

## Hamilton Eye Institute Mouse Eye M430v2 Data Set (Sept08) RMA

Accession number: [GN207](#)

### Summary:

**FINAL RECOMMENDED EYE DATA SET.** The HEIMED September 2008 RMA data release provides estimates of gene expression in whole eyes of 103 lines of young adult mice generated using 221 Affymetrix M430 2.0 arrays. This data set is intended for exploration of the genetics and genomics of the mouse eye, retina, lens, retinal pigment epithelium, cornea, iris and choroid. Data were generated at UTHSC with support from a grant from Dr. Barrett Haik, Director of the Hamilton Eye Institute ([HEI](#)). We used pooled RNA samples, usually two independent pools--one male, one female pool--for most lines of mice. This data set was processed using the [RMA](#) protocol. A total of 2223 probes sets are associated with LRS values greater than 46 (LOD >10).

Users of these mouse eye data may also find the following complementary resources extremely useful:

1. [NEIBank](#) collection of ESTs and SAGE data.
2. [RetNet](#): the Retinal Information Network--tables of genes and loci causing inherited retinal diseases
3. [Mouse Retina SAGE Library](#) from the Cepko laboratory. This site provides extensive developmental data from as early as embryonic day E12.5.
4. [Digital reference of ophthalmology](#) from Columbia provides high quality photographs of human ocular diseases, case studies, and short explanations. This reference does not have a molecular focus.
5. [Mouse Retinal Developmental Gene Expression](#) data sets from the Friedlander laboratory. This site provides extensive developmental data using the Affymetrix U74 v 2 array (predecessor of the M430).
6. [Data sets on differential gene expression in anatomical compartments of the human eye](#) from Pat Brown's lab. View expression signatures for different ocular tissues using the **geneXplorer 2.0**.

### About the cases used to generate this set of data:

This is the complete and final HEIMED data set. HEIMED consists of expression data for 103 genetically defined lines of mice with standard errors of the mean. Almost all animals are young adults between 50 and 80 days of age (Table 1, maximum age is 123 days). We

measured expression in conventional inbred strains, BXD recombinant inbred (RI) strains, reciprocal F1s between C57BL/6J and DBA/2J, and several mutant and knockout lines. We have combined all common strains, F1 hybrids, and mutants into a group called the Mouse Diversity Panel (MDP). Four lines, namely, C57BL/6J (B6), DBA/2J (D2), and the pair of B6D2F1 and D2B6F1 hybrids are common to both the MDP and the BXD set. This is a breakdown of cases that are part of HEIMED:

1. 68 BXD strains. The first 32 of these strains are from the Taylor series of BXD strains generated at the Jackson Laboratory by Benjamin A. Taylor. BXD1 through BXD32 were started in the late 1970s, whereas BXD33 through 42 were started in the 1990s. Only one of these strains, BXD24 (now also known as BXD24b), has retinal degeneration (a spontaneous mutation). The other 36 BXD strains (BXD43 and higher) were bred by Lu Lu, Jeremy Peirce, Lee M. Silver, and Robert W. Williams starting in 1997 using B6D2 generation 10 advanced intercross progeny. This modified breeding protocol doubles the number of recombinations per BXD strain and improves mapping resolution (Peirce et al. 2004). All of the Taylor series of BXD strains and many of the new BXD strains are available from the Jackson Laboratory. All of the new BXD strains (BXD43 and higher) are also available directly from Lu Lu and colleagues at the University of Tennessee Health Science Center in Memphis, TN, USA.
2. 35 MDP lines, including 26 inbred strains representing closely related substrains (e.g., BALB/cJ and BALB/cByJ), many of the most widely used common *Mus musculus domesticus* inbred strains (e.g., C57BL/6J and 129S1/SvImJ), inbred but wild-derived representatives of common subspecies (*Mus musculus domesticus*, e.g., WSB/EiJ; *M. musculus musculus*, e.g., CZECHII/EiJ; *M. musculus molossinus*, e.g., MOLF/EiJ; *M. musculus castaneus*, e.g., CAST/EiJ); and even one different species of mouse (*Mus spicilegus*, PANCEVO/EiJ). The MDP also includes the reciprocal F1 hybrids (B6D2F1 and D2B6F1) and the following 6 KO lines and the *Nyx-nob* mutant:
3. 6 knockouts (KO), including a KO of *Rpe65*, and 5 DeltaGen Inc. knockout lines provided by Dr. Ted Choi. These KO lines have had a bacterial lacZ construct inserted into the gene. The endogenous promoter drives expression of beta-galactosidase. RT-PCR analysis detects a gene transcript in most tissues. The following KOs from DeltaGen were studied: *Gabra1*, *Gabbr1*, *Gnb1*, *Gpr19*, and *Clcn3*. We also included one spontaneous mutant of the *nyctalopin* (*Nyx no b wave "nob"*) gene (Pardue et al., 1998) that is on a BALB/cByJ background.

**Rod photoreceptor degeneration in inbred mice:** Six strains of mice included in HEIMED suffer from severe loss of photoreceptors (mainly rods) and have the equivalent of night blindness in human patients. The death of photoreceptors in these strains occurs by one to two months of age and is often caused by the *retinal degeneration 1 (rd1)* mutant allele in the rod cyclic-GMP phosphodiesterase 6 beta subunit gene (*Pde6b*). The following strains are known to have photoreceptor degeneration: C3H/HeJ, FVB/NJ, MOLF/EiJ, SJL/J and BXD24/TyJ. BXD24/TyJ is now known as BXD24b/TyJ and has nearly complete retinal degeneration. BXD24a/TyJ, a 1988 F80 inbred stock that has been rederived from cryogenic storage, does not have retinal degeneration (stock number 005243) and is an ideal coisogenic control, but is not included in the HEIMED data set.

As expected (Dickerson LW et al., 2002) and as judged from the absence of rhodopsin expression, one of the DeltaGen KO lines (chloride ion channel 3, *Clcn3*) also has retinal degeneration: B6129P2F2N1-Clcn3. Degeneration in this strain is likely to include all rods

and all cones. The cone defect is obvious from the decrease in expression of *Gnat2*, a gene associated with cones and achromatopsia in mice and humans.

Lines of mice were selected using the following criteria:

- genetic and phenotypic diversity, including use by the [Phenome Project](#)
- representation of a fairly wide variety of different subspecies of *Mus*
- their use in making genetic reference populations including recombinant inbred strains, cosomic strains, congenic and recombinant congenic strains
- their use by the [Complex Trait Consortium](#) to make the Collaborative Cross (Tel Aviv/Wellcome, Oak Ridge/DOE, and Perth/UWA)
- genome sequence data from three sources (NHGRI, Celera, and Perlegen-NIEHS)
- interesting mutations or knockouts affecting genes with high expression in the eye
- general availability from The Jackson Laboratory. The only exception are the DeltaGen KO mice.

We have included all eight parents of the Collaborative Cross (129S1/SvImJ, A/J, C57BL/6J, CAST/EiJ, NOD/LtJ, NZO/HILtJ, PWK/PhJ, and WSB/EiJ) in the MDP. Fourteen MDP strains have been partially sequenced by Perlegen for the NIEHS, including including 129S1/SvImJ, A/J, AKR/J, BALB/cByJ, C3H/HeJ, CAST/EiJ, DBA/2J, FVB/NJ, KK/HIJ, MOLF/EiJ, NOD/LtJ, NZW/LacJ, PWD/PhJ, and WSB/EiJ (see the GeneNetwork SNP Browser for data, details, and see [Perlegen's excellent data resources and browser](#)).

1. [129S1/SvImJ](#) : Collaborative Cross strain sequenced by NIEHS; background for many knockouts (R1 ES cell line); Phenome Project A list. This strain (JAX No 002448, aka 129S1/Sv-++Kitl/+) carries hypopigmentation mutations (white bellied chinchilla) of the tyrosinase gene on Chr 7 and a mutant allele of the steel (*Kitl*) gene. It is also a *cone photoreceptor function loss 3* mutant (*Cpfl3* allele) of the *Gnat2* gene that is a model for achromatopsia (JAX Stock Number: [002448](#))
2. [A/J](#): Collaborative Cross strain sequenced by Perlegen/NIEHS; parent of the AXB/BXA panel. A tyrosinase (*Tyr c* allele) albino mutant. This strain is particularly sensitive to light-induced photoreceptor loss (Danciger et al., 2007). (JAX Stock Number: [000646](#))
3. [BALB/cByJ](#): Sequenced by NIEHS; maternal parent of the CXB panel; Phenome Project old group A list. A tyrosinase (*Tyr c* allele) albino mutant and also a tyrosinase related protein 1 (*Tyrp1 b*) brown allele mutant. Small brain, not aggressive (JAX Stock Number: [001026](#))
4. [BALB/cJ](#): Phenome Project A list. A tyrosinase (*Tyr c* allele) albino mutant and also a tyrosinase related protein 1 (*Tyrp1 b*) brown allele mutant. Large brain and aggressive (JAX Stock Number: [000651](#))
5. [BXSJ/MpJ](#): A white-bellied agouti strains with interesting autoimmune disease restricted to males that is associated with a mutation in the *Yaa* gene that causes glomerulonephritis, a dramatic increase in number of peripheral monocytes, and pre-B-cell deficiency (JAX Stock Number: [000740](#))
6. [C3H/HeJ](#): The Heston (He) substrain with a wildtype agouti (A allele) coat color. Sequenced by Perlegen/NIEHS; paternal parent of the BXH panel; Phenome Project old group A list. Important to note for this eye expression dataset, C3H/HeJ is a *Pdeb6 rd1* mutant with near total photoreceptor loss at as early as postnatal day 30. Also a *Tlr4* mutant that is

- endotoxin resistant. (JAX Stock Number: [000659](#))
7. [C57BL/6J](#): Sequenced by NIH/NHGRI; parental strain of AXB/BXA, BXD, and BXH; Phenome Project A list. Single most widely used inbred strain of mouse. (JAX Stock Number: [000664](#))
  8. [C57BLKS/J](#): Black Kaliss strain (non-agouti a allele) derived from C57BL/6J, but genetically contaminated at some point mainly with DBA/2J and then rebred. Now at the Jackson Laboratory. (JAX Stock Number: [000662](#))
  9. [CAST/EiJ](#): A wild-derived inbred *Mus musculus castaneus* strain. Samples of this subspecies were captured in Southeast Asia. One of three wild-derived strains in the Collaborative Cross sequenced by NIEHS; Phenome Project A list. CAST/Ei and CAST/EiJ are the same strain. The addition of the "J" is trivial and was added when stock were transferred from Dr. Eicher's lab to the Jackson Laboratory production facility in about 2004. (JAX Stock Number: [000928](#))
  10. [CBA/CaJ](#): Agouti strain from the Jackson Laboratory. Wildtype pigment genes. (JAX Stock Number: [000654](#))
  11. [CZECHII/EiJ](#): Czech 2 is a wild-derived inbred strain *M. musculus musculus* strain. Samples of this subspecies were caught in the Czech Republic and inbred at the Jackson Laboratory by Eva Eicher. White-bellied agouti. (JAX Stock Number: [001144](#)).
  12. [DBA/2J](#): The dilute, brown, agouti (dba) strain is the oldest inbred strain of mouse. Inbreeding was started in 1909 by Little. A tyrosinase related protein 1 (*Tyrp1 b*) brown allele mutant. A myosin 5a (*Myo5a d*) dilute allele mutant. Sequenced by Perlegen/NIEHS and Celera; paternal parent of the BXD panel; Phenome Project old A group list. (JAX Stock Number: [000671](#))
  13. [FVB/NJ](#): Friend's leukemia virus B (FVB) strain. Sequenced by Perlegen/NIEHS and Celera. *Tyr c* locus albino and a *Pdeb6 rd1* mutant derived from Swiss mice at NIH. This has been the most common strain used to make transgenic mice due to large and easily injected oocytes; Phenome Project A list (JAX Stock Number: [001800](#)).
  14. [KK/HIJ](#): K Kondo's (KK) Kasukabe strain is a homozygous age-related hearing loss (*ahl*) allele mutant of the *Cdh23* gene. A *Tyr c* locus albino strain. Males have a form of type 2 diabetes. Sequenced by Perlegen/NIEHS. (JAX Stock Number: [002106](#))
  15. [LG/J](#): Large (LG) strain. Paternal parent of the Large-by-Small set of RI strains made by James Cheverud and colleagues (the LGXSM panel, not to be confused with the LongXShort or LXS panel). A *Tyr c* locus albino strain. (JAX Stock Number: [000675](#))
  16. [LP/J](#): White-bellied agouti strain with a piebald mutation in the endothelin receptor type B *Ednrb* gene from at the Jackson Laboratory. Some reduction in melanocytes in choroid of eye due to neural crest migration abnormalities. (JAX Stock Number: [000676](#))
  17. [MOLF/EiJ](#): A wild-derived inbred strain derived from *M. musculus molossinus* samples computered in Fukuoka, Japan. This strain has the retinal degeneration *rd1* allele in *Pde6b*. There appears to have been some genetic contamination of this strain with conventional inbred strains in the past several decades (F. Pardo, personal communication to RWW, August 2006). However, the strain is currently fully inbred. (JAX Stock Number: [000550](#))
  18. [NOD/LtJ](#): Non-obese diabetic strain, originally from M. Hattori in Kyoto, Japan. This is the Edward Leiter (Lt) substrain from the Jackson Laboratory. Collaborative Cross strain sequenced by NIEHS; Phenome Project B list. Homozygous age-related hearing loss (*ahl*) allele mutant of the *Cdh23* gene. A *Tyr c* locus albino strain. (JAX Stock Number: [001976](#))
  19. [NZO/HILtJ](#): New Zealand Obese strain. This is a severely obese and hypertensive strain. Males often develop a type 2 diabetes. Collaborative Cross strain. Agouti coat color. (JAX Stock

Number: [002105](#))

20. **NZB/BINJ**: New Zealand Black inbred strain from Bielschowsky (BL, substrain is "B lowercase L N", not "BiN") now maintained at the Jackson Laboratory. (JAX Stock Number: [000648](#))
21. **NZW/LacJ**: New Zealand White strain from the Laboratory Animal Center (Carshalton, UK), now maintained at the Jackson Laboratory. Carries the *Tyr* c locus albino mutation, the pink-eye dilution mutation in the *Oca2* or p locus, and the brown allele at *Tyrp1*. (JAX Stock Number: [001058](#))
22. **PANCEVO/EIJ**: PANCEVO/EIJ is a wild-derived inbred strain from the *Mus spicilegus* samples caught in the Pancevo, Serbia. This species of mouse is also known as the Steppe mouse (taxon identifier [10103](#)). *M. spicilegus* is a colonial [mound-building species](#). No known ocular or retina mutations, but the expression level of *Gnat2* is low in this strain, either due to a 3' UTR length variant or possible achromatosis (cone degeneration) (JAX Stock Number: [001384](#))
23. **PWD/PhJ**: A wild-derived *Mus musculus musculus* agouti strain inbred from samples caught near Prague, Czech Republic. Sequenced by Perlegen/NIEHS; parental strain for a consomic set by Forjet and colleagues. (JAX Stock Number: [004660](#))
24. **PWK/PhJ**: A wild-derived *Mus musculus musculus* inbred strain from samples caught near Lhotka, Czech Republic. Collaborative Cross strain; Phenome Project D list. (JAX Stock Number: [003715](#))
25. **SJL/J**: Swiss Webster inbred strain from Jim Lambert's lab at the Jackson Laboratory. This strain has the retinal degeneration *rd1* allele in *Pde6b*. It also carries both the *Tyr* c albino mutation and the pink-eye dilution mutation in the *Oca2* or p locus. Highly aggressive males. (JAX Stock Number: [000686](#))
26. **WSB/EIJ**: Watkin Star line B (or "wild son-of-a-bitch") is a wild-derived *Mus musculus domesticus* inbred strain from samples caught in Maryland, USA. A Collaborative Cross strain sequenced by NIEHS; Phenome Project C list (JAX Stock Number: [001145](#))
27. B6D2F1 and D2B6F1 (also listed as BDF1 and DBF1 in some graphs and tables): F1 hybrids generated by crossing C57BL/6J with DBA/2J. These black reciprocal F1 can be used to detect dominance effects. Comparison of the two reciprocal F1s can be used to detect parental origin (imprinting) effects. The D2B6F1 animals are currently available from the Jackson Laboratory as a special order.) (JAX Stock Number for B6D2F1 hybrids obtained from the Jackson Laboratory, aka B6D2F1/J [100006](#))

Most of the common inbred strains harbor mutations in genes that control pigmentation (Silvers, [2008](#) and material above in this INFO file). These genes include the albino and chinchilla alleles of the tyrosinase gene (*Tyr*, or human *OCA1*), the brown allele of the tyrosinase related protein 1 (*Tyrp1*), the pink-eye dilution allele of *Oca2* (probe set 1418211), the non-agouti (black) and white-bellied alleles of the agouti signaling protein *Asip*, the steel allele of *Kitlg*, the dilute allele of *Myo5a* (probe set 1419754), and the piebald allele of *Ednrb*. In some of these cases, effects of the mutation are easily detected at the transcript level (*Tyrp1*, *Oca2*, and *Myo5a*), but in the other cases (*Tyr*, *Asip*, *Ednrb*, and *Kitlg*), mutations do not leave a strong imprint on expression.

#### About the tissue used to generate this set of data:

**Tissue preparation protocol.** Animal were killed by rapid cervical dislocation. Eyes were

removed immediately and placed in RNA $\textit{later}$  at room temperature. Usually six eyes from animals with a common sex, age, and strain were stored in a single tube.

Each array was hybridized with a pool of cRNA from 4 to 8 eyes from 2 to 4 animals. RNA was extracted at UTHSC by Zhiping Jia. If tissue was saved for RNA extraction at a later time, eyes were placed directly in RNA $\textit{later}$  (Ambion, Inc.) and treated per the manufacturer's directions. If eyes were used for immediate RNA extraction then we proceeded immediately to the next steps.

#### Dissecting and preparing eyes for RNA extraction

1. Place eyes for RNA extraction in RNA STAT-60 (Tel-Test Inc.) and process per manufacturer's instructions (in brief form below).
2. Store RNA in 75% ethanol at  $-80$  deg. C until use.

Total RNA was extracted with RNA STAT-60 (Tel-Test Inc.) according to the manufacturer's instructions. Briefly we:

1. homogenize tissue samples in the RNA STAT-60 (1 ml/50 to 100 mg tissue)
2. allowed the homogenate to stand for 5 min at room temperature
3. added 0.2 ml of chloroform per 1 ml RNA STAT-60
4. shook the sample vigorously for 15 sec and let the sample sit at room temperature for 3 min
5. centrifuged at 12,000 G for 15 min
6. transferred the aqueous phase to a fresh tube
7. added 0.5 ml of isopropanol per 1 ml RNA STAT-60
8. vortexed and allowed sample to stand at room temperature for 5-10 min
9. centrifuged at 12,000 G for 10-15 min
10. removed the supernatant and washed the RNA pellet with 75% ethanol
11. stored the pellet in 75% ethanol at  $-80$  deg C until use

**Sample Processing.** All samples were processed in the VA Medical Center, Memphis, Rheumatology Disease Research Core Center led by Dr. Weikuan Gu. All arrays were processed by Dr. Yan Jiao. In brief, samples were purified using a standard sodium acetate in alcohol method (recommended by Affymetrix). The RNA quality was checked using a 1% agarose gel. The 18S and 28S bands had to be clear and the 28S band had to be more prominent. RNA concentration was measured using a spectrophotometer. The 260/280 ratios had to be greater than 1.7, and the majority were 1.8 or higher. We used a total of 8 micrograms of RNA as starting amount for cDNA synthesis using a standard Eberwine T7 polymerase method (Superscript II RT, Invitrogen Inc., Affy Part No 900431, GeneChip Expression 3' Amplification One-Cycle cDNA Synthesis Kit). The Affymetrix IVT labeling kit (Affy 900449) was used to generate labeled cRNA. At this point the cRNA was evaluated again using both the 260/280 ratio (values of 2.0 or above were acceptable) and 1% agarose gel inspection of the product (a size range from 200 to 7000 bp is considered suitable for use). We used 45 micrograms of labeled cRNA for fragmentation. Those samples that passed both QC steps (<10% usually fail) were then sheared using a fragmentation buffer included in the Affymetrix GeneChip Sample Cleanup Module (Part No.900371). After fragmentation, samples were either stored at  $-80$  deg. C until use (roughly one third) or were used immediately

for hybridization.

**Dealing with ocular pigmentation:** Variable ocular pigmentation is a potential confound in a study of the whole eye transcriptome. Even the most careful RNA preparations taken from brown and beige colored mice tend to have faint residual pigmentation that affects hybridization signal. To address this problem, Dr. Yan Jiao purified total RNA using the Qiagen RNeasy MinElute Cleanup Kit (Cat No. 74204) all four batches.

**Replication, sex, and sample balance:** Our goal was to obtain data for independent biological sample pools from both sexes for most lines of mice. The four batches of arrays included in this final data set, collectively represent a reasonably well balanced sample of males and females, in general without within-strain-by-sex replication. Two strains are represented by a single male sample pool (BXD29 and A/J). Four lines are represented by two or three male sample pools (all of the five DeltaGen KO line). The SJL/J may be a single mixed sex sample. Users can study possible sex effects by comparing any results of expression data to that of a surrogate measurement that summarizes the overall sex balance of HEIMED. To do this just compare your data to those of probe sets 1427262\_at (*Xist*, high in females) and probe set 1426438\_at (*Ddx3y*, high in males). These two sex-specific probes are quantitative surrogates for the sex balance in this data set.

**Technical duplicates:** One sample, highlighted in the tables below, is a technical duplicate. The pair of technical duplicates were both of high quality. For statistical analysis, they should be combined and treated as single biological sample.

**Batch structure:** This data set consists of four batches (Table 2, far right column). The final September 2008 data set consists of a total of 221 arrays and 220 independent samples.

1. Batch 1: November 2005, n = 78 arrays original arrays of which 76 were accepted into this final data set.
2. Batch 2: January 2006, n = 62 arrays of which 62 were accepted.
3. Batch 3: August 2006, n = 39 arrays of which 36 were accepted. (These three batches, including some arrays that were eventually dropped from the final 2008 data set, were combined to form the September 2006 data set.)
4. Batch 4: Summer 2008, n = 53 arrays of which 47 were accepted.

**Table 1: HEIMED case IDs, including sample tube ID, strain, age, sex, and source of mice** (see [Table 2](#) for information on array quality control)

Index	TubeID	Group	Strain	Age	Sex	Source
1	R2595E.1	GDP	129S1/SvlmJ	59	F	UTHSC RW
2	R2533E.1	GDP	129S1/SvlmJ	60	M	UTHSC RW
3	R0754E.1	GDP	A/J	60	M	JAX
4	R4521E	KO	B6129P2F2N1-Cln3	69	M	TChoi_Deltagen
5	R4522E	KO	B6129P2F2N1-Cln3	69	M	TChoi_Deltagen
6	R4523E	KO	B6129P2F2N1-Cln3	67	M	TChoi_Deltagen
7	R4526E	KO	B6129P2F2N1-Gabbr1	16	F	TChoi_Deltagen
8	R4509E	KO	B6129P2F2N1-Gabbr1	16	M	TChoi_Deltagen
9	R4510E	KO	B6129P2F2N1-Gabbr1	19	M	TChoi_Deltagen
10	R4511E	KO	B6129P2F2N1-Gabbr1	20	M	TChoi_Deltagen
11	R4524E	KO	B6129P2F2N1-Gabbr1	19	M	TChoi_Deltagen
12	R4525E	KO	B6129P2F2N1-Gabbr1	22	M	TChoi_Deltagen
13	R4515E	KO	B6129P2F2N1-Gabra1	67	M	TChoi_Deltagen
14	R4516E	KO	B6129P2F2N1-Gabra1	69	M	TChoi_Deltagen
15	R4517E	KO	B6129P2F2N1-Gabra1	67	M	TChoi_Deltagen
16	R4512E	KO	B6129P2F2N1-Gnb5	22	F	TChoi_Deltagen
17	R4513E	KO	B6129P2F2N1-Gnb5	25	M	TChoi_Deltagen
18	R4514E	KO	B6129P2F2N1-Gnb5	22	M	TChoi_Deltagen
19	R4518E	KO	B6129P2F2N1-Gpr19	70	M	TChoi_Deltagen
20	R4519E	KO	B6129P2F2N1-Gpr19	68	M	TChoi_Deltagen
21	R2601E.1	GDP BXD	B6D2F1	73	F	UTHSC RW
22	R2602E.1	GDP BXD	B6D2F1	73	M	UTHSC RW
23	R1676E.1	GDP	BALB/cByJ	83	F	JAX
24	R1672E.1	GDP	BALB/cByJ	83	M	JAX
25	R4530E	GDP	BALB/cJ	66	F	JAX
26	R4529E	GDP	BALB/cJ	66	M	JAX
27	R2704E.2	BXD	BXD1	59	F	UTHSC RW

28	R2707E.3	BXD	BXD1	59	M	BIDMC GR
29	R1231E.2	BXD	BXD2	64	F	UTHSC RW
30	R2598E.1	BXD	BXD2	61	M	UTHSC RW
31	R2591E.1	BXD	BXD5	60	F	BIDMC GR
32	R2714E.2	BXD	BXD5	58	M	UTHSC RW
33	R2570E.1	BXD	BXD6	65	F	UTHSC RW
34	R2694E.2	BXD	BXD6	58	M	UTHSC RW
35	R2538E.1	BXD	BXD8	77	F	UTHSC RW
36	R2709E.2	BXD	BXD8	61	M	UTHSC RW
37	R2708E.2	BXD	BXD9	60	F	UTHSC RW
38	R2569E.1	BXD	BXD9	67	M	UTHSC RW
39	R2581E.1	BXD	BXD11	65	F	UTHSC RW
40	R2612E.2	BXD	BXD11	70	M	UTHSC RW
41	R2742E.2	BXD	BXD12	71	F	UTHSC RW
42	R2543E.1	BXD	BXD12	63	M	UTHSC RW
43	R2586E.1	BXD	BXD13	60	F	BIDMC GR
44	R877E.2	BXD	BXD13	76	M	UTHSC RW
45	R2557E.1	BXD	BXD14	60	F	BIDMC GR
46	R1128E.2	BXD	BXD14	65	M	UTHSC RW
47	R2701E.3	BXD	BXD15	60	F	BIDMC GR
48	R2716E.2	BXD	BXD15	60	M	UTHSC RW
49	R2711E.2	BXD	BXD16	61	F	UTHSC RW
50	R2567E.1	BXD	BXD16	60	M	BIDMC GR
51	R2720E.2	BXD	BXD18	59	F	UTHSC RW
52	R2559E.1	BXD	BXD18	59	M	BIDMC GR
53	R2560E.1	BXD	BXD19	60	F	BIDMC GR
54	R2713E.2	BXD	BXD19	60	M	UTHSC RW
55	R2584E.1	BXD	BXD20	59	F	BIDMC GR

56	R2731E.2	BXD	BXD20	60	M	UTHSC RW
57	R2702E.2	BXD	BXD21	59	F	UTHSC RW
58	R2541E2.1	BXD	BXD21	61	M	UTHSC RW
59	R2553E.1	BXD	BXD22	58	F	BIDMC GR
60	R2700E.2	BXD	BXD22	59	M	UTHSC RW
61	R2558E-2.1	BXD	BXD23	60	F	BIDMC GR
62	R1086E.2	BXD	BXD23	55	M	UTHSC RW
63	R2719E.2	BXD	BXD24	123	F	UTHSC RW
64	R2589E2.1	BXD	BXD24	59	M	BIDMC GR
65	R2573E-2.1	BXD	BXD25	67	F	UAB
66	R2683E.2	BXD	BXD25	58	M	UTHSC RW
67	R2703E.2	BXD	BXD27	60	F	UTHSC RW
68	R2729E.3	BXD	BXD27	68	M	UTHSC RW
69	R2562E.3	BXD	BXD28	60	F	BIDMC GR
70	R2721E.2	BXD	BXD28	60	M	UTHSC RW
71	R2561E.3	BXD	BXD29	60	M	BIDMC GR
72	R1258E.2	BXD	BXD31	57	F	UTHSC RW
73	R2597E.1	BXD	BXD31	61	M	BIDMC GR
74	R2563E.1	BXD	BXD32	63	F	UTHSC RW
75	R1216E.2	BXD	BXD32	76	M	UTHSC RW
76	R2542E.1	BXD	BXD33	67	F	UTHSC RW
77	R857E.2	BXD	BXD33	77	M	UTHSC RW
78	R1451E.2	BXD	BXD34	61	F	UTHSC RW
79	R2585E.1	BXD	BXD34	60	M	BIDMC GR
80	R2698E.3	BXD	BXD36	58	F	BIDMC GR
81	R2705E.3	BXD	BXD36	57	M	BIDMC GR
82	R2710E.2	BXD	BXD38	55	F	UTHSC RW
83	R2532E.1	BXD	BXD38	62	M	UTHSC RW

84	R2574E.1	BXD	BXD39	70	F	UTHSC RW
85	R2695E.2	BXD	BXD39	59	M	UTHSC RW
86	R2699E.2	BXD	BXD40	59	F	UTHSC RW
87	R2590E.1	BXD	BXD40	60	M	BIDMC GR
88	R2696E.2	BXD	BXD42	58	F	UTHSC RW
89	R2596E.1	BXD	BXD42	59	M	BIDMC GR
90	R994E.2	BXD	BXD43	60	F	UTHSC RW
91	R2607E.1	BXD	BXD43	67	M	UTHSC RW
92	R2594E.1	BXD	BXD44	63	F	UTHSC RW
93	R2610E.2	BXD	BXD44	68	M	UTHSC RW
94	R2732E.2	BXD	BXD45	63	F	UTHSC RW
95	R2592E.1	BXD	BXD45	62	M	UTHSC RW
96	R967E.2	BXD	BXD48	64	F	UTHSC RW
97	R2606E.1	BXD	BXD48	78	M	UTHSC RW
98	R2933E.3	BXD	BXD50	61	F	UTHSC RW
99	R2937E.3	BXD	BXD50	61	M	UTHSC RW
100	R2603E.1	BXD	BXD51	66	F	UTHSC RW
101	R1042E.2	BXD	BXD51	62	M	UTHSC RW
102	R2980E.3	BXD	BXD55	76	F	UTHSC RW
103	R2690E.2	BXD	BXD55	65	M	UTHSC RW
104	R4176E	BXD	BXD56	67	F	UTHSC RW
105	R4175E	BXD	BXD56	53	M	UTHSC RW
106	R1006E.3	BXD	BXD60	60	F	UTHSC RW
107	R2725E.2	BXD	BXD60	61	F	UTHSC RW
108	R1074E.3	BXD	BXD60	59	M	UTHSC RW
109	R2534E2.1	BXD	BXD61	70	F	UTHSC RW
110	R2684E.2	BXD	BXD61	62	M	UTHSC RW
111	R1107E.3	BXD	BXD62	54	F	UTHSC RW

112	R2681E.2	BXD	BXD62	62	M	UTHSC RW
113	R965E.3	BXD	BXD62	54	M	UTHSC RW
114	R1425E.2	BXD	BXD63	61	F	UTHSC RW
115	R2576E.3	BXD	BXD63	70	M	UTHSC RW
116	R943E-2.2	BXD	BXD64	56	F	UTHSC RW
117	R2611E.1	BXD	BXD64	68	M	UTHSC RW
118	R2689E.2	BXD	BXD65	63	F	UTHSC RW
119	R2583E.1	BXD	BXD65	60	M	UTHSC RW
120	R2728E.2	BXD	BXD66	67	F	UTHSC RW
121	R2536E2.1	BXD	BXD66	64	F	UTHSC RW
122	R1207E.2	BXD	BXD66	83	M	UTHSC RW
123	R1192E.2	BXD	BXD67	64	F	UTHSC RW
124	R2727E.3	BXD	BXD67	65	F	UTHSC RW
125	R2691E.3	BXD	BXD67	65	M	UTHSC RW
126	R2551E.1	BXD	BXD68	67	F	UTHSC RW
127	R2726E.2	BXD	BXD68	64	M	UTHSC RW
128	R2593E.1	BXD	BXD69	59	F	UTHSC RW
129	R975E.2	BXD	BXD70	64	F	UTHSC RW
130	R2537E2.1	BXD	BXD70	59	M	UTHSC RW
131	R4531E	BXD	BXD71	87	F	UTHSC RW
132	R4532E	BXD	BXD71	86	M	UTHSC RW
133	R2779E.2	BXD	BXD73	64	F	UTHSC RW
134	R3024E.3	BXD	BXD73	54	M	UTHSC RW
135	R2565E.1	BXD	BXD75	61	F	UTHSC RW
136	R1397E-re.2	BXD	BXD75	58	M	UTHSC RW
137	R2687E.3	BXD	BXD77	60	F	UTHSC RW
138	R2717E.2	BXD	BXD77	107	M	UTHSC RW
139	R1421E.3	BXD	BXD77	62	M	UTHSC RW

140	R2579E.1	BXD	BXD80	65	F	UTHSC RW
141	R2686E.2	BXD	BXD80	61	M	UTHSC RW
142	R2956E.3	BXD	BXD83	58	F	UTHSC RW
143	R2960E.3	BXD	BXD83	58	M	UTHSC RW
144	R2922E.3	BXD	BXD84	61	F	UTHSC RW
145	R2895E.3	BXD	BXD84	67	M	UTHSC RW
146	R2692E.2	BXD	BXD85	63	F	UTHSC RW
147	R2715E.2	BXD	BXD85	91	M	UTHSC RW
148	R1405E.2	BXD	BXD86	58	F	UTHSC RW
149	R1225E.3	BXD	BXD86	58	M	UTHSC RW
150	R2724E.2	BXD	BXD87	63	F	UTHSC RW
151	R2540E.1	BXD	BXD87	63	M	UTHSC RW
152	R1433E.2	BXD	BXD89	63	F	UTHSC RW
153	R2546E.1	BXD	BXD89	66	M	UTHSC RW
154	R2578E2.1	BXD	BXD90	61	F	UTHSC RW
155	R859E.2	BXD	BXD90	72	M	UTHSC RW
156	R2682E.2	BXD	BXD92	66	F	UTHSC RW
157	R1388E.3	BXD	BXD92	62	F	UTHSC RW
158	R1322E.3	BXD	BXD92	55	M	UTHSC RW
159	R2733E.2	BXD	BXD96	67	F	UTHSC RW
160	R2554E.1	BXD	BXD96	67	M	UTHSC RW
161	R2649E.2	BXD	BXD97	74	F	UTHSC RW
162	R2577E.1	BXD	BXD97	55	M	UTHSC RW
163	R2645E.3	BXD	BXD98	66	F	UTHSC RW
164	R2688E.2	BXD	BXD98	67	M	UTHSC RW
165	R4533E	BXD	BXD99	80	F	UTHSC RW
166	R4534E	BXD	BXD99	91	M	UTHSC RW
167	R2885E.3	GDP	BXSB/MpJ	61	F	BIDMC GR

168	R2883E.3	GDP	BXSB/MpJ	61	M	BIDMC GR
169	R1700E.1	GDP	C3H/HeJ	83	F	UTHSC RW
170	R1704E.1	GDP	C3H/HeJ	83	M	UTHSC RW
171	R2605E.1	GDP BXD	C57BL/6J	79	F	UTHSC RW
172	R0871E	GDP BXD	C57BL/6J	65	F	UTHSC RW
173	R0872E.1	GDP BXD	C57BL/6J	66	M	UTHSC RW
174	R0872E	GDP BXD	C57BL/6J	66	M	UTHSC RW
175	R4507E	KO	C57BL/6J-Nyx	57	M	Geisert
176	R4508E	KO	C57BL/6J-Nyx	57	M	Geisert
177	R4505E	KO	C57BL/6J-Rpe65	57	F	Geisert
178	R4506E	KO	C57BL/6J-Rpe65	57	F	Geisert
179	R4535E	GDP	C57BLKS/J	66	F	JAX
180	R4536E	GDP	C57BLKS/J	66	M	JAX
181	R2564E.1	GDP	CAST/EiJ	64	F	JAX
182	R2580E.1	GDP	CAST/EiJ	64	M	JAX
183	R4537E	GDP	CBA/CaJ	66	F	JAX
184	R4538E	GDP	CBA/CaJ	66	M	JAX
185	R4539E	GDP	CZECHII/EiJ	66	F	JAX
186	R4540E	GDP	CZECHII/EiJ	66	M	JAX
187	R2600E.1	GDP BXD	D2B6F1	72	F	UTHSC RW
188	R2604E.1	GDP BXD	D2B6F1	69	M	UTHSC RW
189	R1002E.3	GDP BXD	DBA/2J	72	F	UTHSC RW
190	R4541E	GDP BXD	DBA/2J	65	F	JAX
191	R959E.3	GDP BXD	DBA/2J	60	M	UTHSC RW
192	R2572E.1	GDP BXD	DBA/2J	65	M	UTHSC RW
193	R4542E	GDP BXD	DBA/2J	59	M	JAX
194	R2771E.3	GDP	FVB/NJ	60	F	BIDMC GR
195	R2772E.3	GDP	FVB/NJ	60	M	BIDMC GR

196	R2636E.1	GDP	KK/HIJ	64	F	UTHSC RW
197	R2637E.1	GDP	KK/HIJ	64	M	UTHSC RW
198	R0999E.1	GDP	LG/J	57	F	UTHSC RW
199	R1004E.1	GDP	LG/J	65	M	UTHSC RW
200	R4543E	GDP	LP/J	65	F	JAX
201	R4544E	GDP	LP/J	65	M	JAX
202	R2858E.3	GDP	MOLF/EiJ	60	F	BIDMC GR
203	R2919.3	GDP	MOLF/EiJ	60	M	BIDMC GR
204	R1688E.1	GDP	NOD/LtJ	66	F	JAX
205	R2566E-2.1	GDP	NOD/LtJ	76	M	UTHSC RW
206	R4545E	GDP	NZB/BINJ	61	F	BIDMC GR
207	R4546E	GDP	NZB/BINJ	58	M	BIDMC GR
208	R2535E.1	GDP	NZO/HILtJ	62	F	JAX
209	R2550E.1	GDP	NZO/HILtJ	96	M	JAX
210	R2817E.3	GDP	NZW/LacJ	65	F	BIDMC GR
211	<b>R2810E</b>	GDP	NZW/LacJ	60	M	BIDMC GR
212	R2810E.3	GDP	NZW/LacJ	60	M	BIDMC GR
213	R4547E	GDP	PANCEVO/EiJ	68	F	JAX
214	R4548E	GDP	PANCEVO/EiJ	68	M	JAX
215	R2635E.1	GDP	PWD/PhJ	62	F	JAX
216	R2634E.1	GDP	PWD/PhJ	62	M	JAX
217	R2544E.1	GDP	PWK/PhJ	63	F	JAX
218	R2549E.1	GDP	PWK/PhJ	83	M	JAX
219	R4550E	GDP	SJL/J	65	M+F	JAX
220	R2368E.1	GDP	WSB/EiJ	67	F	UTHSC RW
221	R2547E.1	GDP	WSB/EiJ	67	M	UTHSC RW

### About downloading this data set:

This data set is available as a **bulk download in several formats**. The data are available as

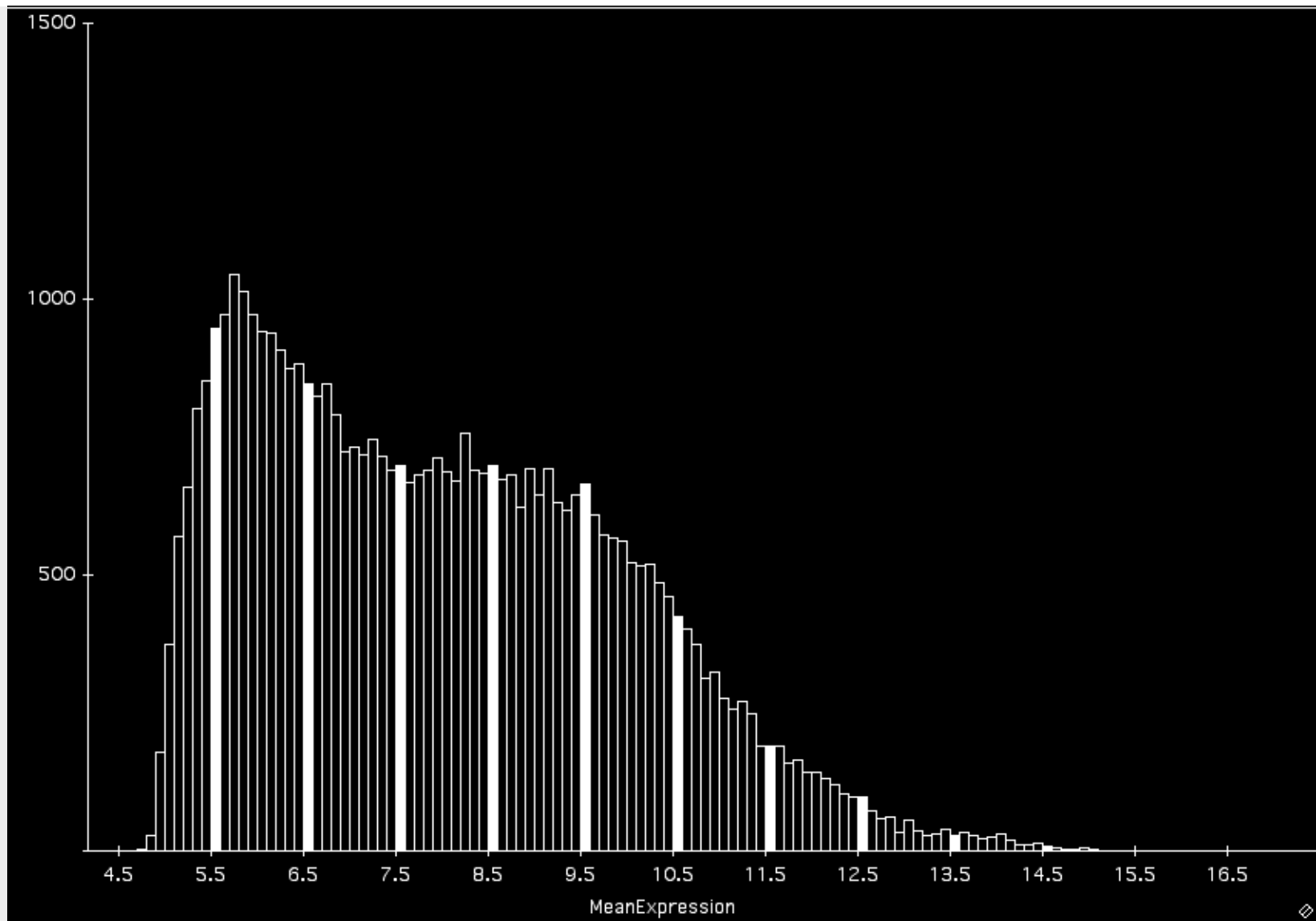
either strain means or the individual arrays. Due to the involved normalization procedures required to correct for batch effects we strongly recommend not using the raw CEL files without special statistical procedures.

### About the array platform:

**Affymetrix Mouse Genome 430 2.0 arrays:** The **430 2.0** array consists of 992936 25-nucleotide probes that estimate the expression of approximately 39,000 transcripts (many probes overlap and target the same transcript). The array sequences were selected late in 2002 using Unigene Build 107. The array nominally contains the same probe sequences as the old M430A and 430B array pair. However, we have found that roughly 75000 probes differ between those on A and B arrays and those on the new 430 2.0.

As part of the development of HEIMED, we have manually annotated individual probe sets by sequence alignment to the mouse genome and transcriptome. Approximately 13,000 probe sets that have comparatively high expression in eye and CNS were curated by one of the authors (RWW) and now have specific information on the part of the transcript targeted by each probe set. The other 33,000 transcripts have corresponding data that was generated by Xusheng Wang using computational methods (BLAT analysis combined with annotated genome sequence).

One example may help explain how to exploit this annotation. The four probe sets for rhodopsin include information on the target location. Only the first probe set targets the last two coding exons. The other three probe sets target different parts of the 3' UTR (mid, distal, and far distal regions). The probe sets can be reordered by from high to low expression using the *Sort By* function in Search Results pages. In the case of rhodopsin, the probe set that targets that last two coding exons and proximal parts of the 3' UTR also has the highest expression. Finally, the HEIMED gene descriptions have been customized to help vision researchers. In the case of rhodopsin, the description appended after the gene name reads "rod photoreceptor pigment, retinitis pigmentosa-associated". For less well known genes this kind of annotation can be extremely useful. For example, the more verbose annotation for *Cerkl* reads "neuronal survival and apoptosis-related, retinal ganglion cell expressed, retinitis pigmentosa 26); alternative 3' UTR of short form message, intron 2".



**Legend:** Distribution of expression values for all probe sets in HEIMED.

**About data values and data processing:**

**Range of Gene Expression in the Eye.** Expression of transcripts in the HEIMED and most other GN data sets is measured on a log<sub>2</sub> scale. Each unit corresponding approximately to a 2-fold difference in hybridization signal intensity. To simplify comparisons among different data sets and cases, log<sub>2</sub> RMA values of each array have been adjusted to an average expression of 8 units and a standard deviation of 2 units (variance stabilized). Values of all 45,101 probe sets in this data set range from a low of 4.8 (*Tcf15*, probe set 1420281\_at) to a high of 15.5

(crystallin gamma C, *Crygc*, probe set 1422674\_s\_at). This corresponds to 10.7 units or a 1 to 1700 dynamic range of expression ( $2^{10.73}$ ).

We calibrated this log intensity scale using Affymetrix spike-in control probe sets. These 18 control probe sets target exogenous bacterial mRNAs that are added to each sample (a graded dose spike cocktail) during preparation at concentrations of 1.5, 5, 25, and 100 pM. (To find these probe sets, search GN's ALL search field using the string "AFFX pM".) A value of 6 or less is equivalent to an mRNA concentration of under 0.4 pM, a value of 8 is equivalent to ~1.5 pM, 9.5 is equivalent to ~5 pM, 11.5 is equivalent to ~25 pM, 13.5 is equivalent to ~100 pM, and a value of 15.5 is equivalent to an mRNA concentration of 400 pM or greater.

This range can be converted to the mRNA molecules per cell in the eye assuming that a value of 8 is equivalent to about 1 mRNA copy per cell (Kanno et al. 2006, see <http://www.biomedcentral.com/1471-2164/7/64>). Since the expression of rhodopsin mRNA is normally 15 units, we predict that there are 27 or ~128 *Rho* mRNAs per cell in the whole eye and ~256 in rods themselves (assuming that rods make up about half of all cells in the eye). For this purpose it may be useful to know that a normal mouse eye contains between 6 and 8 million rod photoreceptors (Guo, Lu, and Williams; GN BXD Phenotype ID 11024).

Note that some probe sets with very low expression still provide reliable data. For example, probe set 1440397\_at (*Cacna2d1*) has expression of only 5.5 units (a value that would be declared as "absent" using conventional Affymetrix procedures), but the values for this calcium channel transcript are associated with a very strong cis QTL with an LRS of 79 (LOD = 17). This strong linkage is definitely not due to chance since the probability of the expression data mapping precisely to the location of the parent gene itself is about  $10e-16$ . This indicates a high signal to noise ratio and the detection of significant strain variation of the correct transcript.

The **standard error of the mean** for the HEIMED data set is computed for 2 to 6 biological replicates. The standard error of such small samples tends to systematically underestimate the population standard error. With  $n = 2$  the underestimate is about 25%, whereas for  $n = 6$  the underestimate is 5%. Gurland and Tripathi (1971) provide a correction and equation for this effect (see Sokal and Rohlf, *Biometry*, 2nd ed., 1981, p 53 for an equation of the correction factor for small samples of  $n < 20$ .) **Probe (cell) level data from the CEL file:** These CEL values produced by GCOS are 75% quantiles from a set of 91 pixel values per cell. The CEL files were processed using the RMA protocol. We processed the first three batches together. The last batch was processed separately and merged as described below.

- Step 1: We added an offset of 1.0 unit to each cell signal to ensure that all values could be logged without generating negative values. We then computed the log base 2 of each cell.
- Step 2: We performed a quantile normalization of the log base 2 values for the total set of arrays using the same initial steps used by the RMA transform.
- Step 3: We computed the Z scores for each cell value.
- Step 4: We multiplied all Z scores by 2.
- Step 5: We added 8 to the value of all Z scores. The consequence of this simple set of transformations is to produce a set of Z scores that have a mean of 8, a variance of 4, and a standard deviation of 2. The advantage of this modified Z score is that a two-fold difference

in expression level corresponds approximately to a 1 unit difference.

- Step 6: Finally, when appropriate, we computed the arithmetic mean of the values for the set of microarrays for each strain. Technical replicates were averaged before computing the mean for independent biological samples.

After RMA processing using Biobase affy10 build running under R version 2.7.1, all array data sets were rank-order normalized. This second round of quantile normalization removes much residual non-linearity across arrays and forces every array to have the same distribution of values as the mean of all arrays. Comparative array data quality was then evaluated in DataDesk. Outlier arrays were flagged by visual inspection in DataDesk, usually by means of an analysis of scatter plots and more quantitatively by generating a correlation matrix of all arrays. Those arrays with mean correlation  $<0.96$  versus all other arrays indicates trouble or a biological outlier). In some cases, outliers were expected, such as samples from strains with retinal degeneration (FVB/NJ, NOD/LtJ, MOLF/EiJ, C3H/HeJ and BXD24), samples from wild subspecies such as WSB/EiJ, CAST/EiJ, PWD/PhJ, and PWK/PhJ, and knockouts. However, when arrays were anomalous both within strain and across strains, they were often simply discarded. The assumption is that anomalous data are much more likely due to experimental and technical errors than to informative biological variation. Approximately 10% of arrays were discarded.

After this process, the acceptable set of arrays was renormalized using all step as above, starting with the original RMA procedure, etc.

We reviewed the data set using a new method developed by RW Williams, Jeremy Peirce, and Hongqiang Li. For the full set of arrays that passed standard QC protocols described above, we computed the strain means for the BXD strains, B6, D2, and F1s. Using this set of strain means we then computed LRS scores for all 45101 probe sets and counted the number of transcripts that generated QTLs with LRS values greater than 50. This value (e.g., 1800) represented the QTL harvest for the full data set. We then dropped a single array from the data set, recomputed strain means, and recomputed the number of transcripts with LRS scores great than 50. This value is expected to typically reduce the number of QTLs that reach the criterion level (e.g., 1750 QTLs  $> 50$ ). This process was repeated for every array to obtain an array-specific difference value--the effect of removing that array on the total QTL count. For example, the loss of a single array might cause a decrease in 50 QTLs. Values ranged from approximately -90 (good arrays) to +40 (bad arrays). This procedure is similar in some ways to a jackknife protocol, although we are not using this procedure to estimate an error term, but rather as a method to polish a data set.

During this process we discovered that nearly 20 arrays in the batch 2 had been mislabeled at some point in processing. We computed the correct strain membership of each array using a large number of Mendelian probe sets (more than 50) and comparing their match to standard SNP and microsatellite markers and the original array data set of November 2005. This allowed us to rescue a large number of arrays that were of high quality.

A third batch of approximately 40 arrays were processed by Yan Jiao and Weikuan Gu in August 2006. These complete data set assembled by Hongqiang Li. This process again included a correction for a batch effect.

For the June 2006 data set Hongqiang Li used a new batch correction method that stabilizes the range of expression in each batch. For each of the three large batches, we extracted the minimum and maximum raw probe expression (CEL file level) value. We then adjusted raw probe values in each batch to have the same range as the first and largest batch (batch 1) using a simple linear interpolation. These procedures generated new correct CEL files which were then used with RMA to generate final probe set estimates.

For the final fourth batch of arrays (Sept 2008) Arthur Centeno and Rob Williams corrected for a systematic difference in probe set expression values between original arrays run in 2005 and 2006 and the new arrays added in 2008 (n = 45 acceptable arrays). This difference is due to unknown technical batch effects that are probably associated with labeling, hybridization, and scanning. We performed a simple correction to normalize values of the new set of arrays to those of the old set (batches 1 through 3). No changes were made to any values of the previous three batches. We corrected only the probe set level (RMA) values and not the CEL files. For this final batch, we corrected for the difference (offset) in probe set expression between the first three batches arrays run in 2005 and 2006 (a total of 174 acceptable arrays) and the new batch (n = 47 acceptable arrays). This difference is due to unknown technical effects that are probably related to various steps in labeling, hybridization, and scanning. The correction was applied as follows: (1) RWW selected 51 high quality arrays with similar expression characteristics (r = 0.97 or better between pairs of arrays) in the old data set (from batches 1, 2, and 3) and 34 high quality arrays in the final batch. RWW used scatterplots of full RMA transcriptome data sets to review many pairs of arrays within these new and old array batches. Strains with retinal degeneration or unusual eye gene expression characteristics were excluded from these selected subsets. The average expression values for each probe set were then computed for both the old and new array subsets. The offset value (old minus new) was added to each probe set across all 47 new arrays. This process forces the average probe set in the new arrays to be very close to that of the previous arrays.

**Table 2: Sample tube ID, strain, original CEL filename, and Affymetrix quality control values. Columns labeled Scale factor, Background Average, Present, Absent, Marginal and 3'/5' ratios for actin and Gapdh were collated from the Affymetrix Report (RPT) files.**

Index	TubeID	Strain	Original CEL	Scale factor	Background Average	Present	Absent	Marginal	AFFX-b-ActinMur (3'/5')	AFFX-GapdhMur (3'/5')	Batch Id	Used for batch control
1	R2595E.1	129S1/SvImJ	R2595E.1.CEL	1.79	115	61.00%	37.50%	1.50%	1.46	0.77	1	Y
2	R2533E.1	129S1/SvImJ	R2533E.1.CEL	2.11	94	57.90%	40.50%	1.60%	1.37	0.78	1	Y

3	R0754E.1	A/J	R0754E.1. CEL	2.72	86	59.80%	38.70%	1.50%	1.36	0.76	1	Y
4	R4521E	B6129P2F2N1- Clcn3	R4521E. CEL	4.83	38.7	63.30%	35.30%	1.40%	1.25	0.77	4	
5	R4522E	B6129P2F2N1- Clcn3	R4522E. CEL	5.76	37.36	62.90%	35.70%	1.40%	1.37	0.83	4	
6	R4523E	B6129P2F2N1- Clcn3	R4523E. CEL	4.88	40.42	63.90%	34.70%	1.40%	1.27	0.77	4	
7	R4526E	B6129P2F2N1- Gabbr1	R4526E. CEL	3.84	44.18	65.00%	33.70%	1.30%	1.34	0.78	4	Y
8	R4509E	B6129P2F2N1- Gabbr1	R4509E. CEL	7.45	34.76	58.90%	39.70%	1.40%	1.45	0.83	4	
9	R4510E	B6129P2F2N1- Gabbr1	R4510E. CEL	8.44	37.44	57.40%	41.10%	1.50%	1.35	0.83	4	
10	R4511E	B6129P2F2N1- Gabbr1	R4511E. CEL	5.91	42.02	61.40%	37.20%	1.40%	1.41	0.83	4	
11	R4524E	B6129P2F2N1- Gabbr1	R4524E. CEL	5.49	42.34	62.40%	36.20%	1.40%	1.29	0.78	4	Y
12	R4525E	B6129P2F2N1- Gabbr1	R4525E. CEL	4.69	41.3	63.10%	35.50%	1.40%	1.27	0.8	4	Y
13	R4515E	B6129P2F2N1- Gabra1	R4515E. CEL	5.75	41.76	62.80%	35.80%	1.40%	1.41	0.81	4	Y
14	R4516E	B6129P2F2N1- Gabra1	R4516E. CEL	7.07	40.73	60.20%	38.40%	1.40%	1.32	0.87	4	Y
15	R4517E	B6129P2F2N1- Gabra1	R4517E. CEL	5.45	38.09	62.70%	35.80%	1.40%	1.34	0.82	4	Y
16	R4512E	B6129P2F2N1- Gnb5	R4512E. CEL	6.56	38.02	59.90%	38.70%	1.50%	1.33	0.83	4	
17	R4513E	B6129P2F2N1- Gnb5	R4513E. CEL	4.15	41.6	63.40%	35.10%	1.50%	1.34	0.82	4	
18	R4514E	B6129P2F2N1- Gnb5	R4514E. CEL	5.86	39.2	61.20%	37.30%	1.50%	1.34	0.81	4	
19	R4518E	B6129P2F2N1- Gpr19	R4518E. CEL	5.58	38.9	62.60%	36.00%	1.30%	1.39	0.79	4	Y

20	R4519E	B6129P2F2N1-Gpr19	R4519E.CEL	5.95	41.91	61.30%	37.30%	1.40%	1.35	0.84	4	Y
21	R2601E.1	B6D2F1	R2601E.1.CEL	2.55	92	58.90%	39.60%	1.50%	1.44	0.78	1	Y
22	R2602E.1	B6D2F1	R2602E.1.CEL	2.6	84	59.70%	38.80%	1.50%	1.37	0.78	1	Y
23	R1676E.1	BALB/cByJ	R1676E.1.CEL	2.69	98	58.90%	39.60%	1.50%	1.46	0.74	1	
24	R1672E.1	BALB/cByJ	R1672E.1.CEL	2.22	111	59.90%	38.60%	1.50%	1.26	0.8	1	Y
25	R4530E	BALB/cJ	R4530E.CEL	6.37	37.53	60.80%	37.80%	1.40%	1.3	0.84	4	Y
26	R4529E	BALB/cJ	R4529E.CEL	5.71	41.33	60.50%	38.00%	1.50%	1.48	0.8	4	Y
27	R2704E.2	BXD1	R2704E.2.CEL	2.066	139.61	56.60%	41.90%	1.50%	1.31	0.81	2	
28	R2707E.3	BXD1	R2707E.3.CEL	1	80	56.40%	42.10%	1.50%	1.43	0.79	3	
29	R1231E.2	BXD2	R1231E.2.CEL	2.197	138.73	57.30%	41.30%	1.40%	1.41	0.77	2	
30	R2598E.1	BXD2	R2598E.1.CEL	1.99	106	60.90%	37.60%	1.50%	1.27	0.78	1	Y
31	R2591E.1	BXD5	R2591E.1.CEL	1.7	136	58.50%	40.00%	1.50%	1.33	0.78	1	Y
32	R2714E.2	BXD5	R2714E.2.CEL	1.404	144.35	60.60%	37.90%	1.50%	1.43	0.79	2	
33	R2570E.1	BXD6	R2570E.1.CEL	1.99	87	58.50%	40.00%	1.50%	1.46	0.76	1	Y
34	R2694E.2	BXD6	R2694E.2.CEL	1.983	97.23	61.60%	37.10%	1.30%	1.39	0.82	2	
35	R2538E.1	BXD8	R2538E.1.CEL	1.91	102	61.20%	37.30%	1.50%	1.52	0.79	1	Y
36	R2709E.2	BXD8	R2709E.2.CEL	1.99	99.79	60.90%	37.60%	1.50%	1.42	0.76	2	

37	R2708E.2	BXD9	R2708E.2. CEL	1.966	126.46	57.70%	40.70%	1.50%	1.4	0.84	2	
38	R2569E.1	BXD9	R2569E.1. CEL	1.75	87	55.10%	43.40%	1.50%	2.82	3.14	1	
39	R2581E.1	BXD11	R2581E.1. CEL	1.94	89	62.10%	36.40%	1.60%	1.55	0.81	1	Y
40	R2612E.2	BXD11	R2612E.2. CEL	1.83	142.03	58.20%	40.50%	1.40%	1.78	0.81	2	
41	R2742E.2	BXD12	R2742E.2. CEL	2.127	134.14	57.00%	41.60%	1.40%	1.64	0.78	2	
42	R2543E.1	BXD12	R2543E.1. CEL	1.61	118	58.60%	39.90%	1.60%	1.43	0.77	1	Y
43	R2586E.1	BXD13	R2586E.1. CEL	2.01	74	56.40%	42.00%	1.60%	2.85	3.81	1	
44	R877E.2	BXD13	R877E.2. CEL	1.558	125.63	61.20%	37.50%	1.20%	1.42	0.81	2	
45	R2557E.1	BXD14	R2557E.1. CEL	1.83	99	62.50%	36.10%	1.40%	1.31	0.78	1	Y
46	R1128E.2	BXD14	R1128E.2. CEL	1.91	115	59.90%	38.80%	1.40%	1.2	0.82	1	Y
47	R2701E.3	BXD15	R2701E.3. CEL	1	88	60.60%	37.90%	1.40%	1.5	0.77	3	
48	R2716E.2	BXD15	R2716E.2. CEL	2.015	150.83	56.40%	42.10%	1.60%	1.42	0.81	2	
49	R2711E.2	BXD16	R2711E.2. CEL	1.953	118.53	59.00%	39.60%	1.50%	1.45	0.8	2	
50	R2567E.1	BXD16	R2567E.1. CEL	2.24	82	56.70%	41.60%	1.70%	1.37	0.75	1	
51	R2720E.2	BXD18	R2720E.2. CEL	2.32	99.93	59.50%	39.00%	1.50%	1.33	0.77	2	
52	R2559E.1	BXD18	R2559E.1. CEL	1.65	104	60.80%	37.70%	1.50%	1.27	0.78	1	Y
53	R2560E.1	BXD19	R2560E.1. CEL	1.79	98	60.90%	37.50%	1.60%	1.35	0.8	1	Y

54	R2713E.2	BXD19	R2713E.2.CEL	1.67	120.82	60.20%	38.30%	1.50%	1.45	0.8	2	
55	R2584E.1	BXD20	R2584E.1.CEL	2.07	84	59.30%	39.10%	1.60%	1.4	0.76	1	Y
56	R2731E.2	BXD20	R2731E.2.CEL	1.825	147	59.00%	39.50%	1.50%	1.4	0.8	2	
57	R2702E.2	BXD21	R2702E.2.CEL	1.811	128.65	59.40%	39.10%	1.40%	1.26	0.8	2	
58	R2541E2.1	BXD21	R2541E2.1.CEL	2.63	125	56.00%	42.40%	1.50%	1.29	0.78	1	
59	R2553E.1	BXD22	R2553E.1.CEL	1.95	111	59.90%	38.50%	1.50%	1.28	0.76	1	Y
60	R2700E.2	BXD22	R2700E.2.CEL	1.858	102.96	61.50%	37.10%	1.30%	1.48	0.79	2	
61	R2558E-2.1	BXD23	R2558E-2.1.CEL	2.233	125.05	58.60%	39.90%	1.50%	1.43	0.77	2	
62	R1086E.2	BXD23	R1086E.2.CEL	2.233	125.05	58.60%	39.90%	1.50%	1.43	0.77	2	
63	R2719E.2	BXD24	R2719E.2.CEL	1.47	140.38	61.50%	37.20%	1.30%	1.38	0.79	2	
64	R2589E2.1	BXD24	R2589E2.1.CEL	2.61	112	57.50%	40.90%	1.60%	1.24	0.8	1	
65	R2573E-2.1	BXD25	R2573E-2.1.CEL	3.15	72	57.90%	40.70%	1.40%	1.77	0.97	1	
66	R2683E.2	BXD25	R2683E.2.CEL	1.777	115.64	58.30%	40.30%	1.40%	2.01	0.79	2	
67	R2703E.2	BXD27	R2703E.2.CEL	1.263	134.78	62.60%	36.10%	1.40%	1.44	0.78	2	
68	R2729E.3	BXD27	R2729E.3.CEL	1	87	57.90%	40.60%	1.50%	1.56	0.84	3	Y
69	R2562E.3	BXD28	R2562E.3.CEL	1.65	116	59.90%	38.40%	1.70%	1.37	0.79	3	Y
70	R2721E.2	BXD28	R2721E.2.CEL	2.065	157.39	56.10%	42.40%	1.50%	1.31	0.81	2	

71	R2561E.3	BXD29	R2561E.3. CEL	1	77	53.30%	45.40%	1.40%	3.36	19.66	3	
72	R1258E.2	BXD31	R1258E.2. CEL	2.063	117.09	59.00%	39.50%	1.50%	1.54	0.78	2	
73	R2597E.1	BXD31	R2597E.1. CEL	2.37	94	60.30%	38.30%	1.50%	1.34	0.77	1	Y
74	R2563E.1	BXD32	R2563E.1. CEL	1.55	102	61.90%	36.70%	1.40%	1.5	0.8	1	
75	R1216E.2	BXD32	R1216E.2. CEL	2.23	111.99	58.80%	39.80%	1.40%	1.35	0.79	2	
76	R2542E.1	BXD33	R2542E.1. CEL	2.13	97	56.50%	41.80%	1.60%	1.91	0.93	1	
77	R857E.2	BXD33	R857E.2. CEL	1.737	113.98	61.90%	36.70%	1.30%	1.6	0.77	2	
78	R1451E.2	BXD34	R1451E.2. CEL	1.843	140.05	59.00%	39.50%	1.50%	1.42	0.81	2	Y
79	R2585E.1	BXD34	R2585E.1. CEL	2.64	75	58.30%	40.00%	1.70%	1.25	0.77	1	
80	R2698E.3	BXD36	R2698E.3. CEL	1	86	59.70%	39.00%	1.30%	1.46	0.78	3	
81	R2705E.3	BXD36	R2705E.3. CEL	1	86	60.20%	38.40%	1.40%	1.46	0.77	3	
82	R2710E.2	BXD38	R2710E.2. CEL	2.112	122.1	58.80%	39.80%	1.40%	1.37	0.78	2	
83	R2532E.1	BXD38	R2532E.1. CEL	2.04	94	59.80%	38.70%	1.50%	1.37	0.8	1	Y
84	R2574E.1	BXD39	R2574E.1. CEL	1.98	91	61.20%	37.30%	1.50%	1.39	0.78	1	
85	R2695E.2	BXD39	R2695E.2. CEL	1.638	122.7	60.80%	37.80%	1.50%	1.42	0.8	2	
86	R2699E.2	BXD40	R2699E.2. CEL	1.827	105.23	61.70%	36.90%	1.40%	1.42	0.81	2	
87	R2590E.1	BXD40	R2590E.1. CEL	2.71	77	59.10%	39.30%	1.50%	1.4	0.77	1	Y

88	R2696E.2	BXD42	R2696E.2. CEL	1.622	118.95	62.00%	36.60%	1.50%	1.53	0.79	2	
89	R2596E.1	BXD42	R2596E.1. CEL	2.63	108	59.00%	39.60%	1.50%	1.24	0.8	1	
90	R994E.2	BXD43	R994E.2. CEL	1.966	113.12	60.80%	37.80%	1.40%	1.66	0.8	2	
91	R2607E.1	BXD43	R2607E.1. CEL	2.43	115	58.60%	40.00%	1.40%	1.31	0.76	1	Y
92	R2594E.1	BXD44	R2594E.1. CEL	1.77	117	59.80%	38.80%	1.40%	1.35	0.85	1	
93	R2610E.2	BXD44	R2610E.2. CEL	1.814	142.91	59.00%	39.50%	1.50%	1.35	0.8	2	
94	R2732E.2	BXD45	R2732E.2. CEL	2.154	122.45	56.50%	42.10%	1.40%	1.8	0.83	2	
95	R2592E.1	BXD45	R2592E.1. CEL	1.85	106	60.10%	38.60%	1.30%	1.43	0.85	1	Y
96	R967E.2	BXD48	R967E.2. CEL	1.948	130.95	57.30%	41.20%	1.50%	1.63	0.81	2	
97	R2606E.1	BXD48	R2606E.1. CEL	2.56	106	58.90%	39.70%	1.40%	1.35	0.83	1	Y
98	R2933E.3	BXD50	R2933E.3. CEL	1	72	52.90%	45.60%	1.50%	2.45	0.98	3	
99	R2937E.3	BXD50	R2937E.3. CEL	1	89	56.90%	41.60%	1.40%	1.81	0.82	3	
100	R2603E.1	BXD51	R2603E.1. CEL	2.49	115	57.70%	40.80%	1.50%	1.24	0.79	1	
101	R1042E.2	BXD51	R1042E.2. CEL	2.352	104.12	58.70%	39.90%	1.40%	1.53	0.82	2	
102	R2980E.3	BXD55	R2980E.3. CEL	1	82	56.90%	41.70%	1.50%	1.77	0.84	3	
103	R2690E.2	BXD55	R2690E.2. CEL	1.887	164.01	56.10%	42.30%	1.60%	1.43	0.8	2	
104	R4176E	BXD56	R4176E. CEL	4.75	43.08	63.00%	35.60%	1.30%	1.39	0.81	4	Y

105	R4175E	BXD56	R4175E. CEL	6	38.49	61.30%	37.30%	1.40%	1.47	0.81	4	Y
106	R1006E.3	BXD60	R1006E.3. CEL	1	98	54.90%	43.70%	1.50%	2.7	0.86	3	
107	R2725E.2	BXD60	R2725E.2. CEL	1.551	148.01	59.80%	38.80%	1.40%	1.43	0.79	2	
108	R1074E.3	BXD60	R1074E.3. CEL	1	118	55.50%	43.10%	1.40%	1.96	0.81	3	
109	R2534E2.1	BXD61	R2534E2.1. CEL	2.47	118	57.90%	40.60%	1.50%	1.42	0.79	1	
110	R2684E.2	BXD61	R2684E.2. CEL	2.01	131.03	57.00%	41.50%	1.50%	1.34	0.78	2	
111	R1107E.3	BXD62	R1107E.3. CEL	1	83	55.20%	43.40%	1.40%	2.43	0.93	3	
112	R2681E.2	BXD62	R2681E.2. CEL	2.086	148.24	57.20%	41.30%	1.50%	1.29	0.81	2	
113	R965E.3	BXD62	R965E.3. CEL	1	93.55	53.30%	45.20%	1.50%	3.11	0.94	3	
114	R1425E.2	BXD63	R1425E.2. CEL	1.7	136	59.30%	39.30%	1.40%	1.43	0.82	2	
115	R2576E.3	BXD63	R2576E.3. CEL	1	84	61.30%	37.40%	1.40%	1.48	0.76	3	
116	R943E-2.2	BXD64	R943E-2.2. CEL	1.591	141.34	60.10%	38.40%	1.50%	1.32	0.76	2	
117	R2611E.1	BXD64	R2611E.1. CEL	2.29	92	58.00%	40.50%	1.50%	1.57	1.06	1	
118	R2689E.2	BXD65	R2689E.2. CEL	1.721	142.44	59.90%	38.60%	1.50%	1.38	0.76	2	
119	R2583E.1	BXD65	R2583E.1. CEL	2.49	70	56.90%	41.50%	1.60%	1.67	1.01	1	
120	R2728E.2	BXD66	R2728E.2. CEL	1.714	137.45	59.40%	39.00%	1.60%	1.38	0.79	2	
121	R2536E2.1	BXD66	R2536E2.1. CEL	2.74	109	56.10%	42.30%	1.70%	1.28	0.79	1	

122	R1207E.2	BXD66	R1207E.2. CEL	1.681	136.86	60.40%	38.10%	1.50%	1.45	0.77	2	
123	R1192E.2	BXD67	R1192E.2. CEL	2.126	123.37	57.90%	40.60%	1.50%	1.5	0.8	2	
124	R2727E.3	BXD67	R2727E.3. CEL	1	82.55	56.10%	42.40%	1.50%	1.97	0.87	2	
125	R2691E.3	BXD67	R2691E.3. CEL	1	90	54.80%	43.80%	1.50%	2.61	0.81	3	
126	R2551E.1	BXD68	R2551E.1. CEL	2.49	92	54.30%	44.10%	1.60%	2.91	1.55	1	
127	R2726E.2	BXD68	R2726E.2. CEL	1.811	153.09	58.70%	39.80%	1.50%	1.39	0.78	2	
128	R2593E.1	BXD69	R2593E.1. CEL	1.67	128	59.20%	39.50%	1.30%	1.47	0.92	1	Y
129	R975E.2	BXD70	R975E.2. CEL	1.841	137.97	58.00%	40.50%	1.40%	1.36	0.79	2	
130	R2537E2.1	BXD70	R2537E2.1. CEL	2.93	99	58.00%	40.50%	1.60%	1.29	0.75	1	
131	R4531E	BXD71	R4531E. CEL	4.77	43.48	62.40%	36.30%	1.40%	1.23	0.77	4	Y
132	R4532E	BXD71	R4532E. CEL	5.89	40.68	60.90%	37.60%	1.50%	1.24	0.79	4	Y
133	R2779E.2	BXD73	R2779E.2. CEL	1.746	121.11	59.60%	39.00%	1.40%	1.5	0.8	2	
134	R3024E.3	BXD73	R3024E.3. CEL	1	78.05	51.70%	46.60%	1.70%	2.3	0.94	3	
135	R2565E.1	BXD75	R2565E.1. CEL	1.79	102	58.00%	40.50%	1.50%	2.31	3.47	1	
136	R1397E- re.2	BXD75	R1397E- re.2.CEL	1.449	189.71	59.60%	39.00%	1.40%	1.39	0.82	2	
137	R2687E.3	BXD77	R2687E.3. CEL	1	80	58.00%	40.60%	1.40%	1.57	0.8	3	Y
138	R2717E.2	BXD77	R2717E.2. CEL	1.797	84.43	61.60%	36.90%	1.40%	1.49	0.76	2	

139	R1421E.3	BXD77	R1421E.3. CEL	1	94	52.40%	46.20%	1.40%	2.29	0.82	3	
140	R2579E.1	BXD80	R2579E.1. CEL	2.42	72	59.20%	39.40%	1.50%	1.73	0.82	1	
141	R2686E.2	BXD80	R2686E.2. CEL	2.342	119.63	56.00%	42.60%	1.50%	1.38	0.79	2	
142	R2956E.3	BXD83	R2956E.3. CEL	1	84	55.40%	43.20%	1.40%	1.39	0.84	3	
143	R2960E.3	BXD83	R2960E.3. CEL	1	80	56.60%	41.90%	1.50%	1.5	0.82	3	Y
144	R2922E.3	BXD84	R2922E.3. CEL	1	91	57.80%	40.80%	1.50%	1.47	0.83	3	Y
145	R2895E.3	BXD84	R2895E.3. CEL	1	75	58.30%	40.20%	1.50%	1.56	0.77	3	Y
146	R2692E.2	BXD85	R2692E.2. CEL	1.423	160.87	60.20%	38.30%	1.40%	1.46	0.79	2	
147	R2715E.2	BXD85	R2715E.2. CEL	1.488	142.6	61.20%	37.30%	1.40%	1.5	0.78	2	
148	R1405E.2	BXD86	R1405E.2. CEL	2.351	119.34	56.40%	42.20%	1.40%	1.64	0.81	2	
149	R1225E.3	BXD86	R1225E.3. CEL	1	71	53.90%	44.60%	1.40%	3.2	1.61	3	
150	R2724E.2	BXD87	R2724E.2. CEL	1.906	113.71	60.70%	37.90%	1.40%	1.45	0.79	2	
151	R2540E.1	BXD87	R2540E.1. CEL	2.33	93	61.10%	37.40%	1.40%	1.22	0.81	1	Y
152	R1433E.2	BXD89	R1433E.2. CEL	1	2.241	57.70%	40.80%	1.50%	1.41	0.78	2	
153	R2546E.1	BXD89	R2546E.1. CEL	1.99	96	58.60%	39.70%	1.70%	1.47	0.78	1	
154	R2578E2.1	BXD90	R2578E2.1. CEL	2.79	92	58.60%	39.80%	1.60%	1.52	0.77	1	Y
155	R859E.2	BXD90	R859E.2. CEL	1.847	152.22	57.90%	40.70%	1.40%	1.36	0.77	2	

156	R2682E.2	BXD92	R2682E.2. CEL	1.547	156.31	60.40%	38.20%	1.40%	1.37	0.77	2	
157	R1388E.3	BXD92	R1388E.3. CEL	1	63	60.00%	38.60%	1.40%	1.85	1.03	3	
158	R1322E.3	BXD92	R1322E.3. CEL	1	80	55.90%	42.60%	1.50%	1.75	0.74	3	
159	R2733E.2	BXD96	R2733E.2. CEL	1.7	113.99	62.10%	36.60%	1.30%	1.4	0.78	2	
160	R2554E.1	BXD96	R2554E.1. CEL	2.18	93	60.20%	38.30%	1.50%	1.46	0.77	1	Y
161	R2649E.2	BXD97	R2649E.2. CEL	2.343	119.04	57.50%	41.20%	1.40%	1.53	0.8	2	
162	R2577E.1	BXD97	R2577E.1. CEL	2.07	77	59.50%	39.10%	1.40%	1.87	1.29	1	
163	R2645E.3	BXD98	R2645E.3. CEL	1	88	59.40%	39.20%	1.50%	1.59	0.81	3	Y
164	R2688E.2	BXD98	R2688E.2. CEL	1.772	145.24	58.50%	40.00%	1.50%	1.48	0.81	2	
165	R4533E	BXD99	R4533E. CEL	1	37.69	60.30%	38.20%	1.40%	1.33	0.89	4	Y
166	R4534E	BXD99	R4534E. CEL	5.69	36.62	62.90%	35.70%	1.40%	1.16	0.8	4	Y
167	R2885E.3	BXSB/MpJ	R2885E.3. CEL	1	76	58.10%	40.60%	1.30%	1.88	1.06	3	
168	R2883E.3	BXSB/MpJ	R2883E.3. CEL	1	71	56.40%	42.00%	1.50%	1.59	0.84	3	Y
169	R1700E.1	C3H/HeJ	R1700E.1. CEL	2.98	69	60.80%	37.90%	1.40%	1.48	0.78	1	
170	R1704E.1	C3H/HeJ	R1704E.1. CEL	2.58	88	60.10%	38.60%	1.30%	1.38	0.84	1	
171	R2605E.1	C57BL/6J	R2605E.1. CEL	1.82	131	60.50%	38.20%	1.30%	1.32	0.8	1	Y
172	R0871E	C57BL/6J	R0871E. CEL	6.24	37.38	61.90%	36.70%	1.40%	1.41	0.8	4	Y

173	R0872E.1	C57BL/6J	R0872E.1. CEL	3.13	89	58.90%	39.60%	1.50%	1.3	0.79	1	Y
174	R0872E	C57BL/6J	R0872E. CEL	3.128	88.58	58.90%	39.60%	1.50%	1.3	0.79	1	
175	R4507E	C57BL/6J-Nyx	R4507E. CEL	8.13	37.5	59.30%	39.30%	1.40%	1.32	0.8	4	Y
176	R4508E	C57BL/6J-Nyx	R4508E. CEL	6.33	37.26	60.90%	37.80%	1.30%	1.24	0.82	4	Y
177	R4505E	C57BL/6J- Rpe65	R4505E. CEL	5.98	37.48	61.80%	36.80%	1.40%	1.45	0.85	4	Y
178	R4506E	C57BL/6J- Rpe65	R4506E. CEL	6.94	37.9	61.10%	37.50%	1.30%	1.5	0.83	4	Y
179	R4535E	C57BLKS/J	R4535E. CEL	6.59	37.28	61.20%	37.30%	1.40%	1.26	0.83	4	Y
180	R4536E	C57BLKS/J	R4536E. CEL	1	40.71	60.30%	38.20%	1.50%	1.25	0.77	4	Y
181	R2564E.1	CAST/EiJ	R2564E.1. CEL	1.94	89	58.50%	39.90%	1.60%	1.6	0.77	1	
182	R2580E.1	CAST/EiJ	R2580E.1. CEL	2.09	95	58.20%	40.10%	1.70%	1.4	0.76	1	
183	R4537E	CBA/CaJ	R4537E. CEL	1	38.45	60.60%	37.90%	1.50%	1.63	0.82	4	Y
184	R4538E	CBA/CaJ	R4538E. CEL	5.89	39.18	61.70%	36.90%	1.40%	1.45	0.8	4	Y
185	R4539E	CZECHII/EiJ	R4539E. CEL	7.73	37.1	58.30%	40.10%	1.50%	1.7	0.95	4	Y
186	R4540E	CZECHII/EiJ	R4540E. CEL	11.04	36.69	53.00%	45.30%	1.70%	1.83	1.32	4	
187	R2600E.1	D2B6F1	R2600E.1. CEL	2.47	95	58.10%	40.20%	1.70%	1.41	0.78	1	Y
188	R2604E.1	D2B6F1	R2604E.1. CEL	2.66	90	59.40%	39.20%	1.50%	1.28	0.79	1	Y
189	R1002E.3	DBA/2J	R1002E.3. CEL	1	102	54.80%	43.70%	1.50%	2.84	0.83	3	

190	R4541E	DBA/2J	R4541E. CEL	1	43.4	61.40%	37.00%	1.50%	1.37	0.73	4	Y
191	R959E.3	DBA/2J	R959E.3. CEL	1	89.97	53.20%	45.30%	1.50%	3.66	1.09	4	
192	R2572E.1	DBA/2J	R2572E.1. CEL	2.41	79	55.50%	42.90%	1.60%	1.37	0.79	1	
193	R4542E	DBA/2J	R4542E. CEL	5.7	39.95	61.00%	37.40%	1.50%	1.23	0.81	4	Y
194	R2771E.3	FVB/NJ	R2771E.3. CEL	1	70	55.30%	43.20%	1.50%	1.69	0.83	3	
195	R2772E.3	FVB/NJ	R2772E.3. CEL	1	76	55.20%	43.40%	1.40%	2.13	1.02	3	
196	R2636E.1	KK/HIJ	R2636E.1. CEL	2.61	93	58.90%	39.50%	1.50%	1.39	0.76	1	Y
197	R2637E.1	KK/HIJ	R2637E.1. CEL	2.19	103	59.40%	39.00%	1.50%	1.3	0.79	1	Y
198	R0999E.1	LG/J	R0999E.1. CEL	2.45	82	59.40%	39.10%	1.50%	1.38	0.79	1	Y
199	R1004E.1	LG/J	R1004E.1. CEL	2.44	92	58.70%	39.80%	1.50%	1.38	0.79	1	Y
200	R4543E	LP/J	R4543E. CEL	6.57	41.99	60.30%	38.20%	1.50%	1.28	0.75	4	Y
201	R4544E	LP/J	R4544E. CEL	4.56	39.9	62.40%	36.10%	1.50%	1.23	0.77	4	Y
202	R2858E.3	MOLF/EiJ	R2858E.3. CEL	1	64	53.80%	44.70%	1.50%	1.59	0.95	3	
203	R2919.3	MOLF/EiJ	R2919.3. CEL	1	64	52.40%	46.00%	1.60%	2.15	1.07	3	
204	R1688E.1	NOD/LtJ	R1688E.1. CEL	2.66	98	58.60%	39.90%	1.50%	1.26	0.8	1	Y
205	R2566E- 2.1	NOD/LtJ	R2566E- 2.1.CEL	3.03	69	59.80%	38.80%	1.50%	1.38	0.75	1	Y
206	R4545E	NZB/BINJ	R4545E. CEL	4.23	43.48	62.10%	36.40%	1.50%	1.33	0.76	4	Y

207	R4546E	NZB/BINJ	R4546E.CEL	6.27	44.22	59.40%	39.10%	1.50%	1.17	0.82	4	Y
208	R2535E.1	NZO/HILtJ	R2535E.1.CEL	1.89	86	60.40%	38.20%	1.40%	1.41	0.85	1	
209	R2550E.1	NZO/HILtJ	R2550E.1.CEL	1.79	87	60.70%	37.80%	1.50%	1.52	0.82	1	
210	R2817E.3	NZW/LacJ	R2817E.3.CEL	1	59	50.90%	47.60%	1.50%	3.59	1.48	3	
211	<b>R2810E</b>	NZW/LacJ	R2810E.CEL								3	
212	R2810E.3	NZW/LacJ	R2810E.3.CEL	1	74	57.00%	41.70%	1.40%	2.15	1.03	4	Y
213	R4547E	PANCEVO/EiJ	R4547E.CEL	5.27	51.34	57.20%	41.10%	1.70%	1.7	0.83	4	
214	R4548E	PANCEVO/EiJ	R4548E.CEL	10.54	37.39	50.30%	48.00%	1.70%	1.68	1.09	4	
215	R2635E.1	PWD/PhJ	R2635E.1.CEL	3.72	80	54.20%	44.10%	1.70%	1.53	0.85	1	
216	R2634E.1	PWD/PhJ	R2634E.1.CEL	3.29	90	55.90%	42.50%	1.60%	1.57	0.81	1	
217	R2544E.1	PWK/PhJ	R2544E.1.CEL	2.2	108	54.90%	43.50%	1.70%	1.36	0.82	1	
218	R2549E.1	PWK/PhJ	R2549E.1.CEL	2.28	84	57.30%	41.20%	1.50%	1.57	0.83	1	
219	R4550E	SJL/J	R4550E.CEL	5.35	40.44	62.30%	36.20%	1.40%	1.24	0.79	4	
220	R2368E.1	WSB/EiJ	R2368E.1.CEL	2.57	86	59.50%	39.10%	1.40%	1.29	0.74	1	Y
221	R2547E.1	WSB/EiJ	R2547E.1.CEL	2.14	90	58.20%	40.10%	1.60%	1.32	0.77	1	Y

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### Information about this text file:

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### GEO Series Data: This section to be used for GEO submission of the whole series of arrays

**GSE Series** No GEO series number

**Status** Public on Feb 3, 2009

**Title** Gene expression landscape of the mammalian eye: A global survey and database of mRNAs of 103 varieties of mice

**Organism(s)** [Mus musculus](#)

**Experiment type** Expression profiling by array

**Summary** The HEIMED September 2008 RMA data release provides estimates of gene expression in whole eyes of 103 lines of young adult mice generated using 221 Affymetrix M430 2.0 arrays. This data set is intended for exploration of the genetics and genomics of the mouse eye, retina, lens, retinal pigment epithelium, cornea, iris and choroid.

**Overall design** We used pooled RNA samples of whole eyes, usually two independent pools--one male, one female pool--for most lines of mice. This data set was processed using the [RMA](#) protocol. A total of 2223 probes sets are associated with LRS values greater than 46 (LOD >10).

**Contributor(s)** Eldon E. Geisert, Lu Lu, Natalie E. Freeman-Anderson, Xusheng Wang, Weikuan Gu, Yan Jiao, Robert W. Williams

**Citation(s)** Eldon E. Geisert, Lu Lu, Natalie E. Freeman-Anderson, Xusheng Wang, Weikuan Gu, Yan Jiao, Robert W. Williams. Gene expression landscape of the mammalian eye: A global survey and database of mRNAs of 103 varieties of mice. *Molecular Vision* 2009; in press. PMID: XXXXXX

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**Country** USA

**Platforms** (1) [GPL1261](#) Affymetrix GeneChip Mouse Genome 430 2.0 Array

**Samples** (221) GSMXXXXX 1\_SampleNameHere, GSMXXXXX 2\_SampleNameHere,  
GSMXXXXX 221\_SampleNameHere,

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