

Figure S1. ROC curve analysis of single lncRNAs for OSCC vs. H. AUC values are presented in the graphs. ROC, receiver operating characteristic; lncRNAs, long non-coding RNAs; OSCC, oral squamous cell carcinoma; H, healthy controls; AUC, area under the ROC curve.

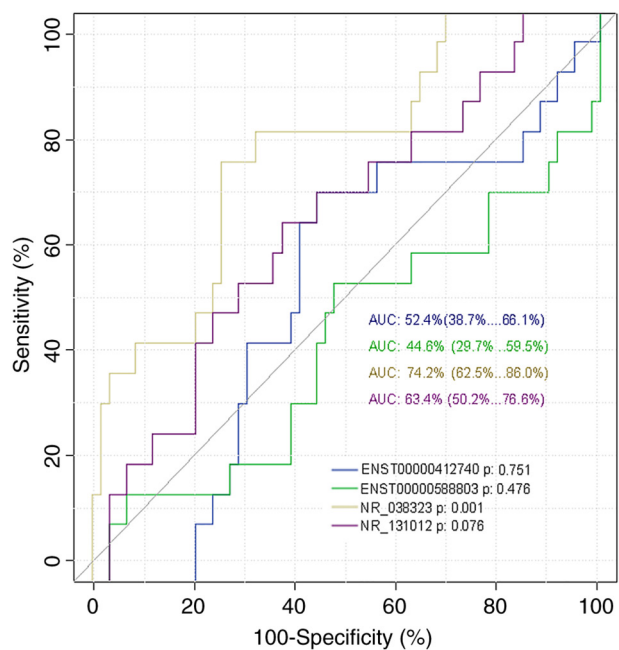


Table SI. General situation of the population for Microarray.

Sample number	Sex	Age	TNM stage	General condition
X474	Female	62	T4aN0M0	-
X574	Female	64	T3N2cM0	-
X602	Female	53	T4N3M0	-
H5	Female	60	-	Healthy
H8	Female	55	-	Healthy
H13	Female	56	-	Healthy

Table SII. TNM staging of 64 patients with OSCC.

	OSCC(N0M0)	OSCC(N)	OSCC(R)	OSCC(RN)	Total
TNM I	5		2		7
TNM II	14		7		21
TNM III	5	9		6	20
TNM IV	2	10	3	1	16
Total	26	19	12	7	64

OSCC, oral squamous cell carcinoma; N0M0, primary squamous cell carcinoma without lymph node metastasis; N, primary squamous cell carcinoma with lymph node metastasis; R, recurrent squamous cell carcinoma without lymph node metastasis; RN, recurrent squamous cell carcinoma with lymph node metastasis.

Table III. Primers of candidate lncRNAs used for RT-qPCR.

lncRNA	Bidirectional primer sequence	AT(°C)	PL(bp)
<i>β-actin (H)</i>	F: 5'GTGGCCGAGGACTTTGATTG3' R: 5'CCTGTAACAACGCATCTCATATT3'	60	73
<i>ENST00000412740</i>	F: 5'CCTGGCAGAGTTTTCTAGTCC3' R: 5'CAGATACTCAAGATGGGTGGTG3'	60	75
<i>NR_131012</i>	F: 5'TAGCGGGTTTTTCAGGGTTC3' R: 5'CCAAATGTCCAAATGATGTGTG3'	60	128
<i>ENST00000427048</i>	F: 5'GATTGTGATGCACTGGGAGC3' R: 5'TCATGCGATGGCAGAAGAC3'	60	70
<i>ENST00000428809</i>	F: 5'GAGGAAGCACACAGTCAACTAA3' R: 5'TGTCCAAACACTAAGCATCAGC3'	60	93
<i>ENST00000588803</i>	F: 5'CAGTGGCACAGGCACAAAAG3' R: 5'ACAGAGGAGGGGTCAATCAAC3'	60	103
<i>NR_037605</i>	F: 5'TGCCTTAAACCAGTTGTGCC3' R: 5'GGAGCTACTTGGAGAAAGTCATG3'	60	202
<i>ENST00000533736</i>	F: 5'GCGTATCGTCTGTTTCTTCGG3' R: 5'GACTGCCTCTACCACGGTATTCT3'	60	111
<i>NR_037901</i>	F: 5'AGTGCCCTTTATGAACGCTT3' R: 5'AGTAATGGGATTGCTGGGTC3'	60	130
<i>uc021qyj.1</i>	F: 5'AGCCCAGGCAGGAACACTTA3' R: 5'TTGGGTGAGAATTTGTCATGGT3'	60	64
<i>NR_038323</i>	F: 5'GGTTACAACAATGTGGTTATCGC3' R: 5'CATTCTTTAGACCACAGCGACG3'	60	51
<i>NR_038835</i>	F: 5'GCAGCAGAACTACCCTCCAGA3' R: 5'CTCAGCCTCGCCATAAAGAT3'	60	91
<i>NR_040026</i>	F: 5'TTCAGCAGTAATGCCAAGGG3' R: 5'AGGGAGGTCATAGATTGGAACA3'	60	100
<i>NR_121182</i>	F: 5'TCAAGTTTTATCACGGACCAGG3' R: 5'CTCACTTGCCTTTGTCCTCATC3'	60	160
<i>NR_024050</i>	F: 5'TTGTCTTGCTCTGAATGTCTGC3' R: 5'AGAGTCAGAGGGTCCTGTAGAA3'	60	93

AT, annealing temperature; PL, product length.

Table SIV. Top 20 dysregulated lncRNAs in OSCC plasma compared to normal plasma (Gold level).

seqname	Upregulated lncRNAs			Downregulated lncRNAs			
	P-value	FDR	Fold change	seqname	P-value	FDR	Fold change
<i>NR_121182</i>	0.000115525	0.001056383	1765.023732	<i>NR_120658</i>	1.4011E-06	0.000113644	938.1336768
<i>NR_037605</i>	0.000409432	0.002373187	1418.509798	<i>NR_024391</i>	0.000497759	0.00268676	540.6557224
<i>NR_038323</i>	4.22299E-05	0.000625734	1407.501782	<i>ENST00000428689</i>	0.000639475	0.003168847	450.6116803
<i>ENST00000533736</i>	0.00052541	0.002772666	1108.149414	<i>ENST00000510562</i>	3.87603E-05	0.000594784	426.1323889
<i>NR_037901</i>	7.78098E-05	0.000843384	959.7284164	<i>ENST00000409758</i>	9.62852E-06	0.00029373	164.8106963
<i>NR_077225</i>	2.12045E-05	0.000435832	656.2546667	<i>NR_104192</i>	5.468E-05	0.000715941	136.1336112
<i>ENST00000476569</i>	3.30819E-07	0.000067742	605.5679045	<i>NR_046160</i>	4.63563E-05	0.000656531	128.6596239
<i>NR_104623</i>	0.002378355	0.007841349	569.9306353	<i>NR_110809</i>	0.01527971	0.032221982	123.9691067
<i>NR_110086</i>	0.000158967	0.001299354	485.7602742	<i>NR_024337</i>	3.37819E-05	0.000548649	107.3548481
<i>NR_024008</i>	1.12252E-05	0.000315798	457.1095764	<i>ENST00000411992</i>	0.002665344	0.008506083	103.9992682
<i>NR_103721</i>	2.30104E-06	0.0001459	393.6771499	<i>NR_038266</i>	0.001752956	0.006277214	96.0951491
<i>ENST00000521793</i>	4.93176E-06	0.000214923	379.0470605	<i>NR_026677</i>	0.001861504	0.006562815	95.1197224
<i>NR_110750</i>	0.00030531	0.001956709	357.7035849	<i>NR_105001</i>	4.43064E-05	0.000634755	95.0629522
<i>NR_038835</i>	6.95458E-07	0.000092149	356.4086398	<i>ENST00000512035</i>	0.002719198	0.008642621	86.4088235
<i>NR_038436</i>	9.15107E-06	0.000288651	352.1337018	<i>NR_121647</i>	1.75019E-05	0.000393097	76.7344881
<i>ENST00000453798</i>	0.000738574	0.003474776	332.0353802	<i>NR_121654</i>	0.000281094	0.001862941	59.337704
<i>NR_026929</i>	1.03759E-05	0.000301209	325.0400166	<i>NR_024423</i>	0.008482331	0.020561316	58.4311846
<i>NR_131216</i>	1.16166E-05	0.000317998	306.7368105	<i>NR_130727</i>	5.49647E-05	0.000717087	54.3634032
<i>NR_104622</i>	0.002217331	0.007447346	301.6888568	<i>NR_110631</i>	9.73309E-06	0.00029373	48.9342121
<i>NR_125929</i>	2.19191E-06	0.00014556	282.2819687	<i>NR_015453</i>	0.002406913	0.00789721	48.4349898

Table SV. Top 20 dysregulated mRNAs in OSCC plasma compared to normal plasma.

seqname	Upregulated mRNAs			Downregulated mRNAs			
	P-value	FDR	Fold change	seqname	P-value	FDR	Fold change
<i>NM_181727</i>	5.4131E-06	0.000358242	1690.026047	<i>NM_004583</i>	1.41465E-08	0.000019278	9181.50369
<i>NM_001099667</i>	5.68249E-06	0.000358636	1042.99192	<i>ENST00000451905</i>	1.39161E-06	0.000187375	7405.631594
<i>NM_002049</i>	1.43842E-05	0.000550257	995.0271172	<i>NM_001282597</i>	1.69929E-05	0.000582528	1924.102891
<i>NM_019851</i>	5.771E-10	0.00000275	967.8592835	<i>uc003afp.3</i>	6.05012E-07	0.00013104	1610.98253
<i>NM_017495</i>	0.000478354	0.003361885	964.5163161	<i>NM_004633</i>	0.001688911	0.007841036	693.9730688
<i>NM_017633</i>	0.002708421	0.010808733	831.76448	<i>NM_001306</i>	1.86413E-05	0.000606604	628.3519274
<i>NM_003154</i>	2.33261E-05	0.000686979	816.0071972	<i>NM_032141</i>	0.000246044	0.002276501	581.9631255
<i>NM_014278</i>	9.80845E-07	0.000153515	808.869396	<i>NM_014845</i>	1.25867E-06	0.000179031	578.8331081
<i>NM_001082486</i>	1.9973E-06	0.00021914	778.2244696	<i>NM_001010980</i>	0.000404901	0.003031189	494.3939459
<i>NM_144659</i>	0.000215761	0.002124177	752.8088092	<i>NM_001564</i>	4.90183E-07	0.000126128	403.3449921
<i>NM_018384</i>	5.695E-10	0.00000275	726.4878367	<i>NM_024100</i>	0.000418297	0.00309746	383.4235393
<i>NM_001083614</i>	0.000106491	0.001395952	701.2493897	<i>NM_021076</i>	0.000197245	0.002022842	343.7115923
<i>NM_139017</i>	1.41598E-08	0.000019278	667.2519625	<i>NM_007352</i>	9.15561E-05	0.001285021	342.4118452
<i>NM_016242</i>	1.12255E-05	0.000477584	634.2980075	<i>NM_015692</i>	0.000282614	0.002411197	278.9780232
<i>ENST00000418535</i>	7.50644E-06	0.000399645	622.8702687	<i>NM_001251</i>	0.000132318	0.00159216	263.3407364
<i>NM_001293626</i>	1.34241E-06	0.000187375	605.7041559	<i>NM_022769</i>	1.97486E-06	0.00021914	235.8636361
<i>NM_031949</i>	5.61149E-07	0.000126128	567.8774575	<i>NM_001004487</i>	0.000116918	0.001479715	234.5060176
<i>NM_006337</i>	2.9741E-06	0.000271536	553.121023	<i>NM_001127</i>	0.001234978	0.006293763	216.8711345
<i>NM_017896</i>	2.07938E-06	0.00021914	534.82583	<i>NM_152431</i>	4.1241E-05	0.000860016	210.9275208
<i>NM_145660</i>	0.00024807	0.00227935	530.5373828	<i>NM_000960</i>	0.001181887	0.006104816	191.3326182

Table SVI. Top 10 GO terms enriched among up-regulated mRNAs.

GO.ID	Term	Count	P-value	Enrichment score
BP				
GO:0007275	Multicellular organismal development	444	8.09221E-06	5.09193312
GO:0010524	Positive regulation of calcium ion transport into cytosol	12	2.18809E-05	4.659935541
GO:0048731	System development	389	2.87144E-05	4.541900928
GO:0060401	Cytosolic calcium ion transport	22	4.28244E-05	4.368308858
GO:0060402	Calcium ion transport into cytosol	21	0.000111095	3.954305892
GO:0010522	Regulation of calcium ion transport into cytosol	16	0.000124524	3.904746387
GO:0032502	Developmental process	494	0.000152539	3.816618053
GO:0044767	Single-organism developmental process	489	0.000170449	3.768405055
GO:0048856	Anatomical structure development	441	0.000194142	3.71188018
GO:0009967	Positive regulation of signal transduction	121	0.0002139	3.669771434
CC				
GO:0002080	Acrosomal membrane	6	0.004691156	2.328720107
GO:0044459	Plasma membrane part	213	0.005002376	2.300823628
GO:0098588	Bounding membrane of organelle	205	0.005346054	2.271966688
GO:0031224	Intrinsic component of membrane	500	0.005852918	2.23262758
GO:0031226	Intrinsic component of plasma membrane	136	0.006076047	2.216378859
GO:0005887	Integral component of plasma membrane	131	0.006291078	2.201274936
GO:0016021	Integral component of membrane	489	0.006506638	2.186643339
GO:0035861	Site of double-strand break	5	0.010682052	1.971345331
GO:0044309	Neuron spine	15	0.010968402	1.959856624
GO:0032580	Golgi cisterna membrane	12	0.014029222	1.852966401
MF				
GO:0016773	Phosphotransferase activity, alcohol group as acceptor	85	0.00012625	3.898769737
GO:0005179	Hormone activity	21	0.000547699	3.261458221
GO:0016301	Kinase activity	88	0.000585852	3.232211911
GO:0016772	Transferase activity, transferring phosphorus-containing groups	99	0.001869393	2.728299324
GO:0004672	Protein kinase activity	68	0.00245727	2.609547137
GO:0030676	Rac guanyl-nucleotide exchange factor activity	5	0.002788329	2.554655917
GO:0005524	ATP binding	148	0.003315297	2.47947753
GO:0008373	Sialyltransferase activity	6	0.004413465	2.355220273
GO:0030554	Adenyl nucleotide binding	151	0.005450622	2.263553931
GO:0032559	Adenyl ribonucleotide binding	149	0.006029415	2.219724828

Table SVII. Top 10 GO terms enriched among down-regulated mRNAs.

GO.ID	Term	Count	P-value	Enrichment score
BP				
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	45	1.92004E-15	14.71668988
GO:0006613	Cotranslational protein targeting to membrane	45	4.41354E-15	14.35521333
GO:0045047	Protein targeting to ER	45	6.62738E-15	14.17865845
GO:0070972	Protein localization to endoplasmic reticulum	49	9.60708E-15	14.01740878
GO:0072599	Establishment of protein localization to endoplasmic reticulum	45	9.89003E-15	14.00480239
GO:0006415	Translational termination	40	6.65716E-14	13.17671126
GO:0006414	Translational elongation	46	1.71717E-13	12.76518584
GO:0019083	Viral transcription	54	1.91828E-13	12.71708908
GO:0019080	Viral gene expression	56	2.18764E-13	12.66002425
GO:0043624	Cellular protein complex disassembly	58	2.38617E-13	12.62229792
CC				
GO:0022626	Cytosolic ribosome	40	6.16437E-14	13.21011163
GO:0044391	Ribosomal subunit	47	9.6904E-13	12.01365846
GO:0044445	Cytosolic part	54	3.88082E-10	9.411076229
GO:0005840	Ribosome	57	4.7347E-10	9.324707092
GO:0022625	Cytosolic large ribosomal subunit	24	6.55126E-10	9.183674909
GO:0015934	Large ribosomal subunit	27	2.11683E-08	7.674313548
GO:0005737	Cytoplasm	1247	1.12331E-07	6.949498973
GO:0030529	Ribonucleoprotein complex	117	1.5921E-07	6.798029857
GO:0031982	Vesicle	486	8.81425E-07	6.054814527
GO:0005829	Cytosol	386	1.76965E-06	5.752112963
MF				
GO:0003735	Structural constituent of ribosome	52	1.302E-13	12.88538741
GO:0005198	Structural molecule activity	109	5.30456E-06	5.275350528
GO:0005515	Protein binding	1052	0.000290507	3.536843247
GO:0015250	Water channel activity	6	0.000354436	3.450462419
GO:0003723	RNA binding	220	0.000395624	3.4027174
GO:0044822	Poly(A) RNA binding	168	0.000630598	3.200247301
GO:0005372	Water transmembrane transporter activity	6	0.000702395	3.153418279
GO:0051287	DNA binding	14	0.001108015	2.955454442
GO:0009055	Electron carrier activity	22	0.002151344	2.667290227
GO:0015144	Carbohydrate transmembrane transporter activity	9	0.002663747	2.574506957

Table SVIII. The KEGG pathways enriched among up-regulated mRNAs.

Pathway ID	Definition	Fisher-P-value	Enrichment score
hsa05100	Bacterial invasion of epithelial cells- <i>Homo sapiens</i> (human)	0.0124945	1.903281
hsa04142	Lysosome- <i>Homo sapiens</i> (human)	0.01407855	1.851442
hsa00051	Fructose and mannose metabolism- <i>Homo sapiens</i> (human)	0.0151138	1.820626
hsa03410	Base excision repair- <i>Homo sapiens</i> (human)	0.01783358	1.748762
hsa04622	RIG-I-like receptor signaling pathway- <i>Homo sapiens</i> (human)	0.03077788	1.511761
hsa04060	Cytokine-cytokine receptor interaction- <i>Homo sapiens</i> (human)	0.03648067	1.437937
hsa00830	Retinol metabolism- <i>Homo sapiens</i> (human)	0.04360679	1.360446
hsa00534	Glycosaminoglycan biosynthesis-heparan sulfate/heparin- <i>Homo sapiens</i> (human)	0.04608181	1.336471

Table SIX. The KEGG pathways enriched among down-regulated mRNAs.

Pathway ID	Definition	Fisher-P-value	Enrichment score
hsa03010	Ribosome- <i>Homo sapiens</i> (human)	7.27343E-13	12.138261
hsa00920	Sulfur metabolism- <i>Homo sapiens</i> (human)	0.004121151	2.384982
hsa00190	Oxidative phosphorylation- <i>Homo sapiens</i> (human)	0.005486373	2.260715
hsa04066	HIF-1 signaling pathway- <i>Homo sapiens</i> (human)	0.01272673	1.895283
hsa04514	Cell adhesion molecules (CAMs)- <i>Homo sapiens</i> (human)	0.01321087	1.879068
hsa05012	Parkinson's disease- <i>Homo sapiens</i> (human)	0.01321087	1.879068
hsa03050	Proteasome- <i>Homo sapiens</i> (human)	0.01522627	1.817407
hsa04721	Synaptic vesicle cycle- <i>Homo sapiens</i> (human)	0.01884585	1.724784
hsa00750	Vitamin B6 metabolism- <i>Homo sapiens</i> (human)	0.02785578	1.555085
hsa04932	Non-alcoholic fatty liver disease (NAFLD)- <i>Homo sapiens</i> (human)	0.02796907	1.553322
hsa04141	Protein processing in endoplasmic reticulum- <i>Homo sapiens</i> (human)	0.03821527	1.417763
hsa04072	Phospholipase D signaling pathway- <i>Homo sapiens</i> (human)	0.04577701	1.339353
hsa05016	Huntington's disease- <i>Homo sapiens</i> (human)	0.04654968	1.332083
hsa04976	Bile secretion- <i>Homo sapiens</i> (human)	0.04827333	1.316293