

Supplemental Information for:

DNA methylation differences during development distinguish sympatric morphs of Arctic charr (*Salvelinus alpinus*)

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Table S1: Samples of the embryos used for DNA (RRBS) and RNA extraction (qPCR), grouped by morph, time, family and sex. Library 5* is the one creating technical effects driving separation in PC2.

Use	Morph	Timepoint	Family	Sample_ID	Sequencing Library	Sex
RRBS	PL	200	17PL30	S1	1	F
RRBS	PL	200	17PL53	S2	1	M
RRBS	PL	200	17PL54	S3	1	M
RRBS	LB	200	17LB1	S4	1	M
RRBS	LB	200	17LB2	S5	1	F
RRBS	LB	200	17LB3	S6	1	M
RRBS	PI	200	17PI1	S7	2	M
RRBS	PI	200	17PI3	S8	2	M
RRBS	PI	200	17PI5	S9	2	M
RRBS	SB	200	17SB1	S10	2	M
RRBS	SB	200	17SB3	S11	2	F
RRBS	SB	200	17SB35	S12	2	F
RRBS	PL	150	17PL30	S13	3	F
RRBS	PL	150	17PL53	S14	3	NA
RRBS	PI	150	17PI5	S15	3	F
RRBS	LB	150	17LB1	S16	3	M
RRBS	LB	150	17LB2	S17	3	M
RRBS	SB	150	17SB35	S18	3	F
RRBS	PI	150	17PI1	S19	4	M
RRBS	PI	150	17PI3	S20	4	F
RRBS	PL	150	17PL54	S21	4	M
RRBS	SB	150	17SB1	S22	4	F
RRBS	SB	150	17SB3	S23	4	M
RRBS	LB	150	17LB3	S24	4	F
RRBS	PL	100	17PL30	S25	5*	F
RRBS	PL	100	17PL34	S26	5*	F
RRBS	PI	100	17PI5	S27	5*	M
RRBS	LB	100	17LB1	S28	5*	F
RRBS	LB	100	17LB2	S29	5*	M
RRBS	SB	100	17SB35	S30	5*	M
RRBS	PI	100	17PI1	S31	6	M
RRBS	PI	100	17PI3	S32	6	F
RRBS	PL	100	17PL54	S33	6	F

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RRBS	SB	100	17SB3	S34	6	M
RRBS	SB	100	17SB20	S35	6	NA
RRBS	LB	100	17LB3	S36	6	F
RRBS	PL	50	17PL23	S37	7	F
RRBS	PL	50	17PL25	S38	7	F
RRBS	PI	50	17PI5	S39	7	NA
RRBS	LB	50	17LB1	S40	7	NA
RRBS	LB	50	17LB2	S41	7	NA
RRBS	SB	50	17SB35	S42	7	NA
RRBS	PI	50	17PI1	S43	8	NA
RRBS	PI	50	17PI3	S44	8	NA
RRBS	PL	50	17PL11	S45	8	F
RRBS	SB	50	17SB1	S46	8	NA
RRBS	SB	50	17SB3	S47	8	NA
RRBS	LB	50	17LB3	S48	8	NA
qPCR	PL	200	17PL30	S49	-	-
qPCR	PL	200	17PL23	S50	-	-
qPCR	PL	200	17PL32	S51	-	-
qPCR	LB	200	17LB1	S52	-	-
qPCR	LB	200	17LB2	S53	-	-
qPCR	LB	200	17LB3	S54	-	-
qPCR	PI	200	17PI1	S55	-	-
qPCR	PI	200	17PI3	S56	-	-
qPCR	PI	200	17PI5	S57	-	-
qPCR	SB	200	17SB1	S58	-	-
qPCR	SB	200	17SB3	S59	-	-
qPCR	SB	200	17SB4	S60	-	-
qPCR	PL	150	17PL30	S61	-	-
qPCR	PL	150	17PL53	S62	-	-
qPCR	PI	150	17PI5	S63	-	-
qPCR	LB	150	17LB1	S64	-	-
qPCR	LB	150	17LB2	S65	-	-
qPCR	SB	150	17SB4	S66	-	-
qPCR	PI	150	17PI1	S67	-	-
qPCR	PI	150	17PI3	S68	-	-
qPCR	PL	150	17PL54	S69	-	-
qPCR	SB	150	17SB1	S70	-	-
qPCR	SB	150	17SB3	S71	-	-

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qPCR	LB	150	17LB3	S72	-	-
qPCR	PL	100	17PL32	S73	-	-
qPCR	PL	100	17PL34	S74	-	-
qPCR	PI	100	17PI5	S75	-	-
qPCR	LB	100	17LB1	S76	-	-
qPCR	LB	100	17LB2	S77	-	-
qPCR	SB	100	17SB35	S78	-	-
qPCR	PI	100	17PI1	S79	-	-
qPCR	PI	100	17PI3	S80	-	-
qPCR	PL	100	17PL26	S81	-	-
qPCR	SB	100	17SB3	S82	-	-
qPCR	SB	100	17SB20	S83	-	-
qPCR	LB	100	17LB3	S84	-	-

Table S2: List of pairwise comparisons for DMR analysis.

Pairwise comparisons DMR analysis	Number of samples
Benthic VS Limnetic	24 VS 24
Benthic VS Limnetic at 50ts	6 VS 6
Benthic VS Limnetic at 100ts	6 VS 6
Benthic VS Limnetic at 150ts	6 VS 6
Benthic VS Limnetic at 200ts	6 VS 6
SB VS PL	12 VS 12
SB VS PL at 50ts	3 VS 3
SB VS PL at 100ts	3 VS 3
SB VS PL at 150ts	3 VS 3
SB VS PL at 200ts	3 VS 3
SB VS PI	12 VS 12
SB VS PI at 50ts	3 VS 3
SB VS PI at 100ts	3 VS 3
SB VS PI at 150ts	3 VS 3
SB VS PI at 200ts	3 VS 3
SB VS LB	12 VS 12
SB VS LB at 50ts	3 VS 3
SB VS LB at 100ts	3 VS 3
SB VS LB at 150ts	3 VS 3
SB VS LB at 200ts	3 VS 3
LB VS PI	12 VS 12
LB VS PI at 50ts	3 VS 3
LB VS PI at 100ts	3 VS 3
LB VS PI at 150ts	3 VS 3
LB VS PI at 200ts	3 VS 3
LB VS PL	12 VS 12
LB VS PL at 50ts	3 VS 3
LB VS PL at 100ts	3 VS 3
LB VS PL at 150ts	3 VS 3
LB VS PL at 200ts	3 VS 3
PL VS PI	12 VS 12
PL VS PI at 50ts	3 VS 3
PL VS PI at 100ts	3 VS 3
PL VS PI at 150ts	3 VS 3
PL VS PI at 200ts	3 VS 3

Table S3: Primers used for qPCR and sexing.

Name	Sequence	Product size (bp)	Use	PCR Efficiency
actb-Fw	5-GAA GAT CAA GAT CAT CGC CC-3	122	qPCR (control)	1.95
actb-Rv	5-CAG ACT CGT CGT ACT CCT GCT-3			
Ub2I3-Fw	5-CGA GAA GGG ACA GGT GTG TC-3	96	qPCR (control)	1.93
Ub2I3-Rv	5-ACC AAC GCA ATC AGG GAC T-3			
HiH2a-F	5-GCA AAG ACA CGT TCA TCC CG-3	187	qPCR	1.99
HiH2a-R	5-TCT TCT TGT TGT CAC GGG CA-3			
Lmtk2-F	5-TTT TCG ACC AAG AGA CCC CC-3	110	qPCR	1.9
Lmtk2-R	5-CCT ATT CAG GTA GCT GGC CG-3			
Nkx23-F2	5-CCG GAG GAT CAG GAA AAC AA-3	156	qPCR	1.93
Nkx23-R2	5-CCG CTC TAA CTC GAA CAC CT-3			
SLC9A3R2-F2	5-GCA CAC ATG TCA AAG AGG TC-3	138	qPCR	1.95
SLC9A3R2-R2	5-CGT TTG TGA TTG GTG AGC CC-3			
ARL16-F1	5-CTA CCT ACG GTG GGC ACC AA-3	145	qPCR	2.49
ARL16-R1	5-CAT GGT ACA AGG GAG GTC CGA-3			
Meis1l-F2	5-CTG AAG AGG GCT GGC TTG AA-3	197	qPCR	2.2
Meis1l-R2	5-GTG GGG CAA GTC TTC GTA CC-3			
HiH3l-F2	5-CAG GAG GCT AGC GAG GCT TA-3	159	qPCR	2.17
HiH3l-R2	5-GGG GGA TTT TGG AGA TCA GGT C-3			
ARMC1-F1	5-TCT CTG CTT CTC ACA ACT GCT T-3	115	qPCR	1.92
ARMC1-R1	5-ATC AAA CCA GCC TCT TCA CAC T-3			
Gli3-F1	5-GCG GTT TTG GAG TTG GTG TC-3	156	qPCR	2.06
Gli3-R1	5-ACG TCA TGG AGA CAG TAC ACG-3			
RASSF4-F2	5-CGA CGA CAA CGA GAG ACT CC-3	143	qPCR	2.21
RASSF4-R2	5-CGT CGT CCT CCT CTA GAC TAC T-3			
NFIX-F1	5-TTT CCC TGC TCC ACA ATG GC-3	197	qPCR	2.17
NFIX-R1	5-GTG TAG GAG AAG GCA CGG AC-3			
MEGF9-F1	5-CCA CCA CTG ACA CGC AAC AAA C-3	191	qPCR	1.95
MEGF9-R1	5-GTC GCA GCT ACA GGG GAT G-3			
MAGUK-F2	5-ACC TAC GAG GAG GTG ACT CG-3	168	qPCR	2.02
MAGUK-R2	5-CTT CTT GGG CCT GGT GGT ATG-3			
Rhoguanin-F1	5-TGA GGC ACA GCT CTG TTA GTG-3	172	qPCR	1.92
Rhoguanin-R1	5-CTT TCC ATG CTG AGG CTG TC-3			
SdY-Fw	5 -CCC AGC ACT GTT TTC TTG TCT CA-3	177	Sexing	-
SdY-Rv2	5 -CTT AAA ACC ACT CCA CCC TCC AT-3			

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Table S4: Statistical differences in methylation distribution between morphs, for each timepoint.

p-values for both Kruskal-Wallis (KW) and pairwise Kolmogorov-Smirnoff (KS) tests are indicated. KW p-values for distribution differences between timepoints were always < 2.2E-16.

50 ts	KW = 3.901E-16		
KS pairwise	LB	SB	PL
LB	-		
SB	7.72E-06	-	
PL	3.49E-10	3.71E-03	-
PI	< 2.2E-16	5.06E-10	4.12E-07
100ts	KW < 2.2E-16		
KS pairwise 100ts	LB	SB	PL
LB	-		
SB	4.81E-09	-	
PL	6.82E-09	< 2.2E-16	-
PI	2.67E-06	< 2.2E-16	0.055
150ts	KW = 3.571E-08		
KS pairwise 150ts	LB	SB	PL
LB	-		
SB	7.32E-05	-	
PL	3.18E-10	9.58E-03	-
PI	1.91E-08	0.240	0.059
200ts	KW = 0.0034		
KS pairwise 200ts	LB	SB	PL
LB	-		
SB	0.093	-	
PL	7.80E-05	4.42E-04	-
PI	0.036	0.943	1.73E-04

Table S5: Variance explained by each principal component.

Principal component	Variance explained (%)	Cumulative variance (%)
PC1	8	8
PC2	3.52	11.52
PC3	3.19	14.71
PC4	2.92	17.63
PC5	2.6	20.23
PC6	2.51	22.74
PC7	2.49	25.23
PC8	2.45	27.68
PC9	2.39	30.07
PC10	2.37	32.44
PC11	2.31	34.75
PC12	2.26	37.01
PC13	2.23	39.24
PC14	2.17	41.41
PC15	2.15	43.56
PC16	2.12	45.68
PC17	2.05	47.73
PC18	2.04	49.77
PC19	2.01	51.78
PC20	2	53.78
PC21	1.96	55.74
PC22	1.94	57.68
PC23	1.91	59.59
PC24	1.89	61.48
PC25	1.86	63.34
PC26	1.86	65.2
PC27	1.84	67.04
PC28	1.81	68.85
PC29	1.8	70.65
PC30	1.77	72.42
PC31	1.75	74.17
PC32	1.75	75.92
PC33	1.72	77.64
PC34	1.71	79.35
PC35	1.69	81.04
PC36	1.67	82.71

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PC37	1.66	84.37
PC38	1.63	86
PC39	1.62	87.62
PC40	1.6	89.22
PC41	1.58	90.8
PC42	1.58	92.38
PC43	1.57	93.95
PC44	1.56	95.51
PC45	1.54	97.05
PC46	1.51	98.56
PC47	1.46	100.02

Table S6: ANOVA results for multiple regressions on PCs, using 3 explanatory variables (Morph, Time and Sex). P-values have been corrected for multiple testing with Bonferroni.

Principal Component	Morph	Time	Sex	Morph X Time
PC1	1	1.06E-28	1	1
PC2	1	1.22E-07	1	1
PC3	0.052	0.003	1	0.369
PC4	9.80E-09	0.982	1	1
PC5	1	1	1	1
PC6	1	1	1	1
PC7	0.197	1	1	1
PC8	0.115	1	1	1
PC9	1	1	1	1
PC10	0.046	1	1	1
PC11	1	1	1	1
PC12	1	1	1	1
PC13	1	1	1	1
PC14	1	1	1	1
PC15	1	1	1	1
PC16	1	1	1	1
PC17	1	1	1	1
PC18	1	1	1	1
PC19	1	1	1	1
PC20	1	1	1	1
PC21	1	1	1	1
PC22	1	1	1	1
PC23	1	1	1	1
PC24	1	1	1	1
PC25	1	1	1	1
PC26	1	1	1	1
PC27	1	1	1	1
PC28	1	1	1	1
PC29	1	1	1	1
PC30	1	1	1	1
PC31	1	1	1	1
PC32	1	1	1	1
PC33	1	1	1	1
PC34	1	1	1	0.369

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PC35	1	1	1	1
PC36	1	1	1	1
PC37	1	1	1	1
PC38	1	1	1	1
PC39	1	1	1	1
PC40	1	1	1	1
PC41	1	1	1	1
PC42	1	1	1	1
PC43	1	1	1	1
PC44	1	1	1	1
PC45	1	1	1	1
PC46	1	1	1	1
PC47	1	1	1	1

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Table S7: Full list of GO enrichment analysis for genes near residues that contributed to timepoint and morph differences (with PCA and glm). GO categories displayed have a p-value < 0.01 with Fisher's test.

Genes near CpGs separating timepoints (PC1)		Annotated	Significant	Expected	weightedFisher
GO.ID	Term				
GO:0006334	nucleosome assembly	152	5	0.46	0.00011
GO:0006189	'de novo' IMP biosynthetic process	10	2	0.03	0.00041
GO:0016559	peroxisome fission	26	2	0.08	0.00287
GO:0045638	negative regulation of myeloid cell differentiation	325	5	0.99	0.00327
GO:0007567	parturition	98	3	0.3	0.00342
GO:0009113	purine nucleobase biosynthetic process	29	2	0.09	0.00356
GO:0035584	calcium-mediated signaling using intracellular calcium source	110	3	0.34	0.00472
GO:0090197	positive regulation of chemokine secretion	34	2	0.1	0.00487
GO:0050847	progesterone receptor signaling pathway	35	2	0.11	0.00516
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	133	3	0.41	0.00797
GO:1900273	positive regulation of long-term synaptic potentiation	134	3	0.41	0.00814
GO:0006525	arginine metabolic process	46	2	0.14	0.00878
Genes near CpGs separating timepoints (glm)		Annotated	Significant	Expected	weightedFisher
GO.ID	Term				
GO:0006334	nucleosome assembly	152	5	0.47	0.00011
GO:0042742	defense response to bacterium	640	9	1.98	0.00017
GO:0006189	'de novo' IMP biosynthetic process	10	2	0.03	0.00042
GO:1900275	negative regulation of phospholipase C activity	14	2	0.04	0.00084
GO:0046148	pigment biosynthetic process	171	4	0.53	0.00199
GO:0015824	proline transport	23	2	0.07	0.00229
GO:0051599	response to hydrostatic pressure	28	2	0.09	0.00339

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GO:0032328	alanine transport	29	2	0.09	0.00363
GO:0051262	protein tetramerization	491	6	1.52	0.00424
GO:0033209	tumor necrosis factor-mediated signaling pathway	356	5	1.1	0.00502
GO:1904468	negative regulation of tumor necrosis factor secretion	35	2	0.11	0.00526
GO:0015816	glycine transport	35	2	0.11	0.00526
GO:0007076	mitotic chromosome condensation	42	2	0.13	0.00751
Genes near CpGs separating morphs (PC4)					
GO.ID	Term	Annotated	Significant	Expected	weightedFisher
GO:0006334	nucleosome assembly	152	5	0.53	0.0002
GO:0016340	calcium-dependent cell-matrix adhesion	9	2	0.03	0.00043
GO:0046548	retinal rod cell development	51	3	0.18	0.00077
GO:0021963	spinothalamic tract morphogenesis	12	2	0.04	0.00078
GO:0032780	negative regulation of ATPase activity	53	3	0.19	0.00086
GO:0106028	neuron projection retraction	14	2	0.05	0.00107
GO:0099557	trans-synaptic signaling by trans-synaptic complex, modulating synaptic transmission	14	2	0.05	0.00107
GO:0055069	zinc ion homeostasis	59	3	0.21	0.00118
GO:1904782	negative regulation of NMDA glutamate receptor activity	16	2	0.06	0.00141
GO:0007216	G protein-coupled glutamate receptor signaling pathway	63	3	0.22	0.00142
GO:1904783	positive regulation of NMDA glutamate receptor activity	18	2	0.06	0.00179
GO:0031938	regulation of chromatin silencing at telomere	21	2	0.07	0.00244
GO:0010961	cellular magnesium ion homeostasis	22	2	0.08	0.00268
GO:0051389	inactivation of MAPKK activity	23	2	0.08	0.00293
GO:1902723	negative regulation of skeletal muscle satellite cell proliferation	24	2	0.08	0.00318
GO:1902725	negative regulation of satellite cell differentiation	24	2	0.08	0.00318
GO:0036109	alpha-linolenic acid metabolic process	24	2	0.08	0.00318
GO:0022038	corpus callosum development	85	3	0.3	0.00334

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GO:0032490	detection of molecule of bacterial origin	25	2	0.09	0.00345
GO:0021554	optic nerve development	86	3	0.3	0.00346
GO:0071679	commissural neuron axon guidance	95	3	0.33	0.00457
GO:0045075	regulation of interleukin-12 biosynthetic process	29	2	0.1	0.00463
GO:0045671	negative regulation of osteoclast differentiation	102	3	0.36	0.00557
GO:0050847	progesterone receptor signaling pathway	35	2	0.12	0.0067
GO:0014719	skeletal muscle satellite cell activation	35	2	0.12	0.0067
GO:0043052	thermotaxis	37	2	0.13	0.00746
GO:0051262	protein tetramerization	491	6	1.72	0.00771
GO:0031648	protein destabilization	120	3	0.42	0.0087
Genes near CpGs separating morphs (glm)					
GO.ID	Term	Annotated	Significant	Expected	weightedFisher
GO:0006334	nucleosome assembly	152	4	0.11	4.20E-06
GO:0042742	defense response to bacterium	640	5	0.46	8.20E-05
GO:0051295	establishment of meiotic spindle localization	30	2	0.02	0.00022
GO:1901223	negative regulation of NIK/NF-kappaB signaling	69	2	0.05	0.00115
GO:0030071	regulation of mitotic metaphase/anaphase transition	118	2	0.09	0.0033
GO:0008205	ecdysone metabolic process	5	1	0	0.00362
GO:0051673	membrane disruption in other organism	5	1	0	0.00362
GO:0000964	mitochondrial RNA 5'-end processing	5	1	0	0.00362
GO:0051663	oocyte nucleus localization involved in oocyte dorsal/ventral axis specification	6	1	0	0.00434
GO:1902956	regulation of mitochondrial electron transport, NADH to ubiquinone	6	1	0	0.00434
GO:0051758	homologous chromosome movement towards spindle pole in meiosis I anaphase	6	1	0	0.00434
GO:1901208	negative regulation of heart looping	7	1	0.01	0.00506
GO:2000321	positive regulation of T-helper 17 cell differentiation	7	1	0.01	0.00506

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GO:1901856	negative regulation of cellular respiration namespace	7	1	0.01	0.00506
GO:0000965	mitochondrial RNA 3'-end processing	7	1	0.01	0.00506
GO:1901211	negative regulation of cardiac chamber formation	7	1	0.01	0.00506
GO:0072068	late distal convoluted tubule development	7	1	0.01	0.00506
GO:0045478	fusome organization	8	1	0.01	0.00579
GO:0031952	regulation of protein autophosphorylation	162	2	0.12	0.00611
GO:1905832	positive regulation of spindle assembly	9	1	0.01	0.00651
GO:0003167	atrioventricular bundle cell differentiation	9	1	0.01	0.00651
GO:0046604	positive regulation of mitotic centrosome separation	9	1	0.01	0.00651
GO:1904801	positive regulation of neuron remodeling	9	1	0.01	0.00651
GO:0075259	spore-bearing structure development	10	1	0.01	0.00723
GO:0070900	mitochondrial tRNA modification	10	1	0.01	0.00723
GO:0071169	establishment of protein localization to chromatin	11	1	0.01	0.00795
GO:0000349	generation of catalytic spliceosome for first transesterification step	11	1	0.01	0.00795
GO:0032621	interleukin-18 production	11	1	0.01	0.00795
GO:0042780	tRNA 3'-end processing	12	1	0.01	0.00867
GO:0090235	regulation of metaphase plate congression	12	1	0.01	0.00867
GO:0045653	negative regulation of megakaryocyte differentiation	12	1	0.01	0.00867
GO:0072019	proximal convoluted tubule development	13	1	0.01	0.00939
GO:0072385	minus-end-directed organelle transport along microtubule	13	1	0.01	0.00939
GO:0070649	formin-nucleated actin cable assembly	13	1	0.01	0.00939

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Table S8: List of all 478 DMRs between timepoints, morphs, or both. The first column is the scaffold name. The second column is the position at which the 1000bp window starts (in base pairs from the beginning of the scaffold). The third column is the distance from the DMR to the closest annotated feature (in base pairs). The fourth column is the Locus-ID of this feature, corresponding to the *Salvelinus sp.* IW2-2015 (assembly ASM291031v2). The fifth column is a more accessible name for each feature/gene.

DMRs between timepoints			Locus-ID	Gene name
Scaffold	Window-start	Dist to Feature		
NW_019942555.1	320001	27100	LOC112068329	39S ribosomal protein L33, mitochondrial-like
NW_019943024.1	212001	5270	LOC112071389	pseudo
NW_019943575.1	17001	4211	LOC112073377	pseudo
NW_019943662.1	46001	-10018	LOC112073686	pseudo
NW_019943912.1	70001	-5888	LOC112074366	zinc finger protein 271-like
NW_019944000.1	20001	NA		NA
NW_019944130.1	70001	NA		NA
NW_019944976.1	57001	0	transfer RNA valine (anticodon AAC)	transfer RNA valine (anticodon AAC)
NW_019946183.1	13001	512	LOC112077787	U5 spliceosomal RNA
NW_019946645.1	1001	5874	LOC112078193	uncharacterized LOC112078193
NW_019942558.1	810001	5283	LOC111955876	zinc finger protein 239
NW_019946655.1	22001	NA		NA
NW_019947228.1	1	NA		NA
NW_019947593.1	10001	NA		NA
NW_019954972.1	1	NA		NA
NW_019957531.1	680001	283	LOC112080403	histone H3-like
NW_019957535.1	1308001	-59866	LOC112080462	uncharacterized LOC112080462
NW_019942632.1	379001	4488	LOC112069034	metabotropic glutamate receptor 7-like

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NW_019957680.1	51001	664	LOC112080981	metastasis-associated protein MTA3-like
NW_019957703.1	66001	-7321	LOC112081032	kinesin light chain 1-like
NC_036838.1	19998001	-4654	LOC111962247	keratin, type I cytoskeletal 18
NC_036839.1	9822001	4994	LOC111974119	kalirin
NC_036839.1	32818001	40975	LOC111971565	pseudo
NC_036839.1	32819001	41975	LOC111971565	pseudo
NC_036842.1	28823001	-24269	LOC111961790	electrogenic sodium bicarbonate cotransporter 4-like
NC_036842.1	62932001	-18186	LOC111962341	cadherin-13
NC_036842.1	70796001	-4926	LOC111962476	guanine nucleotide-binding protein G(i) subunit alpha-1-like
NC_036842.1	79753001	14865	LOC111962594	rho guanine nucleotide exchange factor 11
NC_036843.1	17207001	-74101	Ig4q.2h14orf132	C14orf132 homolog
NC_036848.1	33059001	-627	LOC111967759	probable E3 ubiquitin-protein ligase HECTD2
NC_036849.1	11733001	30426	LOC111968993	uncharacterized protein C14orf132-like
NC_036850.1	3939001	3475	LOC111969554	uncharacterized protein C2orf71
NC_036853.1	20819001	11447	LOC111971876	uncharacterized LOC111971876
NW_019942675.1	94001	-385	transfer RNA proline (anticodon UGG)	transfer RNA proline (anticodon UGG)
NC_036853.1	50968001	0	LOC111971649	histone H2B
NC_036854.1	23549001	4300	LOC111972726	uncharacterized LOC111972726
NC_036855.1	9200001	28046	LOC111974640	uncharacterized LOC111974640
NC_036855.1	12513001	-2922	LOC111974125	Krueppel-like factor 9
NC_036857.1	37116001	1611	LOC111976586	uncharacterized LOC111976586
NC_036857.1	39102001	9729	LOC111976345	pro-neuregulin-3, membrane-bound isoform-like
NC_036857.1	41767001	0	LOC111977305	U1 spliceosomal RNA
NC_036858.1	9989001	-5516	LOC111977797	thyroid hormone receptor alpha
NC_036859.1	7264001	-3563	LOC111978873	semaphorin-6B-like

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NC_036859.1	34108001	6978	cdc73	cell division cycle 73
NC_036860.1	23039001	-2163	LOC111980376	AF4/FMR2 family member 4
NC_036861.1	1515001	2442	LOC111982472	uncharacterized LOC111982472
NC_036862.1	4725001	-64463	LOC111949699	glutamate receptor ionotropic, kainate 4-like
NC_036869.1	24753001	-2878	LOC111955200	protein S100-A1-like
NC_036870.1	23024001	555504	LOC111955604	trafficking protein particle complex subunit 3
NC_036872.1	11006001	-116962	LOC111958098	RING finger and CHY zinc finger domain-containing protein 1
NC_036872.1	11007001	-115962	LOC111958098	RING finger and CHY zinc finger domain-containing protein 1
NW_019942747.1	312001	69075	LOC112069857	SRSF protein kinase 1-like
NC_036875.1	8308001	-29855	LOC111959875	twist-related protein 2
NW_019942872.1	253001	0	transfer RNA isoleucine (anticodon AAU)	transfer RNA isoleucine (anticodon AAU)
NW_019942874.1	212001	19188	LOC112070662	uncharacterized LOC112070662
NW_019942514.1	2792001	7267	LOC112068083	platelet-activating factor receptor-like
NW_019945774.1	54001	14929	LOC112077381	PHD finger protein 3-like
NW_019946655.1	25001	NA		NA
NW_019946715.1	10001	NA		NA
NW_019951255.1	5001	4455	LOC112079873	uncharacterized LOC112079873
NC_036842.1	2068001	0	LOC111961235	uncharacterized LOC111961235
NC_036851.1	30569001	8938	LOC111970155	sorting nexin-6
NC_036857.1	11106001	-349890	LOC111976454	TLD domain-containing protein 2-like
NC_036857.1	29657001	-3034	LOC111976241	vasopressin V2 receptor
NW_019942929.1	52001	0	LOC112070958	pseudo
NC_036860.1	332001	2507	LOC111980429	uncharacterized LOC111980429
NC_036868.1	4731001	2078	LOC111954061	doublecortin domain-containing protein 2-like
NC_036872.1	723001	11931	LOC111958069	pseudo

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NC_036872.1	19702001	-7141	LOC112067915	uncharacterized LOC112067915
NC_036872.1	22840001	42640	LOC111958168	pseudo
NW_019942929.1	53001	166	LOC112070958	pseudo
NC_036875.1	26638001	-27695	LOC111959246	gamma-crystallin M2
NC_036876.1	18483001	-13578	LOC111960330	uncharacterized LOC111960330
NW_019944236.1	38001	2586	LOC112075022	homeodomain-interacting protein kinase 3-like
NW_019944672.1	68001	NA		NA
NW_019944564.1	30001	848	LOC112075615	ribose-5-phosphate isomerase-like
NW_019946656.1	33001	-7566	LOC112078211	uncharacterized LOC112078211
NW_019952667.1	2001	NA		NA
NW_019942747.1	325001	82075	LOC112069857	SRSF protein kinase 1-like
NW_019957703.1	67001	-8321	LOC112081032	kinesin light chain 1-like
NC_036838.1	53256001	-2346	LOC111969907	Kazrin-like
NC_036845.1	594001	355	LOC111964824	nuclear factor 7, brain
NC_036847.1	19050001	44629	ajap1	adherens junctions associated protein 1
NC_036847.1	19693001	-352	LOC111966937	pseudo
NC_036850.1	6286001	40959	LOC111969208	leucine zipper protein 2-like
NC_036855.1	35528001	-40426	efna5	ephrin A5
NW_019942925.1	128001	-724	LOC112070949	5.8S ribosomal RNA
NC_036856.1	13543001	2986	LOC111975301	midnolin
NC_036858.1	1084001	5419	LOC111977496	Extensin-like
NC_036874.1	3430001	-29643	zfpmp2	zinc finger protein ZFPM2
NW_019943090.1	105001	28236	LOC112071715	myoD family inhibitor-like
NW_019943193.1	14001	-11170	LOC112072088	caprin-1-like
NW_019943197.1	14001	-1581	LOC112072110	uncharacterized LOC112072110
NW_019943382.1	17001	-13609	LOC112072777	uncharacterized LOC112072777

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NW_019943695.1	153001	-35617	LOC112073800	pseudo
NW_019943246.1	232001	-39672	LOC112072302	uncharacterized LOC112072302
NC_036838.1	52339001	6424	LOC111969707	ras association domain-containing protein 5
NC_036843.1	5281001	-234617	LOC111963166	ephrin type-B receptor 3-like
NC_036843.1	13605001	0	LOC111963351	BTB/POZ domain-containing protein 6-B-like
NC_036845.1	19089001	-46598	LOC111964695	uncharacterized LOC111964695
NC_036847.1	20588001	-3499	LOC111966564	calcitonin gene-related peptide type 1 receptor
NC_036848.1	15393001	-35675	LOC111967519	probable carboxypeptidase X1
NC_036849.1	26384001	4396	LOC111968882	Prepronociceptin-like
NC_036850.1	16335001	-2193	rnf111	ring finger protein 111
NC_036852.1	11425001	-67587	LOC111971036	uncharacterized LOC111971036
NC_036854.1	43786001	12046	LOC111973108	zinc finger protein 438
NC_036855.1	49658001	-13997	LOC111974302	neuron navigator 2-like
NC_036856.1	8582001	27049	LOC111975447	uncharacterized LOC111975447
NW_019944696.1	9001	39263	LOC112075818	BCL-6 corepressor-like
NC_036857.1	17813001	0	nphp4	Nephrocystin 4
NC_036858.1	15194001	-310	plekha4	pleckstrin homology domain containing A4
NC_036860.1	7897001	0	LOC111981890	MAGUK p55 subfamily member 3
NC_036860.1	26515001	-7371	LOC111980729	disks large homolog 2-like
NC_036860.1	32711001	6043	LOC111981966	opioid-binding protein/cell adhesion molecule-like
NC_036862.1	6747001	68528	LOC111949633	rho GTPase-activating protein 35-like
NC_036862.1	22389001	-1328	LOC111949621	Elastin-like
NC_036862.1	24230001	8760	LOC111982659	Nucleoredoxin-like
NC_036863.1	12468001	0	LOC111950467	protein FAM168A-like
NC_036866.1	9090001	-26142	LOC111952266	uncharacterized LOC111952266

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NW_019944865.1	43001	-53866	LOC112076126	pseudo
NC_036867.1	9941001	22861	LOC111953739	C-C chemokine receptor type 3
NC_036868.1	27349001	70296	LOC111954486	kelch-like protein 29
NC_036870.1	13227001	97266	LOC111955733	cytosolic non-specific dipeptidase
NC_036874.1	15117001	-4019	LOC112067960	uncharacterized LOC112067960
NC_036875.1	6208001	23983	transfer RNA alanine (anticodon CGC)	transfer RNA alanine (anticodon CGC)
NC_036875.1	9806001	8708	tanc1	protein TANC1
NC_036875.1	16315001	1291	LOC111959647	anion exchange protein 3-like
NW_019945363.1	10001	-3641	LOC112076855	histone deacetylase 4-like
NW_019946856.1	29001	4465	mrps33	mitochondrial ribosomal protein S33
NW_019947099.1	21001	NA		NA
NC_036850.1	30001	3647	LOC111969161	uncharacterized LOC111969161
NC_036858.1	34309001	4347	eno4	Enolase 4
NC_036860.1	10197001	-8143	LOC111981463	beta-1,4 N-acetylgalactosaminyltransferase 1
NC_036863.1	46467001	8649	LOC111951100	mitochondrial fission 1 protein
NC_036872.1	19027001	-349	LOC111957498	phosphatidylinositol transfer protein beta isoform
NC_036872.1	35657001	97598	LOC111957439	reticulon-4 receptor-like
NW_019943363.1	46001	-13535	LOC112072732	pseudo
NW_019943980.1	5001	NA		NA
NC_036849.1	10931001	73959	LOC111968562	proton-coupled folate transporter
NW_019942514.1	4759001	53480	cmpk2	cytidine/uridine monophosphate kinase 2
NW_019944279.1	71001	-14236	LOC111958477	protein mab-21-like 2
NW_019945011.1	50001	-11832	LOC112076409	pseudo
NW_019945941.1	14001	-57877	fbxo40	F-box protein 40
NW_019946848.1	9001	NA		NA
NW_019942548.1	402001	4133	LOC112068301	ena/VASP-like protein

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NW_019946938.1	7001	521	LOC112078427	uncharacterized LOC112078427
NW_019947105.1	5001	NA		NA
NW_019957565.1	1104001	0	LOC112080620	multiple epidermal growth factor-like domains protein 9
NC_036838.1	21150001	3875	LOC111962397	Plexin-A1
NW_019942592.1	356001	44907	LOC112068739	taste receptor type 1 member 3-like
NC_036838.1	43676001	91272	fhit	fragile histidine triad
NC_036838.1	55356001	-12065	LOC111978577	pseudo
NC_036839.1	11219001	0	LOC111974293	acid-sensing ion channel 4
NC_036839.1	29941001	-3905	LOC111977983	fibrous sheath CABYR-binding protein
NC_036839.1	41684001	-39190	LOC111971941	pseudo
NC_036840.1	13462001	20854	LOC111951182	Copine-8
NC_036840.1	21684001	-7600	LOC111952471	ER membrane protein complex subunit 4
NC_036842.1	34496001	-8948	LOC111960913	DENN domain-containing protein 1A
NC_036844.1	18912001	0	LOC111964018	tyrosine-protein kinase ABL1
NC_036849.1	17118001	-2906	LOC111968708	solute carrier family 35 member F4
NC_036851.1	11535001	-2266	LOC111969806	forkhead box protein J3
NC_036851.1	30570001	7938	LOC111970155	sorting nexin-6
NC_036854.1	7163001	13477	LOC111973019	N-myc proto-oncogene protein-like
NW_019942793.1	84001	-5446	LOC112070158	pleckstrin homology domain-containing family H member 1-like
NC_036857.1	3438001	9956	LOC111977027	biglycan
NC_036858.1	9055001	-1022	LOC111978135	transcription factor 7-like 2
NC_036859.1	10963001	-7248	LOC111979433	disabled homolog 1
NC_036860.1	54354001	-322	LOC111982133	protocadherin gamma-C5
NC_036860.1	55962001	-60137	LOC111980014	pseudo
NC_036862.1	1353001	15980	LOC111982533	fibroblast growth factor 12-like

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NW_019942846.1	252001	-7867	LOC112070460	cytoplasmic dynein 1 heavy chain 1-like
NC_036863.1	8106001	-51868	LOC111950848	CXADR-like membrane protein
NC_036863.1	15686001	-67813	LOC111950261	rho GTPase-activating protein 32-like
NC_036869.1	7784001	11054	med10	mediator complex subunit 10
NC_036871.1	14120001	1845	LOC111956976	thymocyte selection-associated high mobility group box protein TOX
NC_036873.1	7536001	1667	LOC111958373	hydroperoxide isomerase ALOXE3
NW_019943087.1	3001	-28271	nars2	asparaginyl-tRNA synthetase 2, mitochondrial
NW_019943517.1	14001	-2930	LOC112073214	pseudo
NC_036842.1	17839001	-1312	LOC111961096	transmembrane protein 250-like
NC_036847.1	19049001	43629	ajap1	adherens junctions associated protein 1
NC_036853.1	20133001	41095	LOC111971654	uncharacterized LOC111971654
NC_036857.1	17674001	25232	LOC111976756	pseudo
NC_036861.1	1369001	2868	LOC111982311	small integral membrane protein 28-like
NW_019942747.1	323001	80075	LOC112069857	SRSF protein kinase 1-like
NC_036864.1	234001	-7118	LOC111951489	serine/threonine-protein kinase pim-3
NC_036866.1	41353001	-6180	LOC111952128	iroquois-class homeodomain protein IRX-5-like
NC_036876.1	8226001	159077	LOC111960007	receptor-type tyrosine-protein phosphatase delta-like
NW_019942925.1	120001	-8724	LOC112070949	5.8S ribosomal RNA
NW_019943092.1	90001	11120	LOC112071717	uncharacterized LOC112071717
NW_019944923.1	38001	-2737	LOC112076251	alpha-(1,3)-fucosyltransferase 4-like
NW_019946655.1	23001	NA		NA
NW_019946655.1	24001	NA		NA
NW_019942677.1	185001	-4482	LOC112069370	microtubule-actin cross-linking factor 1-like
NC_036853.1	19414001	-8110	LOC111972251	cytochrome P450 2J2
NC_036854.1	1257001	-3165	LOC111972866	pseudo

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NC_036860.1	52574001	-129223	LOC111981263	T-box transcription factor TBX2b-like
NW_019947025.1	32001	NA		NA
NW_019947025.1	33001	NA		NA
NW_019953566.1	1001	NA		NA
NC_036838.1	30006001	-507	LOC112081245	keratin-associated protein 9-8-like
NC_036846.1	22755001	-43965	LOC111965996	ephrin-B1-like
NW_019942874.1	213001	20188	LOC112070662	uncharacterized LOC112070662
NW_019943197.1	222001	-30012	LOC112072107	C-type lectin domain family 4 member E-like
NW_019943272.1	64001	2901	LOC112072395	Beta-microseminoprotein-like
NW_019943618.1	174001	5727	LOC112073556	collagen alpha-1(XI) chain-like
NW_019944772.1	49001	NA		NA
NW_019944925.1	41001	-8931	LOC112076253	pseudo
NW_019945272.1	15001	-12688	LOC112067792	glutathione hydrolase 1 proenzyme-like
NW_019946126.1	27001	-38803	LOC112077716	pseudo
NW_019947018.1	21001	5364	LOC112078499	zinc finger protein 32-like
NW_019947018.1	22001	6364	LOC112078499	zinc finger protein 32-like
NW_019947960.1	50001	65	LOC112079015	golgin subfamily A member 6-like protein 22
NW_019957527.1	96001	1681	LOC112080376	pseudo
NW_019957527.1	98001	0	LOC112080376	pseudo
NC_036839.1	42797001	178363	LOC111971969	tensin-1-like
NC_036842.1	19256001	63906	LOC111960841	pseudo
NC_036842.1	45957001	-89218	LOC111961137	uncharacterized LOC111961137
NW_019942711.1	306001	4281	LOC112069615	cysteine protease ATG4D-like
NC_036842.1	45976001	-108218	LOC111961137	uncharacterized LOC111961137
NC_036843.1	2511001	41849	qrsl1	glutaminyl-tRNA synthetase (glutamine-hydrolyzing)-like 1
NC_036847.1	27436001	14258	LOC111966749	teashirt homolog 2-like

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NC_036848.1	19503001	47785	LOC111968191	pseudo
NC_036849.1	5161001	116352	LOC111968472	homeobox protein goosecoid
NW_019942721.1	155001	20725	LOC112069693	cyclin-dependent kinase inhibitor 1B-like
NC_036851.1	44198001	-2373	LOC111970450	protein-glutamine gamma-glutamyltransferase 2
NC_036853.1	20134001	42095	LOC111971654	uncharacterized LOC111971654
NC_036853.1	50969001	0	LOC111971341	histone H4
NC_036854.1	46383001	-545636	LOC111973470	cadherin-10-like
NC_036857.1	23171001	-2014	LOC111977020	integrin alpha-5-like
NC_036857.1	26094001	-4119	LOC111976279	uncharacterized LOC111976279
NC_036857.1	41768001	0	LOC111977297	pseudo
NC_036859.1	27070001	0	transfer RNA glycine (anticodon UCC)	transfer RNA glycine (anticodon UCC)
NC_036863.1	5175001	-3750	LOC111951204	gamma-aminobutyric acid receptor subunit beta-2
NC_036863.1	23355001	-9971	LOC111950847	E3 ubiquitin-protein ligase RNFT1
NW_019942747.1	348001	105075	LOC112069857	SRSF protein kinase 1-like
NC_036868.1	25026001	16784	LOC111954566	cholecystokinin
NC_036870.1	1950001	-421	LOC111955687	ATPase inhibitor A, mitochondrial
NC_036870.1	6401001	-18763	LOC111956047	Angiopoietin-1
NC_036870.1	19671001	-32054	LOC111955894	growth factor receptor-bound protein 10
NC_036871.1	23891001	-892	LOC111956362	uncharacterized LOC111956362
NC_036872.1	10391001	6846	LOC111958051	transient receptor potential cation channel subfamily M member 3-like
NC_036872.1	11892001	17728	LOC111957993	uncharacterized LOC111957993
NC_036872.1	26483001	337	trmt2a	tRNA methyltransferase 2 homolog A
NC_036844.1	26361001	-13327	LOC111964129	fibroblast growth factor 11-like
NC_036847.1	11891001	2470	LOC111966395	5-aminolevulinate synthase, erythroid-specific, mitochondrial

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NC_036860.1	73076001	5144	LOC111980282	protein tweety homolog 3
NC_036871.1	29370001	2136	LOC111957248	corticotropin-releasing factor receptor 2-like
NC_036874.1	855001	-12512	LOC111958541	carcinoembryonic antigen-related cell adhesion molecule 1-like
NW_019948565.1	9001	39946	LOC112079234	pseudo
NC_036838.1	8616001	10324	LOC111971021	U7 small nuclear RNA
NC_036842.1	45908001	-40218	LOC111961137	uncharacterized LOC111961137
NC_036849.1	531001	19806	LOC111968410	EMILIN-1
NC_036862.1	28683001	-12175	LOC111982811	Friend leukemia integration 1 transcription factor
NC_036865.1	59001	10816	LOC111951670	cadherin-23-like
NC_036868.1	10316001	17677	LOC111954408	pseudo
NC_036871.1	21214001	15766	LOC111956480	E3 ubiquitin-protein ligase RNF220
NW_019944535.1	78001	12281	LOC112075582	uncharacterized LOC112075582
NW_019953584.1	1001	NA		NA
NW_019943782.1	69001	NA		NA
NW_019944970.1	136001	0	LOC112076326	5.8S ribosomal RNA
NW_019945856.1	77001	NA		NA
NW_019953566.1	2001	NA		NA
NW_019942558.1	955001	-961	LOC112068375	uncharacterized LOC112068375
NC_036838.1	48802001	-11826	LOC111969075	host cell factor 1
NC_036839.1	10428001	12759	LOC111974206	G protein-activated inward rectifier potassium channel 1
NC_036839.1	10882001	42486	LOC111974282	mannose-1-phosphate guanyltransferase alpha-A
NW_019942675.1	95001	0	transfer RNA proline (anticodon UGG)	transfer RNA proline (anticodon UGG)
NC_036851.1	1579001	42336	LOC111969647	Syndecan-4
NC_036851.1	28191001	210	LOC111970676	collagen alpha-1(VII) chain

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NC_036853.1	11463001	11813	LOC111971163	sphingosine 1-phosphate receptor 3-like
NW_019942734.1	48001	-33758	LOC112069779	Iporin-like
NC_036854.1	23112001	9099	LOC111973300	uncharacterized LOC111973300
NC_036855.1	47404001	-73416	LOC111974393	protein kinase C-binding protein NELL1
NW_019942747.1	309001	66075	LOC112069857	SRSF protein kinase 1-like
NC_036858.1	59384001	-55093	LOC111978311	zinc finger protein 503-like
NC_036860.1	17383001	9854	LOC111982089	BEN domain-containing protein 4-like
NC_036860.1	42744001	-95022	LOC111980328	autism susceptibility gene 2 protein-like
NC_036862.1	28681001	-14175	LOC111982811	Friend leukemia integration 1 transcription factor
NC_036863.1	13578001	38096	LOC111950801	opioid-binding protein/cell adhesion molecule-like
NC_036865.1	21253001	41953	LOC111951843	GDNF family receptor alpha-1
NC_036865.1	24650001	82112	LOC111951744	leucine-rich melanocyte differentiation-associated protein-like
NC_036866.1	16496001	6587	LOC111952937	DET1 homolog
NW_019942939.1	197001	14209	LOC112070991	UDP-glucuronosyltransferase 2C1-like
NC_036870.1	16570001	156668	LOC111955512	pseudo
NC_036875.1	30098001	-118060	transfer RNA valine (anticodon UAC)	transfer RNA valine (anticodon UAC)
NC_036875.1	33606001	6515	stam2	signal transducing adaptor molecule 2
NC_036876.1	6158001	-2777	LOC111960109	arf-GAP domain and FG repeat-containing protein 2-like
NW_019943020.1	20001	-7178	LOC112071374	zinc finger protein 239-like
NW_019946533.1	61001	-2538	alkbh7	alkB homolog 7
NW_019948957.1	8001	164	LOC112079356	pseudo
NW_019957698.1	222001	55474	LOC112081025	pseudo
NC_036838.1	26005001	-439	cntn2	Contactin 2
NC_036840.1	26369001	-9700	LOC111953774	uncharacterized LOC111953774

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NC_036842.1	9854001	58810	LOC111961398	retinoic acid receptor alpha
NW_019942971.1	54001	16475	s1pr2	sphingosine-1-phosphate receptor 2
NC_036842.1	43316001	8693	LOC111961133	interferon-induced transmembrane protein 5
NC_036843.1	19820001	-1752	LOC111963439	disheveled-associated activator of morphogenesis 1
NC_036844.1	8936001	-6975	LOC111963858	disabled homolog 2-interacting protein-like
NC_036846.1	69001	1193	LOC111965453	protocadherin beta-16-like
NC_036848.1	35015001	86	LOC111967817	protein quaking-B
NC_036853.1	20144001	52095	LOC111971654	uncharacterized LOC111971654
NC_036855.1	40157001	6170	LOC111974255	E3 ubiquitin-protein ligase znrf3
NC_036856.1	4235001	-283619	LOC111975548	receptor-type tyrosine-protein phosphatase S-like
NC_036857.1	4619001	194262	mafb	MAF bZIP transcription factor B
NC_036860.1	73535001	21157	LOC111980514	stannin
NC_036869.1	14839001	118156	LOC111955262	cytosolic non-specific dipeptidase-like
NC_036872.1	34799001	0	LOC111958271	kelch-like protein 20
NW_019945948.1	14001	227	LOC112077550	CXXC-type zinc finger protein 4-like
NW_019946085.1	124001	-7458	LOC112077671	E3 ubiquitin-protein ligase TRIM71-like
NC_036849.1	14447001	-1370	LOC111968629	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1
NC_036851.1	40913001	13062	LOC111970411	uncharacterized LOC111970411
NC_036857.1	29554001	7113	LOC111976316	uncharacterized LOC111976316
NC_036858.1	39008001	3920	LOC111978462	SH3 and PX domain-containing protein 2A
NC_036859.1	17121001	-3934	LOC111979020	zinc finger protein 521-like
NC_036865.1	23945001	4712	eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2
NC_036866.1	12434001	0	LOC111953085	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

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NC_036867.1	13665001	382	LOC111953336	transcriptional activator GLI3-like
NC_036868.1	9484001	2000	LOC111954346	sodium-dependent glucose transporter 1
NW_019950840.1	3001	NA		NA
NC_036870.1	16247001	-210	LOC111955959	endothelin-2-like
NW_019957557.1	527001	10910	LOC112080559	signal-induced proliferation-associated 1-like protein 1
NC_036839.1	38374001	-188743	cmss1	cms1 ribosomal small subunit homolog (yeast)
NC_036843.1	21887001	-8919	LOC111963473	Galectin-3
NC_036844.1	9555001	-2850	LOC111964483	pseudo
NC_036844.1	13699001	-110260	LOC111964499	netrin receptor UNC5D-like
NC_036845.1	26482001	1989	LOC111965367	rho guanine nucleotide exchange factor 37-like
NW_019944967.1	23001	2185	LOC112076318	NACHT, LRR and PYD domains-containing protein 4A-like
NW_019945627.1	16001	-750	LOC112077177	U2 spliceosomal RNA
NW_019946066.1	10001	NA		NA
NC_036838.1	12041001	-823	LOC111961339	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 2
NC_036842.1	78905001	-133841	LOC111962587	leucine-rich repeat-containing protein 4C-like
NC_036845.1	11935001	-6009	LOC111965085	pseudo
NC_036846.1	23749001	-761	LOC111966006	transmembrane protein 216
NW_019942801.1	258001	-928	LOC112067727	microtubule-associated protein tau-like
NC_036851.1	24113001	13743	tfeb	transcription factor EB
NC_036860.1	49328001	3203	LOC111982191	U7 small nuclear RNA
NC_036871.1	7026001	-26542	LOC111957062	low-density lipoprotein receptor-related protein 8-like
NW_019943971.1	5001	3825	LOC112074509	pseudo

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DMRs between morphs				
Scaffold	Window-start	Dist to Feature	Locus-ID	Gene Name
NW_019944174.1	9001	-24137	LOC112074908	histamine N-methyltransferase-like
NW_019957652.1	17001	175	LOC112080902	ras association domain-containing protein 4-like
NC_036858.1	64900001	-2042	LOC111977992	mismatch repair endonuclease PMS2-like
NW_019957525.1	242001	-41569	LOC112080371	guanylate cyclase soluble subunit alpha-2-like
NC_036862.1	6846001	-62623	LOC111949462	neutral amino acid transporter B(0)-like
NW_019957585.1	40001	NA		NA
NC_036868.1	18078001	5844	atp5mpl	ATP synthase membrane subunit 6.8PL
NW_019942730.1	1001	NA		NA
NC_036844.1	3454001	-36971	LOC111963811	LIM/homeobox protein Lhx2-like
NC_036839.1	22036001	6690	LOC111972899	inactive phospholipase C-like protein 1
NC_036860.1	74186001	39857	baiap3	BAI1 associated protein 3
NW_019944916.1	36001	NA		NA
NW_019945573.1	6001	NA		NA
NW_019948669.1	10001	1769	pcdh9	Protocadherin 9
NC_036841.1	7669001	0	lmtk2	lemur tyrosine kinase 2
NC_036851.1	26497001	-6138	nfya	nuclear transcription factor Y subunit alpha
NW_019944835.1	68001	-62836	LOC112076082	cilia- and flagella-associated protein 251-like
NC_036863.1	23356001	-10971	LOC111950847	E3 ubiquitin-protein ligase RNFT1
NC_036838.1	39341001	-13327	LOC111967420	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1
NC_036841.1	12406001	0	transfer RNA serine (anticodon AGA)	
NC_036842.1	29405001	-20506	LOC111961115	protein CutA homolog
NC_036845.1	23352001	-304352	LOC111964765	matrix-remodeling-associated protein 5-like
NW_019942922.1	163001	-3009	nfix	nuclear factor I X

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NW_019943690.1	15001	44861	LOC112073781	uncharacterized LOC112073781
NW_019947337.1	10001	NA		NA
NW_019943482.1	42001	0	LOC112073110	synaptonemal complex central element protein 3-like
NW_019944324.1	50001	-16390	LOC112067810	uncharacterized LOC112067810
NW_019944976.1	58001	0	transfer RNA valine (anticodon AAC)	NA
NW_019945308.1	27001	NA		NA
NW_019946095.1	29001	427	LOC112077686	FH1/FH2 domain-containing protein 3-like
NW_019946553.1	5001	2301	LOC112078129	Na(+)/H(+) exchange regulatory cofactor NHE-RF2-like
NW_019946988.1	43001	-20643	LOC112078473	solute carrier family 12 member 1-like
NW_019942868.1	417001	15720	LOC112070605	UPF0606 protein KIAA1549L-like
NC_036854.1	19415001	260	LOC111973420	insulinoma-associated protein 1a pseudogene
NC_036858.1	61878001	2719	chat	choline O-acetyltransferase
NC_036868.1	16684001	286	LOC111954466	CD2-associated protein-like
NW_019947409.1	15001	NA		NA
NW_019949599.1	8001	NA		NA
NC_036838.1	1547001	414452	LOC111957030	VPS10 domain-containing receptor SorCS1-like
NC_036838.1	51819001	9396	LOC111969579	contactin-4-like
NC_036849.1	18769001	10692	LOC111968754	regulator of G-protein signaling 6-like
NC_036848.1	48028001	25311	LOC111968064	lutropin-choriogonadotrophic hormone receptor-like
NW_019951751.1	1	0	LOC112079955	hepatocyte nuclear factor 6-like
NC_036857.1	25327001	6751	LOC111976420	trypsin-3-like
NC_036848.1	17280001	-32029	LOC111967556	polycomb group RING finger protein 1
NC_036864.1	10204001	0	LOC112067850	small nuclear ribonucleoprotein F
NW_019948814.1	4001	0	LOC112079300	ADP-ribosylation factor-like protein 16

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NW_019948814.1	5001	0	LOC112079299	ketosamine-3-kinase-like
NC_036872.1	5801001	-112277	LOC111958248	cytochrome c oxidase subunit 7C, mitochondrial
NW_019942523.1	11001	NA		NA
NW_019943690.1	14001	45861	LOC112073781	uncharacterized LOC112073781
NC_036875.1	8928001	0	vil1	villin 1
NC_036842.1	80971001	18552	LOC111962607	transmembrane and TPR repeat-containing protein 2-like
NC_036870.1	25106001	5804	fam221a	family with sequence similarity 221 member A
NC_036843.1	19525001	-223418	LOC111963050	interaptin-like
NC_036848.1	11148001	1643	LOC111967149	protocadherin alpha-C2-like
NC_036858.1	64857001	2555	LOC111977991	vacuolar fusion protein CCZ1 homolog
NW_019942657.1	4001	870	LOC112069229	uncharacterized LOC112069229
NC_036853.1	20050001	-8121	LOC111972008	tumor necrosis factor ligand superfamily member 6
NW_019944660.1	74001	243	LOC112075762	homeobox protein Meis1-like
NC_036846.1	27001	0	LOC111965446	protocadherin beta-16-like
NC_036849.1	4749001	6126	LOC111968468	gamma-aminobutyric acid receptor subunit rho-2-like
NC_036867.1	2054001	6571	LOC111953658	armadillo repeat-containing protein 1
NC_036867.1	2055001	5571	LOC111953658	armadillo repeat-containing protein 1
NC_036868.1	25024001	18784	LOC111954566	cholecystokinin
NW_019949317.1	10001	0	LOC112079456	uncharacterized LOC112079456
NC_036838.1	54895001	16309	LOC111970282	sodium-coupled neutral amino acid transporter 3
NC_036842.1	62921001	-7186	LOC111962341	cadherin-13
NW_019945755.1	44001	5260	LOC112077362	uncharacterized LOC112077362

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NC_036843.1	19530001	-218418	LOC111963050	interaptin-like
NW_019946545.1	58001	0	LOC112078124	CHRNA7-FAM7A fusion protein-like
NC_036842.1	12829001	1910	LOC111962838	uncharacterized LOC111962838
NC_036848.1	48029001	24311	LOC111968064	lutropin-choriogonadotrophic hormone receptor-like
NW_019943136.1	50001	11861	LOC112071877	glucose-fructose oxidoreductase domain-containing protein 1-like
NW_019945121.1	34001	NA		NA
NC_036838.1	16868001	65615	LOC111961781	transcription factor AP-2 gamma-like
NC_036839.1	38434001	-133330	LOC111971760	interleukin-1 receptor accessory protein-like 1
NC_036842.1	56551001	380	LOC111960960	uncharacterized LOC111960960
NW_019942727.1	115001	NA		NA
NC_036848.1	26850001	-57441	LOC111967644	PH and SEC7 domain-containing protein 1-like
NC_036855.1	64253001	-10924	LOC111974783	protein RIC-3
NC_036859.1	25682001	-19101	LOC111979049	long-chain-fatty-acid-CoA ligase 3-like
NC_036863.1	15314001	-49778	jam3	junctional adhesion molecule 3
NC_036865.1	6146001	-2203	LOC111951796	cytoplasmic polyadenylation element-binding protein 3-like
NC_036868.1	11550001	14540	LOC111954519	sodium/potassium-transporting ATPase subunit beta-1-interacting protein 2
NW_019943617.1	82001	4203	LOC112073553	semaphorin-7A-like
NW_019946019.1	43001	-6594	LOC112077610	uncharacterized LOC112077610
NW_019947408.1	1	NA		NA
NC_036869.1	6124001	18324	LOC111954794	extensin-like
NW_019944284.1	49001	454	LOC112075116	homeobox protein Nkx-2.3-like
NW_019950957.1	2001	NA		NA
DMRs between timepoints and morphs				

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Scaffold	Window-start	Dist to Feature	Locus-ID	Gene Name
NW_019944970.1	137001	-570	LOC112076326	5.8S ribosomal RNA
NW_019946655.1	41001	NA		NA
NW_019947147.1	1	0	LOC112078566	5.8S ribosomal RNA
NW_019947337.1	9001	NA		NA
NW_019957589.1	239001	17280	LOC112080706	dnaJ homolog subfamily C member 15-like
NC_036838.1	27806001	-3512	LOC111963368	sodium- and chloride-dependent GABA transporter 2-like
NW_019942669.1	9001	-102708	LOC112069314	spermatid perinuclear RNA-binding protein-like
NC_036851.1	2219001	-22824	abra	actin binding Rho activating protein
NC_036853.1	50964001	0	LOC111971647	histone H3-like
NC_036853.1	50965001	0	LOC111971648	histone H2A-like
NC_036853.1	50966001	0	LOC111971885	histone H1
NC_036853.1	50967001	149	LOC111971649	histone H2B
NC_036854.1	36694001	-21296	ntng1	netrin G1
NC_036857.1	39239001	19325	LOC111977116	uncharacterized LOC111977116
NW_019942721.1	303001	-2435	LOC112069694	DENN domain-containing protein 2A-like
NC_036876.1	19536001	-8058	col25a1	collagen type XXV alpha 1 chain
NW_019947652.1	31001	NA		NA
NC_036840.1	6590001	-1014	fbh1	F-box DNA helicase 1
NC_036866.1	35656001	5727	LOC111952570	ankyrin repeat and BTB/POZ domain-containing protein BTBD11-B
NW_019942669.1	7001	-104708	LOC112069314	spermatid perinuclear RNA-binding protein-like
NW_019952633.1	1	NA		NA
NC_036840.1	18559001	-146345	LOC111956268	5-hydroxytryptamine receptor 2C-like

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NC_036850.1	7487001	21685	LOC111969237	NEDD8-activating enzyme E1 regulatory subunit
NW_019946489.1	9001	NA		NA
NW_019957652.1	18001	1175	LOC112080902	ras association domain-containing protein 4-like
NW_019957652.1	19001	2175	LOC112080902	ras association domain-containing protein 4-like
NC_036858.1	56253001	-7882	LOC111977406	chromobox protein homolog 2-like
NC_036867.1	28906001	68767	LOC111953159	uncharacterized LOC111953159
NC_036876.1	1195001	143	LOC111960022	zinc finger protein 2 homolog
NC_036851.1	2218001	-21824	abra	actin binding Rho activating protein
NC_036865.1	21254001	-42122	LOC111951843	GDNF family receptor alpha-1
NW_019943232.1	205001	7509	LOC111971960	tripartite motif-containing protein 16-like
NW_019942604.1	181001	32096	LOC112068820	C-type natriuretic peptide 4-like
NC_036858.1	39718001	61432	LOC111978430	transcription factor COE3-like
NC_036871.1	29506001	-42583	LOC111957164	aquaporin FA-CHIP
NC_036875.1	6613001	3397	LOC111959710	uncharacterized LOC111959710
NC_036858.1	11864001	-33192	itga3	integrin subunit alpha 3
NC_036870.1	1028001	-1817	LOC111956211	LIX1-like protein
NC_036849.1	10933001	71959	LOC111968562	proton-coupled folate transporter
NW_019947187.1	13001	NA		NA
NW_019943205.1	1001	-78773	LOC112072150	uncharacterized LOC112072150
NC_036848.1	26151001	-3195	LOC111967636	ecto-NOX disulfide-thiol exchanger 2-like
NC_036858.1	15871001	10434	LOC111978815	rho-related GTP-binding protein RhoN
NW_019942914.1	238001	-72188	LOC111963747	uncharacterized LOC111963747
NC_036856.1	8286001	0	LOC111975624	lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial

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NC_036860.1	54990001	-618	LOC111980011	leucine-rich repeat-containing protein 75B-like
NW_019944574.1	19001	10714	LOC112075618	uncharacterized LOC112075618
NC_036846.1	10531001	41847	LOC112081114	leukocyte cell-derived chemotxin-2-like
NC_036851.1	36277001	2329	LOC111970311	caveolin-2-like

Table S9: Distribution of DMRs and non-DMRs on linkage groups from the *Salvelinus* sp. IW2-2015 (assembly ASM291031v2).

	DMRs between timepoints	DMRs between morphs	DMRs between timepoints and morphs	non-DMRs
total	338	91	49	18469
LG1	11	5	1	577
LG2	10	2	0	394
LG3	3	0	2	300
LG4p	0	2	0	236
LG4q.1:29	14	5	0	904
LG4q.2	6	2	0	260
LG5	5	1	0	355
LG6.1	4	1	0	268
LG6.2	3	1	1	227
LG7	6	0	0	343
LG8	4	5	1	519
LG9	7	2	1	300
LG10	4	0	1	225
LG11	8	1	3	496
LG12	1	0	0	127
LG13	8	1	4	475
LG14	6	1	1	449
LG15	6	1	0	616
LG16	3	0	1	346
LG17	13	1	1	400
LG18	7	3	4	678
LG19	5	1	0	368
LG20	14	1	1	748
LG21	2	0	0	53
LG22	7	1	0	348
LG23	7	2	0	461
LG24	1	1	0	76
LG25	4	1	1	225
LG26	4	0	1	421
LG27	2	2	1	382

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LG28	5	4	0	283
LG30	3	1	0	209
LG31	7	1	1	295
LG32	5	0	1	340
LG33	11	1	0	349
LG34	1	0	0	101
LG35	3	0	0	192
LG36	7	1	1	413
LG37	3	0	2	179
Unplaced	118	40	19	4531

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Table S10: Results of ANOVA's and Tukey's HSD tests on methylation data. The first column states the name of the gene of interest. Columns 2, and 7 show ANOVA p-values for each variable (Morph, and Time). Columns 3-6 as well as 8-10 show HSD test results in a compact letter display format: groups with the same letter are not significantly different.

Name	Morph p-value	LB	SB	PI	PL	Time p-value	50ts	100ts	150ts	200ts
LMTK2	0.677	a	a	a	a	0.425	a	a	a	a
H2A-like	0.089	a	a	a	a	3.63E-21	a	b	c	d
SLC9A3R2-like	7.42E-05	b	b	ab	a	0.405	a	a	a	a
NKX23-like	0.073	a	a	a	a	0.673	a	a	a	a
NFIX	7.01E-06	a	bc	b	c	0.648	a	a	a	a
RASSF4-like	2.64E-06	a	ab	bc	c	5.39E-06	c	b	ab	a
ARL16	0.002	ab	b	b	a	0.689	a	a	a	a
MEIS1-like	0.001	b	a	b	ab	0.106	a	a	a	a
H3-like	0.093	a	a	a	a	2.60E-16	a	b	c	d
ARMC1	0.301	a	a	a	a	0.830	a	a	a	a
GLI3-like	0.662	a	a	a	a	0.001	NA	a	a	b
MEGF9	0.056	a	a	a	a	5.53E-16	a	b	c	c
MPP3	0.031	ab	a	b	ab	3.86E-07	a	a	b	b
ARHGEF37-like	0.146	a	a	a	a	5.01E-10	a	a	b	c

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Table S11: Results of ANOVA's and Tukey's HSD tests on gene expression data. The first column states the name of the gene of interest. Columns 2, 7 and 11 show ANOVA p-values for each variable (Morph, Time and Morph x Time interaction). Columns 3,4,5,6 as well as 8,9,10 show HSD test results in a compact letter display format: groups with the same letter are not significantly different.

Name	Morph p-value	LB	SB	PI	PL	Time p-value	100ts	150ts	200ts	Interaction p-value
LMTK2	0.220	a	a	a	a	0.020	b	a	b	0.140
H2A-like	7.32E-06	c	a	b	ab	3.68E-06	b	a	c	0.650
SLC9A3R2-like	2.07E-03	b	a	b	b	1.10E-12	c	b	a	0.970
NKX23-like	0.270	a	a	a	a	9.02E-08	a	a	b	0.620
NFIX	0.030	ab	ab	a	b	1.99E-28	c	b	a	4.47E-03
RASSF4-like	0.300	a	a	a	a	2.06E-05	b	a	b	0.170
ARL16	3.46E-08	c	b	b	a	1.93E-05	b	a	c	0.590
MEIS1-like	0.110	a	a	a	a	6.17E-07	c	b	a	4.48E-03
H3-like	2.69E-05	b	a	b	b	4.43E-08	a	b	c	0.420
ARMC1	1.16E-05	c	a	b	ab	0.210	a	a	a	0.350
GLI3-like	0.020	ab	b	a	ab	0.190	a	a	a	0.050
MEGF9	2.62E-06	b	a	a	a	1.60E-07	b	a	a	0.570
MPP3	0.390	a	a	a	a	2.68E-14	b	a	a	0.060
ARHGEF37-like	4.91E-07	b	a	a	a	5.60E-09	a	b	c	3.51E-03

Table S12: Tests for correlations between average methylation and gene expression. For *GLI3-like* and *NFIX*, the data was not parametric so the Kendall coefficient and test were used. For the other 12 genes, Pearson's correlation and t-tests were implemented.

Gene Name	R	p
H2A	0.1415	0.661
LMTK2	0.0505	0.8827
GLI3-like	0.0556	0.9195
ARHGEF37-like	0.7471	0.0052
MPP3	-0.7846	0.0042
RASSF4-like	0.0212	0.948
H3-like	0.6287	0.0285
ARMC1	-0.1112	0.7309
MEGF9	-0.643	0.0241
NFIX	0.0909	0.7373
NKX23-like	0.0387	0.905
SLC9A3R2-like	-0.0417	0.8977
ARL16	0.3265	0.3002
MEIS1-like	-0.2364	0.4595

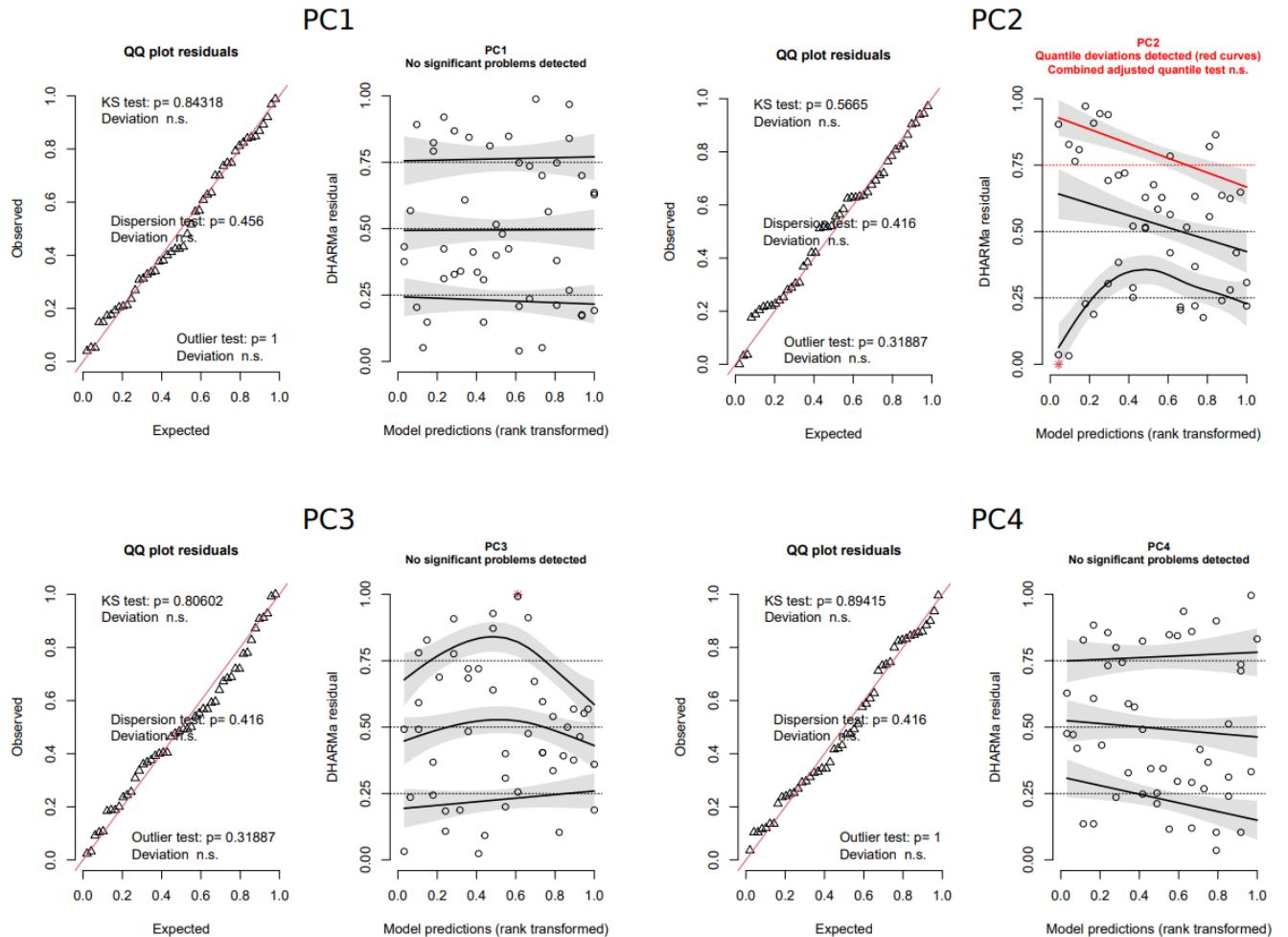


Figure S1: Results of validation analyses of linear models for the first 4 PCs (see labels), using the DHARMA package. For each of the PC's two plots are depicted, on the left a QQ plot with the results of three tests for deviation from normality (with assessment of deviation with associated significance) and on the right plot of residuals against the predicted values from the model.

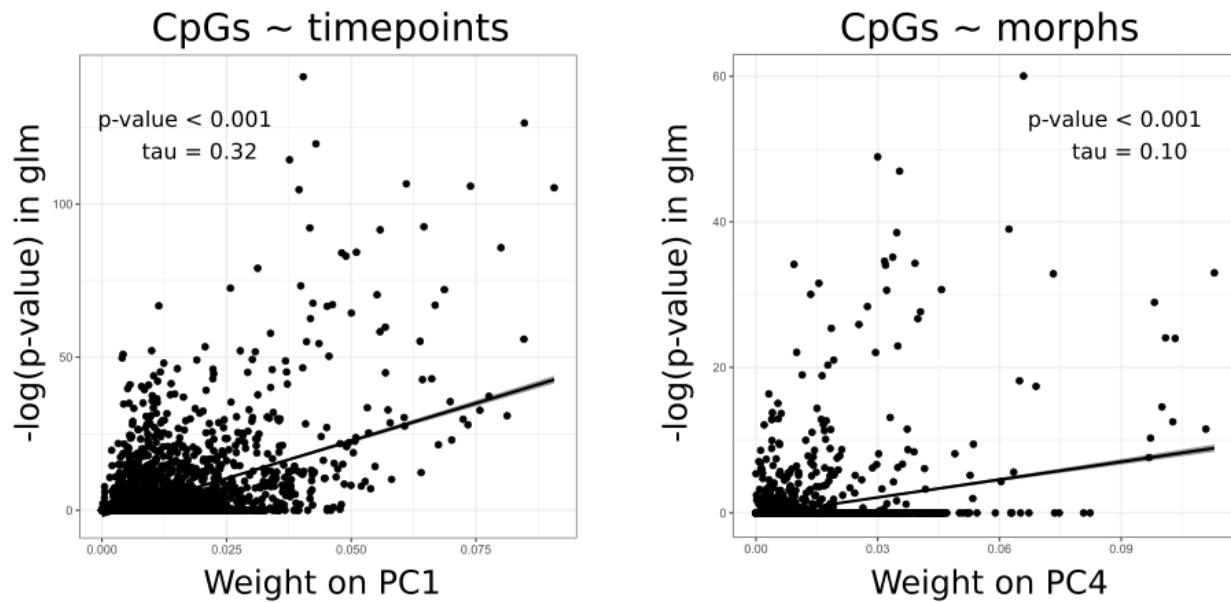
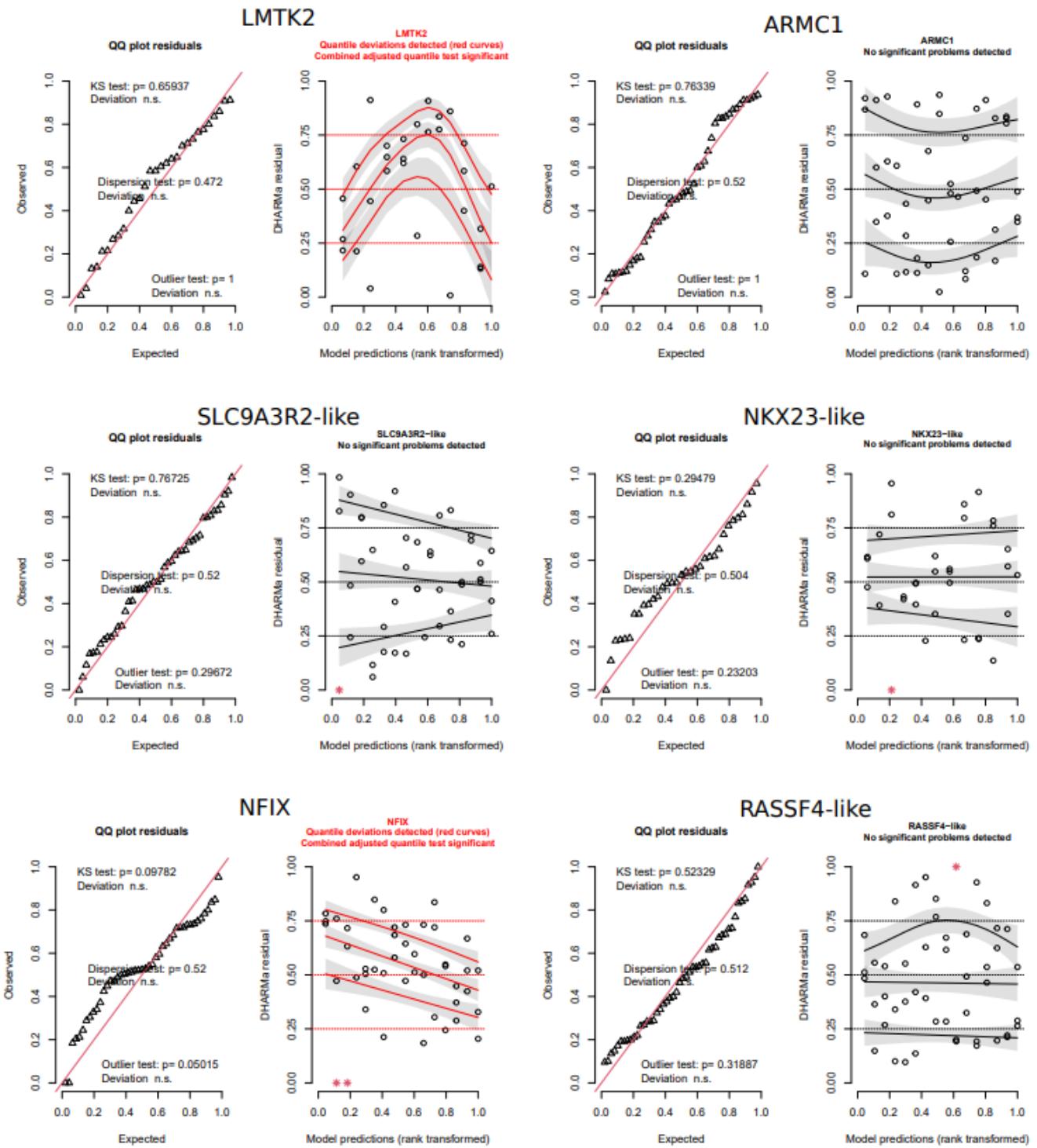
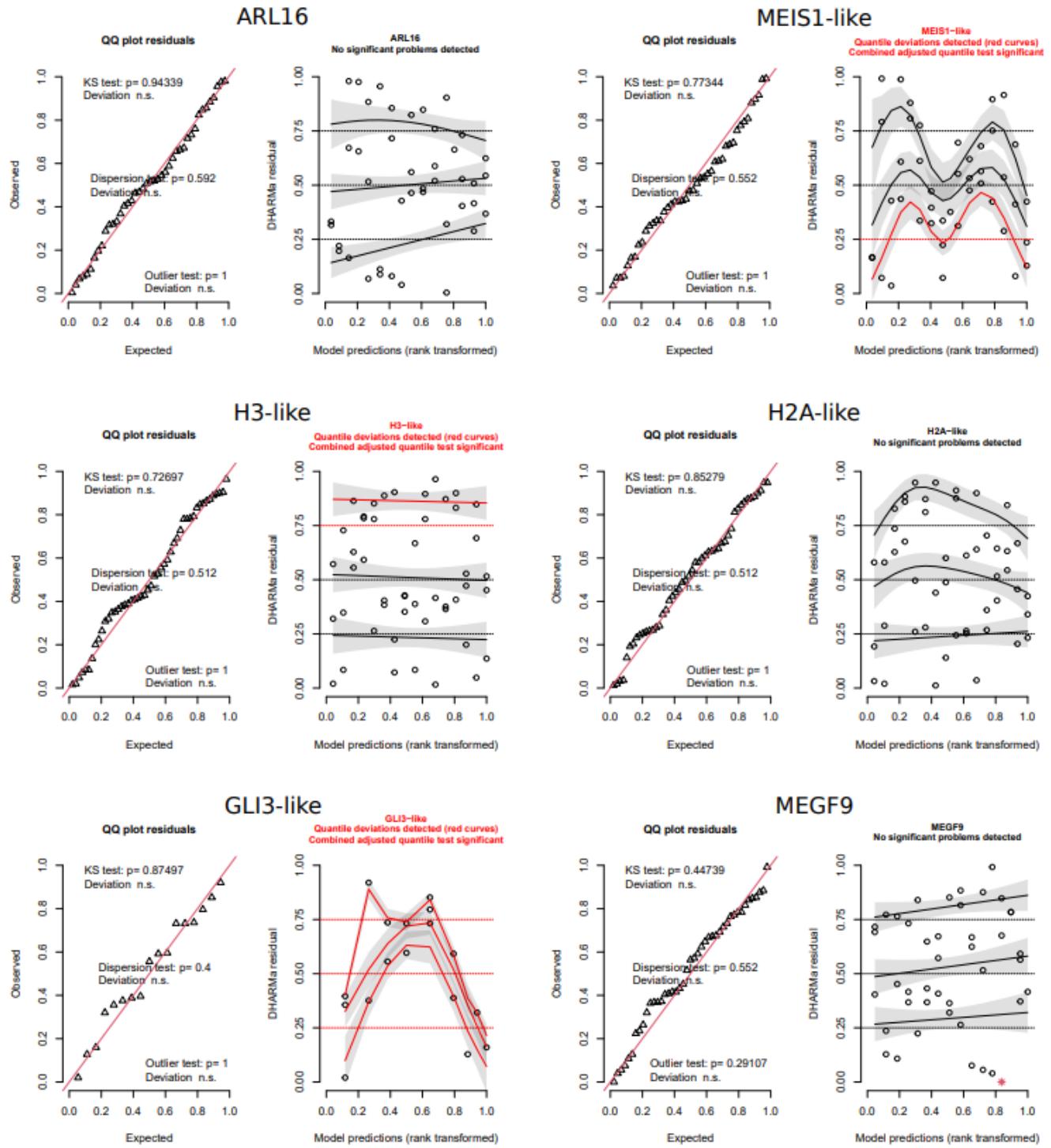


Figure S2: Comparisons between glm and PCA analyses. Contribution of each of the 10340 CpGs to timepoints and morphs. For each CpG, the absolute weight to specific PCs is plotted against the $-\log(p\text{-value})$ in the glm. The regression lines were obtained with kendall correlation. Kendall test results (p-values and tau) are displayed on the graphs.





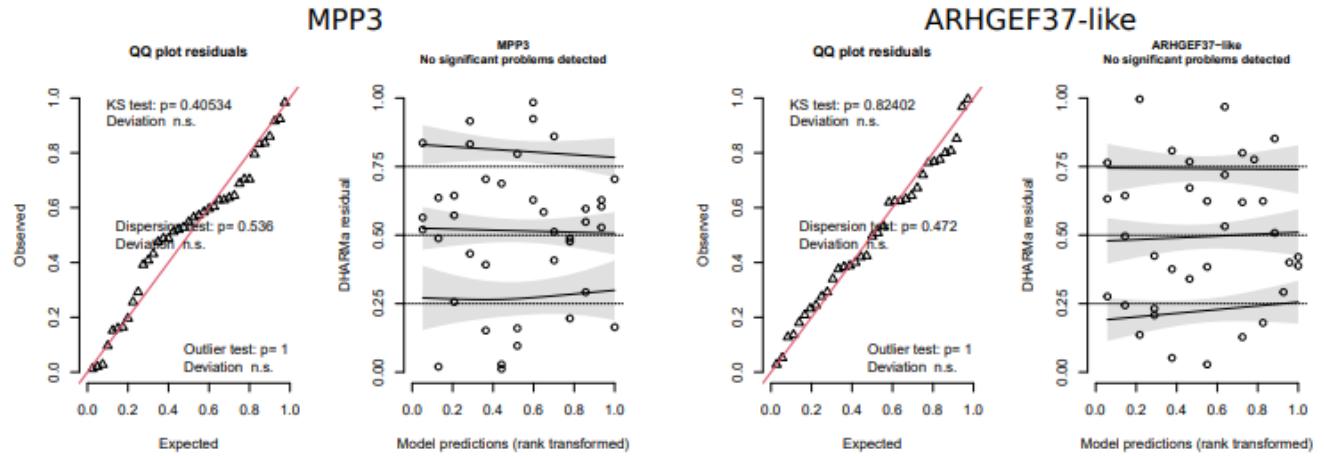
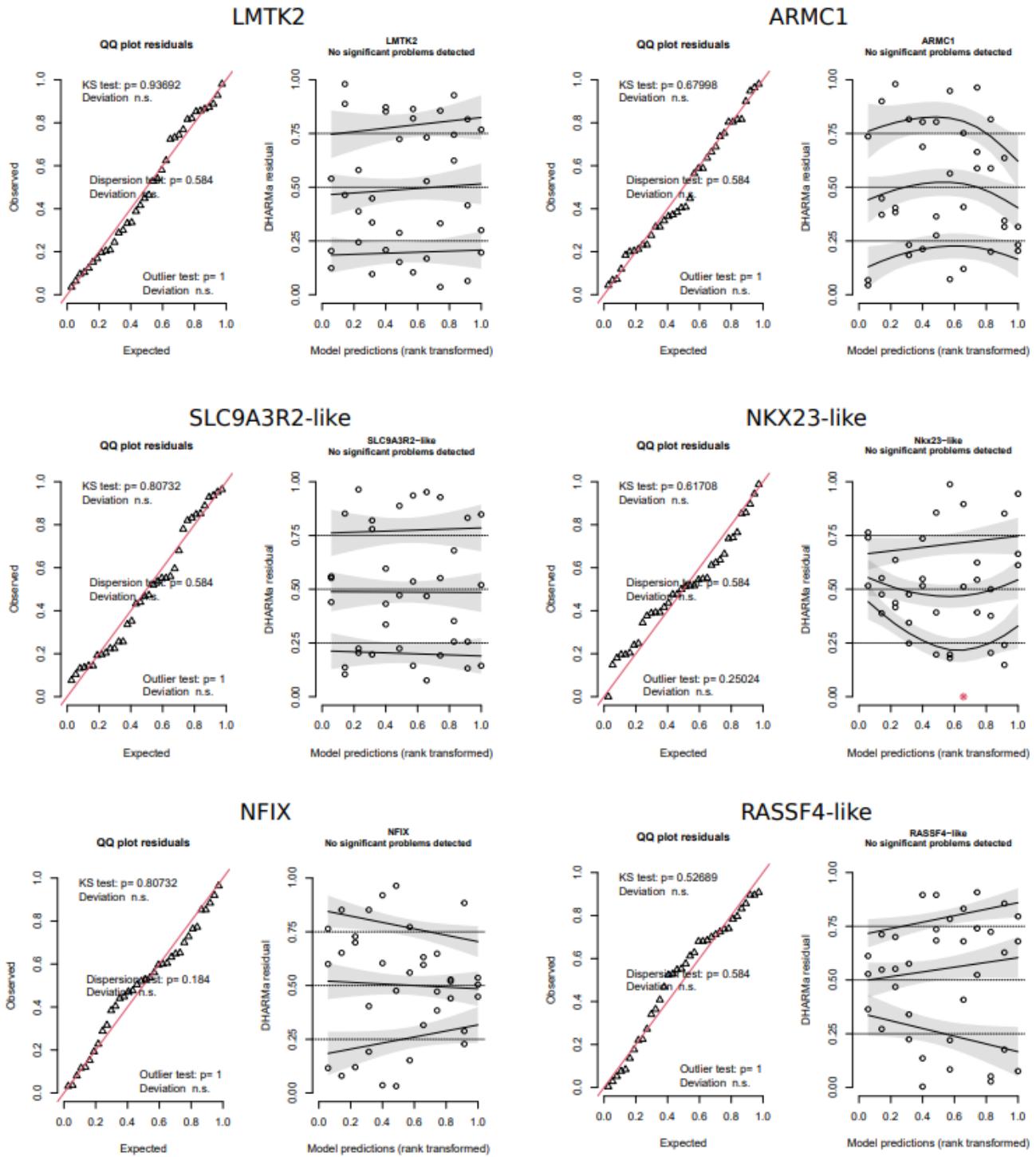
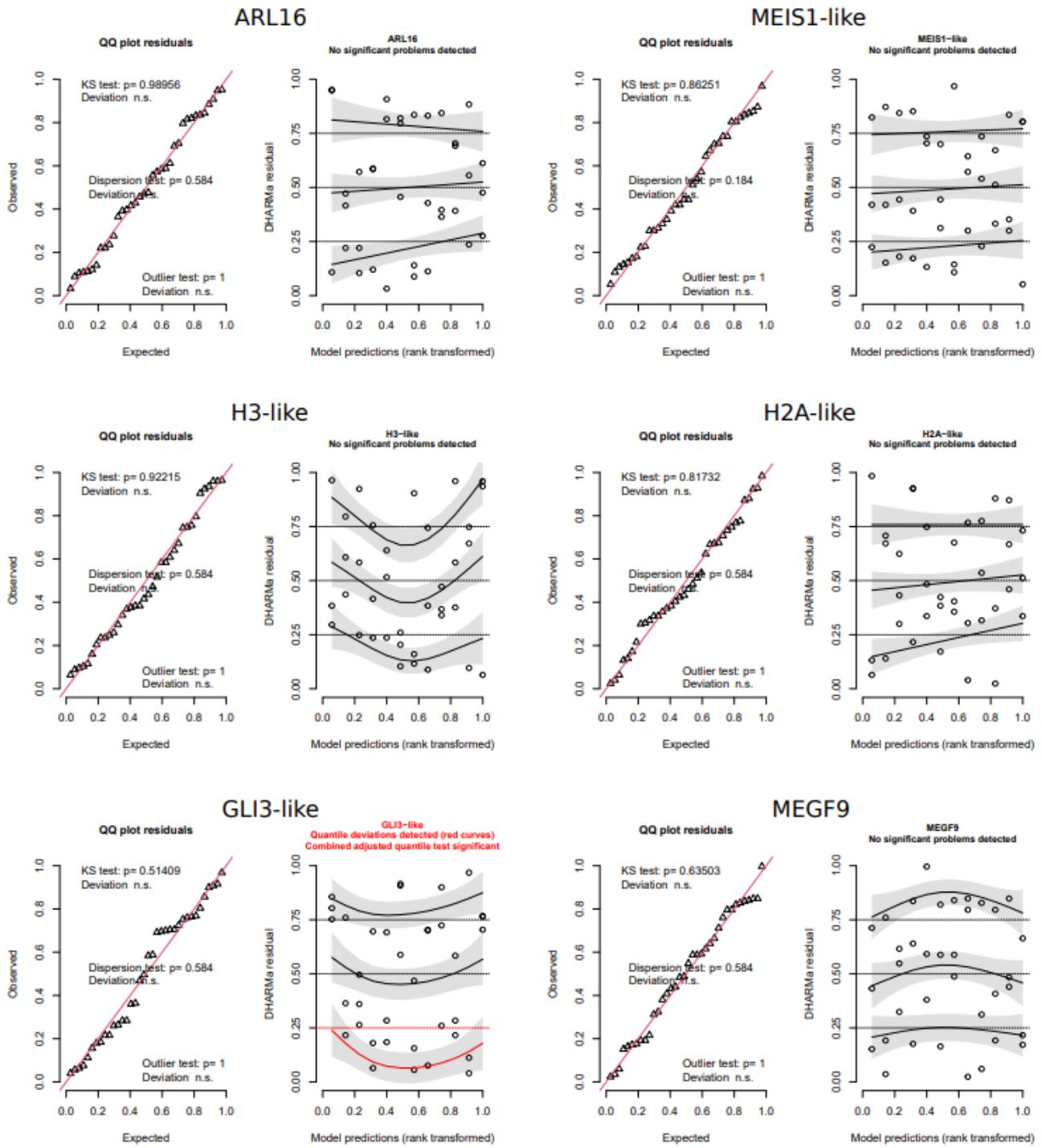


Figure S3: Results of validation analyses of linear models for methylation data on the 14 genes of interest (see labels), using the DHARMA package. For each of the genes two plots are depicted, on the left a QQ plot with the results of three tests for deviation from normality (with assessment of deviation with associated significance) and on the right plot of residuals against the predicted values from the model.



MOLECULAR ECOLOGY



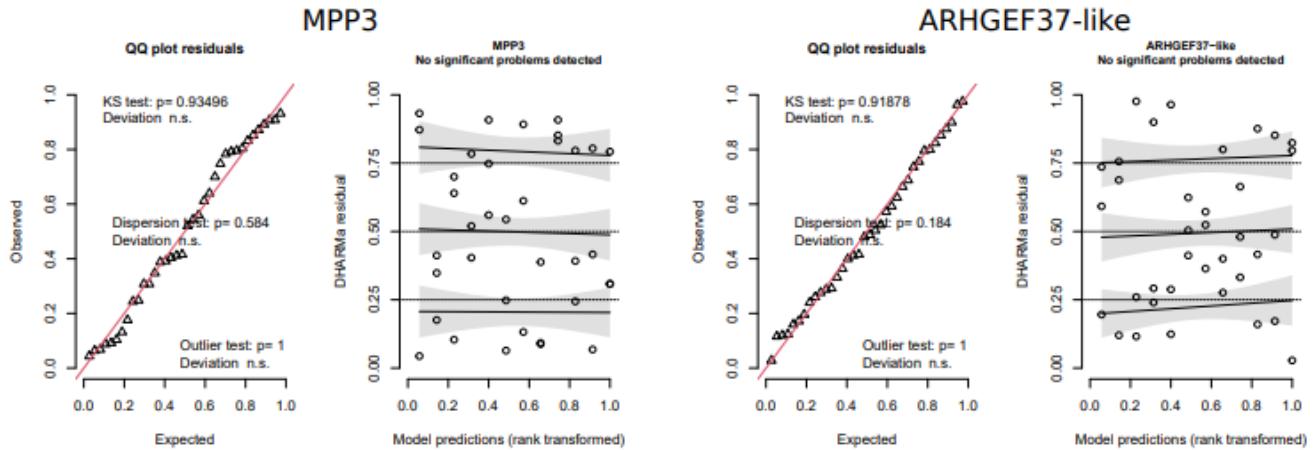


Figure S4: Results of validation analyses of linear models for expression data on the 14 genes of interest (see labels), using the DHARMA package. For each of the genes two plots are depicted, on the left a QQ plot with the results of three tests for deviation from normality (with assessment of deviation with associated significance) and on the right plot of residuals against the predicted values from the model.

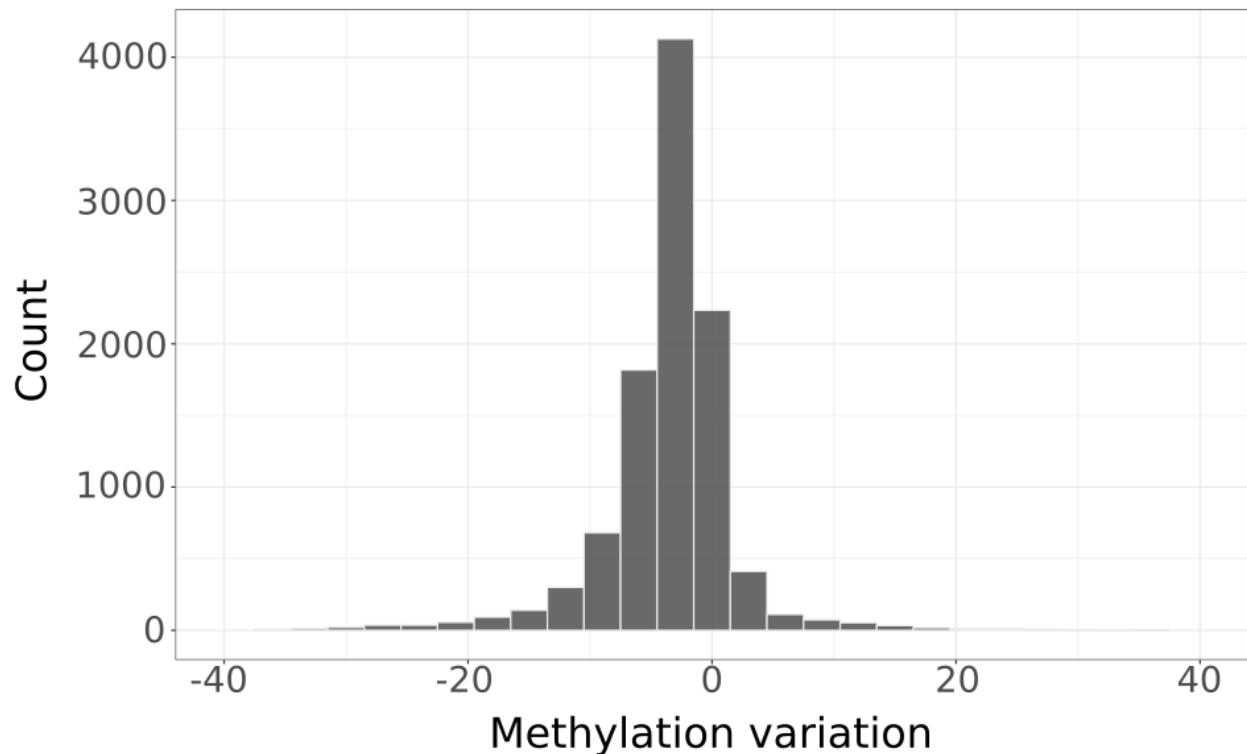
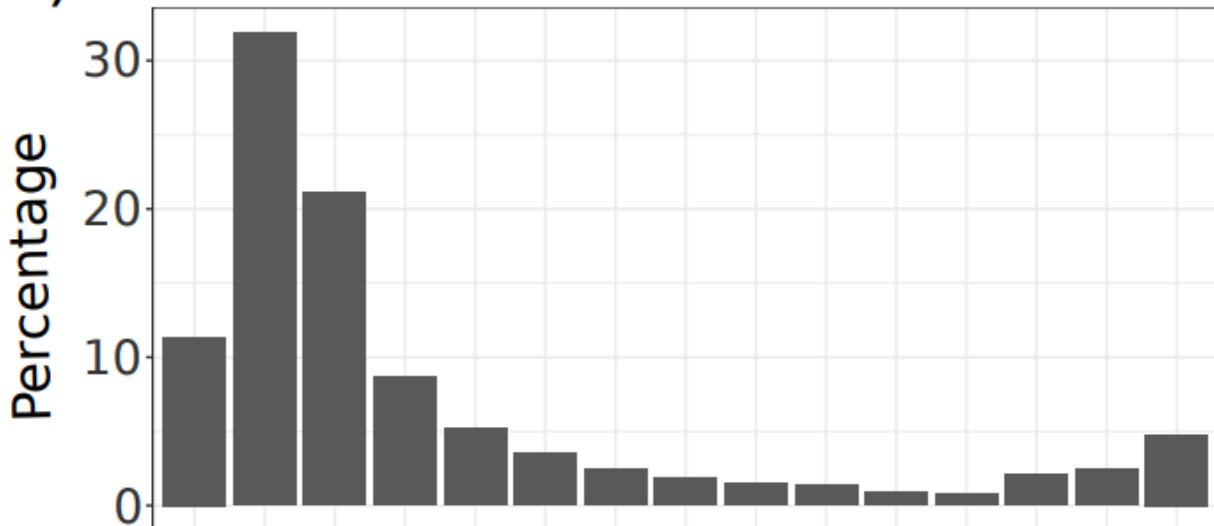


Figure S5: Changes in methylation of 10340 CpGs between 50 and 200 ts. Most of the cytosines show a decrease in methylation over this period, with the mean methylation change being -3.6%.

A)



B)

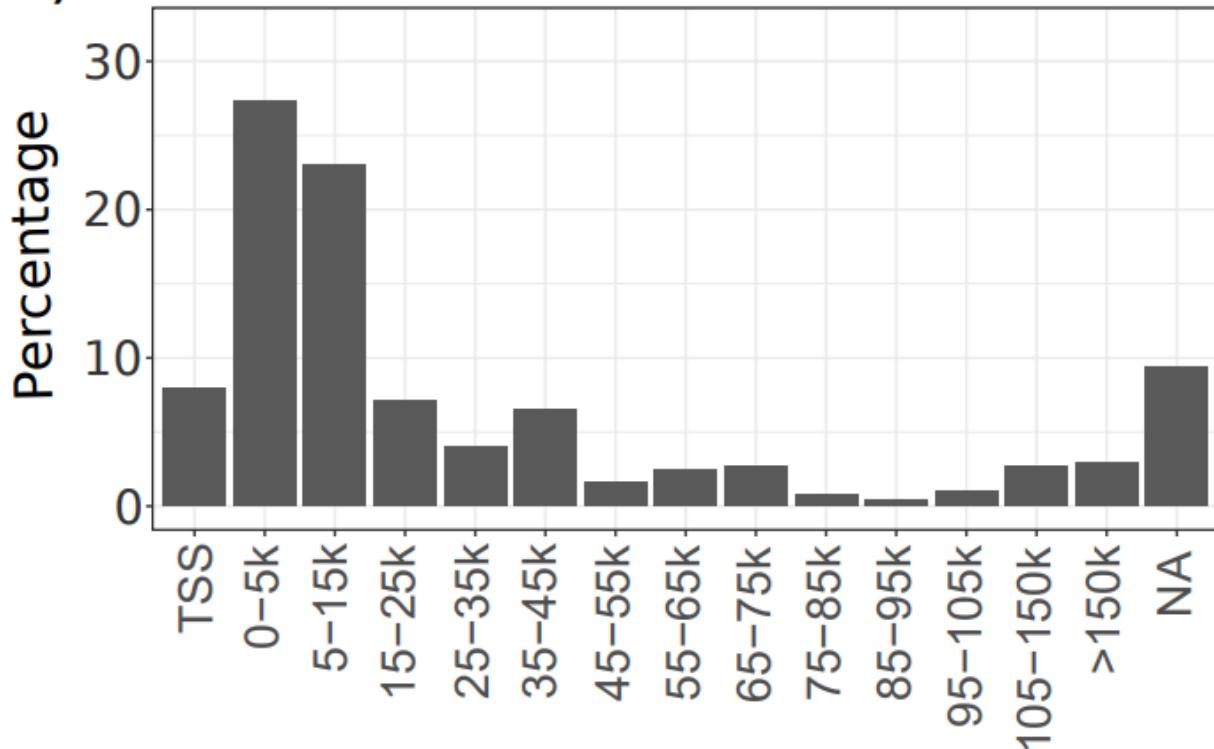


Figure S6: Similar distribution of DMRs and non-DMRs in relation to transcription start sites. Distribution of methylated and differentially methylated

regions in the genome, represented as percentage of regions in each category, binned by their distance to the closest transcription start site (in bp). A) For the 18469 non-DMRs. B) For the 479 DMRs. It appears that differences in methylation arise in CpG islands regardless of their distance to gene bodies.

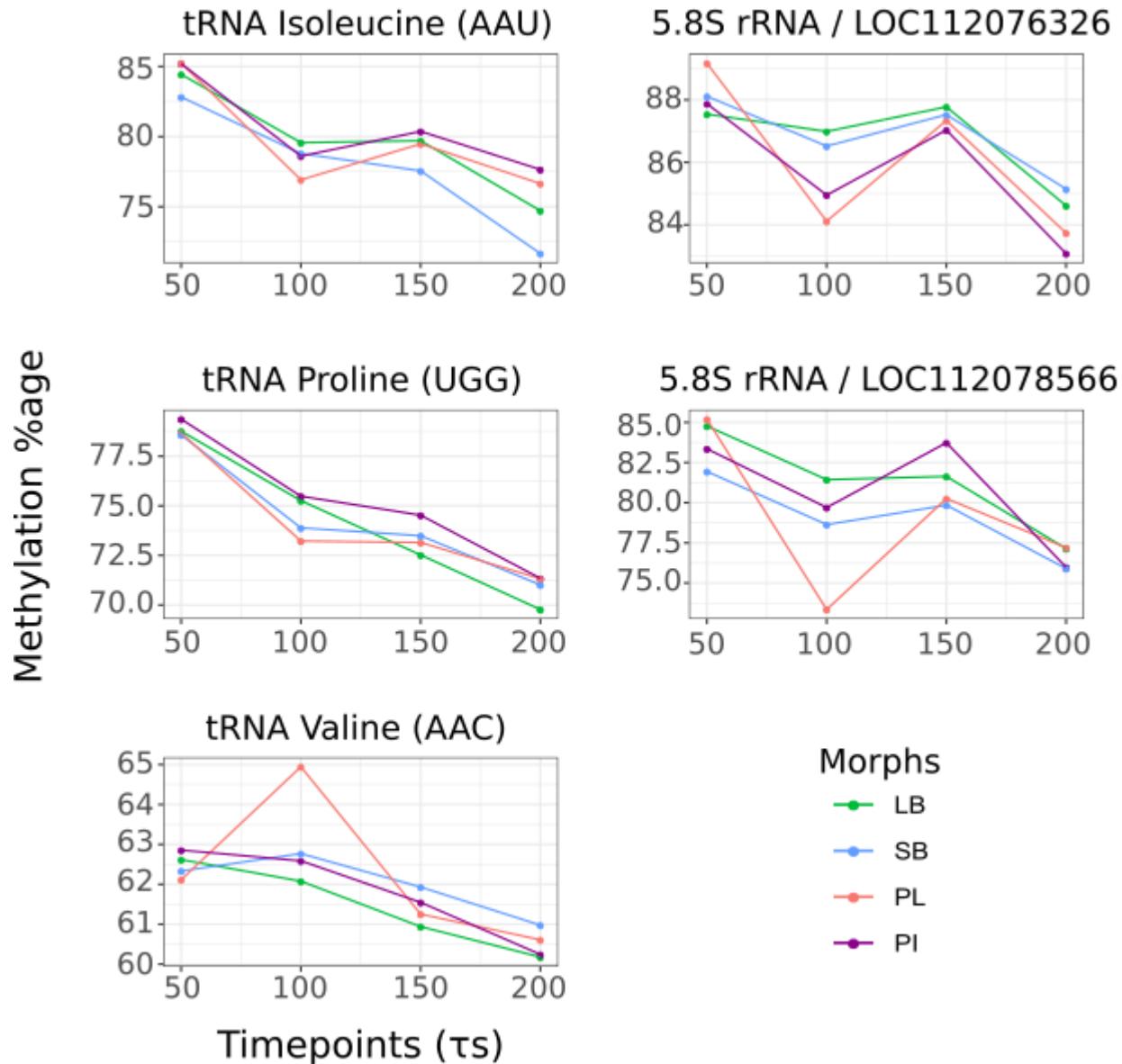
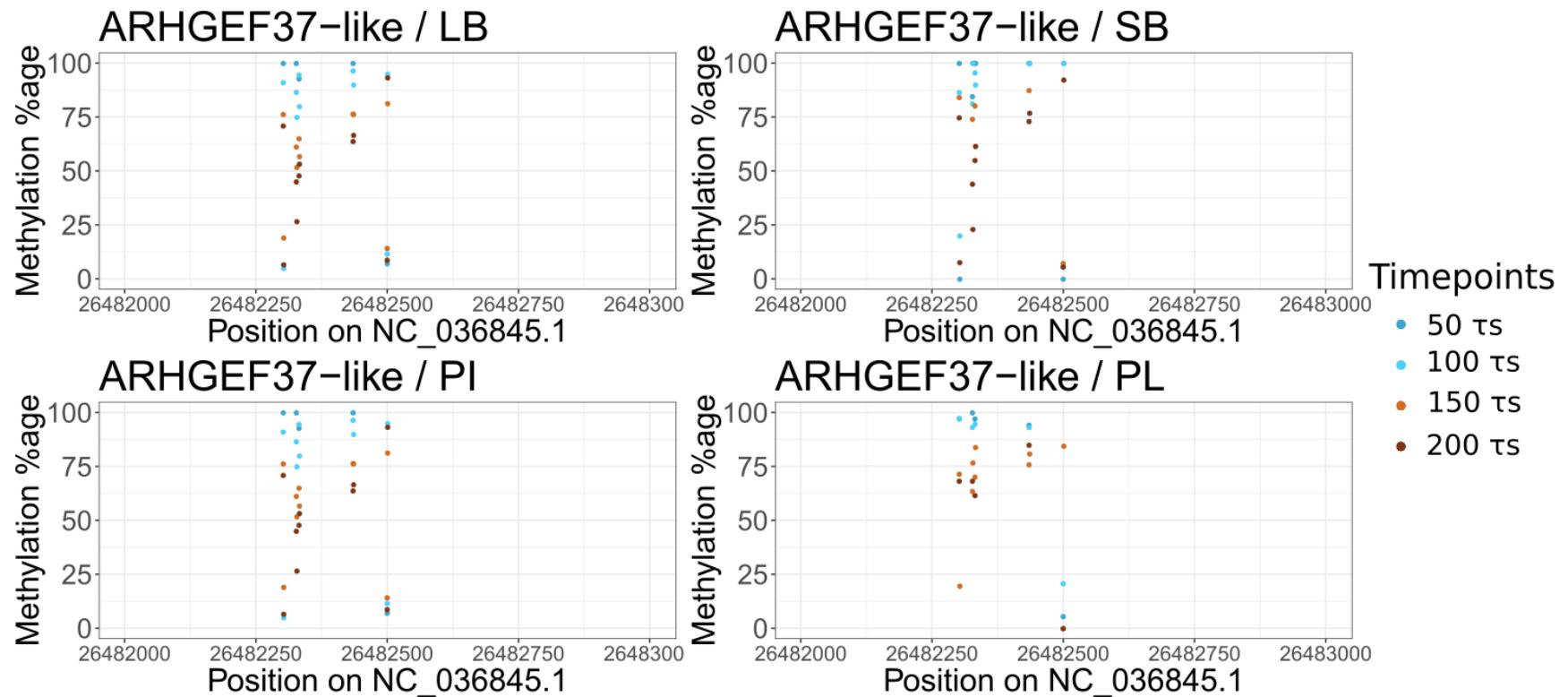
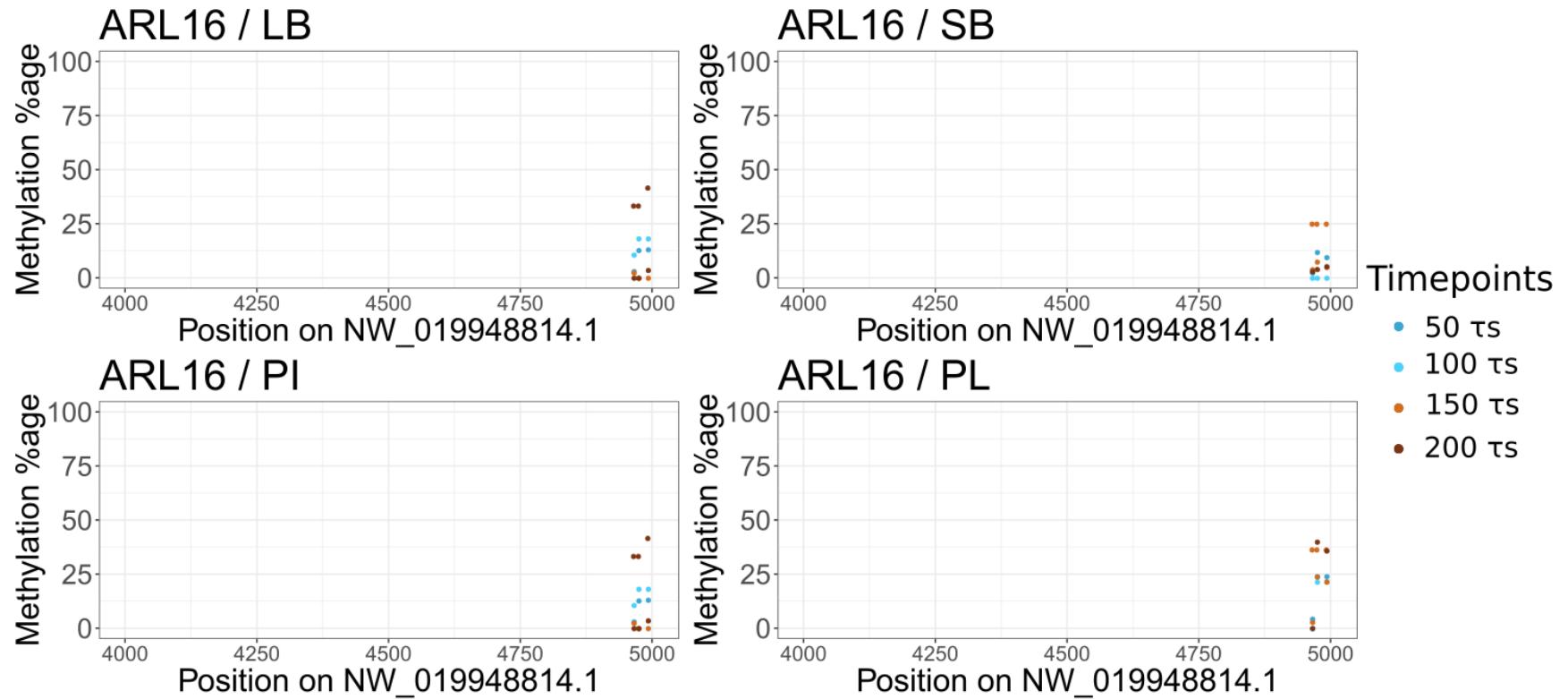


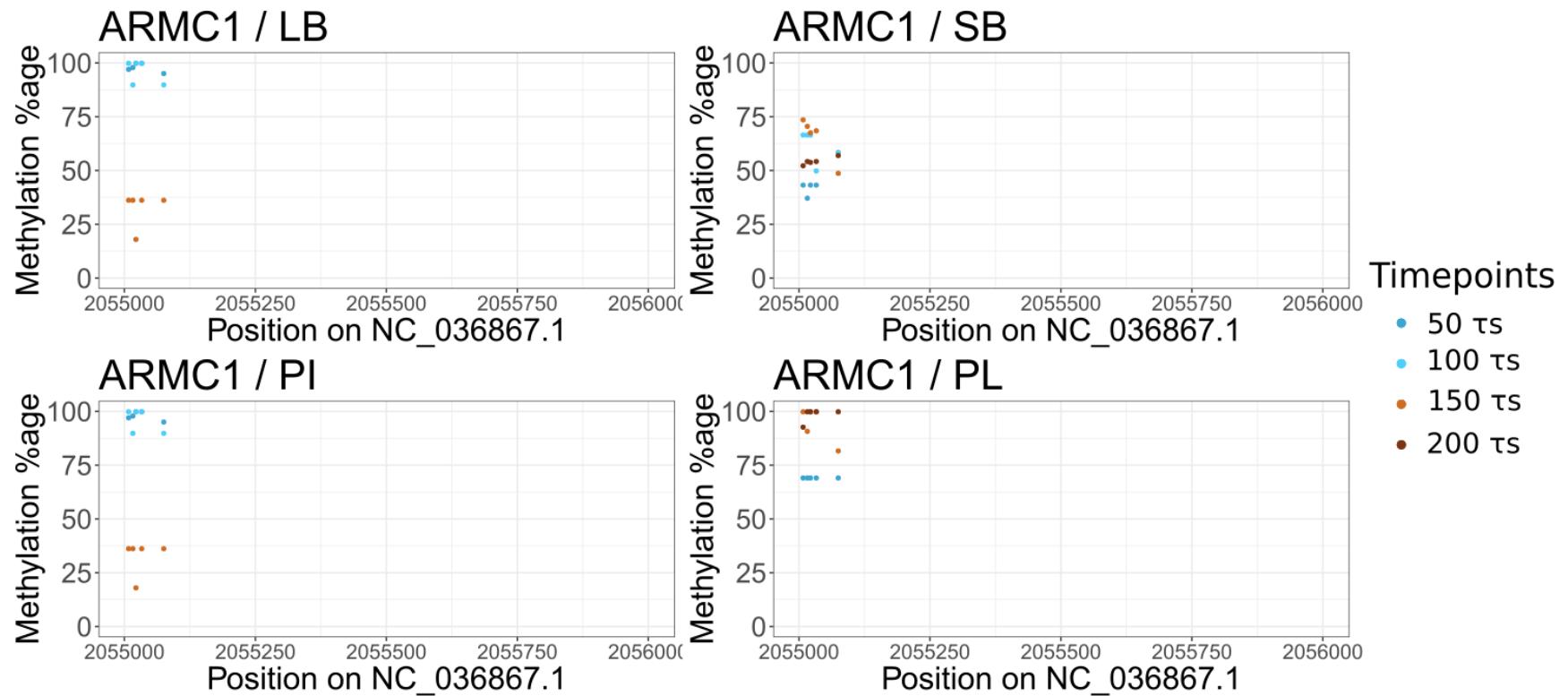
Figure S7: Average methylation of five DMRs located close to tRNA and rRNA sequences for each morph and timepoint.



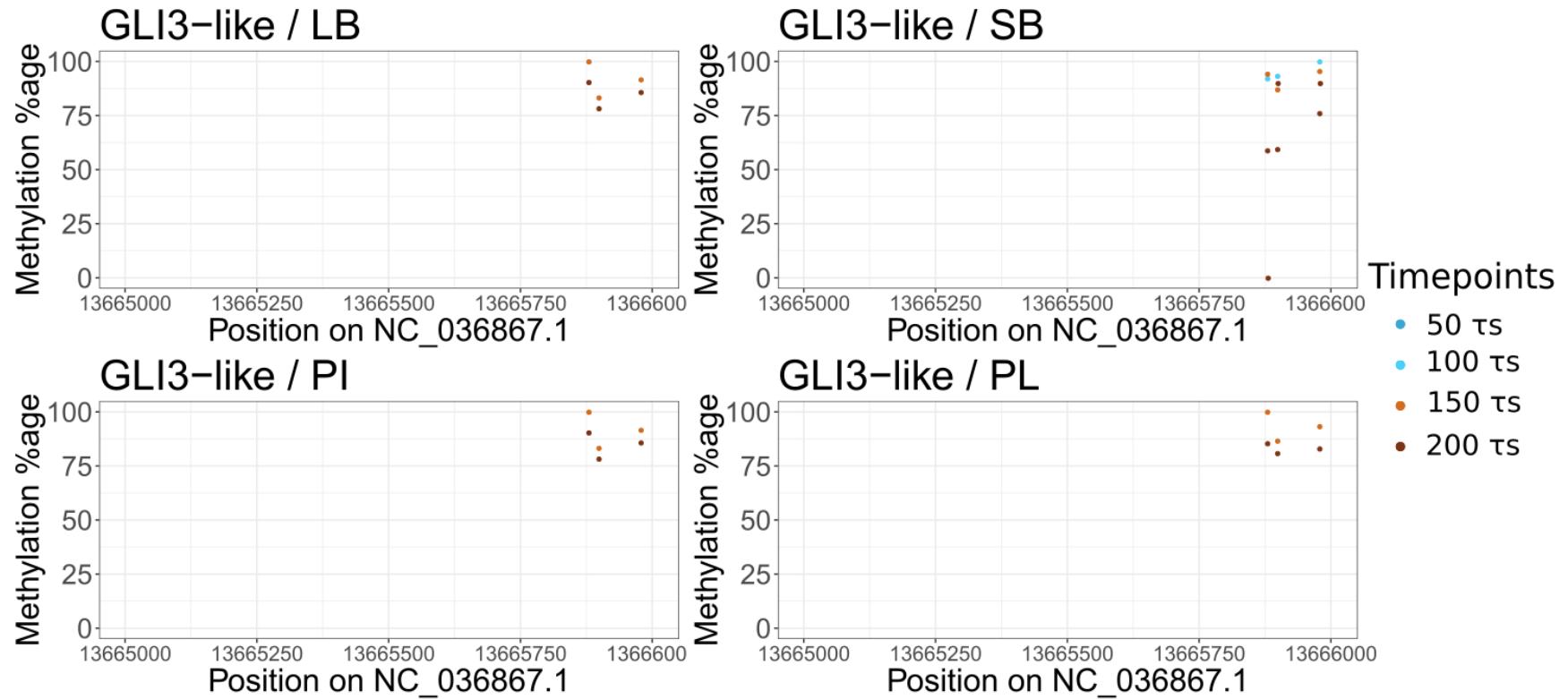
MOLECULAR ECOLOGY



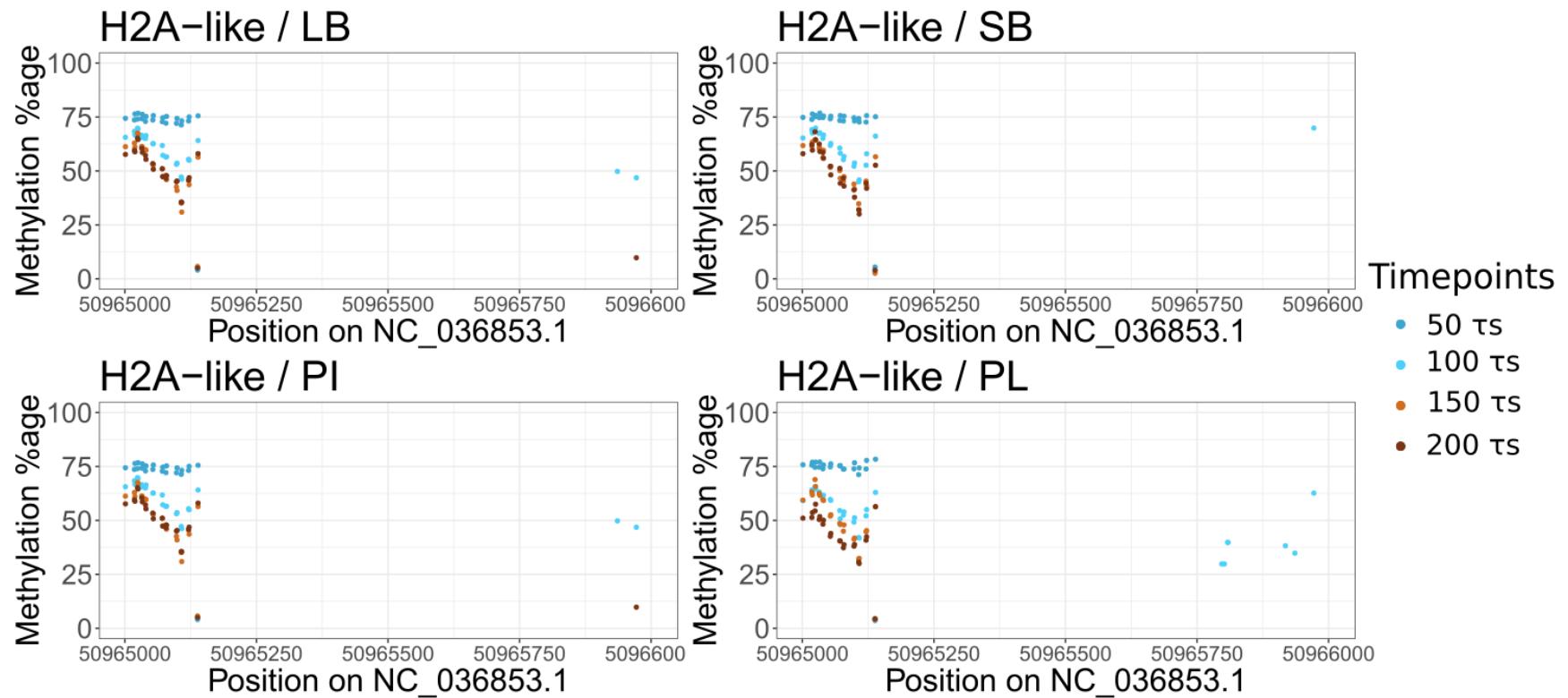
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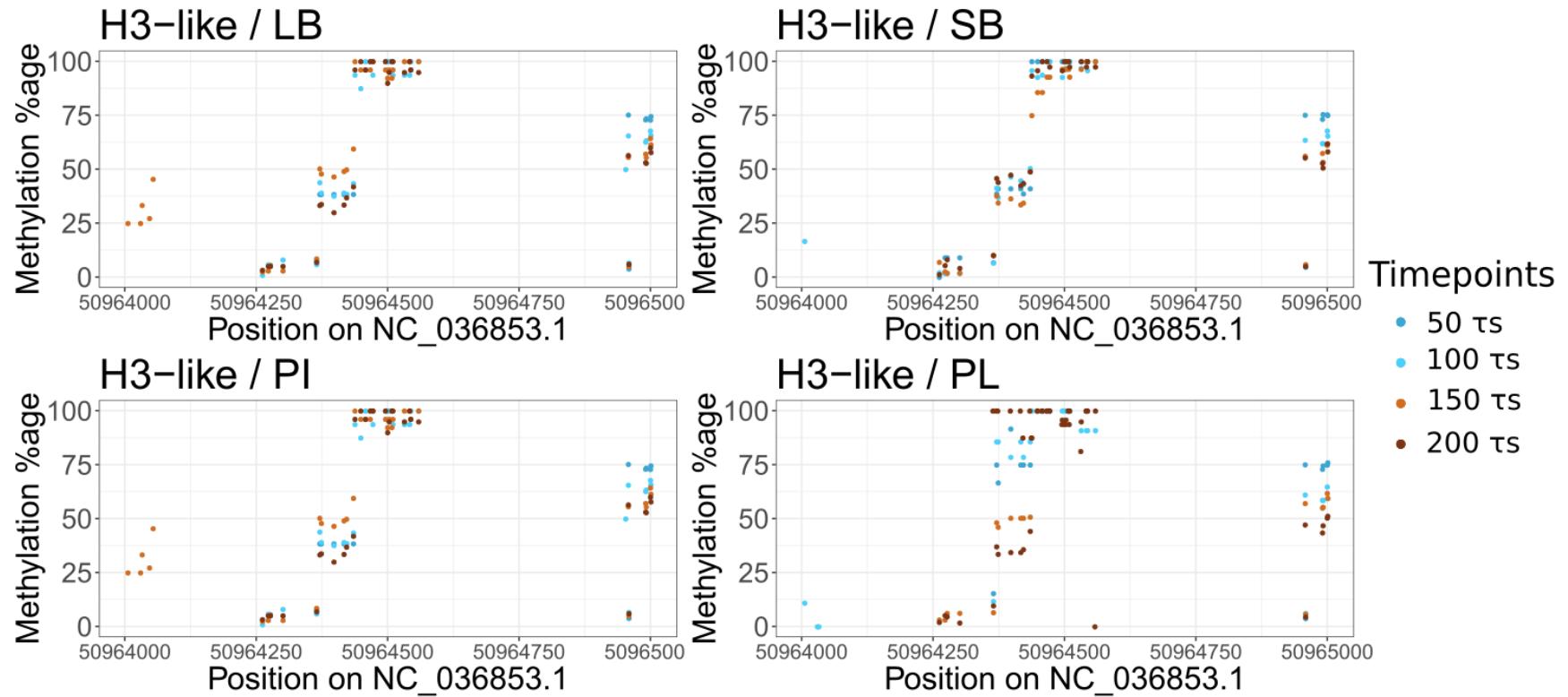
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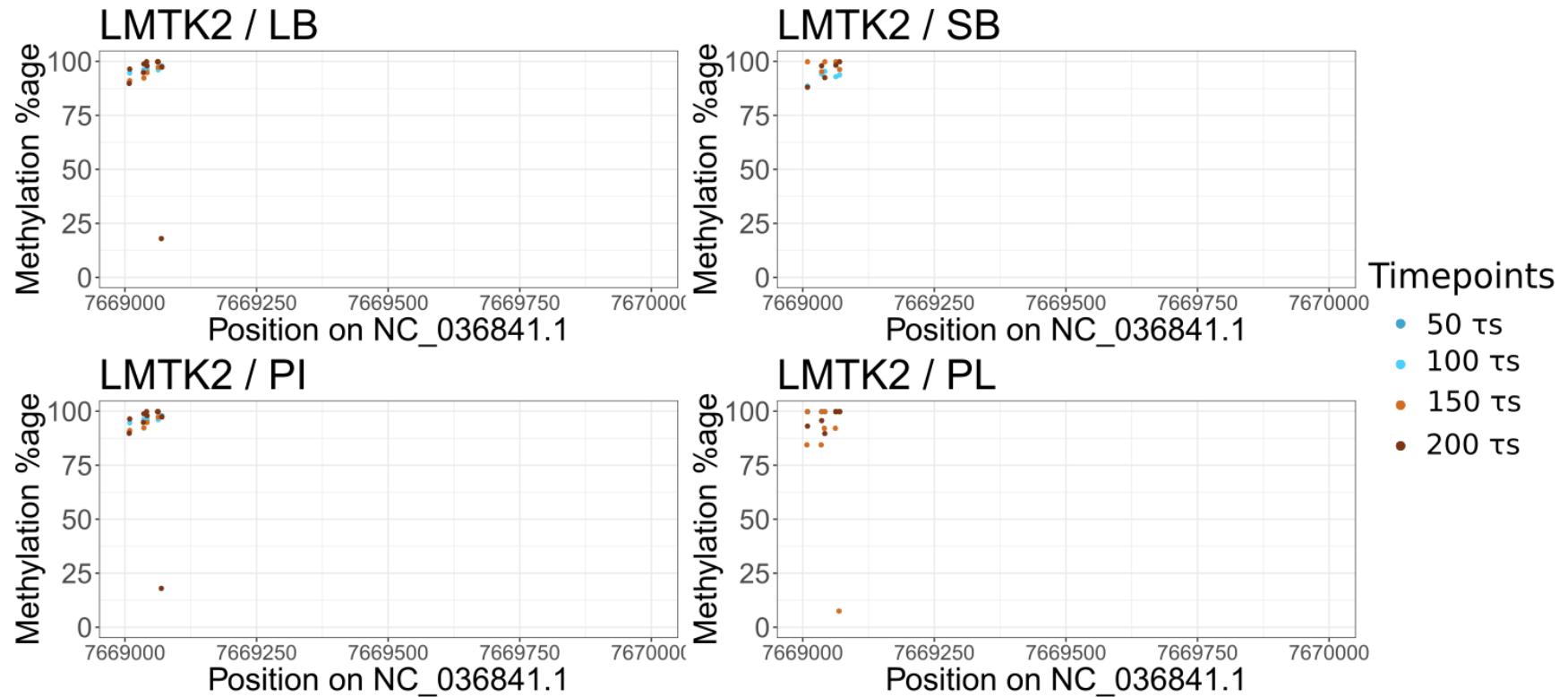
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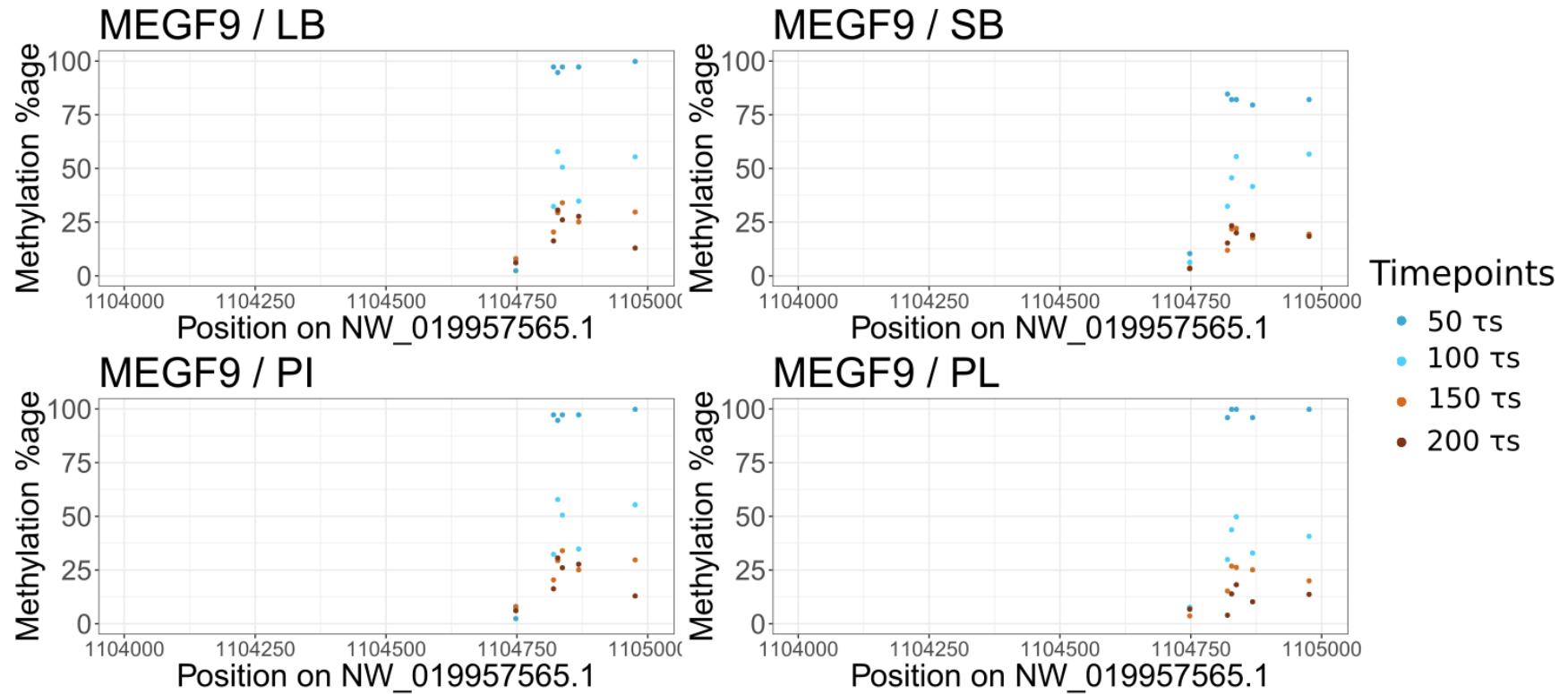
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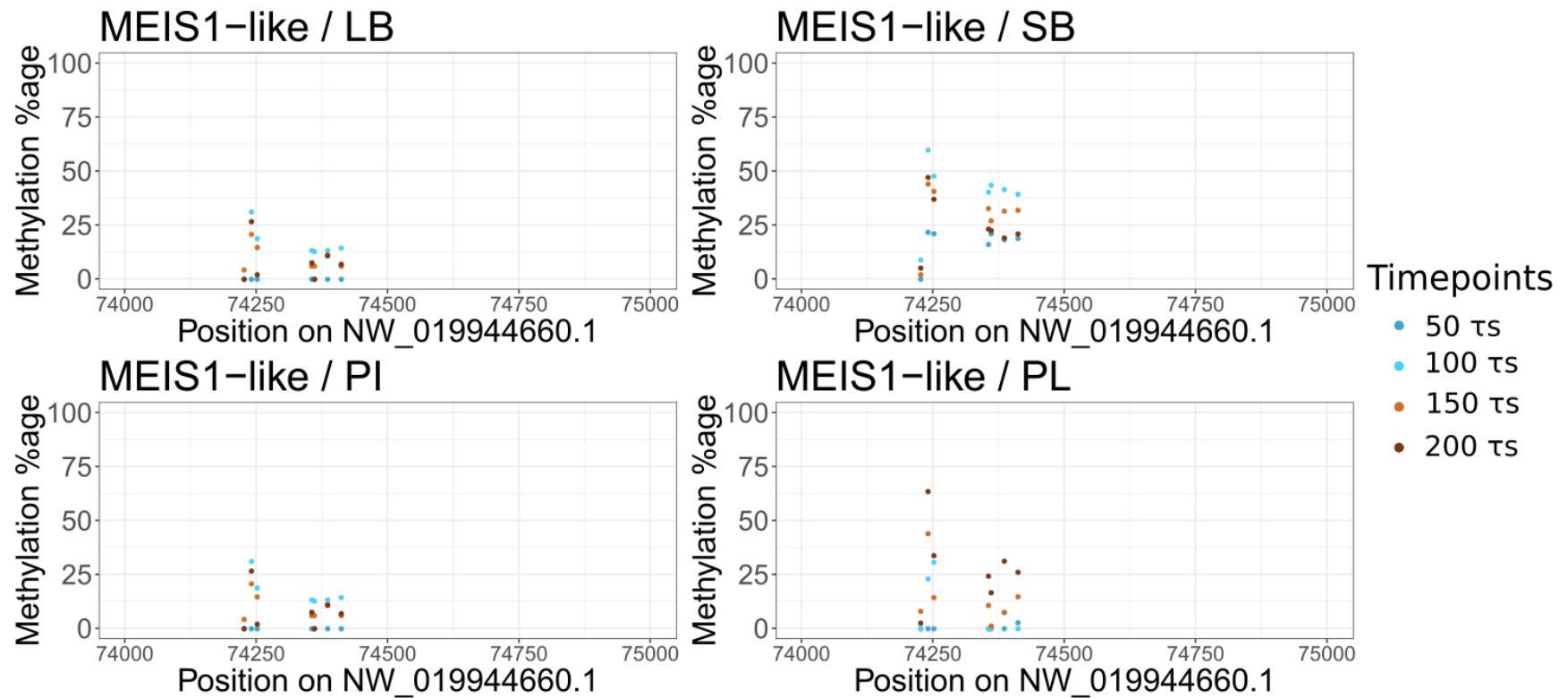
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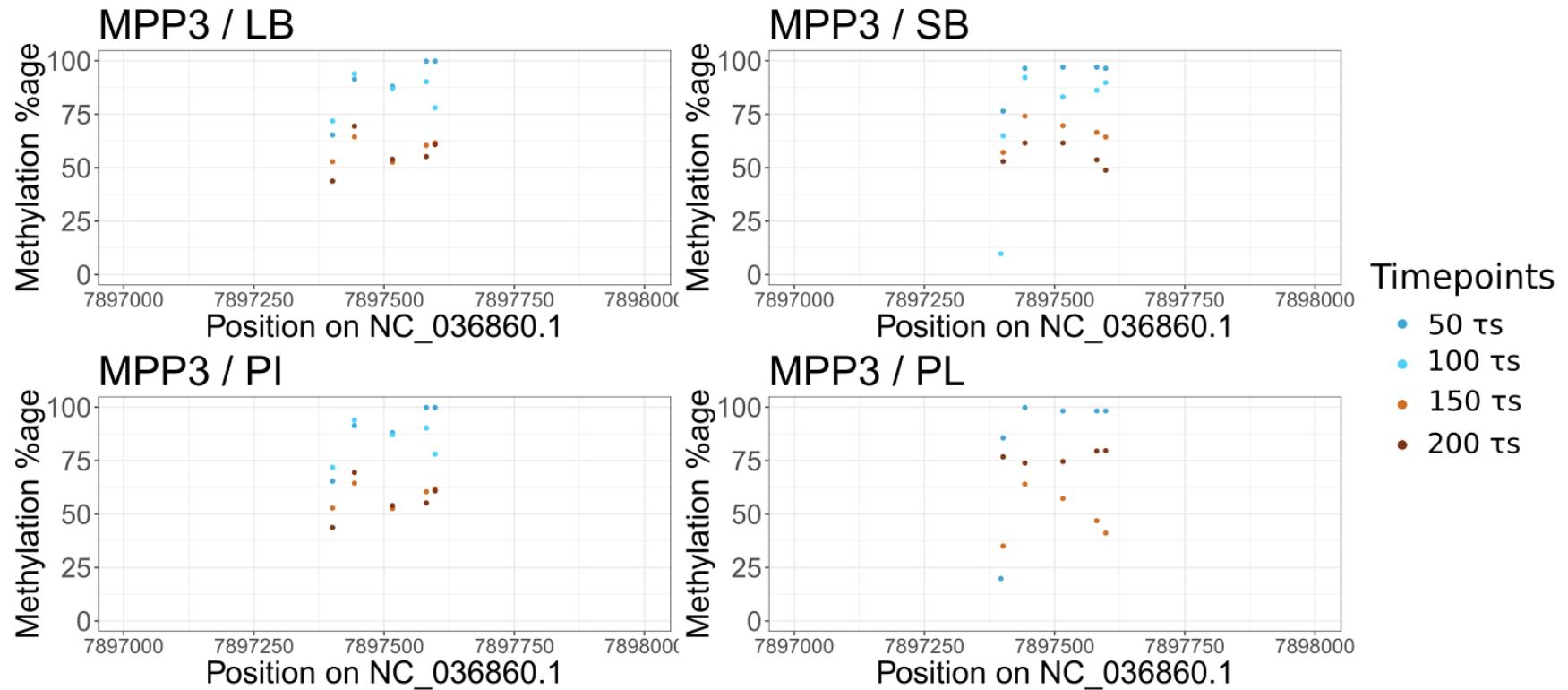
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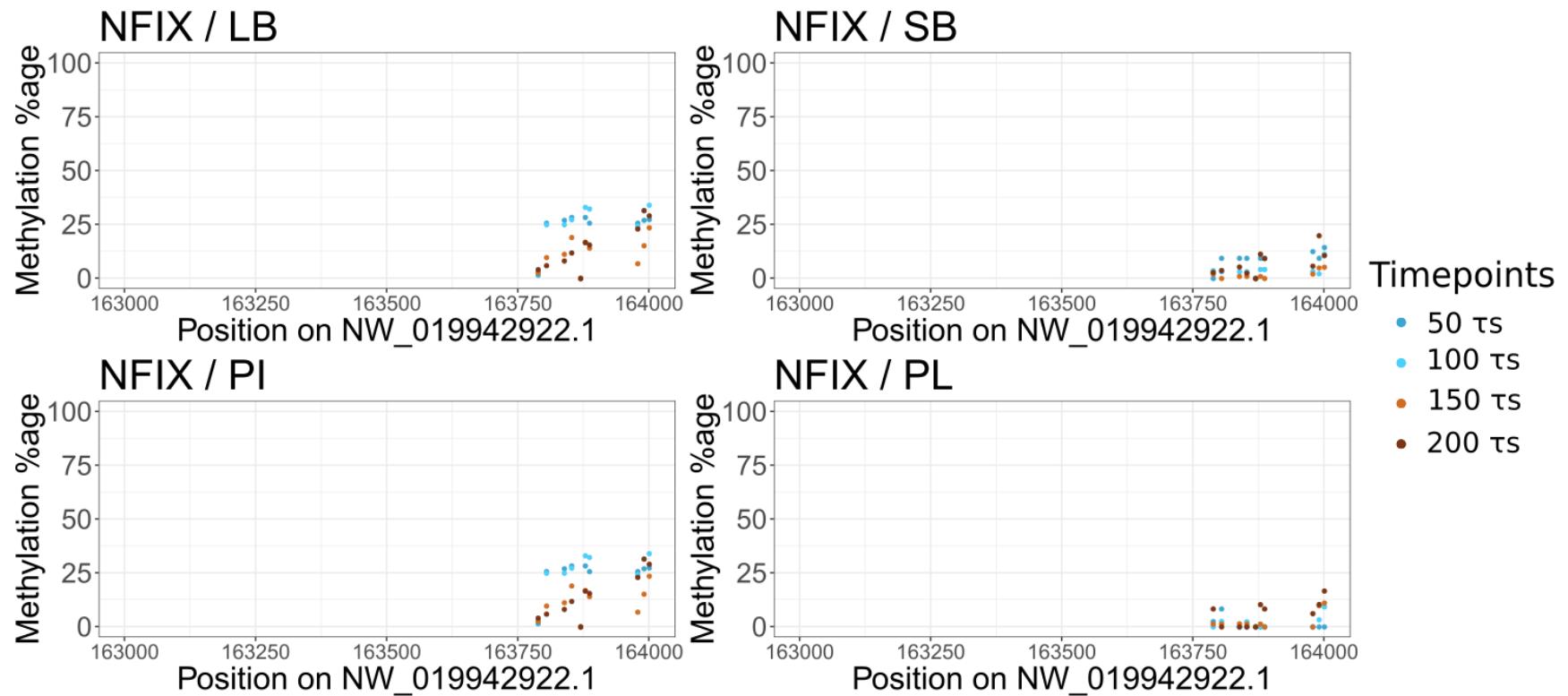
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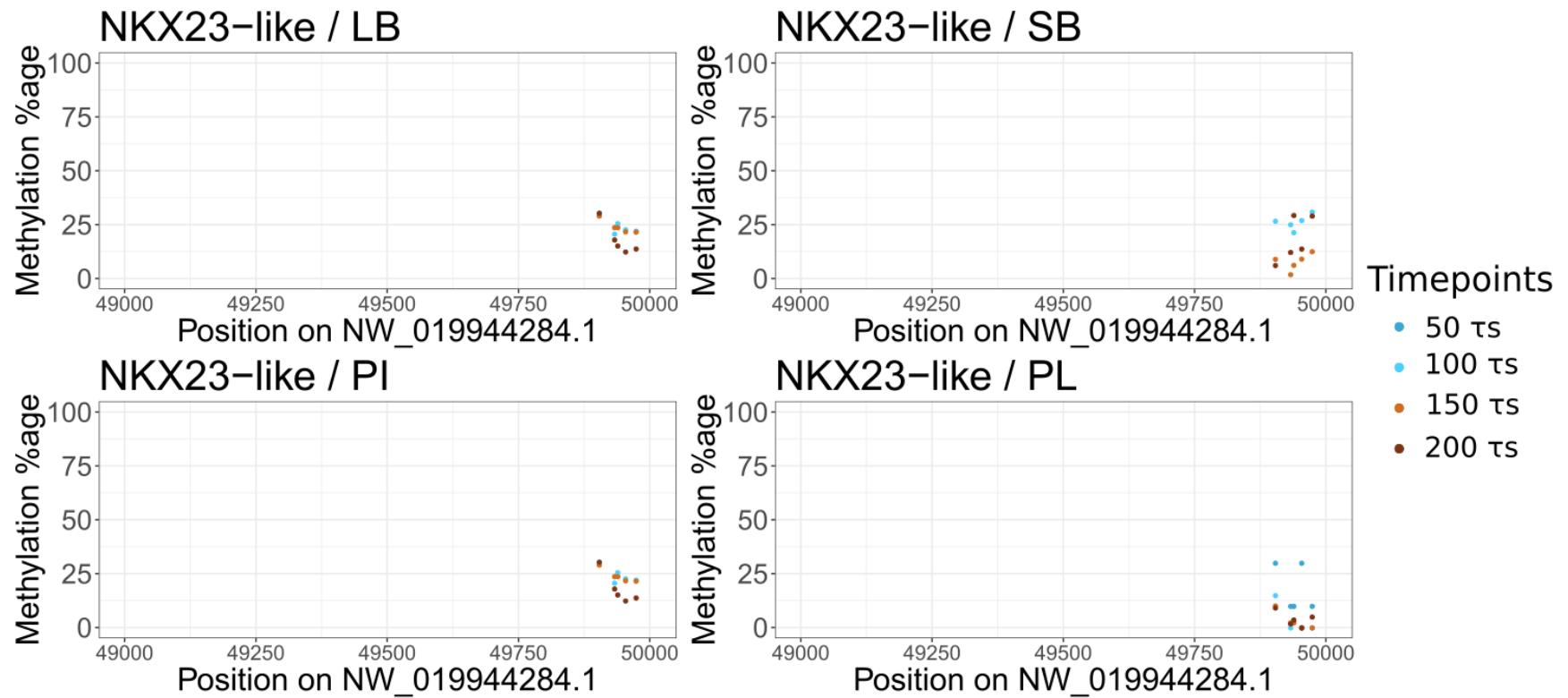
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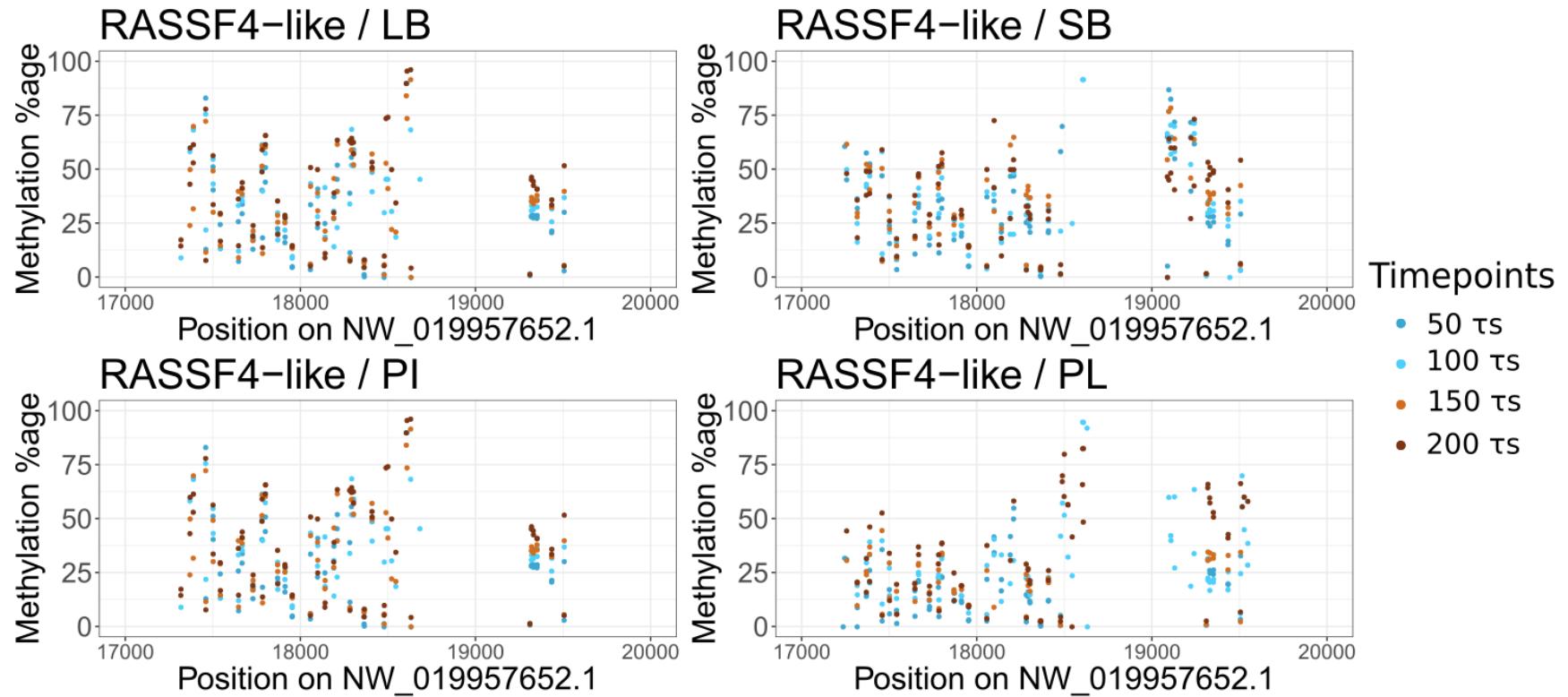
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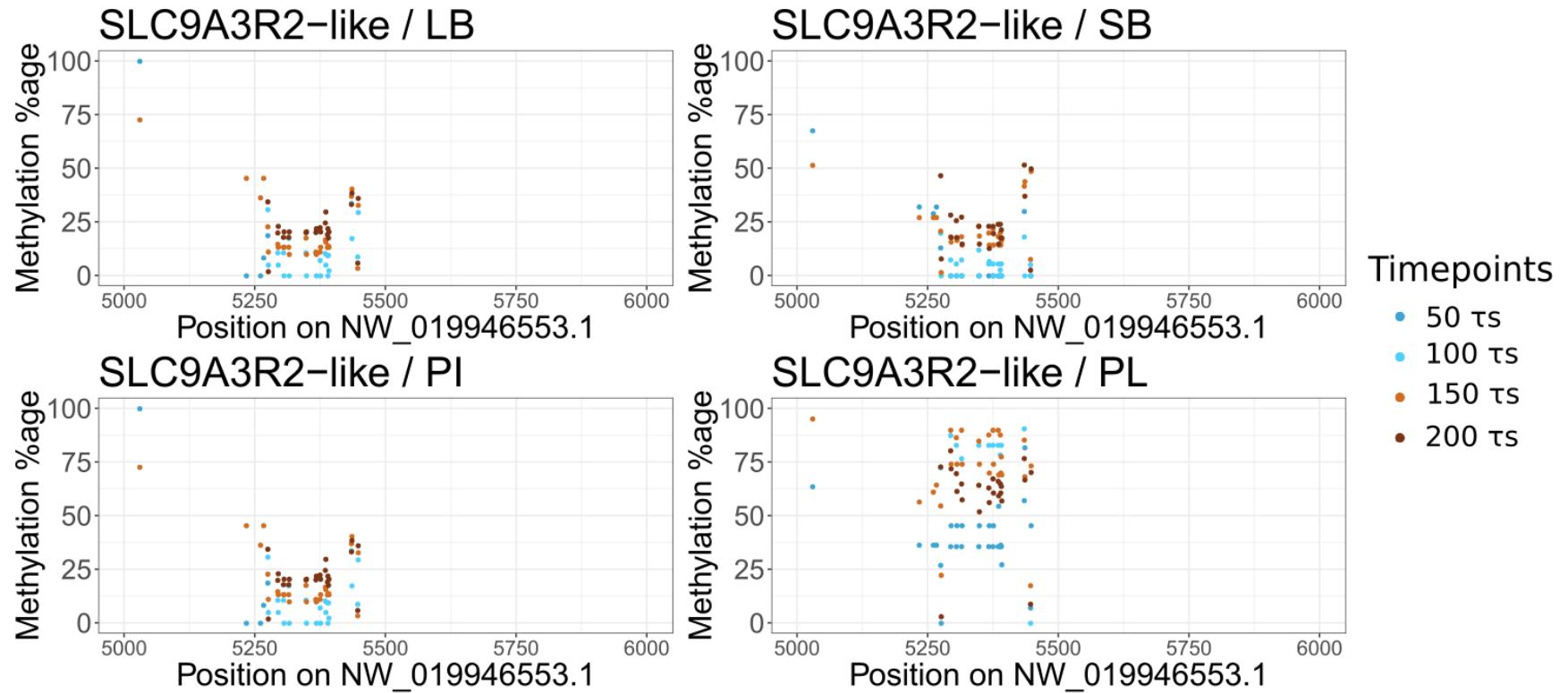
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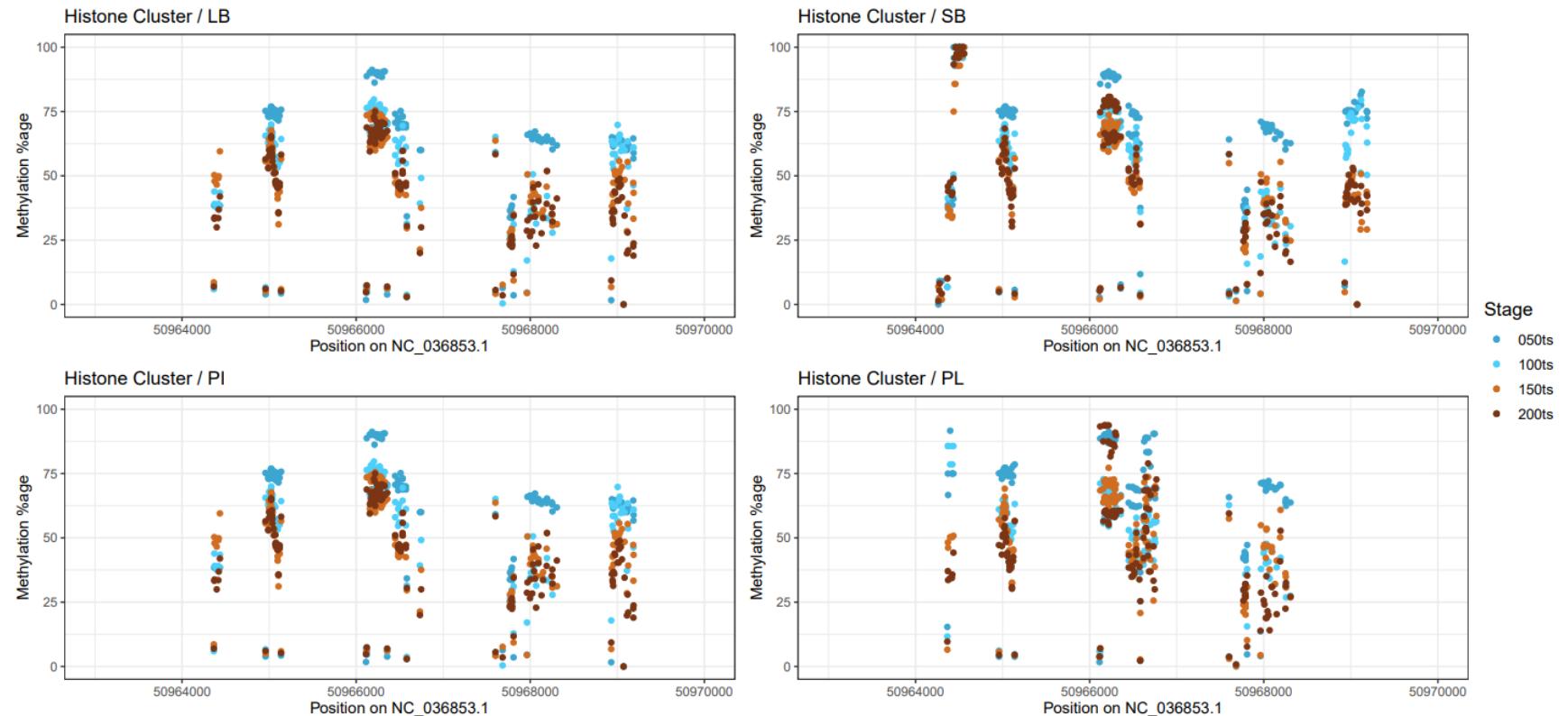


Figure S8: Detailed methylation maps of all 14 DMRs of interest (as well as the histone gene clusters), for each morph and timepoint. Residue-level methylation profiles of regions close to ARHGEF37-like, ARL16, ARMC1, GLI3-like, H2A-like, H3-like, LMTK2, MEGF9, MEIS1-like, MPP3, NKX23-like, NFIX, RASSF4-like, SLC9A3R2-like and the histone gene clusters.

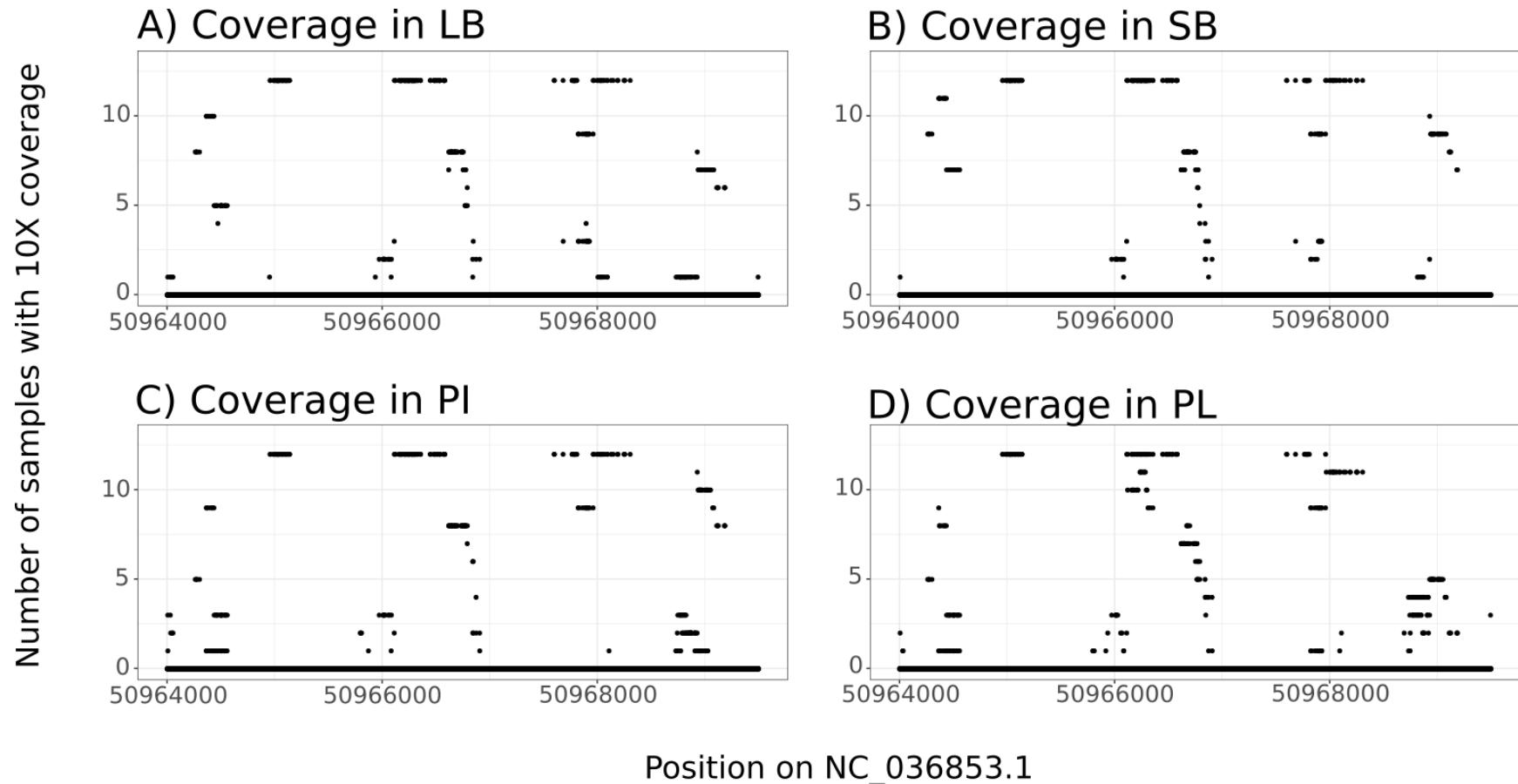


Figure S9: Less coverage of RRBS reads for the PL morph in regions corresponding to histone gene H4. This graph represents the number of samples that have more than 10X coverage for each cytosine in the histone gene cluster. The maximum number of samples is 12 for each morph. H4 is located to the far right of the graph (for reference see Figure 8), and the coverage for the PL morph in this region is less than for other morphs.