Supporting Online Material for

MeCP2, a Key Contributor to Neurological Disease, Activates and Represses Transcription

Maria Chahrour, Sung Yun Jung, Chad Shaw, Xiaobo Zhou, Stephen T. C. Wong,
Jun Qin and Huda Y. Zoghbi*

* To whom correspondence should be addressed. E-mail: hzoghbi@bcm.edu

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Materials and Methods

Microarray data analysis

We used the Affymetrix Mouse Exon 1.0 ST microarray, which carries 1.2 million probe sets covering one million exon clusters, with an average of 40 probes per gene. Exon array data were processed in the R statistical programming environment using locally developed methods and the exonmap package (*S1*). Raw data were first analyzed with RMA normalization as implemented in exonmap to remove between-array effects and to standardize the low-level data. Subsequently, linear models were calculated to analyze genotype effects for each gene. An appropriate gene model was first obtained prior to performing the linear model calculation. Genomic annotations were obtained from UCSC (http://genome.ucsc.edu) in a bulk download using the table browser against the underlying knownGene and refFlat database tables. The probeset coordinate information available from the Affymetrix annotation file was then cross-referenced against the coordinates derived from UCSC. Each array probeset was assigned to its unique exon or intron region grouped within each gene. For genes where the Affymetrix annotation file listed exonic probes but where annotation was not available from UCSC, the corresponding probes were assigned to a single exonic group within the gene that was indicated by the Affymetrix annotation file. The normalized probe level data were then averaged within each exon to produce exon level data for each gene for each animal. A two-way ANOVA with main effects for genotype and exonic region was then calculated for each gene. The ANOVA model was fit using weighted least squares analysis where the weights were determined according to the probe counts within each exon. Since separate wildtype (WT) littermates of different strains were used in the *Mecp2*-null (C57BL/6J) and *MECP2*-Tg (FVB) experiments, a separate linear model was estimated for each gene in each strain (one fit for each WT background). A linear contrast was calculated comparing the WT and mutant cross-exon means for each gene. The cutoff rule for determining genes regulated by MeCP2 was a log scale fold difference of 0.2 in both the *MECP2*-Tg and the *Mecp2*-null lists, or a combined fold difference of 0.4 and a consistent pattern of change for the common genes (*MECP2*-Tg-*Mecp2*-null), and a linear step up false discovery rate (FDR) (*S2*) of less than 0.05 value for the T-statistic corresponding to the linear contrast comparing each WT strain with its corresponding mutant. The gene set determined by this fold change and FDR multiplicity corrected cutoff, corresponds to a median raw marginal p-value of around 0.00015 for the underlying T-statistics. Ultimately, eight sets of genes were determined from our analysis: activated by MeCP2 (upregulated in *MECP2*-Tg, downregulated in *Mecp2*-null), repressed by MeCP2 (downregulated in *MECP2*-Tg, upregulated in *Mecp2*-null), downregulated in both mouse models, upregulated in both mouse models, only altered in *MECP2*-Tg (upregulated or downregulated), and only altered in *Mecp2*-null (upregulated or downregulated). Post-processing of our exon array based gene sets was performed to determine the content of the sets. We utilized the Gene Ontology (GO) analysis for this purpose, using locally developed software and methods. Briefly, the gene ontology vocabulary was obtained from the GO website (9/1/2007 build), and current mouse annotations were also downloaded. The mouse exon array was mapped to entrez identifiers, and these identifiers were mapped to the GO data structure using the available annotations. Using our local ontology analysis system (OntologyTraverser), we tabulated the genes annotated at or below each GO node for the entire exon array. We then used a hypergeometric sampling model to examine the statistical representation of each GO node for genes in our gene sets. In order to make comparisons between sets, we took differences between the standardized scores determined for each gene set. Because of the extreme overlapping structure of the GO, many GO nodes report duplicate or redundant information. To avoid this problem, we calculated the GO covariance structure and used this estimate to compute de-correlated GO scores. Analysis of the de-correlated difference scores revealed substantial content differences between the repressed by MeCP2 and the activated by MeCP2 gene sets. To assess the overlap of the regulated gene sets with CpG island context, we computed the number of genes in each gene set whose transcriptional start site was within 5kb of a CpG island - in either the upstream or downstream direction. The CpG island coordinates were obtained using the UCSC mm8 annotation table cpgIslandExt, and gene coordinates were determined using the knownGene table from UCSC. For genes on the minus strand, we looked within 5kb from the appropriate end of the transcript. Statistical enrichment was determined by using a random model where approximately 34% of randomly selected mouse genes would be expected to overlap a CpG island. The p-values were determined using a normal approximation to the binomial sampling model.

Quantitative real-time RT-PCR

We used only male mice for this study to avoid variability from X-chromosome inactivation (XCI) patterns in female mice; since *Mecp2* is located on the X-chromosome, and the XCI pattern is variable in a mouse colony (*S3*). Total RNA was extracted from the hypothalamus of 6 weeks (wks) old male mice using TRIzol reagent (Invitrogen Corporation, Carlsbad, CA), DNaseI treated, and purified using the RNeasy mini kit according to the manufacturer's protocol (Qiagen, Valencia, CA). cDNA was synthesized from 1 μg of RNA using the RT^2 First Strand Kit (SuperArray Bioscience Corporation, Frederick, MD). Quantitative real-time PCR reactions were performed on 10 ng of cDNA using RT^2 SYBR Green/ROX PCR master mix and commercially available primers (SuperArray Bioscience Corporation, Frederick, MD). All RNA samples were analyzed in triplicate and normalized relative to Gapdh levels.

Sodium bisulfite sequencing

Genomic DNA was isolated from hypothalami of three WT male mice using the Non-Organic DNA Extraction kit according to the manufacturer's protocol (Millipore Corporation, Billerica, MA). Bisulfite treatment of 1 μg of hypothalamic DNA was performed using the CpGenome^{TM} Fast DNA Modification kit (Millipore Corporation, Billerica, MA). Bisulfite-treated DNA (1 μl) was amplified by nested PCR using primers directed against the promoter region of target genes. PCR products were cloned into the pCR2.1-TOPO vector (Invitrogen Corporation, Carlsbad, CA), and for each insert, ~10 clones were sequenced. Nested PCR conditions were as follows: 95°C for 5 minutes, 95°C for 45 seconds, 49°C for 45 seconds, 72 °C for 45 seconds (repeat from step 2 for 35 cycles), 72 °C for 7 minutes, hold at 4°C. We used 5 μl of amplicon from the first round of PCR as the template for the second round. The following primer sequences were used to amplify promoter regions of target genes (*external* for the first round, and *internal* for the second round of the nested PCR):

Grin2a - *external*: Forward 5'-GTTTGTGAGGAGATAAAATTTAGTA-3'
Reverse 5'-CTCTCCTCCACCTTACAAAAACCCT-3'

Grin2a - *internal*: Forward 5'-ATTTTTAAATATTAAGTTATGGATG-3'
Reverse 5'-TATTACCRACCCTTCTAATCTAACA-3'

A2bp1 - *external*: Forward 5'-GTTTTGTTAGTTATAGGATTTA-3'
Reverse 5'-TAAATTCCTCAATTCTCTATATAA-3'

A2bp1 - *internal*: Forward 5'-AGTTYGTATTTGGAGGGGATAGTYG-3'
Reverse 5'-AAACAACRAATTAAAATATTAACT-3'

Sst - *external*: Forward 5'-GGGTTGAGYGATTTTGAGAAGYGTT-3'
Reverse 5'-ATTAATTTTACRAAACTAATAATAC-3'

Sst - *internal*: Forward 5'-AGGGGGATAGTTTTTATTTGTTTTT-3'
Reverse 5'-CACTAATAAAATCTAAAAACRCCTCC-3'

Gprin1 - *external*: Forward 5'-GGGTATGYGYGTTGGGTGTATT-3'
Reverse 5'-TAAACACCTTCTTTCAAACACTTTC-3'

Gprin1 - *internal*: Forward 5'-GTTTGGTGTTTAGTTGGGAGTATYGYGGG-3'
Reverse 5'-AATAACTTATTAAAAAATATCCAAAA-3'

Gamt - *external*: Forward 5'-GGTAAGGAAATTGAGATTTGTAAT-3'
Reverse 5'-CCATCCACCCAAACCCAACCCAATA-3'

Gamt - *internal*: Forward 5'-GTAGAGTATTTTTGGAGGTAGTAGT-3'

Reverse 5’-AACCCACCCTAACCCAAAAAAACCC-3’

E2F1 - external: Forward 5’-GTTTATATTAGAATTGGGAATTTGG-3’

Reverse 5’-CAAATCRTCATCATCTCCACC-3’

E2F1 - internal: Forward 5’-TTAAGTAAGTATTAGTTGGATATA-3’

Reverse 5’-CCCACTAACCCTCRCRATTCTAAC-3’

Chromatin immunoprecipitation

The hypothalamus was dissected from 6 wks old mice and incubated in 1% formaldehyde for 10 minutes at room temperature to cross-link DNA to associated proteins. The tissue was washed twice with ice-cold phosphate buffered saline (PBS) containing 0.125 M glycine and protease inhibitors (PI; complete protease inhibitor cocktail tablets, Roche Applied Science, Indianapolis, IN) and then homogenized in lysis buffer (10 mM Tris-HCl pH 7.5, 10 mM NaCl, 3 mM $MgCl_2$, 0.5% NP40) containing PI. After 10 minutes of incubation on ice, the lysate was centrifuged for 5 minutes at 3,000 rpm and 4°C, and the nuclear pellet was sonicated with a Branson Sonifier 450 for 6 seconds at power level 6. The homogenate was then digested with 300 U of micrococcal nuclease for 5 minutes at 37°C (Worthington Biochemical Corporation, Lakewood, NJ) to generate fragments with an average length of ~100-200 bps, as determined empirically by agarose gel electrophoresis of the fragmented chromatin sample. For immunoprecipitation, 200 µl of chromatin was diluted 1:10 in ChIP dilution buffer (Millipore Corporation, Billerica, MA) and 1% of the diluted sample was set aside for input. The sample was precleared with protein A Dynabeads (Invitrogen Corporation, Carlsbad, CA) at 4°C for 3 hours.

The precleared lysate was incubated overnight with protein A Dynabeads that were pre-blocked with salmon sperm DNA, and 5 μg of rabbit polyclonal anti-MeCP2 antibody (Millipore Corporation, Billerica, MA). Mock immunoprecipitation with 5 μg of nonspecific rabbit immunoglobulin G (IgG) was included as a control. After immunoprecipitation, the beads were washed sequentially at room temperature (for 5 minutes each) with 700 μl of low salt buffer, high salt buffer, LiCl buffer (Millipore Corporation, Billerica, MA), and TE buffer (10 mM Tris-HCl pH 7.4, 1 mM EDTA pH 8.0). Elution was performed twice in 250 μl of fresh elution buffer (1% SDS, 0.1 M NaHCO3) for 15 minutes at room temperature. The eluates were combined, 20 μl of 5 M NaCl was added, and samples were incubated overnight at 65°C to reverse the cross-links. The input DNA was diluted in freshly made elution buffer to a volume of 500 μl, and cross-link reversal was performed. After cross-link reversal, samples were digested with 20 μg of proteinase K for 1 hour at 55°C, and DNA was recovered by standard methods in 30 μl of 10 mM Tris-HCl pH 8.0. One μl of DNA was used for each quantitative real-time PCR. For sequential ChIP (seqChIP) analysis, a primary ChIP was performed with 5 μg of rabbit polyclonal anti-MeCP2 antibody (Millipore Corporation, Billerica, MA), or 5 μg of nonspecific rabbit IgG as a control, and the immunoprecipitated complexes were eluted as described above. Half of the eluate was subjected to a second ChIP using 5 μg of rabbit polyclonal anti-CREB1 antibody (Novus Biologicals, Littleton, CO). Promoters were analyzed by quantitative real-time PCR using 3 μl of DNA. ChIP and seqChIP experiments were performed in triplicate, and all quantitative real-time PCR experiments were performed in triplicate. The quantitative real-time PCR data were analyzed as follows (*S4, S5*). Relative proportions of immunoprecipitated DNA were determined based on the threshold cycle (Ct) value for each PCR reaction. In order to control for variation between ChIP fractions, for every gene promoter studied, a ΔCt value was calculated for each sample (WT, *MECP2*-Tg, *Mecp2*-null) by subtracting the Ct value for the input ($\mathrm{Ct}^{\mathrm{Input}}$) from the Ct value for the immunoprecipitated sample ($\mathrm{Ct}^{\mathrm{antibody}}$ or $\mathrm{Ct}^{\mathrm{IgG}}$). Because the input DNA fraction represents only 1% of the total material (see above), the $\mathrm{Ct}^{\mathrm{Input}}$ value was first adjusted for this dilution factor by subtracting 6.644 cycles (Log_2 of 100). The formula used was:

$\Delta\mathrm{Ct}^{\mathrm{antibody}}$ (or $\Delta\mathrm{Ct}^{\mathrm{IgG}}$) = $[\mathrm{Ct}^{\mathrm{antibody\ (or\ IgG)}} - (\mathrm{Ct}^{\mathrm{Input}} - 6.644)]$.

Next, a ΔΔCt value (*S6*) was calculated for each sample by subtracting the $\Delta\mathrm{Ct}^{\mathrm{IgG}}$ from the corresponding $\Delta\mathrm{Ct}^{\mathrm{antibody}}$. The formula used was:

$\Delta\Delta\mathrm{Ct}^{\mathrm{WT\ (or\ }\mathit{MECP2}\text{-Tg or }\mathit{Mecp2}\text{-null)}} = \Delta\mathrm{Ct}^{\mathrm{antibody}} - \Delta\mathrm{Ct}^{\mathrm{IgG}}$

Fold differences between the specific immunoprecipitation and the IgG background were then determined by raising 2 to the -ΔΔCt power (for example, specific binding in the WT sample = $2^{-\Delta\Delta\mathrm{Ct\ WT}}$). Data were then plotted as fold enrichment over the *Mecp2*-null (for each WT sample: $2^{-\Delta\Delta\mathrm{Ct\ WT}} - 2^{-\Delta\Delta\mathrm{Ct}\ \mathit{Mecp2}\text{-null}}$,

and for each *MECP2*-Tg sample: $2^{-\Delta\Delta\mathrm{Ct}\ \mathit{MECP2}\text{-Tg}} - 2^{-\Delta\Delta\mathrm{Ct}\ \mathit{Mecp2}\text{-null}}$).

Primer and probe sequences used were as follows:

Sst: Forward 5’-GCGTAAAAGCACTGGTGAGATCT-3’

Reverse 5’-GGTCTCCCCTTTTTAAACTCTCTCTCT-3’

Probe 6-FAM-TCCTTGGCTGACGTC-BHQ

Oprk1: Forward 5’-GCACCTTGCTGATCCCAAAC-3’

Reverse 5’-CCACGTTCCTGATGCTCAATT-3’

Probe 6-FAM-CAGTCTTGGAAGGCA-BHQ

Gamt: Forward 5’-ACGGCTCAGCCACGGAG-3’

Reverse 5’-TTGCACTCAAGTGGGTGGG-3’

Probe 6-FAM-TTCTTTAGGGCGCATAG-BHQ

Gprin1: Forward 5’-GCCTTCAGCGGTTCACTCAA-3’

Reverse 5’-CGTCTGTAACTAGTATTAAATCGCCTCAT-3’

Probe 6-FAM-ACTCCTAAACACCTTCT-BHQ

Mef2c: Forward 5’-CACTTGAGCACACGCGTACA-3’

Reverse 5’-ACCCACACAGAACCTTCAAAGTC-3’

Probe 6-FAM-CCAGACATCTTCGGG-BHQ

A2bp1: Forward 5’-CCGCTGCCTGTGGATGAG-3’

Reverse 5’-AAAGCCGAGAGCCAAATCAC-3’

Probe 6-FAM-TGGCTCCTGACAGAA-BHQ

Creb1: Forward 5’-GGCTGGCCGCAAAGC-3’

Reverse 5’-TGGTTCTTTGCTGGGAAGAAAG-3’

Probe 6-FAM-CCACATGCCACCTG-BHQ

For the custom array experiment, ChIP was performed as described above using hypothalamic chromatin from 3 WT males, 3 *MECP2*-Tg males, and 2 *Mecp2*-null males. The input (whole cell extract, WCE) DNA and immunoprecipitated (IP) DNA were differentially labelled and hybridized to the array. The labeling and hybridization were performed using established protocols (Agilent Technologies, Santa Clara, CA). Fluorescence intensity raw data were obtained from scanned images of the array using the Feature Extraction software (Agilent Technologies, Santa Clara, CA). The pre-processing and normalization of the raw signals were carried out using the ChIP Analytics software 1.3 (Agilent Technologies, Santa Clara, CA). Data from all eight samples were subjected to blank subtraction, inter-array and intra-array median normalizations, and the replicate samples for the same genotype were combined to form a single set of output for each probe. For each of the three genotypes (WT, *MECP2*-Tg, *Mecp2*-null), the net signal for a single probe was calculated as the difference between the normalized signals of the IP and WCE channels:

$$I_m = I_m^{IP} - I_m^{WCE}, m = \{'WT', 'MECP2\text{-}Tg', 'Mecp2\text{-}null'\}$$

For each probe, we compared the net signal from the WT and *MECP2*-Tg conditions to that of the *Mecp2*-null condition separately, and the differences in net signals were normalized to the standard deviation of the net signals for the *Mecp2*-null (knock-out, KO) condition. Considering the context information for each probe, a weighted average signal I^* was calculated by including one neighborhood probe up- and downstream of each probe, respectively, and the weight for the center probe was set to 2 while the weight for neighboring probes was 1:

$$\tilde{I}_n = (I_n - I_{KO}) / std(I_{KO}), \qquad n = \{'WT', 'MECP2\text{-}Tg'\}$$

where

$$std(I_{KO}) = \sqrt{\frac{1}{N-1}\sum_{t=1}^{N}\left[I_{KO}(t) - \frac{1}{N}\sum_{t=1}^{N} I_{KO}(t) \right]^2}$$

$$I_n^*(t) = \frac{[\tilde{I}_n(t-1) + 2 * \tilde{I}_n(t) + \tilde{I}_n(t+1)]}{4}.$$

For each, the WT and *MECP2*-Tg conditions, we assumed that the weighted context signal I^* follows a Gaussian distribution with mean and standard deviation estimated from the whole vector. Thus, a p-value was calculated for each probe. At the significant level of 0.05, we picked up probes with significantly large I^* value (indicating that the signals in WT and *MECP2*-Tg conditions are significantly larger than that in the *Mecp2*-null condition), and considered them specific bound probes in WT and *MECP2*-Tg conditions.

Proteomic analysis of MeCP2 complex from mouse brain

Brain tissue preparation and cell harvesting

In order to avoid contamination of protein extracts with mouse immunoglobulins, and to aid dissociation of connective tissue, we performed intracardiac perfusion with aprotinin-PBS prior to collection of mouse brain. All procedures conformed to the Baylor College of Medicine experimental animal handling guidelines. Mice were deeply anesthetized using an intraperitoneal injection of anesthetic (ketamine 37.5 mg, xylazine 1.9 mg, and acepromazine 0.37 mg, in 5 ml of sterile water) at 0.75 - 1.5 ml/kg body weight and intracardiac perfusion was performed through the left ventricle. The whole brain was dissected with the cerebellum and brainstem intact and minced into small pieces on ice to release cells. The cells were further dispersed by aspiration through a large bore pipette and run through a cell strainer (100 µm pore size). Isolated cells were harvested by centrifugation at 1,000 X *g* for 5 minutes at 4°C and washed three times with ice-cold PBS.

Subcellular fractionation

Cytoplasmic fractions (S100) and nuclear extracts (NE) from collected brain cells were prepared by mechanical lysis of the cells. After measuring the packed-cell volume (PCV), the cell pellet was gently resuspended in 2.5 PCVs of lysis solution (10 mM Hepes pH 7.8, 10 mM KCl, 1.5 mM $MgCl_2$, 0.5% NP40, 0.34 M sucrose, 10 mM PMSF, 10 mM 2-mercaptoethanol) and homogenized with a dounce homogenizer. The lysate was centrifuged at 500 X *g* for 10 minutes at 4°C to separate supernatant (for S100) and packed nuclear pellet (for NE). The supernatant was removed and centrifuged at 100K X *g* for 20 minutes to eliminate plasma membrane contamination. For the NE, the packed nuclear pellet was lysed with 1.5 volumes of NETN buffer (25 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 mM EDTA, 0.5% NP40) by sonication and cleared by centrifugation at 100K X *g* for 20 minutes. The cleared supernatant was removed (0.5% NP40 soluble fraction) and the pellet was then solubilized by sonication with 1 volume of RIPA buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl, 1.0% NP40, 0.5% sodium deoxycholic acid, 0.1% SDS) and cleared by 100K X *g* centrifugation for 1 hour (chromatin binding fraction).

Immunoprecipitation

The samples were cleared by centrifugation at 100K X *g* for 20 minutes at 4°C. The supernatant was collected and immunoprecipitation with an anti-MeCP2 antibody was carried out as previously reported (*S7*). Briefly, 10 mg of supernatant was mixed with 7.5 µg of affinity-purified antibody and rotated for 4 hours at 4°C. The sample and antibody mixture was centrifuged at 100K X *g* for 20 minutes at 4°C. To pre-clear the samples, 15 µl of Protein A-Sepharose bead slurry (50%) was added and samples were rotated for 1 hour at 4°C. The immunoprecipitates were washed 3 times with NETN buffer (20 mM Tris-HCl pH 8.0, 100 mM NaCl, 1 mM EDTA, 0.5% NP40). The washed beads were boiled with Laemmli buffer and subjected to SDS-PAGE (4-20% Tris/Glycine NOVEX Gel, Invitrogen). The Coomassie brilliant blue-stained protein bands were excised and destained with 50 mM ammonium bicarbonate solution in 50% methanol. Gel pieces were then washed in HPLC water overnight. After the wash, gel pieces were digested with 100 ng of trypsin in 50 mM NH_4HCO_3 pH 8.5 for 4 hours in a volume of 15 µl. After digestion, peptides were extracted by the addition of 200 µl acetonitrile. The supernatants were dried in a Speed-Vac dryer (Thermo Savant).

Protein identification

<u>Nano-HPLC/MS/MS analysis</u>

Each dried sample was dissolved in 20 µl of 5% methanol/ 95% water/ 0.01% formic acid solution and injected into Surveyor HPLC system (ThermoFinnigan) using autosampler. A 100 mm x 75 µm, C18 column (5 µm, 300 Å pore diameter, PicoFrit™, New objective) with mobile phases of A (0.1% formic acid in water) and B (0.1% formic acid in methanol) was used with a gradient of 5-95% of mobile phase B over 15 minutes followed by 95% phase B for 5 minutes at a flow rate of 200 nl/minute. Peptides were directly eletrosprayed into the mass spectrometer (Finnigan LTQ^{TM}, ThermoFinnigan) using nano-spray source. LTQ were operated in the data-dependant mode acquiring fragmentation spectra of the top 20 strongest ions.

Protein sequence database search and manual verification

The obtained MS/MS spectra were analyzed against NCBI-ref protein sequence database using BioWorks database search engine (BioWorksBrowser ver 3.2, Thermo Electron). All peptide hits with stringent BioWorksBrowser filtering criteria - peptide probability > 5×10^{-5} and Xcorr score > 2.5 for 2+ ions and 4.5 for 3+ ions - were further examined manually and all peptides had to be assigned by consecutive b- or y- ions to eliminate false positives.

Immunoprecipitation from cells

Neuro2a cells were maintained in Dulbecco's modified Eagle's medium (DMEM; Invitrogen Corporation, Carlsbad, CA) containing 10% FBS. Cells in a 6-well plate were transfected with 1 μg of a MeCP2 expression vector (pCDNA3.1-*Mecp2*) using Lipofectamine 2000 according to the manufacture's protocol (Invitrogen Corporation, Carlsbad, CA). For the immunoprecipitation one well of the 6-well plate was used. Cells were lysed in 3 volumes of lysis buffer (25 mM Tris pH 7.8, 1 mM EDTA, 150 mM

NaCl, 0.5% NP40) with sonication. The lysate was centrifuged at 4°C for 30 minutes at 100K X *g*. The supernatant was collected and immunoprecipitated using anti-CREB1 antibody (Abcam, Cambridge, MA) as reported above. Briefly, 1 ml of supernatant was mixed with 3 µg of antibody and rotated for 4 hours at 4°C. The sample and antibody mixture was centrifuged at 100K X *g* for 20 minutes at 4°C. 15 µl of Protein A-Sepharose bead slurry (50%) was added and samples were rotated for 1 hour at 4°C. The immunoprecipitates were washed 3 times with NETN buffer (20 mM Tris-HCl pH 8.0, 100 mM NaCl, 1 mM EDTA, 0.5% NP40). The washed beads were boiled in Laemmli buffer and subjected to SDS-PAGE (4-20% Tris/Glycine NOVEX Gel, Invitrogen Corporation, Carlsbad, CA). In-gel digestion and protein identification were carried out as reported above.

Luciferase assay

Neuro2a cells were transfected, using Lipofectamine 2000 according to the manufacture's protocol (Invitrogen Corporation, Carlsbad, CA), with pGL3-Basic-*Sst*-promoter or pGL3-Basic-*A2bp1*-promoter luciferase reporter constructs (50 ng each), and the pRL-TK vector (10 ng, Promega, Madison, WI) as an internal transfection control. To generate the reporter constructs, mouse genomic DNA was used as a template to amplify the promoter regions of *Sst* and *A2bp1*, with the following primers:

Sst - Forward: 5’-CCGCTCGAGTGGCCTCTGAGACCC-3’
Reverse: 5’-CCGCTCGAGCTTCCTTGCCTCA-3’
A2bp1 - Forward: 5’-CCGCTCGAGAATTGGGTGAAGAAG-3’

Reverse: 5’-CCGCTCGAGGCTTTAAATGGAGGCT-3’

The fragments were cloned into the XhoI site of the pGL3-Basic luciferase reporter vector (Promega, Madison, WI). Cells were transfected with a MeCP2 expression vector (250 ng, pCDNA3.1-*Mecp2*), a CREB1 expression vector (250 ng, pCMV-SPORT6-*Creb1*, Open Biosystems, Huntsville, AL), or both (125 ng each). After 48 hours cells were lysed and subjected to a dual luciferase reporter assay (Promega, Madison, WI). Normalized luciferase activity was obtained by dividing the firefly luciferase activity (from reporter constructs) by the *Renilla* luciferase activity (from pRL-TK vector). All experiments were performed in triplicate.

Western blot analysis

Protein extracts were prepared from hypothalamic tissue of three male mice from each genotype (WT, *MECP2*-Tg, *Mecp2*-null). Hypothalami were collected into 300 µl lysis buffer (10 mM Tris pH 7.5, 150 mM NaCl, 1% Triton X, 1X PI, 1X phosphatase inhibitors 1 and 2, 1 mM PMSF) and briefly homogenized with a dounce homogenizer. The lysate was passed through a 30 G syringe and left on ice for 15 minutes, then centrifuged for 15 minutes at 13,200 rpm and 4°C. The supernatant was quantified and from each sample 10 µg total protein was used for the western blot. Sample buffer (NuPAGE, Invitrogen Corporation, Carlsbad, CA) was added and the samples were boiled for 10 minutes. Western blotting was performed with anti-MeCP2 (1:1000, Millipore Corporation), anti-Sst (1:500, Santa Cruz Biotechnology), anti-CREB1 (1:500, Abcam), and anti-Gapdh (1:5000, Advanced ImmunoChemical Inc) as a loading control.

Supplementary Figures

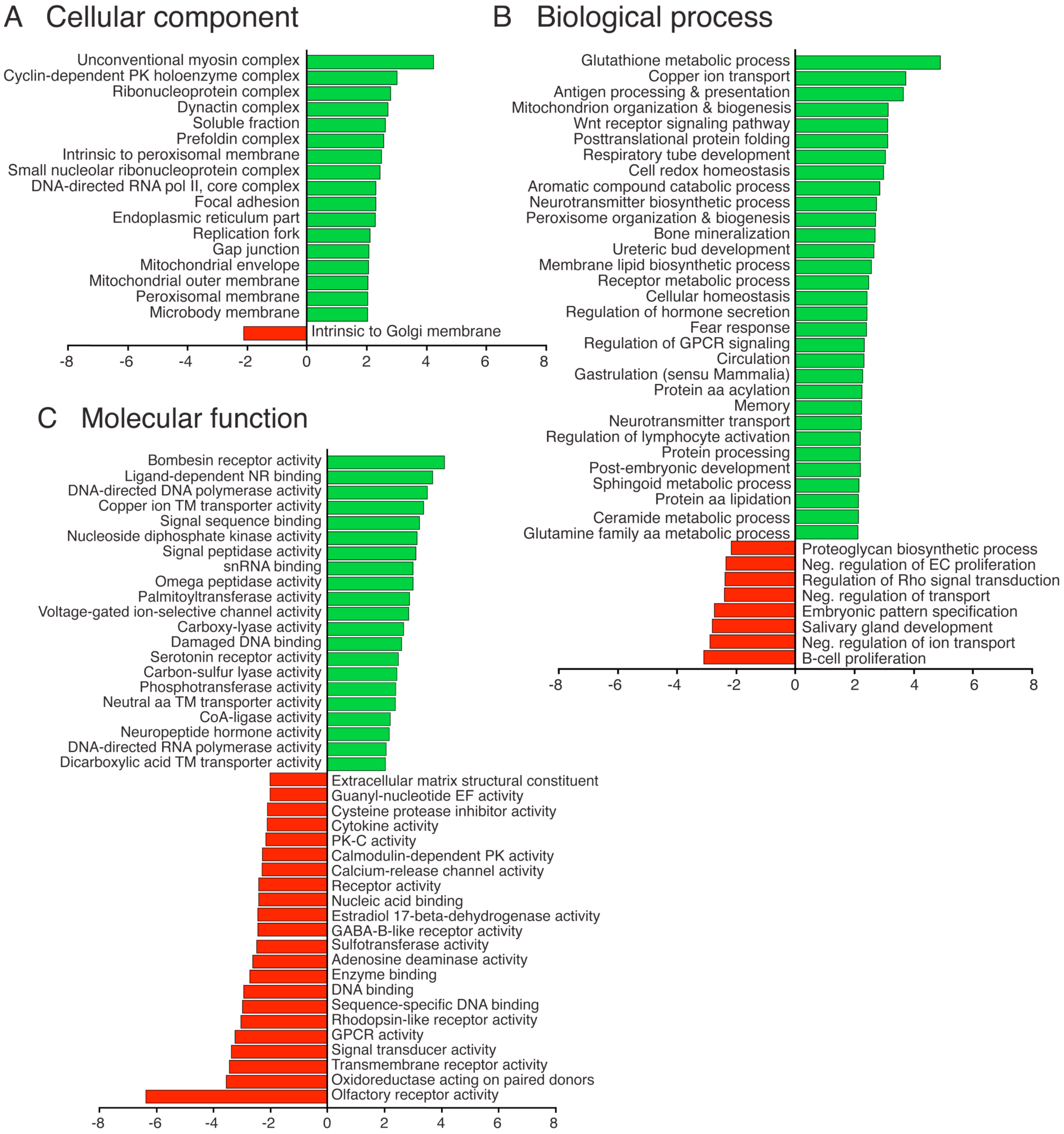

Fig. S1. Gene ontology analysis performed on genes that are differentially expressed in hypothalami of *MECP2*-Tg and *Mecp2*-null mice. Cellular component (**A**), biological process (**B**), and molecular function (**C**) categories that differ significantly between the genes activated by MeCP2 (green) and those repressed by MeCP2 (red) are plotted. The standardized scores (Z values) are presented on the X-axis, and significance was determined by a Z value of more than + or -2 and a count of at least two genes. PK, protein kinase, pol., polymerase, GPCR, G-protein coupled receptor, aa, amino acid, Neg., negative, EC, epithelial cell, NR, nuclear receptor, TM, transmembrane, EF, exchange factor.

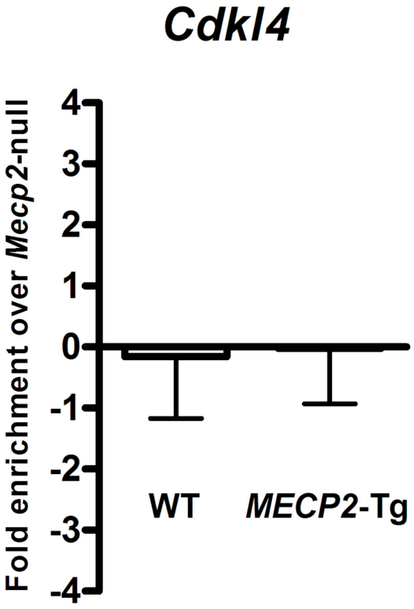

Fig. S2. MeCP2 binding was not detected at the promoter region of *Cdkl4*, a gene downregulated in both *MECP2*-Tg and *Mecp2*-null hypothalami. ChIP with anti-MeCP2 antibody shows that MeCP2 does not bind to the promoter region of *Cdkl4*. Quantitative real-time PCR values were normalized to the input and plotted as fold enrichment over *Mecp2*-null (*N* = 3).

Supplementary Tables

Table S1. The list of genes that are activated by MeCP2 (FDR-adjusted p-value < 0.05).

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
0610009D07Rik	RIKEN cDNA 0610009D07 gene	NM_025323	0.293	-0.301	0.0001	0.2731	0.0003
0610009J22Rik	RIKEN cDNA 0610009J22 gene	NM_027859	0.346	-0.221	0.0000	0.0001	0.0035
0610009O03Rik	RIKEN cDNA 0610009O03 gene	BC064775	0.398	-0.253	0.0000	0.0000	0.0000
0610010B08Rik	RIKEN cDNA 0610010B08 gene	AK002444	0.182	-0.272	0.0047	0.2089	0.0149
0610010F05Rik	RIKEN cDNA 0610010F05 gene	BC065122	0.233	-0.219	0.0000	0.0038	0.0011
0610011F06Rik	RIKEN cDNA 0610011F06 gene	AK192367	0.125	-0.362	0.0266	0.6007	0.0223
0610012D17Rik	RIKEN cDNA 0610012D17 gene	BC053332	0.656	-0.253	0.0125	0.1099	0.0800
0610016J10Rik	RIKEN cDNA 0610016J10 gene	XM_980872	0.425	-0.429	0.0018	0.1049	0.0127
0610031J06Rik	RIKEN cDNA 0610031J06 gene	AK171142	0.306	-0.104	0.0043	0.0317	0.0972
0610038D11Rik	RIKEN cDNA 0610038D11 gene	BC016191	0.282	-0.163	0.0021	0.0112	0.1249
0610039J04Rik	RIKEN cDNA 0610039J04 gene	NM_001035123	0.379	-0.190	0.0019	0.0066	0.1821
0610040D20Rik	RIKEN cDNA 0610040D20 gene	AK013670	0.316	-0.094	0.0076	0.0187	0.2502
0910001L09Rik	RIKEN cDNA 0910001L09 gene	BC056178	0.361	-0.241	0.0189	0.1221	0.1060
1110002N22Rik	RIKEN cDNA 1110002N22 gene	BC094625	0.383	-0.209	0.0114	0.0275	0.2583
1110004B13Rik	RIKEN cDNA 1110004B13 gene	NM_025838	0.581	-0.153	0.0212	0.0198	0.5147
1110008P14Rik	RIKEN cDNA 1110008P14 gene	BC049639	0.524	-0.252	0.0356	0.1027	0.2225
1110012D08Rik	RIKEN cDNA 1110012D08 gene	AK054166	0.391	-0.069	0.0164	0.0075	0.7508
1110014N23Rik	RIKEN cDNA 1110014N23 gene	AK003717	0.451	-0.170	0.0000	0.0000	0.0011
1110015O18Rik	RIKEN cDNA 1110015O18 gene	AK003731	0.739	-0.645	0.0475	0.1130	0.2638

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
1110036O03Rik	RIKEN cDNA 1110036O03 gene	AK029271	0.267	-0.246	0.0000	0.0065	0.0012
1110038D17Rik	RIKEN cDNA 1110038D17 gene	AK034509	0.269	-0.252	0.0000	0.0046	0.0050
1110039B18Rik	RIKEN cDNA 1110039B18 gene	AK053521	0.357	-0.187	0.0000	0.0000	0.0000
1110049F12Rik	RIKEN cDNA 1110049F12 gene	NM_025411	0.632	-0.118	0.0006	0.0020	0.1820
1110061N23Rik	RIKEN cDNA 1110061N23 gene	NM_176834	0.363	-0.088	0.0183	0.0255	0.3902
1110064P04Rik	RIKEN cDNA 1110064P04 gene	NM_172391	0.211	-0.260	0.0046	0.0672	0.0510
1300003B13Rik	RIKEN cDNA 1300003B13 gene	AK079610	0.264	-0.398	0.0433	0.2408	0.1163
1300014I06Rik	RIKEN cDNA 1300014I06 gene	NM_025831	0.340	-0.172	0.0400	0.0471	0.4544
1500005A01Rik	RIKEN cDNA 1500005A01 gene	NM_033146	0.361	-0.245	0.0005	0.0025	0.1284
1500019G21Rik	RIKEN cDNA 1500019G21 gene	NM_024172	0.345	-0.096	0.0358	0.0557	0.3697
1500041B16Rik	RIKEN cDNA 1500041B16 gene	AK019934	0.347	-0.174	0.0002	0.0007	0.1743
1500041N16Rik	RIKEN cDNA 1500041N16 gene	NM_026399	0.332	-0.087	0.0120	0.0082	0.5934
1600002O04Rik	RIKEN cDNA 1600002O04 gene	XM_978850	0.333	-0.338	0.0000	0.0001	0.0024
1700001L19Rik	RIKEN cDNA 1700001L19 gene	BC049693	0.263	-0.375	0.0117	0.2416	0.0315
1700007K13Rik	RIKEN cDNA 1700007K13 gene	AK005731	0.628	-0.541	0.0000	0.0010	0.0216
1700017B05Rik	RIKEN cDNA 1700017B05 gene	AK080676	0.274	-0.213	0.0319	0.0756	0.2647
1700027N10Rik	RIKEN cDNA 1700027N10 gene	AK140720	0.259	-0.288	0.0190	0.2152	0.0582
1700037H04Rik	RIKEN cDNA 1700037H04 gene	AK048328	0.356	-0.234	0.0005	0.0091	0.0436
1700040L02Rik	RIKEN cDNA 1700040L02 gene	NM_028491	0.177	-0.296	0.0077	0.2546	0.0196
1700041C02Rik	RIKEN cDNA 1700041C02 gene	AK224940	0.182	-0.246	0.0013	0.1107	0.0084
1700067C01Rik	RIKEN cDNA 1700067C01 gene	AK138347	0.484	-0.194	0.0000	0.0000	0.1919
1700120C14Rik	RIKEN cDNA 1700120C14 gene	AK007210	0.559	-0.521	0.0030	0.0136	0.1477

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
1810010H24Rik	RIKEN cDNA 1810010H24 gene	AK007422	0.625	-0.180	0.0489	0.0217	0.8103
1810013C15Rik	NA	NM_194348	0.419	-0.126	0.0000	0.0000	0.0000
1810014F10Rik	RIKEN cDNA 1810014F10 gene	AK163708	0.249	-0.356	0.0071	0.2660	0.0172
1810015A11Rik	RIKEN cDNA 1810015A11 gene	AK076869	0.332	-0.226	0.0053	0.0353	0.1069
1810020O05Rik	NA	AK131825	0.550	-0.350	0.0018	0.0054	0.2013
1810022K09Rik	RIKEN cDNA 1810022K09 gene	XM_906582	0.688	-0.327	0.0005	0.0169	0.0235
1810031K17Rik	RIKEN cDNA 1810031K17 gene	AK080437	0.561	-0.011	0.0000	0.0000	0.9661
1810035L17Rik	RIKEN cDNA 1810035L17 gene	BC048513	0.621	-0.147	0.0006	0.0005	0.4910
1810046J19Rik	RIKEN cDNA 1810046J19 gene	NM_025559	0.494	-0.403	0.0004	0.0854	0.0039
1810059G22Rik	RIKEN cDNA 1810059G22 gene	NM_026325	0.337	-0.264	0.0000	0.0016	0.0191
2010007H12Rik	RIKEN cDNA 2010007H12 gene	NM_027242	0.386	-0.076	0.0124	0.0053	0.7653
2010012C16Rik	RIKEN cDNA 2010012C16 gene	NM_025564	0.452	-0.239	0.0205	0.0306	0.3751
2010106G01Rik	RIKEN cDNA 2010106G01 gene	AK155011	0.318	-0.101	0.0005	0.0033	0.1135
2010204K13Rik	RIKEN cDNA 2010204K13 gene	AK077356	0.286	-0.354	0.0391	0.4827	0.0451
2010310D06Rik	RIKEN cDNA 2010310D06 gene	NM_172541	0.377	-0.140	0.0055	0.0123	0.2645
2200002K05Rik	RIKEN cDNA 2200002K05 gene	NM_026955	0.136	-0.452	0.0024	0.4906	0.0024
2210408I21Rik	RIKEN cDNA 2210408I21 gene	XM_889461	0.391	-0.112	0.0116	0.0062	0.6811
2310003H01Rik	RIKEN cDNA 2310003H01 gene	AK165631	0.334	-0.067	0.0329	0.0297	0.5367
2310004I24Rik	RIKEN cDNA 2310004I24 gene	NM_025510	0.252	-0.298	0.0079	0.2754	0.0183
2310005E10Rik	RIKEN cDNA 2310005E10 gene	BC026843	0.186	-0.330	0.0001	0.1844	0.0005
2310008M10Rik	RIKEN cDNA 2310008M10 gene	AK032969	0.425	-0.149	0.0005	0.0021	0.1584
2310014H01Rik	RIKEN cDNA 2310014H01 gene	XM_001003622	0.525	-0.132	0.0122	0.0181	0.3699
2310015A05Rik	RIKEN cDNA 2310015A05 gene	XM_984819	0.440	-0.187	0.0490	0.0677	0.4074

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
2310016C16Rik	RIKEN cDNA 2310016C16 gene	NM_027127	0.447	-0.296	0.0058	0.1050	0.0406
2310022K01Rik	RIKEN cDNA 2310022K01 gene	AK129228	0.344	-0.103	0.0113	0.0066	0.6489
2310022M17Rik	RIKEN cDNA 2310022M17 gene	AK009485	0.348	-0.109	0.0119	0.0114	0.4862
2310030N02Rik	RIKEN cDNA 2310030N02 gene	XM_131300	0.296	-0.182	0.0217	0.1002	0.1466
2310033P09Rik	RIKEN cDNA 2310033P09 gene	NM_024210	0.380	-0.216	0.0008	0.0613	0.0106
2310035K24Rik	RIKEN cDNA 2310035K24 gene	AK002807	0.247	-0.282	0.0137	0.2557	0.0349
2310038H17Rik	RIKEN cDNA 2310038H17 gene	NM_025964	0.442	-0.175	0.0206	0.0285	0.3946
2310042G06Rik	RIKEN cDNA 2310042G06 gene	NM_025531	0.329	-0.161	0.0000	0.0005	0.0464
2310043J07Rik	RIKEN cDNA 2310043J07 gene	XM_977360	0.372	-0.160	0.0155	0.0613	0.1695
2310056P07Rik	RIKEN cDNA 2310056P07 gene	NM_027342	0.572	-0.061	0.0013	0.0006	0.6963
2410008K03Rik	RIKEN cDNA 2410008K03 gene	NM_028022	0.210	-0.254	0.0008	0.0971	0.0063
2410012H22Rik	RIKEN cDNA 2410012H22 gene	XM_990283	0.448	-0.159	0.0134	0.0293	0.2803
2410018G20Rik	RIKEN cDNA 2410018G20 gene	AK011255	0.329	-0.345	0.0010	0.0289	0.0268
2510048L02Rik	RIKEN cDNA 2510048L02 gene	AK016073	0.358	-0.297	0.0005	0.0113	0.0351
2610002F03Rik	RIKEN cDNA 2610002F03 gene	BC046478	0.424	-0.168	0.0464	0.1301	0.2271
2610002M06Rik	RIKEN cDNA 2610002M06 gene	NM_025921	0.360	-0.371	0.0002	0.0261	0.0059
2610024G14Rik	RIKEN cDNA 2610024G14 gene	AK163935	0.370	-0.089	0.0132	0.0075	0.6609
2610036F08Rik	RIKEN cDNA 2610036F08 gene	XM_984127	1.691	-0.333	0.0163	0.0061	0.8218
2610042L04Rik	NA	AK036843	0.424	-0.681	0.0092	0.0892	0.0739
2610209M04Rik	RIKEN cDNA 2610209M04 gene	AK045231	0.220	-0.259	0.0111	0.5377	0.0103
2610301B20Rik	RIKEN cDNA 2610301B20 gene	NM_026005	0.300	-0.161	0.0128	0.0768	0.1169
2610318N02Rik	RIKEN cDNA 2610318N02 gene	XM_913604	0.305	-0.309	0.0177	0.1899	0.0621

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
2610524G07Rik	RIKEN cDNA 2610524G07 gene	NM_025596	0.395	-0.136	0.0000	0.0005	0.0310
2700007P21Rik	RIKEN cDNA 2700007P21 gene	NM_001025102	0.323	-0.185	0.0112	0.0301	0.2349
2700019D07Rik	RIKEN cDNA 2700019D07 gene	AK077304	0.316	-0.200	0.0019	0.0061	0.1953
2700055K07Rik	RIKEN cDNA 2700055K07 gene	NM_026481	0.639	-0.482	0.0000	0.0010	0.0043
2700060E02Rik	RIKEN cDNA 2700060E02 gene	XR_003485	0.418	-0.144	0.0001	0.0002	0.2045
2700069I18Rik	NA	AK012506	0.342	-0.122	0.0399	0.0687	0.3438
2700078K21Rik	RIKEN cDNA 2700078K21 gene	NM_008748	0.468	-0.085	0.0423	0.0521	0.4419
2700081O15Rik	RIKEN cDNA 2700081O15 gene	BC059063	0.407	-0.108	0.0090	0.0054	0.6340
2700097O09Rik	RIKEN cDNA 2700097O09 gene	NM_028314	0.336	-0.214	0.0038	0.0082	0.2609
2810012G03Rik	RIKEN cDNA 2810012G03 gene	NM_175104	0.334	-0.102	0.0480	0.0502	0.4976
2810021G02Rik	RIKEN cDNA 2810021G02 gene	AK009295	0.053	-0.722	0.0256	0.9539	0.0093
2810405K02Rik	RIKEN cDNA 2810405K02 gene	AK012999	0.328	-0.270	0.0002	0.1103	0.0012
2810406K13Rik	RIKEN cDNA 2810406K13 gene	XM_905932	0.477	-0.037	0.0007	0.0002	0.8262
2810409C01Rik	RIKEN cDNA 2810409C01 gene	AK013051	0.744	-0.602	0.0327	0.0300	0.5307
2810410M20Rik	RIKEN cDNA 2810410M20 gene	XM_980210	0.323	-0.274	0.0103	0.0691	0.1059
2810474O19Rik	RIKEN cDNA 2810474O19 gene	BC038922	0.315	-0.227	0.0248	0.1681	0.0995
2900024O10Rik	RIKEN cDNA 2900024O10 gene	NM_028372	0.428	-0.234	0.0018	0.0122	0.1026
2900052N01Rik	RIKEN cDNA 2900052N01 gene	AK049847	0.269	-0.684	0.0214	0.5997	0.0177
2900093B09Rik	RIKEN cDNA 2900093B09 gene	XM_001001044	0.507	-0.298	0.0002	0.0019	0.0746
3110057O12Rik	RIKEN cDNA 3110057O12 gene	BC011312	0.212	-0.311	0.0000	0.0979	0.0001
3300001M20Rik	RIKEN cDNA 3300001M20 gene	BC049083	0.209	-0.194	0.0003	0.0391	0.0071
3300002P09Rik	RIKEN cDNA 3300002P09 gene	AK014377	0.396	-0.321	0.0453	0.0513	0.4708

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
3632451O06Rik	RIKEN cDNA 3632451O06 gene	BC023359	0.202	-0.326	0.0000	0.0664	0.0001
3830408C21Rik	RIKEN cDNA 3830408C21 gene	AK052571	0.533	-0.150	0.0362	0.0275	0.5972
4631403P03Rik	RIKEN cDNA 4631403P03 gene	NM_153793	0.234	-0.242	0.0000	0.0010	0.0006
4632404H22Rik	RIKEN cDNA 4632404H22 gene	AK036417	0.262	-0.216	0.0264	0.1075	0.1634
4632428N05Rik	RIKEN cDNA 4632428N05 gene	NM_028732	0.308	-0.242	0.0010	0.0832	0.0090
4733401H18Rik	RIKEN cDNA 4733401H18 gene	AK014634	0.448	-0.206	0.0001	0.0018	0.0562
4833409A17Rik	RIKEN cDNA 4833409A17 gene	AK154994	0.427	-0.172	0.0001	0.0001	0.2634
4833442J19Rik	RIKEN cDNA 4833442J19 gene	AK132096	0.593	-0.581	0.0000	0.0068	0.0033
4921507P07Rik	RIKEN cDNA 4921507P07 gene	NM_027564	0.229	-0.454	0.0002	0.2892	0.0004
4930423K06Rik	NA	AK086441	0.627	-0.451	0.0262	0.0522	0.3070
4930431L04Rik	RIKEN cDNA 4930431L04 gene	AK015274	0.388	-0.414	0.0000	0.0045	0.0062
4930562D19Rik	NA	NM_177616	0.418	-0.222	0.0000	0.0000	0.0070
4931403E03Rik	NA	XM_144060	0.305	-0.313	0.0128	0.0836	0.1088
4931406I20Rik	RIKEN cDNA 4931406I20 gene	AK172415	0.400	-0.084	0.0000	0.0000	0.1680
4931428F04Rik	RIKEN cDNA 4931428F04 gene	AK016481	0.249	-0.166	0.0187	0.1030	0.1242
4931433A01Rik	RIKEN cDNA 4931433A01 gene	NM_030231	0.093	-0.406	0.0000	0.3316	0.0000
4932417I16Rik	RIKEN cDNA 4932417I16 gene	NM_001033321	0.261	-0.226	0.0017	0.0204	0.0635
4932418E24Rik	RIKEN cDNA 4932418E24 gene	XM_923021	0.288	-0.307	0.0063	0.0832	0.0554
4933406E20Rik	RIKEN cDNA 4933406E20 gene	AK161992	0.395	-0.191	0.0000	0.0000	0.0007
4933427D14Rik	RIKEN cDNA 4933427D14 gene	AK041396	0.269	-0.157	0.0002	0.0013	0.1171
4933434I06Rik	RIKEN cDNA 4933434I06 gene	XM_911600	0.317	-0.329	0.0193	0.2397	0.0523
5033414D02Rik	RIKEN cDNA 5033414D02 gene	AK003543	0.552	-0.124	0.0055	0.0034	0.6052
5033417F24Rik	RIKEN cDNA 5033417F24 gene	AK018199	0.490	-0.271	0.0205	0.0714	0.1892

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
5133400G04Rik	RIKEN cDNA 5133400G04 gene	AK012241	0.436	-0.208	0.0032	0.0116	0.1756
5530401N12Rik	RIKEN cDNA 5530401N12 gene	AK017439	0.615	-0.002	0.0214	0.0052	0.9967
5730494M16Rik	RIKEN cDNA 5730494M16 gene	BC060253	0.235	-0.169	0.0000	0.0008	0.0103
5730536A07Rik	RIKEN cDNA 5730536A07 gene	AK179061	0.490	-0.073	0.0014	0.0006	0.7349
5930412G12Rik	RIKEN cDNA 5930412G12 gene	AK081926	0.421	-0.251	0.0016	0.0683	0.0177
6230416J20Rik	RIKEN cDNA 6230416J20 gene	AK040101	0.201	-0.315	0.0002	0.1463	0.0010
6330403K07Rik	RIKEN cDNA 6330403K07 gene	BC069976	0.123	-0.298	0.0103	0.7209	0.0060
6330404F12Rik	RIKEN cDNA 6330404F12 gene	AK161857	0.259	-0.492	0.0277	0.1503	0.1232
6330406I15Rik	RIKEN cDNA 6330406I15 gene	AB055406	0.273	-0.228	0.0073	0.0468	0.1131
6330407J23Rik	RIKEN cDNA 6330407J23 gene	NM_026138	0.289	-0.128	0.0001	0.0006	0.1128
6330416L07Rik	RIKEN cDNA 6330416L07 gene	AK048043	0.286	-0.171	0.0002	0.0039	0.0452
6330503C03Rik	RIKEN cDNA 6330503C03 gene	AK018206	0.535	-0.301	0.0000	0.0000	0.0029
6330569M22Rik	RIKEN cDNA 6330569M22 gene	AK185112	0.235	-0.177	0.0000	0.0000	0.0000
6430503K07Rik	NA	XM_992712	0.319	-0.219	0.0063	0.0063	0.4631
6430514M23Rik	RIKEN cDNA 6430514M23 gene	AK134916	0.843	-0.742	0.0009	0.0082	0.0805
6430527G18Rik	RIKEN cDNA 6430527G18 gene	XM_977351	0.643	-0.306	0.0047	0.0658	0.0525
6530401C20Rik	RIKEN cDNA 6530401C20 gene	NM_173405	0.183	-0.316	0.0000	0.0558	0.0002
6720458F09Rik	RIKEN cDNA 6720458F09 gene	XM_983239	0.486	-0.120	0.0120	0.0090	0.5624
6720467C03Rik	RIKEN cDNA 6720467C03 gene	AK214863	0.308	-0.207	0.0003	0.0887	0.0027
6720489N17Rik	RIKEN cDNA 6720489N17 gene	XM_904454	1.171	-0.618	0.0302	0.0585	0.3125
7630402I04Rik	NA	AK020189	0.332	-0.437	0.0426	0.4744	0.0506
9030607L17Rik	RIKEN cDNA 9030607L17 gene	BC057953	0.296	-0.209	0.0047	0.0819	0.0424
9030625N01Rik	NA	AK035942	0.327	-0.402	0.0134	0.0619	0.1484

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
9130005N14Rik	RIKEN cDNA 9130005N14 gene	NM_026667	0.433	-0.303	0.0000	0.0009	0.0402
9130401M01Rik	RIKEN cDNA 9130401M01 gene	BC039940	0.528	-0.051	0.0311	0.0153	0.7488
9230110C19Rik	RIKEN cDNA 9230110C19 gene	NM_009534	0.348	-0.297	0.0008	0.0069	0.0845
9330132E09Rik	RIKEN cDNA 9330132E09 gene	XM_892762	0.561	-0.411	0.0000	0.0013	0.0025
9330184L24Rik	RIKEN cDNA 9330184L24 gene	AK034378	0.964	-0.221	0.0234	0.0104	0.7721
9430016H08Rik	RIKEN cDNA 9430016H08 gene	XM_283579	0.418	-0.180	0.0025	0.0089	0.1738
9430023L20Rik	RIKEN cDNA 9430023L20 gene	NM_026566	0.358	-0.056	0.0025	0.0010	0.7404
9430057O19Rik	RIKEN cDNA 9430057O19 gene	AK034894	0.232	-0.287	0.0000	0.0012	0.0000
9530023I19Rik	RIKEN cDNA 9530023I19 gene	AK020568	0.399	-0.511	0.0160	0.1301	0.0848
9530057J20Rik	RIKEN cDNA 9530057J20 gene	AK020613	1.154	-0.214	0.0084	0.0032	0.7864
9530092B13Rik	NA	AK020660	0.131	-0.469	0.0112	0.7355	0.0064
9630010G10Rik	NA	AK035845	0.417	-0.178	0.0219	0.0236	0.4692
9630025I21Rik	RIKEN cDNA 9630025I21 gene	AK079330	0.713	-0.170	0.0196	0.0264	0.4014
9630033F20Rik	RIKEN cDNA 9630033F20 gene	XM_001003452	0.220	-0.229	0.0316	0.2079	0.0999
9630037P07Rik	RIKEN cDNA 9630037P07 gene	XM_001001771	0.657	-0.175	0.0038	0.0090	0.2463
9930012K11Rik	RIKEN cDNA 9930012K11 gene	AK036801	0.310	-0.400	0.0001	0.0137	0.0069
9930021D14Rik	NA	NM_175682	0.347	-0.163	0.0455	0.0837	0.3279
A230058J24Rik	NA	XM_620337	0.347	-0.143	0.0013	0.0018	0.3497
A230060L24Rik	NA	AK038764	0.251	-0.564	0.0076	0.1372	0.0395
A230097K15Rik	NA	AK138410	0.236	-0.232	0.0009	0.0241	0.0305
A230107C01Rik	NA	AK039202	0.663	-0.265	0.0000	0.0000	0.0064
A2m	alpha-2-macroglobulin	XR_005046	0.185	-0.390	0.0001	0.2515	0.0002
A330019N05Rik	RIKEN cDNA A330019N05 gene	AK079058	0.283	-0.247	0.0030	0.0605	0.0377
A430041B07Rik	RIKEN cDNA A430041B07 gene	XM_896986	0.244	-0.200	0.0113	0.1762	0.0438
A430110M15Rik	NA	AK040633	0.454	-0.371	0.0371	0.0308	0.5683

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
A530016O06Rik	RIKEN cDNA A530016O06 gene	AK039191	0.242	-0.252	0.0010	0.0665	0.0114
A530054K11Rik	RIKEN cDNA A530054K11 gene	NM_183146	0.296	-0.211	0.0122	0.0464	0.1768
A530082C11Rik	RIKEN cDNA A530082C11 gene	AK142259	0.358	-0.103	0.0001	0.0002	0.2891
A530094I17Rik	RIKEN cDNA A530094I17 gene	AK041250	0.306	-0.343	0.0175	0.0685	0.1708
A630033E08Rik	RIKEN cDNA A630033E08 gene	BC078460	0.786	-0.448	0.0000	0.0000	0.0051
A630083H20Rik	NA	AK080376	0.522	-0.540	0.0002	0.0476	0.0029
A730008L03Rik	RIKEN cDNA A730008L03 gene	AK046129	0.606	-0.138	0.0000	0.0000	0.0574
A730098D12Rik	RIKEN cDNA A730098D12 gene	AK075709	0.359	-0.158	0.0361	0.1420	0.1660
A830058L05Rik	RIKEN cDNA A830058L05 gene	NM_172486	0.332	-0.359	0.0439	0.2237	0.1269
A830080H07Rik	NA	AK083579	0.481	-0.637	0.0042	0.1934	0.0143
A830093I24Rik	NA	AK044133	0.039	-0.428	0.0273	0.9133	0.0109
A930018M24Rik	NA	XM_907235	0.484	-0.354	0.0135	0.0951	0.1004
Aacs	acetoacetyl-CoA synthetase	NM_030210	0.320	-0.112	0.0000	0.0001	0.0176
Aamp	angio-associated migratory protein	AK183212	0.330	-0.084	0.0054	0.0151	0.2215
Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	NM_026276	0.338	-0.137	0.0001	0.0008	0.0893
Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	NM_153145	0.762	-0.820	0.0000	0.0000	0.0000
Abca8b	ATP-binding cassette, sub-family A(ABC1),member 8b	NM_013851	0.103	-0.367	0.0000	0.1518	0.0000
Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	AK011569	0.321	-0.151	0.0000	0.0009	0.0194
Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	AK040323	0.539	-0.179	0.0000	0.0000	0.0015

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	AK153589	0.285	-0.282	0.0000	0.0304	0.0006
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	NM_011920	0.108	-0.306	0.0009	0.5529	0.0007
Abhd1	abhydrolase domain containing 1	BC013505	0.301	-0.111	0.0441	0.0413	0.5317
Abhd11	abhydrolase domain containing 11	BC069866	0.408	-0.223	0.0011	0.0229	0.0387
Ablim3	actin binding LIM protein family, member 3	NM_198649	0.243	-0.242	0.0000	0.0000	0.0000
Acat2	acetyl-Coenzyme A acetyltransferase 2	NM_153151	0.364	-0.154	0.0000	0.0001	0.0382
Accn2	amiloride-sensitive cation channel 2, neuronal	AB208022	0.284	-0.281	0.0000	0.0000	0.0002
Accn4	amiloride-sensitive cation channel 4, pituitary	NM_183022	0.255	-0.331	0.0002	0.0464	0.0038
Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	J04947	0.318	-0.422	0.0000	0.0000	0.0000
Ache	acetylcholinesterase	AY389978	0.682	-0.581	0.0000	0.0000	0.0000
Acot8	acyl-CoA thioesterase 8	BC052526	0.282	-0.174	0.0036	0.0170	0.1439
Acot9	acyl-CoA thioesterase 9	NM_022816	0.337	-0.242	0.0027	0.0356	0.0572
Acss1	acyl-CoA synthetase short-chain family member 1	NM_080575	0.380	-0.184	0.0000	0.0000	0.0010
Actl6a	actin-like 6A	AK013221	0.449	-0.137	0.0000	0.0000	0.1024
Actl6b	actin-like 6B	NM_031404	0.461	-0.145	0.0000	0.0000	0.0393
Adamts1	a disintegrin-like and metallopeptidse (reprolysin type) with thrombospondin type 1 motif, 1	NM_009621	0.341	-0.329	0.0000	0.0008	0.0027

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Adamts10	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10	AK034565	0.283	-0.439	0.0000	0.0000	0.0000
Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	AK076295	0.273	-0.152	0.0003	0.0179	0.0121
Adamts6	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 6	XM_001002065	0.378	-0.371	0.0000	0.0000	0.0000
Adamtsl2	ADAMTS-like 2	NM_029981	0.186	-0.347	0.0000	0.0069	0.0000
Adamtsl4	NA	NM_144899	0.174	-0.249	0.0000	0.0392	0.0002
Adck4	aarF domain containing kinase 4	NM_133770	0.448	-0.134	0.0000	0.0000	0.0452
Adck5	aarF domain containing kinase 5	BC053696	0.313	-0.120	0.0015	0.0032	0.2604
Adcy3	adenylate cyclase 3	NM_138305	0.198	-0.244	0.0000	0.0029	0.0000
Adcy5	adenylate cyclase 5	NM_001012765	0.307	-0.109	0.0000	0.0000	0.0001
Adcy7	adenylate cyclase 7	NM_001037723	0.249	-0.318	0.0000	0.0000	0.0000
Adcyap1	adenylate cyclase activating polypeptide 1	NM_009625	0.875	-0.724	0.0000	0.0000	0.0000
Adfp	adipose differentiation related protein	NM_007408	0.336	-0.205	0.0002	0.0019	0.0816
Adra2a	adrenergic receptor, alpha 2a	NM_007417	0.377	-0.235	0.0071	0.1165	0.0436
Aebp2	AE binding protein 2	NM_009637	0.256	-0.145	0.0003	0.0021	0.0876
Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, delta)	NM_026644	0.287	-0.226	0.0002	0.0354	0.0051
Agrin	NA	NM_021604	0.339	-0.123	0.0000	0.0000	0.0000
Agrp	agouti related protein	AK138796	0.866	-0.289	0.0017	0.0023	0.3491
AI462493	expressed sequence AI462493	BC029863	0.527	-0.142	0.0472	0.0495	0.4962

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
AI504432	expressed sequence AI504432	AK030783	0.489	-0.409	0.0100	0.1267	0.0555
AI597468	expressed sequence AI597468	AK005698	0.670	-0.156	0.0180	0.0125	0.6005
AI646023	expressed sequence AI646023	NM_198860	0.405	-0.379	0.0000	0.0006	0.0324
AI846148	NA	AK166227	0.260	-0.240	0.0001	0.0057	0.0159
AI848149	expressed sequence AI848149	AK141827	0.799	-0.417	0.0202	0.0235	0.4430
AI851716	expressed sequence AI851716	AK133701	0.353	-0.193	0.0443	0.0591	0.4155
Aifm1	NA	AK165762	0.320	-0.143	0.0000	0.0006	0.0550
Aig1	androgen-induced 1	AK147713	0.351	-0.114	0.0085	0.0106	0.4050
AK122209	cDNA sequence AK122209	NM_001029876	0.225	-0.181	0.0103	0.1002	0.0732
AK129341	cDNA sequence AK129341	AK129341	0.190	-0.241	0.0272	0.3083	0.0550
Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	AK181349	0.377	-0.063	0.0085	0.0183	0.2770
Akr1c14	NA	NM_134072	0.473	-0.424	0.0000	0.0064	0.0048
Akr1e1	aldo-keto reductase family 1, member E1	NM_018859	0.180	-0.367	0.0000	0.1068	0.0001
Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	BC031857	0.300	-0.211	0.0224	0.1309	0.1164
Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	NM_013467	0.223	-0.350	0.0000	0.0249	0.0000
Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	NM_011921	0.198	-0.300	0.0023	0.1279	0.0131
Aldh4a1	aldehyde dehydrogenase 4 family, member A1	NM_175438	0.379	-0.156	0.0000	0.0001	0.0273
Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucosyltransferase)	XM_988003	0.480	-0.112	0.0000	0.0000	0.2851

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Alg6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase)	AK084993	0.276	-0.145	0.0025	0.0105	0.1534
Alg8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	NM_024220	0.325	-0.177	0.0002	0.0017	0.0893
Alox12b	arachidonate 12-lipoxygenase, 12R type	XM_977240	0.366	-0.161	0.0003	0.0006	0.3043
Aloxe3	arachidonate lipoxygenase 3	AK141003	0.465	-0.519	0.0000	0.0000	0.0000
Als2cr4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	AK133112	0.487	-0.196	0.0003	0.0028	0.0826
Amotl2	angiomotin like 2	BC108411	0.303	-0.103	0.0000	0.0000	0.1537
Ampd2	adenosine monophosphate deaminase 2 (isoform L)	AK034844	0.286	-0.143	0.0000	0.0000	0.0001
Amy2-2	NA	XM_911199	0.418	-0.179	0.0373	0.0514	0.4056
Ankrd13d	ankyrin repeat domain 13 family, member D	AK089186	0.214	-0.206	0.0000	0.0163	0.0003
Ankrd15	ankyrin repeat domain 15	AK020911	0.459	-0.184	0.0000	0.0000	0.0235
Ankrd42	NA	NM_028665	0.205	-0.303	0.0000	0.0526	0.0000
Ankrd45	ankyrin repeat domain 45	XM_355251	0.407	-0.135	0.0330	0.0247	0.5984
Anxa1	annexin A1	NM_010730	0.321	-0.151	0.0086	0.0123	0.3686
Anxa4	annexin A4	AK168917	0.328	-0.157	0.0194	0.0267	0.3963
Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	NM_026887	0.431	-0.307	0.0024	0.0055	0.2462
Ap4m1	adaptor-related protein complex AP-4, mu 1	AF242858	0.371	-0.153	0.0000	0.0003	0.0115

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	NM_009685	0.309	-0.092	0.0001	0.0008	0.0751
Apbb3	amyloid beta (A4) precursor protein-binding, family B, member 3	AK171634	0.278	-0.139	0.0000	0.0034	0.0117
Apcdd1	adenomatosis polyposis coli down-regulated 1	NM_133237	0.447	-0.128	0.0003	0.0013	0.1616
Apex2	apurinic/apyrimidinic endonuclease 2	AK080916	0.306	-0.200	0.0000	0.0003	0.0298
Aph1a	anterior pharynx defective 1a homolog (C. elegans)	BC057865	0.396	-0.012	0.0000	0.0000	0.9442
Apoc1	apolipoprotein C-I	NM_007469	0.777	-0.494	0.0012	0.0165	0.0570
Appbp1	amyloid beta precursor protein binding protein 1	AK038756	0.331	-0.236	0.0000	0.0024	0.0008
Ar	androgen receptor	NM_013476	0.208	-0.249	0.0008	0.0548	0.0120
Ard1	N-acetyltransferase ARD1 homolog (S. cerevisiae)	AK078700	0.316	-0.138	0.0000	0.0001	0.0891
Arf2	ADP-ribosylation factor 2	AK042977	0.311	-0.143	0.0036	0.0308	0.0860
Arfip2	ADP-ribosylation factor interacting protein 2	BC079603	0.329	-0.078	0.0005	0.0011	0.2636
Arfrp1	ADP-ribosylation factor related protein 1	AK083490	0.225	-0.185	0.0027	0.0919	0.0216
Arg2	arginase type II	NM_009705	0.622	-0.339	0.0000	0.0000	0.0222
Arhgap8	Rho GTPase activating protein 8	AK028831	0.176	-0.260	0.0107	0.3685	0.0172
Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	XM_989487	0.636	-0.546	0.0000	0.0009	0.0000
Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	NM_008488	0.307	-0.128	0.0000	0.0000	0.0201
Arid3a	AT rich interactive domain 3A (Bright like)	BC016531	0.221	-0.250	0.0000	0.0060	0.0004

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	D87211	0.277	-0.220	0.0020	0.1146	0.0130
Armc5	armadillo repeat containing 5	NM_146205	0.420	-0.187	0.0000	0.0000	0.1506
Armc6	armadillo repeat containing 6	NM_133972	0.448	-0.114	0.0000	0.0000	0.3643
Armcx6	NA	NM_001007578	0.319	-0.314	0.0022	0.0194	0.0816
Arpc1a	actin related protein 2/3 complex, subunit 1A	NM_019767	0.474	-0.120	0.0002	0.0053	0.0352
Arpc5l	actin related protein 2/3 complex, subunit 5-like	AK037305	0.632	-0.212	0.0000	0.0004	0.0450
Arrb2	arrestin, beta 2	AK089542	0.310	-0.165	0.0000	0.0000	0.0003
Arrdc1	arrestin domain containing 1	NM_178408	0.318	-0.145	0.0002	0.0009	0.1599
Arrdc4	arrestin domain containing 4	NM_001042592	0.452	-0.199	0.0000	0.0001	0.0922
Arsa	arylsulfatase A	AK082325	0.200	-0.253	0.0000	0.1164	0.0000
Arts1	NA	AK163954	0.252	-0.262	0.0000	0.0051	0.0023
Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	AK053865	0.348	-0.243	0.0000	0.0000	0.0000
As3mt	arsenic (+3 oxidation state) methyltransferase	NM_020577	0.203	-0.311	0.0003	0.1951	0.0011
Asb2	ankyrin repeat and SOCS box-containing protein 2	AK083400	0.338	-0.171	0.0002	0.0102	0.0178
Asb3	ankyrin repeat and SOCS box-containing protein 3	NM_023906	0.259	-0.196	0.0006	0.0159	0.0320
Asnsd1	NA	XM_977614	0.326	-0.302	0.0000	0.0041	0.0068
Asphd2	NA	AK020319	0.506	-0.082	0.0006	0.0004	0.5603
Atad2	ATPase family, AAA domain containing 2	NM_027435	0.390	-0.185	0.0000	0.0000	0.0601
Atg9a	NA	AK040323	0.363	-0.083	0.0000	0.0000	0.1392
Athl1	NA	AK171694	0.354	-0.160	0.0000	0.0001	0.1131
Atp2a3	ATPase, Ca++ transporting, ubiquitous	NM_016745	0.249	-0.182	0.0000	0.0001	0.0011

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	XM_975732	0.589	-0.023	0.0001	0.0000	0.8605
Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	NM_026536	0.539	-0.310	0.0013	0.0197	0.0502
Atpbd1c	ATP binding domain 1 family, member C	NM_024216	0.467	-0.106	0.0000	0.0000	0.3408
Atxn7l2	ataxin 7-like 2	NM_175183	0.278	-0.138	0.0000	0.0001	0.0787
AU022870	expressed sequence AU022870	AK171671	0.244	-0.216	0.0013	0.0390	0.0260
AU041783	expressed sequence AU041783	NM_146102	0.335	-0.087	0.0000	0.0000	0.3324
AV249152	expressed sequence AV249152	BC056139	0.149	-0.256	0.0001	0.1391	0.0005
AW060207	expressed sequence AW060207	XR_002899	0.211	-0.311	0.0108	0.2291	0.0310
AW146242	expressed sequence AW146242	NM_146168	0.314	-0.219	0.0032	0.0321	0.0735
AW551984	expressed sequence AW551984	NM_178737	0.726	-0.976	0.0000	0.0000	0.0000
AW555464	expressed sequence AW555464	NM_001024602	0.266	-0.186	0.0000	0.0000	0.0000
AW557046	expressed sequence AW557046	AK153592	0.427	-0.438	0.0022	0.0333	0.0493
B130050I23Rik	RIKEN cDNA B130050I23 gene	AK045240	0.331	-0.184	0.0000	0.0000	0.0000
B230216G23Rik	RIKEN cDNA B230216G23 gene	AK009991	0.282	-0.251	0.0210	0.2389	0.0571
B230312A22Rik	RIKEN cDNA B230312A22 gene	BC044832	0.341	-0.168	0.0000	0.0006	0.0037
B230340J04Rik	NA	AK046078	0.383	-0.415	0.0267	0.2634	0.0652
B3bp	NA	NM_001024917	0.176	-0.244	0.0001	0.0603	0.0012
B430211C08Rik	NA	AK016782	1.151	-0.690	0.0000	0.0000	0.0008
B4galt2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	NM_017377	0.342	-0.120	0.0000	0.0000	0.0504

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	AK045602	0.347	-0.115	0.0034	0.0040	0.4037
B630005N14Rik	RIKEN cDNA B630005N14 gene	AK170526	0.401	-0.104	0.0012	0.0018	0.3357
B930025P03Rik	NA	AK047141	0.355	-0.377	0.0022	0.0749	0.0226
Bai2	brain-specific angiogenesis inhibitor 2	AK144268	0.400	-0.058	0.0000	0.0000	0.1629
Bat5	HLA-B associated transcript 5	NM_178592	0.336	-0.107	0.0000	0.0000	0.0349
BC002216	cDNA sequence BC002216	NM_024472	0.420	-0.300	0.0299	0.1741	0.1148
BC004044	cDNA sequence BC004044	AK149780	0.242	-0.207	0.0001	0.0263	0.0030
BC005764	cDNA sequence BC005764	BC098099	0.352	-0.077	0.0000	0.0000	0.3834
BC010787	cDNA sequence BC010787	NM_178577	0.307	-0.370	0.0004	0.1441	0.0021
BC011487	cDNA sequence BC011487	AK020704	0.699	-0.493	0.0000	0.0005	0.0164
BC013491	cDNA sequence BC013491	AK042062	0.390	-0.104	0.0007	0.0004	0.5991
BC013529	cDNA sequence BC013529	NM_145418	0.171	-0.290	0.0000	0.1711	0.0002
BC020077	cDNA sequence BC020077	AK143777	0.218	-0.327	0.0257	0.3039	0.0528
BC021767	NA	XM_619932	0.470	-0.344	0.0063	0.0840	0.0546
BC022687	cDNA sequence BC022687	BC022687	0.377	-0.129	0.0432	0.0419	0.5193
BC023882	cDNA sequence BC023882	AK049414	0.904	-0.195	0.0284	0.0221	0.5811
BC024814	cDNA sequence BC024814	NM_146247	0.265	-0.166	0.0006	0.0139	0.0350
BC025575	cDNA sequence BC025575	NM_199200	0.447	-0.231	0.0000	0.0000	0.0008
BC026585	cDNA sequence BC026585	XM_987821	0.372	-0.134	0.0316	0.0608	0.3136
BC027231	cDNA sequence BC027231	AK137274	0.372	-0.221	0.0013	0.0048	0.1729
BC028799	cDNA sequence BC028799	XM_001000297	0.223	-0.228	0.0235	0.1014	0.1557

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
BC029214	cDNA sequence BC029214	NM_153557	0.304	-0.249	0.0000	0.0004	0.0185
BC031781	cDNA sequence BC031781	NM_145943	0.434	-0.001	0.0000	0.0000	0.9983
BC031853	cDNA sequence BC031853	BC031853	0.239	-0.234	0.0000	0.0001	0.0078
BC034076	NA	AK083701	0.124	-0.298	0.0016	0.2296	0.0044
BC036313	cDNA sequence BC036313	AK148355	0.252	-0.228	0.0000	0.0000	0.0000
BC037034	cDNA sequence BC037034	BC040828	0.351	-0.185	0.0000	0.0000	0.0015
BC043476	cDNA sequence BC043476	XM_900174	0.380	-0.212	0.0395	0.0372	0.5257
BC046404	cDNA sequence BC046404	XM_974701	0.328	-0.120	0.0371	0.0275	0.6077
BC048355	cDNA sequence BC048355	NM_207161	0.205	-0.252	0.0150	0.1592	0.0646
BC049807	cDNA sequence BC049807	AK038795	0.270	-0.521	0.0001	0.0352	0.0024
BC050789	cDNA sequence BC050789	NM_172515	0.196	-0.346	0.0066	0.2746	0.0152
BC052055	cDNA sequence BC052055	AK048916	0.348	-0.169	0.0000	0.0004	0.0165
BC053749	NA	AK052345	0.450	-0.353	0.0000	0.0000	0.0000
BC062115	NA	NM_001024626	0.318	-0.274	0.0375	0.1821	0.1351
BC088983	cDNA sequence BC088983	NM_001009951	0.293	-0.261	0.0177	0.1111	0.1103
Bcam	NA	NM_020486	0.507	-0.399	0.0000	0.0000	0.0000
Bcan	brevican	NM_007529	0.391	-0.112	0.0000	0.0000	0.0016
Bcap31	B-cell receptor-associated protein 31	NM_012060	0.335	-0.218	0.0001	0.1237	0.0005
Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	XM_918156	0.225	-0.183	0.0021	0.0843	0.0192
Bcl2l2	Bcl2-like 2	AK020923	0.374	-0.327	0.0034	0.0277	0.0888
Bcorl1	BCL6 co-repressor-like 1	XM_979298	0.281	-0.146	0.0001	0.0023	0.0448
Bdnf	brain derived neurotrophic factor	AY231132	0.771	-0.491	0.0069	0.0877	0.0574
BE136769	NA	BC028930	1.020	-1.186	0.0394	0.1902	0.1354

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Bet1	blocked early in transport 1 homolog (S. cerevisiae)	NM_009748	0.232	-0.452	0.0415	0.3558	0.0713
Bgn	biglycan	AK086920	0.424	-0.093	0.0008	0.0005	0.5794
Bhlhb9	basic helix-loop-helix domain containing, class B9	AK183392	0.625	-0.224	0.0044	0.0136	0.2032
Bivm	basic, immunoglobulin-like variable motif containing	NM_144558	0.344	-0.231	0.0000	0.0032	0.0066
Bmp4	bone morphogenetic protein 4	X56848	0.447	-0.273	0.0037	0.0206	0.1254
Bola2	bolA-like 2 (E. coli)	BC061197	0.327	-0.225	0.0003	0.0069	0.0387
Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	AK017801	0.481	-0.174	0.0017	0.0115	0.1052
Brca1	breast cancer 1	NM_009764	0.418	-0.157	0.0000	0.0001	0.1392
Brctd1	BRCT domain containing 1	BC100362	0.189	-0.329	0.0116	0.3100	0.0232
Brp16	brain protein 16	NM_021555	0.409	-0.130	0.0000	0.0000	0.2377
Brp44	brain protein 44	NM_027430	0.651	-0.067	0.0419	0.0221	0.7357
Brs3	bombesin-like receptor 3	NM_009766	0.698	-0.386	0.0000	0.0005	0.0413
Brunol6	bruno-like 6, RNA binding protein (Drosophila)	XM_977145	0.496	-0.286	0.0000	0.0004	0.0011
Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	AK004634	0.313	-0.090	0.0004	0.0049	0.0563
Btd	biotinidase	NM_025295	0.415	-0.331	0.0118	0.0308	0.2407
Bxdc2	brix domain containing 2	NM_026396	0.117	-0.341	0.0146	0.6247	0.0110
C030017K20Rik	NA	XM_001000858	0.284	-0.323	0.0405	0.2485	0.1056
C030019F02Rik	RIKEN cDNA C030019F02 gene	NM_021426	0.385	-0.135	0.0005	0.0060	0.0659
C130026L21Rik	RIKEN cDNA C130026L21 gene	AK160721	0.394	-0.337	0.0359	0.1123	0.2059
C1d	NA	NM_020558	0.205	-0.286	0.0098	0.2919	0.0210

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
C1qb	complement component 1, q subcomponent, beta polypeptide	NM_009777	0.416	-0.319	0.0040	0.0751	0.0393
C1qc	NA	BC069926	0.742	-0.140	0.0123	0.0072	0.6501
C1qdc1	C1q domain containing 1	XM_921237	0.214	-0.260	0.0000	0.0086	0.0000
C1qdc2	NA	NM_026125	0.325	-0.364	0.0000	0.0088	0.0011
C1ql1	complement component 1, q subcomponent-like 1	NM_011795	0.572	-0.347	0.0000	0.0016	0.0192
C230086A09Rik	RIKEN cDNA C230086A09 gene	XM_975827	0.138	-0.339	0.0004	0.4277	0.0005
C230094A16Rik	RIKEN cDNA C230094A16 gene	NM_146016	0.200	-0.203	0.0000	0.0000	0.0000
C330001K17Rik	RIKEN cDNA C330001K17 gene	NM_029939	0.371	-0.179	0.0000	0.0004	0.0716
C330011K17Rik	RIKEN cDNA C330011K17 gene	XM_976236	0.339	-0.334	0.0051	0.1986	0.0173
C330016O10Rik	RIKEN cDNA C330016O10 gene	NM_145974	0.137	-0.321	0.0300	0.5709	0.0271
C430004E15Rik	RIKEN cDNA C430004E15 gene	NM_175286	0.434	-0.162	0.0173	0.0214	0.4227
C4b	NA	XM_973068	0.403	-0.023	0.0000	0.0000	0.8148
C530028O21Rik	RIKEN cDNA C530028O21 gene	NM_175696	0.279	-0.199	0.0023	0.1192	0.0136
C630004H02Rik	RIKEN cDNA C630004H02 gene	NM_175454	0.298	-0.134	0.0000	0.0000	0.0003
C77370	expressed sequence C77370	NM_001077354	0.585	-0.539	0.0069	0.0891	0.0563
Cab39	calcium binding protein 39	NM_133781	0.111	-0.354	0.0058	0.5336	0.0053
Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	BC057399	0.496	-0.286	0.0000	0.0000	0.0000
Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	NM_145121	0.426	-0.262	0.0000	0.0000	0.0000
Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	BC055926	0.555	-0.222	0.0000	0.0000	0.0000
Cacybp	calcyclin binding protein	NM_009786	0.250	-0.232	0.0053	0.1459	0.0257

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	NM_023525	0.280	-0.148	0.0000	0.0000	0.0000
Calb1	calbindin-28K	NM_009788	0.698	-0.451	0.0000	0.0000	0.0000
Calb2	calbindin 2	NM_007586	0.269	-0.288	0.0044	0.0957	0.0340
Calcrl	calcitonin receptor-like	NM_018782	0.237	-0.194	0.0021	0.0311	0.0513
Camk1	calcium/calmodulin-dependent protein kinase I	BC042494	0.217	-0.380	0.0002	0.3886	0.0002
Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	AK044660	0.301	-0.101	0.0000	0.0000	0.0684
Camkv	CaM kinase-like vesicle-associated	NM_145621	0.388	-0.065	0.0000	0.0000	0.3160
Caml	calcium modulating ligand	NM_007596	0.587	-0.071	0.0127	0.0058	0.7443
Cand2	cullin-associated and neddylation-dissociated 2 (putative)	NM_025958	0.347	-0.191	0.0000	0.0004	0.0085
Cant1	calcium activated nucleotidase 1	NM_001025617	0.265	-0.187	0.0012	0.0058	0.1330
Capn10	calpain 10	NM_011796	0.302	-0.106	0.0000	0.0000	0.1253
Capn7	calpain 7	NM_009796	0.226	-0.176	0.0000	0.0006	0.0001
Capns1	calpain, small subunit 1	AK132819	0.315	-0.096	0.0000	0.0000	0.0267
Car10	carbonic anhydrase 10	NM_028296	0.198	-0.264	0.0000	0.0199	0.0001
Car11	carbonic anhydrase 11	AK140243	0.273	-0.203	0.0000	0.0002	0.0000
Car4	carbonic anhydrase 4	NM_007607	0.413	-0.536	0.0000	0.0001	0.0000
Car5b	carbonic anhydrase 5b, mitochondrial	NM_019513	0.370	-0.110	0.0032	0.0020	0.5939
Caskin2	cask-interacting protein 2	NM_080643	0.392	-0.137	0.0000	0.0000	0.0202
Casp8ap2	caspase 8 associated protein 2	NM_011997	0.308	-0.187	0.0026	0.0416	0.0480
Cast	calpastatin	XM_990139	0.129	-0.542	0.0000	0.1451	0.0000
Cbln1	cerebellin 1 precursor protein	NM_019626	0.214	-0.288	0.0085	0.2093	0.0272

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Cbln2	cerebellin 2 precursor protein	NM_172633	0.265	-0.284	0.0003	0.0386	0.0066
Cbwd1	COBW domain containing 1	NM_146097	0.197	-0.229	0.0062	0.2342	0.0174
Ccbl1	cysteine conjugate-beta lyase 1	AK039609	0.332	-0.100	0.0075	0.0124	0.3326
Ccbl2	cysteine conjugate-beta lyase 2	AK084398	0.321	-0.256	0.0003	0.0091	0.0247
Ccdc106	NA	NM_146178	0.390	-0.302	0.0001	0.0403	0.0022
Ccdc116	NA	NM_029779	0.425	-0.216	0.0001	0.0003	0.1213
Ccdc28b	NA	AK031278	0.326	-0.284	0.0139	0.1866	0.0508
Ccdc39	NA	NM_026222	0.213	-0.265	0.0000	0.0310	0.0000
Ccdc45	NA	NM_177088	0.399	-0.154	0.0000	0.0000	0.0287
Ccdc49	NA	BC053447	0.250	-0.206	0.0369	0.1391	0.1732
Ccdc5	coiled-coil domain containing 5	NM_146089	0.188	-0.387	0.0001	0.1167	0.0008
Ccdc53	NA	AK028599	0.464	-0.320	0.0000	0.0059	0.0072
Ccdc65	NA	AK135780	0.148	-0.299	0.0012	0.1744	0.0045
Ccdc77	NA	AK014237	0.298	-0.152	0.0333	0.0632	0.3184
Ccdc79	NA	NM_180958	0.386	-0.289	0.0000	0.0034	0.0106
Ccdc84	NA	NM_201372	0.280	-0.195	0.0135	0.0737	0.1276
Ccdc85a	NA	BC020949	0.504	-0.320	0.0000	0.0000	0.0000
Ccdc90b	NA	BC034878	0.694	-0.264	0.0004	0.0015	0.1695
Ccdc98	NA	NM_172405	0.278	-0.217	0.0050	0.0612	0.0606
Ccl3	chemokine (C-C motif) ligand 3	NM_011337	0.510	-0.405	0.0354	0.0830	0.2673
Ccne1	cyclin E1	NM_007633	0.282	-0.174	0.0000	0.0030	0.0090
Ccne2	cyclin E2	NM_009830	0.596	-0.288	0.0000	0.0002	0.0722
Ccnf	cyclin F	NM_007634	0.304	-0.123	0.0000	0.0000	0.2077
Ccng2	cyclin G2	NM_007635	0.419	-0.041	0.0009	0.0003	0.8183
Ccnh	cyclin H	AK137849	0.218	-0.192	0.0122	0.1141	0.0752
Ccnj	cyclin J	NM_172839	0.291	-0.176	0.0109	0.0384	0.1871
Ccrk	cell cycle related kinase	NM_053180	0.609	-0.158	0.0000	0.0000	0.1681
Cd151	CD151 antigen	NM_009842	0.332	-0.236	0.0000	0.0018	0.0014
Cd164	CD164 antigen	NM_016898	0.293	-0.114	0.0000	0.0000	0.2900
Cd200	Cd200 antigen	BC019172	0.175	-0.273	0.0000	0.0323	0.0006
Cd36	CD36 antigen	AK150648	0.766	-0.597	0.0000	0.0000	0.0000
Cd46	NA	NM_010778	0.139	-0.368	0.0195	0.6139	0.0153
Cd53	CD53 antigen	AK088232	0.389	-0.076	0.0000	0.0000	0.7381

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Cd55	NA	NM_010016	0.313	-0.426	0.0001	0.0242	0.0024
Cd63	NA	NM_001042580	0.639	-0.346	0.0000	0.0000	0.0027
Cd68	CD68 antigen	NM_009853	0.254	-0.352	0.0055	0.3014	0.0112
Cd74	NA	NM_010545	0.728	-0.426	0.0000	0.0000	0.0025
Cda	cytidine deaminase	NM_028176	0.273	-0.574	0.0002	0.1156	0.0015
Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	NM_027276	0.367	-0.155	0.0000	0.0000	0.0025
Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	NM_007658	0.283	-0.231	0.0000	0.0012	0.0064
Cdc42se1	CDC42 small effector 1	NM_172395	0.373	-0.252	0.0000	0.0007	0.0394
Cdh23	cadherin 23 (otocadherin)	AK134635	0.325	-0.386	0.0000	0.0000	0.0000
Cdh24	NA	NM_023190	0.274	-0.287	0.0000	0.0034	0.0056
Cdh7	cadherin 7, type 2	NM_172853	0.345	-0.363	0.0000	0.0002	0.0001
Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	AK004852	0.290	-0.154	0.0013	0.0033	0.2256
Cdk5	cyclin-dependent kinase 5	NM_007668	0.330	-0.131	0.0000	0.0000	0.0015
Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	NM_009874	0.298	-0.228	0.0000	0.0012	0.0061
Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	AK155733	0.324	-0.196	0.0001	0.0128	0.0075
Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	AK140808	0.755	-0.288	0.0177	0.0734	0.1622
Cdo1	cysteine dioxygenase 1, cytosolic	NM_033037	0.246	-0.242	0.0253	0.1131	0.1496
Ceecam1	cerebral endothelial cell adhesion molecule 1	NM_207298	0.280	-0.377	0.0000	0.0030	0.0017
Cenpc1	centromere autoantigen C1	NM_007683	0.227	-0.256	0.0001	0.0322	0.0018
Centg1	centaurin, gamma 1	XM_989454	0.448	-0.118	0.0000	0.0000	0.1061
Cep27	NA	AK007106	0.350	-0.209	0.0117	0.0220	0.3107
Cep78	NA	AK050870	0.234	-0.194	0.0003	0.0036	0.0667

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Cept1	choline/ethanolamine phosphotransferase 1	NM_133869	0.338	-0.161	0.0000	0.0007	0.0043
Cetn2	centrin 2	AK151033	0.313	-0.253	0.0105	0.0515	0.1415
Cftr	cystic fibrosis transmembrane conductance regulator homolog	NM_021050	0.588	-0.218	0.0000	0.0000	0.0438
Cgref1	cell growth regulator with EF hand domain 1	XM_181420	0.182	-0.233	0.0476	0.2099	0.1460
Chd3	chromodomain helicase DNA binding protein 3	XM_484041	0.318	-0.115	0.0000	0.0000	0.0000
Chek1	checkpoint kinase 1 homolog (S. pombe)	NM_007691	0.273	-0.246	0.0121	0.0925	0.0922
Chia	chitinase, acidic	NM_023186	0.280	-0.308	0.0014	0.0195	0.0558
Chic2	cysteine-rich hydrophobic domain 2	BC048435	0.311	-0.168	0.0307	0.0585	0.3160
Chka	choline kinase alpha	AK005057	0.432	-0.126	0.0000	0.0000	0.1692
Chmp2b	chromatin modifying protein 2B	NM_026879	0.525	-0.223	0.0102	0.0796	0.0908
Chmp5	chromatin modifying protein 5	BC053709	0.373	-0.140	0.0000	0.0000	0.0204
Chodl	chondrolectin	AK031063	0.535	-0.346	0.0001	0.0029	0.0222
Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	NM_025844	0.405	-0.255	0.0000	0.0000	0.0079
Chrd	chordin	AK220310	0.290	-0.156	0.0000	0.0000	0.0373
Chrm4	cholinergic receptor, muscarinic 4	NM_007699	0.374	-0.643	0.0433	0.2300	0.1220
Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	NM_021369	0.344	-0.952	0.0001	0.0934	0.0005
Chrnb3	cholinergic receptor, nicotinic, beta polypeptide 3	NM_173212	0.309	-0.288	0.0008	0.0555	0.0115
Chuk	conserved helix-loop-helix ubiquitous kinase	NM_007700	0.276	-0.201	0.0000	0.0001	0.0002
Cib1	calcium and integrin binding 1 (calmyrin)	NM_011870	0.292	-0.185	0.0099	0.0362	0.1825

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Cic	capicua homolog (Drosophila)	NM_027882	0.392	-0.111	0.0000	0.0000	0.0052
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	AK018487	0.431	-0.209	0.0000	0.0000	0.0029
Cks1b	CDC28 protein kinase 1b	AK033161	0.465	-0.351	0.0391	0.1000	0.2489
Clcn2	chloride channel 2	AK141656	0.467	-0.268	0.0000	0.0000	0.0000
Cln8	ceroid-lipofuscinosis, neuronal 8	BC021625	0.338	-0.081	0.0344	0.0220	0.6575
Clptm1l	NA	NM_146047	0.310	-0.147	0.0000	0.0001	0.0059
Cmas	cytidine monophospho-N-acetylneuraminic acid synthetase	NM_009908	0.323	-0.108	0.0001	0.0007	0.0522
Cmbl	NA	NM_181588	0.473	-0.195	0.0163	0.0251	0.3634
Cml5	camello-like 5	NM_023493	0.444	-0.600	0.0177	0.3352	0.0323
Cmtm8	NA	NM_027294	0.377	-0.097	0.0071	0.0048	0.5905
Cnih2	cornichon homolog 2 (Drosophila)	XM_975558	0.396	-0.150	0.0000	0.0000	0.1330
Cnot6l	CCR4-NOT transcription complex, subunit 6-like	NM_144910	0.243	-0.190	0.0000	0.0001	0.0000
Cnp1	cyclic nucleotide phosphodiesterase 1	AK161541	0.297	-0.184	0.0021	0.0067	0.1929
Cntnap3	NA	XM_989262	0.635	-0.599	0.0000	0.0000	0.0000
Cntnap5c	NA	XM_975476	0.145	-0.413	0.0000	0.1588	0.0000
Coasy	Coenzyme A synthase	NM_027896	0.445	-0.197	0.0075	0.0719	0.0756
Coch	coagulation factor C homolog (Limulus polyphemus)	NM_007728	0.093	-0.432	0.0007	0.6086	0.0005
Cog4	component of oligomeric golgi complex 4	NM_133973	0.328	-0.152	0.0000	0.0000	0.0004
Cog7	component of oligomeric golgi complex 7	AK163143	0.302	-0.109	0.0000	0.0000	0.0283
Col12a1	procollagen, type XII, alpha 1	AK076278	0.218	-0.455	0.0000	0.0000	0.0000
Colec12	collectin sub-family member 12	NM_130449	0.473	-0.122	0.0000	0.0000	0.2747

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Comt	catechol-O-methyltransferase	AK148311	0.394	-0.182	0.0004	0.0015	0.1626
Copb2	coatomer protein complex, subunit beta 2 (beta prime)	NM_015827	0.279	-0.170	0.0000	0.0000	0.0000
Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	NM_013715	0.736	-0.191	0.0000	0.0000	0.0243
Copz2	coatomer protein complex, subunit zeta 2	NM_019877	0.293	-0.204	0.0054	0.0682	0.0579
Coq4	coenzyme Q4 homolog (yeast)	BC039570	0.349	-0.097	0.0010	0.0010	0.4355
Coro1a	coronin, actin binding protein 1A	AK037801	0.255	-0.309	0.0000	0.0010	0.0000
Coro2a	coronin, actin binding protein 2A	BC068206	0.241	-0.289	0.0000	0.0000	0.0001
Coro7	coronin 7	AK041000	0.332	-0.130	0.0000	0.0000	0.0004
Cova1	cytosolic ovarian carcinoma antigen 1	AK133956	0.211	-0.197	0.0064	0.0728	0.0646
Cox5a	cytochrome c oxidase, subunit Va	NM_007747	0.557	-0.205	0.0097	0.1868	0.0357
Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	BC024343	0.326	-0.300	0.0128	0.4450	0.0160
Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	NM_183406	0.621	-0.426	0.0066	0.0266	0.1659
Cp	ceruloplasmin	NM_001042611	0.338	-0.315	0.0000	0.0000	0.0000
Cpb1	carboxypeptidase B1 (tissue)	NM_029706	0.470	-0.247	0.0004	0.0030	0.0875
Cpne6	copine VI	NM_009947	0.375	-0.315	0.0000	0.0000	0.0000
Cpne7	copine VII	NM_170684	0.352	-0.262	0.0000	0.0000	0.0000
Cpne9	NA	AK047431	0.103	-0.320	0.0000	0.0157	0.0000
Cpsf1	cleavage and polyadenylation specific factor 1	NM_053193	0.314	-0.109	0.0000	0.0000	0.0007
Cpsf2	cleavage and polyadenylation specific factor 2	NM_016856	0.247	-0.154	0.0000	0.0000	0.0029

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Cpsf4	cleavage and polyadenylation specific factor 4	XM_001004468	0.273	-0.234	0.0023	0.0517	0.0346
Cpt1c	carnitine palmitoyltransferase 1c	AK134246	0.303	-0.140	0.0000	0.0000	0.0001
Cpxm2	carboxypeptidase X 2 (M14 family)	AK038874	0.648	-0.207	0.0000	0.0000	0.0629
Creb1	cAMP responsive element binding protein 1	U46027	0.262	-0.180	0.0000	0.0003	0.0118
Creb3	cAMP responsive element binding protein 3	NM_013497	0.364	-0.197	0.0000	0.0000	0.0002
Creld2	NA	NM_145478	0.319	-0.177	0.0100	0.0322	0.2020
Crh	corticotropin releasing hormone	NM_205769	1.020	-0.521	0.0186	0.0430	0.2683
Crhbp	corticotropin releasing hormone binding protein	AK157912	0.269	-0.518	0.0000	0.1160	0.0001
Crip2	cysteine rich protein 2	NM_024223	0.691	-0.370	0.0000	0.0000	0.0002
Crls1	NA	NM_025646	0.264	-0.154	0.0055	0.0095	0.3188
Crsp9	cofactor required for Sp1 transcriptional activation, subunit 9	NM_025426	0.226	-0.267	0.0192	0.1686	0.0768
Crtap	cartilage associated protein	NM_019922	0.400	-0.107	0.0248	0.0275	0.4638
Csdc2	NA	NM_145473	0.171	-0.248	0.0378	0.3391	0.0685
Csk	c-src tyrosine kinase	BC095962	0.409	-0.093	0.0000	0.0000	0.2644
Csnk2b	casein kinase II, beta subunit	BC003775	0.344	-0.118	0.0007	0.0034	0.1273
Cspg2	chondroitin sulfate proteoglycan 2	XM_488510	0.586	-0.451	0.0000	0.0000	0.0000
Cspg4	chondroitin sulfate proteoglycan 4	AK052394	0.251	-0.184	0.0001	0.0021	0.0424
Ctps	cytidine 5'-triphosphate synthase	NM_016748	0.447	-0.201	0.0000	0.0000	0.0018
Ctsc	cathepsin C	NM_009982	0.427	-0.134	0.0044	0.0040	0.4803
Ctsh	cathepsin H	NM_007801	0.023	-0.379	0.0030	0.9261	0.0010
Ctsl	cathepsin L	NM_009984	0.370	-0.252	0.0000	0.0003	0.0030
Ctso	cathepsin O	NM_177662	0.401	-0.074	0.0087	0.0113	0.3938
Ctsz	cathepsin Z	NM_022325	0.303	-0.163	0.0019	0.0051	0.2238

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Cubn	cubilin (intrinsic factor-cobalamin receptor)	XM_993541	0.434	-0.159	0.0000	0.0000	0.0044
Cul4b	cullin 4B	AK170632	0.338	-0.299	0.0000	0.0000	0.0000
Cuta	NA	AK007912	0.205	-0.210	0.0002	0.0034	0.0399
Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	NM_027545	0.388	-0.200	0.0000	0.0000	0.0278
Cxxc4	CXXC finger 4	BC067052	0.379	-0.313	0.0007	0.0082	0.0627
Cyb5	cytochrome b-5	NM_025797	0.276	-0.140	0.0248	0.0351	0.3920
Cyb561	cytochrome b-561	NM_007805	0.566	-0.394	0.0000	0.0000	0.0000
Cyb561d2	cytochrome b-561 domain containing 2	AF131206	0.452	-0.163	0.0277	0.0395	0.3905
Cyb5r1	NA	NM_028057	0.251	-0.266	0.0000	0.0064	0.0006
Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	AK020848	0.338	-0.200	0.0000	0.0000	0.0035
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	NM_024264	0.317	-0.394	0.0000	0.0095	0.0002
Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	AK037031	0.248	-0.158	0.0290	0.1307	0.1472
Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	BC039770	0.274	-0.238	0.0108	0.0392	0.1837
Cyp4f14	cytochrome P450, family 4, subfamily f, polypeptide 14	NM_022434	0.234	-0.424	0.0000	0.0471	0.0005
Cyp4f15	cytochrome P450, family 4, subfamily f, polypeptide 15	NM_134127	0.385	-0.463	0.0000	0.0021	0.0000
Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	XR_003830	0.411	-0.221	0.0001	0.0011	0.0745
Cyp4x1	cytochrome P450, family 4, subfamily x, polypeptide 1	NR_002138	0.194	-0.292	0.0008	0.0353	0.0183
D0H4S114	DNA segment, human D4S114	AK051015	0.668	-0.425	0.0000	0.0001	0.0010
D0HXS9928E	DNA segment, human DXS9928E	NM_138607	0.287	-0.170	0.0308	0.1065	0.1888

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
D10Ertd322e	DNA segment, Chr 10, ERATO Doi 322, expressed	NM_026065	0.223	-0.354	0.0245	0.6187	0.0194
D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	XM_992169	0.251	-0.160	0.0000	0.0002	0.0310
D11Ertd18e	DNA segment, Chr 11, ERATO Doi 18, expressed	NM_026740	0.428	-0.323	0.0000	0.0004	0.0004
D14Ertd581e	DNA segment, Chr 14, ERATO Doi 581, expressed	AK015781	0.162	-0.251	0.0000	0.0971	0.0002
D16Bwg1494e	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	BC058760	0.330	-0.140	0.0257	0.2866	0.0566
D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	AK133778	0.374	-0.230	0.0000	0.0000	0.0000
D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	NM_080837	0.624	-0.262	0.0000	0.0000	0.0432
D19Ertd721e	DNA segment, Chr 19, ERATO Doi 721, expressed	AK015468	0.448	-0.106	0.0001	0.0001	0.4424
D1Bwg1363e	DNA segment, Chr 1, Brigham & Women's Genetics 1363 expressed	NM_001001566	0.278	-0.158	0.0027	0.0420	0.0489
D230017M19Rik	NA	AK084284	0.463	-0.186	0.0141	0.0255	0.3235
D330017J20Rik	RIKEN cDNA D330017J20 gene	AK163706	0.363	-0.071	0.0000	0.0000	0.4915
D330027H18Rik	RIKEN cDNA D330027H18 gene	XM_913212	0.111	-0.353	0.0067	0.1821	0.0253
D3Ucla1	DNA segment, Chr 3, University of California at Los Angeles 1	NM_030685	0.335	-0.205	0.0245	0.0544	0.2793
D430041B17Rik	NA	NM_172737	0.621	-0.204	0.0000	0.0001	0.2061
D630023F18Rik	RIKEN cDNA D630023F18 gene	AK164708	0.092	-0.364	0.0026	0.6284	0.0018

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
D730048A03Rik	RIKEN cDNA D730048A03 gene	AK148615	0.361	-0.943	0.0312	0.6182	0.0249
D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	NM_138589	0.252	-0.153	0.0000	0.0005	0.0617
D830031N03Rik	NA	AK085936	0.348	-0.219	0.0205	0.0969	0.1435
Dach2	dachshund 2 (Drosophila)	AK033050	0.175	-0.337	0.0185	0.3429	0.0329
Dact3	NA	XM_985316	0.349	-0.057	0.0141	0.0098	0.5955
Dad1	defender against cell death 1	BC024378	0.492	-0.092	0.0030	0.0018	0.5983
Dalrd3	DALR anticodon binding domain containing 3	NM_026378	0.252	-0.167	0.0002	0.0430	0.0046
Dap3	death associated protein 3	NM_022994	0.442	-0.153	0.0000	0.0000	0.0099
Dbi	diazepam binding inhibitor	NM_007830	0.699	-0.228	0.0013	0.1319	0.0072
Dbn1	drebrin 1	AK132060	0.426	-0.020	0.0000	0.0000	0.8618
Dcamkl3	doublecortin and CaM kinase-like 3	NM_172928	0.300	-0.119	0.0159	0.0132	0.5410
Dcbld1	discoidin, CUB and LCCL domain containing 1	NM_025705	0.324	-0.240	0.0001	0.0014	0.0379
Dchs1	NA	XM_194371	0.373	-0.122	0.0151	0.0341	0.2730
Dcn	decorin	BC060126	0.584	-0.134	0.0000	0.0000	0.3934
Dctn2	dynactin 2	NM_027151	0.429	-0.120	0.0000	0.0000	0.0091
Dctn3	dynactin 3	BC061120	0.471	-0.086	0.0057	0.0087	0.3460
Dctn6	dynactin 6	NM_011722	0.334	-0.143	0.0188	0.2259	0.0546
Dcx	doublecortin	AK048410	0.290	-0.517	0.0000	0.0009	0.0000
Ddah2	dimethylarginine dimethylaminohydrolase 2	NM_016765	0.284	-0.156	0.0265	0.0839	0.2056
Ddc	dopa decarboxylase	BC060989	0.040	-0.384	0.0000	0.8405	0.0000
Ddit3	DNA-damage inducible transcript 3	NM_007837	0.299	-0.430	0.0148	0.2357	0.0412
Ddr1	discoidin domain receptor family, member 1	BC006836	0.477	-0.237	0.0000	0.0000	0.0000
Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	NM_001033294	0.388	-0.106	0.0000	0.0000	0.2245

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	AK162752	0.418	-0.062	0.0133	0.0062	0.7381
Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	NM_010029	0.136	-0.357	0.0112	0.4793	0.0123
Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	NM_030096	0.265	-0.139	0.0025	0.0103	0.1544
Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	NM_029408	0.316	-0.091	0.0000	0.0002	0.0544
Degs1	degenerative spermatocyte homolog 1 (Drosophila)	AK165352	0.399	-0.058	0.0381	0.0168	0.8010
Dennd2a	DENN/MADD domain containing 2A	AK047138	0.267	-0.199	0.0000	0.0001	0.0001
Denr	density-regulated protein	AK083852	0.475	-0.084	0.0095	0.0096	0.4663
Derl1	Der1-like domain family, member 1	AK028705	0.356	-0.047	0.0016	0.0008	0.6768
Derl2	Der1-like domain family, member 2	AK083725	0.262	-0.253	0.0210	0.2435	0.0558
Dgka	diacylglycerol kinase, alpha	NM_016811	0.468	-0.413	0.0000	0.0000	0.0000
Dgkk	NA	NM_177914	0.568	-0.474	0.0000	0.0000	0.0000
Dgkq	diacylglycerol kinase, theta	AK134745	0.238	-0.167	0.0000	0.0000	0.0000
Dguok	deoxyguanosine kinase	AK167071	0.398	-0.057	0.0097	0.0044	0.7415
Dhrs1	dehydrogenase/reductase (SDR family) member 1	NM_026819	0.543	-0.175	0.0000	0.0000	0.0007
Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	NM_026191	0.330	-0.286	0.0000	0.0000	0.0000
Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	NM_145614	0.339	-0.080	0.0000	0.0000	0.1035

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Dld	dihydrolipoamide dehydrogenase	NM_007861	0.491	-0.209	0.0000	0.0000	0.0002
Dleu7	deleted in lymphocytic leukemia, 7	AK082171	0.727	-0.297	0.0115	0.0580	0.1373
Dll3	delta-like 3 (Drosophila)	NM_007866	0.327	-0.299	0.0000	0.0020	0.0008
Dmc1	NA	NM_010059	0.302	-0.106	0.0016	0.0013	0.4933
Dmpk	dystrophia myotonica-protein kinase	BC024150	0.362	-0.073	0.0000	0.0000	0.2987
Dmrtc1a	NA	AK006548	0.562	-0.334	0.0034	0.0123	0.1760
Dnahc7b	NA	XM_975178	0.503	-0.756	0.0001	0.1835	0.0003
Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	AK147604	0.276	-0.236	0.0374	0.2391	0.1016
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	AK158530	0.529	-0.102	0.0012	0.0009	0.5289
Dnajb10	DnaJ (Hsp40) homolog, subfamily B, member 10	BC085162	0.268	-0.176	0.0030	0.0120	0.1618
Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	XM_986618	0.281	-0.182	0.0000	0.0000	0.0000
Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	AK032207	0.491	-0.434	0.0000	0.0553	0.0000
Dnpep	aspartyl aminopeptidase	AF005051	0.223	-0.181	0.0000	0.0244	0.0010
Doc2a	double C2, alpha	NM_010069	0.228	-0.328	0.0000	0.0030	0.0000
Doc2g	double C2, gamma	AK084565	0.253	-0.187	0.0046	0.0506	0.0675
Dok4	docking protein 4	NM_053246	0.408	-0.295	0.0000	0.0000	0.0002
Dolpp1	dolichyl pyrophosphate phosphatase 1	NM_020329	0.420	-0.043	0.0000	0.0000	0.7431
Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	NM_007875	0.297	-0.199	0.0048	0.0497	0.0712

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Dpp7	dipeptidylpeptidase 7	AK140420	0.534	-0.396	0.0000	0.0000	0.0000
Dpp9	dipeptidylpeptidase 9	AK039652	0.304	-0.145	0.0000	0.0000	0.0001
Dpy19l1	dpy-19-like 1 (C. elegans)	BC031382	0.314	-0.246	0.0000	0.0002	0.0000
Dpy19l4	NA	AK165377	0.227	-0.268	0.0000	0.0022	0.0000
Dpysl3	dihydropyrimidinase-like 3	AK133040	0.335	-0.376	0.0000	0.0000	0.0000
Dpysl4	dihydropyrimidinase-like 4	AK090197	0.286	-0.159	0.0000	0.0003	0.0741
Dpysl5	dihydropyrimidinase-like 5	AK082132	0.310	-0.185	0.0000	0.0000	0.0000
Drg2	developmentally regulated GTP binding protein 2	NM_021354	0.458	-0.084	0.0005	0.0015	0.1952
Dscr1l2	Down syndrome critical region gene 1-like 2	NM_022980	0.386	-0.178	0.0085	0.0492	0.1220
Dscr2	Down syndrome critical region homolog 2 (human)	NM_019537	0.291	-0.147	0.0010	0.0090	0.0787
Dsg1b	desmoglein 1 beta	NM_181682	0.210	-0.232	0.0197	0.1752	0.0754
Dsg1c	NA	AK034104	0.477	-0.760	0.0000	0.0100	0.0000
Dtx4	deltex 4 homolog (Drosophila)	NM_172442	0.251	-0.182	0.0001	0.0027	0.0302
Dusp15	dual specificity phosphatase-like 15	NM_145744	0.454	-0.299	0.0000	0.0003	0.0015
Dusp26	dual specificity phosphatase 26 (putative)	NM_025869	0.253	-0.186	0.0166	0.1538	0.0735
Dvl1	dishevelled, dsh homolog 1 (Drosophila)	NM_010091	0.324	-0.119	0.0000	0.0000	0.0007
Dync2h1	NA	AY452064	0.265	-0.251	0.0000	0.0000	0.0000
E130112L23Rik	RIKEN cDNA E130112L23 gene	BC058405	0.253	-0.148	0.0000	0.0005	0.0013
E130307M08Rik	RIKEN cDNA E130307M08 gene	NM_026530	0.350	-0.197	0.0000	0.0000	0.0000
E2f1	E2F transcription factor 1	AK017841	0.162	-0.373	0.0003	0.3871	0.0004
E2f5	E2F transcription factor 5	NM_007892	0.418	-0.132	0.0093	0.0069	0.5607
E430002G05Rik	RIKEN cDNA E430002G05 gene	NM_173749	0.168	-0.256	0.0000	0.0516	0.0003

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
E430028B21Rik	RIKEN cDNA E430028B21 gene	NM_178668	0.297	-0.193	0.0085	0.0142	0.3333
Ebf4	early B-cell factor 4	AK149248	0.242	-0.253	0.0000	0.0004	0.0000
Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	NM_007898	0.305	-0.353	0.0001	0.0229	0.0032
Ece2	endothelin converting enzyme 2	BC030900	0.250	-0.194	0.0000	0.0000	0.0000
Ecel1	endothelin converting enzyme-like 1	NM_021306	0.550	-0.455	0.0000	0.0000	0.0000
Echdc1	enoyl Coenzyme A hydratase domain containing 1	AK150932	0.273	-0.243	0.0011	0.0160	0.0543
Echdc2	enoyl Coenzyme A hydratase domain containing 2	NM_026728	0.267	-0.385	0.0001	0.0692	0.0012
Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	BC057971	0.443	-0.123	0.0001	0.0007	0.0908
Ecm1	extracellular matrix protein 1	NM_007899	0.156	-0.256	0.0056	0.3268	0.0102
Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	NM_025380	0.456	-0.196	0.0032	0.0222	0.1018
Efcab1	EF hand calcium binding domain 1	AK015866	0.154	-0.388	0.0093	0.3592	0.0154
Efcab5	NA	NM_176965	0.281	-0.182	0.0010	0.0156	0.0479
Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	XM_978001	0.931	-0.317	0.0000	0.0000	0.0337
Efha1	EF hand domain family A1	BC031373	0.411	-0.182	0.0005	0.0211	0.0182
Efhb	EF hand domain family, member B	NM_172497	0.218	-0.298	0.0037	0.1592	0.0159
Efhc2	EF-hand domain (C-terminal) containing 2	NM_028916	0.105	-0.305	0.0053	0.5751	0.0042
Efna3	ephrin A3	U90666	0.508	-0.532	0.0000	0.0005	0.0000
Efnb3	ephrin B3	NM_007911	0.424	-0.135	0.0000	0.0000	0.1380
EG232887	NA	NM_021312	0.339	-0.304	0.0120	0.0536	0.1535

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
EG232930	NA	BC063050	0.145	-0.307	0.0030	0.2824	0.0065
EG245305	NA	AK045713	0.472	-0.421	0.0363	0.0616	0.3465
EG245436	NA	XM_993224	0.322	-0.092	0.0019	0.0032	0.3117
EG432822	NA	NM_026219	0.675	-0.535	0.0200	0.3699	0.0324
EG433158	NA	NM_011368	0.376	-0.345	0.0080	0.0234	0.2176
EG433865	NA	AK131657	0.429	-0.162	0.0010	0.0008	0.5166
EG433923	NA	XM_484885	0.467	-0.098	0.0329	0.1050	0.2030
EG435336	NA	NM_025401	0.442	-0.155	0.0487	0.0486	0.5138
EG621205	NA	XM_992423	0.453	-0.097	0.0000	0.0000	0.2154
EG626327	NA	XM_983802	0.264	-0.256	0.0067	0.0680	0.0714
EG627363	NA	XM_983477	0.540	-0.950	0.0077	0.0622	0.0892
EG628781	NA	XM_921720	0.625	-0.296	0.0074	0.0511	0.1047
EG631304	NA	XM_992966	0.477	-0.174	0.0431	0.0337	0.5918
EG631624	NA	XM_919663	0.614	-0.546	0.0359	0.0927	0.2450
EG633057	NA	XM_001002874	0.628	-0.215	0.0056	0.0095	0.3224
EG637273	NA	XM_001003388	0.315	-0.252	0.0024	0.4314	0.0028
EG640613	NA	NM_011802	0.091	-0.410	0.0447	0.8363	0.0225
EG666114	NA	XM_906812	0.396	-0.241	0.0014	0.0053	0.1704
EG666355	NA	XM_989317	0.994	-0.180	0.0172	0.0049	0.9288
EG667736	NA	XM_976676	0.473	-0.512	0.0020	0.0372	0.0410
EG667979	NA	NM_198410	0.529	-0.115	0.0395	0.0323	0.5742
EG668524	NA	XM_001004842	0.603	-0.188	0.0426	0.1071	0.2513
EG668669	NA	XM_001003013	0.434	-0.727	0.0278	0.2768	0.0637
Egfl9	EGF-like-domain, multiple 9	NM_207666	0.421	-0.241	0.0000	0.0001	0.0031
Ei24	etoposide induced 2.4 mRNA	NM_007915	0.245	-0.187	0.0000	0.0091	0.0018
Eid1	NA	NM_025613	0.520	-0.381	0.0009	0.1298	0.0049
Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	AK049618	0.289	-0.136	0.0178	0.0271	0.3679
Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	NM_026030	0.249	-0.259	0.0004	0.1128	0.0027
Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	AK012186	0.173	-0.288	0.0000	0.0257	0.0002
Eif3s12	eukaryotic translation initiation factor 3, subunit 12	BC027638	0.255	-0.157	0.0273	0.3195	0.0528

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Eif3s2	eukaryotic translation initiation factor 3, subunit 2 (beta)	AK149955	0.799	-0.012	0.0001	0.0000	0.9588
Eif3s5	eukaryotic translation initiation factor 3, subunit 5 (epsilon)	NM_025344	0.547	-0.054	0.0182	0.0107	0.6610
Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	NM_145139	0.303	-0.143	0.0002	0.0023	0.0557
Eif4e2	eukaryotic translation initiation factor 4E member 2	NM_001039170	0.266	-0.321	0.0017	0.1405	0.0087
Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	NM_001039175	0.340	-0.076	0.0002	0.0003	0.3313
Emid2	EMI domain containing 2	AK051600	0.266	-0.183	0.0000	0.0005	0.0448
Emp2	epithelial membrane protein 2	NM_007929	0.332	-0.090	0.0149	0.0127	0.5290
Emp3	epithelial membrane protein 3	NM_010129	0.428	-0.027	0.0484	0.0162	0.9198
Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	NM_010130	0.468	-0.117	0.0000	0.0000	0.3520
Endogl1	endonuclease G-like 1	NM_172456	0.251	-0.175	0.0304	0.1117	0.1791
Eno3	enolase 3, beta muscle	AK002485	0.410	-0.044	0.0090	0.0041	0.7336
Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	AK038460	0.310	-0.136	0.0233	0.0284	0.4338
Ensa	endosulfine alpha	NM_001026212	0.265	-0.195	0.0351	0.2136	0.1080
Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	NM_172117	0.240	-0.221	0.0000	0.0002	0.0000
Epha1	Eph receptor A1	AK017662	0.601	-0.325	0.0000	0.0000	0.0020
Ephb6	Eph receptor B6	NM_007680	0.689	-0.529	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Ephx1	epoxide hydrolase 1, microsomal	NM_010145	0.184	-0.258	0.0119	0.1807	0.0450
Ephx2	epoxide hydrolase 2, cytoplasmic	AY098585	0.151	-0.354	0.0000	0.1970	0.0000
Epor	erythropoietin receptor	NM_010149	0.380	-0.129	0.0024	0.0025	0.4320
Eppb9	endothelial precursor protein B9	AK010355	0.404	-0.124	0.0082	0.0092	0.4298
Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	NM_010153	0.356	-0.457	0.0000	0.0000	0.0000
Ercc1	excision repair cross-complementing rodent repair deficiency, complementation group 1	NM_007948	0.379	-0.115	0.0000	0.0000	0.1850
Erf	Ets2 repressor factor	NM_010155	0.691	-0.345	0.0000	0.0002	0.0135
Ergic3	NA	BC057130	0.454	-0.246	0.0000	0.0000	0.0000
Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	XM_919590	0.199	-0.269	0.0001	0.0400	0.0014
Etfa	electron transferring flavoprotein, alpha polypeptide	NM_145615	0.475	-0.141	0.0004	0.0050	0.0620
Etfdh	electron transferring flavoprotein, dehydrogenase	AK085493	0.430	-0.209	0.0000	0.0000	0.0001
Etnk2	ethanolamine kinase 2	NM_175443	0.345	-0.340	0.0000	0.0268	0.0003
Exosc8	exosome component 8	NM_027148	0.332	-0.181	0.0026	0.0102	0.1618
F11r	F11 receptor	U89915	0.243	-0.264	0.0000	0.0079	0.0021
F13a1	coagulation factor XIII, A1 subunit	NM_028784	0.440	-0.149	0.0002	0.0005	0.2307
Fabp7	fatty acid binding protein 7, brain	NM_021272	1.112	-0.529	0.0002	0.0115	0.0150
Fads1	fatty acid desaturase1	AK192444	0.235	-0.232	0.0000	0.0022	0.0000
Fads2	fatty acid desaturase2	AK032633	0.316	-0.189	0.0000	0.0000	0.0001
Fads3	fatty acid desaturase3	BC071266	0.310	-0.310	0.0000	0.0011	0.0000
Fah	fumarylacetoacetate hydrolase	NM_010176	0.140	-0.262	0.0000	0.1436	0.0001

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Fancb	NA	BC100430	0.275	-0.191	0.0327	0.0880	0.2363
Fancg	Fanconi anemia, complementation group G	NM_053081	0.302	-0.234	0.0000	0.0000	0.0007
Fbln1	fibulin 1	NM_010180	0.526	-0.398	0.0000	0.0000	0.0000
Fbxl19	F-box and leucine-rich repeat protein 19	XM_989561	0.398	-0.059	0.0000	0.0000	0.3106
Fbxl5	F-box and leucine-rich repeat protein 5	NM_178729	0.441	-0.128	0.0000	0.0010	0.0345
Fbxl6	F-box and leucine-rich repeat protein 6	BC011485	0.360	-0.110	0.0005	0.0016	0.1830
Fbxo36	F-box only protein 36	AK036072	0.170	-0.349	0.0123	0.1566	0.0543
Fbxo44	F-box protein 44	NM_173401	0.295	-0.145	0.0151	0.1029	0.1026
Fbxw17	F-box and WD-40 domain protein 17	NM_175401	0.235	-0.210	0.0008	0.1091	0.0056
Fbxw4	F-box and WD-40 domain protein 4	NM_013907	0.462	-0.017	0.0000	0.0000	0.9001
Fbxw9	F-box and WD-40 domain protein 9	AK156709	0.356	-0.110	0.0005	0.0013	0.2235
Fchsd1	FCH and double SH3 domains 1	BC006858	0.396	-0.251	0.0000	0.0000	0.0017
Fgf10	fibroblast growth factor 10	AK045267	0.382	-0.270	0.0463	0.0728	0.3699
Fgf11	fibroblast growth factor 11	BC066859	0.565	-0.633	0.0000	0.0025	0.0053
Fgf13	fibroblast growth factor 13	AF199608	0.431	-0.075	0.0005	0.0004	0.4644
Fibp	fibroblast growth factor (acidic) intracellular binding protein	AK086610	0.416	-0.210	0.0000	0.0002	0.0008
Fjx1	four jointed box 1 (Drosophila)	NM_010218	0.392	-0.341	0.0351	0.0830	0.2649
Fkbp1b	FK506 binding protein 1b	AB107918	0.405	-0.372	0.0013	0.0591	0.0169
Fkbp8	FK506 binding protein 8	AK188492	0.286	-0.148	0.0000	0.0002	0.0003
Fkrp	fukutin related protein	NM_173430	0.397	-0.051	0.0294	0.0148	0.7368
Flna	filamin, alpha	XM_907967	0.506	-0.281	0.0000	0.0000	0.0000
Flot1	flotillin 1	NM_008027	0.518	-0.262	0.0000	0.0000	0.0000
Fmo1	flavin containing monooxygenase 1	AK143940	0.417	-0.369	0.0000	0.0003	0.0000

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Fmr1	fragile X mental retardation syndrome 1 homolog	AK205186	0.327	-0.084	0.0001	0.0002	0.2832
Fndc4	fibronectin type III domain containing 4	NM_022424	0.355	-0.175	0.0007	0.0053	0.0900
Folh1	folate hydrolase	NM_016770	0.416	-0.390	0.0000	0.0000	0.0000
Frat1	frequently rearranged in advanced T-cell lymphomas	NM_008043	0.480	-0.355	0.0095	0.2177	0.0289
Frg1	FSHD region gene 1	AK038143	0.396	-0.146	0.0012	0.0104	0.0831
Frmd3	FERM domain containing 3	NM_172869	0.177	-0.785	0.0000	0.1989	0.0000
Ftsj3	FtsJ homolog 3 (E. coli)	NM_025310	0.258	-0.170	0.0000	0.0000	0.0021
Fuca1	fucosidase, alpha-L-1, tissue	NM_024243	0.273	-0.134	0.0025	0.1092	0.0166
Fuca2	fucosidase, alpha-L-2, plasma	NM_025799	0.280	-0.222	0.0000	0.0140	0.0025
Fundc2	FUN14 domain containing 2	NM_026126	0.528	-0.397	0.0000	0.0139	0.0005
Fut8	fucosyltransferase 8	BC010666	0.307	-0.124	0.0001	0.0025	0.0215
Fuz	NA	XM_001002171	0.576	-0.200	0.0000	0.0000	0.0006
Fxyd5	FXYD domain-containing ion transport regulator 5	BC031112	0.333	-0.128	0.0000	0.0002	0.1824
Fxyd6	FXYD domain-containing ion transport regulator 6	NM_022004	0.135	-0.446	0.0000	0.3465	0.0000
Fxyd7	FXYD domain-containing ion transport regulator 7	NM_022007	1.071	-0.798	0.0000	0.0000	0.0000
Fyttd1	forty-two-three domain containing 1	NM_027226	0.124	-0.353	0.0000	0.3201	0.0000
Fzd8	frizzled homolog 8 (Drosophila)	AK034561	0.587	-0.352	0.0000	0.0008	0.0283
Fzd9	frizzled homolog 9 (Drosophila)	XM_916560	0.317	-0.752	0.0320	0.7030	0.0210
G6pc3	glucose 6 phosphatase, catalytic, 3	NM_175935	0.318	-0.296	0.0000	0.0000	0.0000
Gabarap	gamma-aminobutyric acid receptor associated protein	BC029329	0.734	-0.293	0.0000	0.0056	0.0006

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Gabarapl2	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	NM_026693	0.312	-0.241	0.0052	0.2709	0.0120
Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	NM_008066	0.440	-0.270	0.0000	0.0000	0.0000
Gabra3	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	NM_008067	0.318	-0.357	0.0000	0.0000	0.0000
Gabra5	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 5	NM_176942	0.366	-0.097	0.0001	0.0000	0.5880
Gabrg1	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	AK039068	0.544	-0.481	0.0000	0.0001	0.0000
Gabrq	gamma-aminobutyric acid (GABA-A) receptor, subunit theta	AK156674	0.283	-0.229	0.0000	0.0001	0.0330
Gad1	glutamic acid decarboxylase 1	NM_008077	0.139	-0.325	0.0000	0.0065	0.0000
Gad2	glutamic acid decarboxylase 2	AK136834	0.181	-0.507	0.0000	0.0001	0.0000
Gadd45b	growth arrest and DNA-damage-inducible 45 beta	NM_008655	0.405	-0.159	0.0051	0.0047	0.4823
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	NM_183358	0.492	-0.183	0.0319	0.0628	0.3092
Gal	galanin	NM_010253	1.063	-0.573	0.0000	0.0000	0.0060
Galk1	galactokinase 1	BC016602	0.314	-0.108	0.0218	0.0299	0.3997
Galm	galactose mutarotase	AK085153	0.175	-0.307	0.0473	0.4014	0.0701
Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	NM_013814	0.328	-0.177	0.0000	0.0001	0.0019

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Gamt	guanidinoacetate methyltransferase	NM_010255	0.867	-0.493	0.0000	0.0000	0.0000
Ganab	alpha glucosidase 2 alpha neutral subunit	AK149686	0.180	-0.224	0.0000	0.0007	0.0000
Gap43	growth associated protein 43	AK031908	0.115	-0.376	0.0001	0.2062	0.0001
Gatad1	GATA zinc finger domain containing 1	AK081359	0.362	-0.056	0.0117	0.0090	0.5523
Gats	opposite strand transcription unit to Stag3	XM_622563	0.290	-0.114	0.0000	0.0000	0.0549
Gba2	glucosidase beta 2	BC031397	0.440	-0.191	0.0000	0.0000	0.0000
Gcdh	glutaryl-Coenzyme A dehydrogenase	NM_008097	0.479	-0.119	0.0000	0.0000	0.0926
Gck	glucokinase	NM_010292	0.299	-0.136	0.0182	0.0312	0.3369
Gckr	glucokinase regulatory protein	NM_144909	0.221	-0.220	0.0049	0.0437	0.0822
Gclm	glutamate-cysteine ligase, modifier subunit	NM_008129	0.291	-0.195	0.0000	0.0010	0.0018
Gcs1	glucosidase 1	AK150873	0.517	-0.090	0.0008	0.0007	0.4730
Gdf11	growth differentiation factor 11	NM_010272	0.399	-0.229	0.0000	0.0050	0.0054
Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	AK013104	0.295	-0.259	0.0009	0.0156	0.0438
Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	AK086508	0.459	-0.394	0.0000	0.0000	0.0000
Gemin5	gem (nuclear organelle) associated protein 5	NM_172558	0.232	-0.226	0.0000	0.0000	0.0000
Gfpt1	glutamine fructose-6-phosphate transaminase 1	AK039792	0.254	-0.192	0.0000	0.0000	0.0000
Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	NM_008115	0.408	-0.381	0.0000	0.0008	0.0000
Ggh	gamma-glutamyl hydrolase	XM_989632	0.393	-0.255	0.0354	0.1131	0.2019

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Git1	G protein-coupled receptor kinase-interactor 1	NM_001004144	0.345	-0.090	0.0000	0.0000	0.0011
Gja9	gap junction membrane channel protein alpha 9	NM_010290	0.344	-0.170	0.0206	0.0222	0.4653
Gkap1	G kinase anchoring protein 1	NM_019832	0.301	-0.221	0.0152	0.1322	0.0793
Gla	galactosidase, alpha	AK164231	0.235	-0.229	0.0034	0.0373	0.0664
Glmn	glomulin, FKBP associated protein	NM_133248	0.370	-0.289	0.0000	0.0004	0.0042
Glo1	glyoxalase 1	AK037686	0.201	-0.237	0.0190	0.1301	0.1002
Glra2	glycine receptor, alpha 2 subunit	NM_183427	0.462	-0.555	0.0000	0.0001	0.0000
Glra3	glycine receptor, alpha 3 subunit	AK038618	0.220	-0.757	0.0000	0.1528	0.0000
Glra4	glycine receptor, alpha 4 subunit	NM_010297	0.422	-0.211	0.0040	0.0123	0.2023
Glt8d1	glycosyltransferase 8 domain containing 1	NM_029626	0.407	-0.200	0.0000	0.0008	0.0076
Gm1040	NA	NM_001033457	0.406	-0.318	0.0001	0.0104	0.0057
Gm1673	gene model 1673, (NCBI)	BC100514	0.565	-0.234	0.0057	0.0340	0.1180
Gm1865	NA	XM_284307	0.406	-0.218	0.0000	0.0000	0.0394
Gm237	gene model 237, (NCBI)	XM_979302	0.492	-0.145	0.0290	0.0198	0.6263
Gm440	gene model 440, (NCBI)	NM_198620	0.262	-0.192	0.0000	0.0003	0.0005
Gm527	gene model 527, (NCBI)	NM_001025605	0.461	-0.092	0.0214	0.0134	0.6476
Gm528	NA	XM_986450	0.581	-0.470	0.0000	0.0044	0.0067
Gm561	gene model 561, (NCBI)	NM_001033297	0.571	-0.437	0.0051	0.0680	0.0557
Gm939	NA	XM_355019	0.477	-0.159	0.0453	0.0633	0.4030
Gmip	Gem-interacting protein	NM_198101	0.395	-0.385	0.0000	0.0000	0.0000
Gmppb	GDP-mannose pyrophosphorylase B	AK165816	0.535	-0.274	0.0000	0.0006	0.0131
Gmpr2	guanosine monophosphate reductase 2	BC003886	0.253	-0.150	0.0085	0.0345	0.1670
Gnb4	guanine nucleotide binding protein,beta4	AK020124	0.241	-0.175	0.0023	0.0456	0.0387

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Gng4	guanine nucleotide binding protein (G protein), gamma 4 subunit	NM_010317	0.326	-0.205	0.0040	0.0283	0.1021
Gnpda1	glucosamine-6-phosphate deaminase 1	AK084247	0.374	-0.380	0.0000	0.0034	0.0095
Golga2	golgi autoantigen, golgin subfamily a, 2	AK077516	0.240	-0.175	0.0000	0.0001	0.0000
Golga5	golgi autoantigen, golgin subfamily a, 5	AF026274	0.444	-0.108	0.0001	0.0004	0.1819
Gpc3	glypican 3	AK077942	0.492	-0.100	0.0063	0.0046	0.5601
Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	NM_010271	0.249	-0.167	0.0001	0.0075	0.0160
Gpr101	NA	NM_001033360	0.466	-0.344	0.0033	0.0139	0.1557
Gpr126	NA	NM_001002268	0.203	-0.391	0.0000	0.0390	0.0000
Gpr149	G protein-coupled receptor 149	NM_177346	0.260	-0.636	0.0011	0.3820	0.0016
Gpr153	G protein-coupled receptor 153	NM_178406	0.499	-0.354	0.0000	0.0000	0.0002
Gpr162	G protein-coupled receptor 162	BC016413	0.386	-0.124	0.0001	0.0002	0.2854
Gpr165	G protein-coupled receptor 165	AK045935	0.211	-0.539	0.0000	0.0156	0.0000
Gpr172b	G protein-coupled receptor 172B	AK142597	0.664	-0.416	0.0000	0.0000	0.0023
Gpr173	G-protein coupled receptor 173	NM_027543	0.494	-0.307	0.0002	0.0029	0.0540
Gpr175	G protein-coupled receptor 175	NM_011906	0.380	-0.178	0.0000	0.0000	0.0001
Gpr177	NA	AK031444	0.472	-0.258	0.0000	0.0000	0.0005
Gpr26	G protein-coupled receptor 26	NM_173410	0.428	-0.173	0.0016	0.0023	0.3497
Gpr37l1	G protein-coupled receptor 37-like 1	NM_134438	0.397	-0.122	0.0023	0.0044	0.2867
Gpr4	G protein-coupled receptor 4	NM_175668	0.757	-0.706	0.0278	0.0949	0.1917
Gpr56	G protein-coupled receptor 56	NM_018882	0.459	-0.235	0.0000	0.0000	0.0000
Gpr64	G protein-coupled receptor 64	AK041291	0.212	-0.254	0.0002	0.0476	0.0034
Gpr85	G protein-coupled receptor 85	NM_145066	0.396	-0.250	0.0018	0.0038	0.2588

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Gpr89	G protein-coupled receptor 89	NM_026229	0.320	-0.228	0.0000	0.0000	0.0001
Gprk5	G protein-coupled receptor kinase 5	AK135076	0.515	-0.417	0.0000	0.0000	0.0000
Gprk6	G protein-coupled receptor kinase 6	AK051405	0.245	-0.172	0.0000	0.0000	0.0010
Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	BC071197	0.326	-0.167	0.0000	0.0000	0.0007
Grb7	growth factor receptor bound protein 7	M94450	0.317	-0.239	0.0024	0.0242	0.0721
Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	NM_010349	0.156	-0.290	0.0000	0.1029	0.0000
Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	NM_008168	0.393	-0.141	0.0000	0.0000	0.0000
Grin2d	glutamate receptor, ionotropic, NMDA2D (epsilon4)	NM_008172	0.375	-0.205	0.0000	0.0000	0.0000
Grin3a	glutamate receptor ionotropic, NMDA3A	AK138366	0.357	-0.319	0.0001	0.0009	0.0942
Grm2	G protein-coupled receptor, family C, group 1, member B	XM_909627	0.267	-0.143	0.0401	0.0814	0.3024
Grn	granulin	NM_008175	0.303	-0.178	0.0000	0.0000	0.0001
Grpr	gastrin releasing peptide receptor	NM_008177	0.563	-0.524	0.0248	0.0725	0.2210
Grwd1	glutamate-rich WD repeat containing 1	AB001539	0.369	-0.176	0.0003	0.0046	0.0505
Gsn	gelsolin	BC060377	0.527	-0.142	0.0000	0.0000	0.0079
Gstk1	glutathione S-transferase kappa 1	NM_029555	0.608	-0.158	0.0002	0.0005	0.2104
Gstm4	glutathione S-transferase, mu 4	NM_026764	0.314	-0.212	0.0000	0.0002	0.0064
Gstm6	glutathione S-transferase, mu 6	NM_008184	0.666	-0.450	0.0000	0.0000	0.0000
Gstm7	glutathione S-transferase, mu 7	NM_026672	0.545	-0.337	0.0000	0.0000	0.0002
Gstp1	glutathione S-transferase, pi 1	NM_013541	0.797	-0.248	0.0000	0.0000	0.0011
Gstp2	NA	NM_181796	0.473	-0.368	0.0000	0.0040	0.0020

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Gstt1	glutathione S-transferase, theta 1	NM_008185	0.446	-0.264	0.0013	0.0524	0.0202
Gstt2	glutathione S-transferase, theta 2	BC012707	0.415	-0.381	0.0001	0.0046	0.0229
Gstt3	glutathione S-transferase, theta 3	NM_133994	0.425	-0.207	0.0031	0.0029	0.4640
Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	NM_010363	0.228	-0.180	0.0008	0.0218	0.0285
Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	BC020016	0.320	-0.336	0.0000	0.0103	0.0036
Gtf2h3	general transcription factor IIH, polypeptide 3	NM_181410	0.384	-0.047	0.0015	0.0005	0.7770
Gtf3c5	general transcription factor IIIC, polypeptide 5	NM_148928	0.563	-0.167	0.0000	0.0000	0.0207
Gucy1a2	guanylate cyclase 1, soluble, alpha 2	NM_001033322	0.405	-0.340	0.0000	0.0000	0.0000
Gucy1a3	guanylate cyclase 1, soluble, alpha 3	NM_021896	0.202	-0.251	0.0000	0.0050	0.0001
Gulp1	GULP, engulfment adaptor PTB domain containing 1	NM_028450	0.212	-0.279	0.0066	0.1268	0.0373
Gusb	glucuronidase, beta	BC018202	0.219	-0.234	0.0000	0.0361	0.0002
Gyg	NA	NM_013755	0.300	-0.313	0.0003	0.0777	0.0026
Gyk	glycerol kinase	NM_008194	0.221	-0.189	0.0001	0.0145	0.0082
Gzf1	NA	NM_028986	0.421	-0.215	0.0000	0.0026	0.0141
H13	histocompatibility 13	BC056977	0.295	-0.125	0.0000	0.0000	0.0053
H2afy3	H2A histone family, member Y3	NM_207000	0.619	-0.128	0.0079	0.0043	0.6626
H2-DMa	histocompatibility 2, class II, locus DMa	AK146950	0.549	-0.258	0.0179	0.0201	0.4502
H2-Ke2	H2-K region expressed gene 2	NM_010385	0.124	-0.308	0.0209	0.6969	0.0134
H2-Ke6	H2-K region expressed gene 6	AK169702	0.551	-0.050	0.0426	0.0206	0.7718
H2-M3	histocompatibility 2, M region locus 3	NM_013819	0.565	-0.103	0.0140	0.0056	0.7980
H2-Q2	histocompatibility 2, Q region locus 2	NM_010392	0.437	-0.445	0.0146	0.1201	0.0845

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
H2-T10	histocompatibility 2, T region locus 10	NM_010395	0.139	-0.394	0.0061	0.5830	0.0049
Hap1	huntingtin-associated protein 1	NM_010404	0.388	-0.209	0.0000	0.0000	0.0000
Hars	histidyl-tRNA synthetase	AK014253	0.536	-0.131	0.0000	0.0000	0.0113
Harsl	histidyl-tRNA synthetase-like	NM_080636	0.257	-0.174	0.0002	0.0088	0.0153
Hbp1	high mobility group box transcription factor 1	NM_153198	0.501	-0.067	0.0000	0.0000	0.5482
Hbxip	hepatitis B virus x interacting protein	XM_973046	0.698	-0.102	0.0251	0.0180	0.6071
Hccs	holocytochrome c synthetase	AK028608	0.341	-0.099	0.0046	0.0047	0.4469
Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	NM_181821	0.291	-0.228	0.0072	0.1109	0.0467
Hcn3	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	AF064875	0.559	-0.474	0.0000	0.0000	0.0001
Hcrtr1	hypocretin (orexin) receptor 1	NM_198959	0.694	-0.918	0.0000	0.0000	0.0000
Hcrtr2	hypocretin (orexin) receptor 2	AY336084	0.424	-0.471	0.0000	0.0026	0.0067
Hdac11	histone deacetylase 11	NM_144919	0.314	-0.138	0.0000	0.0000	0.0179
Hdac2	histone deacetylase 2	NM_008229	0.358	-0.281	0.0000	0.0009	0.0000
Hdac6	histone deacetylase 6	XM_973545	0.318	-0.309	0.0000	0.0000	0.0000
Hddc2	HD domain containing 2	AK009957	0.334	-0.350	0.0009	0.0390	0.0191
Hdgf	hepatoma-derived growth factor	NM_008231	0.272	-0.183	0.0000	0.0208	0.0018
Hells	helicase, lymphoid specific	AK014040	0.113	-0.333	0.0010	0.5578	0.0008
Heph	hephaestin	NM_010417	0.331	-0.343	0.0000	0.0001	0.0000
Herc4	hect domain and RLD 4	AK019546	0.258	-0.202	0.0000	0.0001	0.0000
Hes5	hairy and enhancer of split 5 (Drosophila)	NM_010419	0.308	-0.333	0.0003	0.0735	0.0037
Hexa	hexosaminidase A	NM_010421	0.351	-0.129	0.0000	0.0002	0.0611
Hexdc	NA	NM_001001333	0.354	-0.157	0.0000	0.0000	0.0050

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	AK186066	0.362	-0.309	0.0000	0.0008	0.0002
Hist1h2be	histone 1, H2be	NM_178194	0.417	-0.439	0.0006	0.0240	0.0191
Hist2h3c2	histone 2, H3c2	NM_054045	1.004	-0.914	0.0237	0.0586	0.2557
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	NM_145942	0.208	-0.240	0.0000	0.0000	0.0000
Hn1	hematological and neurological expressed sequence 1	NM_008258	0.505	-0.238	0.0045	0.1918	0.0156
Hn1l	NA	NM_198937	0.500	-0.319	0.0004	0.0014	0.1691
Hnmt	histamine N-methyltransferase	AK050129	0.495	-0.509	0.0000	0.0030	0.0036
Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	BC043069	0.340	-0.061	0.0000	0.0000	0.4870
Hnrph3	heterogeneous nuclear ribonucleoprotein H3	XM_897051	0.262	-0.160	0.0197	0.1424	0.0942
Hook1	hook homolog 1 (Drosophila)	AK028714	0.290	-0.236	0.0000	0.0001	0.0000
Hpcal4	hippocalcin-like 4	NM_174998	0.654	-0.442	0.0000	0.0000	0.0001
Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	NM_008278	0.594	-0.140	0.0009	0.0010	0.4015
Hras1	Harvey rat sarcoma virus oncogene 1	BC011083	0.438	-0.155	0.0077	0.0625	0.0889
Hrh3	histamine receptor H 3	NM_133849	0.433	-0.198	0.0003	0.0010	0.1759
Hrsp12	heat-responsive protein 12	AK005016	0.490	-0.218	0.0001	0.0042	0.0108
Hs3st5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	XM_356462	0.304	-0.307	0.0050	0.1056	0.0346
Hsd17b10	NA	NM_016763	0.530	-0.187	0.0004	0.0019	0.1401
Hsf2	heat shock factor 2	NM_008297	0.285	-0.250	0.0000	0.0049	0.0000
Hspa1a	heat shock protein 1A	NM_010479	0.874	-0.671	0.0258	0.0305	0.4446
Hspb1	heat shock protein 1	NM_013560	0.717	-0.370	0.0086	0.1285	0.0478

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Hspb8	heat shock 27kDa protein 8	NM_030704	0.247	-0.215	0.0172	0.1002	0.1188
Hspc171	NA	BC024608	0.459	-0.249	0.0014	0.0250	0.0446
Hspd1	heat shock protein 1 (chaperonin)	BC106112	0.290	-0.199	0.0008	0.1632	0.0031
Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	NM_008308	0.753	-0.598	0.0022	0.0260	0.0643
Htr2a	NA	NM_172812	0.326	-0.236	0.0001	0.0046	0.0097
Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	NM_008312	0.329	-0.252	0.0000	0.0004	0.0004
Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	NM_013561	0.404	-0.291	0.0000	0.0003	0.0622
Htr5a	5-hydroxytryptamine (serotonin) receptor 5A	NM_008314	0.418	-0.302	0.0016	0.0107	0.1022
Htra2	HtrA serine peptidase 2	NM_019752	0.414	-0.043	0.0447	0.0199	0.8045
Hyls1	NA	BC035953	0.511	-0.191	0.0111	0.0128	0.4310
Iars2	isoleucine-tRNA synthetase 2, mitochondrial	AK043729	0.201	-0.216	0.0000	0.0010	0.0000
Ict1	immature colon carcinoma transcript 1	BC079614	0.258	-0.204	0.0004	0.0765	0.0044
Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	NM_010497	0.151	-0.285	0.0000	0.2085	0.0000
Ier3	immediate early response 3	NM_133662	0.372	-0.413	0.0199	0.4461	0.0250
Ier3ip1	immediate early response 3 interacting protein 1	NM_025409	0.557	-0.326	0.0001	0.0003	0.1331
Ifi30	interferon gamma inducible protein 30	NM_023065	0.720	-0.232	0.0000	0.0000	0.3064
Ifit2	interferon-induced protein with tetratricopeptide repeats 2	NM_008332	0.545	-0.323	0.0360	0.0757	0.2934
Ifitm3	interferon induced transmembrane protein 3	NM_025378	0.650	-0.182	0.0206	0.0144	0.6076

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Ift122	NA	NM_031177	0.229	-0.182	0.0000	0.0000	0.0000
Ift140	NA	NM_134126	0.229	-0.198	0.0000	0.0000	0.0004
Ift172	NA	NM_026298	0.309	-0.155	0.0000	0.0000	0.0000
Ift74	NA	BC049156	0.170	-0.259	0.0002	0.0830	0.0019
Igfbp2	insulin-like growth factor binding protein 2	NM_008342	0.875	-0.370	0.0000	0.0000	0.0311
Igfbp4	insulin-like growth factor binding protein 4	NM_010517	0.719	-0.013	0.0040	0.0009	0.9866
Igfbp5	insulin-like growth factor binding protein 5	NM_010518	0.347	-0.222	0.0000	0.0010	0.0046
Igsf1	immunoglobulin superfamily, member 1	NM_177591	0.611	-0.301	0.0000	0.0000	0.0000
Igsf21	immunoglobin superfamily, member 21	NM_198610	0.483	-0.198	0.0000	0.0000	0.0010
Igsf4b	immunoglobulin superfamily, member 4B	NM_053199	0.262	-0.154	0.0001	0.0019	0.0221
Igsf9	immunoglobulin superfamily, member 9	AK053544	0.242	-0.220	0.0000	0.0004	0.0032
Ihpk1	inositol hexaphosphate kinase 1	AK006216	0.389	-0.017	0.0068	0.0021	0.8699
Ik	IK cytokine	NM_011879	0.294	-0.273	0.0000	0.0289	0.0004
Il18	interleukin 18	NM_008360	0.350	-0.163	0.0387	0.0737	0.3186
Ilvbl	ilvB (bacterial acetolactate synthase)-like	AK138031	0.324	-0.216	0.0000	0.0047	0.0000
Impdh1	inosine 5'-phosphate dehydrogenase 1	NM_011829	0.343	-0.091	0.0000	0.0000	0.1751
Impdh2	inosine 5'-phosphate dehydrogenase 2	AK203194	0.501	-0.157	0.0000	0.0000	0.0204
Ing2	NA	NM_023503	0.647	-0.400	0.0085	0.0305	0.1841
Inppl1	inositol polyphosphate phosphatase-like 1	NM_010567	0.321	-0.133	0.0000	0.0000	0.0051
Ints3	NA	AK040147	0.263	-0.138	0.0000	0.0000	0.0001

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Ipp	IAP promoted placental gene	AK042290	0.226	-0.189	0.0193	0.0715	0.1806
Iqcg	IQ motif containing G	XM_001001741	0.299	-0.295	0.0020	0.0661	0.0229
Irf5	interferon regulatory factor 5	AK150598	0.296	-0.157	0.0229	0.0506	0.2814
Isyna1	NA	NM_023627	0.590	-0.213	0.0000	0.0000	0.0001
Itga3	integrin alpha 3	BC062205	0.319	-0.282	0.0000	0.0000	0.0000
Itga7	integrin alpha 7	NM_008398	0.479	-0.196	0.0000	0.0000	0.0000
Itih2	inter-alpha trypsin inhibitor, heavy chain 2	AK149533	0.302	-0.112	0.0014	0.0017	0.3916
Itm2a	integral membrane protein 2A	NM_008409	0.365	-0.249	0.0000	0.0070	0.0003
Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	NM_025922	0.366	-0.066	0.0118	0.0050	0.7646
Jag2	jagged 2	BC009082	0.462	-0.156	0.0000	0.0000	0.0001
Jak3	Janus kinase 3	NM_010589	0.292	-0.200	0.0000	0.0000	0.0052
Jam2	junction adhesion molecule 2	NM_023844	0.333	-0.381	0.0000	0.0001	0.0000
Jmjd3	jumonji domain containing 3	BC075632	0.293	-0.161	0.0000	0.0000	0.0007
Josd2	NA	NM_025368	0.295	-0.207	0.0044	0.1160	0.0276
Jtb	jumping translocation breakpoint	AK146337	0.573	-0.046	0.0067	0.0023	0.8204
Jup	junction plakoglobin	AK086401	0.454	-0.285	0.0000	0.0000	0.0000
Katnal2	NA	BC069977	0.179	-0.263	0.0026	0.1784	0.0098
Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	NM_026962	0.247	-0.480	0.0135	0.3453	0.0239
Kbtbd4	kelch repeat and BTB (POZ) domain containing 4	NM_025991	0.489	-0.220	0.0227	0.0578	0.2491
Kcna3	potassium voltage-gated channel, shaker-related subfamily, member 3	NM_008418	0.375	-0.233	0.0049	0.1038	0.0342

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	AK031890	0.275	-0.218	0.0257	0.3237	0.0493
Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	NM_145922	0.302	-0.189	0.0000	0.0118	0.0022
Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	NM_008423	0.289	-0.205	0.0014	0.0160	0.0662
Kcne1l	potassium voltage-gated channel, Isk-related family, member 1-like	NM_021487	0.481	-0.082	0.0495	0.0304	0.6882
Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	XM_981382	0.375	-0.180	0.0000	0.0000	0.0003
Kcnk4	potassium channel, subfamilyK,member4	NM_008431	0.260	-0.185	0.0002	0.0029	0.0483
Kcnv1	potassium channel, subfamilyV,member1	NM_026200	0.734	-0.190	0.0028	0.0010	0.7969
Kctd5	potassium channel tetramerisation domain containing 5	NM_027008	0.471	-0.109	0.0210	0.0133	0.6407
Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing1	NM_023645	0.190	-0.248	0.0011	0.1327	0.0061
Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	NM_133950	0.553	-0.168	0.0002	0.0002	0.3452
Kif17	kinesin family member 17	AK083171	0.334	-0.193	0.0000	0.0000	0.0168
Kir3dl2	NA	AK046171	0.484	-0.160	0.0001	0.0001	0.3554
Kirrel1	kin of IRRE like 1 (Drosophila)	BC023765	0.450	-0.146	0.0000	0.0000	0.1355
Klc4	NA	NM_029091	0.371	-0.099	0.0000	0.0000	0.1448
Klf6	Kruppel-like factor 6	AY027436	0.299	-0.148	0.0122	0.0410	0.1945
Klf8	NA	BC070442	0.457	-0.273	0.0005	0.0020	0.1658
Klhdc8a	NA	NM_144810	0.266	-0.382	0.0000	0.0264	0.0001

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Klhl1	kelch-like 1 (Drosophila)	AK163473	0.395	-0.468	0.0000	0.0000	0.0000
Klhl12	kelch-like 12 (Drosophila)	NM_153128	0.284	-0.225	0.0000	0.0069	0.0008
Klhl13	kelch-like 13 (Drosophila)	NM_026167	0.256	-0.328	0.0000	0.0769	0.0004
Klhl2	kelch-like 2, Mayven (Drosophila)	AK167903	0.390	-0.053	0.0006	0.0004	0.5713
Klhl23	kelch-like 23 (Drosophila)	NM_177784	0.523	-0.075	0.0004	0.0002	0.6311
Klhl24	NA	NM_029436	0.369	-0.112	0.0000	0.0000	0.0248
Klhl4	kelch-like 4 (Drosophila)	NM_172781	0.246	-0.334	0.0000	0.0653	0.0002
Klk6	kallikrein 6	NM_011177	0.349	-0.373	0.0002	0.0198	0.0070
Klrg1	killer cell lectin-like receptor subfamily G, member 1	NM_016970	0.382	-0.260	0.0258	0.0652	0.2509
Krit1	KRIT1, ankyrin repeat containing	AK050470	0.178	-0.232	0.0000	0.0334	0.0000
Krtcap2	keratinocyte associated protein 2	NM_025327	0.438	-0.226	0.0004	0.0065	0.0504
L1cam	L1 cell adhesion molecule	NM_008478	0.189	-0.317	0.0000	0.0000	0.0000
L3mbtl	NA	BC116639	0.289	-0.359	0.0000	0.0000	0.0000
L3mbtl2	l(3)mbt-like 2 (Drosophila)	AY237002	0.271	-0.205	0.0000	0.0001	0.0000
Lair1	leukocyte-associated Ig-like receptor 1	AF491829	0.381	-0.116	0.0026	0.0017	0.5742
Lama2	laminin, alpha 2	NM_008481	0.367	-0.186	0.0000	0.0000	0.0001
Larp2	NA	BC025528	0.372	-0.278	0.0061	0.0379	0.1151
Lasp1	LIM and SH3 protein 1	NM_010688	0.248	-0.352	0.0000	0.0000	0.0000
Lass4	longevity assurance homolog 4 (S. cerevisiae)	AK036108	0.378	-0.339	0.0000	0.0000	0.0000
Lass5	longevity assurance homolog 5 (S. cerevisiae)	BC043059	0.326	-0.238	0.0000	0.0057	0.0001
Lcat	lecithin cholesterol acyltransferase	NM_008490	0.260	-0.242	0.0001	0.0465	0.0017
Lcorl	NA	BC066151	0.355	-0.411	0.0070	0.1068	0.0470
Lcp2	lymphocyte cytosolic protein 2	AK170491	0.310	-0.119	0.0013	0.0016	0.3842

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Ldb1	LIM domain binding 1	NM_010697	0.383	-0.083	0.0000	0.0000	0.0546
Ldoc1	leucine zipper, down-regulated in cancer 1	NM_001018087	1.025	-1.156	0.0200	0.2584	0.0501
Lemd1	LEM domain containing 1	BC048759	0.635	-0.674	0.0001	0.0056	0.0099
Leng4	leukocyte receptor cluster (LRC) member 4	AK038998	0.324	-0.356	0.0000	0.0069	0.0000
Leprel2	leprecan-like 2	NM_013530	0.289	-0.123	0.0000	0.0000	0.0745
Lfng	lunatic fringe gene homolog (Drosophila)	BC115680	0.699	-0.077	0.0305	0.0152	0.7438
Lig1	ligase I, DNA, ATP-dependent	AK153993	0.321	-0.301	0.0000	0.0017	0.0022
Lims1	LIM and senescent cell antigen-like domains 1	AK087984	0.321	-0.147	0.0006	0.0021	0.1718
Lims2	LIM and senescent cell antigen like domains 2	NM_144862	0.177	-0.231	0.0002	0.1337	0.0013
Llgl1	NA	BC043458	0.331	-0.152	0.0000	0.0000	0.0002
Lmbr1	limb region 1	NM_020295	0.234	-0.263	0.0000	0.0020	0.0000
Lmna	lamin A	AK150501	0.294	-0.207	0.0000	0.0004	0.0001
Lmo1	LIM domain only 1	NM_057173	0.530	-0.090	0.0151	0.0096	0.6264
LOC194612	NA	XM_904918	0.498	-0.312	0.0488	0.0354	0.6219
LOC230765	NA	NM_008228	0.202	-0.239	0.0364	0.3412	0.0656
LOC241715	NA	XR_003863	0.255	-0.212	0.0234	0.1346	0.1178
LOC242546	NA	AK136922	0.271	-0.384	0.0027	0.2597	0.0065
LOC380850	NA	XM_001004736	0.729	-0.472	0.0116	0.0285	0.2527
LOC432459	NA	AK082906	0.586	-0.525	0.0069	0.0400	0.1211
LOC432466	NA	XR_004490	0.435	-0.385	0.0000	0.0000	0.0000
LOC432482	NA	NM_008705	0.416	-0.283	0.0001	0.3885	0.0002
LOC432881	NA	AK135962	0.312	-0.333	0.0000	0.0126	0.0001
LOC432947	NA	NM_029868	0.356	-0.237	0.0045	0.0617	0.0533
LOC433299	NA	XM_905512	0.337	-0.629	0.0037	0.3170	0.0068
LOC433791	NA	XM_485487	1.026	-0.414	0.0007	0.0007	0.4303
LOC434008	NA	NM_001004182	0.307	-0.203	0.0003	0.0270	0.0092
LOC497266	NA	AK090221	0.267	-0.200	0.0267	0.1151	0.1547
LOC544782	NA	AK016732	0.380	-0.183	0.0000	0.0007	0.0124
LOC545344	NA	XR_003455	1.080	-0.950	0.0233	0.3665	0.0385

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
LOC619632	NA	NM_027909	0.491	-0.209	0.0000	0.0000	0.0520
LOC620016	NA	NM_023140	0.472	-0.129	0.0323	0.0909	0.2279
LOC620315	NA	AK013829	0.907	-0.330	0.0207	0.1026	0.1375
LOC620695	NA	XM_885087	0.578	-0.334	0.0231	0.1998	0.0766
LOC620963	NA	NM_170777	0.258	-0.156	0.0395	0.0360	0.5367
LOC622404	NA	NM_001037913	0.379	-0.280	0.0001	0.0029	0.0230
LOC623031	NA	NM_145558	0.533	-0.067	0.0438	0.0345	0.5901
LOC623205	NA	NM_025444	0.720	-0.280	0.0180	0.0464	0.2458
LOC623672	NA	XR_003915	0.394	-0.210	0.0227	0.5693	0.0204
LOC623706	NA	NM_144806	0.348	-0.224	0.0092	0.0451	0.1414
LOC623748	NA	NM_024442	0.458	-0.371	0.0216	0.1234	0.1190
LOC624138	NA	BC022965	0.403	-0.107	0.0012	0.0033	0.2163
LOC624405	NA	XM_993288	0.695	-0.187	0.0068	0.0054	0.5311
LOC624512	NA	XM_620409	0.848	-0.354	0.0338	0.0331	0.5094
LOC625377	NA	NM_030702	0.440	-0.107	0.0156	0.0181	0.4396
LOC627816	NA	XR_004574	0.392	-0.308	0.0430	0.2192	0.1270
LOC627905	NA	AK169456	0.376	-0.294	0.0127	0.0617	0.1414
LOC627995	NA	XM_909683	0.559	-0.374	0.0058	0.0763	0.0555
LOC628205	NA	XM_892939	0.783	-0.563	0.0081	0.0400	0.1405
LOC628935	NA	NM_183250	1.755	-0.629	0.0434	0.3868	0.0671
LOC629315	NA	XM_001001842	0.941	-0.701	0.0160	0.0977	0.1142
LOC629709	NA	NM_175001	0.423	-0.095	0.0426	0.0293	0.6407
LOC630141	NA	NM_172394	0.280	-0.194	0.0023	0.0092	0.1609
LOC630164	NA	XM_903265	0.242	-0.479	0.0021	0.4273	0.0025
LOC631029	NA	XR_003705	0.799	-0.309	0.0303	0.0395	0.4171
LOC631337	NA	XM_979840	0.513	-0.155	0.0001	0.0005	0.0810
LOC631868	NA	XR_002899	0.572	-0.541	0.0016	0.0719	0.0170
LOC632489	NA	XM_977351	0.757	-0.274	0.0215	0.0764	0.1860
LOC632781	NA	XR_002201	0.550	-0.384	0.0114	0.0226	0.2974
LOC633347	NA	AK039689	0.130	-0.696	0.0000	0.7756	0.0000
LOC633402	NA	NM_009491	0.171	-0.523	0.0263	0.7062	0.0169
LOC633983	NA	NM_011072	0.408	-0.131	0.0025	0.0043	0.3101
LOC634142	NA	XR_004271	0.142	-0.698	0.0013	0.8544	0.0005
LOC635169	NA	XM_910141	0.205	-0.305	0.0304	0.5236	0.0310
LOC636781	NA	NM_001004148	0.290	-0.214	0.0000	0.0020	0.0165
LOC637453	NA	XM_985839	0.392	-1.283	0.0031	0.6760	0.0019
LOC638311	NA	NM_178915	0.446	-0.114	0.0030	0.0018	0.6078
LOC638791	NA	AK008133	0.514	-0.197	0.0095	0.0330	0.1890

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
LOC639384	NA	NM_177325	0.292	-0.217	0.0005	0.0140	0.0282
LOC639496	NA	XM_915944	2.560	-0.348	0.0010	0.0004	0.7026
LOC639942	NA	XM_984742	0.278	-0.335	0.0216	0.2645	0.0524
LOC640145	NA	NM_025586	0.635	-0.135	0.0438	0.0912	0.2969
LOC640607	NA	XM_917655	0.822	-0.481	0.0193	0.0666	0.1906
LOC640972	NA	AK032155	0.175	-0.316	0.0344	0.3444	0.0612
LOC664857	NA	BC116882	0.294	-0.230	0.0201	0.1737	0.0778
LOC664985	NA	XM_974465	0.253	-0.282	0.0492	0.1390	0.2256
LOC666532	NA	XM_984410	0.720	-0.382	0.0103	0.0568	0.1263
LOC667016	NA	XR_001959	0.587	-0.394	0.0016	0.0330	0.0385
LOC667301	NA	NM_010281	0.553	-0.291	0.0000	0.0007	0.0041
LOC667666	NA	XM_001002453	0.741	-0.324	0.0003	0.0005	0.3166
LOC667832	NA	BC089574	0.482	-0.344	0.0102	0.1760	0.0395
LOC668166	NA	XM_905081	0.269	-0.210	0.0212	0.0867	0.1643
LOC668523	NA	XR_002193	0.212	-0.277	0.0397	0.0630	0.3655
LOC668584	NA	XR_002211	0.594	-0.349	0.0102	0.0163	0.3480
LOC668600	NA	XR_002215	0.817	-1.471	0.0119	0.1368	0.0606
LOC668644	NA	XM_001002846	0.239	-0.450	0.0201	0.5824	0.0173
LOC669267	NA	BC042494	0.317	-0.241	0.0413	0.3850	0.0643
LOC669344	NA	NM_019755	0.971	-0.264	0.0001	0.0003	0.1706
LOC669532	NA	NM_011368	0.461	-0.195	0.0001	0.0009	0.0897
LOC669617	NA	NM_010655	0.390	-0.235	0.0043	0.0212	0.1377
LOC669789	NA	NM_175235	0.328	-0.179	0.0003	0.0016	0.1258
LOC669868	NA	BC061075	0.553	-0.287	0.0071	0.0226	0.2012
LOC669898	NA	XM_977845	0.710	-0.276	0.0012	0.0012	0.4417
LOC670016	NA	NM_145632	0.644	-0.423	0.0337	0.0575	0.3460
LOC670122	NA	NM_016966	0.313	-0.162	0.0185	0.2422	0.0498
LOC670139	NA	XR_002822	0.383	-0.305	0.0152	0.0764	0.1375
LOC670307	NA	AK165191	0.416	-0.238	0.0000	0.0008	0.0142
LOC670320	NA	NM_008253	0.345	-0.376	0.0413	0.4043	0.0604
LOC670948	NA	XM_984124	0.299	-0.629	0.0096	0.2399	0.0261
LOC670956	NA	XM_984124	0.313	-0.525	0.0086	0.0748	0.0827
LOC671193	NA	XR_001766	0.844	-0.276	0.0216	0.0143	0.6264
LOC671202	NA	XM_922805	0.349	-0.259	0.0285	0.0649	0.2742
LOC671261	NA	NM_009342	0.446	-0.435	0.0031	0.0026	0.4952
LOC671286	NA	AK046045	0.402	-0.453	0.0348	0.3266	0.0658
LOC671344	NA	XR_003384	0.376	-0.193	0.0431	0.0521	0.4486
LOC671359	NA	XM_924014	0.419	-0.161	0.0385	0.0214	0.7128

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
LOC671452	NA	AK075970	0.425	-0.249	0.0234	0.1183	0.1339
LOC671456	NA	NM_198249	0.231	-0.211	0.0362	0.0484	0.4142
LOC671551	NA	XM_981025	0.393	-0.207	0.0489	0.1420	0.2195
LOC671778	NA	NM_023231	0.440	-0.088	0.0001	0.0001	0.4841
LOC671835	NA	XM_899677	0.168	-0.415	0.0000	0.2886	0.0000
LOC671972	NA	BC110673	0.267	-0.301	0.0325	0.6367	0.0249
LOC672170	NA	XM_989079	0.216	-0.192	0.0000	0.0014	0.0137
LOC672337	NA	XM_992735	0.714	-0.674	0.0005	0.0146	0.0283
LOC672472	NA	NM_146193	0.372	-0.185	0.0040	0.0240	0.1171
LOC672587	NA	NM_011413	0.500	-0.045	0.0000	0.0000	0.6831
LOC672609	NA	XM_994751	0.502	-0.676	0.0225	0.3648	0.0373
LOC672630	NA	NM_019755	0.203	-0.377	0.0069	0.2000	0.0232
LOC672697	NA	NM_023538	0.329	-0.257	0.0010	0.0062	0.1096
LOC672851	NA	XM_001001963	0.552	-0.705	0.0055	0.0902	0.0447
LOC673071	NA	NM_010807	0.577	-0.340	0.0006	0.0048	0.0945
LOC673134	NA	XM_001004677	0.446	-0.613	0.0374	0.3938	0.0563
LOC673188	NA	XM_001004903	1.066	-0.925	0.0036	0.0091	0.2309
LOC673354	NA	XM_001005379	0.733	-0.738	0.0000	0.0172	0.0008
LOC673763	NA	XM_001006280	0.309	-0.544	0.0121	0.2828	0.0271
LOC673890	NA	NM_013639	0.745	-0.344	0.0018	0.0038	0.2616
LOC673915	NA	XM_985651	0.199	-0.248	0.0000	0.0103	0.0001
LOC674025	NA	AK043477	0.439	-0.313	0.0031	0.0300	0.0761
LOC674238	NA	XM_973077	0.658	-0.291	0.0278	0.0352	0.4241
LOC674321	NA	AK003189	0.367	-0.236	0.0089	0.2428	0.0240
LOC674483	NA	NM_175135	0.146	-0.275	0.0000	0.1502	0.0001
LOC674618	NA	XM_143339	0.604	-0.501	0.0009	0.0025	0.2154
LOC674888	NA	AK083331	0.265	-0.166	0.0001	0.0024	0.0311
LOC675179	NA	BC066844	0.686	-0.365	0.0425	0.3613	0.0716
LOC675356	NA	XM_976760	0.650	-0.658	0.0000	0.0000	0.0000
LOC675521	NA	XM_001002732	0.340	-0.091	0.0248	0.0217	0.5401
LOC675577	NA	XM_983324	0.255	-0.218	0.0185	0.1327	0.0954
LOC675608	NA	NM_146260	0.342	-0.523	0.0086	0.0993	0.0622
LOC675789	NA	XM_001001282	0.316	-0.531	0.0439	0.5976	0.0382
LOC676620	NA	NM_029097	0.329	-0.073	0.0004	0.0003	0.5126
LOC676690	NA	XM_986626	0.404	-0.327	0.0074	0.0451	0.1178
LOC676708	NA	NM_010392	1.563	-1.780	0.0031	0.1055	0.0217
LOC676779	NA	XM_978325	0.606	-0.274	0.0069	0.0127	0.3084
LOC677369	NA	NM_175628	0.346	-0.374	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
LOC677553	NA	BC019559	0.264	-0.210	0.0204	0.0487	0.2638
LOC677570	NA	NM_022009	0.281	-0.198	0.0000	0.0003	0.0020
Loh11cr2a	loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	NM_172767	0.744	-0.441	0.0000	0.0000	0.0000
Lpo	lactoperoxidase	NM_080420	0.302	-0.178	0.0004	0.0021	0.1276
Lrch2	leucine-rich repeats and calponin homology (CH) domain containing 2	XM_978269	0.164	-0.246	0.0000	0.0186	0.0000
Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	NM_008377	0.283	-0.188	0.0000	0.0000	0.0000
Lrp10	low-density lipoprotein receptor-related protein 10	NM_022993	0.489	-0.364	0.0000	0.0000	0.0017
Lrrc18	NA	NM_026253	0.258	-0.225	0.0454	0.0821	0.3324
Lrrc28	leucine rich repeat containing 28	AK075909	0.347	-0.138	0.0002	0.0013	0.1127
Lrrc41	leucine rich repeat containing 41	AK142801	0.436	-0.120	0.0000	0.0000	0.0368
Lrrc42	leucine rich repeat containing 42	NM_029985	0.491	-0.010	0.0036	0.0008	0.9757
Lrrc47	leucine rich repeat containing 47	NM_201226	0.521	-0.167	0.0005	0.0024	0.1410
Lrrc48	leucine rich repeat containing 48	XM_989154	0.267	-0.223	0.0001	0.0083	0.0058
Lrrc4b	leucine rich repeat containing 4B	NM_198250	0.471	-0.133	0.0120	0.0087	0.5749
Lrrc55	NA	NM_001033346	0.216	-0.245	0.0324	0.1432	0.1488
Lrrc56	NA	AK035366	0.171	-0.231	0.0160	0.1942	0.0550
Lrrc6	leucine rich repeat containing 6 (testis)	NM_019457	0.266	-0.286	0.0105	0.1650	0.0439
Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	AK173256	0.224	-0.360	0.0000	0.0021	0.0000
Lrrn1	leucine rich repeat protein 1, neuronal	NM_008516	0.352	-0.174	0.0424	0.0615	0.3904
Lrsam1	leucine rich repeat and sterile alpha motif containing 1	NM_199302	0.242	-0.172	0.0000	0.0000	0.0003

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Lsm11	U7 snRNP-specific Sm-like protein LSM11	NM_028185	0.246	-0.182	0.0081	0.1918	0.0286
Lsm8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	AK154446	0.678	-0.189	0.0161	0.0173	0.4614
Ltbr	lymphotoxin B receptor	NM_010736	0.518	-0.080	0.0019	0.0009	0.6634
Ly6h	lymphocyte antigen 6 complex, locus H	AK034884	0.873	-0.336	0.0001	0.0494	0.0018
Ly96	lymphocyte antigen 96	NM_016923	0.487	-0.250	0.0492	0.0472	0.5271
Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	BC031547	0.443	-0.078	0.0016	0.0006	0.7439
Lypla3	lysophospholipase 3	AK129099	0.236	-0.269	0.0126	0.3381	0.0229
Lyzs	lysozyme	NM_017372	0.849	-0.429	0.0002	0.0017	0.0773
Lztr1	leucine-zipper-like transcriptional regulator, 1	AK132817	0.414	-0.100	0.0000	0.0000	0.0021
M6pr-ps	NA	AK004656	0.337	-0.120	0.0137	0.0469	0.1937
Mad2l2	MAD2 mitotic arrest deficient-like 2 (yeast)	BC071264	0.405	-0.103	0.0046	0.0058	0.3903
Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	XM_001002362	0.432	-0.083	0.0466	0.0380	0.5805
Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	NM_010757	0.406	-0.235	0.0471	0.0717	0.3786
Maged2	melanoma antigen, family D, 2	AK131598	0.461	-0.241	0.0000	0.0009	0.0190
Magee2	NA	NM_053206	0.553	-0.391	0.0371	0.0566	0.3764
Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	NM_010760	0.957	-0.205	0.0024	0.0025	0.4227

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	NM_030153	0.273	-0.171	0.0000	0.0002	0.0002
Mal2	mal, T-cell differentiation protein 2	NM_178920	0.292	-0.258	0.0186	0.1772	0.0706
Man1a	mannosidase 1, alpha	NM_008548	0.353	-0.208	0.0000	0.0000	0.0653
Man2b1	mannosidase 2, alpha B1	AK054315	0.283	-0.160	0.0000	0.0000	0.0000
Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	NM_025735	0.501	-0.302	0.0000	0.0034	0.0062
Map2k2	mitogen activated protein kinase kinase 2	NM_023138	0.395	-0.014	0.0003	0.0001	0.8915
Map2k3	mitogen activated protein kinase kinase 3	AK176968	0.336	-0.244	0.0002	0.0011	0.0996
Map6d1	NA	NM_198599	0.360	-0.251	0.0247	0.0761	0.2111
Mapk11	mitogen-activated protein kinase 11	BC057626	0.280	-0.270	0.0000	0.0000	0.0001
Mapk3	mitogen activated protein kinase 3	AK155287	0.367	-0.265	0.0000	0.0000	0.0000
Mapk8ip1	mitogen activated protein kinase 8 interacting protein 1	NM_011162	0.314	-0.106	0.0000	0.0000	0.0436
March9	membrane-associated ring finger (C3HC4)9	NM_001033262	0.577	-0.166	0.0000	0.0001	0.2604
Marcks	myristoylated alanine rich protein kinase C substrate	NM_008538	0.279	-0.267	0.0187	0.1680	0.0750
Marcksl1	NA	NM_010807	1.083	-0.582	0.0084	0.1059	0.0565
Mars	methionine-tRNA synthetase	NM_001003913	0.342	-0.068	0.0000	0.0000	0.1817
Mast3	microtubule associated serine/threonine kinase 3	XM_897954	0.388	-0.086	0.0003	0.0004	0.3481
Matn2	matrilin 2	NM_016762	0.422	-0.053	0.0000	0.0000	0.8363
Matn4	matrilin 4	NM_013592	0.444	-0.306	0.0000	0.0001	0.0037

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Mbc2	membrane bound C2 domain containing protein	NM_011843	0.373	-0.342	0.0000	0.0000	0.0000
Mbtd1	mbt domain containing 1	NM_134012	0.361	-0.149	0.0000	0.0000	0.0204
Mcee	methylmalonyl CoA epimerase	NM_028626	0.350	-0.478	0.0000	0.1069	0.0003
Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	XR_004013	0.361	-0.161	0.0119	0.0200	0.3370
Mcoln1	mucolipin 1	BC020377	0.412	-0.029	0.0000	0.0000	0.7565
Mcph1	microcephaly, primary autosomal recessive 1	AK148021	0.236	-0.270	0.0001	0.0296	0.0042
Mdga1	MAM domain containing glycosylphosphatidyl inositol anchor 1	DQ788983	0.540	-0.192	0.0000	0.0000	0.0002
Mecp2	methyl CpG binding protein 2	NM_010788	0.429	-2.450	0.0015	0.0570	0.0202
Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	AK037414	0.499	-0.161	0.0000	0.0002	0.0738
Men1	multiple endocrine neoplasia 1	BC006610	0.370	-0.179	0.0000	0.0000	0.0072
Metrn	meteorin, glial cell differentiation regulator	DQ133463	0.519	-0.129	0.0399	0.0473	0.4530
Mfge8	milk fat globule-EGF factor 8 protein	NM_008594	0.244	-0.203	0.0001	0.0157	0.0032
Mfn1	mitofusin 1	NM_024200	0.265	-0.140	0.0000	0.0000	0.0034
Mfsd1	major facilitator superfamily domain containing 1	NM_025813	0.366	-0.147	0.0000	0.0000	0.0022
Mfsd2	major facilitator superfamily domain containing 2	NM_029662	0.291	-0.306	0.0000	0.0016	0.0000
Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	NM_145926	0.435	-0.034	0.0000	0.0000	0.7303
Mgat4c	NA	AK032009	0.164	-0.380	0.0245	0.5028	0.0263

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Mgat5b	NA	NM_172948	0.317	-0.107	0.0000	0.0000	0.0103
MGC107415	NA	BC096765	0.666	-0.918	0.0017	0.3345	0.0028
MGC38507	NA	XM_001004775	0.329	-0.302	0.0345	0.3884	0.0527
Mgst1	microsomal glutathione S-transferase 1	NM_019946	0.530	-0.188	0.0474	0.0653	0.4076
Mia1	melanoma inhibitory activity 1	BC009815	0.583	-0.225	0.0004	0.0019	0.1430
Midn	midnolin	NM_021565	0.463	-0.200	0.0000	0.0000	0.0009
Mif4gd	NA	NM_027162	0.379	-0.127	0.0001	0.0001	0.2349
Mina	myc induced nuclear antigen	AK014426	0.259	-0.259	0.0001	0.0050	0.0142
Mis12	MIS12 homolog (yeast)	NM_025993	0.264	-0.170	0.0401	0.1772	0.1478
Mkks	McKusick-Kaufman syndrome protein	NM_021527	0.427	-0.091	0.0092	0.0058	0.6157
Mknk2	MAP kinase-interacting serine/threonine kinase 2	AK154235	0.320	-0.157	0.0000	0.0000	0.0097
Mlf1	myeloid leukemia factor 1	AF009515	0.484	-0.315	0.0007	0.0052	0.1002
Mme	membrane metallo endopeptidase	AK033824	0.382	-0.697	0.0000	0.0000	0.0000
Mmp14	matrix metallopeptidase 14 (membrane-inserted)	AK040968	0.478	-0.217	0.0000	0.0001	0.0191
Mmp15	matrix metallopeptidase 15	NM_008609	0.406	-0.405	0.0000	0.0000	0.0000
Mnt	max binding protein	XR_003956	0.362	-0.334	0.0300	0.2322	0.0839
Mobkl1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	AK003346	0.340	-0.112	0.0492	0.0487	0.5165
Morc3	microrchidia 3	NM_001045529	0.289	-0.218	0.0000	0.0002	0.0006
Mospd1	motile sperm domain containing 1	NM_027409	0.385	-0.280	0.0007	0.0095	0.0575
Mospd2	motile sperm domain containing 2	NM_029730	0.320	-0.235	0.0011	0.0235	0.0360
Mpp2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	NM_016695	0.375	-0.220	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Mrc1	mannose receptor, C type 1	NM_008625	0.388	-0.140	0.0000	0.0000	0.1443
Mrg2	myeloid ecotropic viral integration site-related gene 2	XM_983187	0.292	-0.282	0.0007	0.0749	0.0077
Mrm1	NA	NM_145433	0.378	-0.144	0.0076	0.0078	0.4559
Mrpl1	mitochondrial ribosomal protein L1	BC061042	0.258	-0.166	0.0026	0.0161	0.1126
Mrpl23	mitochondrial ribosomal protein L23	NM_011288	0.198	-0.263	0.0012	0.2796	0.0025
Mrpl24	mitochondrial ribosomal protein L24	BC025506	0.303	-0.364	0.0001	0.1594	0.0006
Mrpl43	mitochondrial ribosomal protein L43	NM_053164	0.479	-0.120	0.0381	0.0528	0.4037
Mrpl46	mitochondrial ribosomal protein L46	NM_023331	0.275	-0.289	0.0038	0.2182	0.0112
Mrpl53	mitochondrial ribosomal protein L53	XM_620337	0.446	-0.245	0.0329	0.1236	0.1741
Mrps10	mitochondrial ribosomal protein S10	AK004151	0.375	-0.085	0.0052	0.0024	0.7113
Mrps18a	mitochondrial ribosomal protein S18A	NM_026768	0.401	-0.154	0.0005	0.0028	0.1135
Mrps18c	mitochondrial ribosomal protein S18C	NM_026826	0.491	-0.149	0.0106	0.0232	0.2761
Mrps21	mitochondrial ribosomal protein S21	NM_078479	0.892	-0.270	0.0248	0.3040	0.0512
Mrps22	mitochondrial ribosomal protein S22	BC037653	0.488	-0.316	0.0003	0.0082	0.0311
Mrps25	mitochondrial ribosomal protein S25	NM_025578	0.377	-0.202	0.0003	0.0095	0.0227
Mrps27	mitochondrial ribosomal protein S27	AK172922	0.325	-0.250	0.0000	0.0023	0.0064

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Mrps31	mitochondrial ribosomal protein S31	NM_020560	0.441	-0.280	0.0003	0.0071	0.0364
Msr2	macrophage scavenger receptor 2	NM_030707	0.225	-0.306	0.0074	0.2011	0.0249
Msto1	misato homolog 1 (Drosophila)	NM_144898	0.292	-0.129	0.0000	0.0042	0.0020
Mtch1	mitochondrial carrier homolog 1 (C. elegans)	BC029723	0.349	-0.100	0.0000	0.0000	0.0204
Mterfd2	MTERF domain containing 2	NM_178051	0.308	-0.095	0.0023	0.0009	0.7268
Mthfr	5,10-methylenetetrahydrofolate reductase	AF404274	0.328	-0.165	0.0000	0.0001	0.0026
Mtmr11	myotubularin related protein 11	NM_181409	0.616	-0.363	0.0000	0.0000	0.0000
Mttp	microsomal triglyceride transfer protein	NM_008642	0.229	-0.459	0.0000	0.0612	0.0000
Mtvr2	mammary tumor virus receptor 2	NM_023166	0.453	-0.147	0.0360	0.1177	0.1974
Mtx2	metaxin 2	NM_016804	0.497	-0.099	0.0018	0.0023	0.3744
Mulk	multiple substrate lipid kinase	AK051531	0.141	-0.275	0.0023	0.3174	0.0042
Mvd	mevalonate (diphospho) decarboxylase	AK153439	0.322	-0.111	0.0104	0.0223	0.2792
Mxd1	NA	AK036504	0.261	-0.186	0.0194	0.0948	0.1391
Myc	myelocytomatosis oncogene	NM_010849	0.367	-0.192	0.0206	0.0690	0.1955
Mycbp	c-myc binding protein	NM_019660	0.580	-0.378	0.0003	0.0057	0.0393
Mycl1	NA	NM_008506	0.619	-0.222	0.0003	0.0033	0.0700
Myl6b	NA	NM_172259	0.324	-0.350	0.0008	0.1157	0.0050
Myo1c	myosin IC	NM_008659	0.322	-0.184	0.0000	0.0000	0.0000
Myo3b	NA	NM_177376	0.404	-0.081	0.0000	0.0000	0.4149
Myt1	myelin transcription factor 1	NM_008665	0.183	-0.242	0.0000	0.0049	0.0000
Nagk	N-acetylglucosamine kinase	AJ242911	0.151	-0.297	0.0002	0.5096	0.0001

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	AK158774	0.305	-0.130	0.0084	0.0226	0.2323
Nalp5	NACHT, leucine rich repeat and PYD containing 5	NM_011860	0.295	-0.397	0.0261	0.2285	0.0746
Nanos1	nanos homolog 1 (Drosophila)	NM_178421	0.316	-0.200	0.0347	0.0848	0.2580
Nargl1	NMDA receptor regulated 1-like	NM_025832	0.334	-0.164	0.0001	0.0008	0.0644
Nasp	nuclear autoantigenic sperm protein (histone-binding)	AK008295	0.260	-0.183	0.0000	0.0013	0.0243
Nat5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	AK046153	0.455	-0.169	0.0433	0.2340	0.1195
Nat6	N-acetyltransferase 6	NM_008317	0.265	-0.225	0.0043	0.1107	0.0283
Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	AF043259	0.376	-0.144	0.0492	0.0422	0.5642
Nckap1l	NCK associated protein 1 like	AK077019	0.232	-0.196	0.0000	0.0007	0.0011
Ncln	nicalin homolog (zebrafish)	NM_134009	0.404	-0.134	0.0000	0.0000	0.0524
Ndph	Norrie disease homolog	NM_010883	0.466	-0.108	0.0049	0.0113	0.2542
Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	AK015768	0.143	-0.397	0.0000	0.1796	0.0000
Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	BC061002	0.235	-0.202	0.0166	0.5090	0.0173
Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	NM_025358	0.278	-0.137	0.0003	0.0250	0.0092
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	AK151404	0.303	-0.249	0.0186	0.3480	0.0323

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	AK028334	0.533	-0.264	0.0151	0.1235	0.0848
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	AK028070	0.373	-0.217	0.0001	0.0853	0.0009
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	NM_029272	0.359	-0.045	0.0372	0.0191	0.7417
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	NM_028388	0.284	-0.140	0.0061	0.0286	0.1475
Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	NM_008683	0.511	-0.124	0.0305	0.1192	0.1681
Nek10	NA	XM_977876	0.322	-0.437	0.0003	0.0480	0.0049
Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	BC068168	0.147	-0.268	0.0002	0.2141	0.0006
Neu4	NA	NM_173772	0.376	-0.356	0.0000	0.0192	0.0003
Nf2	neurofibromatosis 2	BC005442	0.303	-0.099	0.0000	0.0001	0.0893
Nfkbil2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	AK139173	0.424	-0.288	0.0000	0.0000	0.0000
Ngb	neuroglobin	NM_022414	0.233	-0.471	0.0000	0.0083	0.0008
Nhs	NA	XM_912343	0.133	-0.271	0.0273	0.3425	0.0491
Nhsl1	NHS-like 1	NM_173390	0.681	-0.225	0.0333	0.0421	0.4275
Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	NM_022988	0.320	-0.193	0.0041	0.0589	0.0514
Nipsnap3a	nipsnap homolog 3A (C. elegans)	NM_025623	0.147	-0.318	0.0018	0.4273	0.0022
Nit1	NA	NM_012049	0.282	-0.132	0.0077	0.0356	0.1477
Nmbr	neuromedin B receptor	NM_008703	0.810	-0.382	0.0000	0.0005	0.0077

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Nme1	expressed in non-metastatic cells 1, protein	AK034899	0.525	-0.224	0.0002	0.0076	0.0235
Nme3	expressed in non-metastatic cells 3	NM_019730	0.401	-0.227	0.0061	0.0183	0.2095
Nme5	expressed in non-metastatic cells 5	BC049625	0.347	-0.371	0.0000	0.0159	0.0013
Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	AK184847	0.436	-0.160	0.0000	0.0000	0.0235
Nol10	nucleolar protein 10	NM_001008421	0.328	-0.111	0.0000	0.0000	0.2304
Nol11	nucleolar protein 11	AK054118	0.261	-0.183	0.0001	0.0237	0.0018
Nov	nephroblastoma overexpressed gene	NM_010930	0.818	-0.036	0.0000	0.0000	0.9047
Nox4	NADPH oxidase 4	AK085509	0.571	-0.428	0.0000	0.0000	0.0001
Npal2	NIPA-like domain containing 2	AK038556	0.271	-0.160	0.0035	0.0079	0.2553
Npas1	neuronal PAS domain protein 1	NM_008718	0.473	-0.417	0.0000	0.0000	0.0001
Npbwr1	NA	XM_984122	0.939	-0.565	0.0012	0.0033	0.2137
Npc2	Niemann Pick type C2	AK151080	0.312	-0.120	0.0128	0.0284	0.2753
Npdc1	neural proliferation, differentiation and control gene 1	BC023887	0.355	-0.102	0.0000	0.0001	0.2802
Npm3	nucleoplasmin 3	NM_008723	0.443	-0.467	0.0228	0.1245	0.1242
Npr1	natriuretic peptide receptor 1	NM_145540	0.416	-0.119	0.0000	0.0000	0.0618
Npy	neuropeptide Y	NM_023456	0.576	-0.184	0.0009	0.0038	0.1458
Nqo1	NAD(P)H dehydrogenase, quinone 1	AK157369	0.708	-0.204	0.0001	0.0001	0.3990
Nr1h3	nuclear receptor subfamily 1, group H, member 3	NM_013839	0.342	-0.095	0.0311	0.0273	0.5431
Nr2f6	nuclear receptor subfamily 2, group F, member 6	AK144475	0.449	-0.062	0.0013	0.0005	0.7259
Nradd	neurotrophin receptor associated death domain	NM_026012	0.545	-0.423	0.0110	0.0953	0.0816
Nrarp	Notch-regulated ankyrin repeat protein	NM_025980	0.604	-0.598	0.0066	0.0809	0.0594

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Nsd1	nuclear receptor-binding SET-domain protein 1	AK179504	0.398	-0.123	0.0001	0.0006	0.0833
Nt5c	5',3'-nucleotidase, cytosolic	BC024368	0.327	-0.279	0.0005	0.0763	0.0055
Nt5c3l	NA	NM_026561	0.266	-0.138	0.0072	0.0239	0.1952
Nt5dc2	NA	NM_027289	0.340	-0.194	0.0004	0.0017	0.1338
Ntf3	neurotrophin 3	NM_008742	0.608	-0.255	0.0089	0.0033	0.8102
Nts	neurotensin	NM_024435	0.990	-0.677	0.0000	0.0003	0.0140
Ntsr1	neurotensin receptor1	NM_018766	0.371	-0.319	0.0000	0.0004	0.0102
Nudt10	nudix (nucleoside diphosphate linked moiety X)-type motif 10	NM_001031664	0.369	-0.181	0.0009	0.0065	0.0954
Nudt12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	NM_026497	0.241	-0.237	0.0267	0.1741	0.1031
Nudt14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	AK003991	0.218	-0.262	0.0226	0.3939	0.0340
Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	NM_026675	0.370	-0.105	0.0118	0.0116	0.4810
Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	XM_992328	0.482	-0.047	0.0027	0.0011	0.7520
Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	AK018345	0.283	-0.165	0.0012	0.0080	0.1006
Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	BC033046	0.252	-0.307	0.0062	0.1167	0.0383
Nufip1	nuclear fragile X mental retardation protein interacting protein	NM_013745	0.498	-0.129	0.0001	0.0001	0.3286
Nup155	nucleoporin 155	NM_133227	0.229	-0.198	0.0000	0.0000	0.0000
Nxph3	neurexophilin 3	NM_130858	0.253	-0.390	0.0041	0.1425	0.0204

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Nxph4	neurexophilin 4	NM_183297	0.790	-1.120	0.0000	0.0053	0.0000
Oatl1	ornithine aminotransferase-like 1	NM_172478	0.242	-0.260	0.0040	0.1571	0.0176
Oaz2	ornithine decarboxylase antizyme 2	NM_010952	0.484	-0.327	0.0086	0.0240	0.2267
Odc1	ornithine decarboxylase, structural 1	NM_013614	0.312	-0.238	0.0202	0.1935	0.0693
Odf2l	outer dense fiber of sperm tails 2-like	AK048931	0.217	-0.307	0.0005	0.0941	0.0042
Odf4	outer dense fiber of sperm tails 4	XM_976840	0.217	-0.381	0.0283	0.4085	0.0406
Ogfr	opioid growth factor receptor	NM_031373	0.409	-0.130	0.0084	0.0561	0.1074
Olfm2	olfactomedin 2	NM_173777	0.225	-0.307	0.0114	0.2266	0.0331
Olig1	oligodendrocyte transcription factor 1	NM_016968	0.413	-0.130	0.0214	0.0276	0.4167
Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	AK136208	0.383	-0.135	0.0001	0.0004	0.1617
Oprk1	opioid receptor, kappa 1	AK039151	0.884	-0.903	0.0000	0.0000	0.0000
Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	AK078405	0.612	-0.037	0.0002	0.0000	0.8523
Ormdl1	ORM1-like 1 (S. cerevisiae)	NM_145517	0.630	-0.559	0.0019	0.1152	0.0122
Oxgr1	NA	NM_001001490	0.784	-0.387	0.0001	0.0006	0.0949
Oxt	oxytocin	NM_011025	0.383	-0.436	0.0244	0.3719	0.0395
P140	NA	AK129422	0.323	-0.095	0.0000	0.0000	0.0722
P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	AK140283	0.261	-0.222	0.0154	0.1203	0.0887
P2ry1	purinergic receptor P2Y, G-protein coupled 1	AK033660	0.354	-0.416	0.0001	0.0118	0.0087
Pabpc1	poly A binding protein, cytoplasmic1	AK005009	0.267	-0.133	0.0037	0.0147	0.1635

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	NM_008776	0.555	-0.471	0.0000	0.0017	0.0001
Pak1ip1	PAK1 interacting protein 1	AK017959	0.351	-0.137	0.0000	0.0000	0.1443
Panx1	pannexin 1	AK089764	0.371	-0.307	0.0000	0.0000	0.0026
Panx2	pannexin 2	NM_001002005	0.257	-0.269	0.0200	0.1214	0.1131
Papd4	PAP associated domain containing 4	XR_004961	0.123	-0.532	0.0463	0.8145	0.0243
Papd5	NA	XM_134422	0.370	-0.454	0.0004	0.0414	0.0070
Pappa	pregnancy-associated plasma protein A	NM_021362	0.215	-0.398	0.0000	0.0129	0.0000
Pappa2	pappalysin 2	XM_355248	0.425	-0.137	0.0000	0.0000	0.2516
Paqr4	progestin and adipoQ receptor family member IV	NM_023824	0.506	-0.134	0.0000	0.0000	0.1422
Paqr6	progestin and adipoQ receptor family member VI	XM_987704	0.528	-0.258	0.0000	0.0000	0.0128
Parg	poly (ADP-ribose) glycohydrolase	AK160742	0.223	-0.185	0.0000	0.0011	0.0111
Pbx2	pre B-cell leukemia transcription factor 2	AK141763	0.488	-0.173	0.0000	0.0000	0.0287
Pbxip1	pre-B-cell leukemia transcription factor interacting protein 1	NM_146131	0.336	-0.130	0.0000	0.0000	0.1058
Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	M83741	0.589	-0.195	0.0236	0.0619	0.2414
Pcbp1	poly(rC) binding protein 1	NM_011865	0.480	-0.067	0.0474	0.0180	0.8685
Pcbp4	poly(rC) binding protein 4	NM_021567	0.319	-0.150	0.0000	0.0000	0.0007
Pcdh11x	protocadherin 11 X-linked	AY861426	0.277	-0.639	0.0000	0.0328	0.0000
Pcdh18	protocadherin 18	AK014140	0.438	-0.487	0.0000	0.0005	0.0002
Pcdh19	protocadherin 19	XM_205287	0.178	-0.323	0.0103	0.6249	0.0076

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Pcdh21	protocadherin 21	NM_130878	0.313	-0.383	0.0000	0.0016	0.0004
Pcdh8	protocadherin 8	AK006960	0.453	-0.086	0.0268	0.0170	0.6515
Pcdhb11	protocadherin beta 11	NM_053136	0.451	-0.206	0.0427	0.0422	0.5114
Pcdhb16	protocadherin beta 16	NM_053141	0.466	-0.290	0.0274	0.0525	0.3171
Pcdhb19	protocadherin beta 19	NM_053144	0.199	-0.327	0.0056	0.5066	0.0056
Pcdhb3	protocadherin beta 3	NM_053128	0.575	-0.154	0.0138	0.0091	0.6116
Pcdhb7	protocadherin beta 7	NM_053132	0.410	-0.187	0.0322	0.0363	0.4616
Pcdhb9	protocadherin beta 9	NM_053134	0.749	-0.506	0.0034	0.0212	0.1134
Pcgf1	polycomb group ring finger 1	AK008048	0.266	-0.168	0.0018	0.0361	0.0388
Pcgf2	polycomb group ring finger 2	NM_009545	0.432	-0.292	0.0000	0.0003	0.0000
Pcgf6	polycomb group ring finger 6	AK132448	0.362	-0.246	0.0000	0.0017	0.0000
Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	NM_028994	0.293	-0.167	0.0000	0.0010	0.0115
Pcmtd2	NA	NM_153594	0.380	-0.291	0.0000	0.0000	0.0000
Pcna	proliferating cell nuclear antigen	NM_011045	0.448	-0.265	0.0024	0.0705	0.0257
Pcp4l1	Purkinje cell protein 4-like 1	XM_917594	0.245	-0.324	0.0096	0.2491	0.0249
Pcsk1	proprotein convertase subtilisin/kexin type1	NM_013628	0.482	-0.601	0.0000	0.0000	0.0000
Pctk3	PCTAIRE-motif protein kinase 3	AK004998	0.354	-0.288	0.0000	0.0000	0.0000
Pcyox1l	NA	NM_172832	0.326	-0.092	0.0004	0.0002	0.5367
Pdcl3	phosducin-like 3	NM_026850	0.245	-0.165	0.0280	0.5247	0.0286
Pde1b	phosphodiesterase 1B, Ca2+-calmodulin dependent	NM_008800	0.385	-0.209	0.0000	0.0000	0.0000
Pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta	XM_974388	0.350	-0.162	0.0006	0.0017	0.2005
Pdgfa	platelet derived growth factor, alpha	AK017169	0.392	-0.127	0.0000	0.0000	0.0977
Pdgfb	platelet derived growth factor, B polypeptide	NM_011057	0.470	-0.161	0.0000	0.0000	0.0930
Pdgfc	platelet-derived growth factor, C polypeptide	BC006027	0.391	-0.084	0.0042	0.0026	0.5999

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Pdgfra	platelet derived growth factor receptor, alpha polypeptide	AK145097	0.269	-0.368	0.0000	0.0001	0.0000
Pdia4	protein disulfide isomerase associated 4	NM_009787	0.355	-0.140	0.0000	0.0000	0.0392
Pdia6	protein disulfide isomerase associated 6	XM_907880	0.324	-0.109	0.0000	0.0001	0.0194
Pdzd4	NA	AK084004	0.453	-0.185	0.0000	0.0000	0.0064
Pdzd7	NA	NM_177605	0.401	-0.117	0.0149	0.0132	0.5192
Pemt	phosphatidylethanolamine N-methyltransferase	NM_008819	0.555	-0.140	0.0000	0.0000	0.4894
Penk1	preproenkephalin 1	NM_001002927	0.404	-0.577	0.0002	0.0314	0.0065
Pex13	peroxisomal biogenesis factor 13	NM_023651	0.345	-0.102	0.0018	0.0029	0.3190
Pex16	peroxisome biogenesis factor 16	NM_145122	0.295	-0.129	0.0049	0.0143	0.2132
Pex5	peroxisome biogenesis factor 5	NM_008995	0.262	-0.139	0.0000	0.0001	0.0115
Pex6	peroxisomal biogenesis factor 6	NM_145488	0.539	-0.092	0.0000	0.0000	0.0440
Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	NM_008824	0.183	-0.295	0.0038	0.2617	0.0090
Pgam2	phosphoglycerate mutase 2	NM_018870	0.320	-0.331	0.0137	0.0937	0.1028
Pgam5	NA	NM_028273	0.457	-0.060	0.0014	0.0008	0.6116
Pgcp	NA	NM_018755	0.258	-0.169	0.0001	0.0005	0.1118
Pggt1b	protein geranylgeranyltransferase type I, beta subunit	BC048404	0.294	-0.112	0.0324	0.0391	0.4418
Pgpep1	pyroglutamyl-peptidase I	AK003373	0.542	-0.204	0.0001	0.0005	0.1334
Pgr	progesterone receptor	AK036862	0.138	-0.307	0.0000	0.1821	0.0001
Pgr15l	NA	NM_001033361	0.815	-0.638	0.0000	0.0000	0.0260
Pgrmc1	progesterone receptor membrane component 1	NM_016783	0.411	-0.143	0.0045	0.0155	0.1867

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Phca	phytoceramidase, alkaline	NM_025408	0.340	-0.298	0.0011	0.0422	0.0214
Phf16	PHD finger protein 16	AK077755	0.259	-0.270	0.0017	0.0551	0.0235
Phf23	PHD finger protein 23	NM_030064	0.545	-0.202	0.0000	0.0000	0.0297
Phka1	phosphorylase kinase alpha 1	X73876	0.328	-0.146	0.0000	0.0000	0.0000
Pigs	phosphatidylinositol glycan, class S	AK158128	0.322	-0.162	0.0000	0.0003	0.0342
Pigt	phosphatidylinositol glycan, class T	NM_133779	0.341	-0.062	0.0000	0.0000	0.4019
Pik4cb	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	BC059895	0.262	-0.208	0.0000	0.0014	0.0000
Pim2	proviral integration site 2	NM_145737	0.316	-0.225	0.0000	0.0026	0.0014
Pip5kl1	phosphatidylinositol-4-phosphate 5-kinase-like 1	AK133244	0.423	-0.506	0.0000	0.0002	0.0000
Pitpnm1	phosphatidylinositol membrane-associated 1	AK155377	0.373	-0.087	0.0000	0.0000	0.0166
Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	NM_001039051	0.253	-0.299	0.0439	0.3646	0.0733
Pla2g3	NA	BC079556	0.273	-0.179	0.0070	0.0187	0.2330
Pla2g4e	NA	AK049063	0.137	-0.531	0.0005	0.0267	0.0160
Plag1	pleiomorphic adenoma gene 1	NM_019969	0.173	-0.328	0.0500	0.5376	0.0505
Plat	plasminogen activator, tissue	NM_008872	0.289	-0.142	0.0000	0.0023	0.0008
Plcd4	phospholipase C, delta 4	AK039149	0.240	-0.238	0.0000	0.0001	0.0000
Plcxd2	NA	XM_001000738	0.270	-0.338	0.0195	0.1163	0.1151
Plcz1	phospholipase C, zeta 1	AK005949	0.516	-0.266	0.0001	0.0004	0.1789
Pld2	phospholipase D2	NM_176893	0.601	-0.345	0.0000	0.0000	0.0000
Pld4	phospholipase D family, member 4	BC058565	0.354	-0.234	0.0007	0.0121	0.0438
Pldn	pallidin	NM_019788	0.318	-0.199	0.0074	0.0548	0.0978
Plek	pleckstrin	NM_019549	0.217	-0.201	0.0051	0.1140	0.0324

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Plekhh3	NA	NM_146030	0.366	-0.060	0.0000	0.0000	0.6792
Plk3	polo-like kinase 3 (Drosophila)	NM_013807	0.161	-0.315	0.0000	0.0893	0.0000
Plk4	polo-like kinase 4 (Drosophila)	AK045082	0.588	-0.441	0.0000	0.0000	0.0000
Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	NM_011122	0.500	-0.222	0.0000	0.0000	0.0001
Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	NM_011962	0.399	-0.179	0.0000	0.0000	0.0005
Plxna2	plexin A2	NM_008882	0.390	-0.137	0.0000	0.0000	0.0000
Plxna3	plexin A3	NM_008883	0.605	-0.491	0.0000	0.0000	0.0000
Plxnb2	plexin B2	XM_001003816	0.356	-0.149	0.0053	0.0405	0.0939
Plxnb3	plexin B3	AK048728	0.452	-0.269	0.0000	0.0000	0.0000
Plxnc1	plexin C1	NM_018797	0.190	-0.287	0.0000	0.0005	0.0000
Pmpcb	peptidase (mitochondrial processing) beta	NM_028431	0.326	-0.137	0.0027	0.0145	0.1284
Pnma3	paraneoplastic antigen MA3	NM_153169	0.632	-0.225	0.0140	0.0211	0.3669
Pno1	NA	NM_025443	0.423	-0.115	0.0404	0.0493	0.4437
Pnp	purine-nucleoside phosphorylase	XM_972632	0.276	-0.211	0.0050	0.0311	0.1139
Pnpla3	NA	NM_054088	0.200	-0.207	0.0054	0.1128	0.0344
Pnpla6	NA	AK089095	0.259	-0.193	0.0000	0.0000	0.0000
Pola2	polymerase (DNA directed), alpha 2	NM_008893	0.288	-0.175	0.0008	0.0087	0.0635
Pold4	polymerase (DNA-directed), delta 4	NM_027196	0.430	-0.350	0.0004	0.0117	0.0291
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	AK145365	0.366	-0.195	0.0204	0.0959	0.1435
Polg2	polymerase (DNA directed), gamma 2, accessory subunit	AF006072	0.185	-0.216	0.0389	0.2761	0.0896
Polh	polymerase (DNA directed), eta (RAD 30 related)	NM_030715	0.375	-0.106	0.0043	0.0040	0.4727
Polm	polymerase (DNA directed), mu	AK137747	0.349	-0.315	0.0000	0.0002	0.0017

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	NM_027231	0.363	-0.177	0.0100	0.1299	0.0543
Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	BC055278	0.474	-0.224	0.0003	0.0319	0.0084
Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	NM_145632	0.697	-0.018	0.0354	0.0098	0.9719
Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	AK013084	0.276	-0.184	0.0003	0.0012	0.1441
Polr3h	polymerase (RNA) III (DNA directed) polypeptide H	NM_030229	0.468	-0.024	0.0021	0.0005	0.9226
Pomp	NA	AK044283	0.638	-0.065	0.0003	0.0002	0.5878
Pomt1	protein-O-mannosyltransferase1	NM_172661	0.324	-0.154	0.0000	0.0000	0.0036
Pomt2	protein-O-mannosyltransferase2	AK085703	0.348	-0.221	0.0000	0.0000	0.0000
Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	NM_025390	0.441	-0.131	0.0063	0.0079	0.3985
Postn	periostin, osteoblast specific factor	NM_015784	0.375	-0.555	0.0000	0.0009	0.0000
Pot1a	NA	NM_133931	0.376	-0.205	0.0000	0.0000	0.0005
Pot1b	NA	AK013364	0.348	-0.142	0.0002	0.0003	0.3548
Pp11r	placental protein 11 related	AK169457	0.317	-0.191	0.0071	0.0156	0.2711
Ppa1	NA	AK033434	0.326	-0.127	0.0000	0.0000	0.0668
Ppap2c	phosphatidic acid phosphatase type 2c	NM_015817	0.556	-0.406	0.0000	0.0000	0.0023
Ppcs	phosphopantothenoyl cysteine synthetase	NM_026494	0.556	-0.371	0.0011	0.0357	0.0251
Ppef1	NA	XM_987222	0.557	-0.385	0.0000	0.0001	0.0197
Ppic	peptidylprolyl isomerase C	NM_008908	0.429	-0.062	0.0412	0.0176	0.8148
Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3	NM_027351	0.393	-0.211	0.0010	0.0369	0.0208

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	NM_008014	0.385	-0.052	0.0117	0.0170	0.3714
Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	AK158681	0.282	-0.144	0.0002	0.0181	0.0076
Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	NM_029632	0.269	-0.266	0.0212	0.0633	0.2173
Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	BC044775	0.318	-0.082	0.0047	0.0045	0.4684
Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit1A	NM_021391	0.662	-0.286	0.0000	0.0000	0.0336
Ppp1r3a	protein phosphatase 1, regulatory (inhibitor) subunit3A	NM_080464	0.575	-0.279	0.0054	0.0045	0.5150
Ppp4c	protein phosphatase 4, catalytic subunit	NM_019674	0.286	-0.154	0.0052	0.0774	0.0494
Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	XM_917944	0.379	-0.176	0.0000	0.0005	0.0289
Prcp	prolylcarboxypeptidase (angiotensinase C)	BC089575	0.229	-0.336	0.0000	0.0120	0.0002
Prdx1	peroxiredoxin 1	NM_011034	0.189	-0.437	0.0067	0.8190	0.0030
Prdx4	peroxiredoxin 4	NM_016764	0.503	-0.221	0.0002	0.0011	0.1045
Prim1	DNA primase, p49 subunit	AK160831	0.443	-0.319	0.0000	0.0000	0.0060
Prkcsh	protein kinase C substrate 80K-H	NM_008925	0.280	-0.144	0.0000	0.0000	0.0317
Prkd2	protein kinase D2	BC096444	0.334	-0.134	0.0096	0.0119	0.4080
Prkdc	protein kinase, DNA activated, catalytic polypeptide	NM_011159	0.215	-0.226	0.0000	0.0000	0.0000
Prkrip1	Prkr interacting protein 1 (IL11 inducible)	BC027503	0.399	-0.255	0.0185	0.0594	0.2027
Prlhr	NA	NM_201615	0.775	-0.311	0.0492	0.0339	0.6439

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Prmt1	NA	AK146927	0.409	-0.169	0.0000	0.0000	0.0223
Prmt2	NA	NM_133182	0.310	-0.287	0.0000	0.1279	0.0000
Prph1	peripherin 1	NM_013639	0.847	-0.278	0.0000	0.0000	0.0584
Prss12	protease, serine, 12 neurotrypsin (motopsin)	NM_008939	0.154	-0.280	0.0222	0.3088	0.0449
Prtn3	proteinase 3	NM_011178	0.319	-0.334	0.0031	0.1061	0.0212
Psat1	phosphoserine aminotransferase 1	NM_177420	0.283	-0.168	0.0012	0.0123	0.0688
Psd	pleckstrin and Sec7 domain containing	AK158685	0.587	-0.166	0.0000	0.0000	0.0036
Psd2	pleckstrin and Sec7 domain containing 2	NM_028707	0.345	-0.224	0.0000	0.0000	0.0000
Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	NM_008949	0.387	-0.385	0.0000	0.0064	0.0059
Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	NM_025959	0.211	-0.210	0.0000	0.1793	0.0002
Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	NM_025550	0.226	-0.185	0.0001	0.0378	0.0019
Psme1	proteasome (prosome, macropain) 28 subunit, alpha	NM_026808	0.298	-0.211	0.0001	0.0013	0.0330
Psme2	proteasome (prosome, macropain) 28 subunit, beta	NM_011190	0.184	-0.308	0.0172	0.4879	0.0191
Pspc1	paraspeckle protein 1	AK160722	0.311	-0.148	0.0000	0.0005	0.0516
Ptcd2	pentatricopeptide repeat domain 2	NM_026873	0.444	-0.127	0.0002	0.0019	0.0862
Ptchd1	NA	XM_911319	0.456	-0.323	0.0000	0.0003	0.0030
Ptdss1	phosphatidylserine synthase 1	NM_008959	0.395	-0.069	0.0000	0.0000	0.2907
Ptdss2	phosphatidylserine synthase 2	NM_013782	0.317	-0.143	0.0000	0.0000	0.0016

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Pter	phosphotriesterase related	NM_008961	0.337	-0.287	0.0127	0.0929	0.0963
Ptgs1	prostaglandin-endoperoxide synthase 1	AY547265	0.406	-0.190	0.0004	0.0032	0.0808
Pthr2	parathyroid hormone receptor 2	NM_139270	0.620	-0.432	0.0000	0.0000	0.0004
Ptn	pleiotrophin	AK133835	0.238	-0.235	0.0052	0.3830	0.0076
Ptplad1	NA	NM_021345	0.248	-0.198	0.0000	0.0002	0.0029
Ptplad2	NA	NM_025760	0.249	-0.366	0.0219	0.2695	0.0521
Ptpn5	protein tyrosine phosphatase, non-receptor type 5	NM_013643	0.318	-0.232	0.0000	0.0000	0.0000
Ptprf	protein tyrosine phosphatase, receptor type, F	NM_011213	0.337	-0.211	0.0000	0.0000	0.0000
Ptprs	protein tyrosine phosphatase, receptor type, S	S59186	0.344	-0.151	0.0000	0.0000	0.0000
Pts	6-pyruvoyl-tetrahydropterin synthase	AK160842	0.398	-0.270	0.0043	0.0529	0.0601
Pus3	pseudouridine synthase 3	AK017552	0.293	-0.166	0.0047	0.0304	0.1111
Pus7	NA	XM_980945	0.096	-0.326	0.0001	0.5056	0.0001
Pwp1	PWP1 homolog (S. cerevisiae)	NM_133993	0.352	-0.100	0.0000	0.0001	0.2203
Pxdn	NA	AK122223	0.300	-0.153	0.0000	0.0000	0.0014
Pxmp3	peroxisomal membrane protein 3	NM_008994	0.324	-0.393	0.0131	0.2028	0.0434
Pycrl	pyrroline-5-carboxylate reductase-like	NM_025412	0.342	-0.193	0.0004	0.0278	0.0125
Qpctl	glutaminyl-peptide cyclotransferase-like	NM_175530	0.222	-0.184	0.0042	0.0511	0.0609
R74862	expressed sequence R74862	AK034864	0.284	-0.337	0.0464	0.1429	0.2077
Rab13	RAB13, member RAS oncogene family	AK080805	0.372	-0.285	0.0003	0.0384	0.0073
Rab15	RAB15, member RAS oncogene family	NM_134050	0.267	-0.237	0.0000	0.0037	0.0017

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Rab34	RAB34, member of RAS oncogene family	XM_984679	0.576	-0.211	0.0001	0.0143	0.0054
Rab3b	RAB3B, member RAS oncogene family	NM_023537	0.494	-0.382	0.0000	0.0003	0.0009
Rab40c	Rab40c, member RAS oncogene family	NM_139154	0.415	-0.118	0.0073	0.0191	0.2377
Rab4b	RAB4B, member RAS oncogene family	NM_019394	0.352	-0.207	0.0048	0.0260	0.1284
Rab7l1	RAB7, member RAS oncogene family-like 1	AK137928	0.366	-0.068	0.0402	0.0222	0.7162
Rabep1	rabaptin, RAB GTPase binding effector protein 1	BC009814	0.288	-0.180	0.0000	0.0004	0.0004
Rabepk	Rab9 effector protein with kelch motifs	AK153022	0.222	-0.186	0.0001	0.0177	0.0069
Rabggta	Rab geranylgeranyl transferase, a subunit	NM_019519	0.301	-0.201	0.0000	0.0000	0.0000
Rabl2a	RAB, member of RAS oncogene family-like 2A	AK051232	0.267	-0.142	0.0066	0.0574	0.0841
Rabl4	RAB, member of RAS oncogene family-like 4	NM_025931	0.432	-0.285	0.0002	0.0543	0.0027
Rac3	RAS-related C3 botulinum substrate 3	NM_133223	0.927	-0.566	0.0000	0.0002	0.0003
Rad1	RAD1 homolog (S. pombe)	AK168588	0.475	-0.216	0.0122	0.0299	0.2553
Rad51c	Rad51 homolog c (S. cerevisiae)	AK136204	0.201	-0.202	0.0028	0.0067	0.2405
Rai1	retinoic acid induced 1	NM_001037764	0.441	-0.081	0.0000	0.0000	0.4340
Rai12	retinoic acid induced 12	BC115853	0.350	-0.111	0.0007	0.0038	0.1253
Ralgds	ral guanine nucleotide dissociation stimulator	NM_009058	0.488	-0.202	0.0000	0.0000	0.0000
Ramp2	receptor (calcitonin) activity modifying protein 2	NM_019444	0.589	-0.114	0.0276	0.0275	0.4991

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Ranbp1	RAN binding protein 1	NM_011239	0.443	-0.305	0.0000	0.0023	0.0072
Rangap1	RAN GTPase activating protein 1	NM_011241	0.301	-0.117	0.0000	0.0000	0.0003
Rap2a	RAS related protein 2a	AK018024	0.308	-0.149	0.0141	0.0219	0.3602
Rap2c	RAP2C, member of RAS oncogene family	NM_172413	0.544	-0.145	0.0009	0.0008	0.4344
Rap2ip	Rap2 interacting protein	BC046319	0.449	-0.057	0.0000	0.0000	0.2411
Rara	retinoic acid receptor, alpha	BC038266	0.332	-0.078	0.0053	0.0028	0.6528
Rasa4	RAS p21 protein activator 4	AK133565	0.445	-0.118	0.0000	0.0000	0.2223
Rasal1	RAS protein activator like 1 (GAP1 like)	NM_013832	0.267	-0.244	0.0000	0.0001	0.0000
Rasgrp2	RAS, guanyl releasing protein 2	BC051474	0.540	-0.430	0.0000	0.0000	0.0000
Raver1	NA	AK052443	0.318	-0.130	0.0012	0.0125	0.0708
Rbm13	RNA binding motif protein 13	NM_026453	0.246	-0.252	0.0001	0.0307	0.0033
Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	NM_134083	0.419	-0.041	0.0000	0.0000	0.7240
Rcn1	reticulocalbin 1	NM_009037	0.556	-0.440	0.0000	0.0003	0.0000
Rcor2	REST corepressor 2	NM_054048	0.917	-0.375	0.0000	0.0000	0.0040
Rdbp	RD RNA-binding protein	NM_001045863	0.252	-0.208	0.0009	0.0314	0.0225
Rdh11	retinol dehydrogenase 11	NM_021557	0.219	-0.228	0.0014	0.1309	0.0075
Rdh12	retinol dehydrogenase 12	AK164157	0.330	-0.369	0.0012	0.0641	0.0144
Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	AK039931	0.616	-0.500	0.0092	0.0927	0.0709
Rdh5	retinol dehydrogenase 5	NM_134006	0.183	-0.306	0.0365	0.4631	0.0447
Rfc3	replication factor C (activator 1) 3	AK165891	0.509	-0.255	0.0000	0.0026	0.0125

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Rfx5	NA	NM_017395	0.236	-0.372	0.0000	0.0764	0.0001
Rgag1	NA	AK220382	0.662	-0.872	0.0157	0.0781	0.1377
Rgl2	ral guanine nucleotide dissociation stimulator-like 2	NM_009059	0.253	-0.166	0.0000	0.0000	0.0100
Rgs11	regulator of G-protein signaling 11	XM_990503	0.617	-0.398	0.0000	0.0000	0.0000
Rgs19	regulator of G-protein signaling 19	XM_990290	0.219	-0.268	0.0298	0.3044	0.0610
Rgs20	regulator of G-protein signaling 20	NM_021374	0.556	-0.439	0.0000	0.0056	0.0036
Rhbdf1	rhomboid family 1 (Drosophila)	NM_010117	0.465	-0.285	0.0000	0.0000	0.0000
Rhbdl3	NA	AJ313479	0.564	-0.388	0.0000	0.0000	0.0001
Rhoc	ras homolog gene family, member C	NM_007484	0.631	-0.334	0.0000	0.0002	0.0206
Rhof	ras homolog gene family, member f	NM_175092	0.394	-0.256	0.0000	0.0002	0.0091
Rhov	ras homolog gene family, member V	NM_145530	0.604	-0.212	0.0074	0.0055	0.5575
Rhpn1	rhophilin, Rho GTPase binding protein 1	AK085338	0.279	-0.189	0.0000	0.0019	0.0032
Rhpn2	rhophilin, Rho GTPase binding protein 2	NM_027897	0.200	-0.203	0.0009	0.0591	0.0113
Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	AK171093	0.317	-0.093	0.0000	0.0000	0.2147
Riok2	RIO kinase 2 (yeast)	NM_025934	0.252	-0.194	0.0000	0.0053	0.0005
Rit1	Ras-like without CAAX 1	NM_009069	0.465	-0.091	0.0011	0.0004	0.7400
Rkhd1	ring finger (C3HC4 type) and KH domain containing 1	AK149801	0.343	-0.272	0.0020	0.0796	0.0194
Rnd1	Rho family GTPase 1	NM_172612	0.347	-0.562	0.0000	0.0117	0.0001
Rnd2	Rho family GTPase 2	AK075970	0.580	-0.269	0.0000	0.0000	0.0001
Rnf122	ring finger protein 122	AK162034	0.258	-0.234	0.0005	0.1042	0.0039
Rnf13	ring finger protein 13	AK082296	0.340	-0.097	0.0005	0.0028	0.1187
Rnf14	ring finger protein 14	AK011316	0.329	-0.078	0.0004	0.0009	0.2674

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Rnf2	ring finger protein 2	Y12880	0.387	-0.131	0.0026	0.0114	0.1511
Rnh1	ribonuclease/angiogenin inhibitor 1	NM_145135	0.451	-0.212	0.0003	0.0357	0.0074
Rnpc3	RNA-binding region (RNP1, RRM) containing 3	NM_007446	0.353	-0.221	0.0000	0.0049	0.0011
Rnpep	arginyl aminopeptidase (aminopeptidase B)	NM_145417	0.353	-0.359	0.0000	0.0001	0.0000
Rnu3b4	NA	NR_002843	0.411	-0.486	0.0309	0.6509	0.0229
Robo3	roundabout homolog 3 (Drosophila)	AK031746	0.372	-0.050	0.0360	0.0138	0.8484
Rp2h	retinitis pigmentosa 2 homolog (human)	NM_133669	0.579	-0.193	0.0002	0.0006	0.1742
Rpa2	replication proteinA2	NM_011284	0.449	-0.122	0.0004	0.0007	0.3024
Rpl13	ribosomal proteinL13	XR_001880	0.783	-0.100	0.0104	0.0114	0.4459
Rpl14	ribosomal proteinL14	BC092249	0.426	-0.136	0.0056	0.0172	0.2080
Rpl35	ribosomal proteinL35	BC085091	0.405	-0.174	0.0205	0.0146	0.5984
Rpp14	ribonuclease P 14 subunit (human)	NM_025938	0.428	-0.160	0.0263	0.0462	0.3377
Rpp40	ribonuclease P 40 subunit (human)	NM_145938	0.206	-0.344	0.0262	0.4311	0.0350
Rprm	reprimo, TP53 dependent G2 arrest mediator candidate	NM_023396	0.322	-0.199	0.0427	0.0558	0.4227
Rps19bp1	NA	NM_175109	0.339	-0.100	0.0109	0.0093	0.5165
Rps6ka4	ribosomal protein S6 kinase, polypeptide 4	NM_019924	0.288	-0.144	0.0000	0.0000	0.0022
Rps6ka6	ribosomal protein S6 kinase polypeptide 6	NM_025949	0.237	-0.288	0.0000	0.0476	0.0002
Rps6kl1	ribosomal protein S6 kinase-like 1	NM_146244	0.270	-0.131	0.0000	0.0010	0.0115
Rragd	Ras-related GTP binding D	AF490406	0.414	-0.138	0.0000	0.0003	0.0814
Rras	Harvey rat sarcoma oncogene, subgroupR	NM_009101	0.272	-0.220	0.0035	0.1045	0.0242
Rras2	related RAS viral (r-ras) oncogene homolog 2	XM_978422	0.917	-0.101	0.0235	0.0145	0.6558
Rrn3	RRN3 RNA polymerase I transcription factor homolog (yeast)	NM_001039521	0.312	-0.129	0.0000	0.0000	0.0191

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Rshl3	radial spokehead-like 3	XM_993152	0.561	-0.241	0.0115	0.0199	0.3284
Rspo3	NA	NM_028351	0.423	-0.143	0.0036	0.0037	0.4419
Rtbdn	NA	NM_144929	0.363	-0.353	0.0001	0.0043	0.0111
Rttn	rotatin	AK052059	0.218	-0.218	0.0000	0.0000	0.0000
Rusc1	RUN and SH3 domain containing 1	AK170012	0.403	-0.115	0.0000	0.0000	0.0103
Rusc2	RUN and SH3 domain containing 2	NM_199057	0.317	-0.090	0.0001	0.0002	0.1324
Rutbc2	RUN and TBC1 domain containing 2	NM_172718	0.294	-0.265	0.0000	0.0000	0.0000
S100a10	S100 calcium binding protein A10 (calpactin)	AK051143	1.007	-0.639	0.0000	0.0007	0.0020
Sacm1l	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae)	NM_030692	0.297	-0.178	0.0000	0.0000	0.0000
Samd10	sterile alpha motif domain containing 10	NM_172676	0.232	-0.198	0.0056	0.0613	0.0667
Samd14	NA	NM_178049	0.685	-0.377	0.0000	0.0000	0.0000
Sar1a	NA	NM_009120	0.583	-0.128	0.0001	0.0004	0.1554
Sar1b	NA	NM_025535	0.459	-0.069	0.0021	0.0010	0.6666
Sardh	sarcosine dehydrogenase	NM_138665	0.341	-0.217	0.0000	0.0000	0.0000
Sart2	squamous cell carcinoma antigen recognized by T cells 2	NM_172508	0.448	-0.173	0.0008	0.0025	0.1931
Sat2	spermidine/spermine N1-acetyl transferase 2	BC061227	0.666	-0.294	0.0000	0.0000	0.0274
Sbk1	SH3-binding kinase 1	XM_992744	0.578	-0.217	0.0000	0.0002	0.0145
Sccpdh	saccharopine dehydrogenase (putative)	AK081021	0.246	-0.187	0.0000	0.0019	0.0140
Scml2	sex comb on midleg-like 2 (Drosophila)	XM_981005	0.131	-0.535	0.0000	0.4102	0.0000
Scn3b	sodium channel, voltage-gated, type III, beta	NM_153522	0.330	-0.375	0.0000	0.0001	0.0001

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Scn7a	sodium channel, voltage-gated, type VII, alpha	NM_009135	0.456	-0.582	0.0000	0.0000	0.0000
Scn9a	sodium channel, voltage-gated, type IX, alpha	XM_920936	0.146	-0.469	0.0000	0.2501	0.0000
Scp2	sterol carrier protein 2, liver	NM_011327	0.226	-0.214	0.0005	0.0284	0.0137
Scrg1	scrapie responsive gene 1	AJ223206	0.353	-0.453	0.0011	0.0221	0.0384
Scube3	signal peptide, CUB domain, EGF-like 3	NM_001004366	0.341	-0.231	0.0000	0.0000	0.0000
Scye1	small inducible cytokine subfamily E, member 1	NM_007926	0.264	-0.184	0.0063	0.1355	0.0331
Sdc2	syndecan 2	NM_008304	0.224	-0.271	0.0226	0.2686	0.0540
Sdc3	syndecan 3	AK179937	0.311	-0.218	0.0000	0.0001	0.0020
Sec22c	NA	NM_178677	0.591	-0.138	0.0000	0.0000	0.3625
Sec24c	SEC24 related gene family, member C (S. cerevisiae)	NM_172596	0.284	-0.148	0.0000	0.0000	0.0000
Sec61g	NA	NM_011343	0.528	-0.660	0.0177	0.0734	0.1618
Selk	NA	XM_910190	0.609	-0.182	0.0003	0.0057	0.0362
Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	AK077231	0.437	-0.032	0.0000	0.0000	0.8173
Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	AK163828	0.324	-0.186	0.0000	0.0009	0.0295
Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F	AK172610	0.391	-0.330	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	NM_013658	0.451	-0.478	0.0000	0.0000	0.0000
Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	NM_011350	0.403	-0.285	0.0000	0.0000	0.0000
Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	NM_013662	0.463	-0.118	0.0029	0.0030	0.4346
Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	NM_011351	0.431	-0.220	0.0000	0.0000	0.0000
Senp3	SUMO/sentrin specific peptidase 3	XR_003084	0.526	-0.238	0.0002	0.0139	0.0092
Senp5	SUMO/sentrin specific peptidase 5	NM_177103	0.330	-0.087	0.0000	0.0000	0.3273
Sep15	selenoprotein	NM_053102	0.417	-0.200	0.0002	0.0005	0.2176
Sept3	septin 3	NM_011889	0.348	-0.203	0.0000	0.0000	0.0000
Sept6	septin 6	NM_019942	0.367	-0.117	0.0005	0.0044	0.0802
Sepx1	selenoprotein X 1	AK003112	0.365	-0.090	0.0075	0.0043	0.6445
Serf2	small EDRK-rich factor 2	BC092136	0.275	-0.203	0.0134	0.4097	0.0188
Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	NM_025429	0.166	-0.440	0.0394	0.6279	0.0311
Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b	NM_173052	0.820	-0.604	0.0000	0.0004	0.0007
Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	XR_004911	0.337	-0.220	0.0001	0.0050	0.0185

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	NM_011454	0.318	-0.443	0.0452	0.2731	0.1056
Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	NM_009256	0.389	-0.501	0.0008	0.0529	0.0122
Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	NM_008871	0.465	-0.175	0.0000	0.0000	0.1154
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	NM_011340	0.243	-0.330	0.0012	0.0977	0.0095
Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	NM_009776	0.426	-0.136	0.0030	0.0064	0.2620
Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1	NM_009250	0.166	-0.256	0.0001	0.1867	0.0004
Sez6	seizure related gene 6	AK032277	0.361	-0.178	0.0000	0.0000	0.0000
Sfrp5	secreted frizzled-related sequence protein 5	NM_018780	0.454	-0.365	0.0000	0.0001	0.0021
Sgpl1	sphingosine phosphate lyase 1	NM_009163	0.317	-0.189	0.0000	0.0003	0.0000
Sh2d5	SH2 domain containing 5	XM_914492	0.300	-0.230	0.0000	0.0001	0.0003
Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	NM_019989	0.288	-0.226	0.0045	0.0558	0.0600
Sh3bp2	SH3-domain binding protein 2	NM_011893	0.222	-0.276	0.0029	0.0879	0.0249
Sh3bp5l	SH3 binding domain protein 5 like	NM_024480	0.342	-0.077	0.0067	0.0072	0.4437
Sh3glb2	SH3-domain GRB2-like endophilin B2	NM_139302	0.385	-0.127	0.0000	0.0000	0.0272
Sh3yl1	Sh3 domain YSC-like 1	BC061488	0.374	-0.356	0.0002	0.0047	0.0403
Shc1	src homology 2 domain-containing transforming protein C1	AK036980	0.567	-0.313	0.0000	0.0000	0.0000
Shc4	NA	AK036946	0.306	-0.198	0.0000	0.0005	0.0551

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Shd	src homology 2 domain-containing transforming protein D	NM_009168	0.345	-0.275	0.0002	0.0357	0.0041
Shf	NA	NM_001013829	0.238	-0.234	0.0000	0.0744	0.0004
Shfm1	split hand/foot malformation (ectrodactyly) type 1	NM_009169	0.526	-0.121	0.0018	0.0038	0.2584
Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)	NM_028230	0.191	-0.223	0.0005	0.0311	0.0130
Siae	NA	AF156856	0.203	-0.229	0.0000	0.0003	0.0000
Sidt1	SID1 transmembrane family, member 1	AK046836	0.417	-0.295	0.0000	0.0000	0.0000
Sim1	single-minded homolog 1 (Drosophila)	NM_011376	0.189	-0.235	0.0077	0.1505	0.0362
Six5	sine oculis-related homeobox 5 homolog (Drosophila)	NM_011383	0.252	-0.347	0.0037	0.1792	0.0140
Six6os1	Six6 opposite strand transcript 1	AK044729	0.367	-0.436	0.0000	0.0013	0.0000
Skap1	NA	AK040068	0.174	-0.229	0.0335	0.2010	0.1100
Skap2	NA	NM_018773	0.257	-0.144	0.0123	0.0273	0.2753
Slbp	stem-loop binding protein	AK131729	0.394	-0.254	0.0096	0.1678	0.0397
Slc10a4	NA	NM_173403	0.247	-0.378	0.0264	0.1702	0.1045
Slc12a5	solute carrier family 12, member 5	NM_020333	0.307	-0.125	0.0000	0.0000	0.0000
Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	NM_172892	0.637	-0.122	0.0000	0.0000	0.4532
Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	NM_001004148	0.321	-0.316	0.0046	0.0774	0.0438
Slc16a11	solute carrier family 16 (monocarboxylic acid transporters), member 11	NM_153081	0.450	-0.513	0.0000	0.0286	0.0000

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Slc16a4	solute carrier family 16 (monocarboxylic acid transporters), member 4	BC025441	0.148	-0.267	0.0049	0.3376	0.0085
Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9	NM_025807	0.320	-0.153	0.0054	0.0120	0.2640
Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	AK034368	0.029	-0.465	0.0000	0.8220	0.0000
Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	NM_018861	0.282	-0.208	0.0000	0.0116	0.0012
Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	NM_009201	0.396	-0.183	0.0044	0.0122	0.2215
Slc1a6	solute carrier family 1 (high affinity aspartate/glutamate transporter),member6	NM_009200	0.244	-0.252	0.0003	0.0492	0.0049
Slc22a17	solute carrier family 22 (organic cation transporter), member 17	NM_010112	0.330	-0.081	0.0000	0.0000	0.0995
Slc22a21	solute carrier family 22 (organic cation transporter), member 21	AK080177	0.292	-0.259	0.0048	0.1472	0.0230
Slc22a5	solute carrier family 22 (organic cation transporter), member 5	NM_011396	0.290	-0.231	0.0000	0.0009	0.0006
Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	NM_153150	0.302	-0.262	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14	AK148277	0.202	-0.252	0.0000	0.1257	0.0000
Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	NM_020520	0.379	-0.147	0.0000	0.0001	0.0721
Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	BC050887	0.338	-0.129	0.0000	0.0000	0.0994
Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	NM_172685	0.328	-0.239	0.0007	0.0043	0.1094
Slc25a33	NA	NM_027460	0.449	-0.127	0.0000	0.0000	0.1928
Slc25a39	NA	NM_026542	0.306	-0.114	0.0013	0.0034	0.2158
Slc26a6	solute carrier family 26, member 6	AK053088	0.426	-0.161	0.0000	0.0001	0.0661
Slc27a3	solute carrier family 27 (fatty acid transporter),member3	NM_011988	0.658	-0.345	0.0000	0.0000	0.0012
Slc27a4	solute carrier family 27 (fatty acid transporter),member4	NM_011989	0.374	-0.201	0.0000	0.0000	0.0000
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	NM_008302	0.344	-0.269	0.0000	0.0000	0.0000
Slc29a4	solute carrier family 29 (nucleoside transporters), member 4	NM_146257	0.243	-0.324	0.0000	0.0104	0.0040
Slc2a5	solute carrier family 2 (facilitated glucose transporter),member5	NM_019741	0.142	-0.286	0.0022	0.2856	0.0046
Slc30a10	solute carrier family 30, member 10	NM_001033286	0.356	-0.175	0.0072	0.0575	0.0914
Slc30a7	solute carrier family 30 (zinc transporter), member 7	NM_023214	0.434	-0.218	0.0000	0.0000	0.0040

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Slc31a1	solute carrier family 31, member 1	NM_175090	0.475	-0.203	0.0022	0.0059	0.2204
Slc32a1	solute carrier family 32 (GABA vesicular transporter),member1	XM_979351	0.341	-0.086	0.0420	0.0240	0.7052
Slc35a1	solute carrier family 35 (CMP-sialic acid transporter),member1	AK005650	0.278	-0.189	0.0089	0.0512	0.1233
Slc35a2	solute carrier family 35 (UDP-galactose transporter),member2	NM_078484	0.347	-0.151	0.0087	0.0491	0.1253
Slc35b1	solute carrier family 35, member B1	NM_016752	0.415	-0.101	0.0114	0.0321	0.2261
Slc35b3	solute carrier family 35, member B3	AK141280	0.332	-0.238	0.0000	0.0006	0.0121
Slc35c1	solute carrier family 35, member C1	NM_145832	0.417	-0.229	0.0028	0.0086	0.1951
Slc35e4	solute carrier family 35, member E4	NM_153142	0.411	-0.125	0.0043	0.0180	0.1593
Slc35f1	solute carrier family 35, member F1	NM_178675	0.277	-0.239	0.0000	0.0016	0.0115
Slc35f5	solute carrier family 35, member F5	NM_028787	0.305	-0.111	0.0000	0.0000	0.1283
Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter),member1	AK163990	0.293	-0.145	0.0001	0.0003	0.1163
Slc37a4	solute carrier family 37 (glycerol-6-phosphate transporter),member4	NM_008063	0.410	-0.001	0.0009	0.0002	0.9973
Slc38a3	solute carrier family 38, member 3	NM_023805	0.404	-0.159	0.0000	0.0000	0.0001
Slc38a5	solute carrier family 38, member 5	NM_172479	0.371	-0.196	0.0000	0.0022	0.0156
Slc39a12	solute carrier family 39 (zinc transporter), member 12	NM_001012305	0.274	-0.205	0.0000	0.2028	0.0000
Slc39a6	solute carrier family 39 (metal ion transporter),member6	NM_139143	0.336	-0.140	0.0000	0.0002	0.0417
Slc44a2	solute carrier family 44, member 2	AK043924	0.247	-0.155	0.0000	0.0003	0.0038
Slc45a1	NA	NM_173774	0.310	-0.106	0.0007	0.0073	0.0707

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Slc4a2	solute carrier family 4 (anion exchanger), member 2	NM_009207	0.320	-0.259	0.0000	0.0000	0.0000
Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	NM_001033270	0.333	-0.158	0.0000	0.0000	0.0064
Slc5a5	solute carrier family 5 (sodium iodide symporter),member 5	NM_053248	0.418	-0.168	0.0000	0.0000	0.1087
Slc5a7	solute carrier family 5 (choline transporter),member7	AK164116	0.340	-0.320	0.0008	0.0350	0.0192
Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	NM_144512	0.702	-0.130	0.0000	0.0000	0.1834
Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	NM_175328	0.487	-0.316	0.0000	0.0000	0.0000
Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine),member 3	NM_010020	0.133	-0.444	0.0023	0.3145	0.0043
Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	NM_201353	0.370	-0.237	0.0000	0.0000	0.0000
Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	NM_133987	0.211	-0.248	0.0000	0.0525	0.0000
Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	NM_008135	0.260	-0.187	0.0000	0.0000	0.0000
Slc7a10	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10	BC027516	0.492	-0.207	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	AK141558	0.513	-0.474	0.0000	0.0017	0.0000
Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	NM_144852	0.417	-0.278	0.0000	0.0082	0.0022
Slc8a2	solute carrier family 8 (sodium/calcium exchanger),member 2	NM_148946	0.397	-0.117	0.0003	0.0001	0.6448
Slc9a5	NA	XM_915379	0.346	-0.337	0.0000	0.0000	0.0000
Slco1c1	solute carrier organic anion transporter family, member 1c1	NM_021471	0.271	-0.202	0.0000	0.0006	0.0020
Slco2a1	solute carrier organic anion transporter family, member 2a1	NM_033314	0.525	-0.223	0.0000	0.0000	0.0433
Slitrk4	SLIT and NTRK-like family, member 4	NM_178740	0.517	-0.470	0.0000	0.0005	0.0082
Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	NM_053123	0.215	-0.355	0.0000	0.0000	0.0000
Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	XM_620137	0.191	-0.295	0.0018	0.3007	0.0034
Smc2	NA	BC021847	0.434	-0.361	0.0000	0.0000	0.0000
Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	NM_001009927	0.442	-0.011	0.0221	0.0058	0.9759
Smpd3	sphingomyelin phosphodiesterase 3, neutral	NM_021491	0.297	-0.122	0.0264	0.0541	0.2991
Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A	NM_020561	0.260	-0.255	0.0010	0.2310	0.0027

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Smtn	smoothelin	NM_013870	0.448	-0.301	0.0000	0.0000	0.0000
Snapc1	small nuclear RNA activating complex, polypeptide 1	NM_178392	0.246	-0.228	0.0002	0.0525	0.0034
Snf8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	AK180940	0.698	-0.106	0.0009	0.0021	0.2426
Snrpa1	small nuclear ribonucleoprotein polypeptide A'	AK152546	0.487	-0.217	0.0006	0.0020	0.1680
Snrpb	small nuclear ribonucleoprotein B	NM_009225	0.415	-0.037	0.0008	0.0002	0.8436
Snupn	NA	BC023317	0.116	-0.289	0.0111	0.4920	0.0118
Snx26	sorting nexin 26	NM_178252	0.547	-0.376	0.0000	0.0000	0.0000
Snx7	sorting nexin 7	XM_001005105	0.133	-0.344	0.0003	0.4820	0.0003
Snx8	sorting nexin 8	BC019142	0.381	-0.073	0.0001	0.0001	0.4844
Sord	NA	NM_146126	0.117	-0.289	0.0000	0.0351	0.0003
Spag6	sperm associated antigen 6	AK054199	0.681	-0.542	0.0000	0.0000	0.0000
Spast	NA	AK044900	0.207	-0.195	0.0000	0.0018	0.0010
Spata6	spermatogenesis associated 6	NM_026470	0.362	-0.261	0.0000	0.0023	0.0041
Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	BC020050	0.544	-0.208	0.0008	0.0127	0.0482
Speer8-ps1	spermatogenesis associated glutamate (E)-rich protein 8, pseudogene 1	NR_001584	0.284	-0.541	0.0366	0.0759	0.2969
Spfh1	SPFH domain family, member 1	BC021793	0.228	-0.214	0.0001	0.0244	0.0018
Spin2	NA	NM_001005370	0.447	-0.447	0.0118	0.1983	0.0399
Spink10	NA	BC049733	0.829	-0.523	0.0000	0.0001	0.0240
Spint2	serine protease inhibitor, Kunitz type 2	AF099020	0.438	-0.307	0.0000	0.0055	0.0007
Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3	AJ278998	0.310	-0.113	0.0000	0.0003	0.0419

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Spred3	sprouty-related, EVH1 domain containing 3	NM_182927	0.242	-0.201	0.0372	0.0600	0.3598
Sptlc1	serine palmitoyltransferase, long chain base subunit 1	NM_009269	0.293	-0.138	0.0000	0.0000	0.0455
Sra1	steroid receptor RNA activator 1	NM_025291	0.533	-0.180	0.0007	0.0024	0.1860
Srd5a2l	steroid 5 alpha-reductase 2-like	NM_020611	0.421	-0.232	0.0002	0.0030	0.0485
Srp14	signal recognition particle 14	NM_009273	0.685	-0.167	0.0069	0.0076	0.4325
Srpk3	NA	NM_019684	0.242	-0.288	0.0001	0.0217	0.0023
Srpx2	sushi-repeat-containing protein, X-linked 2	NM_026838	0.192	-0.334	0.0002	0.1614	0.0009
Ssbp1	single-stranded DNA binding protein 1	AK090272	0.435	-0.224	0.0026	0.0211	0.0889
Ssbp4	single stranded DNA binding protein 4	NM_133772	0.398	-0.073	0.0000	0.0000	0.3438
Ssh3	slingshot homolog 3 (Drosophila)	AK038981	0.446	-0.235	0.0000	0.0000	0.0000
Ssr2	signal sequence receptor, beta	NM_025448	0.256	-0.179	0.0063	0.1920	0.0226
Ssr4	signal sequence receptor, delta	AK142600	0.392	-0.160	0.0035	0.0533	0.0491
Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	NM_020491	0.425	-0.199	0.0113	0.0167	0.3674
Sst	somatostatin	NM_009215	0.668	-0.501	0.0045	0.1518	0.0206
Sstr1	somatostatin receptor 1	NM_009216	0.160	-0.308	0.0093	0.4208	0.0123
Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	NM_026899	0.566	-0.004	0.0265	0.0068	0.9889
Ssx9	NA	NM_199063	4.517	-0.016	0.0059	0.0013	0.9855

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
St6galnac6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	AK030648	0.553	-0.237	0.0000	0.0000	0.0072
St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase4	NM_009183	0.296	-0.149	0.0044	0.0085	0.2910
Stard3	START domain containing 3	AK160480	0.382	-0.268	0.0000	0.0000	0.0001
Stard3nl	STARD3 N-terminal like	AK018331	0.487	-0.113	0.0170	0.0284	0.3449
Stard4	StAR-related lipid transfer (START) domain containing 4	NM_133774	0.425	-0.174	0.0004	0.0109	0.0289
Stat6	signal transducer and activator of transcription 6	AK149563	0.319	-0.169	0.0000	0.0000	0.0098
Stc1	stanniocalcin 1	NM_009285	0.514	-0.630	0.0000	0.0010	0.0005
Stch	stress 70 protein chaperone, microsome-associated, human homolog	M33214	0.312	-0.171	0.0008	0.0201	0.0311
Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	AK029842	0.257	-0.160	0.0000	0.0000	0.0032
Stk38	serine/threonine kinase 38	AK020024	0.302	-0.127	0.0000	0.0001	0.0673
Stmn1	stathmin 1	AB064953	0.471	-0.238	0.0000	0.0030	0.0007
Stoml1	stomatin-like 1	AK148324	0.330	-0.101	0.0120	0.0201	0.3370
Stra13	stimulated by retinoic acid 13	NM_016665	0.346	-0.289	0.0001	0.0030	0.0142
Stra6	stimulated by retinoic acid gene 6	AK083120	0.362	-0.157	0.0008	0.0011	0.3715
Stx1a	syntaxin 1A (brain)	AK144399	0.250	-0.348	0.0000	0.0219	0.0000
Stx3	syntaxin 3	NM_001025307	0.279	-0.382	0.0000	0.0060	0.0000
Stx5a	syntaxin 5A	AK002722	0.321	-0.112	0.0000	0.0008	0.0417
Stxbp2	syntaxin binding protein 2	NM_011503	0.273	-0.213	0.0000	0.0000	0.0001
Styk1	serine/threonine/tyrosine kinase 1	NM_172891	0.610	-0.273	0.0000	0.0002	0.1178

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Styx	phosphoserine/threonine/tyrosine interaction protein	BC085089	0.467	-0.100	0.0002	0.0001	0.6011
Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit	NM_019879	0.581	-0.052	0.0184	0.0217	0.4359
Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	AK167339	0.292	-0.109	0.0177	0.0220	0.4204
Sumf1	sulfatase modifying factor 1	NM_145937	0.327	-0.154	0.0000	0.0002	0.0166
Surf2	surfeit gene 2	NM_013678	0.497	-0.089	0.0063	0.0050	0.5320
Surf4	surfeit gene 4	NM_011512	0.378	-0.209	0.0000	0.0006	0.0267
Sv2a	synaptic vesicle glycoprotein 2 a	NM_022030	0.271	-0.163	0.0000	0.0000	0.0001
Syap1	synapse associated protein 1	NM_025932	0.423	-0.161	0.0014	0.0043	0.1952
Sycp3	synaptonemal complex protein 3	NM_011517	0.264	-0.482	0.0026	0.3482	0.0043
Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	NM_019666	0.347	-0.212	0.0000	0.0001	0.0000
Syngr3	synaptogyrin 3	NM_011522	0.219	-0.190	0.0004	0.0512	0.0071
Syt10	synaptotagmin X	NM_018803	0.064	-0.345	0.0001	0.6283	0.0001
Syt3	synaptotagmin III	NM_016663	0.348	-0.148	0.0000	0.0000	0.0059
Syt5	synaptotagmin V	NM_016908	0.335	-0.366	0.0000	0.0023	0.0000
Sytl5	NA	NM_177704	0.241	-0.317	0.0001	0.0361	0.0018
Tac1	tachykinin 1	NM_009311	0.895	-0.872	0.0000	0.0000	0.0000
Tacc3	transforming, acidic coiled-coil containing protein 3	AK076282	0.316	-0.209	0.0000	0.0006	0.0537
Tacr3	tachykinin receptor 3	NM_021382	0.380	-0.609	0.0000	0.0174	0.0000
Tacstd2	tumor-associated calcium signal transducer 2	NM_020047	0.641	-0.356	0.0210	0.0195	0.5154
Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_177342	0.168	-0.239	0.0066	0.2698	0.0156

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Taf6l	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	AK077149	0.572	-0.235	0.0000	0.0000	0.0059
Tagln3	transgelin 3	AK012333	0.429	-0.112	0.0006	0.0017	0.2166
Taldo1	transaldolase 1	NM_011528	0.299	-0.350	0.0003	0.1749	0.0010
Tasp1	NA	AK050603	0.303	-0.178	0.0001	0.0020	0.0214
Tbc1d10a	TBC1 domain family, member 10a	BC037230	0.323	-0.184	0.0004	0.0015	0.1532
Tbc1d10b	TBC1 domain family, member 10b	NM_144522	0.366	-0.095	0.0000	0.0000	0.1095
Tbc1d12	TBC1D12: TBC1 domain family, member 12	NM_145952	0.338	-0.129	0.0000	0.0001	0.0616
Tbc1d20	TBC1 domain family, member 20	BC086617	0.336	-0.126	0.0061	0.0134	0.2687
Tbccd1	NA	BC082558	0.465	-0.095	0.0006	0.0005	0.4668
Tbl3	transducin (beta)-like 3	AK081572	0.396	-0.092	0.0000	0.0000	0.1547
Tbrg1	transforming growth factor beta regulated gene 1	NM_025289	0.420	-0.135	0.0000	0.0006	0.0562
Tbx18	T-box18	AK012980	0.309	-0.113	0.0374	0.0334	0.5420
Tceal5	NA	NM_177919	0.454	-0.276	0.0323	0.1308	0.1624
Tcf19	transcription factor 19	NM_025674	0.333	-0.320	0.0430	0.0833	0.3150
Tcirg1	T-cell, immune regulator 1	NM_016921	0.284	-0.196	0.0000	0.0000	0.0001
Tegt	testis enhanced gene transcript	NM_026669	0.317	-0.106	0.0001	0.0001	0.2802
Tekt2	tektin 2	NM_011902	0.245	-0.358	0.0052	0.0681	0.0557
Telo2	NA	NM_027880	0.341	-0.106	0.0000	0.0000	0.0638
Tep1	telomerase associated protein 1	NM_009351	0.233	-0.216	0.0017	0.0309	0.0421
Tex261	testis expressed gene 261	AK170049	0.535	-0.129	0.0000	0.0000	0.2916
Tex264	testis expressed gene 264	AK159046	0.311	-0.175	0.0009	0.0125	0.0530
Tfpi	tissue factor pathway inhibitor	AF004833	0.315	-0.389	0.0018	0.1383	0.0092
Tgfb1	transforming growth factor, beta 1	NM_011577	0.261	-0.177	0.0235	0.0759	0.2027

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Tgfb1i1	transforming growth factor beta 1 induced transcript 1	DQ143891	0.175	-0.269	0.0008	0.1046	0.0054
Th	tyrosine hydroxylase	AK139568	0.177	-0.444	0.0000	0.0414	0.0000
Thbs3	thrombospondin 3	NM_013691	0.544	-0.309	0.0000	0.0000	0.0000
Them4	thioesterase superfamily member 4	AK139993	0.943	-0.353	0.0002	0.0008	0.1350
Thoc6	NA	BC089551	0.305	-0.137	0.0001	0.0010	0.0749
Thop1	thimet oligopeptidase 1	BC031722	0.351	-0.120	0.0000	0.0001	0.0515
Thpo	thrombopoietin	BC003803	0.450	-0.283	0.0025	0.0037	0.3465
Thra	thyroid hormone receptor alpha	BC046795	0.375	-0.070	0.0000	0.0000	0.1875
Thrap4	thyroid hormone receptor associated protein 4	NM_011869	0.261	-0.142	0.0000	0.0000	0.0000
Thrap5	thyroid hormone receptor associated protein 5	NM_198107	0.328	-0.116	0.0000	0.0000	0.0579
Thrap6	thyroid hormone receptor associated protein 6	NM_027212	0.580	-0.207	0.0361	0.0551	0.3757
Thumpd3	THUMP domain containing 3	NM_008188	0.303	-0.198	0.0139	0.0657	0.1454
Timm17b	translocator of inner mitochondrial membrane 17b	NM_011591	0.320	-0.121	0.0001	0.0000	0.6076
Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	NM_025616	0.407	-0.162	0.0000	0.0000	0.0127
Timm8a1	NA	NM_013898	0.581	-0.288	0.0018	0.0089	0.1305
Tiprl	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	NM_145513	0.298	-0.151	0.0035	0.0088	0.2320
Tlcd1	NA	AK002703	0.292	-0.246	0.0000	0.0009	0.0161
Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	NM_011599	0.420	-0.087	0.0000	0.0000	0.2748

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	NM_019725	0.490	-0.340	0.0000	0.0000	0.0000
Tll1	tolloid-like	NM_009390	0.348	-0.363	0.0000	0.0000	0.0000
Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	0.341	-0.065	0.0479	0.0233	0.7737
Tm7sf2	transmembrane 7 superfamily member 2	AK003717	0.483	-0.262	0.0000	0.0000	0.0033
Tm9sf2	transmembrane 9 superfamily member 2	NM_080556	0.216	-0.335	0.0000	0.0121	0.0000
Tmbim4	transmembrane BAX inhibitor motif containing 4	NM_026617	0.405	-0.147	0.0002	0.0009	0.1201
Tmc4	transmembrane channel-like gene family 4	NM_027203	0.414	-0.157	0.0000	0.0001	0.1872
Tmco3	transmembrane and coiled-coil domains 3	AK083321	0.339	-0.123	0.0000	0.0000	0.0073
Tmco5	NA	NM_026104	0.298	-0.415	0.0346	0.3903	0.0524
Tmem126a	NA	AK210038	0.342	-0.726	0.0033	0.2684	0.0077
Tmem128	NA	AK076679	0.391	-0.215	0.0001	0.0035	0.0131
Tmem132a	NA	NM_133804	0.561	-0.279	0.0000	0.0000	0.0000
Tmem132e	NA	AK134540	0.373	-0.397	0.0000	0.0000	0.0000
Tmem141	NA	NM_001040130	0.424	-0.342	0.0000	0.0011	0.0045
Tmem147	NA	BC035323	0.428	-0.130	0.0004	0.0048	0.0683
Tmem150	NA	NM_144916	0.510	-0.321	0.0000	0.0000	0.0005
Tmem158	NA	NM_001002267	0.509	-0.299	0.0009	0.0021	0.2483
Tmem160	NA	NM_026938	0.342	-0.251	0.0092	0.0557	0.1168
Tmem17	transmembrane protein 17	NM_153596	0.423	-0.130	0.0297	0.0250	0.5548
Tmem176a	NA	AK165660	0.295	-0.229	0.0477	0.1443	0.2108
Tmem176b	NA	AK156042	0.325	-0.140	0.0004	0.0029	0.1082
Tmem180	NA	NM_029186	0.303	-0.110	0.0003	0.0008	0.2093
Tmem181	NA	AK137412	0.223	-0.357	0.0163	0.1676	0.0662
Tmem24	transmembrane protein 24	NM_027909	0.454	-0.163	0.0000	0.0000	0.0002
Tmem38a	transmembrane protein 38a	NM_144534	0.638	-0.208	0.0000	0.0000	0.0018

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Tmem38b	transmembrane protein 38B	NM_028053	0.355	-0.179	0.0029	0.0054	0.2977
Tmem41b	transmembrane protein 41B	NM_153525	0.269	-0.185	0.0004	0.0042	0.0645
Tmem43	transmembrane protein 43	NM_028766	0.469	-0.202	0.0000	0.0000	0.0000
Tmem45a	transmembrane protein 45a	NM_019631	0.532	-0.205	0.0049	0.0061	0.3951
Tmem48	transmembrane protein 48	NM_028355	0.218	-0.202	0.0000	0.0046	0.0007
Tmem55b	transmembrane protein 55b	AK169026	0.499	-0.121	0.0001	0.0013	0.0580
Tmem58	transmembrane protein 58	AK134719	0.232	-0.185	0.0040	0.0586	0.0512
Tmem62	transmembrane protein 62	NM_010761	0.439	-0.310	0.0000	0.0000	0.0000
Tmem67	transmembrane protein 67	AK077246	0.255	-0.229	0.0000	0.0000	0.0000
Tmem74	NA	AK045145	0.396	-0.418	0.0315	0.0720	0.2730
Tmem80	NA	AK049405	0.286	-0.211	0.0108	0.0751	0.1021
Tmem85	NA	NM_026519	0.295	-0.132	0.0141	0.0351	0.2531
Tmem87b	NA	AK044356	0.283	-0.157	0.0001	0.0005	0.1037
Tmod3	tropomodulin 3	NM_016963	0.308	-0.142	0.0000	0.0000	0.0201
Tmpo	thymopoietin	U39073	0.307	-0.109	0.0206	0.0189	0.5173
Tmtc4	NA	AK036741	0.278	-0.342	0.0000	0.0002	0.0000
Tnc	tenascin C	NM_011607	0.203	-0.209	0.0000	0.0039	0.0028
Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	AK206708	0.277	-0.153	0.0003	0.0010	0.1827
Tnfrsf23	tumor necrosis factor receptor superfamily, member 23	NM_024290	0.493	-0.331	0.0011	0.0028	0.2173
Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	NM_009401	0.241	-0.165	0.0055	0.0220	0.1663
Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1	XM_914945	0.363	-0.129	0.0122	0.0085	0.5885
Tnks1bp1	tankyrase 1 binding protein 1	AK081682	0.380	-0.172	0.0000	0.0000	0.0013
Tnnt1	troponin T1, skeletal, slow	NM_011618	0.393	-0.571	0.0000	0.1012	0.0002

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	AK043707	0.317	-0.163	0.0000	0.0000	0.0000
Tnrc5	trinucleotide repeat containing 5	NM_028065	0.294	-0.135	0.0001	0.0004	0.1048
Tomm40l	NA	NM_001037170	0.302	-0.144	0.0001	0.0047	0.0215
Topbp1	topoisomerase (DNA) II beta binding protein	AK031389	0.317	-0.208	0.0000	0.0000	0.0000
Tor1b	torsin family 1, member B	AK169692	0.310	-0.176	0.0006	0.0071	0.0619
Tor2a	torsin family 2, member A	NM_152800	0.338	-0.106	0.0005	0.0003	0.5654
Tpd52l2	tumor protein D52-like 2	AK013085	0.422	-0.102	0.0283	0.0330	0.4486
Tpm2	tropomyosin 2, beta	BC014809	0.430	-0.536	0.0000	0.0009	0.0001
Tra2a	NA	BC058764	0.301	-0.194	0.0007	0.1100	0.0047
Tradd	TNFRSF1A-associated via death domain	BC028542	0.444	-0.438	0.0000	0.0010	0.0038
Traf4	Tnf receptor associated factor 4	AK046015	0.344	-0.285	0.0001	0.0181	0.0031
Trappc1	NA	BC115818	0.417	-0.251	0.0059	0.2754	0.0133
Trhr	thyrotropin releasing hormone receptor	NM_013696	0.294	-0.651	0.0035	0.4188	0.0044
Trim13	tripartite motif protein 13	NM_023233	0.428	-0.272	0.0202	0.1406	0.0979
Trim24	tripartite motif protein 24	NM_145076	0.285	-0.333	0.0000	0.0003	0.0000
Trim36	tripartite motif-containing 36	NM_178872	0.229	-0.199	0.0182	0.1112	0.1132
Trim39	tripartite motif protein 39	AK166148	0.339	-0.163	0.0430	0.1316	0.2095
Trim46	tripartite motif protein 46	NM_183037	0.326	-0.188	0.0000	0.0000	0.0001
Trim8	tripartite motif protein 8	NM_053100	0.393	-0.210	0.0000	0.0000	0.0104
Trip10	thyroid hormone receptor interactor 10	AY081142	0.197	-0.218	0.0025	0.0460	0.0409
Trit1	tRNA isopentenyltransferase 1	NM_025873	0.220	-0.184	0.0211	0.1144	0.1257
Trmt11	NA	NM_028604	0.298	-0.178	0.0002	0.0014	0.0874

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Trmt12	tRNA methyltranferase 12 homolog (S. cerevisiae)	NM_026642	0.247	-0.404	0.0349	0.5116	0.0373
Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	NM_027296	0.323	-0.210	0.0066	0.0752	0.0641
Trp53bp1	transformation related protein 53 binding protein 1	AK148123	0.213	-0.195	0.0000	0.0000	0.0000
Trpc3	transient receptor potential cation channel, subfamily C, member 3	NM_019510	0.439	-0.203	0.0000	0.0000	0.0011
Trpc6	transient receptor potential cation channel, subfamily C, member 6	NM_013838	0.313	-0.100	0.0058	0.0030	0.6712
Trpc7	transient receptor potential cation channel, subfamily C, member 7	NM_012035	0.274	-0.371	0.0000	0.0102	0.0017
Trpv2	transient receptor potential cation channel, subfamily V, member 2	NM_011706	0.429	-0.360	0.0000	0.0000	0.0000
Tsc22d4	TSC22 domain family 4	AK006262	0.449	-0.197	0.0000	0.0001	0.1246
Tsga14	testis specific gene A14	AK160804	0.323	-0.273	0.0001	0.0251	0.0036
Tsga2	testis specific gene A2	NM_025290	0.426	-0.321	0.0171	0.2227	0.0506
Tspan17	tetraspanin 17	NM_028841	0.581	-0.385	0.0000	0.0001	0.0001
Tspan4	tetraspanin 4	AK051376	0.290	-0.298	0.0000	0.1128	0.0003
Tspan6	tetraspanin 6	NM_019656	0.557	-0.389	0.0000	0.0000	0.0000
Tspyl5	testis-specific protein, Y-encoded-like 5	XM_139378	0.450	-0.175	0.0131	0.0130	0.4820
Tssc4	tumor-suppressing subchromosomal transferable fragment 4	NM_138631	0.521	-0.209	0.0139	0.0824	0.1181

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Tst	thiosulfate sulfurtransferase, mitochondrial	NM_009437	0.665	-0.332	0.0068	0.0901	0.0549
Ttc26	NA	AK035185	0.247	-0.376	0.0000	0.0133	0.0000
Ttc27	NA	AK084905	0.323	-0.093	0.0000	0.0002	0.1640
Ttc8	tetratricopeptide repeat domain 8	NM_029553	0.334	-0.214	0.0000	0.0000	0.0016
Ttll12	NA	NM_183017	0.261	-0.165	0.0000	0.0001	0.0103
Ttpa	tocopherol (alpha) transfer protein	BC043705	0.375	-0.387	0.0046	0.0212	0.1475
Ttrap	Traf and Tnf receptor associated protein	AK167707	0.260	-0.220	0.0233	0.1342	0.1177
Tubb2b	NA	NM_023716	0.277	-0.217	0.0084	0.1632	0.0357
Tubb2c	NA	NM_146116	0.335	-0.242	0.0000	0.0025	0.0062
Tubb5	tubulin, beta 5	NM_011655	0.254	-0.194	0.0018	0.1286	0.0102
Tubd1	tubulin, delta 1	NM_019756	0.335	-0.101	0.0109	0.0082	0.5637
Tusc3	tumor suppressor candidate 3	NM_030254	0.433	-0.061	0.0305	0.0264	0.5465
Txlna	taxilin alpha	NM_001005506	0.249	-0.173	0.0001	0.0064	0.0136
Txn1	thioredoxin 1	NM_011660	0.647	-0.048	0.0137	0.0051	0.8181
Txndc1	thioredoxin domain containing 1	AK137059	0.433	-0.199	0.0000	0.0000	0.0023
Txnl1	thioredoxin-like 1	NM_016792	0.527	-0.155	0.0000	0.0002	0.0342
Txnl5	thioredoxin-like 5	BC030344	0.506	-0.277	0.0135	0.0305	0.2735
Tyro3	TYRO3 protein tyrosine kinase 3	NM_019392	0.406	-0.307	0.0000	0.0000	0.0000
Tyrobp	TYRO protein tyrosine kinase binding protein	NM_011662	0.322	-0.387	0.0028	0.1518	0.0129
Tyrp1	tyrosinase-related protein 1	NM_031202	0.248	-0.354	0.0158	0.0768	0.1413
U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	XR_003610	0.526	-0.135	0.0341	0.0416	0.4396
Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	NM_001033293	0.266	-0.139	0.0000	0.0009	0.0144
Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	AK163966	0.919	-0.263	0.0000	0.0010	0.0298

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	NM_009458	0.518	-0.220	0.0052	0.0391	0.0950
Ube2h	ubiquitin-conjugating enzyme E2H	NM_009459	0.181	-0.226	0.0195	0.3852	0.0299
Ubiad1	UbiA prenyltransferase domain containing 1	NM_027873	0.379	-0.104	0.0188	0.0079	0.7849
Ubxd1	UBX domain containing 1	NM_024432	0.398	-0.053	0.0092	0.0057	0.6195
Ubxd4	UBX domain containing 4	BC004632	0.297	-0.280	0.0295	0.1729	0.1139
Ubxd5	UBX domain containing 5	NM_026257	0.274	-0.296	0.0000	0.0040	0.0004
Ubxd6	UBX domain containing 6	BC024492	0.229	-0.173	0.0099	0.1008	0.0701
Uchl3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	AB033370	0.478	-0.159	0.0302	0.0811	0.2368
Uckl1	uridine-cytidine kinase 1-like 1	XM_990895	0.261	-0.145	0.0000	0.0030	0.0129
Uevld	UEV and lactate/malate dehyrogenase domains	AK086750	0.414	-0.130	0.0000	0.0001	0.1081
Ufc1	ubiquitin-fold modifier conjugating enzyme 1	BC055109	0.601	-0.075	0.0176	0.0105	0.6537
Ugp2	UDP-glucose pyrophosphorylase 2	NM_139297	0.366	-0.178	0.0000	0.0014	0.0231
Ulk2	Unc-51 like kinase 2 (C. elegans)	NM_013881	0.271	-0.155	0.0000	0.0000	0.0000
Unc119	unc-119 homolog (C. elegans)	AF030169	0.219	-0.188	0.0029	0.1533	0.0131
Unc13a	unc-13 homolog A (C. elegans)	AY753536	0.322	-0.168	0.0000	0.0000	0.0000
Unc13b	unc-13 homolog B (C. elegans)	XM_973550	0.491	-0.450	0.0000	0.0000	0.0000
Uqcrb	ubiquinol-cytochrome c reductase binding protein	XM_484346	0.649	-0.332	0.0496	0.1431	0.2207

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Urm1	ubiquitin related modifier 1 homolog (S. cerevisiae)	AK165008	0.489	-0.158	0.0010	0.0031	0.1854
Uros	uroporphyrinogen III synthase	AK135314	0.306	-0.184	0.0001	0.0046	0.0232
Usf1	upstream transcription factor 1	BC049784	0.434	-0.203	0.0005	0.0271	0.0154
Usp16	ubiquitin specific peptidase 16	NM_024258	0.278	-0.226	0.0000	0.0035	0.0025
Usp38	ubiquitin specific peptidase 38	NM_027554	0.332	-0.212	0.0000	0.0012	0.0020
Utp18	UTP18, small subunit (SSU) processome component, homolog (yeast)	AK032265	0.308	-0.112	0.0075	0.0293	0.1715
Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	AK084039	0.277	-0.224	0.0000	0.0000	0.0000
Uxt	ubiquitously expressed transcript	AK038495	0.383	-0.135	0.0031	0.0030	0.4533
V2r5	vomeronasal 2, receptor 32	XM_975880	0.692	-0.336	0.0382	0.0362	0.5210
Vash2	vasohibin 2	AK078596	0.283	-0.264	0.0008	0.0719	0.0086
Vat1	vesicle amine transport protein 1 homolog (T californica)	BC099678	0.271	-0.221	0.0004	0.0018	0.1325
Vbp1	von Hippel-Lindau binding protein 1	AK167742	0.344	-0.297	0.0006	0.0354	0.0134
Vcam1	vascular cell adhesion molecule 1	AK085320	0.337	-0.329	0.0000	0.0001	0.0002
Vdac2	voltage-dependent anion channel 2	AK159561	0.339	-0.095	0.0001	0.0001	0.3568
Vdac3	voltage-dependent anion channel 3	NM_011696	0.478	-0.117	0.0000	0.0000	0.0458
Vgf	VGF nerve growth factor inducible	NM_001039385	0.504	-0.547	0.0003	0.0323	0.0076
Vil1	villin 1	XM_992366	0.324	-0.258	0.0000	0.0008	0.0383
Vps54	vacuolar protein sorting 54 (yeast)	AK032728	0.297	-0.178	0.0000	0.0002	0.0024

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Vstm2	V-set and transmembrane domain containing2A	AK134954	0.051	-0.505	0.0000	0.7359	0.0000
Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	NM_016800	0.381	-0.150	0.0001	0.0011	0.0776
Vwa1	von Willebrand factor A domain containing 1	NM_147776	0.363	-0.204	0.0010	0.0302	0.0254
Wbp1	WW domain binding protein 1	AK184383	0.313	-0.205	0.0000	0.0006	0.0035
Wbp5	WW domain binding protein 5	U92454	0.651	-0.316	0.0267	0.1636	0.1098
Wbscr27	Williams Beuren syndrome chromosome region 27 (human)	NM_024479	0.416	-0.467	0.0000	0.0003	0.0000
Wdr1	WD repeat domain 1	NM_011715	0.297	-0.153	0.0000	0.0000	0.0000
Wdr12	WD repeat domain12	XM_981875	0.330	-0.122	0.0000	0.0000	0.2069
Wdr17	WD repeat domain17	AK044241	0.179	-0.382	0.0000	0.0037	0.0000
Wdr24	WD repeat domain24	NM_173741	0.532	-0.104	0.0092	0.0084	0.4938
Wdr26	WD repeat domain26	XM_977731	0.337	-0.112	0.0000	0.0000	0.0066
Wdr32	WD repeat domain32	AK165246	0.349	-0.088	0.0002	0.0002	0.3983
Wdr44	WD repeat domain44	AK043684	0.159	-0.279	0.0002	0.1687	0.0008
Wdr5	WD repeat domain 5	NM_080848	0.615	-0.132	0.0000	0.0000	0.1460
Wdr53	WD repeat domain53	NM_026898	0.320	-0.365	0.0037	0.0714	0.0391
Wdr54	WD repeat domain54	BC083332	0.329	-0.144	0.0000	0.0000	0.0304
Wdr61	WD repeat domain61	NM_023191	0.298	-0.159	0.0200	0.0917	0.1475
Wdr77	WD repeat domain77	AK078856	0.294	-0.123	0.0000	0.0001	0.1195
Wdr78	WD repeat domain 8	AK030997	0.319	-0.435	0.0000	0.0003	0.0000
Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	XM_898331	0.213	-0.200	0.0000	0.0012	0.0000
Wnt5a	wingless-related MMTV integration site 5A	AK032977	0.349	-0.236	0.0087	0.1383	0.0445
Wnt7b	wingless-related MMTV integration site 7B	NM_009528	0.316	-0.089	0.0106	0.0072	0.5941
Xpo1	exportin 1, CRM1 homolog (yeast)	NM_001035226	0.524	-0.222	0.0000	0.0000	0.0005

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Xtrp3s1	solute carrier family 6 (neurotransmitter transporter), member 20A	NM_139142	0.441	-0.032	0.0000	0.0000	0.7519
Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	AK083653	0.254	-0.370	0.0018	0.1146	0.0113
Yeats4	YEATS domain containing 4	NM_026570	0.318	-0.282	0.0000	0.0003	0.0025
Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	AK051466	0.177	-0.304	0.0000	0.0844	0.0001
Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)	NM_026553	0.559	-0.221	0.0001	0.0006	0.0842
Yipf2	Yip1 domain family, member 2	NM_138303	0.311	-0.133	0.0003	0.0009	0.2297
Yipf3	Yip1 domain family, member 3	AK042644	0.407	-0.059	0.0001	0.0001	0.4387
Ykt6	YKT6 homolog (S. Cerevisiae)	NM_019661	0.266	-0.166	0.0006	0.0315	0.0168
Ypel3	yippee-like 3 (Drosophila)	NM_026875	0.513	-0.100	0.0000	0.0000	0.5778
Ypel4	yippee-like 4 (Drosophila)	AK043577	0.220	-0.213	0.0000	0.0212	0.0013
Zbtb26	zinc finger and BTB domain containing 26	NM_199025	0.458	-0.357	0.0111	0.0300	0.2334
Zbtb7b	zinc finger and BTB domain containing7B	XM_989013	0.373	-0.192	0.0001	0.0042	0.0253
Zc3h8	zinc finger CCCH type containing 8	AK132679	0.425	-0.207	0.0177	0.0391	0.2772
Zcchc12	zinc finger, CCHC domain containing 12	NM_028325	0.385	-0.174	0.0071	0.0102	0.3657
Zcchc9	zinc finger, CCHC domain containing 9	NM_145453	0.365	-0.228	0.0012	0.0338	0.0277
Zcwpw1	zinc finger, CW type with PWWP domain 1	NM_001005426	0.488	-0.260	0.0000	0.0000	0.0017
Zdhhc12	zinc finger, DHHC domain containing 12	NM_001037762	0.217	-0.215	0.0245	0.1295	0.1277
Zdhhc13	zinc finger, DHHC domain containing 13	NM_028031	0.344	-0.075	0.0000	0.0000	0.2905
Zdhhc15	zinc finger, DHHC domain containing 15	NM_175358	0.509	-0.475	0.0000	0.0000	0.0000

Table S1. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Zdhhc2	zinc finger, DHHC domain containing 2	AK044652	0.437	-0.250	0.0000	0.0000	0.0010
Zdhhc20	zinc finger, DHHC domain containing 20	NM_029492	0.266	-0.255	0.0000	0.0000	0.0000
Zdhhc22	zinc finger, DHHC-type containing 22	AK080584	0.238	-0.323	0.0012	0.2777	0.0026
Zdhhc3	zinc finger, DHHC domain containing 3	NM_026917	0.308	-0.106	0.0000	0.0000	0.3068
Zdhhc6	zinc finger, DHHC domain containing 6	AK168497	0.342	-0.169	0.0006	0.0068	0.0694
Zdhhc7	zinc finger, DHHC domain containing 7	AK089681	0.470	-0.111	0.0001	0.0001	0.5891
Zfp110	zinc finger protein 110	NM_022981	0.274	-0.169	0.0140	0.0226	0.3497
Zfp120	zinc finger protein 120	NM_181266	0.534	-0.261	0.0013	0.0172	0.0579
Zfp125	zinc finger protein 125	AJ005350	0.553	-0.378	0.0086	0.1408	0.0433
Zfp191	zinc finger protein 191	XM_975695	0.324	-0.154	0.0235	0.0828	0.1879
Zfp219	zinc finger protein 219	BC052050	0.439	-0.187	0.0000	0.0001	0.0995
Zfp259	zinc finger protein 259	AK168061	0.385	-0.033	0.0002	0.0000	0.7824
Zfp263	zinc finger protein 263	AK182706	0.515	-0.220	0.0001	0.0020	0.0442
Zfp313	zinc finger protein 313	NM_030743	0.350	-0.138	0.0000	0.0002	0.0311
Zfp322a	zinc finger protein 322a	NM_172586	0.273	-0.409	0.0035	0.2359	0.0093
Zfp330	zinc finger protein 330	AK037748	0.302	-0.118	0.0050	0.0124	0.2405
Zfp369	zinc finger protein 369	NM_178364	0.242	-0.213	0.0012	0.0931	0.0099
Zfp37	zinc finger protein 37	AK043700	0.498	-0.328	0.0235	0.1821	0.0869
Zfp397	zinc finger protein 397	NM_027007	0.224	-0.252	0.0118	0.1664	0.0486
Zfp40	zinc finger protein 40	NM_009555	0.291	-0.430	0.0000	0.0778	0.0000
Zfp444	zinc finger protein 444	AK012846	0.332	-0.106	0.0085	0.0078	0.4921
Zfp446	zinc finger protein 446	AK044666	0.232	-0.172	0.0130	0.1107	0.0827
Zfp518	zinc finger protein 518	XM_976746	0.205	-0.225	0.0393	0.2181	0.1172

Table S1. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Zfp52	zinc finger protein 52	NM_144515	0.598	-0.582	0.0000	0.0075	0.0001
Zfp54	zinc finger protein 54	NM_011760	0.370	-0.494	0.0001	0.0201	0.0042
Zfp57	zinc finger protein 57	NM_009559	0.698	-0.769	0.0000	0.0000	0.0001
Zfp598	zinc finger protein 598	AK138860	0.296	-0.156	0.0000	0.0010	0.0086
Zfp617	zinc finger protein 617	AK143880	0.084	-0.453	0.0264	0.8119	0.0132
Zfp711	zinc finger protein 711	XM_898101	0.216	-0.352	0.0244	0.2579	0.0612
Zfp715	zinc finger protein 715	AK011730	0.240	-0.208	0.0024	0.0185	0.0933
Zfp748	zinc finger protein 748	NM_001035231	0.252	-0.469	0.0484	0.5713	0.0448
Zfp758	zinc finger protein 758	NM_145484	0.428	-0.252	0.0000	0.0004	0.0079
Zfp760	zinc finger protein 760	NM_001008501	0.327	-0.197	0.0076	0.0204	0.2334
Zfp82	zinc finger protein 82	XM_001002250	0.272	-0.198	0.0462	0.0647	0.4026
Zfp92	zinc finger protein 92	NM_009566	0.310	-0.290	0.0222	0.0522	0.2678
Zfyve1	zinc finger, FYVE domain containing 1	NM_183154	0.371	-0.079	0.0000	0.0000	0.2064
Zfyve16	zinc finger, FYVE domain containing 16	AK080779	0.113	-0.299	0.0001	0.2882	0.0001
Zik1	zinc finger protein interacting with K protein 1	NM_009577	0.566	-0.374	0.0001	0.0011	0.0424
Zmat2	zinc finger, matrin type 2	NM_025594	0.338	-0.105	0.0306	0.0655	0.2888
Zmpste24	zinc metallopeptidase, STE24 homolog (S. cerevisiae)	NM_172700	0.285	-0.225	0.0000	0.0214	0.0016
Zmym1	zinc finger, MYM domain containing 1	AK132399	0.375	-0.185	0.0003	0.0010	0.1846
Zmym3	zinc finger, MYM-type 3	AK082075	0.292	-0.193	0.0000	0.0000	0.0000
Zmynd19	zinc finger, MYND domain containing 19	XM_987306	0.340	-0.160	0.0120	0.0673	0.1243
Znrf4	zinc and ring finger 4	AK007069	0.652	-0.507	0.0496	0.0465	0.5356
Zpbp	zona pellucida binding protein	NM_015785	0.343	-0.126	0.0169	0.0194	0.4418
Zscan21	zinc finger SCAN domain containing 21	NM_001044704	0.317	-0.114	0.0451	0.0403	0.5462

Table S2. The list of genes that are repressed by MeCP2 (FDR-adjusted p-value < 0.05).

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
1200009I06Rik	RIKEN cDNA 1200009I06 gene	NM_028807	-0.390	0.063	0.0004	0.0002	0.6948
1600021P15Rik	NA	NM_177718	-0.331	0.190	0.0195	0.0695	0.1856
1700006F04Rik	RIKEN cDNA 1700006F04 gene	AK005671	-0.696	0.526	0.0067	0.1291	0.0373
1700018C11Rik	RIKEN cDNA 1700018C11 gene	NM_029324	-0.603	0.127	0.0033	0.0015	0.7070
1700030F04Rik	NA	AK006540	-0.755	0.334	0.0028	0.0065	0.2434
1810015C04Rik	RIKEN cDNA 1810015C04 gene	AK007506	-0.303	0.105	0.0058	0.0064	0.4320
2010300C02Rik	RIKEN cDNA 2010300C02 gene	XM_916039	-0.398	0.490	0.0103	0.0046	0.7474
2210019I11Rik	RIKEN cDNA 2210019I11 gene	AK133519	-0.339	0.233	0.0177	0.0094	0.6921
2310005E17Rik	RIKEN cDNA 2310005E17 gene	AK009168	-0.513	0.100	0.0464	0.0168	0.8876
2410066E13Rik	RIKEN cDNA 2410066E13 gene	NM_026629	-0.360	0.180	0.0247	0.0585	0.2647
2700071J12Rik	NA	AK012511	-0.593	0.856	0.0219	0.2643	0.0533
2810473G09Rik	NA	AK170452	-0.475	0.100	0.0022	0.0014	0.5715
2900056L01Rik	RIKEN cDNA 2900056L01 gene	AK013704	-0.604	0.065	0.0305	0.0103	0.8868
4930403O15Rik	RIKEN cDNA 4930403O15 gene	AK015069	-0.334	0.361	0.0039	0.3441	0.0065
4930404K13Rik	NA	AK015085	-0.833	0.588	0.0027	0.0423	0.0482
4930443B20Rik	RIKEN cDNA 4930443B20 gene	AK015368	-0.408	0.342	0.0346	0.0275	0.5799
4930487H11Rik	NA	AK015638	-0.152	0.701	0.0261	0.7382	0.0155
4930519N16Rik	RIKEN cDNA 4930519N16 gene	BC016199	-0.284	0.325	0.0396	0.1806	0.1435
4930563M20Rik	NA	AK019781	-0.762	1.063	0.0443	0.1405	0.2027
4933432G23Rik	NA	AK017021	-0.352	0.331	0.0065	0.2655	0.0156
5033415L01Rik	NA	AK017175	-1.213	0.117	0.0434	0.0149	0.9043
5830408B19Rik	RIKEN cDNA 5830408B19 gene	AK017909	-0.257	0.196	0.0207	0.1367	0.1036
5830408C22Rik	RIKEN cDNA 5830408C22 gene	AK037533	-0.275	0.284	0.0038	0.0321	0.0860

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
9430013L17Rik	RIKEN cDNA 9430013L17 gene	AK020414	-0.084	0.351	0.0122	0.8621	0.0052
A2bp1	NA	AK158194	-0.225	0.289	0.0000	0.0000	0.0000
A430090L17Rik	RIKEN cDNA A430090L17 gene	XM_977267	-0.330	0.271	0.0112	0.0728	0.1094
A530065N20	NA	AK080130	-0.376	0.333	0.0494	0.1165	0.2665
A730017D01Rik	RIKEN cDNA A730017D01 gene	AK031243	-0.557	0.392	0.0439	0.1016	0.2715
A730054J21Rik	RIKEN cDNA A730054J21 gene	BC023483	-0.369	0.242	0.0069	0.1836	0.0257
AB112350	cDNA sequence AB112350	NM_178728	-0.448	0.072	0.0017	0.0019	0.4105
Acbd7	NA	XM_990697	-0.066	0.418	0.0311	0.7978	0.0164
Accn1	amiloride-sensitive cation channel 1, neuronal (degenerin)	NM_007384	-0.213	0.308	0.0000	0.0042	0.0000
Adam2	a disintegrin and metallopeptidase domain 2	AK161261	-0.258	0.219	0.0071	0.0252	0.1846
Adamtsl1	ADAMTS-like 1	AK045085	-0.327	0.166	0.0000	0.0000	0.0249
Adarb1	adenosine deaminase, RNA-specific, B1	NM_001024838	-0.256	0.150	0.0000	0.0000	0.0013
Adarb2	adenosine deaminase, RNA-specific, B2	AK051460	-0.420	0.103	0.0000	0.0000	0.1775
Aff1	AF4/FMR2 family, member 1	AK082878	-0.140	0.359	0.0000	0.1616	0.0000
Aff3	AF4/FMR2 family, member 3	AK014322	-0.283	0.133	0.0077	0.0464	0.1187
Agc1	aggrecan 1	NM_007424	-0.319	0.103	0.0044	0.0030	0.5778
Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	NM_027907	-0.552	0.055	0.0000	0.0000	0.5312
AI851790	expressed sequence AI851790	NM_182807	-0.169	0.301	0.0000	0.1037	0.0000
AI875142	NA	AK079091	-0.331	0.528	0.0187	0.0371	0.3033
Akap13	A kinase (PRKA) anchor protein 13	XM_979405	-0.228	0.219	0.0124	0.2824	0.0280
Akr1c6	aldo-keto reductase family 1,member C6	NM_054080	-0.415	0.312	0.0126	0.0246	0.3037

Table S2. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Aqp7	aquaporin 7	NM_007473	-0.286	0.122	0.0344	0.0365	0.4813
Arhgap10	Rho GTPase activating protein 10	AF297030	-0.183	0.336	0.0000	0.0776	0.0000
Arhgap26	Rho GTPase activating protein 26	NM_175164	-0.284	0.172	0.0000	0.0000	0.0000
Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	NM_027871	-0.257	0.146	0.0028	0.0293	0.0715
Asah2	N-acylsphingosine amidohydrolase 2	AK046540	-0.362	0.044	0.0000	0.0000	0.6104
Atp1b4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	NM_133690	-0.380	0.165	0.0212	0.0184	0.5372
Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	NM_015803	-0.277	0.140	0.0000	0.0000	0.0000
Atxn7l4	ataxin 7-like 4	NM_028139	-0.471	0.205	0.0010	0.0150	0.0500
Auts2	autism susceptibility candidate 2	AK038536	-0.211	0.381	0.0000	0.0013	0.0000
AY702103	cDNA sequence AY702103	AK133160	-0.245	0.192	0.0486	0.2728	0.1139
B230120H23Rik	RIKEN cDNA B230120H23 gene	AK162819	-0.330	0.220	0.0000	0.0014	0.0235
B230209C24Rik	RIKEN cDNA B230209C24 gene	AK045534	-0.408	0.111	0.0001	0.0007	0.1397
B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	NM_020283	-0.406	0.286	0.0055	0.0721	0.0557
Bach2	BTB and CNC homology 2	BC099420	-0.342	0.214	0.0004	0.0063	0.0438
Bard1	BRCA1 associated RING domain 1	NM_007525	-0.253	0.293	0.0078	0.1188	0.0466
Bbx	bobby sox homolog (Drosophila)	AK167724	-0.458	0.078	0.0000	0.0000	0.4241
BC016495	cDNA sequence BC016495	AK050579	-0.444	0.172	0.0098	0.0273	0.2282
BC018465	cDNA sequence BC018465	NM_144890	-0.239	0.167	0.0257	0.0566	0.2814
BC056349	NA	NM_177757	-0.276	0.319	0.0004	0.0180	0.0166

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
BC057079	cDNA sequence BC057079	XM_989294	-0.204	0.254	0.0000	0.0000	0.0000
Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	AK140949	-0.177	0.405	0.0025	0.1590	0.0110
Bcl6	B-cell leukemia /lymphoma 6	AK036975	-0.185	0.341	0.0001	0.1213	0.0004
Best3	NA	NM_001007583	-0.284	0.214	0.0130	0.0321	0.2544
Bmper	BMP-binding endothelial regulator	NM_028472	-0.178	0.228	0.0000	0.0504	0.0000
C030044C12Rik	RIKEN cDNA C030044C12 gene	AK030860	-0.298	0.345	0.0342	0.1930	0.1164
C130030J05	NA	AK048019	-0.288	0.244	0.0218	0.0550	0.2518
C130089L09Rik	RIKEN cDNA C130089L09 gene	AK081955	-0.223	0.207	0.0068	0.1234	0.0395
C230071H17Rik	NA	AK048805	-0.730	0.352	0.0047	0.0033	0.5592
C230079O03	NA	AK048899	-0.690	0.027	0.0297	0.0081	0.9724
C230081A13Rik	RIKEN cDNA C230081A13 gene	AK173328	-0.381	0.235	0.0002	0.0040	0.0302
C330020E22Rik	NA	AK079836	-0.464	0.512	0.0185	0.2032	0.0604
C530014P21Rik	NA	AK085434	-0.327	0.476	0.0169	0.0595	0.1868
C630007B19Rik	RIKEN cDNA C630007B19 gene	NM_182808	-0.473	0.564	0.0000	0.0003	0.0000
C630035N08Rik	RIKEN cDNA C630035N08 gene	NM_175427	-0.542	0.364	0.0029	0.0075	0.2274
C920021L13Rik	NA	AK044447	-0.549	0.209	0.0102	0.0125	0.4114
Cabp7	calcium binding protein 7	NM_138948	-0.066	0.498	0.0326	0.8158	0.0165
Caln1	calneuron 1	AF282251	-0.236	0.182	0.0028	0.0455	0.0463
Camk1d	calcium/calmodulin-dependent protein kinase ID	NM_177343	-0.429	0.379	0.0000	0.0000	0.0000
Camk4	calcium/calmodulin-dependent protein kinase IV	AK043457	-0.343	0.112	0.0000	0.0000	0.0707
Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	AK035556	-0.253	0.205	0.0000	0.0000	0.0000
Car8	carbonic anhydrase8	NM_007592	-0.329	0.092	0.0002	0.0001	0.5029

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Casq2	calsequestrin 2	NM_009814	-0.336	0.085	0.0271	0.0151	0.6966
Ccbe1	collagen and calcium binding EGF domains 1	AK028377	-0.198	0.209	0.0327	0.1542	0.1405
Ccdc11	coiled-coil domain containing 11	NM_028948	-0.470	0.367	0.0273	0.1270	0.1435
Ccdc27	NA	NM_001033455	-0.251	0.246	0.0108	0.0517	0.1445
Ccl1	chemokine (C-C motif) ligand 1	BC042744	-0.353	0.202	0.0145	0.0181	0.4159
Cdh12	NA	NM_001008420	-0.551	0.211	0.0000	0.0000	0.0020
Cdh13	cadherin 13	AK029195	-0.312	0.205	0.0000	0.0000	0.0031
Cdh6	cadherin 6	NM_007666	-0.550	0.269	0.0000	0.0000	0.0013
Cdk6	cyclin-dependent kinase 6	NM_009873	-0.265	0.250	0.0428	0.2127	0.1305
Ceacam16	CEA-related cell adhesion molecule 16	NM_001033419	-0.391	0.102	0.0319	0.0161	0.7424
Ceacam18	CEA-related cell adhesion molecule 1	NM_028236	-0.255	0.170	0.0443	0.0549	0.4399
Chrnd	cholinergic receptor, nicotinic, delta polypeptide	AK081344	-0.157	0.278	0.0192	0.2312	0.0543
Chrne	cholinergic receptor, nicotinic, epsilon polypeptide	NM_009603	-0.275	0.307	0.0021	0.0525	0.0305
Chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	AK051290	-0.290	0.220	0.0004	0.0137	0.0212
Clstn2	calsyntenin 2	NM_022319	-0.339	0.428	0.0000	0.0000	0.0000
Clybl	citrate lyase beta like	NM_029556	-0.325	0.102	0.0071	0.0221	0.2045
Cnksr3	Cnksr family member 3	BC031194	-0.296	0.163	0.0001	0.0075	0.0088
Col4a2	procollagen, type IV, alpha 2	NM_009932	-0.251	0.249	0.0000	0.0000	0.0000
Colec11	collectin sub-family member 11	NM_027866	-0.290	0.223	0.0165	0.0799	0.1413
Coro6	coronin, actin binding protein 6	NM_139128	-0.412	0.229	0.0000	0.0000	0.0000

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	AK053197	-0.225	0.272	0.0000	0.0000	0.0000
Ctrb1	chymotrypsinogen B1	NM_025583	-0.406	0.039	0.0313	0.0099	0.9152
Cxcl12	chemokine (C-X-C motif) ligand 12	NM_021704	-0.258	0.151	0.0195	0.1418	0.0939
Cyp11b1	cytochrome P450, family 11, subfamily b, polypeptide 1	XM_001006812	-0.216	0.328	0.0097	0.3222	0.0183
Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	NM_027816	-0.229	0.187	0.0140	0.2105	0.0447
D230039L06Rik	NA	NM_177724	-0.217	0.297	0.0033	0.0778	0.0312
D930030D11Rik	NA	AK164171	-0.295	0.335	0.0024	0.1876	0.0086
D930044I17Rik	NA	AK086664	-0.669	0.532	0.0035	0.0358	0.0713
Dab1	disabled homolog 1 (Drosophila)	BC051993	-0.243	0.404	0.0000	0.0347	0.0000
Dcc	deleted in colorectal carcinoma	NM_007831	-0.317	0.200	0.0000	0.0000	0.0000
Dgkg	diacylglycerol kinase, gamma	AK037612	-0.349	0.325	0.0000	0.0000	0.0000
Dgkh	diacylglycerol kinase, eta	XM_895030	-0.292	0.325	0.0000	0.0000	0.0000
Dlgap2	discs, large (Drosophila) homolog-associated protein 2	NM_172910	-0.306	0.362	0.0000	0.0002	0.0008
Dpy19l3	dpy-19-like 3 (C. elegans)	NM_178704	-0.327	0.079	0.0000	0.0000	0.1557
Drd3	dopamine receptor 3	NM_007877	-0.419	0.191	0.0003	0.0011	0.1681
E2f8	E2F transcription factor 8	AY957576	-0.221	0.197	0.0236	0.1319	0.1214
E430014B02Rik	NA	AK088368	-0.156	0.405	0.0406	0.7822	0.0227
EG224276	NA	NM_019643	-0.155	0.514	0.0304	0.6946	0.0203
EG239502	NA	NM_153093	-0.670	0.233	0.0017	0.0119	0.1014
EG243423	NA	AF086602	-0.423	0.329	0.0367	0.0511	0.4029
EG434181	NA	BC100510	-0.263	0.284	0.0204	0.0216	0.4727
EG436081	NA	XM_983082	-0.467	0.971	0.0018	0.0058	0.1920

Table S2. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
EG666606	NA	XM_986444	-0.371	0.302	0.0364	0.0405	0.4693
EG668311	NA	XM_923724	-0.416	0.367	0.0444	0.0770	0.3431
Egln3	EGL nine homolog 3 (C. elegans)	BC044926	-0.325	0.297	0.0018	0.0417	0.0342
Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	AK028389	-0.298	0.107	0.0000	0.0000	0.0049
Elmod1	ELMO domain containing 1	AK029207	-0.336	0.148	0.0000	0.0000	0.0187
Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	NM_007703	-0.548	0.002	0.0294	0.0074	0.9971
Epb4.1	erythrocyte protein band 4.1	AK148569	-0.306	0.098	0.0000	0.0000	0.1534
Epha4	Eph receptor A4	AK132203	-0.192	0.227	0.0000	0.0011	0.0000
Epha6	Eph receptor A6	NM_007938	-0.267	0.199	0.0000	0.0000	0.0005
Ero1lb	ERO1-like beta (S. cerevisiae)	AK006886	-0.259	0.249	0.0000	0.0013	0.0004
Etv6	ets variant gene 6 (TEL oncogene)	NM_007961	-0.296	0.170	0.0018	0.0063	0.1804
F730043M19Rik	NA	AK089514	-0.529	0.382	0.0018	0.0457	0.0310
Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	BC060620	-0.290	0.185	0.0000	0.0000	0.0001
Fkbp5	FK506 binding protein 5	AK159389	-0.072	0.349	0.0000	0.6916	0.0000
Flnb	filamin, beta	XM_977444	-0.250	0.156	0.0000	0.0000	0.0000
Flrt3	fibronectin leucine rich transmembrane protein 3	AK045146	-0.558	0.772	0.0000	0.0047	0.0000
Flt3	FMS-like tyrosine kinase 3	NM_010229	-0.340	0.142	0.0000	0.0000	0.0017
Fndc1	fibronectin type III domain containing 1	XM_974498	-0.335	0.202	0.0000	0.0000	0.0092
Foxp1	forkhead box P1	AK040800	-0.214	0.189	0.0000	0.0005	0.0000
Fras1	Fraser syndrome 1 homolog (human)	NM_175473	-0.384	0.136	0.0000	0.0000	0.0000

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Fryl	NA	AK164590	-0.365	0.124	0.0000	0.0000	0.0000
Fscn3	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	AF176024	-0.271	0.270	0.0077	0.1403	0.0387
Fstl4	follistatin-like 4	NM_177059	-0.463	0.459	0.0000	0.0000	0.0000
Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	NM_010279	-0.111	0.331	0.0000	0.1420	0.0000
Gimap4	GTPase, IMAP family member 4	NM_174990	-0.474	0.239	0.0276	0.0423	0.3707
Glp1r	glucagon-like peptide 1 receptor	XM_001000702	-0.208	0.404	0.0000	0.0795	0.0000
Gm944	gene model 944, (NCBI)	AK220564	-0.239	0.235	0.0042	0.2312	0.0117
Gpc6	glypican 6	AK141752	-0.350	0.297	0.0000	0.0007	0.0001
Gpr133	G protein-coupled receptor 133	XM_924876	-0.258	0.462	0.0000	0.0298	0.0000
Greb1	NA	NM_015764	-0.368	0.224	0.0000	0.0000	0.0015
Grin2a	glutamate receptor, ionotropic,NMDA2A(epsilon1)	XM_988553	-0.469	0.581	0.0000	0.0000	0.0000
Grip1	glutamate receptor interacting protein 1	NM_133442	-0.405	0.077	0.0000	0.0000	0.2297
Grm1	glutamate receptor, metabotropic 1	NM_016976	-0.230	0.230	0.0000	0.0000	0.0000
Gsdmdc2	NA	XM_979344	-0.492	0.108	0.0367	0.0146	0.8351
Guca2a	guanylate cyclase activator 2a (guanylin)	NM_008190	-0.242	0.536	0.0062	0.3650	0.0098
Gucy1b2	NA	XM_981583	-0.316	0.184	0.0029	0.0170	0.1177
Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	NM_010408	-0.330	0.265	0.0000	0.0535	0.0001
Hdac9	histone deacetylase9	AK133334	-0.288	0.296	0.0000	0.0000	0.0000
Hrc	histidine rich calcium binding protein	NM_010473	-0.241	0.225	0.0216	0.1107	0.1330

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	NM_011828	-0.249	0.173	0.0112	0.2868	0.0245
Hs6st3	heparan sulfate 6-O-sulfotransferase 3	NM_015820	-0.417	0.629	0.0000	0.0316	0.0000
Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2	NM_008290	-0.467	0.305	0.0212	0.0357	0.3437
Ifna6	interferon alpha family, gene 6	NM_008334	-0.734	0.959	0.0037	0.0956	0.0282
Igf1r	NA	NM_010513	-0.359	0.181	0.0000	0.0000	0.0000
Igl-V1	immunoglobulin lambda chain, variable 1	AK008094	-0.268	0.243	0.0489	0.0371	0.6077
Il1rap	interleukin 1 receptor accessory protein	NM_008364	-0.464	0.221	0.0000	0.0000	0.0360
Il1rn	interleukin 1 receptor antagonist	NM_001039701	-0.422	0.005	0.0210	0.0052	0.9910
Iqgap2	IQ motif containing GTPase activating protein 2	AK147360	-0.181	0.433	0.0000	0.0185	0.0015
Itpr1	inositol 1,4,5-triphosphate receptor 1	NM_010585	-0.600	0.429	0.0000	0.0000	0.0000
Iyd	NA	NM_027391	-0.632	0.128	0.0193	0.0117	0.6528
Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	NM_010598	-0.383	0.172	0.0000	0.0000	0.0000
Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1	NM_010600	-0.381	0.344	0.0000	0.0055	0.0000
Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	NM_172805	-0.362	0.314	0.0000	0.0001	0.0000
Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	NM_133207	-0.389	0.159	0.0000	0.0000	0.0018

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Kcnip4	Kv channel interacting protein 4	NM_030265	-0.309	0.118	0.0000	0.0000	0.0313
Kctd16	potassium channel tetramerisation domain containing 16	XM_993798	-0.257	0.468	0.0065	0.4205	0.0085
Klf17	NA	NM_029416	-0.087	0.362	0.0258	0.6246	0.0202
Klk1	kallikrein 1	NM_010639	-0.429	0.393	0.0001	0.0072	0.0078
Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	AK129011	-0.533	0.126	0.0001	0.0000	0.4765
Krt33a	NA	NM_027983	-0.316	0.326	0.0163	0.1662	0.0666
Krt82	NA	NM_053249	-0.258	0.298	0.0112	0.0558	0.1385
Lamb1-1	laminin B1 subunit1	AK051131	-0.405	0.174	0.0000	0.0000	0.0006
Lamc2	laminin, gamma 2	AF106279	-0.313	0.146	0.0000	0.0000	0.1220
Lass6	longevity assurance homolog 6 (S. cerevisiae)	AK136463	-0.246	0.221	0.0001	0.0103	0.0107
Lcn12	lipocalin 12	AK020307	-0.230	0.197	0.0411	0.1040	0.2504
Lct	lactase	XM_129479	-0.107	0.649	0.0310	0.3949	0.0463
Lmo3	LIM domain only 3	BC057086	-0.212	0.218	0.0359	0.0832	0.2697
Lmo7	LIM domain only 7	AK143133	-0.530	0.115	0.0000	0.0000	0.0995
LOC331000	NA	XM_990270	-0.232	0.226	0.0455	0.1186	0.2423
LOC385333	NA	XR_002718	-0.354	0.415	0.0459	0.1141	0.2541
LOC385448	NA	XR_002972	-0.563	0.486	0.0488	0.1146	0.2670
LOC436147	NA	NM_009485	-0.298	0.164	0.0428	0.0406	0.5262
LOC630557	NA	NM_016678	-0.245	0.197	0.0001	0.0528	0.0017
LOC632536	NA	XR_002466	-0.049	0.477	0.0318	0.9182	0.0127
LOC635671	NA	XM_975990	-0.440	0.437	0.0152	0.1395	0.0751
LOC636534	NA	AK054457	-0.318	0.153	0.0150	0.0411	0.2327
LOC638024	NA	NM_010678	-0.311	0.392	0.0098	0.3797	0.0149
LOC638275	NA	XM_001003348	-0.293	0.180	0.0186	0.0759	0.1638
LOC638935	NA	AK168685	-0.445	0.064	0.0264	0.0094	0.8609
LOC639376	NA	NM_175367	-0.268	0.302	0.0337	0.1851	0.1199
LOC640277	NA	XM_888068	-0.572	0.566	0.0037	0.0305	0.0887
LOC665446	NA	X00696	-0.313	0.666	0.0441	0.6205	0.0361
LOC666218	NA	XM_985665	-0.294	0.354	0.0172	0.2896	0.0374

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
LOC667574	NA	XM_991287	-0.688	0.292	0.0321	0.0160	0.7465
LOC668978	NA	XR_002277	-0.586	0.565	0.0222	0.1125	0.1341
LOC669001	NA	NM_010100	-0.208	0.273	0.0159	0.2557	0.0404
LOC669205	NA	XM_895977	-0.437	0.537	0.0000	0.0008	0.0000
LOC669222	NA	XM_975713	-0.559	0.831	0.0423	0.0712	0.3513
LOC669253	NA	XM_974035	-0.995	0.845	0.0030	0.0113	0.1692
LOC669755	NA	XM_977157	-0.550	0.283	0.0210	0.2141	0.0648
LOC669896	NA	XR_002712	-0.290	0.352	0.0442	0.0717	0.3617
LOC670350	NA	XM_485079	-0.355	0.327	0.0293	0.3280	0.0550
LOC671893	NA	XM_989719	-0.352	0.328	0.0394	0.0765	0.3136
LOC672708	NA	XM_909592	-0.424	0.863	0.0175	0.5428	0.0165
LOC673364	NA	XM_903363	-0.146	0.746	0.0500	0.8526	0.0243
LOC673990	NA	XM_001004045	-0.203	0.424	0.0446	0.2322	0.1241
LOC674047	NA	M16122	-0.447	0.123	0.0496	0.0304	0.6895
LOC674102	NA	XR_002296	-0.111	0.551	0.0488	0.7915	0.0271
LOC674213	NA	XR_001648	-0.372	0.232	0.0492	0.1480	0.2123
LOC674611	NA	XM_980076	-0.266	0.172	0.0001	0.0181	0.0056
LOC675875	NA	XM_985738	-0.471	0.227	0.0180	0.0178	0.4886
LOC676038	NA	NM_001004173	-0.285	0.160	0.0083	0.0183	0.2730
LOC676216	NA	XR_004894	-0.159	0.411	0.0409	0.7250	0.0259
LOC676553	NA	XM_484184	-0.367	0.602	0.0431	0.2134	0.1310
LOC676870	NA	XM_001003209	-0.321	0.152	0.0001	0.0010	0.0487
Lonrf1	NA	XM_146279	-0.350	0.314	0.0030	0.0270	0.0816
Lphn2	latrophilin 2	AK084598	-0.722	0.412	0.0000	0.0000	0.0000
Lpp	LIM domain containing preferred translocation partner in lipoma	AK029335	-0.238	0.200	0.0000	0.0048	0.0073
Lrp1b	low density lipoprotein-related protein 1B (deleted in tumors)	NM_053011	-0.258	0.186	0.0000	0.0000	0.0000
Lrrc20	leucine rich repeat containing 20	NM_153542	-0.173	0.277	0.0001	0.1990	0.0003

Table S2. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Lrrtm1	leucine rich repeat transmembrane neuronal 1	BC027803	-0.215	0.212	0.0458	0.2493	0.1178
Lrrtm2	leucine rich repeat transmembrane neuronal 2	NM_178005	-0.432	0.106	0.0018	0.0072	0.1590
Lrrtm4	leucine rich repeat transmembrane neuronal 4	AK033053	-0.340	0.315	0.0007	0.0132	0.0392
Ly75	lymphocyte antigen 75	NM_013825	-0.366	0.137	0.0000	0.0000	0.0795
Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2	XM_001000904	-0.328	0.185	0.0000	0.0000	0.0000
Map3k1	mitogen activated protein kinase kinase kinase 1	XM_981580	-0.296	0.144	0.0000	0.0001	0.0112
Map3k5	mitogen activated protein kinase kinase kinase 5	XM_981337	-0.664	0.281	0.0000	0.0000	0.0004
Mctp2	NA	XM_978331	-0.515	0.116	0.0000	0.0000	0.3979
Mef2c	myocyte enhancer factor 2C	BC026841	-0.543	0.433	0.0000	0.0000	0.0000
Mep1b	meprin 1 beta	NM_008586	-0.288	0.173	0.0450	0.0879	0.3132
Mfsd4	NA	NM_172510	-0.305	0.231	0.0001	0.0016	0.0248
Mkl2	MKL/myocardin-like 2	NM_153588	-0.291	0.205	0.0000	0.0000	0.0000
Mpdz	multiple PDZ domain protein	BC043464	-0.347	0.139	0.0000	0.0000	0.0001
Mpped1	NA	AK159045	-0.187	0.400	0.0000	0.0521	0.0001
Mreg	NA	AY628210	-0.249	0.371	0.0160	0.1910	0.0562
Mrvi1	MRV integration site 1	NM_010826	-0.360	0.193	0.0000	0.0002	0.0017
Mtus1	mitochondrial tumor suppressor 1	NM_001005864	-0.434	0.095	0.0000	0.0000	0.2346
Mup4	major urinary protein 4	NM_008648	-0.377	0.395	0.0500	0.3905	0.0768
Myo1b	myosin IB	NM_010863	-0.407	0.299	0.0000	0.0000	0.0000
Nanog	Nanog homeobox	NM_028016	-0.436	0.151	0.0310	0.0505	0.3570

Table S2. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	NM_031881	-0.348	0.146	0.0000	0.0000	0.0000
Negr1	neuronal growth regulator 1	NM_001039094	-0.234	0.185	0.0000	0.0000	0.0001
Neil3	nei like 3 (E. coli)	AK042059	-0.070	0.397	0.0285	0.7687	0.0159
Nexn	nexilin	AK162232	-0.582	0.128	0.0020	0.0010	0.6522
Ngfb	nerve growth factor, beta	NM_013609	-0.795	0.385	0.0038	0.0116	0.2034
Nos1	nitric oxide synthase 1, neuronal	NM_008712	-0.296	0.191	0.0000	0.0000	0.0000
Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	AK122290	-0.248	0.235	0.0001	0.0981	0.0004
Nphs2	nephrosis 2 homolog, podocin (human)	NM_130456	-0.120	0.436	0.0404	0.5519	0.0390
Npnt	nephronectin	AF397008	-0.277	0.368	0.0000	0.0144	0.0000
Odz3	odd Oz/ten-m homolog 3 (Drosophila)	NM_011857	-0.599	0.372	0.0000	0.0000	0.0000
Olfm3	olfactomedin 3	NM_153157	-0.451	0.137	0.0009	0.0030	0.1896
Olfr1038	NA	NM_147013	-0.577	0.153	0.0391	0.0157	0.8363
Olfr161	NA	NM_146860	-0.367	0.400	0.0139	0.0669	0.1430
Olfr225	NA	NM_001011740	-0.591	0.792	0.0465	0.4640	0.0570
Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	NM_138648	-0.202	0.460	0.0089	0.3832	0.0133
Osbpl3	oxysterol binding protein-like 3	NM_027881	-0.492	0.409	0.0000	0.0000	0.0000
Padi2	peptidyl arginine deiminase, type II	XM_001004735	-0.232	0.194	0.0028	0.0087	0.1965
Pax1	paired box gene 1	AB080657	-0.350	0.153	0.0074	0.0136	0.3133
Pcdh9	protocadherin 9	XM_001003348	-0.301	0.131	0.0191	0.0585	0.2115
Pcolce2	procollagen C-endopeptidase enhancer 2	NM_029620	-0.406	0.075	0.0004	0.0002	0.6682

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Pde3a	phosphodiesterase 3A, cGMP inhibited	AK042725	-0.246	0.355	0.0000	0.0435	0.0001
Pde7b	phosphodiesterase 7B	NM_013875	-0.358	0.292	0.0000	0.0000	0.0000
Pdlim5	PDZ and LIM domain 5	XM_976375	-0.262	0.141	0.0000	0.0006	0.0267
Phactr1	phosphatase and actin regulator 1	BC025873	-0.321	0.203	0.0000	0.0000	0.0064
Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	NM_008846	-0.227	0.319	0.0000	0.0034	0.0000
Pkd2l1	polycystic kidney disease 2-like 1	NM_181422	-0.357	0.146	0.0036	0.0077	0.2645
Pla2g4f	NA	NM_001024145	-0.143	0.262	0.0144	0.3618	0.0239
Plagl1	pleiomorphic adenoma gene-like 1	BC065150	-0.353	0.311	0.0001	0.0190	0.0032
Plcb1	phospholipase C, beta 1	AK129166	-0.349	0.327	0.0000	0.0000	0.0000
Plcb4	phospholipase C, beta 4	AK080865	-0.499	0.124	0.0000	0.0000	0.0042
Plcl4	NA	NM_175556	-0.133	0.354	0.0000	0.0056	0.0000
Pld5	NA	BC100428	-0.212	0.224	0.0004	0.0418	0.0070
Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	AK034403	-0.633	0.202	0.0000	0.0000	0.0000
Pou6f2	POU domain, class 6, transcription factor 2	BC094915	-0.375	0.337	0.0000	0.0068	0.0027
Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	NM_008904	-0.401	0.163	0.0000	0.0001	0.0086
Ppm1l	protein phosphatase 1 (formerly 2C)-like	NM_178726	-0.291	0.231	0.0000	0.0521	0.0000
Prkca	protein kinase C, alpha	NM_011101	-0.334	0.440	0.0000	0.0000	0.0000
Prkcd	protein kinase C, delta	AB201454	-0.285	0.236	0.0000	0.0000	0.0000

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Prkce	protein kinase C, epsilon	NM_011104	-0.425	0.262	0.0000	0.0000	0.0000
Prkg1	protein kinase, cGMP-dependent, type I	NM_001013833	-0.246	0.207	0.0001	0.0034	0.0123
Prox1	prospero-related homeobox 1	NM_008937	-0.280	0.142	0.0278	0.0933	0.1943
Ptprg	protein tyrosine phosphatase, receptor type, G	XM_976892	-0.314	0.181	0.0000	0.0000	0.0000
Ptprk	protein tyrosine phosphatase, receptor type, K	NM_008983	-0.209	0.221	0.0000	0.0000	0.0000
Ptprm	protein tyrosine phosphatase, receptor type, M	NM_008984	-0.449	0.299	0.0000	0.0000	0.0000
Pvalb	parvalbumin	NM_013645	-0.980	0.273	0.0000	0.0012	0.0260
Pvt1	plasmacytoma variant translocation 1	AK144873	-0.421	0.140	0.0017	0.0082	0.1345
Pygm	muscle glycogen phosphorylase	NM_011224	-0.458	0.131	0.0000	0.0000	0.0000
Rab37	RAB37, member of RAS oncogene family	NM_021411	-0.420	0.120	0.0000	0.0000	0.3100
Rasgef1b	RasGEF domain family, member 1B	NM_181318	-0.367	0.338	0.0000	0.0000	0.0000
Rasgrp1	RAS guanyl releasing protein 1	AK013548	-0.407	0.209	0.0000	0.0000	0.0000
Rassf3	Ras association (RalGDS/AF-6) domain family 3	NM_138956	-0.401	0.306	0.0005	0.0125	0.0300
Rbms3	RNA binding motif, single stranded interacting protein	AK041098	-0.786	0.314	0.0000	0.0000	0.0000
Reln	reelin	NM_011261	-0.260	0.162	0.0000	0.0000	0.0000
Rerg	RAS-like, estrogen-regulated, growth-inhibitor	AK133734	-0.339	0.252	0.0018	0.0339	0.0406
Rfpl4	ret finger protein-like 4	AK136022	-0.338	0.121	0.0359	0.0221	0.6712
Rgs5	regulator of G-protein signaling 5	U67188	-0.525	0.028	0.0000	0.0000	0.9064

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Rnd3	Rho family GTPase 3	AK048635	-0.254	0.241	0.0415	0.0740	0.3361
Rnf182	ring finger protein 182	NM_183204	-0.295	0.451	0.0478	0.1283	0.2358
Robo2	roundabout homolog 2 (Drosophila)	NM_175549	-0.337	0.115	0.0000	0.0000	0.0078
Ror1	receptor tyrosine kinase-like orphan receptor 1	NM_013845	-0.205	0.350	0.0033	0.2677	0.0077
Rora	RAR-related orphan receptor alpha	XM_903197	-0.375	0.295	0.0000	0.0000	0.0000
Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	AK030051	-0.333	0.170	0.0000	0.0002	0.0005
Rreb1	NA	NM_001013392	-0.666	0.685	0.0000	0.0000	0.0000
Runx2	runt related transcription factor2	AF005936	-0.231	0.323	0.0047	0.2891	0.0100
Runx3	runt related transcription factor3	NM_019732	-0.276	0.164	0.0222	0.0460	0.2969
Ryr2	ryanodine receptor 2, cardiac	NM_023868	-0.296	0.280	0.0000	0.0000	0.0000
Satb1	special AT-rich sequence binding protein 1	AK040502	-0.375	0.270	0.0000	0.0001	0.0000
Sdk1	sidekick homolog 1 (chicken)	AK030635	-0.355	0.554	0.0000	0.0000	0.0000
Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	NM_011348	-0.305	0.115	0.0079	0.0106	0.3849
Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	AK043386	-0.401	0.468	0.0000	0.0000	0.0000

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Sftpa1	surfactant associated protein A1	NM_023134	-0.429	0.312	0.0054	0.0360	0.1072
Shbg	sex hormone binding globulin	NM_011367	-0.275	0.399	0.0152	0.1214	0.0870
Shc3	src homology 2 domain-containing transforming protein C3	NM_009167	-0.327	0.117	0.0000	0.0000	0.0010
Sipa1l1	signal-induced proliferation-associated 1 like 1	AK051853	-0.182	0.308	0.0000	0.0011	0.0000
Slc24a2	solute carrier family 24 (sodium/potassium/ calcium exchanger), member 2	AK038800	-0.389	0.121	0.0000	0.0000	0.0646
Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	NM_015829	-0.402	0.101	0.0000	0.0000	0.2666
Slc25a37	solute carrier family 25, member 37	AK021203	-0.449	0.146	0.0391	0.0286	0.6142
Slc26a3	solute carrier family 26, member 3	XM_988690	-0.290	0.190	0.0092	0.0328	0.1862
Slc2a13	NA	NM_001033633	-0.363	0.294	0.0000	0.0000	0.0000
Slc4a1	solute carrier family 4 (anion exchanger), member 1	NM_011403	-0.229	0.242	0.0030	0.1514	0.0136
Slit3	slit homolog 3 (Drosophila)	NM_011412	-0.538	0.611	0.0000	0.0000	0.0000
Smoc2	SPARC related modular calcium binding 2	AK040109	-0.205	0.314	0.0030	0.0534	0.0432
Sorbs2	NA	XM_919733	-0.394	0.124	0.0000	0.0000	0.0045
Sorl1	sortilin-related receptor, LDLR class A repeats-containing	AK029071	-0.246	0.189	0.0000	0.0000	0.0000
Sox5	SRY-box containing gene 5	AK087772	-0.374	0.177	0.0000	0.0001	0.0246

Table S2. Continued.

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (Total)	FDR-adjusted p-value (*MECP2*-Tg over WT)	FDR-adjusted p-value (*Mecp2*-null over WT)
Spag4l	sperm associated antigen 4-like	XM_975479	-0.350	0.535	0.0003	0.1755	0.0013
Spdyb	NA	AK015441	-0.132	0.318	0.0178	0.2953	0.0378
Spnb1	spectrin beta 1	NM_013675	-0.260	0.250	0.0000	0.0000	0.0000
Spock1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	NM_009262	-0.321	0.201	0.0000	0.0001	0.0000
Ssbp2	single-stranded DNA binding protein 2	AK005150	-0.248	0.180	0.0000	0.0000	0.0000
St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	NM_012028	-0.360	0.354	0.0000	0.0011	0.0076
Steap2	six transmembrane epithelial antigen of prostate 2	BC043459	-0.455	0.148	0.0000	0.0001	0.1506
Syngr4	synaptogyrin 4	XM_001003608	-0.506	0.265	0.0029	0.0075	0.2238
Synj2	synaptojanin 2	AF026123	-0.405	0.107	0.0000	0.0000	0.0049
Syt2	synaptotagmin II	NM_009307	-0.329	0.127	0.0003	0.0006	0.2435
Tanc1	NA	AK030022	-0.224	0.252	0.0000	0.0000	0.0000
Tcf4	transcription factor4	AK014343	-0.239	0.328	0.0000	0.0001	0.0000
Tcfcp2l1	transcription factor CP2-like 1	NM_023755	-0.256	0.213	0.0044	0.0419	0.0776
Tera	NA	NM_019643	-0.565	0.444	0.0000	0.0011	0.0014
Tgfbr3	transforming growth factor, beta receptor III	AK133234	-0.291	0.172	0.0000	0.0002	0.0109
Tiam1	T-cell lymphoma invasion and metastasis 1	AK136856	-0.425	0.288	0.0000	0.0000	0.0000
Tmem16b	NA	AK044763	-0.179	0.233	0.0062	0.1302	0.0342
Tmprss4	transmembrane protease, serine 4	NM_145403	-0.354	0.134	0.0019	0.0019	0.4328

Table S2. Continued.

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	NM_009399	-0.334	0.137	0.0002	0.0002	0.3897
Trps1	trichorhinophalangeal syndrome I (human)	XM_987804	-0.270	0.144	0.0089	0.0669	0.0951
Tshz1	NA	XM_917016	-0.204	0.283	0.0020	0.1013	0.0147
Tshz2	NA	AK220569	-0.586	0.256	0.0001	0.0006	0.1167
Tshz3	NA	NM_172298	-0.305	0.314	0.0037	0.0419	0.0659
Tspan5	tetraspanin 5	XM_987462	-0.309	0.295	0.0000	0.0001	0.0000
Unc5d	unc-5 homolog D (C. elegans)	NM_153135	-0.206	0.358	0.0000	0.0007	0.0000
Vamp1	vesicle-associated membrane protein 1	BC057587	-0.440	0.159	0.0000	0.0001	0.0373
Wwc2	NA	NM_133791	-0.395	0.214	0.0000	0.0000	0.0000
Zfp516	zinc finger protein 516	NM_183033	-0.237	0.221	0.0005	0.0539	0.0081
Zfp521	zinc finger protein 521	NM_145492	-0.306	0.213	0.0003	0.0092	0.0295
Zfp533	zinc finger protein 533	AK033075	-0.543	0.320	0.0000	0.0000	0.0000
Zfp804a	NA	BC035535	-0.418	0.080	0.0023	0.0013	0.6289
Zfpm2	zinc finger protein, multitype 2	NM_011766	-0.073	0.364	0.0032	0.7437	0.0016

Table S3. The list of genes that are upregulated in both *MECP2*-Tg and *Mecp2*-null mouse hypothalami (FDR-adjusted p-value < 0.05).

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
9030625A04Rik	RIKEN cDNA 9030625A04 gene	AK053693	0.430	0.324	0.0066	0.0424	0.1125
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	NM_007505	0.274	0.050	0.0000	0.0001	0.1375
Bai1	brain-specific angiogenesis inhibitor 1	AK046831	0.228	0.073	0.0000	0.0000	0.0022
Calcr	calcitonin receptor	NM_007588	0.213	0.238	0.0004	0.0576	0.0057
Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	NM_007390	0.256	0.170	0.0005	0.0050	0.0730
LOC621446	NA	NM_010879	0.238	0.217	0.0249	0.1194	0.1404
Rxrb	retinoid X receptor beta	BC019432	0.276	0.091	0.0119	0.0568	0.1435
Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	AF314821	0.207	0.051	0.0000	0.0000	0.1299
Spnb3	spectrin beta 3	NM_021287	0.222	0.092	0.0000	0.0000	0.0382

Table S4. The list of genes that are downregulated in both *MECP2*-Tg and *Mecp2*-null mouse hypothalami (FDR-adjusted p-value < 0.05).

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (Total)**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
2900073C16Rik	NA	AK013770	-0.957	-0.481	0.0175	0.1273	0.0944
9030617O03Rik	RIKEN cDNA 9030617O03 gene	BC021385	-0.200	-0.250	0.0010	0.1168	0.0064
B830045N13Rik	RIKEN cDNA B830045N13 gene	AK083233	-0.180	-0.276	0.0000	0.0536	0.0001
Cdkl4	cyclin-dependent kinase-like 4	NM_001033443	-0.411	-0.244	0.0016	0.0010	0.1499
Eltd1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	-0.283	-0.244	0.0000	0.0031	0.0021
Mak	male germ cell-associated kinase	BC050009	-0.311	-0.280	0.0002	0.0153	0.0106
Nol8	nucleolar protein 8	BC026402	-0.158	-0.222	0.0000	0.0841	0.0002
Ret	ret proto-oncogene	BC059012	-0.155	-0.277	0.0000	0.0422	0.0000
Sgk	serum/glucocorticoid regulated kinase	BC070401	-0.329	-0.306	0.0000	0.0010	0.0006
St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	BC026197	-0.184	-0.203	0.0160	0.1329	0.0829
Vit	vitrin	NM_028813	-0.231	-0.291	0.0010	0.0950	0.0081
Xdh	xanthine dehydrogenase	AK164764	-0.250	-0.211	0.0000	0.0063	0.0061

Table S5. The list of genes specifically misregulated in *MECP2*-Tg hypothalami (FDR-adjusted p-value < 0.05).

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
0610025P10Rik	RIKEN cDNA 0610025P10 gene	AK002679	0.234	0.0000
1110007C09Rik	RIKEN cDNA 1110007C09 gene	BC047205	0.250	0.0089
1110007L15Rik	RIKEN cDNA 1110007L15 gene	BC019557	0.251	0.0143
1110020G09Rik	RIKEN cDNA 1110020G09 gene	NM_001040395	0.264	0.0004
1110051M20Rik	RIKEN cDNA 1110051M20 gene	BC049648	0.273	0.0001
1110059P08Rik	RIKEN cDNA 1110059P08 gene	AK085518	0.249	0.0192
1200004M23Rik	RIKEN cDNA 1200004M23 gene	NM_026169	0.220	0.0390
1200015F23Rik	RIKEN cDNA 1200015F23 gene	XM_980736	0.225	0.0006
1500012F01Rik	NA	XM_983517	0.638	0.0101
1600002H07Rik	RIKEN cDNA 1600002H07 gene	BC063767	0.289	0.0476
1700020C11Rik	RIKEN cDNA 1700020C11 gene	NM_026443	0.515	0.0017
1700021K19Rik	RIKEN cDNA 1700021K19 gene	BC037474	0.213	0.0000
1700027J05Rik	RIKEN cDNA 1700027J05 gene	BC030395	0.241	0.0000
1810007P19Rik	RIKEN cDNA 1810007P19 gene	AK007366	0.229	0.0372
1810008A18Rik	RIKEN cDNA 1810008A18 gene	BC022775	0.252	0.0389
1810020D17Rik	RIKEN cDNA 1810020D17 gene	BC062811	0.606	0.0129
1810030O07Rik	RIKEN cDNA 1810030O07 gene	AK085228	0.259	0.0195
1810043G02Rik	RIKEN cDNA 1810043G02 gene	AK153233	0.207	0.0149
2310003L22Rik	RIKEN cDNA 2310003L22 gene	BC005630	0.346	0.0466
2310021P13Rik	RIKEN cDNA 2310021P13 gene	AB093273	0.276	0.0000
2310022B05Rik	RIKEN cDNA 2310022B05 gene	NM_175149	0.313	0.0000
2310035C23Rik	RIKEN cDNA 2310035C23 gene	AK040168	0.211	0.0000
2310044H10Rik	RIKEN cDNA 2310044H10 gene	AY761096	0.242	0.0475
2310066E14Rik	RIKEN cDNA 2310066E14 gene	XM_994701	0.312	0.0001
2400003C14Rik	RIKEN cDNA 2400003C14 gene	AK122215	0.288	0.0011
2600009E05Rik	RIKEN cDNA 2600009E05 gene	NM_029832	0.264	0.0165
2610003J06Rik	RIKEN cDNA 2610003J06 gene	NM_028101	0.242	0.0090
2610018I03Rik	RIKEN cDNA 2610018I03 gene	NM_027394	0.221	0.0244
2610019A05Rik	RIKEN cDNA 2610019A05 gene	AK031715	0.252	0.0117
2610027L16Rik	RIKEN cDNA 2610027L16 gene	NM_026403	0.261	0.0010
2610042O14Rik	RIKEN cDNA 2610042O14 gene	AK032098	0.330	0.0083
2610206B13Rik	RIKEN cDNA 2610206B13 gene	NM_026047	0.255	0.0047
2610529C04Rik	RIKEN cDNA 2610529C04 gene	NM_025952	0.257	0.0429
2700050L05Rik	RIKEN cDNA 2700050L05 gene	NM_178115	0.295	0.0000
2810050O03Rik	NA	AK012940	0.380	0.0348
2810403A07Rik	RIKEN cDNA 2810403A07 gene	AK173057	0.343	0.0000

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
2810439F02Rik	RIKEN cDNA 2810439F02 gene	AK005781	0.279	0.0232
2900046G09Rik	RIKEN cDNA 2900046G09 gene	NM_133778	0.688	0.0020
4632415K11Rik	RIKEN cDNA 4632415K11 gene	NM_028883	0.236	0.0213
4833418A01Rik	RIKEN cDNA 4833418A01 gene	AK079462	0.210	0.0292
4930452B06Rik	RIKEN cDNA 4930452B06 gene	NM_028934	0.226	0.0146
4930471M23Rik	RIKEN cDNA 4930471M23 gene	NM_175675	0.217	0.0054
4930579J09Rik	RIKEN cDNA 4930579J09 gene	NM_133689	0.219	0.0497
4933417O08Rik	RIKEN cDNA 4933417O08 gene	AK016850	0.354	0.0179
4933424C08Rik	RIKEN cDNA 4933424C08 gene	AK048826	0.660	0.0209
4933428G09Rik	RIKEN cDNA 4933428G09 gene	AK032498	0.257	0.0381
5031439G07Rik	RIKEN cDNA 5031439G07 gene	AK138575	0.239	0.0084
5630401D24Rik	RIKEN cDNA 5630401D24 gene	NM_144877	0.276	0.0333
5730403B10Rik	RIKEN cDNA 5730403B10 gene	AK035791	0.245	0.0175
5730405I09Rik	RIKEN cDNA 5730405I09 gene	NM_026484	0.227	0.0244
5730410I19Rik	RIKEN cDNA 5730410I19 gene	NM_025666	0.262	0.0108
5730472N09Rik	RIKEN cDNA 5730472N09 gene	AK140122	0.255	0.0000
5730593N15Rik	RIKEN cDNA 5730593N15 gene	AK019987	0.314	0.0085
6030443O07Rik	RIKEN cDNA 6030443O07 gene	AK031688	0.203	0.0046
6330407G11Rik	RIKEN cDNA 6330407G11 gene	BC096040	0.308	0.0282
6330500D04Rik	RIKEN cDNA 6330500D04 gene	AK134538	0.218	0.0001
6330514A18Rik	RIKEN cDNA 6330514A18 gene	NM_183152	0.249	0.0048
6430598A04Rik	RIKEN cDNA 6430598A04 gene	AK080821	0.242	0.0012
6720456H20Rik	RIKEN cDNA 6720456H20 gene	AK141246	0.218	0.0086
6820408C15Rik	RIKEN cDNA 6820408C15 gene	NM_177656	0.246	0.0379
8430427H17Rik	RIKEN cDNA 8430427H17 gene	AK157863	0.204	0.0491
9030625A04Rik	RIKEN cDNA 9030625A04 gene	AK053693	0.430	0.0424
9130206N08Rik	RIKEN cDNA 9130206N08 gene	BC111864	0.235	0.0008
9130227C08Rik	RIKEN cDNA 9130227C08 gene	NM_027143	0.224	0.0115
9130404D14Rik	RIKEN cDNA 9130404D14 gene	NM_146119	0.279	0.0075
A630076J17Rik	RIKEN cDNA A630076J17 gene	AK080367	0.332	0.0474
A730028G07Rik	RIKEN cDNA A730028G07 gene	AK042831	0.578	0.0340
Aaas	achalasia, adrenocortical insufficiency, alacrimia	BC026604	0.261	0.0002
Aarsl	alanyl-tRNA synthetase like	NM_198608	0.212	0.0005
Abca17	NA	AK031613	0.235	0.0072

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	NM_013850	0.217	0.0000
Abca9	ATP-binding cassette transporter sub-family A member 9	NM_147220	0.210	0.0028
Abcc10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	NM_145140	0.200	0.0006
Abhd12	NA	AK018261	0.227	0.0003
Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	NM_178890	0.209	0.0190
Acot7	acyl-CoA thioesterase 7	AB088411	0.208	0.0073
Acp2	acid phosphatase 2, lysosomal	NM_007387	0.222	0.0010
Actn4	actinin alpha 4	NM_021895	0.230	0.0000
Actr10	ARP10 actin-related protein 10 homolog (S. cerevisiae)	AK090043	0.233	0.0012
Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	NM_146107	0.350	0.0020
Actr3	ARP3 actin-related protein 3 homolog (yeast)	XR_002077	0.221	0.0017
Adcy6	adenylate cyclase 6	NM_007405	0.336	0.0000
Adcy8	adenylate cyclase 8	NM_009623	0.295	0.0000
Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	NM_001025372	0.279	0.0000
Adipor1	adiponectin receptor 1	NM_028320	0.227	0.0006
Adprhl2	ADP-ribosylhydrolase like 2	NM_133883	0.277	0.0178
Adsl	adenylosuccinate lyase	NM_009634	0.225	0.0147
Aebp1	AE binding protein 1	NM_009636	0.305	0.0001
Aes	amino-terminal enhancer of split	X73361	0.270	0.0024
Aggf1	angiogenic factor with G patch and FHA domains 1	BC027286	0.237	0.0061
Agpat7	NA	NM_207206	0.214	0.0023
Ahdc1	AT hook, DNA binding motif, containing 1	AK149347	0.318	0.0011
Ak3l1	adenylate kinase 3 alpha-like 1	XM_992477	0.357	0.0308
Akt1	thymoma viral proto-oncogene 1	NM_009652	0.295	0.0000
Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	NM_009022	0.562	0.0000
Alkbh8	NA	AK034664	0.202	0.0041
Amfr	autocrine motility factor receptor	AF124144	0.211	0.0004

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Anapc2	anaphase promoting complex subunit 2	NM_175300	0.300	0.0002
Ankmy2	ankyrin repeat and MYND domain containing 2	AK037644	0.266	0.0011
Ankrd10	ankyrin repeat domain 10	NM_133971	0.411	0.0015
Ankrd13b	ankyrin repeat domain 13b	NM_172945	0.304	0.0000
Ankrd54	NA	AK084500	0.408	0.0001
Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	NM_007456	0.202	0.0039
Ap2a1	adaptor protein complex AP-2, alpha 1 subunit	NM_001077264	0.303	0.0000
Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	NM_007459	0.263	0.0000
Apc2	adenomatosis polyposis coli 2	NM_011789	0.257	0.0000
Apeh	acylpeptide hydrolase	BC034199	0.257	0.0000
Apip	APAF1 interacting protein	NM_019735	0.353	0.0004
Apoa1bp	apolipoprotein A-I binding protein	NM_144897	0.262	0.0142
Aprt	adenine phosphoribosyl transferase	NM_009698	0.284	0.0245
Arfgap1	ADP-ribosylation factor GTPase activating protein 1	AK030520	0.255	0.0034
Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	NM_172415	0.201	0.0001
Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	NM_172520	0.225	0.0116
Arl8a	NA	NM_026823	0.239	0.0008
Armc1	armadillo repeat containing 1	XM_887464	0.304	0.0108
Armc9	NA	AK164041	0.244	0.0000
Armcx2	armadillo repeat containing, X-linked 2	AK172960	0.251	0.0317
Ars2	NA	NM_031405	0.275	0.0002
Asb6	ankyrin repeat and SOCS box-containing protein 6	BC085485	0.224	0.0415
Asrgl1	asparaginase like 1	NM_025610	0.237	0.0000
Atg10	NA	NM_025770	0.353	0.0068
Atg4d	NA	NM_153583	0.242	0.0075
Atp13a2	ATPase type 13A2	BC025028	0.230	0.0000
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	NM_007505	0.274	0.0001

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	NM_025313	0.271	0.0006
Atp6v0b	ATPase, H+ transporting, V0 subunit B	BC009169	0.321	0.0000
Atp6v0c	ATPase, H+ transporting, V0 subunit C	NM_009729	0.249	0.0459
Atp6v0d1	ATPase, H+ transporting, V0 subunit D isoform 1	AK138796	0.204	0.0008
Atp9a	ATPase, class II, type 9A	NM_015731	0.260	0.0000
Atxn7l3	ataxin 7-like 3	XM_001003471	0.328	0.0001
AU014645	expressed sequence AU014645	AK166458	0.230	0.0000
Avil	advillin	NM_009635	0.232	0.0210
Avp	arginine vasopressin	AK138179	0.909	0.0016
Aytl1	NA	NM_173014	0.298	0.0015
Azin1	antizyme inhibitor 1	BC046814	0.209	0.0031
B4galnt1	NA	BC022180	0.242	0.0025
B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	AK155471	0.259	0.0084
Bace1	beta-site APP cleaving enzyme 1	AK079814	0.264	0.0000
Bap1	Brca1 associated protein 1	NM_027088	0.216	0.0001
Bat3	HLA-B-associated transcript 3	AK170134	0.243	0.0000
Bbs2	Bardet-Biedl syndrome 2 homolog (human)	NM_026116	0.313	0.0003
BC018242	cDNA sequence BC018242	BC023082	0.248	0.0002
BC024868	cDNA sequence BC024868	NM_199149	0.231	0.0022
BC032265	cDNA sequence BC032265	AK078838	0.361	0.0000
BC038286	cDNA sequence BC038286	BC038286	0.304	0.0001
BC057552	cDNA sequence BC057552	NM_172502	0.234	0.0363
BC057893	cDNA sequence BC057893	AK089417	0.203	0.0146
Bcar1	breast cancer anti-estrogen resistance 1	AK079554	0.261	0.0180
Bcat2	branched chain aminotransferase 2, mitochondrial	AK002831	0.253	0.0025
Bcdin3	NA	NM_144913	0.332	0.0069
Bcl2l1	Bcl2-like 1	U51279	0.232	0.0224
Bcl9l	B-cell CLL/lymphoma 9-like	XM_990658	0.242	0.0330

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Bcor	Bcl6 interacting corepressor	AK053309	0.225	0.0070
Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	AK028851	0.236	0.0023
Bmi1	B lymphoma Mo-MLV insertion region 1	XM_982861	0.279	0.0175
Bmp1	bone morphogenetic protein 1	NM_011359	0.200	0.0001
Bmp7	bone morphogenetic protein 7	NM_007557	0.302	0.0067
Bop1	block of proliferation 1	NM_013481	0.275	0.0014
Brcc3	NA	AK038919	0.234	0.0028
Brwd2	bromodomain and WD repeat domain containing 2	BC042568	0.252	0.0000
Bzrap1	benzodiazapine receptor associated protein 1	AK043747	0.236	0.0000
C2	complement component 2 (within H-2S)	NM_013484	0.312	0.0209
C230078M14Rik	NA	NM_172851	0.239	0.0139
C230088H06Rik	NA	AK089842	0.367	0.0004
C4a	NA	XM_994603	0.246	0.0197
C78339	expressed sequence C78339	AK090371	0.374	0.0027
Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	AK134542	0.252	0.0000
Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	NM_021415	0.279	0.0000
Calm3	calmodulin 3	NM_007590	0.232	0.0047
Camta2	NA	BC023962	0.201	0.0003
Capn1	calpain 1	AK150084	0.218	0.0006
Capn3	calpain 3	AK040360	0.227	0.0019
Cars	cysteinyl-tRNA synthetase	NM_013742	0.209	0.0000
Casd1	NA	NM_145398	0.205	0.0030
Caskin1	CASK interacting protein 1	NM_027937	0.305	0.0000
Casp2	caspase 2	AK052396	0.263	0.0001
Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	X95399	0.233	0.0343
Cbx5	chromobox homolog 5 (Drosophila HP1a)	AK083928	0.296	0.0037
Cc2d1b	coiled-coil and C2 domain containing 1B	NM_177045	0.212	0.0020
Ccar1	cell division cycle and apoptosis regulator 1	BC055954	0.245	0.0022

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Ccdc120	NA	NM_207202	0.211	0.0232
Ccdc132	NA	AK134533	0.285	0.0001
Ccdc22	coiled-coil domain containing 22	BC057686	0.247	0.0029
Ccdc52	NA	XM_001002919	0.235	0.0014
Ccdc64	NA	BC049161	0.215	0.0063
Ccnd1	cyclin D1	AK017834	0.306	0.0008
Cct2	chaperonin subunit 2 (beta)	NM_007636	0.266	0.0011
Cct3	chaperonin subunit 3 (gamma)	AK158254	0.309	0.0279
Cct6a	chaperonin subunit 6a (zeta)	NM_009838	0.266	0.0051
Cd81	CD 81 antigen	NM_133655	0.316	0.0052
Cd82	NA	NM_007656	0.242	0.0097
Cd97	CD97 antigen	NM_011925	0.245	0.0124
Cdan1	congenital dyserythropoietic anemia, type I (human)	XM_985468	0.201	0.0006
Cdc25b	cell division cycle 25 homolog B (S. cerevisiae)	NM_023117	0.214	0.0058
Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	NM_001004721	0.266	0.0002
Cdh22	cadherin 22	XM_982809	0.271	0.0081
Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	NM_144926	0.256	0.0000
Cdk10	cyclin-dependent kinase (CDC2-like) 10	XR_002479	0.357	0.0000
Cdk4	cyclin-dependent kinase 4	XM_917659	0.403	0.0391
Cdk5r2	NA	NM_009872	0.292	0.0045
Cdt1	NA	NM_026014	0.316	0.0121
Centa1	centaurin, alpha 1	BC079634	0.283	0.0000
Centb5	centaurin, beta 5	BC026407	0.280	0.0000
Centg3	centaurin, gamma 3	NM_139153	0.243	0.0000
Cep63	NA	XM_898001	0.225	0.0334
Cga	glycoprotein hormones, alpha subunit	BC087926	0.966	0.0067
Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	NM_007390	0.256	0.0050
Ciapin1	cytokine induced apoptosis inhibitor1	NM_134141	0.300	0.0227
Clcn7	chloride channel 7	AK150395	0.233	0.0000
Clk2	CDC-like kinase 2	AK161259	0.223	0.0063
Clk3	CDC-like kinase 3	AK145880	0.270	0.0050

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	AK179220	0.269	0.0169
Clptm1	cleft lip and palate associated transmembrane protein 1	NM_019649	0.228	0.0000
Cnih4	cornichon homolog 4 (Drosophila)	AK144157	0.243	0.0047
Cno	cappuccino	NM_133724	0.204	0.0443
Col1a2	procollagen, type I, alpha 2	AK157724	0.296	0.0000
Col3a1	procollagen, type III, alpha 1	NM_009930	0.285	0.0000
Copb1	coatomer protein complex, subunit beta 1	AK082977	0.237	0.0003
Cpne5	copine V	AK079192	0.219	0.0013
Cpt1a	carnitine palmitoyltransferase 1a, liver	AK050213	0.213	0.0001
Cpxm1	carboxypeptidase X 1 (M14 family)	NM_019696	0.313	0.0029
Crebl1	cAMP responsive element binding protein-like 1	NM_017406	0.232	0.0001
Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	AK052795	0.284	0.0287
Crmp1	collapsin response mediator protein 1	NM_007765	0.209	0.0003
Csnk1e	casein kinase 1, epsilon	AK158709	0.263	0.0000
Cspg3	chondroitin sulfate proteoglycan 3	XM_912383	0.226	0.0019
Cspg5	chondroitin sulfate proteoglycan 5	AK031799	0.246	0.0012
Ctbp1	C-terminal binding protein 1	AK149906	0.210	0.0000
Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NM_146012	0.267	0.0019
Ctnnb1	catenin (cadherin associated protein), beta 1, 88kDa	AK020013	0.263	0.0056
Ctnnbl1	catenin, beta like 1	BC050787	0.278	0.0055
Ctsd	cathepsin D	NM_009983	0.258	0.0000
Ctss	cathepsin S	NM_021281	0.309	0.0070
Cxxc1	CXXC finger 1 (PHD domain)	NM_028868	0.243	0.0018
Cyb561d1	cytochrome b-561 domain containing 1	AK005419	0.226	0.0345
Cybasc3	cytochrome b, ascorbate dependent 3	AK040692	0.267	0.0029
Cygb	cytoglobin	NM_030206	0.218	0.0218
Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	AK078893	0.225	0.0089

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	BC054833	0.392	0.0000
D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	BC025117	0.228	0.0176
D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	NM_138601	0.216	0.0063
D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	AK143016	0.234	0.0056
D230025D16Rik	NA	NM_145604	0.225	0.0000
D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed	XM_913983	0.356	0.0025
D630014H12Rik	NA	AK085349	0.223	0.0376
D630037F22Rik	RIKEN cDNA D630037F22 gene	AK035346	0.224	0.0013
Dapk3	death-associated kinase 3	BC012210	0.201	0.0048
Dazap1	DAZ associated protein 1	NM_133188	0.208	0.0287
Dbil5	diazepam binding inhibitor-like 5	NM_021294	0.406	0.0435
Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	NM_010023	0.264	0.0370
Ddb2	damage specific DNA binding protein 2	NM_028119	0.248	0.0430
Ddn	dendrin	XM_912147	0.837	0.0095
Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	AK050950	0.265	0.0210
Ddx51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	AK085040	0.276	0.0000
Def8	differentially expressed in FDCP 8	NM_054046	0.244	0.0015
Dennd2d	DENN/MADD domain containing 2D	AK050033	0.314	0.0218
Dennd4b	NA	NM_201407	0.213	0.0000
Dgat1	diacylglycerol O-acyltransferase 1	NM_010046	0.241	0.0140
Dgat2	diacylglycerol O-acyltransferase 2	NM_026384	0.274	0.0011
Dgcr2	DiGeorge syndrome critical region gene 2	NM_030558	0.220	0.0007
Dgke	diacylglycerol kinase, epsilon	AK044596	0.233	0.0076
Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	NM_026987	0.239	0.0017
Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	NM_028136	0.244	0.0000
Diras1	DIRAS family, GTP-binding RAS-like 1	NM_145217	0.311	0.0485

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Dlgap3	discs, large (Drosophila) homolog-associated protein 3	BC098311	0.224	0.0002
Dlgh4	discs, large homolog 4 (Drosophila)	NM_007864	0.255	0.0000
Dmwd	dystrophia myotonica-containing WD repeat motif	BC089027	0.258	0.0059
Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	AK053314	0.227	0.0308
Dnajc18	DnaJ (Hsp40) homolog, subfamily C, member 18	NM_029669	0.293	0.0001
Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	AK167991	0.260	0.0255
Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	AK008092	0.218	0.0065
Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9	NM_134081	0.369	0.0324
Dock11	dedicator of cytokinesis 11	NM_001009947	0.237	0.0003
Dock6	dedicator of cytokinesis 6	AK129348	0.244	0.0130
Drd1ip	dopamine receptor D1 interacting protein	NM_026769	0.210	0.0121
Dtnb	dystrobrevin, beta	AK157158	0.312	0.0000
Dullard	Dullard homolog (Xenopus laevis)	XM_978384	0.274	0.0129
Dus1l	dihydrouridine synthase 1-like (S. cerevisiae)	AK179747	0.281	0.0002
Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	AK166183	0.250	0.0034
Dvl3	dishevelled 3, dsh homolog (Drosophila)	AK052151	0.215	0.0000
Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	NM_001012324	0.274	0.0278
Edc4	NA	NM_181594	0.275	0.0000
Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	AK075585	0.310	0.0000
Efhd2	EF hand domain containing 2	XM_992220	0.316	0.0422
Efnb2	ephrin B2	NM_010111	0.296	0.0021
Efs	embryonal Fyn-associated substrate	NM_010112	0.241	0.0067
Eftud2	elongation factor Tu GTP binding domain containing 2	NM_011431	0.222	0.0001
EG216185	NA	NM_020024	0.278	0.0272
EG381065	NA	XM_001006374	0.320	0.0376

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
EG544864	NA	XM_974939	0.518	0.0181
EG545216	NA	NM_178072	0.358	0.0109
EG627022	NA	NM_027978	0.241	0.0449
Egfl7	EGF-like domain 7	NM_198725	0.265	0.0334
Egln1	EGL nine homolog 1 (C. elegans)	NM_053207	0.219	0.0121
Ehbp1l1	NA	NM_053252	0.207	0.0213
Ehmt2	euchromatic histone lysine N-methyltransferase 2	NM_145830	0.312	0.0000
Eif2c4	eukaryotic translation initiation factor 2C, 4	AK032475	0.201	0.0093
Eif3s8	eukaryotic translation initiation factor 3, subunit 8	XM_993422	0.251	0.0027
Elavl3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	AK090281	0.200	0.0182
Elk1	ELK1, member of ETS oncogene family	NM_007922	0.328	0.0156
Elmod2	ELMO domain containing 2	NM_178736	0.206	0.0031
Eml3	echinoderm microtubule associated protein like 3	NM_144872	0.241	0.0152
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	U91511	0.295	0.0178
Ephb2	Eph receptor B2	NM_010142	0.253	0.0000
Epn1	epsin 1	BC106134	0.290	0.0264
Epn3	epsin 3	AK158031	0.230	0.0094
Ercc2	excision repair cross-complementing rodent repair deficiency, complementation group 2	NM_007949	0.325	0.0000
Esrra	estrogen related receptor, alpha	NM_007953	0.313	0.0050
Ets2	E26 avian leukemia oncogene 2, 3' domain	NM_011809	0.307	0.0000
Exosc4	exosome component 4	BC012277	0.370	0.0432
Extl1	exostoses (multiple)-like 1	NM_019578	0.257	0.0211
Extl3	exostoses (multiple)-like 3	NM_018788	0.244	0.0056
F8	coagulation factor VIII	NM_007977	0.282	0.0012
Faf1	Fas-associated factor 1	NM_007983	0.211	0.0121
Fam18b	NA	XM_974979	0.303	0.0041
Farsla	phenylalanine-tRNA synthetase-like, alpha subunit	AK016506	0.251	0.0131

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Fasn	fatty acid synthase	NM_007988	0.262	0.0000
Fbxl18	F-box and leucine-rich repeat protein 18	NM_001033312	0.212	0.0435
Fbxl3	F-box and leucine-rich repeat protein 3	NM_015822	0.209	0.0396
Fbxo18	F-box protein 18	AK083118	0.238	0.0002
Fbxo6	NA	NM_015797	0.258	0.0500
Fbxw2	F-box and WD-40 domain protein 2	AK133758	0.341	0.0033
Fbxw8	F-box and WD-40 domain protein 8	NM_172721	0.226	0.0025
Fchsd2	FCH and double SH3 domains 2	NM_199012	0.214	0.0000
Fgfr3	fibroblast growth factor receptor 3	NM_008010	0.217	0.0001
Fhit	fragile histidine triad gene	BC012662	0.242	0.0461
Fhl1	four and a half LIM domains 1	BC059009	0.281	0.0228
Flcn	folliculin	NM_146018	0.211	0.0024
Flot2	flotillin 2	NM_008028	0.259	0.0001
Fmnl3	formin-like 3	NM_011711	0.202	0.0031
Foxk2	forkhead box K2	AK139325	0.238	0.0106
Fpgt	fucose-1-phosphate guanylyltransferase	AK030969	0.284	0.0222
Frs3	fibroblast growth factor receptor substrate 3	NM_144939	0.257	0.0499
Fsd1	fibronectin type 3 and SPRY domain-containing protein	NM_183178	0.259	0.0039
Fuk	fucokinase	NM_172283	0.257	0.0000
Fus	c("fusion, derived from t(12", "16) malignant liposarcoma (human)")	BC058247	0.230	0.0101
Fvt1	follicular lymphoma variant translocation 1	NM_027534	0.237	0.0006
Fxr2	NA	NM_011814	0.277	0.0000
Gabre	gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	NM_017369	0.416	0.0051
Galntl4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like4	NM_173739	0.294	0.0047
Gars	glycyl-tRNA synthetase	AK190416	0.274	0.0004
Gas8	growth arrest specific 8	AK140135	0.293	0.0136
Gbl	NA	AF237676	0.259	0.0002
Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	AK141371	0.293	0.0065

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	NM_025638	0.206	0.0001
Gdpd5	glycerophosphodiester phosphodiesterase domain containing 5	NM_201352	0.230	0.0001
Gfap	glial fibrillary acidic protein	AK140151	0.332	0.0000
Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	AK051911	0.266	0.0006
Ggcx	gamma-glutamyl carboxylase	NM_019802	0.240	0.0010
Ggnbp2	gametogenetin binding protein 2	NM_153144	0.205	0.0470
Ghitm	growth hormone inducible transmembrane protein	AK168678	0.240	0.0036
Gins4	NA	AK016667	0.224	0.0045
Gm705	NA	XM_984028	0.748	0.0332
Gm719	NA	XM_907647	0.344	0.0183
Gmeb2	glucocorticoid modulatory element binding protein 2	NM_198169	0.204	0.0036
Gmfb	glia maturation factor, beta	NM_022023	0.217	0.0172
Gna11	guanine nucleotide binding protein, alpha 11	XM_988472	0.238	0.0023
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	BC065159	0.244	0.0011
Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	NM_010306	0.310	0.0047
Gna-rs1	guanine nucleotide binding protein, related sequence 1	BC013243	0.303	0.0287
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	NM_019690	0.250	0.0011
Gnb2	guanine nucleotide binding protein, beta 2	AK002604	0.372	0.0158
Gnpat	glyceronephosphate O-acyltransferase	NM_010322	0.286	0.0000
Gnptg	N-acetylglucosamine-1-phosphotransferase, gamma subunit	NM_172529	0.222	0.0005
Gorasp1	golgi reassembly stacking protein 1	AK017293	0.277	0.0002
Gpaa1	GPI anchor attachment protein 1	NM_010331	0.251	0.0018
Gpbp1	GC-rich promoter binding protein 1	AK145318	0.294	0.0001
Gpc1	glypican 1	NM_016696	0.299	0.0000
Gpr137	NA	AK143450	0.256	0.0021

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Gps1	G protein pathway suppressor 1	NM_145370	0.275	0.0049
Gramd3	NA	AK038289	0.223	0.0012
Grb14	growth factor receptor bound protein 14	NM_016719	0.215	0.0389
Grik3	glutamate receptor, ionotropic, kainate 3	XM_993378	0.262	0.0000
Gsk3a	NA	NM_001031667	0.247	0.0009
Gtf2h1	general transcription factor II H, polypeptide 1	BC052837	0.272	0.0003
Gtf3c4	general transcription factor IIIC, polypeptide 4	BC061476	0.217	0.0059
Gtpbp2	GTP binding protein 2	NM_019581	0.226	0.0036
Gtpbp3	GTP binding protein 3	NM_032544	0.262	0.0072
Gtpbp6	GTP binding protein 6 (putative)	NM_145147	0.334	0.0012
Gucy1b3	guanylate cyclase 1, soluble, beta 3	NM_017469	0.233	0.0010
Hcfc1	host cell factor C1	NM_008224	0.224	0.0000
Hdac5	histone deacetylase 5	AK156008	0.277	0.0000
Heatr1	HEAT repeat containing 1	NM_144835	0.211	0.0005
Heatr3	NA	BC048074	0.315	0.0000
Hectd3	HECT domain containing 3	NM_175244	0.239	0.0000
Hiatl1	hippocampus abundant transcript-like 1	NM_133680	0.234	0.0001
Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	NM_176958	0.281	0.0022
Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	AK161118	0.309	0.0000
Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	XR_003344	0.219	0.0447
Hps4	Hermansky-Pudlak syndrome 4 homolog (human)	BC107023	0.286	0.0002
Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	AK076088	0.205	0.0088
Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	NM_008292	0.234	0.0000
Hsp90ab1	NA	NM_008302	0.202	0.0493
Htf9c	HpaII tiny fragments locus 9c	AK080170	0.207	0.0463
Icam5	intercellular adhesion molecule 5, telencephalin	NM_008319	0.597	0.0000
Icmt	isoprenylcysteine carboxyl methyltransferase	NM_133788	0.221	0.0079

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Icosl	icos ligand	AK220220	0.314	0.0347
Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	NM_173011	0.257	0.0021
Idh3b	isocitrate dehydrogenase 3 (NAD+) beta	AK046059	0.273	0.0000
Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	NM_008323	0.260	0.0049
Ifrd2	interferon-related developmental regulator 2	NM_025903	0.205	0.0307
Igsf4c	immunoglobulin superfamily, member 4C	NM_153112	0.281	0.0001
Igsf8	immunoglobulin superfamily, member 8	BC060087	0.408	0.0001
Ilk	integrin linked kinase	NM_010562	0.218	0.0463
Imp4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	NM_178601	0.258	0.0000
Impad1	inositol monophosphatase domain containing 1	NM_177730	0.276	0.0025
Ints8	NA	AK036255	0.202	0.0102
Ipo13	importin 13	NM_146152	0.220	0.0007
Ipo4	importin 4	BC085150	0.240	0.0000
Iqcb1	IQ calmodulin-binding motif containing 1	AK087791	0.201	0.0251
Iqsec2	IQ motif and Sec7 domain 2	AY451401	0.224	0.0008
Ireb2	iron responsive element binding protein 2	AK034218	0.224	0.0001
Irf3	interferon regulatory factor 3	NM_016849	0.235	0.0398
Itfg3	NA	NM_207217	0.244	0.0000
Itgb1	integrin beta 1 (fibronectin receptor beta)	U37029	0.323	0.0000
Itgb5	integrin beta 5	NM_010580	0.305	0.0000
Itm2c	integral membrane protein 2C	NM_022417	0.211	0.0325
Jakmip1	NA	NM_178394	0.308	0.0001
Jazf1	NA	AK047180	0.251	0.0353
Jmjd4	jumonji domain containing 4	BC049148	0.216	0.0494
Josd1	NA	NM_028792	0.281	0.0089
Jph3	junctophilin 3	NM_020605	0.321	0.0018
Jph4	junctophilin 4	NM_007455	0.299	0.0013
Kcnip2	Kv channel-interacting protein 2	NM_145704	0.202	0.0090

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6	NM_001033525	0.259	0.0208
Kctd15	potassium channel tetramerisation domain containing 15	NM_146188	0.295	0.0378
Khk	ketohexokinase	NM_008439	0.290	0.0030
Kif21b	kinesin family member 21B	AK089400	0.217	0.0000
Kirrel3	kin of IRRE like 3 (Drosophila)	NM_026324	0.215	0.0001
Klhdc8b	NA	BC060089	0.323	0.0010
Klhl22	kelch-like 22 (Drosophila)	AK012046	0.299	0.0016
Kns2	kinesin 2	NM_001025362	0.227	0.0044
Kptn	kaptin	AK081226	0.258	0.0464
Lamp2	lysosomal membrane glycoprotein 2	AK051989	0.214	0.0217
Lars	leucyl-tRNA synthetase	XM_901173	0.224	0.0001
Lass2	longevity assurance homolog 2 (S. cerevisiae)	NM_029789	0.329	0.0001
Lcmt1	leucine carboxyl methyltransferase 1	BC010316	0.296	0.0089
Lepre1	leprecan 1	NM_001042411	0.242	0.0199
Lig3	ligase III, DNA, ATP-dependent	U66057	0.200	0.0074
Limd1	LIM domains containing 1	NM_013860	0.273	0.0500
Limk2	LIM motif-containing protein kinase 2	AK161560	0.225	0.0010
Lman2l	lectin, mannose-binding 2-like	AK041656	0.274	0.0015
Lmln	leishmanolysin-like (metallopeptidase M8 family)	NM_172823	0.236	0.0002
Lmtk3	lemur tyrosine kinase 3	NM_001005511	0.288	0.0000
LOC385211	NA	AK049536	0.572	0.0270
LOC630776	NA	AK049585	0.239	0.0079
LOC631002	NA	XM_919014	2.292	0.0000
LOC631981	NA	XM_354985	0.364	0.0012
LOC632799	NA	NM_133910	0.334	0.0288
LOC634390	NA	NM_028840	0.306	0.0034
LOC635658	NA	NM_025788	0.273	0.0088
LOC636848	NA	NM_007789	0.228	0.0030
LOC637661	NA	AK044685	0.241	0.0001
LOC638576	NA	AK203333	0.300	0.0062
LOC641104	NA	NM_019770	0.520	0.0289
LOC641141	NA	AK080118	0.277	0.0022

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
LOC666313	NA	XM_982985	0.303	0.0203
LOC666405	NA	AK146086	0.221	0.0120
LOC668047	NA	AK020104	0.217	0.0199
LOC669930	NA	NM_054063	0.706	0.0400
LOC670116	NA	NM_024195	0.355	0.0239
LOC670579	NA	NM_029097	0.254	0.0000
LOC671402	NA	XR_004532	0.549	0.0081
LOC671511	NA	AK132671	0.384	0.0021
LOC672350	NA	XM_890293	0.214	0.0077
LOC672466	NA	XM_993654	0.266	0.0273
LOC673058	NA	XM_001003979	0.819	0.0345
LOC674856	NA	XM_994883	0.257	0.0022
LOC677007	NA	AK087038	0.367	0.0154
Lonrf3	LON peptidase N-terminal domain and ring finger 3	NM_028894	0.304	0.0237
Lphn1	latrophilin 1	AK157878	0.259	0.0000
Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	NM_153388	0.270	0.0302
Lrig2	leucine-rich repeats and immunoglobulin-like domains 2	NM_001025067	0.218	0.0005
Lrp4	low density lipoprotein receptor-related protein 4	NM_172668	0.225	0.0000
Lrrc14	leucine rich repeat containing 14	NM_145471	0.326	0.0161
Lrrc23	NA	NM_013588	0.314	0.0311
Lrrc24	NA	NM_198119	0.296	0.0273
Lrrc40	leucine rich repeat containing 40	NM_024194	0.265	0.0009
Lrrc45	leucine rich repeat containing 45	NM_026877	0.250	0.0004
Lrrc59	NA	NM_133807	0.268	0.0004
Lsm14a	NA	NM_025948	0.222	0.0000
Lsm14b	NA	NM_177727	0.240	0.0007
Lss	lanosterol synthase	AK054393	0.250	0.0002
Ltb4dh	leukotriene B4 12-hydroxydehydrogenase	BC014865	0.365	0.0183
Lzic	leucine zipper and CTNNBIP1 domain containing	NM_026963	0.286	0.0069
Lzts2	leucine zipper, putative tumor suppressor 2	NM_145503	0.251	0.0028
Magel2	melanoma antigen, family L, 2	XM_622091	0.276	0.0066

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Mamdc2	MAM domain containing 2	AK004794	0.270	0.0180
Man2c1	mannosidase, alpha, class 2C, member 1	NM_028636	0.267	0.0000
Map3k10	mitogen activated protein kinase kinase kinase 10	XM_194344	0.291	0.0000
Map3k11	mitogen activated protein kinase kinase kinase 11	NM_022012	0.227	0.0339
Map4k2	mitogen activated protein kinase kinase kinase kinase 2	NM_009006	0.213	0.0000
Mapk8	mitogen activated protein kinase 8	NM_016700	0.236	0.0180
Mapkbp1	mitogen activated protein kinase binding protein 1	AK122323	0.213	0.0000
Mark3	MAP/microtubule affinity-regulating kinase 3	AK220557	0.252	0.0002
Matk	megakaryocyte-associated tyrosine kinase	AK079816	0.216	0.0030
Mbd6	methyl-CpG binding domain protein6	NM_033072	0.255	0.0153
Mboat5	NA	NM_145130	0.231	0.0005
Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	AK083618	0.272	0.0012
Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	NM_010442	0.276	0.0034
Mcrs1	microspherule protein 1	NM_016766	0.295	0.0000
Mdh1b	malate dehydrogenase 1B, NAD (soluble)	NM_029696	0.288	0.0002
Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	NM_008617	0.306	0.0005
Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	AK149867	0.237	0.0001
Mett10d	NA	NM_026197	0.320	0.0001
Mettl2	methyltransferase like 2	AK048040	0.224	0.0064
Mettl9	NA	AK188768	0.359	0.0180
Mgrn1	mahogunin, ring finger 1	AK034100	0.222	0.0000
Mib1	mindbomb homolog 1 (Drosophila)	AK080847	0.209	0.0003
Mib2	mindbomb homolog 2 (Drosophila)	BC058086	0.268	0.0000
Mier2	NA	NM_027422	0.258	0.0002
Mink1	misshapen-like kinase 1 (zebrafish)	NM_001045959	0.238	0.0000
Mir16	NA	NM_019580	0.321	0.0016

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Mizf	NA	XM_993174	0.226	0.0036
Mllt1	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	NM_022328	0.303	0.0018
Mllt6	myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog (Drosophila)	NM_139311	0.244	0.0002
Mlx	NA	NM_011550	0.259	0.0329
Mmel1	NA	NM_013783	0.204	0.0094
Mmp2	matrix metallopeptidase 2	AK217488	0.200	0.0437
Mms19l	MMS19 (MET18 S. cerevisiae)-like	NM_028152	0.283	0.0000
Mov10	Moloney leukemia virus 10	AK159295	0.225	0.0008
Mrpl10	mitochondrial ribosomal protein L10	AK078499	0.268	0.0360
Mrpl37	mitochondrial ribosomal protein L37	AK030828	0.218	0.0203
Mrpl4	mitochondrial ribosomal protein L4	AK216490	0.213	0.0036
Mst1r	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	NM_009074	0.231	0.0029
Mta2	metastasis-associated gene family, member 2	AK183116	0.214	0.0003
Mtap1s	NA	AK158860	0.234	0.0080
Mtf2	metal response element binding transcription factor 2	NM_013827	0.274	0.0008
Mthfsd	NA	NM_172761	0.269	0.0004
Mtm1	X-linked myotubular myopathy gene1	AK220524	0.245	0.0019
Mtmr4	myotubularin related protein 4	NM_133215	0.223	0.0000
Mvk	mevalonate kinase	AK009261	0.249	0.0188
Mxd4	Max dimerization protein 4	NM_001015039	0.362	0.0163
Mxra8	matrix-remodelling associated 8	NM_024263	0.375	0.0010
Myo5b	myosin Vb	BC030481	0.227	0.0006
Nab2	Ngfi-A binding protein 2	NM_008668	0.259	0.0084
Nat12	NA	XM_988793	0.290	0.0430
Nat8l	NA	NM_001001985	0.231	0.0425
Ndg2	NA	NM_175329	0.229	0.0184
Ndor1	NADPH dependent diflavin oxidoreductase 1	NM_178239	0.278	0.0000
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	AK046292	0.215	0.0146
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	NM_025316	0.236	0.0036

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Nelf	nasal embryonic LHRH factor	NM_020276	0.212	0.0000
Neu1	neuraminidase 1	NM_010893	0.225	0.0276
Neud4	neuronal d4 domain family member	AK142419	0.291	0.0061
Nicn1	nicolin 1	NM_025449	0.217	0.0169
Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	NM_008698	0.238	0.0001
Nle1	notchless homolog 1 (Drosophila)	AK187952	0.214	0.0064
Nlgn2	neuroligin 2	XM_908969	0.220	0.0010
Nlgn3	neuroligin 3	BC069040	0.233	0.0003
Nol1	nucleolar protein 1	NM_138747	0.216	0.0271
Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_011939	0.251	0.0086
Nope	neighbor of Punc E11	NM_020043	0.202	0.0002
Notch3	Notch gene homolog 3 (Drosophila)	NM_008716	0.223	0.0000
Npcd	NA	NM_030689	0.249	0.0089
Nploc4	NA	NM_199469	0.240	0.0000
Nptx2	neuronal pentraxin 2	NM_016789	0.393	0.0003
Nr1h2	nuclear receptor subfamily 1, group H, member 2	XM_001002072	0.278	0.0012
Nr5a1	nuclear receptor subfamily 5, group A, member 1	D10584	0.273	0.0212
Nras	neuroblastoma ras oncogene	NM_010937	0.261	0.0015
Nrf1	nuclear respiratory factor 1	NM_010938	0.225	0.0007
Nsfl1c	NA	AK039136	0.282	0.0104
Nsg2	neuron specific gene family member2	AK160712	0.294	0.0260
Nsun5	NOL1/NOP2/Sun domain family, member 5	BC051209	0.283	0.0029
Nt5m	5',3'-nucleotidase, mitochondrial	NM_134029	0.221	0.0189
Ntn2l	netrin 2-like (chicken)	NM_010947	0.331	0.0028
Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	NM_008746	0.267	0.0000
Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	XM_974561	0.264	0.0296
Numbl	numb-like	NM_010950	0.274	0.0002
Nup133	nucleoporin 133	AK040528	0.292	0.0000
Nup85	NA	NM_001002929	0.261	0.0269
Nxt1	NTF2-related export protein 1	NM_019761	0.235	0.0257

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Ogn	osteoglycin	NM_008760	0.497	0.0090
Olfml2a	olfactomedin-like 2A	NM_172854	0.448	0.0165
Olfr1258	NA	NM_146978	0.238	0.0339
Olfr297	NA	AK215451	0.208	0.0364
Orc5l	origin recognition complex, subunit 5-like (S. cerevisiae)	NM_011959	0.228	0.0198
ORF61	open reading frame 61	BC080302	0.349	0.0000
Osbp	oxysterol binding protein	XM_982920	0.234	0.0002
P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	NM_011026	0.226	0.0026
P4hb	prolyl 4-hydroxylase, beta polypeptide	NM_011032	0.220	0.0401
Pacsin3	protein kinase C and casein kinase substrate in neurons 3	NM_030880	0.291	0.0044
Parc	p53-associated parkin-like cytoplasmic protein	XM_924078	0.209	0.0000
Parp2	poly (ADP-ribose) polymerase family, member 2	NM_009632	0.241	0.0017
Pcdh1	protocadherin 1	NM_029357	0.513	0.0108
Pcdhb2	protocadherin beta 2	NM_053127	0.705	0.0311
Pcdhb8	protocadherin beta 8	NM_053133	0.565	0.0159
Pcdhgc5	NA	NM_033587	0.221	0.0100
Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	NM_008786	0.267	0.0031
Pcnxl3	pecanex-like 3 (Drosophila)	XM_001005672	0.261	0.0000
Pcolce	procollagen C-endopeptidase enhancer protein	XM_132440	0.360	0.0006
Pcyox1	prenylcysteine oxidase 1	NM_025823	0.248	0.0092
Pdcd2l	NA	NM_026549	0.204	0.0147
Pde2a	phosphodiesterase 2A, cGMP-stimulated	AK158354	0.216	0.0000
Pde3b	phosphodiesterase 3B, cGMP-inhibited	XM_912421	0.208	0.0080
Pde4a	phosphodiesterase 4A, cAMP specific	NM_183408	0.241	0.0002
Pde7a	phosphodiesterase 7A	BC062909	0.287	0.0068
Pdlim7	PDZ and LIM domain 7	AK049902	0.297	0.0022
Perq1	PERQ amino acid rich, with GYF domain 1	NM_031408	0.288	0.0000
Pex7	peroxisome biogenesis factor 7	NM_008822	0.336	0.0003

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Pfkl	phosphofructokinase, liver, B-type	NM_008826	0.323	0.0013
Pgd	phosphogluconate dehydrogenase	XM_001003312	0.260	0.0008
Pgea1	PKD2 interactor, golgi and endoplasmic reticulum associated 1	NM_028634	0.256	0.0009
Pgs1	NA	AK016901	0.376	0.0009
Phex	phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophosphatemia, vitamin D resistant rickets)	NM_011077	0.243	0.0063
Phf8	PHD finger protein 8	AK040969	0.204	0.0004
Phldb1	pleckstrin homology-like domain, family B, member 1	AK122336	0.223	0.0000
Pick1	NA	AK090155	0.210	0.0184
Pigo	phosphatidylinositol glycan, class O	NM_020035	0.250	0.0000
Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypeptide	NM_020272	0.302	0.0408
Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	NM_181585	0.228	0.0006
Pim1	proviral integration site 1	AK154127	0.276	0.0063
Pim3	proviral integration site 3	AK182442	0.283	0.0063
Pink1	PTEN induced putative kinase 1	XM_990170	0.331	0.0007
Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	NM_008844	0.211	0.0001
Pip5k2b	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	XM_991611	0.266	0.0323
Pkig	protein kinase inhibitor, gamma	AK135505	0.310	0.0404
Pkn1	protein kinase N1	AK171297	0.281	0.0000
Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	BC054740	0.431	0.0013
Pla2g6	phospholipase A2, group VI	NM_016915	0.205	0.0027
Plcb3	phospholipase C, beta 3	AK047029	0.244	0.0000
Plcxd1	phosphatidylinositol-specific phospholipase C, X domain containing 1	NM_207279	0.310	0.0192
Plekhq1	NA	NM_153119	0.324	0.0128
Plxdc1	plexin domain containing 1	AK040620	0.521	0.0000
Plxnb1	plexin B1	AK010831	0.258	0.0000
Pnpla2	patatin-like phospholipase domain containing 2	NM_025802	0.252	0.0026

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Pold2	polymerase (DNA directed), delta 2, regulatory subunit	NM_008894	0.262	0.0003
Poldip2	polymerase (DNA-directed), delta interacting protein 2	NM_026389	0.328	0.0000
Polg	polymerase (DNA directed), gamma	AK162462	0.208	0.0001
Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	NM_153798	0.209	0.0011
Polrmt	polymerase (RNA) mitochondrial (DNA directed)	NM_172551	0.232	0.0000
Pols	polymerase (DNA directed) sigma	NM_198600	0.208	0.0125
Pon2	paraoxonase 2	AK210368	0.327	0.0089
Por	P450 (cytochrome) oxidoreductase	NM_008898	0.201	0.0000
Porcn	porcupine homolog (Drosophila)	BC027292	0.205	0.0023
Ppan	peter pan homolog (Drosophila)	NM_145610	0.255	0.0173
Ppapdc1a	NA	XM_355946	0.201	0.0106
Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	AF369981	0.257	0.0368
Ppox	protoporphyrinogen oxidase	AK134341	0.298	0.0000
Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	AK089067	0.299	0.0001
Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	XM_976397	0.274	0.0031
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	NM_172994	0.284	0.0000
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	NM_138748	0.260	0.0044
Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	NM_012024	0.215	0.0015
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	NM_024459	0.437	0.0025
Ppt2	palmitoyl-protein thioesterase 2	NM_152922	0.279	0.0001
Pqlc1	PQ loop repeat containing 1	AK017854	0.369	0.0204
Prdx5	peroxiredoxin 5	NM_012021	0.231	0.0058
Prei3	preimplantation protein 3	NM_025283	0.254	0.0008
Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	NM_008924	0.314	0.0001
Prmt7	NA	NM_145404	0.205	0.0160
Pros1	protein S (alpha)	NM_011173	0.266	0.0012

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Prosapip1	NA	NM_197945	0.272	0.0051
Prpf19	NA	NM_134129	0.297	0.0023
Psen2	presenilin 2	NM_011183	0.273	0.0243
Psma1	proteasome (prosome, macropain) subunit, alpha type 1	AK162439	0.358	0.0001
Psmb2	proteasome (prosome, macropain) subunit, beta type 2	NM_011970	0.582	0.0000
Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	NM_027357	0.203	0.0000
Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	AK145487	0.384	0.0024
Ptov1	prostate tumor over expressed gene 1	BC062108	0.455	0.0000
Ptpn23	protein tyrosine phosphatase, non-receptor type 23	AK173178	0.226	0.0000
Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	XM_988289	0.214	0.0000
Pwp2	NA	BC117903	0.203	0.0018
Pygb	brain glycogen phosphorylase	NM_153781	0.286	0.0000
Pygl	liver glycogen phosphorylase	NM_133198	0.265	0.0109
Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1	AK015536	0.352	0.0076
Rab25	RAB25, member RAS oncogene family	NM_016899	0.387	0.0311
Rab33b	RAB33B, member of RAS oncogene family	NM_016858	0.253	0.0161
Rab3a	RAB3A, member RAS oncogene family	NM_009001	0.316	0.0275
Ranbp17	RAN binding protein 17	AK163271	0.216	0.0002
Rapgefl1	NA	XM_994457	0.237	0.0015
Rbbp4	retinoblastoma binding protein 4	AK141176	0.334	0.0370
Rbbp7	retinoblastoma binding protein 7	AK132101	0.358	0.0001
Rbm10	RNA binding motif protein 10	XM_920975	0.331	0.0001
Rbm14	RNA binding motif protein 14	NM_009032	0.214	0.0490
Rbm18	RNA binding motif protein 18	AK036220	0.305	0.0166
Rbm39	NA	AK155976	0.276	0.0000
Rcc2	regulator of chromosome condensation 2	NM_173867	0.283	0.0000
Rchy1	ring finger and CHY zinc finger domain containing 1	AF276959	0.394	0.0199

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Rcn2	reticulocalbin 2	NM_011992	0.272	0.0297
Rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)	AK034180	0.225	0.0192
Reep3	NA	NM_178606	0.240	0.0022
Rfng	radical fringe gene homolog (Drosophila)	NM_009053	0.270	0.0300
Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	AK146481	0.240	0.0342
Rhbdd2	NA	NM_146002	0.212	0.0220
Rhot2	ras homolog gene family, member T2	BC023927	0.346	0.0000
Rimbp2	NA	XM_001002187	0.207	0.0137
Rims4	regulating synaptic membrane exocytosis 4	NM_183023	0.265	0.0284
Rin1	Ras and Rab interactor 1	NM_145495	0.264	0.0240
Ring1	ring finger protein 1	NM_013543	0.318	0.0040
Rmnd5b	NA	NM_025346	0.202	0.0090
Rnf10	ring finger protein 10	NM_016698	0.316	0.0000
Rnf166	ring finger protein 166	AK165700	0.212	0.0217
Rnf31	ring finger protein 31	AK131160	0.259	0.0000
Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	AK138067	0.290	0.0000
RP23-136K12.4	NA	AK166638	0.235	0.0011
Rpn1	ribophorin I	NM_133933	0.281	0.0007
Rragc	Ras-related GTP binding C	BC037732	0.269	0.0004
Rrp9	NA	NM_145620	0.210	0.0086
Rtcd1	RNA terminal phosphate cyclase domain 1	AK190960	0.253	0.0166
Rtn2	reticulon 2 (Z-band associated protein)	NM_013648	0.265	0.0000
Sae2	NA	NM_016682	0.282	0.0000
Sall2	sal-like 2 (Drosophila)	NM_015772	0.284	0.0021
Saps1	NA	NM_172894	0.243	0.0000
Sbf1	SET binding factor 1	XM_922582	0.268	0.0000
Scamp4	secretory carrier membrane protein 4	AK078226	0.237	0.0069
Scarb1	scavenger receptor class B, member 1	NM_016741	0.272	0.0001
Scg5	NA	NM_009162	0.246	0.0077
Scgn	secretagogin, EF-hand calcium binding protein	NM_145399	0.379	0.0347

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Scrib	scribbled homolog (Drosophila)	NM_134089	0.212	0.0000
Sdc4	syndecan 4	BC002312	0.325	0.0185
Sec11a	NA	BC010484	0.274	0.0055
Sec14l2	SEC14-like 2 (S. cerevisiae)	NM_144520	0.232	0.0009
Sec23b	SEC23B (S. cerevisiae)	AK029661	0.241	0.0097
Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	AK054318	0.280	0.0020
Serinc3	NA	AK145604	0.265	0.0002
Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	NM_009252	0.210	0.0333
Sfi1	Sfi1 homolog, spindle assembly associated (yeast)	XM_986858	0.203	0.0001
Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	NM_173374	0.223	0.0049
Sfrs14	splicing factor, arginine/serine-rich14	AK137294	0.208	0.0006
Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	AF250135	0.292	0.0078
Sfrs9	splicing factor, arginine/serine rich 9	NM_025573	0.539	0.0000
Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	NM_024499	0.205	0.0019
Shkbp1	Sh3kbp1 binding protein 1	BC061477	0.299	0.0000
Shq1	SHQ1 homolog (S. cerevisiae)	NM_181590	0.274	0.0187
Sidt2	SID1 transmembrane family, member 2	AK152371	0.258	0.0000
Sin3a	transcriptional regulator, SIN3A (yeast)	NM_011378	0.202	0.0004
Sin3b	transcriptional regulator, SIN3B (yeast)	AK173005	0.210	0.0001
Sirt1	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	XM_975350	0.214	0.0451
Skiv2l	superkiller viralicidic activity 2-like (S. cerevisiae)	NM_021337	0.236	0.0000
Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	NM_054055	0.296	0.0159
Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	NM_021301	0.348	0.0000
Slc15a4	solute carrier family 15, member 4	NM_133895	0.272	0.0393

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	AK044409	0.270	0.0000
Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	AK138577	0.217	0.0445
Slc20a1	solute carrier family 20, member 1	AK089184	0.245	0.0000
Slc22a6	solute carrier family 22 (organic anion transporter), member 6	AK035971	0.371	0.0005
Slc22a8	solute carrier family 22 (organic anion transporter), member 8	NM_031194	0.217	0.0068
Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	AF314821	0.207	0.0000
Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	NM_013770	0.244	0.0075
Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	AK187524	0.350	0.0035
Slc25a19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	NM_026071	0.285	0.0240
Slc25a21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	NM_172577	0.321	0.0448
Slc25a46	NA	NM_026165	0.235	0.0022
Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	AK137700	0.273	0.0000
Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	NM_007854	0.245	0.0400
Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6	BC025498	0.270	0.0025
Slc2a8	solute carrier family 2, (facilitated glucose transporter), member 8	NM_019488	0.249	0.0040
Slc30a4	solute carrier family 30 (zinc transporter), member 4	NM_011774	0.243	0.0392
Slc30a5	solute carrier family 30 (zinc transporter), member 5	AK051654	0.295	0.0000
Slc35c2	solute carrier family 35, member C2	AK158331	0.217	0.0035
Slc39a10	solute carrier family 39 (zinc transporter), member 10	BC052880	0.211	0.0002

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Slc41a3	solute carrier family 41, member 3	NM_001037493	0.245	0.0149
Slc43a2	solute carrier family 43, member 2	AK090207	0.207	0.0001
Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	NM_133661	0.247	0.0356
Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	NM_011405	0.304	0.0421
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	NM_023449	0.229	0.0065
Slc9a7	NA	NM_177353	0.204	0.0009
Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1`	NM_007958	0.233	0.0025
Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	AK159259	0.288	0.0042
Smc3	NA	NM_007790	0.237	0.0000
Smek1	NA	AK031629	0.238	0.0201
Smg5	NA	NM_178246	0.295	0.0000
Smn1	survival motor neuron 1	NM_011420	0.336	0.0052
Smox	spermine oxidase	AJ567473	0.237	0.0066
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	XM_988429	0.279	0.0000
Snrpd3	small nuclear ribonucleoprotein D3	NM_026095	0.421	0.0252
Snta1	syntrophin, acidic 1	NM_009228	0.320	0.0009
Snx15	sorting nexin 15	NM_026912	0.207	0.0351
Snx17	sorting nexin 17	NM_153680	0.323	0.0105
Socs7	suppressor of cytokine signaling 7	NM_138657	0.243	0.0324
Solh	small optic lobes homolog (Drosophila)	NM_015830	0.222	0.0019
Sorcs2	sortilin-related VPS10 domain containing receptor 2	NM_030889	0.258	0.0000
Sp3	trans-acting transcription factor 3	BC027797	0.210	0.0391
Spag7	sperm associated antigen 7	NM_172561	0.235	0.0494
Sparc	secreted acidic cysteine rich glycoprotein	AK082283	0.222	0.0044
Sphk2	sphingosine kinase 2	NM_203280	0.329	0.0000

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Spnb3	spectrin beta 3	NM_021287	0.222	0.0000
Sppl3	NA	BC078437	0.289	0.0001
Spred1	sprouty protein with EVH-1 domain 1, related sequence	BC057874	0.218	0.0022
Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	NM_029035	0.290	0.0465
Src	Rous sarcoma oncogene	AK017629	0.208	0.0017
Srf	serum response factor	NM_020493	0.274	0.0001
Sri	sorcin	NM_025618	0.217	0.0009
Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	NM_178750	0.212	0.0017
Ssr3	signal sequence receptor, gamma	AK029353	0.300	0.0000
Ssrp1	structure specific recognition protein 1	NM_182990	0.219	0.0145
St5	suppression of tumorigenicity 5	NM_029811	0.234	0.0221
St7	Suppression of tumorigenicity 7	BC060630	0.211	0.0457
St7l	suppression of tumorigenicity 7-like	AK172218	0.214	0.0143
St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	NM_009181	0.323	0.0374
Stab1	stabilin 1	NM_138672	0.217	0.0000
Stag3	stromal antigen 3	AK145898	0.215	0.0073
Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	AK144987	0.261	0.0002
Statip1	signal transducer and activator of transcription interacting protein 1	AK044699	0.222	0.0000
Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	AF459099	0.214	0.0008
Stk11ip	serine/threonine kinase 11 interacting protein	BC035530	0.205	0.0001
Stk25	serine/threonine kinase 25 (yeast)	NM_021537	0.262	0.0065
Stk40	serine/threonine kinase 40	NM_028800	0.240	0.0053
Stmn3	stathmin-like 3	AK149129	0.453	0.0135
Strn4	striatin, calmodulin binding protein 4	NM_133789	0.289	0.0000
Stub1	STIP1 homology and U-Box containing protein 1	NM_019719	0.282	0.0400
Stx18	syntaxin 18	AK169273	0.265	0.0025
Stxbp4	syntaxin binding protein 4	AK012293	0.231	0.0143
Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	NM_011506	0.243	0.0049

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Suds3	NA	NM_178622	0.273	0.0069
Sufu	suppressor of fused homolog (Drosophila)	NM_001025391	0.225	0.0473
Sumf2	sulfatase modifying factor 2	NM_026445	0.268	0.0283
Supt3h	suppressor of Ty 3 homolog (S. cerevisiae)	BC096051	0.231	0.0283
Svop	NA	NM_026805	0.246	0.0000
Sybl1	synaptobrevin like 1	NM_011515	0.241	0.0045
Syn2	synapsin II	BC053427	0.239	0.0000
Syt13	synaptotagmin XIII	AK129357	0.243	0.0025
Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	NM_133932	0.291	0.0007
Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_009315	0.298	0.0003
Tapbp	TAP binding protein	NM_001025313	0.219	0.0014
Tarsl1	threonyl-tRNA synthetase-like 1	NM_027931	0.206	0.0230
Taz	tafazzin	AK183640	0.239	0.0098
Tbc1d14	TBC1 domain family, member 14	XM_993814	0.230	0.0181
Tbc1d22a	TBC1 domain family, member 22a	NM_145476	0.245	0.0012
Tbc1d22b	NA	XM_993756	0.211	0.0001
Tbcd	tubulin-specific chaperone d	NM_029878	0.207	0.0000
Tbkbp1	NA	NM_198100	0.327	0.0000
Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	AK140144	0.278	0.0000
Tcea1	transcription elongation factorA(SII)1	D00925	0.230	0.0076
Tcfcp2	transcription factor CP2	AK147898	0.214	0.0117
Tcfe2a	transcription factor E2a	NM_011548	0.202	0.0003
Tdh	L-threonine dehydrogenase	XR_002703	0.362	0.0068
Tdpoz4	NA	NM_207272	0.458	0.0455
Tesc	NA	NM_021344	0.375	0.0244
Tesk1	testis specific protein kinase 1	NM_011571	0.215	0.0113
Tfip11	tuftelin interacting protein 11	NM_018783	0.246	0.0010
Tfpt	TCF3 (E2A) fusion partner	NM_023524	0.310	0.0008
Thap7	THAP domain containing 7	AK007329	0.402	0.0277
Thg1l	NA	BC092541	0.243	0.0366
Timm44	translocator of inner mitochondrial membrane 44	NM_011592	0.282	0.0001

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Tjap1	NA	NM_028751	0.262	0.0023
Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	AK122524	0.279	0.0003
Tlk2	tousled-like kinase 2 (Arabidopsis)	BC066198	0.209	0.0011
Tm7sf3	transmembrane 7 superfamily member 3	NM_026281	0.228	0.0002
Tmcc2	transmembrane and coiled-coil domains 2	AK172720	0.211	0.0032
Tmco6	NA	AK046207	0.253	0.0083
Tmed4	transmembrane emp24 protein transport domain containing 4	NM_134020	0.228	0.0382
Tmem1	transmembrane protein 1	XM_359259	0.225	0.0000
Tmem106b	NA	AK018015	0.325	0.0001
Tmem143	NA	AK010209	0.240	0.0223
Tmem145	NA	BC058129	0.259	0.0013
Tmem161a	NA	NM_145597	0.229	0.0032
Tmem161b	NA	BC060067	0.221	0.0385
Tmem164	NA	AK081890	0.249	0.0011
Tmem167	NA	AK019962	0.273	0.0137
Tmem175	NA	AK076446	0.304	0.0063
Tmem183a	NA	AK006183	0.246	0.0008
Tmem25	transmembrane protein 25	NM_027865	0.241	0.0020
Tmem45b	transmembrane protein 45b	NM_144936	0.455	0.0312
Tmem55a	transmembrane protein 55A	NM_028264	0.256	0.0178
Tmem8	transmembrane protein 8 (five membrane-spanning domains)	AK079893	0.224	0.0115
Tnrc4	trinucleotide repeat containing 4	AK030259	0.281	0.0001
Tns3	tensin 3	XM_990368	0.347	0.0000
Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	BC057096	0.265	0.0205
Tor1a	torsin family 1, member A (torsin A)	NM_144884	0.276	0.0358
Trabd	NA	NM_001002005	0.218	0.0020
Trap1	TNF receptor-associated protein 1	AK178868	0.248	0.0128
Trappc2	trafficking protein particle complex 2	NM_025432	0.320	0.0063
Trappc4	trafficking protein particle complex 4	AK005276	0.309	0.0289
Trappc6b	trafficking protein particle complex 6B	AK037638	0.278	0.0374
Trim23	tripartite motif protein 23	AK039280	0.265	0.0017

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Trim28	tripartite motif protein 28	NM_011588	0.238	0.0000
Trim3	tripartite motif protein 3	XM_001000076	0.304	0.0003
Trp53i11	Trp53 inducible protein 11	BC024710	0.253	0.0070
Trp53inp1	transformation related protein 53 inducible nuclear protein 1	NM_021897	0.371	0.0467
Trpt1	NA	AK038830	0.239	0.0483
Tsen54	tRNA splicing endonuclease 54 homolog (SEN54, S. cerevisiae)	NM_029557	0.208	0.0237
Tsg101	tumor susceptibility gene 101	NM_021884	0.205	0.0249
Tsta3	tissue specific transplantation antigen P35B	NM_031201	0.294	0.0189
Ttyh1	tweety homolog 1 (Drosophila)	AK031550	0.303	0.0000
Tubgcp2	tubulin, gamma complex associated protein 2	NM_133755	0.203	0.0044
Tubgcp6	NA	AK052441	0.565	0.0289
Tusc4	tumor suppressor candidate 4	NM_018879	0.284	0.0037
Txndc5	thioredoxin domain containing 5	NM_145367	0.297	0.0286
Txnrd2	thioredoxin reductase 2	NM_013711	0.218	0.0289
Ube2g2	ubiquitin-conjugating enzyme E2G 2	NM_019803	0.354	0.0045
Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	NM_145578	0.216	0.0017
Ube2q1	NA	BC082275	0.208	0.0052
Ube3a	ubiquitin protein ligase E3A	AK018028	0.202	0.0145
Ube3b	ubiquitin protein ligase E3B	AK216199	0.235	0.0000
Ube3c	ubiquitin protein ligase E3C	NM_133907	0.210	0.0001
Ubqln4	ubiquilin 4	NM_033526	0.230	0.0000
Ubxd2	UBX domain containing 2	NM_026390	0.228	0.0001
Uck1	uridine-cytidine kinase 1	NM_011675	0.275	0.0024
Unc50	unc-50 homolog (C. elegans)	NM_026123	0.297	0.0193
Unc5b	unc-5 homolog B (C. elegans)	NM_029770	0.211	0.0012
Upf1	NA	AK046599	0.247	0.0000
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	NM_025899	0.284	0.0003
Usf2	upstream transcription factor 2	NM_011680	0.234	0.0065
Usp37	ubiquitin specific peptidase 37	AK173210	0.229	0.0001
Usp47	ubiquitin specific peptidase 47	NM_133758	0.231	0.0000
Usp5	ubiquitin specific peptidase 5 (isopeptidase T)	NM_013700	0.218	0.0019

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Vapb	vesicle-associated membrane protein, associated protein B and C	NM_019806	0.253	0.0304
Vash1	vasohibin 1	BC086688	0.231	0.0024
Vav1	vav 1 oncogene	NM_011691	0.203	0.0189
Vim	vimentin	BC089335	0.253	0.0006
Vipr2	vasoactive intestinal peptide receptor 2	NM_009511	0.271	0.0491
Vps26b	NA	NM_178027	0.275	0.0035
Vps36	vacuolar protein sorting 36 (yeast)	AK005810	0.334	0.0000
Wars	tryptophanyl-tRNA synthetase	AK190440	0.265	0.0437
Wdhd1	WD repeat and HMG-box DNA binding protein 1	AK052690	0.229	0.0076
Wdr13	WD repeat domain 13	NM_026137	0.299	0.0000
Wdr3	WD repeat domain 3	NM_175552	0.222	0.0002
Wdr34	WD repeat domain 34	NM_001008498	0.216	0.0006
Wdr36	WD repeat domain 36	AK156822	0.209	0.0017
Wdr4	WD repeat domain 4	NM_021322	0.298	0.0009
Wdr40a	WD repeat domain 40A	AK083369	0.260	0.0137
Wdr6	WD repeat domain 6	NM_031392	0.269	0.0001
Wdr74	WD repeat domain 74	NM_134139	0.269	0.0136
Wdr82	NA	BC019115	0.305	0.0001
Wrb	tryptophan rich basic protein	AK021091	0.322	0.0092
Wwp2	WW domain containing E3 ubiquitin protein ligase 2	AK141281	0.210	0.0001
Xab1	XPA binding protein 1	BC020174	0.299	0.0022
Xbp1	X-box binding protein 1	NM_013842	0.209	0.0067
Xpnpep3	NA	AK035269	0.247	0.0036
Xpo7	exportin 7	NM_023045	0.210	0.0000
Yif1b	Yip1 interacting factor homolog B (S. cerevisiae)	NM_029887	0.299	0.0014
Ypel2	yippee-like 2 (Drosophila)	NM_001005341	0.258	0.0076
Zbtb33	zinc finger and BTB domain containing 33	NM_020256	0.541	0.0425
Zc3h7b	NA	AK129268	0.226	0.0000
Zdhhc16	zinc finger, DHHC domain containing 16	AK005255	0.218	0.0304
Zfp179	zinc finger protein 179	AK131651	0.203	0.0005
Zfp251	zinc finger protein 251	AK047148	0.262	0.0435

Table S5. Continued.

Upregulated genes (940):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
Zfp276	zinc finger protein (C2H2 type) 276	BC048688	0.275	0.0003
Zfp469	zinc finger protein 469	NM_178242	0.297	0.0000
Zfp68	zinc finger protein 68	NM_001044747	0.270	0.0168
Zfp687	zinc finger protein 687	NM_030074	0.313	0.0001
Zfp692	zinc finger protein 692	NM_182996	0.217	0.0024
Zfpl1	zinc finger like protein 1	NM_024231	0.254	0.0157
Zfx	zinc finger protein X-linked	L19714	0.211	0.0124
Zfyve27	zinc finger, FYVE domain containing 27	NM_177319	0.243	0.0000
Zgpat	zinc finger, CCCH-type with G patch domain	NM_144894	0.243	0.0029
Zmiz2	NA	NM_001005867	0.209	0.0010
Zyx	zyxin	BC054775	0.219	0.0405

Downregulated genes (247):

Gene Symbol	Gene Name	Entrez ID	Fold Change *MECP2*-Tg over WT	FDR-adjusted p-value (*MECP2*-Tg over WT)
1700015C15Rik	RIKEN cDNA 1700015C15 gene	AK005986	-1.090	0.0313
1700034O15Rik	RIKEN cDNA 1700034O15 gene	NM_029671	-0.641	0.0350
1700041C23Rik	NA	AK006669	-0.738	0.0407
1700051A21Rik	NA	AK035540	-0.338	0.0398
1700052K07Rik	NA	AK006770	-0.427	0.0354
1810054D07Rik	RIKEN cDNA 1810054D07 gene	AK049108	-0.222	0.0010
2010110K18Rik	NA	AK029153	-0.208	0.0323
3300002A11Rik	RIKEN cDNA 3300002A11 gene	AK014365	-0.302	0.0358
4732479N06Rik	RIKEN cDNA 4732479N06 gene	AK129030	-0.208	0.0200
4930478L05Rik	RIKEN cDNA 4930478L05 gene	AK030550	-0.335	0.0361
4930519B02Rik	RIKEN cDNA 4930519B02 gene	XM_125512	-0.239	0.0308
4930535O05Rik	NA	AK015983	-0.309	0.0476
4930542N06Rik	RIKEN cDNA 4930542N06 gene	AK051451	-0.412	0.0475
6330527O06Rik	RIKEN cDNA 6330527O06 gene	NM_029530	-0.371	0.0100
6330577E15Rik	RIKEN cDNA 6330577E15 gene	NM_026377	-0.240	0.0180
7530416G11Rik	NA	AK078701	-0.238	0.0221
9430070O13Rik	RIKEN cDNA 9430070O13 gene	AK020482	-0.390	0.0051

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
A830006F12Rik	RIKEN cDNA A830006F12 gene	AK083856	-0.296	0.0038
Abca15	NA	AK029712	-0.219	0.0294
Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	NM_011076	-0.271	0.0001
Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	NM_001033336	-0.269	0.0000
Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	NM_011994	-0.237	0.0177
Ablim1	actin-binding LIM protein 1	AK171860	-0.245	0.0000
Acvr1c	activin A receptor, type IC	NM_001033369	-0.508	0.0000
Adam29	NA	NM_175939	-0.624	0.0421
Adamts13	NA	AB071302	-0.227	0.0080
Adamts3	NA	XM_977798	-0.259	0.0020
Adrbk2	adrenergic receptor kinase, beta 2	NM_177078	-0.244	0.0014
Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	NM_009646	-0.214	0.0293
AK220484	cDNA sequence AK220484	XM_977373	-0.283	0.0001
Anubl1	AN1, ubiquitin-like, homolog (Xenopus laevis)	BC019579	-0.303	0.0006
Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	BC038035	-0.206	0.0028
Arhgap21	Rho GTPase activating protein 21	AK122508	-0.218	0.0020
Arhgap22	Rho GTPase activating protein 22	NM_153800	-0.212	0.0068
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	AK016387	-0.213	0.0342
Atp10d	ATPase, Class V, type 10D	AK085120	-0.280	0.0000
Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	NM_026482	-0.233	0.0000
Atxn7l1	ataxin 7-like 1	NM_001033436	-0.323	0.0110
B230208N19Rik	RIKEN cDNA B230208N19 gene	NM_008069	-0.214	0.0065
B230220E17Rik	RIKEN cDNA B230220E17 gene	XM_354862	-0.254	0.0008
Baz2b	NA	AK147737	-0.301	0.0000
BC003331	cDNA sequence BC003331	NM_145511	-0.238	0.0017
BC026657	cDNA sequence BC026657	XM_912620	-0.293	0.0016
BC030499	cDNA sequence BC030499	BC030499	-0.325	0.0310
BC033606	cDNA sequence BC033606	XM_911052	-0.220	0.0484
BC055107	cDNA sequence BC055107	NM_183187	-0.206	0.0243

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Bmf	Bcl2 modifying factor	AK089218	-0.245	0.0347
C920006C10Rik	RIKEN cDNA C920006C10 gene	AK030074	-0.235	0.0000
Cab39l	calcium binding protein 39-like	BC034159	-0.438	0.0003
Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	L20343	-0.249	0.0009
Cacng2	calcium channel, voltage-dependent, gamma subunit 2	AK164203	-0.391	0.0199
Capn8	calpain 8	NM_130890	-0.210	0.0389
Car7	carbonic anhydrase 7	NM_053070	-0.306	0.0306
Cat	catalase	AK183520	-0.226	0.0000
Cd6	CD6 antigen	NM_001037801	-0.289	0.0003
Cdh15	cadherin 15	XM_001002605	-0.281	0.0413
Cdkl4	cyclin-dependent kinase-like 4	NM_001033443	-0.414	0.0053
Cit	citron	AK145037	-0.210	0.0000
Clmn	calmin	NM_053155	-0.236	0.0004
Cobll1	Cobl-like 1	AK037010	-0.304	0.0055
Col19a1	procollagen, type XIX, alpha 1	AK019854	-0.253	0.0001
Col24a1	procollagen, type XXIV, alpha 1	BC092542	-0.222	0.0001
Creb5	cAMP responsive element binding protein 5	AK170766	-0.371	0.0108
Ctps2	cytidine 5'-triphosphate synthase 2	AK085381	-0.210	0.0046
Cutl2	cut-like 2 (Drosophila)	NM_007804	-0.216	0.0000
Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	NM_133969	-0.265	0.0134
D430015B01Rik	RIKEN cDNA D430015B01 gene	NM_153574	-0.250	0.0018
Ddef1	development and differentiation enhancing	XM_977047	-0.234	0.0000
Depdc6	DEP domain containing 6	AK145208	-0.317	0.0009
Dmbt1	deleted in malignant brain tumors 1	NM_007769	-0.234	0.0015
Dnahc5	dynein, axonemal, heavy chain 5	NM_133365	-0.204	0.0000
Dock4	dedicator of cytokinesis 4	AK031713	-0.208	0.0000
Dock9	dedicator of cytokinesis 9	AK034324	-0.254	0.0000
Dst	dystonin	DQ023311	-0.243	0.0000
Dync1i1	NA	NM_010063	-0.213	0.0016
Ebf1	early B-cell factor 1	NM_007897	-0.278	0.0075
EG216818	NA	XM_001001019	-0.429	0.0286
Eltd1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	-0.283	0.0031

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Emb	embigin	AK148540	-0.280	0.0001
Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	NM_008813	-0.203	0.0113
Epb4.1l3	erythrocyte protein band 4.1-like 3	AK173080	-0.298	0.0000
Epb4.1l4a	erythrocyte protein band 4.1-like 4a	BC089158	-0.239	0.0002
Eps15	epidermal growth factor receptor pathway substrate 15	NM_007943	-0.204	0.0001
Erbb4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	XM_993491	-0.286	0.0000
Erg	avian erythroblastosis virus E-26 (v-ets) oncogene related	AK050922	-0.298	0.0134
Esrrg	estrogen-related receptor gamma	NM_011935	-0.352	0.0008
Extl2	exotoses (multiple)-like 2	AF200973	-0.348	0.0023
Fat1	NA	XM_896341	-0.210	0.0004
Fbn1	fibrillin 1	AF007248	-0.205	0.0000
Fbxl21	F-box and leucine-rich repeat protein 21	NM_178674	-0.280	0.0379
Fbxo8	F-box only protein 8	NM_015791	-0.207	0.0075
Fcrl1	Fc receptor-like 1	AK041750	-0.340	0.0206
Fgd6	FYVE, RhoGEF and PH domain containing 6	NM_053072	-0.244	0.0375
Fgf12	fibroblast growth factor 12	AK148215	-0.245	0.0009
Fgfr2	fibroblast growth factor receptor 2	NM_010207	-0.213	0.0010
Fmn1	formin 1	NM_010230	-0.214	0.0082
Fnbp1	formin binding protein 1	NM_001038700	-0.230	0.0005
Frmd4b	FERM domain containing 4B	NM_145148	-0.261	0.0000
Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	NM_010250	-0.244	0.0000
Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	AK041791	-0.201	0.0492
Ggta1	glycoprotein galactosyltransferase alpha 1, 3	XM_915541	-0.341	0.0213
Glra1	glycine receptor, alpha 1 subunit	NM_020492	-0.251	0.0218
Glul	glutamate-ammonia ligase (glutamine synthase)	XR_003500	-0.242	0.0013
Gm498	NA	XM_917182	-0.266	0.0464
Gpr113	NA	NM_001014394	-0.350	0.0484
Gpr155	G protein-coupled receptor 155	XM_001002587	-0.246	0.0140

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Gria1	glutamate receptor, ionotropic, AMPA1 (alpha 1)	AK135107	-0.214	0.0011
Gtdc1	glycosyltransferase-like domain containing 1	AK028468	-0.209	0.0460
Hivep1	human immunodeficiency virus type I enhancer binding protein 1	NM_007772	-0.285	0.0047
Ibrdc2	IBR domain containing 2	NM_146042	-0.246	0.0056
Igsf4a	immunoglobulin superfamily, member 4A	AB021966	-0.218	0.0014
Il12rb1	interleukin 12 receptor, beta 1	NM_008353	-0.241	0.0050
Il6st	interleukin 6 signal transducer	AK170020	-0.274	0.0000
Inadl	InaD-like (Drosophila)	NM_172696	-0.290	0.0000
Indol1	NA	AK082385	-0.303	0.0334
Itga1	integrin alpha 1	AK137169	-0.230	0.0061
Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	NM_001025581	-0.259	0.0023
Kcnip3	NA	NM_019789	-0.273	0.0455
Kera	keratocan	NM_008438	-0.592	0.0479
Kif13b	kinesin family member 13B	XM_001001137	-0.278	0.0000
Klhl14	kelch-like 14 (Drosophila)	XM_905416	-0.269	0.0448
LOC240895	NA	XR_003742	-0.222	0.0400
LOC381484	NA	XM_909129	-0.885	0.0238
LOC381806	NA	NM_001013775	-0.906	0.0287
LOC382469	NA	XR_003768	-0.348	0.0399
LOC382471	NA	XR_003850	-1.015	0.0170
LOC547223	NA	XM_974408	-0.754	0.0265
LOC622459	NA	AK138811	-0.430	0.0275
LOC635295	NA	XR_002040	-0.434	0.0183
LOC635583	NA	XM_979222	-0.295	0.0220
LOC665232	NA	XR_003071	-0.264	0.0320
LOC667763	NA	AK040590	-0.272	0.0239
LOC670900	NA	XM_356148	-0.325	0.0376
LOC671029	NA	BC046394	-0.282	0.0475
LOC672056	NA	XR_003685	-0.835	0.0234
LOC673340	NA	XR_004199	-0.344	0.0255
LOC674183	NA	XM_990669	-0.253	0.0485
LOC674649	NA	XR_002534	-0.407	0.0320

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
LOC675182	NA	XM_140042	-1.378	0.0036
LOC677555	NA	AB071302	-0.288	0.0479
Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	AK132436	-0.207	0.0000
Lrp12	low density lipoprotein-related protein 12	NM_172814	-0.215	0.0497
Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	NM_008515	-0.214	0.0017
Lrrk2	leucine-rich repeat kinase 2	NM_025730	-0.243	0.0000
Ltbp1	latent transforming growth factor beta binding protein 1	NM_206958	-0.220	0.0006
Lyl1	lymphoblastomic leukemia	NM_008535	-0.207	0.0328
Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	AK163800	-0.228	0.0000
Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	NM_133853	-0.221	0.0374
Mak	male germ cell-associated kinase	BC050009	-0.311	0.0153
Mansc1	MANSC domain containing 1	NM_026345	-0.465	0.0026
March1	membrane-associated ring finger (C3HC4) 1	AK086052	-0.278	0.0010
Mbnl2	muscleblind-like 2	AK220470	-0.205	0.0001
Mcf2	mcf.2 transforming sequence	AK045424	-0.273	0.0001
Megf9	NA	AK155926	-0.242	0.0391
Miox	myo-inositol oxygenase	NM_019977	-0.331	0.0426
Mitf	microphthalmia-associated transcription factor	AK052895	-0.227	0.0345
Mmachc	NA	NM_025962	-0.344	0.0446
Mr1	major histocompatibility complex, class I-related	AF010453	-0.282	0.0364
Mtmr7	myotubularin related protein 7	AK148768	-0.245	0.0006
Muc10	mucin 10, submandibular gland salivary mucin	NM_008644	-0.342	0.0474
Mybl1	myeloblastosis oncogene-like 1	NM_008651	-0.319	0.0057
Mybphl	NA	NM_026831	-0.227	0.0398
Myh6	myosin, heavy polypeptide 6, cardiac muscle, alpha	NM_010856	-0.229	0.0029
Mylip	myosin regulatory light chain interacting protein	NM_153789	-0.243	0.0327

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Myo15	myosin XV	AK030528	-0.220	0.0001
Myo1e	myosin IE	NM_181072	-0.206	0.0077
Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	AK078224	-0.220	0.0002
Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	XM_973147	-0.256	0.0048
Oas3	2'-5' oligoadenylate synthetase 3	BC025152	-0.234	0.0054
Odf3l1	NA	NM_198673	-0.341	0.0381
Olfr1337	NA	NM_146309	-0.799	0.0362
Olfr1357	NA	NM_001011737	-0.428	0.0049
Olfr137	NA	NM_146488	-0.308	0.0344
Olfr735	NA	NM_001011754	-0.561	0.0251
Oxr1	oxidation resistance 1	BC098491	-0.219	0.0008
Padi1	peptidyl arginine deiminase, type I	NM_011059	-0.265	0.0046
Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	NM_011864	-0.407	0.0128
Parva	parvin, alpha	AK162796	-0.270	0.0000
Pex2	peroxin 2	AK044552	-0.218	0.0062
Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	NM_001077495	-0.208	0.0109
Pip	prolactin induced protein	NM_008843	-0.361	0.0407
Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	NM_008845	-0.211	0.0189
Pla2g1b	phospholipase A2, group IB, pancreas	AK019009	-0.428	0.0224
Plch1	NA	NM_183191	-0.226	0.0015
Plekha5	pleckstrin homology domain containing, family A member 5	BC014853	-0.242	0.0000
Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	NM_177606	-0.294	0.0000
Pou2f3	POU domain, class 2, transcription factor 3	AK153697	-0.255	0.0300
Pparg	peroxisome proliferator activated receptor gamma	U01841	-0.357	0.0416
Prlr	prolactin receptor	NM_011169	-0.467	0.0257
Prtg	NA	AK045117	-0.290	0.0007
Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	NM_008950	-0.287	0.0474

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Rai14	retinoic acid induced 14	NM_030690	-0.299	0.0058
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	NM_019688	-0.211	0.0000
Rasgrp3	RAS, guanyl releasing protein 3	AK173041	-0.318	0.0013
Rbms1	RNA binding motif, single stranded interacting protein 1	BC057866	-0.288	0.0073
Rgs6	regulator of G-protein signaling 6	AK053087	-0.287	0.0000
Rgs9	regulator of G-protein signaling 9	AF011358	-0.206	0.0010
Rhbg	Rhesus blood group-associated B glycoprotein	NM_021375	-0.243	0.0221
Ribc2	RIB43A domain with coiled-coils 2	XM_001002357	-0.298	0.0327
Rsrc1	arginine/serine-rich coiled-coil 1	BC027501	-0.221	0.0189
Scn1a	sodium channel, voltage-gated, type I, alpha	XM_899643	-0.334	0.0000
Scn4b	sodium channel, type IV, beta	NM_001013390	-0.249	0.0338
Scn5a	sodium channel, voltage-gated, type V, alpha	NM_021544	-0.219	0.0014
Scn8a	sodium channel, voltage-gated, type VIII, alpha	NM_001077499	-0.244	0.0000
Scpep1	serine carboxypeptidase 1	NM_029023	-0.305	0.0006
Setdb2	NA	XM_001002736	-0.387	0.0095
Sgk	serum/glucocorticoid regulated kinase	BC070401	-0.329	0.0010
Sh3d19	SH3 domain protein D19	D89677	-0.230	0.0018
Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	BC026364	-0.269	0.0094
Shox2	short stature homeobox 2	AK032007	-0.364	0.0376
Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	AK038847	-0.346	0.0000
Slc7a9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	AF192310	-0.300	0.0322
Slc9a3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	AK033564	-0.235	0.0363
Smoc1	SPARC related modular calcium binding 1	AK040931	-0.291	0.0005
Spata21	NA	XM_991770	-0.237	0.0024
Spna1	spectrin alpha 1	NM_011465	-0.212	0.0025
Spp1	secreted phosphoprotein 1	AK165965	-0.459	0.0082

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Srgap1	SLIT-ROBO Rho GTPase activating protein 1	AY057898	-0.228	0.0008
Srpk2	serine/arginine-rich protein specific kinase 2	U92456	-0.290	0.0000
St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	NM_001035228	-0.259	0.0014
St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	NM_011372	-0.311	0.0285
Stard5	StAR-related lipid transfer (START) domain containing 5	AK142503	-0.220	0.0239
Stat1	signal transducer and activator of transcription 1	NM_009283	-0.218	0.0081
Stk32b	serine/threonine kinase 32B	AJ250840	-0.311	0.0154
Stxbp3a	syntaxin binding protein 3A	U19521	-0.231	0.0296
Syne1	synaptic nuclear envelope 1	AK122550	-0.227	0.0000
Tbc1d4	TBC1 domain family, member 4	XM_919052	-0.275	0.0003
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	AF363724	-0.268	0.0013
Tfrc	transferrin receptor	BC067403	-0.308	0.0030
Tgfbr2	transforming growth factor, beta receptor II	NM_009371	-0.215	0.0413
Tjp1	tight junction protein 1	AK161324	-0.225	0.0001
Tmem132d	NA	NM_172885	-0.240	0.0092
Tmem2	transmembrane protein 2	AK156343	-0.205	0.0045
Tmod1	tropomodulin 1	AK132878	-0.390	0.0002
Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	AK034121	-0.359	0.0188
Top1mt	DNA topoisomerase 1, mitochondrial	XM_994430	-0.267	0.0044
Tph2	tryptophan hydroxylase 2	NM_173391	-0.295	0.0259
Trp53bp2	transformation related protein 53 binding protein 2	NM_173378	-0.217	0.0053
Trpm3	transient receptor potential cation channel, subfamily M, member 3	AK046308	-0.244	0.0000
Ttf2	transcription termination factor, RNA polymerase II	NM_001013026	-0.235	0.0175
Ttll5	tubulin tyrosine ligase like family 5	XM_994418	-0.253	0.0000
Ubd	ubiquitin D	NM_023137	-0.831	0.0463
Usp25	ubiquitin specific peptidase 25	NM_013918	-0.232	0.0012

Table S5. Continued.

Downregulated genes (247):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *MECP2*-Tg over WT**	**FDR-adjusted p-value (*MECP2*-Tg over WT)**
Utrn	utrophin	AK134424	-0.225	0.0000
Vil2	villin 2	NM_009510	-0.263	0.0008
Xdh	xanthine dehydrogenase	AK164764	-0.250	0.0063
Zmat4	zinc finger, matrin type 4	AK043510	-0.258	0.0089

Table S6. The list of genes specifically misregulated in *Mecp2*-null hypothalami (FDR-adjusted p-value < 0.05).

Upregulated genes (85):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
1700081B01Rik	NA	AK006961	0.407	0.0362
1700112M02Rik	NA	AK007185	0.581	0.0239
4732456N10Rik	NA	NM_053249	0.246	0.0375
4930401O12Rik	NA	AK015040	0.607	0.0409
9930013L23Rik	RIKEN cDNA 9930013L23 gene	BC056981	0.307	0.0000
9930021J17Rik	RIKEN cDNA 9930021J17 gene	BC094511	0.302	0.0227
Adcy1	adenylate cyclase 1	BC050125	0.273	0.0000
Angpt2	angiopoietin 2	NM_007426	0.280	0.0125
Bace2	beta-site APP-cleaving enzyme 2	NM_019517	0.318	0.0073
BC016201	cDNA sequence BC016201	BC051415	0.245	0.0122
BC048507	cDNA sequence BC048507	XM_621326	0.261	0.0407
Bhlhb2	basic helix-loop-helix domain containing, class B2	NM_011498	0.287	0.0016
Bpil1	bactericidal/permeability-increasing protein-like 1	AK009346	0.242	0.0373
Btbd14a	BTB (POZ) domain containing 14A	AK043047	0.241	0.0004
C1ql3	C1q-like 3	NM_153155	0.352	0.0239
Calcr	calcitonin receptor	NM_007588	0.238	0.0057
Camk2a	calcium/calmodulin-dependent protein kinase II alpha	NM_177407	0.212	0.0109
Cdh16	cadherin 16	AK164546	0.249	0.0421
Cdh4	cadherin 4	NM_009867	0.306	0.0000
Chrm3	cholinergic receptor, muscarinic 3, cardiac	NM_033269	0.348	0.0003
Chst11	carbohydrate sulfotransferase 11	NM_021439	0.329	0.0001
Col25a1	procollagen, type XXV, alpha 1	NM_198711	0.201	0.0000
Col4a1	procollagen, type IV, alpha 1	NM_009931	0.217	0.0000
Cpne4	copine IV	NM_028719	0.249	0.0000
Crispld2	cysteine-rich secretory protein LCCL domain containing 2	NM_030209	0.259	0.0054
Csmd1	CUB and Sushi multiple domains1	XM_979853	0.289	0.0000
Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	BC059246	0.390	0.0222
D230005D02Rik	RIKEN cDNA D230005D02 gene	AK082388	0.220	0.0000
D630021H01Rik	NA	AK052676	0.920	0.0023
D930015E06Rik	RIKEN cDNA D930015E06 gene	AK028803	0.222	0.0000
E130310K16Rik	RIKEN cDNA E130310K16 gene	AK141456	0.291	0.0489
Efna5	ephrin A5	NM_207654	0.334	0.0013
EG433623	NA	XR_004819	0.200	0.0090

Table S6. Continued.

Upregulated genes (85):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
G6pc2	glucose-6-phosphatase, catalytic, 2	NM_021331	0.403	0.0444
Gpr44	G protein-coupled receptor 44	NM_009962	0.310	0.0425
Habp2	hyaluronic acid binding protein 2	NM_146101	0.342	0.0044
Hba-a1	hemoglobin alpha, adult chain 1	AK011056	0.483	0.0402
Homer2	homer homolog 2 (Drosophila)	BC038314	0.221	0.0257
Hoxc13	homeo box C13	NM_010464	0.224	0.0100
Hpn	hepsin	NM_008281	0.203	0.0187
Il1f6	interleukin 1 family, member 6	NM_019450	0.377	0.0500
Irak1	interleukin-1 receptor-associated kinase 1	NM_008363	0.557	0.0000
Isl1	ISL1 transcription factor, LIM/homeodomain (islet 1)	NM_021459	0.237	0.0246
Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	AK082310	0.284	0.0000
Kcnk9	NA	NM_001033876	0.414	0.0299
Kif24	kinesin family member 24	NM_024241	0.273	0.0439
Klre1	killer cell lectin-like receptor family E member 1	NM_153590	0.338	0.0111
Ksr1	NA	NM_013571	0.250	0.0000
LOC622552	NA	AK038993	0.513	0.0183
LOC632784	NA	XM_907012	0.328	0.0340
LOC633879	NA	NM_001033251	0.744	0.0190
LOC636466	NA	XM_994280	0.244	0.0099
LOC669490	NA	NM_011856	0.216	0.0000
LOC670210	NA	NM_053171	0.369	0.0023
Loxl2	lysyl oxidase-like 2	NM_033325	0.319	0.0024
Lsp1	lymphocyte specific 1	AK075783	0.217	0.0250
Lypd1	Ly6/Plaur domain containing 1	BC058599	0.293	0.0057
Mgll	monoglyceride lipase	NM_011844	0.273	0.0000
Mical2	NA	AK220353	0.254	0.0001
Mkl1	MKL (megakaryoblastic leukemia)/myocardin-like 1	AK155937	0.207	0.0043
Nr1d1	nuclear receptor subfamily 1, group D, member 1	NM_145434	0.236	0.0000
Nrn1	neuritin 1	NM_153529	0.281	0.0005
Nrp2	neuropilin 2	NM_010939	0.203	0.0000
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	AK031198	0.244	0.0000
Olfr1340	NA	NM_146304	0.218	0.0375

Table S6. Continued.

Upregulated genes (85):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
Olfr820	NA	NM_146675	0.637	0.0448
Pcbp3	poly(rC) binding protein 3	NM_021568	0.220	0.0006
Pgm5	NA	AK076484	0.269	0.0037
Plxna4	plexin A4	XM_984204	0.208	0.0000
Prkcq	protein kinase C, theta	AK085546	0.231	0.0000
Ptk2b	PTK2 protein tyrosine kinase 2 beta	BC024594	0.234	0.0347
Rassf8	Ras association (RalGDS/AF-6) domain family 8	AK142231	0.218	0.0205
Rorb	RAR-related orphan receptor beta	BC024768	0.225	0.0000
Sec14l1	SEC14-like 1 (S. cerevisiae)	AK047396	0.250	0.0000
Sh2d6	NA	XM_911211	0.201	0.0308
Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	AK079049	0.216	0.0082
Sorcs3	sortilin-related VPS10 domain containing receptor 3	NM_025696	0.254	0.0000
Tex101	testis expressed gene 101	DQ222040	0.359	0.0429
Tnfrsf19l	tumor necrosis factor receptor superfamily, member 19-like	NM_177073	0.212	0.0018
Tspan9	tetraspanin 9	NM_175414	0.334	0.0000
Umodl1	NA	NM_177465	0.255	0.0021
Usp3	ubiquitin specific peptidase 3	AK158516	0.216	0.0004
Ust	uronyl-2-sulfotransferase	NM_177387	0.279	0.0002
Zbtb16	zinc finger and BTB domain containing 16	NM_001033324	0.467	0.0003
Zfp496	zinc finger protein 496	NM_172941	0.218	0.0064

Downregulated genes (284):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
1110049B09Rik	RIKEN cDNA 1110049B09 gene	XM_976214	-0.224	0.0113
1110057K04Rik	RIKEN cDNA 1110057K04 gene	AK162914	-0.211	0.0337
1200016E24Rik	RIKEN cDNA 1200016E24 gene	AK075710	-0.286	0.0288
1700024D23Rik	RIKEN cDNA 1700024D23 gene	NM_029911	-0.323	0.0066
1700027A23Rik	RIKEN cDNA 1700027A23 gene	AK006407	-0.298	0.0472
1810048J11Rik	RIKEN cDNA 1810048J11 gene	AK076035	-0.252	0.0000
2310005N01Rik	RIKEN cDNA 2310005N01 gene	BC108404	-0.202	0.0158

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
2310057J16Rik	RIKEN cDNA 2310057J16 gene	BC048787	-0.213	0.0000
2410187C16Rik	RIKEN cDNA 2410187C16 gene	AK010831	-0.240	0.0235
2610110G12Rik	RIKEN cDNA 2610110G12 gene	AK028297	-0.246	0.0015
2700012I20Rik	RIKEN cDNA 2700012I20 gene	AK012238	-0.453	0.0460
2700085E05Rik	RIKEN cDNA 2700085E05 gene	BC055356	-0.218	0.0018
3830406C13Rik	RIKEN cDNA 3830406C13 gene	NM_146051	-0.258	0.0091
4921504I05Rik	RIKEN cDNA 4921504I05 gene	BC061080	-0.687	0.0432
4930455F23Rik	RIKEN cDNA 4930455F23 gene	XM_001002779	-0.202	0.0080
4930480G23Rik	RIKEN cDNA 4930480G23 gene	AK015599	-0.490	0.0192
4930528D03Rik	RIKEN cDNA 4930528D03 gene	AK015923	-0.480	0.0451
4932432K03Rik	RIKEN cDNA 4932432K03 gene	AK053266	-0.203	0.0374
4933426K21Rik	RIKEN cDNA 4933426K21 gene	XM_132812	-0.330	0.0078
5730591J02Rik	RIKEN cDNA 5730591J02 gene	AK054421	-0.211	0.0407
6330503K22Rik	RIKEN cDNA 6330503K22 gene	NM_182995	-0.217	0.0004
6430524H05Rik	NA	NM_001033531	-0.244	0.0011
9030617O03Rik	RIKEN cDNA 9030617O03 gene	BC021385	-0.250	0.0064
9430022A06Rik	NA	AK158576	-0.534	0.0102
9430087C24Rik	NA	AK035088	-0.389	0.0309
A330021E22Rik	RIKEN cDNA A330021E22 gene	AK164190	-0.220	0.0004
A430106J12Rik	RIKEN cDNA A430106J12 gene	AK040472	-0.224	0.0000
A430107O13Rik	RIKEN cDNA A430107O13 gene	XM_485730	-0.216	0.0221
A430108E01Rik	RIKEN cDNA A430108E01 gene	AK031601	-0.224	0.0159
A830018L16Rik	RIKEN cDNA A830018L16 gene	AK135047	-0.280	0.0017
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	NM_008991	-0.208	0.0000
Acly	ATP citrate lyase	AK162364	-0.206	0.0000
Acsl5	acyl-CoA synthetase long-chain family member 5	NM_027976	-0.297	0.0000
Agtr2	angiotensin II receptor, type 2	NM_007429	-0.493	0.0461
AI427515	expressed sequence AI427515	AK035009	-0.266	0.0000
Aldh1l2	aldehyde dehydrogenase 1 family, member L2	NM_153543	-0.331	0.0000
Alox8	NA	NM_009661	-0.408	0.0000
Ankra2	ankyrin repeat, family A (RFXANK-like), 2	BC066113	-0.202	0.0229
Ankrd55	NA	AK081197	-0.336	0.0000
Anln	anillin, actin binding protein (scraps homolog, Drosophila)	AK046102	-0.221	0.0074
Apex1	apurinic/apyrimidinic endonuclease 1	NM_009687	-0.216	0.0122

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Aqp4	aquaporin 4	AK039777	-0.200	0.0043
Arhgap1	Rho GTPase activating protein 1	BC006592	-0.222	0.0025
Arrdc2	arrestin domain containing 2	NM_027560	-0.209	0.0041
Arsg	NA	NM_028710	-0.228	0.0003
Arsk	NA	AK033968	-0.220	0.0413
Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	AK146254	-0.228	0.0000
Asl	argininosuccinate lyase	NM_133768	-0.208	0.0007
Aspa	aspartoacylase (aminoacylase) 2	NM_023113	-0.285	0.0281
Atp7a	ATPase, Cu++ transporting, alpha polypeptide	NM_009726	-0.201	0.0065
Atxn3	NA	NM_029705	-0.206	0.0064
B830045N13Rik	RIKEN cDNA B830045N13 gene	AK083233	-0.276	0.0001
Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	NM_130452	-0.278	0.0118
BC022224	cDNA sequence BC022224	XM_001002312	-0.228	0.0316
BC052040	cDNA sequence BC052040	BC052040	-0.273	0.0049
BC056474	cDNA sequence BC056474	AK147129	-0.231	0.0336
BC068110	NA	NM_001013778	-0.268	0.0012
BC068171	cDNA sequence BC068171	XM_903797	-0.226	0.0201
Blmh	bleomycin hydrolase	NM_178645	-0.230	0.0000
Brwd3	bromodomain and WD repeat domain containing 3	XM_897923	-0.231	0.0000
Bud13	NA	NM_146000	-0.221	0.0122
Bzw1	basic leucine zipper and W2 domains 1	XR_002994	-0.304	0.0042
C130022K22Rik	RIKEN cDNA C130022K22 gene	NM_172730	-0.271	0.0374
C130090K23Rik	RIKEN cDNA C130090K23 gene	NM_145560	-0.238	0.0244
Camk1g	calcium/calmodulin-dependent protein kinase I gamma	NM_144817	-0.228	0.0003
Ccdc104	NA	NM_025740	-0.273	0.0000
Cckbr	cholecystokinin B receptor	AK039721	-0.242	0.0017
Ccnc	cyclin C	BC062376	-0.245	0.0086
Cd59a	CD59a antigen	NM_007652	-0.469	0.0013
Cdh10	cadherin 10	AK048368	-0.234	0.0010
Cdh20	cadherin 20	NM_011800	-0.212	0.0021
Cetn4	centrin 4	BC087905	-0.453	0.0017
Clgn	calmegin	NM_009904	-0.469	0.0000

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
Cntn6	contactin 6	NM_017383	-0.256	0.0000
Crabp1	cellular retinoic acid binding protein I	BC065787	-0.311	0.0189
Crnkl1	Crn, crooked neck-like 1 (Drosophila)	NM_025820	-0.243	0.0112
Ctns	cystinosis, nephropathic	NM_031251	-0.251	0.0001
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	XM_897712	-0.216	0.0308
D530005L17Rik	NA	BC027370	-0.207	0.0104
Dhx57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	BC079618	-0.200	0.0000
Dimt1	NA	NM_025447	-0.322	0.0015
Dlec1	NA	AK045848	-0.234	0.0041
Drg1	developmentally regulated GTP binding protein 1	AK090156	-0.204	0.0073
Dsc2	desmocollin 2	AK172168	-0.295	0.0081
Dync2li1	NA	XM_984615	-0.284	0.0008
Dysf	dysferlin	AJ242954	-0.207	0.0001
E030013G06Rik	RIKEN cDNA E030013G06 gene	NM_177697	-0.229	0.0001
E130008D07Rik	NA	AK053296	-0.364	0.0393
E130119H09Rik	RIKEN cDNA E130119H09 gene	XR_004505	-0.279	0.0406
Eea1	early endosome antigen 1	BC021363	-0.201	0.0000
Efcbp1	EF hand calcium binding protein 1	AK005641	-0.227	0.0004
EG627232	NA	XM_891890	-0.217	0.0295
EG635680	NA	AK049064	-0.221	0.0238
Ell2	elongation factor RNA polymerase II 2	AK033541	-0.253	0.0186
Eltd1	EGF, latrophilin seven transmembrane domain containing 1	NM_133222	-0.244	0.0021
Endod1	NA	NM_028013	-0.267	0.0073
Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	NM_007647	-0.254	0.0000
Etf1	eukaryotic translation termination factor 1	AK038771	-0.215	0.0157
Exoc3	NA	NM_177333	-0.201	0.0006
Fancc	Fanconi anemia, complementation group C	L08266	-0.319	0.0034
Fastkd1	NA	NM_177244	-0.326	0.0000
Fbxo25	F-box only protein 25	NM_025785	-0.209	0.0025

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
Fgd4	FYVE, RhoGEF and PH domain containing 4	AK043656	-0.201	0.0000
Fkbp3	FK506 binding protein 3	NM_013902	-0.245	0.0097
Fstl5	follistatin-like 5	NM_178673	-0.259	0.0105
G6pd2	glucose-6-phosphate dehydrogenase 2	NM_008062	-0.200	0.0315
Gab3	growth factor receptor bound protein 2-associated protein 3	XM_903329	-0.440	0.0001
Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	NM_016722	-0.227	0.0006
Galnt6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6	XM_001000202	-0.204	0.0090
Garnl3	GTPase activating RANGAP domain-like 3	AK133163	-0.247	0.0000
Gbp6	NA	AK152380	-0.243	0.0449
Gcc2	NA	AK008992	-0.221	0.0000
Glrb	glycine receptor, beta subunit	NM_010298	-0.235	0.0469
Gmps	guanine monphosphate synthetase	NM_001033300	-0.235	0.0017
Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	NM_010305	-0.284	0.0000
Gpr116	G protein-coupled receptor 116	XM_001003162	-0.293	0.0000
Gramd2	NA	NM_001033498	-0.226	0.0271
Grb10	growth factor receptor bound protein 10	AK169000	-0.212	0.0000
Grm3	glutamate receptor, metabotropic 3	NM_181850	-0.261	0.0007
Gtf2h2	general transcription factor II H, polypeptide 2	BC016231	-0.236	0.0007
Gtpbp8	NA	AK078242	-0.236	0.0015
Guk1	guanylate kinase 1	NM_008193	-0.207	0.0022
Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	AK029861	-0.224	0.0000
Hint3	histidine triad nucleotide binding protein 3	NM_025798	-0.284	0.0409
Hisppd1	NA	AK051955	-0.272	0.0000
Hmgb2l1	high mobility group box 2-like 1	AK014640	-0.204	0.0021
Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	NM_080634	-0.218	0.0000
Hsp90aa1	NA	AK158753	-0.218	0.0001
Ide	insulin degrading enzyme	AK029089	-0.250	0.0020

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Ift81	NA	NM_009879	-0.227	0.0011
Ighv1-77	NA	XM_894825	-0.433	0.0441
Il10rb	interleukin 10 receptor, beta	AK040938	-0.246	0.0246
Il33	NA	AK020353	-0.323	0.0001
Impg2	NA	NM_174876	-0.215	0.0407
Intu	NA	NM_178386	-0.221	0.0317
Itga4	integrin alpha 4	AK037794	-0.234	0.0003
Kcnq4	potassium voltage-gated channel, subfamily Q, member 4	XM_978045	-0.281	0.0034
Kif9	kinesin family member 9	AK029776	-0.216	0.0290
Lgi1	leucine-rich repeat LGI family, member 1	NM_020278	-0.208	0.0052
LOC385336	NA	XM_001002232	-0.675	0.0201
LOC620376	NA	AK045385	-0.277	0.0436
LOC620499	NA	XM_974591	-0.241	0.0496
LOC623241	NA	XR_003922	-0.336	0.0308
LOC670389	NA	XM_916746	-0.284	0.0399
LOC671429	NA	NM_009086	-0.247	0.0073
LOC671598	NA	AK088688	-0.291	0.0365
LOC671909	NA	XM_902375	-0.217	0.0047
LOC675766	NA	XM_994803	-0.229	0.0117
LOC675977	NA	XM_983830	-0.499	0.0299
Lrfn3	leucine rich repeat and fibronectin type III domain containing 3	NM_175478	-0.202	0.0278
Lrrc9	NA	AK031279	-0.248	0.0014
Lta4h	leukotriene A4 hydrolase	AK199829	-0.219	0.0077
Mak	male germ cell-associated kinase	BC050009	-0.280	0.0106
Mast2	microtubule associated serine/threonine kinase 2	NM_008641	-0.202	0.0000
Mctp1	NA	AK054478	-0.223	0.0062
Mmp16	matrix metallopeptidase 16	AK052039	-0.239	0.0034
Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	NM_019579	-0.258	0.0000
Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	AK161013	-0.213	0.0069
Mrpl39	mitochondrial ribosomal protein L39	NM_017404	-0.228	0.0003
Mrpl47	mitochondrial ribosomal protein L47	XM_994072	-0.282	0.0476

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	Gene Name	Entrez ID	Fold Change *Mecp2*-null over WT	FDR-adjusted p-value (*Mecp2*-null over WT)
Mrpl52	mitochondrial ribosomal protein L52	NM_026851	-0.264	0.0354
Msl31	male-specific lethal-3 homolog 1 (Drosophila)	AK053927	-0.202	0.0015
Mtif2	mitochondrial translational initiation factor 2	NM_133767	-0.205	0.0071
N6amt2	NA	NM_026526	-0.248	0.0266
Nadk	NAD kinase	AK186958	-0.218	0.0014
Narg1	NMDA receptor-regulated gene 1	AK172501	-0.200	0.0012
Narg2	NMDA receptor-regulated gene 2	NM_145618	-0.262	0.0094
Ncoa7	nuclear receptor coactivator 7	BC080670	-0.256	0.0000
Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	AK132938	-0.236	0.0131
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	NM_019443	-0.278	0.0414
Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	XM_973975	-0.233	0.0000
Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	NM_011848	-0.238	0.0080
Nit2	nitrilase family, member 2	NM_023175	-0.266	0.0094
Nol8	nucleolar protein 8	BC026402	-0.222	0.0002
Npat	nuclear protein in the AT region	XM_917387	-0.263	0.0001
Npl	N-acetylneuraminate pyruvate lyase	NM_028749	-0.254	0.0357
Npsr1	NA	NM_175678	-0.471	0.0000
Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	AK040377	-0.236	0.0000
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	NM_010941	-0.228	0.0003
Nucb2	nucleobindin 2	NM_016773	-0.308	0.0000
Odz1	odd Oz/ten-m homolog 1 (Drosophila)	AK034286	-0.226	0.0000
Olfr1116	NA	NM_207632	-0.525	0.0154
Otof	otoferlin	NM_031875	-0.332	0.0000
P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	NM_033321	-0.234	0.0449
Pb1	NA	BC055456	-0.202	0.0000
Pdia3	protein disulfide isomerase associated 3	NM_007952	-0.213	0.0016
Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase3	NM_133232	-0.209	0.0000

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Phf10	PHD finger protein 10	NM_024250	-0.265	0.0009
Phkb	phosphorylase kinase beta	AK089493	-0.214	0.0000
Pkn2	protein kinase N2	AK083425	-0.215	0.0000
Pls3	plastin 3 (T-isoform)	NM_145629	-0.238	0.0000
Pnpla7	NA	AK148380	-0.227	0.0000
Pnpt1	polyribonucleotide nucleotidyltransferase 1	XM_975791	-0.228	0.0001
Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	AK163324	-0.208	0.0076
Ppm1m	protein phosphatase 1M	AK046387	-0.208	0.0019
Pqbp1	polyglutamine binding protein 1	NM_019478	-0.226	0.0232
Prdx3	peroxiredoxin 3	NM_007452	-0.222	0.0002
Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	NM_011871	-0.238	0.0180
Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	BC033575	-0.207	0.0033
Psip1	PC4 and SFRS1 interacting protein 1	NM_133948	-0.227	0.0001
Ptpn9	protein tyrosine phosphatase, non-receptor type 9	NM_019651	-0.209	0.0001
Pycr1	pyrroline-5-carboxylate reductase1	NM_144795	-0.238	0.0315
Qdpr	quininoid dihydropteridine reductase	NM_024236	-0.213	0.0000
Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains1	NM_001045513	-0.235	0.0025
Rassf4	Ras association (RalGDS/AF-6) domain family 4	AK160584	-0.221	0.0199
Rbbp8	retinoblastoma binding protein 8	AK163908	-0.265	0.0023
Rec8L1	REC8-like 1 (yeast)	NM_020002	-0.222	0.0006
Ret	ret proto-oncogene	BC059012	-0.277	0.0000
Rgs2	regulator of G-protein signaling 2	NM_009061	-0.304	0.0058
Ric3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	NM_001038624	-0.242	0.0118
Rif1	Rap1 interacting factor 1 homolog (yeast)	XR_003484	-0.255	0.0000
Rnf20	ring finger protein 20	NM_182999	-0.225	0.0000
Rock1	Rho-associated coiled-coil forming kinase 1	BC066873	-0.269	0.0000
Rpgr	retinitis pigmentosa GTPase regulator	AK029864	-0.213	0.0020

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	AK015701	-0.285	0.0000
Rpp30	ribonuclease P/MRP 30 subunit (human)	AK004137	-0.337	0.0229
Rrp12	NA	NM_199447	-0.209	0.0000
Rxfp1	NA	AK137655	-0.257	0.0308
S100pbp	NA	AK043160	-0.237	0.0041
Scg3	secretogranin III	NM_009130	-0.274	0.0000
Sclt1	NA	XM_982400	-0.239	0.0011
Scn3a	sodium channel, voltage-gated, type III, alpha	XM_001001591	-0.293	0.0000
Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	BC005458	-0.207	0.0000
Sgk	serum/glucocorticoid regulated kinase	BC070401	-0.306	0.0006
Sgk2	serum/glucocorticoid regulated kinase 2	AK050009	-0.257	0.0426
Slc25a31	solute carrier family 25 mitochondrial carrier, adenine nucleotide translocator, member31	NM_178386	-0.229	0.0313
Slc39a4	solute carrier family 39 (zinc transporter), member 4	NM_028064	-0.268	0.0234
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	NM_016917	-0.316	0.0007
Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	NM_177909	-0.260	0.0004
Slco1a4	solute carrier organic anion transporter family, member 1a4	NM_030687	-0.308	0.0001
Slco4c1	solute carrier organic anion transporter family, member 4C1	NM_172658	-0.353	0.0372
Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	NM_018817	-0.201	0.0000
Smc6	NA	BC048790	-0.267	0.0000
Sncg	synuclein, gamma	NM_011430	-0.424	0.0046
Snx14	sorting nexin 14	AK213239	-0.230	0.0000
Spag1	sperm associated antigen 1	AK032601	-0.203	0.0112
Spag4	sperm associated antigen 4	AK220494	-0.228	0.0192
St18	suppression of tumorigenicity 18	AK147664	-0.217	0.0177
St6gal2	beta galactoside alpha 2,6 sialyltransferase 2	AK129462	-0.266	0.0097

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	NM_133810	-0.262	0.0232
Stmn2	stathmin-like 2	NM_025285	-0.244	0.0004
Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	NM_033618	-0.227	0.0000
Susd2	sushi domain containing 2	BC066833	-0.201	0.0010
Sytl2	synaptotagmin-like 2	NM_001040087	-0.264	0.0002
Tbc1d19	TBC1 domain family, member 19	AK177065	-0.228	0.0000
Tbc1d8b	NA	XM_907570	-0.282	0.0073
Tdrkh	tudor and KH domain containing protein	BC057030	-0.200	0.0018
Tek	endothelial-specific receptor tyrosine kinase	NM_013690	-0.213	0.0001
Terf1	telomeric repeat binding factor 1	AK036615	-0.224	0.0058
Thnsl2	NA	NM_178413	-0.217	0.0317
Thoc1	THO complex 1	AK042548	-0.255	0.0008
Thoc2	THO complex 2	XM_359343	-0.231	0.0000
Tmem100	NA	NM_026433	-0.484	0.0298
Tmem77	NA	NM_026013	-0.272	0.0002
Tmem87a	NA	NM_147153	-0.221	0.0029
Tmem98	NA	AK148132	-0.245	0.0288
Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	NM_025394	-0.240	0.0133
Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	NM_028109	-0.222	0.0351
Trim62	tripartite motif-containing 62	NM_178110	-0.272	0.0011
Tro	trophinin	NM_001002272	-0.220	0.0010
Trpm6	transient receptor potential cation channel, subfamily M, member 6	XM_987699	-0.325	0.0000
Ttc12	tetratricopeptide repeat domain 12	NM_172770	-0.240	0.0156
Ttc16	tetratricopeptide repeat domain 16	AK089384	-0.215	0.0203
Ube1l2	NA	NM_010323	-0.332	0.0000
Ube2j2	ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	NR_002889	-0.305	0.0136
Ube2r2	ubiquitin-conjugating enzyme E2R 2	XM_001002125	-0.228	0.0037
Ubn1	ubinuclein 1	NM_026666	-0.227	0.0082
Usp1	ubiquitin specific peptdiase 1	XR_002561	-0.358	0.0110
Vit	vitrin	NM_028813	-0.291	0.0081
Wbp4	WW domain binding protein 4	NM_018765	-0.266	0.0003

Table S6. Continued.

Downregulated genes (284):

Gene Symbol	**Gene Name**	**Entrez ID**	**Fold Change *Mecp2*-null over WT**	**FDR-adjusted p-value (*Mecp2*-null over WT)**
Wdr31	WD repeat domain 31	NM_023597	-0.238	0.0271
Wif1	Wnt inhibitory factor 1	NM_011915	-0.296	0.0038
Wwp1	WW domain containing E3 ubiquitin protein ligase 1	NM_177327	-0.276	0.0043
Xdh	xanthine dehydrogenase	AK164764	-0.211	0.0061
Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	NM_009533	-0.316	0.0000
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	NM_010247	-0.227	0.0036
Yipf4	Yip1 domain family, member 4	AK086213	-0.204	0.0053
Zfp108	zinc finger protein 108	NM_018791	-0.237	0.0335
Zfp28	zinc finger protein 28	NM_175247	-0.235	0.0432
Zfp291	zinc finger protein 291	XM_620753	-0.237	0.0000
Zfp426	zinc finger protein 426	AK036912	-0.258	0.0015
Zfp694	NA	XM_982941	-0.217	0.0256
Zranb3	zinc finger, RAN-binding domain containing 3	BC117922	-0.236	0.0014
Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	BC067405	-0.209	0.0016

Table S7. Expression of 66 genes was confirmed by quantitative real-time RT-PCR ($p < 0.05$). Fold change values from the microarray experiment are also included.

***MECP2*-Tg**			***Mecp2*-null**			**Fold change values observed in the microarray experiment**	
Gene	**Fold Change over WT**	**p-value**	**Gene**	**Fold Change over WT**	**p-value**	**Fold Change *MECP2*-Tg / WT**	**Fold Change *Mecp2*-null / WT**
Gpr165	7.35	0.0000	Gpr165	-3.55	0.0000	0.211	-0.539
Npbwr1	4.61	0.0100	Npbwr1	-3.11	0.0000	0.939	-0.565
Agrp	3.76	0.0006	Agrp	-1.40	0.0076	0.866	-0.289
Trrap	3.47	0.0084	Trrap	-1.62	0.0002	0.110	-0.024
AW551984	3.29	0.0029	AW551984	-2.39	0.0000	0.726	-0.976
Htr1a	3.21	0.0065	Htr1a	-2.55	0.0000	0.753	-0.598
Crh	3.21	0.0001	Crh	-2.06	0.0002	1.020	-0.521
Gpr56	3.16	0.0005	Gpr56	-1.33	0.0218	0.459	-0.235
Pgr15l	2.83	0.0280	Pgr15l	-3.35	0.0000	0.815	-0.638
Gpr17	2.71	0.0029	Gpr17	-1.51	0.0012	0.591	-0.166
Hcrtr1	2.70	0.0000	Hcrtr1	-3.07	0.0000	0.694	-0.918
Gpr153	2.60	0.0127	Gpr153	-1.74	0.0000	0.499	-0.354
Gprin1	2.59	0.0009	Gprin1	-1.45	0.0010	0.533	-0.063
Htr2a	2.53	0.0209	Htr2a	-1.44	0.0001	0.326	-0.236
Oprk1	2.51	0.0000	Oprk1	-2.46	0.0000	0.884	-0.903
C1ql4	2.51	0.0010	C1ql4	-1.65	0.0010	0.644	-0.442
Nts	2.45	0.0439	Nts	-1.83	0.0001	0.990	-0.677
Creb1	2.39	0.0055	Creb1	-1.90	0.0000	0.262	-0.180
Oxtr	2.38	0.0014	Oxtr	-1.37	0.0072	0.257	-0.111
Ldoc1	2.36	0.0000	Ldoc1	-4.21	0.0000	1.025	-1.156
Gabrq	2.35	0.0152	Gabrq	-1.34	0.0110	0.283	-0.229
Nisch	2.26	0.0336	Nisch	-1.84	0.0001	0.120	-0.065
Gprk5	2.22	0.0413	Gprk5	-1.37	0.0008	0.515	-0.417
Gabra3	2.18	0.0203	Gabra3	-1.42	0.0006	0.318	-0.357
Gamt	2.13	0.0261	Gamt	-1.71	0.0000	0.867	-0.493
Gps1	2.11	0.0270	Gps1	-1.24	0.0083	0.275	-0.066
Adcyap1	2.10	0.0000	Adcyap1	-1.95	0.0001	0.875	-0.724
Gad2	2.07	0.0400	Gad2	-1.59	0.0147	0.181	-0.507
Htr1d	1.94	0.0145	Htr1d	-1.23	0.0280	0.252	-0.277
Sst	1.86	0.0000	Sst	-1.66	0.0001	0.668	-0.501
Fabp7	1.79	0.0000	Fabp7	-1.46	0.0011	1.112	-0.529
Gpr126	1.65	0.0435	Gpr126	-1.21	0.0359	0.203	-0.391
Hcrtr2	1.64	0.0010	Hcrtr2	-1.51	0.0003	0.424	-0.471

Table S7. Continued.

MECP2-Tg			*Mecp2*-null			Fold change values observed in the microarray experiment	
Gene	**Fold Change over WT**	**p-value**	**Gene**	**Fold Change over WT**	**p-value**	**Fold Change *MECP2*-Tg / WT**	**Fold Change *Mecp2*-null / WT**
Rhbdl3	1.63	0.0001	Rhbdl3	-1.57	0.0012	0.564	-0.388
Fxyd7	1.63	0.0009	Fxyd7	-1.96	0.0000	1.071	-0.798
Npy	1.58	0.0017	Npy	-1.23	0.0343	0.576	-0.184
Arhgdig	1.47	0.0009	Arhgdig	-1.95	0.0000	0.636	-0.546
Snx26	1.46	0.0238	Snx26	-1.69	0.0056	0.547	-0.376
Brunol6	1.45	0.0000	Brunol6	-1.29	0.0025	0.496	-0.286
E2f1	1.44	0.0002	E2f1	-1.55	0.0001	0.162	-0.373
Npas1	1.42	0.0063	Npas1	-1.61	0.0001	0.473	-0.417
Arg2	1.41	0.0160	Arg2	-1.31	0.0033	0.622	-0.339
Bdnf	1.39	0.0392	Bdnf	-1.83	0.0000	0.771	-0.491
Ar	1.36	0.0004	Ar	-1.43	0.0010	0.208	-0.249
Hes5	1.34	0.0489	Hes5	-1.89	0.0001	0.308	-0.333
Taf6l	1.29	0.0024	Taf6l	-1.30	0.0024	0.572	-0.235
Ppargc1a	-1.19	0.0402	Ppargc1a	1.40	0.0000	-0.401	0.163
A2bp1	-1.25	0.0052	A2bp1	1.24	0.0004	-0.225	0.289
Pou6f2	-1.29	0.0092	Pou6f2	1.40	0.0000	-0.375	0.337
Satb1	-1.29	0.0004	Satb1	1.29	0.0000	-0.375	0.270
Prox1	-1.34	0.0118	Prox1	1.28	0.0006	-0.280	0.142
Crim1	-1.34	0.0010	Crim1	1.58	0.0001	-0.225	0.272
Kcnh1	-1.35	0.0007	Kcnh1	1.29	0.0132	-0.381	0.344
Tspan5	-1.42	0.0006	Tspan5	1.37	0.0000	-0.309	0.295
Chst8	-1.46	0.0000	Chst8	1.48	0.0065	-0.290	0.220
Rasgef1b	-1.48	0.0000	Rasgef1b	1.37	0.0000	-0.367	0.338
Pde7b	-1.50	0.0000	Pde7b	1.28	0.0001	-0.358	0.292
Odz3	-1.50	0.0001	Odz3	1.47	0.0002	-0.599	0.372
Sema5a	-1.52	0.0005	Sema5a	1.49	0.0051	-0.401	0.468
Il1rap	-1.54	0.0001	Il1rap	1.20	0.0056	-0.464	0.221
Tiam1	-1.74	0.0000	Tiam1	1.50	0.0108	-0.425	0.288
Grin2a	-1.88	0.0000	Grin2a	1.47	0.0000	-0.469	0.581
Mef2c	-1.90	0.0000	Mef2c	1.68	0.0000	-0.543	0.433
C630007B19Rik	-1.90	0.0000	C630007B19Rik	1.26	0.0072	-0.473	0.564
Rreb1	-2.22	0.0000	Rreb1	1.81	0.0000	-0.666	0.685
Itpr1	-2.35	0.0109	Itpr1	1.48	0.0032	-0.600	0.429

Table S8. MeCP2-interacting proteins identified by co-immunopurification from WT brain extracts, but not *Mecp2*-null brain extracts.

Protein	Accession number
Creb1	NP_598589
H2A histone family, member Y	NP_036145
Histone cluster 1, H2bb	NP_783595
Lamin A isoform C2	NP_062263
Lens epithelium-derived growth factor	NP_598709
Regulator of chromosome condensation 1	NP_598639
Synaptopodin isoform A	NP_796314
Transcription factor A, mitochondrial	NP_033386
Transcriptional activator protein Pur-alpha	P42669

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