

Supplementary Table S1: Variants identified in pre-treatment and post-treatment tumor targeted next-generation sequencing (NGS).

Pre-treatment (~30% tumor content)	Allelic fraction	Post-treatment (~80% tumor content)	Allelic fraction
EGFR c.2238_2252delATTAAGAGA AGCAAC (p.L747_T751del), exon 19	22% (133/603)	EGFR c.2238_2252delATTAAGAGA AGCAAC (p.L747_T751del), exon 19	11% (37/336)
TP53 c.796G>A (p.G266R), exon 8	25% (74/296)	TP53 c.796G>A (p.G266R), exon 8	22% (31/141)
BRCA1 c.4036G>A (p.E1346K), exon 10	29% (168/581)	BRCA1 c.4036G>A (p.E1346K), exon 10	34% (101/297)
GLI3 c.93G>C (p.E31D), exon 2	10% (54/538)	GLI3 c.93G>C (p.E31D), exon 2	7% (24/339)
JAK3 c.2681-4C>T ()	69% (157/227)	JAK3 c.2681-4C>T ()	61% (51/84)
PTPRD c.239C>T (p.S80L), exon 11	45% (233/518)	PTPRD c.239C>T (p.S80L), exon 11	46% (151/328)
SMAD4 c.1091T>G (p.L364W), exon 9	27% (148/548)	SMAD4 c.1091T>G (p.L364W), exon 9	21% (68/325)
Not Detected	N/A	REL c.1324G>T (p.G442C), exon 11	10% (44/437)
Not Detected	N/A	MET c.3683A>T (p.D1228V), exon 19	43% (309/718)

Note: paired germline NGS was not performed so some variants, such as the high allelic fraction JAK3 mutation, may be germline in nature and not somatic