

Title: Establishing molecular biomarkers for efficient demarcation of tumor and non-tumor tissue in Oral Squamous Cell Carcinoma

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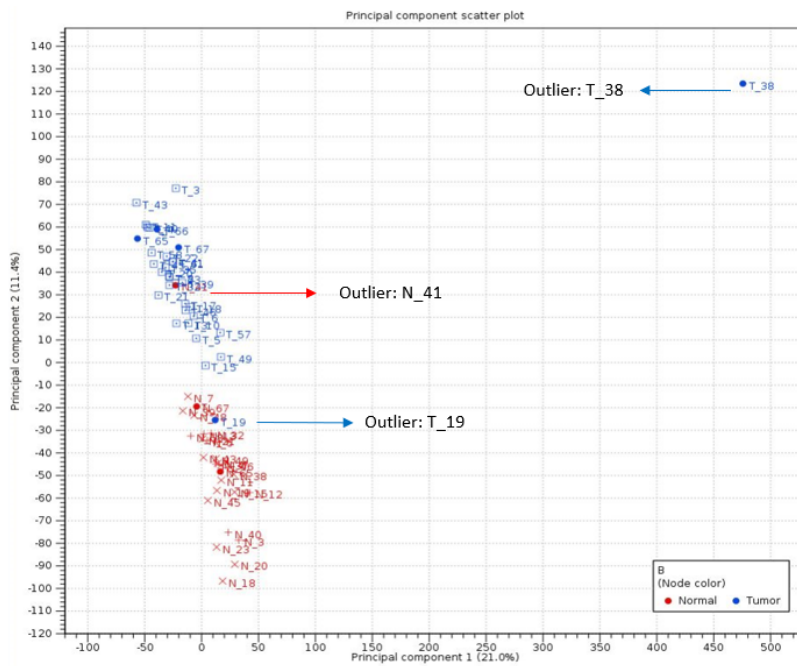
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Supplementary table. 1 Sample information/ details.

	Tumour samples	Normal samples	Age	Sex	Stage	Consumption type
1	T_3	N_3	44	Male	Stage-4	Pan-masala
2	T_4	N_4	40	Male	Stage-1	Tobacco
3	T_5		54	Female	Stage-4	None
4	T_6	N_6	55	Male	Stage-4	Tobacco chewing
5		N_7	-	Male	Stage-1	None
6	T_8	-	34	Male	Stage-1	None
7	T_10	-	60	Male	Stage-3	Tobacco, smoking
8	T_11	N_11	50	Male	Stage-2	Tobacco chewing (2 pk/day)
9	-	N_12	64	Male	Stage-4	Bidi, gutkha
10	T_13	N_13	60	Male	Stage-4	Bidi, gutkha
11	T_15	N_15	55	Male	Stage-2	Tobacco chewing
12	T_17	-	51	Male	Stage-1	Tobacco chewing
13	T_18	N_18	44	Male	Stage-2	Tobacco chewing
14	-	N_19	51	Male	Stage-1	Tobacco chewing
15	T_20	N_20	-	Male	Stage-2	Tobacco chewing
16	T_21	N_21	53	Male	Stage-1	Tobacco chewing
17	T_22	-	-	Male	Stage-2	Tobacco chewing
18	T_23	N_23	38	Male	Stage-2	Tobacco chewing
19	T_32	N_32	42	Male	Stage-4	Tobacco chewing
20	T_35	-	42	Male	Stage-1	Tobacco Chewing
21	-	N_37	46	Male	Stage-4	-
22	-	N_38	36	Male	Stage-2	-
23	T_39	N_39	56	Male	Stage-2	-
24	T_40	N_40	37	Male	Stage-4	-
25	T_41	-	53	Male	Stage-1	-
26	T_43	N_43	39	Male	stage-3	-
27	T_45	N_45	49	Male	stage-2	-
28	T_46	N_46	49	Male	stage-1	-
29	-	N_48	46	Male	stage-2	-
30	T_49	N_49	41	Male	stage-2	-
31	T_57	-	71	Male	stage-1	-
32	T_58	N_58	48	Male	stage-4	-
33	T_61	-	40	Male	stage-3	-
34	T_65	N_65	52	Male	-	-
35	T_66	-	-	-	-	-
36	T_67	N_67	-	-	-	-

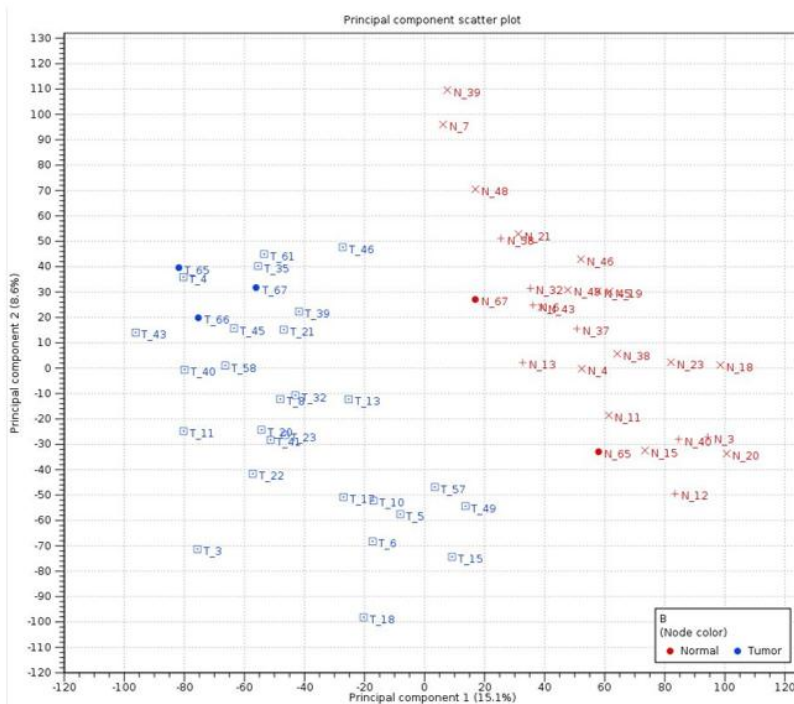
Supplementary fig. 1 (a) PCA plot of 32 tumor and 27 adjacent normal samples identifying 3 outliers in the dataset. **(b)** PCA plot after removing the identified outliers.

(a)



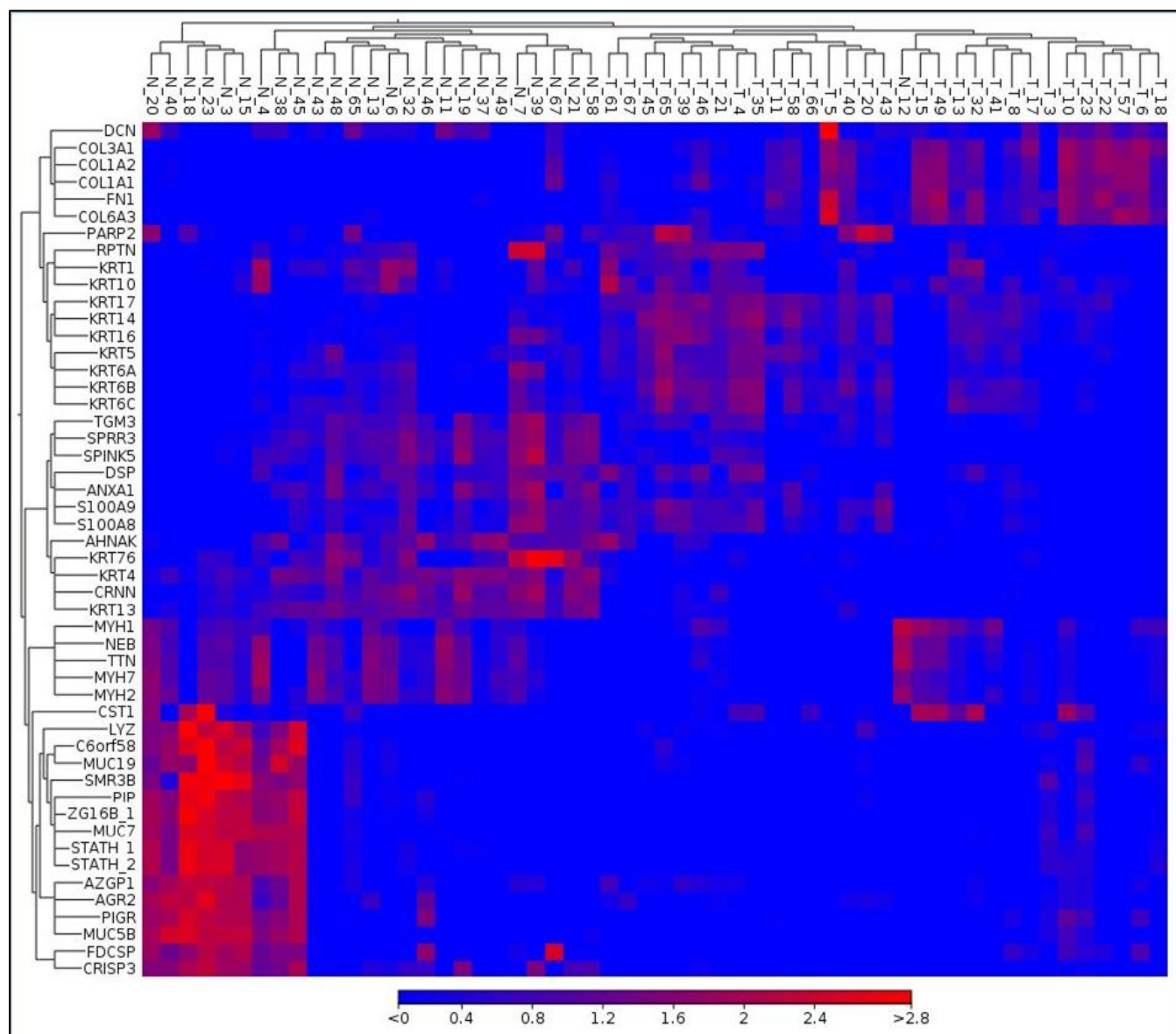
Outliers: T_19, T_38, N_41

(b)



After removing outliers

Supplementary fig. 2 Heat map for visualizing gene expression levels in all the tumor and adjacent normal samples.



Supplementary table. 2 (a) top 100 upregulated genes and **(b)** top 100 downregulated genes sorted based on their log2 fold change. Genes marked with * are significant in HNSC (based on TCGA database validation).

(a)

	Name	Max group mean	Log2 fold change	FDR p-value
1	<i>MAGEA6</i>	5.084	8.683	0.000
2	<i>MAGEA1</i>	2.094	8.032	0.000
3	<i>MAGEC1</i>	0.425	7.921	0.000
4	<i>MMP1*</i>	520.547	7.904	0.000
5	<i>CT45A10</i>	2.542	7.839	0.000
6	<i>PTPRN</i>	1.003	7.504	0.000
7	<i>TMPRSS15</i>	0.331	7.498	0.000
8	<i>GAGE1</i>	0.608	7.374	0.000
9	<i>CT45A1</i>	2.120	7.371	0.000
10	<i>MAGEA4</i>	4.724	7.330	0.000
11	<i>MMP10*</i>	64.527	7.254	0.000
12	<i>MAGEA3</i>	4.201	7.249	0.000
13	<i>CT45A3</i>	1.386	7.132	0.000
14	<i>PAGE5</i>	1.975	6.980	0.000
15	<i>GAGE12J</i>	1.537	6.975	0.000
16	<i>SSX2B</i>	0.532	6.795	0.000
17	<i>IL24*</i>	18.206	6.694	0.000
18	<i>MAGEA9</i>	0.953	6.693	0.000
19	<i>MMP13*</i>	74.945	6.676	0.000
20	<i>MAGEA11</i>	1.140	6.462	0.000
21	<i>LHX1 2</i>	0.217	6.439	0.000
22	<i>XAGE1A</i>	1.014	6.373	0.000
23	<i>SPANXA1</i>	1.812	6.240	0.000
24	<i>DEFB4B 1</i>	23.109	6.235	0.000
25	<i>HSPA1A 1</i>	0.300	6.234	0.000
26	<i>IL11*</i>	3.953	6.163	0.000
27	<i>GAGE2A</i>	1.197	6.107	0.000
28	<i>CDSN 5</i>	0.743	5.917	0.000
29	<i>CDSN 4</i>	0.737	5.901	0.000
30	<i>SPANXD</i>	0.863	5.895	0.000
31	<i>MMP11 1</i>	13.560	5.871	0.000
32	<i>SAGE1</i>	0.157	5.870	0.000
33	<i>PRAME 1</i>	0.483	5.829	0.000
34	<i>MAGEA10</i>	0.180	5.774	0.000
35	<i>CSAG3*</i>	2.353	5.758	0.000
36	<i>CDSN 1</i>	1.614	5.739	0.000
37	<i>TDO2 2</i>	10.161	5.728	0.000
38	<i>PRAME 2</i>	0.419	5.678	0.000
39	<i>HTR2C</i>	0.115	5.670	0.000
40	<i>TRIML2</i>	0.456	5.659	0.000
41	<i>TDO2 1</i>	9.756	5.652	0.000
42	<i>AMTN</i>	35.367	5.651	0.000
43	<i>MMP11 2</i>	13.367	5.620	0.000
44	<i>IGF2BP1</i>	0.328	5.603	0.000

45	<i>MAGEA2</i>	0.151	5.590	0.000
46	<i>MMP3*</i>	181.501	5.567	0.000
47	<i>MAGEA9B</i>	0.301	5.566	0.000
48	<i>ISG15*</i>	259.294	5.548	0.000
49	<i>GAGE12B</i>	0.788	5.483	0.000
50	<i>LHX1 1</i>	0.102	5.436	0.000
51	<i>CA9*</i>	2.328	5.385	0.000
52	<i>CCL11</i>	6.444	5.351	0.000
53	<i>LIN28B</i>	0.056	5.323	0.000
54	<i>LHX5</i>	0.127	5.269	0.000
55	<i>CNGB1</i>	2.705	5.228	0.000
56	<i>MMP12*</i>	71.452	5.210	0.000
57	<i>PAEP</i>	1.064	5.208	0.000
58	<i>CT45A2</i>	0.234	5.188	0.000
59	<i>LOC102723971</i>	0.152	5.171	0.000
60	<i>MAGEB2</i>	1.393	5.146	0.000
61	<i>CSAG1</i>	0.384	5.141	0.000
62	<i>XAGE1B</i>	0.400	5.066	0.000
63	<i>GPR50</i>	0.379	5.047	0.000
64	<i>DNAH17*</i>	2.084	5.043	0.000
65	<i>POTEF</i>	0.192	5.020	0.000
66	<i>ZP4</i>	0.143	4.991	0.000
67	<i>CTAG2</i>	0.290	4.904	0.000
68	<i>ADAM12*</i>	8.897	4.900	0.000
69	<i>MAGEA2B</i>	0.096	4.900	0.000
70	<i>GAGE13</i>	0.496	4.881	0.000
71	<i>CSF2</i>	6.511	4.860	0.000
72	<i>FGG</i>	0.084	4.760	0.000
73	<i>CXCL6</i>	15.278	4.758	0.000
74	<i>CT45A8</i>	0.217	4.738	0.000
75	<i>METTL11B</i>	0.099	4.738	0.000
76	<i>GAST</i>	1.409	4.667	0.000
77	<i>SPANXB1</i>	0.944	4.638	0.000
78	<i>SLC37A4 1</i>	0.073	4.638	0.000
79	<i>DAZ3</i>	0.066	4.584	0.000
80	<i>KLF17</i>	0.057	4.569	0.000
81	<i>CXCL11*</i>	37.445	4.561	0.000
82	<i>CDSN 6</i>	7.655	4.557	0.000
83	<i>NETO1</i>	0.232	4.536	0.000
84	<i>HOXC11</i>	0.248	4.512	0.000
85	<i>LOC105375816</i>	0.109	4.494	0.000
86	<i>CER1</i>	0.185	4.467	0.000
87	<i>SI00A7A*</i>	23.728	4.455	0.000
88	<i>HOXA9</i>	0.187	4.439	0.000
89	<i>KHDC1L*</i>	3.978	4.426	0.000
90	<i>GRP</i>	0.151	4.420	0.000
91	<i>KRT82</i>	0.062	4.407	0.000
92	<i>SOST</i>	1.449	4.373	0.000
93	<i>PII5</i>	11.585	4.356	0.000
94	<i>BEST2</i>	0.242	4.353	0.000
95	<i>BRDT</i>	0.045	4.340	0.000
96	<i>COL22A1</i>	1.448	4.337	0.000
97	<i>DAZ4</i>	0.042	4.327	0.000

98	<i>MLXIP 2</i>	0.019	4.275	0.000
99	<i>SOHLH1</i>	0.032	4.270	0.000
100	<i>NLRP7 3</i>	0.081	4.259	0.000

(b)

	Name	Max group mean	Log2 fold change	FDR p- value
1	<i>PRR27 1</i>	10.980	-10.709	0.000
2	<i>ZG16B 1</i>	2841.185	-10.598	0.000
3	<i>ZG16B 2</i>	2845.669	-10.578	0.000
4	<i>PIP*</i>	1426.734	-10.546	0.000
5	<i>PRR4 2</i>	467.942	-10.339	0.000
6	<i>LPO</i>	29.192	-10.315	0.000
7	<i>C6orf58</i>	176.418	-10.252	0.000
8	<i>SMR3B</i>	678.331	-10.170	0.000
9	<i>STATH 1</i>	1133.550	-10.100	0.000
10	<i>PRR4 3</i>	469.622	-10.088	0.000
11	<i>SLC13A2</i>	2.559	-10.064	0.000
12	<i>PRR27 2</i>	11.302	-9.983	0.000
13	<i>CLDN22</i>	3.324	-9.936	0.000
14	<i>PRR4 1</i>	467.381	-9.934	0.000
15	<i>KRT36</i>	41.508	-9.836	0.000
16	<i>STATH 2</i>	1127.723	-9.733	0.000
17	<i>OPRPN</i>	79.627	-9.661	0.000
18	<i>MUC5B</i>	162.193	-9.284	0.000
19	<i>MUC19</i>	14.255	-9.208	0.000
20	<i>LACRT</i>	16.915	-9.150	0.000
21	<i>MUC7</i>	344.789	-9.130	0.000
22	<i>ADIPOQ</i>	7.245	-9.096	0.000
23	<i>CIDEA</i>	4.650	-9.066	0.000
24	<i>HTN1 1</i>	128.625	-8.995	0.000
25	<i>PLIN1</i>	12.508	-8.929	0.000
26	<i>TFF3*</i>	131.549	-8.626	0.000
27	<i>CRISP3*</i>	504.455	-8.597	0.000
28	<i>HTN1 2</i>	125.931	-8.596	0.000
29	<i>TFF1</i>	15.588	-8.537	0.000
30	<i>KRT76</i>	116.356	-8.490	0.000
31	<i>ITLN1</i>	14.637	-8.462	0.000
32	<i>MUC21 7</i>	9.481	-8.433	0.000
33	<i>CST4</i>	58.055	-8.340	0.000
34	<i>SCGB1D2</i>	5.274	-8.334	0.000
35	<i>TTR</i>	12.384	-8.242	0.000
36	<i>KRTAP13-2</i>	4.048	-8.231	0.000
37	<i>BPIFB2</i>	266.892	-8.184	0.000
38	<i>SCGB2A2</i>	23.066	-8.168	0.000
39	<i>CAPN9</i>	1.356	-8.111	0.000
40	<i>GP2</i>	1.433	-8.107	0.000
41	<i>HMGCS2</i>	11.063	-8.071	0.000
42	<i>LRRC31</i>	0.806	-8.035	0.000
43	<i>CST2</i>	15.410	-8.021	0.000

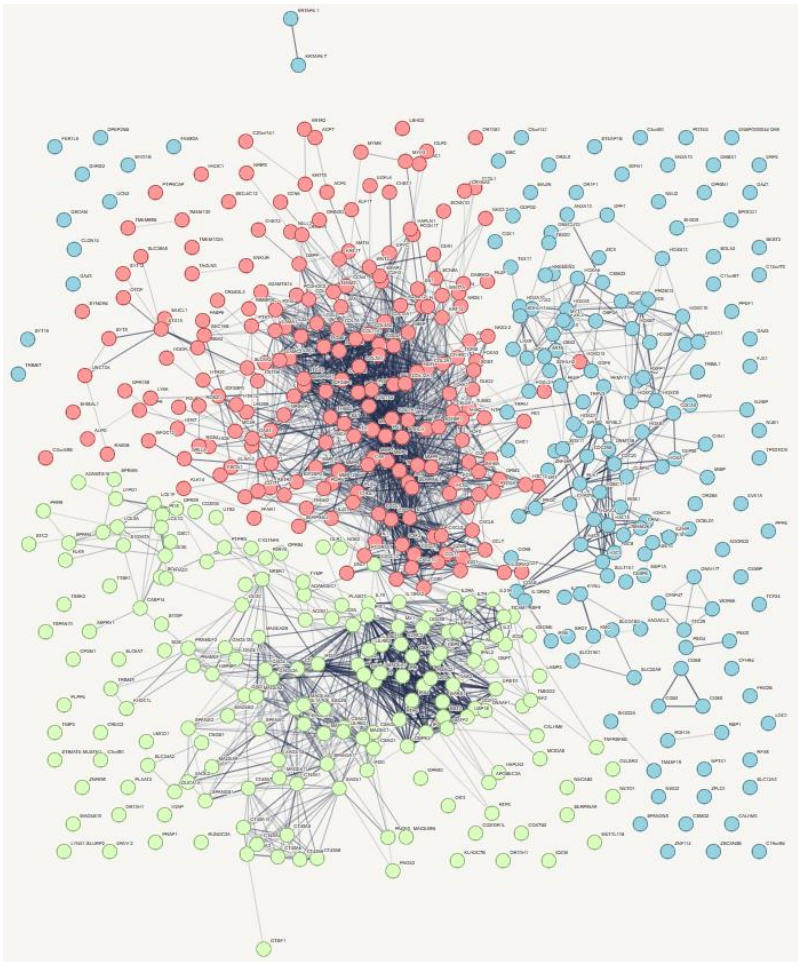
44	<i>SCGB3A1*</i>	52.109	-7.991	0.000
45	<i>LRRC26</i>	1.957	-7.952	0.000
46	<i>CST5</i>	2.189	-7.921	0.000
47	<i>PPP1R1B*</i>	11.291	-7.888	0.000
48	<i>PRB3 1</i>	3.821	-7.870	0.000
49	<i>DMBT1</i>	45.352	-7.737	0.000
50	<i>ADH1B*</i>	18.877	-7.687	0.000
51	<i>ODAM</i>	22.801	-7.600	0.000
52	<i>WIF1</i>	3.546	-7.597	0.000
53	<i>KRTAP13-1</i>	2.412	-7.593	0.000
54	<i>MGAM2 2</i>	0.270	-7.573	0.000
55	<i>MUC21 1</i>	58.839	-7.573	0.000
56	<i>TRARG1</i>	1.233	-7.565	0.000
57	<i>MYOC</i>	5.881	-7.468	0.000
58	<i>TSPAN8</i>	22.127	-7.420	0.000
59	<i>PIGR*</i>	543.607	-7.395	0.000
60	<i>KRT4*</i>	5263.881	-7.326	0.000
61	<i>HEPACAM</i>	0.416	-7.309	0.000
62	<i>BPIFB6</i>	0.675	-7.138	0.000
63	<i>CHRM1</i>	3.444	-7.074	0.000
64	<i>KRT85</i>	1.480	-7.072	0.000
65	<i>MUC21 4</i>	27.141	-7.068	0.000
66	<i>SPDEF</i>	7.887	-7.065	0.000
67	<i>SCGB1D1</i>	1.984	-7.049	0.000
68	<i>CSN3</i>	1.352	-7.036	0.000
69	<i>CSN2 1</i>	0.789	-7.012	0.000
70	<i>MUC21 2</i>	27.207	-7.005	0.000
71	<i>KRTAP3-1 1</i>	1.451	-6.984	0.000
72	<i>PRB3 2</i>	3.887	-6.969	0.000
73	<i>DCT</i>	9.186	-6.936	0.000
74	<i>KRT84</i>	35.592	-6.868	0.000
75	<i>KRTAP3-3 1</i>	1.044	-6.781	0.000
76	<i>KRTAP3-3 2</i>	1.035	-6.774	0.000
77	<i>SCGB2A1</i>	5.626	-6.748	0.000
78	<i>LMAN1L</i>	1.668	-6.747	0.000
79	<i>TOX3</i>	0.738	-6.679	0.000
80	<i>ERN2</i>	2.817	-6.660	0.000
81	<i>DHRS7C</i>	4.676	-6.647	0.000
82	<i>CLCNKB</i>	0.557	-6.614	0.000
83	<i>RBP4</i>	2.404	-6.604	0.000
84	<i>MUC22 4</i>	0.113	-6.594	0.000
85	<i>KLK1</i>	10.935	-6.511	0.000
86	<i>FAM3B*</i>	13.387	-6.505	0.000
87	<i>TMEM213</i>	1.193	-6.468	0.000
88	<i>MUC21 3</i>	10.096	-6.456	0.000
89	<i>KRTAP3-2 2</i>	1.307	-6.450	0.000
90	<i>GRIA2</i>	0.596	-6.434	0.000
91	<i>ENTPD8</i>	0.855	-6.424	0.000
92	<i>FLOT1 2</i>	0.954	-6.419	0.000
93	<i>NPY5R</i>	0.119	-6.403	0.000
94	<i>KRTAP3-2 1</i>	1.232	-6.375	0.000
95	<i>ELAPOR1</i>	17.254	-6.349	0.000
96	<i>FDCSP</i>	453.363	-6.339	0.000

97	<i>AGR2</i>	212.646	-6.319	0.000
98	<i>DNASE2B</i>	0.456	-6.316	0.000
99	<i>KRTAP3-1 2</i>	1.502	-6.314	0.000
100	<i>Cl4orf180 2</i>	0.196	-6.155	0.000

Supplementary fig. 3 (a) PPI network and K-mean clustering for the upregulated genes. Out of the 704 upregulated genes, 217 genes are in Cluster 1 (red), 177 genes are in Cluster 2 (green), and 170 genes are in Cluster 3 (blue).

(b) for each of these three different clusters, the top 20 nodes were identified through Cytohubba in Cytoscape. Marked with * are genes significant in HNSC and marked with ** are genes significant in HNSC present in the top 100. Cluster 1 contains a significant number of genes associated with HNSC.

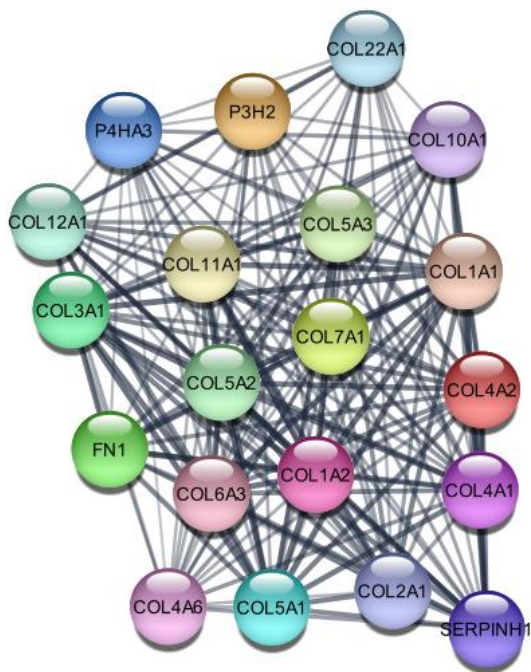
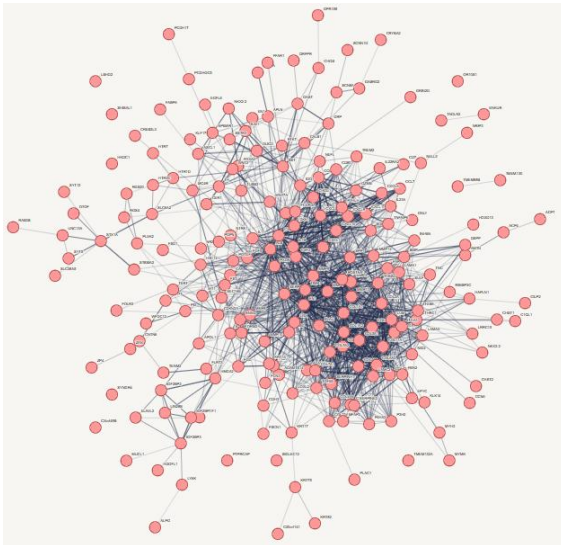
(a)



Clusters:		
Color	Cluster ID	Gene count
Red	Cluster 1	217
Green	Cluster 2	177
Blue	Cluster 3	170

(b)

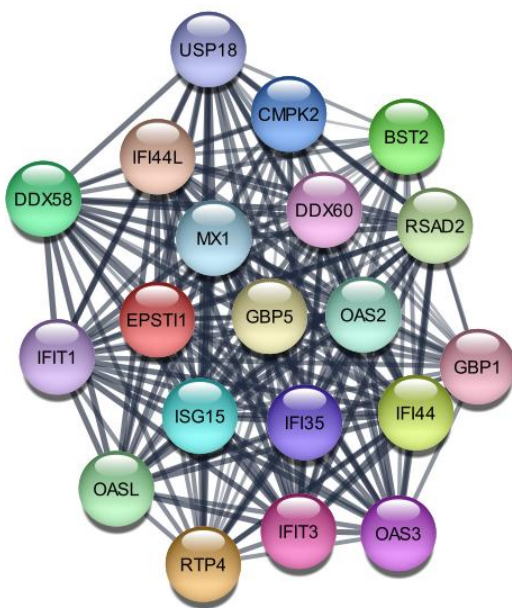
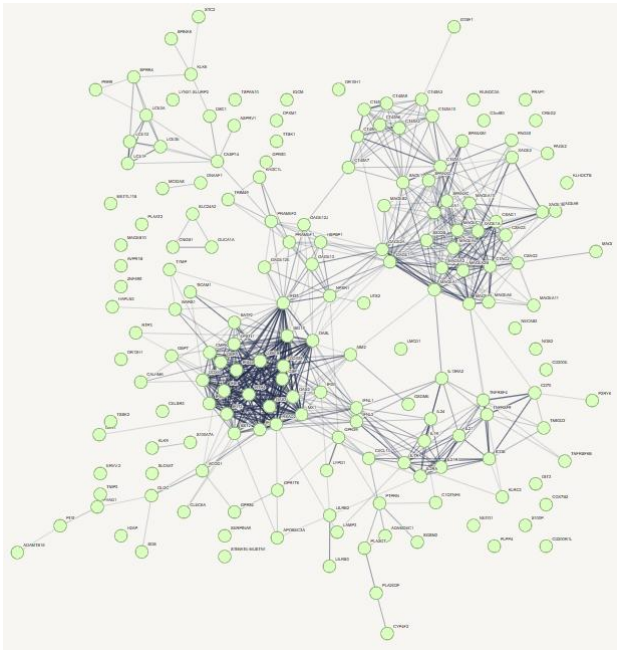
Cluster 1



Cluster 1: Cytohubba (top 20 nodes)

P4HA3, COL10A1, COL3A1*, COL5A2*, COL6A3*, COL5A1*, COL11A1*, COL2A1, COL5A3, COL4A2*, COL4A6*, COL22A1, COL4A1*, COL1A2*, COL12A1*, COL7A1*, P3H2*, FN1*, SERPINH1*, COL1A1**

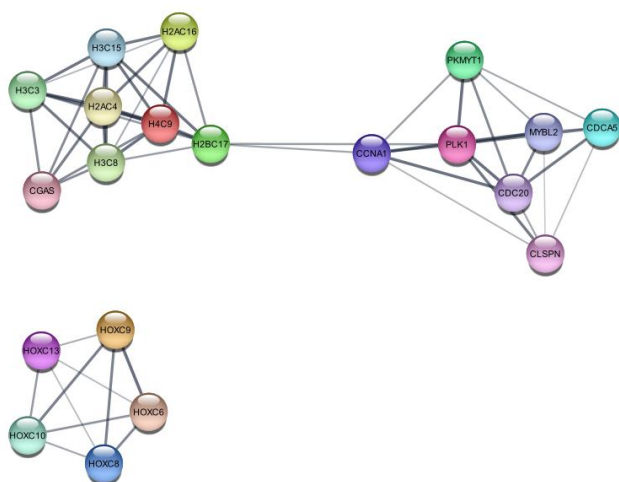
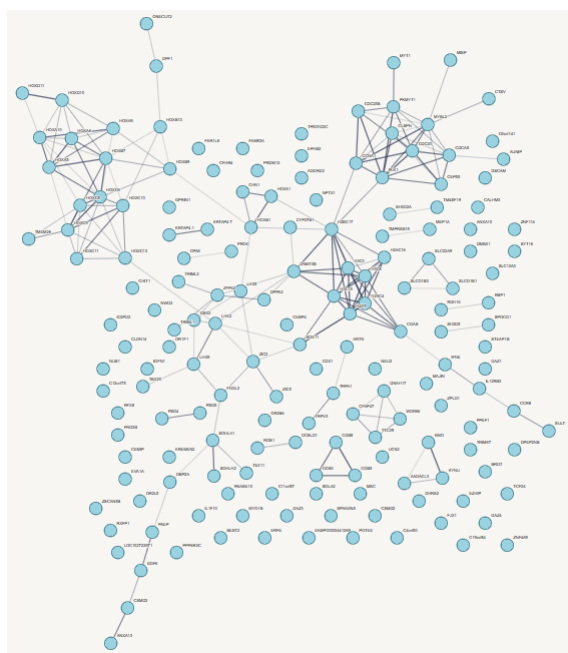
Cluster 2



Cluster 2: Cytohubba (top 20 nodes)

*GBP5**, *USP18*, *MX1*, *RTP4*, *IFI35*, *ISG15***, *DDX58*, *OAS2*, *EPSTI1**, *IFI44**, *RSAD2**, *GBP1*, *IFIT3**, *BST2**, *DDX60*, *IFI44L*, *OASL**, *IFIT1*, *OAS3*, *CMPK2*

Cluster 3



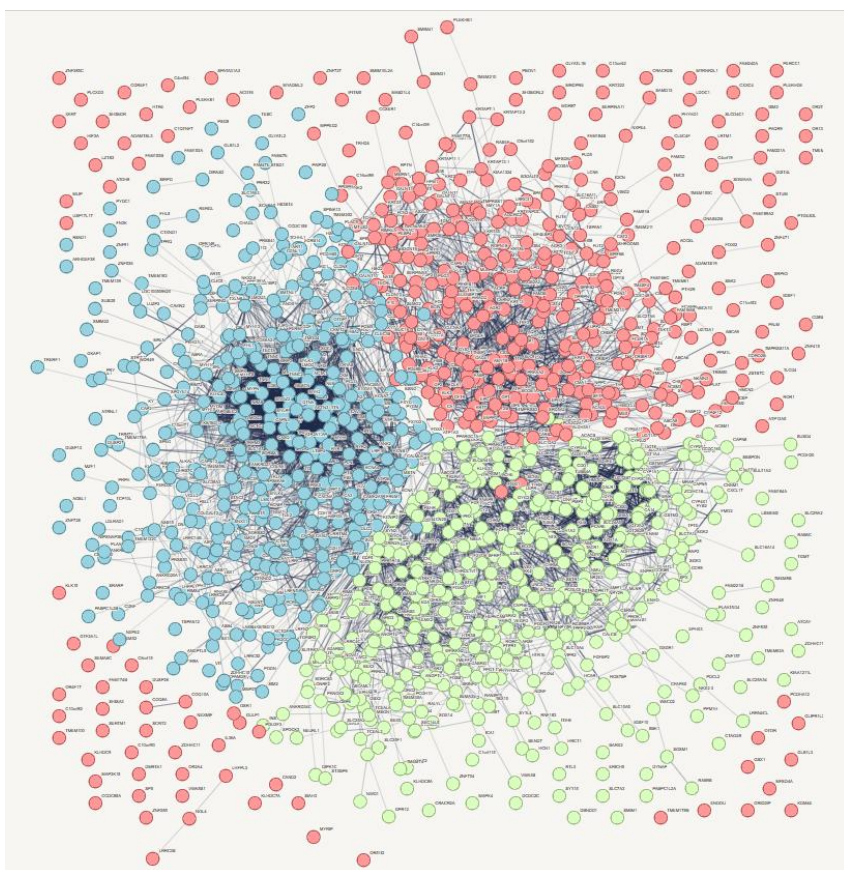
Cluster 3: Cytohubba (top 20 nodes)

*HOXC10**, *HOXC9*, *H3C8*, *CDC20*, *CCNA1*, *H2AC4*, *H4C9*, *HOXC6*, *H2AC16*, *HOXC13**, *MYBL2**, *CLSPN*, *PKMYT1**, *H2BC17*, *CDCA5**, *CGAS*, *H3C3*, *PLK1*, *HOXC8*, *H3C15*

Supplementary fig. 4 (a) PPI network and K-mean clustering for the downregulated genes. Out of the 1540 downregulated genes, 443 genes are in Cluster 1 (red), 440 genes are in Cluster 2 (green) and 419 genes are in Cluster 3 (blue).

(b) for each of these three different clusters, the top 20 nodes were identified through Cytohubba in Cytoscape. Marked with * are genes significant in HNSC and marked with ** are genes significant in HNSC present in the top 100. Cluster 3 contains a significant number of genes associated with HNSC.

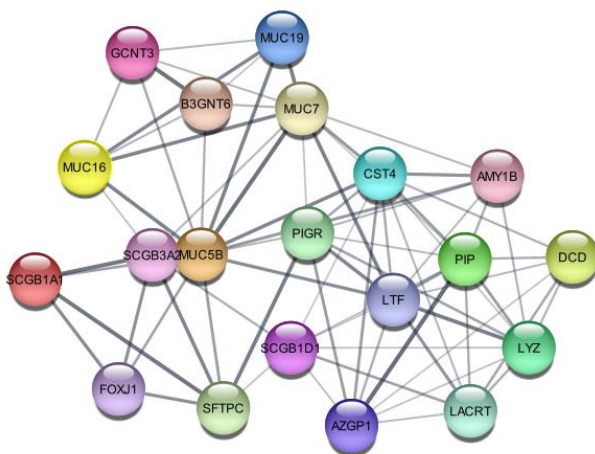
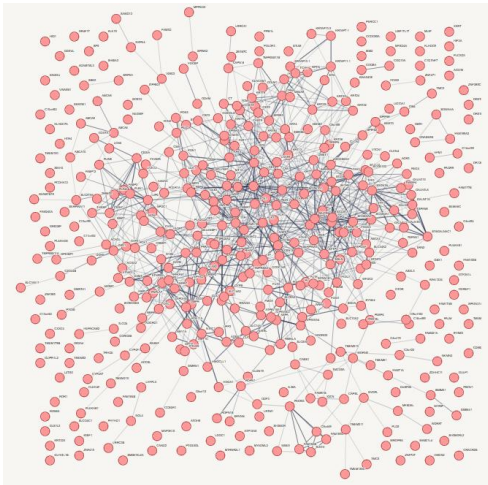
(a)



Clusters:		
Color	Cluster ID	Gene count
Red	Cluster 1	443
Green	Cluster 2	440
Blue	Cluster 3	419

(b)

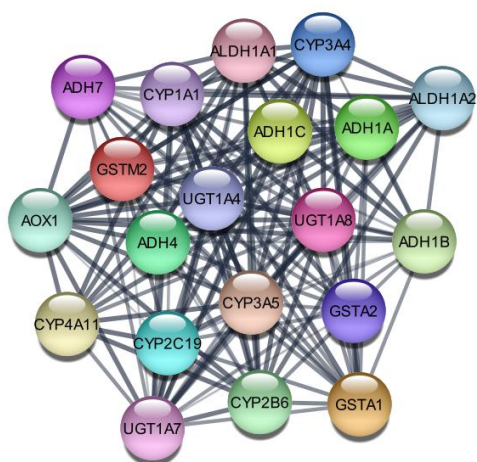
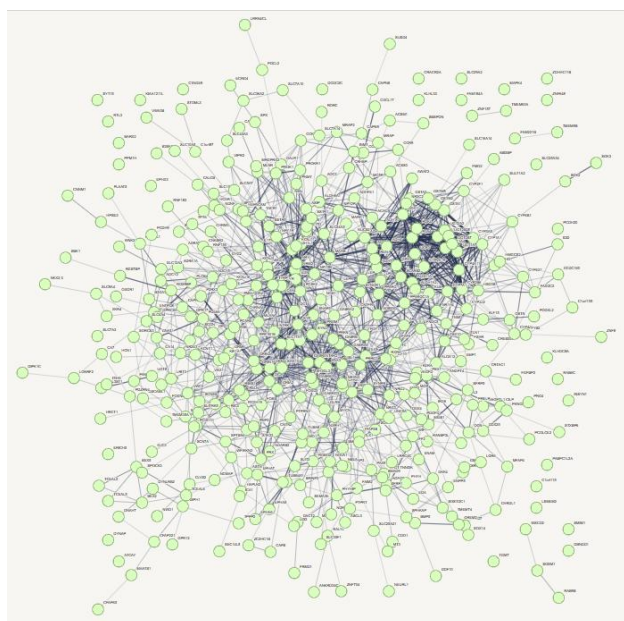
Cluster 1



Cluster 1: Cytohubba (top 20 nodes)

*AZGP1**, *GCNT3**, *SCGB1A1*, *MUC16*, *CST4*,
MUC5B, *LYZ*, *SFTPC*, *PIP***, *MUC19*, *MUC7*, *LTF**,
SCGB3A2, *LACRT*, *PIGR***, *SCGB1D1*, *DCD*,
B3GNT6, *AMY1B*, *FOXJ1*

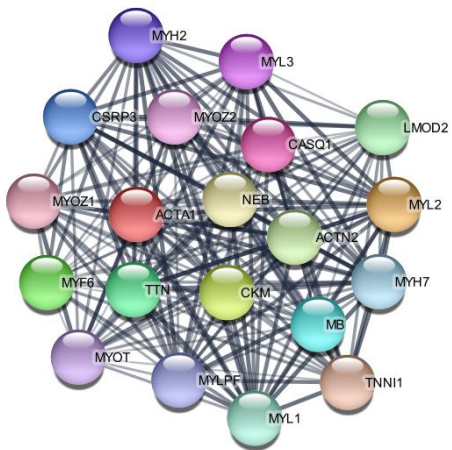
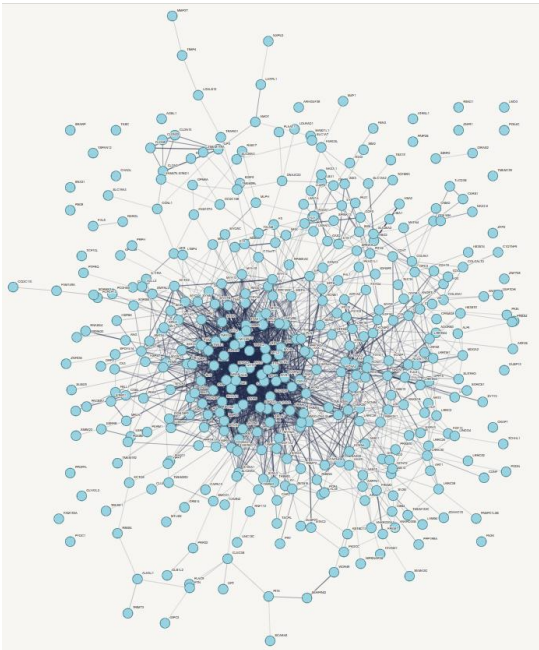
Cluster 2



Cluster 2: Cytohubba (top 20 nodes)

CYP2B6, ADH7, ALDH1A1*, ADH1B**, GSTM2, UGT1A8, CYP3A4, ADH1A, UGT1A4, ADH4, CYP2C19, CYP1A1, GSTA1*, ALDH1A2, CYP3A5*, CYP4A11, ADH1C, GSTA2, UGT1A7*, AOX1*

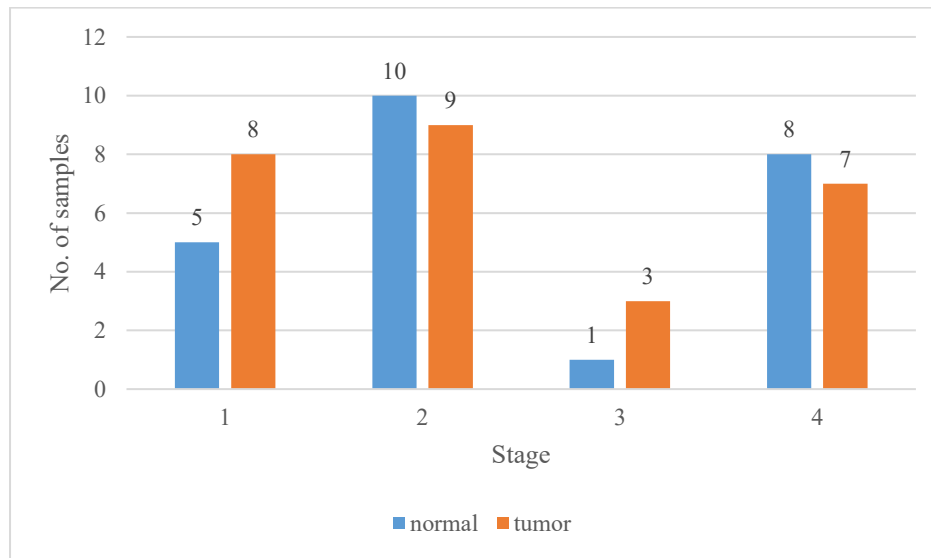
Cluster 3



Cluster 3: Cytohubba (top 20 nodes)

MYL3, MYH2, CSRP3*, MYOZ1*, MYF6, CASQ1*, MYOZ2, MB*, MYL2*, MYLPPF*, NEB*, MYH7*, TTN, ACTN2*, MYL1*, LIMOD2*, TNNI1*, MYOT*, CKM*, ACTA1**

Supplementary fig. 5 Graph showing the number of adjacent normal and tumor samples in each stage of cancer.



Supplementary table. 3 (a) total number of upregulated and downregulated genes for each of the four stages. **(b)** examining the log₂ fold change of the significant upregulated and downregulated genes for each cancer stage, marked with * are the genes with significant log₂ fold change i.e. >2 and <-2.

(a)

Stage of cancer	No. of Upregulated genes	No. of downregulated genes
Stage 1	424	967
Stage 2	824	1247
Stage 3	99	194
Stage 4	516	1218

(b)

Upregulated genes				
Gene	Stage 1	Stage 2	Stage 3	Stage 4
<i>MMP1</i>	6.781*	9.612*	10.013*	7.635*
<i>MMP10</i>	5.992*	8.099*	13.213*	7.825*
<i>IL24</i>	5.186*	7.676*	11.700*	6.911*
<i>MMP13</i>	5.701*	9.562*	9.293*	10.387*
<i>IL11</i>	5.939*	6.730*	9.676*	6.150*
<i>CSAG3</i>	3.301*	7.586*	9.583*	6.014*
<i>MMP3</i>	4.541*	6.226*	4.104*	6.210*
<i>ISG15</i>	3.813*	6.395*	6.913*	5.288*
<i>CA9</i>	4.286*	4.524*	5.294*	5.751*
<i>MMP12</i>	3.924*	7.311*	4.529*	5.912*
<i>DNAH17</i>	5.633*	6.060*	6.815*	3.900*
<i>ADAM12</i>	4.758*	5.224*	5.776*	5.601*
<i>CXCL11</i>	3.569*	5.912*	7.233*	4.643*
<i>SI00A7A</i>	4.753*	6.957*	3.435*	3.357*
<i>KHDC1L</i>	3.789*	5.581*	8.239*	3.137*

Downregulated genes				
Gene	Stage 1	Stage 2	Stage 3	Stage 4
<i>PIP</i>	- 8.754*	- 10.743*	-0.680	- 8.688*
<i>TFF3</i>	- 3.444*	-9.341*	5.277*	- 9.270*
<i>CRISP3</i>	- 6.453*	- 10.289*	3.823*	- 8.358*
<i>SCGB3A1</i>	- 8.159*	-8.802*	5.842*	- 9.075*
<i>PPP1R1B</i>	- 6.211*	-9.442*	-1.697	- 6.731*
<i>ADH1B</i>	- 7.468*	-6.927*	- 7.292*	- 7.572*
<i>PIGR</i>	- 6.765*	-8.995*	6.202*	- 6.669*
<i>KRT4</i>	- 8.670*	-8.223*	- 4.175*	- 7.568*
<i>FAM3B</i>	- 5.371*	-8.610*	- 5.078*	- 5.994*

Supplementary table. 4 (a) the number of upregulated and downregulated genes for each of the 20 sample pairs. **(b)** examining the log2 fold change of the significant upregulated and downregulated genes for each sample pair, marked with * are the genes with significant log2 fold change i.e. >2 and <-2.

(a)

	Sample pair	No. of Upregulated genes	No. of downregulated genes
1	N3 & T3	1123	1329
2	N4 & T4	535	1832
3	N6 & T6	1103	1071
4	N11 & T11	1051	1983
5	N13 & T13	494	904
6	N15 & T15	1101	978
7	N18 & T18	1818	1705
8	N20 & T20	1212	2529
9	N21 & T21	833	748
10	N23 & T23	1639	1630
11	N32 & T32	695	897
12	N39 & T39	1843	1154
13	N40 & T40	1122	1692
14	N43 & T43	909	1378

15	N45 & T45	782	1110
16	N46 & T46	1028	1263
17	N49 & T49	1067	924
18	N58 & T58	589	943
19	N65 & T65	811	1977
20	N67 & T67	954	1534

(b)

Upregulated genes																				
Gene	N 3 T 3	N 4 T 4	N 6 T 6	N 11 T 11	N 13 T 13	N 15 T 15	N 18 T 18	N 20 T 20	N 21 T 21	N 23 T 23	N 32 T 32	N 39 T 39	N 40 T 40	N 43 T 43	N 45 T 45	N 46 T 46	N 49 T 49	N 58 T 58	N 65 T 65	N 67 T 67
<i>MMP 1</i>	10 .1 9*	1. 89	12 .1 7*	8.18 *	4.78 *	8.15 *	12.0 4*	8.78 *	9.59 *	11.7 5*	10.4 1*	5.25 *	7.51 *	9.59 *	6.05 *	7.65 *	8.74 *	7.67 *	7.06 *	5.90 *
<i>MMP 10</i>	6. 36 *	2. 78 *	9. 26 *	9.36 *	4.39 *	5.65 *	9.37 *	6.01 *	7.76 *	14.7 2*	8.62 *	9.94 *	5.49 *	9.97 *	6.73 *	4.40 *	13.3 6*	8.59 *	11.2 9*	4.40 *
<i>IL24</i>	8. 01 *	2. 08 *	7. 30 *	7.42 *	3.85 *	3.17 *	11.4 68*	10.3 5*	10.9 6*	13.6 8*	10.6 4*	9.28 *	10.8 8*	11.3 3*	4.40 *	3.62 *	8.69 *	11.8 0*	11.3 5*	5.28 *
<i>MMP 13</i>	9. 01 *	- 0. 67	11 .5 5*	9.35 *	8.97 *	8.27 *	9.30 *	10.1 7*	5.94 *	10.0 3*	12.0 5*	3.85 *	7.20 *	6.71 *	13.3 8*	0.24	10.5 3*	9.20 *	7.94 *	- 4.72 *
<i>IL11</i>	5. 57 *	4. 09 *	5. 23 *	10.9 7*	6.94 *	2.30 *	10.4 3*	7.40 *	9.71 *	7.96 *	7.08 *	-	8.99 *	8.96 *	6.11 *	3.87 *	3.78 *	4.46 *	5.76 *	3.86 *
<i>CSAG 3</i>	8. 31 *	2. 34 *	9. 27 *	5.45 *	-	6.39 *	7.88 *	8.27 *	6.85 *	6.30 *	-	8.65 *	10.2 2*	9.81 *	8.56 *	5.46 *	11.7 0*	4.05 *	6.65 *	- 4.90 *
<i>MMP 3</i>	2. 07 *	1. 22	7. 03 *	7.51 *	5.62 *	1.02	8.96 *	4.60 *	3.00 *	8.37 *	7.64 *	6.09 *	4.81 *	4.81 *	4.31 *	6.34 *	8.97 *	8.63 *	5.02 *	3.73 *
<i>ISG15</i>	4. 58 *	1. 70	5. 64 *	6.86 *	2.49 *	6.04 *	3.03 *	3.68 *	4.86 *	2.76 *	5.50 *	10.1 0*	6.87 *	8.41 *	6.30 *	3.31 *	4.92 *	3.11 *	4.88 *	-1.31
<i>CA9</i>	4. 17 *	8. 99 *	5. 39 *	0.75	1.14	-	-	7.47 *	-	9.81 *	9.49 *	8.06 *	10.8 4*	5.51 *	-	1.32	- 4.16 *	5.01 *	7.90 *	8.22 *
<i>MMP 12</i>	9. 51 *	1. 86	5. 41 *	6.32 *	2.99 *	4.15 *	13.8 0*	7.79 *	12.4 2*	6.89 *	7.78 *	11.4 8*	7.78 *	5.29 *	5.97 *	0.37	7.04 *	5.27 *	6.86 *	1.99
<i>DNA H17</i>	6. 40 *	5. 53 *	1. 75	5.59 *	8.17 *	3.40 *	6.06 *	3.88 *	6.52 *	7.20 *	5.52 *	9.35 *	6.53 *	5.99 *	6.28 *	2.70 *	6.58 *	6.24 *	9.37 *	5.68 *
<i>ADA M12</i>	5. 41 *	1. 75	7. 05 *	4.28 *	4.92 *	5.17 *	5.16 *	3.88 *	4.04 *	5.11 *	5.43 *	3.93 *	5.68 *	3.34 *	2.27 *	4.28 *	5.96 *	4.99 *	1.21	2.06 *
<i>CXCL 11</i>	8. 26 *	1. 97	3. 38 *	3.09 *	0.53	6.23 *	12.0 1*	5.75 *	11.7 2*	2.10 *	5.90 *	8.10 *	12.8 1*	8.56 *	4.78 *	8.13 *	5.27 *	0.88	3.57 *	- 9.61 *
<i>S100A 7A</i>	9. 28 *	0. 97	2. 18 *	9.92 *	3.01 *	4.48 *	4.35 *	8.26 *	11.6 6*	10.9 3*	2.92 *	12.4 8*	10.7 7*	0.58	7.21 *	8.27 *	4.84 *	11.6 0*	5.64 *	3.82 *
<i>KHD CIL</i>	0. 97	2. 36 *	2. 45 *	- 0.23	3.15 *	5.53 *	5.22 *	7.44 *	8.16 *	8.58 *	- 0.09	8.87 *	7.63 *	8.80 *	7.03 *	9.36 *	6.41 *	7.07 *	9.56 *	6.24 *

Downregulated genes																				
Gene	N 3 T 3	N 4 T 4	N 6 T 6	N 11 T 11	N 13 T 13	N 15 T 15	N 18 T 18	N 20 T 20	N 21 T 21	N 23 T 23	N 32 T 32	N 39 T 39	N 40 T 40	N 43 T 43	N 45 T 45	N 46 T 46	N 49 T 49	N 58 T 58	N 65 T 65	N 67 T 67
<i>PIP</i>	- 9.30 *	- 15. 00 *	- 1.3 4	-	-	- 15.9 9*	- 14.9 7*	- 8.13 *	- 3.89 *	- 10.2 0*	- 0.67	0.65	- 9.83 *	1.05	- 11.9 7*	- 10.0 6*	-	-	- 2.87 *	-
<i>TFF3</i>	- 8.37 *	- 4.4 4*	- 6.6 1*	- 7.21 *	- 6.69 *	- 8.29 *	- 15.0 1*	- 12.1 9*	- 0.37	- 8.55 *	0.75	0.65	- 12.4 3*	-	- 13.8 7*	- 3.85 *	- 0.47	0.08	- 2.18 *	- 6.87 *
<i>CRIS P3</i>	- 10.0 9*	- 7.9 5*	- 2.1 9*	- 3.33 *	- 5.53 *	- 12.6 1*	- 11.8 6*	- 9.83 *	- 6.84 *	- 9.45 *	- 5.27 *	- 10.5 2*	- 12.4 7*	1.47	- 17.5 9*	- 1.85	- 4.68 *	- 6.46 *	0.47	2.58 *
<i>SCG B3A1</i>	- 11.5 2*	- 10. 05 *	-	-	-	- 11.2 6*	- 13.0 5*	- 7.48 *	-	- 8.75 *	-	4.31 *	- 11.9 3*	-	- 12.1 9*	- 8.35 *	-	- 3.22 *	-	-
<i>PPP1 R1B</i>	- 11.7 9*	- 9.3 1*	- 0.2 0	- 5.16 *	- 4.58 *	- 11.7 1*	- 14.0 6*	- 9.87 *	- 7.65 *	- 9.85 *	- 5.48 *	- 1.27	- 8.52 *	- 6.24 *	- 11.7 4*	- 9.10 *	- 8.08 *	- 5.39 *	- 6.53 *	-
<i>ADH 1B</i>	- 11.5 5*	- 12. 62 *	- 12. 16 *	- 11.5 9*	- 5.91 *	- 2.13 *	- 10.0 9*	- 11.9 8*	- 7.48 *	- 11.2 4*	- 10.5 2*	- 4.06 *	- 12.7 4*	- 12.7 5*	- 12.1 9*	- 13.5 9*	- 5.73 *	- 9.25 *	- 10.9 5*	- 0.08
<i>PIGR</i>	- 8.47 *	- 10. 11 *	5.1 5*	2.53 *	- 2.46 *	- 14.2 4*	- 12.6 3*	- 10.9 8*	- 0.02	- 7.09 *	0.86	2.37 *	- 10.0 4*	0.09	- 10.2 8*	- 11.6 0*	- 2.46 *	0.21	- 1.48	1.85
<i>KRT4</i>	- 6.71 *	- 6.8 7*	- 5.6 4*	- 10.7 1*	- 7.46 *	- 9.20 *	- 4.36 *	- 7.24 *	- 9.69 *	- 6.82 *	- 7.83 *	- 8.63 *	- 3.49 *	- 9.04 *	- 5.95 *	- 7.69 *	- 10.2 8*	- 12.9 5*	- 7.74 *	- 3.97 *
<i>FAM 3B</i>	- 5.37 *	- 3.6 2*	- 5.7 1*	- 9.46 *	- 9.89 *	- 11.4 9*	- 7.55 *	- 12.3 1*	- 4.86 *	- 7.13 *	- 5.01 *	- 11.6 2*	- 8.71 *	- 4.93 *	- 11.4 6*	- 12.6 9*	- 12.1 9*	- 10.1 9*	- 3.64 *	- 6.15 *