

SUPPLEMENTARY TABLE S2. SURFACE MARKER EXPRESSION WITH GENE ID/CD NOMENCLATURE

<i>CD</i>	<i>Gene ID</i>	<i>Undifferentiated</i>	<i>Adipogenic</i>	<i>Osteogenic</i>
CD1a	CD1A	0.256	0.012	0.175
CD1b	CD1B	0.389	0.094	0
CD1d	CD1D	0.187	4.15	0
CD2	CD2	0.979	0.662	0.037
CD3	CD3	0.837	0.268	2.55
CD4	CD4	0.215	1.83	0.011
CD4v4	CD4	0.221	1.09	0.404
CD5	CD5	0.489	0.558	2.83
CD6	CD6	0.254	0.557	0.199
CD7	CD7	0.306	0.295	0.397
CD8a	CD8A	0.769	0.162	0.826
CD8b	CD8B	0.247	0.681	2.87
CD9	CD9	72.8	18.4	15.8
CD10	MME	98.2	83.9	81.3
CD11a	ITGAL	0.349	0.277	3.21
CD11b	ITGAM	0.695	0.198	2.95
CD11c	ITGAX	0.909	8.11	3.44
CD13	ANPEP	99.1	94.5	95.7
CD14	CD14	0.262	5.51	4.15
CD15	FUT4	0.303	1.87	0.678
CD15s	FUT4	0.182	0.507	0.707
CD16	FCGR3	0.678	0.535	0.201
CD18	ITGB2	0.168	12.13	5.21
CD19	CD19	0.026	0.493	0.759
CD20	MS4A1	0.044	0.285	0.975
CD21	CR2	0	0.187	0.642
CD22	CD22	0.221	0.069	0.056
CD23	FCER2	0.725	0.642	0.528
CD24	CD24	0.126	0.723	2.89
CD25	IL2RA	0.422	0.13	0.273
CD26	DPP4	96.8	34.7	34.4
CD27	CD27	0.205	0.066	0.031
CD28	CD28	0.721	0.738	0.924
CD29	ITGB1	93.5	62.2	23.9
CD30	TNFRSF8	0.269	0.652	0.983
CD31	PECAM1	0.773	6.71	0.244
CD32	FCGR2	0.013	6.63	3.54
CD33	CD33	0.628	0.313	0.992
CD34	CD34	14.8	37.4	12.6
CD35	CR1	0.5	0.865	0.092
CD36	CD36	17.7	56.7	4.7
CD37	CD37	0.782	0.578	0
CD38	CD38	0.22	0.113	0.621
CD39	ENTPD1	0.64	0.675	0.214
CD40	CD40	16.1	28.2	1.45
CD41a	ITGA2B	0.929	0.839	0.218
CD41b	CD41B	0.141	0.475	0.712
CD42a	GP9	0.551	0.768	0.423
CD42b	GP1BA	0.269	0.132	0.172
CD43	SPN	0.659	2.51	2.87
CD44	CD44	99.6	88.8	91.9
CD45	PTPRC	0.908	9.5	2.11
CD45RA	PTPRC	0.048	0.489	0.133
CD45RB	PTPRC	0.728	1.53	7.15
CD45RO	PTPRC	0.17	5.65	3.64
CD46	CD46	99.8	75.8	7.4
CD47	CD47	95.7	65.3	87.3
CD48	CD48	0.264	0.963	0.506
CD49a	ITGA1	87.4	68.6	9.11
CD49b	ITGA2	60.8	26.2	5.51
CD49c	ITGA3	55.3	15.1	2.26
CD49d	ITGA4	90.8	25.9	< 1

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SUPPLEMENTARY TABLE S2. (CONTINUED)

<i>CD</i>	<i>Gene ID</i>	<i>Undifferentiated</i>	<i>Adipogenic</i>	<i>Osteogenic</i>
CD49e	ITGA5	99.8	91.2	55.5
CD50	ICAM3	0.939	0.653	1.58
CD51/61	ITGAV	97.8	66.8	59.1
CD53	CD53	0.881	5.12	3.67
CD54	ICAM1	94.8	20.8	29.4
CD55	CD55	99.9	50.7	8.77
CD56	NCAM1	0.682	0.355	0.565
CD57	B3GAT1	0.308	0.93	1.66
CD58	CD58	99.3	55.9	19.8
CD59	CD59	100	88.4	96.2
CD61	ITGB3	91.7	74.5	61.4
CD62E	SELE	0.186	0.178	0.892
CD62L	SELL	0.016	0.398	0.133
CD62P	SELP	0	0.529	0.32
CD63	CD63	70.2	92.3	82.1
CD64	FCGR1	0.639	0.764	3.87
CD66(a.c.d.e)	CECAM1	0.594	0.785	2.55
CD66b	CECAM8	0.655	0.366	0.882
CD66f	PSG1	0.039	0.944	0.418
CD69	CD69	0.59	0.376	0.818
CD70	CD70	0.836	0.497	0.219
CD71	TFRC	41.9	17.8	3.34
CD72	CD72	0.141	0.115	0.371
CD73	NT5E	99.2	79.4	75.3
CD74	CD74	0.92	0.208	0.114
CD75	ST6GAL1	0.389	0.412	0.332
CD77	A4GALT	0.486	6.76	0.652
CD79b	CD79b	0.496	0.43	0.612
CD80	CD80	0.982	0.838	0.884
CD81	CD81	99.8	91.5	96.6
CD83	CD83	0.014	0.365	0.04
CD84	CD84	0.818	6.45	4.85
CD85	LILRA5	0.896	3.65	3.11
CD86	CD86	0.83	6.36	2.55
CD87	PLAUR	0.94	0.502	0.994
CD88	C5AR1	0.395	1.81	0.094
CD89	FCAR	0.837	0.023	0.83
CD90	THY1	98.8	94.9	93.5
CD91	LRP1	16.3	7.09	0.528
CDw93	CD93	0.655	0.434	0.921
CD94	KLRD1	0.044	0.498	0.467
CD95	FAS	98.2	56.8	83.2
CD97	CD97	2.22	12.8	0.704
CD98	SLC7A5	99.8	85.7	88.3
CD99	CD99	99.1	68.3	4.64
CD99R	CD99	32.8	13.8	0.159
CD100	SEMA4D	0.123	0.903	0.386
CD102	ICAM2	1.95	0.59	5.33
CD103	ITGAE	0	0.028	0.583
CD105	ENG	95.2	50.8	0.929
CD106	VCAM1	2.67	2.41	0.633
CD107a	LAMP1	4.89	28.3	30.5
CD107b	LAMP2	1.53	29.9	14.2
CD108	SEMA7A	9.75	0.292	2.85
CD109	CD109	22.8	3.45	0.036
CD112	PVRL2	0.179	0.927	0.804
CD114	CSF3R	0.586	0.974	0
CD116	CSF2RA	0.036	0.284	0.507
CD117	KIT	0.184	0.556	0.961
CD118	LIFR	0.077	0.495	0.143
CD119	IFNGR1	1.33	9.51	0.002
CD120a	TNFRSF1A	0.31	14.8	0.24

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SUPPLEMENTARY TABLE S2. (CONTINUED)

<i>CD</i>	<i>Gene ID</i>	<i>Undifferentiated</i>	<i>Adipogenic</i>	<i>Osteogenic</i>
CD121a	IL1R1	0.496	0.287	0.674
CD121b	IL1R2	0.691	0.193	0.207
CD122	IL2RB	0.932	0.043	0.652
CD123	IL3RA	0.218	0.549	0.327
CD124	IL4R	0.099	0.359	0.435
CD126	IL6R	0.335	0.884	0.022
CD127	IL7R	0.226	0.552	0.142
CD128b	CXCR2	0	0.672	0.969
CD130	IL6ST	13.3	5.86	0.069
CD134	TNFRSF4	0.671	0.378	0.888
CD135	FLT3	0.866	0.896	0.553
CD137	TNFRSF9	0.214	0.606	0.017
CD137L	TNFSF9	0.966	0.034	0.095
CD138	SDC1	66.8	1.75	0.107
CD140a	PDGFRA	59.1	26.3	3.98
CD140b	PDGFRB	97.4	49.3	3.53
CD141	THBD	62.7	28.3	0.563
CD142	F3	86.2	59.8	1.91
CD144	CDH5	0.253	0.178	0.742
CD146	MCAM	11.8	41.2	0.474
CD147	BSG	100	98.4	99.6
CD150	SLAMF1	0.762	0.525	0.114
CD151	CD151	98.6	74.9	3.67
CD152	CTLA4	0.198	0.829	2.58
CD153	TNFSF8	0.337	0.439	0.141
CD154	CD40L	0.584	0.971	0.5
CD158a	KIR2DL1	0.031	0.731	0.342
CD158b	KIR2DL3	0.076	0.434	0.497
CD161	KLRB1	0.15	0.329	0.557
CD162	SEPLG	0.978	7.31	0.036
CD163	CD163	0	5.99	0.888
CD164	CD164	5.07	44.1	84
CD165	CD165	85.8	33.6	0.0642
CD166	ALCAM	98.5	35.7	0.769
CD171	L1CAM	2.54	0.5	2.98
CD172b	SIRPB1	0.574	0.002	0.719
CD177	CD177	0.5	0.136	0.785
CD178	FASLG	0.462	0.316	0.627
CD180	CD180	0.459	0.73	0.641
CD181	CXCR1	0.136	0.654	0.145
CD183	CXCR3	0.494	0.357	0.578
CD184	CXCR4	0.362	0.601	0.466
CD193	CCR3	5.98	1.3	0.211
CD195	CCR5	0.57	0.261	1.33
CD196	CCR6	0	0.592	0.964
CD197	CCR7	0.318	0.608	0.453
CD200	CD200	6.9	12.3	1.49
CD205	LY75	0.197	0.289	0.372
CD206	MRC1	0.38	4.51	0.655
CD209	CD209	0.067	2.99	0.126
CD220	INSR	0.645	0.155	0.063
CD221	IGF1R	0.916	0.172	0.673
CD226	CD226	0.381	0.142	0.254
CD227	MUC1	46.2	8.74	0.814
CD229	LY9	0.779	0.996	0.95
CD231	TSPAN7	0.525	0.42	0.371
CD235a	GYP A	0.038	0.076	1.53
CD243	ABCB1	2.43	15.4	3.35
CD244	CD244	0.615	0.613	1.25
CD255	TNFSF12	0.53	0.332	0.399
CD268	TNFRSF13C	0.143	0.19	0.032
CD271	NGFR	0.837	77.6	0.962

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SUPPLEMENTARY TABLE S2. (CONTINUED)

<i>CD</i>	<i>Gene ID</i>	<i>Undifferentiated</i>	<i>Adipogenic</i>	<i>Osteogenic</i>
CD273	PDCDILG2	38.6	0.353	0.139
CD274	CD274	0.781	0.131	0.282
CD275	ICOSLG	0.115	2.01	0.401
CD278	ICOS	0.501	0.837	0.18
CD279	PDCD1	0.343	0.543	0.399
CD282	TLR2	0.446	5.26	0.443
CD305	LAIR1	0.83	7.44	4.01
CD309	KDR	0.261	0.393	0.117
CD314	KLRK1	0.682	0.945	0.446
CD321	F11R	0.919	36.8	5.31
CDw327	SIGLEC6	0.052	0.509	0.061
CDw328	SIGLEC7	0.628	3.99	0.33
CDw329	SIGLEC9	0.861	5.15	1.09
CD335	NCR1	0.7	0.638	0.617
CD336	NCR2	0.86	0.872	0.537
CD337	NCR3	0.878	0.888	0.276
CD338	ABCDG2	0.109	0.373	0.449
CD340	ERBB2	23.2	3.88	0.415
abTCR	IP26	0.279	0.713	0.052
B2-uGlob	B2M	99.9	68.3	82.3
BLTR-1	BLTR1	0.629	1.3	0.109
CLIP	CLIP1	0.974	0.799	0.464
CMRF-44	CMRF-44	0.468	3.15	0.113
CMRF-56	CMRF-56	0.041	2.43	0.318
EGF-r	EGFR	79.6	33.8	0.776
Fmlp-r	FPR2	0.722	4.51	0.491
gd TCR	CD3D	0.25	0.34	0.903
Hem. prog. cell		11.5	11.8	3.01
HLA-A,B,C	HLAA	98.7	92.4	97.3
HLA-A2	HLAA	67.1	66.8	70.5
HLA-DQ	HLA-DQ	0.002	4.51	3.11
HLA-DR	HLA-DR	2.41	10.8	3.95
HLA-DR,DP,DO	HLA-DR	0.773	8.34	4.72
Invariant NKT	912	0.037	0.064	0.524
GD2	B4GALNT1	0.083	1.67	23.8
MIC A/B	MIC	0.533	0.397	2.39
NKB1	KIR3DL1	0.01	0.473	0.495
SSEA-1	FUT4	0.413	3.67	0.514
SSEA-4	SSEA-4	6.34	16.3	4.04
TRA-1-60	PODXL	0.728	0.901	0.685
TRA-1-81	PODXL	0	0.317	0.208
Vb 23		0.101	0.222	0.517
Vb 8	COX5BP8	0	0.476	0.213
CD49f	ITGA6	1.5	33.6	0.152
CD104	ITGB4	1	4.26	2.59
CD120b	TNFRSF1B	0.921	4.58	2.81
CD132	IL2RG	0.185	6.31	3.25
CD201	PROCR	92.4	31.4	34.9
CD210	IL10RA	0.56	1.83	0.845
CD212	IL12RB1	0.243	0.147	0.793
CD267	TNFRSF13B	0.033	0.933	0.448
CD294	PTGDR2	0.854	0.338	0.227
CD326	CD326	0.738	0.361	1.7
Cutaneous T-cell lymphoma associated antigen 1	CTAGE1	0	0.13	0.953
INT B7	INTB7	0.028	0.2	0.518
SSEA-3	SSEA-3	0.219	1.75	0.857

Mean percentage of positive cells for each surface marker (with gene ID and CD nomenclature) assayed across each of the three donor hASC populations.

hASC, human adipose-derived stromal cell.