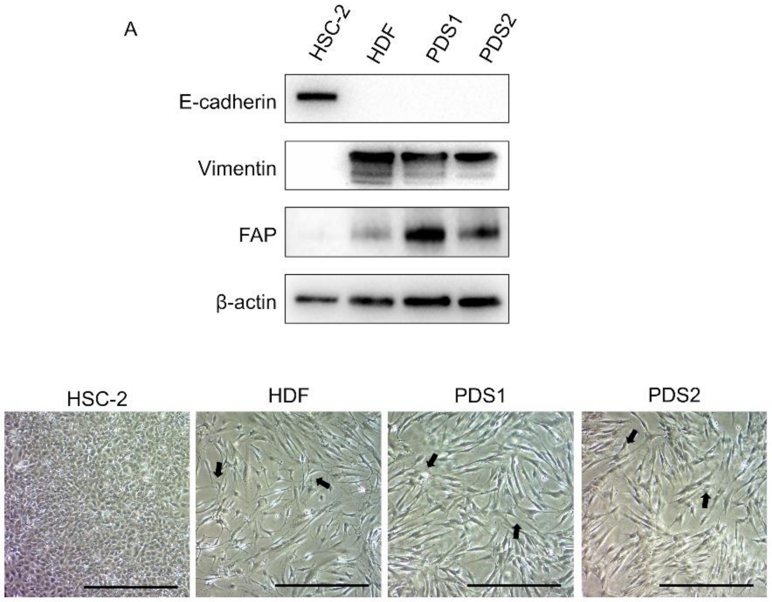
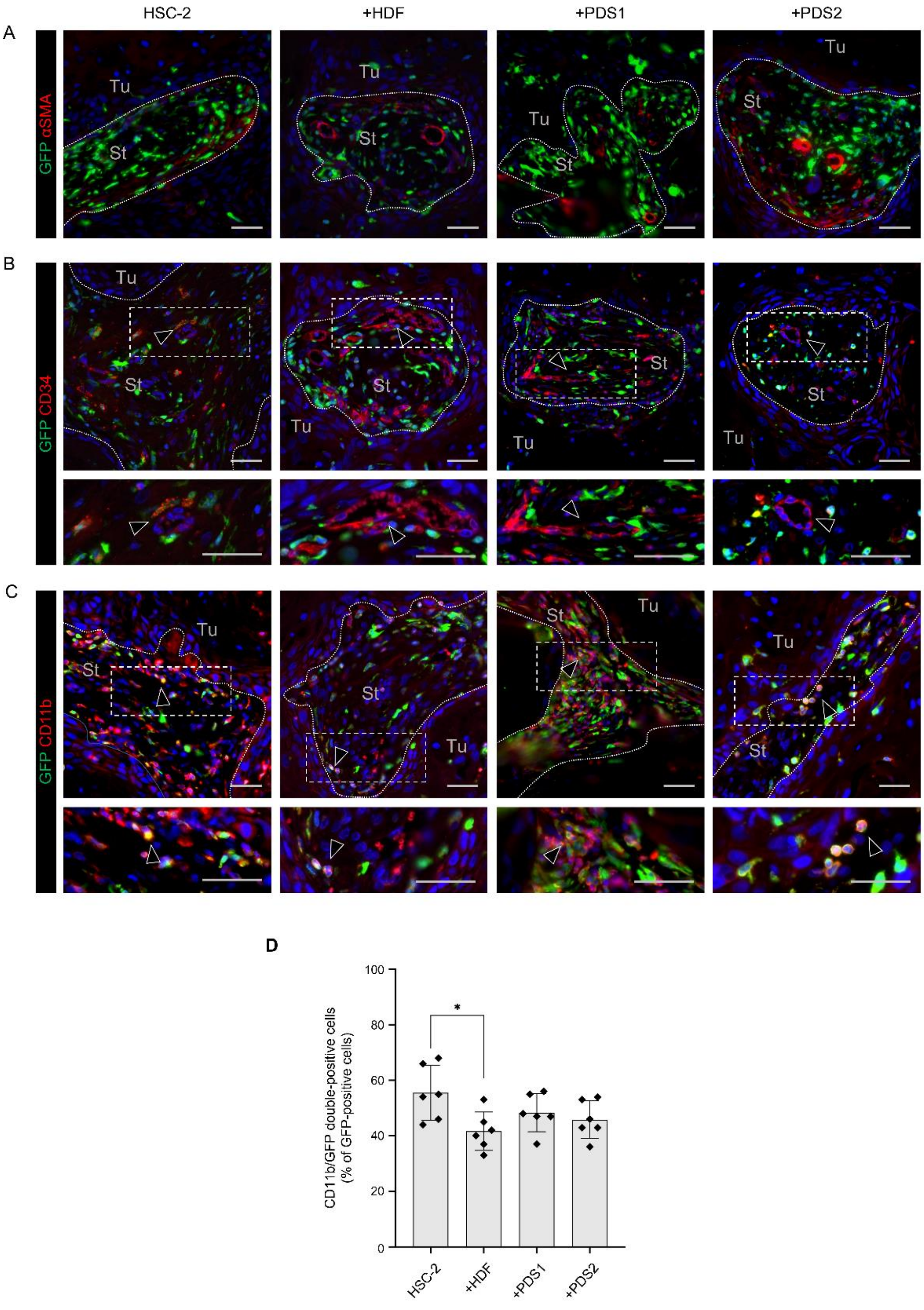
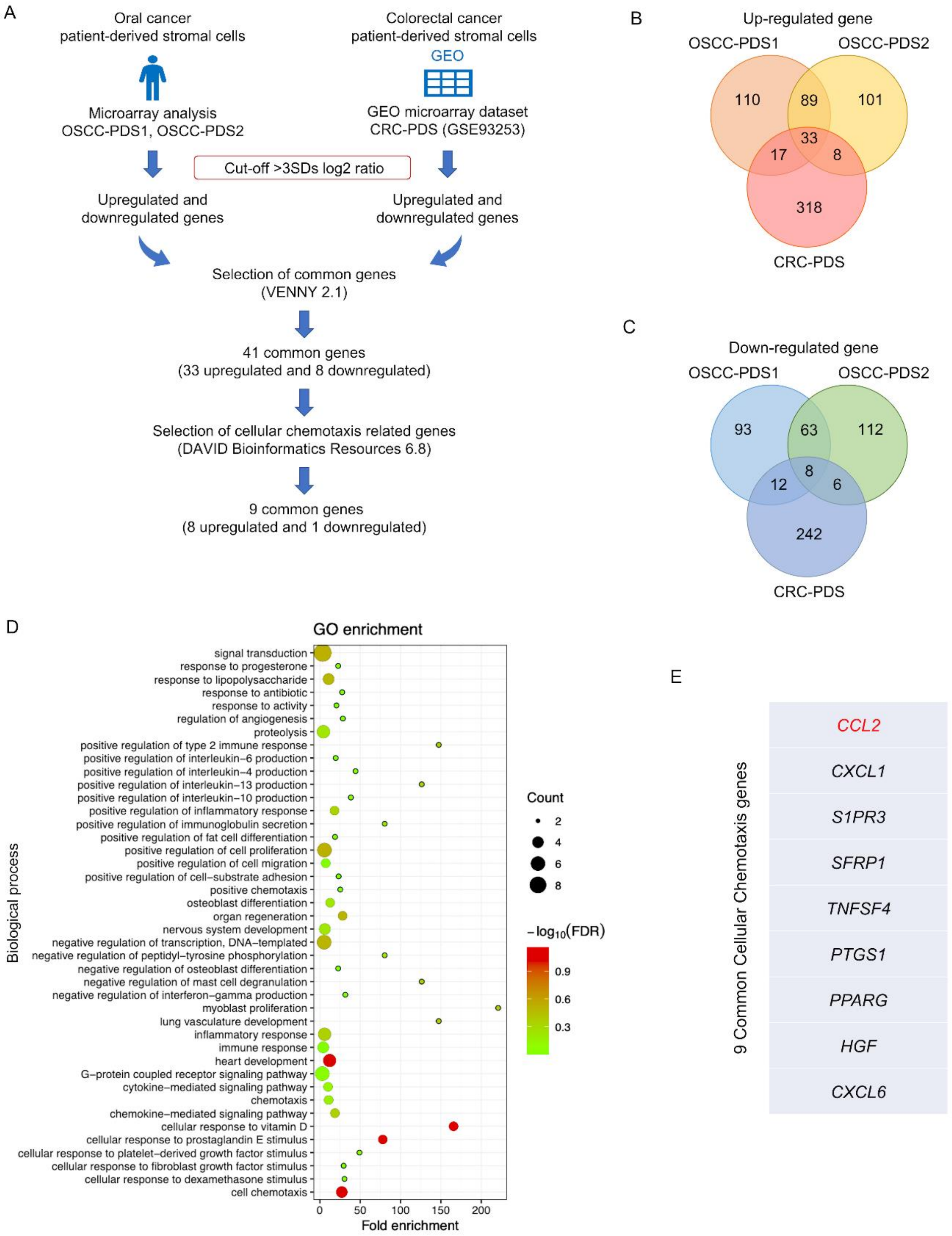


Supplementary Figure 1. Isolation of PDS from oral squamous cell carcinoma tissue specimens: (A) Western blot showing E-cadherin, vimentin, and fibroblast activated protein (FAP) expression in HSC-2, HDF, PDS1, and PDS2. HSC-2 and HDF were used for positive control of E-cadherin and vimentin, respectively. Whole-cell lysate and culture supernatant were prepared from the cells cultured in a serum-free medium for 24 h. 20 µg protein sample was applied per lane. All antigen-antibody reactions were performed using the same membrane. There was no contamination of tumor cells (no expression of E-cadherin) in the isolated PDSs, showing the expression of vimentin and FAP. **(B)** Representative images of HSC-2, HDF, isolated PDS1, and PDS2. Arrows indicate the intercellular connection of cells. Scale bars, 500 µm.

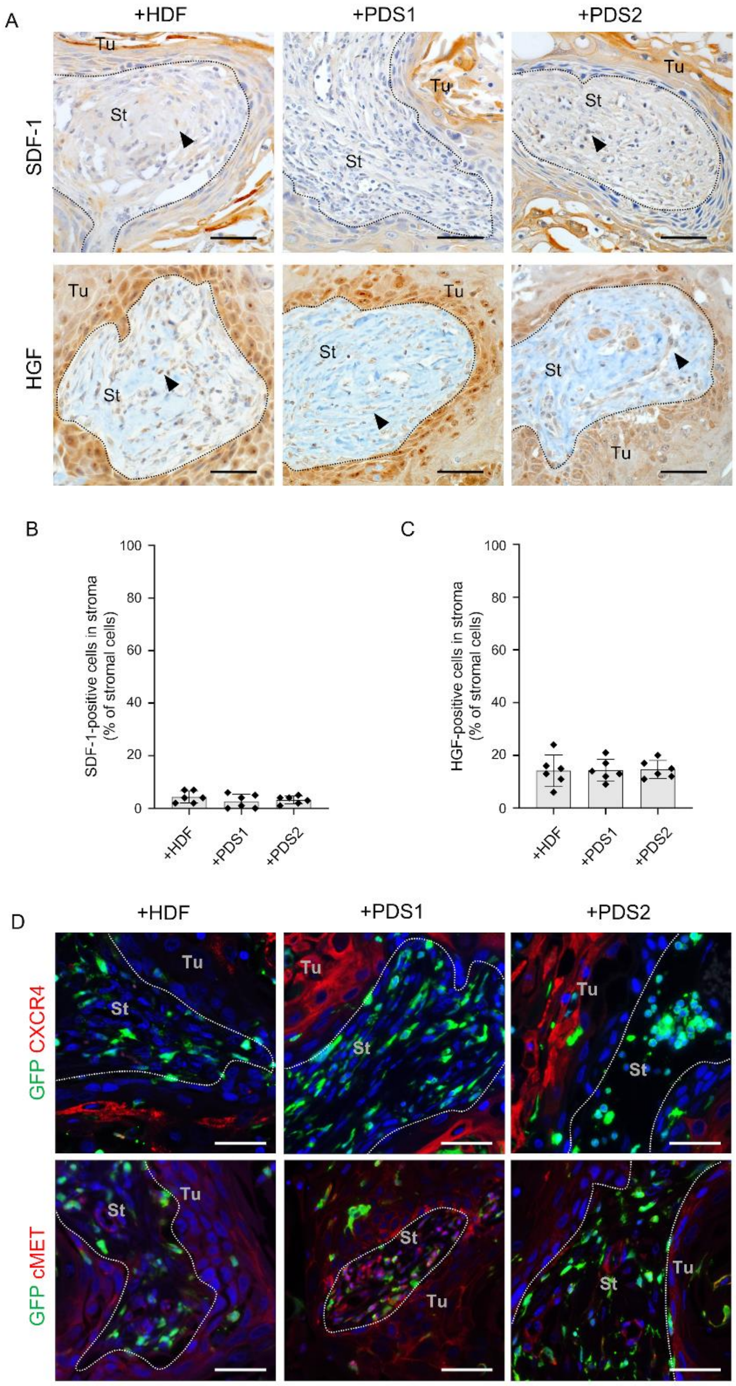


Supplementary Figure 2. The resident stroma influences the potential of BMDCs differentiation into TAMs but not on CAFs and TECs in OSCC. The tumor tissue sections of HSC-2, +HDF, +PDS1, and +PDS2 were analyzed for αSMA-positive CAFs, CD34-positive TECs, and CD11b-positive TAMs co-staining with GFP-positive BMDCs. **(A)** Representative images of double-fluorescent IHC for GFP (green) and αSMA (red). **(B)** Representative images of double-fluorescent IHC for GFP (green) and CD34 (red). Images on the bottom, high-magnified images. Arrowheads indicate CD34-positive vessel loop formation. **(C)** Representative images of double-fluorescent IHC for GFP (green) and CD11b (red). Insets are high-magnified images. Arrowheads indicate CD11b/GFP double-positive cells. **(D)** The rate of CD11b/GFP double-positive cells (% of GFP-positive cells). Dotted lines represent the boundary of the tumor (Tu) and stroma (St) area. Nuclei are stained with DAPI. Scale bars, 50 µm. HSC-2, HSC-2 alone xenograft. +HDF, HSC-2+HDF co-xenograft. +PDS1, HSC-2+PDS1 co-xenograft. +PDS2, HSC-2+PDS2 co-xenograft (5 fields per mouse, n = 6). All data are shown as Mean ± SD. Statistical analyses were performed using one-way ANOVA followed by Tukey's multiple comparison post hoc test; * $P < 0.05$.

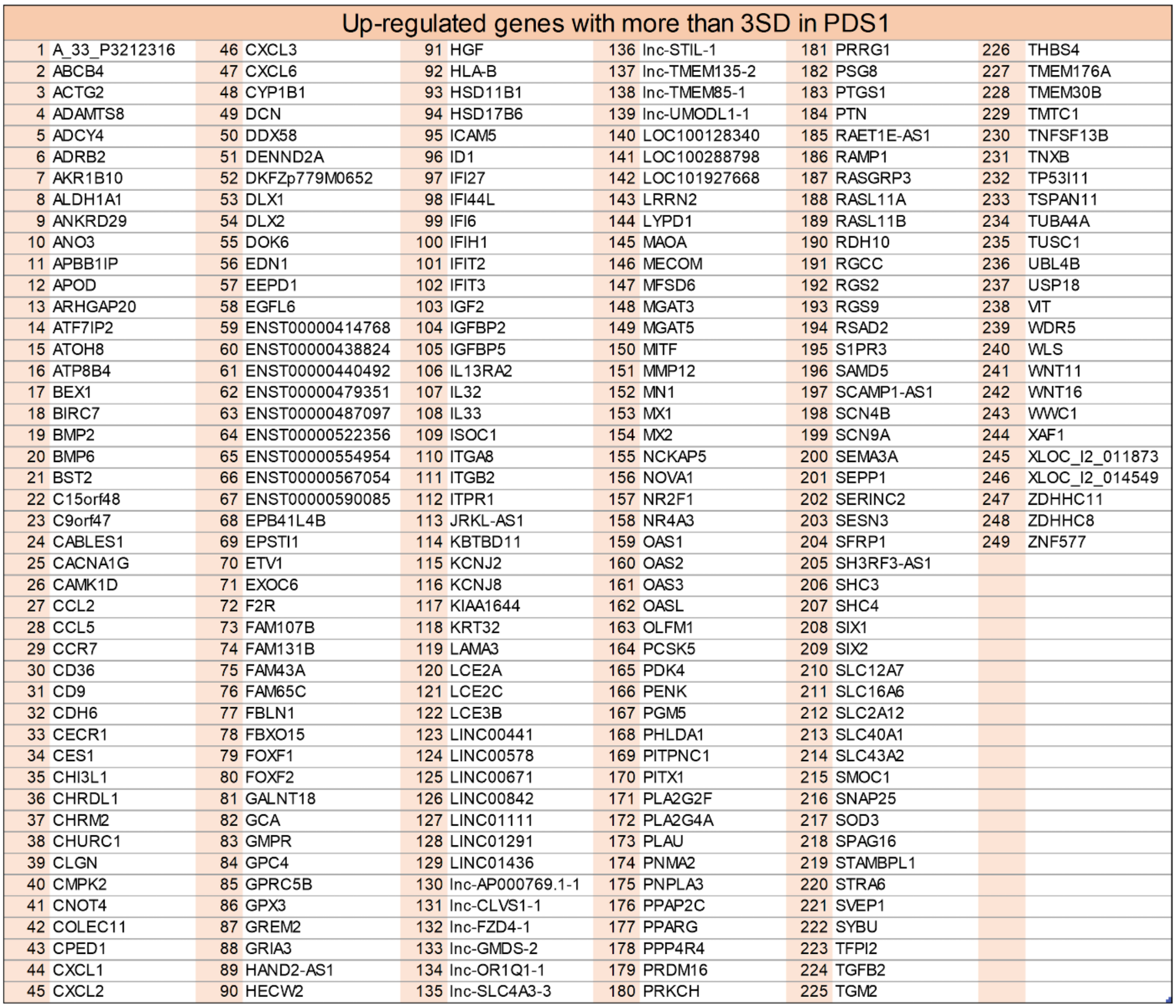
Supplementary Figure 3. The biological process enrichment analysis of common 193 differentially expressed genes (DEGs) of oral cancer PDS1 and PDS2. The biological process enrichment analysis was performed using DAVID and presented with a bubble plot. The color of each bubble represented the false discovery rate (FDR), and the size of the bubble represented the count of the genes.



Supplementary Figure 4. Gene expression profiles of OSCC-PDSs and CRC-PDS shared 9 cellular chemotaxis-related genes. **(A)** Flow chart of cellular chemotaxis-related genes screening. We analyzed the differentially expressed genes (DEGs) of oral squamous cell carcinoma (OSCC) PDS1 and PDS2 compared to HDF (upper left). We screened the GEO database and analyzed the DEGs of other cancer. We selected colorectal cancer (CRC) PDS from GEO (GSE93253), which has the same stroma isolation method. (Upper right). Then we compared DEGs of OSCC-PDSs and CRC-PDSs and selected the common DEGs by Venny 2.1. Then, we observed the cellular chemotaxis-related genes by DAVID bioinformatics Resources 6.8. **(B)** Venn diagram for commonly upregulated gene expression among OSCC-PDS1, OSCC-PDS2, and CRC-PDS. **(C)** Venn diagram for commonly downregulated gene expression among OSCC-PDS1, OSCC-PDS2, and CRC-PDS. **(D)** The biological process enrichment analysis of common 41 DEGs was performed using DAVID and presented with a bubble plot. The color of each bubble represented the false discovery rate (FDR), and the size of the bubble represented the count of the genes. **(E)** Table of 9 common cellular chemotaxis-related genes. *CCL2* is included in the shared DEG of OSCC-PDS and CRC-PDS.



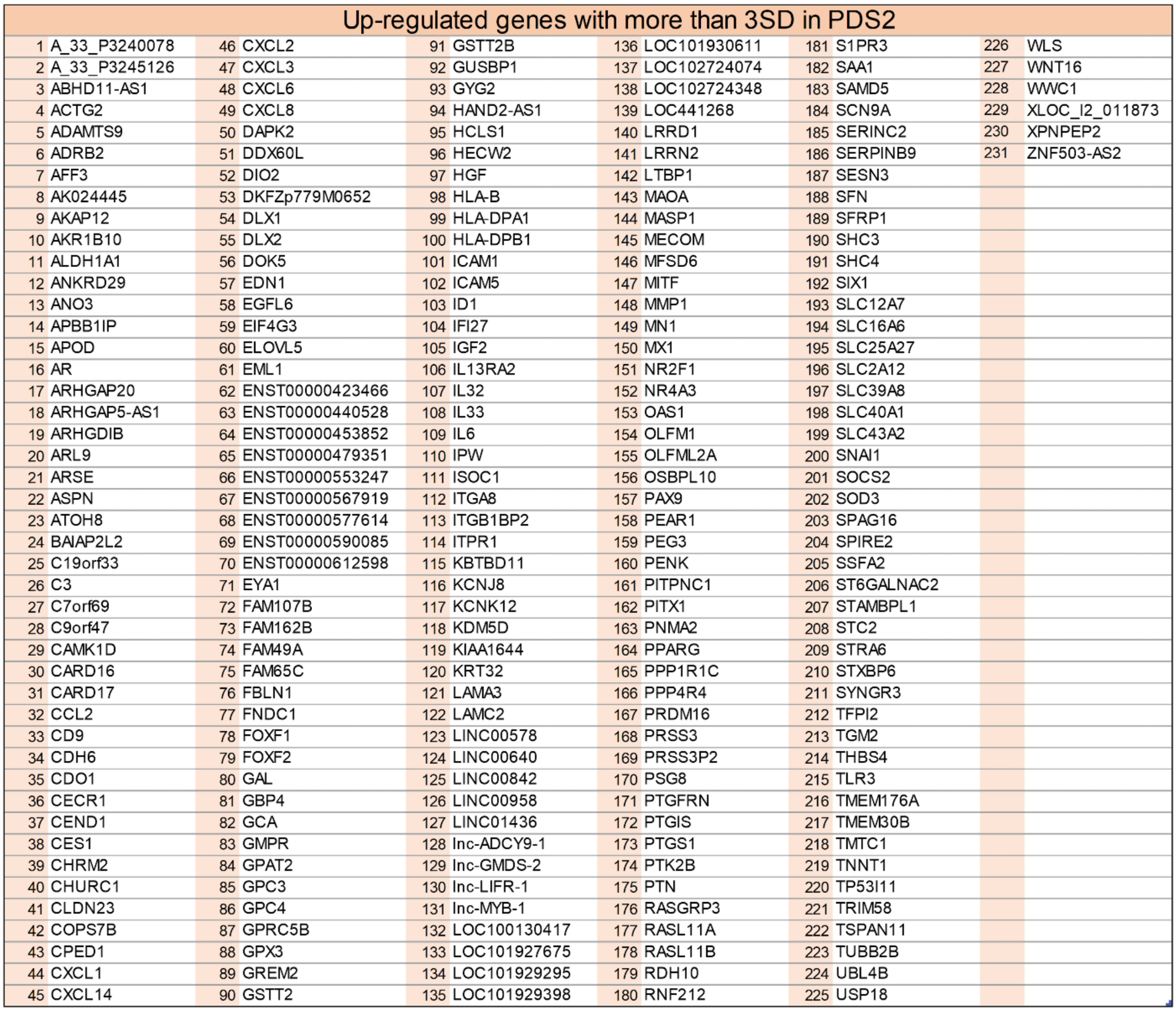
Supplementary Figure 5. SDF1 and HGF are the weak stromal secreted factors for BMDCs recruitment in OSCC. (A) IHC features of SDF-1 (upper panels) and HGF (lower panel). Arrows indicate positive stromal cells. Dotted lines represent the boundary of the tumor (Tu) and stroma (St) area. Scale bars, 50 μm. **(B)** The rate of SDF-1-positive cells in the stroma. **(C)** The rate of HGF-positive cells in the stroma. The positive cells were calculated as the percentage of total stromal cells using Image J software. **(D)** Representative images of double-fluorescent IHC for GFP (green) and CXCR4 (red) (upper panels) or cMet (red) (lower panels). Dotted lines represent the boundary of the tumor (Tu) and stroma (St) area. Nuclei are stained with DAPI. Scale bars, 50 μm. +HDF, HSC-2+HDF co-xenograft. +PDS1, HSC-2+PDS1 co-xenograft. +PDS2, HSC-2+PDS2 co-xenograft (5 fields per mouse, n = 6). All data are shown as Mean ± SD. Statistical analyses were performed using one-way ANOVA followed by Tukey's multiple comparison post hoc test.



Up-regulated genes with more than 3SD in PDS1

1	A_33_P3212316
2	ABCB4
3	ACTG2
4	ADAMTS8
5	ADCY4
6	ADRB2
7	AKR1B10
8	ALDH1A1
9	ANKRD29
10	ANO3
11	APBB1IP
12	APOD
13	ARHGAP20
14	ATF7IP2
15	ATOH8
16	ATP8B4
17	BEX1
18	BIRC7
19	BMP2
20	BMP6
21	BST2
22	C15orf48
23	C9orf47
24	CABLES1
25	CACNA1G
26	CAMK1D
27	CCL2
28	CCL5
29	CCR7
30	CD36
31	CD9
32	CDH6
33	CECR1
34	CES1
35	CHI3L1
36	CHRDL1
37	CHRM2
38	CHURC1
39	CLGN
40	CMPK2
41	CNOT4
42	COLEC11
43	CPED1
44	CXCL1
45	CXCL2
46	CXCL3
47	CXCL6
48	CYP1B1
49	DCN
50	DDX58
51	DENND2A
52	DKFZp779M0652
53	DLX1
54	DLX2
55	DOK6
56	EDN1
57	EEPD1
58	EGFL6
59	ENST00000414768
60	ENST00000438824
61	ENST00000440492
62	ENST00000479351
63	ENST00000487097
64	ENST00000522356
65	ENST00000554954
66	ENST00000567054
67	ENST00000590085
68	EPB41L4B
69	EPSTI1
70	ETV1
71	EXOC6
72	F2R
73	FAM107B
74	FAM131B
75	FAM43A
76	FAM65C
77	FBLN1
78	FBXO15
79	FOXF1
80	FOXF2
81	GALNT18
82	GCA
83	GMPR
84	GPC4
85	GPRC5B
86	GPX3
87	GREM2
88	GRIA3
89	HAND2-AS1
90	HECW2
91	HGF
92	HLA-B
93	HSD11B1
94	HSD17B6
95	ICAM5
96	ID1
97	IFI27
98	IFI44L
99	IFI6
100	IFIH1
101	IFIT2
102	IFIT3
103	IGF2
104	IGFBP2
105	IGFBP5
106	IL13RA2
107	IL32
108	IL33
109	ISOC1
110	ITGA8
111	ITGB2
112	ITPR1
113	JRKL-AS1
114	KBTBD11
115	KCNJ2
116	KCNJ8
117	KIAA1644
118	KRT32
119	LAMA3
120	LCE2A
121	LCE2C
122	LCE3B
123	LINC00441
124	LINC00578
125	LINC00671
126	LINC00842
127	LINC01111
128	LINC01291
129	LINC01436
130	lnc-AP000769.1-1
131	lnc-CLVS1-1
132	lnc-FZD4-1
133	lnc-GMDS-2
134	lnc-OR1Q1-1
135	lnc-SLC4A3-3
136	lnc-STIL-1
137	lnc-TMEM135-2
138	lnc-TMEM85-1
139	lnc-UMODL1-1
140	LOC100128340
141	LOC100288798
142	LOC101927668
143	LRRN2
144	LYPD1
145	MAOA
146	MECOM
147	MFSD6
148	MGAT3
149	MGAT5
150	MITF
151	MMP12
152	MN1
153	MX1
154	MX2
155	NCKAP5
156	NOVA1
157	NR2F1
158	NR4A3
159	OAS1
160	OAS2
161	OAS3
162	OASL
163	OLFM1
164	PCSK5
165	PDK4
166	PENK
167	PGM5
168	PHLDA1
169	PITPNC1
170	PITX1
171	PLA2G2F
172	PLA2G4A
173	PLAU
174	PNMA2
175	PNPLA3
176	PPAP2C
177	PPARG
178	PPP4R4
179	PRDM16
180	PRKCH
181	PRRG1
182	PSG8
183	PTGS1
184	PTN
185	RAET1E-AS1
186	RAMP1
187	RASGRP3
188	RASL11A
189	RASL11B
190	RDH10
191	RGCC
192	RGS2
193	RGS9
194	RSAD2
195	S1PR3
196	SAMD5
197	SCAMP1-AS1
198	SCN4B
199	SCN9A
200	SEMA3A
201	SEPP1
202	SERINC2
203	SESN3
204	SFRP1
205	SH3RF3-AS1
206	SHC3
207	SHC4
208	SIX1
209	SIX2
210	SLC12A7
211	SLC16A6
212	SLC2A12
213	SLC40A1
214	SLC43A2
215	SMOC1
216	SNAP25
217	SOD3
218	SPAG16
219	STAMBPL1
220	STRA6
221	SVEP1
222	SYBU
223	TFPI2
224	TGFB2
225	TGM2
226	THBS4
227	TMEM176A
228	TMEM30B
229	TMTC1
230	TNFSF13B
231	TNXB
232	TP53I11
233	TSPAN11
234	TUBA4A
235	TUSC1
236	UBL4B
237	USP18
238	VIT
239	WDR5
240	WLS
241	WNT11
242	WNT16
243	WWC1
244	XAF1
245	XLOC_l2_011873
246	XLOC_l2_014549
247	ZDHHC11
248	ZDHHC8
249	ZNF577

Supplementary Table 1. Upregulated genes with more than 3SDs in PDS1. Gene expression of PDS1 was analyzed by the Agilent microarray method. Comparing with HDF, fold-change, 3SDs Log2(fold-change) were calculated.



Up-regulated genes with more than 3SD in PDS2

1	A_33_P3240078
2	A_33_P3245126
3	ABHD11-AS1
4	ACTG2
5	ADAMTS9
6	ADRB2
7	AFF3
8	AK024445
9	AKAP12
10	AKR1B10
11	ALDH1A1
12	ANKRD29
13	ANO3
14	APBB1IP
15	APOD
16	AR
17	ARHGAP20
18	ARHGAP5-AS1
19	ARHGDIB
20	ARL9
21	ARSE
22	ASPN
23	ATOH8
24	BAIAP2L2
25	C19orf33
26	C3
27	C7orf69
28	C9orf47
29	CAMK1D
30	CARD16
31	CARD17
32	CCL2
33	CD9
34	CDH6
35	CDO1
36	CECR1
37	CEND1
38	CES1
39	CHRM2
40	CHURC1
41	CLDN23
42	COPS7B
43	CPED1
44	CXCL1
45	CXCL14
46	CXCL2
47	CXCL3
48	CXCL6
49	CXCL8
50	DAPK2
51	DDX60L
52	DIO2
53	DKFZp779M0652
54	DLX1
55	DLX2
56	DOK5
57	EDN1
58	EGFL6
59	EIF4G3
60	ELOVL5
61	EML1
62	ENST00000423466
63	ENST00000440528
64	ENST00000453852
65	ENST00000479351
66	ENST00000553247
67	ENST00000567919
68	ENST00000577614
69	ENST00000590085
70	ENST00000612598
71	EYA1
72	FAM107B
73	FAM162B
74	FAM49A
75	FAM65C
76	FBLN1
77	FNDC1
78	FOXF1
79	FOXF2
80	GAL
81	GBP4
82	GCA
83	GMPR
84	GPAT2
85	GPC3
86	GPC4
87	GPRC5B
88	GPX3
89	GREM2
90	GSTT2
91	GSTT2B
92	GUSBP1
93	GYG2
94	HAND2-AS1
95	HCLS1
96	HECW2
97	HGF
98	HLA-B
99	HLA-DPA1
100	HLA-DPB1
101	ICAM1
102	ICAM5
103	ID1
104	IFI27
105	IGF2
106	IL13RA2
107	IL32
108	IL33
109	IL6
110	IPW
111	ISOC1
112	ITGA8
113	ITGB1BP2
114	ITPR1
115	KBTBD11
116	KCNJ8
117	KCNK12
118	KDM5D
119	KIAA1644
120	KRT32
121	LAMA3
122	LAMC2
123	LINC00578
124	LINC00640
125	LINC00842
126	LINC00958
127	LINC01436
128	lnc-ADCY9-1
129	lnc-GMDS-2
130	lnc-LIFR-1
131	lnc-MYB-1
132	LOC100130417
133	LOC101927675
134	LOC101929295
135	LOC101929398
136	LOC101930611
137	LOC102724074
138	LOC102724348
139	LOC441268
140	LRRD1
141	LRRN2
142	LTBP1
143	MAOA
144	MASP1
145	MECOM
146	MFSD6
147	MITF
148	MMP1
149	MN1
150	MX1
151	NR2F1
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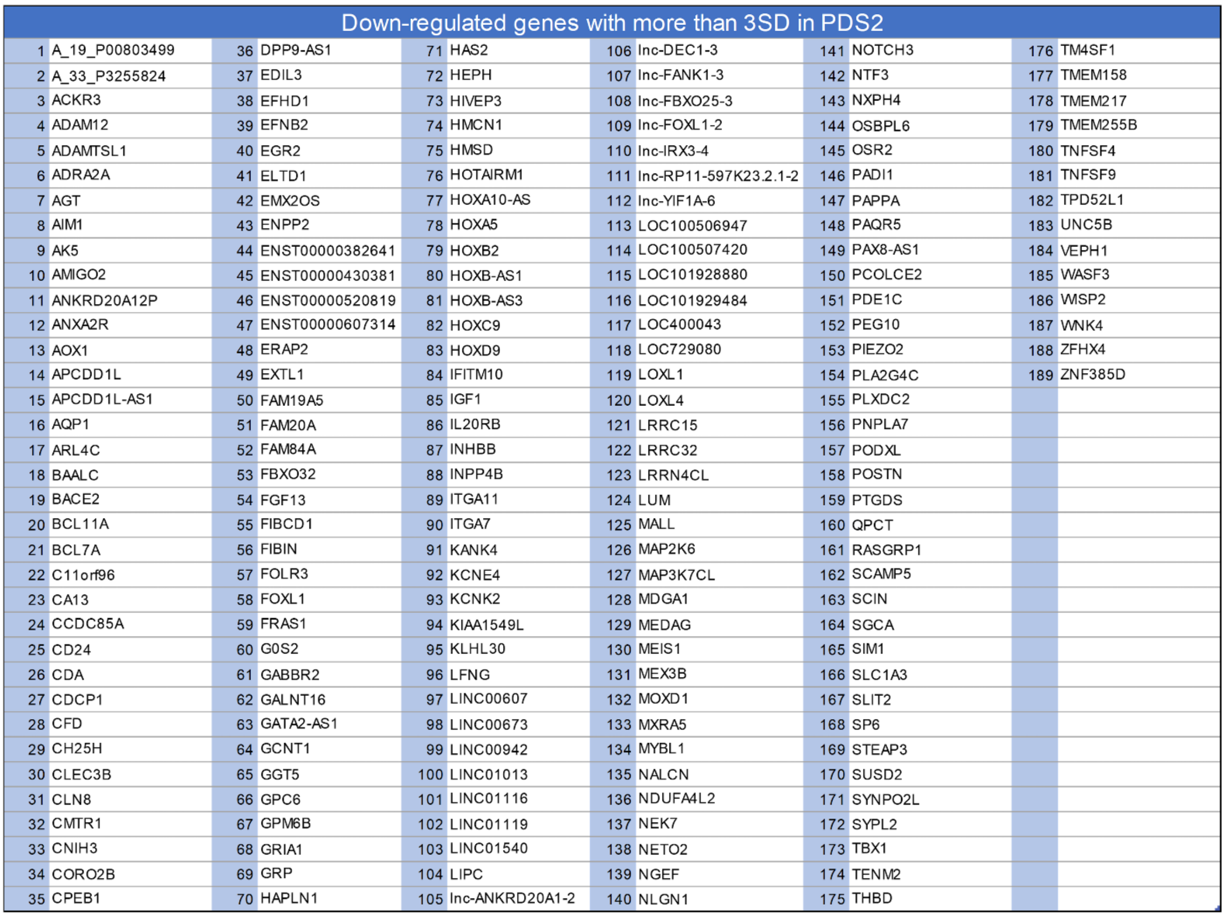
154	OLFM1
155	OLFML2A
156	OSBPL10
157	PAX9
158	PEAR1
159	PEG3
160	PENK
161	PITPNC1
162	PITX1
163	PNMA2
164	PPARG
165	PPP1R1C
166	PPP4R4
167	PRDM16
168	PRSS3
169	PRSS3P2
170	PSG8
171	PTGFRN
172	PTGIS
173	PTGS1
174	PTK2B
175	PTN
176	RASGRP3
177	RASL11A
178	RASL11B
179	RDH10
180	RNF212
181	S1PR3
182	SAA1
183	SAMD5
184	SCN9A
185	SERINC2
186	SERPINB9
187	SESN3
188	SFN
189	SFRP1
190	SHC3
191	SHC4
192	SIX1
193	SLC12A7
194	SLC16A6
195	SLC25A27
196	SLC2A12
197	SLC39A8
198	SLC40A1
199	SLC43A2
200	SNAI1
201	SOCS2
202	SOD3
203	SPAG16
204	SPIRE2
205	SSFA2
206	ST6GALNAC2
207	STAMBPL1
208	STC2
209	STRA6
210	STXBP6
211	SYNGR3
212	TFPI2
213	TGM2
214	THBS4
215	TLR3
216	TMEM176A
217	TMEM30B
218	TMTC1
219	TNNT1
220	TP53I11
221	TRIM58
222	TSPAN11
223	TUBB2B
224	UBL4B
225	USP18
226	WLS
227	WNT16
228	WWC1
229	XLOC_l2_011873
230	XPNPEP2
231	ZNF503-AS2

Supplementary Table 2. Upregulated genes with more than 3SDs in PDS2. Gene expression of PDS2 was analyzed by the Agilent microarray method. Comparing with HDF, fold-change, 3SDs Log2(fold-change) were calculated.

Down-regulated genes with more than 3SD in PDS1											
1	A_19_P00803499	31	COL15A1	61	FRMD4A	91	KCNE4	121	LRRC15	151	SKAP2
2	ACAN	32	COL4A5	62	GALNT16	92	KCNG1	122	LRRC17	152	SLC27A5
3	ADAM12	33	CRYBB2	63	GATA2-AS1	93	KCNJ6	123	LYPD6	153	SLC6A9
4	ADAMTSL1	34	CRYBB2P1	64	GFRA1	94	KCNK1	124	LYPD6B	154	SLC7A5
5	ADH1A	35	CXCL12	65	GLS	95	KCNK2	125	LZTS1	155	SPP1
6	ADH1C	36	DC378344	66	GNG4	96	KIF26B	126	MALL	156	SYPL2
7	ADM2	37	DNAH12	67	GPR162	97	KRT18	127	MAP2K6	157	SYT1
8	ADRA1D	38	DPEP3	68	GRP	98	KRT18P55	128	MEOX2	158	SYTL2
9	ADRA2A	39	DPT	69	GRPR	99	KRT19	129	MEST	159	TBX1
10	AGT	40	EGR2	70	HAPLN1	100	KRT19P2	130	MEX3B	160	TENM2
11	AMIGO2	41	ELTD1	71	HAS1	101	LFNG	131	MOCS3	161	TES
12	ANXA2R	42	EMB	72	HECTD2	102	LIMCH1	132	MYOD1	162	TGFB3
13	APCDD1L	43	EMX2OS	73	HEPH	103	LINC00673	133	NETO2	163	THC2596076
14	AQP1	44	ENST00000382641	74	HIVEP3	104	LINC01013	134	NNMT	164	TINAGL1
15	ATP7B	45	ENST00000430381	75	HMCN1	105	LINC01116	135	NTF3	165	TMEM217
16	BAALC	46	ENST00000432694	76	HMSD	106	LINC01119	136	NXPH4	166	TNFSF4
17	BACE2	47	ENST00000438158	77	HNF4A-AS1	107	LINC01133	137	PCBP3	167	TNFSF9
18	BHLHE40	48	ENST00000520524	78	HOTAIRM1	108	LIPC	138	PCOLCE2	168	TPD52L1
19	BRINP1	49	ENST00000619960	79	HOXA10-AS	109	lnc-ADA-1	139	PDE11A	169	ULBP1
20	C10orf10	50	EPB41L3	80	HOXA13	110	lnc-ATIC-2	140	PDE1A	170	UNC5B
21	C11orf96	51	ERAP2	81	HOXB-AS3	111	lnc-CCDC69-1	141	PDK3	171	WISP2
22	CA12	52	FADS2	82	HOXC4	112	lnc-EBF1-2	142	PLA2G4C	172	WNK4
23	CARD9	53	FAM19A5	83	HOXC6	113	lnc-FANK1-3	143	PLAC8	173	WNT2
24	CCDC8	54	FAM20A	84	HOXD-AS2	114	lnc-IRX3-4	144	PPP1R13L	174	XLOC_l2_011265
25	CDCA7	55	FBXO32	85	IGF2BP1	115	lnc-SCRG1-1	145	PRAME	175	XLOC_l2_014835
26	CGNL1	56	FIBCD1	86	IL20RB	116	lnc-YIF1A-6	146	RBMS3-AS3	176	XLOC_l2_015849
27	CH25H	57	FIBIN	87	IRX2	117	LOC100130938	147	REP15		
28	CMKLR1	58	FOS	88	ITGA11	118	LOC100507420	148	SCD		
29	CMTR1	59	FOXL2	89	ITGA9	119	LOC401557	149	SGCA		
30	COL12A1	60	FOXL2NB	90	ITGB2	120	LOXL4	150	SHROOM3		

Supplementary Table 3. Downregulated genes with more than 3SDs in PDS1. Gene expression of PDS1 was analyzed by the Agilent microarray method. Comparing with HDF, fold-change, 3SDs Log2(fold-change) were calculated.



Down-regulated genes with more than 3SD in PDS2											
1	A_19_P00803499	36	DPP9-AS1	71	HAS2	106	lnc-DEC1-3	141	NOTCH3	176	TM4SF1
2	A_33_P3255824	37	EDIL3	72	HEPH	107	lnc-FANK1-3	142	NTF3	177	TMEM158
3	ACKR3	38	EFHD1	73	HIVEP3	108	lnc-FBXO25-3	143	NXPH4	178	TMEM217
4	ADAM12	39	EFNB2	74	HMCN1	109	lnc-FOXL1-2	144	OSBPL6	179	TMEM255B
5	ADAMTSL1	40	EGR2	75	HMSD	110	lnc-IRX3-4	145	OSR2	180	TNFSF4
6	ADRA2A	41	ELTD1	76	HOTAIRM1	111	lnc-RP11-597K23.2.1-2	146	PADI1	181	TNFSF9
7	AGT	42	EMX2OS	77	HOXA10-AS	112	lnc-YIF1A-6	147	PAPPA	182	TPD52L1
8	AIM1	43	ENPP2	78	HOXA5	113	LOC100506947	148	PAQR5	183	UNC5B
9	AK5	44	ENST00000382641	79	HOXB2	114	LOC100507420	149	PAX8-AS1	184	VEPH1
10	AMIGO2	45	ENST00000430381	80	HOXB-AS1	115	LOC101928880	150	PCOLCE2	185	WASF3
11	ANKRD20A12P	46	ENST00000520819	81	HOXB-AS3	116	LOC101929484	151	PDE1C	186	WISP2
12	ANXA2R	47	ENST00000607314	82	HOXC9	117	LOC400043	152	PEG10	187	WNK4
13	AOX1	48	ERAP2	83	HOXD9	118	LOC729080	153	PIEZO2	188	ZFHX4
14	APCDD1L	49	EXTL1	84	IFITM10	119	LOXL1	154	PLA2G4C	189	ZNF385D
15	APCDD1L-AS1	50	FAM19A5	85	IGF1	120	LOXL4	155	PLXDC2		
16	AQP1	51	FAM20A	86	IL20RB	121	LRRC15	156	PNPLA7		
17	ARL4C	52	FAM84A	87	INHBB	122	LRRC32	157	PODXL		
18	BAALC	53	FBXO32	88	INPP4B	123	LRRN4CL	158	POSTN		
19	BACE2	54	FGF13	89	ITGA11	124	LUM	159	PTGDS		
20	BCL11A	55	FIBCD1	90	ITGA7	125	MALL	160	QPCT		
21	BCL7A	56	FIBIN	91	KANK4	126	MAP2K6	161	RASGRP1		
22	C11orf96	57	FOLR3	92	KCNE4	127	MAP3K7CL	162	SCAMP5		
23	CA13	58	FOXL1	93	KCNK2	128	MDGA1	163	SCIN		
24	CCDC85A	59	FRAS1	94	KIAA1549L	129	MEDAG	164	SGCA		
25	CD24	60	G0S2	95	KLHL30	130	MEIS1	165	SIM1		
26	CDA	61	GABBR2	96	LFNG	131	MEX3B	166	SLC1A3		
27	CDCP1	62	GALNT16	97	LINC00607	132	MOXD1	167	SLIT2		
28	CFD	63	GATA2-AS1	98	LINC00673	133	MXRA5	168	SP6		
29	CH25H	64	GCNT1	99	LINC00942	134	MYBL1	169	STEAP3		
30	CLEC3B	65	GGT5	100	LINC01013	135	NALCN	170	SUSD2		
31	CLN8	66	GPC6	101	LINC01116	136	NDUFA4L2	171	SYNPO2L		
32	CMTR1	67	GPM6B	102	LINC01119	137	NEK7	172	SYPL2		
33	CNIH3	68	GRIA1	103	LINC01540	138	NETO2	173	TBX1		
34	CORO2B	69	GRP	104	LIPC	139	NGEF	174	TENM2		
35	CPEB1	70	HAPLN1	105	lnc-ANKRD20A1-2	140	NLGN1	175	THBD		

Supplementary Table 4. Downregulated genes with more than 3SDs in PDS2. Gene expression of PDS2 was analyzed by the Agilent microarray method. Comparing with HDF, fold-change, 3SDs Log2(fold-change) were calculated.

Types of cells	Recruited BMDCs and subsets			
	HSC-2 alone	**HSC-2+HDF**	**HSC-2+PDS1**	**HSC-2+PDS2**
BMDCs (GFP-positive)	Low	High*	High****	High***
CAFs (αSMA-positive)	n.d	n.d	n.d	n.d
TECs (CD34-positive)	n.d	n.d	n.d	n.d
TAMs (CD11b-positive)	High	Low*	Low	Low
MDSCs (GR1/CD11b/Arg1 triple-positive)	Low	Low	$^{\Phi}$ High****	$^{\Phi}$ High****

Supplementary Table 5. Summarizing the data of BMDC infiltration and subsets in OSCC tumor models. Significant difference (* $P < 0.05$, *** $P < 0.001$, **** $P < 0.0001$) presented between the control group (HSC-2) and tumor/stroma co-xenografted groups (HSC-2+HDF, HSC-2+PDS1, and HSC-2+PDS2). n.d., not differentiated. $^{\Phi}$, significant difference ($P < 0.0001$) presented between HSC-2+PDS1/2 and HSC-2+HDF.

Primary antibody	**Immunized animal**	**Antigen retrieval**	**Dilution**	**Supplier**
GFP	Goat	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:500	Abcam (ab6673)
αSMA	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:200	Abcam (ab7817)
CD34	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:200	Abcam (ab81289)
CD11b	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:500	Abcam (ab133357)
GR1	Rat	0.1% Trypsin at 37°C for 5 min	1:200	Biolegend (#108401)
Arginase 1 (Arg1)	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:100	Cell signaling technology (#93668)
CCL2	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:500	Abcam (ab25124)
CCR2	Rabbit	Microwave heating in 0.01 mol/L Tris-EDTA buffer (pH 9.0) at 100°C for 1 min	1:250	Abcam (ab273050)
SDF-1	Rabbit	Microwave heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 1 min	1:200	Abcam (ab9797)
HGF	Rabbit	Cooker heating in 0.01 mol/L Tris-EDTA buffer (pH 9.0) at 100°C for 8 min	1:200	Abcam (ab83760)
cMet	Rabbit	Cooker heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 8 min	1:200	Abcam (ab51067)
CXCR4	Rabbit	Cooker heating in 0.01 mol/L citrate buffer (pH 6.0) at 100°C for 8 min	1:300	Abcam (ab124824)

Supplementary Table 6. Antibodies used in immunohistochemistry

Secondary antibody	**Immunized animal**	**Fluorescent dye**	**Supplier**
Anti-goat IgG	Donkey	Alexa Fluor 488	Thermo (Ref: A11055)
Anti-rabbit IgG	Donkey	Alexa Fluor 568	Thermo (Ref: A10042)

Supplementary Table 7. Antibodies used in double-fluorescent immunohistochemistry