

Supplemental material for:

## **Placental effects on maternal brain revealed by disrupted placental gene expression in mouse hybrids**

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### **Supplemental material in this pdf:**

Supplemental Fig. S1: Diagnostic plots for DESeq2 analysis for hybrid vs. Dom placenta.  
Supplemental Fig. S2: Diagnostic plots for DESeq2 analysis for hybrid vs. Spret placenta.  
Supplemental Fig. S3: Diagnostic plots for DESeq2 analysis for Dom vs. Spret placenta.  
Supplemental Fig. S4: Diagnostic plots for DESeq2 analysis for MPoA-hy vs. MPoA-dom.  
Supplemental Fig. S5: Diagnostic plots for DESeq2 analysis for MPoA-hy vs. MPoA-spret.  
Supplemental Fig. S6: Diagnostic plots for DESeq2 analysis for MPoA-dom vs. MPoA-spret.  
Supplemental Table S4: PAML4 CodeML likelihood ratio test results.  
Supplemental Table S5: Sequence ID information for evolutionary analysis.

### **Additional supplemental material in separate files:**

Supplemental Dataset S1: Result summary and gene lists for placental DESeq2 analysis.  
Supplemental Dataset S2: Result summary and gene lists for MPoA DESeq2 analysis.  
Supplemental Dataset S3: Result summary and gene lists for placenta-MPoA co-expression analysis.

Figure S1. Diagnostic plots for DESeq2 differential expression analysis for hybrid vs. *Dom* placenta.

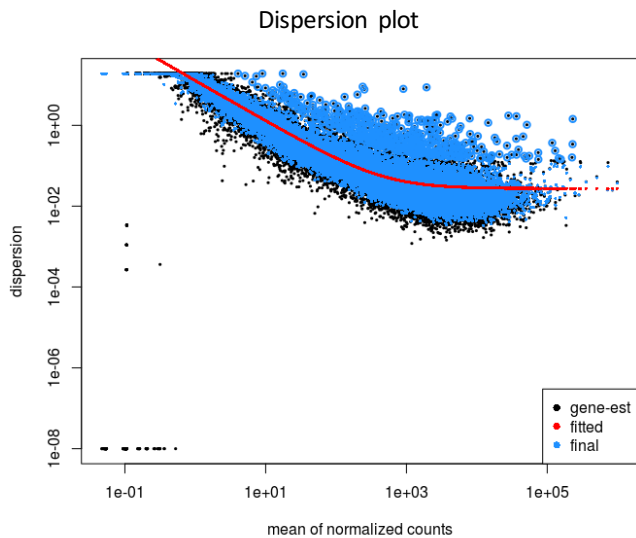
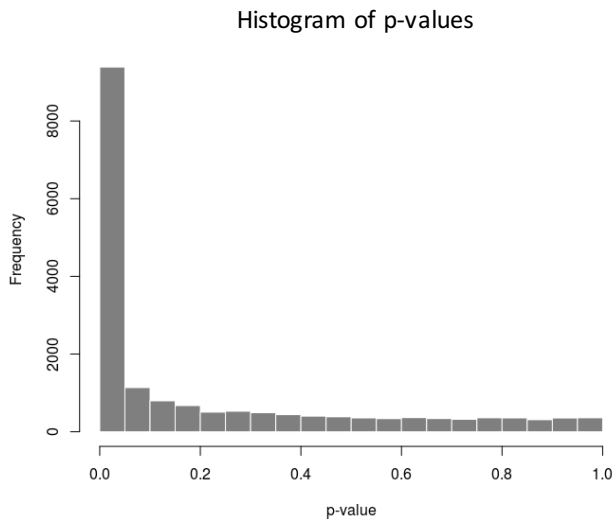
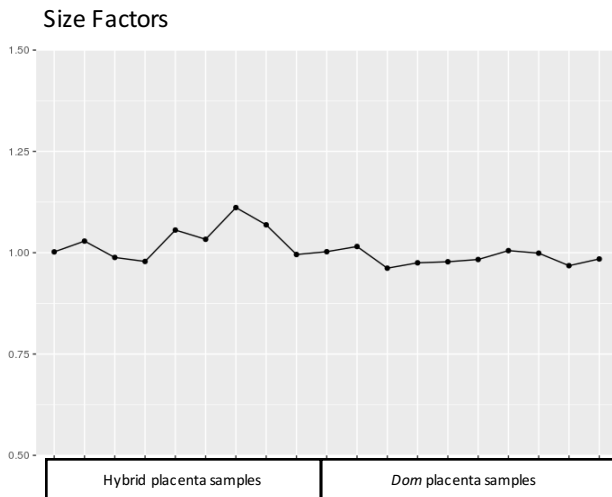
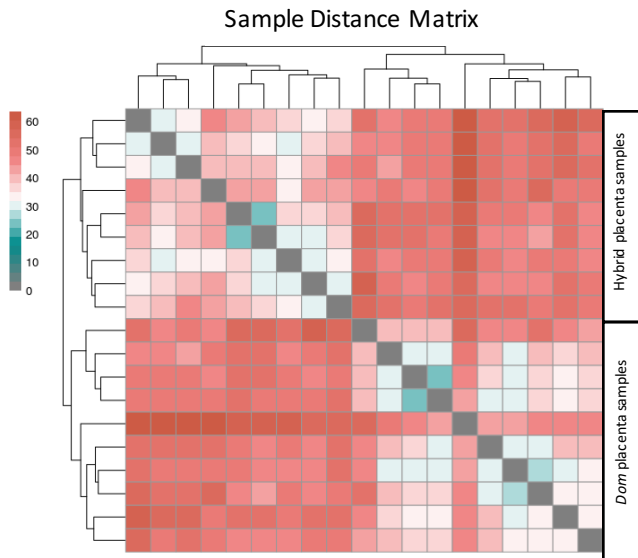
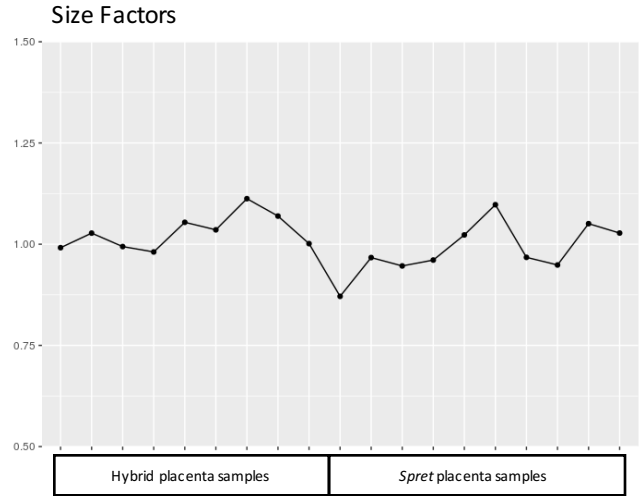
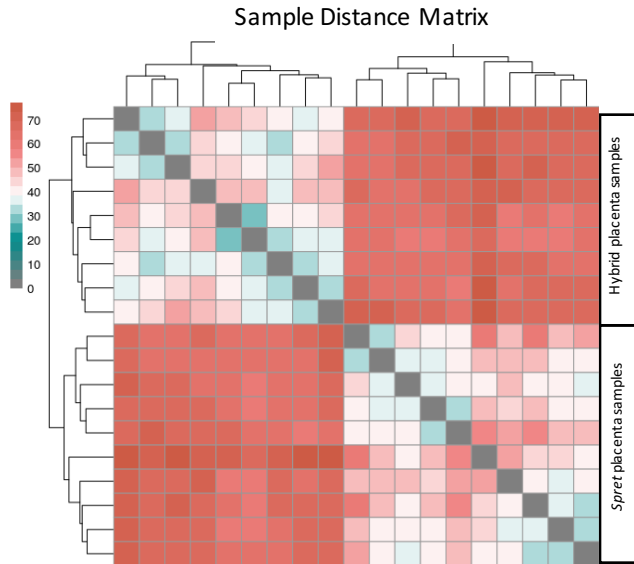
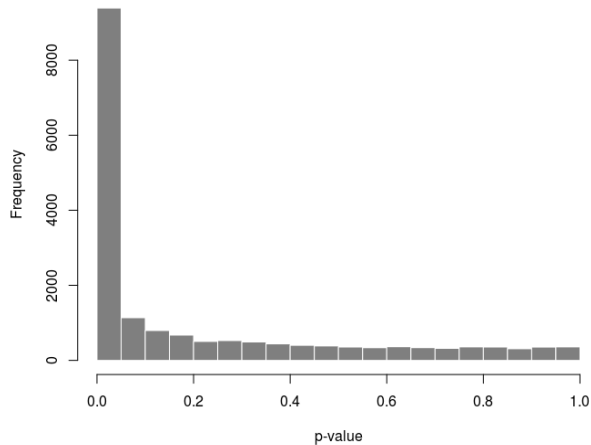


Figure S2. Diagnostic plots for DESeq2 differential expression analysis for hybrid vs. *Spret* placenta.



### Histogram of p-values



### Dispersion plot

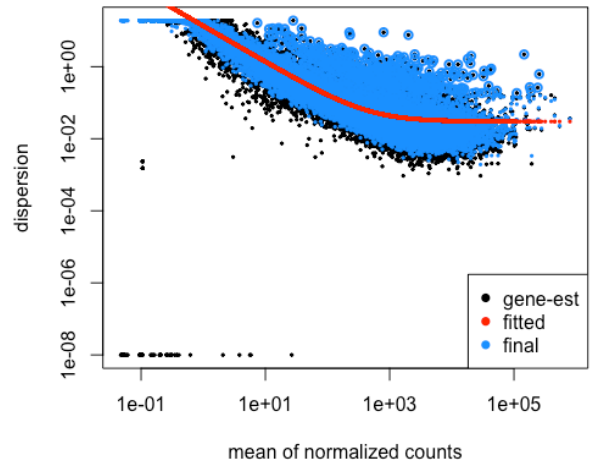


Figure S3. Diagnostic plots for DESeq2 differential expression analysis for *Dom* vs. *Spret* placenta.

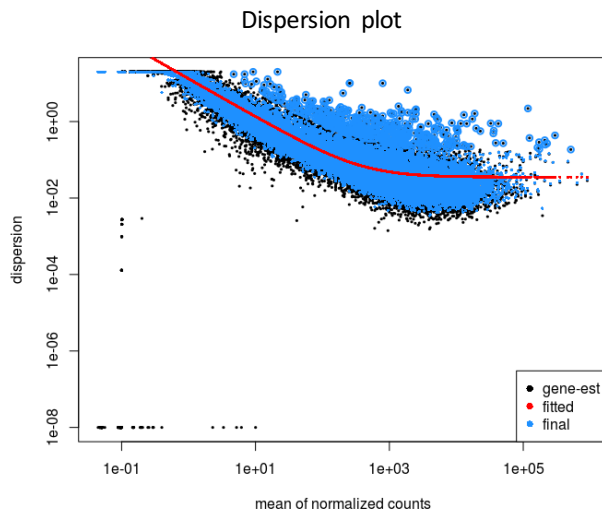
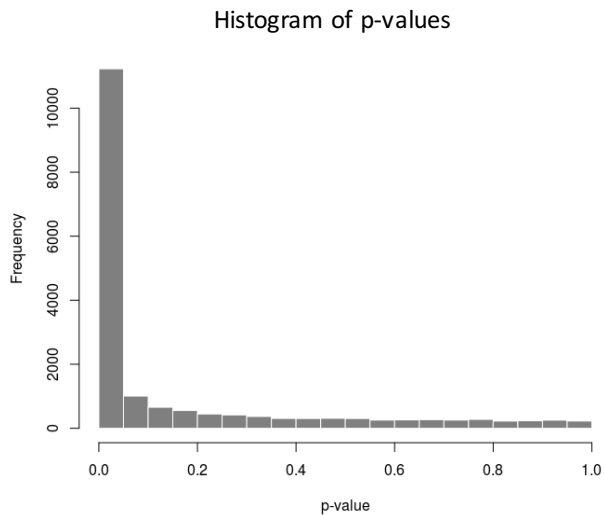
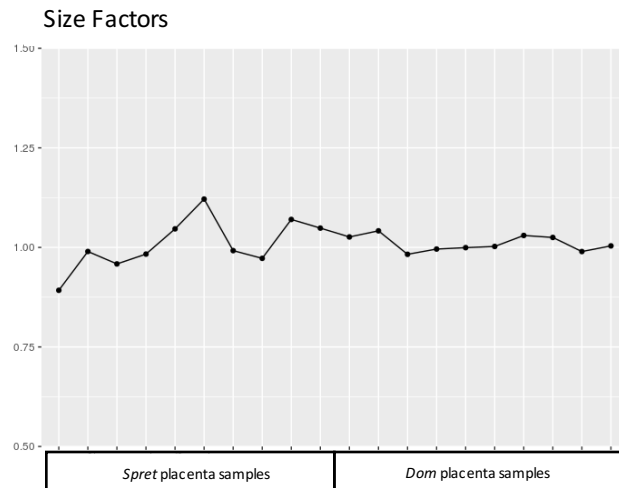
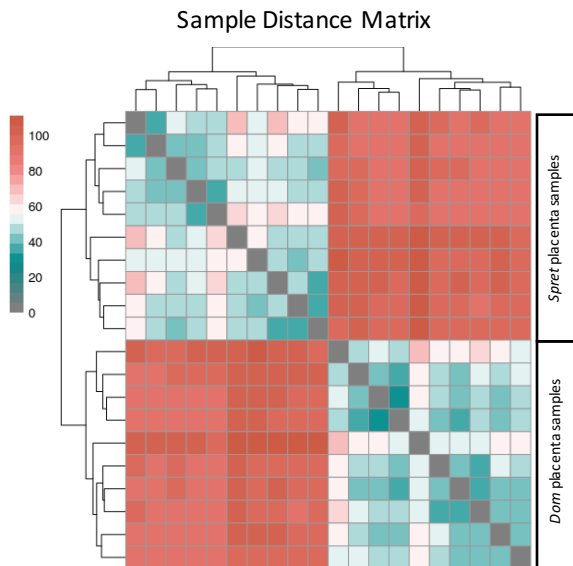


Figure S4. Diagnostic plots for DESeq2 differential expression analysis for MPoA-*hy* vs. MPoA-*dom*.

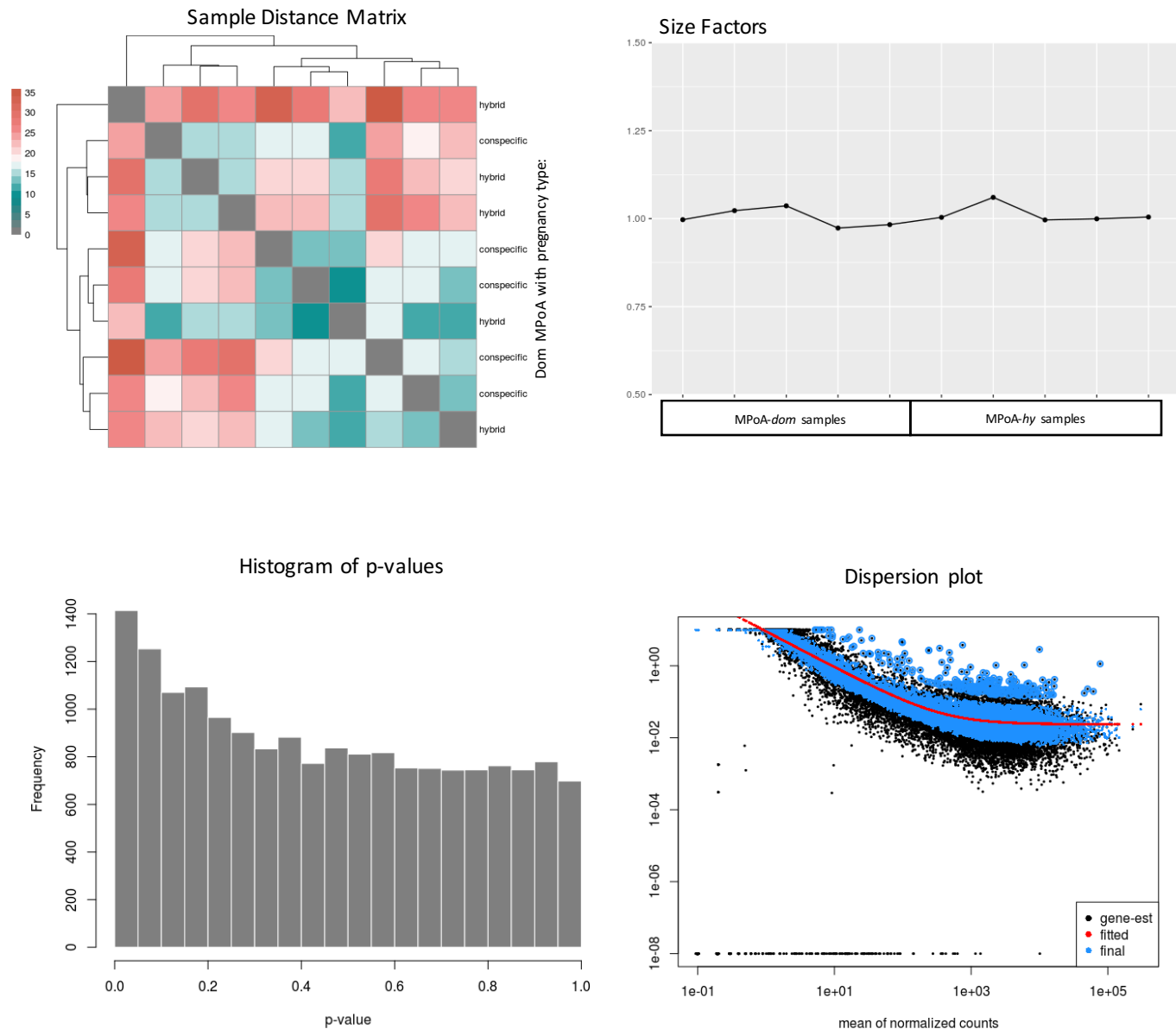
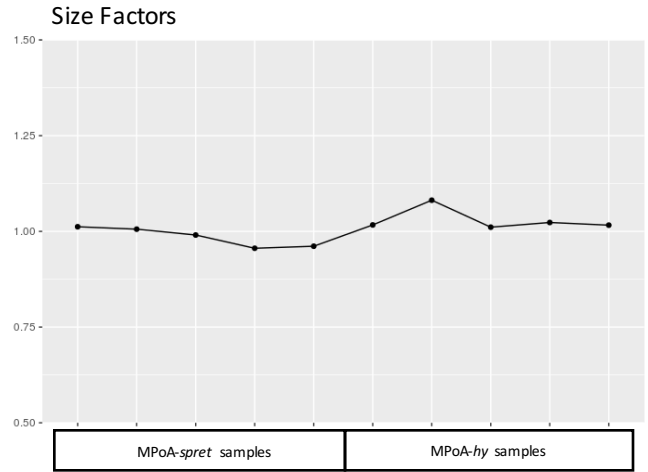
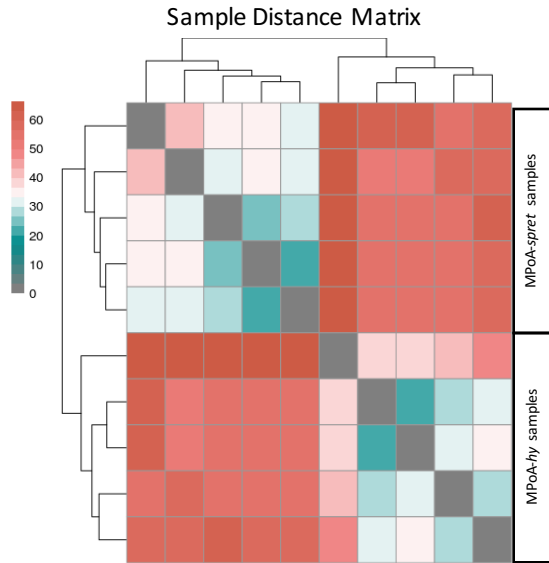
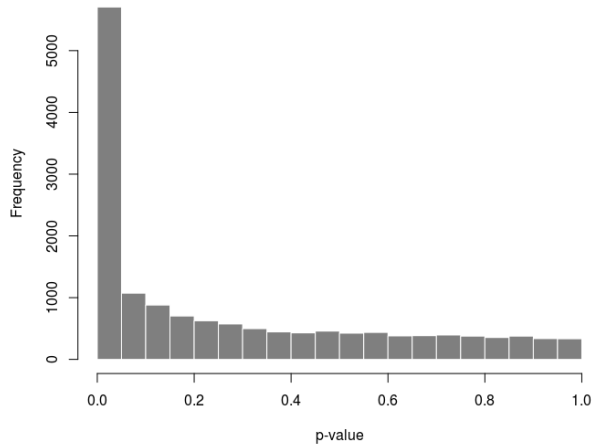


Figure S5. Diagnostic plots for DESeq2 differential expression analysis for MPoA-*hy* vs. MPoA-*spret*.



### Histogram of p-values



### Dispersion plot

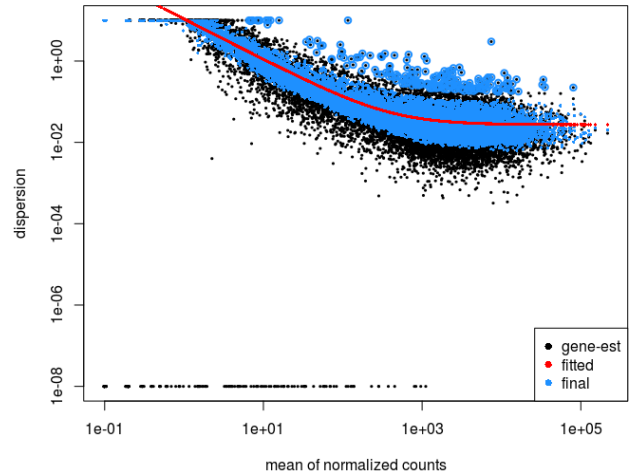


Figure S6. Diagnostic plots for DESeq2 differential expression analysis for MPoA-*dom* vs. MPoA-*spret*.

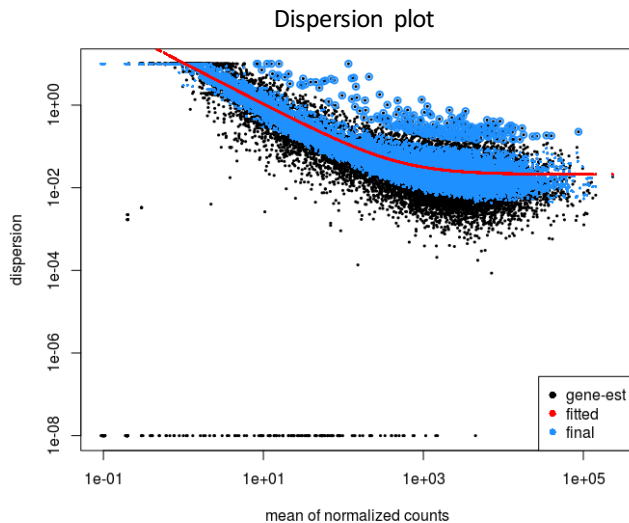
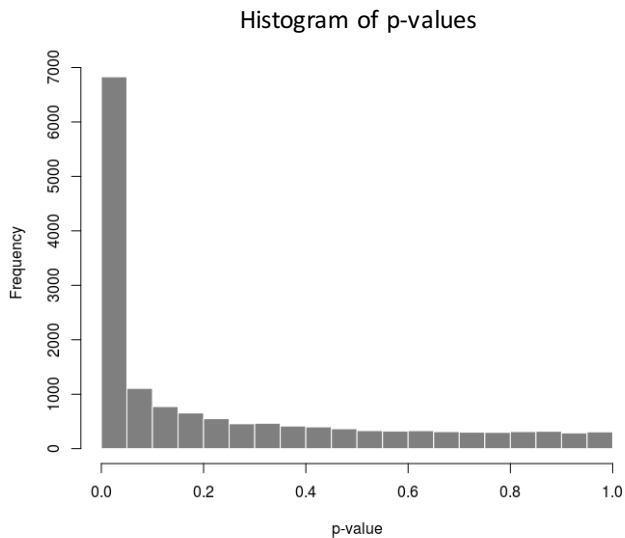
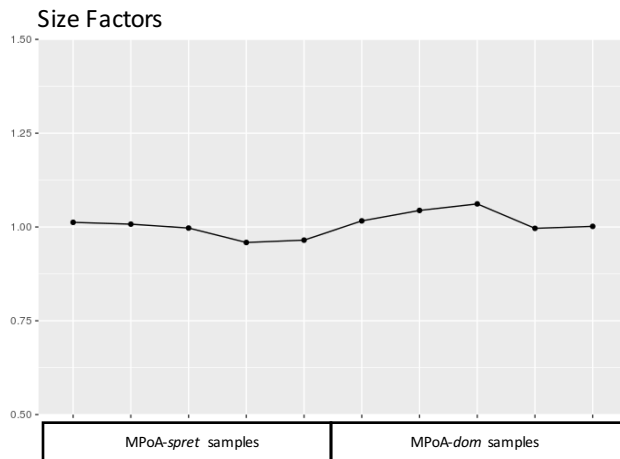
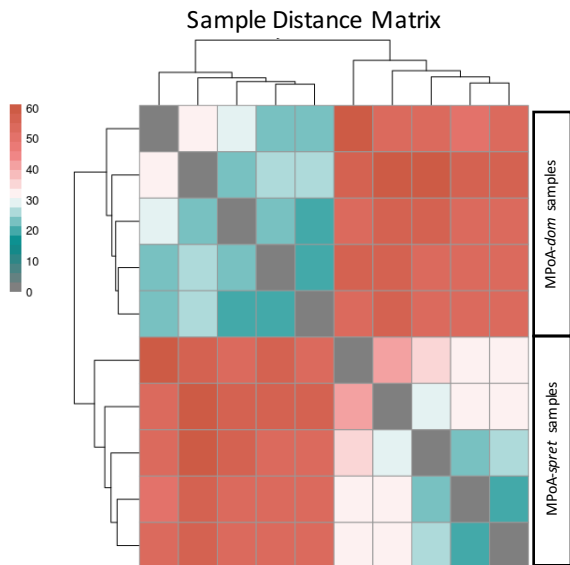


Table S1. PAML4 Codeml likelihood ratio test results

	M0 lnL	MC lnL	2Δ(M0-MC)	<i>p</i>	interpretation	dN/dS	Foreground dN/ dS	Background dN/dS
<i>Ctsr</i>	1380.921675	1377.454646	6.93405800000028	0.01	differing rates across tree	M2	>10	0.26
<i>Pri8a6</i>	1164.593902	1160.842685	7.50243399999999	0.01	differing rates across tree	M2	3.78	0.25
<i>Tpbpb</i>	754.456437	752.675798	3.56127800000013	0.1	whole tree evolves at same rate	M0		1.43

M=Model, for explanation of compared models see methods, lnL=log likelihood of Model fit, dN/dS nonsynonymous to synonymous substitution rate ratio (evolutionary rate)

Table S2. Sequence ID information for evolutionary analysis

	<i>Ctsr</i>	<i>Pri8a6</i>	<i>Tpbpb</i>	<i>Tpbpa</i>
<i>Musc</i>	MGP_PWKPhJ_G0019675	MGP_PWKPhJ_G0019422	MGP_PWKPhJ_G0019671	
<i>Cast</i>	MGP_CASTEiJ_G0019922	MGP_CASTEiJ_G0019668	MGP_CASTEiJ_G0019917	
<i>Dom</i>	MGP_WSBEiJ_G0019983	MGP_WSBEiJ_G0019728	MGP_WSBEiJ_G0019979	MGP_WSBEiJ_G0019980
<i>Spret</i>	MGP_SPRETEiJ_G0019504	MGP_SPRETEiJ_G0019238	MGP_SPRETEiJ_G0019499	
<i>Car</i>	MGP_CAROLIEiJ_G0018624	MGP_CAROLIEiJ_G0018369	MGP_CAROLIEiJ_G0018621	
<i>Pah</i>	XM_021179921.1	XM_021180719.1	XM_021215385.1 ( <i>Tpbpa</i> -like)	XM_021216022.1 ( <i>Tpbpa</i> -like)

Ensembl gene stable ID of included sequences for *Mus m. castaneus* (*Cast*), *Mus m. musculus* (*Musc*), *Mus m. domesticus* (*Dom*), *Mus spretus* (*Spret*), *Mus caroli* (*Car*).  
NCBI sequence ID of included sequences for *Mus pahari* (*Pah*).

% identity to <i>Dom-Tpbpa</i> : 84.3%	% identity to <i>Dom-Tpbpa</i> : 92.2%
% identity to <i>Dom-Tpbpb</i> : 90.6%	% identity to <i>Dom-Tpbpb</i> : 82.7%