S5 Table. Verified mutated gene list of HD827, with known VAF

Name	Chromosome	Position	Gene	Variant type	Variant	Expected frequency (%VAF)
HD827	chr1	115256530	*NRAS*	SNV	p.Q61K	12.50
	chr10	43613843	*RET*[a)]	SNV	p.L769L	60.00
	chr12	25398281	*KRAS*	SNV	p.G13D	15.00
	chr12	25398284	*KRAS*	SNV	p.G12D	6.00
	chr13	28578214	*FLT3*	INDEL	p.P986fs*>8	10.00
	chr13	32913558	*BRCA2*	INDEL	p.K1691fs*15	32.50
	chr17	7579472	*TP53*[a)]	SNV	p.P72R	92.50
	chr3	41266101	*CTNNB1*	SNV	p.S33Y	32.50
	chr3	41266133	*CTNNB1*	INDEL	p.S45del	10.00
	chr3	178936091	*PIK3CA*	SNV	p.E545K	9.00
	chr3	178952085	*PIK3CA*	SNV	p.H1047R	17.50
	chr4	55599321	*KIT**	SNV	p.D816V	10.00
	chr4	55602765	*KIT*	SNV	p.L862L	7.50
	chr4	153244155	*FBXW7*	INDEL	p.S668fs*39	32.50
	chr5	112175770	*APC*[a)]	SNV	p.T1493T	35.00
	chr7	55241707	*EGFR*	SNV	p.G719S	24.50
	chr7	55242464	*EGFR*	INDEL	p.E746_A750del	2.00
	chr7	55249063	*EGFR*[a)]	SNV	p.Q787Q	15.00
	chr7	55249071	*EGFR*	SNV	p.T790M	1.00
	chr7	55259515	*EGFR*	SNV	p.L858R	3.00
	chr7	116339847	*MET*	INDEL	p.L238fs*25	7.00
	chr7	116436022	*MET*[a)]	SNV	p.A1357A	7.00
	chr7	140453136	*BRAF*	SNV	p.V600E	10.50
	chr9	139409754	*NOTCH1*	SNV	p.P668S	30.00

VAF, variant of allele frequency. [a)]Excluded from the validation process (germline filter).