

Supplementary Materials

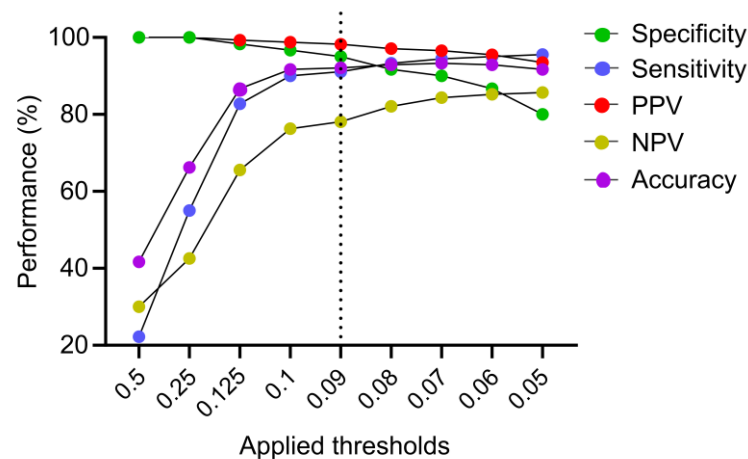


Figure S1: DEEPGENTM performance metrics at different thresholds. DEEPGENTM assay was performed with Seraseq™ ctDNA Mutation Mix v2 samples with validated minor allelic frequencies of 0.0%, 0.125%, 0.25% and 0.5% (20 ng input, n=3). Calculated are the sensitivity, specificity, the PPV and the NPA value as well as the accuracy for the DEEPGENTM assays at various VAF thresholds. A threshold of 0.09% was chosen to give the best assay performance.

Table S1: Overview of the 20 validated targets representing the overlap between the SeraCare mutation panel and the DEEPGENTM mutation panel. DEEPGENTM assay was performed with Seraseq™ ctDNA Mutation Mix v2 samples with validated minor allelic frequencies of 0.0%, 0.125%, 0.25% and 0.5% (20 ng input, n=3). Detected mutations are indicated as (1), not detected as (0). False negative and false positive values are highlighted in bold.

Chr.	Gene	Location	Mutation	0.0% VAF			0.125% VAF			0.25% VAF			0.5% VAF		
				Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3	Rep 1	Rep 2	Rep 3
3	CTNNB1	41266124	A/G	0	0	0	1	1	1	1	1	1	1	1	1
3	FOXL2	138665163	G/C	0	0	0	1	0	1	1	1	1	1	1	1
3	PIK3CA	178936091	G/A	0	0	0	1	0	0	1	1	1	1	1	1
3	PIK3CA	178952085	A/G	0	0	0	0	1	1	1	1	1	1	1	1
4	FGFR3	1803568	C/G	0	0	0	1	1	1	1	1	1	1	1	1
4	KIT	55599321	A/T	0	0	0	1	1	1	1	1	1	1	1	1
5	APC	112175639	C/T	0	0	0	1	1	0	1	1	1	1	1	1
7	EGFR	55242466	GAATTAAGAGAAGCA/-	0	0	0	1	0	0	1	1	1	1	1	1
7	EGFR	55249071	C/T	0	1	0	1	0	1	1	1	1	1	1	1
7	EGFR	55259515	T/G	0	0	0	1	1	0	1	1	1	1	1	1
7	BRAF	140453136	A/T	0	1	0	0	1	1	1	1	1	1	0	1

9	JAK2	5073770	G/T	0	0	0	1	1	0	1	1	1	1	1	1
10	RET	43617416	T/C	0	0	0	0	0	1	1	1	1	1	1	1
12	KRAS	25398284	C/T	0	0	0	1	1	1	1	1	1	1	1	1
14	AKT1	105246551	C/T	0	0	0	1	1	1	1	1	1	1	1	1
17	TP53	7577120	C/T	0	0	1	1	1	1	1	1	1	1	1	1
17	TP53	7577538	C/T	0	0	0	1	1	1	1	0	1	1	1	1
17	TP53	7578406	C/T	0	0	0	1	1	1	1	1	1	1	1	1
19	GNA11	3118942	A/T	0	0	0	1	1	1	1	1	1	1	1	1
20	GNAS	57484420	C/T	0	0	0	1	0	1	1	1	1	1	1	1

Table S2: DEEPGEN™ sensitivity at different input amounts. Seraseq™ ctDNA Mutation Mix v2 reference standard with validated minor allelic frequencies of 0.125% VAF and various cfDNA input (5ng and 20ng) was used for sequencing. Detected mutations are indicated as (1), not detected as (0). False negatives were highlighted in bold.

Chr.	Gene	Location	Mutation	5 ng				20 ng		
				Rep 1	Rep 2	Rep 3	Rep 4	Rep1	Rep 2	Rep 3
3	CTNNB1	41266124	A/G	1	0	0	1	1	1	1
3	FOXL2	138665163	G/C	0	1	0	0	1	0	1
3	PIK3CA	178936091	G/A	1	0	1	1	1	0	0
3	PIK3CA	178952085	A/G	1	1	1	1	0	1	1
4	FGFR3	1803568	C/G	1	1	1	0	1	1	1
4	KIT	55599321	A/T	0	0	0	1	1	1	1
5	APC	112175639	C/T	1	0	1	0	1	1	0
7	EGFR	55242466	GAATTAAGAGAAGCA/-	0	1	1	1	1	0	0
7	EGFR	55249071	C/T	1	1	1	1	1	0	1
7	EGFR	55259515	T/G	1	1	1	1	1	1	0
7	BRAF	140453136	A/T	0	1	0	1	0	1	1
9	JAK2	5073770	G/T	1	0	1	1	1	1	0
10	RET	43617416	T/C	1	0	1	0	0	0	1
12	KRAS	25398284	C/T	1	0	0	1	1	1	1
14	AKT1	105246551	C/T	1	0	1	0	1	1	1
17	TP53	7577120	C/T	1	1	1	1	1	1	1
17	TP53	7577538	C/T	0	1	0	1	1	1	1
17	TP53	7578406	C/T	1	1	1	0	1	1	1
19	GNA11	3118942	A/T	1	0	0	0	1	1	1
20	GNAS	57484420	C/T	1	0	0	1	1	0	1

Table S3: Intra-assay reproducibility. Six independent runs of the DEEPGEN™ assay using Seraseq™ ctDNA Mutation Mix v2 with 20 validated minor allelic frequencies of 0.5% were performed. Shown is the genome position of the 20 variants and their respective VAF [in %] of all six replicates. Shown as well is the average VAF [in %], highlighted in bold and the SD.

Chr.	Gene	Location	Mutation	Rep 1	Rep 2	Rep 3	Rep 4	Rep 5	Rep 6	Average	SD
3	CTNNB1	41266124	A/G	0.11	0.36	0.30	0.37	0.79	0.56	0.41	0.22
3	FOXL2	138665163	G/C	0.37	0.51	0.68	0.69	0.60	0.58	0.57	0.12
3	PIK3CA	178936091	G/A	0.13	0.11	0.22	0.17	0.21	0.51	0.22	0.14
3	PIK3CA	178952085	A/G	0.58	0.57	0.50	0.73	0.61	0.43	0.57	0.10
4	FGFR3	1803568	C/G	0.28	0.61	0.68	0.69	0.78	0.58	0.61	0.16
4	KIT	55599321	A/T	0.29	0.40	0.54	0.37	0.25	0.54	0.40	0.12
5	APC	112175639	C/T	0.41	0.27	0.39	0.33	0.41	0.30	0.35	0.06
7	EGFR	55242466	GAATTAAGAGAAGCA/-	0.33	0.52	0.21	0.43	0.68	0.67	0.47	0.18
7	EGFR	55249071	C/T	0.52	0.46	0.54	0.76	0.39	0.53	0.53	0.12
7	EGFR	55259515	T/G	0.70	0.42	0.59	0.79	0.52	0.61	0.61	0.12
7	BRAF	140453136	A/T	0.53	0.29	0.38	0.00	0.62	0.37	0.37	0.20
9	JAK2	5073770	G/T	0.17	0.55	0.17	0.15	0.46	0.40	0.32	0.17
10	RET	43617416	T/C	0.45	0.74	0.41	0.56	0.63	0.49	0.55	0.12
12	KRAS	25398284	C/T	0.58	0.75	0.40	0.52	0.59	0.34	0.53	0.14
14	AKT1	105246551	C/T	0.23	0.22	0.24	0.51	0.48	0.54	0.37	0.15
17	TP53	7577120	C/T	0.68	0.55	0.55	0.95	0.77	0.58	0.68	0.15
17	TP53	7577538	C/T	0.20	0.31	0.30	0.39	0.35	0.31	0.31	0.06
17	TP53	7578406	C/T	0.53	0.58	0.42	0.57	0.57	0.84	0.59	0.13
19	GNA11	3118942	A/T	0.74	0.50	0.59	0.64	0.89	0.47	0.64	0.15
20	GNAS	57484420	C/T	0.44	0.26	0.82	0.53	0.38	0.70	0.52	0.20

Table S4: Comparison of Quantgene's DEEPGEN™ with the AVENIO assay over 13 validated targets with four different VAFs (0%, 0.125%, 0.25%, 0.5%). Detected mutations are indicated as (1), not detected as (0). False negatives were highlighted in bold.

Chr.	Gene	Location	Mutation	0% VAF		0.125% VAF		0.25% VAF		0.5% VAF	
				DEEPGEN™	AVENIO	DEEPGEN™	AVENIO	DEEPGEN™	AVENIO	DEEPGEN™	AVENIO
5	APC	112175639	C/T	0	0	1	1	1	1	1	1
7	BRAF	140453136	A/T	0	0	0	0	1	1	1	1
3	CTNNB1	41266124	A/G	0	0	1	0	1	1	1	1
7	EGFR	55249071	C/T	0	0	1	0	1	1	1	1
7	EGFR	55259515	T/G	0	0	1	0	1	1	1	1

4	KIT	55599321	A/T	0	0	1	0	1	1	1	1
12	KRAS	25398284	C/T	0	0	1	1	1	1	1	1
3	PIK3CA	178936091	G/A	0	0	0	0	1	0	1	1
3	PIK3CA	178952085	A/G	0	0	1	0	1	0	1	1
10	RET	43617416	T/C	0	0	0	1	1	1	1	1
17	TP53	7577120	C/T	0	0	1	0	1	0	1	1
17	TP53	7577538	C/T	0	0	1	0	1	0	1	1
17	TP53	7578406	C/T	0	0	1	0	1	0	1	1
