

Supplementary Table 7: Methylation profiling of all diseased SSc twins. Most significant differentially methylated cytosines in skin fibroblasts from twins discordant for SSc. Only CpGs with $P < 10E-05$ that mapped to a gene body are listed here. Genes with the most significant differences in methylation levels ($P < 5.0E-06$) between diseased and healthy twins are shown in red font. This table is sorted in *W* Beta value. Blue shading: decreased methylation (*W* Beta < -0.20); red shading: increased methylation (*W* Beta > 0.20). Chr: chromosome; bp: base pair; MZ: monozygotic; DZ: dizygotic; *W* Beta: Beta value for the meta-analysis of the MZ and DZ analyses; Meta *P*-value: *p*-value for the meta-analysis of the MZ and DZ analyses.

CpG	Chr	Position (bp)	RefGene	MZ P-value	DZ P-value	MZ Beta	DZ Beta	W Beta	Meta P-value
cg11841394	12	114841536	TBX5	1.32E-05	7.43E-03	-0.7	-0.87	-0.74	3.50E-07
cg09042277	12	114840854	TBX5	1.27E-05	2.04E-02	-0.71	-0.89	-0.74	7.77E-07
cg23820885	12	114840942	TBX5	2.40E-05	7.27E-03	-0.66	-0.83	-0.7	6.40E-07
cg16805360	12	114845223	TBX5	3.23E-04	1.43E-02	-0.66	-0.88	-0.7	1.61E-05
cg15864691	7	27217606	HOXA10	8.53E-04	2.79E-02	-0.66	-0.83	-0.7	7.31E-05
cg21907579	12	114845868	TBX5	2.29E-04	9.19E-02	-0.67	-0.77	-0.69	5.14E-05
cg02566861	17	46679516	LOC404266	1.00E-03	5.26E-03	-0.61	-0.91	-0.67	2.78E-05
cg00642359	12	114841708	TBX5	6.97E-05	1.32E-02	-0.62	-0.79	-0.65	3.07E-06
cg14264795	12	114845180	TBX5	2.07E-04	9.18E-02	-0.61	-0.77	-0.64	4.64E-05
cg14688579	2	223168453	CCDC140	1.38E-04	5.99E-02	-0.58	-0.8	-0.63	2.12E-05
cg09636715	7	27217057	HOXA10	7.06E-04	7.00E-03	-0.58	-0.83	-0.63	2.28E-05
cg21611810	12	114841870	TBX5	2.94E-05	9.34E-02	-0.59	-0.75	-0.62	7.20E-06
cg10724867	7	27218867	HOXA10	4.69E-04	3.29E-02	-0.57	-0.81	-0.62	4.45E-05
cg14935646	7	27215464	HOXA10	5.13E-04	2.42E-02	-0.54	-0.85	-0.61	3.87E-05
cg09233651	12	114838567	TBX5	2.57E-04	1.05E-01	-0.55	-0.78	-0.6	6.48E-05
cg05516617	7	27221689	HOXA11	6.09E-04	4.07E-02	-0.56	-0.74	-0.6	6.86E-05
cg27157482	7	27215606	HOXA10	1.28E-03	1.56E-02	-0.54	-0.84	-0.6	7.43E-05
cg02483701	7	27215610	HOXA10	9.67E-04	2.75E-02	-0.54	-0.85	-0.6	8.25E-05
cg19476053	2	223167463	CCDC140	1.60E-03	6.69E-03	-0.54	-0.82	-0.59	5.45E-05
cg10035294	2	223164925	PAX3	6.06E-04	5.82E-02	-0.54	-0.78	-0.59	9.08E-05
cg07119829	2	223168487	CCDC140	5.66E-04	2.87E-02	-0.55	-0.68	-0.58	4.88E-05
cg13496838	2	223164747	PAX3	1.09E-03	6.07E-03	-0.53	-0.73	-0.57	3.34E-05
cg14509967	17	46679135	LOC404266	1.32E-03	1.45E-02	-0.53	-0.73	-0.57	7.28E-05
cg03877376	12	114846162	TBX5	1.71E-06	9.40E-02	-0.57	-0.48	-0.55	4.94E-07
cg17462200	12	114841980	TBX5	4.32E-06	9.73E-02	-0.52	-0.69	-0.55	1.22E-06
cg03803541	17	46681401	LOC404266; HOXB6	8.28E-04	3.85E-03	-0.53	-0.65	-0.55	1.84E-05
cg04435975	17	46683047	LOC404266; HOXB6	1.41E-03	1.77E-03	-0.54	-0.59	-0.55	2.11E-05
cg19787532	12	114841880	TBX5	4.66E-05	9.56E-02	-0.5	-0.7	-0.54	1.15E-05
cg09411999	7	27214383	HOXA10	2.81E-04	1.20E-02	-0.49	-0.74	-0.54	1.23E-05
cg26196480	12	114846347	TBX5	5.69E-05	1.48E-01	-0.53	-0.52	-0.53	2.16E-05
cg00590029	12	114838618	TBX5	9.68E-05	1.06E-01	-0.47	-0.68	-0.52	2.55E-05
cg18878432	17	46683409	LOC404266; HOXB6	1.02E-03	9.62E-03	-0.49	-0.57	-0.51	4.20E-05
cg00182639	12	114841671	TBX5	1.94E-04	3.16E-02	-0.45	-0.66	-0.5	1.75E-05
cg17645823	12	114846321	TBX5	1.01E-05	6.20E-02	-0.5	-0.47	-0.49	1.72E-06
cg05343665	12	15790461	EPS8	3.44E-05	3.79E-01	-0.5	-0.47	-0.49	4.16E-05
cg22045225	12	114841792	TBX5	1.23E-05	5.22E-02	-0.44	-0.49	-0.45	1.77E-06
cg09486778	2	223169609	CCDC140	1.58E-03	1.13E-02	-0.4	-0.64	-0.45	7.50E-05
cg27480727	2	223164831	PAX3	1.30E-03	9.75E-03	-0.42	-0.49	-0.44	5.54E-05
cg15825116	2	223169586	CCDC140	1.41E-03	1.03E-02	-0.38	-0.58	-0.42	6.26E-05
cg20099830	12	114842031	TBX5	9.37E-05	8.99E-02	-0.42	-0.3	-0.4	2.12E-05
cg18066690	8	48344060	KIAA0146	6.50E-04	4.29E-02	-0.36	-0.57	-0.4	7.65E-05
cg06856840	15	80446451	FAH	1.54E-04	1.24E-01	-0.38	-0.32	-0.36	4.63E-05
cg19673155	10	72995181	UNC5B	5.54E-05	1.20E-01	-0.32	-0.36	-0.33	1.69E-05
cg17790273	17	49040709	SPAG9	3.73E-04	4.54E-02	-0.3	-0.43	-0.33	4.55E-05
cg20162206	18	30353125	KLHL14	1.54E-03	1.62E-02	-0.32	-0.41	-0.33	9.26E-05
cg05999049	17	46692859	HOXB8	3.03E-05	2.16E-02	-0.32	-0.25	-0.31	1.95E-06
cg13852093	18	74770815	MBP	4.32E-04	2.72E-03	-0.24	-0.45	-0.28	7.17E-06
cg24825767	10	18453319	CACNB2	1.88E-04	4.71E-02	-0.25	-0.35	-0.27	2.36E-05
cg25483907	3	41723017	ULK4	3.74E-05	9.11E-02	-0.24	-0.28	-0.24	8.85E-06
cg27105598	2	205520167	PARD3B	1.06E-04	1.59E-01	-0.26	-0.18	-0.24	4.19E-05
cg09447811	3	121972621	CASR	8.46E-04	2.14E-02	-0.24	-0.25	-0.24	5.96E-05
cg16867817	7	82057703	CACNA2D1	1.11E-04	3.13E-01	-0.22	-0.31	-0.24	9.29E-05
cg18761976	15	91807630	SV2B	7.16E-04	4.62E-03	-0.21	-0.21	-0.21	1.77E-05
cg23390920	12	97858120	RMST	1.52E-03	6.45E-03	-0.2	-0.23	-0.21	5.04E-05
cg19898108	12	54383692	HOXC10	5.53E-05	3.72E-01	-0.23	-0.09	-0.2	6.17E-05
cg16991569	1	63142359	DOCK7	2.07E-03	1.68E-03	-0.24	-0.01	-0.19	3.19E-05
cg02088470	10	1551251	ADARB2	3.27E-04	1.27E-01	-0.2	-0.16	-0.19	9.74E-05

cg03861217	2	155652401	KCNJ3	4.16E-04	6.64E-02	-0.19	-0.16	-0.18	6.95E-05
cg09434534	3	118865026	IGSF11	8.22E-05	1.28E-01	-0.18	-0.12	-0.17	2.65E-05
cg18979491	20	36974445	LBP	6.29E-04	2.96E-02	-0.14	-0.27	-0.16	5.56E-05
cg01185093	7	5343176	SLC29A4	1.97E-04	1.53E-01	-0.18	-0.09	-0.16	7.19E-05
cg22220722	1	20306641	PLA2G2A	9.00E-05	2.44E-01	-0.15	-0.14	-0.15	5.73E-05
cg04757411	13	76259545	LMO7	8.00E-05	2.68E-01	-0.14	-0.2	-0.15	5.73E-05
cg21387752	17	46680288	LOC404266; HOXB6	7.66E-04	1.64E-02	-0.12	-0.22	-0.14	4.45E-05
cg25924807	3	2696551	CNTN4	1.09E-03	2.60E-02	-0.13	-0.19	-0.14	8.97E-05
cg04147642	6	32054659	TNXB	9.19E-06	4.13E-01	-0.11	-0.12	-0.12	1.47E-05
cg16425829	12	119632544	HSPB8	2.81E-04	2.95E-02	-0.11	-0.15	-0.12	2.41E-05
cg14504586	9	134744872	MED27	1.16E-03	7.90E-03	-0.1	-0.19	-0.12	4.25E-05
cg16803613	12	7583651	CD163L1	1.16E-04	1.03E-01	-0.12	-0.07	-0.11	2.95E-05
cg00477978	11	6463746	HPX	3.24E-04	1.16E-01	-0.1	-0.11	-0.1	8.91E-05
cg09707903	12	19286583	PLEKHA5	2.52E-02	1.83E-05	-0.1	-0.11	-0.1	8.94E-05
cg16576052	14	68038799	PLEKHH1	3.75E-04	1.01E-02	-0.09	-0.11	-0.09	1.48E-05
cg00100538	4	184067792	WWC2	1.21E-05	1.87E-01	-0.08	-0.09	-0.08	6.64E-06
cg14257656	17	4500399	SMTNL2	3.93E-04	4.70E-02	-0.09	-0.01	-0.07	4.93E-05
cg26339943	4	145571234	HHIP	3.72E-03	3.42E-03	-0.07	-0.05	-0.07	9.47E-05
cg03214697	22	30901532	SEC14L4; SEC14L4	2.18E-04	3.06E-02	-0.03	-0.03	-0.03	1.92E-05
cg05089903	7	1862491	MAD1L1	5.12E-03	6.94E-04	-0.03	-0.01	-0.03	5.79E-05
cg11358634	11	67159532	RAD9A	2.91E-06	2.57E-01	-0.01	-0.01	-0.01	2.73E-06
cg07515251	2	74730404	LBX2	1.71E-05	1.83E-01	-0.01	-0.01	-0.01	8.95E-06
cg16409497	12	66217818	HMGA2; RPSAP52	4.03E-04	4.41E-02	-0.01	-0.01	-0.01	4.80E-05
cg21587412	3	107244153	BBX	9.22E-04	1.76E-02	-0.01	0	-0.01	5.71E-05
cg02302400	8	56987044	SNORD54; RPS20	1.05E-04	2.59E-01	-0.01	0	-0.01	7.04E-05
cg25227352	11	61129331	CYBASC3; TMEM13	8.05E-05	3.75E-01	-0.01	-0.01	-0.01	8.74E-05
cg16729415	15	35047203	GJD2	5.05E-05	5.34E-01	-0.01	0	-0.01	9.48E-05
cg07219542	1	110210770	GSTM2	1.88E-05	3.55E-01	-0.01	0	0	2.23E-05
cg13937608	10	6131228	RBM17	1.36E-04	1.50E-01	0	0	0	5.00E-05
cg11709662	15	49913013	C15orf33; DTWD1	4.18E-05	3.86E-01	0	0	0	5.07E-05
cg01454815	16	23193933	SCNN1G	5.97E-04	4.82E-02	0	0	0	7.69E-05
cg01682615	4	2845235	ADD1	1.43E-03	1.76E-02	0	-0.01	0	9.11E-05
cg20465008	1	17766219	RCC2	1.07E-03	4.48E-03	0.01	0.01	0.01	2.69E-05
cg18871670	3	134205507	CEP63; ANAPC13	3.21E-05	3.38E-01	0.01	0.02	0.01	3.36E-05
cg09081385	12	120972070	RNF10	1.12E-03	2.11E-02	0.01	0.01	0.01	7.92E-05
cg20267828	6	128222390	THEMIS	1.13E-03	3.11E-03	0.02	0.03	0.02	2.28E-05
cg08442149	10	1767484	ADARB2	1.46E-04	9.00E-02	0.11	0.1	0.11	3.24E-05
cg02810692	3	54962954	LRTM1	4.93E-04	1.20E-02	0.1	0.19	0.12	2.23E-05
cg22118465	3	52486691	TNNC1	1.14E-04	1.11E-01	0.14	0.12	0.13	3.12E-05
cg12649539	6	42111545	C6orf132	6.04E-05	1.00E-01	0.11	0.29	0.14	1.54E-05
cg21550785	2	29439093	ALK	8.16E-04	2.30E-02	0.15	0.23	0.16	6.05E-05
cg27406618	10	50341989	FAM170B	4.46E-03	8.07E-04	0.16	0.23	0.17	5.30E-05
cg25067162	17	41277974	BRCA1; NBR2	5.47E-05	2.82E-01	0.23	0.06	0.19	4.31E-05
cg07066794	14	89014677	PTPN21	1.11E-04	1.86E-01	0.18	0.28	0.2	5.17E-05
cg00979527	1	4749733	AJAP1	7.18E-05	1.68E-01	0.21	0.18	0.21	3.08E-05
cg04066190	6	10407470	TFAP2A	1.60E-05	1.12E-01	0.24	0.2	0.23	4.85E-06
cg16235582	11	78673212	ODZ4	5.50E-05	3.85E-01	0.25	0.12	0.23	6.44E-05
cg18438300	7	72847175	FZD9	7.38E-05	2.27E-01	0.25	0.2	0.24	4.39E-05
cg01203812	1	3081078	PRDM16	9.18E-04	2.91E-02	0.3	0.19	0.28	8.14E-05
cg03207151	12	54442288	HOXC4	3.83E-04	3.54E-02	0.26	0.45	0.3	3.83E-05
cg06994420	2	66672553	MEIS1	5.01E-04	2.33E-03	0.37	0.36	0.37	7.67E-06
cg18210860	13	78470739	EDNRB	2.80E-03	2.63E-03	0.39	0.38	0.39	5.87E-05
cg26880445	8	9952965	MSRA	1.40E-03	3.97E-03	0.38	0.49	0.41	3.40E-05
cg09535924	2	66671659	MEIS1	5.88E-04	1.91E-02	0.44	0.4	0.43	3.76E-05
cg14775296	2	66672841	MEIS1	3.30E-04	2.02E-02	0.5	0.52	0.5	2.14E-05
cg23551720	17	46633726	HOXB3	8.82E-04	3.71E-02	0.58	0.45	0.55	9.35E-05
cg04196862	17	46669455	HOXB5; LOC404266	8.88E-04	6.55E-04	0.56	0.72	0.59	6.89E-06
cg27008363	12	54449761	HOXC4	4.31E-04	3.40E-02	0.57	0.84	0.62	4.19E-05
cg05987823	12	54428592	HOXC4; HOXC5	6.43E-04	3.50E-02	0.59	0.74	0.62	6.46E-05