Supplementary Table S1. Description of the 51 CpG sites with a differential DNA methylation status between the asymptomatic/paucisymptomatic (n=104) and severe (n=103) groups in the discovery cohort.

CpG ID	Chromosome location (GRCh37, hg19)	Gene	Discovery cohort		Validation cohort		Entire cohort	
			Adjusted P value	Odds ratio	Adjusted P value	Odds ratio	Adjusted P value	Odds ratio
cg17515347	1:159047163	AIM2	1.11E-10	2.03E+08	8.25E-20	9.06E+16	8.19E-30	6.39E+27
cg24145401	1:159047177	AIM2	2.70E-10	6.17E+07	3.57E-21	7.87E+18	1.65E-30	4.65E+28
cg04736673	10:61647141	CCDC6	1.99E-04	1.90E+00	7.20E-08	4.97E+03	7.20E-12	4.71E+07
cg02003183	14:103415882	CDC42BPB	6.08E-12	1.03E+10	2.24E-09	1.84E+05	8.41E-21	2.27E+17
cg15355235	18:35001518	CELF4	9.53E-03	1.53E-02	1.47E-03	1.38E-01	2.52E-05	6.81E+00
cg10947500	6:118985774	CEP85L	9.99E-07	1.77E+03	9.32E-08	3.80E+03	1.30E-14	3.63E+10
cg19225688	2:218990043	CXCR2	1.04E-09	1.09E+07	1.37E-15	6.56E+11	1.01E-24	5.62E+21
cg02872426	6:110736772	DDO	4.73E-09	1.55E+06	2.14E-05	1.27E+01	1.41E-14	3.33E+10
cg09516963	12:68042445	DYRK2	3.79E-10	3.99E+07	1.25E-10	3.71E+06	1.18E-20	1.57E+17
cg15148145	2:164539743	FIGN	1.68E-10	1.16E+08	2.55E-06	1.19E+02	5.83E-17	1.23E+13
cg05030953	6:31241000	HLA-C	6.79E-07	2.90E+03	2.13E-01	6.13E-04	6.73E-06	2.76E+01
cg08309069	6:31240651	HLA-C	4.28E-09	1.77E+06	2.25E-02	6.96E-03	1.28E-09	2.14E+05
cg13452062	1:79088559	IFI44L	1.55E-06	1.01E+03	5.31E-11	9.10E+06	1.75E-16	3.73E+12
cg26931608	1:170036455	KIFAP3	4.10E-11	7.52E+08	6.54E-08	5.50E+03	1.06E-19	1.37E+16
cg07796016	1:152779584	LCE1C	6.14E-03	2.58E-02	4.46E-04	5.01E-01	4.13E-06	4.62E+01
cg13571460	9:124989337	LHX6	1.69E-03	1.26E-01	5.91E-02	2.41E-03	1.53E-04	9.81E-01
cg07381806	19:2094327	MOBKL2A	8.19E-11	3.00E+08	4.78E-08	7.62E+03	1.31E-18	8.42E+14
cg14893161	1:205819251	PM20D1	4.97E-03	3.34E-02	1.43E-03	1.42E-01	7.95E-06	2.32E+01
cg17178900	1:205818956	PM20D1	3.60E-03	4.94E-02	3.76E-03	4.95E-02	1.41E-05	1.26E+01
cg23256579	12:11002403	PRR4	1.26E-12	8.87E+10	4.60E-09	8.71E+04	1.11E-21	2.12E+18
cg27615582	12:11002411	PRR4	2.67E-12	3.23E+10	2.59E-08	1.44E+04	2.40E-20	7.14E+16
cg10188795	10:52158244	SGMS1	1.15E-10	1.92E+08	4.31E-20	2.23E+17	7.58E-30	7.09E+27
cg24795173	10:108751940	SORCS1	2.64E-04	1.32E+00	1.23E-02	1.34E-02	5.33E-06	3.53E+01
cg14859874	1:154238265	UBAP2L	1.07E-05	8.28E+01	1.72E-02	9.34E-03	3.78E-07	5.68E+02
cg12682382	8:74787918	UBE2W	3.27E-05	1.95E+01	1.42E-08	2.70E+04	1.82E-13	2.23E+09
cg26063719	10:17273187	VIM	7.68E-12	7.09E+09	6.58E-18	2.68E+14	2.66E-29	1.40E+27
cg06760111	3:21551522	ZNF385D	4.45E-09	1.68E+06	9.63E-07	3.32E+02	4.95E-16	1.21E+12
cg01097406	16:89675127	-	1.27E-03	1.80E-01	3.86E-03	4.81E-02	4.46E-06	4.26E+01
cg01808126	16:47049977	-	2.24E-04	1.63E+00	5.60E-04	3.92E-01	7.65E-08	3.01E+03
cg02025944	4:80998921	-	1.26E-06	1.31E+03	7.92E-03	2.19E-02	1.60E-08	1.54E+04
cg02159489	17:79459563	-	4.73E-04	6.27E-01	1.02E-02	1.66E-02	5.73E-06	3.27E+01
cg02779288	15:93157567	-	2.14E-04	1.72E+00	2.87E-05	9.31E+00	3.61E-09	7.23E+04
cg06601098	16:11319090	-	2.26E-09	4.01E+06	4.01E-05	6.53E+00	1.24E-13	3.34E+09
cg08689926	22:50322930	-	3.53E-02	3.38E-03	3.44E-01	3.76E-04	2.25E-01	3.89E-04
cg10537261	11:102183505	-	5.57E-13	2.76E+11	1.29E-09	3.28E+05	2.98E-23	1.21E+20
cg10841563	9:83280018	-	3.74E-04	8.47E-01	2.88E-04	8.01E-01	6.03E-08	3.85E+03
cg11671940	10:28781637	-	6.28E-05	8.36E+00	7.51E-06	3.84E+01	1.97E-10	1.49E+06
cg11822515	5:151841890	-	3.60E-03	4.93E-02	1.61E-02	1.01E-02	9.21E-05	1.70E+00
cg13023205	17:81060243	-	1.06E-03	2.27E-01	1.40E-04	1.73E+00	1.15E-07	1.97E+03
cg15532640	12:129554566	-	9.05E-04	2.76E-01	8.00E-01	1.88E-04	1.32E-02	7.61E-03
cg16814680	8:91681699	-	8.31E-03	1.80E-02	5.09E-02	2.84E-03	5.89E-04	2.27E-01
cg18523915	2:85728591	-	7.26E-06	1.37E+02	1.71E-05	1.60E+01	2.41E-11	1.34E+07
cg18826637	2:145116633	-	5.10E-10	2.73E+07	3.98E-01	3.27E-04	8.71E-08	2.63E+03
cg19214707	7:3157722	-	2.01E-02	6.42E-03	5.89E-03	3.03E-02	2.59E-04	5.56E-01
cg20190576	8:109955223	-	4.37E-05	1.34E+01	1.06E-03	1.96E-01	2.23E-08	1.09E+04
cg21139150	21:46976175	-	9.51E-03	1.53E-02	6.99E-02	2.01E-03	1.37E-03	9.02E-02
cg22117893	13:114212078	-	9.97E-04	2.44E-01	1.01E-04	2.45E+00	8.48E-08	2.70E+03
cg24630035	5:120389062	-	6.14E-05	8.58E+00	1.98E-04	1.20E+00	3.56E-09	7.34E+04
cg24976744	5:120518655	-	1.26E-12	8.86E+10	4.79E-07	6.88E+02	2.99E-20	5.57E+16
cg25134647	12:25454990	-	4.21E-02	2.78E-03	7.29E-01	1.99E-04	8.57E-02	1.03E-03
cg26035071	1:209982407	-	2.72E-03	6.98E-02	1.40E-03	1.46E-01	4.68E-06	4.05E+01