

Proliferation of tumor cell lines z-score = 2.7 (increased)			
Genes in dataset	Prediction	$\Delta\Delta Ct$	p-value
<i>MMP9</i>	Increased	4.960	1.20E-10
<i>SIK1</i>	Increased	4.219	1.05E-26
<i>AREG</i>	Increased	3.486	8.61E-15
<i>ENC1</i>	Increased	3.190	6.76E-20
<i>PBK</i>	Increased	2.770	1.84E-07
<i>MNDA</i>	Increased	2.525	2.47E-12
<i>IL12RB2</i>	Increased	2.364	4.83E-17
<i>TYMS</i>	Increased	1.889	2.47E-13
<i>PFKFB3</i>	Increased	1.756	2.50E-11
<i>CD38</i>	Increased	1.688	7.78E-15
<i>CCNE1</i>	Increased	1.648	3.17E-16
<i>DTL</i>	Increased	1.610	6.68E-09
<i>NAMPT</i>	Increased	1.610	3.62E-16
<i>E2F8</i>	Increased	1.510	9.92E-11
<i>PER1</i>	Increased	1.475	1.15E-11
<i>NFKB1A</i>	Increased	1.429	2.38E-20
<i>MK167</i>	Increased	1.220	9.68E-09
<i>PRC1</i>	Increased	1.150	1.10E-12
<i>CHEK1</i>	Increased	1.110	5.31E-13
<i>ADAM9</i>	Increased	1.090	3.46E-08
<i>ODC1</i>	Increased	1.069	1.48E-14
<i>DUSP10</i>	Increased	1.060	2.45E-12
<i>KIF11</i>	Increased	0.994	4.33E-09
<i>VAV3</i>	Increased	0.950	1.42E-11
<i>PTGER4</i>	Increased	0.861	1.34E-13
<i>ZNF267</i>	Increased	0.791	1.27E-10
<i>MXD1</i>	Increased	0.670	1.40E-08
<i>NR4A3</i>	Increased	0.551	1.96E-03
<i>PTP4A1</i>	Increased	0.529	2.85E-05
<i>NCAFG</i>	Increased	0.334	1.62E-02
<i>DNAJA3</i>	Increased	-0.428	2.10E-03
<i>FGF9</i>	Increased	-1.980	1.72E-14
<i>NR4A2</i>	Increased	Upregulated*	
<i>SGK1</i>	Increased	NA	
<i>TOP2A</i>	Increased	0.230	NS
<i>TAF1D</i>	Increased	0.130	NS
<i>TTK</i>	Increased	0.090	NS
<i>MMP8</i>	Decreased	3.622	1.01E-14
<i>LTF</i>	Decreased	3.48	1.16E-11
<i>S100A8</i>	Decreased	3.11	5.04E-12
<i>CD83</i>	Decreased	2.20	6.94E-17
<i>TNFAIP3</i>	Decreased	2.14	1.53E-20
<i>SAT1</i>	Decreased	1.403	7.31E-15
<i>DUSP5</i>	Decreased	1.078	6.33E-09
<i>SOD2</i>	Decreased	0.696	9.68E-07
<i>NRAS</i>	Decreased	0.542	3.90E-06
<i>MYC</i>	Decreased	-0.946	4.04E-10
<i>VIPR1</i>	Decreased	NA	
<i>HRH2</i>	Decreased	0.07	NS
<i>FABP5</i>	Decreased	0.060	NS
<i>BUB1B</i>	Affected	1.75	1.48E-07
<i>BCL6</i>	Affected	1.07	1.21E-11
<i>CD55</i>	Affected	0.93	1.48E-09
<i>PLK4</i>	Affected	0.72	4.60E-06
<i>ADCY3</i>	Affected	-0.56	1.49E-06
<i>ID3</i>	Affected	NA	

Apoptosis z-score=-1.9 (decreased)			
Genes in dataset	Prediction	$\Delta\Delta Ct$	p-value
<i>MMP9</i>	Decreased	4.96	1.20E-10
<i>AREG</i>	Decreased	3.49	8.61E-15
<i>CSTA</i>	Decreased	2.81	2.21E-06
<i>PBK</i>	Decreased	2.77	1.84E-07
<i>TNFAIP3</i>	Decreased	2.14	1.53E-20
<i>TYMS</i>	Decreased	1.89	2.47E-13
<i>CD38</i>	Decreased	1.69	7.78E-15
<i>NAMPT</i>	Decreased	1.61	3.62E-16
<i>NFKB1A</i>	Decreased	1.43	2.38E-20
<i>MCM10</i>	Decreased	1.34	4.16E-08
<i>SRGN</i>	Decreased	1.162	2.14E-12
<i>CHEK1</i>	Decreased	1.11	5.31E-13
<i>HERPUD1</i>	Decreased	0.99	2.05E-09
<i>VAV3</i>	Decreased	0.95	1.42E-11
<i>SOD2</i>	Decreased	0.70	9.68E-07
<i>MXD1</i>	Decreased	0.67	1.40E-08
<i>NR4A3</i>	Decreased	0.55	1.96E-03
<i>NRAS</i>	Decreased	0.54	3.90E-06
<i>RNASEL</i>	Decreased	-0.32	2.55E-02
<i>DNAJA3</i>	Decreased	-0.43	2.10E-03
<i>MYC</i>	Decreased	-0.95	4.04E-10
<i>UBASH3A</i>	Decreased	-1.33	2.53E-13
<i>FGF9</i>	Decreased	-1.98	1.72E-14
<i>NR4A2</i>	Decreased	Upregulated*	
<i>SGK1</i>	Decreased	NA	
<i>ID3</i>	Decreased	NA	
<i>OLR1</i>	Increased	3.480	5.80E-13
<i>S100A8</i>	Increased	3.112	5.04E-12
<i>PMAIP1</i>	Increased	2.640	3.10E-13
<i>CCNE1</i>	Increased	1.648	3.17E-16
<i>PER1</i>	Increased	1.475	1.15E-11
<i>SAT1</i>	Increased	1.403	7.31E-15
<i>MAP3K8</i>	Increased	1.300	3.89E-10
<i>GADD45B</i>	Increased	1.208	1.11E-13
<i>BCL6</i>	Increased	1.070	1.21E-11
<i>CD55</i>	Increased	0.926	1.48E-09
<i>HSPB1</i>	Increased	-1.439	1.92E-09
<i>CCR8</i>	Increased	-2.500	2.47E-15
<i>TOP2A</i>	Increased	0.230	NS
<i>TNFRSF10D</i>	Increased	0.150	NS
<i>TTK</i>	Increased	0.090	NS
<i>LTF</i>	Affected	3.484	1.16E-11
<i>ENC1</i>	Affected	3.190	6.76E-20
<i>ODC1</i>	Affected	1.069	1.48E-14
<i>ADORA2A</i>	Affected	-1.248	7.13E-09
<i>AKTIP</i>	Affected	-0.007	NS

Interphase of tumors cell lines (G1/S/G2) z-score=1.8 (increased)			
Genes in dataset	Prediction	$\Delta\Delta Ct$	p-value
<i>CCNE1</i>	Increased	1.65	3.17E-16
<i>E2F8</i>	Increased	1.51	9.92E-11
<i>NFKB1A</i>	Increased	1.43	2.38E-20
<i>MCM10</i>	Increased	1.34	4.16E-08
<i>CHEK1</i>	Increased	1.11	5.31E-13
<i>RBBP8</i>	Increased	0.80	1.01E-08
<i>MXD1</i>	Increased	0.67	1.40E-08
<i>MYC</i>	Decreased	-0.95	4.04E-10
<i>ID3</i>	Decreased	NA	
<i>MMP9</i>	Affected	4.96	1.20E-10
<i>TYMS</i>	Affected	1.89	2.47E-13
<i>DTL</i>	Affected	1.61	6.68E-09
<i>ZBTB10</i>	Affected	1.17	3.48E-13

Cytostasis (arrest) z-score=2.2 (increased)			
Genes in dataset	Prediction	$\Delta\Delta Ct$	p-value
<i>PER1</i>	Increased	1.48	1.15E-11
<i>NFKB1A</i>	Increased	1.43	2.38E-20
<i>GADD45B</i>	Increased	1.21	1.11E-13
<i>BCL6</i>	Increased	1.07	1.21E-11
<i>MXD1</i>	Increased	0.67	1.40E-08
<i>TOP2A</i>	Increased	0.23	NS
<i>NRAS</i>	Affected	0.54	3.90E-06

Mitosis z-score=-1.187 (decreased)			
Genes in dataset	Prediction	$\Delta\Delta Ct$	p-value
<i>CHEK1</i>	Decreased	1.11	5.31E-13
<i>KIF11</i>	Decreased	0.99	4.33E-09
<i>RBBP8</i>	Decreased	0.80	1.01E-08
<i>FGF9</i>	Decreased	-1.98	1.72E-14
<i>BUB1B</i>	Increased	1.75	1.48E-07
<i>CCNE1</i>	Increased	1.65	3.17E-16
<i>SKA3</i>	Affected	2.77	6.37E-04
<i>PTP4A1</i>	Affected	0.53	2.85E-05
<i>TOP2A</i>	Affected	0.23	NS
<i>TTK</i>	Affected	0.09	NS

Additional file 8. Ingenuity functional prediction analysis of the signature of T_{CM} cells in HIV infection. Ingenuity functional prediction analysis was made with IPA software. $\Delta\Delta Ct$ and p-values represent RT-PCR validation values. * Upregulation was inferred in the absence of a $\Delta\Delta Ct$ value, based on amplification in patients' cells ($\Delta Ct=6.5$), but no amplification in cells from controls. NS: Not significant. NA: no amplification.