

mod/ENCODE Transcription
Comparison Paper
Figure Slide Pack

15 Feb 2013

Transcriptome Comparison Group

Exhibit 1: Data Sets

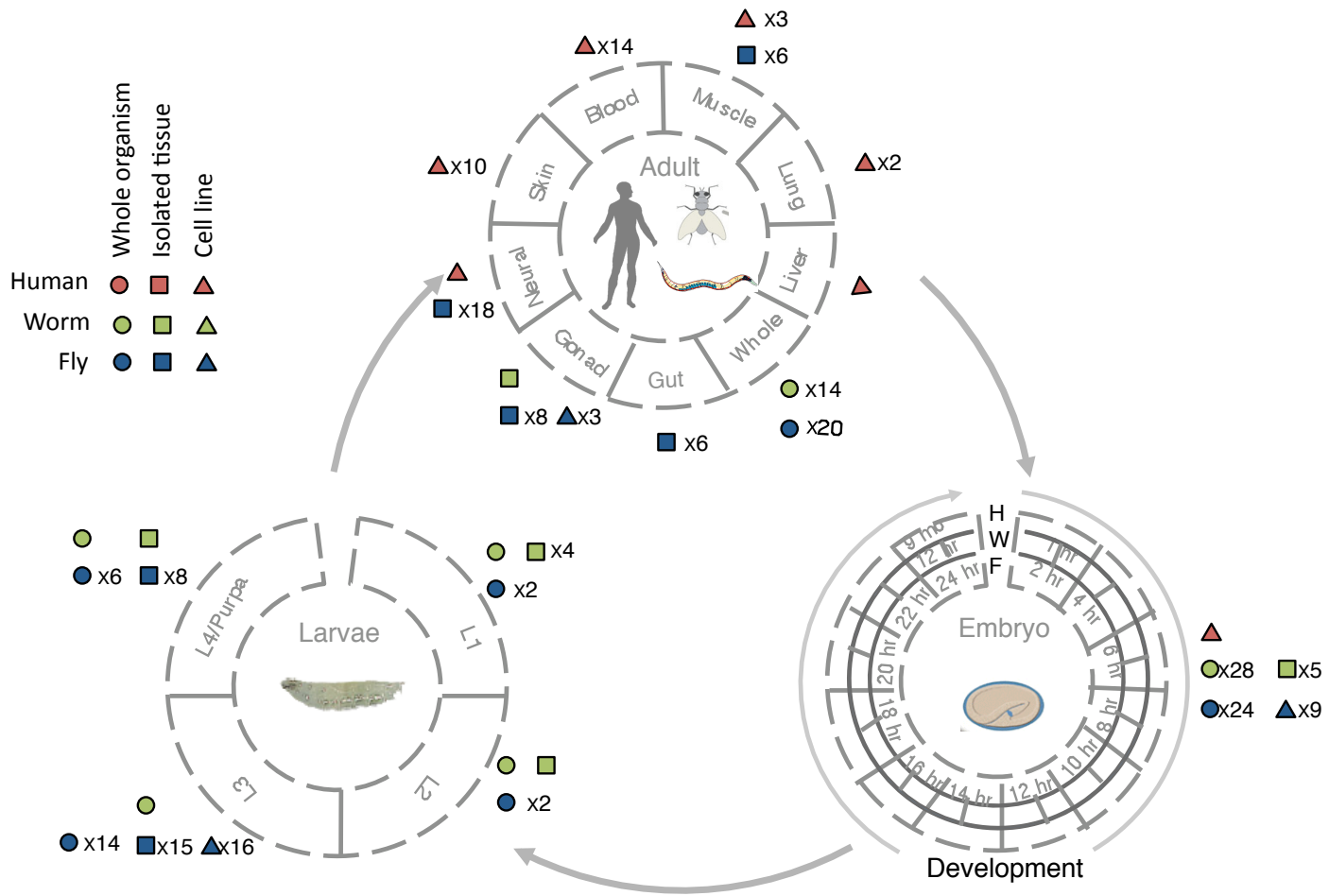


Exhibit 2: Summary Statistics for Protein Coding Genes

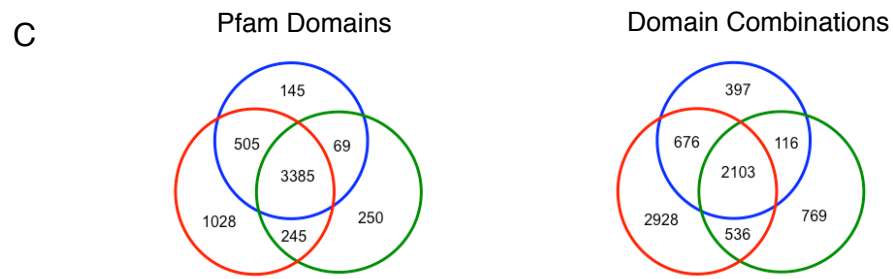
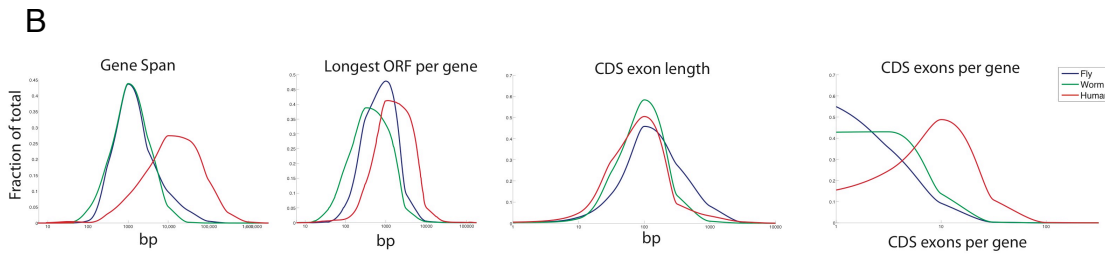
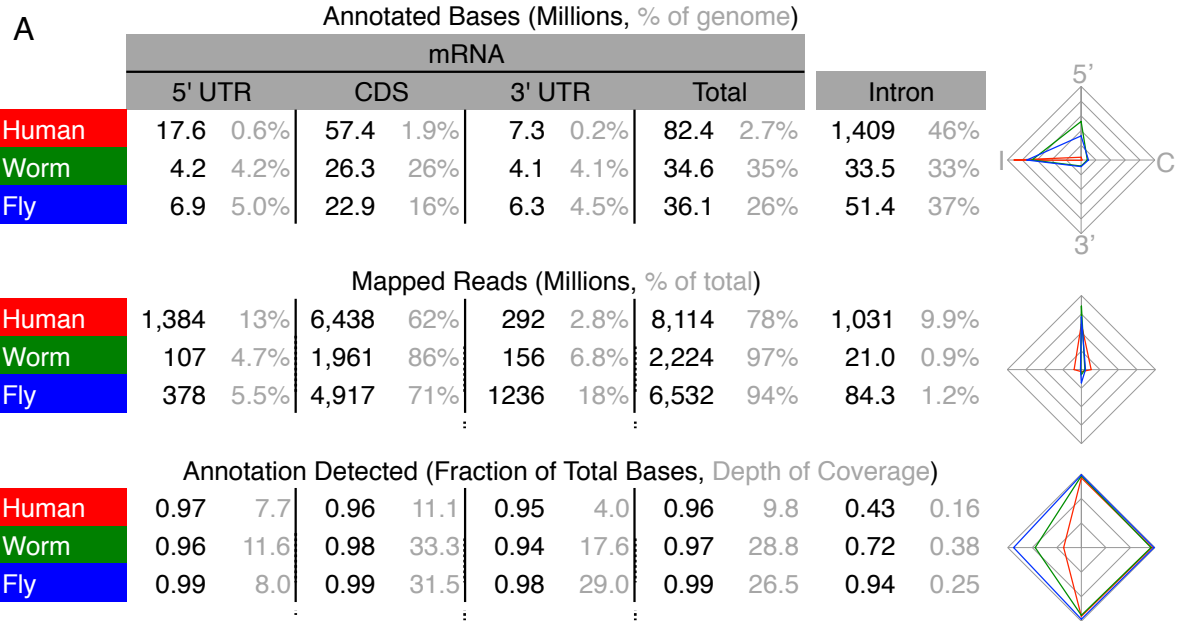


Exhibit 2: Summary Statistics for Protein Coding Genes

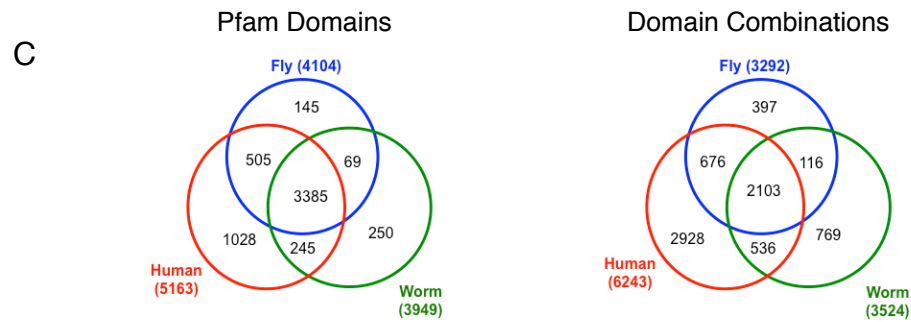
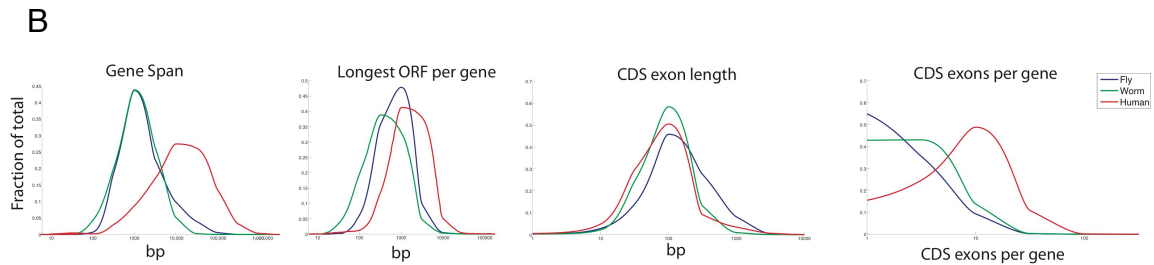
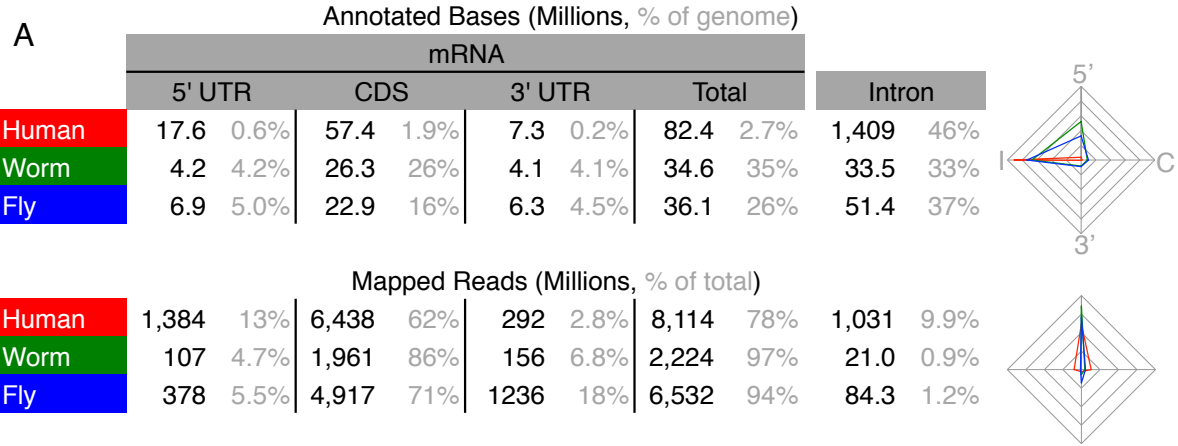


Exhibit 3: Splicing Figure

Figure 2 - 1/21/13

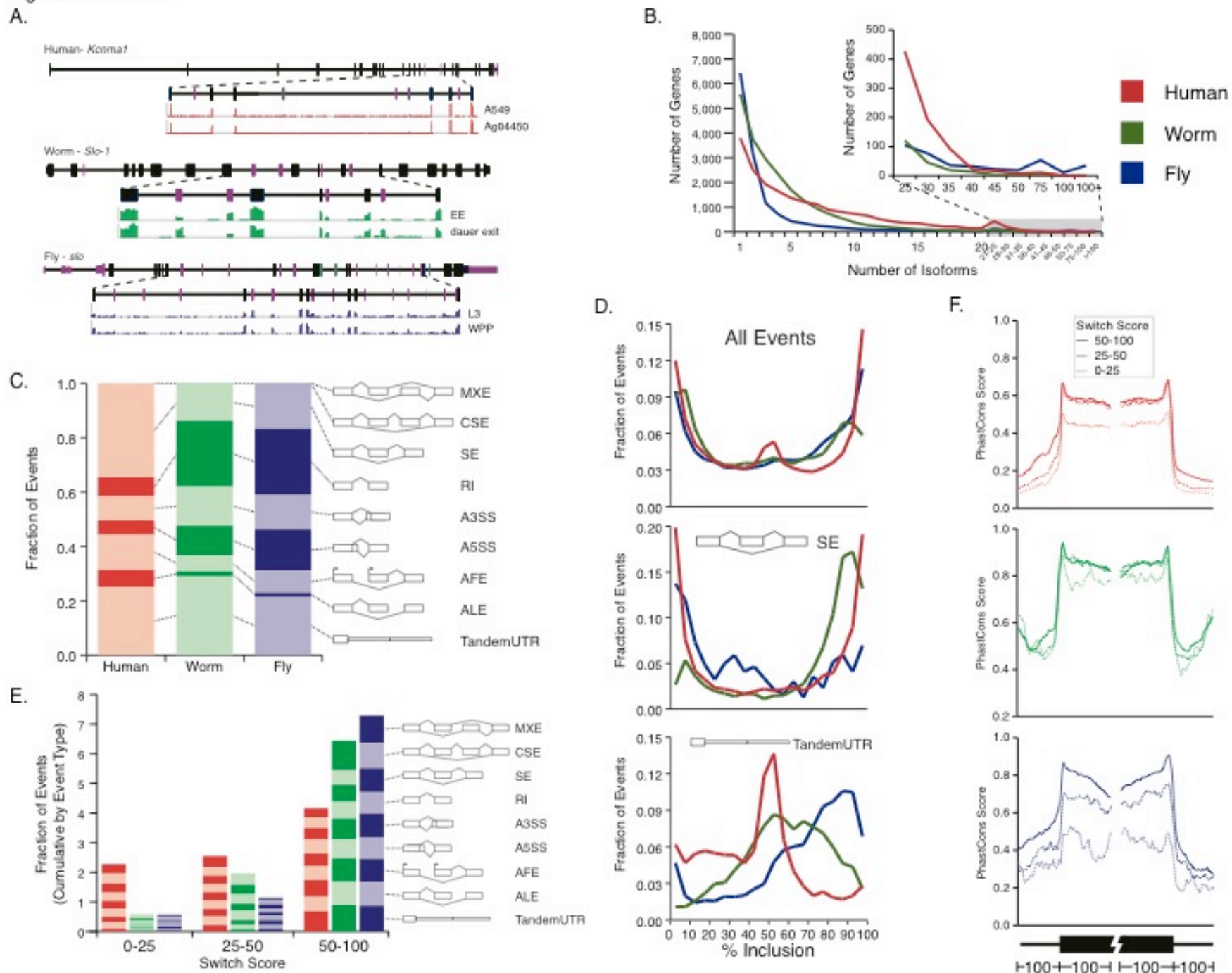
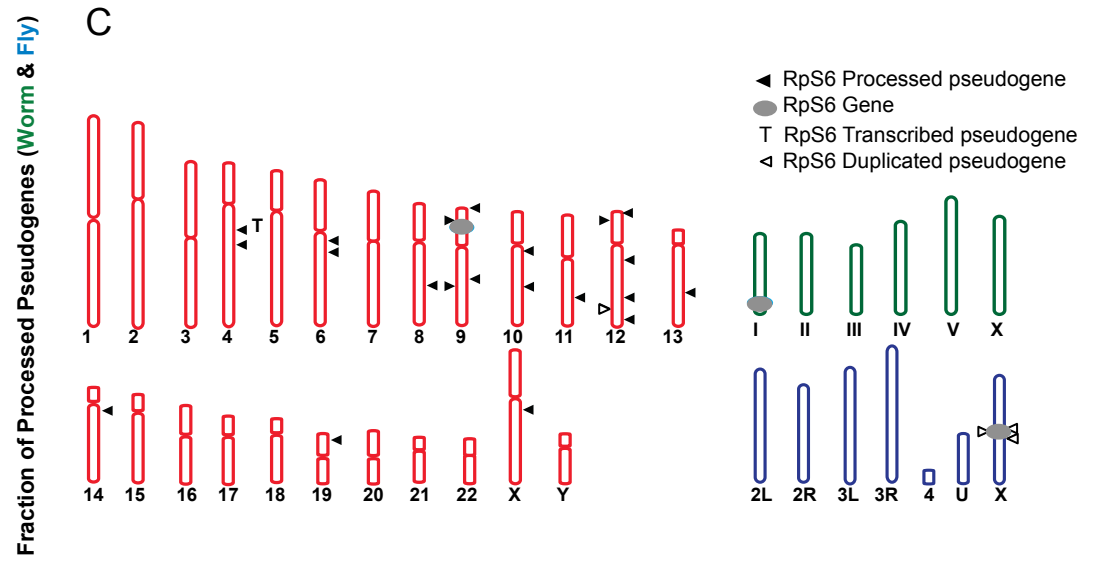
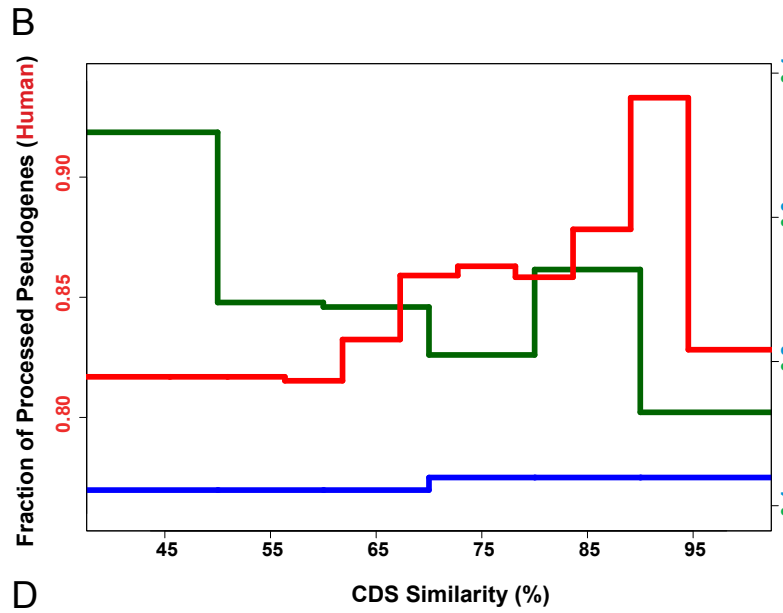
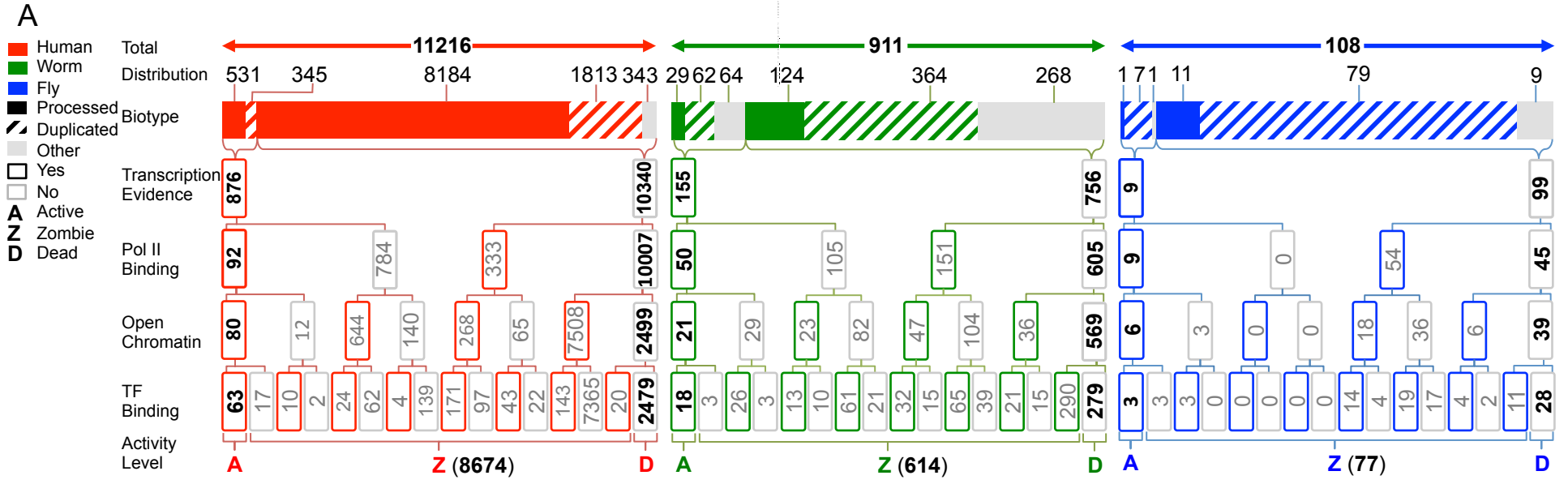


Exhibit 4: Pseudogenes



D

Type	Human	Worm	Fly
7tm	414		
RRM	235		
IG	180	1	3
TF	176		5
IG	171		2
Ribo	144		
Ribo	132		
TF	123		
Struct	117		
Kin	93	2	3
Ploop	93		
Ploop	86		
Ribo	86		
Ubiqu	84		
TF	83		
Ribo	82		
Ribo	76		
H	74		3
H	71		7
Ribo	69	1	
Ribo	68		
Ribo	68		
GAPDH	66		
Ribo	64		1
Ribo	64		1
Struct	62		
GAPDH	61		
Ribo	60		
Ribo	59		
Kin	58	2	2
Ploop	58	1	
Ribo	57		
Ubiqu	55	1	
Ribo	55		
Ubiqu	54		
Ribo	54		
Struct	53		
TF	50		
Struct	49		
Struct	48		
Ribo	48		
Ribo	47		
TF	46		
Ploop	45		2
Ploop	44		2
Ploop	44		
Ribo	43	1	
Ploop	42		1
Struct	41		
Struct	41		
Kin	40		
Ubiqu	39		
Ubiqu	38		
7tm	36		
7tm	36		
7tm	36		
7tm	36		
Ubiqu	35		
7tm	34		
Struct	33		
7tm	33		
7tm	33		
7tm	33		
SAP	30		30
Motor	10		10
Kin	9		9
Kin	8		8

Exhibit 5: Comparison of ncRNAs

A)

		Human			Worm			Fly			
		Elements	Genome Coverage (Kb [%])	Mapped Reads (fraction)	Elements	Genome Coverage (Kb [%])	Mapped Reads (fraction)	Elements	Genome Coverage (Kb [%])	Mapped Reads (fraction)	
Annotated ncRNAs	Comparable ncRNAs	piRNA loci	88	1,272 [0.04]	3.2 e-4	35,322	449 [0.45]	6.7 e-3	21	1,604 [1.2]	1.6 e-3
		pri-miRNA	58	1,158 [0.04]	3.6 e-4	44	16 [0.02]	6.6 e-6	43	316 [0.25]	1.7 e-4
		pre-miRNAs	1,756	162 [0.006]	2.7 e-3	221	20 [0.02]	2.1 e-4	235	22 [0.02]	7.2 e-5
		tRNAs	624	47 [0.002]	3.0 e-4	638	45 [0.04]	1.3 e-5	308	22 [0.02]	1.4 e-6
		snoRNAs	1,521	168 [0.006]	3.3 e-4	141	16 [0.02]	2.9 e-4	287	34 [0.03]	2.9 e-4
		snRNAs	1,944	210 [0.007]	4.6 e-5	114	14 [0.01]	4.9 e-5	47	7 [0.006]	8.5 e-5
		lncRNAs	10,840	10,581 [0.37]	2.2 e-2	417	184 [0.18]	8.3 e-4	558	868 [0.68]	1.3 e-2
	Other ncRNAs	9,281	2,624 [0.091]	3.9 e-3	2,935	530 [0.53]	2.9 e-3	398	381 [0.30]	2.1 e-3	
	Total	26,112	16,103 [0.56]	2.9 e-2	39,832	1,268 [1.26]	1.1 e-2	1,897	3,022 [2.35]	1.6 e-2	
Transcriptionally Unannotated Regions		294,956	2,749,660 [96.1]	2.0 e-1	146,913	64,232 [64.1]	5.1 e-2	60,267	89,630 [69.8]	5.5 e-2	
TARs	Total	718,537	923,774 [32.3]	2.0 e-1	235,915	37,482 [37.4]	4.6 e-2	76,757	47,542 [37.0]	5.5 e-2	
	Overlapping TEs	1,633,407	455,803 [15.9]	8.0 e-2	65,600	5,621 [5.6]	2.3 e-3	38,595	7,414 [5.8]	2.9 e-2	
	Overlapping Introns	1,300,035	360,778 [12.6]	1.2 e-1	173,253	18,347 [18.3]	2.5 e-2	79,012	28,857 [22.5]	1.9 e-2	
	incRNA ncRNAs	104,001	13,844 [0.51]	1.2 e-2	2,509	390 [0.77]	2.5 e-4	599	164 [0.004]	2.4 e-5	

A)

		Elements	Genome Coverage		Mapped Reads (fraction)	Elements	Genome Coverage		Mapped Reads (fraction)	Elements	Genome Coverage		Mapped Reads (fraction)	
			Kb	%			Kb	%			Kb	%		
Annotated ncRNAs	Comparable ncRNAs	piRNA loci	88	1,272	0.04	3.2 e-4	35,322	449	0.45	6.7 e-3	21	1,604	1.2	1.6 e-3
		pri-miRNA	58	1,158	0.04	3.6 e-4	44	16	0.02	6.6 e-6	43	316	0.25	1.7 e-4
		pre-miRNAs	1,756	162	0.006	2.7 e-3	221	20	0.02	2.1 e-4	235	22	0.02	7.2 e-5
		tRNAs	624	47	0.002	3.0 e-4	638	45	0.04	1.3 e-5	308	22	0.02	1.4 e-6
		snoRNAs	1,521	168	0.006	3.3 e-4	141	16	0.02	2.9 e-4	287	34	0.03	2.9 e-4
		snRNAs	1,944	210	0.007	4.6 e-5	114	14	0.01	4.9 e-5	47	7	0.006	8.5 e-5
		lncRNAs	10,840	10,581	0.37	2.2 e-2	417	184	0.18	8.3 e-4	558	868	0.68	1.3 e-2
	Other ncRNA	9,281	2,624	0.091	3.9 e-3	2,935	530	0.53	2.9 e-3	398	381	0.30	2.1 e-3	
Total	26,112	16,103	0.56	2.9 e-2	39,832	1,268	1.26	1.1 e-2	1,897	3,022	2.35	1.6 e-2		
Transcriptionally Unannotated Regions		294,956	2,749,660	96.1	2.0 e-1	146,913	64,232	64.1	5.1 e-2	60,267	89,630	69.8	5.5 e-2	
TARs	Total	718,537	923,774	32.3	2.0 e-1	235,915	37,482	37.4	4.6 e-2	76,757	47,542	37.0	5.5 e-2	
	Overlapping TEs	1,633,407	455,803	15.9	8.0 e-2	65,600	5,621	5.6	2.3 e-3	38,595	7,414	5.8	2.9 e-2	
	Overlapping Introns	1,300,035	360,778	12.6	1.2 e-1	173,253	18,347	18.3	2.5 e-2	79,012	28,857	22.5	1.9 e-2	
	Supervised ncRNA Predictions	104,001	13,844	0.51	1.2 e-2	2,509	390	0.77	2.5 e-4	599	164	0.004	2.4 e-5	

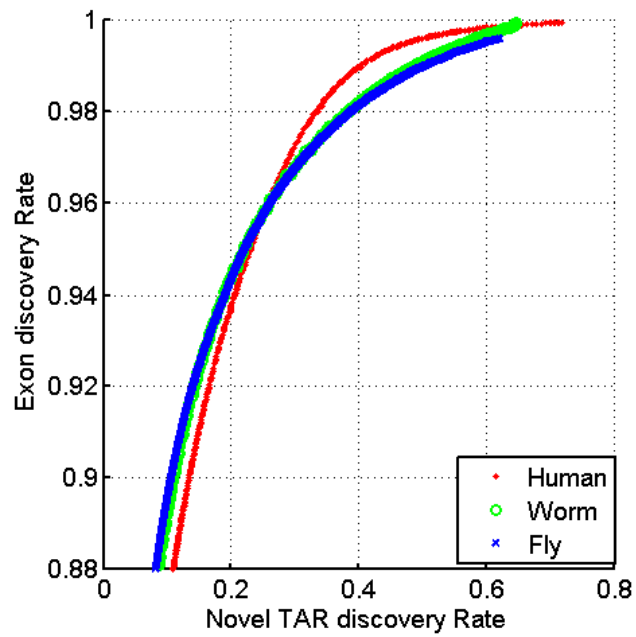
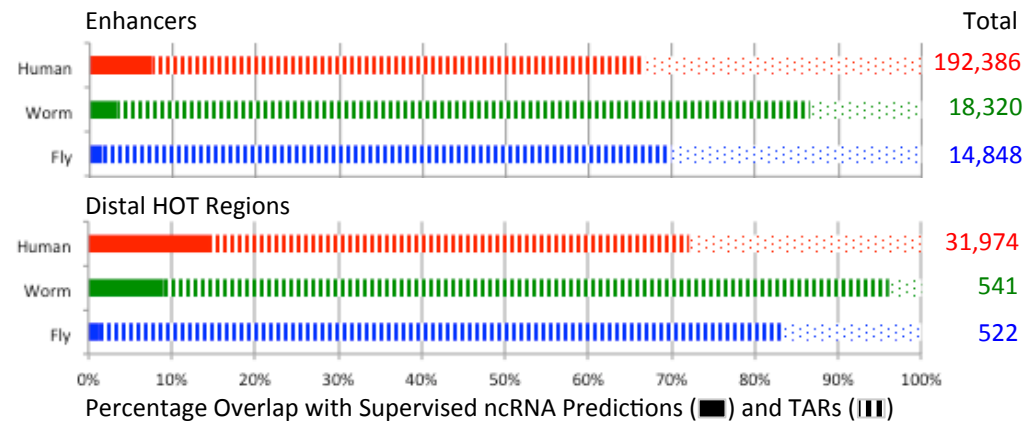
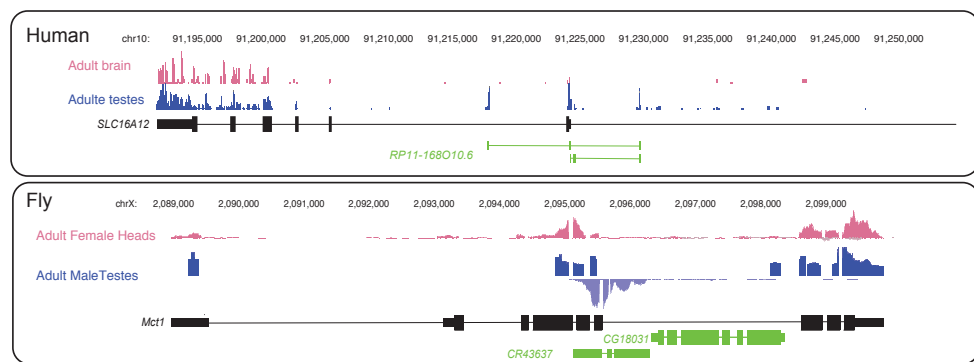
B)**C)****D)**

Exhibit 6: Expression Clustering of Coding Genes and ncRNAs

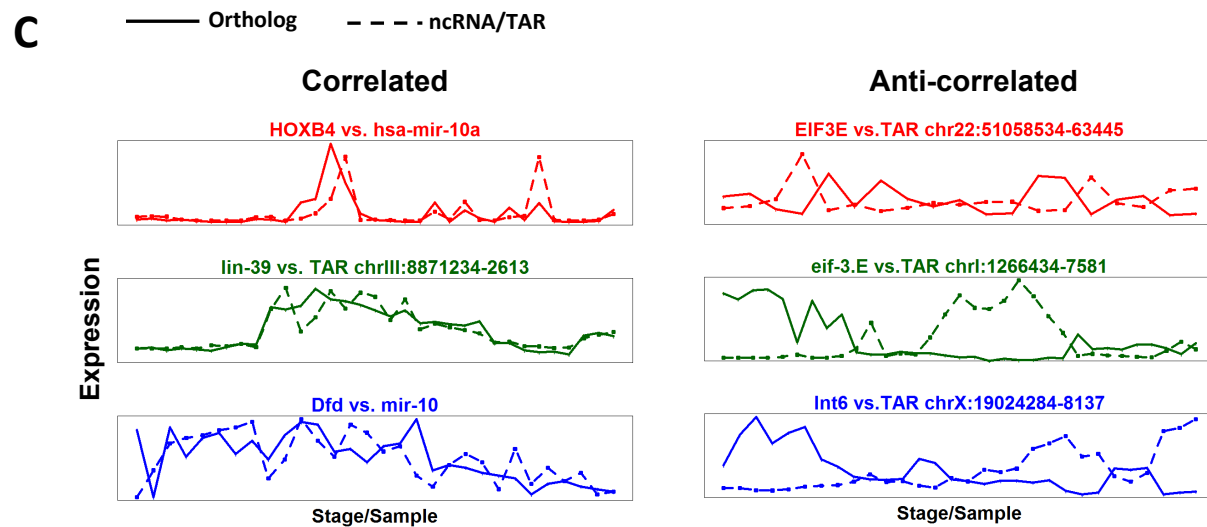
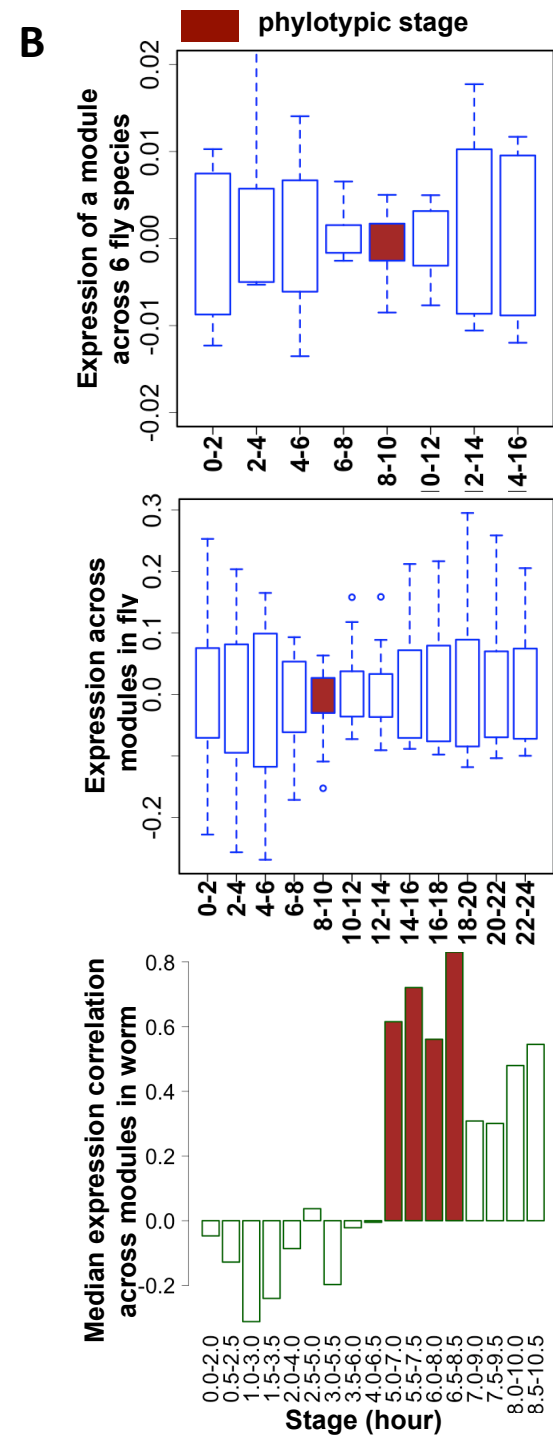
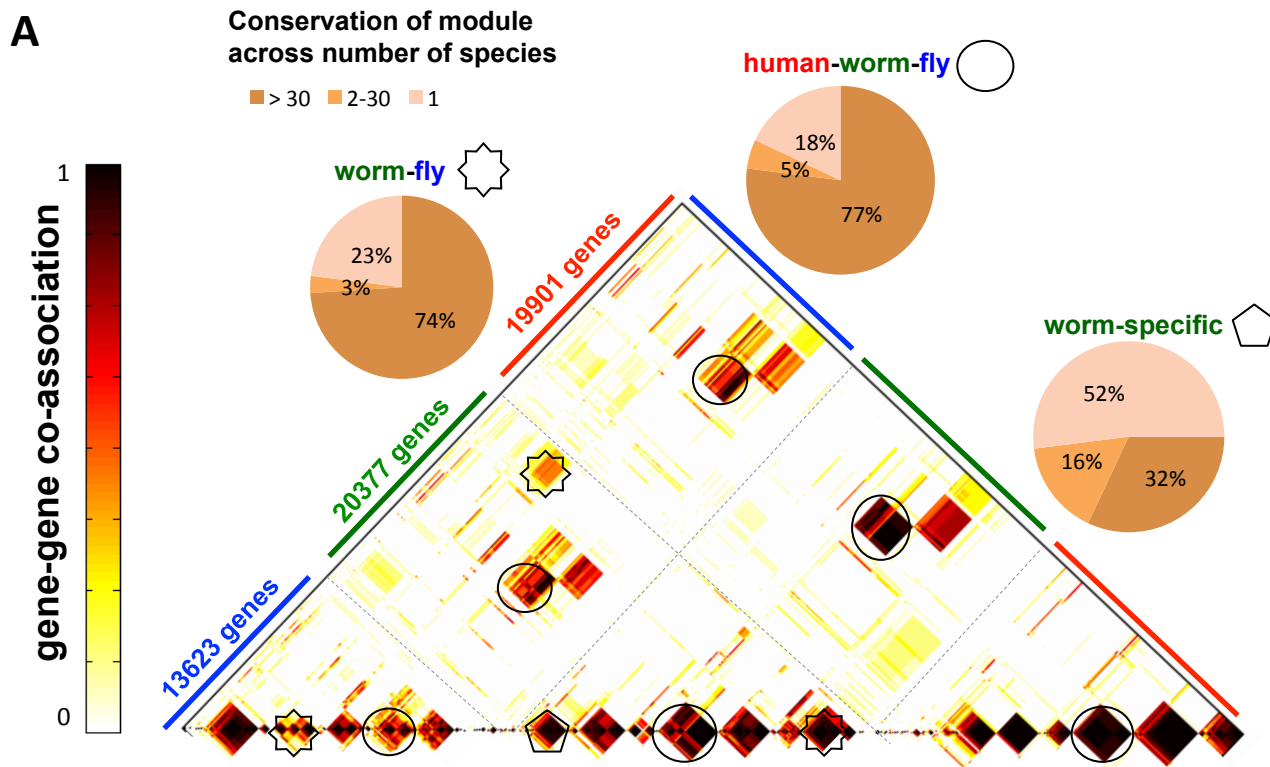
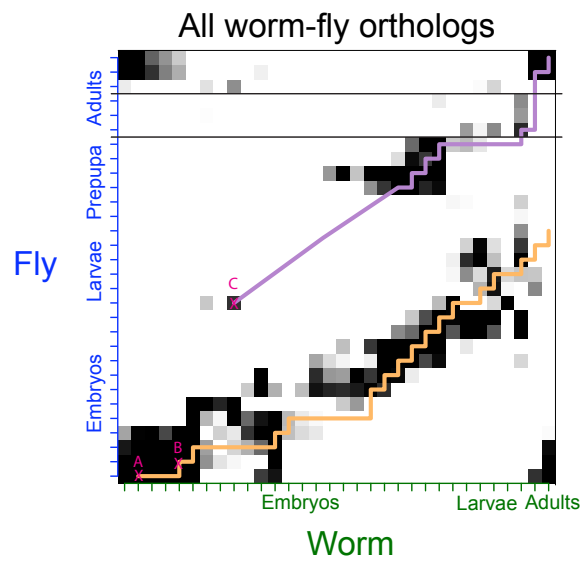


Exhibit 7: Stage Mapping of Worm and Fly Developmental Timecourses



— phylotypic stage

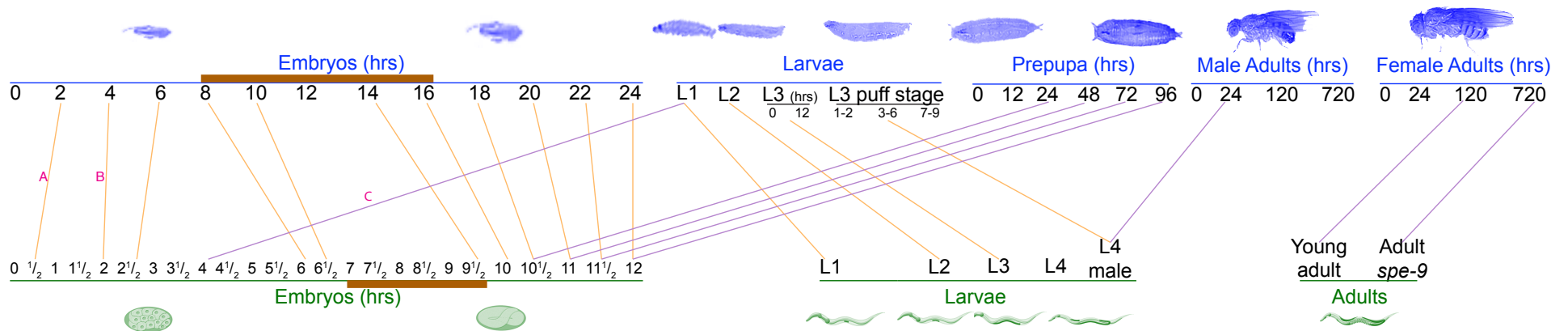
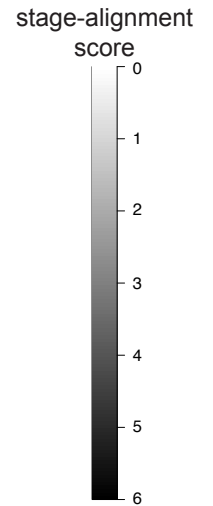
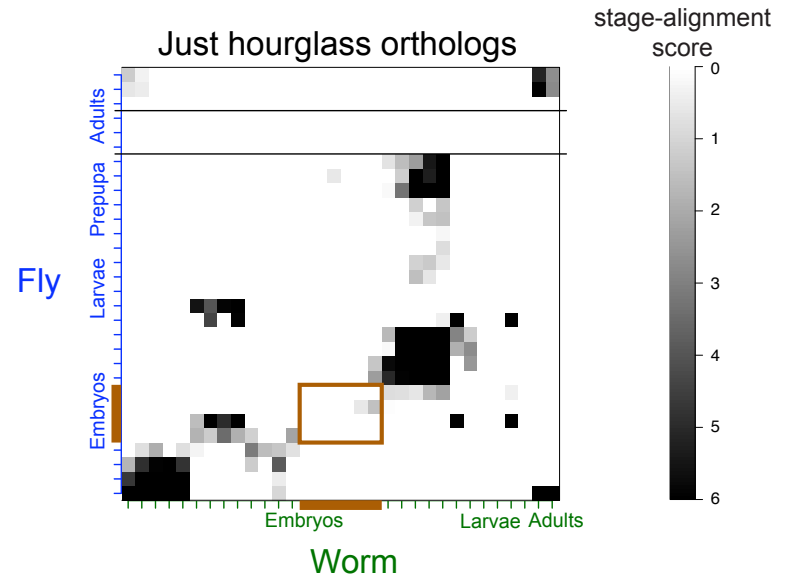


Exhibit 8: Histone and TF Models for Gene Expression

