

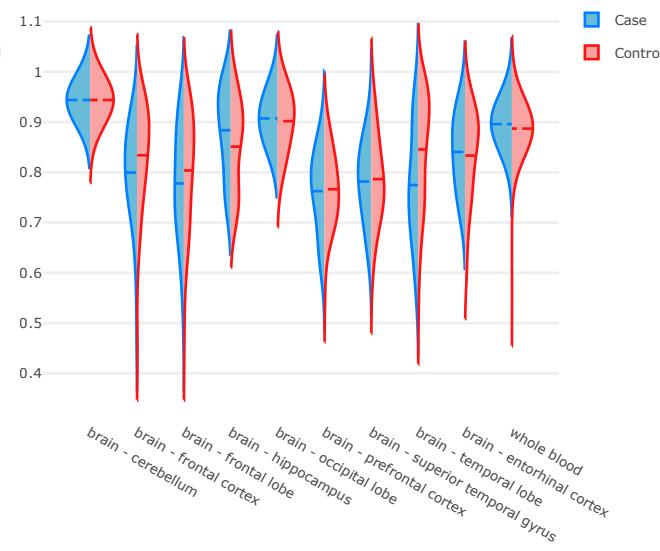
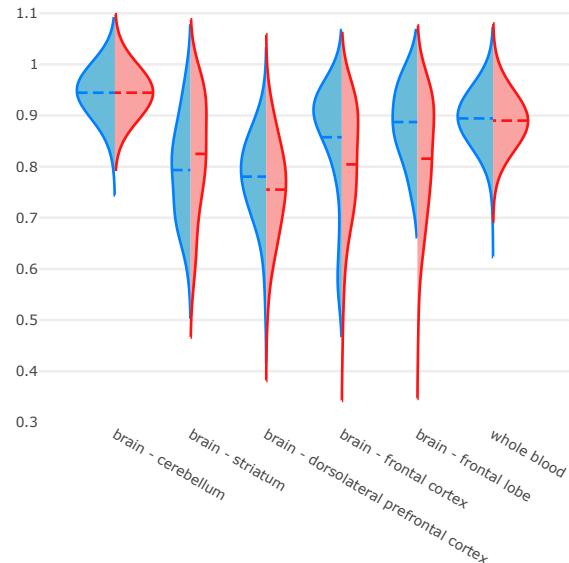
	Genomic CpG ID	Chr Coordinat (hg19)	Associate CpG in d Genes	Feature	Cor BA7	Blood-BA10	Cor BA20	Cor All Brain	Mean Cor All	SD Mean	Percentile of Mean	Percentile of Mean	Mean Change	Mean Change	Percentile rank of Blood	Percentile rank of Brain	Var in Blood	Var in Brain	Var in BA7	Var in BA10	Var in BA20
1	cg0192052	1.69E+08	3 ACTRT3	intragenic	-0.28529	-0.16471	-0.49706	-0.31569	0.168248	-	90%	0	0.02	<50% (Blo	75-90% (Bri	0.027148	0.095309	0.066311	0.074639	0.10182	
2	cg0629427	1.24E+08	7 GPR37	intragenic	-0.28824	-0.00294	-0.05294	-0.11471	0.152346	-	<50%	0.02	0.06	50-75% (Bri	90% (Brain	0.072983	0.249145	0.178842	0.278994	0.163316	
3	cg0819357	1.7E+08	3 LRRC34	intragenic	0.447059	0.558824	0.441176	0.482353	0.066291	90%	-	0.04	0.04	75-90% (Bri	90% (Brain	0.127189	0.136379	0.120043	0.138222	0.126796	
4	cg0083255	1.7E+08	3 LRRC34	intragenic	0.529412	0.1	0.126471	0.251961	0.240644	75-90%	-	0.02	0.01	50-75% (Bri	50-75% (Bri	0.072089	0.065075	0.073866	0.03225	0.055494	
5	cg1235852	1.7E+08	3 LRRC34	promoter	-0.12647	-0.06765	0.047059	-0.04902	0.088252	-	<50%	0	0	0 <50% (Blo	<50% (Brai	0.016803	0.017184	0.01909	0.015699	0.012274	
6	cg0809563	1.7E+08	3 LRRC34	promoter	0.264706	0.002941	-0.17353	0.031373	0.220497	<50%	-	0	0	0 <50% (Blo	<50% (Brai	0.008852	0.013789	0.015128	0.014062	0.010161	
7	cg1232414	1.7E+08	3 LRRC34	promoter	0.402941	0.220588	-0.17647	0.14902	0.296262	50-75%	-	0.02	0.01	75-90% (Bri	50-75% (Bri	0.101411	0.128388	0.098344	0.110964	0.104191	
8	cg0336996	1.7E+08	3 LRRC34	promoter	0.008824	0.023529	0.202941	0.078431	0.108079	<50%	-	0.03	0.02	75-90% (Bri	75-90% (Bri	0.126303	0.119049	0.07667	0.147694	0.0675	
9	cg1817109	1.7E+08	3 None	intergenic	-0.20882	-0.18235	-0.11471	-0.16863	0.048537	-	50-75%	0.01	0.01	<50% (Blo	<50% (Bri	0.0293	0.136339	0.118085	0.095679	0.13315	
10	cg1100555	1.06E+08	10 OBFC1	intragenic	0.288235	0.144118	0.214706	0.215686	0.072064	50-75%	-	0.02	0.04	50-75% (Bri	90% (Brain	0.094638	0.290632	0.281379	0.269243	0.284652	
11	cg0062441	1282357	5 TERT	intragenic	-0.07059	-0.02059	-0.10882	-0.06667	0.044248	-	<50%	0.02	0.04	50-75% (Bri	90% (Brain	0.072427	0.142684	0.149954	0.169352	0.119533	
12	cg0393537	1282703	5 TERT	intragenic	0.055882	-0.05588	-0.59118	-0.19706	0.34586	-	50-75%	0.01	0.04	50-75% (Bri	90% (Brain	0.056818	0.166135	0.148556	0.194885	0.112009	
13	cg0738002	1296007	5 TERT	promoter	-0.28824	0.173529	0.011765	-0.03431	0.234306	-	<50%	0.02	0	50-75% (Bri	50-75% (Bri	0.100413	0.0651	0.067849	0.059821	0.054737	
14	cg057513462405935	20 ZBTB46	intragenic	-0.58235	0.132353	-0.23235	-0.22745	0.357378	-	50-75%	0.02	0.01	50-75% (Bri	75-90% (Bri	0.063213	0.096965	0.063702	0.086945	0.117883		
15	cg14251262406428	20 ZBTB46	intragenic	0.267647	0.529412	0.455882	0.417647	0.135006	90%	-	0.06	0.01	90% (Blo	50-75% (Bri	0.215439	0.116059	0.110012	0.093078	0.124745		
16	cg026309162436995	20 ZBTB46	promoter	0.055882	0.138235	-0.04412	0.05	0.091319	<50%	-	0.02	0.01	50-75% (Bri	50-75% (Bri	0.074256	0.083229	0.057636	0.098675	0.054512		
17	cg21291962437035	20 ZBTB46	promoter	0.073529	-0.2	0.032353	-0.03137	0.14748	-	<50%	0	0.04	<50% (Blo	90% (Brain	0.029687	0.230601	0.094223	0.231544	0.091153		

Tabular values for the significant CpG sites observed with Summary-based Mendelian Randomization, mined from BECon as displayed in Figure 4

Schizophrenia

Alzheimer's disease

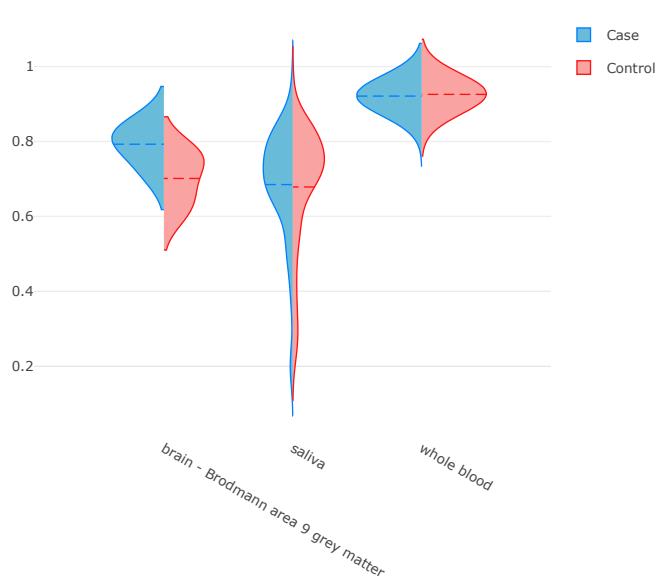
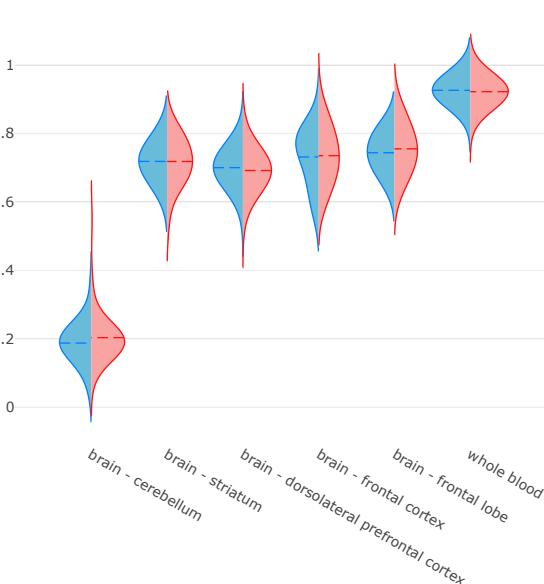
beta/m-value - methylation intensity



Schizophrenia

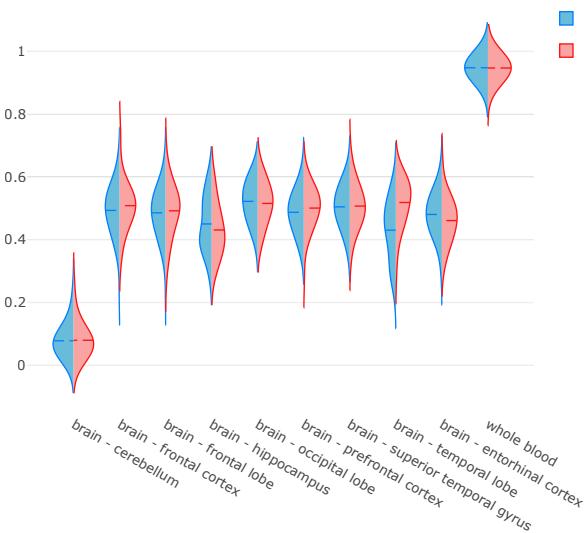
Parkinson's disease

beta/m-value - methylation intensity

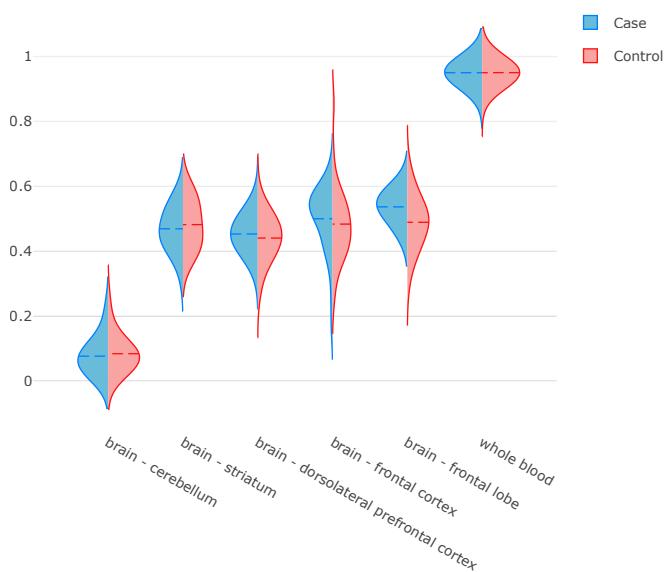


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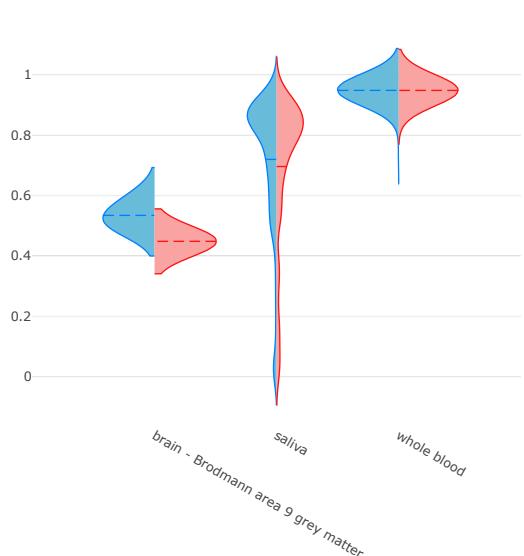
Alzheimer's disease



schizophrenia



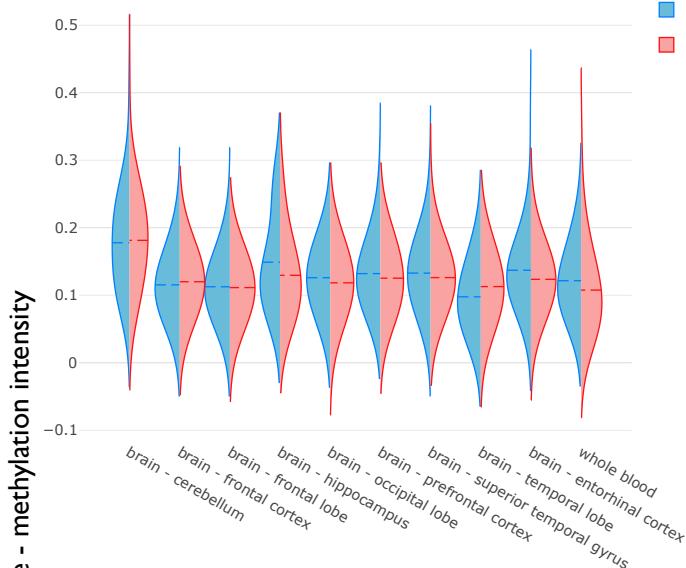
Parkinson's disease



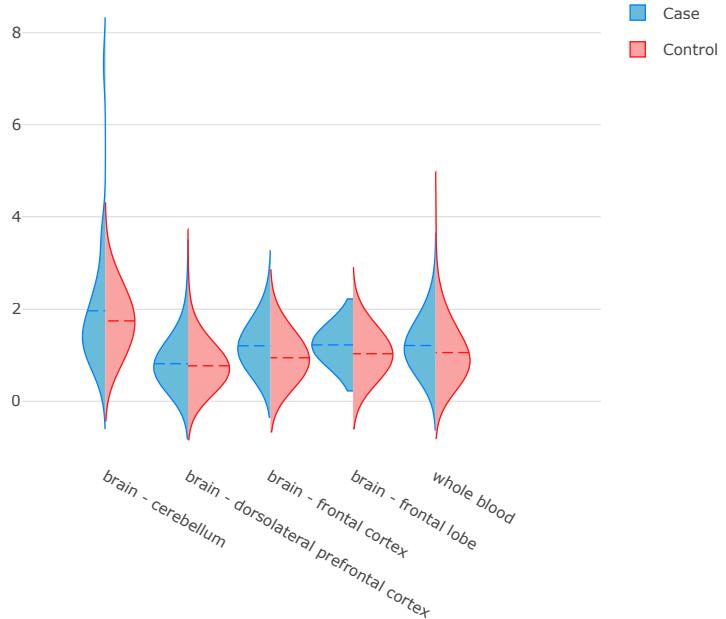
beta/m-value - methylation intensity

cg00832555

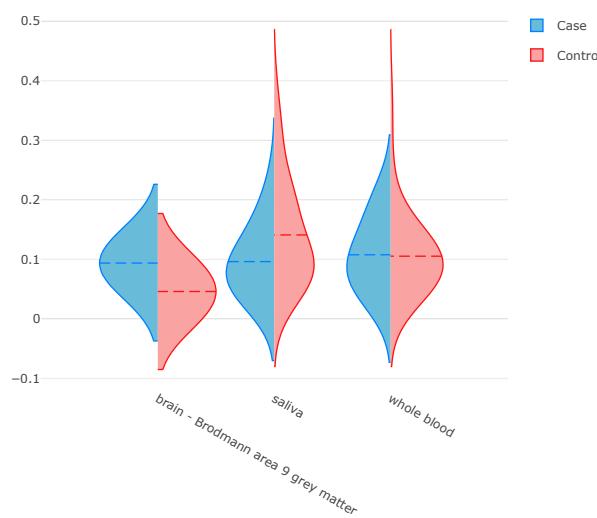
Alzheimer's disease



schizophrenia



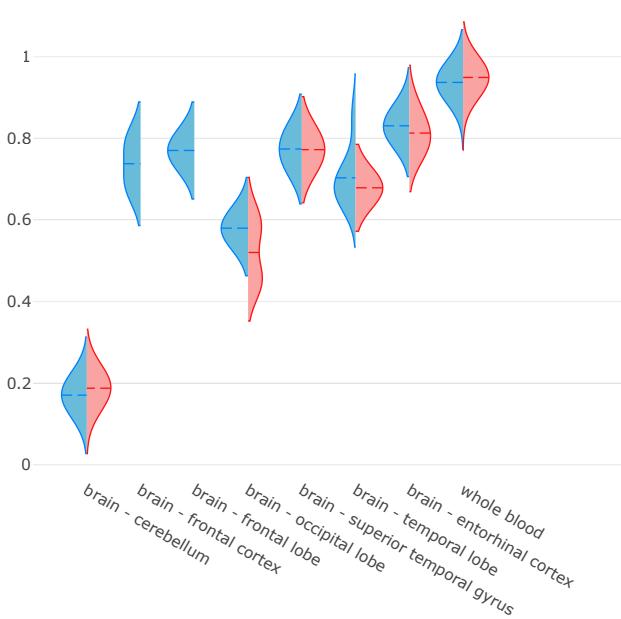
Parkinson's disease



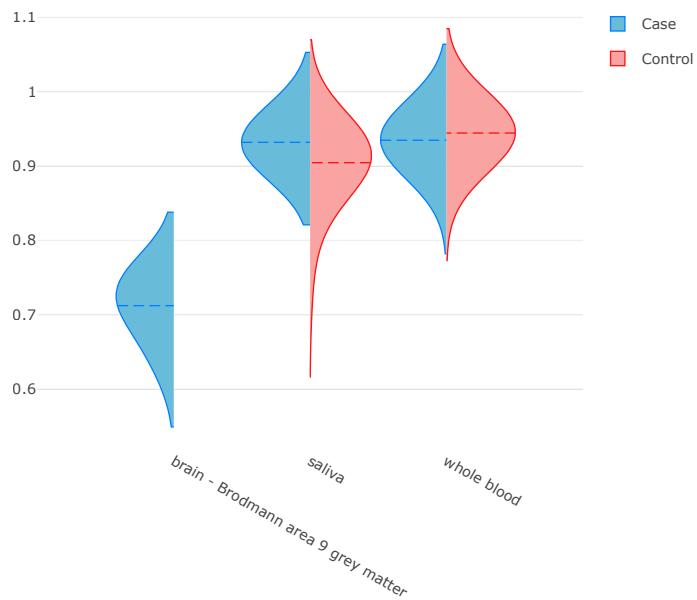
cg01920524

Alzheimer's disease

beta/m-value - methylation intensity



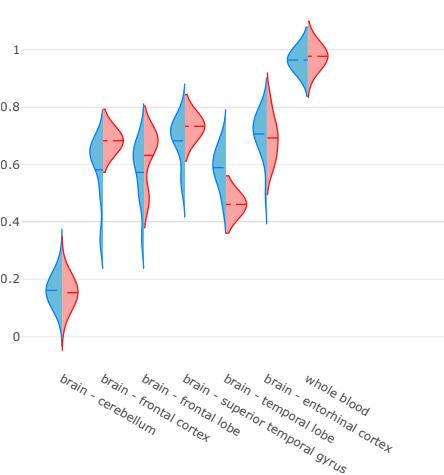
Parkinson's disease



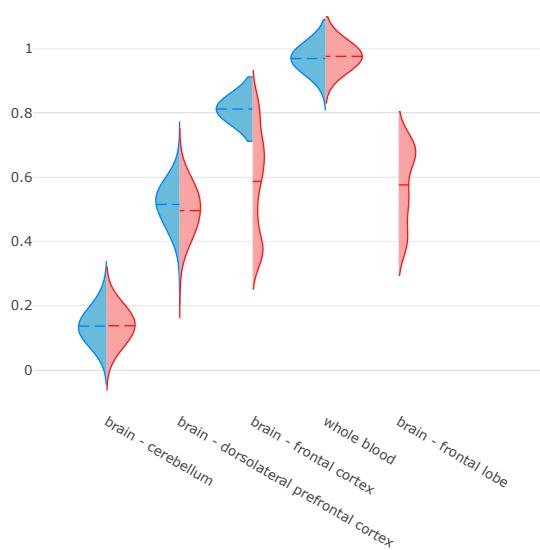
cg21291985

beta/m-value - methylation intensity

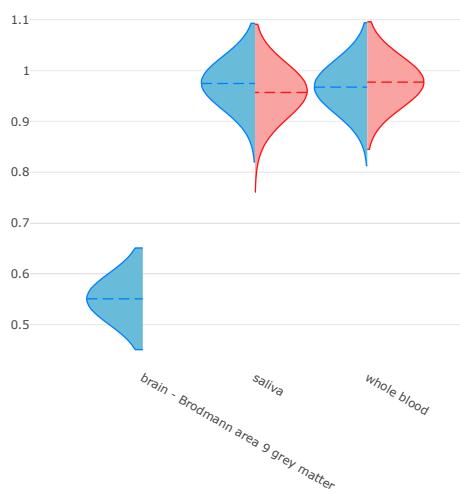
Alzheimer's disease



schizophrenia



Parkinson's disease



cg08095637

