

Table S13. Expression of 42 selected mRNA tested in the excised CRC (patient 2).

Biomarker	Normalised expression ratios *				Log-transformed normalised expression ratios				Confidence Limits		P-value	
	1st repeat	2nd repeat	3rd repeat	Average	1st repeat	2nd repeat	3rd repeat	Average	SD	SEM		From
BAD	9.840	10.010	10.370	10.073	3.2987	3.3234	3.3743	3.3321	0.0315	0.0182	3.2538	3.4104
TLR2	9.160	8.990	8.890	9.013	3.1953	3.1683	3.1522	3.1720	0.0178	0.0103	3.1277	3.2162
BCL2L1	8.840	8.740	9.010	8.863	3.1440	3.1276	3.1715	3.1477	0.0181	0.0105	3.1027	3.1927
BID	5.910	6.260	6.300	6.157	2.5632	2.6462	2.6554	2.6216	0.0415	0.0239	2.5185	2.7246
PDGFRB	4.700	4.950	4.550	4.733	2.2327	2.3074	2.1859	2.2420	0.0501	0.0289	2.1176	2.3664
EGF	4.110	4.940	4.750	4.600	2.0391	2.3045	2.2479	2.1972	0.1141	0.0659	1.9137	2.4807
BAX	3.450	5.730	4.270	4.483	1.7866	2.5185	2.0942	2.1331	0.3001	0.1732	1.3876	2.8786
IRS2	4.340	4.540	4.490	4.457	2.1177	2.1827	2.1667	2.1557	0.0277	0.0160	2.0870	2.2244
CDK2	4.120	4.100	4.340	4.187	2.0426	2.0356	2.1177	2.0653	0.0371	0.0214	1.9730	2.1576
CDK6	3.680	3.590	4.340	3.870	1.8797	1.8440	2.1177	1.9471	0.1215	0.0701	1.6453	2.2489
CCND1	3.860	3.400	3.040	3.433	1.9486	1.7655	1.6041	1.7727	0.1407	0.0813	1.4231	2.1224
CCNE1	3.780	3.510	2.950	3.413	1.9184	1.8115	1.5607	1.7635	0.1499	0.0865	1.3911	2.1359
PDGFC	3.160	3.030	3.550	3.247	1.6599	1.5993	1.8278	1.6957	0.0967	0.0558	1.4556	1.9358
CDK4	3.300	2.890	3.320	3.170	1.7225	1.5311	1.7312	1.6616	0.0923	0.0533	1.4321	1.8910
VEGFC	3.170	2.900	2.900	2.990	1.6645	1.5361	1.5361	1.5789	0.0605	0.0350	1.4285	1.7293
MMP2	2.240	2.620	2.860	2.573	1.1635	1.3896	1.5160	1.3564	0.1458	0.0842	0.9941	1.7186
TSC2	2.710	2.370	2.280	2.453	1.4383	1.2449	1.1890	1.2907	0.1068	0.0617	1.0254	1.5561
CREB1	2.270	2.350	2.470	2.363	1.1827	1.2327	1.3045	1.2400	0.0500	0.0289	1.1157	1.3642
CCNA1	2.320	2.590	2.120	2.343	1.2141	1.3730	1.0841	1.2237	0.1181	0.0682	0.9302	1.5172
MAPK3	2.410	2.260	2.270	2.313	1.2690	1.1763	1.1827	1.2093	0.0423	0.0244	1.1043	1.3144
TGFB1	1.910	1.910	1.930	1.917	0.9336	0.9336	0.9486	0.9386	0.0071	0.0041	0.9210	0.9562
EGFR	1.660	1.520	1.510	1.563	0.7312	0.6041	0.5945	0.6433	0.0623	0.0360	0.4885	0.7980
PIK3CA	1.720	1.550	1.400	1.557	0.7824	0.6323	0.4854	0.6334	0.1212	0.0700	0.3322	0.9346
STAT1	1.570	1.270	1.730	1.523	0.6508	0.3448	0.7908	0.5955	0.1862	0.1075	0.1328	1.0581
MDM2	1.830	1.010	1.440	1.427	0.8718	0.0144	0.5261	0.4708	0.3522	0.2034	-0.4043	1.3459
CDH1	1.560	1.050	1.190	1.267	0.6415	0.0704	0.2510	0.3210	0.2384	0.1376	-0.2712	0.9132
CDKN1A	1.570	1.020	1.160	1.250	0.6508	0.0286	0.2141	0.2978	0.2608	0.1506	-0.3501	0.9458
SHC1	1.240	1.280	1.230	1.250	0.3103	0.3561	0.2987	0.3217	0.0248	0.0143	0.2601	0.3833
KRAS	1.100	0.940	1.650	1.230	0.1375	-0.0893	0.7225	0.2569	0.3420	0.1974	-0.5927	1.1065
TGFB3	0.570	1.570	1.470	1.203	-0.8110	0.6508	0.5558	0.1319	0.6678	0.3856	-1.5272	1.7909
CDKN1B	1.300	0.920	1.310	1.177	0.3785	-0.1203	0.3896	0.2159	0.2378	0.1373	-0.3748	0.8067
HRAS	1.410	0.930	1.130	1.157	0.4957	-0.1047	0.1763	0.1891	0.2453	0.1416	-0.4202	0.7985
PIK3R3	1.130	1.010	1.250	1.130	0.1763	0.0144	0.3219	0.1709	0.1256	0.0725	-0.1412	0.4830
E2F3	1.440	1.100	0.760	1.100	0.5261	0.1375	-0.3959	0.0892	0.3779	0.2182	-0.8497	1.0282
SMAD4	1.100	0.940	1.210	1.083	0.1375	-0.0893	0.2750	0.1077	0.1502	0.0867	-0.2654	0.4809
CCND2	0.720	0.900	1.560	1.060	-0.4739	-0.1520	0.6415	0.0052	0.4688	0.2706	-1.1594	1.1698
CCND3	1.160	0.860	1.110	1.043	0.2141	-0.2176	0.1506	0.0490	0.1903	0.1099	-0.4238	0.5218
CTNNB1	0.790	0.800	0.970	0.853	-0.3401	-0.3219	-0.0439	-0.2353	0.1355	0.0782	-0.5720	0.1014
FN1	0.830	0.740	0.960	0.843	-0.2688	-0.4344	-0.0589	-0.2540	0.1537	0.0887	-0.6358	0.1277
FGFR1	0.860	0.610	0.670	0.713	-0.2176	-0.7131	-0.5778	-0.5028	0.2091	0.1207	-1.0224	0.0167
TGFB2	0.610	0.500	0.590	0.567	-0.7131	-1.0000	-0.7612	-0.8248	0.1254	0.0724	-1.1364	-0.5131
BCL2	0.300	0.140	0.190	0.210	-1.7370	-2.8365	-2.3959	-2.3231	0.4518	0.2609	-3.4456	-1.2006

* Gene expression ratios (tumor v matching normal tissue) normalised to the endogenous levels of three reference RNAs (housekeeping gene GAPDH mRNA, 18S and 28S rRNAs). Measured in triplicate. Significantly upregulated mRNA (red), downregulated mRNAs (blue).