

Table 2. Summary of previously reported comparative genomic hybridization (CGH) profiles of all chromosomal arms for a variety of head and neck tumor sites and stages generated by six different studies

Ref.	1p	1q	2p	2q	3p	3q	4p	4q	5p	5q	6p	6q	7p	7q	8p	8q	9p	9q	10p	10q	11p	11q	12p	12q	13q	14q	15q	16p	16q	17p	17q	18p	18q	19p	19q	20p	20q	21q	22q
7	-	+	+	-	-	+	-	-	+	+	-	-	+	E	-	+	-	+	-	E	-	E	E	E	-	+	E	-	+	+	+	+	-	-	-	+	+	-	-
8	+	+	+	+	-	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
5	-	+	+	-	-	+	-	-	+	-	E	-	+	+	-	+	-	-	-	-	+	-	-	-	-	E	+	-	+	+	E	-	+	+	+	+	-	+	
3	+	+	NR	+	-	-	NR	E	+	-	NR	NR	+	-	-	+	-	+	-	NR	NR	E	NR	NR	-	+	-	-	NR	-	NR	NR	-	-	-	NR	+	NR	+
4	NR	+	+	+	-	+	-	+	+	+	+	+	+	+	-	+	-	NR	+	+	+	+	+	-	+	+	NR	NR	NR	NR	+	NR	+	NR	NR	+	+	-	-
27	+	+	+	+	-	+	-	-	+	+	+	+	NR	+	-	+	NR	+	NR	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	NR	+			
Malignant data	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

+, Chromosomal arms demonstrating an increase in copy number, as reported by the respective study. -, Chromosomal arms demonstrating a decrease in copy number. Those cases in which defining a chromosomal arm as having a copy number aberration because of an ambiguous CGH profile for that particular arm were reported as indeterminate (I). In the setting of equivocal decreases or increases in copy number on a particular chromosomal arm, that entire arm is reported as equivocal (E). NR, not reported. Results from our *in silico* analysis of seven malignant lesions using all 9,724 annotated genes and their average expression Z scores are shown in the bottom row for comparison. Large, bold characters in the bottom row indicate that 95% confidence interval excludes no change in expression relative to normal controls.