

Supplemental Table 7: Summary of somatic genomic alterations in combined BETRNet and TCGA cohorts

		SNV				CNV_High_Gain				CNV_Two_Copy_Loss				Total % Altered			
Gene_ID	Pathway	HM	IM	LM	MM	HM	IM	LM	MM	HM	IM	LM	MM	HM	IM	LM	MM
TP53	p53	72%	81%	74%	65%	NA	NA	NA	NA	6%	3%	0%	10%	78%	84%	74%	75%
ATM	p53	6%	0%	4%	0%	NA	NA	NA	NA	3%	3%	0%	5%	9%	3%	4%	5%
ARID1A	Chromatin remodeling	22%	10%	11%	5%	NA	NA	NA	NA	0%	6%	0%	0%	22%	16%	11%	5%
ARID1B	Chromatin remodeling	0%	0%	7%	0%	NA	NA	NA	NA	0%	0%	0%	5%	0%	0%	7%	5%
ERBB2	ERBB/MET	19%	12%	0%	0%	28%	23%	4%	15%	NA	NA	NA	NA	41%	32%	4%	15%
ERBB4	ERBB/MET	0%	8%	10%	0%	0%	0%	0%	0%	NA	NA	NA	NA	0%	8%	10%	0%
EGFR	ERBB/MET	0%	0%	0%	0%	6%	13%	0%	0%	NA	NA	NA	NA	6%	13%	0%	0%
MET	ERBB/MET	0%	0%	0%	0%	3%	0%	4%	0%	NA	NA	NA	NA	3%	0%	4%	0%
KRAS	ERBB/MET	6%	3%	0%	0%	6%	13%	15%	0%	NA	NA	NA	NA	12%	16%	15%	0%
NRAS	ERBB/MET	0%	0%	0%	0%	3%	3%	0%	0%	NA	NA	NA	NA	3%	3%	0%	0%
CDKN2B	Cell cycle	0%	0%	0%	0%	NA	NA	NA	NA	9%	13%	15%	15%	12%	15%	10%	19%
CDKN2A	Cell cycle	9%	13%	26%	0%	NA	NA	NA	NA	13%	13%	15%	15%	22%	26%	41%	15%
CDK6	Cell cycle	3%	0%	0%	0%	0%	16%	7%	5%	NA	NA	NA	NA	3%	16%	7%	5%
RB1	Cell cycle	6%	0%	4%	5%	NA	NA	NA	NA	0%	3%	0%	0%	6%	3%	4%	5%