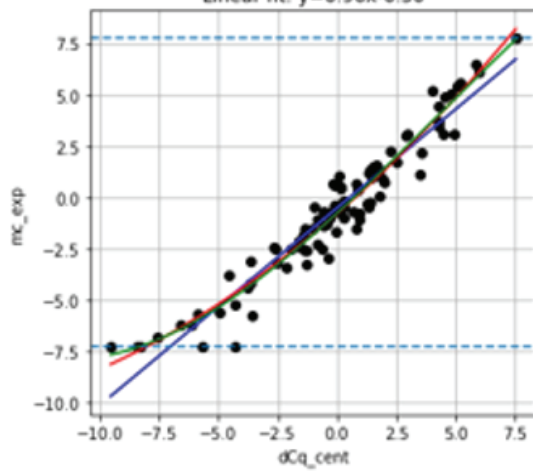


Supplementary Figure S1

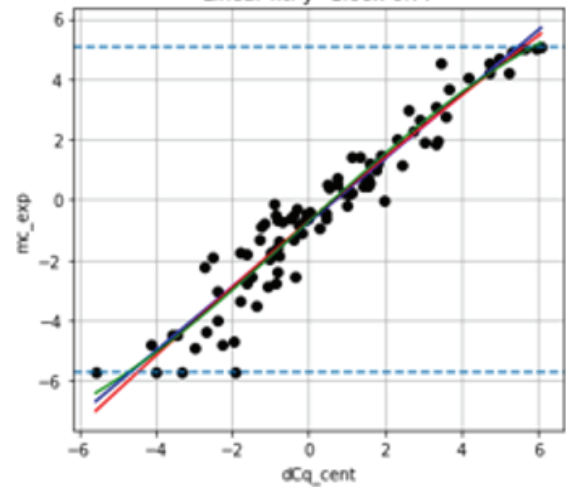
A

ADAM12.E10E11.NM_003474.4
 Pearson r (within bounds)= 0.961 (95%CI 0.941-0.974) p=8.3651e-52
 Linear fit: $y=0.96x-0.50$



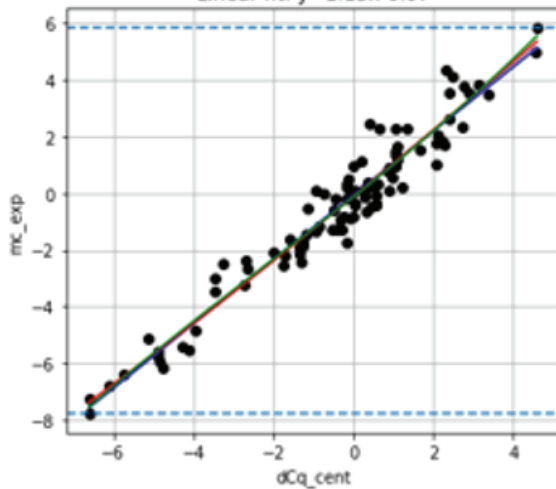
B

CD274.E4E5.NM_014143.3
 Pearson r (within bounds)= 0.959 (95%CI 0.939-0.973) p=2.1373e-53
 Linear fit: $y=1.06x-0.77$



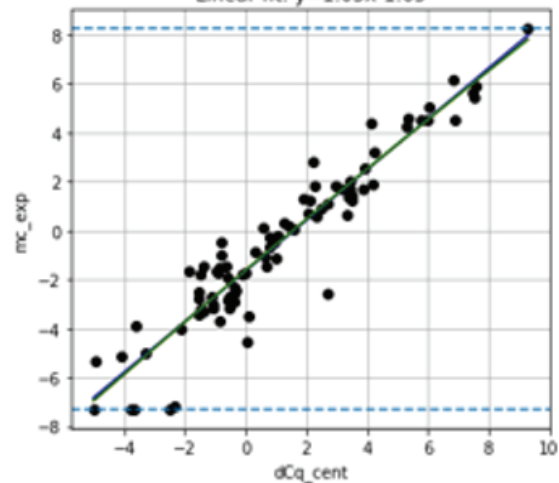
C

NM_001067:TOP2A.E21E22
 Pearson r (within bounds)= 0.969 (95%CI 0.954-0.979) p=8.5062e-59
 Linear fit: $y=1.13x-0.07$



D

NM_005018:PDCD1.E1E2
 Pearson r (within bounds)= 0.946 (95%CI 0.918-0.964) p=8.6717e-43
 Linear fit: $y=1.03x-1.65$



IRS Target	Within LOQ bound Pearson correlation coefficient (r)	Lower LOQ (12nRPM)	Upper LOQ (12nRPM)	Linear Range (fold)
<i>ADAM12</i>	0.961	-7.26	7.79	33,855x
<i>PD-L1</i>	0.959	-5.72	5.05	1,757x
<i>TOP2A</i>	0.969	-7.76	5.83	12,368x
<i>PD-1</i>	0.946	-7.30	8.24	47,803x

Supplementary Figure S1. Accuracy and linearity of Immunotherapy Response Score (IRS) expression components by quantitative transcriptional profiling vs. qRT-PCR

A-D. Normalized target gene expression for all four expression components of IRS (*ADAM12* [A], *PD-L1* [CD274; B], *TOP2A* [C] and *PD-1* [*PDCDI*; D] were determined by quantitative transcriptional profiling (performed in parallel with clinical StrataNGS CGP testing; y axis [mc_exp]) and qRT-PCR (x axis [dCq_cent]) from replicate RNA aliquots of 96 FFPE tumor tissues. Median-centered log₂ values for each target gene are plotted. Blue, red, and green lines are linear (1st), 2nd order, and 3rd order models, respectively. Polynomial terms were not significant (all p>0.05) for any of the genes. Blue dashed lines are lower and upper limit of quantification (LOQ). The amplicon name, within LOQ bound Pearson correlation coefficient (*r*) with 95% confidence interval (CI), p-value, and linear fit equation are shown for each IRS expression component gene. The table below the individual plots shows the linear range (from lower to upper LOQ) for each gene.