

Supplementary material

Supplementary Table S1: Individual sequencing results for PBMC-derived and MBD-captured methyl-DNA from free-ranging females and under human care.

Animal_Id	Status	Batch	Raw single end reads	%GC	Clean single end reads	Mapped reads	Mapping efficiency [%]
F_1	Free-ranging	1	22889851	52	22372654	22372654	83,66
F_2	Free-ranging	1	26349606	54	26216984	26216984	96,08
F_3	Free-ranging	1	32213939	48	32103436	32103436	95,4
F_4	Free-ranging	1	20895459	47	20767583	20767583	95,95
F_5	Free-ranging	1	25034844	56	24631774	24631774	96,78
F_6	Free-ranging	2	40410591	55	39629442	39629442	98,61
F_7	Free-ranging	2	44418720	54	43438663	43438663	98,48
F_8	Free-ranging	2	39272835	55	38211109	38211109	93,04
C_1	Human care	1	27695035	52	27594177	27594177	95,8
C_2	Human care	1	32228340	52	32109179	32109179	96,85
C_3	Human care	1	31035479	52	30948725	30948725	94,73
C_4	Human care	1	25929318	52	25866751	25866751	96,14
C_5	Human care	2	69587963	53	69458113	69458113	95,41
C_6	Human care	2	40415509	54	39625842	39625842	95,95
C_7	Human care	2	62283749	54	60889584	60889584	97,7

Supplementary Table S2: Annotated genes overlapped by DMRs, including their Gene Ontology (GO) terms

Gene ID	Gene name (info STRING)	GOterm_names	GOterm_ID
CFAP299 CSTF3	Cilia and flagella associated protein 299 Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	nucleus, cytoplasm, protein binding nucleus, protein binding, RNA processing, mRNA processing, RNA binding, nucleoplasm, mRNA binding, mRNA cleavage, mRNA polyadenylation, RNA 3'-endprocessing regulation of cell adhesion, cytoplasm, nucleoplasm, cytosol, cell cortex	GO:0005634, GO:0005737, GO:0005515 GO:0005634, GO:0005515, GO:0006396, GO:0006397, GO:0003723, GO:0005654, GO:0003729, GO:0006378, GO:0006379, GO:0031123 GO:0030155, GO:0005737, GO:0005654, GO:0005829, GO:0005938
CYTIP	Cytohesin-interacting protein isoform x1; Cytohesin 1 interacting protein	Golgi apparatus, carbohydrate binding, membrane, integral component of membrane, transferase activity, glycosyltransferase activity, metal ion binding, Golgi apparatus, polypeptide N-acetylgalactosaminyltransferase activity, O-glycan processing, Golgi membrane, polypeptide N-acetylgalactosaminyltransferase activity, protein O-linked glycosylation, polypeptide N-acetylgalactosaminyltransferase activity, Golgi membrane, protein glycosylation, protein O-linked glycosylation via threonine, protein O-linked glycosylation via serine, polypeptide N-acetylgalactosaminyltransferase activity	GO:0005794, GO:0030246, GO:0016020, GO:0016021, GO:0016740, GO:0016757, GO:0046872, GO:0005794, GO:0004653, GO:0016268, GO:0000139, GO:0004653, GO:0006493, GO:0004653, GO:0000139, GO:0006486, GO:0018243, GO:0018242, GO:0004653
<u>GALNT13^c</u>	Polypeptide N-acetylgalactosaminyltransferase 13 isoform x3; Polypeptide N-acetylgalactosaminyltransferase 13		
<u>GLIS3^a</u>	Zinc finger protein glis3 isoform x1; Uncharacterized protein; GLIS family zinc finger 3	nucleus, regulation of transcription by RNA polymerase II, RNA polymerase II transcription regulatory region sequence-specific DNA binding, metal ion binding, DNA binding, negative regulation of transcription by competitive promoter, DNA-binding transcription factor activity, RNA polymerase II-specific, RNA polymerase II cis-regulatory region sequence-specific DNA binding, transcription by RNA polymerase II, DNA-binding transcription repressor activity, RNA polymerase II-specific	GO:0005634, GO:0006357, GO:0000977, GO:0046872, GO:0003677, GO:0043565, GO:0045944, GO:0005515, GO:0000122, GO:0000981, GO:0000978, GO:0006366, GO:0001228, GO:0001227
GPR107	G protein-coupled receptor 107	integral component of membrane, membrane, Golgi apparatus, nucleoplasm, plasma membrane, clathrin-coated vesicle, clathrin-dependent endocytosis, clathrin heavy chain binding, early endosome	GO:0016021, GO:0016020, GO:0005794, GO:0005654, GO:0005886, GO:0030136, GO:0072583, GO:0032050, GO:0005769
<u>KLC1^a</u>	Kinesin light chain 1 isoform x1; Uncharacterized protein; Kinesin light chain 1	protein binding, kinesin complex, cytoplasm, membrane, cytoskeleton, cytoplasmic vesicle, cell projection, microtubule, growth cone, cytosol, motor activity, stress granule disassembly regulation of transcription, DNA-templated, metal ion binding	GO:0005515, GO:0005871, GO:0005737, GO:0016020, GO:0005856, GO:0031410, GO:0042995, GO:0005874, GO:0030426, GO:0005829, GO:0003774, GO:0035617, GO:0006355, GO:0046872
LOC106960912 LOC113594259 LOC113594259 LOC113595181	Zinc finger protein 708-like isoform X1 uncharacterized LOC113594259 uncharacterized LOC113594259 uncharacterized LOC113595181	NA NA NA NA	NA NA NA NA
NRG3	Pro-neuregulin-3, membrane-bound isoform isoform X5; Uncharacterized protein; Neuregulin 3	nervous system development, membrane, integral component of membrane, signaling receptor binding	GO:0007399, GO:0016020, GO:0016021, GO:0005102
<u>SLC9A9^b</u>	Solute carrier family 9 (sodium/hydrogen exchanger), member 9; Belongs to the monovalent cation:proton antiporter 1 (CPA1) transporter (TC 2.A.36) family	proton antiporter activity, proton antiporter activity, integral component of membrane, regulation of pH, sodium ion transport, cation transport, transmembrane transport, antiporter activity, membrane, integral component of membrane, sodium ion transport, ion transport, endosome, protein binding, regulation of intracellular pH, potassium ion transmembrane transport, sodium ion import across plasma membrane	GO:0015299, GO:0015385, GO:0016021, GO:0006885, GO:0006814, GO:0006812, GO:0055085, GO:0015297, GO:0016020, GO:0016021, GO:0006814, GO:0006811, GO:0005768, GO:0005515, GO:0051453, GO:0071805, GO:0098719
<u>TTL1^{a,b}</u>	Low quality protein; probable tubulin polyglutamylase ttl1; Tubulin tyrosine ligase-like family, member 1	cytoplasm, nucleotide binding, ATP binding, cytoskeleton, cellular protein modification process, microtubule, ligase activity, protein polyglutamylation, extracellular region, microtubule cytoskeleton organization, cilium, tubulin binding, tubulin-glutamic acid ligase activity, immune response in nasopharyngeal-associated lymphoid tissue, epithelial cilium movement involved, sperm axoneme assembly, cerebellar Purkinje cell differentiation, flagellated sperm motility, axoneme assembly, mucociliary clearance, regulation of blastocyst development, ciliary basal body	GO:0005737, GO:0000168, GO:0005524, GO:0005856, GO:0006484, GO:0005874, GO:0016874, GO:0018095, GO:0005576, GO:0000226, GO:0005929, GO:0015631, GO:0070740, GO:0002365, GO:0003351, GO:0007288, GO:0021702, GO:0030317, GO:0035082, GO:0120197, GO:0120222, GO:0036064
<u>WARS2^b</u>	Tryptophanyl tRNA synthetase 2, mitochondrial; Belongs to the class-I aminoacyl-tRNA synthetase family	ATP binding, nucleotide binding, aminoacyl-tRNA ligase activity, tRNA aminoacylation for protein translation, tryptophan-tRNA ligase activity, tryptophanyl-tRNA aminoacylation, translation, nucleoplasm, plasma membrane, mitochondrion, mitochondrial matrix, ligase activity, mitochondrial tryptophanyl-tRNA aminoacylation, vasculogenesis	GO:0005524, GO:0000168, GO:0004812, GO:0006418, GO:0004830, GO:0006436, GO:0006412, GO:0005854, GO:0005886, GO:0005739, GO:0005759, GO:0016874, GO:0070183, GO:0001570

Genes in bold are of functional interest in a: immune function, b: energy balance, c: homeostasis (ion transporter). Gene ontologies (GOterms) are listed in supplementary table S2. 1: DMR overlapping intron 1. Genes in bold and underlined have additional biological relevant criteria.