

Supplementary Table S1: Detailed qPCR assay information.

Gene	Ref Seq.	Forward primer [5'-3'] Reverse primer [5'-3']	Amplicon length [bp] Bp between primers	<sup>1</sup> nT or nU	<sup>2</sup> PCR E <sub>amp</sub> <sup>3</sup> PCR E <sub>UTP</sub>	<sup>4</sup> Molecules/reaction <sup>5</sup> T or U
<i>APAF1</i>	<a href="#">NM_013229.2</a>	ATGGAACAGTGAAGGTATGGAA AGCAGAGGTAGATGAAAACCTGGT	125 79	51	100.8% 94.1%	1 U
<i>ATM</i>	<a href="#">NM_000051.3</a>	CCGTCAGCAAAGAAGTAGAAGGA GCTAAGTGTGGGATAGAGCGA	182 138	86	109.2% 97.7%	1 U
<i>ATR</i>	<a href="#">NM_001184.3</a>	GGATGCCACTGCTTGTATGA TCCACTCGGACCTGTTAGC	152 112	63	105.5% 97.6%	1 U
<i>BBC3</i>	<a href="#">NM_001127240.2</a>	TACGAGCGGCGGAGACAAG CTGGGTAAGGGCAGGAGTC	95 57	21	109.2% 101.7%	4096 T
<i>BCL2L1</i>	<a href="#">NM_138578.2</a>	TGCGTGGAAAAGCGTAGACAA ACAAAAGTATCCCAGCGCC	125 85	39	117.8% 94.5%	1 T
<i>BID</i>	<a href="#">NM_197966.2</a>	GCCAGAAATGGGATGGACTGA TCTCTAGGAACGCTGTTGACAT	127 84	38	102.4% 94.0%	4096 T
<i>CASP3</i>	<a href="#">NM_004346.3</a>	GGCGTGCATAAAATACCACTG GCGTCAAAGGAAAAGGACTCAAA	216 171	91	106.4% 89.9%	1024 U
<i>CAV1</i>	<a href="#">NM_001753.4</a>	GCAACATCTACAAGCCCAACA GCCTTCCAAATGCCCTCAAAA	196 154	72	96.3% 91.8%	1024 U
<i>CCNA2</i>	<a href="#">NM_001237.3</a>	AAGACGAGACGGGTTTC GGCTGTTTACTGTTCCTTCC	89 50	27	102.5% 95.4%	1 T
<i>CCNB2</i>	<a href="#">NM_004701.3</a>	CGACCCTTGCCACTACACTT TGACTTCCAATACTTCATTCTCTG	244 200	111	101.7% 95.7%	1 U
<i>CCND1</i>	<a href="#">NM_053056.2</a>	AGAGGGCGGAGGAGAACAAA TGAGGCGGTAGTAGGACAGG	182 143	58	101.5% 93.7%	1 T
<i>CCND3</i>	<a href="#">NM_001760.4</a>	CTGTTTCGCTGCCGAGTATG GCATGTGCGGCTTGATCTC	186 147	38	94.1% 89.8%	<sup>7</sup> N.I. <sup>7</sup> N.I.
<i>CCNE1</i>	<a href="#">NM_001238.3</a>	CCGGTATATGGCGACACAAG TACGCAAACCTGGTCAACTT	123 83	57	98.1% 94.0%	1 U
<i>CCNG1</i>	<a href="#">NM_004060.3</a>	CCTTGGGTGTGTTGGACTGA GCTATTTCTCCTTTCAAGTGGCA	250 207	129	101.8% 88.4%	1 U
<i>CCNH</i>	<a href="#">NM_001239.3</a>	TGAGGAGGAAGAATGGACTGA GTTACTGTGAAAGGGAAAAGAAAACA	189 143	104	107.9% 107.4%	1 T
<i>CDC25A</i>	<a href="#">NM_001789.2</a>	GTCGCTGTACCAACCT CGGAGGAGCCATTCTCT	116 80	38	106.6% 90.4%	1 T
<i>CDC25B</i>	<a href="#">NM_021873.3</a>	GGCGGGACATCAAGACTG GGGTAGTAGAGGCTGGGGTA	209 170	71	- -	4096 T
<i>CDC45</i>	<a href="#">NM_001178010.2</a>	CTTTGAGTATGACCTCCGCCT AACTTCTGCTTCACTGCTTCA	174 131	54	131.6% 120.4%	1 T
<i>CDC6</i>	<a href="#">NM_001254.3</a>	ACTTGGTGCTGATTGGTATTGC TGCGAACATCTCCTGAAACA	237 195	113	93.7% 89.2%	4 U
<i>CDC7</i>	<a href="#">NM_003503.3</a>	ACACCAGGATTCAGAGCACCC TCGTCCACTAAGCAAAGAAAGAA	108 65	36	95.3% 98.3%	4 U
<i>CDK1</i>	<a href="#">NM_001786.4</a>	AGAAAGTGAAGAGGAAAGGGTTC AGCACATCCTGAAGACTGACTA	99 54	35	97.6% 87.9%	4 U
<i>CDK6</i>	<a href="#">NM_001259.7</a>	CGTGGTCAGGTTGTTTGATGT CGGTGTGAATGAAGAAAGTCC	195 153	86	97.6% 88.1%	4096 T
<i>CDK7</i>	<a href="#">NM_001799.3</a>	GCCAGAGATAAGAACACCAACC TCCAAAAGCATCAAGGAGACCA	162 118	81	93.4% 100.7%	4 U
<i>CDKN1A</i>	<a href="#">NM_000389.4</a>	TTAGCAGCGGAACAGGAGT GCCGAGAGAAAACAGTCCAG	225 185	87	99.1% 93.7%	4 U
<i>CDKN1B</i>	<a href="#">NM_004064.4</a>	TCTGAGGACACGCATTTGGT CTTAATTCGAGCTGTTTACGTTTGA	240 195	91	107.5% 94.5%	4 T
<i>CDKN2C</i>	<a href="#">NM_001262.2</a>	AGTTCCTGGTGAAGCACACGG CCTCATTCTCCCATAGAGCCT	96 53	21	119.2% 98.5%	4 T
<i>CDT1</i>	<a href="#">NM_030928.3</a>	GACTCGTGCTGCCCTACAA ACTCCTCAAAAACGCCTACG	153 115	42	94.9% 88.6%	1024 U
<i>COL1A1</i>	<a href="#">NM_000088.3</a>	CGGAGCAGACGGGAGTTTC TGTACGCAGGTGATTGGTGG	247 208	78	105.5% 92.7%	4096 T
<i>DBF4</i>	<a href="#">NM_006716.3</a>	GCCAGAAAATCCAAATGTAAGCC TTCAACTCGCCCTCCAGAT	118 74	48	103.4% 92.1%	4 U
<i>E2F1</i>	<a href="#">NM_005225.2</a>	TGCCAAGAAGTCCAAGAACCA GTCAACCCTCAAGCCGTC	81 41	12	121.4% 89.2%	16384 U
<i>E2F4</i>	<a href="#">NM_001950.3</a>	CGGACCAACCTTCTACTCT GGGGCAAACACTTCTGAGGA	156 116	54	- -	<sup>7</sup> N.I. <sup>7</sup> N.I.
<i>E2F5</i>	<a href="#">NM_001951.3</a>	TGATACTTTGGCTGTGAGGCA CAGCACCTACACCTTTCCAC	119 78	55	106.3% 103.1%	4 T
<i>E2F7</i>	<a href="#">NM_203394.2</a>	CCTTTAGCCACCCAGTATTT ATCCCTCTCTGACCCCTGACC	237 196	86	96.8% 86.9%	1024 U
<i>EGFR</i>	<a href="#">NM_005228.4</a>	AGAGCGACTGCCTGGTCT TACGGGGACACTTCTTCACG	159 121	50	94.6% 92.3%	4096 T
<i>EWSR1</i>	<a href="#">NM_013986.3</a>	ATACTACTCCAAGTCCCTCC TCCATCCTGCGGTCTTGTA	197 158	65	95.1% 93.8%	1024 T

<i>FN1</i>	<a href="#">NM_212482.2</a>	CTGAGGGCAGAAGACACA CCACGACCATTCCCAACACA	205 164	77	105.3% 86.8%	16384 U
<i>GTSE1</i>	<a href="#">NM_016426.6</a>	TGCGGAGAAGCCCAAGAAAGAG TGCGAGATTGCTGGTAGAGCC	229 186	78	89.5% 101.5%	4 T
<i>HIF1A</i>	<a href="#">NM_001530.3</a>	CGATTTTGGCAGCAACGACACA CGTTTCAGCGGTGGGTAATGGA	142 120	74	107.0% 91.8%	1024 T
<i>ID1</i>	<a href="#">NM_002165.3</a>	CTGAGGGGAGAACAAGACCGAT CCCCCTAAAGTCTCTGGTGA	132 91	30	106.6% 90.0%	1024 T
<i>IFNAR1</i>	<a href="#">NM_000629.2</a>	GTGAGAAAACAAAACCAGGAAATAC TGACAAACGGGAGAGCAAAT	84 39	28	99.8% 102.2%	4 T
<i>IFNAR2</i>	<a href="#">NM_207585.2</a>	GGATTTCAGCGGGAACACA CCTTTTATTTCCGGTTCCTCTCT	227 184	114	6 -	4 T
<i>IFNGR1</i>	<a href="#">NM_000416.2</a>	TCCAGTTGTTGCTGCTTTACT AACGGCTCTTCACAGACCAC	231 190	125	104.2% 84.2%	16 U
<i>IFNGR2</i>	<a href="#">NM_001329128.1</a>	TTTTCGTTGCTGTCGGTGTC TGGGCTGAGTTGGGCTTTT	139 100	57	103.7% 91.0%	16 U
<i>IGF2BP3</i>	<a href="#">NM_006547.2</a>	TCCCAAAAAGCCAAAGGATTTCG GCTCTCCACCCTCCATACTG	107 64	36	108.3% 96.1%	16 U
<i>IL6ST</i>	<a href="#">NM_002184.3</a>	GAGGTGTGAGTGGGATGGTG GCGGATTGGGCTCACTTA	248 208	124	91.8% 95.0%	16 U
<i>IRF9</i>	<a href="#">NM_006084.4</a>	CCATCAAAGCAGACGACAG GCCCTCCTCCTCATTATT	122 82	36	96.6% 95.7%	1024 U
<i>JAK1</i>	<a href="#">NM_002227.3</a>	CTGGAGTATCTGTTTCTCAGG GCTCGGTCTTGGGCTCTC	76 36	20	6 -	16 T
<i>LOX</i>	<a href="#">NM_002317.6</a>	CCAGTACAGCATAACAGGGCA TGGCATCAAAGCAGGTCATAG	192 152	84	97.3% 90.5%	16384 T
<i>MCM10</i>	<a href="#">NM_182751.2</a>	CTTCTCTGGTCTGCGGCTC AGTTTTTCCACTATTCACACTCT	197 154	83	101.9% 97.8%	16 U
<i>MCM4</i>	<a href="#">NM_005914.4</a>	GCCAAACGCCTCCATCG GGCACTCATCCCGTAGTAAG	96 58	28	105.5% 92.9%	16 U
<i>MCM5</i>	<a href="#">NM_006739</a>	ACTTCACCAAGCAGAAATACCCG GGCAGAGGTCCAGCAACAT	206 163	56	97.2% 93.7%	16 T
<i>MCM6</i>	<a href="#">NM_005915.5</a>	AGCGGAACTTTCTGTGCTT CTTCTAAACTGCGGGGGATAC	220 179	102	96.6% 85.4%	16 T
<i>MCM7</i>	<a href="#">NM_005916.4</a>	AACTGTGCGTGGAATCGTCA GAGACTGGATCGGCTGGTAG	110 70	32	105.0% 95.1%	16 T
<i>MCM8</i>	<a href="#">NM_032485.5</a>	TCTTCCACAAAGTGCCTGT CCGACCTGCTTCTCTCTGAT	142 101	50	96.8% 96.8%	16 T
<i>MCM9</i>	<a href="#">NM_017696.2</a>	AGGCTGGGCATTAGTTCTT ATGGTGGTCTTGTGTTTCTG	163 123	64	98.2% 99.6%	16 T
<i>MDM2</i>	<a href="#">NM_002392.5</a>	ATCAGCAGGAATCATCGGAC GTGGCGTTTTCTTGTGCTT	221 181	105	100.2% 87.6%	64 U
<i>MDM4</i>	<a href="#">NM_002393.4</a>	TGCCGCTTTTGAAGATTTTGC GAGAGGGCTTGGGCTTTTCA	203 162	89	97.6% 97.7%	64 U
<i>MMP2</i>	<a href="#">NM_004530.5</a>	GTCCGTGTGAAGTATGGGAAC CCCTGGAAGCGGAATGGAAC	236 194	84	103.0% 95.8%	16384 T
<i>MUC1</i>	<a href="#">NM_002456.5</a>	CTGGTCTGTGTTCTGGTTGC CCACTGCTGGTITGTGTAA	250 210	90	104.2% 88.4%	1024 T
<i>MYC</i>	<a href="#">NM_002467.5</a>	GGAGGCTATTCTGCCATTT GGCTGCTGTTTTCCACTAC	122 82	33	108.2% 93.3%	1024 T
<i>ORC1</i>	<a href="#">NM_004153.3</a>	CAAGCCTAGAAGCCACG TACATGCACCTCCGGTATG	207 169	77	109.1% 99.7%	64 U
<i>ORC2</i>	<a href="#">NM_006190.4</a>	ACCTAGCGGTGACTGTATCTG CTCCACAAAGTGAACCTCCA	122 80	50	101.4% 92.6%	16384 U
<i>ORC4</i>	<a href="#">NM_181741.3</a>	ACACATGCTATTGATGCTTGCT TGCTACACAGTTGGCTTGCT	95 53	31	103.7% 96.6%	64 U
<i>ORC5</i>	<a href="#">NM_002553.3</a>	TGCCAGAATGCCCACTT TGATGTCTCTCCAAACAAGGA	87 46	22	106.7% 91.8%	64 U
<i>ORC6</i>	<a href="#">NM_014321.3</a>	GAAGCCCAGCAAAGGAAATG AAATCCCAAAGCCGCAAGT	223 182	108	96.2% 89.7%	1024 U
<i>OSMR</i>	<a href="#">NM_003999.2</a>	TGTCATCTGGTGGGGAAT CTCAGGGAACCTGGCATCGT	142 103	54	95.7% 92.9%	64 U
<i>PCNA</i>	<a href="#">NM_002592.2</a>	GTGGAGAATTGGAATGGAA ACCGTTGAGAGAGTGGAGTG	160 118	74	96.2% 98.0%	64 T
<i>PDGFA</i>	<a href="#">NM_002607.5</a>	CACCACCGCAGCGTCAA CCGTGTCCTTCCCGATAA	145 108	51	102.9% 94.1%	1024 T
<i>PIAS1</i>	<a href="#">NM_001320687.1</a>	ACCTGTCTTCCCTATCTCCC GGTGTGTAATGCTGATTGTCTCC	237 192	111	106.4% 97.7%	64 T
<i>PIAS3</i>	<a href="#">NM_006099.3</a>	GAGCCGACATCCAAGTTTTAG CCAGAAAGTGAGAAGGGGTCC	144 102	54	106.2% 101.0%	64 T
<i>PPARG</i>	<a href="#">NM_138712.3</a>	TACTCCACATTACGAAGACAT CTCCATAGTGAATCCAGAAG	236 194	110	97.1% 97.1%	4096 U
<i>PPM1D</i>	<a href="#">NM_003620.3</a>	AAGGTTTTACCTGTCCG GCCATTCGCCAGTTTCTTC	100 61	26	111.9% 103.0%	64 T

<i>RB1</i>	<a href="#">NM_000321.2</a>	AAAGGACCGAGAAGGACCA AAGGCTGAGGTTGCTTGTGT	180 141	85	103.4% 99.6%	64 T
<i>RCHY1</i>	<a href="#">NM_015436.3</a>	ACTGTGGAATTTGTAGGATTGGT ACATGAGCAACAACACGGGA	172 129	82	102.2% 98.5%	64 T
<i>RPS10</i>	<a href="#">NM_001014.5</a>	AGCCGCAGAGATGTTGATG CCTCGGACTTGAGAGACTG	177 138	69	91.6% 89.3%	4096 U
<i>RRM2B</i>	<a href="#">NM_015713.4</a>	TGTGACTTTGCTTGCCTGATG TGCCGTGAAAACCTTTGAGAATCC	222 177	109	102.5% 92.1%	256 U
<i>SESN1</i>	<a href="#">NM_014454.2</a>	GGGAGTGAAGACGCACAGAT GCCGCAGCCATTATCCAA	197 158	95	109.6% 94.0%	256 U
<i>SHISA5</i>	<a href="#">NM_016479.4</a>	GTGGTGAGGTGTGTATGGCTT AGGTCGCTCCGAACCTGA	249 209	84	104.0% 93.1%	256 U
<i>SIAH1</i>	<a href="#">NM_003031.3</a>	CGCTCTCCGCCACAGAAT GGACACTCAAAAAGACTCGCCA	143 101	44	104.7% 90.2%	256 T
<i>SKP2</i>	<a href="#">NM_005983.3</a>	CCCCAGAACTGCTCTCAA ACTCATCAGACGCTAGGCCGA	250 210	97	100.4% 93.2%	256 U
<i>SOCS2</i>	<a href="#">NM_003877.4</a>	CATGACCCTGCGGTGCTT AAGTTCTTCTGGTGCCTCTTTT	209 167	57	67.1% 69.9%	<sup>7</sup> N.I. <sup>7</sup> N.I.
<i>SORT1</i>	<a href="#">NM_002959.6</a>	ATGGGAAGAAATCCACAAGCAG ATTCCAGAGCCCAAGGTACG	113 69	39	101.0% 92.6%	4096 U
<i>SOX9</i>	<a href="#">NM_000346.3</a>	GCTCTGGAGACTTCTGAACGA CCGTTCTTACCAGCTTCTCT	132 91	29	98.3% 94.0%	4096 U
<i>STAT1</i>	<a href="#">NM_139266.2</a>	GTTATGGGACCGCACCTTCA CACCAACAGTCTCAACTTCACAG	148 105	46	107.5% 92.1%	256 U
<i>STAT2</i>	<a href="#">NM_005419.3</a>	AGCACCAGGATGATGACAAGG GGGGGATTTCGGGGATAGAGG	162 121	59	101.2% 84.3%	256 T
<i>STAT3</i>	<a href="#">NM_139276.2</a>	GCCAGAGAGCCAGGAGCATC GGGACATCGGCAGGTCAAT	119 80	37	105.8% 98.9%	256 U
<i>STAT5B</i>	<a href="#">NM_012448.3</a>	CTGCGAGTCTGCTACTGCTA GAGTCAGGGTTCTGTGGGTA	186 146	61	106.0% 94.7%	256 T
<i>STAT6</i>	<a href="#">NM_001178078.1</a>	GAACATCCAGCCATTCTCTGC TTGGTCCCTTCCACGGTCA	202 161	76	96.8% 87.2%	256 T
<i>SUZ12</i>	<a href="#">NM_015355.3</a>	AGCCATCACCAAAGTCAAGAA GCTTTTTACCTGTGGAACTTG	126 83	52	<sup>6</sup> -	4096 U
<i>TGFB1</i>	<a href="#">NM_000660.6</a>	AACAATTCCTGGCGATACCTCA AAGCCCTCAATTTCCCTCC	125 83	33	95.9% 89.9%	16384 U
<i>TGFB2</i>	<a href="#">NM_001135599.3</a>	AAGACCCACATCTCTGCTAA TCGTGTATCCATTTCCACCTT	182 139	74	96.2% 95.9%	16384 T
<i>TGFB3</i>	<a href="#">NM_003239.4</a>	GCGTGAGTGGCTGTTGAGA AGGATTAGATGAGGGTTGTGGTG	216 174	91	90.0% 92.2%	16384 T
<i>TP53/INP1</i>	<a href="#">NM_033285.3</a>	GCCCAAGTAGTCCAGAGTG AGTTGTATGAGCAGCAAGAGC	86 45	28	103.0% 93.9%	<sup>7</sup> N.I. <sup>7</sup> N.I.
<i>TYK2</i>	<a href="#">NM_003331.4</a>	AGCTTGACTGTACGATCCG GACTTCTCGCCTTGGTCTC	185 144	55	99.4% 92.7%	256 T
<i>VIM</i>	<a href="#">NM_003380.4</a>	CAGATGCGTGAAATGGAAGA TGGAAGAGGCAGAGAAATCC	222 182	92	110.1% 91.5%	4096 U
<i>ZMAT3</i>	<a href="#">NM_022470.3</a>	TATCGAAGGGAGGGGAGCAA TTAAGGAGCCCATCTGCGG	247 207	105	108.0% 98.8%	256 T
<b>TATAA Universal DNA Spike I</b>	n/a	n/a n/a	300 n/a	n/a	Not tested Not tested	<sup>7</sup> N.I. <sup>7</sup> N.I.

<sup>1</sup> *n<sub>T</sub>* or *n<sub>U</sub>*: Total number of thymidines or uraciles in sequence between primers.

<sup>2</sup> *PCR E<sub>dTTP</sub>*: Amplification efficiency using dTTP in preamplification.

<sup>3</sup> *PCR E<sub>dUTP</sub>*: Amplification efficiency using dUTP in preamplification.

<sup>4</sup> *Molecules/reaction*: Number of amplicons per reaction. Related to data in Figure 3.

<sup>5</sup> *T* or *U*: Whether amplicon contains thymine (T) or uracil (U). Related to data in Figure 3.

<sup>6</sup> -: Failed amplification.

<sup>7</sup> *N.I.*: Not included.