

**Table S12.** Expression of 42 selected mRNA tested in the excised CRC (patient 1).

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
IRS2	15.400	15.150	16.680	15.743	3.9449	3.9212	4.0600	3.9754	0.0606	0.0350	3.8247	4.1260
BID	7.330	7.940	7.230	7.500	2.8738	2.9891	2.8540	2.9056	0.0596	0.0344	2.7576	3.0537
PIK3R3	5.280	6.240	6.020	5.847	2.4005	2.6415	2.5898	2.5439	0.1036	0.0598	2.2866	2.8013
TLR2	3.520	4.660	3.560	3.913	1.8156	2.2203	1.8319	1.9559	0.1871	0.1080	1.4912	2.4207
FN1	3.400	4.290	3.330	3.673	1.7655	2.1010	1.7355	1.8673	0.1657	0.0956	1.4558	2.2789
CDK2	2.620	3.830	3.990	3.480	1.3896	1.9373	1.9964	1.7744	0.2732	0.1577	1.0957	2.4532
PDGFRB	3.790	3.170	3.090	3.350	1.9222	1.6645	1.6276	1.7381	0.1310	0.0757	1.4125	2.0637
FGFR1	2.610	2.750	2.710	2.690	1.3840	1.4594	1.4383	1.4273	0.0317	0.0183	1.3484	1.5061
SHC1	2.230	2.790	2.800	2.607	1.1570	1.4803	1.4854	1.3742	0.1536	0.0887	0.9927	1.7558
E2F3	2.810	2.790	2.200	2.600	1.4906	1.4803	1.1375	1.3694	0.1641	0.0947	0.9619	1.7770
BCL2L1	2.310	2.860	2.120	2.430	1.2079	1.5160	1.0841	1.2693	0.1816	0.1049	0.8181	1.7205
CTNNB1	2.380	2.310	2.520	2.403	1.2510	1.2079	1.3334	1.2641	0.0521	0.0301	1.1347	1.3935
CDK4	2.290	2.260	2.530	2.360	1.1953	1.1763	1.3391	1.2369	0.0727	0.0420	1.0564	1.4175
CDK6	2.320	2.570	2.100	2.330	1.2141	1.3618	1.0704	1.2154	0.1190	0.0687	0.9199	1.5110
CDKN1B	1.500	1.900	1.720	1.707	0.5850	0.9260	0.7824	0.7645	0.1398	0.0807	0.4171	1.1118
BAD	1.550	1.710	1.750	1.670	0.6323	0.7740	0.8074	0.7379	0.0759	0.0438	0.5493	0.9264
TGFB1	1.800	1.830	1.220	1.617	0.8480	0.8718	0.2869	0.6689	0.2703	0.1561	-0.0026	1.3404
VEGFC	1.790	1.570	1.390	1.583	0.8400	0.6508	0.4751	0.6553	0.1490	0.0860	0.2851	1.0254
CREB1	1.700	1.850	1.140	1.563	0.7655	0.8875	0.1890	0.6140	0.3046	0.1759	-0.1427	1.3708
CCND1	1.670	1.600	1.000	1.423	0.7398	0.6781	0.0000	0.4726	0.3352	0.1935	-0.3600	1.3053
MDM2	1.610	1.630	0.660	1.300	0.6871	0.7049	-0.5995	0.2642	0.6107	0.3526	-1.2531	1.7814
MMP2	1.620	1.140	0.870	1.210	0.6960	0.1890	-0.2009	0.2280	0.3672	0.2120	-0.6842	1.1403
EGF	0.790	1.600	1.090	1.160	-0.3401	0.6781	0.1243	0.1541	0.4162	0.2403	-0.8798	1.1881
STAT1	1.060	1.300	0.930	1.097	0.0841	0.3785	-0.1681	0.0829	0.1988	0.1148	-0.3747	0.6133
CCND2	0.890	1.500	0.890	1.093	-0.1681	0.5850	-0.1681	0.0714	0.3550	0.2050	-0.7991	0.9649
CDKN1A	1.180	1.130	0.870	1.060	0.2388	0.1763	-0.2009	0.0264	0.1942	0.1121	-0.4111	0.5539
CCNE1	0.730	1.080	1.340	1.050	-0.4540	0.1110	0.4222	0.0264	0.3627	0.2094	-0.8747	0.9275
CDH1	0.560	1.540	0.880	0.993	-0.8365	0.6229	-0.1844	-0.1327	0.5969	0.3446	-1.6156	1.3503
TGFB2	0.880	0.830	1.030	0.913	-0.1844	-0.2688	0.0426	-0.1369	0.1315	0.0759	-0.4636	0.1899
CCNA1	1.000	0.660	1.010	0.890	0.0000	-0.5995	0.0144	-0.1950	0.2860	0.1651	-0.9056	0.5156
BAX	0.850	1.220	0.540	0.870	-0.2345	0.2869	-0.8890	-0.2789	0.4811	0.2777	-1.4740	0.9163
TSC2	0.680	0.930	0.910	0.840	-0.5564	-0.1047	-0.1361	-0.2657	0.2059	0.1189	-0.7773	0.2459
TGFB3	0.890	0.930	0.600	0.807	-0.1681	-0.1047	-0.7370	-0.3366	0.2843	0.1641	-1.0429	0.3697
MAPK3	0.440	0.790	0.620	0.617	-1.1844	-0.3401	-0.6897	-0.7381	0.3464	0.2000	-1.5986	0.1225
PDGFC	0.610	0.650	0.540	0.600	-0.7131	-0.6215	-0.8890	-0.7412	0.1110	0.0641	-1.0169	-0.4655
BCL2	0.540	0.780	0.310	0.543	-0.8890	-0.3585	-1.6897	-0.9790	0.5472	0.3159	-2.3384	0.3804
SMAD4	0.470	0.540	0.510	0.507	-1.0893	-0.8890	-0.9714	-0.9832	0.0822	0.0475	-1.1874	-0.7790
EGFR	0.290	0.470	0.410	0.390	-1.7859	-1.0893	-1.2863	-1.3871	0.2932	0.1693	-2.1155	-0.6588
KRAS	0.340	0.450	0.330	0.373	-1.5564	-1.1520	-1.5995	-1.4360	0.2016	0.1164	-1.9367	-0.9352
CCND3	0.220	0.310	0.430	0.320	-2.1844	-1.6897	-1.2176	-1.6972	0.3947	0.2279	-2.6779	-0.7165
PIK3CA	0.140	0.380	0.370	0.297	-2.8365	-1.3959	-1.4344	-1.8889	0.6702	0.3869	-3.5540	-0.2239
HRAS	0.200	0.330	0.310	0.280	-2.3219	-1.5995	-1.6897	-1.8704	0.3214	0.1856	-2.6689	-1.0718

\* 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).