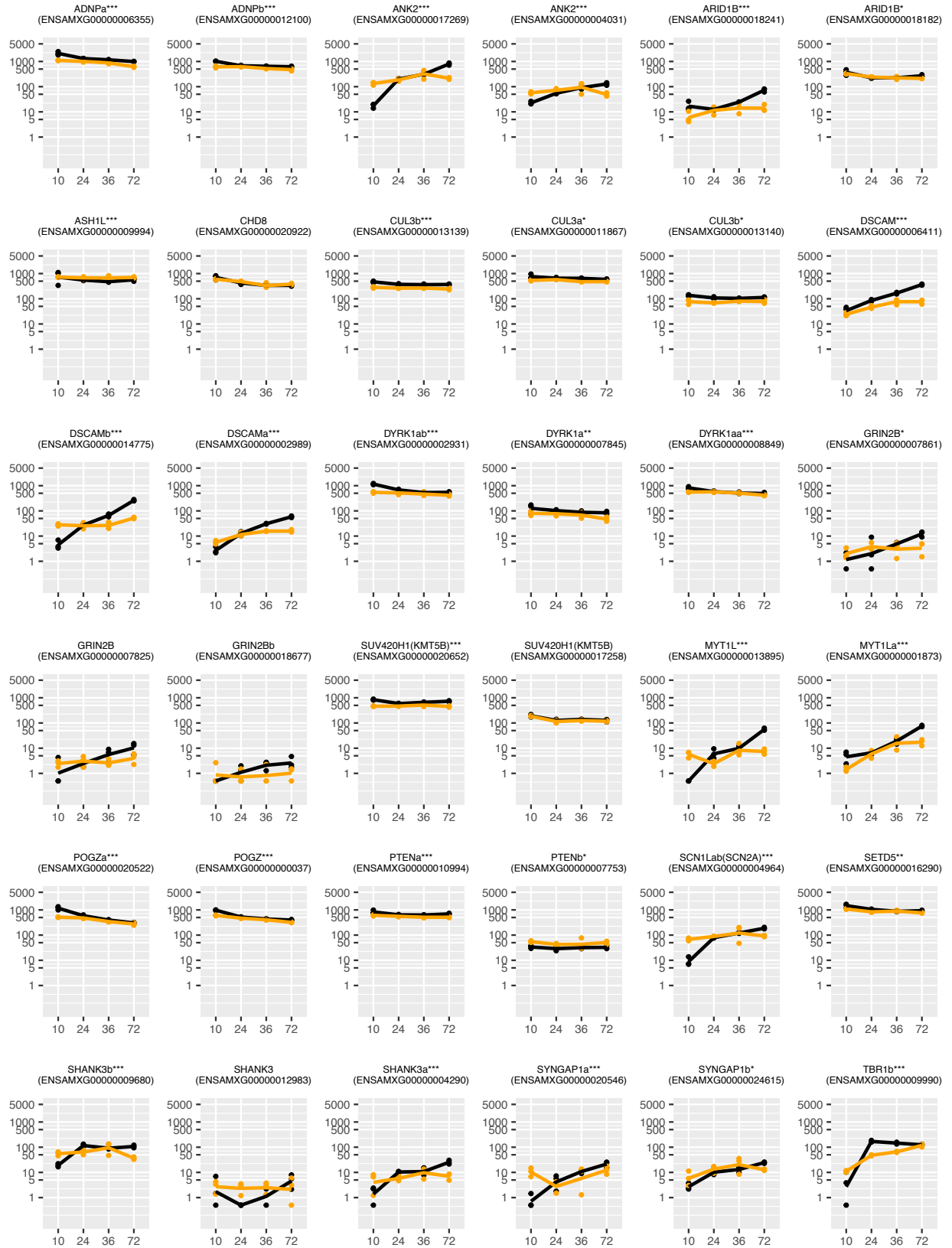


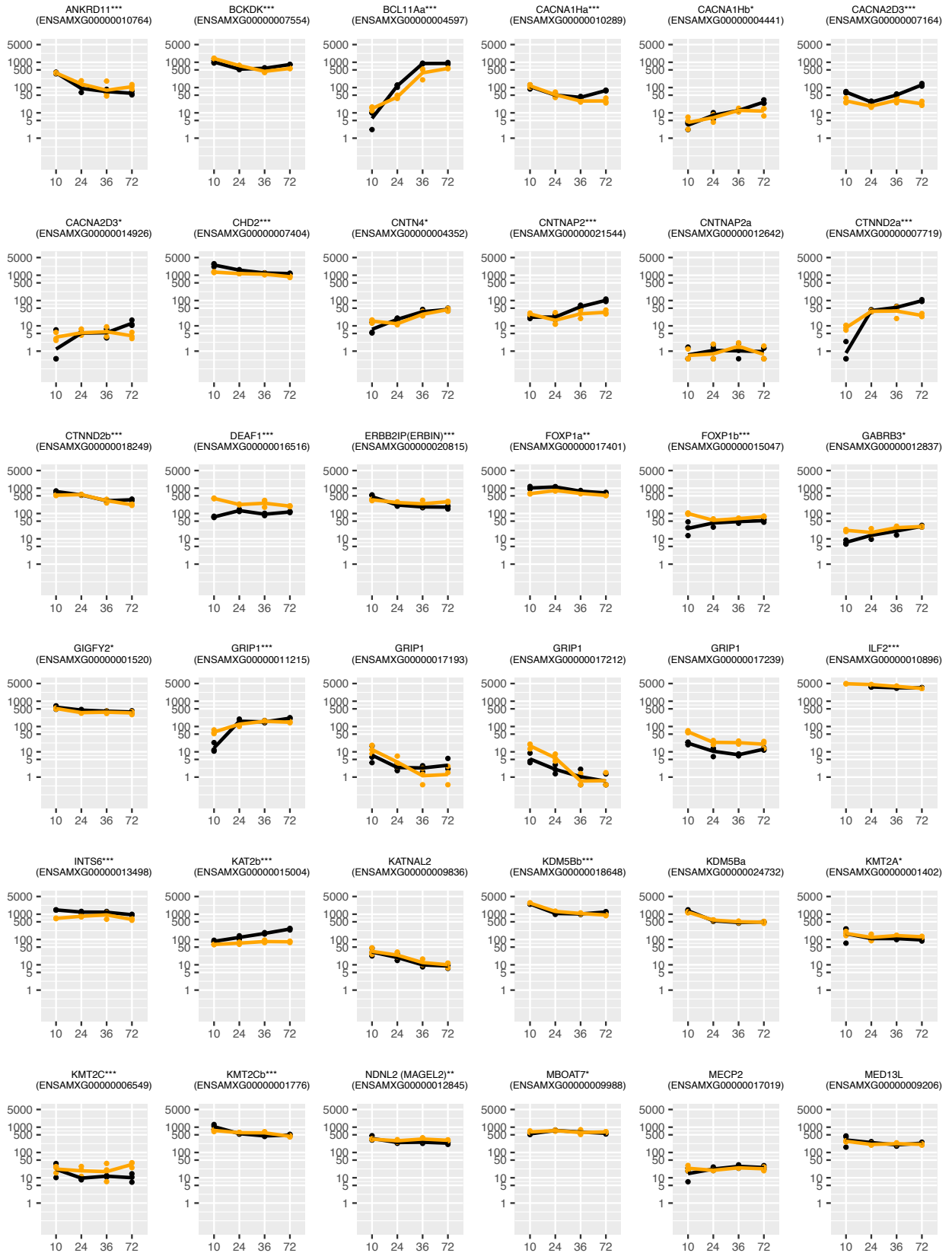
SFARI Gene Category 1 (page 1 of 1)



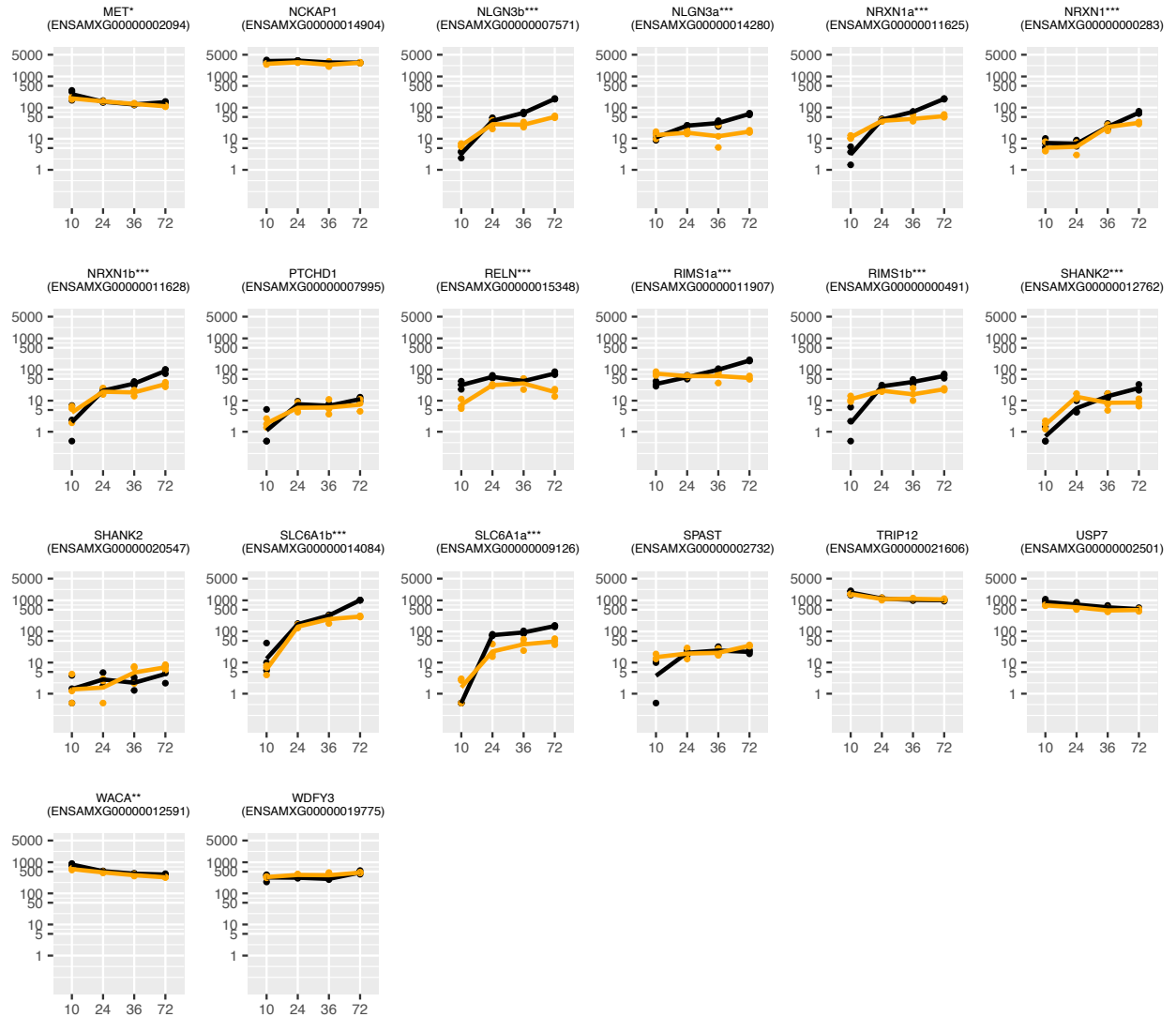
Additional file 2.1—associated with Table 1. Many of the ASD-risk genes listed in SFARI Gene Category 1 had significantly different expression between surface fish and cavefish at the stages of 10, 24, 36 and 72 hours post fertilization (hpf).

A set of 36 *A. mexicanus* genes (all paralogs of 18 out of 19 orthologs in Category 1) that are orthologs of human SFARI Gene Category 1 is shown (https://gene.sfari.org/autdb/GS_Home.do). Y-axis: normalized count of the number of sequence reads (Fragments Per Kilobase Million; FPKM). X-axis: hours post fertilization. Yellow dots and line represent the gene expression of cavefish, and the black dots and line represent that of surface fish. Each dot represents one of 3 replicates in each data point (morph and age). *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$ in the lower P-value between the age $\times$ morph interaction and the expression difference at 72 hpf after applying Benjamini-Hochberg correction[1]. See also Additional file 1.

SFARI Gene Category 2 (page 1 of 2)



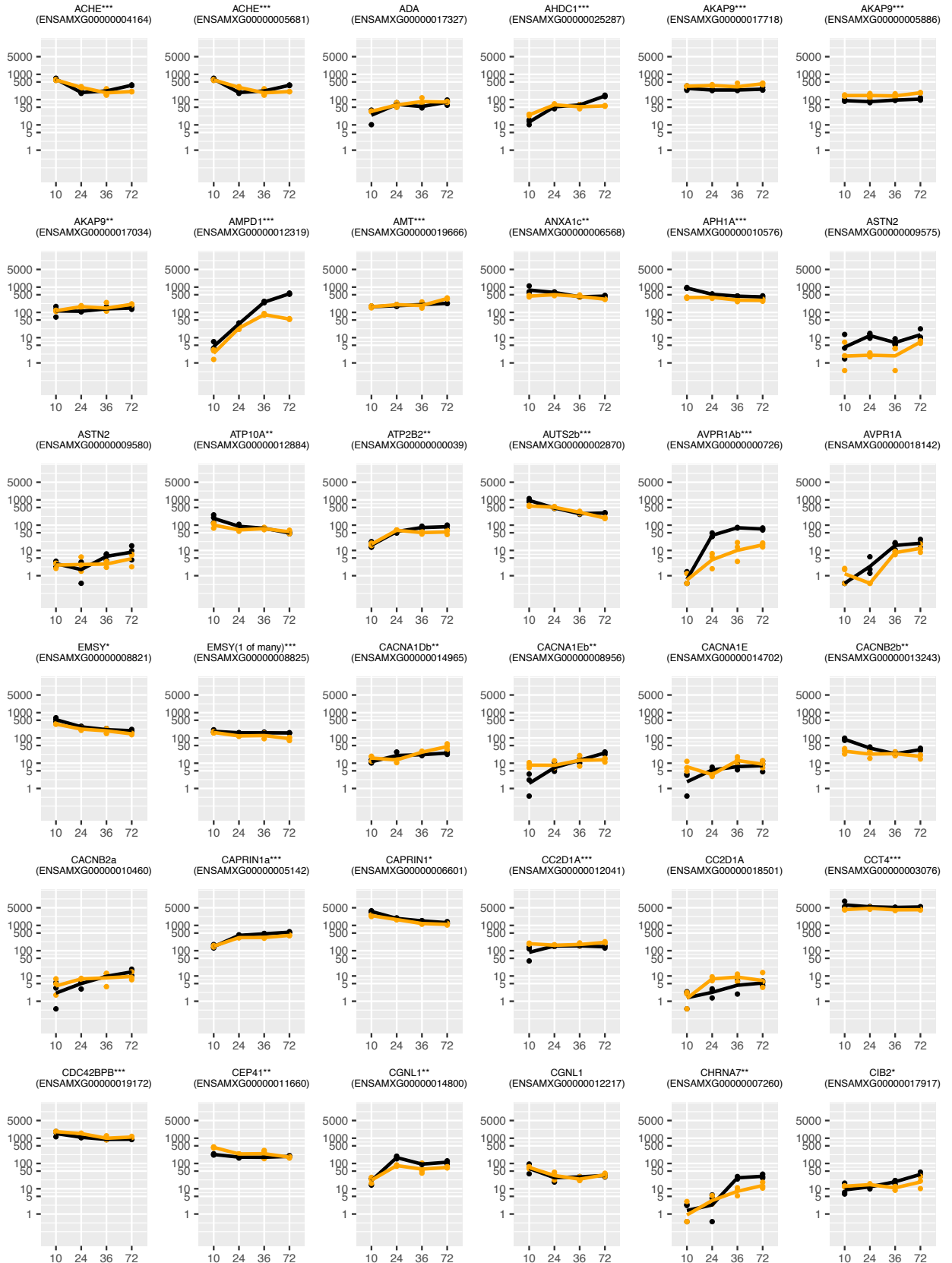
SFARI Gene Category 2 (page 2 of 2)



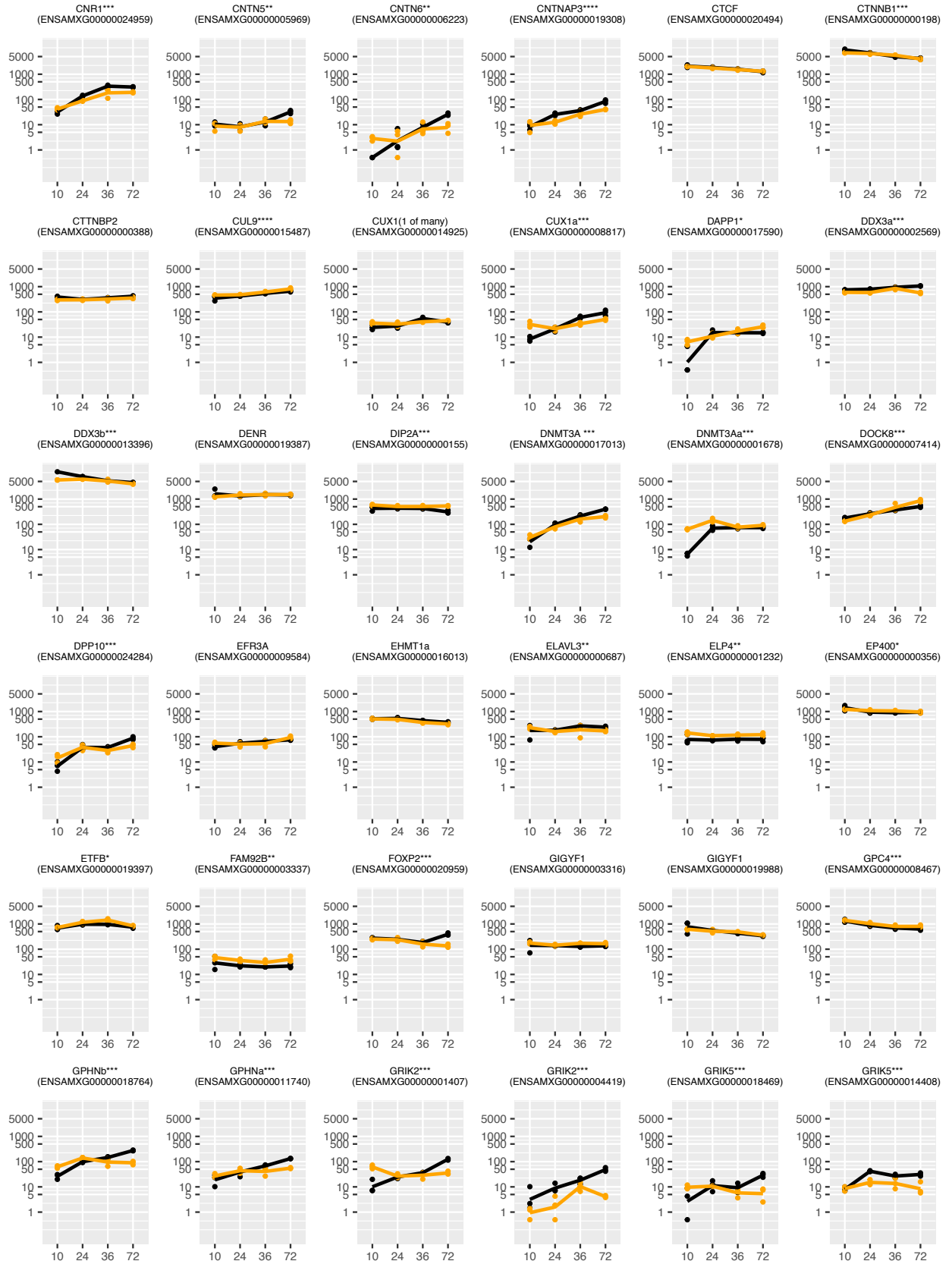
Additional file 2.2—associated with Table 1. Many of the ASD-risk genes listed in SFARI Gene Category 2 had significantly different expression in surface fish and cavefish at the stages of 10, 24, 36 and 72 hours post fertilization (hpf).

A set of 56 (all paralogs of 40 out of 43 orthologs in Category 2) *A. mexicanus* genes that are orthologs of human SFARI Gene Category 2 is shown (https://gene.sfari.org/autdb/GS_Home.do). Y-axis: normalized count of the number of sequence reads (Fragments Per Kilobase Million; FPKM). X-axis: hours post fertilization. Yellow dots and line represent the gene expression of cavefish, and the black dots and line represent that of surface fish. Each dot represents one of 3 replicates in each data point (morph and age). *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$ in the lower P-value of between the age $\times$ morph interaction and the expression difference at 72 hpf after applying Benjamini-Hochberg correction [1]. See also Additional file 1.

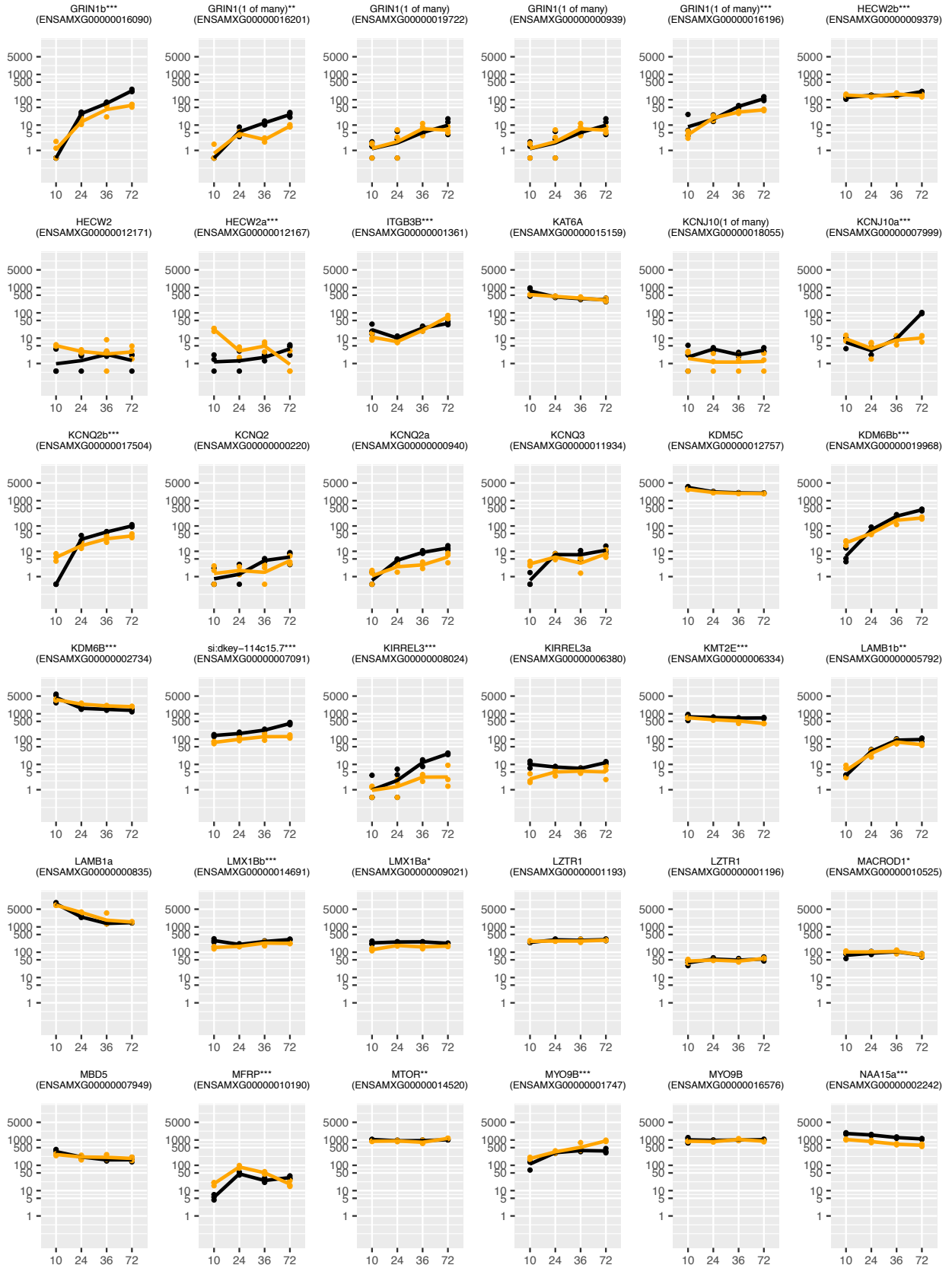
SFARI Gene Category 1 (page 1 of 6)



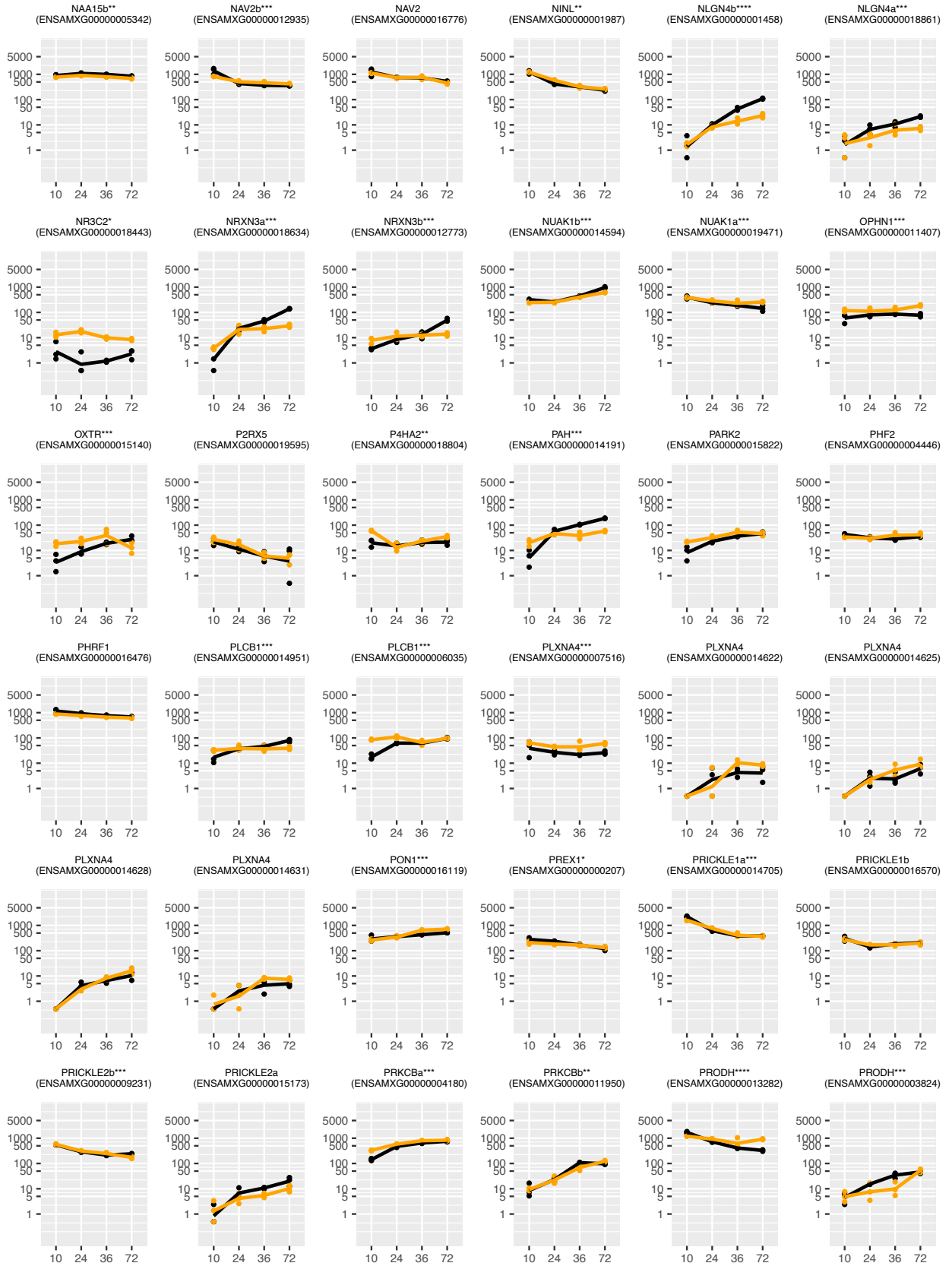
SFARI Gene Category 3 (page 2 of 6)



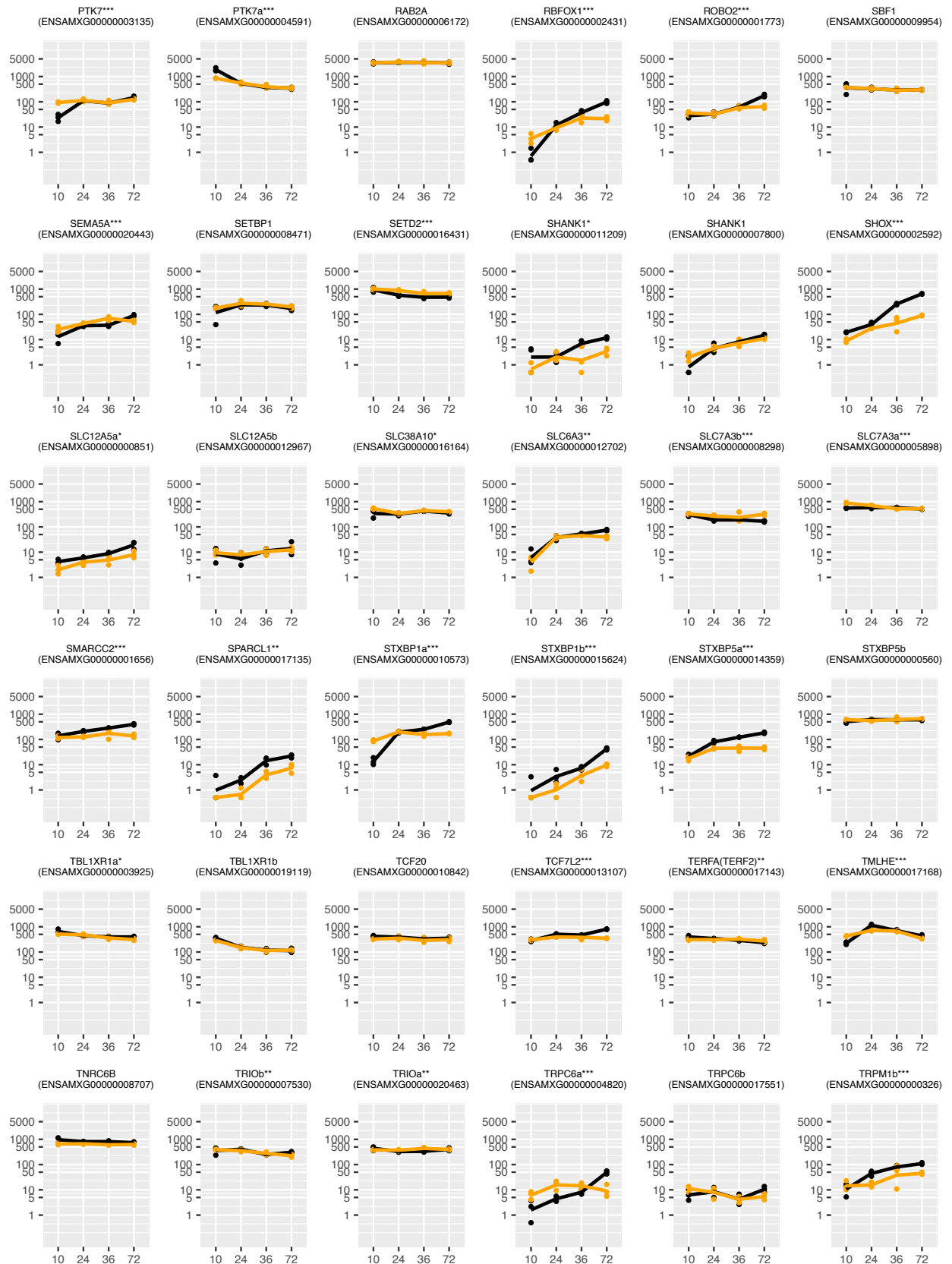
SFARI Gene Category 3 (page 3 of 6)



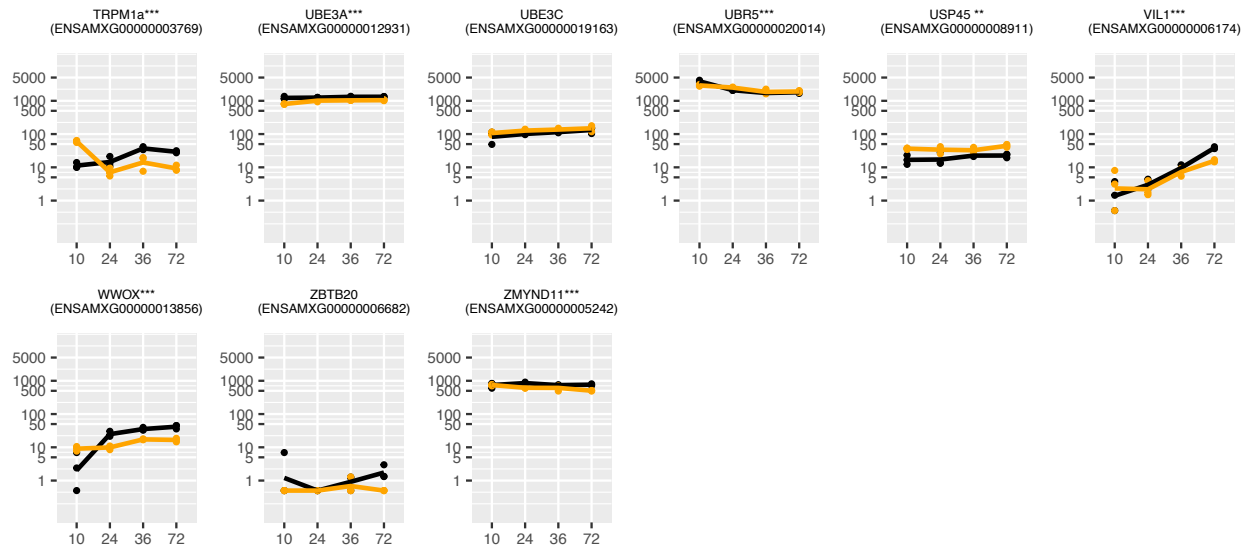
SFARI Gene Category 3 (page 4 of 6)



SFARI Gene Category 3 (page 5 of 6)



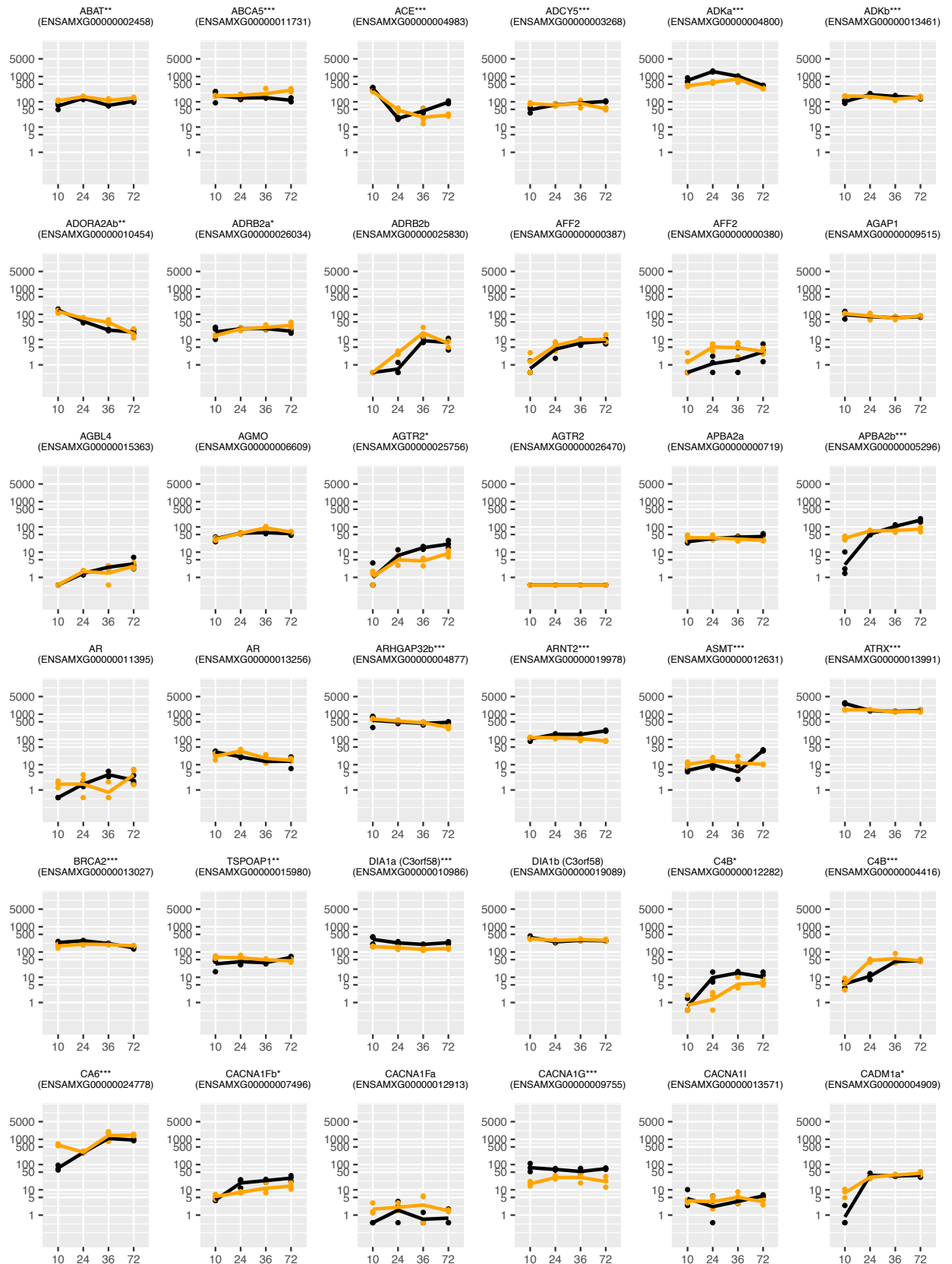
SFARI Gene Category 3 (page 6 of 6)



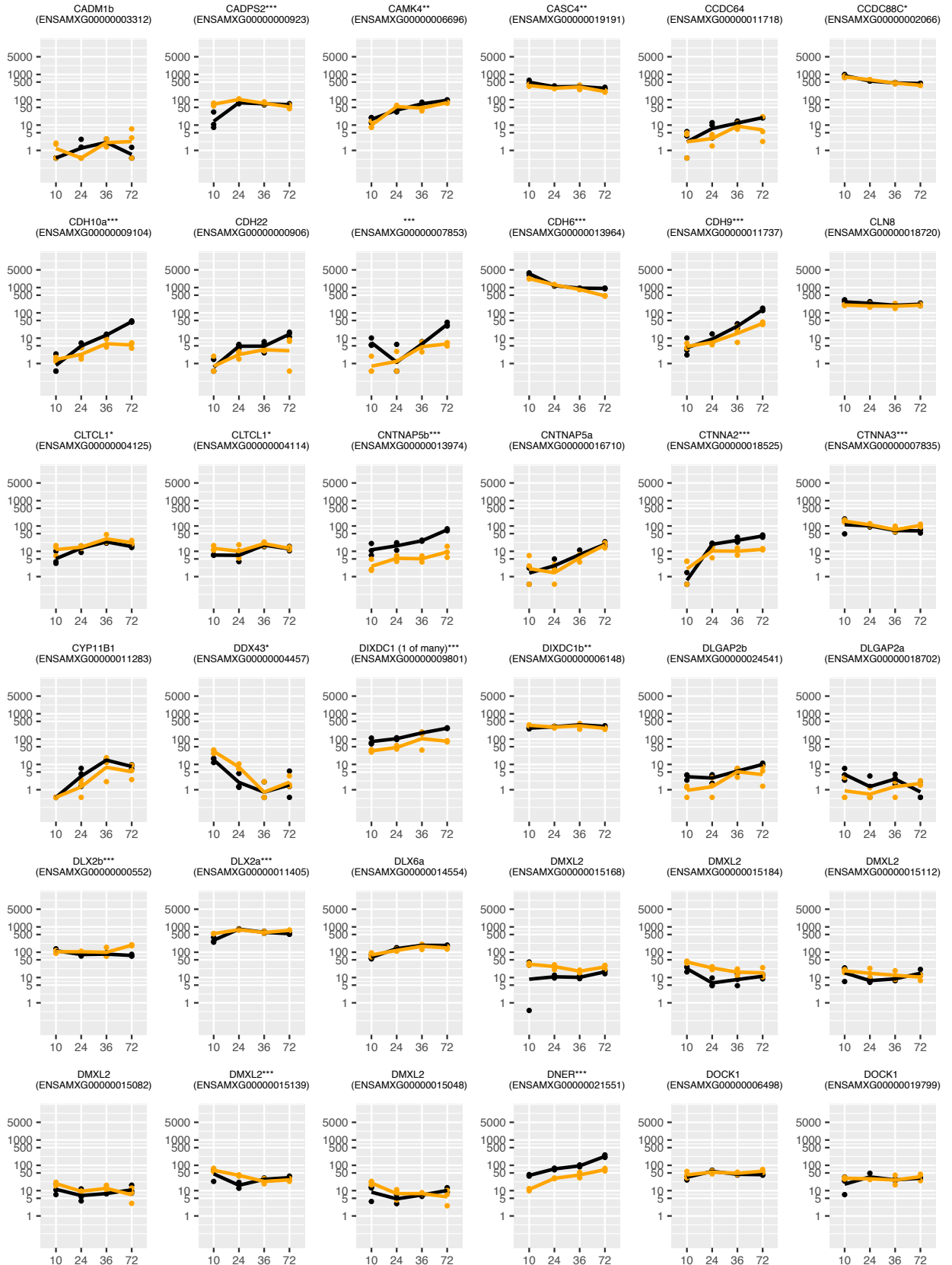
Additional file 2.3—associated with Table 1. Many of the ASD-risk genes listed in SFARI Gene Category 3 had significantly different expression in surface fish and cavefish at the stages of 10, 24, 36 and 72 hours post fertilization (hpf).

A set of 189 (all paralogs of 132 out of 139 orthologs in Category 3) *A. mexicanus* genes, orthologs of human SFARI Gene Category 3 is shown (https://gene.sfari.org/autdb/GS_Home.do). Y-axis: normalized count of the number of sequence reads (Fragments Per Kilobase Million; FPKM). X-axis: hours post fertilization. Yellow dots and line represent the gene expression of cavefish, and the black dots and line represent that of surface fish. Each dot represents one of 3 replicates in each data point (morph and age). *: P < 0.05, **: P < 0.01, ***: P < 0.001 in the lower P-value of between the age × morph interaction and the expression difference at 72 hpf after applying Benjamini-Hochberg correction [1]. See also Additional file 1.

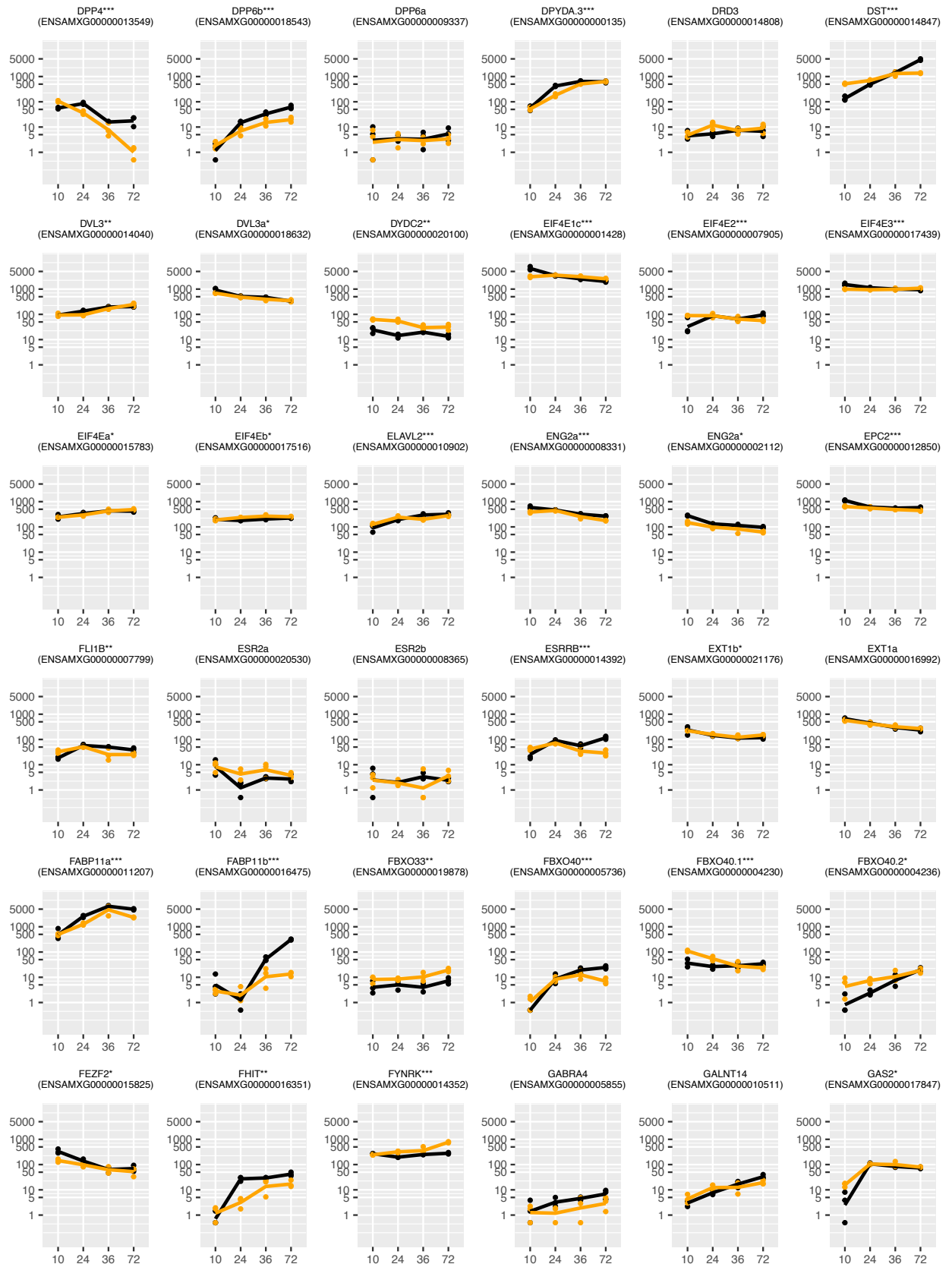
SFARI Gene Category 4 (page 1 of 9)



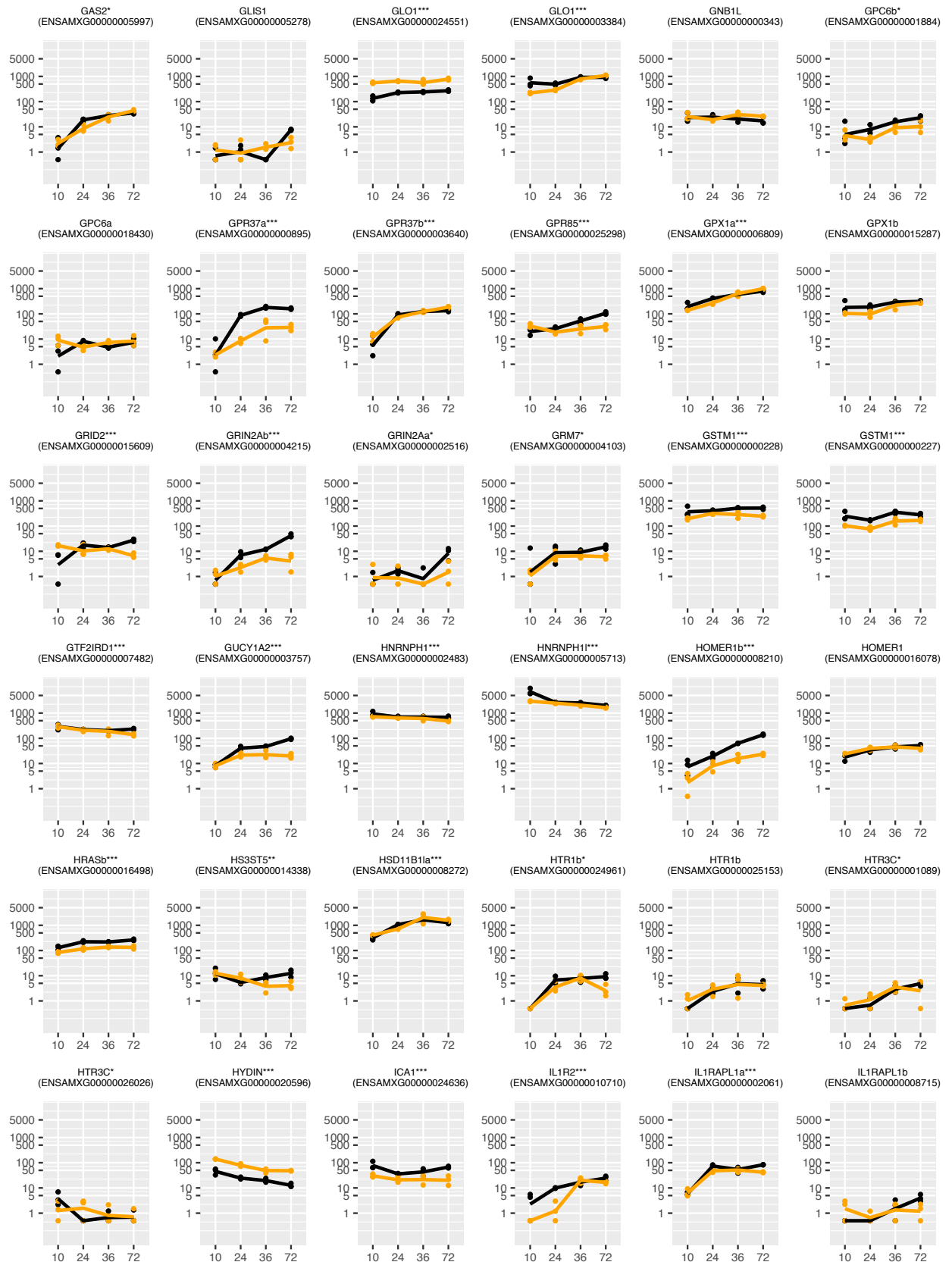
SFARI Gene Category 4 (page 2 of 9)



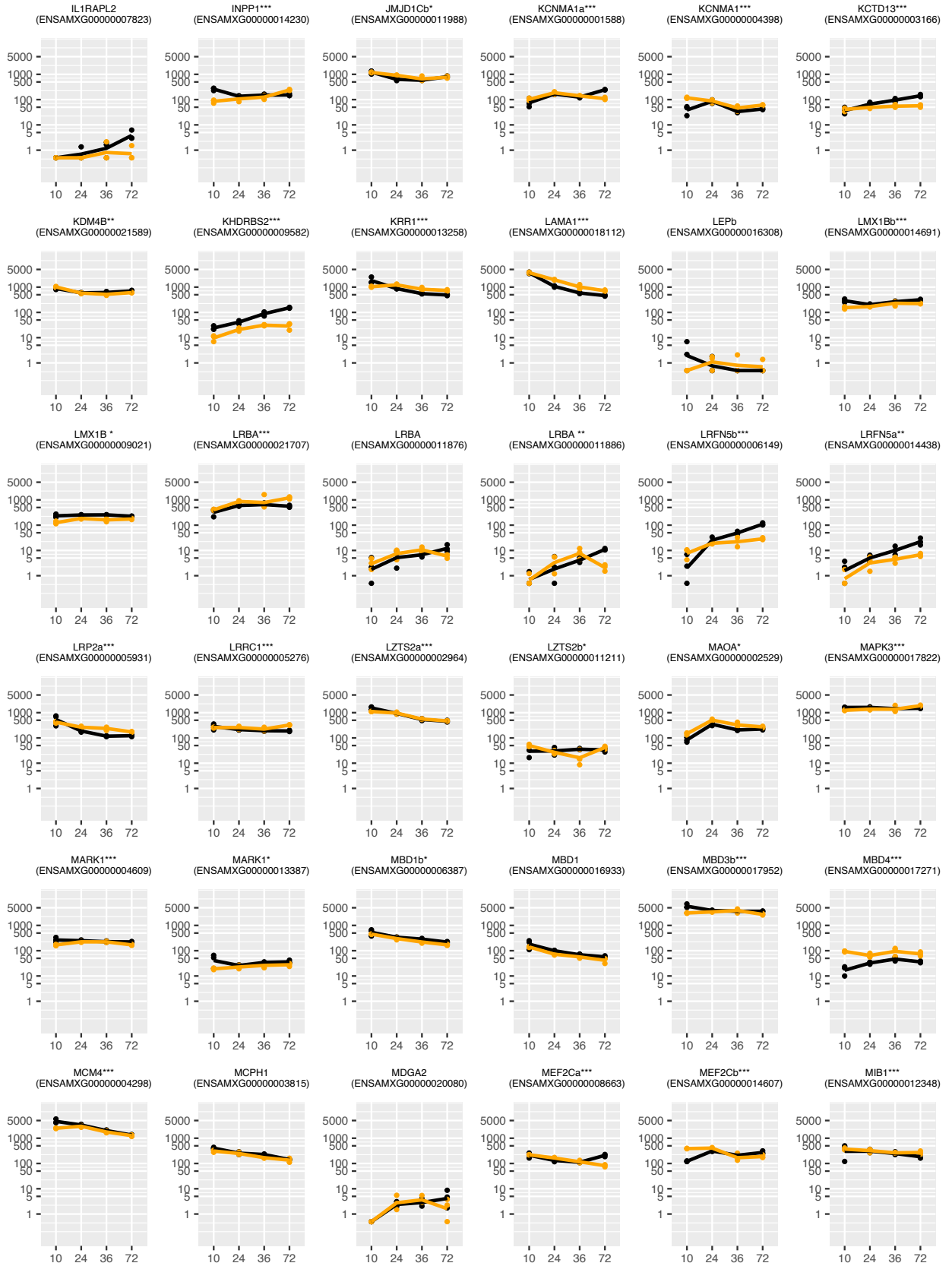
SFARI Gene Category 4 (page 3 of 9)



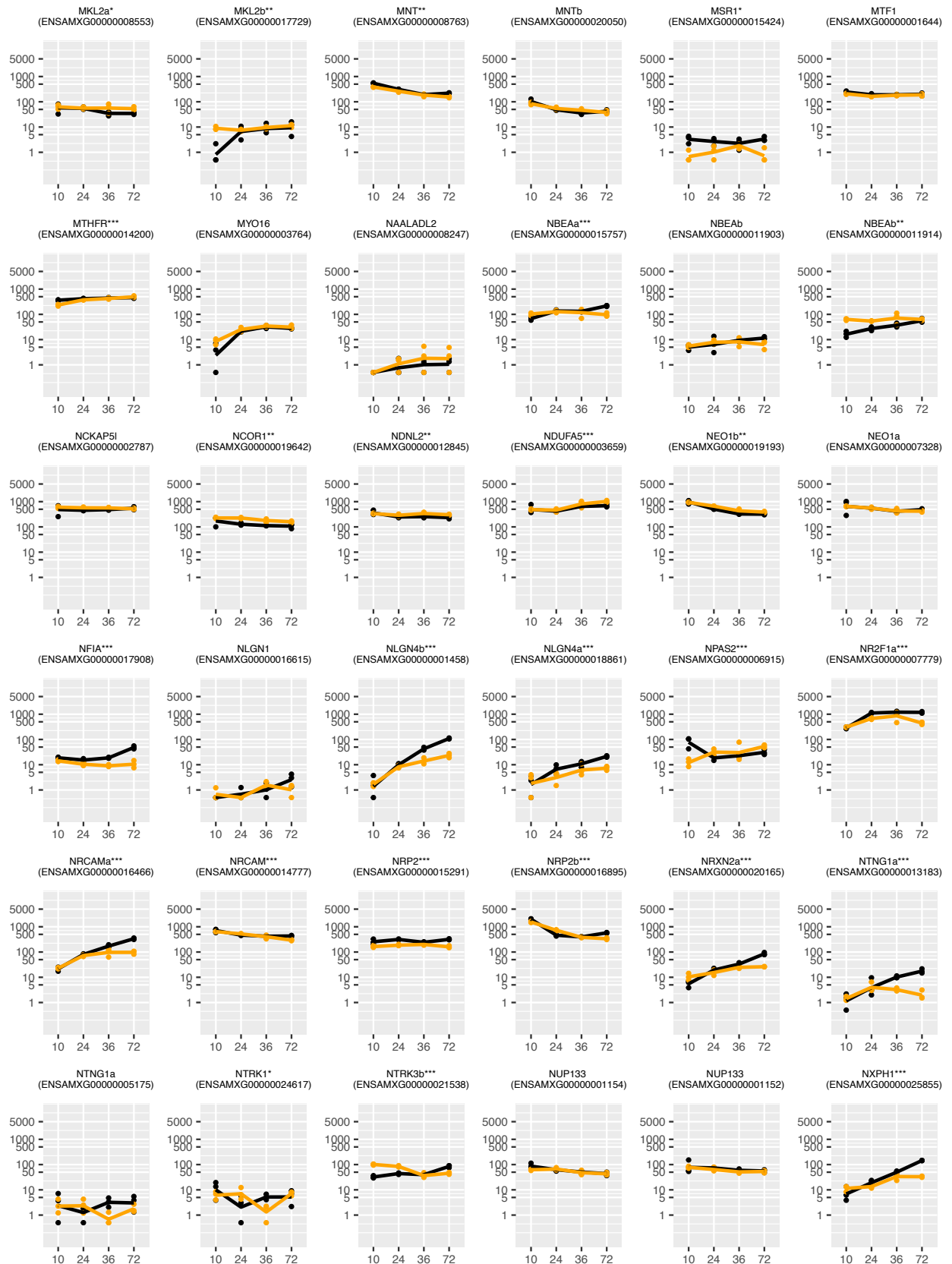
SFARI Gene Category 4 (page 4 of 9)



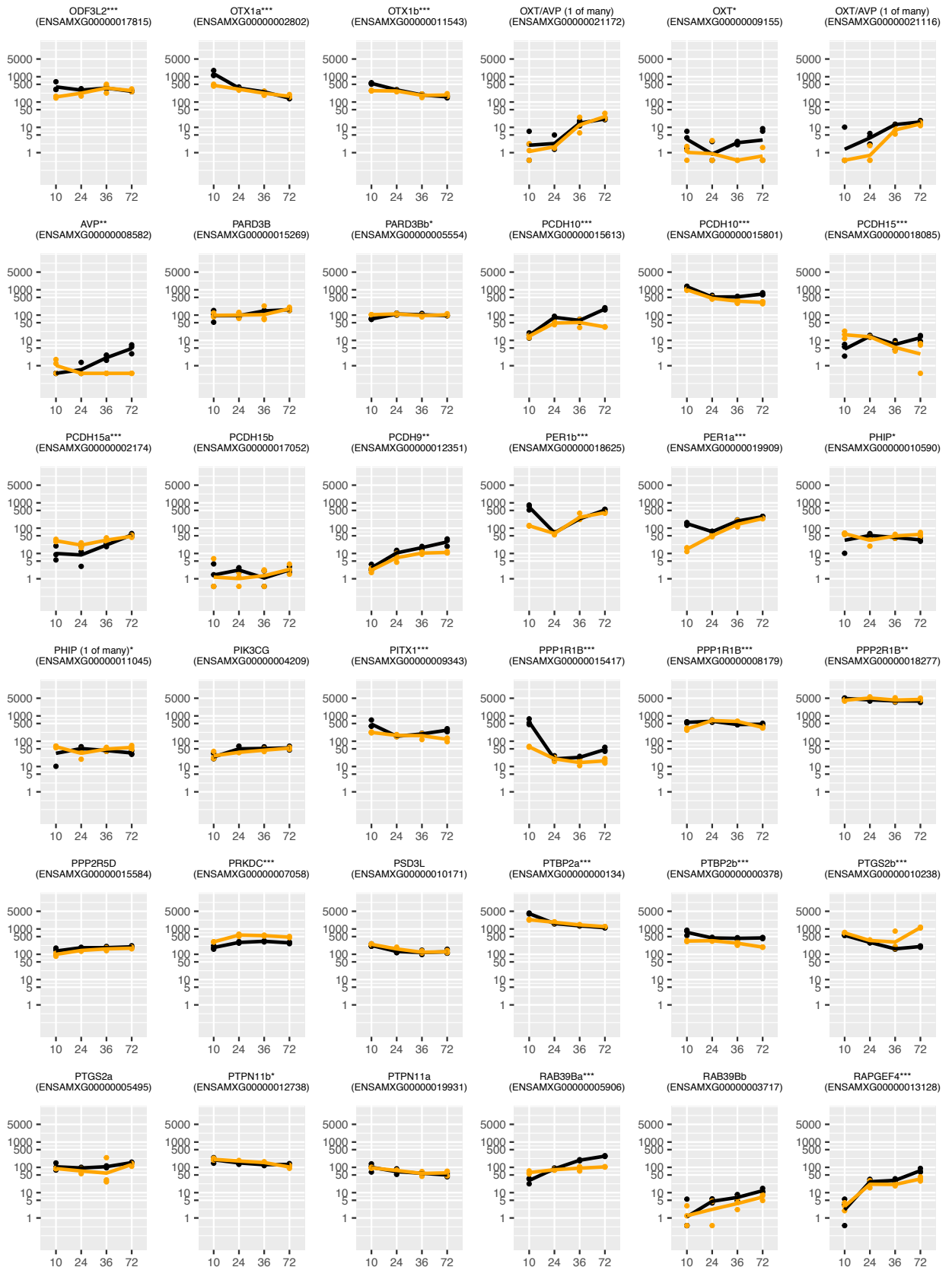
SFARI Gene Category 4 (page 5 of 9)



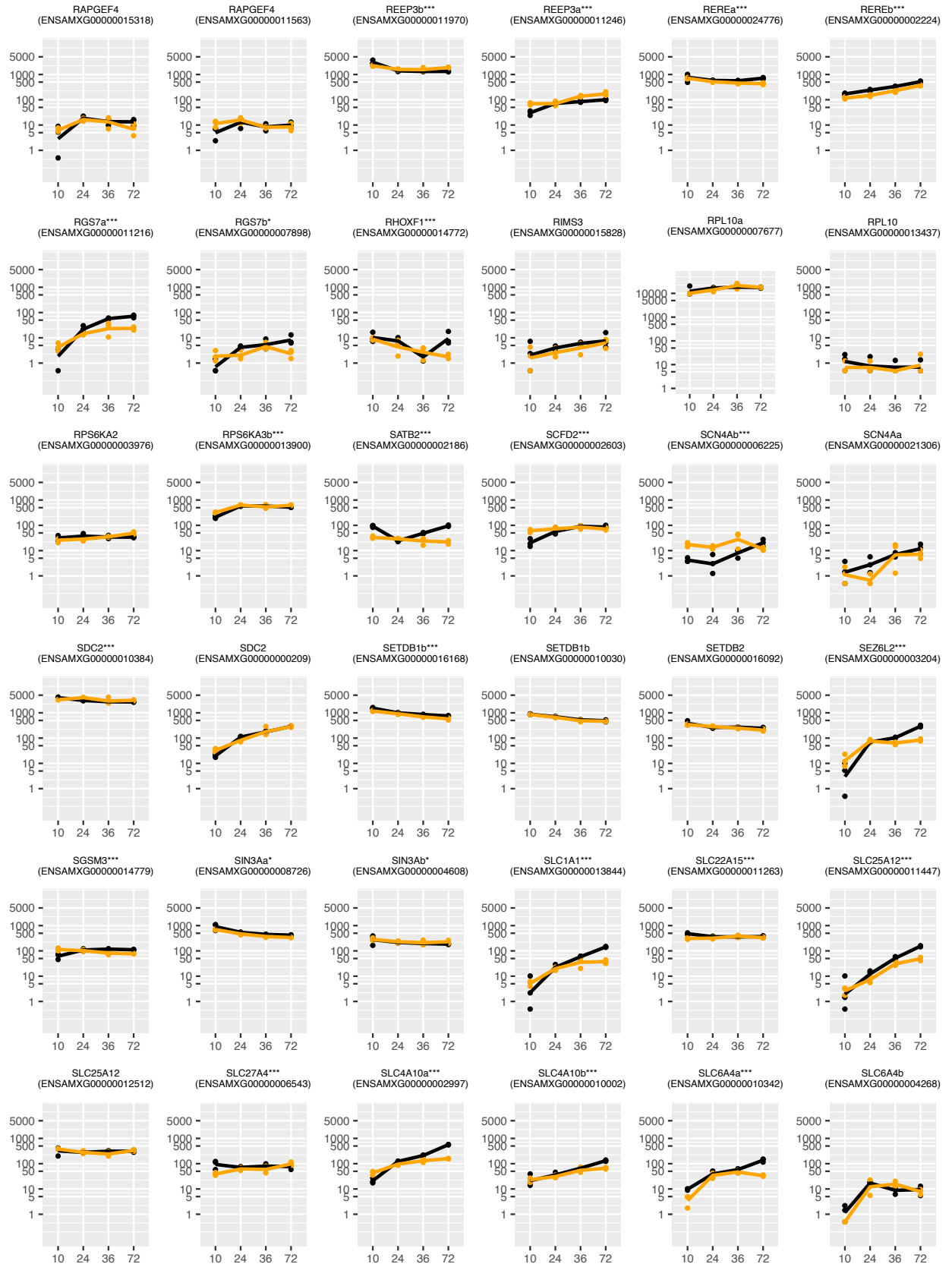
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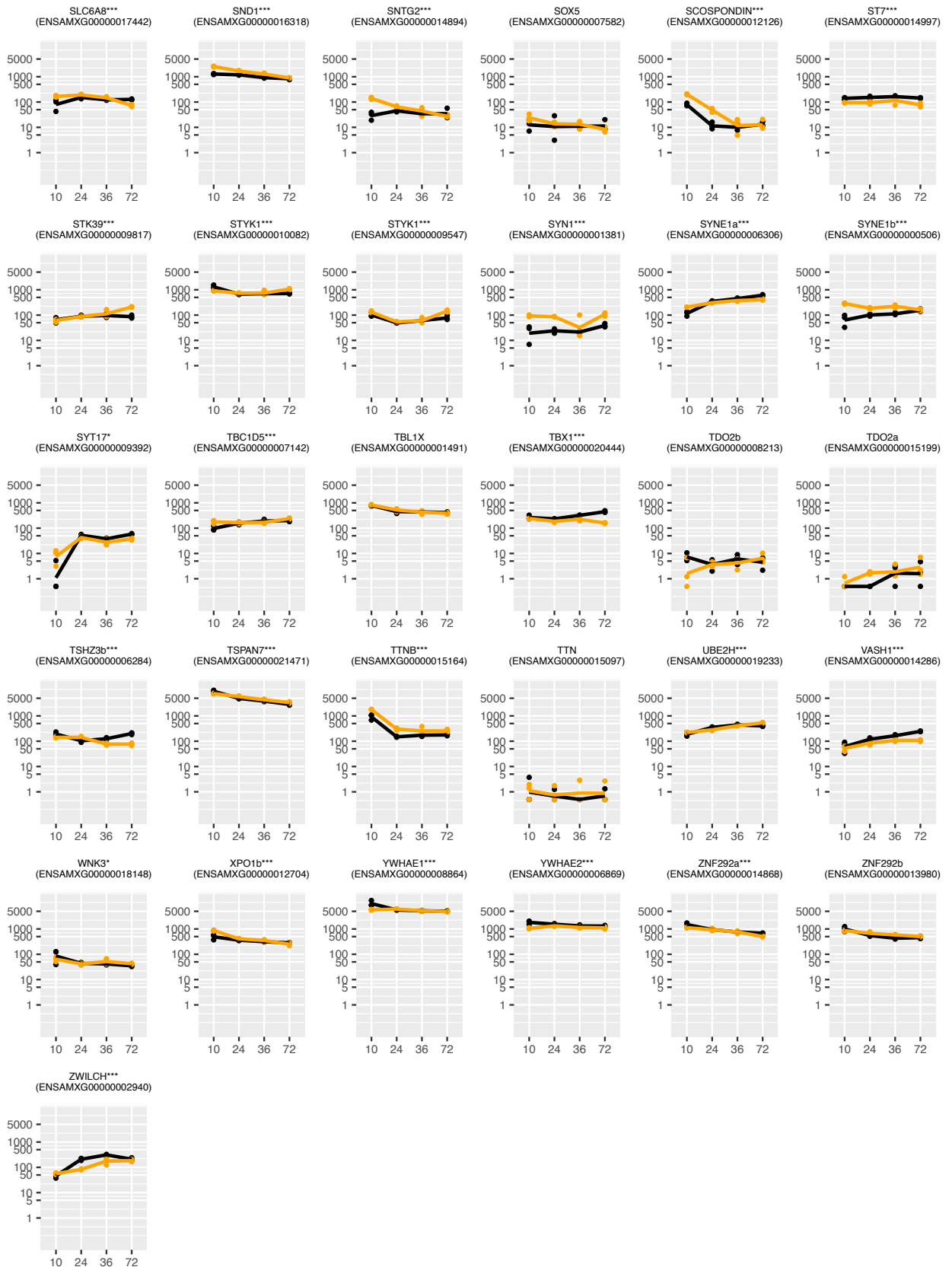
SFARI Gene Category 4 (page 7 of 9)



SFARI Gene Category 4 (page 8 of 9)



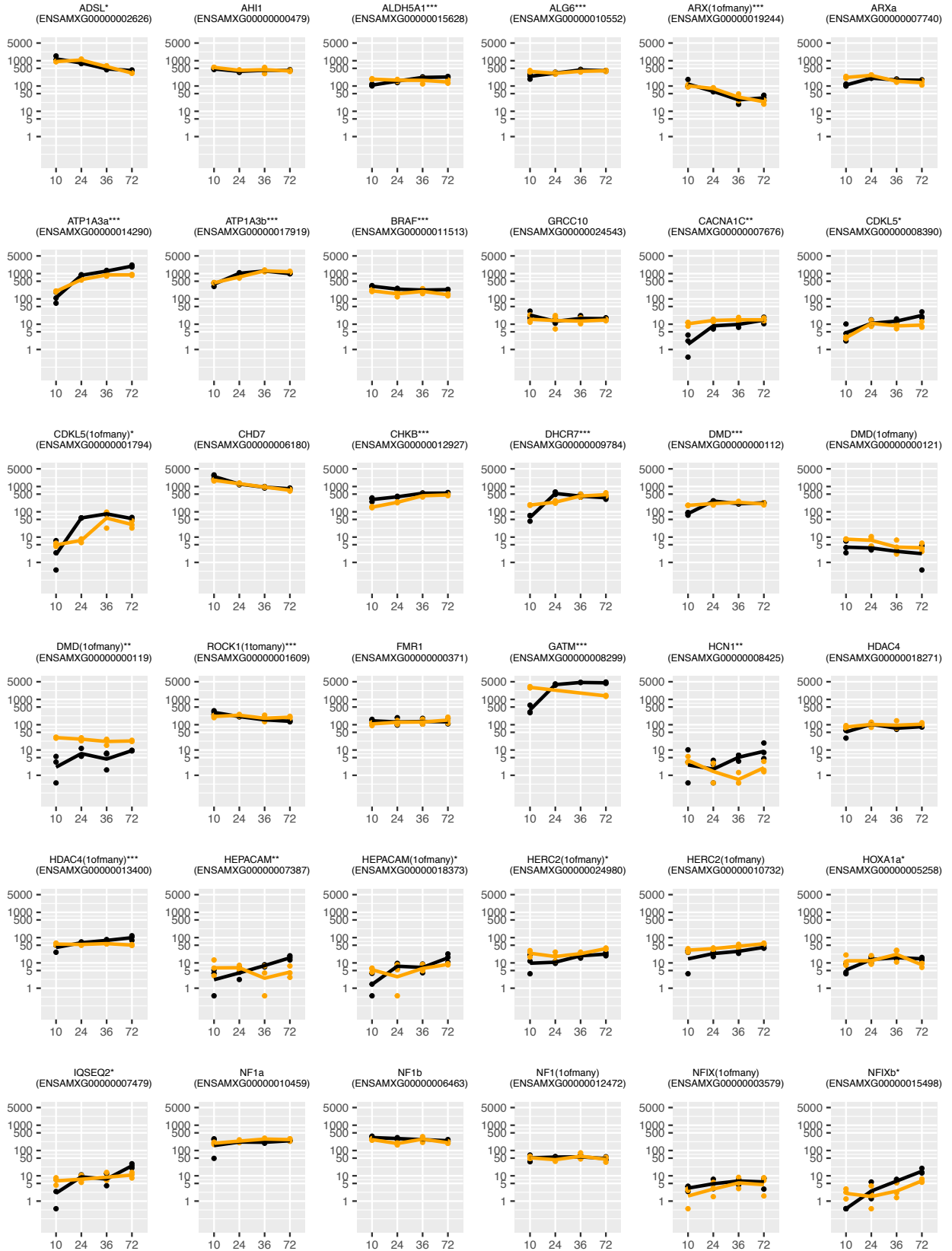
SFARI Gene Category 4 (page 9 of 9)



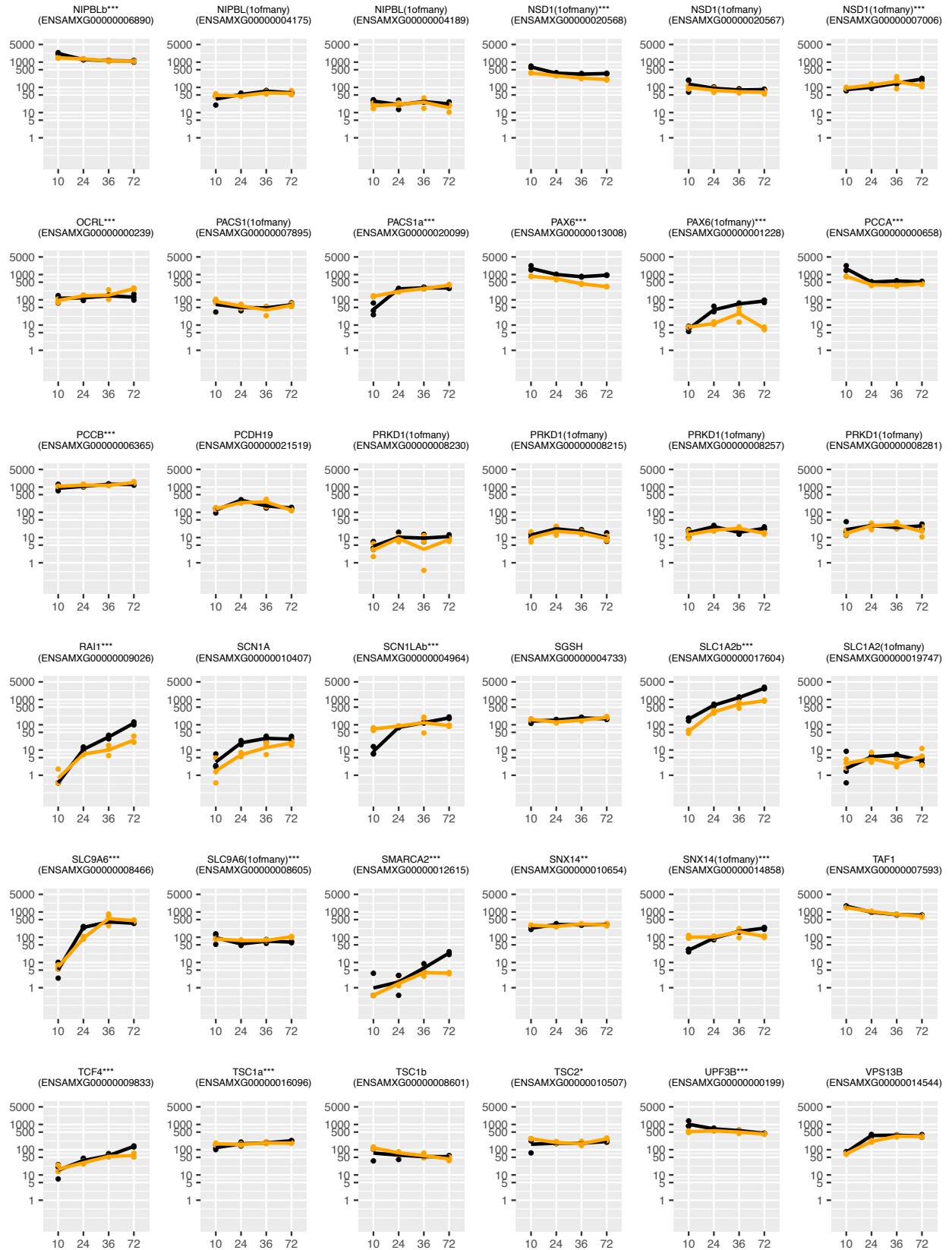
Additional file 2.4—associated with Table 1. Many of the ASD-risk genes listed in SFARI Gene Category 4 had significantly different expression in surface fish and cavefish at the stages of 10, 24, 36 and 72 hours post fertilization (hpf).

A set of 319 (all paralogs of 219 out of 244 orthologs in Category 4) *A. mexicanus* genes that are orthologs of human SFARI Gene Category 4 is shown (https://gene.sfari.org/autdb/GS_Home.do). Y-axis: normalized count of the number of sequence reads (Fragments Per Kilobase Million; FPKM). X-axis: hours post fertilization. Yellow dots and line represent the gene expression of cavefish, and the black dots and line represent that of surface fish. Each dot represents one of 3 replicates in each data point (morph and age). *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$ in the lower P-value of between the age $\times$ morph interaction and the expression difference at 72 hpf after applying Benjamini-Hochberg correction [1]. See also Additional file 1.

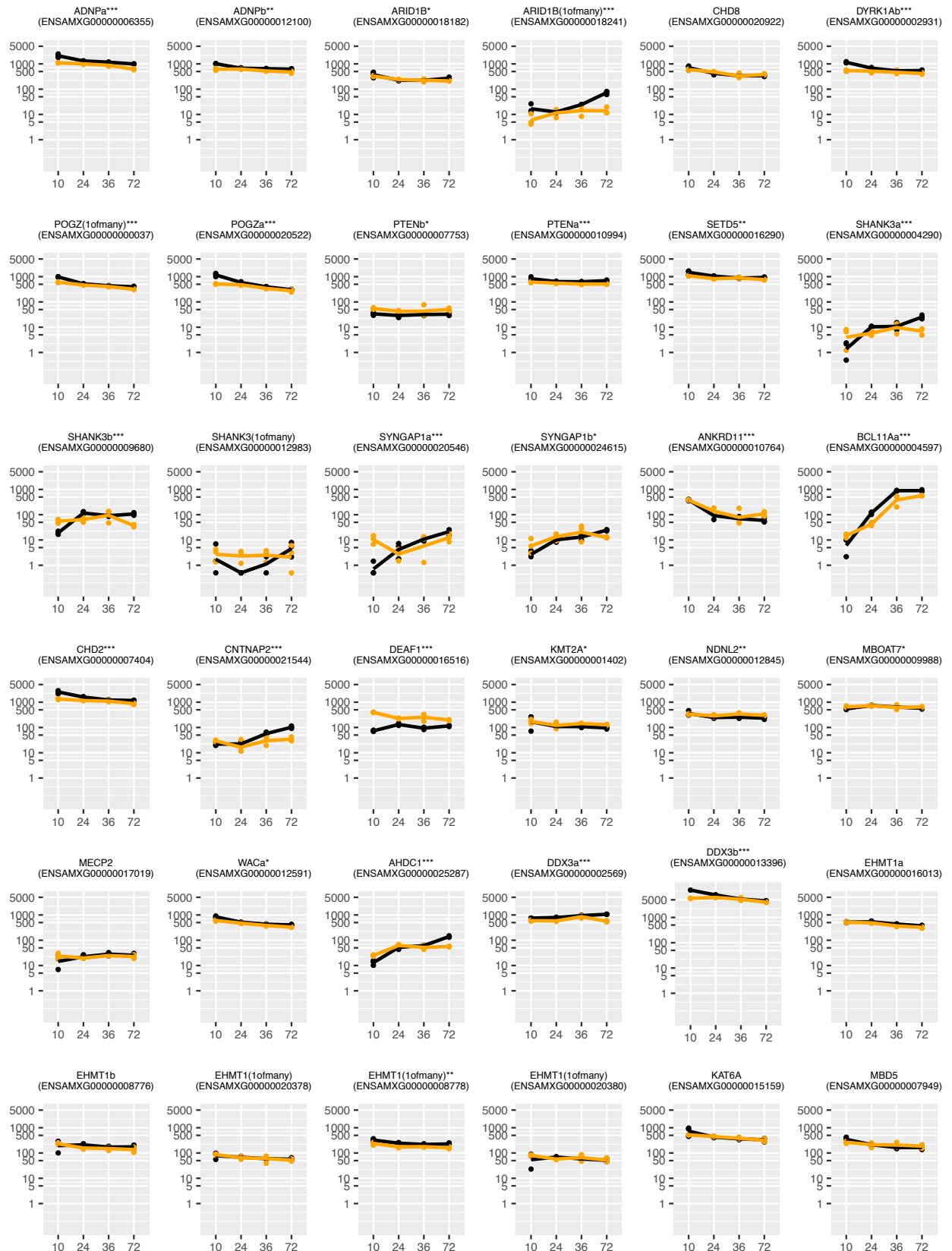
SFARI Gene Category S (Syndromic) (page 1 of 4)



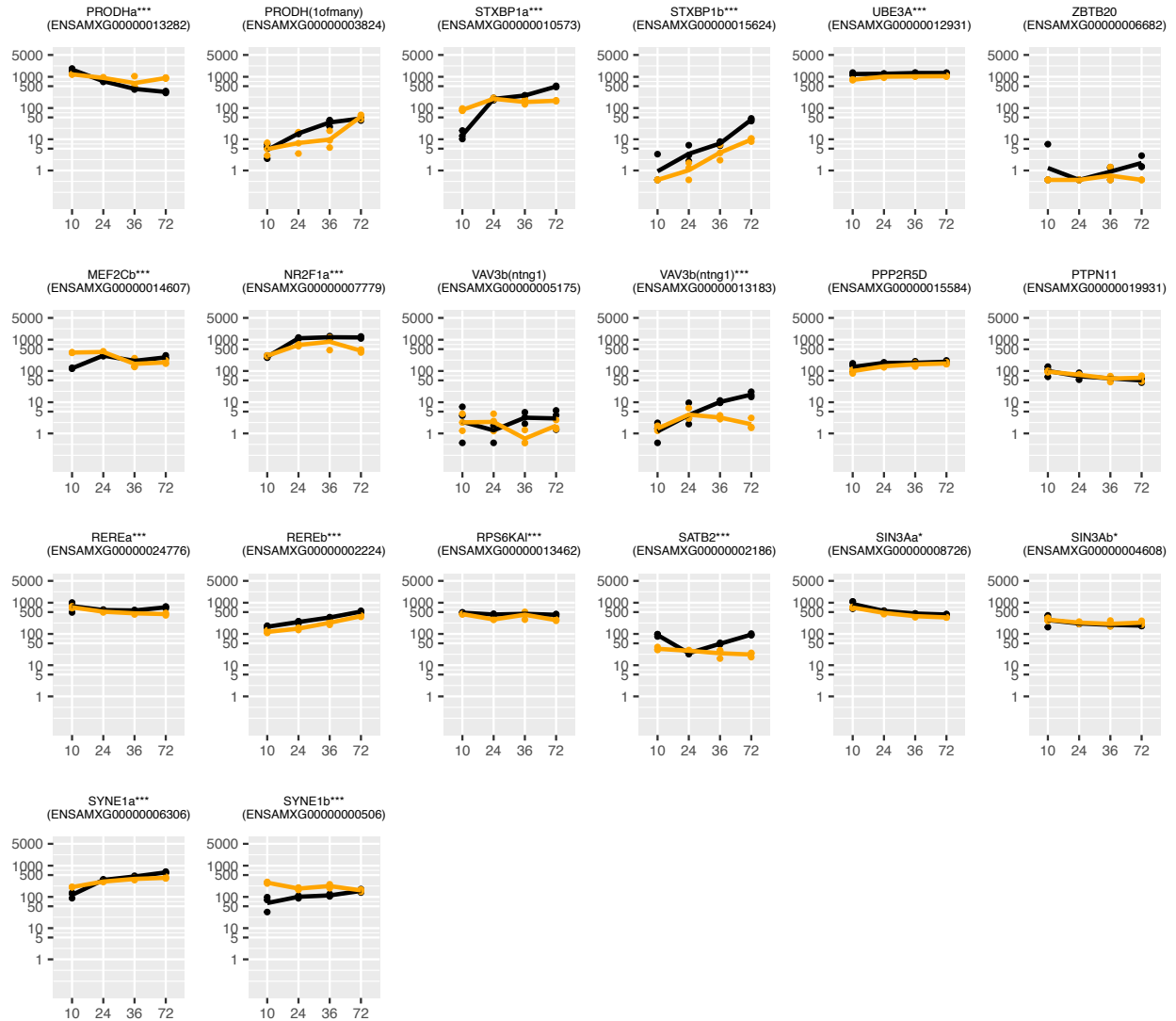
SFARI Gene Category S (Syndromic) (page 2 of 4)



SFARI Gene Category S (Syndromic) (page 3 of 4)



SFARI Gene Category S (Syndromic) (page 4 of 4)



Additional file 2.5—associated with Table 1. Many of the ASD-risk genes listed in SFARI Gene Category S (Syndromic) had significantly different expression in surface fish and cavefish at the stages of 10, 24, 36 and 72 hours post fertilization (hpf).

A set of 128 (all paralogs of 85 out of 89 orthologs in Category S including genes which are also listed in Category 1-4. See also Additional file 1) *A. mexicanus* genes that are orthologs of human SFARI Gene Category S (Syndromic) is shown (https://gene.sfari.org/autdb/GS_Home.do). Y-axis: normalized count of the number of sequence reads (Fragments Per Kilobase Million; FPKM). X-axis: hours post fertilization. Yellow dots and line represent the gene expression of cavefish, and the black dots and line represent that of surface fish. Each dot represents one of 3 replicates in each data point (morph and age). *: $P < 0.05$, **: $P < 0.01$, ***: $P < 0.001$ in the lower P-value of between the age $\times$ morph interaction and the expression difference at 72 hpf after applying Benjamini-Hochberg correction[1]. See also Additional file 1.

References:

1. Love MI, Anders S, Kim V, Huber W, Love MI, Anders S, Kim V, Huber W: **RNA-Seq workflow: gene-level exploratory analysis and differential expression.** *F1000Research* 2016, **4**:1070.