

S11 Table. REACTOME analysis (WES VAF > 4% and RNA VAF > 4%)

	Pathway name	#Entities found	#Entities total	Entities FDR	Submitted entities found
P1	Regulation of TP53 expression	2	4	0.46675	TP53
	Association of TriC/CCT with target proteins during biosynthesis	4	40	0.46675	USP11;PIM1;FKBP9;TP53
	Regulation of TP53 activity through phosphorylation	6	95	0.46675	SLC25A16;RBBP8;RAD17;TP53;TAF1
	Ovarian tumour domain proteases	4	43	0.46675	ZRANB1;NAF1;NOD2;TP53
	RNA Polymerase II transcription pre-initiation and promoter opening	4	47	0.46675	GTF2A2;SPAG1;TAF1
	Regulation of TP53 activity	8	178	0.46675	SLC25A16;RBBP8;PIP4K2A;RAD17;TP53;TAF1
P5	FGFR2 mutant receptor activation	6	48	5.78E-07	FGFR2
	Signalling by FGFR in disease	7	89	5.78E-07	NARS2;FGFR2
	Signalling by FGFR2 IIIa TM	5	24	5.78E-07	FGFR2
	Signalling by FGFR2 in disease	6	62	1.20E-06	FGFR2
	PI3K cascade	5	58	2.08E-05	NARS2;FGFR2
P8	RAS signalling downstream of NF1 loss-of-function variants	2	5	0.050366	KRAS
	CD209 (DC-SIGN) signalling	3	29	0.050366	EP300;KRAS
	RAF activation	3	30	0.050366	BRAF;KRAS
	NOTCH3 intracellular domain regulates transcription	3	36	0.050366	PLXND1;EP300
	Signalling to ERKs	3	37	0.050366	BRAF;KRAS

WES, whole exome sequencing; VAF, variant allele frequency.