

different sense oligonucleotides for TVN-PAT assays confirmed the location of the main polyadenylation site for genes that were assessed by ePAT. No amplicon was observed when reverse-transcriptase was omitted. (D) cDNA species missing a significant poly(A) tail are not detected by ePAT. Degradation of poly(A) tails may result in decreased intensity of bands as well as appearance of smears.

References

1. Proudfoot, N.J. Ending the message: poly(A) signals then and now. *Genes Dev* **2011**, *25*, 1770-1782, doi:10.1101/gad.17268411.
2. Sheets, M.D.; Ogg, S.C.; Wickens, M.P. Point mutations in AAUAAA and the poly (A) addition site: effects on the accuracy and efficiency of cleavage and polyadenylation in vitro. *Nucleic Acids Res* **1990**, *18*, 5799-5805, doi:10.1093/nar/18.19.5799.
3. Beilharz, T.H.; Preiss, T. Transcriptome-wide measurement of mRNA polyadenylation state. *Methods* **2009**, *48*, 294-300, doi:10.1016/j.ymeth.2009.02.003.

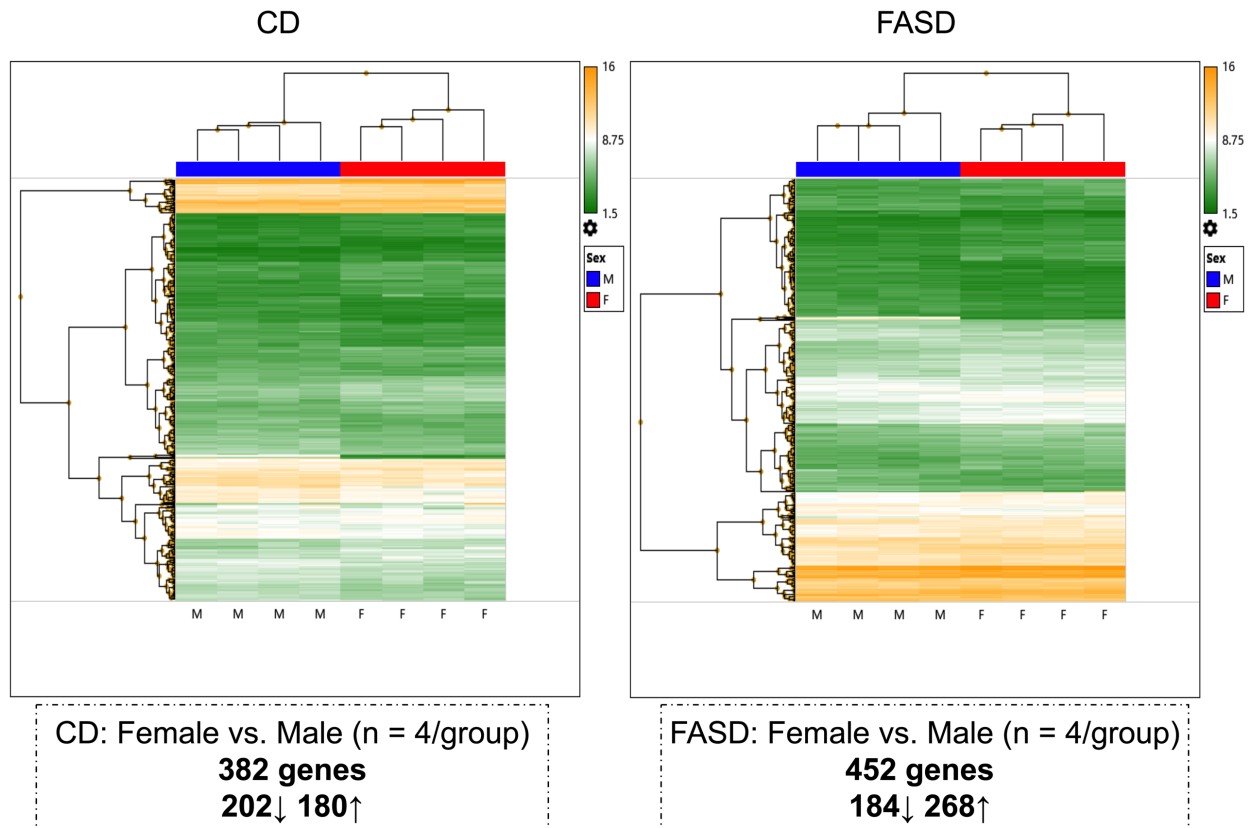


Figure S2. Hierarchical clustering showing distinct sex expression pattern in P30 cortex. 382 genes (202 down-regulated, 180 up-regulated) were differentially expressed in CD females compared to CD males, and 452 genes (184 down-regulated, 268 up-regulated) were differentially expressed in FASD females compared to FASD males.

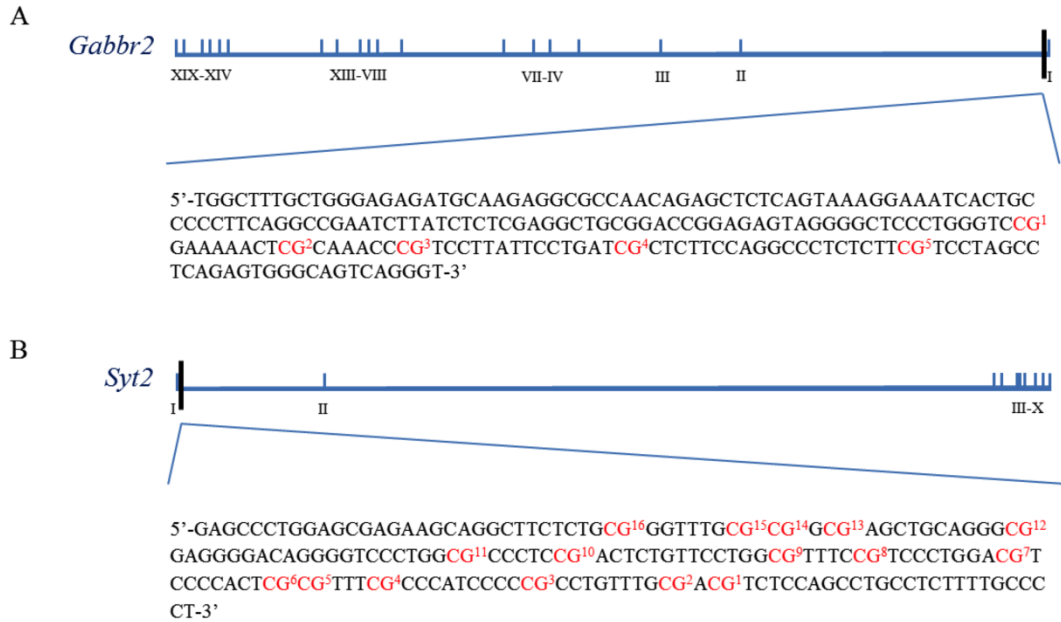


Figure S3. Schematic representation of CpGs analyzed by quantitative bisulfite pyrosequencing. (A) CpGs 1 to 5 of *Gabbr2* are included between positions 46990041-46990248 of genome assembly GRCm39 (mm39) from Genome Reference Consortium. Numbering of CpGs was arbitrarily assigned and matches the numbering in Figure 3A. (B) CpGs 1 to 16 are included between positions 134574702-134574775 of genome assembly GRCm39 (mm39) from Genome Reference Consortium. Numbering of CpGs was arbitrarily assigned and matches the numbering in Figure 3B and Figure 10.

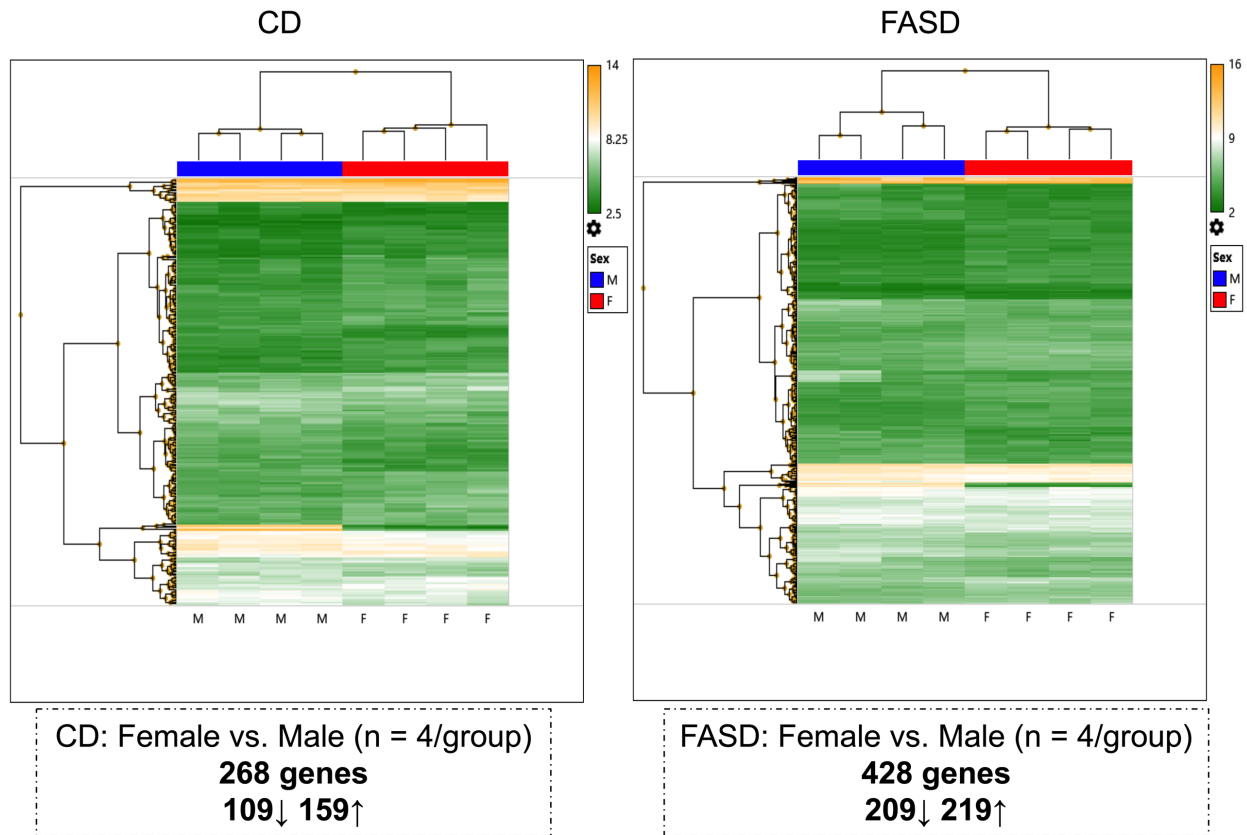


Figure S4. Hierarchical clustering showing distinct sex expression pattern in E17.5 cerebrum. 268 genes (109 down-regulated, 159 up-regulated) were differentially expressed in CD females compared to CD males, and 428 genes (209 down-regulated, 219 up-regulated) were differentially expressed in FASD females compared to FASD males.

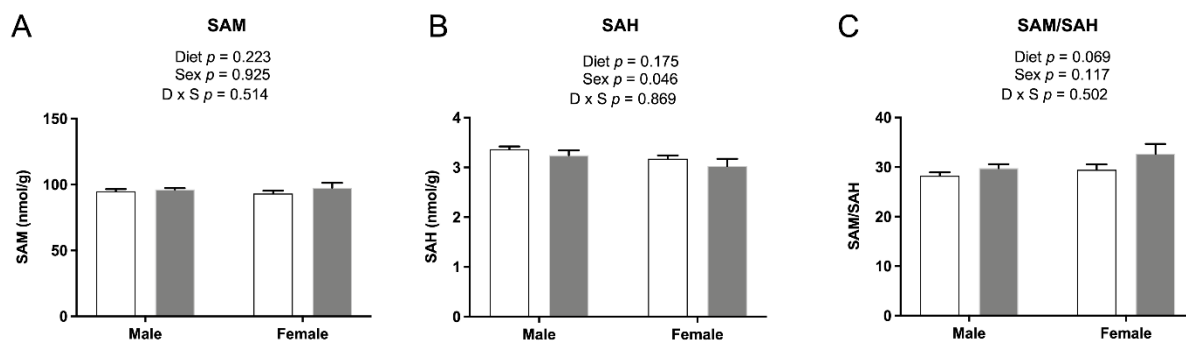


Figure S5. Concentration of methyl metabolites in E17.5 cerebrum. (A) SAM, (B) SAH, (C) SAM/SAH ratio. Values are means \pm SEM of 7-8 per group. p values from 2-factor ANOVA are indicated at the top of each graph. CD: control diet, FASD: folic acid supplemented diet, D: diet, S: sex, D x S: diet x sex interaction. SAM, S-adenosylmethionine, SAH, S-adenosylhomocysteine.

Table S1. Composition of Control Diet (CD) and Folic Acid Supplemented Diet (FASD).

Diet Composition	CD (TD.01369) (2mg/kg Folic Acid) (g/kg)	FASD (TD.08278) (10mg/kg Folic Acid) (g/kg)
L-Alanine	3.5	3.5
L-Arginine HCl	12.1	12.1
L-Asparagine	6.0	6.0
L-Aspartic Acid	3.5	3.5
L-Cystine	3.5	3.5
L-Glutamic Acid	40.0	40.0
Glycine	23.3	23.3
L-Histidine HCl, monohydrate	4.5	4.5
L-Isoleucine	8.2	8.2
L-Leucine	11.1	11.1
L-Lysine HCl	18.0	18.0
L-Methionine	3.3	3.3
L-Phenylalanine	7.5	7.5
L-Proline	3.5	3.5
L-Serine	3.5	3.5
L-Threonine	8.2	8.2
L-Tryptophan	1.8	1.8
L-Tyrosine	5.0	5.0
L-Valine	8.2	8.2
Sucrose	349.53	349.422
Corn Starch	150.0	150.0
Maltodextrin	150.0	150.0
Soybean Oil	80.0	80.0
Cellulose	30.0	30.0
Mineral Mix, AIN-93-M-MX	35.0	35.0
Calcium Phosphate, monobasic, monohydrate	8.2	8.2
Succinylsulfathiazole	10.0	10.0
Vitamin Mix, AIN-93-VX	10.0	10.0
Choline Bitartrate	2.5	2.5
Vitamin K, menadione sodium bisulfite	0.05	0.05
tert-Butylhydroquinone (TBHQ), antioxidant	0.02	0.02
Folic Acid	-	0.008
Red food color	-	0.1

Table S2. Oligonucleotide primer sets used for qRT-PCR analysis (including normalizer genes) and PCR conditions.

Gene	Sense Primer	Antisense primer	Amplicon size (bp)	Annealing temperature (°C)	Primer molarity (μM)
<i>Actb</i>	CTGACGGCCAGGTCATCACTA	TAGTTTCATGGATGCCACAGGAT	105	60	0.4
<i>Angpt2</i>	AGAGTCCAACCTACAGGATTCACC	GACCACATGCGTCAAACCAC	170	60	0.6
<i>Arnt</i>	TGCACAGGCTACATCAAGGC	GGGAGAACTAGTTACCTGCAGCC	126	60	0.6
<i>B2m</i>	ATGCTATCCAGAAAACCCCTCAA	GCGGGTGGAAGTGTGTACG	102	60	0.4
<i>Chrm1</i>	GGTCCCATGGAAACCCTGAAT	GCCAGCAGCCTCATTCAATC	77	60	0.4
<i>Colla1</i>	CTGACGCATGGCCAAGAAGA	CCCTTGGGTCCCTCGACTC	260	60	0.6
<i>Col4a2</i>	CGTGACAAATACCGGGGTGA	GTCCGTAAAAACCGAGCCCT	178	60	0.6
<i>Eef2</i>	TGTCAGTCATCGCCCATGTG	CATCCTTGCGAGTGTCACTGA	123	60	0.6
<i>Esys1</i>	CTACCCAGGGGCATTATCCG	GGGATCCGATTTGCCCTCAA	99	60	0.4
<i>Gabbr2</i>	CTTCTTCGGAGTCACGGGTC	GTTGTACTCGCCGACCTTCA	109	60	0.4
<i>Gabrb1</i>	TCTTTTCCCGTGATGGTTGC	CGGGGGCCCTCCAAAG	141	60	0.6
<i>Gabrd</i>	TCAAATCGGCTGGCCAGTTCCC	GCACGGCTGCCTGGCTAATCC	147	60	0.4
<i>Gapdh</i>	CAGGAGCGAGACCCCACTAACAT	AAGACACCAGTAGACTCCACGAC	74	62	0.4
<i>Grina</i>	CCCTACCCTCAAGGAGGCTAC	CTGGCGAATGTTCTTGTTCC	192	60	0.6
<i>Htr1a</i>	CAACAACACCACAACGTCCC	GCTGAAGGTCACGTTGGAGA	76	60	0.4
<i>Igf1</i>	CTGGACCAGAGACCCTTTGC	CTCCGAATGCTGGAGCCATA	112	60	0.4
<i>Nono</i>	AAAGCAGGCGAAGTTTTTCATTC	ATTTCCGCTAGGGTTCGTGTT	77	60	0.6
<i>Nrp1</i>	CAGTGGCACAGGTGATGACT	CCGTATGTCGGGAAGTCTGA	108	60	0.6
<i>Ogt</i>	TCATCACTTTGAAAAGGCTGTC	AAGGCACGAAGATAAGCTGC	123	60	0.6
<i>Parn</i>	CCCATGCACTGGGTTCCAA	TCCTGCTCTCTCCTTTTGCG	156	60	0.6
<i>Rnh1</i>	CCAGATACAGTGCTGCGTGA	AGGCTGCTGCAACCACTATT	68	60	0.6
<i>Sdha</i>	GCTGTGGCCCTGAGAAAGATC	ATCATGGCCGTCTCTGAAATTC	100	60	0.4
<i>Sfrp1</i>	TACCACGGAAGCCTCTAAGC	GGCCTCTGACTCAACTCGT	73	60	0.6
<i>Sfrp4</i>	AGCCCTGATCGGTGCAAGT	ATTGCAACCACTCCTCTGGAC	117	60	0.6
<i>Slc32a1</i>	CCATTCAGGGCATGTTTCGTG	GAGGAACAACCCAGGTAGC	71	60	0.6
<i>Syt2</i>	GGCGGCGAGATGTGATACT	GGGTGTCTATGATGGCATCAA	69	60	0.4
<i>Tbp</i>	ACCGTGAATCTTGGCTGTAAAC	GCAGCAAATCGCTTGGGATTA	86	60	0.6
<i>Tfrc</i>	GTTTCTGCCAGCCCCCTTATTAT	GCAAGGAAAGGATATGCAGCA	152	60	0.6
<i>Tph2</i>	GCTACCTGAGCCCAAGAGAC	GCATGTATCTGGTTCCGGGG	113	60	0.4
<i>Tubal1</i>	CCAGGGCTTCTTGGTTTTC	CTACCATGAAGGCACAATC	218	60	0.6

<i>Ubc</i>	AGCCCAGTGTTACCACCAAG	ACCCAAGAACAAGCACAAGG	97	60	0.6
<i>Vegfa(120aa)</i>	CTTCCTACAGCACAGCAGATG	TGGCTTGTCACATTTTCTGGC	73	60	0.6
<i>Vegfa(164aa)</i>	AGCACAGCAGATGTGAATGCAG	AGGCTCACAGTGATTTTCTGGC	65	60	0.6
<i>Ywhaz</i>	TGCTGGTGATGACAAGAAAGGA	TGAGGGCCAGACCCAGTCT	119	60	0.4

Table S3. Full gene names.

Abbreviation	Full name
<i>Actb</i>	actin beta
<i>Arnt</i>	aryl hydrocarbon receptor nuclear translocator
<i>B2m</i>	beta-2-microglobulin
<i>Chrm1</i>	cholinergic receptor muscarinic 1
<i>Colla1</i>	collagen type I alpha 1
<i>Col4a2</i>	collagen type IV alpha 2
<i>Eef2</i>	eukaryotic translation elongation factor 2
<i>Esyt1</i>	extended synaptotagmin 1
<i>Gabbr2</i>	gamma-aminobutyric acid (GABA) B receptor 2
<i>Gabbr1</i>	gamma-aminobutyric acid type A receptor subunit beta1
<i>Gabrd</i>	gamma-aminobutyric acid type A receptor delta subunit
<i>Gapdh</i>	glyceraldehyde-3-phosphate dehydrogenase
<i>Grina</i>	glutamate ionotropic receptor NMDA type subunit associated protein 1
<i>Htr1a</i>	5-hydroxytryptamine receptor 1A
<i>Igf1</i>	insulin like growth factor 1
<i>Nono</i>	non-POU domain containing octamer binding
<i>Nrp1</i>	neuropilin 1
<i>Ogt</i>	O-linked N-acetylglucosamine (GlcNAc) transferase
<i>Parn</i>	poly(A)-specific ribonuclease
<i>Rnh1</i>	ribonuclease inhibitor 1
<i>Sdha</i>	succinate dehydrogenase complex flavoprotein subunit A
<i>Sfrp1</i>	secreted frizzled-related protein 1
<i>Sfrp4</i>	secreted frizzled-related protein 4
<i>Slc32a1</i>	solute carrier family 32 member 1
<i>Syt2</i>	synaptotagmin 2
<i>Tbp</i>	TATA-box binding protein
<i>Tfrc</i>	transferrin receptor
<i>Tph2</i>	tryptophan hydroxylase 2
<i>Tuba1a</i>	tubulin alpha 1A
<i>Ubc</i>	ubiquitin C
<i>Vegf</i>	vascular endothelial growth factor
<i>Ywhaz</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta

Table S4. Oligonucleotide combinations used for quantitative bisulfite pyrosequencing methylation analysis of *Gabbr2* and *Syt2* genes in the genomic segments described in Figure S3, as well as for *Chrm1*, *Igf1*, *Sfrp1* and *Sfrp4* genes.

Oligonucleotide sequence ^a and orientation ^b		Amplified segment	Amplicon size (bp)
TGGTTTTGTTGGGAGAGATGTAAGA	(S)	Mouse <i>Gabbr2</i> promoter region	208
5'Biot- ACCCTAACTACCCACTCTAAACTA	(A)		
GAGGATAGGAGAGTAGGGGT	(SEQ1)		
TTTTTGGGTAGGAAAAATT	(SEQ2)		
5'Biot- AAACCCTAAAACCAAAAACAACTTCTCTAC	(S)	Mouse <i>Syt2</i> promoter region	183
AGGGGTAAAAGAGGTAGGTTG	(A)		
CCACAATATTTATTTAAACAATTC	(SEQ1)		
AAATAGGAGGGGGATGGG	(SEQ2)		
GTTTAGGGAAGGAAAAGTTAGGAATAGAGT	(SEQ3)		
TGTTTTTTTTTTTTGTTGTGAGGGAGTTAAA	(S)	Mouse <i>Chrm1</i> promoter region	107
5'-biot-AAACCAACCCTCTAAATCTAATCCAAATTAA	(A)		
TTTGTTTGAAAATGATATATTGG	(SEQ1)		
ATTGGGTAAGTGGTTGGTAGTAT	(S)	Mouse <i>Igf1</i> promoter region	174
5'biot-ACCTTCTTTCATAATTCACCTTCTTATCT	(A)		
GTTGGTAGTATGGTTTAAG	(SEQ1)		
GGAGTTTTGATTTTTTGTGTA	(SEQ2)		
ATGGGTAGGTTGAATTTAGGG	(S)	Mouse <i>Sfrp1</i> promoter region	161
5'biot-CTAATACCCACATAATCAATACTCTTCT	(A)		
ATTTAGGGAGTTTTTTTAAATT	(SEQ1)		
TGTTTGTGGTTGTGTTTGTAGGTGA	(SEQ2)		
GTAGAATTATGGTTTTTGGTTGTGG	(S)	Mouse <i>Sfrp4</i> promoter region	137
5'biot-TCCCCTAACCTAACTCAACAACCTTA	(A)		
TGGAGAGGTAGAGATGATGT	(SEQ1)		
TGTAGGAGAGGTTGGGGGTG	(SEQ2)		

^a 5'Biot- designates a 5'-biotinylated oligonucleotide.

^b (S), sense PCR primer; (A), antisense PCR primer; (SEQ1), (SEQ2) and (SEQ3), sequencing primer, same polarity as the non-biotinylated PCR primer.

Table S5. Oligonucleotide primer sets used for ePAT analysis of polyadenylated mRNAs.

Oligonucleotide ^(a)	Sequence	Orientation ^(b)
PAT anchor primer	GCGAGCTCCGCGGCCGCGTTTTTTTTTTTTT	(A)
TVN anchor primer	GCGAGCTCCGCGGCCGCGTTTTTTTTTTTTTVN	(A)
<i>Eef2</i> - 141 bp	GTGGGGTAAGTGCCTCCAG	(S)
<i>Eef2</i> - 169 bp	GCCAAGTGGAGTTCCCCCAG	(S)
<i>Eef2</i> - 172 bp	ATGGCCAAGTGGAGTTCCC	(S)
<i>Eef2</i> - 176 bp	GTCCATGGCCAAGTGGAGT	(S)
<i>Nono</i> - 113 bp	CAGATACCTTCAGTTTGGAAAGTT	(S)
<i>Nono</i> - 123 bp	TGAATTGTTCCAGATACCTTCAGT	(S)
<i>Nono</i> - 159 bp	TAGGTAGCTACGCTGTGCAT	(S)
<i>Tfrc</i> - 125 bp	TGTCTTTGCTGAAATGCCCTT	(S)
<i>Tfrc</i> - 126 bp	CTGTCTTTGCTGAAATGCCCT	(S)
<i>Tfrc</i> - 127 bp	ACTGTCTTTGCTGAAATGCCC	(S)
<i>Tfrc</i> - 139 bp	TGCCAACCTATACTGTCTTTGCT	(S)

^a For gene-specific sense primers, the bp number indicates the expected size for the TVN amplicon.

^b (S), sense; (A), antisense.

Table S6. 15 genes showing a diet effect for both sexes in P30 pups

ID	Gene Symbol	Description	Chromosome	Group
TC0100000637.mm.2	<i>Plcd4</i>	phospholipase C, delta 4	chr1	Multiple_Complex
TC0100000640.mm.2	<i>Tll4</i>	tubulin tyrosine ligase-like family, member 4	chr1	Multiple_Complex
TC0200001779.mm.2	<i>Rtf1</i>	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	chr2	Multiple_Complex
TC0200003177.mm.2	<i>C330006A16Rik</i>	RIKEN cDNA C330006A16 gene	chr2	Multiple_Complex
TC0300000841.mm.2	<i>Gm4858</i>	predicted gene 4858	chr3	Coding
TC0300001362.mm.2	<i>Tacr3</i>	tachykinin receptor 3	chr3	Coding
TC0600000409.mm.2	<i>Wee2</i>	WEE1 homolog 2 (S. pombe)	chr6	Coding
TC0600002743.mm.2	<i>Trh</i>	thyrotropin releasing hormone	chr6	Coding
TC0700001409.mm.2	<i>Ucp2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	chr7	Multiple_Complex
TC0X00001955.mm.2	<i>Klhl13</i>	kelch-like 13	chrX	Multiple_Complex
TC0X00002274.mm.2	<i>Gpr101</i>	G protein-coupled receptor 101	chrX	Multiple_Complex
TC1200001912.mm.2	<i>Six1</i>	sine oculis-related homeobox 1	chr12	Multiple_Complex
TC1500000346.mm.2	<i>Trhr</i>	thyrotropin releasing hormone receptor	chr15	Coding
TC1600000508.mm.2	<i>Gm5483</i>	predicted gene 5483	chr16	Multiple_Complex
TC1600000741.mm.2	<i>Senp7</i>	SUMO1/sentrin specific peptidase 7	chr16	Multiple_Complex

Table S7. 23 genes showing sex differences for both diets in P30 pups.

ID	Gene Symbol	Description	Chromosome	Group
TC0100000637.mm.2	<i>Plcd4</i>	phospholipase C, delta 4	chr1	Multiple_Complex
TC0100000640.mm.2	<i>Ttl4</i>	tubulin tyrosine ligase-like family, member 4	chr1	Multiple_Complex
TC0200001340.mm.2	<i>Olfrl261</i>	olfactory receptor 1261	chr2	Coding
TC0400001715.mm.2	<i>Eif4g3</i>	eukaryotic translation initiation factor 4 gamma, 3	chr4	Multiple_Complex
TC0400004191.mm.2	<i>Slc6a9</i>	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	chr4	Multiple_Complex
TC0500001205.mm.2	<i>Wscd2</i>	WSC domain containing 2	chr5	Multiple_Complex
TC0600002714.mm.2	<i>Cfap100</i>	cilia and flagella associated protein 100	chr6	Multiple_Complex
TC0700001409.mm.2	<i>Ucp2</i>	uncoupling protein 2 (mitochondrial, proton carrier)	chr7	Multiple_Complex
TC0700002178.mm.2	<i>Sbk2</i>	SH3-binding domain kinase family, member 2	chr7	Multiple_Complex
TC0700002373.mm.2	<i>Sult2a4</i>	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member 4	chr7	Coding
TC0X00000190.mm.2	<i>Kdm6a</i>	lysine (K)-specific demethylase 6A	chrX	Multiple_Complex
TC0X00002643.mm.2	<i>Eif2s3x</i>	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	chrX	Multiple_Complex
TC0Y00000005.mm.2	<i>Kdm5d</i>	lysine (K)-specific demethylase 5D	chrY	Multiple_Complex
TC0Y00000006.mm.2	<i>Eif2s3y</i>	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	chrY	Multiple_Complex
TC0Y00000066.mm.2	<i>Gm21768</i>	predicted gene, 21768	chrY	Coding
TC0Y00000233.mm.2	<i>Uty</i>	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	chrY	Multiple_Complex
TC0Y00000235.mm.2	<i>Ddx3y</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	chrY	Multiple_Complex
TC1100002004.mm.2	<i>Endov</i>	endonuclease V	chr11	Multiple_Complex
TC1200001912.mm.2	<i>Six1</i>	sine oculis-related homeobox 1	chr12	Multiple_Complex
TC1300000020.mm.2	<i>Akr1c19</i>	aldo-keto reductase family 1, member C19	chr13	Multiple_Complex

TC1600001788.mm.2	<i>Olf190</i>	olfactory receptor 190	chr16	Coding
TC1900000467.mm.2	<i>Papss2</i>	3-phosphoadenosine 5-phosphosulfate synthase 2; 3'-phosphoadenosine 5'-phosphosulfate synthase 2	chr19	Multiple_Complex
TC1900000928.mm.2	<i>Gm960</i>	predicted gene 960	chr19	Coding

Table S8. Five genes showing a diet effect for both sexes in E17.5 embryos.

ID	Gene Symbol	Description	Chromosome	Group
TC0200001276.mm.2	<i>Olfrl112</i>	olfactory receptor 1112	chr2	Coding
TC0400002381.mm.2	<i>Spacal</i>	sperm acrosome associated 1	chr4	Coding
TC0X00002031.mm.2	<i>Gm2964</i>	predicted gene 2964 [Source:MGI Symbol;Acc:MGI:3781142]; predicted gene 2964	chrX	Coding
TC0Y00000067.mm.2	<i>Gm20840</i>	predicted gene, 20840	chrY	Coding
TC1100001293.mm.2	<i>Bcas3</i>	breast carcinoma amplified sequence 3	chr11	Multiple_Complex

Table S9. Three genes showing a diet effect for both P30 and E17.5 males.

ID	Gene Symbol	Description	Chromosome	Group
TC0X00002805.mm.2	<i>Magee2</i>	melanoma antigen, family E, 2	chrX	Coding
TC1000003019.mm.2	<i>Irak3</i>	interleukin-1 receptor-associated kinase 3	chr10	Multiple_Complex
TC1100001848.mm.2	<i>Kcnj16</i>	potassium inwardly-rectifying channel, subfamily J, member 16	chr11	Coding

Table S10. 12 genes showing a diet effect in both P30 and E17.5 females.

ID	Gene Symbol	Description	Chromosome	Group
TC0200003300.mm.2	<i>Dnm1</i>	dynamain 1	chr2	Multiple_Complex
TC0200003747.mm.2	<i>Gm11084</i>	predicted gene 11084 [Source:MGI Symbol;Acc:MGI:377 9315]	chr2	Coding
TC0400000982.mm.2	<i>Inadl</i>	InaD-like (Drosophila)	chr4	Multiple_Complex
TC0500000947.mm.2	<i>Prdm8</i>	PR domain containing 8	chr5	Multiple_Complex
TC0600000014.mm.2	<i>Peg10</i>	paternally expressed 10	chr6	Coding
TC0900000151.mm.2	<i>Olfir851</i>	olfactory receptor 851	chr9	Coding
TC1100001251.mm.2	<i>1700020L24R ik</i>	RIKEN cDNA 1700020L24 gene	chr11	Coding
TC1100001448.mm.2	<i>Colla1</i>	collagen, type I, alpha 1	chr11	Multiple_Complex
TC1600000288.mm.2	<i>Eif4g1</i>	eukaryotic translation initiation factor 4, gamma 1	chr16	Multiple_Complex
TC1600002145.mm.2	<i>Dscam</i>	Down syndrome cell adhesion molecule	chr16	Coding
TC1700000576.mm.2	<i>LOC1008615 96</i>	PREDICTED: zinc finger protein 791-like (LOC100861596), mRNA.	chr17	Coding
TSUnmapped00000005.m m.2	<i>Amot</i>	angiomotin	chrX	Coding

Table S11. 15 genes showing sex differences for both diets in E17.5 embryos.

ID	Gene Symbol	Description	Chromosome	Group
TC0200002550.mm.2	<i>Eya2</i>	eyes absent 2 homolog (Drosophila)	chr2	Multiple_Complex
TC0500000690.mm.2	<i>Spata18</i>	spermatogenesis associated 18	chr5	Coding
TC0500003743.mm.2	<i>Psmg3</i>	proteasome (prosome, macropain) assembly chaperone 3	chr5	Multiple_Complex
TC0600000409.mm.2	<i>Wee2</i>	WEE1 homolog 2 (S. pombe)	chr6	Coding
TC0600002413.mm.2	<i>Vmn1r33</i>	vomer nasal 1 receptor 33	chr6	Coding
TC0900000679.mm.2	<i>Pstpip1</i>	proline-serine-threonine phosphatase-interacting protein 1	chr9	Multiple_Complex
TC0900002044.mm.2	<i>Slc37a2</i>	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	chr9	Multiple_Complex
TC0X00000190.mm.2	<i>Kdm6a</i>	lysine (K)-specific demethylase 6A	chrX	Multiple_Complex
TC0Y00000005.mm.2	<i>Kdm5d</i>	lysine (K)-specific demethylase 5D	chrY	Multiple_Complex
TC0Y00000006.mm.2	<i>Eif2s3y</i>	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	chrY	Multiple_Complex
TC0Y00000233.mm.2	<i>Uty</i>	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	chrY	Multiple_Complex
TC0Y00000235.mm.2	<i>Ddx3y</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	chrY	Multiple_Complex
TC1100002084.mm.2	<i>Limk2</i>	LIM motif-containing protein kinase 2	chr11	Multiple_Complex
TC1200000716.mm.2	<i>Rps26</i>	ribosomal protein S26	chr12	Multiple_Complex
TC1900000026.mm.2	<i>Cdk2ap2</i>	CDK2-associated protein 2	chr19	Multiple_Complex