



**Supplementary Figure S1.** The microarray data were analyzed by algorithm 'DIANA-mirExTra'. The score indicates the frequency of seed sequences of indicated miRNAs found in the 3'UTR of genes down-regulated by miR-125b in microarray analysis. Only the top ten miRNAs are shown.

Supplementary table S1. MicroRNAs deregulated in cSCC compared to healthy skin.

Up-regulated genes			
Gene names	Score (d)	Fold change	q-value (%)
hsa-miR-31	4,21	135,17	0,00
hsa-miR-21	3,70	3,80	0,00
hsa-miR-135b	3,14	32,25	0,00
hsa-miR-223	2,65	4,64	2,44
Down-regulated genes			
Gene names	Score (d)	Fold change	q-value (%)
hsa-let-7c	-7,86	0,11	0,00
hsa-miR-328	-6,55	0,08	0,00
hsa-miR-195	-5,98	0,14	0,00
hsa-miR-30a-3p	-5,15	0,11	0,00
hsa-miR-29c	-5,13	0,21	0,00
hsa-miR-143	-4,88	0,11	0,00
hsa-miR-125b	-4,69	0,15	0,00
hsa-miR-375	-4,68	0,07	0,00
hsa-miR-497	-4,62	0,15	0,00
hsa-let-7g	-4,49	0,27	0,00
hsa-miR-199b	-4,39	0,13	0,00
hsa-miR-26a	-4,23	0,23	0,00
hsa-miR-199a	-4,20	0,24	0,00
hsa-miR-30e-5p	-4,06	0,21	0,00
hsa-miR-10a	-3,96	0,14	0,00
hsa-miR-99a	-3,78	0,14	0,00
hsa-miR-196a	-3,68	0,24	0,00
hsa-miR-218	-3,68	0,17	0,00
hsa-miR-23b	-3,66	0,24	0,00
hsa-miR-100	-3,62	0,15	0,00
hsa-miR-149	-3,44	0,12	0,00
hsa-miR-140	-3,39	0,32	0,00
hsa-miR-30e-3p	-3,32	0,28	0,00
hsa-miR-145	-3,22	0,19	0,00
hsa-miR-214	-3,15	0,28	0,00
hsa-miR-335	-3,10	0,22	0,00
hsa-miR-26b	-2,99	0,32	0,00
hsa-miR-196b	-2,98	0,23	0,00
hsa-miR-101	-2,95	0,27	0,00
hsa-miR-615	-2,89	0,22	0,00
hsa-miR-10b	-2,77	0,27	0,00
hsa-let-7b	-2,66	0,35	0,00
hsa-miR-29a	-2,60	0,42	0,00
hsa-miR-197	-2,59	0,39	0,00
hsa-miR-125a	-2,58	0,33	0,00
hsa-miR-451	-2,55	0,14	0,00
hsa-miR-126	-2,48	0,30	0,00
hsa-miR-486	-2,47	0,15	0,00
hsa-miR-30c	-2,42	0,37	0,00
hsa-miR-211	-2,40	0,28	0,00
hsa-miR-130a	-2,24	0,44	0,00
hsa-miR-152	-2,17	0,52	0,00
hsa-let-7a	-2,16	0,39	0,00
hsa-miR-99b	-2,15	0,39	0,00
hsa-miR-30b	-2,12	0,43	0,00
hsa-miR-127	-1,82	0,48	0,83
hsa-let-7d	-1,78	0,48	0,83
hsa-miR-378	-1,71	0,38	1,53
hsa-let-7f	-1,70	0,54	1,53
hsa-miR-148a	-1,66	0,47	1,53
hsa-miR-23a	-1,57	0,51	1,53
hsa-miR-423	-1,56	0,51	1,53
hsa-miR-139	-1,44	0,49	1,53
hsa-miR-16	-1,27	0,58	2,4

Supplementary table S2. MicroRNA families deregulated in cSCC compared to healthy skin.

<i>miRNA families</i>	<i>Deregulated members in SCC</i>	<i>Genomic loci</i>
<b>let-7</b>	let-7a	9:96938239-96938318 [+]/ 11: 122022937-122023016 [-] / 22: 46508629-46508702 [+]
	let-7b	22: 46509566-46509648 [+]
	let-7c	21: 17912148-17912231 [+]
	let-7d	9: 96941116-96941202 [+]
	let-7f	9: 96938629-96938715 [+] / X: 53584153-53584235 [-]
	let-7g	3: 52302294-52302377 [-]
<b>miR-125b</b>	miR-125a	19: 52196507-52196592 [+]
	miR-125b	11: 121970465-121970552 [-] / 21: 17962557-17962645 [+]
<b>miR-10</b>	miR-10a	17: 46657200-46657309 [-]
	miR-10b	2: 177015031-177015140 [+]
<b>miR-199</b>	miR-199a	19: 10928102-10928172 [-] / 1: 172113675-172113784 [-]
	miR-199b	9: 131007000-131007109 [-]
<b>miR-99</b>	miR-99a	21: 17911409-17911489 [+]
	miR-99b	19: 52195865-52195934 [+]
	miR-100	11: 122022937-122023016 [-]
<b>miR-16</b>	miR-16	13: 50623109-50623197 [-] / 3: 160122533-160122613 [+]
	miR-195	17: 6920934-6921020 [-]
<b>miR-30</b>	miR-30a	6: 72113254-72113324 [-]
	miR-30b	8: 135812763-135812850 [-]
	miR-30c	1: 41222956-41223044 [+]/ 6: 72086663-72086734 [-]
	miR-30e	1: 41220027-41220118 [+]
<b>miR-196</b>	miR-196a	17: 46709852-46709921 [-] / 12: 54385522-54385631 [+]
	miR-196b	7: 27209099-27209182 [-]
<b>miR-23</b>	miR-23a	19: 13947401-13947473 [-]
	miR-23b	9: 97847490-97847586 [+]
<b>miR-29</b>	miR-29a	7: 130561506-130561569 [-]
	miR-29b	7: 130562218-130562298 [-] / 1: 207975788-207975868 [-]
<b>miR-26</b>	miR-26a	3: 38010895-38010971 [+]/ 12: 58218392-58218475 [-]
	miR-26b	2: 219267369-219267445 [+]
<b>miR-148</b>	miR-148a	7: 25989539-25989606 [-]
	miR-152	17: 46114527-46114613 [-]

Note: the miRNAs with close genomic loci (<10kb) are highlighted in same color.

**Table S3: miR-125b regulated transcripts**

The potential targets of miR-125b predicted by miRWalk are labeled in red.

Pre-miR-125b				Pre-miR-Ctrl				Fold change (miR-125b vs miR-Ctrl)	p-value	Gene Assignment		
Sample 1	Sample 2	Sample 3	Mean	Sample 1	Sample 2	Sample 3	Mean			ID	Symbol	Name
20	23	22	22	37	40	32	36	-1.65	0.004	NM_006674	HCP5	HLA complex P5
187	210	274	224	394	314	379	363	-1.62	0.018	NM_022156	DUS1L	dihydrouridine synthase 1-like ( <i>S. cerevisiae</i> )
47	50	38	45	77	60	76	71	-1.58	0.017	NM_001920	DCN	decorin
32	32	21	29	46	41	40	42	-1.49	0.029	NM_002427	MMP13	matrix metalloproteinase 13 (collagenase 3)
20	22	21	21	30	28	33	31	-1.48	0.002	NM_001012642	GRAMD2	GRAM domain containing 2
56	35	40	43	62	60	69	64	-1.47	0.039	NM_032681	SPRY5	SPRY domain containing 5
73	56	63	64	92	84	107	94	-1.47	0.022	NM_013275	ANKRD11	ankyrin repeat domain 11
430	490	581	500	676	859	671	735	-1.47	0.036	NM_005949	MT1F	metallothionein 1F
35	29	36	33	53	52	40	49	-1.46	0.029	NM_005268	GJB5	gap junction protein, beta 5, 31.1kDa
42	34	40	39	56	51	64	57	-1.46	0.016	NR_026869	NCRNA00052	non-protein coding RNA 52
43	45	57	49	73	72	66	70	-1.45	0.012	NM_130459	TOR2A	torsin family 2, member A
40	32	33	35	46	59	48	51	-1.44	0.027	NM_002423	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)
54	56	75	61	95	84	86	88	-1.44	0.022	NM_002257	KLK1	kallikrein 1
84	79	90	84	133	97	128	119	-1.42	0.041	NM_005985	SNAI1	snail homolog 1 ( <i>Drosophila</i> )
644	627	571	614	855	885	859	866	-1.41	0.000	NM_001127605	LIPA	lipase A, lysosomal acid, cholesterol esterase
280	258	293	277	381	393	383	386	-1.39	0.001	NM_001102402	PCTP	phosphatidylcholine transfer protein
689	730	1034	818	1164	1125	1093	1127	-1.38	0.049	NM_138442	CCDC124	coiled-coil domain containing 124
323	324	305	317	448	425	436	436	-1.38	0.000	NM_001150	ANPEP	alanyl (membrane) aminopeptidase
170	187	219	192	295	232	264	264	-1.37	0.037	NM_014232	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)
118	120	148	129	193	152	185	177	-1.37	0.039	NM_000116	TAZ	tafazzin
341	359	426	375	540	504	498	514	-1.37	0.009	NM_078467	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
79	83	98	86	135	114	104	118	-1.36	0.043	NM_006103	WFDC2	WAP four-disulfide core domain 2
64	66	74	68	96	96	87	93	-1.36	0.005	NM_182757	RNF144B	ring finger protein 144B
94	104	110	103	132	150	137	139	-1.35	0.007	NM_002781	PSG5	pregnancy specific beta-1-glycoprotein 5
23	19	24	22	31	29	31	30	-1.35	0.008	XM_001714063	LOC642776	hypothetical protein LOC642776
44	39	54	46	64	56	64	61	-1.34	0.038	AK128439	VAC14	Vac14 homolog ( <i>S. cerevisiae</i> )
48	46	48	47	60	72	59	63	-1.34	0.018	BC002752	C11orf67	chromosome 11 open reading frame 67
68	67	80	72	89	107	92	96	-1.34	0.025	NM_004389	CTNNA2	catenin (cadherin-associated protein), alpha 2
41	33	34	36	47	45	52	48	-1.33	0.026	NM_030915	LBH	limb bud and heart development homolog (mouse)
129	123	111	121	154	168	161	161	-1.33	0.004	NM_080740	ZNF280A	zinc finger protein 280A
135	124	105	121	167	152	164	161	-1.33	0.017	NM_033285	TP53INP1	tumor protein p53 inducible nuclear protein 1
73	60	71	68	91	92	87	90	-1.33	0.006	NM_015892	CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15
224	252	275	250	322	363	309	332	-1.32	0.021	NM_001785	CDA	cytidine deaminase
72	71	81	75	106	101	89	99	-1.32	0.014	NM_148886	SMCR7	Smith-Magenis syndrome chromosome region, candidate 7
342	322	313	326	458	438	396	431	-1.32	0.007	NM_024111	CHAC1	ChaC, cation transport regulator homolog 1 ( <i>E. coli</i> )
149	166	185	167	222	209	227	219	-1.32	0.011	NM_001860	SLC31A2	solute carrier family 31 (copper transporters), member 2
79	83	94	85	117	101	118	112	-1.31	0.020	NM_015299	KHNYN	KH and NYN domain containing
168	148	159	158	209	200	214	208	-1.31	0.002	NM_007260	LYPLA2	lysophospholipase II
40	39	49	42	58	59	50	56	-1.31	0.032	NM_001040167	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
88	82	86	85	114	102	118	111	-1.30	0.008	NM_014901	RNF44	ring finger protein 44
												serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
43	35	33	37	51	46	46	48	-1.30	0.035	NM_002615	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
62	65	73	67	77	98	85	87	-1.30	0.048	NM_017421	COQ3	coenzyme Q3 homolog, methyltransferase ( <i>S. cerevisiae</i> )
47	44	37	42	57	52	57	55	-1.30	0.021	NM_199136	C7orf46	chromosome 7 open reading frame 46
58	64	57	60	72	79	80	77	-1.30	0.006	NM_020405	PLXDC1	plexin domain containing 1
98	120	115	111	136	151	146	144	-1.30	0.015	NM_001252	CD70	CD70 molecule
234	230	204	223	287	299	279	288	-1.29	0.004	NM_003474	ADAM12	ADAM metalloproteinase domain 12
709	715	843	756	920	1078	935	977	-1.29	0.029	NM_175617	MT1E	metallothionein 1E
83	101	116	100	127	125	136	129	-1.29	0.045	NM_017410	HOXC13	homeobox C13

143	148	167	152	209	189	192	197	-1.29	0.010	NM_152739	HOXA9	homeobox A9
88	92	121	101	126	133	130	130	-1.29	0.049	NM_001003927	EVI2A	ecotropic viral integration site 2A
39	43	54	45	56	60	60	59	-1.29	0.049	NR_027471	LOC440173	hypothetical LOC440173
307	359	403	356	463	497	416	458	-1.29	0.049	NM_020992	PDLIM1	PDZ and LIM domain 1
43	36	43	41	48	55	54	52	-1.29	0.023	XM_001714030	LOC642838	similar to hCG1742442
79	75	90	81	105	96	112	104	-1.28	0.021	NM_020127	TUFT1	tuftelin 1
627	600	736	654	793	924	802	840	-1.28	0.035	NM_002488	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
92	88	115	98	117	132	130	126	-1.28	0.046	NM_001870	CPA3	carboxypeptidase A3 (mast cell)
348	377	373	366	459	473	473	469	-1.28	0.001	NM_020453	ATP10D	ATPase, class V, type 10D
35	40	39	38	51	49	46	49	-1.28	0.008	NM_001134407	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A
74	66	68	69	98	89	78	89	-1.28	0.038	NM_032681	SPRYD5	SPRY domain containing 5
47	44	46	46	62	57	57	58	-1.28	0.002	NM_001033551	TOM1L2	target of myb1-like 2 (chicken)
81	75	86	81	100	111	97	103	-1.28	0.016	NM_014415	ZBTB11	zinc finger and BTB domain containing 11
701	764	683	716	897	996	845	913	-1.27	0.018	NR_015379	UCA1	urothelial cancer associated 1 (non-protein coding)
21	26	26	24	28	30	33	31	-1.27	0.037	NM_017893	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G

76	84	90	83	98	114	106	106	-1.27	0.019	NM_004106	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
85	74	96	85	108	103	113	108	-1.27	0.028	NM_014729	TOX	thymocyte selection-associated high mobility group box
29	30	25	28	40	34	32	35	-1.27	0.050	NM_001178061	SEMA6C	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C
163	158	183	168	223	211	205	213	-1.27	0.008	NM_198723	TCEA2	transcription elongation factor A (SII), 2
23	30	27	27	31	34	37	34	-1.27	0.049	NM_203370	C3orf54	chromosome 3 open reading frame 54
200	197	242	213	276	253	282	270	-1.27	0.027	NM_001141969	DAXX	death-domain associated protein
63	77	63	68	82	91	84	86	-1.27	0.028	NM_032740	SFT2D3	SFT2 domain containing 3
194	192	235	207	267	246	273	262	-1.27	0.028	NM_001141969	DAXX	death-domain associated protein
24	23	24	24	29	28	33	30	-1.27	0.012	AF258550	LOC100129503	hypothetical protein LOC100129503
113	94	87	98	130	121	120	124	-1.26	0.034	NM_152321	ERP27	endoplasmic reticulum protein 27
204	204	248	219	281	258	289	276	-1.26	0.030	NM_001141969	DAXX	death-domain associated protein
62	65	58	62	79	83	72	78	-1.26	0.011	NM_016835	MAPT	microtubule-associated protein tau
197	207	243	216	277	281	259	272	-1.26	0.022	NM_001134375	CCNJ	cyclin J
127	133	135	131	170	159	169	166	-1.26	0.001	NM_015997	C1orf66	chromosome 1 open reading frame 66
88	82	95	88	116	102	115	111	-1.26	0.017	NR_002592	SNORD96A	small nucleolar RNA, C/D box 96A
83	84	84	84	108	103	103	105	-1.25	0.000	NM_000355	TCN2	transcobalamin II
390	388	460	413	528	531	495	518	-1.25	0.016	NM_004656	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
29	27	28	28	40	34	32	35	-1.25	0.044	NM_021133	RNASEL	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)
183	179	220	194	246	255	229	243	-1.25	0.032	NM_015533	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)
133	145	170	150	199	172	192	188	-1.25	0.048	NM_001080826	SGK223	homolog of rat pragma of Rnd2
96	91	92	93	118	117	114	116	-1.25	0.000	NM_178858	SFXN2	sideroflexin 2
56	52	54	54	74	60	67	67	-1.25	0.032	NM_023072	ZSWIM4	zinc finger, SWIM-type containing 4
398	382	387	389	484	514	462	487	-1.25	0.004	NM_000326	RLBP1	retinaldehyde binding protein 1
39	33	41	38	48	45	48	47	-1.25	0.020	NM_005420	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1
162	154	169	162	207	204	196	202	-1.25	0.002	NM_023948	MOSPD3	motile sperm domain containing 3
222	236	252	237	283	275	329	296	-1.25	0.035	NM_144576	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)
41	35	43	40	50	53	46	49	-1.25	0.036	NM_145047	OSCP1	organic solute carrier partner 1
219	239	224	227	294	268	289	284	-1.25	0.005	NM_016472	C14orf129	chromosome 14 open reading frame 129 mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction
75	76	93	81	105	97	103	102	-1.25	0.038	NM_016069	TIMM16	factor signal transduction
112	104	115	111	136	132	146	138	-1.25	0.006	NM_153631	HOXA3	homeobox A3
41	37	40	39	46	51	51	49	-1.25	0.009	ENST00000377425	AQP7	aquaporin 7
106	93	88	96	115	121	121	119	-1.25	0.015	NM_004727	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
294	283	356	311	405	379	379	388	-1.25	0.034	NM_025232	REEP4	receptor accessory protein 4
119	130	141	130	157	165	164	162	-1.25	0.010	AK291605	FAM115A	family with sequence similarity 115, member A
202	182	196	193	242	236	245	241	-1.25	0.002	NM_053025	MYLK	myosin light chain kinase
69	71	72	71	89	91	84	88	-1.24	0.002	NM_033544	RCCD1	RCC1 domain containing 1
178	142	182	168	194	216	216	209	-1.24	0.048	NM_198476	C19orf54	chromosome 19 open reading frame 54
280	264	227	257	318	312	329	320	-1.24	0.019	NM_000888	ITGB6	integrin, beta 6
448	419	435	434	543	561	516	540	-1.24	0.002	NM_002466	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
161	153	169	161	203	201	196	200	-1.24	0.001	NM_153603	COG7	component of oligomeric golgi complex 7
181	193	186	187	242	230	225	232	-1.24	0.002	NM_005155	PPT2	palmitoyl-protein thioesterase 2
179	190	184	184	238	226	222	229	-1.24	0.002	NM_005155	PPT2	palmitoyl-protein thioesterase 2
117	117	117	117	144	147	146	145	-1.24	0.000	NM_003427	ZNF76	zinc finger protein 76 (expressed in testis)
210	213	242	222	295	251	279	275	-1.24	0.032	NM_022822	KLC2	kinesin light chain 2
83	80	71	78	96	103	90	96	-1.24	0.021	NM_014211	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi
46	37	39	40	49	53	48	50	-1.24	0.034	NM_024584	CCDC121	coiled-coil domain containing 121
67	60	56	61	76	74	77	76	-1.24	0.010	NM_145176	SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12
111	122	128	120	147	135	165	149	-1.24	0.048	NM_205767	C19orf70	chromosome 19 open reading frame 70
113	124	108	115	142	145	140	142	-1.24	0.005	NM_003275	TMOD1	tropomodulin 1
54	50	45	50	61	58	65	61	-1.24	0.018	NM_000808	GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3
119	125	127	124	153	160	145	153	-1.24	0.004	NM_024701	ASB13	ankyrin repeat and SOCS box-containing 13
107	88	106	100	125	117	130	124	-1.24	0.033	NM_022909	CENPH	centromere protein H
471	426	501	466	550	547	631	576	-1.24	0.036	NM_017612	ZCCHC8	zinc finger, CCHC domain containing 8

43	38	42	41	47	53	52	51	-1.24	0.013	<a href="#">XM_001714030</a>	LOC642838	similar to hCG1742442
56	53	55	55	71	68	63	67	-1.24	0.009	<a href="#">NM_004934</a>	CDH18	cadherin 18, type 2
73	62	67	67	86	83	80	83	-1.23	0.014	<a href="#">NM_145252</a>	ZG16B	zymogen granule protein 16 homolog B (rat)
75	71	64	70	93	89	77	86	-1.23	0.044	<a href="#">NM_032709</a>	PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2
93	84	90	89	117	105	108	110	-1.23	0.009	<a href="#">NM_145111</a>	FAM200A	family with sequence similarity 200, member A
67	65	72	68	82	87	82	84	-1.23	0.005	<a href="#">NR_002803</a>	RPL13P5	ribosomal protein L13 pseudogene 5
1484	1348	1160	1331	1644	1666	1608	1639	-1.23	0.032	<a href="#">NM_006472</a>	<a href="#">TXNIP</a>	thioredoxin interacting protein
33	31	34	33	40	45	37	40	-1.23	0.035	<a href="#">NM_001195</a>	BFSP1	beaded filament structural protein 1, filensin
169	155	164	163	182	201	218	200	-1.23	0.029	<a href="#">NM_000968</a>	RPL4	ribosomal protein L4
126	123	121	123	155	153	147	152	-1.23	0.001	<a href="#">NM_020204</a>	<a href="#">LHX9</a>	LIM homeobox 9
86	77	80	81	104	93	102	100	-1.23	0.012	<a href="#">NM_004205</a>	<a href="#">USP2</a>	ubiquitin specific peptidase 2
165	169	200	178	211	235	209	219	-1.23	0.042	<a href="#">NM_018073</a>	TRIM68	tripartite motif-containing 68
169	191	188	183	229	235	208	224	-1.23	0.017	<a href="#">NM_005371</a>	METTL1	methyltransferase like 1
294	285	346	308	365	399	370	378	-1.23	0.032	<a href="#">NM_016352</a>	CPA4	carboxypeptidase A4

96	99	105	100	132	127	109	123	-1.22	0.037	NM_032501	ACSS1	acyl-CoA synthetase short-chain family member 1
271	295	343	303	388	374	350	371	-1.22	0.046	NM_015926	TEX264	testis expressed 264
90	95	90	92	109	119	109	112	-1.22	0.005	NM_080424	SP110	SP110 nuclear body protein
146	152	148	148	195	174	175	181	-1.22	0.010	NM_005133	RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
261	236	247	248	310	272	326	303	-1.22	0.035	NM_032510	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)
727	733	847	769	1009	891	915	939	-1.22	0.033	NM_005053	RAD23A	RAD23 homolog A (S. cerevisiae)
40	37	39	39	43	49	50	47	-1.22	0.019	XM_001715084	LOC100132426	similar to hCG1742442
42	46	44	44	60	49	53	54	-1.22	0.041	NM_207396	RNF207	ring finger protein 207
1557	1714	1861	1711	2040	2185	2030	2085	-1.22	0.021	NM_012106	ARL2BP	ADP-ribosylation factor-like 2 binding protein
180	189	207	192	242	223	237	234	-1.22	0.013	NM_025069	ZNF703	zinc finger protein 703
57	58	70	62	77	77	71	75	-1.22	0.045	NM_178836	PLD6	phospholipase D family, member 6
77	75	68	73	90	92	85	89	-1.21	0.010	NM_012219	MRAS	muscle RAS oncogene homolog
165	165	171	167	199	206	203	203	-1.21	0.000	NM_052897	MBD6	methyl-CpG binding domain protein 6
133	136	162	144	177	174	172	174	-1.21	0.028	BC033660	DBF4B	DBF4 homolog B (S. cerevisiae)
685	694	779	719	850	930	835	872	-1.21	0.022	NM_006941	SOX10	SRY (sex determining region Y)-box 10
163	167	164	165	191	207	201	200	-1.21	0.002	NM_003102	SOD3	superoxide dismutase 3, extracellular
175	193	203	190	250	209	233	230	-1.21	0.050	NM_025010	KLHL18	kelch-like 18 (Drosophila)
67	76	80	75	85	91	95	90	-1.21	0.032	NM_002145	HOXB2	homeobox B2
217	231	247	232	264	269	307	280	-1.21	0.041	NM_022778	CCDC21	coiled-coil domain containing 21
88	81	75	81	94	98	103	98	-1.21	0.021	NM_004099	STOM	stomatin
191	183	195	190	234	223	231	229	-1.21	0.001	NM_001188	BAK1	BCL2-antagonist/killer 1
71	59	67	65	77	75	85	79	-1.21	0.043	NM_022717	SNRNP35	small nuclear ribonucleoprotein 35kDa (U11/U12)
121	117	118	119	142	158	129	143	-1.21	0.043	NR_029192	LOC100133315	transient receptor potential cation channel, subfamily C, member 2-like
521	592	649	587	747	690	687	708	-1.21	0.045	NM_002229	JUNB	jun B proto-oncogene
352	372	394	372	471	442	433	449	-1.21	0.010	NM_014516	CNOT3	CCR4-NOT transcription complex, subunit 3
484	533	589	536	629	661	646	646	-1.21	0.026	NM_032822	FAM136A	family with sequence similarity 136, member A
67	63	59	63	79	74	74	76	-1.20	0.010	NM_000530	MPZ	myelin protein zero
78	66	63	69	79	87	83	83	-1.20	0.048	NM_001040260	DCLK2	doublecortin-like kinase 2
105	100	110	105	131	116	131	126	-1.20	0.022	NM_014840	NUAK1	NUAK family, SNF1-like kinase, 1
30	28	30	29	32	38	36	35	-1.20	0.041	NM_153336	PSTK	phosphoserine-tRNA kinase
515	472	449	479	616	565	544	575	-1.20	0.029	NM_001024847	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)
106	115	124	115	136	143	134	138	-1.20	0.017	NM_032575	GLIS2	GLIS family zinc finger 2
238	217	265	240	288	291	285	288	-1.20	0.026	NM_031484	MARVELD1	MARVEL domain containing 1
285	256	297	280	341	310	356	336	-1.20	0.037	NM_022566	MESDC1	mesoderm development candidate 1
152	140	142	145	180	169	172	174	-1.20	0.005	NM_006129	BMP1	bone morphogenetic protein 1
378	397	421	399	475	499	462	479	-1.20	0.008	NM_002611	PDK2	pyruvate dehydrogenase kinase, isozyme 2
326	301	288	305	357	374	366	366	-1.20	0.008	NM_173473	ANAPC16	anaphase promoting complex subunit 16
93	101	92	95	76	86	77	79	1.20	0.019	XM_002345769	HSBP1P2	heat shock factor binding protein 1 pseudogene 2
182	189	183	185	146	165	151	154	1.20	0.007	CR590757	RPL22P15	ribosomal protein L22 pseudogene 15
135	122	117	125	108	102	101	104	1.20	0.024	NM_019100	DMAP1	DNA methyltransferase 1 associated protein 1
351	349	302	334	290	278	259	276	1.21	0.035	NR_024060	FAM27A	family with sequence similarity 27, member A
57	58	52	56	44	49	46	46	1.21	0.016	NM_152379	C1orf131	chromosome 1 open reading frame 131
647	664	641	651	534	558	520	537	1.21	0.001	NM_001146276	NCEH1	neutral cholesterol ester hydrolase 1
866	875	739	827	684	716	644	682	1.21	0.041	NM_001040058	SPP1	secreted phosphoprotein 1
371	370	317	353	306	293	273	291	1.21	0.036	NR_024060	FAM27A	family with sequence similarity 27, member A
55	64	62	61	48	54	47	50	1.21	0.035	NM_018378	FBXL8	F-box and leucine-rich repeat protein 8
338	328	279	315	272	258	246	259	1.22	0.047	NR_027421	FAM27C	family with sequence similarity 27, member C
316	330	294	313	225	264	280	257	1.22	0.044	NM_012403	ANP32C	acidic (leucine-rich) nuclear phosphoprotein 32 family, member C
39	39	37	38	29	35	30	31	1.22	0.020	NM_007030	TPPP	tubulin polymerization promoting protein
793	807	801	800	670	671	621	654	1.22	0.001	BC071678	RPS18P9	ribosomal protein S18 pseudogene 9
80	73	86	80	61	69	65	65	1.22	0.030	NM_001444	FABP5	fatty acid binding protein 5 (psoriasis-associated)
40	47	48	45	36	39	35	37	1.22	0.045	NM_003322	TULP1	tubby like protein 1
171	185	171	176	134	157	140	143	1.23	0.018	BC034580	SLC44A5	solute carrier family 44, member 5
39	34	39	37	28	30	33	30	1.23	0.038	NM_006665	HPSE	heparanase
63	67	61	64	52	56	49	52	1.23	0.013	NM_174936	PCSK9	proprotein convertase subtilisin/kexin type 9
497	458	456	471	407	325	414	382	1.23	0.049	NM_014399	TSPAN13	tetraspanin 13



89	95	98	94	77	76	75	76	1.24	0.002	NM_173808	NEGR1	neuronal growth regulator 1
430	464	435	443	360	315	398	358	1.24	0.032	NM_057159	LPAR1	lysophosphatidic acid receptor 1
1230	1205	996	1144	923	940	908	924	1.24	0.042	NM_002273	KRT8	keratin 8
233	241	196	223	180	178	183	180	1.24	0.037	NM_019007	ARMCX6	armadillo repeat containing, X-linked 6
54	50	45	50	41	42	37	40	1.24	0.034	AB042555	PDE4DIP	phosphodiesterase 4D interacting protein
42	41	44	42	32	37	33	34	1.24	0.014	NM_001145678	C5orf36	chromosome 5 open reading frame 36
95	90	95	93	80	82	63	75	1.25	0.040	NM_014580	SLC2A8	solute carrier family 2 (facilitated glucose transporter), member 8
536	593	543	557	483	423	436	447	1.25	0.013	NR_002918	SNORA48	small nucleolar RNA, H/ACA box 48
206	191	184	194	142	171	153	155	1.25	0.023	NM_001004419	CLEC2D	C-type lectin domain family 2, member D
2696	2926	2713	2778	2316	2020	2336	2224	1.25	0.012	NR_000020	SNORD33	small nucleolar RNA, C/D box 33
158	151	143	151	131	107	123	120	1.25	0.021	NM_201649	SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9
142	138	146	142	117	103	119	113	1.25	0.007	NM_002354	EPCAM	epithelial cell adhesion molecule
906	986	855	916	753	710	727	730	1.25	0.010	ENST00000447487	RPS27	ribosomal protein S27

200	194	187	193	151	148	163	154	1.26	0.003	NM_006408	AGR2	anterior gradient homolog 2 ( <i>Xenopus laevis</i> )
171	160	147	159	138	110	132	126	1.26	0.040	NM_001039140	C20orf27	chromosome 20 open reading frame 27
56	66	61	61	48	45	53	49	1.26	0.032	NM_001263	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
182	191	199	191	151	161	142	151	1.26	0.006	NM_005320	HIST1H1D	histone cluster 1, H1d
38	40	41	40	33	34	27	31	1.27	0.029	NM_004769	ACCN3	amiloride-sensitive cation channel 3
750	838	770	786	550	658	653	620	1.27	0.020	NR_002183	FAM10A4	ST13-like tumor suppressor
482	526	589	533	446	377	437	420	1.27	0.041	NM_003535	HIST1H3J	histone cluster 1, H3j
42	39	39	40	34	34	26	31	1.27	0.047	NM_001102651	ZNF554	zinc finger protein 554
407	372	433	404	311	295	348	318	1.27	0.022	NM_014331	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
109	118	110	112	97	80	88	88	1.27	0.012	NM_024042	METRN	meteorin, glial cell differentiation regulator
43	49	39	44	36	33	35	34	1.27	0.041	NM_003044	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
112	124	103	113	82	96	87	89	1.28	0.030	XR_038419	LOC645181	similar to PDGFA associated protein 1
88	92	95	92	62	77	76	72	1.28	0.016	NR_002726	HNRNPA3P1	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1
141	152	142	145	120	105	113	113	1.29	0.005	NM_014256	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
48	40	45	44	33	33	36	34	1.29	0.016	NM_173664	ARL10	ADP-ribosylation factor-like 10
179	194	198	190	151	166	125	147	1.29	0.032	NM_032328	EFCAB2	EF-hand calcium binding domain 2
92	105	111	103	76	90	72	79	1.30	0.038	NM_001824	CKM	creatine kinase, muscle
134	127	118	126	93	97	100	97	1.31	0.005	NM_004650	PNPLA4	patatin-like phospholipase domain containing 4
51	50	42	48	36	32	41	36	1.32	0.039	NM_015645	C1QTNF5	C1q and tumor necrosis factor related protein 5
252	232	234	239	185	183	176	181	1.32	0.001	NM_017527	LY6K	lymphocyte antigen 6 complex, locus K
152	179	153	161	133	131	102	122	1.32	0.042	NM_001037161	ACOT1	acyl-CoA thioesterase 1
59	61	59	60	46	49	41	45	1.32	0.005	NM_002447	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
226	245	237	236	170	196	168	178	1.33	0.005	NM_012067	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
486	460	397	448	354	319	340	338	1.33	0.018	NM_006579	EBP	emopamil binding protein (sterol isomerase)
64	72	67	68	49	61	43	51	1.33	0.047	NM_175075	C8orf42	chromosome 8 open reading frame 42
48	40	45	44	30	37	34	33	1.33	0.023	NR_003667	SUGT1P1	suppressor of G2 allele of SKP1 pseudogene 1 ( <i>S. cerevisiae</i> )
135	167	167	156	106	126	120	117	1.34	0.034	NM_004202	TMSB4Y	thymosin beta 4, Y-linked
57	59	66	61	43	54	40	45	1.34	0.034	NM_031895	CACNG8	calcium channel, voltage-dependent, gamma subunit 8
143	155	169	156	114	122	109	115	1.35	0.008	NM_004878	PTGES	prostaglandin E synthase
91	84	93	89	78	53	65	66	1.36	0.037	NM_001080431	SLC45A4	solute carrier family 45, member 4
97	85	75	86	65	62	62	63	1.36	0.023	NM_017805	RASIP1	Ras interacting protein 1
96	98	97	97	62	79	71	71	1.37	0.006	NM_025211	GKAP1	G kinase anchoring protein 1
50	39	41	44	30	34	30	31	1.39	0.031	NM_001034173	ALDH1L2	aldehyde dehydrogenase 1 family, member L2
50	45	43	46	31	33	35	33	1.40	0.006	NM_000499	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1
2114	2418	1898	2143	1518	1509	1531	1519	1.41	0.015	BC037964	DHX37	DEAH (Asp-Glu-Ala-His) box polypeptide 37
384	340	306	343	254	261	214	243	1.41	0.021	NM_080430	SELM	selenoprotein M
58	50	44	51	39	30	38	36	1.41	0.044	NM_007332	TRPA1	transient receptor potential cation channel, subfamily A, member 1
84	93	70	82	60	63	50	58	1.42	0.038	NM_001354	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)
149	161	154	155	117	111	98	109	1.42	0.002	XR_040249	LOC124685	hCG1644301
46	39	47	44	29	35	27	31	1.43	0.021	NM_014364	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic
51	48	52	50	40	33	32	35	1.44	0.005	NM_004098	EMX2	empty spiracles homeobox 2
65	71	55	63	38	50	43	44	1.46	0.026	NM_198472	C10orf125	chromosome 10 open reading frame 125
65	64	48	59	45	41	35	40	1.46	0.038	NM_013376	SERTAD1	SERTA domain containing 1
59	75	63	66	41	55	39	45	1.47	0.040	ENST00000309775	LOC100291851	similar to Putative ubiquitin-like protein FUBI-like protein ENSP00000310146
133	133	117	128	89	88	83	87	1.47	0.002	NM_080875	MIB2	mindbomb homolog 2 ( <i>Drosophila</i> )
108	150	120	126	80	96	78	85	1.49	0.039	NM_198849	SLAH3	seven in absentia homolog 3 ( <i>Drosophila</i> )
57	54	48	53	39	37	30	35	1.49	0.010	NM_080390	TCEAL2	transcription elongation factor A (SII)-like 2
534	646	543	574	362	463	281	369	1.56	0.032	J04755	FTHL5	ferritin, heavy polypeptide-like 5
163	166	170	166	90	96	119	101	1.64	0.002	NM_002852	PTX3	pentraxin 3, long
260	251	216	242	142	119	178	147	1.65	0.012	NM_006528	TFPI2	tissue factor pathway inhibitor 2

| 63 71 75 70 | 36 46 37 40 | 1.75 0.003 | [NM\\_194249](#) DND1 dead end homolog 1 (zebrafish)