Cytoband	Gene Symbo	Fold-Change (LM vs	Chromosome Location
13q12.11	LATS2	-1.57	chr13.21548578.21635655
16p13.3	FBXL16	1.65	chr16.742499.743126
1p36.11	RCAN3	-2.46	chr1.24862824.24867531
1p36.21	RP1-21O18.	-2.00	chr1.14925199.15393109
2q37.3	ASB1	-2.20	chr2.239335625.239360891
2q33.3	FAM119A	-2.14	chr2.208473838.208474361
2q24.1	NR4A2	-1.77	chr2.157180950.157189213
2q23.3	RND3	-1.68	chr2.151324711.151344169
4p14	---	-2.42	chr4.39124003.39125224
4p14	APBB2	-2.27	chr4.40812044.40816815
4p12	ATP10D	-1.95	chr4.47560039.47595436
4p16.2	CYTL1	-3.64	chr4.5016317.5021200
4p12	FRYL	-1.48	chr4.48501281.48522706
4p14	KLHL5	-1.97	chr4.39064545.39124044
4p13	LIMCH1	-3.64	chr4.41614936.41702062
4p11	OCIAD2	-1.87	chr4.48887398.48908801
4p12	SLAIN2	-1.80	chr4.48343433.48428219
4p14	UBE2K	-2.29	chr4.39781731.39784409
4q12	---	-1.96	chr4.56294071.56294744
4q12	---	-1.85	chr4.56294561.56298429
4q26	---	-1.66	chr4.114374777.114375243
4q31.22	ABCE1	-1.90	chr4.146019485.146050332
4q22.1	ABCG2	-2.08	chr4.89013200.89079754
4q13.3	ADAMTS3	-1.94	chr4.73146686.73434517
4q21.3	AFF1	-2.12	chr4.87928139.88062191
4q31.22	ANAPC10	-2.05	chr4.145916319.146019342
4q28.1	ANKRD50	-1.56	chr4.125585205.125593586
4q21.21	ANTXR2	-1.91	chr4.80825359.80826841
4q31.3	ARFIP1	-1.82	chr4.153701111.153833062
4q26	CAMK2D	-2.17	chr4.114373569.114683203
4q13.3	CXCL1	-4.44	chr4.74735108.74736954
4q13.3	CXCL2	-5.84	chr4.74962800.74964893
4q13.3	CXCL5	-3.03	chr4.74862997.74864447
4q31.3	FBXW7	-2.07	chr4.153242410.153243031
4q27	FGF2	-1.60	chr4.123747862.123819377
4q32.1	GLRB	-2.00	chr4.157997402.158092418
4q21.22	HPSE	-2.08	chr4.84213614.84256306
4q13.3	IL8	-4.05	chr4.74606368.74607739
4q31.21	INPP4B	-2.62	chr4.142949893.143352533
4q12	KDR	-1.79	chr4.55944648.55991763
4q31.3	LRBA	-1.98	chr4.151185598.151388930
4q31.1	MAML3	-1.96	chr4.140637908.140638418
4q32.1	MAP9	-2.28	chr4.156263809.156264473
4q13.3	MTHFD2L	-2.57	chr4.75065510.75168813
4q22.1	NAP1L5	-2.61	chr4.89617065.89618072
4q32.1	PDGFC	-2.49	chr4.157682763.157892547
4q32.1	PLRG1	-2.06	chr4.155456157.155456711
4q31.23	PRMT10	-1.85	chr4.148558944.148575570
4q25	SGMS2	-1.85	chr4.108834104.108836188
4q31.3	SH3D19	-1.77	chr4.152041187.152069170
4q13.3	SLC4A4	-1.92	chr4.72204816.72437800
4q31.22	SMAD1	-2.02	chr4.146479198.146480329
4q31.21	SMARCA5	-2.34	chr4.144474160.144475891
4q12	SRP72	-1.76	chr4.57349374.57357735
4q22.1	TIGD2	-2.39	chr4.90035004.90036195
4q31.21	USP38	-2.13	chr4.144127298.144142743

FIG. S5. Integration of DNA copy number alteration and gene expression in RCC cell lines. Genes with altered mRNA expression and variations in the corresponding genomic region within the identified aberrant regions.