

Table 2. List of up and down-regulated genes between primary and metastatic colorectal carcinomas
($P < 0.05$, $fc > 2.0$)

NO	UGCluster	Symbol	Name	P-value	P / M (fc)
1	Hs.95582	SOX15	SRY (sex determining region Y)-box 15	0.000276	-14.43
2	Hs.75285	ITIH2	Inter-alpha (globulin) inhibitor H2	0.000032	-14.29
3	Hs.39311		CDNA clone IMAGE:5295612	0.002214	-9.15
4	Hs.469593	LIMS1	LIM and senescent cell antigen-like domains 1	0.000068	-7.89
5	Hs.368783	NAT5	N-acetyltransferase 5 (ARD1 homolog, <i>S. cerevisiae</i>)	0.000160	-6.48
6	Hs.525557	SERPINA1	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), m	0.007210	-4.49
7	Hs.73849	APOC3	Apolipoprotein C-III	0.003717	-4.24
8	Hs.534293	SERPINA3	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), m	0.000276	-4.11
9	Hs.492203	TERT	Telomerase reverse transcriptase	0.000071	-4.08
10	Hs.76452	CRP	C-reactive protein, pentraxin-related	0.000032	-3.32
11	Hs.313	SPP1	Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activat	0.020921	-3.25
12	Hs.154654	CYP1B1	Cytochrome P450, family 1, subfamily B, polypeptide 1	0.001696	-3.20
13	Hs.391835	C8B	Complement component 8, beta polypeptide	0.005584	-2.99
14	Hs.427202	TTR	Transthyretin (prealbumin, amyloidosis type I)	0.004639	-2.88
15	Hs.1498	HRG	Histidine-rich glycoprotein	0.002680	-2.85
16	Hs.306812	BUCS1	Butyryl Coenzyme A synthetase 1	0.000110	-2.84
17	Hs.512677	SAA4	Serum amyloid A4, constitutive	0.031232	-2.80
18	Hs.421281	WNT8B	Wingless-type MMTV integration site family, member 8B	0.000568	-2.60
19	Hs.13776	DO	Dombrock blood group	0.000110	-2.42
20	Hs.409412	PARP2	Ribonuclease P RNA component H1	0.043308	-2.40
21	Hs.522543	ADAMTSL2	ADAMTS-like 2	0.000451	-2.39
22	Hs.133527	TM4SF4	Transmembrane 4 L six family member 4	0.001946	-2.34
23	Hs.445358	APOH	Apolipoprotein H (beta-2-glycoprotein I)	0.003235	-2.33
24	Hs.75615	APOC2	Apolipoprotein C-II	0.017926	-2.27
25	Hs.494997	C5	Complement component 5	0.000068	-2.26
26	Hs.167584	SLC2A2	Solute carrier family 2 (facilitated glucose transporter), member 2	0.006862	-2.24
27	Hs.182385	HPN	Hepsin (transmembrane protease, serine 1)	0.004639	-2.23
28	Hs.76716	ITIH3	Inter-alpha (globulin) inhibitor H3	0.000041	-2.22
29	Hs.498720	CCDC3	Coiled-coil domain containing 3	0.003235	-2.18
30	Hs.111227	ZIC3	Zic family member 3 heterotaxy 1 (odd-paired homolog, <i>Drosophila</i>)	0.000725	-2.17
31	Hs.195040	HSD11B1	Hydroxysteroid (11-beta) dehydrogenase 1	0.011623	-2.14
32	Hs.24321		CDNA: FLJ21462 fis, clone COL04744	0.016703	-2.11
33	Hs.478553	EIF4A2	Eukaryotic translation initiation factor 4A, isoform 2	0.036389	-2.11
34	Hs.551573		Data not found	0.024236	-2.11
35	Hs.506908	AADAC	Arylacetamide deacetylase (esterase)	0.002680	-2.09
36	Hs.368549	ADH1A	Alcohol dehydrogenase 1A (class I), alpha polypeptide	0.043308	-2.06
37	Hs.12056	ASGR1	Asialoglycoprotein receptor 1	0.002680	-2.05
38	Hs.284712	BAAT	Bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	0.006769	-2.04
39	Hs.513266	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	0.000139	-2.03
40	Hs.442530	TBXA2R	Thromboxane A2 receptor	0.009740	-2.01
41	Hs.180903	384D8-2	Kleisin beta	0.001941	2.03
42	Hs.75765	CXCL2	Chemokine (C-X-C motif) ligand 2	0.007827	2.10
43	Hs.483444	CXCL14	Chemokine (C-X-C motif) ligand 14	0.003893	2.11
44	Hs.62886	SPARCL1	SPARC-like 1 (mast9, hevin)	0.019349	2.12
45	Hs.24976	ART3	ADP-ribosyltransferase 3	0.037667	2.13
46	Hs.512842	MFAP5	Microfibrillar associated protein 5	0.031232	2.14
47	Hs.282265	FABP2	Fatty acid binding protein 2, intestinal	0.043308	2.18
48	Hs.459538	ALDH1A3	Aldehyde dehydrogenase 1 family, member A3	0.002214	2.21
49	Hs.465929	CNN1	Calponin 1, basic, smooth muscle	0.019349	2.24
50	Hs.65029	GAS1	Growth arrest-specific 1	0.013823	2.30
51	Hs.53973	VIP	Vasoactive intestinal peptide	0.000207	2.32
52	Hs.2490	CASP1	Caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	0.007912	2.35
53	Hs.66744	TWIST1	Twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (<i>Drosophila</i>)	0.000812	2.36
54	Hs.111732	FCGBP	Fc fragment of IgG binding protein	0.036389	2.36
55	Hs.513617	MMP2	Matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	0.003235	2.36

56	Hs.112405	S100A9	S100 calcium binding protein A9 (calgranulin B)	0.005584	2.38
57	Hs.551722		Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5, 5' end	0.011074	2.45
58	Hs.35861	RIS1	Ras-induced senescence 1	0.000276	2.56
59	Hs.445818	SPON1	Spondin 1, extracellular matrix protein	0.028240	2.58
60	Hs.155591	FOXF1	Forkhead box F1	0.000889	2.61
61	Hs.646	CPA3	Carboxypeptidase A3 (mast cell)	0.009740	2.72
62	Hs.202354	DIO2	Deiodinase, iodothyronine, type II	0.000139	3.01
63	Hs.2936	MMP13	Matrix metalloproteinase 13 (collagenase 3)	0.047913	3.09
64	Hs.524894	GJB2	Gap junction protein, beta 2, 26kDa (connexin 26)	0.000086	3.19
65	Hs.50813	ITLN1	Intelectin 1 (galactofuranose binding)	0.015314	3.26
66	Hs.89690	CXCL3	Chemokine (C-X-C motif) ligand 3	0.004669	3.26
67	Hs.126256	IL1B	Interleukin 1, beta	0.000712	3.26
68	Hs.411311	IL24	Interleukin 24	0.000175	3.29
69	Hs.546367		Data not found	0.004669	3.32
70	Hs.336046	IL13RA2	Interleukin 13 receptor, alpha 2	0.000222	3.43
71	Hs.40098	GREM1	Gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	0.001814	3.72
72	Hs.505141		Tetraspanin 11	0.000068	3.73
73	Hs.101302	COL12A1	Collagen, type XII, alpha 1	0.003717	3.75
74	Hs.375129	MMP3	Matrix metalloproteinase 3 (stromelysin 1, progelatinase)	0.000999	3.84
75	Hs.481022	SFRP2	Secreted frizzled-related protein 2	0.006995	4.27
76	Hs.152213	WNT5A	Wingless-type MMTV integration site family, member 5A	0.000086	4.38
77	Hs.211426	THBS4	Thrombospondin 4	0.001823	4.38
78	Hs.523594	CTSK	Cathepsin K (pseudodysostosis)	0.000568	5.31
79	Hs.423	PAP	Regenerating islet-derived 3 alpha	0.028240	6.23
80	Hs.83169	MMP1	Matrix metalloproteinase 1 (interstitial collagenase)	0.000429	7.08

P-value, between 12 primary colon carcinomas and paired metastatic tumors from Mann-Whitney rank-sum test.

P / M (fc), average ratio in intensity of 12 primary colon carcinoma / average ratio of intensity of paired metastatic tumors.

Secretory genes described in SPD(<http://spd.cib.pku.edu.cn>.) are shown in boldface