S5 Table. Comparison of expected variants with identified variants in Horizon HD753

No	Variant type	Chromosome number	Gene	Variant	Expected allelic frequency (%)	GliomaSCAN, allelic frequency (%)
1	SNV high GC	chr.19	*GNA11*	Q209L	5.6	4.4
2	SNV high GC	chr.14	*AKT1*	E17K	5.0	4.0
3	SNV low GC	chr.3	*PIK3CA*	E545K	5.6	4.5
4	Long insertion	chr.7	*EGFR*	V769_D770ins ASV	5.6	3.8
5	Long deletion	chr.7	*EGFR*	ΔE746 - A750	5.0	2.0
6	CNV	chr.2	*MYC-N*	Amplification	9.5	17.5
7	CNV	ch.8	*MYC-C*	Amplification	9.8	19.8
8	SNV low GC	chr.12	*KRAS*	G13D	5.6	4.4
9	SNV high GC	chr.9	*NOTCH1*	P668S	5.0	6.8
10	Short deletion	chr.7	*MET*	V237fs	2.5	2.3
11	Short deletion	chr.13	*FLT3*	S985fs	5.6	3.9
12	Short deletion	chr.13	*BRCA2*	A1689fs	5.6	5.7
13	SNV	chr.7	*EGFR*	G719S	5.3	4.5
14	SNV	chr.7	*BRAF*	V600E	18.2	15.8
15	SNV	chr.3	*PIK3CA*	H1047R	16.7	14.6

SNV, single nucleotide variant; Chr, chromosome; CNV, copy number variant.