

Table S4. Frequencies of mutated genes in 22 colorectal cancer patients identified by exome sequencing.

Gene	missense	nonsense	splicing	frameshift_indel	nonframeshift_indel	mutated_sample_num	total_sample_num	mutation_frequency
APC	0	19	0	8	0	18	22	0.818181818
TP53	7	2	0	0	0	9	22	0.409090909
KRAS	6	0	0	0	0	6	22	0.272727273
FBXW7	2	2	0	2	0	3	22	0.136363636
TRIO	2	0	1	0	0	3	22	0.136363636
USH2A	3	0	0	0	0	3	22	0.136363636
GOLGA2	0	0	0	0	3	3	22	0.136363636
FAT4	3	0	0	0	0	3	22	0.136363636
SYNE1	2	0	0	0	0	2	22	0.090909091
MUC16	2	0	0	0	0	2	22	0.090909091
NF1	1	0	0	1	0	2	22	0.090909091
HMCN1	2	0	0	0	0	2	22	0.090909091
ERLIN1	2	0	0	0	0	2	22	0.090909091
SMC4	1	0	0	1	0	2	22	0.090909091
PDE10A	2	0	0	0	0	2	22	0.090909091
LRRC7	2	0	0	0	0	2	22	0.090909091
PRICKLE1	2	0	0	0	0	2	22	0.090909091
PRPF8	2	0	0	0	0	2	22	0.090909091
ASB3	0	1	1	0	0	2	22	0.090909091
CDH9	1	0	1	0	0	2	22	0.090909091
MTMR8	0	2	0	0	0	2	22	0.090909091
DPP10	2	0	0	0	0	2	22	0.090909091
AASDH	0	0	0	2	0	2	22	0.090909091
DDX58	2	0	0	0	0	2	22	0.090909091
CEACAM5	0	0	1	1	0	2	22	0.090909091
GPR161	2	0	0	0	0	2	22	0.090909091
ASTN1	2	0	0	0	0	2	22	0.090909091
DNAH9	1	0	0	0	1	2	22	0.090909091
CSMD2	2	0	0	0	0	2	22	0.090909091
AIM2	1	0	0	1	0	2	22	0.090909091
NLRP13	2	1	0	0	0	2	22	0.090909091
ACADL	1	1	0	0	0	2	22	0.090909091
RSPO2	2	0	0	0	0	2	22	0.090909091
DOCK2	2	0	0	0	0	2	22	0.090909091
BICC1	2	0	0	0	0	2	22	0.090909091
HERC2	2	0	0	0	0	2	22	0.090909091
MAGEC1	2	0	0	0	0	2	22	0.090909091

CCR3	1	0	0	1	0	2	22	0.090909091
ANAPC4	2	0	0	0	0	2	22	0.090909091
LRP2	2	0	0	0	0	2	22	0.090909091
LRRC27	2	0	0	0	0	2	22	0.090909091
DNAH10	2	0	0	0	0	2	22	0.090909091
ATP2B2	2	0	0	0	0	2	22	0.090909091
IGSF10	2	0	0	1	0	2	22	0.090909091
PSG9	2	0	0	0	0	2	22	0.090909091
TMPRSS13	0	0	0	0	2	2	22	0.090909091
GLIPR1L1	2	0	0	0	0	2	22	0.090909091
SGCZ	2	0	0	0	0	2	22	0.090909091
FGF13	1	1	0	0	0	2	22	0.090909091
ZNF133	2	0	0	0	0	2	22	0.090909091
VCAN	2	0	0	0	0	2	22	0.090909091
ANKRD26	2	0	0	0	0	2	22	0.090909091
HIST1H4B	1	0	0	0	0	1	22	0.045454545
HMG5	1	0	0	0	0	1	22	0.045454545
CPO	1	0	0	0	0	1	22	0.045454545
PCSK2	1	0	0	0	0	1	22	0.045454545
INVS	1	0	0	0	0	1	22	0.045454545
CPAMD8	1	0	0	0	0	1	22	0.045454545
LAPTM5	1	0	0	0	0	1	22	0.045454545
CCDC147	1	0	0	0	0	1	22	0.045454545
FKBP7	1	0	0	0	0	1	22	0.045454545
OR2L2	1	0	0	0	0	1	22	0.045454545
LIFR	1	0	0	0	0	1	22	0.045454545
ASS1	1	0	0	0	0	1	22	0.045454545
OR2L8	1	0	0	0	0	1	22	0.045454545
SEMA4G	1	0	0	0	0	1	22	0.045454545
SMG6	1	0	0	0	0	1	22	0.045454545
DLG5	0	0	0	1	0	1	22	0.045454545
CASS4	1	0	0	0	0	1	22	0.045454545
C11orf35	1	0	0	0	0	1	22	0.045454545
COMMD3	0	0	1	0	0	1	22	0.045454545
SPR	0	0	0	1	0	1	22	0.045454545
ALMS1	0	1	0	0	0	1	22	0.045454545
LRRTM1	1	0	0	0	0	1	22	0.045454545
IRAK1	1	0	0	0	0	1	22	0.045454545
IFNA16	1	0	0	0	0	1	22	0.045454545
GRIN3A	1	0	0	0	0	1	22	0.045454545
WDR7	1	0	0	0	0	1	22	0.045454545
FAM59A	1	0	0	0	0	1	22	0.045454545

SLITRK4	1	0	0	0	0	1	22	0.045454545
SLITRK5	1	0	0	0	0	1	22	0.045454545
DIAPH3	1	0	0	0	0	1	22	0.045454545
FAM120C	1	0	0	0	0	1	22	0.045454545
SLC45A2	0	0	0	1	0	1	22	0.045454545
ABLIM3	1	0	0	0	0	1	22	0.045454545
NMS	1	0	0	0	0	1	22	0.045454545
GPR39	1	0	0	0	0	1	22	0.045454545
ZNF670	1	0	0	0	0	1	22	0.045454545
HCN1	1	0	0	0	0	1	22	0.045454545
PARP12	1	0	0	0	0	1	22	0.045454545
AKAP9	1	0	0	0	0	1	22	0.045454545
FDXACB1	1	0	0	0	0	1	22	0.045454545
STARD8	0	1	0	0	0	1	22	0.045454545
C7orf51	1	0	0	0	0	1	22	0.045454545
EIF5A2	0	0	0	1	0	1	22	0.045454545
GPR112	1	0	0	0	0	1	22	0.045454545
STARD5	1	0	0	0	0	1	22	0.045454545
HSD17B10	1	0	0	0	0	1	22	0.045454545
GPR158	1	0	0	0	0	1	22	0.045454545
MMP10	0	0	0	1	0	1	22	0.045454545
DTL	1	0	0	0	0	1	22	0.045454545
DSTYK	1	0	0	0	0	1	22	0.045454545
ITGA1	1	0	0	0	0	1	22	0.045454545
CAPRIN1	0	1	0	0	0	1	22	0.045454545
MX1	1	0	0	0	0	1	22	0.045454545
CYP2C9	1	0	0	0	0	1	22	0.045454545
GTF3C1	1	0	0	0	0	1	22	0.045454545
GTF3C5	1	0	0	0	0	1	22	0.045454545
DENND4C	1	0	0	0	0	1	22	0.045454545
OR2W3	1	0	0	0	0	1	22	0.045454545
TMEM132D	1	0	0	0	0	1	22	0.045454545
OR5D14	1	0	0	0	0	1	22	0.045454545
OR5D16	1	0	0	0	0	1	22	0.045454545
XPO1	1	0	0	0	0	1	22	0.045454545
APOB	1	0	0	0	0	1	22	0.045454545
LILRB2	1	0	0	0	0	1	22	0.045454545
RWDD2B	1	0	0	0	0	1	22	0.045454545
WDR49	1	0	0	0	0	1	22	0.045454545
SPG11	0	1	0	0	0	1	22	0.045454545
MST1	1	0	0	0	0	1	22	0.045454545
L3MBTL4	0	1	0	0	0	1	22	0.045454545

LSR	1	0	0	0	0	1	22	0.045454545
TTN	1	0	0	0	0	1	22	0.045454545
VSX2	1	0	0	0	0	1	22	0.045454545
GRM4	1	0	0	0	0	1	22	0.045454545
JAGN1	1	0	0	0	0	1	22	0.045454545
GRM7	0	0	0	1	0	1	22	0.045454545
GRM1	1	0	0	0	0	1	22	0.045454545
SDK1	1	0	0	0	0	1	22	0.045454545
ALPK3	1	0	0	0	0	1	22	0.045454545
KIF6	1	0	0	0	0	1	22	0.045454545
KCNQ5	1	0	0	0	0	1	22	0.045454545
GTF2IRD1	1	0	0	0	0	1	22	0.045454545
CUX2	1	0	0	0	0	1	22	0.045454545
GPAM	1	0	0	0	0	1	22	0.045454545
FSIP2	1	0	0	0	0	1	22	0.045454545
ZEB2	1	0	0	0	0	1	22	0.045454545
KCNH5	1	0	0	0	0	1	22	0.045454545
KCNH7	0	0	0	1	0	1	22	0.045454545
KCNH3	1	0	0	0	0	1	22	0.045454545
ZNF823	1	0	0	0	0	1	22	0.045454545
SH3D19	0	1	0	0	0	1	22	0.045454545
CABP5	1	0	0	0	0	1	22	0.045454545
CDC73	1	0	0	0	0	1	22	0.045454545
MAGOHB	1	0	0	0	0	1	22	0.045454545
KCNH8	0	0	0	0	1	1	22	0.045454545
CBL	1	0	0	0	0	1	22	0.045454545
C10orf68	1	0	0	0	0	1	22	0.045454545
KRT17	1	0	0	0	0	1	22	0.045454545
AKAP8	1	0	0	0	0	1	22	0.045454545
SLC35B3	0	0	1	0	0	1	22	0.045454545
WDFY3	1	0	0	0	0	1	22	0.045454545
FBXO31	1	0	0	0	0	1	22	0.045454545
UTP20	1	0	0	0	0	1	22	0.045454545
MYBBP1A	1	0	0	0	0	1	22	0.045454545
GOSR2	1	0	0	0	0	1	22	0.045454545
VWF	1	0	0	0	0	1	22	0.045454545
GOSR1	1	0	0	0	0	1	22	0.045454545
ZNF292	1	0	0	0	0	1	22	0.045454545
SYT4	1	0	0	0	0	1	22	0.045454545
KLHL26	1	0	0	0	0	1	22	0.045454545
C12orf29	1	0	0	0	0	1	22	0.045454545
GPM6A	1	0	0	0	0	1	22	0.045454545

SMAD4	1	0	0	0	0	1	22	0.045454545
SLC2A14	1	0	0	0	0	1	22	0.045454545
KLHL28	0	0	1	0	0	1	22	0.045454545
RET	1	0	0	0	0	1	22	0.045454545
CAMK4	1	0	0	0	0	1	22	0.045454545
SPTA1	1	0	0	0	0	1	22	0.045454545
CDH12	0	1	0	0	0	1	22	0.045454545
TRIM59	1	0	0	0	0	1	22	0.045454545
PLP1	1	0	0	0	0	1	22	0.045454545
CLCA1	1	0	0	0	0	1	22	0.045454545
CTH	0	0	0	1	0	1	22	0.045454545
CLCA4	1	0	0	0	0	1	22	0.045454545
SCLT1	0	0	1	0	0	1	22	0.045454545
NCOA4	1	0	0	0	0	1	22	0.045454545
C12orf59	1	0	0	0	0	1	22	0.045454545
SMC5	1	0	0	0	0	1	22	0.045454545
RBM12	0	1	0	0	0	1	22	0.045454545
C2orf15	1	0	0	0	0	1	22	0.045454545
TM9SF2	1	0	0	0	0	1	22	0.045454545
S100A4	1	0	0	0	0	1	22	0.045454545
C2orf18	1	0	0	0	0	1	22	0.045454545
MAGI2	1	0	0	0	0	1	22	0.045454545
SLC25A40	1	0	0	0	0	1	22	0.045454545
LAMA2	1	0	0	0	0	1	22	0.045454545
GRID1	1	0	0	0	0	1	22	0.045454545
ZNF83	0	0	0	1	0	1	22	0.045454545
OR6K2	1	0	0	0	0	1	22	0.045454545
PPEF2	1	0	0	0	0	1	22	0.045454545
LEPR	1	0	0	0	0	1	22	0.045454545
SS18	1	0	0	0	0	1	22	0.045454545
MBNL1	1	0	0	0	0	1	22	0.045454545
ALG12	1	0	0	0	0	1	22	0.045454545
TMEM63A	1	0	0	0	0	1	22	0.045454545
KIAA2022	1	0	0	0	0	1	22	0.045454545
OR9I1	1	0	0	0	0	1	22	0.045454545
ZFYVE26	1	0	0	0	0	1	22	0.045454545
GPR155	1	0	0	0	0	1	22	0.045454545
APBA2	1	0	0	0	0	1	22	0.045454545
F8	1	0	0	0	0	1	22	0.045454545
SUCLA2	1	0	0	0	0	1	22	0.045454545
TAS2R5	1	0	0	0	0	1	22	0.045454545
NTN4	1	0	0	0	0	1	22	0.045454545

CCDC113	1	0	0	0	0	1	22	0.045454545
SSTR1	1	0	0	0	0	1	22	0.045454545
ABCA4	1	0	0	0	0	1	22	0.045454545
ATP1A4	1	0	0	0	0	1	22	0.045454545
SSTR4	1	0	0	0	0	1	22	0.045454545
ABCA1	1	0	0	0	0	1	22	0.045454545
CDK5RAP2	1	0	0	0	0	1	22	0.045454545
KIF4A	1	0	0	0	0	1	22	0.045454545
TUBGCP5	1	0	0	0	0	1	22	0.045454545
ATP11B	0	1	0	0	0	1	22	0.045454545
ERC1	1	0	0	0	0	1	22	0.045454545
PTPRZ1	1	0	0	0	0	1	22	0.045454545
CTNNB1	1	0	0	0	0	1	22	0.045454545
ZNF14	1	0	0	0	0	1	22	0.045454545
ZNF493	1	0	0	0	0	1	22	0.045454545
PGLYRP4	0	0	0	1	0	1	22	0.045454545
MYOC	1	0	0	0	0	1	22	0.045454545
C10orf81	1	0	0	0	0	1	22	0.045454545
GYG1	1	0	0	0	0	1	22	0.045454545
OR8A1	1	0	0	0	0	1	22	0.045454545
OIP5	1	0	0	0	0	1	22	0.045454545
RGS22	1	0	0	0	0	1	22	0.045454545
IMPG2	1	0	0	0	0	1	22	0.045454545
PDE1C	1	0	0	0	0	1	22	0.045454545
SULF1	1	0	0	0	0	1	22	0.045454545
C20orf114	1	0	0	0	0	1	22	0.045454545
HNF1B	1	0	0	0	0	1	22	0.045454545
CERKL	1	0	0	0	0	1	22	0.045454545
MTTP	1	0	0	0	0	1	22	0.045454545
KLF3	1	0	0	0	0	1	22	0.045454545
VWCE	1	0	0	0	0	1	22	0.045454545
LRRIQ1	1	0	0	0	0	1	22	0.045454545
PSMC2	1	0	0	0	0	1	22	0.045454545
JAG1	0	0	1	0	0	1	22	0.045454545
HSD17B4	0	1	0	0	0	1	22	0.045454545
POTEB	1	0	0	0	0	1	22	0.045454545
PSMC6	0	0	0	1	0	1	22	0.045454545
HECW1	1	0	0	0	0	1	22	0.045454545
ITIH5L	1	0	0	0	0	1	22	0.045454545
ITGB4	1	0	0	0	0	1	22	0.045454545
CD44	1	0	0	0	0	1	22	0.045454545
PCDH15	1	0	0	0	0	1	22	0.045454545

SLC24A2	1	0	0	0	0	1	22	0.045454545
HEATR8	1	0	0	0	0	1	22	0.045454545
IL33	0	0	1	0	0	1	22	0.045454545
ACSM1	1	0	0	0	0	1	22	0.045454545
HGF	0	1	0	0	0	1	22	0.045454545
ATP8B3	1	0	0	0	0	1	22	0.045454545
NBN	1	0	0	0	0	1	22	0.045454545
DMXL2	1	0	0	0	0	1	22	0.045454545
SCGBL	1	0	0	0	0	1	22	0.045454545
RAB25	1	0	0	0	0	1	22	0.045454545
CFH	1	0	0	0	0	1	22	0.045454545
BNC2	1	0	0	0	0	1	22	0.045454545
GLRA2	1	0	0	0	0	1	22	0.045454545
OLFM2	1	0	0	0	0	1	22	0.045454545
ARMCX1	1	0	0	0	0	1	22	0.045454545
E2F8	1	0	0	0	0	1	22	0.045454545
ITLN1	1	0	0	0	0	1	22	0.045454545
ADNP2	0	1	0	0	0	1	22	0.045454545
MAP3K15	1	0	0	0	0	1	22	0.045454545
ZNF543	0	1	0	0	0	1	22	0.045454545
SYBU	1	0	0	0	0	1	22	0.045454545
SLC1A6	1	0	0	0	0	1	22	0.045454545
WDR72	1	0	0	0	0	1	22	0.045454545
FAM126A	1	0	0	0	0	1	22	0.045454545
SLC1A2	1	0	0	0	0	1	22	0.045454545
LILRA1	0	1	0	0	0	1	22	0.045454545
SYTL2	1	0	0	0	0	1	22	0.045454545
MCF2	0	0	0	1	0	1	22	0.045454545
RAD18	1	0	0	0	0	1	22	0.045454545
UPRT	0	1	0	0	0	1	22	0.045454545
HYLS1	1	0	0	0	0	1	22	0.045454545
CATSPER1	1	0	0	0	0	1	22	0.045454545
HPS5	1	0	0	0	0	1	22	0.045454545
ARAF	1	0	0	0	0	1	22	0.045454545
TNRC6B	1	0	0	0	0	1	22	0.045454545
TNRC6A	0	0	0	1	0	1	22	0.045454545
ARAP3	1	0	0	0	0	1	22	0.045454545
CLSTN2	1	0	0	0	0	1	22	0.045454545
ASB2	1	0	0	0	0	1	22	0.045454545
PGCP	1	0	0	0	0	1	22	0.045454545
ADAMTS2	1	0	0	0	0	1	22	0.045454545
ARHGEF7	1	0	0	0	0	1	22	0.045454545

ZNF331	1	0	0	0	0	1	22	0.045454545
CDH8	1	0	0	0	0	1	22	0.045454545
NAALAD2	0	0	1	0	0	1	22	0.045454545
RELN	1	0	0	0	0	1	22	0.045454545
MTMR9	1	0	0	0	0	1	22	0.045454545
CDH7	1	0	0	0	0	1	22	0.045454545
C5orf43	1	0	0	0	0	1	22	0.045454545
C17orf46	1	0	0	0	0	1	22	0.045454545
MRPL37	1	0	0	0	0	1	22	0.045454545
NCKIPSD	1	0	0	0	0	1	22	0.045454545
PLBD1	1	0	0	0	0	1	22	0.045454545
OR5111	1	0	0	0	0	1	22	0.045454545
MCHR2	0	0	0	1	0	1	22	0.045454545
XYLT1	0	0	1	0	0	1	22	0.045454545
UTP14A	0	0	1	0	0	1	22	0.045454545
REV3L	1	0	0	0	0	1	22	0.045454545
KIRREL2	1	0	0	0	0	1	22	0.045454545
EFHA1	1	0	0	0	0	1	22	0.045454545
KIFC3	1	0	0	0	0	1	22	0.045454545
STK17A	1	0	0	0	0	1	22	0.045454545
SYT9	1	0	0	0	0	1	22	0.045454545
LRRC4C	1	0	0	0	0	1	22	0.045454545
ARID1A	0	0	0	1	0	1	22	0.045454545
NRXN3	0	0	1	0	0	1	22	0.045454545
ZNF280B	1	0	0	0	0	1	22	0.045454545
APOL1	0	0	0	1	0	1	22	0.045454545
LSAMP	1	0	0	0	0	1	22	0.045454545
GATAD1	1	0	0	0	0	1	22	0.045454545
WNT7A	1	0	0	0	0	1	22	0.045454545
TMEM40	0	0	1	0	0	1	22	0.045454545
FOXP2	1	0	0	0	0	1	22	0.045454545
FOXP1	1	0	0	0	0	1	22	0.045454545
TRPC4	1	0	0	0	0	1	22	0.045454545
ALG3	1	0	0	0	0	1	22	0.045454545
CNTN3	1	0	0	0	0	1	22	0.045454545
NOS3	1	0	0	0	0	1	22	0.045454545
CNTN4	1	0	0	0	0	1	22	0.045454545
ADAM7	1	0	0	0	0	1	22	0.045454545
OR4C13	1	0	0	0	0	1	22	0.045454545
LHCGR	0	1	0	0	0	1	22	0.045454545
CABIN1	1	0	0	0	0	1	22	0.045454545
KIAA0802	1	0	0	0	0	1	22	0.045454545

DDX50	1	0	0	0	0	1	22	0.045454545
EXO1	1	0	0	0	0	1	22	0.045454545
TIMELESS	1	0	0	0	0	1	22	0.045454545
PRKG2	1	0	0	0	0	1	22	0.045454545
TNS3	0	0	0	1	0	1	22	0.045454545
TNS1	1	0	0	0	0	1	22	0.045454545
FAM135A	1	0	0	0	0	1	22	0.045454545
ANGPT4	1	0	0	0	0	1	22	0.045454545
RAD54L2	1	0	0	0	0	1	22	0.045454545
GCA	1	0	0	0	0	1	22	0.045454545
TCF4	1	0	0	0	0	1	22	0.045454545
RASGEF1A	1	0	0	0	0	1	22	0.045454545
ZNF180	1	0	0	0	0	1	22	0.045454545
NPFRR2	1	0	0	0	0	1	22	0.045454545
KIAA0895L	1	0	0	0	0	1	22	0.045454545
SEMA4D	1	0	0	0	0	1	22	0.045454545
RAG2	1	0	0	0	0	1	22	0.045454545
SHE	1	0	0	0	0	1	22	0.045454545
SMYD2	1	0	0	0	0	1	22	0.045454545
PHEX	1	0	0	0	0	1	22	0.045454545
GALNT2	1	0	0	0	0	1	22	0.045454545
LARS	1	0	0	0	0	1	22	0.045454545
SDSL	1	0	0	0	0	1	22	0.045454545
PTPRG	1	0	0	0	0	1	22	0.045454545
DNAH5	1	0	0	0	0	1	22	0.045454545
DOPEY2	1	0	0	0	0	1	22	0.045454545
BCKDK	1	0	0	0	0	1	22	0.045454545
COX18	1	0	0	0	0	1	22	0.045454545
TMEM217	1	0	0	0	0	1	22	0.045454545
GPR98	1	0	0	0	0	1	22	0.045454545
FBXL20	1	0	0	0	0	1	22	0.045454545
BTK	1	0	0	0	0	1	22	0.045454545
HDAC3	1	0	0	0	0	1	22	0.045454545
CD72	1	0	0	0	0	1	22	0.045454545
CCDC48	0	1	0	0	0	1	22	0.045454545
AMPD3	1	0	0	0	0	1	22	0.045454545
ZFHX4	1	0	0	0	0	1	22	0.045454545
AMPD1	1	0	0	0	0	1	22	0.045454545
ATM	0	1	0	0	0	1	22	0.045454545
EGFLAM	1	0	0	0	0	1	22	0.045454545
CYLC1	0	0	0	1	0	1	22	0.045454545
FABP4	1	0	0	0	0	1	22	0.045454545

KIF17	1	0	0	0	0	1	22	0.045454545
ATR	1	0	0	0	0	1	22	0.045454545
HNRNPH1	0	0	1	0	0	1	22	0.045454545
EPCAM	0	1	0	0	0	1	22	0.045454545
RNF113B	1	0	0	0	0	1	22	0.045454545
FLT1	1	0	0	0	0	1	22	0.045454545
MYH3	1	0	0	0	0	1	22	0.045454545
ZBTB11	1	0	0	0	0	1	22	0.045454545
COG6	1	0	0	0	0	1	22	0.045454545
INS-IGF2	1	0	0	0	0	1	22	0.045454545
GAS2L3	1	0	0	0	0	1	22	0.045454545
NLRP9	0	1	0	0	0	1	22	0.045454545
RPS6KB2	1	0	0	0	0	1	22	0.045454545
QSOX2	1	0	0	0	0	1	22	0.045454545
FANCC	1	0	0	0	0	1	22	0.045454545
FANCB	1	0	0	0	0	1	22	0.045454545
GABRG2	1	0	0	0	0	1	22	0.045454545
VGLL3	1	0	0	0	0	1	22	0.045454545
TTC27	1	0	0	0	0	1	22	0.045454545
CADM3	1	0	0	0	0	1	22	0.045454545
ACVR2A	0	0	0	1	0	1	22	0.045454545
GRIA1	1	0	0	0	0	1	22	0.045454545
KLHL14	1	0	0	0	0	1	22	0.045454545
OR2K2	1	0	0	0	0	1	22	0.045454545
MTMR11	1	0	0	0	0	1	22	0.045454545
PUS7	1	0	0	0	0	1	22	0.045454545
GNB3	1	0	0	0	0	1	22	0.045454545
FAM105A	1	0	0	0	0	1	22	0.045454545
MTOR	1	0	0	0	0	1	22	0.045454545
MED27	1	0	0	0	0	1	22	0.045454545
TSEN54	1	0	0	0	0	1	22	0.045454545
ANO3	1	0	0	0	0	1	22	0.045454545
TAOK3	1	0	0	0	0	1	22	0.045454545
CYP24A1	0	0	1	0	0	1	22	0.045454545
GRIK3	1	0	0	0	0	1	22	0.045454545
HAS1	1	0	0	0	0	1	22	0.045454545
RPL10A	0	0	0	1	0	1	22	0.045454545
KCNRG	1	0	0	0	0	1	22	0.045454545
TGFB2	1	0	0	0	0	1	22	0.045454545
FGD4	1	0	0	0	0	1	22	0.045454545
BPI	1	0	0	0	0	1	22	0.045454545
SF3B1	0	0	1	0	0	1	22	0.045454545

PRKAA1	1	0	0	0	0	1	22	0.045454545
SF3B2	1	0	0	0	0	1	22	0.045454545
PRSS1	1	0	0	0	0	1	22	0.045454545
NLRP14	1	0	0	0	0	1	22	0.045454545
KIAA0430	1	0	0	0	0	1	22	0.045454545
SLC5A5	1	0	0	0	0	1	22	0.045454545
COL3A1	1	0	0	0	0	1	22	0.045454545
SORBS1	1	0	0	0	0	1	22	0.045454545
SMARCA1	0	1	0	0	0	1	22	0.045454545
ACCS	1	0	0	0	0	1	22	0.045454545
LOXL4	1	0	0	0	0	1	22	0.045454545
PHACTR3	1	0	0	0	0	1	22	0.045454545
IL18RAP	1	0	0	0	0	1	22	0.045454545
CTCF	1	0	0	0	0	1	22	0.045454545
MMRN1	1	0	0	0	0	1	22	0.045454545
FYN	0	1	0	0	0	1	22	0.045454545
OR5F1	1	0	0	0	0	1	22	0.045454545
ADCK1	1	0	0	0	0	1	22	0.045454545
DNAJC14	0	1	0	0	0	1	22	0.045454545
MED13	1	0	0	0	0	1	22	0.045454545
MED14	1	0	0	0	0	1	22	0.045454545
ABCB4	0	0	0	1	0	1	22	0.045454545
NBAS	1	0	0	0	0	1	22	0.045454545
PACSIN3	1	0	0	0	0	1	22	0.045454545
RP1	2	0	0	0	0	1	22	0.045454545
MATN4	1	0	0	0	0	1	22	0.045454545
INTS5	1	0	0	0	0	1	22	0.045454545
INTS4	1	0	0	0	0	1	22	0.045454545
DIRC1	1	0	0	0	0	1	22	0.045454545
CARD11	1	0	0	0	0	1	22	0.045454545
INTS8	1	0	0	0	0	1	22	0.045454545
ATP10D	0	0	0	1	0	1	22	0.045454545
BOD1L	1	0	0	0	0	1	22	0.045454545
CD4	1	0	0	0	0	1	22	0.045454545
FCGR2A	0	0	1	0	0	1	22	0.045454545
SMAD3	1	0	0	0	0	1	22	0.045454545
DBC1	1	0	0	0	0	1	22	0.045454545
EBF1	1	0	0	0	0	1	22	0.045454545
CADPS	1	0	0	0	0	1	22	0.045454545
CTNNA1	1	0	0	0	0	1	22	0.045454545
CHST12	0	0	0	1	0	1	22	0.045454545
CHST15	1	0	0	0	0	1	22	0.045454545

SUSD1	1	0	0	0	0	1	22	0.045454545
WDR47	1	0	0	0	0	1	22	0.045454545
CSTF1	1	0	0	0	0	1	22	0.045454545
NSUN4	1	0	0	0	0	1	22	0.045454545
CSTF3	0	0	0	1	0	1	22	0.045454545
NOTCH3	1	0	0	0	0	1	22	0.045454545
CACNG8	1	0	0	0	0	1	22	0.045454545
USP45	1	0	0	0	0	1	22	0.045454545
ZNF790	0	0	0	1	0	1	22	0.045454545
ZNF91	1	0	0	0	0	1	22	0.045454545
BACH2	1	0	0	0	0	1	22	0.045454545
MMP2	1	0	0	0	0	1	22	0.045454545
PCDHB1	1	0	0	0	0	1	22	0.045454545
EP300	0	1	0	0	0	1	22	0.045454545
TM7SF3	0	1	0	0	0	1	22	0.045454545
RAB3IP	0	1	0	0	0	1	22	0.045454545
NUDT15	1	0	0	0	0	1	22	0.045454545
LRRRC16B	1	0	0	0	0	1	22	0.045454545
MYL6	0	0	0	1	0	1	22	0.045454545
TRPM1	0	1	0	0	0	1	22	0.045454545
CHN1	1	0	0	0	0	1	22	0.045454545
N4BP2L2	1	0	0	0	0	1	22	0.045454545
POLR3B	1	0	0	0	0	1	22	0.045454545
PPIL6	1	0	0	0	0	1	22	0.045454545
MYL1	1	0	0	0	0	1	22	0.045454545
CCNT1	1	0	0	0	0	1	22	0.045454545
SYNE2	1	0	0	0	0	1	22	0.045454545
PAM	1	0	0	0	0	1	22	0.045454545
SOX30	1	0	0	0	0	1	22	0.045454545
TRIM63	1	0	0	0	0	1	22	0.045454545
PPP1R3A	1	0	0	0	0	1	22	0.045454545
MPP3	1	0	0	0	0	1	22	0.045454545
MAP3K3	1	0	0	0	0	1	22	0.045454545
DNMT1	1	0	0	0	0	1	22	0.045454545
CACNA1E	1	0	0	0	0	1	22	0.045454545
PROX1	1	0	0	0	0	1	22	0.045454545
GSTA4	1	0	0	0	0	1	22	0.045454545
C10orf96	1	0	0	0	0	1	22	0.045454545
ZNF471	1	0	0	0	0	1	22	0.045454545
CUL5	1	0	0	0	0	1	22	0.045454545
MBNL2	0	1	0	0	0	1	22	0.045454545
C15orf43	1	0	0	0	0	1	22	0.045454545

SETDB1	1	0	0	0	0	1	22	0.045454545
CUL2	1	0	0	0	0	1	22	0.045454545
MAPRE2	1	0	0	0	0	1	22	0.045454545
KIAA0319L	1	0	0	0	0	1	22	0.045454545
ERBB3	1	0	0	0	0	1	22	0.045454545
PRMT8	1	0	0	0	0	1	22	0.045454545
HUWE1	1	0	0	0	0	1	22	0.045454545
CASZ1	0	1	0	0	0	1	22	0.045454545
ZNF200	1	0	0	0	0	1	22	0.045454545
FPR1	1	0	0	0	0	1	22	0.045454545
IDH1	2	0	0	0	0	1	22	0.045454545
FPR3	1	0	0	0	0	1	22	0.045454545
CDH26	0	1	0	0	0	1	22	0.045454545
POSTN	1	0	0	0	0	1	22	0.045454545
TRPS1	1	0	0	0	0	1	22	0.045454545
ERBB4	1	0	0	0	0	1	22	0.045454545
MTPAP	1	0	0	0	0	1	22	0.045454545
FNDC3B	1	0	0	0	0	1	22	0.045454545
ADCY6	1	0	0	0	0	1	22	0.045454545
RBM43	0	0	0	1	0	1	22	0.045454545
ADCY2	1	0	0	0	0	1	22	0.045454545
SLTM	0	1	0	0	0	1	22	0.045454545
KIF5A	1	0	0	0	0	1	22	0.045454545
MYLK	0	0	1	0	0	1	22	0.045454545
RNF182	0	1	0	0	0	1	22	0.045454545
UTRN	0	0	1	0	0	1	22	0.045454545
PKD2	1	0	0	0	0	1	22	0.045454545
RNF213	1	0	0	0	0	1	22	0.045454545
CSRP2BP	1	0	0	0	0	1	22	0.045454545
DMD	0	1	0	0	0	1	22	0.045454545
C4orf22	0	0	0	1	0	1	22	0.045454545
GRIA4	1	0	0	0	0	1	22	0.045454545
NTSR1	1	0	0	0	0	1	22	0.045454545
CRTC3	1	0	0	0	0	1	22	0.045454545
CDYL2	1	0	0	0	0	1	22	0.045454545
FAM13C	1	0	0	0	0	1	22	0.045454545
SEPT6	0	0	1	0	0	1	22	0.045454545
XRCC5	1	0	0	0	0	1	22	0.045454545
ERAL1	1	0	0	0	0	1	22	0.045454545
PCDHB8	1	0	0	0	0	1	22	0.045454545
PCDHB3	1	0	0	0	0	1	22	0.045454545
ADAD1	1	0	0	0	0	1	22	0.045454545

LIMCH1	1	0	0	0	0	1	22	0.045454545
PPM1L	1	0	0	0	0	1	22	0.045454545
PCDHB5	1	0	0	0	0	1	22	0.045454545
SCNN1G	1	0	0	0	0	1	22	0.045454545
TIAM1	1	0	0	0	0	1	22	0.045454545
JMJD1C	0	1	0	0	0	1	22	0.045454545
TRPM5	1	0	0	0	0	1	22	0.045454545
TRPM6	0	0	0	1	0	1	22	0.045454545
CARD6	1	0	0	0	0	1	22	0.045454545
FCN1	1	0	0	0	0	1	22	0.045454545
SPANXN2	0	0	0	1	0	1	22	0.045454545
GBP2	0	0	0	1	0	1	22	0.045454545
EHBP1	1	0	0	0	0	1	22	0.045454545
UNC5D	0	1	0	0	0	1	22	0.045454545
HERC3	1	0	0	0	0	1	22	0.045454545
TRRAP	1	0	0	0	0	1	22	0.045454545
RPUSD2	1	0	0	0	0	1	22	0.045454545
DDX60	1	0	0	0	0	1	22	0.045454545
GIMAP4	1	0	0	0	0	1	22	0.045454545
PWP2	1	0	0	0	0	1	22	0.045454545
PCDHGA7	1	0	0	0	0	1	22	0.045454545
PTPN5	1	0	0	0	0	1	22	0.045454545
MRPL9	1	0	0	0	0	1	22	0.045454545
ABCA12	1	0	0	0	0	1	22	0.045454545
ABCA13	1	0	0	0	0	1	22	0.045454545
ESR2	1	0	0	0	0	1	22	0.045454545
OTOA	1	0	0	0	0	1	22	0.045454545
PALB2	0	0	0	1	0	1	22	0.045454545
C19orf47	1	0	0	0	0	1	22	0.045454545
PTCD2	1	0	0	0	0	1	22	0.045454545
SI	1	0	0	0	0	1	22	0.045454545
ST8SIA1	1	0	0	0	0	1	22	0.045454545
MELK	1	0	0	0	0	1	22	0.045454545
C20orf43	1	0	0	0	0	1	22	0.045454545
OR6N1	1	0	0	0	0	1	22	0.045454545
PHF2	1	0	0	0	0	1	22	0.045454545
TOP3B	1	0	0	0	0	1	22	0.045454545
OR51F1	1	0	0	0	0	1	22	0.045454545
MYOM2	1	0	0	0	0	1	22	0.045454545
PMP2	0	0	0	0	1	1	22	0.045454545
KMO	0	0	0	1	0	1	22	0.045454545
LCLAT1	1	0	0	0	0	1	22	0.045454545

C6orf57	0	1	0	0	0	1	22	0.045454545
KRT1	1	0	0	0	0	1	22	0.045454545
UPF1	1	0	0	0	0	1	22	0.045454545
ADAMTS18	1	0	0	0	0	1	22	0.045454545
KCNA3	1	0	0	0	0	1	22	0.045454545
SCPEP1	1	0	0	0	0	1	22	0.045454545
FLG2	1	0	0	0	0	1	22	0.045454545
SPRR3	1	0	0	0	0	1	22	0.045454545
STAT4	1	0	0	0	0	1	22	0.045454545
SEC23A	1	0	0	0	0	1	22	0.045454545
CAPN6	1	0	0	0	0	1	22	0.045454545
CPXM1	1	0	0	0	0	1	22	0.045454545
ZNF385B	1	0	0	0	0	1	22	0.045454545
CASK	1	0	0	0	0	1	22	0.045454545
FHL2	1	0	0	0	0	1	22	0.045454545
GTF2A1L	1	0	0	0	0	1	22	0.045454545
C20orf70	1	0	0	0	0	1	22	0.045454545
SLC6A13	1	0	0	0	0	1	22	0.045454545
EPS15	2	0	0	0	0	1	22	0.045454545
ZIM3	1	0	0	0	0	1	22	0.045454545
PDYN	1	0	0	0	0	1	22	0.045454545
RIMBP2	1	0	0	0	0	1	22	0.045454545
ACACB	1	0	0	0	0	1	22	0.045454545
CCDC30	0	1	0	0	0	1	22	0.045454545
EFNA4	0	0	0	0	1	1	22	0.045454545
SLFN11	1	0	0	0	0	1	22	0.045454545
EIF2C3	1	0	0	0	0	1	22	0.045454545
APPL1	1	0	0	0	0	1	22	0.045454545
GPR64	1	0	0	0	0	1	22	0.045454545
ADAM29	0	0	0	1	0	1	22	0.045454545
AJAP1	1	0	0	0	0	1	22	0.045454545
IL19	1	0	0	0	0	1	22	0.045454545
KCNJ1	0	1	0	0	0	1	22	0.045454545
VASH1	1	0	0	0	0	1	22	0.045454545
TUSC3	1	0	0	0	0	1	22	0.045454545
PLXNA4	1	0	0	0	0	1	22	0.045454545
C9orf135	1	0	0	0	0	1	22	0.045454545
MYO16	1	0	0	0	0	1	22	0.045454545
KIAA1217	1	0	0	0	0	1	22	0.045454545
SEPP1	0	0	0	1	0	1	22	0.045454545
CDH10	1	0	0	0	0	1	22	0.045454545
INSC	0	0	0	0	1	1	22	0.045454545

CYFIP1	1	0	0	0	0	1	22	0.045454545
RNF38	0	0	1	0	0	1	22	0.045454545
C17orf47	1	0	0	0	0	1	22	0.045454545
TCN1	1	0	0	0	0	1	22	0.045454545
TRMT2B	0	0	0	1	0	1	22	0.045454545
SNX24	1	0	0	0	0	1	22	0.045454545
BMPR1A	1	0	0	0	0	1	22	0.045454545
MAP2K7	1	0	0	0	0	1	22	0.045454545
MDH2	1	0	0	0	0	1	22	0.045454545
PEX13	1	0	0	0	0	1	22	0.045454545
DCLRE1B	1	0	0	0	0	1	22	0.045454545
TMEM159	1	0	0	0	0	1	22	0.045454545
SPTBN1	1	0	0	0	0	1	22	0.045454545
AP3B1	1	0	0	0	0	1	22	0.045454545
VEPH1	1	0	0	0	0	1	22	0.045454545
NXN	1	0	0	0	0	1	22	0.045454545
FAM171B	1	0	0	0	0	1	22	0.045454545
NEFH	0	0	0	0	1	1	22	0.045454545
RMI1	1	0	0	0	0	1	22	0.045454545
SPAG6	1	0	0	0	0	1	22	0.045454545
NIPBL	1	0	0	0	0	1	22	0.045454545
KCNS2	1	0	0	0	0	1	22	0.045454545
OR51T1	1	0	0	0	0	1	22	0.045454545
SPOCD1	1	0	0	0	0	1	22	0.045454545
RENBP	1	0	0	0	0	1	22	0.045454545
PIGA	0	1	0	0	0	1	22	0.045454545
BEND2	1	0	0	0	0	1	22	0.045454545
ATP1B3	1	0	0	0	0	1	22	0.045454545
TMEM198	1	0	0	0	0	1	22	0.045454545
CYP2A7	1	0	0	0	0	1	22	0.045454545
CASQ1	1	0	0	0	0	1	22	0.045454545
IL21R	1	0	0	0	0	1	22	0.045454545
ZNF804A	1	0	0	0	0	1	22	0.045454545
MCM9	1	0	0	0	0	1	22	0.045454545
ZNF804B	1	0	0	0	0	1	22	0.045454545
PCDHA2	1	0	0	0	0	1	22	0.045454545
HS1BP3	1	0	0	0	0	1	22	0.045454545
CASP8	1	0	0	0	0	1	22	0.045454545
ANKFN1	1	0	0	0	0	1	22	0.045454545
BCL9	0	0	0	1	0	1	22	0.045454545
CDR2	1	0	0	0	0	1	22	0.045454545
HIST1H2BE	1	0	0	0	0	1	22	0.045454545

RSPH6A	0	0	0	0	1	1	22	0.045454545
PLAUR	1	0	0	0	0	1	22	0.045454545
ABCC3	1	0	0	0	0	1	22	0.045454545
AOC3	1	0	0	0	0	1	22	0.045454545
TIMP2	1	0	0	0	0	1	22	0.045454545
KIAA1841	1	0	0	0	0	1	22	0.045454545
PCDHGB1	1	0	0	0	0	1	22	0.045454545
FAM155A	1	0	0	0	0	1	22	0.045454545
MS4A2	1	0	0	0	0	1	22	0.045454545
MS4A1	1	0	0	0	0	1	22	0.045454545
SPINT1	0	0	0	1	0	1	22	0.045454545
CXorf58	1	0	0	0	0	1	22	0.045454545
PCCA	1	0	0	0	0	1	22	0.045454545
DOK3	1	0	0	0	0	1	22	0.045454545
PFKM	1	0	0	0	0	1	22	0.045454545
MYO1G	1	0	0	0	0	1	22	0.045454545
TTYH2	1	0	0	0	0	1	22	0.045454545
ACTC1	1	0	0	0	0	1	22	0.045454545
SERPINB6	1	0	0	0	0	1	22	0.045454545
SLC4A5	1	0	0	0	0	1	22	0.045454545
ZNF667	1	0	0	0	0	1	22	0.045454545
HIST1H1B	1	0	0	0	0	1	22	0.045454545
KIAA1244	1	0	0	0	0	1	22	0.045454545
RNASE9	0	0	0	1	0	1	22	0.045454545
SLC41A3	1	0	0	0	0	1	22	0.045454545
COG5	0	0	1	0	0	1	22	0.045454545
C14orf50	1	0	0	0	0	1	22	0.045454545
DISP1	1	0	0	0	0	1	22	0.045454545
KLHL4	1	0	0	0	0	1	22	0.045454545
VPS13D	1	0	0	0	0	1	22	0.045454545
GPR22	1	0	0	0	0	1	22	0.045454545
SERPINB4	1	0	0	0	0	1	22	0.045454545
SERPINB7	1	0	0	0	0	1	22	0.045454545
SOCS5	0	0	0	1	0	1	22	0.045454545
C12orf12	0	0	0	0	1	1	22	0.045454545
CX3CR1	1	0	0	0	0	1	22	0.045454545
MBTPS1	1	0	0	0	0	1	22	0.045454545
EIF4G1	1	0	0	0	0	1	22	0.045454545
KCTD14	1	0	0	0	0	1	22	0.045454545
ACSL6	1	0	0	0	0	1	22	0.045454545
WDR59	1	0	0	0	0	1	22	0.045454545
ACSL5	1	0	0	0	0	1	22	0.045454545

NFS1	1	0	0	0	0	1	22	0.045454545
L3MBTL3	0	1	0	0	0	1	22	0.045454545
DARS2	1	0	0	0	0	1	22	0.045454545
XRN1	0	1	0	0	0	1	22	0.045454545
XRN2	1	0	0	0	0	1	22	0.045454545
GLS	1	0	0	0	0	1	22	0.045454545
PSG7	1	0	0	0	0	1	22	0.045454545
SLC19A2	1	0	0	0	0	1	22	0.045454545
ALDH1L1	1	0	0	0	0	1	22	0.045454545
ZNF560	0	0	0	1	0	1	22	0.045454545
KIAA1409	1	0	0	0	0	1	22	0.045454545
TRIM38	1	0	0	0	0	1	22	0.045454545
CCDC60	1	0	0	0	0	1	22	0.045454545
ANKRD55	1	0	0	0	0	1	22	0.045454545
ZNF844	1	0	0	0	0	1	22	0.045454545
HP	1	0	0	0	0	1	22	0.045454545
FMN1	0	0	1	0	0	1	22	0.045454545
DCLK2	1	0	0	0	0	1	22	0.045454545
SLAIN1	0	1	0	0	0	1	22	0.045454545
NOX5	0	1	0	0	0	1	22	0.045454545
SPRYD5	1	0	0	0	0	1	22	0.045454545
DPPA4	1	0	0	0	0	1	22	0.045454545
TLR2	1	0	0	0	0	1	22	0.045454545
FAM200A	1	0	0	0	0	1	22	0.045454545
FLG	1	0	0	0	0	1	22	0.045454545
PTN	0	0	0	1	0	1	22	0.045454545
CHD3	1	0	0	0	0	1	22	0.045454545
IGF2R	0	1	0	0	0	1	22	0.045454545
PREX2	1	0	0	0	0	1	22	0.045454545
CHD4	1	0	0	0	0	1	22	0.045454545
CHD6	1	0	0	0	0	1	22	0.045454545
TSC2	1	0	0	0	0	1	22	0.045454545
NKAPL	1	0	0	0	0	1	22	0.045454545
THBS2	1	0	0	0	0	1	22	0.045454545
SOHLH1	1	0	0	0	0	1	22	0.045454545
MED12L	1	0	0	0	0	1	22	0.045454545
PRPS1L1	1	0	0	0	0	1	22	0.045454545
GUCY1A3	0	1	0	0	0	1	22	0.045454545
GUCY1A2	1	0	0	0	0	1	22	0.045454545
PIK3R3	0	1	0	0	0	1	22	0.045454545
HTR2C	1	0	0	0	0	1	22	0.045454545
MYST3	1	0	0	0	0	1	22	0.045454545

PSME4	0	0	1	0	0	1	22	0.045454545
TROAP	2	0	0	0	0	1	22	0.045454545
DCHS2	1	0	0	0	0	1	22	0.045454545
C1QL4	1	0	0	0	0	1	22	0.045454545
MRPL15	1	0	0	0	0	1	22	0.045454545
TFEC	1	0	0	0	0	1	22	0.045454545
NHSL2	1	0	0	0	0	1	22	0.045454545
ANKRD27	1	0	0	0	0	1	22	0.045454545
NPHS2	1	0	0	0	0	1	22	0.045454545
POLR2C	1	0	0	0	0	1	22	0.045454545
NELL2	1	0	0	0	0	1	22	0.045454545
TRIM42	1	0	0	0	0	1	22	0.045454545
OR7C2	0	0	0	1	0	1	22	0.045454545
NLE1	0	1	0	0	0	1	22	0.045454545
HENMT1	1	0	0	0	0	1	22	0.045454545
TAF1	1	0	0	0	0	1	22	0.045454545
G6PC	1	0	0	0	0	1	22	0.045454545
SHROOM3	1	0	0	0	0	1	22	0.045454545
PAK1	1	0	0	0	0	1	22	0.045454545
BPIL1	1	0	0	0	0	1	22	0.045454545
RBM23	0	0	0	0	1	1	22	0.045454545
RBM20	1	0	0	0	0	1	22	0.045454545
ACTR5	1	0	0	0	0	1	22	0.045454545
VPS72	1	0	0	0	0	1	22	0.045454545
BTN3A1	1	0	0	0	0	1	22	0.045454545
SORCS1	0	0	1	0	0	1	22	0.045454545
EPHA5	1	0	0	0	0	1	22	0.045454545
NEB	1	0	0	0	0	1	22	0.045454545
SDCBP	1	0	0	0	0	1	22	0.045454545
FZD8	1	0	0	0	0	1	22	0.045454545
C10orf72	1	0	0	0	0	1	22	0.045454545
MAPK3	1	0	0	0	0	1	22	0.045454545
UGT2B10	0	1	0	0	0	1	22	0.045454545
ALDH18A1	1	0	0	0	0	1	22	0.045454545
DUSP6	1	0	0	0	0	1	22	0.045454545
RAP2C	1	0	0	0	0	1	22	0.045454545
RBL2	1	0	0	0	0	1	22	0.045454545
PCDH9	1	0	0	0	0	1	22	0.045454545
CCDC13	1	0	0	0	0	1	22	0.045454545
MARK3	0	1	0	0	0	1	22	0.045454545
FERMT2	1	0	0	0	0	1	22	0.045454545
TOMM70A	1	0	0	0	0	1	22	0.045454545

BAI3	1	0	0	0	0	1	22	0.045454545
KCNB2	1	0	0	0	0	1	22	0.045454545
OR8B8	1	0	0	0	0	1	22	0.045454545
HNRNPUL2	1	0	0	0	0	1	22	0.045454545
THNSL1	1	0	0	0	0	1	22	0.045454545
HEY1	1	0	0	0	0	1	22	0.045454545
XKR4	1	0	0	0	0	1	22	0.045454545
FHOD3	1	0	0	0	0	1	22	0.045454545
RGS12	1	0	0	0	0	1	22	0.045454545
SOS2	1	0	0	0	0	1	22	0.045454545
SOS1	1	0	0	0	0	1	22	0.045454545
MIS18BP1	1	0	0	0	0	1	22	0.045454545
METTL1	1	0	0	0	0	1	22	0.045454545
RIN1	1	0	0	0	0	1	22	0.045454545
SYNGR4	1	0	0	0	0	1	22	0.045454545
SLC12A5	1	0	0	0	0	1	22	0.045454545
C9orf3	1	0	0	0	0	1	22	0.045454545
MAGEB18	1	0	0	0	0	1	22	0.045454545
CD53	0	1	0	0	0	1	22	0.045454545
KCTD1	0	1	0	0	0	1	22	0.045454545
AUTS2	1	0	0	0	0	1	22	0.045454545
MED4	1	0	0	0	0	1	22	0.045454545
KALRN	1	0	0	0	0	1	22	0.045454545
IL12B	1	0	0	0	0	1	22	0.045454545
CNTNAP1	1	0	0	0	0	1	22	0.045454545
OR52M1	1	0	0	0	0	1	22	0.045454545
ODZ1	1	0	0	0	0	1	22	0.045454545
BTN2A2	1	0	0	0	0	1	22	0.045454545
SEC31B	1	0	0	0	0	1	22	0.045454545
UBOX5	1	0	0	0	0	1	22	0.045454545
GRIN2B	0	0	0	1	0	1	22	0.045454545
TCEB3B	1	0	0	0	0	1	22	0.045454545
GRHL1	1	0	0	0	0	1	22	0.045454545
PRPF18	0	0	1	0	0	1	22	0.045454545
CMPK2	1	0	0	0	0	1	22	0.045454545
LTN1	0	0	0	1	0	1	22	0.045454545
SLC38A11	1	0	0	0	0	1	22	0.045454545
C10orf18	1	0	0	0	0	1	22	0.045454545
DGKI	1	0	0	0	0	1	22	0.045454545
ZNF419	1	0	0	0	0	1	22	0.045454545
FSHR	1	0	0	0	0	1	22	0.045454545
TF	1	0	0	0	0	1	22	0.045454545

TG	0	0	0	1	0	1	22	0.045454545
VPS13A	0	1	0	0	0	1	22	0.045454545
DGKG	1	0	0	0	0	1	22	0.045454545
HSD11B1	1	0	0	0	0	1	22	0.045454545
DPY19L3	1	0	0	0	0	1	22	0.045454545
TRAF7	1	0	0	0	0	1	22	0.045454545
ORC6	1	0	0	0	0	1	22	0.045454545
MMP9	1	0	0	0	0	1	22	0.045454545
ACAP1	0	0	0	0	1	1	22	0.045454545
PTGIS	1	0	0	0	0	1	22	0.045454545
KIAA1432	0	1	0	0	0	1	22	0.045454545
ARMC4	1	0	0	0	0	1	22	0.045454545
RASA2	0	0	0	1	0	1	22	0.045454545
C20orf85	1	0	0	0	0	1	22	0.045454545
PLEKHG1	0	1	0	0	0	1	22	0.045454545
PREX1	0	1	0	0	0	1	22	0.045454545
AMTN	1	0	0	0	0	1	22	0.045454545
PTPRD	1	0	0	0	0	1	22	0.045454545
PTPRC	0	0	1	0	0	1	22	0.045454545
PTPRM	1	0	0	0	0	1	22	0.045454545
PTPRH	0	1	0	0	0	1	22	0.045454545
