Supporting Information

Table S1. Linear models for the decline in similarity (Spearman's rho correlation coefficient) between pheasant and each species over divergence time. Separate models are run for each tissue and sex.

Variable	**Estimate**	**SE**	**T value**	**P value**
Female Spleen				
Intercept	0.82	0.02	35.7	**<0.0001**
Chromosome	-0.09	0.03	-2.79	0.032
Divergence time	-0.82	0.34	-2.37	0.055
Chromosome*Divergence time	-1.25	0.49	-2.57	**0.043**
Male Spleen				
Intercept	0.80	0.03	29.1	**<0.0001**
Chromosome	-0.06	0.04	-1.64	0.152
Divergence time	-0.87	0.42	-2.10	0.081
Chromosome*Divergence time	-1.39	0.89	-2.35	0.057
Female Gonad				
Intercept	0.85	0.01	66.2	**<0.0001**
Chromosome	-0.02	0.02	-1.13	0.301
Divergence time	-1.21	0.19	-6.25	0.001
Chromosome*Divergence time	-0.77	0.27	-2.12	**0.030**
Male Gonad				
Intercept	0.84	0.03	32.1	**<0.0001**
Chromosome	0.02	0.04	0.57	0.590
Divergence time	-1.80	0.39	-4.58	0.004
Chromosome*Divergence time	-0.09	0.57	-0.16	0.877

S1 Figure. **Pairwise gene expression divergence between each focal species and the estimated ancestral gene expression levels at the nearest node in the female and male gonad for (a) female-biased genes and (b) male-biased genes**. Genes were classified as female- or male-biased if they had a significant two-fold difference in expression between males and females for the ancestral expression at the ancestral node common to all 6 species (shown by a circle on the phylogeny). Expression in females shown in red and males in blue. Autosomes are shaded dark and Z chromosome shaded light. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

S2 Figure. **Pairwise gene expression divergence between each focal species and the estimated ancestral gene expression levels at the nearest node in the female and male gonad for (a) gene with low expression and (b) genes with high expression**. Mean gene expression between males and females, across all 6 species was used to rank genes as lowly expression (lowest 50 % genes) and highly expressed (top 50 % of genes). Expression in females shown in red and males in blue. Autosomes are shaded dark and Z chromosome shaded light. Wilcoxon tests for significant differences between autosomal and Z chromosome divergence denoted by * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Fig. S1

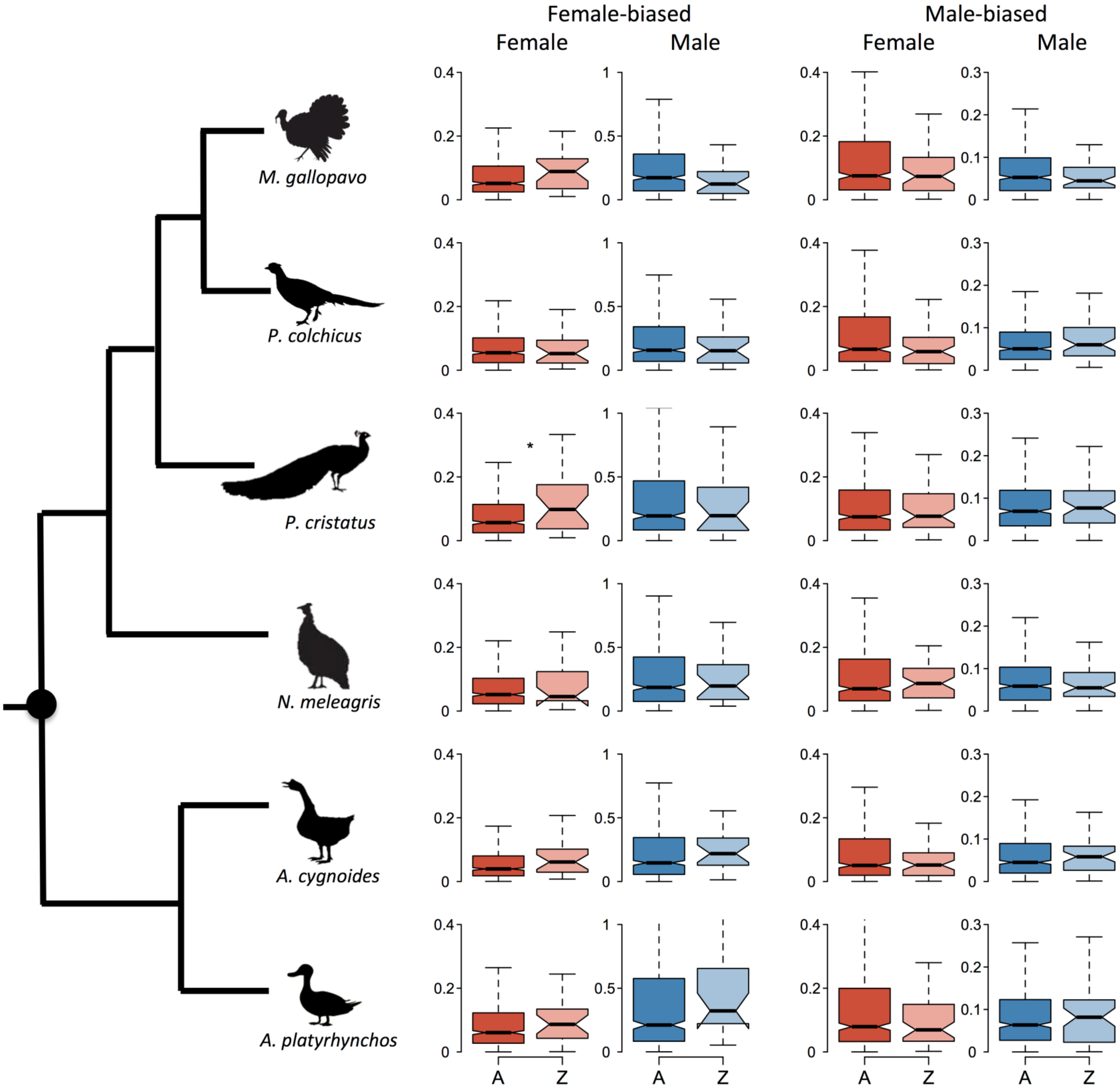
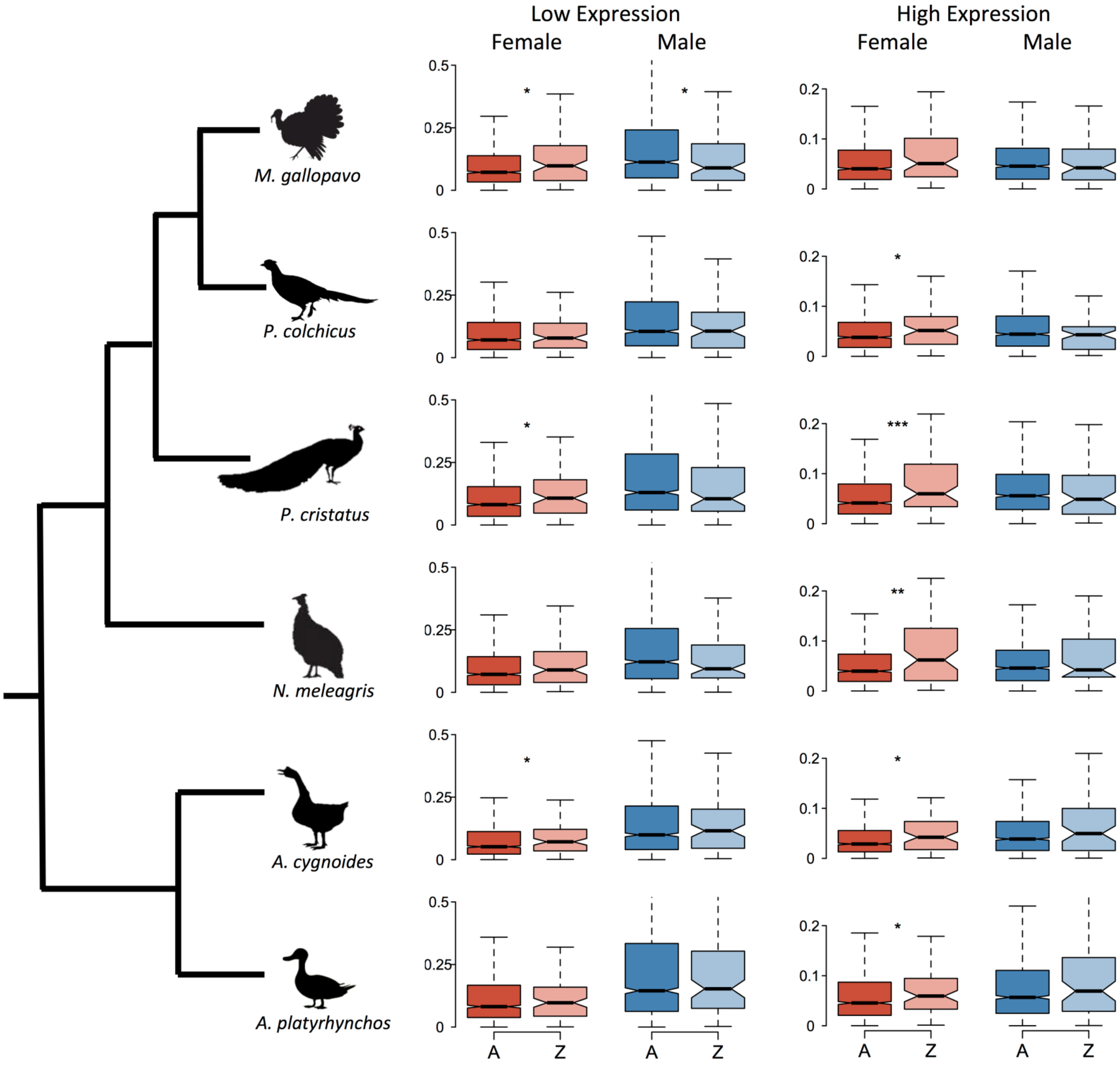

Female-biased
Male-biased
Female
Male
Female
Male
M. gallopavo
P. colchicus
P. cristatus
N. meleagris
A. cygnoides
A. platyrhynchos
0.4
0.2
0
1
0.5
0
0.3
0.2
0.1
*
A
Z
A
Z
A
Z
A
Z

Fig. S2


Low Expression
High Expression
Female
Male
Female
Male
M. gallopavo
P. colchicus
P. cristatus
N. meleagris
A. cygnoides
A. platyrhynchos
0.5
0.25
0
0.2
0.1
0
*
*
*
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*
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*
*
A
Z
A
Z
A
Z
A
Z