

**Table SI.** Clinical features of 65 laryngeal squamous cell carcinoma samples that underwent reverse transcription-quantitative PCR analysis.

<b>Parameter</b>	<b>Number of cases (%)</b>
Age, years	
≤60	29 (44.6)
>60	36 (55.4)
Sex	
Female	2 (3.1)
Male	63 (96.9)
Primary site	
Glottic	28 (43.1)
Supraglottic	25 (38.5)
Subglottic	6 (9.2)
Transglottic	6 (9.2)
Differentiation	
High	13 (20.0)
Medium	27 (41.5)
Low	25 (38.5)
T staging <sup>a</sup>	
T1	15 (23.1)
T2	20 (30.8)
T3	16 (24.6)
T4	14 (21.5)
Cervical lymph node metastasis	
N0	49 (75.4)
N+	16 (24.6)
Distant metastasis	
M0	65 (100.0)
M1	0 (0.0)
Clinical stage	
I	15 (23.1)
II	17 (26.2)
III	13 (20.0)
IV	20 (30.8)

<sup>a</sup>TNM staging is referring to the AJCC 8th edition TNM Staging Criteria.

**Table SII.** Primer sequences for quantitative PCR analysis.

<b>Primer name</b>	<b>Forward, 5'-3'</b>	<b>Reverse, 5'-3'</b>
miR-488-3p	TTGAAAGGCTATTTCTTGGTC	Universal primer provided by miRNA First-Strand cDNA Synthesis Kit
ACVR1C	AGTGTGAAACTTGTGCCATAGC	ATTTCCCAGTAAACCAGACCAA
ABCA12	TCTTTTCTTCGCAATGGTTCTT	TCTTTTCTTCGCAATGGTTCTT
TNFSF11	CAACATATCGTTGGATCACAGCA	GACAGACTCACTTTATGGGAACC
SYT14	CAGTCCTGAGCCCTGAAGATA	CAGTCCTGAGCCCTGAAGATA
18s rRNA	CCTGGATACCGCAGCTAGGA	GCGGCGCAATACGAATGCCCC
U6 RNA	TCGCTTCGGCAGCACATAT	ATTTGCGTGTTCATCCTTGC
Primer-01	CTCTTAAAGTTTTGCCTCGTC	CTACCAATATGAAGGAATCCAC
Primer-NC	GCGTGGCTGGAGAGGGTAT	AACGGCCTTTTACACACTTCTT

ACVR1C, activin A receptor type 1C; miR, microRNA; NC, negative control.