Figure S1. Algorithm of the clustering method for microarray data.
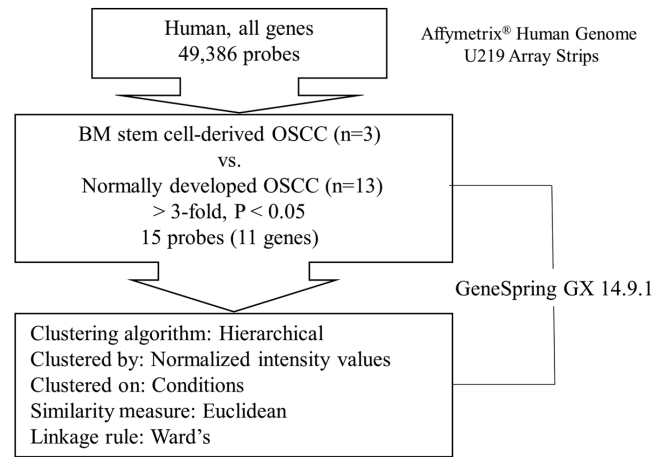
Figure S2. Expression of marker genes detected in the current microarray analysis was analyzed in head and neck squamous cell carcinoma (528 cases) from the cancer genome atlas database.

Gene	%	Alteration frequency
KRT8	4%	0% (0/528)
ABCC3	4%	1.9% (10/528)
GCLC	6%	4.7% (25/528)
RYBP	4%	1.7% (9/528)
TMEM97	5%	3.2% (17/528)
SLC1A3	5%	1.7% (9/528)
IRS2	6%	2.7% (14/528)
KYNU	2.3%	1.3% (7/528)
CSAG2	0.4%	0% (0/528)
CDA	1.7%	1.7% (9/528)
CCL21	5%	3.6% (19/528)

Genetic alteration

■ mRNA High ■ mRNA Low ■ No alterations

Samples per patient   0 ◢ 2