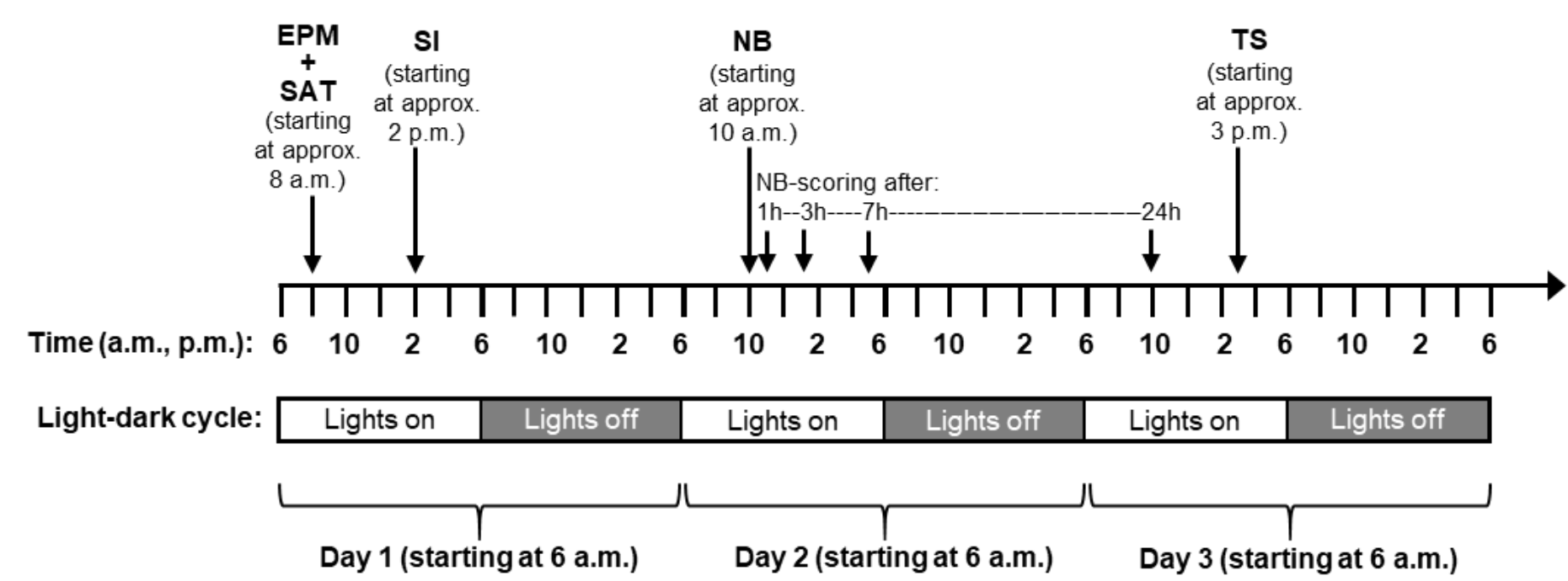


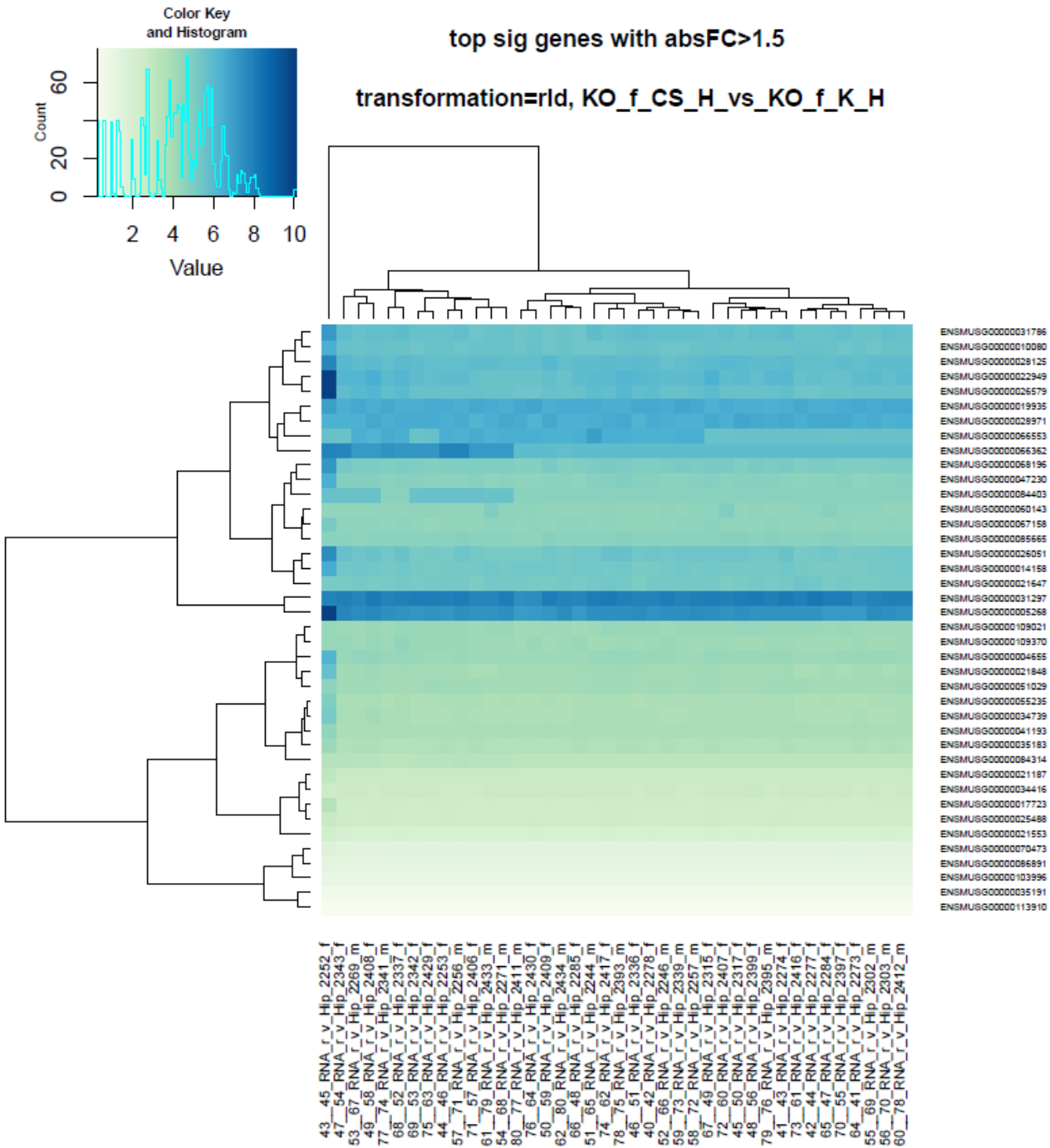
Supplemental Figures

Suppl. Fig. 1

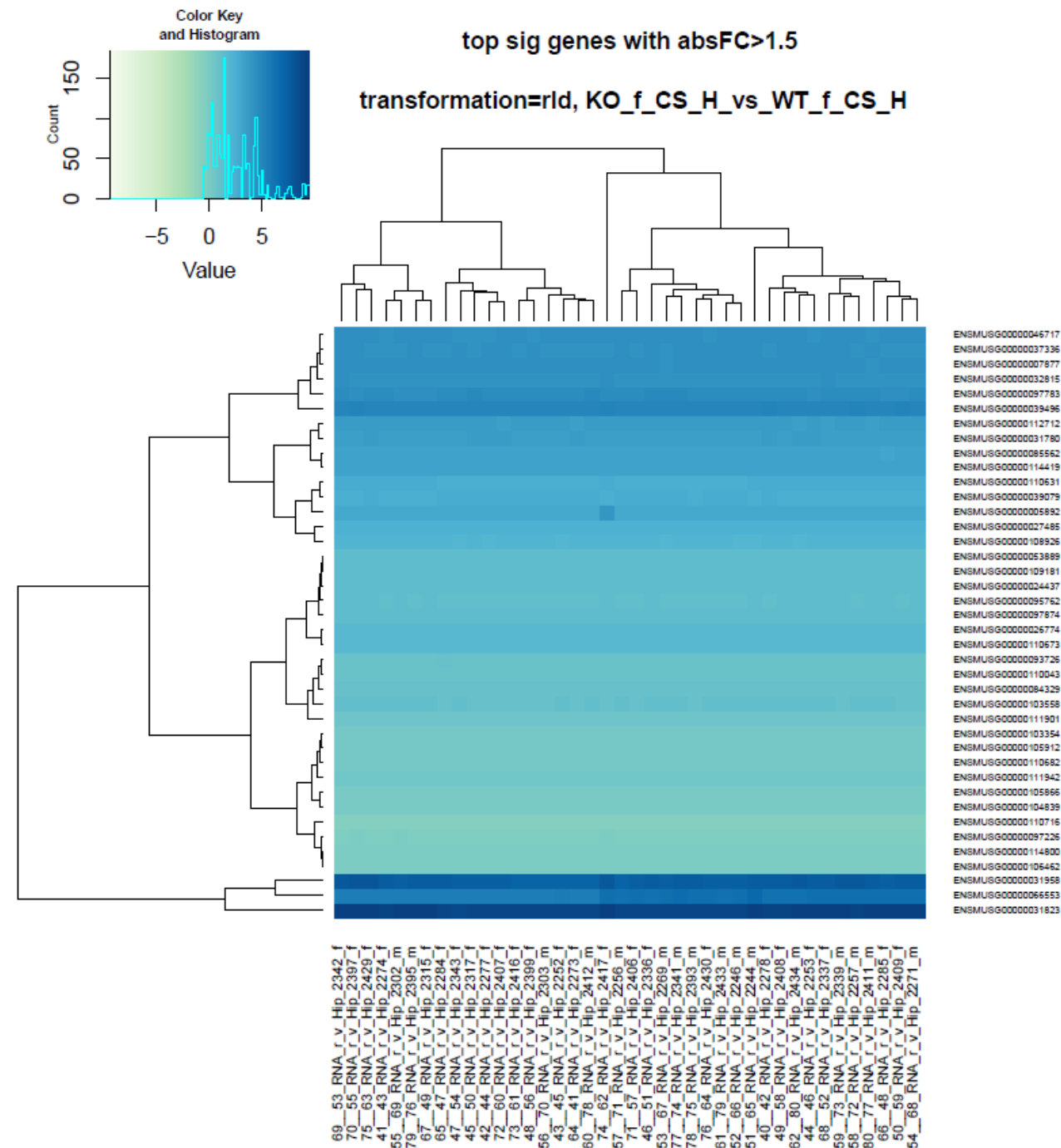


**Supplemental Fig. 1 Timeline of behavioural testing.** *Zdhhc7* wildtype and knockout mice (n=182) after control or chronic stress conditions at 14 weeks of age went through the following behavioural tests: elevated plus maze (EPM) test for the evaluation of anxiety-like behaviour and locomotion; spontaneous alternation test (SAT) for the evaluation of basal spatial working memory and locomotion; social interaction (SI) test for the assessment of depression-like behaviour; nest building (NB) test for the assessment of attention and general stress load; tail suspension (TS) test for the evaluation of depression-like behaviour.

Suppl.  
Fig. 2 A

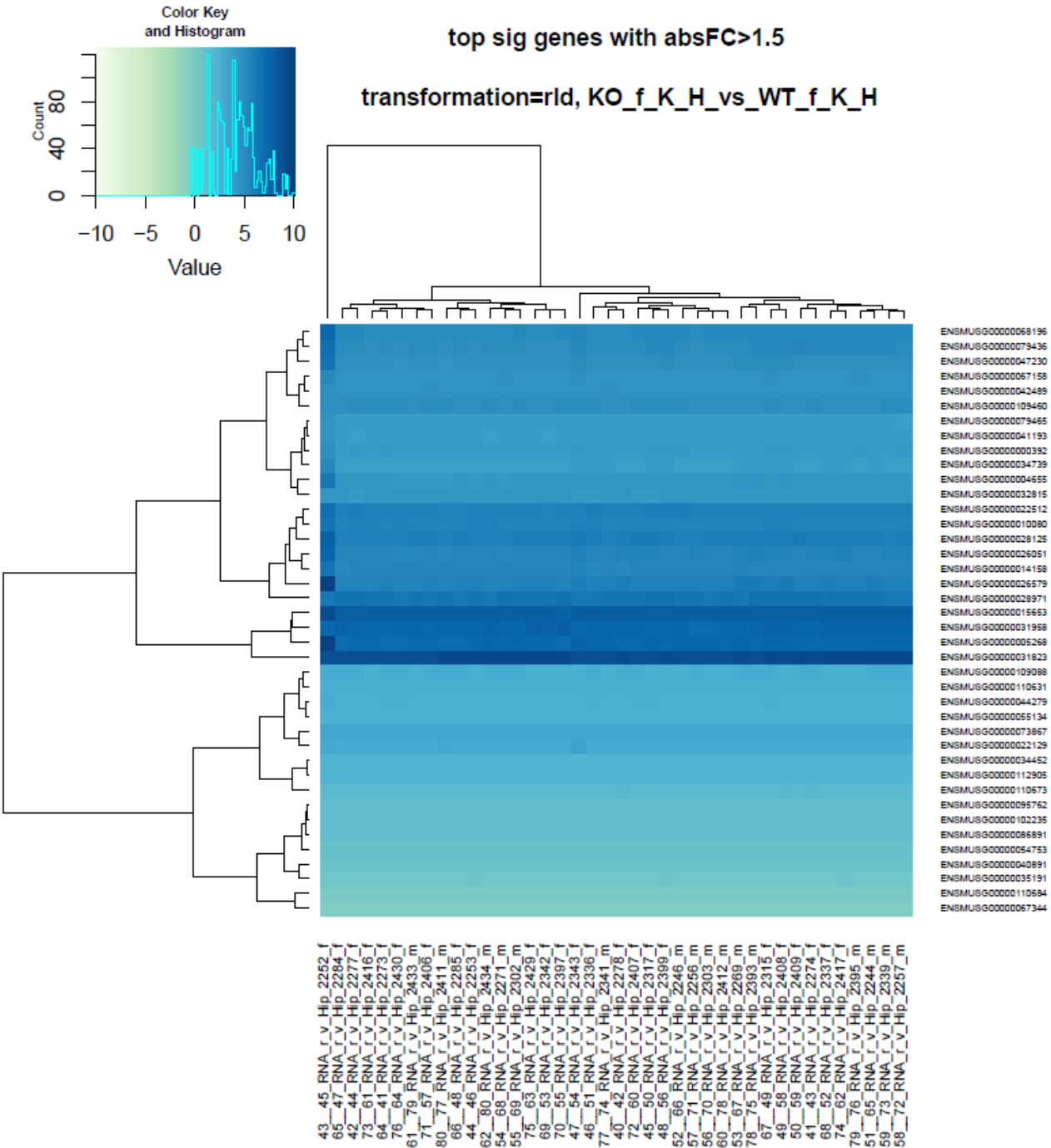


Suppl.  
Fig. 2 B

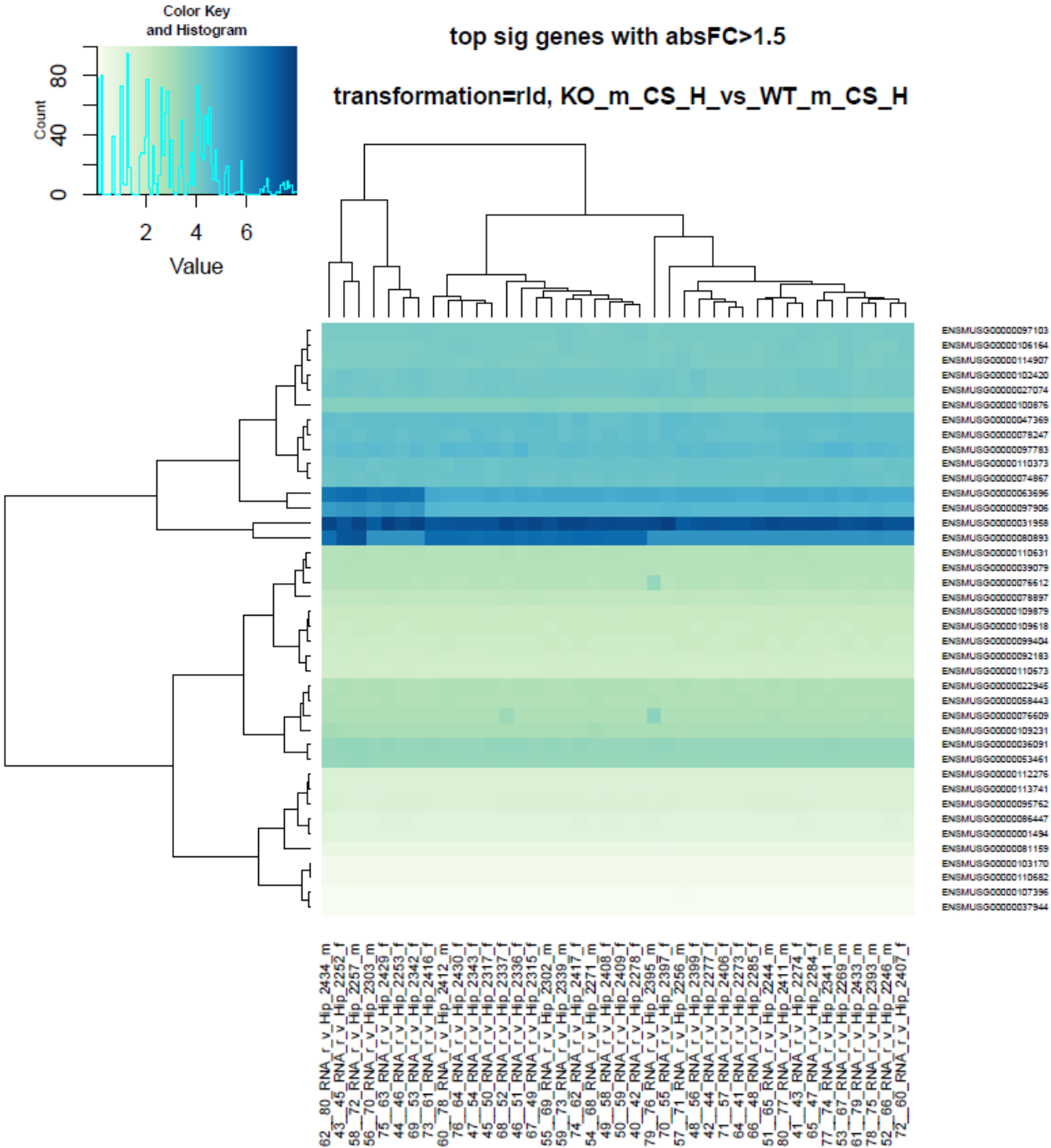


Supplemental Fig. 2 Heatmap and dendrogram illustrating hippocampal genes in different group comparisons: to be continued below

Suppl.  
Fig. 2 C

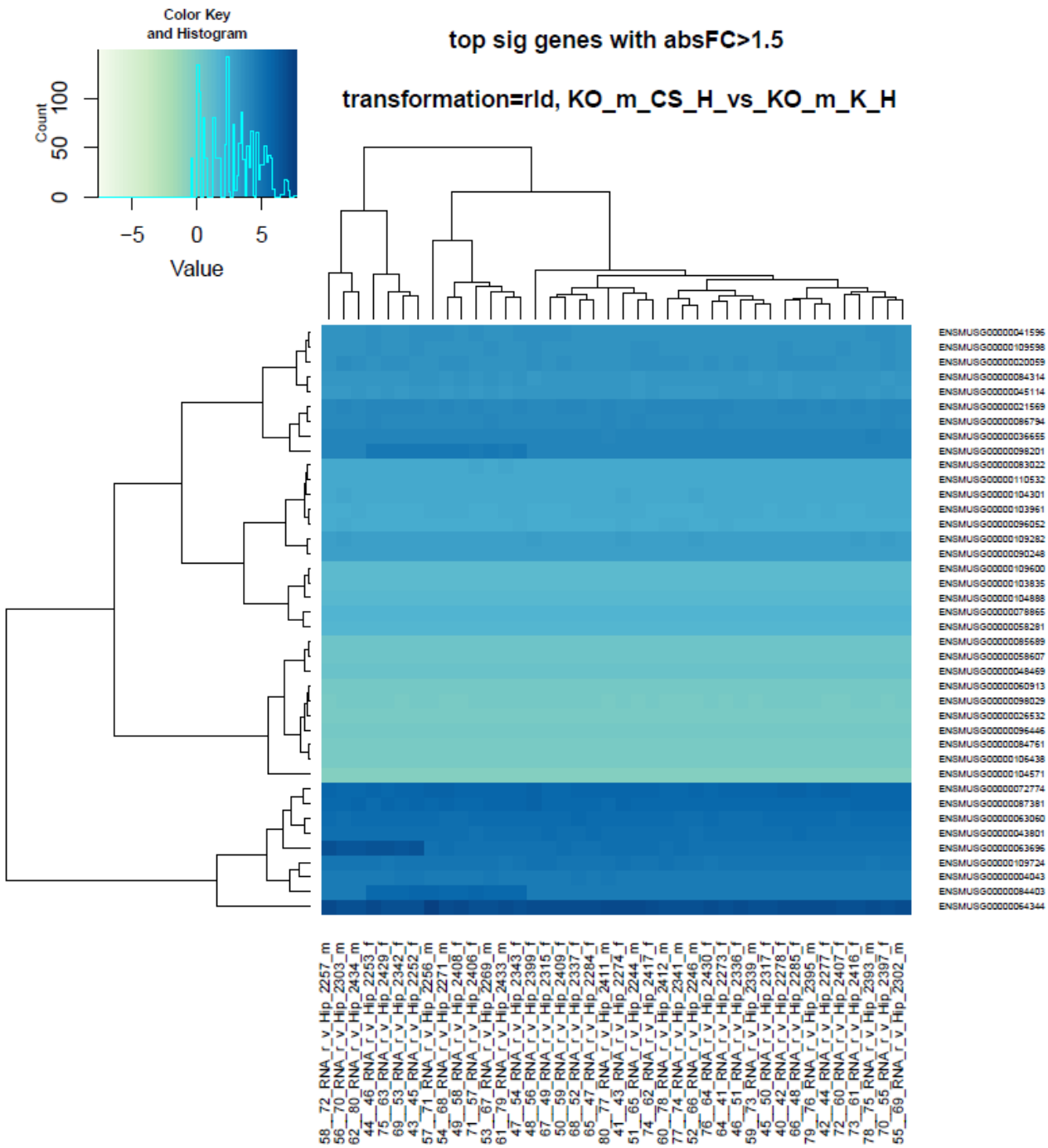


Suppl.  
Fig. 2 D

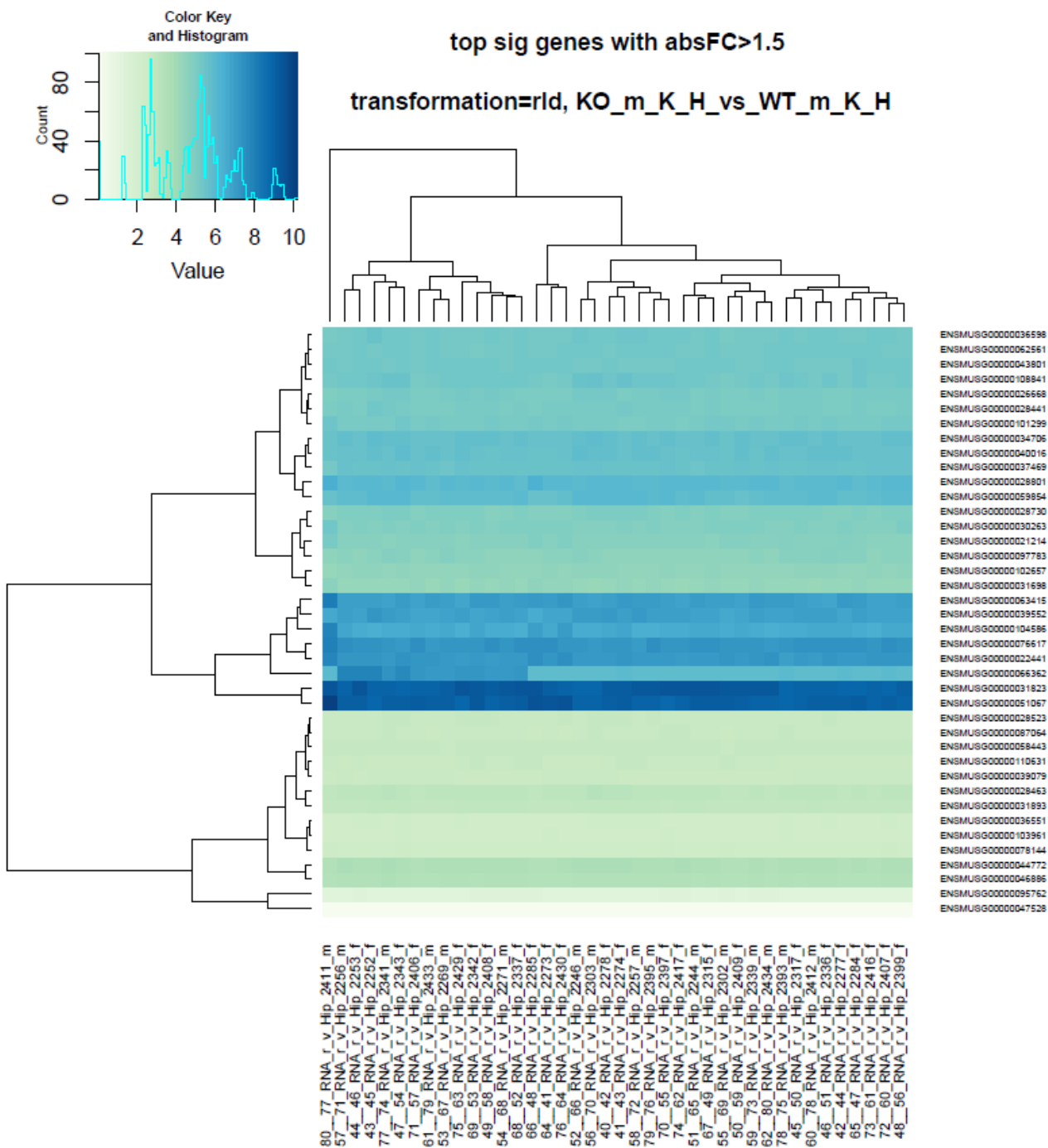


Supplemental Fig. 2 Heatmap and dendrogram illustrating hippocampal genes in different group comparisons: to be continued below

Suppl.  
Fig. 2 E

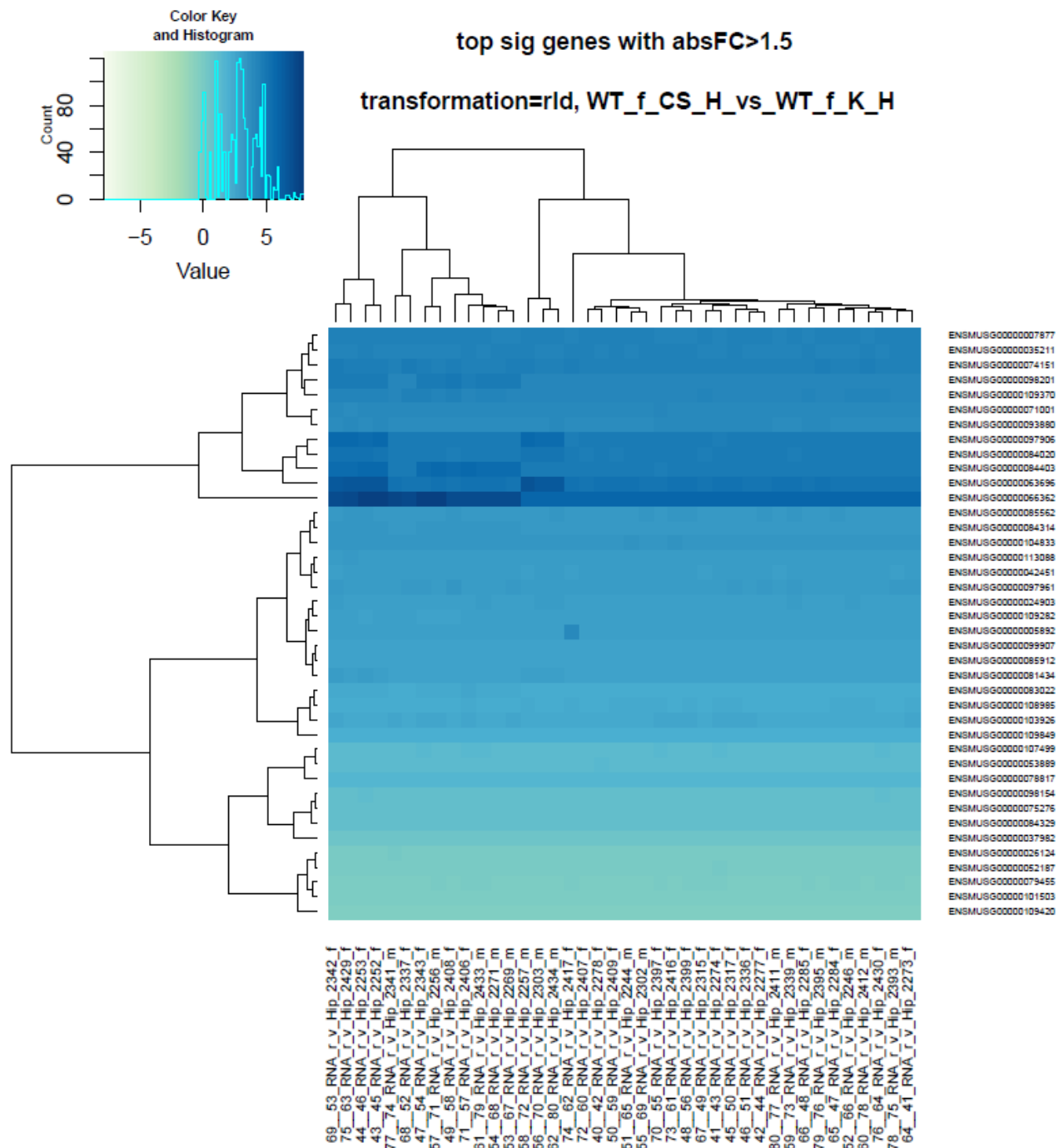


Suppl.  
Fig. 2 F

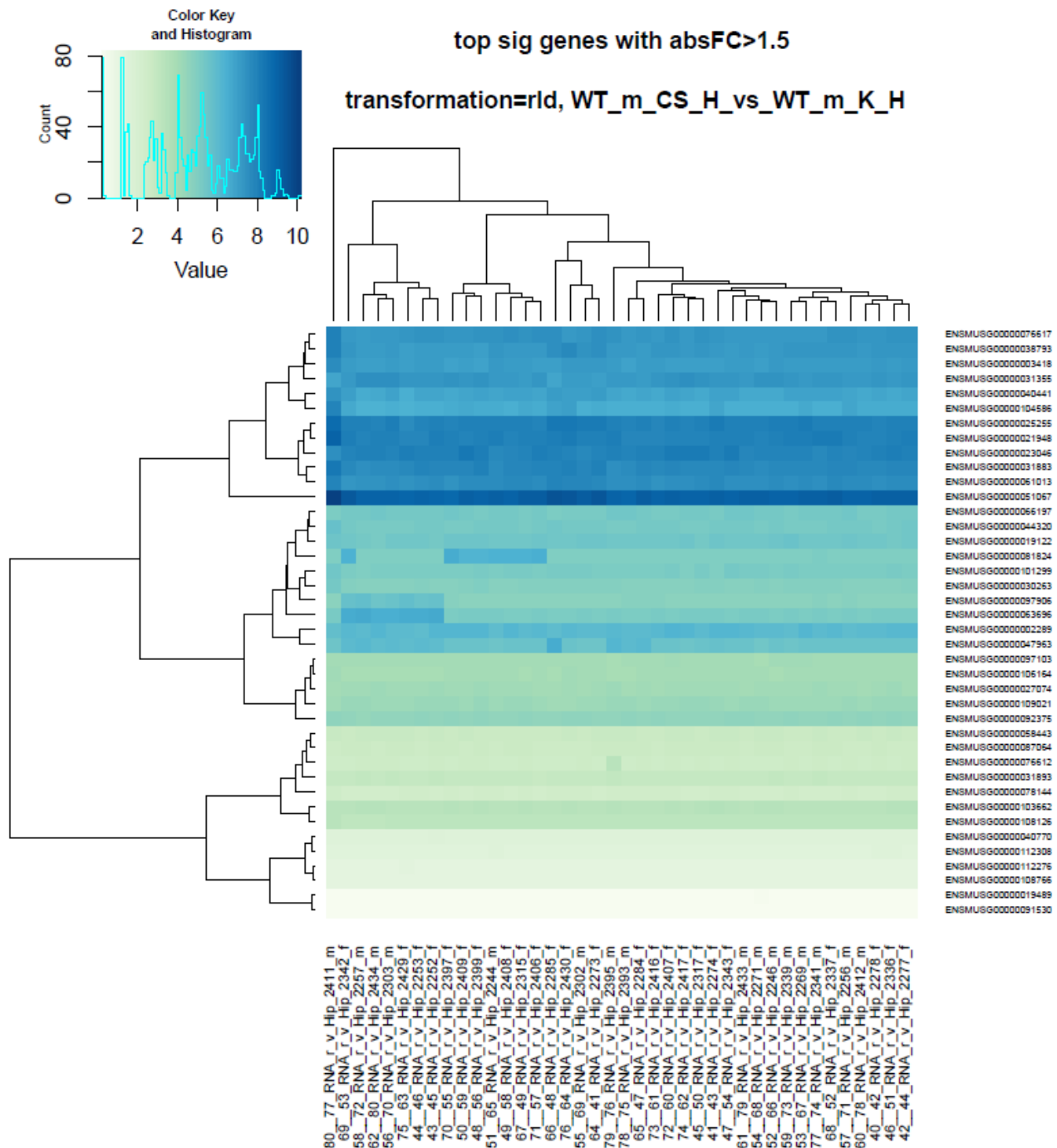


Supplemental Fig. 2 Heatmap and dendrogram illustrating hippocampal genes in different group comparisons: to be continued below

**Suppl.  
Fig. 2 G**

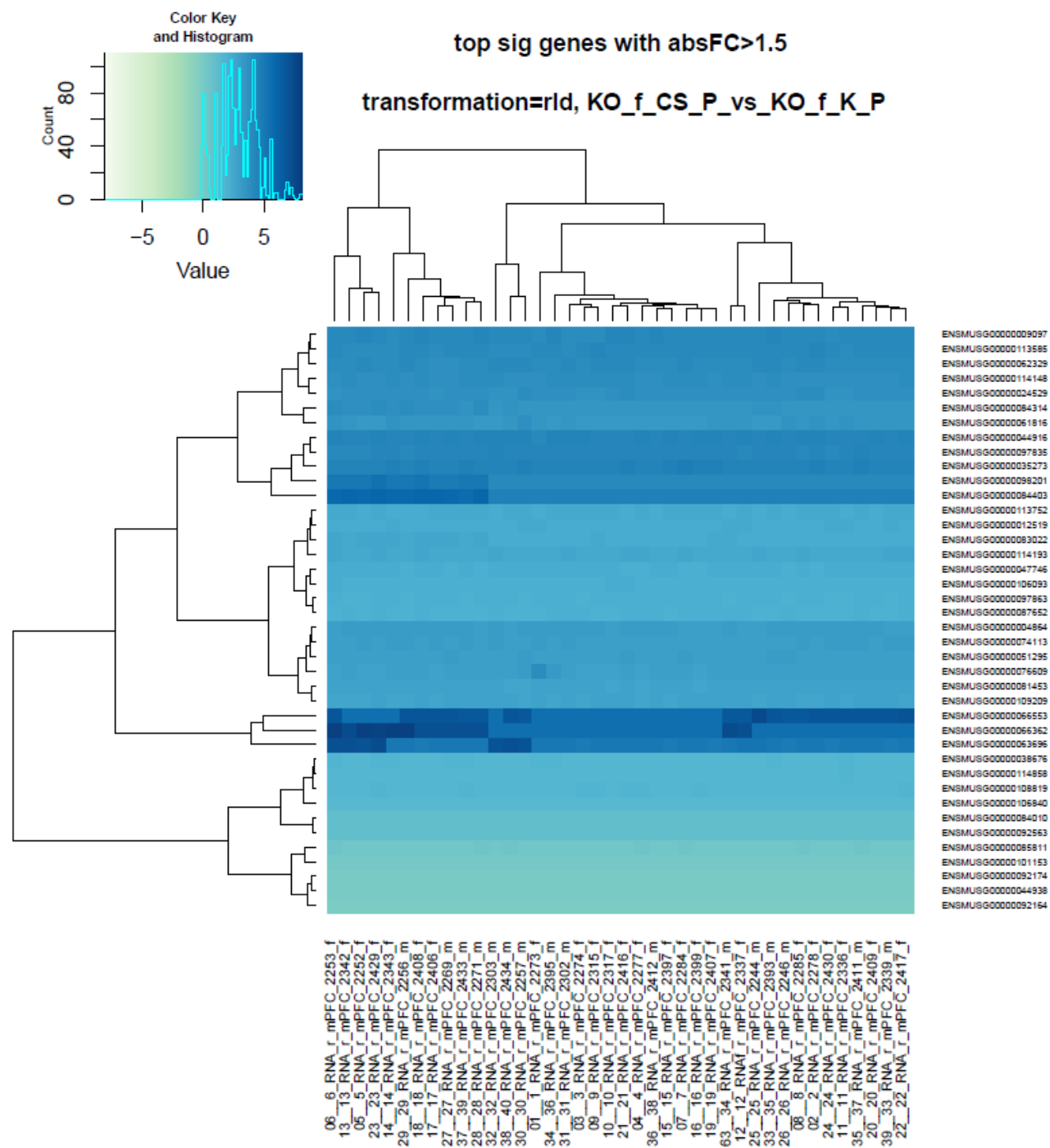


**Suppl.  
Fig. 2 H**

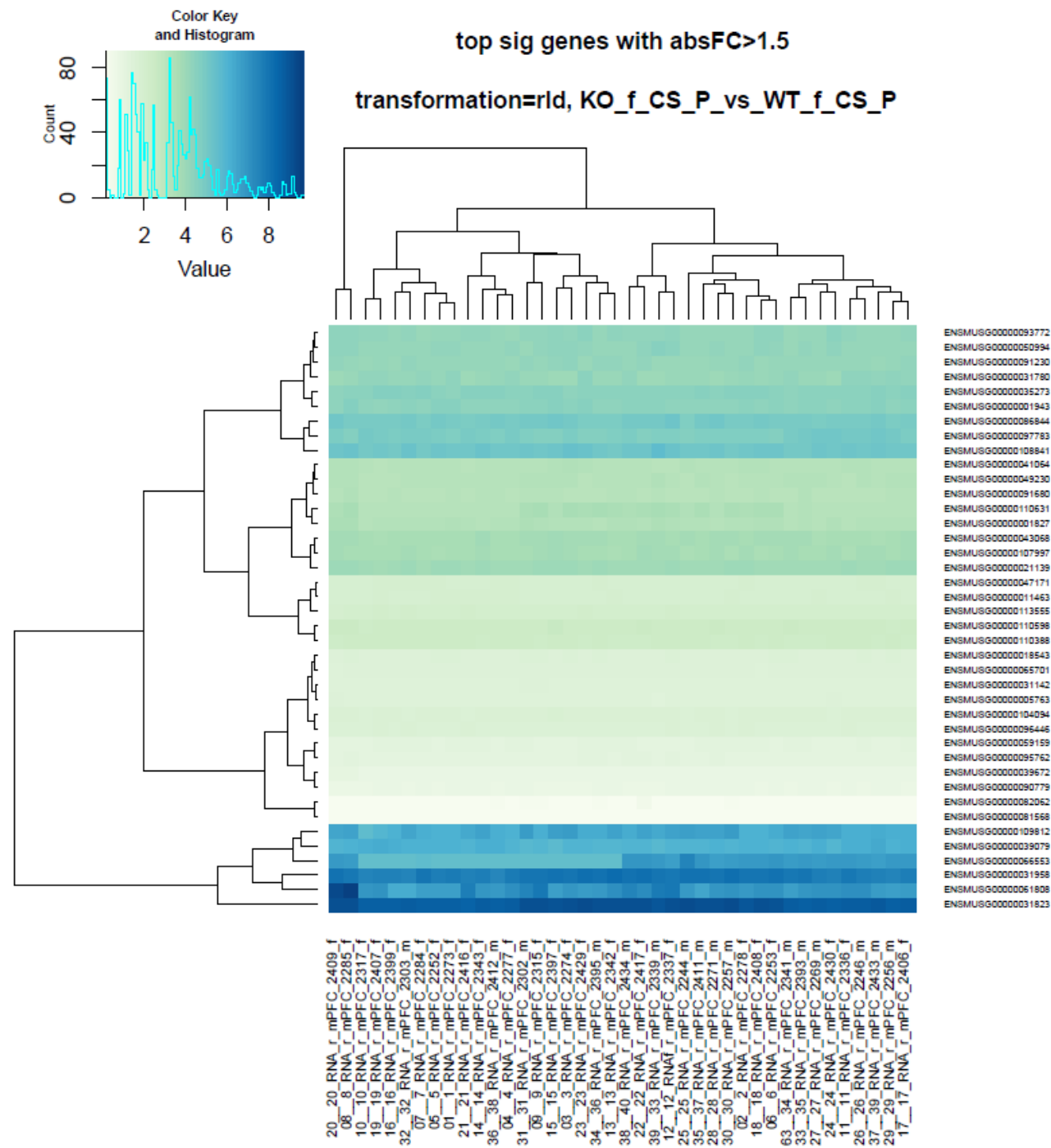


**Supplemental Fig. 2 Heatmap and dendrogram illustrating hippocampal genes in different group comparisons.** Top significant genes (ensemble IDs; statistics: Wald test) with absolute Fold changes (FC) > 1.5 were plotted against RNA-seq based gene expression data (normalized (rld transformation) counts) from *Zdhhc7* mice (N=40) from eight groups (1. C-WT-m, N=4; 2. CS-WT-m, N=4; 3. C-KO-m, N=4; 4. CS-KO-m, N=4; 5. C-WT-f, N=6; 6. CS-WT-f, N=6; 7. C-KO-f, N=6; 8. CS-KO-f N=6); for individual sample allocation to groups see GEO data deposition (GSE281404). Individual group comparisons were displayed in different parts of **Fig.:** **A)** KO\_f\_CS\_H vs. KO\_f\_K\_H, **B)** KO\_f\_CS\_H vs. WT\_f\_CS\_H, **C)** KO\_f\_K\_H vs. WT\_f\_K\_H, **D)** KO\_m\_CS\_H vs. WT\_m\_CS\_H, **E)** KO\_m\_CS\_H vs. KO\_m\_K\_H, **F)** KO\_m\_K\_H vs. WT\_m\_K\_H, **G)** WT\_f\_CS\_H vs. WT\_f\_K\_H, **H)** WT\_m\_CS\_H vs. WT\_m\_K\_H.

Suppl.  
Fig. 3 A

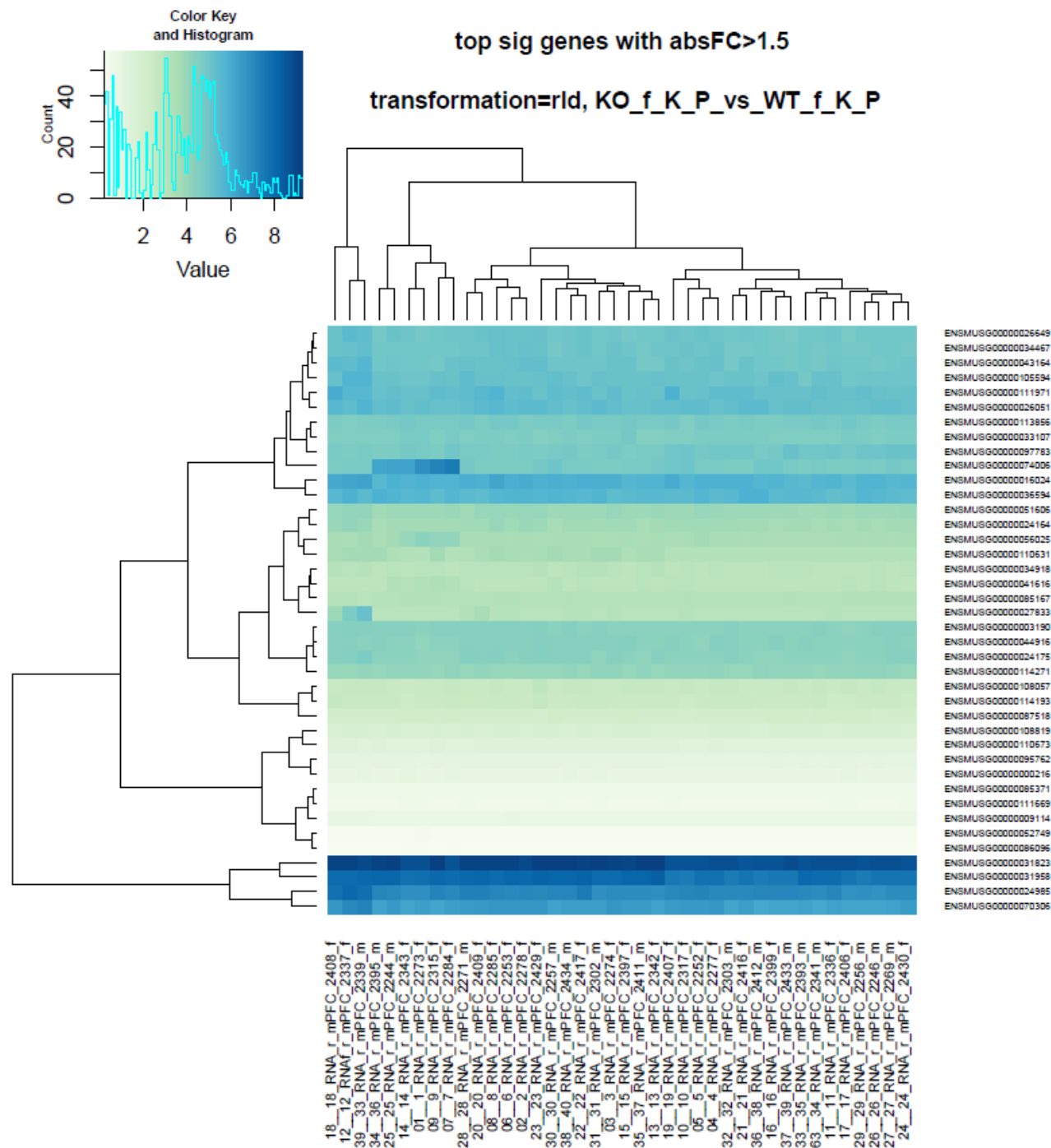


Suppl.  
Fig. 3 B

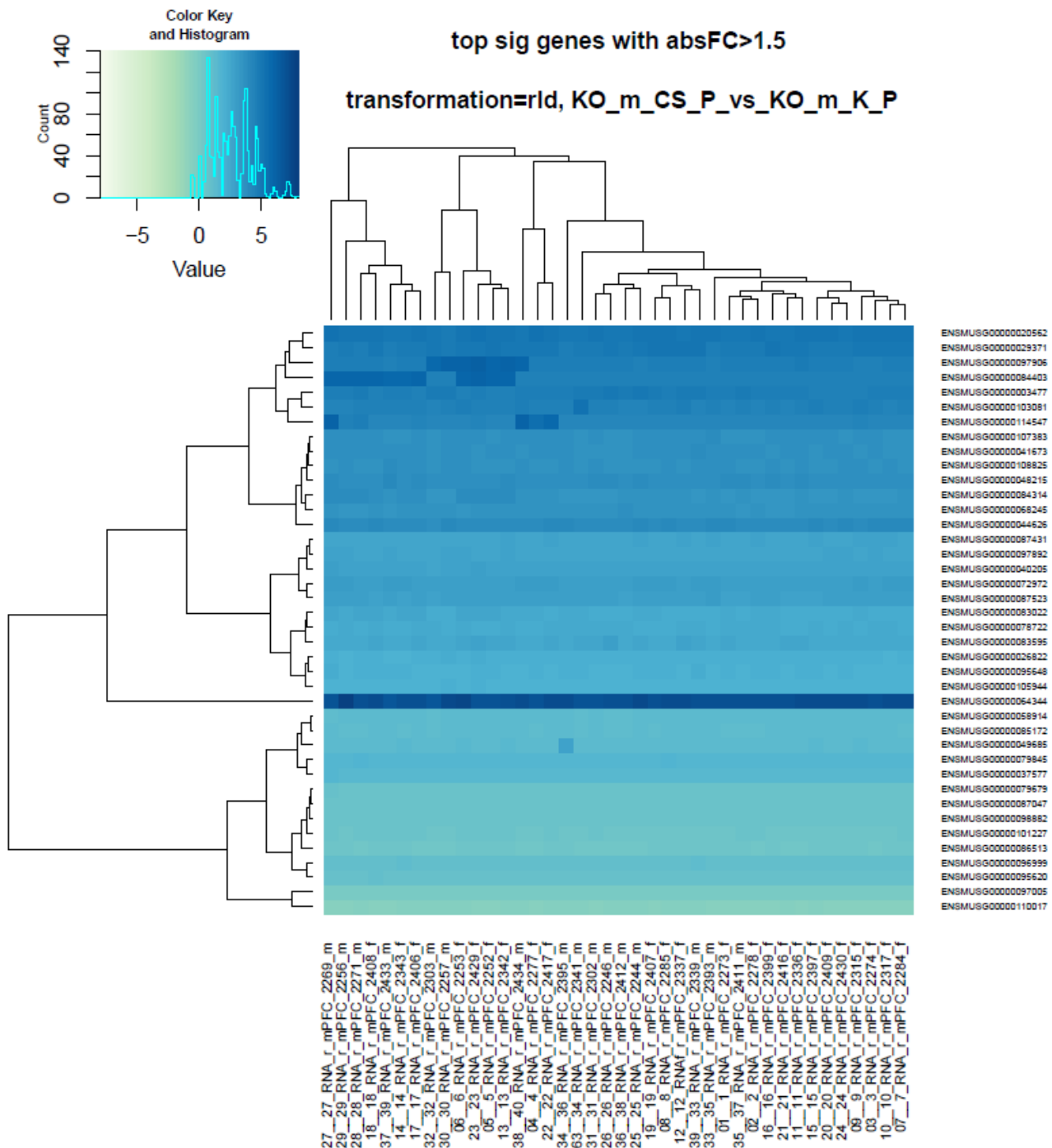


Supplemental Fig. 3 Heatmap and dendrogram illustrating prefrontal cortex genes in different group comparisons: to be continued below

Suppl.  
Fig. 3 C

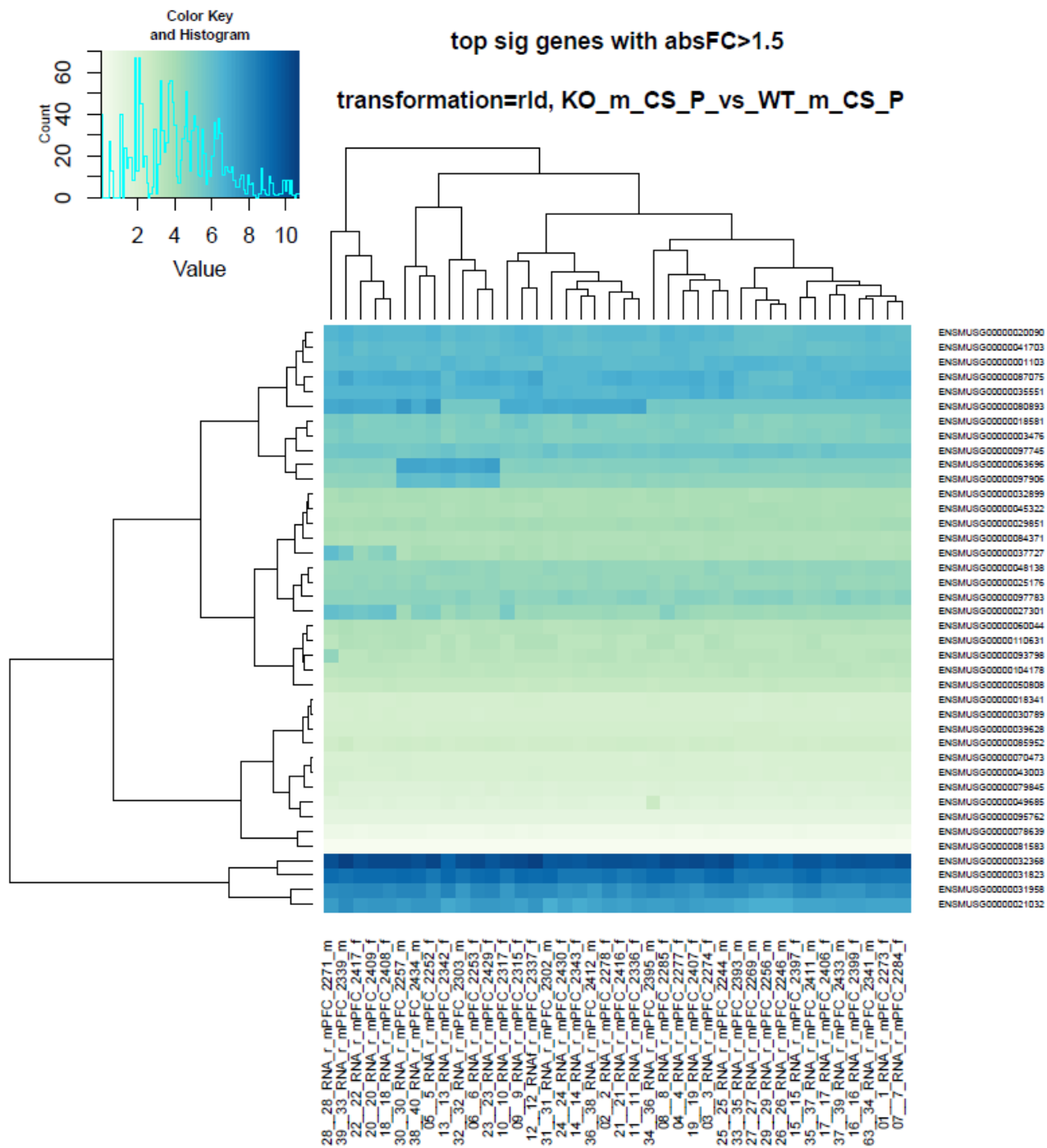


Suppl.  
Fig. 3 D

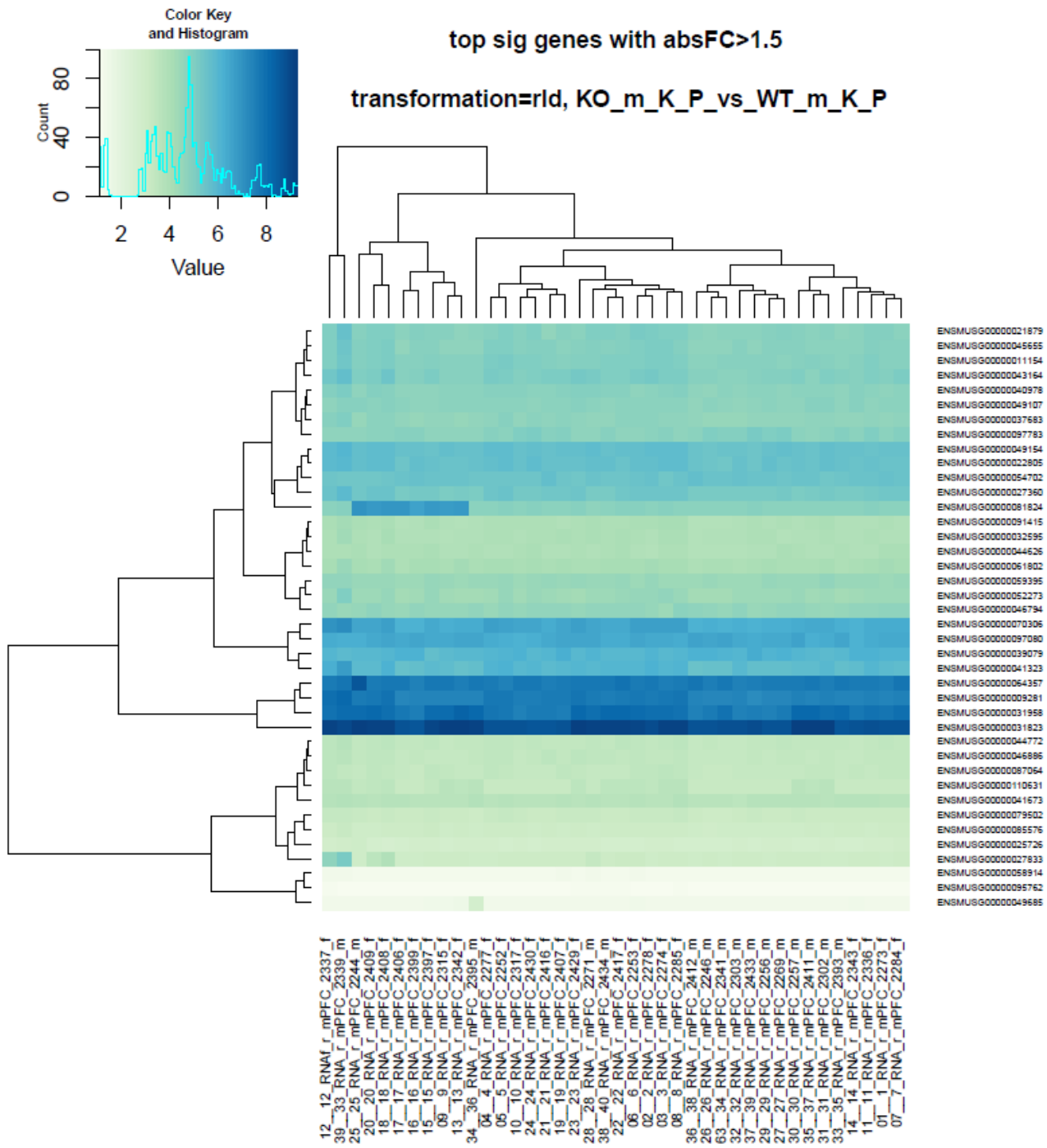


Supplemental Fig. 3 Heatmap and dendrogram illustrating prefrontal cortex genes in different group comparisons: to be continued below

Suppl.  
Fig. 3 E

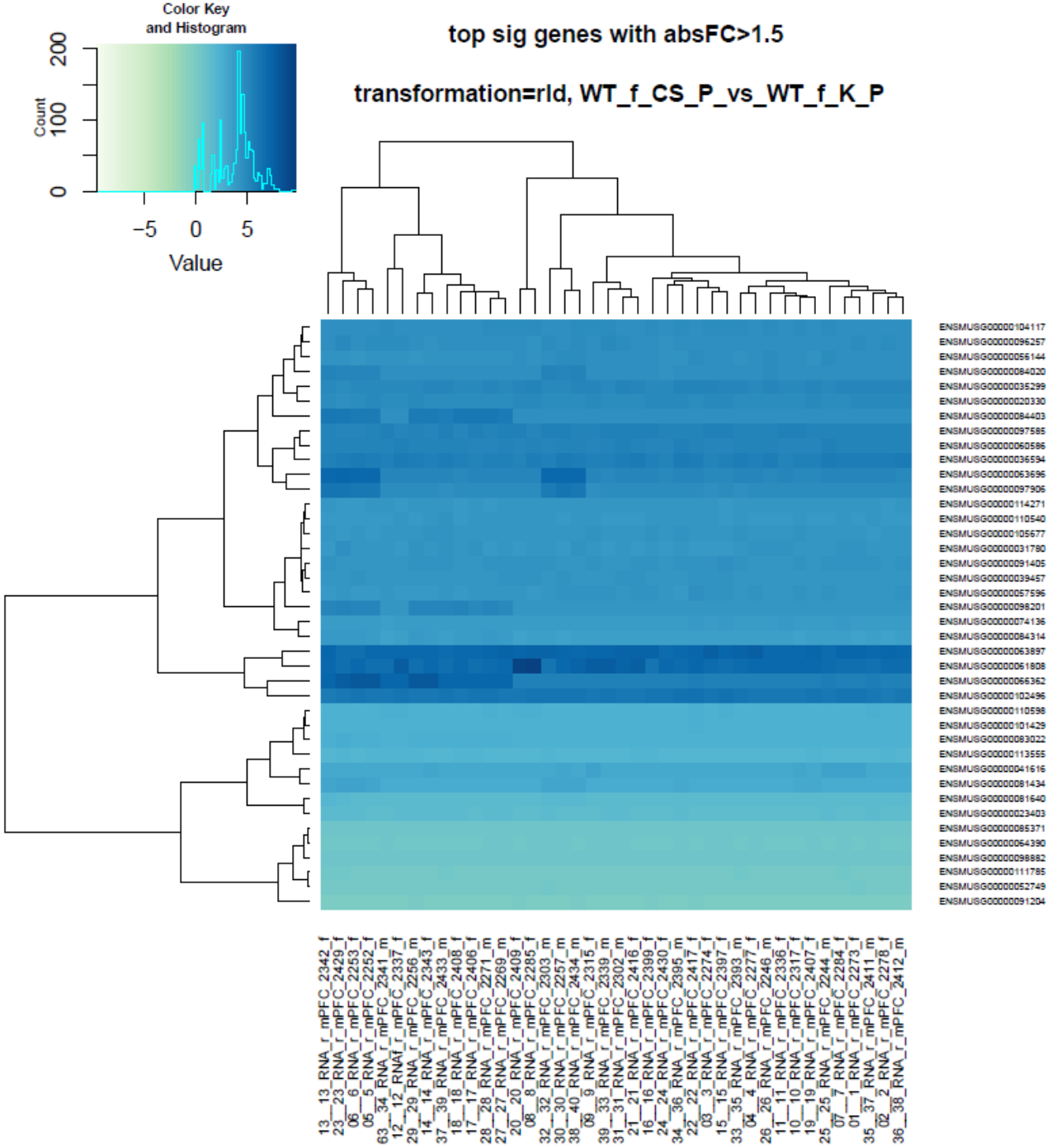


Suppl.  
Fig. 3 F

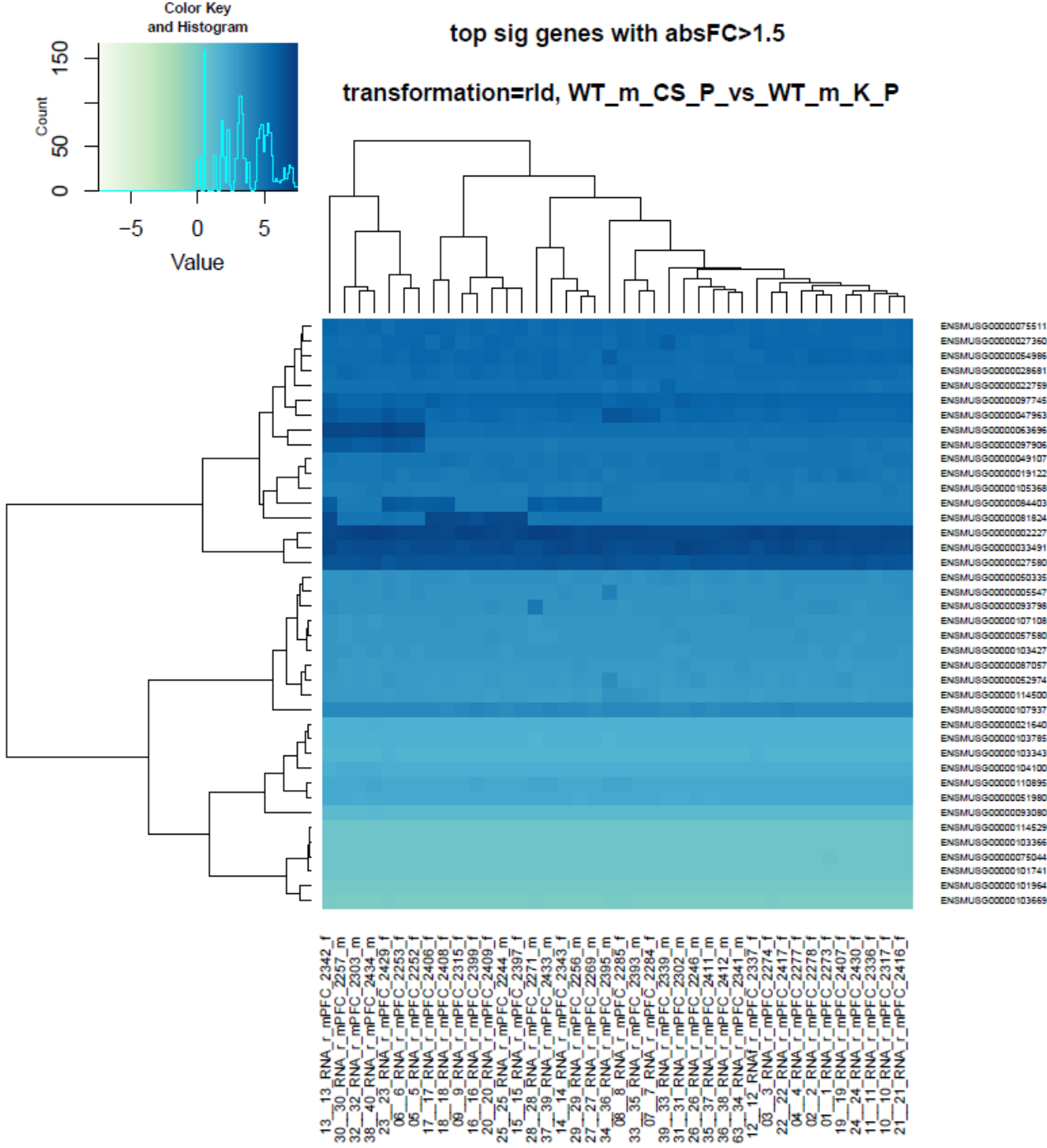


Supplemental Fig. 3 Heatmap and dendrogram illustrating prefrontal cortex genes in different group comparisons: to be continued below

Suppl.  
Fig. 3 G

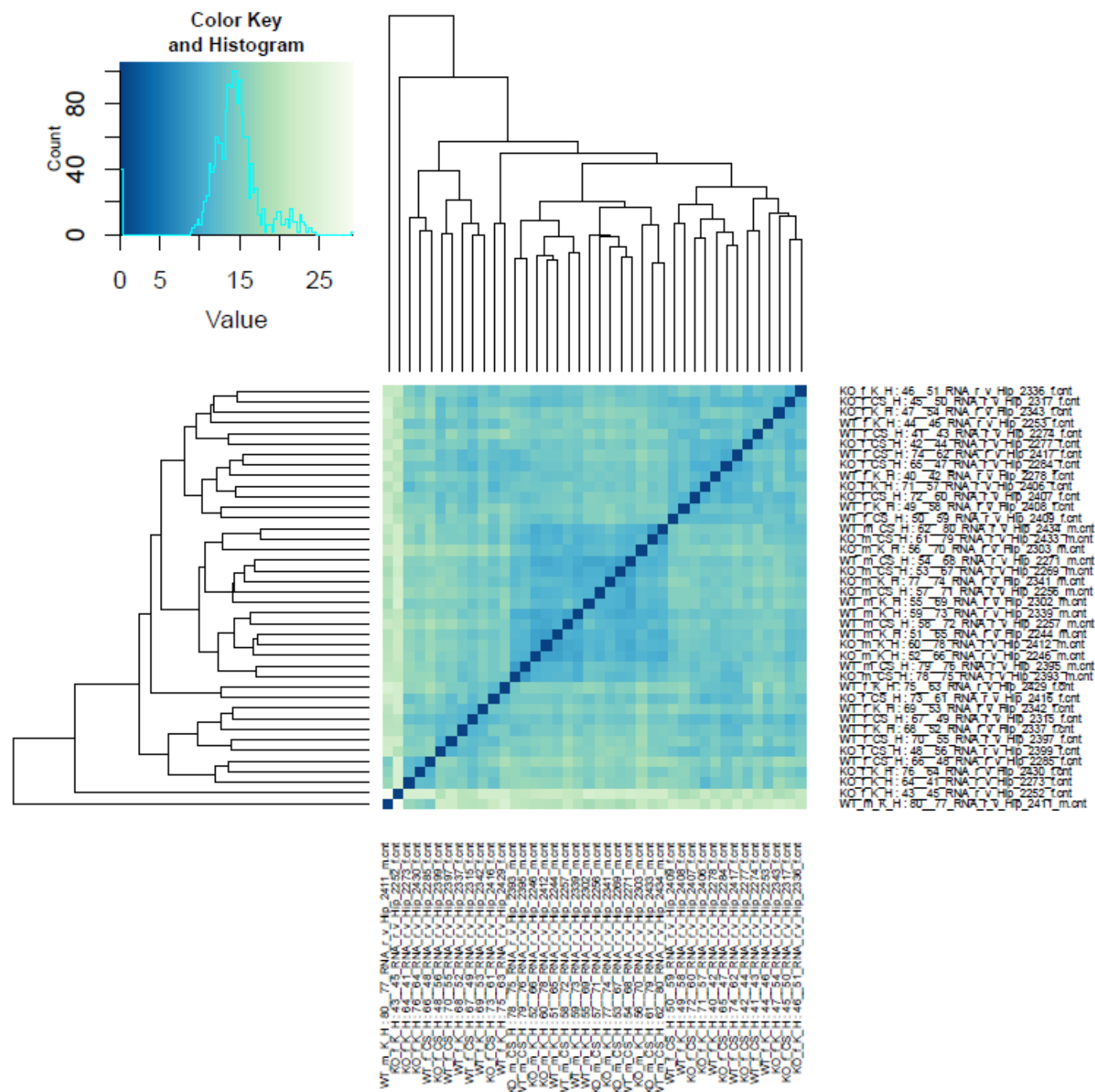


Suppl.  
Fig. 3 H

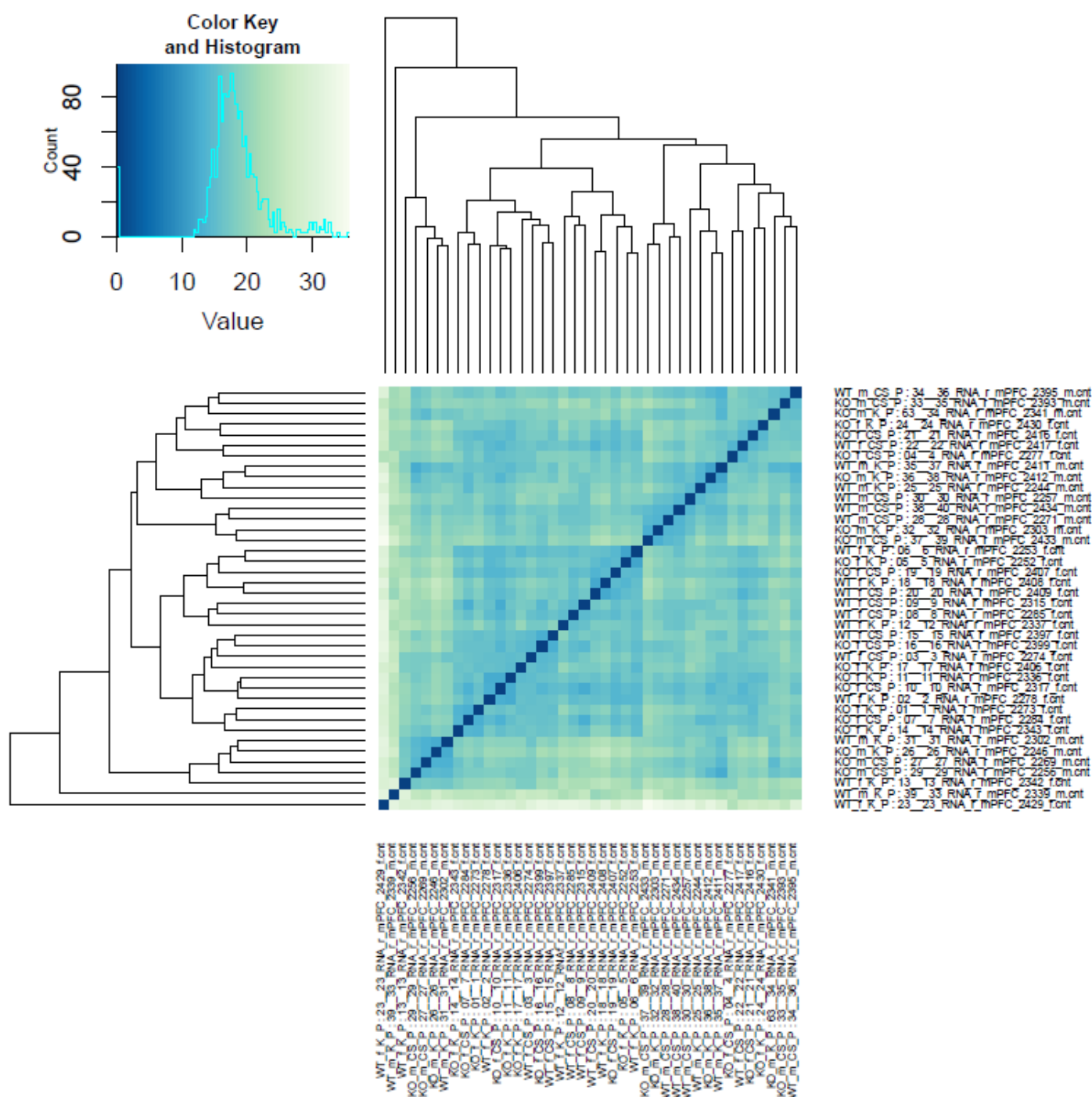


**Supplemental Fig. 3 Heatmap and dendrogram illustrating prefrontal cortex genes in different group comparisons.** Top significant genes (ensemble IDs; statistics: Wald test) with absolute Fold changes (FC) > 1.5 were plotted against RNA-seq based gene expression data (normalized (rld transformation) counts) from *Zdhc7* mice (N=40) from eight groups (1. C-WT-m, N=4; 2. CS-WT-m, N=4; 3. C-KO-m, N=4; 4. CS-KO-m, N=4; 5. C-WT-f, N=6; 6. CS-WT-f, N=6; 7. C-KO-f, N=6; 8. CS-KO-f N=6); for individual sample allocation to groups see GEO data deposition (GSE281404). Individual group comparisons were displayed in different parts of **Fig.:** **A)** KO\_f\_CS\_P\_vs.\_KO\_f\_K\_P, **B)** KO\_f\_CS\_P\_vs.\_WT\_f\_CS\_P, **C)** KO\_f\_K\_P\_vs.\_WT\_f\_K\_P, **D)** KO\_m\_CS\_P\_vs.\_KO\_m\_K\_P, **E)** KO\_m\_CS\_P\_vs.\_WT\_m\_CS\_P, **F)** KO\_m\_K\_P\_vs.\_WT\_m\_K\_P, **G)** WT\_f\_CS\_P\_vs.\_WT\_f\_K\_P, **H)** WT\_m\_CS\_P\_vs.\_WT\_m\_K\_P.

Suppl.  
Fig. 4 A

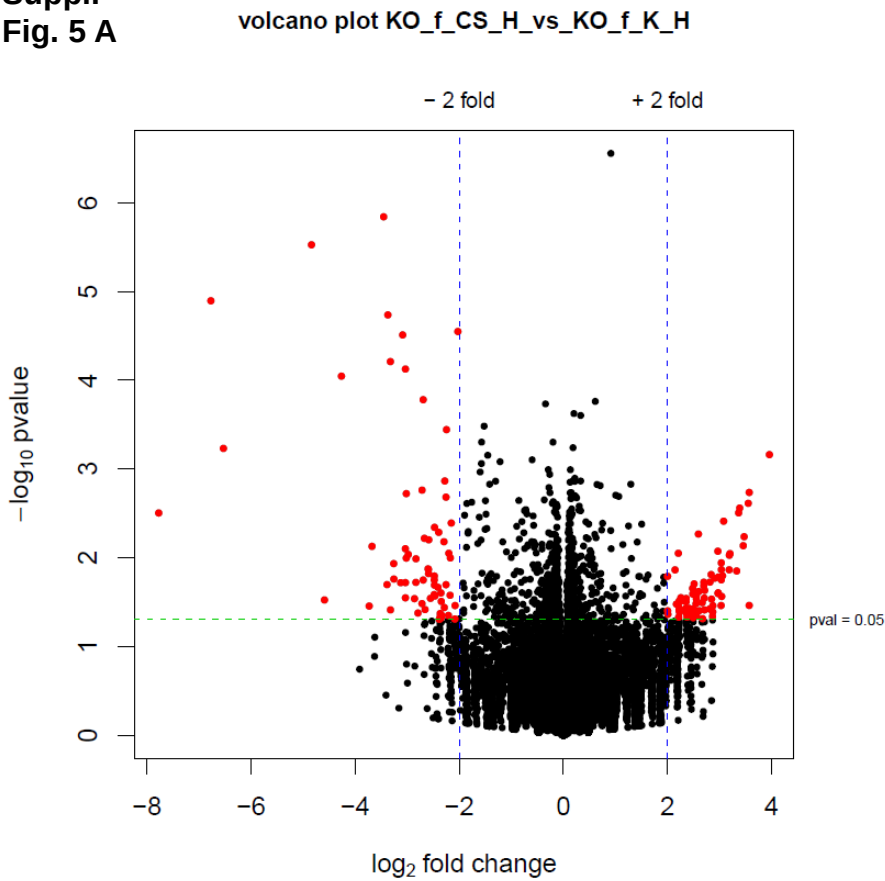


Suppl.  
Fig. 4 B

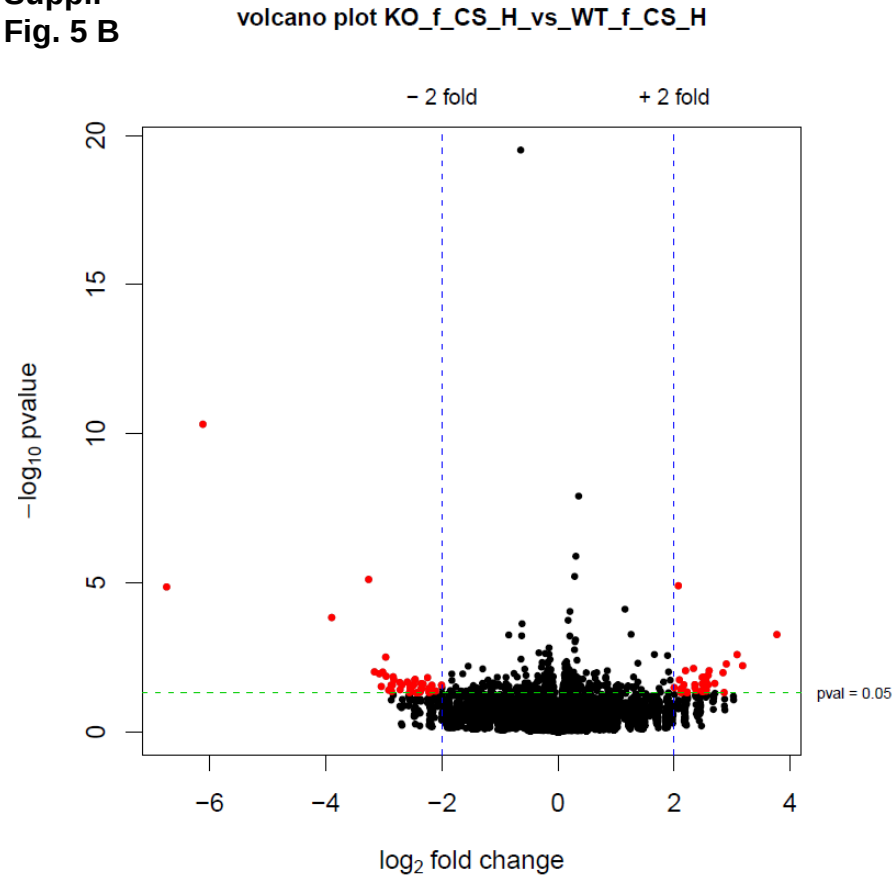


**Supplemental Fig. 4 Heatmap and dendrogram illustrating hippocampal (Fig. A) and prefrontal cortex (Fig. B) gene counts sample by sample.** RNA-seq based gene expression data (normalized (rld transformation) counts) from *Zdhhc7* mice (N=40) from eight groups (1. C-WT-m, N=4; 2. CS-WT-m, N=4; 3. C-KO-m, N=4; 4. CS-KO-m, N=4; 5. C-WT-f, N=6; 6. CS-WT-f, N=6; 7. C-KO-f, N=6; 8. CS-KO-f N=6) were plotted against each other; for individual sample allocation to groups see GEO data deposition (GSE281404).

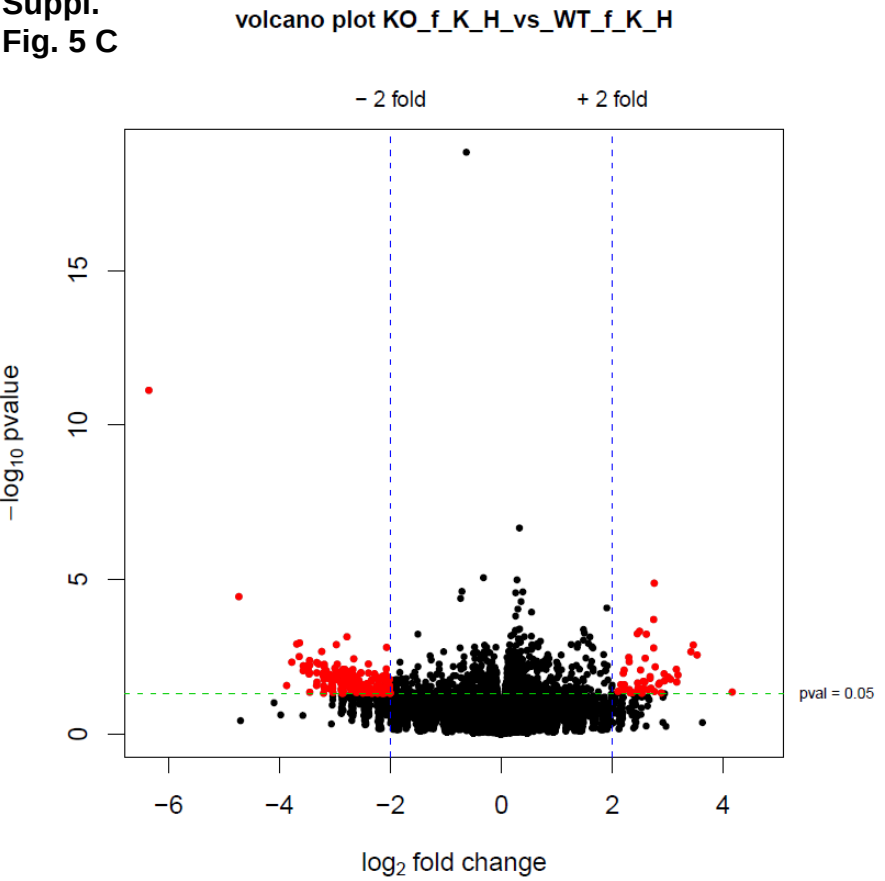
Suppl.  
Fig. 5 A



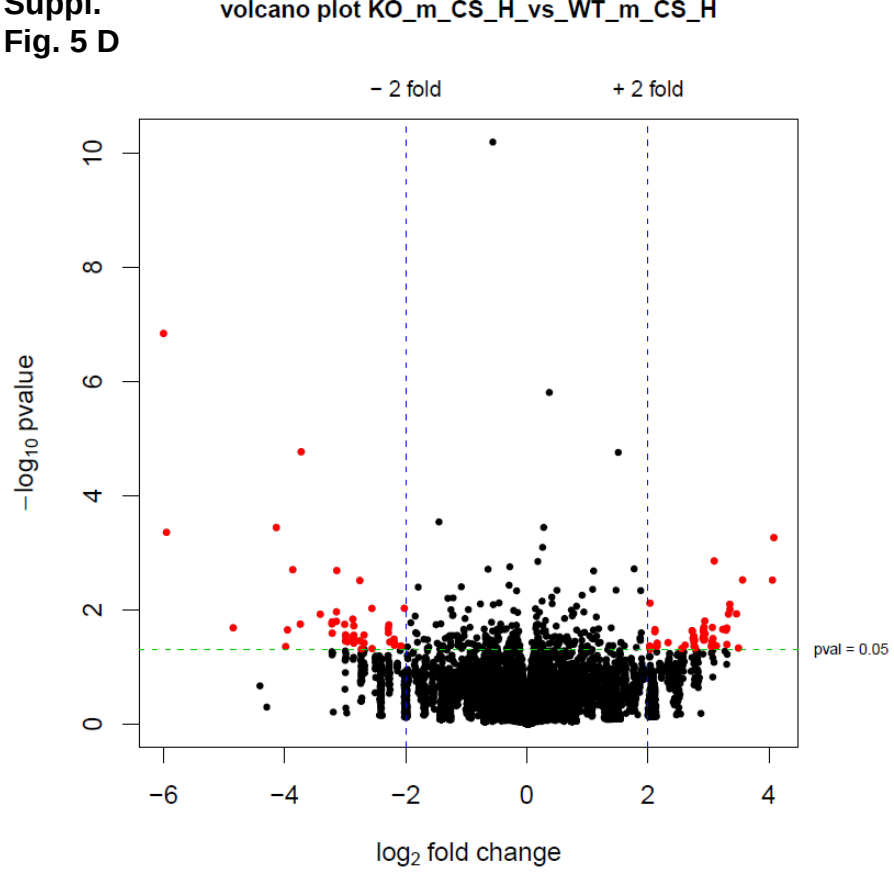
Suppl.  
Fig. 5 B



Suppl.  
Fig. 5 C

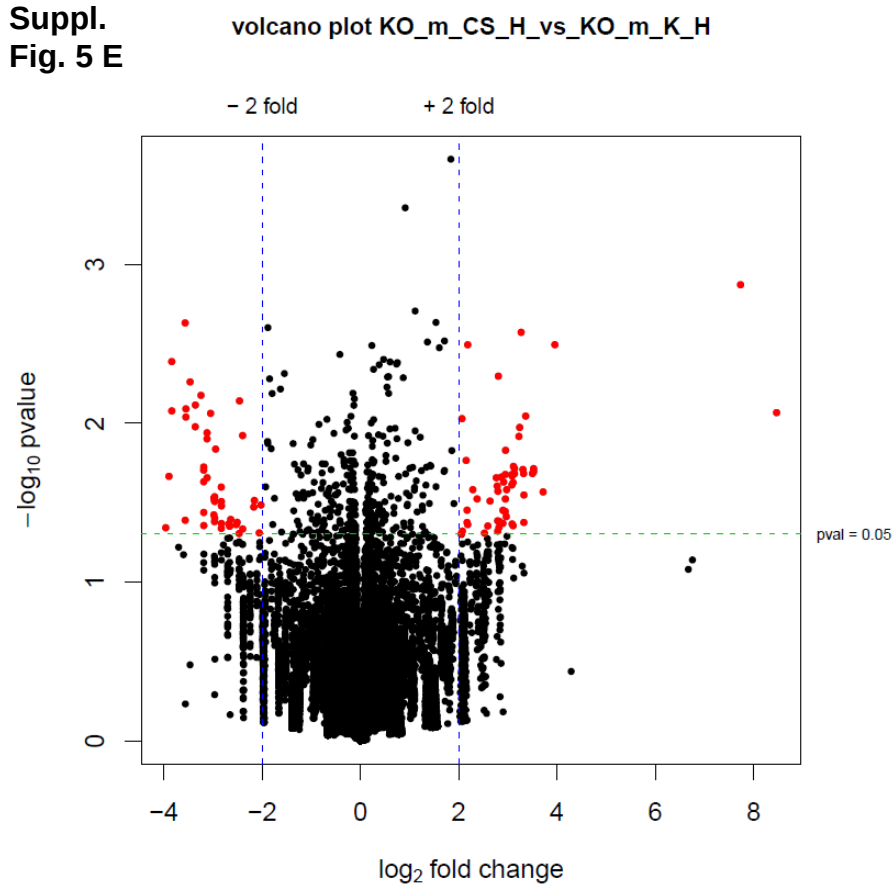


Suppl.  
Fig. 5 D

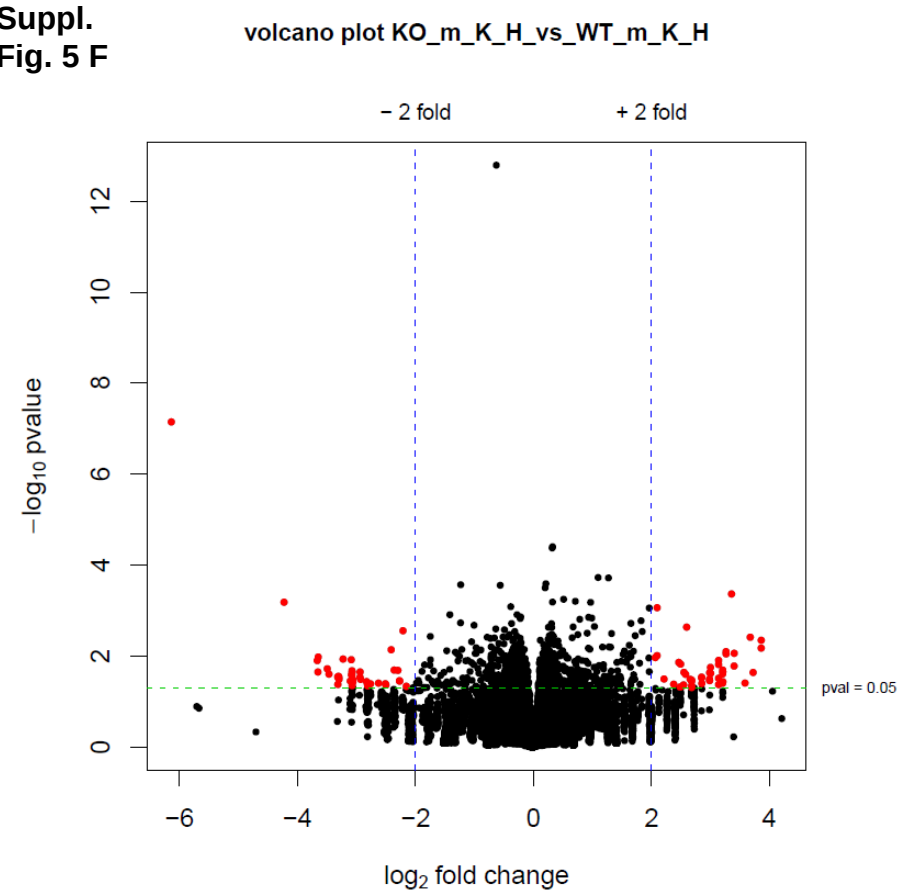


Supplemental Fig. 5 Volcanoplots illustrating hippocampal genes in different group comparisons: to be continued below

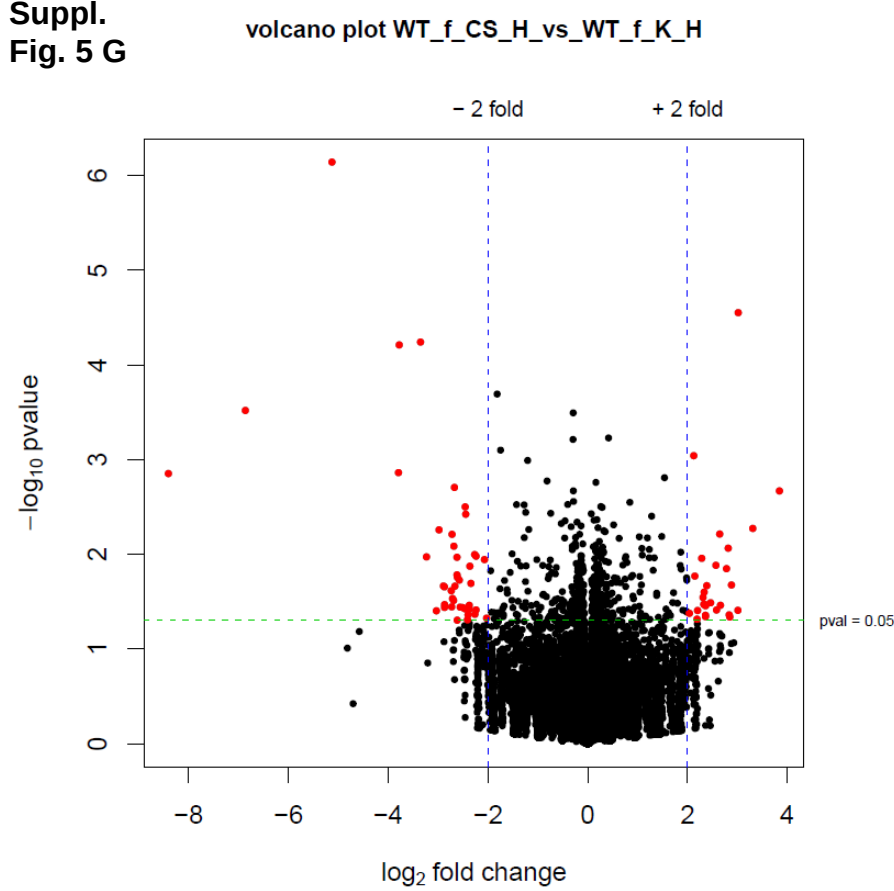
Suppl.  
Fig. 5 E



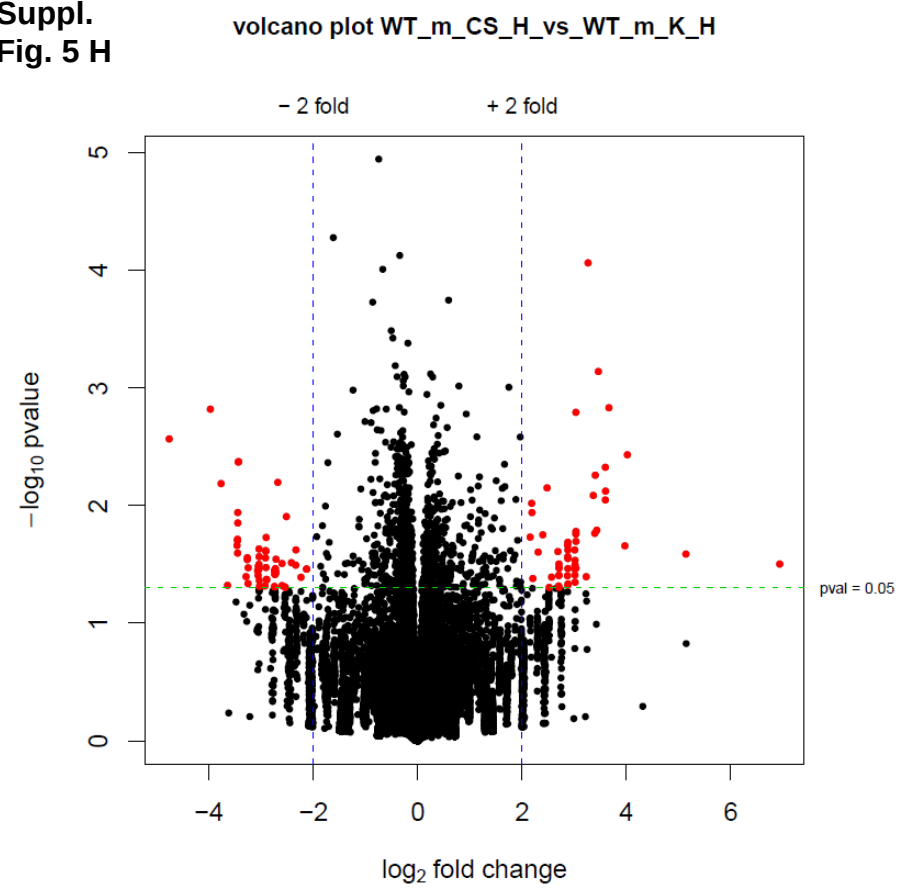
Suppl.  
Fig. 5 F



Suppl.  
Fig. 5 G

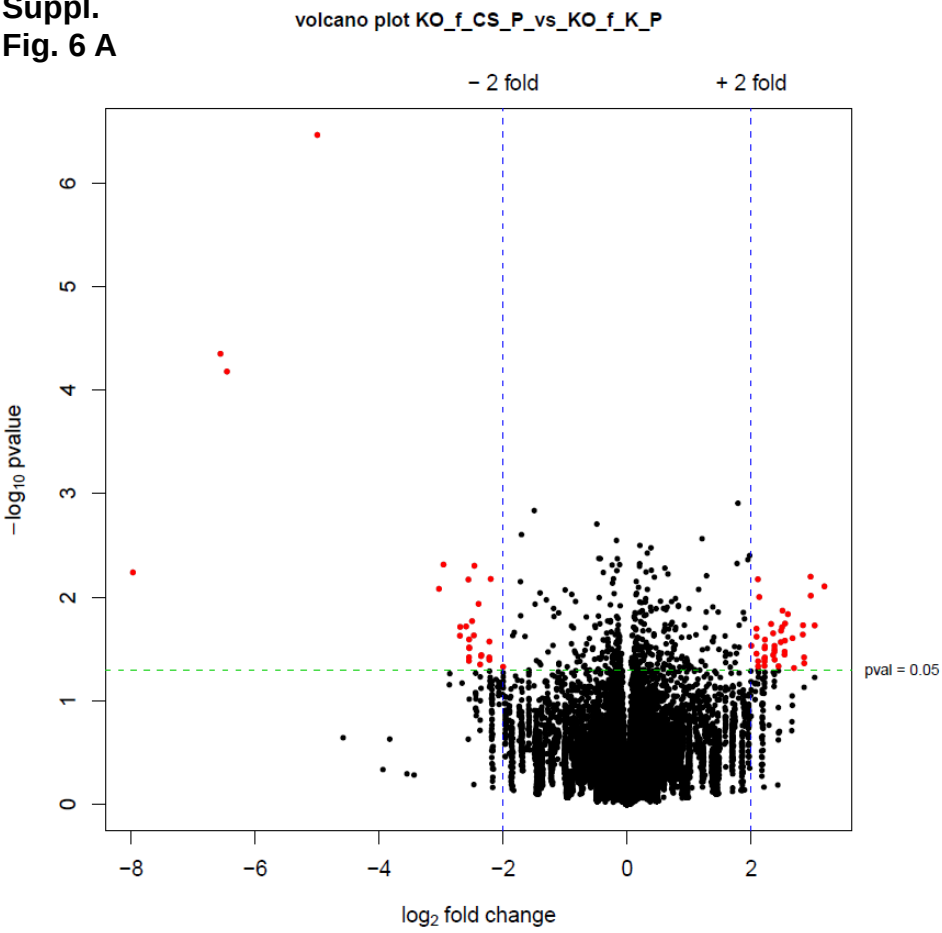


Suppl.  
Fig. 5 H

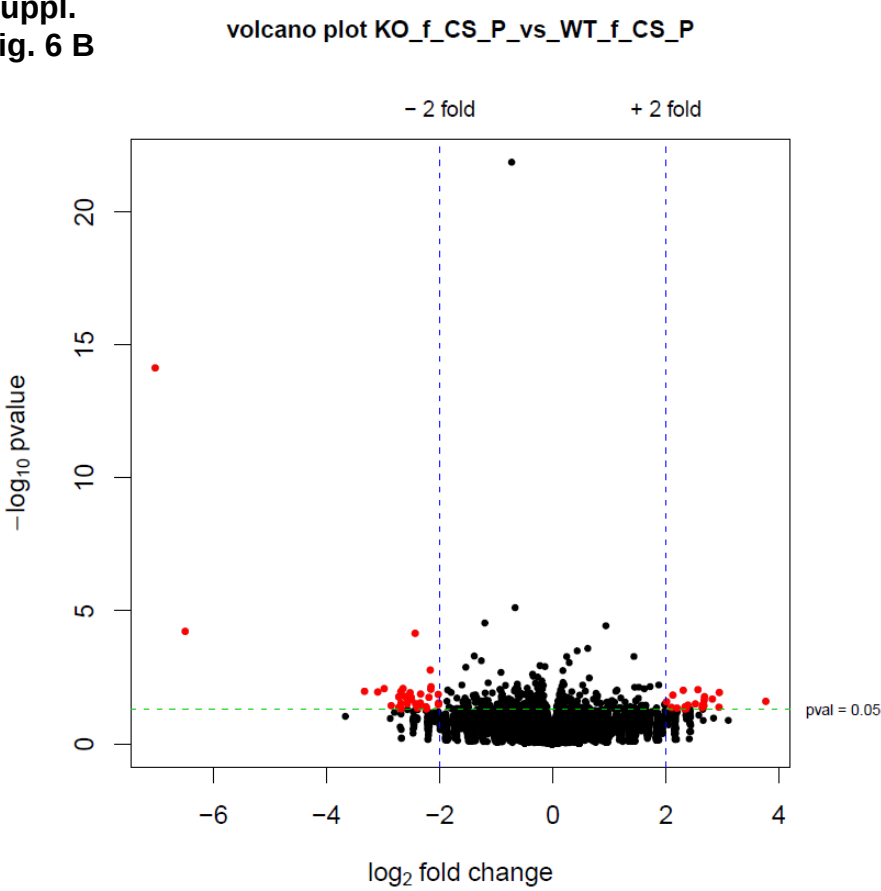


**Supplemental Fig. 5 Volcanoplots illustrating hippocampal genes in different group comparisons.** Differentially expressed genes via DESeq2 with top significant candidates highlighted in red (statistics: Wald test, alpha-level of significance (uncorrected for multiple testing): 0.05) are plotted against  $\log_2$  fold change. Data were based on RNA-seq gene expression data (normalized (rld transformation) counts) from *Zdhc7* mice (N=40) from eight groups (1. C-WT-m, N=4; 2. CS-WT-m, N=4; 3. C-KO-m, N=4; 4. CS-KO-m, N=4; 5. C-WT-f, N=6; 6. CS-WT-f, N=6; 7. C-KO-f, N=6; 8. CS-KO-f N=6); for individual sample allocation to groups see GEO data deposition (GSE281404). Individual group comparisons were displayed in different parts of **Fig.:** **A)** KO\_f\_CS\_H\_vs.\_KO\_f\_K\_H, **B)** KO\_f\_CS\_H\_vs.\_WT\_f\_CS\_H, **C)** KO\_f\_K\_H\_vs.\_WT\_f\_K\_H, **D)** KO\_m\_CS\_H\_vs.\_WT\_m\_CS\_H, **E)** KO\_m\_CS\_H\_vs.\_KO\_m\_K\_H, **F)** KO\_m\_K\_H\_vs.\_WT\_m\_K\_H, **G)** WT\_f\_CS\_H\_vs.\_WT\_f\_K\_H, **H)** WT\_m\_CS\_H\_vs.\_WT\_m\_K\_H.

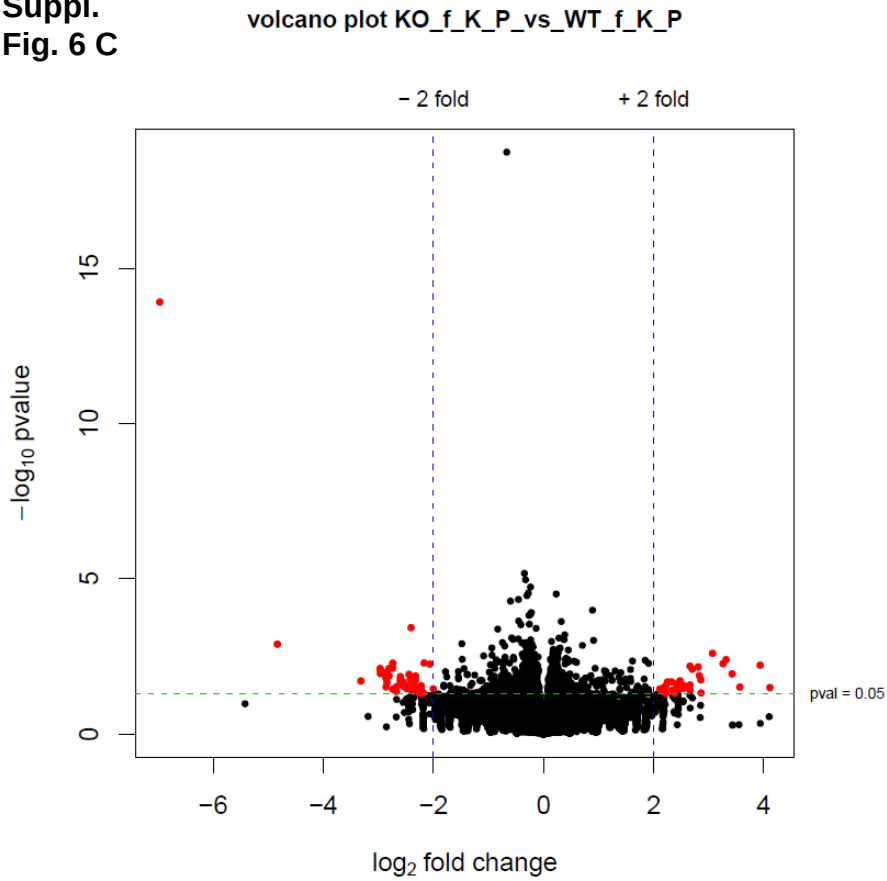
Suppl.  
Fig. 6 A



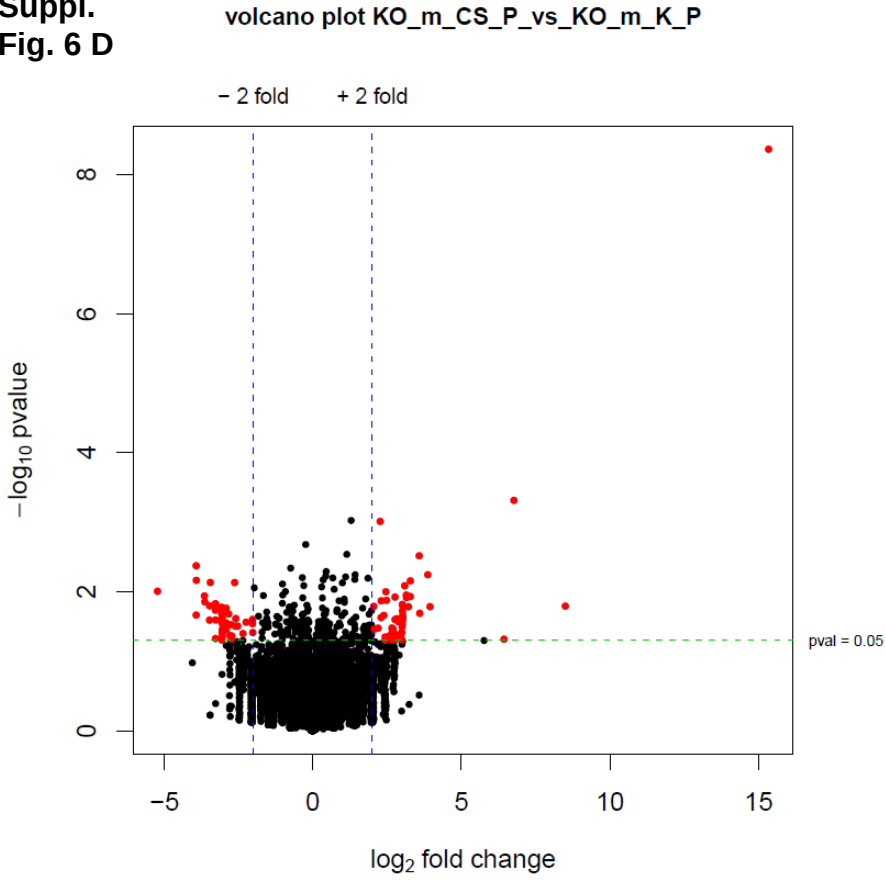
Suppl.  
Fig. 6 B



Suppl.  
Fig. 6 C

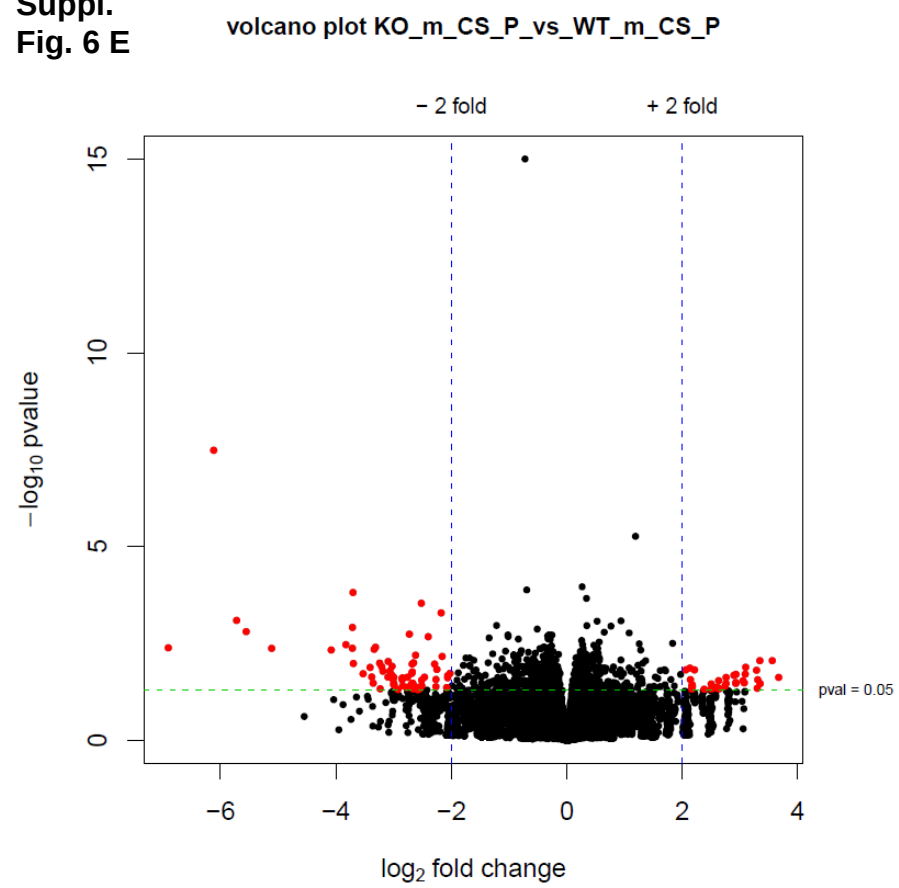


Suppl.  
Fig. 6 D

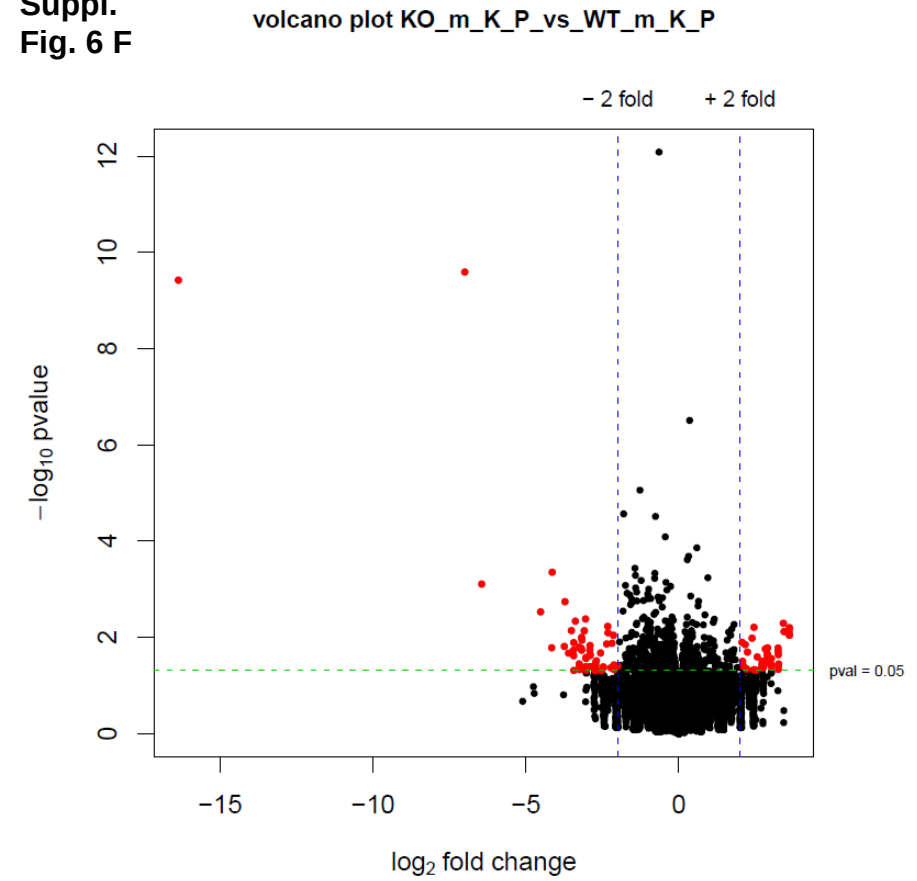


Supplemental Fig. 6 Volcanoplots illustrating prefrontal cortex genes in different group comparisons: to be continued below

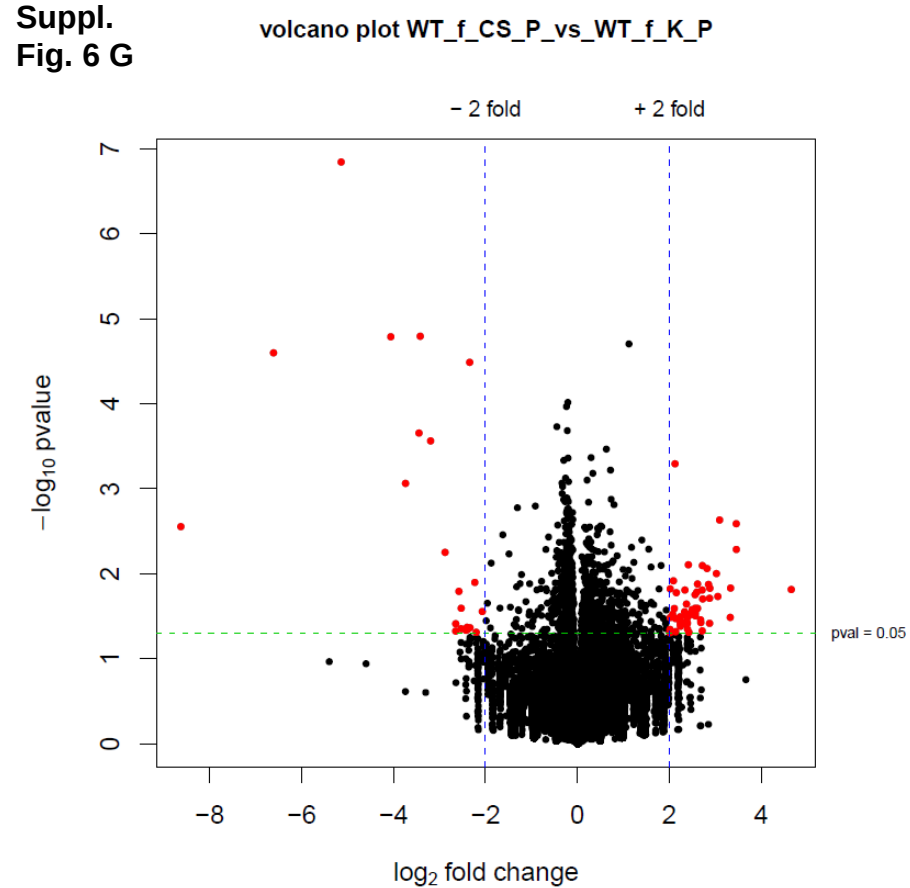
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Fig. 6 E



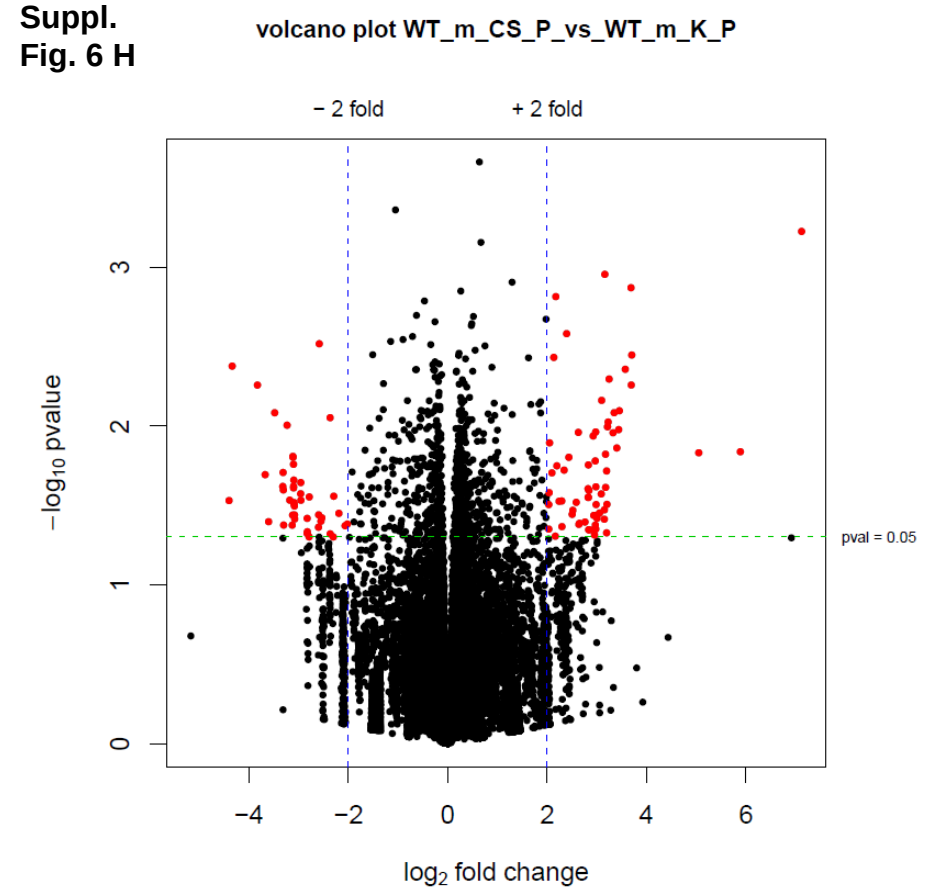
Suppl.  
Fig. 6 F



Suppl.  
Fig. 6 G



Suppl.  
Fig. 6 H



**Supplemental Fig. 6 Volcanoplots illustrating prefrontal cortex genes in different group comparisons.** Differentially expressed genes via DESeq2 with top significant candidates highlighted in red (statistics: Wald test, alpha-level of significance (uncorrected for multiple testing): 0.05) are plotted against  $\log_2$  fold change. Data were based on RNA-seq gene expression data (normalized (rld transformation) counts) from *Zdhhc7* mice (N=40) from eight groups (1. C-WT-m, N=4; 2. CS-WT-m, N=4; 3. C-KO-m, N=4; 4. CS-KO-m, N=4; 5. C-WT-f, N=6; 6. CS-WT-f, N=6; 7. C-KO-f, N=6; 8. CS-KO-f N=6); for individual sample allocation to groups see GEO data deposition (GSE281404). Individual group comparisons were displayed in different parts of **Fig.:** **A)** KO\_f\_CS\_P\_vs.\_KO\_f\_K\_P, **B)** KO\_f\_CS\_P\_vs.\_WT\_f\_CS\_P, **C)** KO\_f\_K\_P\_vs.\_WT\_f\_K\_P, **D)** KO\_m\_CS\_P\_vs.\_KO\_m\_K\_P, **E)** KO\_m\_CS\_P\_vs.\_WT\_m\_CS\_P, **F)** KO\_m\_K\_P\_vs.\_WT\_m\_K\_P, **G)** WT\_f\_CS\_P\_vs.\_WT\_f\_K\_P, **H)** WT\_m\_CS\_P\_vs.\_WT\_m\_K\_P.