

Figure S1. STR loci in Ca9-22 cell lines. The identical signals for STR of Ca9-22 cells in the present study are indicated. The assay was evaluated from 10 different STR loci (TH01, D21S11, D5S818, D13S317, D7S820, D16S539, CSF1PO, AMEL, vWA and TPOX). STR, short tandem repeat.

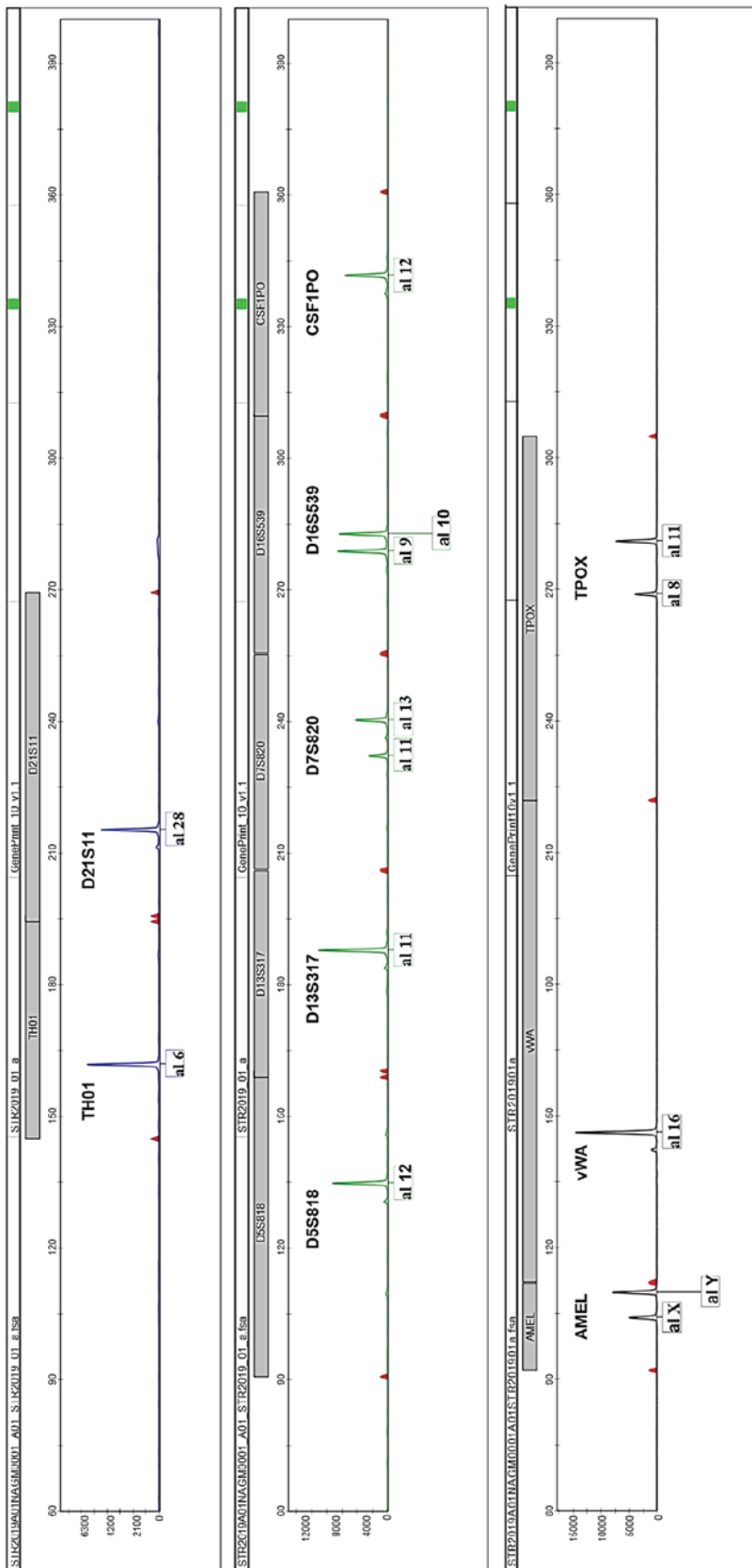


Figure S2. Migration of oral cancer cells in response to IL-6. (A) siPLOD2-transfected oral cancer cells (HSC-2, HSC-3 and Ca9-22, green fluorescence protein-positive cells) were seeded in the COL-I-coated plate. Cell migration with IL-6 treatment (0.5 ng/ml) was detected with a wound healing assay using a 24-well plate. Images were taken 0 and 12 h after wound formation (scale bar, 400 μ m). (B) The wound width was estimated using fluorescence microscopic images. Results are presented as the mean \pm SD (n=3). *P<0.05, **P<0.01 vs. siControl + IL-6 group. IL-, interleukin; PLOD2, procollagen-lysine 2-oxoglutarate 5-dioxygenase 2; si, small interfering RNA.

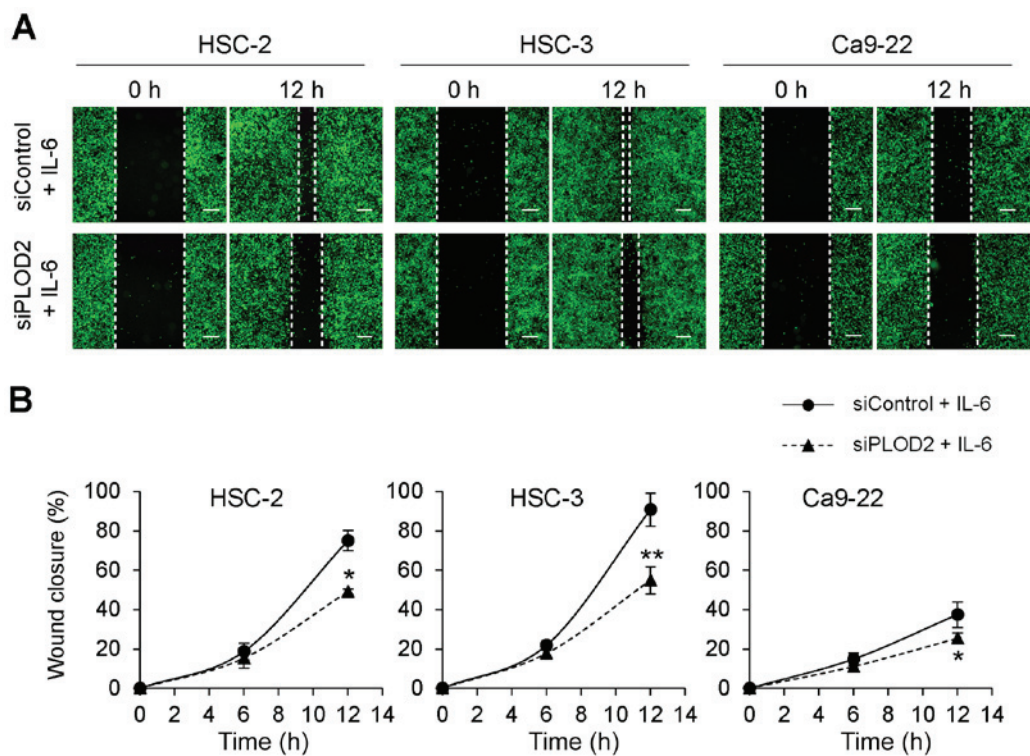


Table SI. STR profiles of oral cancer cell lines.

STR marker	Cell lines							
	Ca9-22 ^a	Ca9-22 ^b	HSC-2 ^a	HSC-2 ^b	HSC-2 ^c	HSC-3 ^a	HSC-3 ^b	MSK-922 ^d
AMEL	X, Y	X, Y	X, Y	X	X, Y	X, Y	X, Y	X, X
TH01	6	6	6, 7	6, 7	6, 7	6, 9.3	6, 9.3	8, 8
D5S818	12	12	10, 12	10, 12	10, 12	11, 13	11, 13	11, 11
D13S317	11	11	11, 12	11, 12	11, 12	12	12	12, 12
D7S820	11, 13	11, 13	9, 12	9, 12	9, 12	13	13	11, 11
D16S539	9, 10	9, 10	12	12	12	9	9	9, 11
CSF1PO	12	12	12, 13	12, 13	12, 13	11	11	10, 12
vWA	16	16	16, 18	16, 18	16, 18	14, 17	14, 17	17, 17
TPOX	8, 11	8, 11	8	8	8	8	8	8, 8
E.V. ^e	1.00 (Ca9-22 ^a vs. Ca9-22 ^b)	1.00 (HSC-2 ^a vs. HSC-2 ^{b,c})	1.00 (HSC-3 ^a vs. HSC-3 ^b)	-	-	-	-	-
	0.30 (Ca9-22 ^a vs. MSK-922)	0.20 (HSC-2 ^a vs. MSK-922)	0.37 (HSC-3 ^a vs. MSK-922)	-	-	-	-	-
Others	Used in the present study	ID, JCRB0625	Used in the present study	ID, JCRB0622	ID, RCB1945	Used in the present study	ID, JCRB0623	(23)

The number of repeat units at each STR marker is indicated. Homozygous alleles are shown as one value, and heterozygous alleles are shown as two values, which corresponds to one or two peaks in the STR electropherogram, respectively. ^aUsed in present study; ^bSTR profiles from JCRB cell bank; ^cSTR profiles from RIKEN bioresource research center; ^dInformation from Zhao *et al* (29); ^eEvaluation Value = 2 x number of shared alleles/(number of query alleles + number of reference alleles). STR, short tandem repeat; X, X chromosome; Y, Y chromosome; JCRB, Japanese Collection of Research Bioresources; -, not applicable.