

**Table S1** The top 10 up and down regulated DElncRNAs, DEmiRNAs and DEMRNAs in UCEC patients for TCGA (above three ones) database and CPTAC database (lower three ones)

lncRNA	logFC	logCPM	PValue	FDR
RP11-679B19.1	-4.609665565	6.530968909	1.6397E-194	1.3475E-190
MBNL1-AS1	-3.741748824	8.755912505	4.6355E-187	1.9047E-183
LINC01197	-3.950847703	6.400468962	2.2879E-158	6.2672E-155
LINC01016	-6.306247501	6.066382992	1.3589E-155	2.7919E-152
RP11-613D13.8	-5.037151715	5.178629807	1.079E-154	1.7735E-151
MIR202HG	-8.211270213	5.501504991	1.7643E-154	2.4165E-151
MEF2C-AS1	-4.234988486	5.146458797	1.0996E-146	1.291E-143
LINC00702	-4.632384251	6.619106924	2.4588E-143	2.5258E-140
RP11-535A5.1	-5.379666932	4.124845545	6.5591E-136	5.9892E-133
ACTA2-AS1	-4.167647477	7.842288237	3.699E-128	3.0398E-125
RP6-65G23.3	2.424491976	8.170464715	5.29E-39	3.50E-37
TFAP2A-AS1	3.540784393	7.623581464	1.97E-34	9.91E-33
TRPM2-AS	3.118967302	9.378205266	9.78E-32	4.39E-30
RP11-57A19.2	3.319194854	7.989516924	8.17E-31	3.42E-29
LINC00858	4.094175485	6.893728812	1.46E-29	5.75E-28
RP4-635E18.6	2.234532646	6.072501653	4.71E-29	1.78E-27
RP11-443B20.1	2.070790115	7.52494364	9.07E-29	3.39E-27
FAM83H-AS1	2.522429397	11.54381403	3.41E-28	1.24E-26
RP11-303E16.2	2.025677626	9.317319558	6.46E-27	2.19E-25
RP11-465N4.4	2.070113718	7.780077623	9.77E-27	3.26E-25
hsa-mir-202	-9.053278925	3.426902818	2.20E-266	1.50E-263
hsa-mir-139	-3.303204309	4.724789121	1.69E-113	5.75E-111
hsa-mir-101-2	-2.594505882	12.32873184	1.79E-109	4.04E-107
hsa-mir-101-1	-2.592962483	12.31864278	5.58E-109	9.46E-107
hsa-mir-140	-2.572395288	9.538938356	5.43E-107	7.37E-105
hsa-mir-143	-3.416483965	16.51631794	2.00E-93	2.26E-91
hsa-mir-145	-3.262670245	11.43527602	1.60E-91	1.55E-89
hsa-mir-542	-2.880683315	8.124890384	1.97E-86	1.67E-84
hsa-mir-100	-3.345617451	12.11361639	5.29E-81	3.99E-79
hsa-mir-424	-3.156111844	8.33177413	1.11E-73	7.52E-72
hsa-mir-183	4.428895958	14.26832082	2.97E-54	7.75E-53
hsa-mir-96	3.835747829	5.71119686	9.55E-47	2.16E-45
hsa-mir-182	3.764054615	15.34495864	6.73E-43	1.34E-41
hsa-mir-1307	2.058708346	11.19105576	5.45E-37	9.02E-36
hsa-mir-200a	2.689505063	11.15480027	5.16E-36	7.78E-35

**Table S1** (continued)

**Table S1** (continued)

lncRNA	logFC	logCPM	PValue	FDR
hsa-mir-130b	2.202502881	6.142857397	4.44E-31	6.15E-30
hsa-mir-429	2.854246283	8.851947393	4.63E-31	6.17E-30
hsa-mir-877	3.113467805	2.349670899	3.81E-29	4.79E-28
hsa-mir-210	2.816111439	10.81766962	7.66E-28	9.29E-27
hsa-mir-200b	2.275598674	10.85998217	1.76E-26	2.06E-25
CSRP1	-2.907945921	8.455452802	1.87E-216	3.37E-212
MYLK	-4.311931235	7.238331211	3.99E-210	3.60E-206
PPP1R12B	-4.210166343	6.30001368	2.82E-208	1.70E-204
GSTM5	-5.021590783	2.409866329	1.27E-197	5.73E-194
TNS1	-3.416332066	7.035411869	4.60E-190	1.66E-186
CBX7	-3.278024706	4.409436085	5.20E-185	1.56E-181
SYNPO2	-4.539556297	5.8953856	4.30E-184	1.11E-180
GPRASP1	-3.723657127	2.942139577	6.97E-179	1.57E-175
RERG	-4.793611622	3.7151094	3.44E-176	6.90E-173
LYVE1	-3.675154124	1.345640227	4.74E-172	8.55E-169
TBC1D7	2.050198189	4.901671184	1.75E-58	7.83E-57
CDC6	3.188311841	4.802656544	3.02E-55	1.26E-53
PRAME	4.160544447	8.019274758	5.88E-54	2.36E-52
C16orf59	3.02543474	4.058818372	5.76E-52	2.15E-50
ASF1B	3.235057427	5.677795682	1.13E-50	4.08E-49
POC1A	2.930270522	4.555914044	5.24E-50	1.85E-48
PKMYT1	3.676875293	4.805974699	9.59E-50	3.39E-48
RNFT2	2.811744393	3.879030558	6.08E-49	2.08E-47
HN1	2.61482313	7.325508943	2.09E-48	7.02E-47
KIFC1	3.374364309	5.934283212	5.34E-48	1.78E-46
RP11-254F19.2	-4.707311483	5.299971932	9.17E-43	1.04E-38
RP11-324I22.3	-3.236228261	4.464039034	4.10E-40	2.32E-36
RP11-720L2.2	-3.360306188	3.613693572	7.97E-37	3.01E-33
MBNL1-AS1	-2.890098457	8.535109417	1.73E-35	4.90E-32
RP11-380D23.1	-3.929502134	5.467847224	2.12E-33	4.79E-30
CTD-2647E9.3	-2.738058426	4.601971327	1.32E-32	2.50E-29
ATP1B3-AS1	-2.512165702	6.170458397	2.81E-32	4.55E-29
RP11-753H16.5	-2.672739403	4.498713319	5.95E-32	7.48E-29
RP11-22H5.2	-3.19419286	4.452740583	1.96E-31	2.22E-28
XXyac-YX65C7_A.2	-3.149517791	5.176243387	2.29E-30	2.16E-27

**Table S1** (continued)

**Table S1** (continued)

lncRNA	logFC	logCPM	PValue	FDR
RP11-465B22.8	3.229998114	7.44524169	3.78E-29	2.67E-26
U47924.27	3.141678103	6.86806041	7.44E-29	4.95E-26
U47924.29	2.826951987	4.603599682	1.26E-25	5.08E-23
FAM83H-AS1	3.958170755	9.389238858	1.58E-25	5.95E-23
C1orf147	2.572962546	5.607313286	3.35E-24	9.26E-22
RP11-22C11.2	2.919838778	5.988782	5.27E-24	1.41E-21
RP11-473M20.5	2.866837745	6.693075791	8.41E-24	2.07E-21
RP4-569M23.2	2.53751859	7.512388024	3.11E-23	6.28E-21
AC073046.25	2.057664512	6.150134287	6.21E-23	1.12E-20
RP11-435O5.2	2.150224405	6.393448529	7.01E-23	1.24E-20
hsa-mir-133a-1	-3.123679701	7.778774524	2.21E-13	5.47E-12
hsa-mir-133a-2	-3.121359147	7.77946003	2.54E-13	6.13E-12
hsa-mir-873	-3.100210187	3.341201683	2.78E-11	3.95E-10
hsa-mir-133b	-2.855327099	1.945475308	1.80E-08	1.61E-07
hsa-mir-202	-2.724034421	0.84631269	1.69E-07	1.25E-06
hsa-mir-1-2	-2.643892028	10.72815455	1.09E-09	1.25E-08
hsa-mir-1-1	-2.63294447	10.64051555	1.56E-09	1.74E-08
hsa-mir-143	-2.534166876	15.66352197	1.80E-15	6.25E-14
hsa-mir-139	-2.516027773	7.164410618	9.63E-17	4.39E-15
hsa-mir-876	-2.507773051	0.232650124	8.96E-07	5.18E-06
hsa-mir-200b	4.504168715	14.3696645	1.92E-34	1.66E-31
hsa-mir-200c	3.993082006	14.32096226	1.80E-30	6.69E-28
hsa-mir-182	5.161618639	12.60503609	2.31E-30	6.69E-28
hsa-mir-183	4.927002062	11.65678037	2.07E-28	4.49E-26
hsa-mir-429	4.227596071	11.253198	3.26E-27	5.66E-25
hsa-mir-1307	2.450045098	7.96356071	5.24E-26	7.57E-24
hsa-mir-200a	4.095845848	12.12704419	1.30E-25	1.61E-23
hsa-mir-96	4.666652668	7.180974872	9.79E-23	7.71E-21
hsa-mir-425	2.465213335	10.47962229	7.67E-19	5.54E-17
hsa-mir-556	3.757866523	2.532672262	3.01E-17	1.74E-15
CREM	-2.439362866	5.301819805	9.92E-51	1.83E-46
ATP8B4	-3.013257354	5.260889567	5.71E-46	5.27E-42
KLF2	-3.196350652	3.485181239	8.88E-44	3.28E-40
NR4A3	-4.135574937	5.18026954	2.25E-42	5.94E-39
ZNF331	-2.366012989	5.798425479	1.71E-41	3.95E-38

**Table S1** (continued)

**Table S1** (continued)

lncRNA	logFC	logCPM	PValue	FDR
CRISPLD2	-3.569809933	6.619459698	2.28E-41	4.67E-38
GPRASP1	-2.359715433	5.886424608	1.45E-40	2.69E-37
C11orf96	-3.85102415	4.853093905	3.08E-38	4.75E-35
FAM65C	-2.41825427	3.810645708	3.74E-36	4.32E-33
TCEAL4	-2.046345618	6.309624404	3.64E-36	4.32E-33
ST14	3.02398522	7.566481661	9.61E-36	1.04E-32
CDC42BPG	3.044699757	4.766226251	1.64E-32	9.17E-30
LLGL2	2.44927257	6.740518983	3.42E-32	1.71E-29
FAM83H	3.431407861	5.968257159	1.28E-31	5.72E-29
DPP3	2.01130707	5.799654989	1.39E-30	4.77E-28
MAP3K9	2.483993143	5.543775372	1.73E-30	5.81E-28
MYO10	2.304734505	7.862393745	3.23E-29	8.29E-27
KDF1	2.460145427	3.701162092	5.35E-29	1.27E-26
STXBP2	2.226110239	4.541972622	1.28E-28	2.86E-26
MARVELD2	2.480561709	5.529167599	1.34E-28	2.94E-26

DElncRNAs, different expressed long noncoding RNAs; DEmiRNAs, different expressed microRNAs; DErnRNAs, different expressed messenger RNA; UCEC, uterine corpus endometrial carcinoma; TCGA, The Cancer Genome Atlas; CPTAC, Clinical Proteomic Tumor Analysis Consortium; lncRNA, long noncoding RNA; mRNA, messenger RNA; miRNA, microRNA; logFC, Log2 foldchange; logCPM, Log2 counts-per-million; FDR, false discovery rate.

**Table S2** Top 20 GO, KEGG results for TCGA (up) and CPTAC (down) databases

ID	Description	P value	Count
GO:0015267	channel activity	1.66E-28	245
GO:0022803	passive transmembrane transporter activity	2.49E-28	245
GO:0005216	ion channel activity	3.29E-24	217
GO:0022836	gated channel activity	1.65E-23	179
GO:0005261	cation channel activity	7.49E-20	170
GO:0046873	metal ion transmembrane transporter activity	2.34E-17	199
GO:0030546	signaling receptor activator activity	5.49E-17	221
GO:0048018	receptor ligand activity	6.53E-17	219
GO:0005539	glycosaminoglycan binding	1.27E-14	119
GO:0015079	potassium ion transmembrane transporter activity	9.93E-14	87
GO:0008528	G protein-coupled peptide receptor activity	2.41E-13	83
GO:0001653	peptide receptor activity	5.20E-13	84
GO:0015276	ligand-gated ion channel activity	1.20E-12	78
GO:0022834	ligand-gated channel activity	1.20E-12	78

**Table S2** (continued)

**Table S2** (continued)

ID	Description	P value	Count
GO:0034987	immunoglobulin receptor binding	3.03E-12	52
GO:0005244	voltage-gated ion channel activity	3.66E-12	100
GO:0022832	voltage-gated channel activity	3.66E-12	100
GO:0008201	heparin binding	4.09E-12	89
GO:0099094	ligand-gated cation channel activity	4.68E-12	64
GO:0022843	voltage-gated cation channel activity	6.62E-12	77
hsa04080	Neuroactive ligand-receptor interaction	3.78E-24	181
hsa04020	Calcium signaling pathway	3.86E-12	116
hsa04270	Vascular smooth muscle contraction	2.28E-09	69
hsa04024	cAMP signaling pathway	2.42E-09	100
hsa04060	Cytokine-cytokine receptor interaction	2.52E-09	128
hsa04512	ECM-receptor interaction	8.39E-08	48
hsa04713	Circadian entrainment	1.61E-07	51
hsa04950	Maturity onset diabetes of the young	2.40E-07	20
hsa05414	Dilated cardiomyopathy	3.13E-07	50
hsa04911	Insulin secretion	3.36E-07	46
hsa05144	Malaria	3.75E-07	31
hsa05032	Morphine addiction	9.68E-07	47
hsa04022	cGMP-PKG signaling pathway	2.35E-06	74
hsa04970	Salivary secretion	5.86E-06	46
hsa04726	Serotonergic synapse	6.90E-06	54
hsa04061	Viral protein interaction with cytokine and cytokine receptor	1.06E-05	48
hsa04510	Focal adhesion	1.68E-05	83
hsa04514	Cell adhesion molecules	1.77E-05	65
hsa04930	Type II diabetes mellitus	3.45E-05	26
hsa05226	Gastric cancer	3.68E-05	64
GO:0022803	passive transmembrane transporter activity	3.53E-19	225
GO:0015267	channel activity	6.04E-19	224
GO:0030546	signaling receptor activator activity	2.62E-18	227
GO:0048018	receptor ligand activity	3.03E-18	225
GO:0022836	gated channel activity	2.16E-17	167
GO:0046873	metal ion transmembrane transporter activity	2.80E-16	198
GO:0005216	ion channel activity	3.03E-16	199
GO:0005125	cytokine activity	2.03E-15	123
GO:0015079	potassium ion transmembrane transporter activity	2.07E-14	89

**Table S2** (continued)

**Table S2** (continued)

ID	Description	P value	Count
GO:0005539	glycosaminoglycan binding	1.07E-13	118
GO:0005261	cation channel activity	1.55E-13	156
GO:0005201	extracellular matrix structural constituent	3.24E-12	90
GO:0008201	heparin binding	9.61E-12	89
GO:0005267	potassium channel activity	1.04E-11	69
GO:0022843	voltage-gated cation channel activity	1.43E-11	77
GO:0004714	transmembrane receptor protein tyrosine kinase activity	3.67E-11	42
GO:0015077	monovalent inorganic cation transmembrane transporter activity	1.35E-10	164
GO:0005244	voltage-gated ion channel activity	1.69E-10	97
GO:0022832	voltage-gated channel activity	1.69E-10	97
GO:0005249	voltage-gated potassium channel activity	2.40E-10	53
hsa04080	Neuroactive ligand-receptor interaction	1.73E-13	158
hsa04060	Cytokine-cytokine receptor interaction	7.31E-11	134
hsa04020	Calcium signaling pathway	2.00E-07	104
hsa04061	Viral protein interaction with cytokine and cytokine receptor	9.27E-07	51
hsa04972	Pancreatic secretion	5.20E-06	50
hsa00830	Retinol metabolism	6.40E-06	37
hsa04974	Protein digestion and absorption	7.39E-06	50
hsa04657	IL-17 signaling pathway	1.30E-05	46
hsa04512	ECM-receptor interaction	2.59E-05	43
hsa04024	cAMP signaling pathway	3.29E-05	88
hsa04713	Circadian entrainment	3.60E-05	46
hsa04270	Vascular smooth muscle contraction	3.79E-05	59
hsa04976	Bile secretion	5.13E-05	43
hsa04610	Complement and coagulation cascades	5.79E-05	41
hsa05150	Staphylococcus aureus infection	6.22E-05	45
hsa02010	ABC transporters	9.42E-05	25
hsa05226	Gastric cancer	0.000120482	63
hsa04726	Serotonergic synapse	0.000125788	51
hsa05414	Dilated cardiomyopathy	0.000143664	44

Gene ontology: GO; Kyoto encyclopedia of genes and genomes: KEGG; The Cancer Genome Atlas: TCGA; Clinical Proteomic Tumor Analysis Consortium: CPTAC; Extracellular matrix: ECM; Cyclic Adenosine monophosphate: cAMP; Cyclic guanosine monophosphate; cGMP; Interleukin 17: IL-17.