

Supplementary Table S4. Comparison of studies identifying a metastatic signature in HNSCC

Study	No. of Normal (N), Primary (P), Metastatic (M) Samples	No. Samples Used to Develop Metastatic Signature	Gene Expression Array	No. of Transcripts Interrogated	Comparison	Statistic	Journal/ Figure with Gene List
Colella (this study)	28 N, 28 P, 14 M (matched)	14 HNSCC primaries and metastases	Affymetrix HuGeneFL & U95Av2	5,600 & 9,600 genes 4,509 common genes	matched metastases (14) vs. primaries (14)	46 genes, sign test & >1.5 fold diff.	This paper; Table 1
Chung (Chung <i>et al.</i> , 2004)	60 P	26 primaries (no oral SCC)	Agilent Human1 cDNA array (30 tumor pool as ref.)	12,814 cDNAs	LN+ (18) vs. LN- (8)	500 top genes in 10 permutations of training/test set	<i>Cancer Cell</i> 2004; Supplemental Figure S2
Cromer (Cromer <i>et al.</i> , 2004)	34 P, 4 N (unmatched)	30 late stage hypopharyngeal primaries (all LN+)	Affymetrix U95A	9,600 genes 12,500 transcripts	mets (15) vs. no mets (10) (all were LN+ and had complete resection)	164 genes, union of t-test and >1.5 fold diff. in 1/2 of samples	<i>Oncogene</i> 2004; Supplementary Table
Roepman (Roepman <i>et al.</i> , 2005)	82 P	82 HNSCC primaries (+22 for validation set)	Qiagen Human Array-ready oligo set (vs. common ref. pool)	21,329 genes	LN+ (44) or M+ (1) vs. LN-/M- (37)	Iteratively generated test/training sets, optimal classifier: 102 genes	<i>Nature Genet.</i> 2005; Supplementary Table 2
O'Donnell (O'Donnell <i>et al.</i> , 2005)	18 P	18 HNSCC primaries (+4 for validation set)	Affymetrix U133A	14,500 genes, 18,400 transcripts	LN+ (11) vs. LN- (7)	116 genes (SAM with low-expression genes omitted)	<i>Oncogene</i> 2005; Supplementary Figure 1
Hunter (Hunter <i>et al.</i> , 2005)		16 HNSCC cell lines	Affymetrix U133A+B	33,000 genes 39,000 transcripts	mortal (7) vs. immortal (9) HNSCC cell cultures	160 genes, SAM	<i>Cancer Res.</i> 2006; Table S3
Schmalbach (Schmalbach <i>et al.</i> , 2004)	20 P	20 OSCC/OPSCC primaries	Affymetrix U95Av2	9,600 genes 12,500 transcripts	LN+ (13) vs. LN- (7)	101 genes, 57 of these showed diff. between N, P also	<i>Arch. Otol. HN Surg.</i> 2004; Figure 3