase	p-value	0.0144415		0.0048434	0.0165936																									0.0004363	0.0301304							
		RHO	-0.077064		-0.088715	-0.075478																									-0.11063	-0.068336							
	PWY-6125 superpathway of guanosine nucleotides de novo biosynthesis II	p-value	4.10E-06	1.25E-05	1.09E-06	1.95E-06	0.0067915	0.0089485			0.0420848			0.0370523			0.0455226	0.0289371													0.0245156		0.0043086						
		RHO	0.144565	0.1371824	0.1529002	0.1493003	0.0852522	0.0823369			0.064069			0.0657204			0.0630345	0.0688383													0.0708694		0.0898868						
	PWY-5920 superpathway of heme biosynthesis from glycine	p-value	0.0152583			0.0012024				0.0059817																	0.0310866	0.0371574		0.0422326									
		RHO	-0.076439			-0.101908				0.0865664																	0.067946	0.065684		-0.072796									
	PWY-5532 adenosine nucleotides degradation IV	p-value	4.62E-06	0.0003814	8.56E-08	6.93E-06						0.0015585	0.0455039	0	0.0173193													0.023807	0.0061738	0.0098458	0.0039516	0.0200283						0.0134433	
		RHO	-0.143794	-0.111741	-0.167757	-0.141141						-0.099568	-0.06304	-0.012879	-0.074983													-0.071224	-0.086241	-0.092431	-0.090745	-0.073285						-0.088872	
	PWY-5384 sucrose degradation IV_sucrose phosphorylase	p-value	0.0001002	0.0008182	8.67E-05	0.0001114	0.0037414	0.0158908									0.0115805	0.016488		0.0112185											1.63E-06	0.0018396							
		RHO	-0.122277	-0.105296	-0.123369	-0.121471	-0.091284	-0.075975									-0.079532	-0.075551		-0.079882											-0.150406	-0.098046							
	PWY-5345 superpathway of L-methionine biosynthesis_by sulfhydrylation	p-value																								0.0276421		0.0114468	0.0133516							0.0176786		0.0280387	
		RHO																								-0.069404		0.0796601	0.0779484							-0.074745		-0.079016	
	PWY-4722 creatinine degradation II	p-value	0.0006155	0.0001545	0.0006736	0.0011545						0.0344268																								0	0.0488685		
		RHO	-0.107741	-0.118958	-0.106971	-0.102271						-0.066659																								0.0105243	0.0620889		
	PWY0-41 allantoin degradation IV_anaerobic	p-value	0.0002983	0.0062613	3.68E-05	0.0009741						0.0159943				0.0499023															0.0066764								
		RHO	-0.113745	-0.086096	-0.129663	-0.103774						-0.0759				0.0618077															-0.08543								
	PWY0-166 superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis_E. coli	p-value	0.0004167	0.0001129	0.0001035	0.0003935	0.0373654							0.0241589			0.036186	0.016961										0.0010981			0.0421176								
		RHO	0.1110105	0.1213755	0.1220369	0.1114847	0.0656123							0.0710467			0.0660237	0.0752249										0.1027161			0.0640588								
	PWY0-162 superpathway of pyrimidine ribonucleotides de novo biosynthesis	p-value	2.58E-06	9.99E-06	1.81E-06	6.35E-07	0.0089343	0.010363			0.0376711							0.0337731										0.0340177			0.0367405		0.0031565						
		RHO	0.1475319	0.1387019	0.1497622	0.1561672	0.082354	0.0807504			0.0655074							0.0669023										0.0668109			0.0658289		0.0929418						
	PWY0-1061 superpathway of L-alanine biosynthesis	p-value				0.0458179					0.0254985																	0.0076528											
		RHO				-0.062949					-0.070392																	0.0840006											
	POLYISOPRENSYN-PWY polyisoprenoid biosynthesis_E. coli	p-value	0.0001761	0.0002503	1.91E-05	7.58E-05	0.0119498	0.0199601																				0.0071868					0.0090032						
		RHO	0.1179411	0.1151581	0.1342815	0.1243782	0.079185	0.0733254																				0.0846611					0.0822716						
	P461-PWY hexitol fermentation to lactate formate ethanol and acetate	p-value																	0.0339246											0.0074283	0.0166553								
		RHO																	0.0668456											-0.095847	0.0754348								
	P162-PWY L-glutamate degradation V_via hydroxyglutarate	p-value	0.0032268	0.0177184	0.000115	0.0155878				0.0332151														0.0011838				0.0239293	0.0162592					0.0190408					
		RHO	-0.092728	-0.074719	-0.121233	-0.076195				0.0671131														-0.102048				-0.071162	-0.075712					0.0738795					
	METHYLGALLATE-DEGRADATION-PWY methylgallate degradation	p-value	2.91E-07	7.84E-06	3.59E-07	7.44E-08	0.0004258	0.00029			0.0031711	0.0292324	0.0349545	0.0412248	0.0194418										0.0308269						1.67E-06	6.13E-05	0.0444281						
		RHO	-0.160784	-0.14032	-0.159555	-0.168537	-0.110833	-0.113974			-0.092897	-0.068712	-0.066466	-0.064339	-0.073635										-0.068051						-0.150255	-0.125952	-0.063356						
	METH-ACETATE-PWY methanogenesis from acetate	p-value	2.95E-07	1.34E-07	3.14E-08	3.18E-07	0.000272	0.0010052				0.0378403		0.0135062				0.0109611					0.0051277	0.010667				0.009489			8.01E-07	0.0064457							
		RHO	-0.160695	-0.165224	-0.173271	-0.160256	-0.114489	-0.103497				-0.06545		-0.077819				-0.080137					-0.088139	-0.080435				-0.081706			-0.154776	-0.085795							
	KDO-NAGLIPASYN-PWY superpathway of_Kdo2-lipid A biosynthesis	p-value				0.0277355																						0.0031827								0.0398035			
		RHO				-0.069362																						0.0928618								-0.064796			
	HEXITOLDEGSUPER-PWY superpathway of hexitol degradation_bacteria	p-value																	0.0134087											0.0040697									
		RHO																	0.0779005											-0.102818									
	GLUTORN-PWY L-ornithine biosynthesis	p-value	1.16E-07	2.11E-06	2.89E-07	1.82E-09	0.0001247	0.0011861						0.0206513			0.0365515	0.0071688			0.0243126			0.0294247								0.0491144		0.0242947					
		RHO	0.1660578	0.1488156	0.1608146	0.188031	0.1206151	0.1020308						0.0729232			0.065895	0.0846873			0.07097			0.068631								0.0620216		0.0709789					
	GLCMANNANAUT-PWY superpathway of N-acetylglucosamine N-acetylmannosamine and N-acetylneuraminate degradation	p-value			0.0477322																																		
		RHO			-0.062404																																		
	GALLATE-DEGRADATION-I-PWY gallate degradation II	p-value	2.91E-07	7.84E-06	3.59E-07	7.44E-08	0.0004259	0.0002901			0.0031726	0.0292318	0.0349538	0.0412222	0.0194414										0.0308261								0.0444273						
		RHO	-0.160785	-0.140321	-0.159556	-0.168538	-0.110829	-0.113972			-0.092892	-0.068713	-0.066466	-0.06434	-0.073635										-0.068051								-0.063357						
	FUCCAT-PWY fucose degradation	p-value			0.0466648																																		
		RHO			-0.062705																																		

	FASYN-ELONG-PWY fatty acid elongation - saturated	p-value	0.0002419	0.0004893	5.69E-05	0.0001186	0.032351														0.0431249							0.034273	0.0473927				0.0281095					
		RHO	0.1154303	0.109675	0.1264921	0.1209972	0.0674456														0.0637487							0.066716	0.0624991				0.0691971					
	DENOVOPURINE2-PWY superpathway of purine nucleotides de novo biosynthesis II	p-value	8.27E-06	2.05E-05	4.67E-06	2.31E-06	0.0102163	0.0108783			0.0371107							0.0404894										0.0303415					0.0036089					
		RHO	0.1399678	0.1337925	0.1437212	0.1482424	0.0809056	0.0802199			0.0657002							0.0645735										0.0682491					0.0916374					
	CODH-PWY reductive acetyl coenzyme A pathway	p-value	7.55E-12	4.52E-13	2.83E-12	5.22E-11	4.37E-05	0.0004363			0.0321351			6.11E-05		0.0137506	0.0005578	3.02E-05	0.020173	0.0014578	0.0116322			0.0282659				0.0068359		0.0098832	0.0023359		0.0030031					
		RHO	0.2135367	0.225459	0.2177669	0.2049249	0.1284215	0.1106306			0.0675298			0.1259666		0.0776175	0.1085742	0.1310609	0.0732002	0.1001758	0.0794829			0.0691286				0.0851842		0.0923848	0.0958172		0.0934227					
	ARGSYN-PWY L-arginine biosynthesis I_via L-ornithine	p-value	8.44E-07	8.82E-07	1.96E-06	1.24E-07	0.0001786	0.0010888						0.007157			0.0165396	0.0032978						0.0051482		0.0446694								0.0259522				
		RHO	0.1544564	0.1541896	0.1492804	0.1656796	0.11783	0.1027918						0.0847045			0.075515	0.0925171						0.0880982		0.0632849								0.070177				