Supplementary Table 1 – Results of the internal validation phase from 2X parallel runs for 4 different NGS panels for 9 tested cell lines.

Cell line	Illumina		ThermoFisher		Qiagen		Foundation Medicine	
	RUN1	RUN2	RUN1	RUN2	RUN1	RUN2	RUN1	RUN2
NCI-H2009	18.801	18.147	19.31	18.41	13.69	12.92	15.13	15.13
NCI-H2126	17.864	16.479	16.81	16.74	8.38	8.38	13.87	13.87
NCI-H2171	4.248	3.92	9.24	9.19	1.52	1.52	10.09	10.09
NCI-H1437	6.282	7.058	7.54	7.56	5.33	5.33	5.04	5.04
NCI-H23	15.667	13.298	23.5	24.26	9.11	9.88	27.74	27.74
NCI-H322	8.651	8.632	10.9	10.9	6.09	5.32	25.22	25.22
SKMEL2	18.003	25.174	17.56	17.53	16.71	16.72	34.04	44.13
C33A	66.942	64.147	36.23	37.49	25.08	25.08	69.35	69.35
IGROV1	112.715	113.429	71.6	61.73	51.66	51.66	71.87	76.91

Supplementary Table 2 – Description of the participating NGS methods at the pilot EQA scheme

Company	Panel Name	Type of NGS approach	Type of variants used to infer TMB	Number of gene
IDT	Custom panel	Gene targated	Non synonimous mutations, Indels	423
Twist Bioscience	Custom panel	Gene targated	Non-synonymous mutations, Splice variants, Indels	350
Twist Bioscience	Custom panel	Gene targated	Synonymous and non-synonymous mutations, Indels	645
Agilent	Custom panel	Gene targated	Non synonimous mutations, Indels	431
Illumina	TruSight Oncology 500	Gene targated	Non synonimous mutations, Indels	523
Thermo Fisher Scientific	Oncomine Tumor Mutation Load	Gene targated	Non synonimous and synonimous mutations, Indels	409
Thermo Fisher Scientific	Oncomine Tumor Mutation Load	Gene targated	Non synonimous mutations, Indels	409
Thermo Fisher Scientific	Oncomine Comprehensive Assay Plus	Gene targated	Non synonimous mutations, Indels	514
IDT	IDT xGen Pan-Cancer Panel v2.4	Clinical exome	Non synonimous mutations	523
Agilent	Custom Panel	Clinical exome	Non synonimous mutations, Indels	431
Twist Bioscience	Twist human Exome plus	Whole exome sequencing	Non-synonymous mutations, Splice variants, Indels	22000
Roche	Nimblegen (Roche) SeqCap EZ MedExome	Whole exome sequencing	Synonymous and non-synonymous mutations, Indels	22334