Table S9. Comparison of the promoter DNA hypermethylation detection in all primary tissues from HNSCC and non-cancerous patients from three cohorts using four different DNA methylation detection techniques

		Discovery Cohort	Validation Cohort		TCGA
		DNA methylation array 27K	Bisulfite Sequensing	QMSP	DNA methylation array 450
		%	%	%	%
ZNF14	Detection in tumor samples	41	43.8	44.1	40.5
	Detection in normal	0	0	0	0
ZNF160	Detection in tumor samples	25	46.9	39	34.8
	Detection in normal	0	14.3	0	0
ZNF420	Detection in tumor samples	34	25	32.2	48
	Detection in normal	0	0	0	0

For the array data the detection cut-off for each gene was set as normal mean plus 3 standard deviations. For QMSP data the cut of was DNA methylation detection at 38 PCR cycles.