

PMLB: copy number alteration - Illumina Human Omni-Quad version 1 Beadchips, Targeted capture

Molecular Methods Description:

Copy number alterations profiled on Illumina Human Omni-Quad version 1 Beadchips.

Analysis Description:

Data was processed using the Bioconductor DNACopy package version 1.50 and mapped to hg19 gene coordinates using the Bioconductor CNTools package version 1.3.2.

- TCGA serous ovarian copy number data (Broad Institute's Firehose pipeline) was used to correct for germline events and outliers that would confound somatic signal.

Table:

ABCA13	154664	ERBB2	2064	MYH9	4627
ADAMTSL3	57188	ERBB3	2065	MYO3A	53904
AHNAK	79026	ERBB4	2066	NCOA3	8202
AKAP9	10142	FAT1	2195	NCOR1	9611
AKT1	207	FAT3	120114	NCOR2	9612
ALK	238	FBXW7	55294	NF1	4763
APC	324	FCGBP	8857	NOTCH1	4851
APOB	338	FGFR2	2263	NRAS	4893
ARID1A	8289	GATA3	2625	PDGFRA	5156
ARID2	196528	GNAS	2778	PIK3CA	5290
ATM	472	GRIN2A	2903	PIK3CG	5294
ATR	545	HNF1	6927	PIK3R1	5295
BRAF	673	HNF1A	PKHD1	5314	BRCA1
672	HRNR	388697	PKHD1L1	93035	BRCA2
675	HUWE1	10075	PPP2R1A	5518	CASP8
841	JAK2	3717	PREX2	80243	CDH1
999	JAK3	3718	PTEN	5728	CDK12
51755	KIT	3815	PTPRD	5789	CDKN2A
1029	KRAS	3845	RB1	5925	CHEK2
11200	LAMA2	3908	RET	5979	COL6A3
1293	LRP1B	53353	RICTOR	253260	CREBBP
1387	LRP2	4036	ROS1	6098	CSMD1

64478	LRRK2	120892	RYR1	6261	CSMD2
114784	MACF1	23499	RYR2	6262	CSMD3
114788	MAP2	4133	RYR3	6263	CTNNB1
1499	MAP2K4	6416	SETD2	29072	DDR2
4921	MAP3K1	4214	SF3B1	23451	DNAH11
8701	MDN1	23195	SMAD4	4089	DNAH2
146754	MET	4233	SMARCA4	6597	DNAH3
55567	MLH1	4292	SPEN	23013	DNAH5
1767	MLL3	58508	SPTA1	6708	DNAH9
1770	MSH2	4436	SYNE1	23345	DST
667	MSH6	2956	SYNE2	23224	DYNC1H1
1778	MTOR	2475	TP53	7157	EGFR
1956	MUC4	4585	TSC1	7248	EPHA3
2042	MUC5AC	4586	TSC2	7249	EPHA5
2044	MYH1	4619	UBR5	51366	EPHA7
2045	MYH2	4620	ZFHX4	79776	