

Supplemental Table 6: Summary of somatic genomic alterations in TCGA EACs

		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%	70%	69%	NA	NA	NA	NA	4%	4%	0%	13%	76%	85%	70%	82%
ATM	p53	8%	0%	5%	0%	NA	NA	NA	NA	4%	0%	0%	6%	12%	0%	5%	6%
ARID1A	Chromatin remodeling	24%	8%	5%	6%	NA	NA	NA	NA	0%	4%	0%	0%	24%	12%	5%	6%
ARID1B	Chromatin remodeling	0%	0%	5%	0%	NA	NA	NA	NA	0%	0%	0%	6%	0%	0%	5%	6%
ERBB2	ERBB/MET	12%	8%	0%	0%	20%	27%	5%	13%	NA	NA	NA	NA	28%	31%	5%	13%
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%	8%	12%	0%	0%	NA	NA	NA	NA	8%	12%	0%	0%
MET	ERBB/MET	0%	0%	0%	0%	4%	0%	0%	0%	NA	NA	NA	NA	4%	0%	0%	0%
KRAS	ERBB/MET	8%	4%	0%	0%	8%	8%	20%	0%	NA	NA	NA	NA	16%	12%	20%	0%
NRAS	ERBB/MET	0%	0%	0%	0%	0%	4%	0%	0%	NA	NA	NA	NA	0%	4%	0%	0%
CDKN2B	Cell cycle	0%	0%	0%	0%	NA	NA	NA	NA	12%	15%	10%	19%	12%	15%	10%	19%
CDKN2A	Cell cycle	8%	15%	25%	0%	NA	NA	NA	NA	16%	15%	10%	19%	24%	30%	35%	19%
CDK6	Cell cycle	4%	0%	0%	0%	0%	19%	5%	6%	NA	NA	NA	NA	4%	19%	5%	6%
RB1	Cell cycle	8%	0%	5%	0%	NA	NA	NA	NA	0%	4%	0%	0%	8%	4%	5%	0%