

Supplementary Table 1. Summary of candidate DNAm sites in DPREG

CpG methylated region	N Systolic	Beta Systolic	Standard Error Systolic	Unadjusted p-value Systolic	N Diastolic	Beta Diastolic	Standard Error Diastolic	Unadjusted p-value Diastolic	CHR	Base pair position	Gene
cg00101629	93	-4.691E-04	3.348E-04	0.166	93	1.410E-04	4.438E-04	0.752	1	15068966	KAZN
cg01142526	93	4.310E-05	1.369E-04	0.754	93	1.050E-04	1.789E-04	0.560	5	177541754	N4BP3
cg01476222	93	3.538E-04	2.782E-04	0.208	93	1.490E-05	3.681E-04	0.968	11	36522143	TRAF6
cg01621943	93	-2.370E-05	3.177E-04	0.941	93	-5.374E-04	4.112E-04	0.196	17	53531409	
cg03152187	93	3.657E-04	2.242E-04	0.108	93	4.801E-04	2.935E-04	0.107	17	75417165	SEPT9
cg03254336	93	-3.221E-04	2.964E-04	0.281	93	-3.197E-04	3.893E-04	0.415	10	114635839	
cg03272932	93	-1.220E-04	3.256E-04	0.709	93	-2.141E-04	4.259E-04	0.617	16	87588893	
cg03706951	93	-8.030E-05	4.133E-04	0.846	93	-5.158E-04	5.379E-04	0.341	17	39465518	KRTAP16-1
cg03901454	93	-2.265E-04	3.199E-04	0.482	93	-5.144E-04	4.160E-04	0.221	16	87588683	
cg04212285	93	-4.715E-04	5.295E-04	0.377	93	-6.200E-06	6.994E-04	0.993	7	157342638	PTPRN2
cg04549583	93	-1.244E-04	1.501E-04	0.410	93	-6.380E-05	1.972E-04	0.747	2	12146219	LOC100506457
cg06320380	93	-4.890E-06	1.469E-04	0.974	93	8.690E-05	1.921E-04	0.653	2	218770208	TNS1
cg09964921	93	4.599E-04	3.592E-04	0.205	93	4.792E-04	4.721E-04	0.314	21	35885767	KCNE1
cg10131972	93	3.384E-04	1.817E-04	0.067	93	4.618E-04	2.387E-04	0.057	22	19879787	TXNRD2
cg13250001	93	2.554E-04	1.791E-04	0.159	93	1.576E-04	2.369E-04	0.508	3	119810597	GSK3B
cg13290254	93	-2.366E-04	3.965E-04	0.553	93	-2.429E-04	5.161E-04	0.639	12	125197730	
cg13514049	93	1.010E-04	3.573E-04	0.778	93	-2.280E-04	4.672E-04	0.627	9	110495709	
cg16447680	93	-1.955E-04	2.885E-04	0.501	93	-1.736E-04	3.784E-04	0.648	12	55379100	TESPA1
cg18721397	93	-5.389E-04	8.616E-04	0.534	93	-6.201E-04	1.129E-03	0.585	5	32584912	SUB1
cg19787650	93	-4.340E-05	3.259E-04	0.894	93	-1.101E-04	4.265E-04	0.797	8	130998171	FAM49B
cg19921917	93	-6.820E-04	5.935E-04	0.255	93	-1.343E-03	7.683E-04	0.085	4	169418224	PALLD
cg20253872	93	3.760E-04	2.526E-04	0.141	93	5.068E-04	3.287E-04	0.128	1	110166571	AMPD2
cg20519581	93	1.723E-04	4.290E-04	0.689	93	4.804E-04	5.567E-04	0.391	20	48959844	
cg23471393	93	-3.861E-04	4.740E-04	0.418	93	-2.447E-04	6.089E-04	0.689	17	79797038	

Supplementary Table 2. Summary of preterm birth associated DNAm sites compared to previous research (Parets, 2013)

CpG methylated region	N Systolic	Beta Systolic	Standard Error Systolic	Unadjusted p-value Systolic	N Diastolic	Beta Diastolic	Standard Error Diastolic	Unadjusted p-value Diastolic	CHR	Base pair position	Gene
cg00078085	93	1.699E-04	2.975E-04	5.700E-01	93	2.598E-04	3.892E-04	5.069E-01	3	8810592	OXTR
cg00385883	93	5.820E-05	1.442E-04	6.880E-01	93	4.190E-05	1.889E-04	8.253E-01	3	8808259	OXTR
cg02192228	93	5.517E-04	5.180E-04	2.908E-01	93	2.245E-04	6.827E-04	7.434E-01	3	8809536	OXTR
cg03257388	93	3.889E-04	8.554E-04	6.509E-01	93	-2.962E-04	1.121E-03	7.924E-01	3	8809213	OXTR
cg03987506	93	-1.526E-04	2.908E-04	6.016E-01	93	-2.162E-04	3.805E-04	5.720E-01	3	8810549	OXTR
cg04523291	93	2.110E-04	8.290E-04	7.999E-01	93	-9.230E-05	1.086E-03	9.325E-01	3	8809501	OXTR
cg09353063	93	2.900E-05	1.732E-04	8.678E-01	93	-2.756E-04	2.246E-04	2.243E-01	3	8811092	OXTR
cg11171527	93	3.938E-04	2.348E-04	9.841E-02	93	5.851E-04	3.057E-04	6.014E-02	3	8810206	OXTR
cg11589699	93	4.026E-04	1.658E-04	1.801E-02	93	6.419E-04	2.129E-04	3.684E-03	3	8806317	OXTR
cg12695586	93	1.704E-04	2.095E-04	4.191E-01	93	1.609E-04	2.748E-04	5.604E-01	3	8810077	OXTR
cg13079193	93	2.251E-04	3.383E-04	5.081E-01	93	4.001E-04	4.417E-04	3.684E-01	3	8802718	OXTR
cg15317815	93	9.224E-04	9.272E-04	3.236E-01	93	5.584E-04	1.220E-03	6.487E-01	3	8809306	OXTR
cg17285225	93	-9.690E-05	1.085E-04	3.753E-01	93	-9.310E-05	1.424E-04	5.158E-01	3	8811004	OXTR
cg19619174	93	7.590E-05	1.397E-04	5.890E-01	93	8.590E-05	1.803E-04	6.355E-01	3	8810139	OXTR
cg23391006	93	-9.370E-05	8.000E-05	2.458E-01	93	5.140E-06	1.037E-04	9.606E-01	3	8811279	OXTR
cg26455676	93	4.510E-05	3.654E-04	9.023E-01	93	4.526E-04	4.755E-04	3.447E-01	3	8797459	OXTR
cg00425217	93	1.272E-04	1.769E-04	4.747E-01	93	3.465E-04	2.289E-04	1.350E-01	19	13205470	NFIX
cg00689651	93	6.150E-05	2.338E-04	7.935E-01	93	-2.710E-05	3.062E-04	9.298E-01	19	13209548	NFIX
cg01001422	93	4.630E-05	5.635E-04	9.348E-01	93	2.825E-04	7.383E-04	7.033E-01	19	13135631	NFIX
cg01617040	93	2.599E-04	1.991E-04	1.966E-01	93	4.403E-04	2.587E-04	9.360E-02	19	13172859	NFIX
cg02297936	93	1.019E-04	2.224E-04	6.482E-01	93	3.953E-04	2.880E-04	1.746E-01	19	13208599	NFIX
cg03214274	93	1.729E-04	1.810E-04	3.430E-01	93	1.205E-04	2.377E-04	6.139E-01	19	13179476	NFIX
cg03330161	93	-2.258E-04	2.379E-04	3.460E-01	93	-1.884E-04	3.125E-04	5.488E-01	19	13181605	NFIX
cg03759890	93	-2.569E-04	3.583E-04	4.761E-01	93	-3.976E-04	4.684E-04	3.991E-01	19	13143279	NFIX
cg04189679	93	3.600E-05	3.033E-04	9.060E-01	93	1.607E-04	3.967E-04	6.867E-01	19	13138055	NFIX
cg05502283	93	-7.270E-05	1.760E-04	6.811E-01	93	-1.824E-04	2.270E-04	4.247E-01	19	13203715	NFIX
cg06623219	93	-1.500E-05	2.985E-04	9.602E-01	93	3.909E-04	3.882E-04	3.178E-01	19	13207502	NFIX
cg06623668	93	-1.994E-04	3.048E-04	5.153E-01	93	1.020E-05	4.001E-04	9.798E-01	19	13138816	NFIX
cg06744585	93	-4.192E-04	6.097E-04	4.942E-01	93	-8.442E-04	7.914E-04	2.901E-01	19	13135808	NFIX
cg07111635	93	-1.330E-03	2.300E-03	5.651E-01	93	-3.912E-03	2.984E-03	1.945E-01	19	13163575	NFIX
cg07240953	93	4.289E-04	4.933E-04	3.878E-01	93	8.319E-04	6.419E-04	1.997E-01	19	13194770	NFIX

cg07788061	93	4.170E-04	2.084E-04	4.962E-02	93	7.497E-04	2.659E-04	6.404E-03	19	13207239	NFIX
cg08052226	93	-8.102E-04	4.310E-04	6.472E-02	93	-3.103E-04	5.690E-04	5.874E-01	19	13207993	NFIX
cg08740546	93	-2.361E-04	3.084E-04	4.467E-01	93	-2.614E-04	3.983E-04	5.140E-01	19	13155548	NFIX
cg09331335	93	-2.010E-04	2.069E-04	3.349E-01	93	-3.712E-04	2.675E-04	1.701E-01	19	13209485	NFIX
cg09883779	93	1.995E-04	2.268E-04	3.823E-01	93	2.044E-04	2.975E-04	4.946E-01	19	13177929	NFIX
cg10300991	93	-5.122E-04	2.272E-04	2.760E-02	93	-2.906E-04	3.055E-04	3.450E-01	19	13174538	NFIX
cg10809147	93	1.040E-05	1.955E-04	9.577E-01	93	3.712E-04	2.482E-04	1.397E-01	19	13169186	NFIX
cg11758861	93	-2.470E-05	1.583E-04	8.765E-01	93	1.040E-05	2.073E-04	9.603E-01	19	13135514	NFIX
cg11796565	93	-3.806E-04	4.282E-04	3.775E-01	93	-5.719E-04	5.597E-04	3.108E-01	19	13205681	NFIX
cg12685962	93	2.785E-04	3.427E-04	4.194E-01	93	1.972E-04	4.501E-04	6.627E-01	19	13144918	NFIX
cg12891836	93	-2.749E-04	2.051E-04	1.847E-01	93	-2.542E-04	2.704E-04	3.507E-01	19	13161341	NFIX
cg13077190	93	1.110E-05	1.558E-04	9.432E-01	93	-1.007E-04	2.029E-04	6.214E-01	19	13162891	NFIX
cg13649253	93	1.454E-04	2.258E-04	5.219E-01	93	-1.021E-04	2.931E-04	7.287E-01	19	13198798	NFIX
cg17145190	93	1.101E-04	1.721E-04	5.245E-01	93	1.826E-04	2.223E-04	4.145E-01	19	13197029	NFIX
cg17344906	93	5.832E-04	5.114E-04	2.583E-01	93	4.568E-04	6.693E-04	4.974E-01	19	13202507	NFIX
cg17368800	93	3.216E-04	1.989E-04	1.108E-01	93	4.599E-04	2.595E-04	8.116E-02	19	13188366	NFIX
cg17976191	93	-2.350E-05	2.416E-04	9.228E-01	93	-3.761E-04	3.118E-04	2.321E-01	19	13135527	NFIX
cg18299835	93	3.870E-05	1.868E-04	8.364E-01	93	1.639E-04	2.439E-04	5.042E-01	19	13207445	NFIX
cg18427308	93	-1.306E-04	2.203E-04	5.554E-01	93	1.420E-04	2.839E-04	6.187E-01	19	13142463	NFIX
cg18480977	93	1.218E-04	1.758E-04	4.910E-01	93	1.906E-04	2.307E-04	4.118E-01	19	13182850	NFIX
cg19611364	93	-1.112E-04	4.268E-04	7.953E-01	93	-1.959E-04	5.509E-04	7.233E-01	19	13135494	NFIX
cg20116828	93	-6.500E-05	3.105E-04	8.349E-01	93	4.443E-04	4.034E-04	2.748E-01	19	13207602	NFIX
cg23518986	93	-1.131E-04	1.131E-04	3.211E-01	93	-1.557E-04	1.451E-04	2.875E-01	19	13209470	NFIX
cg24158442	93	1.112E-04	2.817E-04	6.942E-01	93	-2.617E-04	3.679E-04	4.795E-01	19	13140977	NFIX
cg24277817	93	8.570E-05	6.176E-04	8.900E-01	93	1.619E-04	7.987E-04	8.400E-01	19	13135662	NFIX
cg24339219	93	-1.918E-04	1.546E-04	2.192E-01	93	1.375E-04	2.038E-04	5.022E-01	19	13149516	NFIX
cg25343560	93	6.109E-04	4.419E-04	1.716E-01	93	2.606E-04	5.851E-04	6.576E-01	19	13155130	NFIX
cg25394801	93	-1.077E-04	2.848E-04	7.066E-01	93	-8.710E-06	3.732E-04	9.815E-01	19	13147655	NFIX
cg25417223	93	4.278E-04	5.411E-04	4.321E-01	93	-5.944E-04	6.995E-04	3.987E-01	19	13209306	NFIX
cg26767614	93	-2.307E-04	2.391E-04	3.381E-01	93	-2.722E-04	3.134E-04	3.884E-01	19	13136168	NFIX
cg27635771	93	2.770E-05	2.435E-04	9.097E-01	93	2.105E-04	3.178E-04	5.102E-01	19	13170076	NFIX
cg01427268	93	6.737E-04	3.171E-04	3.748E-02	93	7.604E-04	4.154E-04	7.180E-02	4	160252652	RAPGEF2
cg01779906	93	1.013E-03	4.907E-04	4.303E-02	93	1.742E-03	6.270E-04	7.164E-03	4	160195650	RAPGEF2
cg02898059	93	4.688E-04	2.535E-04	6.898E-02	93	6.061E-04	3.289E-04	7.001E-02	4	160264661	RAPGEF2

cg02903498	93	-5.870E-04	6.291E-04	3.543E-01	93	1.371E-03	8.131E-04	9.666E-02	4	160263268	RAPGEF2
cg02968883	93	-1.951E-04	7.800E-05	1.498E-02	93	-1.057E-04	1.078E-04	3.308E-01	4	160277142	RAPGEF2
cg03351978	93	4.223E-04	3.568E-04	2.409E-01	93	5.685E-04	4.627E-04	2.237E-01	4	160230280	RAPGEF2
cg03431482	93	6.330E-05	2.935E-04	8.298E-01	93	3.418E-04	3.823E-04	3.746E-01	4	160215429	RAPGEF2
cg04250661	93	-1.591E-04	4.013E-04	6.930E-01	93	-4.689E-04	5.159E-04	3.668E-01	4	160199879	RAPGEF2
cg04399899	93	6.180E-07	3.113E-04	9.984E-01	93	-5.620E-05	4.020E-04	8.893E-01	4	160189254	RAPGEF2
cg04696208	93	-2.933E-04	3.021E-04	3.354E-01	93	3.310E-05	3.969E-04	9.337E-01	4	160266334	RAPGEF2
cg05187155	93	3.590E-06	1.682E-04	9.831E-01	93	2.114E-04	2.189E-04	3.376E-01	4	160280029	RAPGEF2
cg05924733	93	1.528E-04	1.928E-04	4.309E-01	93	1.380E-05	2.534E-04	9.569E-01	4	160277162	RAPGEF2
cg07187641	93	3.054E-04	2.783E-04	2.766E-01	93	1.178E-04	3.636E-04	7.471E-01	4	160212040	RAPGEF2
cg08872866	93	1.568E-04	3.170E-04	6.226E-01	93	-3.030E-05	4.157E-04	9.421E-01	4	160279539	RAPGEF2
cg09051794	93	-2.618E-04	5.437E-04	6.318E-01	93	-2.046E-04	7.125E-04	7.749E-01	4	160216717	RAPGEF2
cg09495517	93	-1.632E-04	2.235E-04	4.681E-01	93	-5.810E-05	2.936E-04	8.436E-01	4	160266803	RAPGEF2
cg09614179	93	-6.060E-05	2.054E-04	7.690E-01	93	-6.240E-05	2.690E-04	8.172E-01	4	160264255	RAPGEF2
cg12305855	93	-2.387E-04	3.329E-04	4.760E-01	93	-1.690E-04	4.368E-04	7.002E-01	4	160216262	RAPGEF2
cg13155469	93	-9.357E-04	4.501E-04	4.162E-02	93	-9.844E-04	5.952E-04	1.030E-01	4	160270640	RAPGEF2
cg13216597	93	2.134E-04	3.287E-04	5.184E-01	93	3.139E-04	4.299E-04	4.680E-01	4	160217706	RAPGEF2
cg13258313	93	-6.820E-05	1.366E-04	6.194E-01	93	7.410E-05	1.789E-04	6.800E-01	4	160266429	RAPGEF2
cg14559229	93	3.829E-04	4.945E-04	4.416E-01	93	4.086E-04	6.376E-04	5.239E-01	4	160201600	RAPGEF2
cg16055817	93	1.039E-03	1.074E-03	3.367E-01	93	6.020E-05	1.425E-03	9.664E-01	4	160277110	RAPGEF2
cg16882824	93	-3.080E-05	2.229E-04	8.905E-01	93	4.320E-06	2.918E-04	9.882E-01	4	160193163	RAPGEF2
cg19135406	93	-6.730E-05	4.381E-04	8.784E-01	93	-4.890E-04	5.762E-04	3.992E-01	4	160219852	RAPGEF2
cg24435971	93	-1.037E-04	1.681E-04	5.394E-01	93	-1.512E-04	2.199E-04	4.941E-01	4	160215959	RAPGEF2
cg24884856	93	-4.260E-05	4.576E-04	9.261E-01	93	4.438E-04	6.047E-04	4.657E-01	4	160203265	RAPGEF2
cg25121721	93	5.119E-04	5.321E-04	3.397E-01	93	6.450E-04	6.970E-04	3.582E-01	4	160218463	RAPGEF2
cg26204575	93	1.139E-04	1.899E-04	5.506E-01	93	-5.480E-05	2.491E-04	8.264E-01	4	160213440	RAPGEF2
cg01030886	93	-7.900E-05	3.741E-04	8.334E-01	93	-7.980E-06	4.899E-04	9.870E-01	12	65766936	MSRB3
cg01104960	93	-9.820E-05	4.292E-04	8.198E-01	93	5.870E-05	5.621E-04	9.171E-01	12	65674264	MSRB3
cg01531701	93	5.098E-04	4.975E-04	3.094E-01	93	-4.557E-04	6.427E-04	4.808E-01	12	65675516	MSRB3
cg04034644	93	3.046E-04	3.162E-04	3.390E-01	93	2.400E-05	4.165E-04	9.542E-01	12	65825192	MSRB3
cg04094162	93	5.216E-04	3.875E-04	1.830E-01	93	5.002E-04	5.121E-04	3.323E-01	12	65675289	MSRB3
cg04104959	93	1.828E-04	4.862E-04	7.082E-01	93	1.386E-04	6.370E-04	8.285E-01	12	65674363	MSRB3
cg04204737	93	2.815E-04	3.088E-04	3.654E-01	93	2.588E-04	4.054E-04	5.255E-01	12	65707425	MSRB3
cg04525892	93	-2.986E-04	2.265E-04	1.922E-01	93	-3.072E-04	2.979E-04	3.062E-01	12	65822627	MSRB3

cg05475386	93	-3.914E-04	4.025E-04	3.345E-01	93	-1.090E-04	5.301E-04	8.377E-01	12	65723693	MSRB3
cg05697394	93	-2.069E-04	3.668E-04	5.746E-01	93	7.520E-05	4.811E-04	8.763E-01	12	65701642	MSRB3
cg06700060	93	7.470E-06	2.582E-04	9.770E-01	93	2.705E-04	3.365E-04	4.245E-01	12	65859647	MSRB3
cg09387650	93	-3.482E-04	3.377E-04	3.065E-01	93	-3.030E-05	4.453E-04	9.460E-01	12	65713650	MSRB3
cg09421347	93	-2.940E-05	8.410E-05	7.279E-01	93	2.330E-05	1.101E-04	8.334E-01	12	65673222	MSRB3
cg10442759	93	-7.690E-05	7.590E-05	3.146E-01	93	3.530E-05	9.990E-05	7.249E-01	12	65673274	MSRB3
cg12269782	93	-1.937E-04	2.566E-04	4.531E-01	93	-1.419E-04	3.340E-04	6.725E-01	12	65737799	MSRB3
cg12708266	93	3.641E-04	3.168E-04	2.548E-01	93	4.548E-04	4.151E-04	2.773E-01	12	65702725	MSRB3
cg12747525	93	1.332E-04	2.856E-04	6.427E-01	93	-1.353E-04	3.768E-04	7.206E-01	12	65675358	MSRB3
cg14571669	93	-4.651E-04	5.500E-04	4.009E-01	93	-5.424E-04	7.208E-04	4.544E-01	12	65756576	MSRB3
cg14609260	93	-1.045E-03	4.728E-04	3.060E-02	93	-9.616E-04	6.251E-04	1.289E-01	12	65859092	MSRB3
cg18130328	93	4.120E-05	2.458E-04	8.675E-01	93	1.855E-04	3.212E-04	5.656E-01	12	65720609	MSRB3
cg19365956	93	2.680E-05	3.025E-04	9.297E-01	93	1.533E-04	3.956E-04	6.996E-01	12	65721370	MSRB3
cg20315554	93	5.155E-04	5.028E-04	3.091E-01	93	4.613E-04	6.541E-04	4.832E-01	12	65676662	MSRB3
cg20845085	93	1.248E-04	2.465E-04	6.144E-01	93	4.586E-04	3.189E-04	1.553E-01	12	65728847	MSRB3
cg21614762	93	4.458E-04	5.963E-04	4.574E-01	93	7.984E-04	7.781E-04	3.087E-01	12	65674271	MSRB3
cg22559881	93	1.350E-05	4.450E-04	9.759E-01	93	-6.384E-04	5.703E-04	2.671E-01	12	65700713	MSRB3
cg24890392	93	-6.770E-05	2.323E-04	7.717E-01	93	4.320E-05	2.979E-04	8.853E-01	12	65721645	MSRB3
cg03279206	93	-6.970E-05	1.796E-04	6.994E-01	93	-1.746E-04	2.345E-04	4.593E-01	20	3064001	AVP
cg04360210	93	1.811E-04	8.950E-05	4.721E-02	93	1.634E-04	1.189E-04	1.741E-01	20	3064015	AVP
cg14065127	93	-9.660E-05	7.950E-05	2.290E-01	93	-1.643E-04	1.034E-04	1.169E-01	20	3063238	AVP
cg25551168	93	3.801E-04	1.997E-04	6.147E-02	93	6.416E-04	2.586E-04	1.573E-02	20	3065343	AVP
cg25673357	93	1.820E-05	1.094E-04	8.687E-01	93	2.265E-04	1.408E-04	1.127E-01	20	3063586	AVP
cg06404175	93	-1.928E-04	1.909E-04	3.161E-01	93	-2.710E-04	2.496E-04	2.817E-01	20	3052692	OXT
cg09774842	93	-7.160E-05	1.840E-04	6.986E-01	93	1.552E-04	2.444E-04	5.275E-01	20	3052483	OXT
cg12099952	93	-1.857E-04	1.265E-04	1.469E-01	93	-1.227E-04	1.674E-04	4.662E-01	20	3053037	OXT
cg19592472	93	-3.076E-04	7.124E-04	6.674E-01	93	-2.597E-04	9.333E-04	7.817E-01	20	3052274	OXT
cg26955850	93	-4.213E-04	5.073E-04	4.093E-01	93	-1.005E-03	6.571E-04	1.312E-01	20	3052345	OXT
cg01071966	93	1.621E-04	2.384E-04	4.991E-01	93	1.311E-04	3.127E-04	6.763E-01	5	76248923	CRHBP
cg02882540	93	-3.207E-04	3.313E-04	3.367E-01	93	-5.272E-04	4.331E-04	2.280E-01	5	76256334	CRHBP
cg03286609	93	4.870E-05	5.562E-04	9.305E-01	93	-4.362E-04	7.264E-04	5.503E-01	5	76252218	CRHBP
cg04306063	93	7.020E-05	1.376E-04	6.117E-01	93	1.608E-04	1.795E-04	3.736E-01	5	76249502	CRHBP
cg05620787	93	4.710E-04	2.657E-04	8.108E-02	93	6.752E-04	3.465E-04	5.569E-02	5	76264831	CRHBP
cg07380705	93	2.990E-05	1.776E-04	8.668E-01	93	-1.050E-05	2.326E-04	9.642E-01	5	76249897	CRHBP

cg08792780	93	-1.774E-04	3.246E-04	5.866E-01	93	1.430E-05	4.258E-04	9.734E-01	5	76249094	CRHBP
cg10593758	93	2.551E-04	2.247E-04	2.605E-01	93	1.329E-04	2.963E-04	6.552E-01	5	76248743	CRHBP
cg13157757	93	-3.420E-05	2.036E-04	8.672E-01	93	-1.451E-04	2.661E-04	5.875E-01	5	76250351	CRHBP
cg13777717	93	-3.286E-04	3.126E-04	2.972E-01	93	-5.251E-04	4.078E-04	2.025E-01	5	76250527	CRHBP
cg16545105	93	-4.050E-05	4.200E-04	9.236E-01	93	-4.749E-04	5.471E-04	3.886E-01	5	76248749	CRHBP
cg17448335	93	-4.320E-05	7.530E-05	5.683E-01	93	-4.580E-05	9.860E-05	6.439E-01	5	76249776	CRHBP
cg18419716	93	-6.850E-05	6.791E-04	9.199E-01	93	-3.153E-04	8.825E-04	7.220E-01	5	76254194	CRHBP
cg18493242	93	-8.478E-04	4.544E-04	6.665E-02	93	-8.965E-04	5.996E-04	1.398E-01	5	76255050	CRHBP
cg20214624	93	-4.296E-04	3.716E-04	2.519E-01	93	-1.312E-04	4.906E-04	7.900E-01	5	76254375	CRHBP
cg21199406	93	2.267E-04	2.208E-04	3.084E-01	93	7.020E-05	2.855E-04	8.066E-01	5	76250201	CRHBP
cg22323744	93	1.587E-04	2.852E-04	5.799E-01	93	4.509E-04	3.705E-04	2.281E-01	5	76248711	CRHBP
cg26269677	93	6.706E-04	7.236E-04	3.575E-01	93	-1.648E-04	9.395E-04	8.613E-01	5	76251688	CRHBP
cg00601836	93	-4.518E-04	1.110E-03	6.854E-01	93	-8.192E-04	1.446E-03	5.730E-01	6	152130332	ESR1
cg00655307	93	3.810E-05	8.120E-05	6.405E-01	93	1.657E-04	1.039E-04	1.156E-01	6	152128743	ESR1
cg00920970	93	-1.300E-04	1.181E-04	2.751E-01	93	-1.160E-04	1.537E-04	4.532E-01	6	152129388	ESR1
cg00975240	93	-1.156E-04	3.459E-04	7.392E-01	93	1.250E-04	4.530E-04	7.835E-01	6	152370564	ESR1
cg01735235	93	-4.630E-05	3.694E-04	9.005E-01	93	-2.701E-04	4.826E-04	5.776E-01	6	152135407	ESR1
cg01777019	93	-1.300E-04	1.237E-04	2.970E-01	93	-1.833E-04	1.617E-04	2.612E-01	6	152128805	ESR1
cg01901499	93	-2.390E-04	2.088E-04	2.567E-01	93	-1.707E-04	2.750E-04	5.370E-01	6	152376804	ESR1
cg02285263	93	-4.390E-05	1.494E-04	7.699E-01	93	7.090E-05	1.956E-04	7.182E-01	6	152129749	ESR1
cg02404255	93	-1.491E-04	3.150E-04	6.376E-01	93	-5.999E-04	4.072E-04	1.456E-01	6	152419175	ESR1
cg02720618	93	-1.103E-04	1.021E-04	2.839E-01	93	1.174E-04	1.380E-04	3.982E-01	6	152129791	ESR1
cg03037684	93	1.380E-03	5.804E-04	2.045E-02	93	7.070E-04	7.798E-04	3.680E-01	6	152421333	ESR1
cg03732055	93	6.217E-04	7.228E-04	3.929E-01	93	1.465E-03	9.357E-04	1.223E-01	6	152201038	ESR1
cg04418936	93	-5.440E-06	2.951E-04	9.854E-01	93	-1.000E-05	3.864E-04	9.793E-01	6	152388255	ESR1
cg04525653	93	-3.727E-04	2.280E-04	1.070E-01	93	-3.749E-04	3.006E-04	2.169E-01	6	152375589	ESR1
cg04718764	93	-4.763E-04	4.061E-04	2.451E-01	93	-3.708E-04	5.347E-04	4.906E-01	6	152235927	ESR1
cg05171584	93	-2.066E-04	2.765E-04	4.577E-01	93	1.411E-04	3.629E-04	6.988E-01	6	152128535	ESR1
cg06877423	93	-1.569E-04	4.540E-04	7.308E-01	93	-1.926E-04	5.944E-04	7.470E-01	6	152200760	ESR1
cg08157080	93	-2.678E-04	2.595E-04	3.059E-01	93	-4.930E-06	3.492E-04	9.888E-01	6	152406734	ESR1
cg09414638	93	-4.837E-04	6.251E-04	4.419E-01	93	2.313E-04	8.212E-04	7.791E-01	6	152239860	ESR1
cg09495438	93	-5.820E-04	3.100E-04	6.499E-02	93	-1.171E-03	4.022E-04	4.933E-03	6	152168125	ESR1
cg10804487	93	-1.090E-05	2.581E-04	9.663E-01	93	-1.404E-04	3.375E-04	6.788E-01	6	152136586	ESR1
cg10939667	93	2.241E-04	2.421E-04	3.581E-01	93	1.782E-04	3.181E-04	5.773E-01	6	152201611	ESR1

cg11251858	93	1.931E-04	1.845E-04	2.994E-01	93	1.962E-04	2.423E-04	4.210E-01	6	152129036	ESR1
cg11813455	93	8.640E-05	1.199E-04	4.738E-01	93	2.114E-04	1.557E-04	1.793E-01	6	152128515	ESR1
cg12001846	93	-5.421E-04	1.083E-03	6.185E-01	93	-5.568E-04	1.419E-03	6.961E-01	6	152212815	ESR1
cg12209876	93	-1.423E-04	1.736E-04	4.152E-01	93	-2.901E-04	2.258E-04	2.034E-01	6	152381560	ESR1
cg12519939	93	8.910E-05	1.838E-04	6.295E-01	93	-6.440E-05	2.407E-04	7.898E-01	6	152265431	ESR1
cg13889536	93	1.990E-05	2.746E-04	9.424E-01	93	1.961E-04	3.588E-04	5.867E-01	6	152417832	ESR1
cg15358019	93	4.774E-04	4.740E-04	3.177E-01	93	9.081E-04	6.159E-04	1.452E-01	6	152136221	ESR1
cg15390122	93	-4.660E-05	6.321E-04	9.414E-01	93	-4.001E-04	8.262E-04	6.299E-01	6	152130188	ESR1
cg15561702	93	3.631E-04	3.277E-04	2.719E-01	93	-1.308E-04	4.376E-04	7.660E-01	6	152136576	ESR1
cg15626350	93	6.719E-04	9.165E-04	4.662E-01	93	1.510E-05	1.204E-03	9.900E-01	6	152130207	ESR1
cg15980539	93	2.070E-05	4.900E-05	6.735E-01	93	6.440E-05	6.380E-05	3.166E-01	6	152128865	ESR1
cg18024141	93	-1.398E-04	2.510E-04	5.796E-01	93	-2.458E-04	3.280E-04	4.564E-01	6	152232729	ESR1
cg18206764	93	6.408E-04	5.820E-04	2.750E-01	93	1.517E-03	7.783E-04	5.563E-02	6	152283837	ESR1
cg18509675	93	1.780E-05	1.880E-04	9.249E-01	93	3.834E-04	2.421E-04	1.182E-01	6	152411260	ESR1
cg19369424	93	-1.126E-04	2.716E-04	6.799E-01	93	-1.870E-04	3.501E-04	5.950E-01	6	152264237	ESR1
cg19411146	93	1.130E-04	2.445E-04	6.456E-01	93	4.281E-04	3.127E-04	1.757E-01	6	152128471	ESR1
cg20253551	93	-3.360E-05	1.120E-04	7.648E-01	93	4.740E-05	1.466E-04	7.476E-01	6	152129400	ESR1
cg21017124	93	-2.635E-04	2.283E-04	2.528E-01	93	-3.438E-04	2.989E-04	2.544E-01	6	152320157	ESR1
cg21950534	93	3.612E-04	1.623E-04	2.959E-02	93	4.972E-04	2.117E-04	2.196E-02	6	152128483	ESR1
cg21969073	93	4.500E-05	9.930E-05	6.520E-01	93	8.560E-05	1.301E-04	5.129E-01	6	152129018	ESR1
cg23009221	93	2.532E-04	1.879E-04	1.826E-01	93	2.289E-04	2.476E-04	3.585E-01	6	152128588	ESR1
cg23467008	93	-6.250E-05	1.011E-04	5.389E-01	93	-1.316E-04	1.318E-04	3.218E-01	6	152128537	ESR1
cg24170716	93	3.338E-04	7.550E-04	6.599E-01	93	-1.326E-04	9.896E-04	8.938E-01	6	152411971	ESR1
cg24900983	93	5.990E-05	1.780E-04	7.375E-01	93	-1.396E-04	2.326E-04	5.505E-01	6	152128528	ESR1
cg27301701	93	-3.599E-04	2.387E-04	1.366E-01	93	-5.115E-04	3.117E-04	1.057E-01	6	152222460	ESR1
cg27316393	93	-7.180E-05	1.155E-04	5.367E-01	93	-4.140E-05	1.516E-04	7.856E-01	6	152128675	ESR1
cg27491370	93	-3.096E-04	3.296E-04	3.510E-01	93	-5.978E-04	4.285E-04	1.678E-01	6	152400061	ESR1