

**Table S3. Similarities and differences in associations with coding sequence evolution in an ant (*C. floridanus*) and a fly (*D. melanogaster*) in linear models generated from traits with data in both taxa, limited to common orthologs (n = 2102)**

	<i>C. floridanus</i> model coefficient	<i>D. melanogaster</i> model coefficient	Consistent significant relationship with X between species?
<b>X</b>	<b>dS (R<sup>2</sup> = 0.26)</b>	<b>dS (R<sup>2</sup> = 0.34)</b>	
H3K9ac	-0.38****	-0.08	No
Exon count	-0.20****	0.07*	No
H3K4me1	-0.06*	-0.15****	Yes, negative
H3K27me3	-0.04	-0.03	No
H3K36me3	-0.03	0.17****	No
Intron length	-0.02	-0.13****	No
Expression level	0.01	-0.27****	No
H3K9me3	0.03	0.10****	No
H3K27ac	0.04	-0.01	No
RNA Pol II	0.09**	-0.09**	No
H3K4me3	0.20****	0.52****	Yes, positive
Exon length	0.26****	0.29****	Yes, positive
<b>X</b>	<b>dN (R<sup>2</sup> = 0.16)</b>	<b>dN (R<sup>2</sup> = 0.15)</b>	
H3K9ac	-0.26****	0.05	No
H3K36me3	-0.15****	-0.05	No
Expression level	-0.07**	-0.25****	Yes, negative
H3K4me3	-0.04	0.09	No
H3K9me3	-0.03	0.03	No
Intron length	0.01	-0.06*	No
H3K4me1	0.04	-0.01	No
Exon count	0.06	0.21****	No
H3K27ac	0.12**	-0.01	No
RNA Pol II	0.14****	-0.04	No
H3K27me3	0.17****	-0.15****	No
Exon length	0.36****	0.35****	Yes, positive
<b>X</b>	<b>dN/dS (R<sup>2</sup> = 0.12)</b>	<b>dN/dS (R<sup>2</sup> = 0.09)</b>	
H3K36me3	-0.15****	-0.11**	Yes, negative
H3K9ac	-0.14****	0.08	No
H3K4me3	-0.12**	-0.10	Yes, negative
Expression level	-0.08**	-0.17****	Yes, negative
H3K9me3	-0.04	0.00	No
Intron length	0.02	-0.02	No
H3K4me1	0.07*	0.04	No
RNA Pol II	0.11**	0.00	No
H3K27ac	0.11**	0.00	No
Exon count	0.13****	0.20****	Yes, positive
H3K27me3	0.20****	-0.14****	No
Exon length	0.30****	0.27****	Yes, positive

\*P < 0.05, \*\*P < 10<sup>-2</sup>, \*\*\*P < 10<sup>-3</sup>, \*\*\*\*P < 10<sup>-4</sup>