Supplemental Material to:

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Distinctive patterns of DNA methylation associated with Parkinson disease: Identification of concordant epigenetic changes in brain and peripheral blood leukocytes

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Supplemental Material

Supplementary Table 1. Demographic characterization of the studied cohort.
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Supplementary Table 1-A. Clinical and demographic characteristics of the studied cohort

Group	Age (y)	Gender F/ M (n)	Brain weight (g)	MMSE[1]	Education (yrs)
Control	89 ± 4	4 / 2 (6)	1,144 ± 199	27.8 ± 1.3	15 ± 2
Parkinson's	80 ± 8	0 / 5 (5)	1,246 ± 104	15.2 ± 10	17 ± 3

1. Mini-Mental State Examination.

Supplementary Table 1-B. Individual clinical profile and drug treatment of PD patients

Case ID	First PD diagnosis	Disease Duration (y)	Drug Treatment *	Date started on medication
1	2004	7	Sinemet Rasagiline	2004 2009
2	1981	26	Sinemet Deprenyl Comtan	1983 1989 2000
3	1984	16	ENA-713	1995
4	1999	9	Clonazepan Memantine	1996 2004
5	2002	7	Sinemet Rivastigmine	2007 2008

* Record of medication most relevant to PD pathology

Supplementary Table 2. Autosomal genes showing differential methylation in the brain of PD cases. Analysis of differential methylation was performed with Genome Studio using Illumina custom model. Genes with Delta β value > |0.20| at $p<0.01$ and FDR $q<0.001$. * Denotes genes for which more than one DM independent probe was detected showing opposite methylation changes.

TargetID	*ACCESSION#*	*GENE NAME*	*DiffScore*	*Delta Beta*	*CHR*	*CpG Context*
Genes with decreased methylation in PD						
cg05084668	NM_001015050	ALG1L	-143.090	-0.233	3	
cg20959002	NM_133463	AMZ1	-159.666	-0.241	7	S_Shelf
cg09785377	NM_001136015	ANXA2	-142.532	-0.234	15	
cg14460215	NM_001163	APBA1	-243.590	-0.312	9	S_Shore
cg27057480	NM_021226	ARHGAP22	-165.823	-0.258	10	S_Shore
cg10738003	NM_015313	ARHGEF12	-229.619	-0.301	11	
cg16655091	NM_016529	ATP8A2	-137.037	-0.244	13	S_Shelf
cg25165144	NM_173593	B4GALNT3	-129.592	-0.207	12	
cg05483487	NM_173593	B4GALNT3	-115.847	-0.205	12	
cg24859648	NM_178477	BANF2	-163.008	-0.236	20	
cg18861767	NR_024572	C10orf58	-112.505	-0.222	10	
cg09175792	NM_199459	C10orf71	-171.287	-0.201	10	Island
cg08085267	NM_152347	C17orf57	-101.182	-0.210	17	S_Shore
cg09385306	NM_198077	C1orf52	-88.117	-0.201	1	N_Shore
cg01784345	NM_032261	C21orf56	-141.770	-0.211	21	N_Shore
cg18457108	NM_152531	C3orf21	-116.696	-0.219	3	
cg18391209	NM_001143962	CAPN8	-260.688	-0.318	1	S_Shelf
cg10482512	NM_004367	CCR6	-96.688	-0.210	6	
cg16744961	NM_172004	CLECL1	-136.458	-0.244	12	
cg05340866	NM_014141	CNTNAP2	-155.009	-0.256	7	N_Shelf
cg14782559	NM_080679	COL11A2	-115.460	-0.224	6	S_Shelf
cg22508145	NM_015692	CPAMD8	-161.492	-0.252	19	
cg20208879	NM_004389	CTNNA2	-209.601	-0.270	2	
cg05195318	NM_001037333	CYFIP2	-127.259	-0.209	5	
cg09746326	NM_001014283	DCUN1D2	-285.361	-0.307	13	
cg14506194	NR_026597	DIRC3	-168.849	-0.223	2	
cg03327352	NM_147192	DMBX1	-342.878	-0.370	1	
cg07437923	NM_001135110	DNAJA3	-342.878	-0.445	16	
cg24407607	NM_013352	DSE	-171.169	-0.255	6	
cg17279365	NM_206594	ESRRG	-135.385	-0.230	1	

cg24345856	NM_001014980	FAM132A	-162.147	-0.232	1	S_Shore
cg09281805	NM_001037165	FOXK1	-253.377	-0.317	7	
cg07525313	NM_002031	FRK	-342.878	-0.386	6	
cg13291296	NM_145290	GPR125	-306.262	-0.308	4	
cg11478607	NM_000853	GSTT1	-280.913	-0.240	22	Island
cg01238044	NM_000853	GSTT1	-162.218	-0.219	22	N_Shore
cg01647917	NM_005317	GZMM	-143.690	-0.220	19	S_Shore
cg00211215	NM_002124	HLA-DRB1*	-342.878	-0.409	6	Island
cg15568074	NM_002124	HLA-DRB1*	-160.212	-0.259	6	Island
cg16514085	NM_002124	HLA-DRB1*	-110.013	-0.219	6	Island
cg25046571	NM_002127	HLA-G	-122.637	-0.227	6	N_Shore
cg07629625	NM_001105521	JAKMIP3	-342.878	-0.495	10	
cg03084184	NM_001105521	JAKMIP3	-253.038	-0.311	10	
cg09518270	NM_172362	KCNH1	-166.731	-0.254	1	S_Shore
cg05522042	NM_014732	KIAA0513	-160.380	-0.259	16	
cg22336867	NM_002307	LGALS7	-342.878	-0.368	19	S_Shelf
cg24730756	NR_028415	LOC100292680	-140.498	-0.244	12	
cg04234412	NM_001144931	LOC391322	-267.675	-0.317	22	Island
cg15083522	NM_001143757	LRRC27	-342.878	-0.382	10	
cg21829038	NM_024652	LRRK1*	-156.769	-0.216	15	Island
cg12543766	NM_012301	MAGI2	-261.794	-0.306	7	S_Shelf
cg05093818	NM_138982	MAPK10	-88.353	-0.201	4	
cg08238375	NM_002387	MCC	-113.551	-0.216	5	
cg25340688	NR_030583	MIR886	-134.531	-0.241	5	Island
cg26328633	NR_030583	MIR886	-113.944	-0.225	5	Island
cg06536614	NR_030583	MIR886	-94.768	-0.206	5	Island
cg04481923	NR_030583	MIR886	-95.385	-0.206	5	Island
cg00124993	NR_030583	MIR886	-96.393	-0.205	5	Island
cg18678645	NR_030583	MIR886	-92.209	-0.202	5	Island
cg19712277	NM_033467	MMEL1*	-190.273	-0.226	1	Island
cg04528326	NM_007208	MRPL3	-127.621	-0.221	3	N_Shelf
cg00295418	NM_003970	MYOM2	-146.225	-0.249	8	
cg05891136	NM_003970	MYOM2	-97.240	-0.206	8	
cg05023192	NM_004544	NDUFA10	-126.818	-0.229	2	S_Shore
cg15075357	NM_015102	NPHP4	-137.161	-0.245	1	
cg04152793	NM_001144059	NTM	-127.991	-0.223	11	
cg11881038	NM_001145283	OPRM1	-262.959	-0.318	6	
cg01463139	NM_001004473	OR10K1	-106.787	-0.219	1	
cg16035267	NM_030959	OR12D3	-237.267	-0.280	6	
cg00045070	NM_174936	PCSK9	-129.340	-0.238	1	N_Shore

cg11594160	NM_005027	PIK3R2	-162.084	-0.229	19	S_Shore
cg06012903	NM_002847	PTPRN2	-123.859	-0.223	7	S_Shore
cg23657215	NM_138499	PWWP2B	-110.682	-0.222	10	S_Shore
cg18443741	NM_024854	PYROXD1	-122.462	-0.232	12	S_Shelf
cg11508056	NM_019034	RHOF	-118.393	-0.211	12	
cg27308738	NM_014631	SH3PXD2A	-133.025	-0.236	10	N_Shelf
cg16733676	NM_213651	SLC25A24	-182.809	-0.253	1	N_Shore
cg22841866	NM_133489	SLC26A10	-91.812	-0.202	12	Island
cg05509228	NM_022138	SMOC2	-144.912	-0.222	6	Island
cg04798314	NM_001167740	SMYD3	-98.302	-0.208	1	N_Shore
cg17174466	NM_001100422	SPATS2L	-125.633	-0.217	2	
cg17671604	NM_020971	SPTBN4	-135.959	-0.242	19	N_Shelf
cg00030117	NM_001008410	STEAP3	-342.878	-0.358	2	N_Shore
cg16956665	NM_152713	STT3A	-159.901	-0.258	11	
cg17386240	NM_000358	TGFBI	-162.268	-0.256	5	
cg20926353	NM_005077	TLE1	-118.007	-0.207	9	Island
cg07876831	NM_017905	TMCO3	-126.706	-0.207	13	N_Shelf
cg14361804	NM_001244	TNFSF8	-118.296	-0.230	9	
cg24697433	NM_006510	TRIM27	-103.339	-0.210	6	
cg20089799	NM_006675	TSPAN9	-148.536	-0.253	12	
cg03206401	NM_207312	TUBA3E	-96.370	-0.210	2	Island
cg20106077	NM_182552	WDR27	-150.634	-0.219	6	N_Shore
cg02823311	NM_020196	XAB2	-177.112	-0.234	19	Island
cg03900028	NM_015852	ZNF117	-177.587	-0.273	7	
Genes with increased methylation in PD						
cg10760240	NM_012138	AATF	342.878	0.224	17	
cg01491428	NM_001089	ABCA3	342.878	0.264	16	Island
cg09998151	NM_004274	AKAP6	103.863	0.216	14	
cg05890457	NM_014629	ARHGEF10	342.878	0.319	8	
cg24166916	NM_000046	ARSB	342.878	0.220	5	S_Shore
cg17056069	NM_001135191	ASAP2	342.878	0.235	2	
cg00095677	NM_174954	ATP2A3	342.878	0.235	17	
cg00713204	NM_017869	BANP	342.878	0.254	16	N_Shore
cg14655569	NM_015250	BICD2	342.878	0.266	9	N_Shelf
cg00231519	NM_153810	C10orf46	119.059	0.223	10	S_Shore
cg16706502	NM_080664	C14orf126	342.878	0.298	14	S_Shore
cg23813394	NM_004369	COL6A3	127.621	0.236	2	
cg16471877	NM_017421	COQ3	118.170	0.219	6	
cg11128983	NM_001008220	CPLX2	131.466	0.200	5	N_Shore
cg00861214	NM_175710	CR1L	342.878	0.244	1	

cg11229715	NM_003590	CUL3	94.918	0.209	2	
cg08002427	NM_001372	DNAH9	114.432	0.220	17	S_Shore
cg04212500	NM_005702	ERAL1	342.878	0.237	17	S_Shelf
cg09438069	NM_005245	FAT1	113.270	0.214	4	
cg04888234	NM_032738	FCRLA	99.076	0.210	1	
cg16140565	NM_001166243	FHIT	342.878	0.254	3	
cg01801090	NR_029435	FLJ31306	342.878	0.240	14	N_Shelf
cg25203245	NM_152432	FLJ32810	342.878	0.316	11	
cg10058204	NR_026835	FLJ37201	342.878	0.254	10	
cg03812172	NM_033508	GCK	129.769	0.223	7	N_Shore
cg02891314	NM_005110	GFPT2	342.878	0.316	5	Island
cg13944838	NM_005110	GFPT2	342.878	0.263	5	Island
cg23221052	NM_005110	GFPT2	342.878	0.279	5	Island
cg23248424	NM_005110	GFPT2	342.878	0.308	5	Island
cg15242686	NR_003081	GSTTP1	108.769	0.218	22	
cg01500431	NR_003082	GSTTP2	342.878	0.222	22	S_Shelf
cg09510698	NR_001435	HLA-DPB2	342.878	0.272	6	
cg24470466	NM_002122	HLA-DQA1	342.878	0.437	6	
cg24969496	NM_002122	HLA-DQA1	102.246	0.213	6	
cg08964730	NM_002123	HLA-DQB1	342.878	0.223	6	S_Shore
cg12867728	NM_002124	HLA-DRB1*	110.059	0.222	6	N_Shelf
cg13910785	NM_002124	HLA-DRB1*	342.878	0.350	6	N_Shelf
cg21810411	NM_002124	HLA-DRB1*	120.061	0.223	6	N_Shelf
cg24760581	NM_002124	HLA-DRB1*	117.666	0.224	6	
cg26590106	NM_002124	HLA-DRB1*	342.878	0.263	6	N_Shelf
cg01341801	NM_002125	HLA-DRB5	342.878	0.271	6	N_Shore
cg17369694	NM_002125	HLA-DRB5	342.878	0.231	6	
cg18111114	NM_002125	HLA-DRB5	342.878	0.343	6	
cg11752699	NR_001298	HLA-DRB6	98.266	0.207	6	
cg22627029	NR_001298	HLA-DRB6	134.390	0.231	6	
cg25140213	NR_001298	HLA-DRB6	342.878	0.284	6	
cg03648908	NM_002222	ITPR1	92.341	0.205	3	
cg03796003	NM_018992	KCTD5	342.878	0.429	16	Island
cg00729708	NM_178842	LASS3	119.661	0.230	15	Island
cg10879348	NM_004987	LIMS1	117.005	0.211	2	
cg11008123	NR_015451	LOC283267	342.878	0.375	11	
cg25450321	NM_024652	LRRK1*	342.878	0.294	15	N_Shelf
cg13275129	NM_032427	MAML2	119.788	0.204	11	
cg02228913	NM_016835	MAPT	342.878	0.238	17	N_Shelf
cg24801230	NM_001123067	MAPT	342.878	0.249	17	S_Shelf

cg21209485	NM_033467	MMEL1*	342.878	0.284	1	S_Shore
cg04627110	NM_206813	MOG	342.878	0.357	6	
cg12279734	NM_006792	MORF4	342.878	0.226	4	
cg25755428	NM_001031727	MRI1	342.878	0.258	19	Island
cg18346634	NM_000911	OPRD1	342.878	0.263	1	S_Shore
cg10701801	NM_148909	OSBPL9	105.855	0.213	1	
cg21069494	NM_002626	PFKL	129.769	0.223	21	S_Shelf
cg26584456	NM_005729	PPIF	342.878	0.298	10	
cg08600378	NM_001105577	PRHOXNB	342.878	0.340	13	
cg02978201	NM_002761	PRM1	114.901	0.222	16	
cg02901522	NR_003367	PVT1	134.390	0.241	8	
cg12532878	NM_007368	RASA3	94.839	0.206	13	N_Shore
cg03570263	NM_170769	RNF39	115.872	0.218	6	S_Shore
cg13251750	NM_175739	SERPINA9	86.518	0.201	14	
cg19223824	NM_020708	SLC12A5	342.878	0.284	20	N_Shelf
cg17662493	NM_148674	SMC1B	342.878	0.273	22	N_Shelf
cg09050820	NM_001145121	TCP10L2	104.445	0.209	6	N_Shore
cg15290312	NM_003255	TIMP2	125.152	0.225	17	Island
cg01012836	NM_052907	TMEM132B	105.780	0.208	12	
cg16112880	NM_016456	TMEM9	342.878	0.274	1	Island
cg26365090	NM_001098796	TOX2	128.553	0.232	20	
cg02627240	NM_022445	TPK1	342.878	0.239	7	
cg03422583	NM_025204	TRABD	118.352	0.203	22	N_Shore
cg03187614	NM_006778	TRIM10	342.878	0.352	6	
cg25569462	NM_173553	TRIML2	107.227	0.208	4	N_Shore
cg01891583	NM_003470	USP7	87.287	0.201	16	
cg15365500	NM_005715	UST	342.878	0.272	6	
cg13564529	NM_001134398	VAV2	342.878	0.374	9	
cg15625495	NM_005997	VPS72	342.878	0.245	1	
cg07456585	NM_182894	VSX2	134.390	0.240	14	N_Shore
cg21171335	NM_144668	WDR66	342.878	0.238	12	Island
cg22618164	NM_144668	WDR66	110.475	0.203	12	Island
cg19471911	NM_001130145	YAP1	91.716	0.206	11	
cg07878625	NR_015357	ZNF783	342.878	0.213	7	N_Shore

Supplementary Table 3. Autosomal genes showing differential methylation on PBLs from PD cases. Analysis of differential methylation was performed with Genome Studio using Illumina custom model. Genes with Delta β value > |0.20 | at p<0.01 and FDR q<0.001. * Denotes genes for which more than one DM independent probe was detected showing opposite methylation changes.

TargetID	*ACCESSION#*	*GENE NAME*	*DiffScore*	*Delta Beta*	*CHR*	*CpG Context*
Genes with decerased methylation in PD						
cg06131755	NM_005891	ACAT2	-135.396	-0.206	6	Island
cg25736982	NM_005891	ACAT2	-115.981	-0.201	6	Island
cg20959002	NM_133463	AMZ1	-178.400	-0.253	7	S_Shelf
cg09785377	NM_001136015	ANXA2	-156.458	-0.244	15	
cg14460215	NM_001163	APBA1	-195.225	-0.283	9	S_Shore
cg10738003	NM_015313	ARHGEF12	-226.177	-0.300	11	
cg16655091	NM_016529	ATP8A2	-110.950	-0.221	13	S_Shelf
cg24859648	NM_178477	BANF2	-274.720	-0.291	20	
cg08253809	NM_017924	C14orf119	-116.598	-0.227	14	S_Shelf
cg13966843	NM_006781	C6orf10	-173.991	-0.220	6	
cg18391209	NM_001143962	CAPN8	-234.488	-0.305	1	S_Shelf
cg11070193	NM_198137	CATSPER4	-97.137	-0.207	1	
cg20415053	NM_198137	CATSPER4	-117.531	-0.226	1	
cg04246708	NM_001139459	CNST	-213.902	-0.294	1	S_Shore
cg05340866	NM_014141	CNTNAP2	-164.915	-0.261	7	N_Shelf
cg14782559	NM_080679	COL11A2	-97.924	-0.209	6	S_Shelf
cg22508145	NM_015692	CPAMD8	-146.686	-0.245	19	
cg05092371	NM_001037631	CTLA4	-112.911	-0.201	2	
cg20208879	NM_004389	CTNNA2	-149.883	-0.234	2	
cg09746326	NM_001014283	DCUN1D2	-329.196	-0.305	13	
cg25709790	NM_001127454	DFNA5	-139.792	-0.229	7	
cg24068006	NM_014974	DIP2C	-142.297	-0.209	10	S_Shore
cg03327352	NM_147192	DMBX1	-333.136	-0.354	1	
cg07437923	NM_001135110	DNAJA3	-344.873	-0.511	16	
cg24407607	NM_013352	DSE;DSE	-181.425	-0.259	6	
cg22459517	NM_133180	EPS8L1	-109.244	-0.218	19	
cg24345856	NM_001014980	FAM132A	-119.584	-0.207	1	S_Shore
cg00167275	NM_019054	FAM35A	-161.156	-0.205	10	Island
cg21190982	NM_015962	FCF1	-104.844	-0.217	14	S_Shore
cg01620164	NM_018086	FIGN	-111.409	-0.221	2	N_Shelf

cg09281805	NM_001037165	FOXK1	-301.844	-0.340	7	
cg07525313	NM_002031	FRK	-304.474	-0.341	6	
cg26303777	NM_004481	GALNT2	-149.005	-0.240	1	
cg02981003	NM_001083909	GPR123	-142.339	-0.211	10	N_Shore
cg01238044	NM_000853	GSTT1	-227.818	-0.268	22	N_Shore
cg11478607	NM_000853	GSTT1	-154.384	-0.210	22	Island
cg01647917	NM_005317	GZMM	-157.727	-0.233	19	S_Shore
cg06071033	NM_005477	HCN4	-87.429	-0.200	15	S_Shore
cg05341252	NM_002123	HLA-DQB1*	-160.031	-0.251	6	Island
cg13423887	NM_002123	HLA-DQB1*	-235.455	-0.302	6	Island
cg00211215	NM_002124	HLA-DRB1*	-344.873	-0.438	6	Island
cg09139047	NM_002124	HLA-DRB1*	-150.066	-0.211	6	Island
cg09949906	NM_002124	HLA-DRB1*	-99.879	-0.211	6	S_Shore
cg11404906	NM_002124	HLA-DRB1*	-322.447	-0.345	6	N_Shore
cg15568074	NM_002124	HLA-DRB1*	-100.602	-0.208	6	Island
cg16514085	NM_002124	HLA-DRB1*	-335.781	-0.351	6	Island
cg06316104	NM_002127	HLA-G	-116.038	-0.211	6	S_Shore
cg25046571	NM_002127	HLA-G	-125.877	-0.229	6	N_Shore
cg02856402	NM_001127205	HMOX2	-344.873	-0.493	16	
cg03084184	NM_001105521	JAKMIP3	-189.470	-0.276	10	
cg07629625	NM_001105521	JAKMIP3	-344.873	-0.449	10	
cg09518270	NM_172362	KCNH1	-193.384	-0.267	1	S_Shore
cg05522042	NM_014732	KIAA0513	-207.146	-0.283	16	
cg10909185	NM_001039548	KLHL35	-130.201	-0.231	11	Island
cg22336867	NM_002307	LGALS7	-344.873	-0.380	19	S_Shelf
cg24730756	NR_028415	LOC100292680	-242.560	-0.288	12	
cg11716267	NM_001145710	LOC375190	-111.143	-0.213	2	
cg04234412	NM_001144931	LOC391322	-297.451	-0.328	22	Island
cg04824771	NM_001144931	LOC391322	-159.389	-0.200	22	Island
cg15083522	NM_001143757	LRRC27	-344.873	-0.406	10	
cg21829038	NM_024652	LRRK1*	-318.922	-0.305	15	Island
cg12543766	NM_012301	MAGI2	-121.104	-0.228	7	S_Shelf
cg12252547	NM_052886	MAL2	-132.265	-0.237	8	N_Shore
cg05093818	NM_138982	MAPK10	-88.256	-0.201	4	
cg08238375	NM_002387	MCC	-110.904	-0.209	5	
cg00124993	NR_030583	MIR886	-170.540	-0.254	5	Island
cg04481923	NR_030583	MIR886	-145.842	-0.241	5	Island
cg06536614	NR_030583	MIR886	-203.039	-0.281	5	Island
cg08745965	NR_030583	MIR886	-103.105	-0.202	5	S_Shore
cg16615357	NR_030583	MIR886	-87.763	-0.201	5	S_Shore

cg18797653	NR_030583	MIR886	-97.781	-0.208	5	S_Shore
cg25340688	NR_030583	MIR886	-186.941	-0.272	5	Island
cg26328633	NR_030583	MIR886	-198.858	-0.282	5	Island
cg26896946	NR_030583	MIR886	-130.947	-0.234	5	Island
cg19712277	NM_033467	MMEL1	-155.590	-0.220	1	Island
cg04528326	NM_007208	MRPL3	-119.455	-0.214	3	N_Shelf
cg17959722	NM_032477	MRPL41	-113.051	-0.204	9	Island
cg05891136	NM_003970	MYOM2	-92.312	-0.201	8	
cg11132120	NM_006312	NCOR2	-166.066	-0.209	12	N_Shelf
cg05023192	NM_004544	NDUFA10	-116.007	-0.222	2	S_Shore
cg23174406	NM_152905	NEDD1	-146.140	-0.250	12	S_Shelf
cg11787167	NM_001164749	NPAS3	-129.550	-0.222	14	S_Shelf
cg15075357	NM_015102	NPHP4	-147.520	-0.251	1	
cg04152793	NM_001144059	NTM	-111.433	-0.219	11	
cg11881038	NM_001145283	OPRM1	-188.558	-0.278	6	
cg01463139	NM_001004473	OR10K1	-122.955	-0.232	1	
cg16035267	NM_030959	OR12D3*	-229.789	-0.275	6	
cg10155537	NM_001001918	OR14C36	-95.906	-0.207	1	
cg00045070	NM_174936	PCSK9	-121.196	-0.230	1	N_Shore
cg11594160	NM_005027	PIK3R2	-189.222	-0.223	19	S_Shore
cg07586008	NM_003660	PPFIA3	-109.005	-0.208	19	Island
cg23256579	NM_007244	PRR4	-96.265	-0.206	12	
cg23657215	NM_138499	PWWP2B	-176.470	-0.271	10	S_Shore
cg18443741	NM_024854	PYROXD1	-196.842	-0.283	12	S_Shelf
cg05338731	NM_004914	RAB36	-105.430	-0.216	22	S_Shore
cg27308738	NM_014631	SH3PXD2A	-97.766	-0.208	10	N_Shelf
cg17221813	NM_022082	SLC17A9	-148.649	-0.247	20	Island
cg19142181	NM_022082	SLC17A9	-180.217	-0.265	20	Island
cg16733676	NM_213651	SLC25A24	-179.869	-0.241	1	N_Shore
cg05509228	NM_022138	SMOC2	-199.613	-0.246	6	Island
cg04798314	NM_001167740	SMYD3	-170.227	-0.267	1	N_Shore
cg17174466	NM_001100422	SPATS2L	-189.912	-0.264	2	
cg00030117	NM_001008410	STEAP3	-254.295	-0.296	2	N_Shore
cg16956665	NM_152713	STT3A	-187.954	-0.261	11	
cg07876831	NM_017905	TMCO3	-129.282	-0.203	13	N_Shelf
cg14361804	NM_001244	TNFSF8	-109.856	-0.221	9	
cg10985055	NM_003449	TRIM26	-110.021	-0.219	6	
cg24697433	NM_006510	TRIM27	-131.567	-0.217	6	
cg21610927	NM_007118	TRIO	-110.257	-0.201	5	
cg20089799	NM_006675	TSPAN9	-298.950	-0.330	12	

cg03206401	NM_207312	TUBA3E	-97.540	-0.210	2	Island
cg14417873	NM_001134398	VAV2*	-103.469	-0.205	9	
cg20106077	NM_182552	WDR27	-161.272	-0.225	6	N_Shore
cg02823311	NM_020196	XAB2	-171.766	-0.230	19	Island
cg03900028	NM_015852	ZNF117	-233.084	-0.305	7	
Genes with increased methylation in PD						
cg10760240	NM_012138	AATF	344.873	0.241	17	
cg01491428	NM_001089	ABCA3	344.873	0.294	16	Island
cg03108651	NR_024514	ADAMTS13	135.693	0.205	9	N_Shore
cg18662228	NM_014914	AGAP1	97.199	0.208	2	Island
cg04073914	NM_032717	AGPAT9	100.245	0.212	4	S_Shelf
cg09998151	NM_004274	AKAP6	344.873	0.285	14	
cg05890457	NM_014629	ARHGEF10	344.873	0.356	8	
cg17056069	NM_001135191	ASAP2	344.873	0.257	2	
cg00095677	NM_174954	ATP2A3	344.873	0.257	17	
cg00713204	NM_017869	BANP	344.873	0.313	16	N_Shore
cg10610477	NM_022893	BCL11A	344.873	0.219	2	
cg14655569	NM_015250	BICD2	344.873	0.296	9	N_Shelf
cg21782309	NM_003957	BRSK2	344.873	0.204	11	S_Shore
cg00231519	NM_153810	C10orf46	135.693	0.235	10	S_Shore
cg08584759	NM_153256	C10orf47	344.873	0.244	10	Island
cg24694947	NM_152324	C13orf16	344.873	0.210	13	S_Shelf
cg18075755	NM_031911	C1QTNF7	106.825	0.209	4	
cg14560110	NM_001004306	CCDC144NL	107.759	0.203	17	Island
cg05638648	NM_130444	COL18A1	344.873	0.218	21	S_Shelf
cg19218082	NM_001846	COL4A2	96.815	0.204	13	S_Shore
cg17713488	NM_015719	COL5A3	96.890	0.203	19	S_Shore
cg23813394	NM_004369	COL6A3	344.873	0.292	2	
cg16471877	NM_017421	COQ3	344.873	0.260	6	
cg11128983	NM_001008220	CPLX2	344.873	0.223	5	N_Shore
cg00861214	NM_175710	CR1L	344.873	0.283	1	
cg11229715	NM_003590	CUL3	117.597	0.227	2	
cg08002427	NM_001372	DNAH9	344.873	0.260	17	S_Shore
cg26893861	NM_004090	DUSP3	118.828	0.218	17	
cg05130642	NM_031308	EPPK1	344.873	0.204	8	Island
cg04212500	NM_005702	ERAL1	344.873	0.264	17	S_Shelf
cg00156497	NM_172105	EYA4	96.001	0.205	6	
cg05990366	NM_181709	FAM101A	344.873	0.249	12	
cg26296371	NM_006567	FARS2	113.547	0.215	6	
cg09438069	NM_005245	FAT1	344.873	0.263	4	

cg04888234	NM_032738	FCRLA	111.597	0.220	1	
cg16140565	NM_001166243	FHIT	344.873	0.292	3	
cg01801090	NR_029435	FLJ31306	344.873	0.283	14	N_Shelf
cg25203245	NM_152432	FLJ32810	344.873	0.339	11	
cg10058204	NR_026835	FLJ37201	344.873	0.289	10	
cg16464924	NM_001079804	GAA	91.925	0.205	17	Island
cg00675157	NM_000807	GABRA2	344.873	0.242	4	
cg01055691	NM_002045	GAP43	129.799	0.236	3	N_Shore
cg03812172	NM_033508	GCK	135.693	0.232	7	N_Shore
cg02891314	NM_005110	GFPT2	344.873	0.249	5	Island
cg13944838	NM_005110	GFPT2	344.873	0.281	5	Island
cg23221052	NM_005110	GFPT2	344.873	0.250	5	Island
cg23248424	NM_005110	GFPT2	128.086	0.232	5	Island
cg03088219	NM_201591	GPM6A	344.873	0.335	4	
cg16908938	NM_148903	GREB1	115.731	0.218	2	
cg11141652	NR_003081	GSTTP1	344.873	0.265	22	
cg15242686	NR_003081	GSTTP1	344.873	0.249	22	
cg22666875	NR_003081	GSTTP1	344.873	0.259	22	
cg01500431	NR_003082	GSTTP2	344.873	0.207	22	S_Shelf
cg15070894	NR_001317	HCG4P6	118.171	0.218	6	Island
cg25644740	NR_001317	HCG4P6	344.873	0.273	6	Island
cg08506353	NR_001435	HLA-DPB2	344.873	0.242	6	
cg09510698	NR_001435	HLA-DPB2	344.873	0.301	6	
cg15019001	NR_001435	HLA-DPB2	344.873	0.255	6	
cg09411910	NM_002122	HLA-DQA1	122.379	0.223	6	
cg11784298	NM_002122	HLA-DQA1	111.758	0.223	6	
cg22933800	NM_002122	HLA-DQA1	344.873	0.249	6	
cg24470466	NM_002122	HLA-DQA1	344.873	0.465	6	
cg14323910	NM_002123	HLA-DQB18	90.084	0.203	6	N_Shelf
cg13910785	NM_002124	HLA-DRB1*	344.873	0.387	6	N_Shelf
cg21810411	NM_002124	HLA-DRB1*	128.858	0.232	6	N_Shelf
cg24760581	NM_002124	HLA-DRB1*	344.873	0.251	6	
cg01341801	NM_002125	HLA-DRB5	344.873	0.348	6	N_Shore
cg17369694	NM_002125	HLA-DRB5	344.873	0.269	6	
cg23365293	NM_002125	HLA-DRB5	96.995	0.206	6	Island
cg26981746	NM_002125	HLA-DRB5	113.346	0.224	6	Island
cg27362989	NM_002125	HLA-DRB5	120.241	0.229	6	S_Shelf
cg11752699	NR_001298	HLA-DRB6	124.798	0.226	6	
cg19774683	NR_001298	HLA-DRB6	344.873	0.377	6	
cg22627029	NR_001298	HLA-DRB6	344.873	0.234	6	

cg25140213	NR_001298	HLA-DRB6	344.873	0.278	6	
cg02772880	NM_017558	HYDIN	122.765	0.230	16	N_Shelf
cg25790212	NM_014987	IGSF9B	344.873	0.249	11	Island
cg18689402	NM_002222	ITPR1	344.873	0.203	3	
cg03796003	NM_018992	KCTD5	344.873	0.465	16	Island
cg26749518	NM_012315	KLK9	128.086	0.228	19	Island
cg00729708	NM_178842	LASS3	132.753	0.238	15	Island
cg06679270	NM_178842	LASS3	344.873	0.248	15	Island
cg11008123	NR_015451	LOC283267	344.873	0.355	11	
cg16503053	NM_015116	LRCH1	344.873	0.223	13	
cg25450321	NM_024652	LRRK1*	344.873	0.315	15	N_Shelf
cg06950937	NM_003550	MAD1L1	344.873	0.214	7	Island
cg13275129	NM_032427	MAML2	344.873	0.238	11	
cg02228913	NM_016835	MAPT	344.873	0.281	17	N_Shelf
cg24801230	NM_001123067	MAPT	344.873	0.310	17	S_Shelf
cg00993903	NM_001128919	MARK3	344.873	0.270	14	
cg06738063	NM_001040000	MLLT4	344.873	0.244	6	
cg21209485	NM_033467	MMEL1	344.873	0.334	1	S_Shore
cg04627110	NM_206813	MOG	344.873	0.336	6	
cg12279734	NM_006792	MORF4	344.873	0.263	4	
cg25755428	NM_001031727	MRI1	344.873	0.284	19	Island
cg06112835	NM_181514	MRPL21	111.670	0.223	11	
cg01552920	NM_001145113	MYADML2	344.873	0.276	17	
cg00501169	NM_001143989	NBPF4	344.873	0.213	1	
cg16919708	NM_001012393	OPCML	129.799	0.238	11	
cg18346634	NM_000911	OPRD1	344.873	0.277	1	S_Shore
cg02246922	NM_030959	OR12D3*	92.697	0.206	6	
cg10701801	NM_148909	OSBPL9	112.772	0.216	1	
cg22026089	NM_013377	PDZRN4	104.563	0.217	12	
cg22466012	NM_001130081	PLD1	344.873	0.261	3	
cg25465065	NM_007221	PMF1	98.700	0.211	1	
cg08600378	NM_001105577	PRHOXNB	344.873	0.299	13	
cg14001750	NM_002737	PRKCA	135.693	0.235	17	S_Shelf
cg02978201	NM_002761	PRM1	344.873	0.247	16	
cg24073023	NM_001042359	PTPN20B	115.053	0.222	10	
cg02901522	NR_003367	PVT1	344.873	0.289	8	
cg12532878	NM_007368	RASA3	344.873	0.250	13	N_Shore
cg03570263	NM_170769	RNF39	128.086	0.230	6	S_Shore
cg08900396	NM_006987	RPH3AL	344.873	0.203	17	N_Shelf
cg08477332	NM_020672	S100A14	96.961	0.206	1	

cg07249765	NR_027816	SDK1	110.376	0.209	7	
cg13251750	NM_175739	SERPINA9	92.156	0.204	14	
cg19223824	NM_020708	SLC12A5	344.873	0.316	20	N_Shelf
cg07664579	NM_001044	SLC6A3	111.850	0.223	5	S_Shelf
cg17662493	NM_148674	SMC1B	344.873	0.289	22	N_Shelf
cg09289202	NM_006374	STK25	94.263	0.201	2	N_Shelf
cg14422932	NM_018401	STK32B	344.873	0.229	4	
cg16112880	NM_016456	TMEM9	344.873	0.249	1	Island
cg00872984	NM_019105	TNXB	135.693	0.244	6	Island
cg07524919	NM_019105	TNXB	107.351	0.218	6	Island
cg14188106	NM_019105	TNXB	109.641	0.221	6	Island
cg26365090	NM_001098796	TOX2	344.873	0.265	20	
cg02627240	NM_022445	TPK1	344.873	0.263	7	
cg03187614	NM_006778	TRIM10	344.873	0.397	6	
cg13446859	NM_007028	TRIM31	111.459	0.217	6	
cg25569462	NM_173553	TRIML2	118.671	0.226	4	N_Shore
cg01891583	NM_003470	USP7	118.450	0.228	16	
cg15365500	NM_005715	UST	344.873	0.270	6	
cg13564529	NM_001134398	VAV2*	344.873	0.426	9	
cg07456585	NM_182894	VSX2	344.873	0.260	14	N_Shore
cg19471911	NM_001130145	YAP1	344.873	0.250	11	
cg07878625	NR_015357	ZNF783	344.873	0.229	7	N_Shore

Supplementary Table 4. Differentially methylated autosomal genes that co-varied in brain and blood DNA from PD patients, complete list. Analysis of differential methylation was performed with Genome Studio using Illumina custom model. Genes with Delta Beta value > |0.20| at p<0.01 and FDR q<0.001. * Denotes genes for which more than one DM independent probe was detected showing opposite methylation changes.

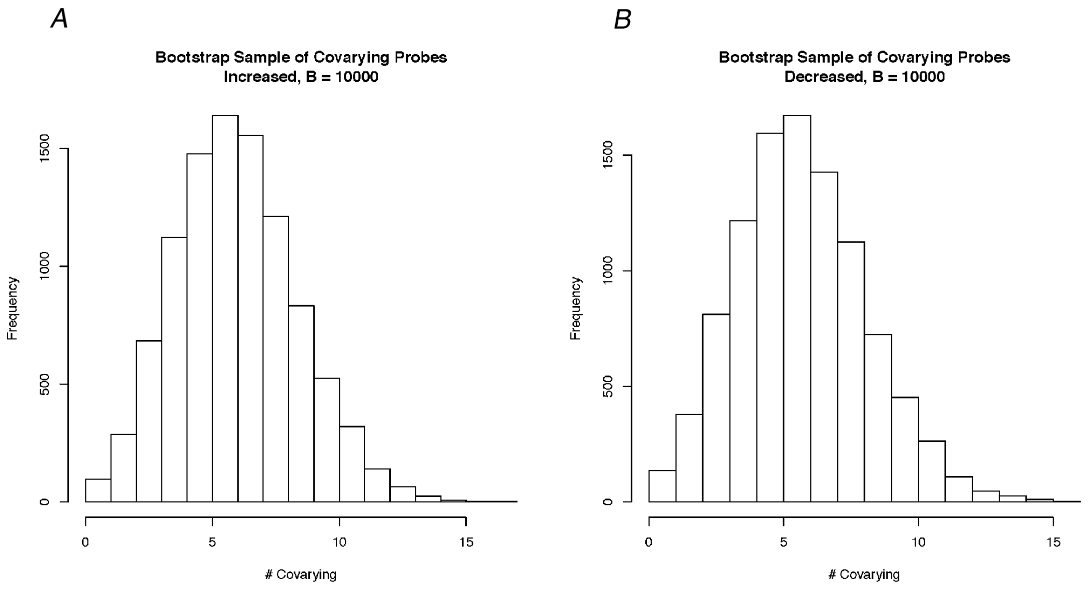
GENE NAME	Delta Beta Brain	Delta Beta Blood
Genes with increased methylation in PD		
KCTD5	0.429	0.465
LOC283267	0.375	0.355
VAV2	0.374	0.426
MOG	0.357	0.336
TRIM10	0.352	0.397
PRHOXNB	0.340	0.299
HLA-DQA1	0.325	0.290
ARHGEF10	0.319	0.356
FLJ32810	0.316	0.339
LRRK1*	0.294	0.315
GFPT2	0.291	0.253
SLC12A5	0.284	0.316
MMEL1*	0.284	0.334
HLA-DRB5	0.282	0.255
TMEM9	0.274	0.249
SMC1B	0.273	0.289
HLA-DPB2	0.272	0.266
UST	0.272	0.270
BICD2	0.266	0.296
ABCA3	0.264	0.294
OPRD1	0.263	0.277
MRI1	0.258	0.284
FLJ37201	0.254	0.289
FHIT	0.254	0.292
BANP	0.254	0.313
MAPT	0.247	0.295
CR1L	0.244	0.283
PVT1	0.241	0.289
HLA-DRB6	0.240	0.279

VSX2	0.240	0.260
FLJ31306	0.240	0.283
TPK1	0.239	0.263
ERAL1	0.237	0.264
COL6A3	0.236	0.292
ATP2A3	0.235	0.257
ASAP2	0.235	0.257
TOX2	0.232	0.265
LASS3	0.230	0.243
MORF4	0.226	0.263
AATF	0.224	0.241
HLA-DQB1	0.223	0.203
GCK	0.223	0.232
C10orf46	0.223	0.235
PRM1	0.222	0.247
GSTTP2	0.222	0.207
DNAH9	0.220	0.260
COQ3	0.219	0.260
RNF39	0.218	0.230
GSTTP1	0.218	0.258
AKAP6	0.216	0.285
FAT1	0.214	0.263
OSBPL9	0.213	0.216
ZNF783	0.213	0.229
FCRLA	0.210	0.220
CUL3	0.209	0.227
TRIML2	0.208	0.226
YAP1	0.206	0.250
RASA3	0.206	0.250
ITPR1	0.205	0.203
MAML2	0.204	0.238
USP7	0.201	0.228
SERPINA9	0.201	0.204
CPLX2	0.200	0.223
Genes with decreased methylation in PD		
DNAJA3	-0.445	-0.511
JAKMIP3	-0.403	-0.362
FRK	-0.386	-0.341
LRRC27	-0.382	-0.406
DMBX1	-0.370	-0.354

LGALS7	-0.368	-0.380
STEAP3	-0.358	-0.296
OPRM1	-0.318	-0.278
CAPN8	-0.318	-0.305
LOC391322	-0.317	-0.264
FOXK1	-0.317	-0.340
APBA1	-0.312	-0.283
DCUN1D2	-0.307	-0.305
MAGI2	-0.306	-0.228
ARHGEF12	-0.301	-0.300
HLA-DRB1*	-0.296	-0.294
OR12D3	-0.280	-0.275
ZNF117	-0.273	-0.305
CTNNA2	-0.270	-0.234
KIAA0513	-0.259	-0.283
STT3A	-0.258	-0.261
CNTNAP2	-0.256	-0.261
DSE	-0.255	-0.259
KCNH1	-0.254	-0.267
SLC25A24	-0.253	-0.241
TSPAN9	-0.253	-0.330
CPAMD8	-0.252	-0.245
NPHP4	-0.245	-0.251
ATP8A2	-0.244	-0.221
LOC100292680	-0.244	-0.288
AMZ1	-0.241	-0.253
GSTT1	-0.239	-0.239
PCSK9	-0.238	-0.230
BANF2	-0.236	-0.291
SH3PXD2A	-0.236	-0.208
XAB2	-0.234	-0.230
ANXA2	-0.234	-0.244
FAM132A	-0.232	-0.207
PYROXD1	-0.232	-0.283
TNFSF8	-0.230	-0.221
NDUFA10	-0.229	-0.222
PIK3R2	-0.229	-0.223
MYOM2	-0.228	-0.201
HLA-G	-0.227	-0.220
MMEL1*	-0.226	-0.220

COL11A2	-0.224	-0.209
NTM	-0.223	-0.219
SMOC2	-0.222	-0.246
PWWP2B	-0.222	-0.271
MRPL3	-0.221	-0.214
GZMM	-0.220	-0.233
WDR27	-0.219	-0.225
OR10K1	-0.219	-0.232
SPATS2L	-0.217	-0.264
LRRK1*	-0.216	-0.305
MCC	-0.216	-0.209
MIR886	-0.214	-0.242
TUBA3E	-0.210	-0.210
TRIM27	-0.210	-0.217
SMYD3	-0.208	-0.267
TMCO3	-0.207	-0.203
MAPK10	-0.201	-0.201

Supplementary Figure 1. Bootstrap analysis of differentially methylated probes



We detected 2,908 probes in brain and 3,897 probes in PBLs showing differential methylation in PD samples. The majority of these probes showed decreased methylation in PD: 2,591 in the brain and 3,421 in blood. The remaining DM probes gained methylation, 317 probes in the brain and 476 in PBLs (Table 1). Stepwise selection of probes located only on autosomal chromosomes yielded 131 probes gaining methylation in brain and 206 in blood in PD, while 148 probes lost methylation in brain and 174 in blood. From these pool of differentially methylated autosomal probes, a total of N=124 probes associated with annotated genes (63 with increased and 61 with decreased methylation) showed concordant methylation changes in both tissues (brain and blood).

We tested the probability of selecting the same 124 probes from both pools of differentially methylated probes in PD brain and blood only by chance by performing bootstrap analysis [1]. We independently analyzed probes sets with increased (A) and decreased (B) methylation in PD. We generated a random sample from the 131 probes with increased methylation in brain and from the 206 that gained methylation in PD blood, and computed how many probes were present on both sets. The procedure was repeated 10,000 times. For the 10,000 iterations, most of the bootstrapped samples had a low number of co-varying probes, with N=6 being the value that reached the highest frequency (P<0.001). Similar results were obtained when the same procedure was performed for the group of 148 probes showing decreased methylation in brain and 174 probes that lost methylation in PD blood, and testing for the probability of finding the same 61 probes in both sets. The results obtained from bootstrap analysis preclude the possibility that we could select the same 124 probes by chance.

1. Efron, B. and Tibshirani, R. (1993) An Introduction to the Bootstrap. Chapman and Hall, New York, London.

Supplementary Figure 2. Validation of array findings by methylation-sensitive restriction/qPCR technique. Methylation levels of 5 selected genes showing increased (*MRI1* and *TMEM9*) or decreased methylation (*GSST1*, *TUBA3E* and *KCNH1*) on the array analysis was also determined by a qPCR-based method in brain and blood samples from PD patients (n=5) and control subjects (n=6) as an independent validation assay. Significant differences in methylation levels were determined in brain or blood groups by Student's *t* test, two-tailed (* p<0.005; ** p<0.01 and ***p<0.001).