

Supplementary Table 2. Differentially expressed genes in comparisons between tumor and ANT tissues in patients with HCV-related HCC down-regulated genes

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Gene	Description
	ANT	T			
NM_017931.2	11794.398	5889.6681	-2.0025574	TTC38	tetratricopeptide repeat domain 38
NM_006459.3,NM_001100626.1	1309.0339	640.57011	-2.043545	ERLIN1	ER lipid raft associated 1
NM_032470.3,NM_019105.6 XM_003960362.1 NR_001284.2	371.29253	178.70647	-2.0776669	TNXB LOC101060681 TNXA	tenascin XB tenascin-X-like tenascin XA (pseudogene)
NM_001242401.3,NM_001242406.2,NM_001242405.2,NM_001242404.2,NM_001242403.2,NM_001242402.2,NM_001242400.2,NM_001242399.2,NM_000163.4,NM_001242462.1,NM_001242461.1,NM_001242460.1	6155.9549	2911.379	-2.1144464	GHR	growth hormone receptor
NM_015675.3	15820.061	7446.8692	-2.1243908	GADD45B	growth arrest and DNA-damage-inducible, beta
NM_003407.3	2497.061	1163.1494	-2.1468101	ZFP36	ZFP36 ring finger protein
NM_012084.3	641.94294	294.9589	-2.176381	GLUD2	glutamate dehydrogenase 2
NM_005891.2	2130.0591	975.85903	-2.1827529	ACAT2	acetyl-CoA acetyltransferase 2
NM_001198688.1,NM_001198687.1,NM_001003680.3	878.5322	395.38734	-2.2219533	LEPR	leptin receptor
NM_018286.2,NM_001099640.1	567.41152	255.00551	-2.2250969	TMEM100	transmembrane protein 100
NM_001220496.1,NM_001220494.1,NM_080661.3	1712.1736	761.24961	-2.2491618	GLYATL1	glycine-N-acetyltransferase-like 1
NM_016546.2	3914.6039	1732.8488	-2.2590568	C1RL	complement component 1, r subcomponent-like
NM_001008410.1,NM_182915.2,NM_018234.2	1816.2602	790.96293	-2.2962646	STEAP3	STEAP family member 3, metalloreductase
NM_001164664.1,NM_015183.2	244.55183	104.29258	-2.3448631	MAST4	microtubule associated serine/threonine kinase family member 4
NM_015002.2,NM_033624.2	1447.5482	616.02869	-2.3498064	FBXO21	F-box protein 21
NM_152766.3	3529.6956	1502.0057	-2.3499881	TMEM256	transmembrane protein 256
NM_001256307.1,NM_001256306.1,NM_001256305.1,NM_001256301.1,NM_001145816.2,NM_000860.5	5514.9816	2342.4948	-2.3543197	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)
NM_001130410.1,NM_001607.3,NR_024024.1	3376.5324	1431.9937	-2.357924	ACAA1	acetyl-CoA acyltransferase 1

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Family with sequence similarity
	ANT	T		
NM_176782.2	1431.7172	606.31171	-2.361355	family with sequence similarity 151, member A
NM_031481.1	6928.4984	2905.8682	-2.3843126	solute carrier family 25 (glutamate carrier), member 18
NM_000320.2	1613.5368	672.9953	-2.3975455	quinoid dihydropteridine reductase
NM_001165921.1,NM_001165920.1,NM_000934.3	1941.7051	809.67212	-2.3981376	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2
NM_001195803.1,NM_001195802.1,NM_001195800.1,NM_001195799.1,NM_001195798.1,NM_000527.4	5736.9556	2384.1192	-2.4063208	low density lipoprotein receptor
NM_138424.1	349.26037	143.62497	-2.4317524	kinesin family member 12
NM_001127707.1,NM_001127706.1,NM_001127705.1,NM_001127704.1,NM_001127703.1,NM_001127702.1,NM_001127701.1,NM_001002236.2,NM_001002235.2,-NM_000295.4	6065.4548	2488.9626	-2.4369409	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1
NM_000177.4,NM_198252.2,NM_001127663.1,NM_001127662.1,NM_001127661.1,NM_001127660.1,NM_001127659.1,NM_001127658.1,NM_001127657.1,NM_001127656.1,NM_001127655.1,NM_001127654.1,NM_001127653.1,NM_001127652.1,NM_001127651.1,NM_001127650.1,NM_001127649.1,NM_001127648.1,NM_001127647.1,NM_001127646.1,NM_001127645.1,NM_001127644.1,NM_001127643.1,NM_001127642.1,NM_006100.3	5727.3208	2311.7035	-2.4775326	gelsolin
NM_001271148.1,NM_001271147.1,NM_001271146.1,NM_001271145.1,NM_001271144.1,NM_006100.3	1432.0167	572.98211	-2.4992346	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
NM_001033083.1	1922.9666	768.62209	-2.5018363	phenazine biosynthesis-like protein domain containing
NM_080825.3	653.40293	260.75723	-2.5057903	chromosome 20 open reading frame 144
NM_000670.3	20506.753	8168.7869	-2.5103792	alcohol dehydrogenase 4 (class II), pi polypeptide
NM_001134707.1,NM_007101.3	1667.2778	663.40057	-2.5132294	sarcosine dehydrogenase
NM_003641.3	5615.7337	2234.0237	-2.5137306	interferon induced transmembrane protein 1

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Gene	Description
	ANT	T			
NM_016337.2	859.45601	338.31269	-2.5404191	EVL	Enah/Vasp-like
NM_003891.2,NM_001256134.1	3296.2612	1293.2011	-2.5489162	PROZ	protein Z, vitamin K-dependent plasma glycoprotein
XR_171578.1,XR_108661.1, XR_133426.1	3015.2836	1174.5784	-2.56712	LOC100505985	uncharacterized LOC100505985
NM_152404.3	375.76314	145.22391	-2.5874743	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1
NM_001193335.1,NM_017680.4	930.5568	359.27936	-2.5900648	ASPN	asporin
NM_004277.4,NM_001204052.1, NM_001204051.1	322.41284	124.39267	-2.5918958	SLC25A27	solute carrier family 25, member 27
NM_201541.1,NM_201540.1,NM_201539.1,NM_201538.1,NM_201537.1,NM_016250.2,NM_201536.1, NM_201535.1	13522.47	5126.5176	-2.6377496	NDRG2	NDRG family member 2
NM_001204963.1,NM_001204961.1,NM_002585.3	278.82041	105.67334	-2.6385122	PBX1	pre-B-cell leukemia homeobox 1
NM_005074.3	1359.9811	511.85421	-2.6569696	SLC17A1	solute carrier family 17 (sodium phosphate), member 1
NM_013410.3,NM_203464.2, NM_001005353.2	1598.949	599.32135	-2.6679327	AK4	adenylate kinase 4
NM_004673.3	484.56681	179.78187	-2.6953041	ANGPTL1	angiotensin-like 1
NM_032219.2	215.44837	79.363024	-2.7147198	MFSD7	major facilitator superfamily domain containing 7
NM_000229.1	3932.0806	1443.1091	-2.7247285	LCAT	lecithin-cholesterol acyltransferase
NM_000067.2	23699.453	8614.5664	-2.7510907	CA2	carbonic anhydrase II
NM_020676.5	1301.0226	470.39949	-2.7657823	ABHD6	abhydrolase domain containing 6
NM_000242.2	7695.338	2771.8021	-2.7762942	MBL2	mannose-binding lectin (protein C) 2, soluble
NM_001177433.1,NM_001177431.1, ,NM_001177428.1,NM_021625.4, NM_147204.2	2888.7859	1034.8313	-2.7915524	TRPV4	transient receptor potential cation channel, subfamily V, member 4
NM_012342.2	882.7321	315.79656	-2.7952556	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Gene	Description
	ANT	T			
NM_001178137.1,NM_014912.4	NP_00117608.1,NP_055727.3	771.98814	275.77712	-2.799319	CPEB3 cytoplasmic polyadenylation element binding protein 3
NM_001243743.1,NM_000136.2	NP_001230672.1,NP_000127.2	504.20825	176.72393	-2.8530842	FANCC Fanconi anemia, complementation group C
NM_001206961.1,NM_001206960.1,NM_015900.3	NP_001193890.1,NP_001193889.1,NP_056984.1	754.69898	262.08178	-2.8796317	PLA1A phospholipase A1 member A
NM_001010924.1	NP_001010924.1	581.63047	201.50766	-2.8863939	FAM171A1 family with sequence similarity 171, member A1
NM_021229.3	NP_067052.2	1297.3784	446.33116	-2.9067618	NTN4 netrin 4
NM_181712.4	NP_859063.3	246.88106	83.474139	-2.9575754	KANK4 KN motif and ankyrin repeat domains 4
NM_006623.3	NP_006614.2	1075.3361	362.38033	-2.9674242	PHGDH phosphoglycerate dehydrogenase
NM_005252.3	NP_005243.1	9709.4447	3269.4143	-2.969781	FOS FBJ murine osteosarcoma viral oncogene homolog
NM_000429.2	NP_000420.1	19342.161	6464.862	-2.9918909	MATIA methionine adenosyltransferase I, alpha
NM_001242393.1,NM_001076552.2,NM_018677.3	NP_001229322.1,NP_001070020.2,NP_061147.1	2325.1607	775.78595	-2.9971679	ACSS2 acyl-CoA synthetase short-chain family member 2
NM_173054.2,NM_005045.3	NP_774959.1,NP_005036.2	4928.8875	1644.2696	-2.9976152	RELN reelin
NM_133503.2,NM_001920.3,NM_504.2,NM_133505.2	NP_598010.1,NP_001911.1,NP_598011.1,NP_598012.1	3915.5927	1300.6857	-3.0104065	DCN decorin
NM_001199241.1,NM_001032998.1,NM_003937.2	NP_001186170.1,NP_001028170.1,NP_003928.1	3467.1998	1148.44	-3.0190517	KYNU kynureninase
NR_027462.1,NR_027463.1,NM_001146280.1,NM_001040.3,NM_001146281.1	-NP_001139752.1,NP_001031.2,NP_001139753.1	4605.6506	1525.328	-3.0194493	SHBG sex hormone-binding globulin
NM_031938.5,NM_001256400.1,NM_001256398.1,NM_001037290.2	NP_114144.4,NP_001243329.1,NP_001243327.1,NP_001032367.2	1872.9536	614.31832	-3.0488324	BCO2 beta-carotene oxygenase 2
NM_203417.1,NM_004414.5,NM_203418.1	NP_981962.1,NP_004405.3,NP_981963.1	4206.758	1373.308	-3.0632298	RCAN1 regulator of calcineurin 1
NM_003246.2	NP_003237.2	655.29331	211.5528	-3.0975402	THBS1 thrombospondin 1
NM_033071.3,NM_182961.3	NP_149062.1,NP_892006.3	498.35889	159.99192	-3.1149003	SYNE1 spectrin repeat containing, nuclear envelope 1

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)			
	ANT	T				
NM_003235.4	NP_003226.4	4257.4329	1357.3547	-3.1365661	TG	thyroglobulin
NM_001032365.2,NM_001032364.2,NM_013430.2,NM_005265.2,NM_199127.2	NP_001027537.1,NP_001027536.1,NP_038347.2,NP_005256.2,NP_954578.2	1119.0697	356.194	-3.1417421	GGT1 GGTLC2	gamma-glutamyltransferase 1 gamma-glutamyltransferase light chain 2
NM_001128203.1,NM_007069.3	NP_001121675.1,NP_009000.2	381.4698	120.99986	-3.1526465	PLA2G16	phospholipase A2, group XVI
NM_002666.4,NM_001145311.1	NP_002657.3,NP_001138783.1	414.10291	129.68364	-3.1931776	PLIN1	perilipin 1
NM_000672.3	NP_000663.1	16272.526	5084.9849	-3.2001129	ADH6	alcohol dehydrogenase 6 (class V)
NM_006206.4	NP_006197.1	979.21989	304.75924	-3.2130934	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide
NM_001242889.1,NM_001242888.1,NM_001242887.1,NM_001242886.1,NM_001082971.1,NM_000790.3	NP_001229818.1,NP_001229817.1,NP_001229816.1,NP_001229815.1,NP_001076440.1,NP_000781.1	5073.7061	1575.2621	-3.2208647	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)
NM_001261447.1,NM_001261448.1,NM_201592.2,NM_201591.2,NM_005277.4,NR_048571.1	NP_001248376.1,NP_001248377.1,NP_963886.1,NP_963885.1,NP_005268.1,-	422.31994	130.74774	-3.2300363	GPM6A	glycoprotein M6A
NM_001024455.3	NP_001019626.1	526.20086	161.58017	-3.2565929	RGAG4	retrotransposon gag domain containing 4
NM_004022.2,NM_004018.2,NM_004017.2,NM_004016.2,NM_004013.2,NM_004006.2,NM_000109.3,NM_004020.3,NM_004023.2,NM_004021.2,NM_004015.2,NM_004007.2,NM_004014.2,NM_004012.3,NM_004011.3,NM_004010.3,NM_004009.3	NP_004013.1,NP_004009.1,NP_004008.1,NP_004007.1,NP_004004.1,NP_003997.1,NP_000100.2,NP_004011.2,NP_004014.1,NP_004012.1,NP_004006.1,NP_003998.1,NP_004005.1,NP_004003.1,NP_004002.2,NP_004001.1,NP_004000.1	4546.1191	1369.1327	-3.3204371	DMD	dystrophin
NM_024669.2	NP_078945.2	486.4526	146.36051	-3.3236602	ANKRD55	ankyrin repeat domain 55
NR_003669.1 NM_005952.3 NM_175617.3 NM_005946.2 NM_005953.3 NM_005947.2 NR_001447.2 NM_005951.2	- NP_005943.1 NP_783316.2 NP_005937.2 NP_005944.1 NP_005938.1 NP_005942.1	1198.6118	355.32001	-3.3733304	MT1P1 MT1X MT1E MT1A MT2A MT1B MT1L MT1H	metallothionein 1I, pseudogene metallothionein 1X metallothionein 1E metallothionein 1A metallothionein 2A metallothionein 1B metallothionein 1H pseudogene metallothionein 1H
NM_001102654.1,NM_002527.4	NP_001096124.1,NP_002518.1	671.48017	199.03069	-3.373752	NTF3	neurotrophin 3

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)			
	ANT	T				
NM_000917.3,NM_001142596.1,NM_001142595.1,NM_001017962.2	NP_000908.2,NP_001136068.1,NP_001136067.1,NP_001017962.1	488.12414	144.08352	-3.3877861	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I
NM_001018049.1,NM_002571.2	NP_001018059.1,NP_002562.2	389.84221	114.63205	-3.4008135	PAEP	progesteragen-associated endometrial protein
NM_006918.4,NM_001024956.2	NP_008849.2,NP_001020127.1	13360.581	3889.042	-3.4354427	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, <i>S. cerevisiae</i>)-like
NM_006774.4,NM_001199219.1	NP_006765.4,NP_001186148.1	5065.9221	1472.9572	-3.4392868	INMT	indolethylamine N-methyltransferase
NM_000014.4	NP_000005.2	952.37374	276.49788	-3.4444416	A2M	alpha-2-macroglobulin
NM_016205.2,NR_036641.1	NP_057289.1,-	651.23948	187.56624	-3.4720506	PDGFC	platelet derived growth factor C
NM_001130715.1,NM_001130716.1,NM_016619.2	NP_001124187.1,NP_001124188.1,NP_057703.1	1262.4688	361.40278	-3.4932459	PLAC8	placenta-specific 8
NM_018945.3	NP_061818.1	777.13469	222.17001	-3.497928	PDE7B	phosphodiesterase 7B
NM_145739.2,NM_032523.3,NM_001201482.1,NM_001201481.1,NM_001201480.1	NP_665682.1,NP_115912.1,NP_001188411.1,NP_001188410.1,NP_001188409.1	345.4992	98.335523	-3.513473	OSBPL6	oxysterol binding protein-like 6
NM_000767.4	NP_000758.1	23938.48	6795.8671	-3.5225056	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6
NM_000270.3	NP_000261.2	1032.3415	293.01659	-3.5231502	PNP	purine nucleoside phosphorylase
NM_001127710.1,NM_001127709.1,NM_001127708.1,NM_005807.3	NP_001121182.1,NP_001121181.1,NP_001121180.1,NP_005798.2	21227.197	5961.9495	-3.5604455	PRG4	proteoglycan 4
NM_001145320.1,NM_014694.3	NP_001138792.1,NP_055509.2	1045.2012	290.74264	-3.594936	ADAMTSL2	ADAMTS-like 2
NM_006169.2	NP_006160.1	58060.646	16079.999	-3.6107369	NNMT	nicotinamide N-methyltransferase
NM_014883.3,NM_001265580.1,NM_001265579.1,NM_001265578.1,NM_001015045.2	NP_055698.2,NP_001252509.1,NP_001252508.1,NP_001252507.1,NP_001015045.1	449.81396	124.33364	-3.6177977	FAM13A	family with sequence similarity 13, member A
NM_01847.4,NM_001167749.1	NP_060887.2,NP_001161221.1	534.72711	146.59818	-3.6475699	ADCY10	adenylate cyclase 10 (soluble)
NM_002899.3,NM_001130993.1,NM_001130992.1	NP_002890.2,NP_001124465.1,NP_001124464.1	2040.0501	558.43519	-3.6531547	RBP1	retinol binding protein 1, cellular
NM_014291.3	NP_055106.1	643.62671	174.81688	-3.6817195	GCAT	glycine C-acyltransferase

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Description
	ANT	T		
NM_001074.2 NM_001144767.1, NM_001075.4 NM_053039.1, NM_001207004.1	10256.254	2736.5104	-3.7479316	UGT2B7 UGT2B10 UGT2B28 UDP glucuronosyltransferase 2 fam- ily, polypeptide B7 UDP glucuron- osyltransferase 2 family,
NM_032709.2	749.79354	199.99469	-3.7490672	PYROXD2 pyridine nucleotide-disulphide oxidoreductase domain 2
NM_021197.2	355.58004	94.065857	-3.780118	WFDC1 WAP four-disulfide core domain 1
NM_004616.2	3618.1868	957.08034	-3.780442	TSPAN8 tetraspanin 8
NM_144488.4 NM_144489.2 NM_02 1106.3 NM_130795.2 NM_134427.1	2159.6426	564.92278	-3.8228987	RG53 regulator of G-protein signaling 3
NM_001039752.3	567.41839	147.03741	-3.8590069	SLC22A10 solute carrier family 22, member 10
NM_000767.4 NR_001278.1	17121.551	4413.1684	-3.8796506	CYP2B6 CYP2B7P1 cytochrome P450, family 2, subfamily B, polypeptide 6 cytochrome P450, family 2, subfamily B
NM_001128085.1 NM_000049.2	461.80555	118.676	-3.8913136	ASPA aspartoacylase
NM_000771.3	9003.5322	2302.3244	-3.9106271	CYP2C9 cytochrome P450, family 2, subfamily C, polypeptide 9
NM_024605.3	1332.7007	339.68089	-3.9233903	ARHGAP10 Rho GTPase activating protein 10
NM_000668.4	33570.594	8503.4877	-3.9478617	ADH1B alcohol dehydrogenase 1B (class I), beta polypeptide
NM_054033.2 NM_004116.3	610.40374	153.90215	-3.9661808	FKBP1B FK506 binding protein 1B, 12.6 kDa
NM_001528.2	3299.7633	825.77665	-3.9959514	HGFAC HGF activator
NM_152470.2 NM_001256758.1	659.0222	164.37102	-4.0093575	RNF165 ring finger protein 165
NM_180991.4	523.67395	130.50228	-4.0127571	SLCO4C1 solute carrier organic anion trans- porter family, member 4C1
NM_000301.3	1064.479	263.76443	-4.0357184	PLG plasminogen
NM_000769.1	9056.0622	2230.1266	-4.0607838	CYP2C19 cytochrome P450, family 2, subfamily C, polypeptide 19
NM_202000.2 NM_005622.3	4178.4363	1017.3065	-4.1073522	ACSM3 acyl-CoA synthetase medium-chain family member 3
NM_001122848.2 NM_001122847.2, NM_001206931.1 NM_003044.4	1216.3067	294.29242	-4.1329868	SLC6A12 solute carrier family 6 (neurotrans- mitter transporter, betaine/GABA), member 12

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	
	ANT	T		
NM_020130.4	NP_064515.1	318.1123	-4.1542617	C8orf4 chromosome 8 open reading frame 4
NM_021800.2,NM_201262.1	NP_068572.1,NP_957714.1	103.06195	-4.1643671	DNAJC12 DnaJ (Hsp40) homolog, subfamily C, member 12
NM_000050.4,NM_054012.3	NP_000041.2,NP_446464.1	3673.4962	-4.2093401	ASS1 argininosuccinate synthase 1
NM_001145252.1,NM_002621.2	NP_001138724.1,NP_002612.1	288.99392	-4.2486772	CFP complement factor properdin
NM_201648.2	NP_964011.2	3535.3028	-4.260166	GLYAT glycine-N-acyltransferase
NM_000078.2	NP_000069.2	338.82301	-4.2775729	CETP cholesteryl ester transfer protein, plasma
NM_020872.1	NP_065923.1	89.154566	-4.3292606	CNTN3 contactin 3 (plasmacytoma associated)
NM_145870.2,NM_001513.3, NM_145871.2	NP_665877.1,NP_001504.2, NP_665878.2	274.09191	-4.3625307	GSTZ1 glutathione S-transferase zeta 1
NM_006632.3,NM_001098486.1	NP_006623.2,NP_001091956.1	1000.3194	-4.4020217	SLC17A3 solute carrier family 17 (sodium phosphate), member 3
NM_001190907.1,NM_001190906.1,N M_005989.3	NP_001177836.1,NP_001177835.1,NP_ 005980.1	370.27196	-4.4384421	AKR1D1 aldo-keto reductase family 1, member D1
NM_152349.2	NP_689562.1	206.10827	-4.4714397	KRT222 keratin 222
NM_021154.3,NM_058179.2	NP_066977.1,NP_478059.1	3242.5353	-4.4807465	PSAT1 phosphoserine aminotransferase 1
NM_001114171.1,NM_006732.2	NP_001107643.1,NP_006723.2	513.95605	-4.5758342	FOSB FBJ murine osteosarcoma viral oncogene homolog B
NM_152637.2	NP_689850.2	1248.2097	-4.6768014	METTL7B methyltransferase like 7B
NM_001199771.1,NM_002905.3 NR_037658.1	NP_001186700.1,NP_002896.2 -	553.95728	-4.8249286	RDH5 BLOC1S1-RDH5 retinol dehydrogenase 5 (11-cis/9-cis) BLOC1S1-RDH5 readthrough
NM_015837.2,NM_004108.2	NP_056652.1,NP_004099.2	411.3217	-5.1577049	FCN2 ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)
NM_144646.3	NP_653247.1	439.51443	-5.3387685	IGJ immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
NM_005953.3	NP_005944.1	4903.2893	-5.3972258	MT2A metallothionein 2A
NM_152855.2,NM_020070.3 NM_00 1256296.1,NM_001178126.1 NR_02 4448.2 NR_029395.1	NP_690594.1,NP_064455.1 NP_00124 3225.1,NP_001171597.1 -	444.81177	-5.4824981	IGLL1 IGLL5 GUSBP1 IGLL3P immunoglobulin lambda-like polypeptide 1 immunoglobulin lambda-like polypeptide 5

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	Gene	Description
	ANT	T			
NM_001190997.2,NM_016615.4	NP_001177926.1,NP_057699.2	2031.6294 365.26825	-5.5620203	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
NM_001100877.1,NM_001100876.1,NM_174933.3	NP_001094347.1,NP_001094346.1,NP_777593.2	1097.5755 192.86634	-5.6908605	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1
NM_001167930.1,NM_134470.3	NP_001161402.1,NP_608273.1	1131.1978 188.88832	-5.9887124	IL1RAP	interleukin 1 receptor accessory protein
NM_001146006.1,NM_004970.2,NR_027389.1	NP_001139478.1,NP_004961.1,-	3515.3608 579.14912	-6.0698717	IGFALS	insulin-like growth factor binding protein, acid labile subunit
NM_016228.3,NM_182662.1	NP_057312.1,NP_872603.1	6368.845 1043.315	-6.1044318	AADAT	aminoadipate aminotransferase
NR_038343.2	-	954.47085 155.1764	-6.1508765	MAG12-AS3	MAG12 antisense RNA 3
NM_152338.3	NP_689551.2	3127.8467 506.84676	-6.1711881	ZG16	zymogen granule protein 16
NM_019844.3	NP_062818.1	1796.45 290.30392	-6.1881702	SLCO1B3	solute carrier organic anion transporter family, member 1B3
NM_001136503.1	NP_001129975.1	4705.3917 759.27895	-6.1971845	C19orf77	chromosome 19 open reading frame 77
NM_017460.5,NM_001202855.2	NP_059488.2,NP_001189784.1	14183.301 2266.8655	-6.25679	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4
NM_144717.3	NP_653318.2	728.89594 112.87426	-6.4575923	IL20RB	interleukin 20 receptor beta
NM_000015.2	NP_000006.2	8566.234 1270.6352	-6.7416944	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)
NM_016593.3	NP_057677.2	5033.3289 733.19955	-6.8648827	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1
NM_002346.2,NM_001127213.1	NP_002337.1,NP_001120685.1	2854.7492 406.65654	-7.0200499	LY6E	lymphocyte antigen 6 complex, locus E
NM_001005783.1,NM_016527.2	NP_001005783.1,NP_057611.1	18918.594 2658.7413	-7.1156207	HAO2	hydroxyacid oxidase 2 (long chain)
NM_006829.2	NP_006820.1	5744.5613 789.92997	-7.2722412	C10orf116	chromosome 10 open reading frame 116
NM_001128432.1,NM_020973.3	NP_001121904.1,NP_066024.1	12490.183 1695.2275	-7.3678505	GBA3	glucosidase, beta, acid 3 (cytosolic)
NM_001136493.1,NM_032793.3	NP_001129965.1,NP_116182.2	14210.688 1851.3032	-7.6760455	MFSD2A	major facilitator superfamily domain containing 2A
NM_001937.4	NP_001928.2	788.8827 101.89405	-7.7421864	DPT	dermatopontin

Supplementary Table 2. Continued

Annotation	Normalized Intensity		Fold change (T/ANT ratio)	
	ANT	T		
NM_003251.3	5470.0592	695.27622	-7.8674621	thyroid hormone responsive
NM_194294.2	2351.9846	283.58503	-8.2937543	indoleamine 2,3-dioxygenase 2
NM_000348.3	8085.0484	959.92997	-8.4225398	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
NM_001178006.1, NM_000331.4, NM_199161.3	3841.246	431.52984	-8.901461	serum amyloid A1
NM_000612.4, NM_001007139.4, NM_001127598.1, NR_003512.2	11073.054	1224.3552	-9.0439885	insulin-like growth factor 2 (somatomedin A) INS-IGF2
NM_007289.2, NM_007288.2, NM_007287.2, NM_000902.3	1780.3813	140.80211	-12.644564	membrane metallo-endoropeptidase
NM_176870.2, NR_036677.1	15281.01	809.92841	-18.867113	metallothionein 1M metallothionein 1J, pseudogene
NM_005952.3	25432.772	1323.486	-19.216502	metallothionein 1X
NM_001680.4	4251.9126	137.48589	-30.926176	FXYD domain containing ion transport regulator 2

ANT, adjacent non-tumor tissues; HCV, hepatitis C virus; HCC, hepatocellular carcinoma.