

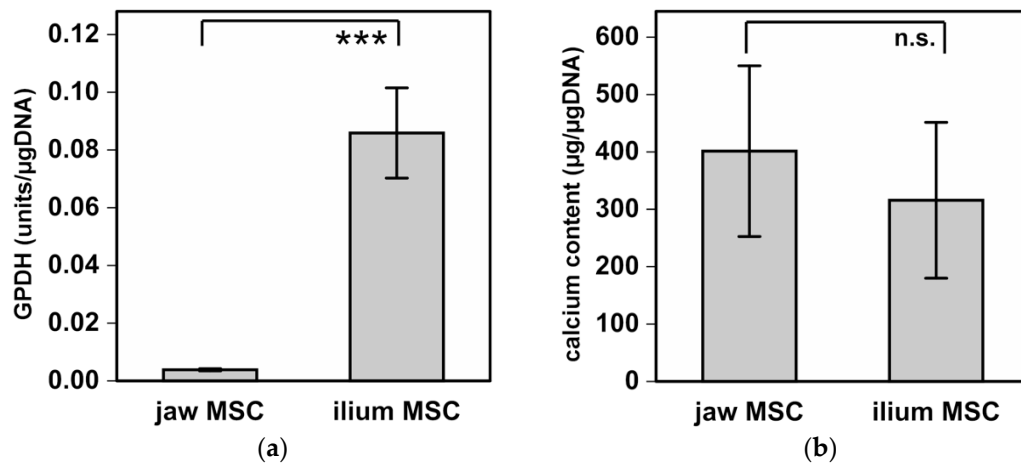


Figure S1. Comparison of differentiation levels between jaw and ilium MSCs. (a) GPDH activity at day 28 after adipogenic induction. (b) Calcium content at day 28 after osteogenic induction. Data are presented as mean $\pm$ standard error. $n = 5$, jaw MSC; $n = 10$, ilium MSC. *** $p < 0.001$; n.s., not significant (Student's t-test).

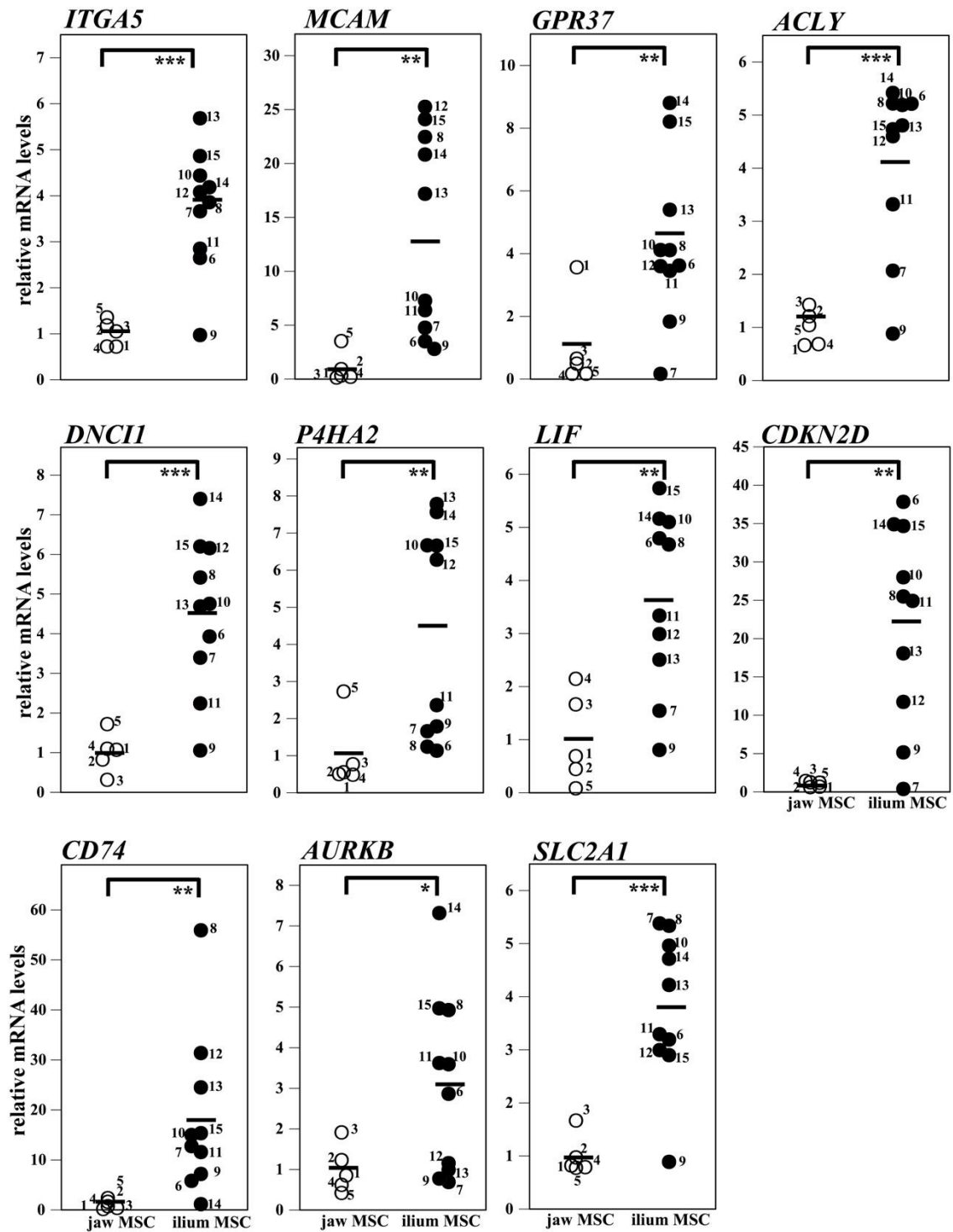


Figure S2. Comparison of expression levels between jaw and ilium MSCs of the predictor genes before adipogenic induction. 1–5 (open circles), jaw MSCs; 6–15 (closed circles), ilium MSCs. Bars represent mean values for each group. Student's t-test; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

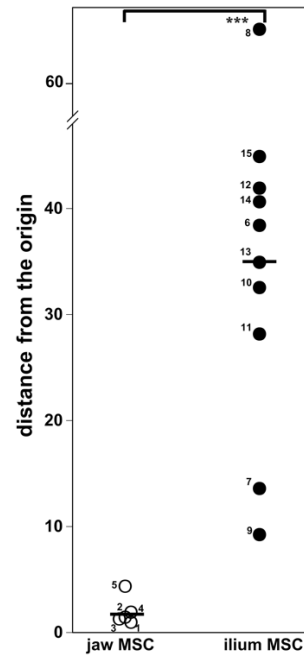


Figure S3. 3D analysis of *CDKN2D*, *CD74* and *MCAM* mRNA expression. Using SPSS, the scatter plots were drawn and distances between the origin and each point were calculated. The distances in jaw MSCs (open circles, Nos. 1-5) were compared with those in ilium MSCs (closed circles, 6-15). Bars indicated mean values for each group. Student's t-test; *** $p < 0.001$.

Table S1. Donor information.

donor ID number	tissue	age	sex	disease/operation
1	jaw bone marrow	63	Female	dental implant
2	jaw bone marrow	36	Male	fracture
3	jaw bone marrow	36	Female	fracture
4	jaw bone marrow	20	Male	jaw movement for orthodontic treatment
5	jaw bone marrow	28	Female	cyst removal
6	illium bone marrow	63	Male	periodontitis
7	illium bone marrow	39	Male	periodontitis
8	illium bone marrow	25	Male	periodontitis
9	illium bone marrow	64	Male	rebuilding of mandible
10	illium bone marrow	59	Male	arteriosclerosis of obliterated
11	illium bone marrow	55	Male	arteriosclerosis of obliterated
12	illium bone marrow	61	Male	diabetes mellitus
13	illium bone marrow	53	Male	Buerger's disease
14	illium bone marrow	81	Male	arteriosclerosis of obliterated
15	illium bone marrow	65	Male	arteriosclerosis of obliterated

Table S2. Correlation between gene expression levels before induction and GPDH activities after adipogenic induction in 15 MSCs.

donor ID number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	r		Probe Set ID
GPDH (units/ugDNA)	0.0039	0.0049	0.0044	0.0030	0.0030	0.0351	0.0221	0.0897	0.0437	0.0809	0.0971	0.0856	0.1302	0.0732	0.1911			
ITGA5	0.72	1.17	1.04	0.71	1.29	2.64	3.66	3.85	0.97	4.43	2.84	0.77	5.68	4.18	4.86	0.826	***	Hs00233743 m1
MCAM	0.19	0.90	0.11	0.30	2.77	3.49	4.75	22.44	2.79	7.25	6.37	25.23	17.17	20.81	24.10	0.812	***	Hs00174838 m1
GPB37	3.55	0.48	0.64	0.16	0.14	3.61	0.16	0.41	1.83	4.11	3.45	3.59	5.39	8.80	8.20	0.782	**	Hs00173744 m1
PSMCS6	0.78	1.28	0.95	1.05	0.90	2.34	0.41	2.58	0.48	2.09	1.49	1.81	2.16	3.03	3.42	0.769	**	Hs00267687 m1
ACLY	0.66	1.20	1.42	0.68	0.99	5.21	2.06	5.21	0.88	5.19	3.32	4.60	4.80	5.41	4.73	0.737	**	Hs00153764 m1
DNC1I	1.09	0.82	0.31	1.06	1.62	3.93	3.39	5.41	1.05	4.75	2.24	6.15	4.68	7.39	6.20	0.732	**	Hs00189392 m1
PH4A2	0.55	0.50	0.76	0.47	2.58	1.13	1.65	1.24	1.79	6.66	2.36	6.28	7.78	7.56	6.66	0.720	**	Hs00188349 m1
LIF	0.68	0.44	1.66	2.13	0.07	4.79	1.54	0.67	0.80	5.10	3.33	2.99	2.50	5.16	5.73	0.708	**	Hs00171455 m1
ZNF185	1.15	0.92	0.98	0.81	1.04	0.95	0.54	1.20	0.24	0.93	0.89	2.01	1.38	1.98	1.78	0.708	**	Hs00200253 m1
CDKN2D	0.64	0.59	1.22	1.33	0.82	37.81	0.35	25.47	5.13	27.98	24.88	11.71	18.05	34.87	34.65	0.703	**	Hs00176481 m1
DPPYSL3	1.17	1.03	0.84	0.46	1.48	1.18	0.93	1.53	0.36	1.75	0.87	1.59	1.92	1.43	1.96	0.664	**	Hs00181665 m1
INPP5E	0.54	1.45	1.48	1.20	0.32	2.64	0.63	2.45	0.60	1.71	1.16	1.28	2.25	2.36	2.79	0.650	**	Hs00219878 m1
UBE2C	1.17	1.43	1.36	0.42	0.60	2.01	0.45	3.20	0.41	2.32	3.21	0.97	0.86	4.22	3.86	0.612	*	Hs00853610 g1
E2F1	0.82	0.95	1.42	1.04	0.74	3.14	0.94	3.98	0.54	2.25	2.60	1.48	1.38	4.02	3.50	0.608	*	Hs00153451 m1
CNCN81	0.94	1.35	1.33	0.51	0.84	1.78	0.38	2.47	0.39	1.54	1.92	0.83	0.80	3.34	3.47	0.598	*	Hs00259126 m1
CD74	0.68	1.57	0.33	0.12	1.97	5.77	12.72	55.89	7.15	14.94	11.53	31.35	24.47	1.11	15.32	0.561	*	Hs00269961 m1
COL7A1	0.59	1.56	1.41	0.38	1.01	4.45	0.99	1.84	0.66	1.45	1.38	1.16	3.05	3.24	3.90	0.561	*	Hs00164310 m1
AURKB	0.84	1.22	1.91	0.61	0.39	2.86	0.68	0.49	0.77	3.59	3.62	1.15	0.99	7.31	4.92	0.556	*	Hs00177782 m1
AMD1	0.80	0.95	1.26	0.73	1.24	1.57	0.60	1.16	0.29	1.15	0.95	1.37	1.27	1.83	1.99	0.545	*	Hs00750876 s1
CDC20	1.17	1.38	1.51	0.32	0.59	2.09	1.17	3.20	0.27	1.93	2.45	0.90	0.73	4.16	3.37	0.526	*	Hs00415851 g1
SLC2A1	0.78	0.97	1.66	0.81	0.75	3.19	5.38	5.33	0.89	4.96	3.29	2.99	4.22	4.71	2.90	0.526	*	Hs00197884 m1
MCM7	0.75	1.20	1.26	0.80	0.97	2.61	1.50	2.43	0.36	1.47	2.03	1.04	1.08	2.88	2.72	0.517	*	Hs00428518 m1
TRIP13	0.93	1.12	1.70	0.54	0.69	2.04	3.34	2.32	0.38	1.42	1.78	0.74	0.81	2.85	2.61	0.501		Hs00188500 m1
HLA-DR4	0.56	1.42	0.01	0.18	2.33	6.16	11.93	103.25	13.07	54.58	22.80	126.90	64.33	0.61	19.08	0.498		Hs00219578 m1
LRP8	0.62	1.56	1.09	0.57	1.10	6.60	1.53	1.52	0.76	3.46	1.55	3.37	3.93	6.25	4.62	0.493		Hs00182998 m1
UBE2S	0.82	1.27	1.37	0.67	0.85	1.65	0.65	1.15	0.20	1.46	1.15	0.78	1.04	2.00	2.24	0.492		Hs00819350 m1
PRKAG1	0.84	1.26	1.06	0.81	1.01	1.49	0.37	1.42	0.25	1.13	0.70	1.01	1.16	1.37	1.74	0.460		Hs00176952 m1
IFI44	1.09	1.19	0.99	1.06	0.65	0.89	0.41	1.15	0.24	1.07	0.92	0.72	0.53	0.92	2.26	0.454		Hs00197427 m1
EFEMP1	0.50	1.48	0.40	1.18	1.45	1.26	2.02	9.93	2.11	3.36	4.13	1.60	5.10	2.74	1.14	0.437		Hs00251661 m1
RRM2	1.01	1.11	1.72	0.50	0.65	1.82	0.41	2.49	0.30	1.68	1.81	0.63	0.62	2.75	2.26	0.436		Hs00357247 g1
TAF1D	0.75	1.31	0.98	0.93	1.02	2.52	0.55	1.18	0.44	1.30	1.19	1.38	1.53	1.76	1.81	0.427		Hs00225533 m1
IL13R2A	1.19	1.30	0.91	0.25	1.28	5.52	0.10	1.32	0.24	0.33	0.72	7.79	2.88	6.13	4.67	0.411		Hs00152924 m1
ICAM1	0.32	1.52	0.06	2.23	0.87	0.83	2.54	2.15	0.23	0.73	0.87	2.06	3.67	0.76	2.06	0.393		Hs00277001 m1
ARGH2B1	2.66	1.45	0.19	0.50	0.18	1.09	8.46	12.46	0.19	2.19	0.92	1.82	1.94	6.30	5.34	0.347		Hs00171288 m1
TGDM	0.51	0.30	0.09	0.70	3.33	4.96	19.72	27.47	1.90	15.53	8.21	5.03	7.32	5.67	4.73	0.324		Hs00190278 m1
HGF	0.91	1.45	0.55	1.43	0.65	1.23	0.62	0.95	0.23	1.51	0.70	1.80	0.75	1.08	1.66	0.305		Hs00300159 m1
PROS1	0.61	1.02	0.24	1.89	1.25	1.17	0.19	0.79	0.46	1.86	1.03	0.70	1.86	0.71	1.30	0.301		Hs00165590 m1
CTGF	0.67	0.82	0.45	1.93	1.14	3.35	1.02	1.02	1.47	1.77	1.89	2.10	1.86	1.75	0.289			Hs00170014 m1
ITGA3	0.55	0.72	0.92	0.73	2.06	2.28	0.93	1.50	0.11	0.68	0.50	1.68	0.84	1.41	2.22	0.286		Hs00233722 m1
KCTD12	1.20	0.90	1.47	0.56	0.85	1.86	0.94	1.07	0.31	1.39	0.50	1.31	0.86	0.98	1.91	0.286		Hs00540818 s1
TRIB2	0.93	0.86	0.50	1.87	0.84	1.23	0.83	1.32	0.28	1.32	0.97	0.83	0.83	1.15	1.55	0.279		Hs00222224 m1
LAM43	0.90	0.63	1.79	0.54	1.12	2.07	0.23	0.29	0.72	1.00	0.51	1.01	1.80	0.84	1.71	0.239		Hs00165042 m1
MCM5	0.81	1.12	1.30	0.99	0.76	1.20	0.85	1.43	0.22	0.88	1.09	0.54	0.48	1.81	1.65	0.234		Hs00198823 m1
TK1	0.71	1.55	1.63	0.53	0.57	2.18	0.77	2.20	0.21	1.12	1.16	0.70	0.45	2.39	1.80	0.233		Hs00177406 m1
MGP	1.50	1.71	0.01	0.56	1.22	0.75	0.61	0.79	0.42	4.83	0.26	1.02	3.27	0.18	1.05	0.232		Hs00179899 m1
HLA-DRB	1.00	1.00	1.00	0.96	0.72	1.00	33.48	1.83	56.93	180.53	9.18	763.47	45.31	1.42	32.79	0.197		Hs00734212 m1
NPR3	0.39	0.49	0.26	3.76	1.12	1.75	0.90	5.97	0.91	7.99	1.98	1.19	0.93	1.28	1.00	0.188		Hs00168558 m1
IGFBP7	0.64	0.87	0.55	2.14	0.80	0.59	0.51	0.98	0.30	1.21	1.19	0.35	0.69	0.65	1.52	0.187		Hs00266026 m1
MICA	0.78	0.53	0.60	1.75	1.37	1.10	0.49	1.06	0.41	1.15	0.69	0.70	1.55	2.49	1.09	0.186		Hs00741286 m1
IGF1	1.00	1.14	0.23	1.51	1.13	1.18	0.24	0.28	0.42	1.56	0.73	0.88	1.46	0.42	1.17	0.181		Hs00153126 m1
TCF19	0.70	0.97	1.79	0.74	0.79	0.98	0.79	1.09	0.27	0.85	0.95	0.53	0.48	1.90	1.64	0.178		Hs00232525 m1
GMFG	0.32	1.57	0.70	0.94	1.49	1.50	0.37	8.25	0.03	0.38	0.70	0.69	0.22	0.30	0.50	0.100		Hs00178167 m1
PLEC1	0.76	0.97	1.21	0.82	1.24	1.60	1.16	1.05	0.29	0.53	0.52	0.86	1.11	1.21	1.39	0.080		Hs00356977 m1
PRG1	0.26	0.36	0.52	0.72	3.23	0.58	1.36	1.45	0.24	0.85	0.58	1.31	1.25	1.02	0.94	0.040		Hs00160444 m1
BM1I	0.72	0.94	1.38	0.90	1.07	1.15	0.36	0.54	0.27	0.85	0.56	0.70	1.01	0.96	1.19	0.035		Hs00180411 m1
NFE2L3	0.80	1.97	1.29	0.72	0.22	1.04	1.07	2.38	0.12	0.77	0.64	0.79	0.39	1.15	0.71	-0.074		Hs00852569 g1
VLDLR	0.46	1.18	1.54	0.60	1.23	0.68	0.56	0.45	0.10	0.68	0.32	0.34	2.23	0.62	0.38	-0.080		Hs00182461 m1
ITGA6	1.30	1.15	0.94	0.22	1.38	0.87	0.06	0.05	0.01	0.13	0.13	0.45	0.63	1.48	1.26	-0.091		Hs00173952 m1
SLC16A4	0.94	1.49	1.41	0.43	0.73	1.54	0.58	1.32	0.19	0.54	0.41	0.84	0.63	0.62	1.06	-0.095		Hs00190794 m1
TFPI2	0.41	0.76	0.17	3.17	0.51	0.39	1.10	1.19	0.18	0.34	0.12	1.02	0.27	1.09	1.08	-0.099		Hs00197918 m1
CD97	0.38	1.37	1.92	1.05	0.28	1.67	0.56	0.90	0.25	0.61	0.48	0.69	0.62	1.45	1.01	-0.118		Hs00173542 m1
PGR	1.56	1.69	1.32	0.17	0.25	12.80	0.17	0.39	0.24	0.72	0.17	0.75	0.23	0.79	0.30	-0.180		Hs00172183 m1
HNRPU	1.00	0.92	0.96	1.15	0.97	1.00	0.44	0.85	0.19	0.62	0.57	0.55	0.75	0.82	0.92	-0.207		Hs00244919 m1
RAB3B	0.56	0.96	2.38	0.64	0.46	3.46	0.09	0.17	0.10	0.27	0.29	0.49	0.42	0.79	0.88	-0.222		Hs00267896 m1
EDG2	1.93	2.09	0.81	0.02	0.14	8.87	0.02	0.02	0.08	0.11	0.02	0.08	0.11	0.02	0.33	-0.234		Hs00173857 m1
SLCO1A2	0.06	0.06	0.06	4.80	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.52	0.06	0.06	-0.239		Hs00366488 m1
SPRY2	0.91	0.95	1.32	1.29	0.53	1.37	0.39	0.85	0.19	0.46	0.37	0.45	0.48	0.77	1.00	-0.244		Hs00183386 m1
API52	0.81	1.04	0.82	1.60	0.74	1.04	0.20	0.55	0.13	0.34	0.32	0.64	0.34	0.70	0.84			