

Table S1 Included studies of microarray based differential gene expression profiles of HNSCC (Pre-malignancy)

FAU	PMID	Tumor	Site	Premalignancy	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
Kondoh[1]	16979924	27	o=27	19	LP,o=19	IntelliGene HS cDNA array (Takara)	16600	cluster,LDA	qRT-PCR	n	genbank	12 [§]	15 [§]	n	n
Odani [2]	16465365	2	o=2	4	LP,o=4	Affymetrix human genome focus array	8800	fold,rank	qRT-PCR	n	probe_set	10 [§]	8 [§]	n	n
Carinci¶[3]	16164832	8	o=8	9	DS, o=9	Ontario Cancer Institute cDNA array	19200	SAM,FDR,FatiGO,cluster	n	n,70%	UniGene	24	9	n	y
		Premalignancy	Site	Normal	Site										
Banerjee[4]	15956244	8	DS,o=8	6	N=6	Affymetrix HG-U133A	21722	fold,cluster	qRT-PCR,IHC	n	probe_set	1334	183	n	y
Carinci[5]	15792608	5	mild DS,o=5	11	N=11	Ontario Cancer Institute cDNA array	19200	SAM,FDR,FatiGO	n	n	UniGene	161 ^a	109 ^a	n	n
		4	severe DS, o=4	5	mild DS, o=5							63 ^a	118 ^a		
Ha [6]	12912957	7	DS,o=6,L=1	11	mN=5,N=6	Affymetrix HG-U95A.v2	12686	SAM,FDR, cluster,PCA	qRT-PCR	n,85%	genbank	108	226	n	y

Abbreviations: N, normal epithelial sample; mN, matched normal epithelial sample; o, oral cavity; p, pharynx; L, larynx; LP, leukoplakia; DS, dysplasia; y, yes; n, no; cluster, hierarchical clustering analysis, (<http://rana.lbl.gov/EisenSoftware.htm>); LDA, Fisher's linear discriminant analysis; rank, Wilcoxon's signed rank test; SAM, (<http://www-stat.stanford.edu/~tibs/SAM/>); FDR, false discovery rate; PCA, principal components analysis; FatiGO, (<http://fatiGO.bioinfo.cnio.es>); IHC, immunohistochemistry.

Notes: †: Tumor percentage. ‡: Dataset IDs are of GEO (<http://www.ncbi.nlm.nih.gov/geo/>) or ArrayExpress ([http://www.ebi.ac.uk/microarray-as/aer/#ae-main\[0\]](http://www.ebi.ac.uk/microarray-as/aer/#ae-main[0])). *: the original identifier reported in the article; Genbank accession; Affymetrix probe sets; UniGene cluster ID. §: reversed up- or down- differential gene expression profiles. ¶: This article was included in the Tumor v.s. Normal analysis, instead of the Pre-malignancy stage. a : Only genes, whose expression profiles were reported consistently with the same direction (up- or dn-) in the article, were included in the analysis.

Table S1 Included studies of microarray based differential gene expression profiles of HNSCC (TvN)

FAU	PMID	Tumor	Site	Normal	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
Ye[7]	18254958	53	o=53	22	mN=22	Affymetrix HG-U133A plus2	47000	PCA, RMA ,FDR, cluster	qRT-PCR,IHC	n,80%	probe_set	188 [§]	177 [§]	GSE9844	y
Suhr[8]	17914555	15	o=15	15	mN=15	Operon Human Genome Array-Ready Oligo Set v3	34580	t.test, cluster	qRT-PCR	n,70%	oligo_ID	190	73	n	y
Braakhuis[9]	16679350	19	o=15,p=2,L=2	8	N=8	Sigma-Genosys Human Oligo Library	18861	t.test,SAM,FDR, cluster,DEGOS	n	n,60%	genbank	25	25	n	n
Ziober[10]	17062667	13	o=13,p=4, L=4,s=1	13	mN=13	Affymetrix HG-U133A	22283	SAM, ANOVA, cluster,PCA,SVM, ,	qRT-PCR,IHC	n,80%	g_name	91	5	n	y
Kainuma[11]	16864496	17	o=7,p=7,L=3	17	mN=17	Intelligene Human Cancer Chip v.2.0	425	fold,cluster	n	n	g_symbol	7	3	n	y
Gottschlich [12]	16865276	6	p=4,L=2	4	N=4	Scienion cDNA array	1344	u.test, cluster	RT-PCR	n	g_symbol	19	3	n	n
Tomioka[13]	16519767	9	o=9	9	mN=9	IntelliGene HS cDNA array	16617	fold,cluster	RT-PCR	n	genbank	28	19	n	y
Dysvik[14]	16489063	117	pooled, o=104,p=5, L=6,s=2	117	pooled, mN=117	Research Genetics IMAGE cDNA array	15000	t.test, cluster	qRT-PCR,IHC	n,70%	UniGene	27 ^a	46 ^a	y	y
Jarvinen[15]	16715129	10	L=10	0	0	Agilent Human1A oligo array	15496	ECN	IHC	n,50%	gene_ID	40	0	y	n
Roesch Ely [16]	15819419	4	pL=4	4	mN=4	custom cDNA array (IMAGE)	5200	fold, t.test	qRT-PCR, TMA_IHC,MS	n,40%	g_symbol	0	5	n	y

Table S1: TvN (1)

Yu et al., HNSCC transcriptome

Belbin[17]	15655179	9	o=9	9	mN=9	custom cDNA array (IMAGE)	17840	fold, bounded prob score	TMA_IHC	n,70%	genbank	140	59	p	y
Schlingemann [18]	16205657	4	p=4	4	mN=4	Affymetrix HG-U133A	22283	DWD,gcRMA,FDR, bayes,t.test	qRT-PCR	n,80%	UniGene	36	41	GSE1722	y
		4	p=4	4	mN=4	custom oligo array (Operon)	26791	DWD,gcRMA,FDR, bayes,t.test,DAVID	qRT-PCR	n,80%	UniGene	30	47	GSE1722	y
Kornberg[19]	15805883	7	o=5,p=2	7	mN=7	Affymetrix HG-U95A.v2, HG-U133A	10599	t.test,cluster	RT-PCR,IHC	n,80%	genbank	52	55	n	y
Carinci[3]	16164832	8	o=8	9	DS,o=9	Ontario Cancer Institute cDNA array	19200	SAM,FDR,FatiGO, cluster	n	n,70%	UniGene	24	9	n	y
Laytragoon- Lewin[20]	15865097	16	o=8,p=7,L=1	16	mN=16	GEArray Q series	100	fold,t.test	n	n	g_symbol	4	8	n	n
Chin[21]	15499618	7	o=5,p=2	7	mN=7	Ontario Cancer Institute cDNA array	19200	fold,u.test	IHC,survival	n	genbank	25	25	n	y
Shimada[22]	15870709	4	o=4	4	mN=4	custom cDNA array	2304	fold	qRT-PCR,IHC	n,80%	UniGene	16	0	n	y
Irie[23]	15221650	11	o=11	11	mN=11	Clontech Atlas 1.2 Human Cancer Array	1176	fold	n	y	g_symbol	5	5	n	n
Cromer[24]	14676830	34	p=34	4	N=4	Affymetrix HG-U95A	12558	SAM,cluster, LD,NN	qRT-PCR	n,70%	genbank	64	55	GSE2379	y
Schmalbach [25]	15023835	20	o=20	4	N=4	Affymetrix HG-U95A.v2	12625	fold,t.test,FDR	IHC	n,70%	probe_set	24	37	n	y

Table S1: TvN (2)

Yu et al., HNSCC transcriptome

Ginos[26]	14729608	41	o=18,p=5,L=1 5,sinus=3	13	N=13	Affymetrix HG-U133A	22283	fold,t.test,cluster Bayesian prob	qRT-PCR,IHC	n,50%	probe_set	1658 ^s	1232 ^s	p	y
Marcus[27]	15546137	20	op=20	4	N=4	Affymetrix HG-U95A.v2	12625	fold,t.test permutation	chemotaxis TMA_IHC surv	n,70%	probe_set	68	12	n	y
Toruner[28]	15381369	16	o=16	4	mN=4	Affymetrix HG-U133A	22283	fold,SAM,cluster	qRT-PCR	y	genbank	33	20	GSE3524	y
Kuriakose[29]	15170515	22	o=13,p=4,L=4, sinus=1	22	mN=22	Affymetrix HG-U95A.v2	12625	t.test,u.test,SAM PPV,MDMR,WEPO	qRT-PCR	n	probe_set	18	24	GSE6631	y
Tsai[30]	14969821	10	o=10	10	mN=10	MillenniaChip v.2 cDNA array	1117	fold,cluster	RT-PCR Northern	n	UniGene	29	55	n	n
Whipple[31]	15280706	26	o=21,p=5	18	o=18	Affymetrix Test 1, HuGene FL	7023	PCA,t.test,LLR	test.set(23)	n,60%	genbank	31	19	n	n
Ha[6]	12912957	7	o=6,L=1	11	mN=5,N=6	Affymetrix HG-U95A.v2	12625	SAM,FDR,PCA cluster	qRT-PCR	n,85%	genbank	965 ^s	1106 ^s	n	y
Banerjee[32]	14633702	2	o=2	2	mN=2	BD Atlas Plastic cDNA microarray	96	fold	RT-PCR,IHC	n	g_symbol	5	0	n	y
Nagata[33]	12866027	15	o=15	58	pooled	Intelligene Human Cancer Chip v.2.1	557	fold,u.test,SAM,FDR cluster	qRT-PCR,IHC	n	genbank	14	19	n	y
Sok[34]	12874079	9	o=5,p=2,L=1, sinus=1	9	mN=9	Affymetrix HG-U95A	12558	fold,t.test,Bayesian cluster	n	n	genbank	92	135	n	y
Gonzalez[35]	12874078	3	o=3	3	mN=3	Incyte Genomics UniGEM V,Research Genetics GF204	9350 5760	upper and lower 2.5 percentile of log(fold)	RT-PCR,IHC	n	g_symbol	2	7	n	n

Table S1: TvN (3)

Yu et al., HNSCC transcriptome

Leethanakul [36]	12618197	5	o=5	5	mN=5	custom cDNA array	384	chisq.test	n	y	UniGene	23	23	n	n
Kuo[37]	12703240	5	o=5	5	mN=5	custom cDNA array	4132	variance,cluster,t.test	n	y	g_symbol	9	0	n	n
Ibrahim[38]	12457720	22	o=22	22	mN=22	Atlas human cancer cDNA array	588	fold	RT-PCR,IHC	n	genbank	35 ^a	18 ^a	n	n
Hwang[39]	12618198	5	o=5	5	mN=5	Affymetrix Test 1, HuGene FL	7023	Wilks' lambda LOOCV,FDA	qRT-PCR	y	genbank	15	30	n	n
El-Naggar[40]	12444558	12	o=11,p=1	12	mN=12	Research Genetics GF200,GF211	5453 4324	fold, ranking top 1 percentile t.test, cluster	qRT-PCR,IHC	n,90%	genbank	13	1	n	y
Mendez[41]	12237917	26	o=21,p=5	18	o=18	Affymetrix Test 1, HuGene FL	7023	regression,cluster	qRT-PCR	n,60%	probe_set	239	75	n	y
Squire[42]	12211052	5	o=5	5	mN=5	Clontech Atlas Human Cancer Array	588	fold	CGH,SKY	n	g_symbol	10	3	n	n
Alevizos[43]	11593428	5	o=5	5	mN=5	Affymetrix Test 1, HuGene FL	7023	fold, consistency SOM,cluster	qRT-PCR	y	genbank	16	23	n	y
Leethanakul [44]	10918578	5	o=3,p=1,L=1	5	mN=5	Clontech Atlas Human Cancer Array	588	fold	n	y	genbank	59	0	n	n
Villaret[45]	10718422	16	pooled,o=12,p=1,L=1,LN=3	22	pooled	custom cDNA array	985	fold,t.test	n	n	g_symbol	12	0	n	n

Table S1: TvN (4)

Yu et al., HNSCC transcriptome

Abbreviations: N, normal epithelial sample; mN, matched normal epithelial sample; o, oral cavity; p, pharynx; L, larynx; s, sinus; DS, dysplasia; y, yes; n, no; cluster, hierarchical clustering analysis, (<http://rana.lbl.gov/EisenSoftware.htm>); DEGOS, deviations from gaussian-order statistics; SAM, (<http://www-stat.stanford.edu/~tibs/SAM/>); FDR, false discovery rate; PCA, principal components analysis; FatiGO, (<http://fatiGO.bioinfo.cnio.es>); u.test, Mann-Whitney U test; ECN, Expression annotation of Copy Number tool; DWD, 'Distance Weighted Discrimination; DAVID, Database for Annotation, Visualization and Integrated Discovery, (<http://david.niaid.nih.gov/david/>); LD, local density; NN, nearest neighbor; PPV, Predict Parameter Value (Gene Spring); MDMR, Minimum Distance to Modal Ranking; WEPO, WEighted Punishment on Overlap; LLR, log likelihood ratio; LOOCV, leave-one-out cross-validation; FDA, Fisher discriminant analysis; TMA_IHC, tissue microarray immunohistochemistry; MS, surface enhanced laser desorption ionisation-time of flight mass spectrometry.

Notes: †: Tumor percentage. ‡: Dataset IDs are of GEO (<http://www.ncbi.nlm.nih.gov/geo/>) or ArrayExpress ([http://www.ebi.ac.uk/microarray-as/aer/#ae-main\[0\]](http://www.ebi.ac.uk/microarray-as/aer/#ae-main[0])). *: the original identifier reported in the article; Genbank accession; Affymetrix probe sets; UniGene cluster ID. §: gene lists extracted from supplementary materials. a: Only genes, whose expression profiles were reported consistently with the same direction (up- or dn-) in the article, were included in the analysis. ¶: This gene list was not included in the analysis.

Additional information: Ye et al. performed analysis including data from Zoiber and Toruner et al.; Whipple et al. performed analysis using the same data of Mendez et al.; Hwang et al performed analysis using the same data of Alevizos et al.

Table S1 Included studies of microarray based differential gene expression profiles of HNSCC (Metastatic v.s. Primary)

FAU	PMID	pN+	Site	pN-	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
Mendez[46]	17573689	6	pN+,o=6	5	pN-,o=5	Affymetrix human genome focus array	8795	z.score,NFD, cluster,PCA	IHC	y	probe_set	73	87	n	n
Carinci[47]	17900511	11	L=11	11	L=11	Ontario Cancer Institute cDNA array	19200	t.test,FDR	RT-PCR, cell assay	n,70%	genbank	1	38	n	n
Nguyen[48]	17391312	13	pN+,o=13	17	pN-,o=17	Affymetrix HG-U133A plus2	47000	fold,t.test,cluster	qRT-PCR test.set(13)	y	genbank	52	33	n	y
Zhou[49]	17132224	11	pN+,o=11	14	pN-,o=14	Affymetrix HG-U133A	22283	fold,t.test, clusterl,MDS	qRT-PCR	n,80%	probe_set	17	16	n	n
Kato[50]	17016585	5	pN+,o=5	10	pN-,o=10	AceGene Human oligo chip	10800	SAM,cluster	test.set(8)	n	genbank	21		n	n
Roepman[51]	16489042	29	pN+,o=21,p=8	15	pN-,o=14,p=1	UMC Utrecht H.S 25K array v.1	21329	fold,t.test,SNR, multiple training	test.set(22)	n,50%	genbank	429§	396§	E-UMCU -11	y
Belbin[17]	15655179	4	pN+,o=4	5	pN-,o=5	custom cDNA array (IMAGE)	17840	fold, bounded prob score	TMA_IHC	n,70%	genbank	64	59	n	y

O'Donnell[52]	15558013	11	pN+,o=11	7	pN-,o=7	Affymetrix HG-U133A	22283	SAM,PCA,SVM	qRT-PCR,IHC test.set(4)	n	gene_name	11	19	GSE2280	y
Roepman[53]	15640797	45	pN+,o=34, p=11	37	pN-,o=33, p=4	UMC Utrecht H.S 25K array v.1	21329	fold,t.test,SNR	test.set(22)	n,50%	genbank	26	81	E-UMCU -11	y
Irie[23]	15221650	4	pN+,o=4	7	pN-,o=7	Clontech Atlas 1.2 Human Cancer Array	1176	fold	n	y	gene_sym	10	10	n	n
Chung[54]	15144956	18	pN+,pL=8	8	pN-,pL=8	Agilent Human 1 cDNA array	12814	intrinsic,cluster PAM,KNN	IHC,survival	n	genbank	16	49	GSE686	y
Schmalbach [25]	15023835	13	pN+,o=13	7	pN-,o=7	Affymetrix HG-U95A.v2	12625	fold,t.test,FDR	IHC	n,70%	probe_set	24	37	n	y
Warner[55]	15170668	12	pN+	8	pN-	Ontario Cancer Institute cDNA array	19200	SOM,BTSVQ	qRT-PCR	n,80%	uniGene	23		n	n
Nagata[33]	12866027	8	pN+,o=8	7	pN-,o=7	Intelligene Human Cancer Chip v.2.1	557	fold,u.test,SAM,FDR cluster	qRT-PCR,IHC	n	genbank	15	4	n	y
FAU	PMID	dMeta+	Site	dMeta-	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
Vachani[56]	17504990	10	lung=10	18	o=18	Affymetrix HG-U133A	22283	DWD, cluster,PDA	test.set(72 vs 50)	n,70%	uniGene	73	27	n	y
Braakhuis[9]	16679350	11	dM,o=7,p=3, L=1	8	nM,o=2,p=5, L=1	Sigma-Genosys Human Oligo Library	18861	t.test,SAM,FDR, cluster,DEGOS	n	n,60%	genbank	25	25	n	n
Giri[57]	16289374	7	dM,o=2,p=1, L=1,sinus=3	8	nR,o=5,p=1, L=1,sinus=1	custom oligo array	18861	fold,t.test,cluster	qRT-PCR	n,85%	gene_sym	22	28	n	n
Carinci[3]	16164832	11	dM,o=11	8	nM,o=8	Ontario Cancer Institute cDNA array	19200	z.score,cluster,FatiGO	n	n,70%	uniGene	89	66	n	y
Talbot[58]	15833835	21	lung=21	31	1st,o=31	Affymetrix HG-U95A.v2	12625	cluster,bootstrap	qRT-PCR test.set(12)	n,70%	genbank	10	40	n	n
Cromer[24]	14676830	15	dM,p=15	11	nM,p=11	Affymetrix HG-U95A	12558	SAM,cluster,NN	qRT-PCR	n,70%	genbank	13	14	GSE2379	y

FAU	PMID	recur+	Site	recur-	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
Pramana[59]	17931799	38	o=14,p=71, L=7	54	o=14,p=71, L=7	custom oligo array (Operon v3.0)	34580	fold,SAM,cluster GSEA	cross.val,survival	n,50%	gene_sym	33		n	n
Ginos[26]	14729608	16	o=10,p=3,L=3	25	o=8,p=2, L=12,s=3	Affymetrix HG-U133A	22283	t.test,cluster	qRT-PCR,IHC	n,50%	gene_name	64	13	p	y
FAU	PMID	surv gr1	Site	surv gr2	Site	company	features	analysis	validation	LCD [†]	identifier*	up	dn	dataset [‡]	FC
<i>Pramana[59]</i>	<i>17931799</i>	<i>35</i>	<i>Rsp+</i>	<i>35</i>	<i>Rsp-</i>	<i>custom oligo array (Operon v3.0)</i>	<i>34580</i>	<i>fold,SAM,cluster GSEA</i>	<i>cross.val,survival</i>	<i>n,50%</i>	<i>gene_sym</i>	<i>11</i>		<i>n</i>	<i>n</i>
Ganly[60]	17416856	26	Rsp+	9	Rsp-	custom cDNA array (IMAGE)	1152	fold,t.test	qRT-PCR,IHC, survival	n	geneID	6	11	n	n
Winter[61]	17409455	59	o=12,p=35,L=9,other=3			Affymetrix HG-U133A plus2	47000	SAM,FDR,cluster	test.set(60),survival	n,90%	probe_set	129	81	y	n
Chung[62]	16912200	15	o=5,p=7,L=3	14	o=8,p=4,L=2	Affymetrix X3P	47000	intrinsic,GSEA	RT-PCR,survival	n,70%	probe_set	26	18	GSE283 7	n
<i>Chung[54]</i>	<i>15144956</i>	<i>23</i>	<i>o=7,p=7,L=9</i>	<i>51</i>	<i>o=10,p=19, L=19</i>	<i>Agilent Human 1 cDNA array</i>	<i>12814</i>	<i>intrinsic,cluster PAM,KNN</i>	<i>IHC, survival</i>	<i>n</i>	<i>genbank</i>	<i>28</i>	<i>92</i>	<i>GSE686</i>	<i>y</i>
Belbin[63]	11861402	8	gr1,o=5,p=2, L=1	9	gr2,o=7,p=1, L=1	custom cDNA array	9216	fold,cluster,t.test	survival	n,70%	genbank	337	1	p	y

Abbreviations: N, normal epithelial sample; mN, matched normal epithelial sample; o, oral cavity; p, pharynx; L, larynx; s, sinus; DS, dysplasia; y, yes; n, no; cluster, hierarchical clustering analysis, (<http://rana.lbl.gov/EisenSoftware.htm>); NFD, number of false discovery; MDS, multidimensional scaling; SNR, signal-to-noise ratio; SVM, support vector machine; DEGOS, deviations from gaussian-order statistics; SAM, (<http://www-stat.stanford.edu/~tibs/SAM/>); FDR, false discovery rate; PCA, principal components analysis; GSEA, gene set enrichment analysis; FatiGO, (<http://fati.go.bioinfo.cnio.es>); u.test, Mann-Whitney U test; DWD, 'Distance Weighted Discrimination; SOM, self-organizing map; BTSVQ, binary tree-structured vector quantization; PDA, penalized discriminant analysis; PAM, prediction analysis of microarray; KNN, K-Nearest Neighbor; DAVID, Database for Annotation, Visualization and Integrated Discovery, (<http://david.niaid.nih.gov/david/>); NN, nearest neighbor; FDA, Fisher discriminant analysis; TMA_IHC, tissue microarray immunohistochemistry.

Notes: †: Tumor percentage. ‡: Dataset IDs are of GEO (<http://www.ncbi.nlm.nih.gov/geo/>) or ArrayExpress ([http://www.ebi.ac.uk/microarray-as/aer/#ae-main\[0\]](http://www.ebi.ac.uk/microarray-as/aer/#ae-main[0])). *: the original identifier reported in the article; Genbank accession; Affymetrix probe sets; UniGene cluster ID. §: gene lists extracted from supplementary materials. a: Only genes, whose expression profiles were reported consistently with the same direction (up- or dn-) in the article, were included in the analysis.

Table S1: Meta (3)

Yu et al., HNSCC transcriptome

1. Kondoh N, Ohkura S, Arai M, Hada A, Ishikawa T, et al. (2007) Gene expression signatures that can discriminate oral leukoplakia subtypes and squamous cell carcinoma. *Oral Oncol* 43: 455-462.
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