

Supplementary table 2: Frequencies of common and specific gains and losses in Sawtooth/8/16 and Firestorm/Amplifier IMPC subsets.

Pos SNP Start	Pos SNP End	Chr	Cytoband	Sawtooth/8/16 (%)	Firestorm/Amplifier (%)	Genes of interest
Common regions						
<i>Gains</i>						
36872094	146293414	8	p11.23-q24.3	83	53	
<i>Losses</i>						
315843	35282003	8	p23.3-p12	62	66	
46534977	90163275	16	q11.2-q24.3	74	40	
Specific regions						
<i>Gains</i>						
552621	35205717	16	p13.3-p11.1	71	8	
25899668	28036350	17	q11.2	0	44	
35306175	38327133	17	q12-q21.1	0	59	
47177747	81049725	17	q21.32-q25.3	18	62	
46889933	62912463	20	q13.13-q13.33	18	51	
<i>Losses</i>						
34811050	114150717	1	p34.3-p13.2	8	49	
70106360	170918031	6	q13-q27	50*	23*	
2310130	22235650	17	p13.3-p11.1	15	74	
32541260	35320846	17	q12	13	43	
41982253	46948218	17	q21.31-31.32	13	41	
34734484	77828600	18	q12.2-q23	11	42	
Amplifications						
94690198	132251807	8	q22.1-q24.22	2	35	<i>RAD54B, CCNE2, TP53INP1, RAD21, M</i>
37251066	38303547	17	q12-q21.1	0	37	<i>STARD3, ERBB2, GRB7</i>
48579452	49994258	17	q21.33	5	20	
57486793	62354992	17	q22-q23.3	6	46	<i>PPM1D, BCAS3, TBX2, TBX4, TLK1, TL</i>
48483623	49500894	20	q13.13	0	23	<i>BCAS4</i>
50796522	53259964	20	q13.2	0	30	<i>ZNF217, BCAS1</i>

Legends: Recurrent gains, losses or amplifications regions after exclusion of genomic variant according to the DGV database, observed in more than 40% of cases. Pos SNP Start/ pos SNP End: position of the SNP that represent the boundaries of gains, losses or amplifications. Genomic positions are provided according to human genome 19 references in bp; Chr: chromosome; IMPC: invasive micropapillary carcinoma; *: losses associated with loss of heterozygosity (LOH).