

Fig. 1

			Human			Worm			Fly			
			Elements	Genome Coverage		Elements	Genome Coverage		Elements	Genome Coverage		
				Kb	%		Kb	%		Kb	%	
Sequenced Genome	mRNAs (exons)		20,007	86,560	3.0	21,192	34,437	34.3	13,940	35,970	28.0	
	Pseudogenes		11,216	27,089	0.95	881	1,343	1.3	145	155	0.12	
	Annotated ncRNAs		22,154	17,770	0.62	41,466	2,611	2.6	2,155	3,279	2.6	
	Annotated ncRNAs	Comparable ncRNAs	miRNAs	1,756	162	0.006	221	20	0.02	236	22	0.02
			tRNAs	624	47	0.002	609	45	0.04	314	22	0.02
			snoRNAs	1,521	168	0.006	141	16	0.02	287	34	0.03
			snRNAs	1,944	210	0.007	114	14	0.01	47	7	0.006
			lncRNAs	10,840	10,581	0.37	233	184	0.18	852	868	0.68
	Regions excluding mRNAs, Pseudogenes and Annotated ncRNAs		283,816	2,731,811	95.5	143,372	63,520	63.3	60,108	89,445	69.6	
	Transcription Detected (TARs)		708,253	916,401	32.0	232,150	37,029	36.9	83,618	44,256	34.5	
	Supervised Predictions		104,016	13,835	0.48	2,525	392	0.39	599	164	0.13	

Fig. 2

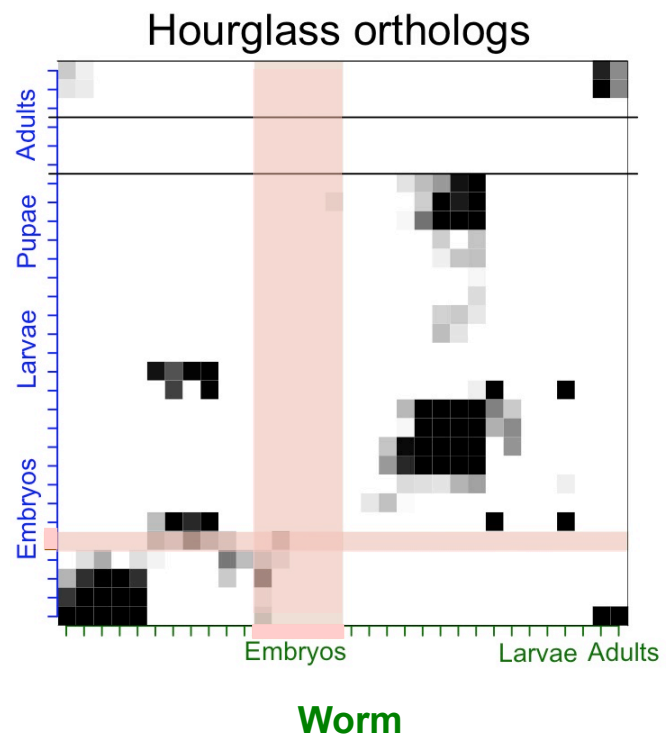
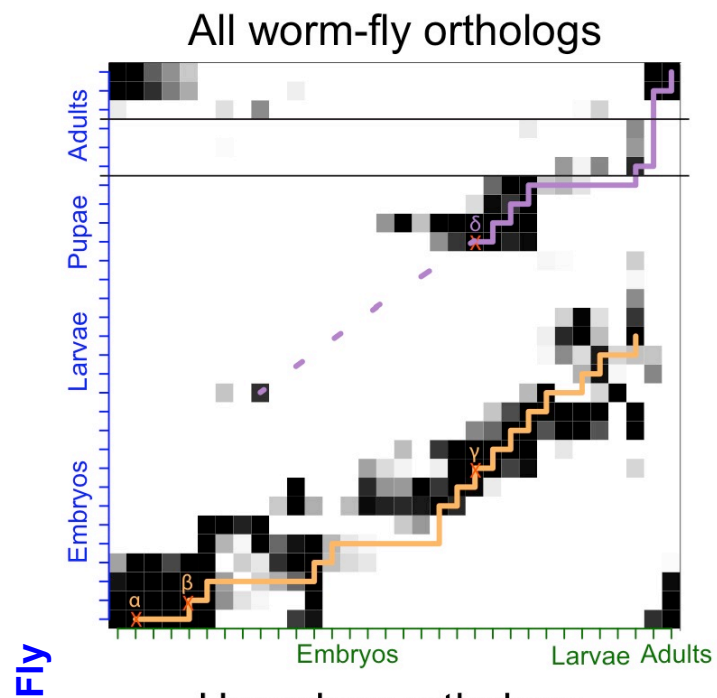
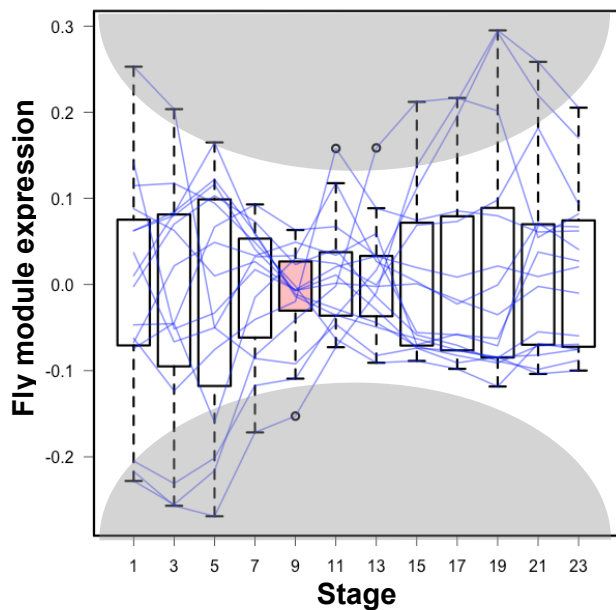
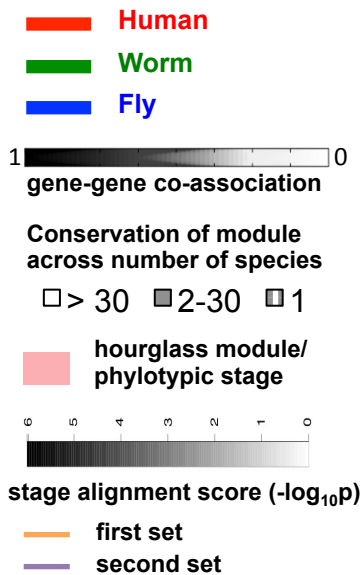
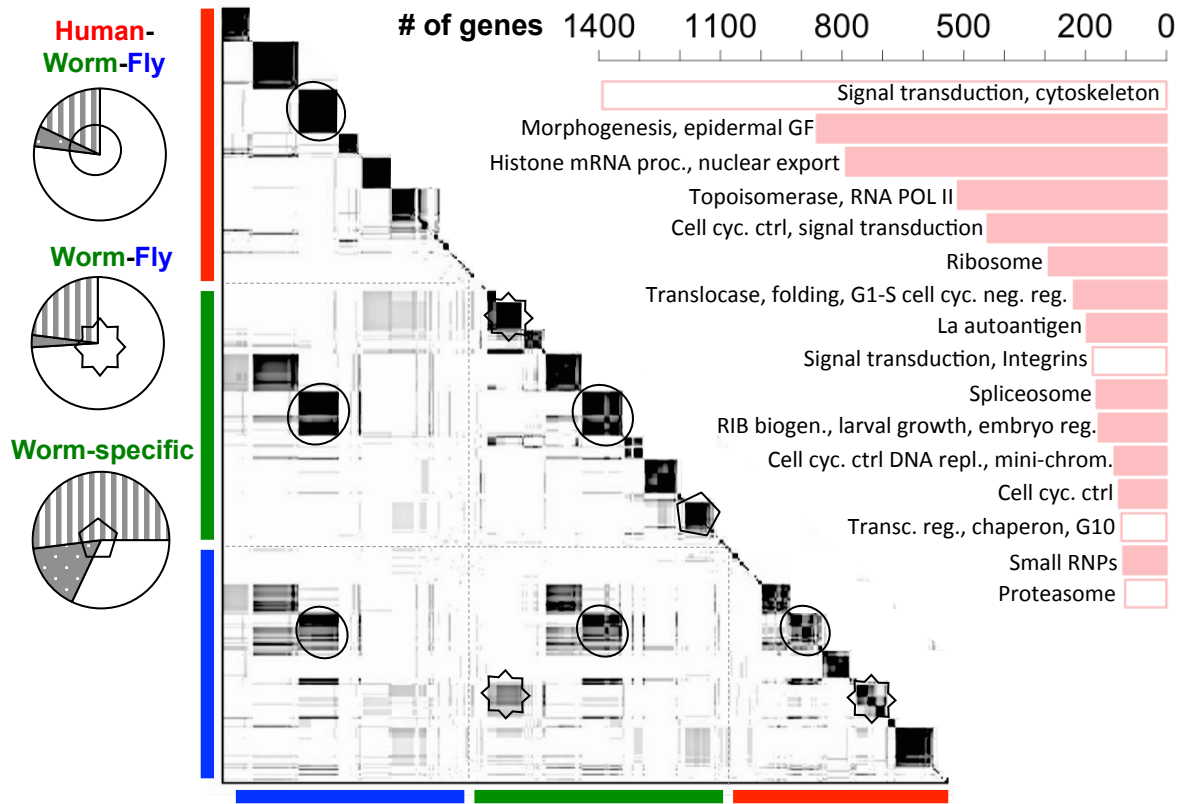
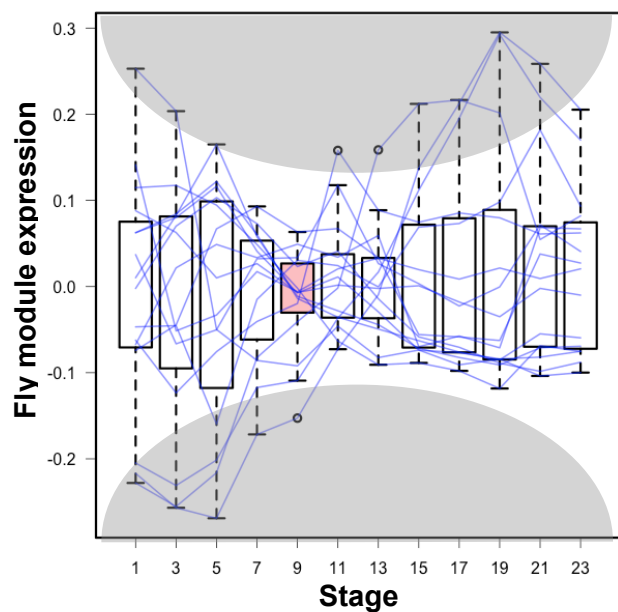
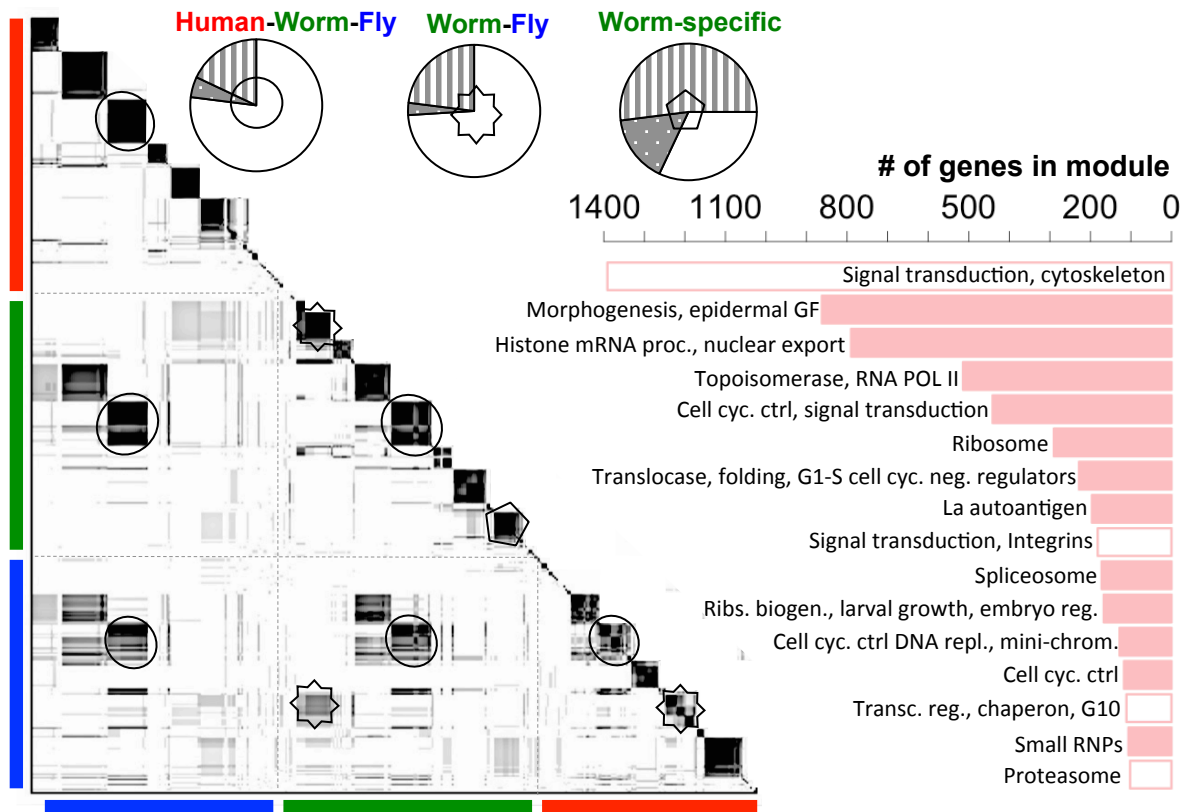
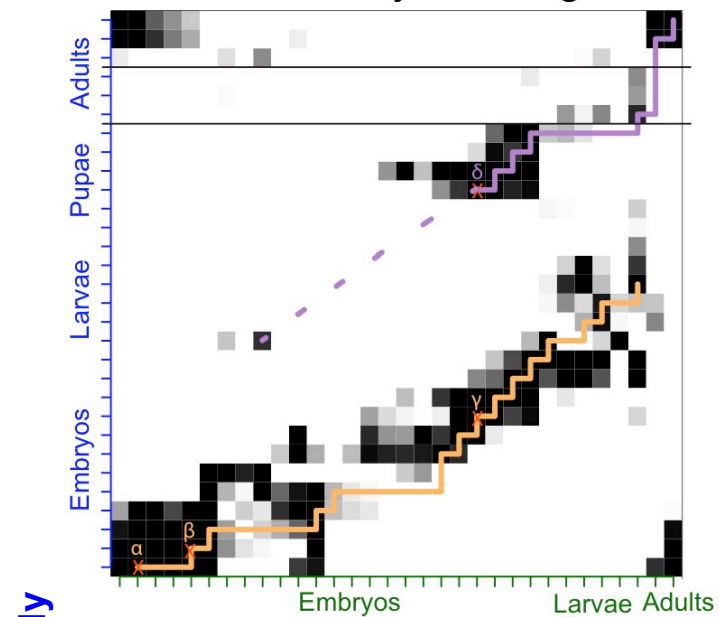


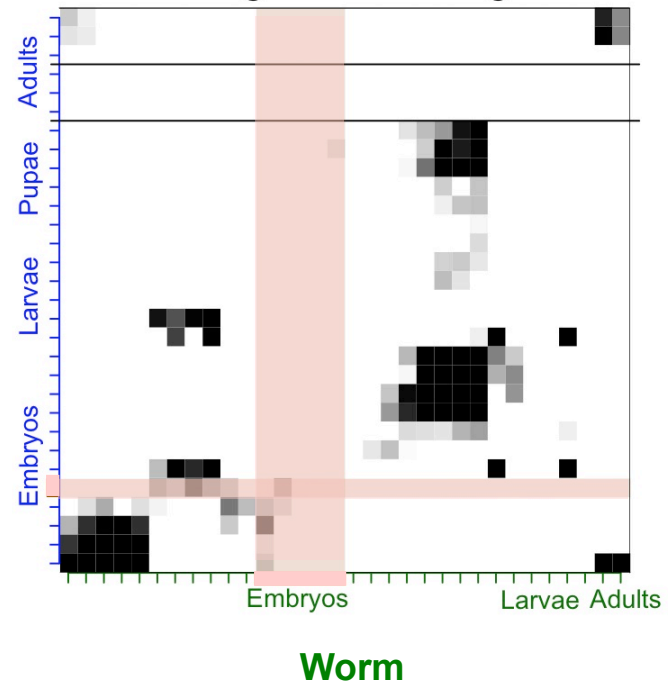
Fig. 3



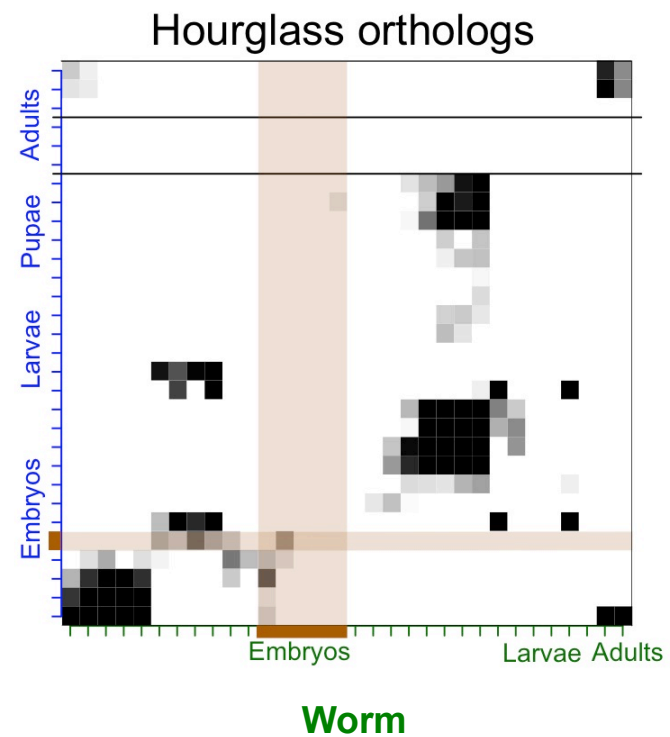
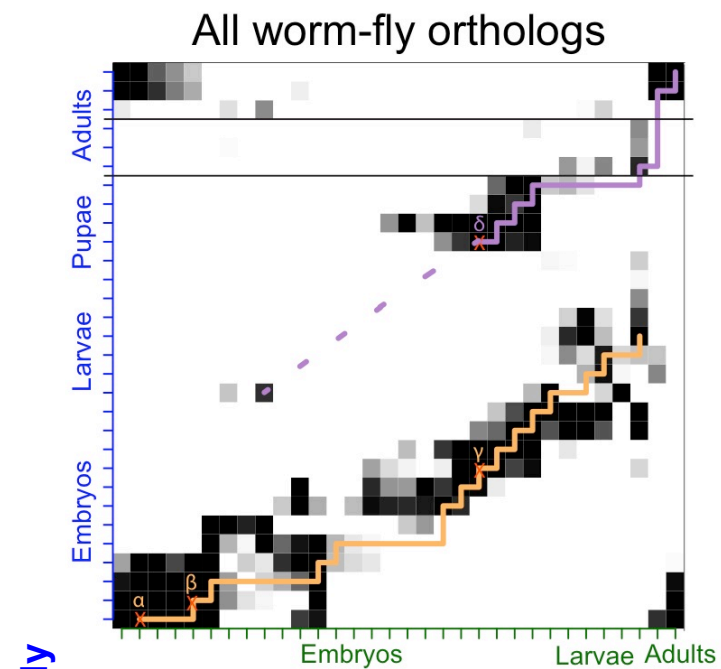
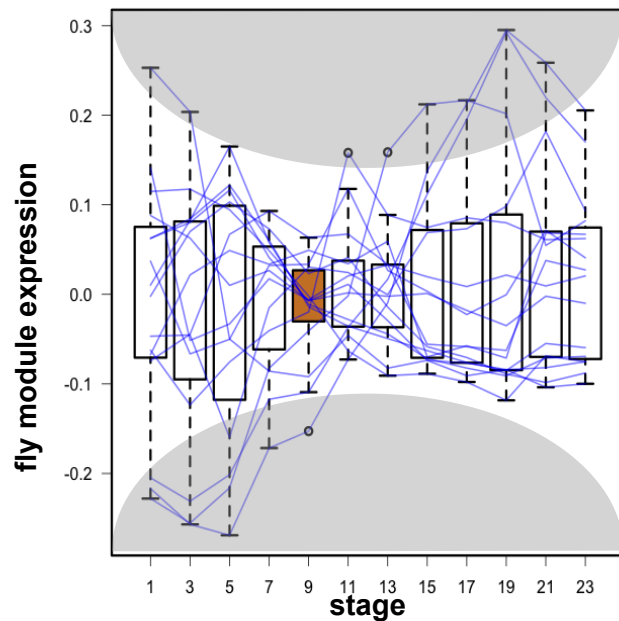
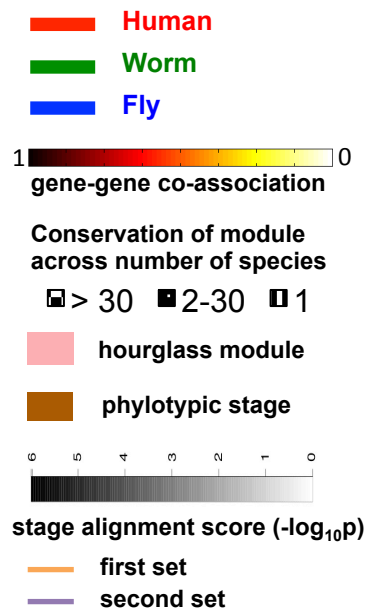
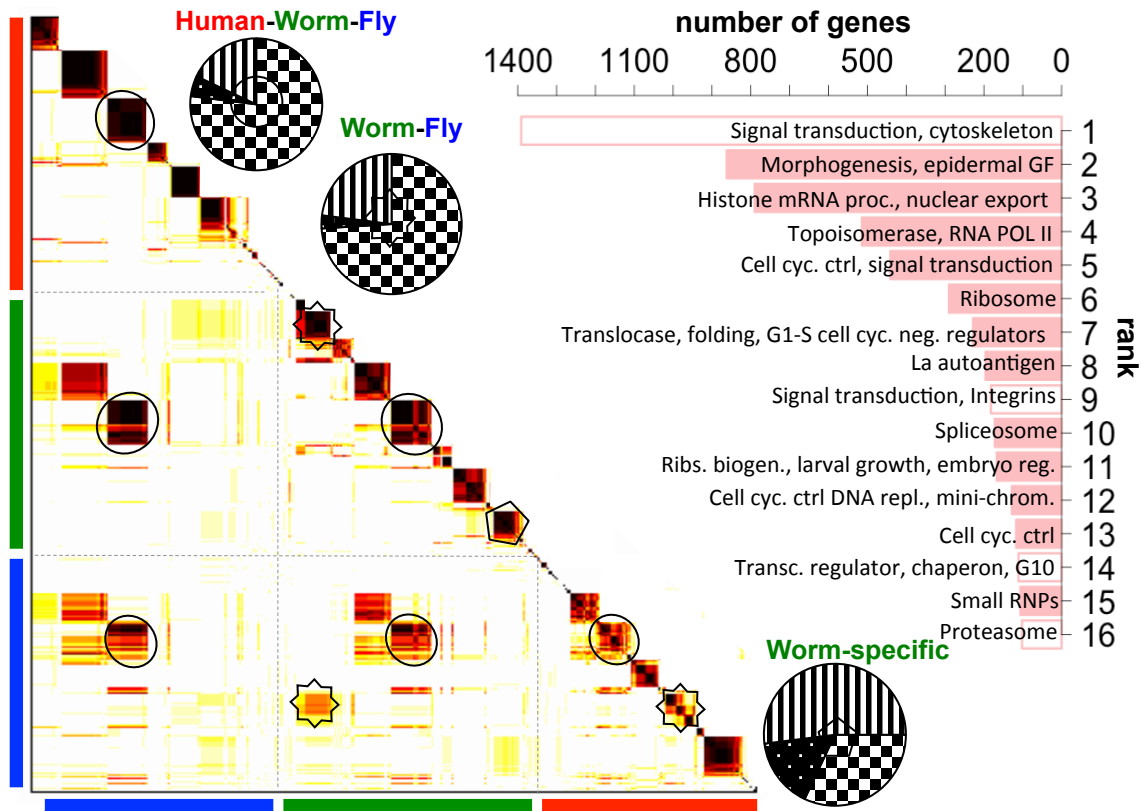
All worm-fly orthologs



Hourglass orthologs



backup



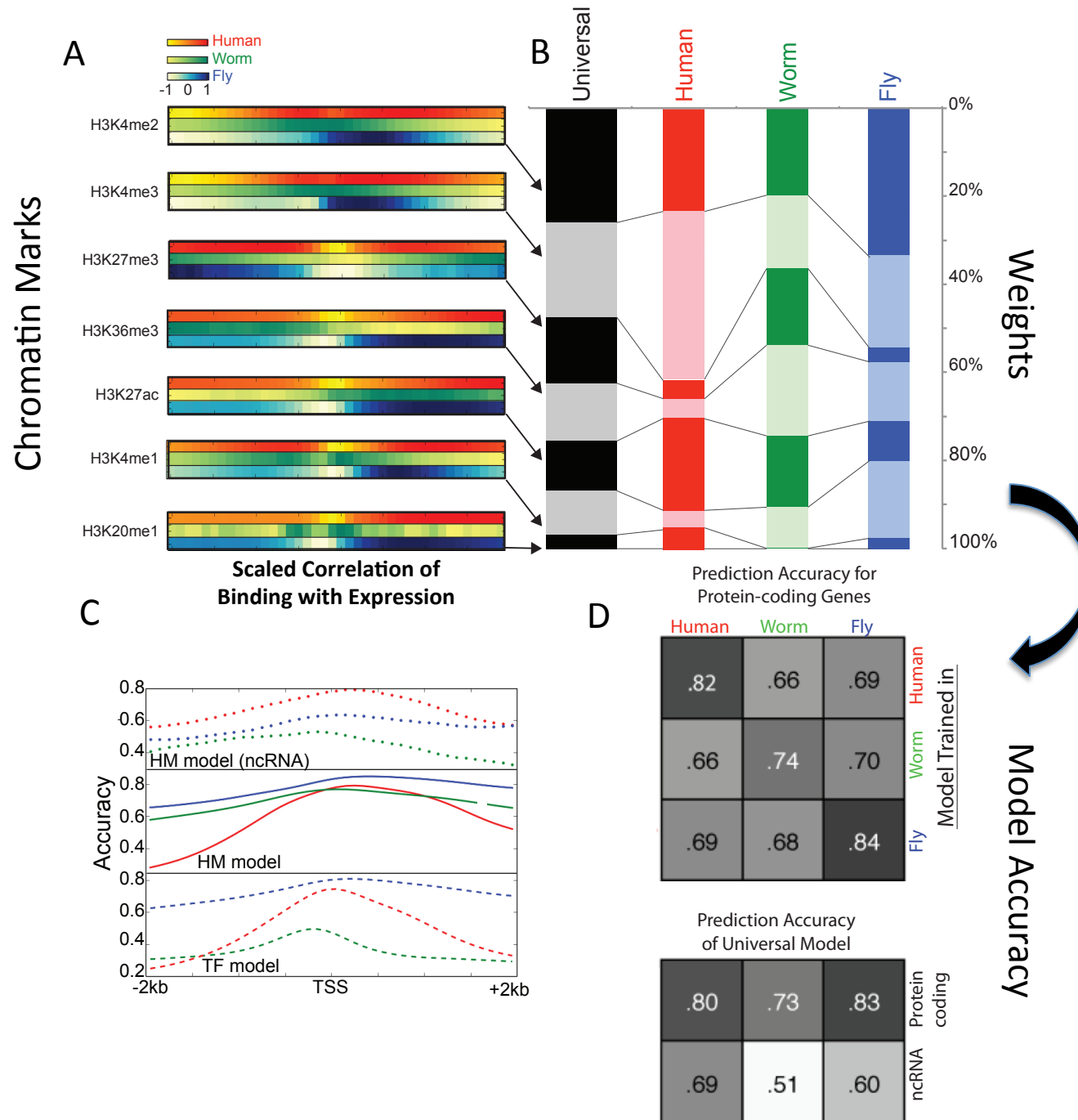


Fig. 4

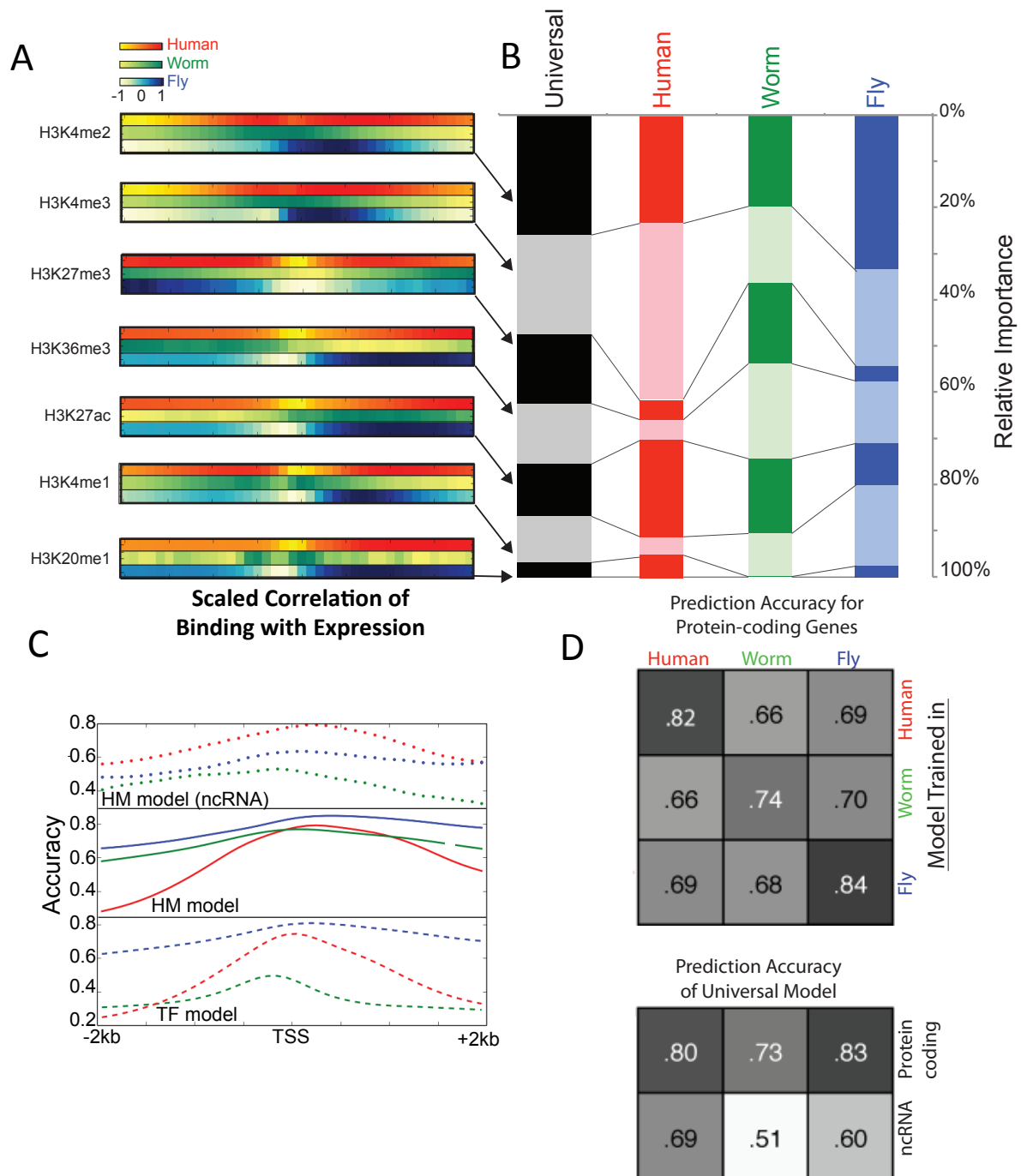


Fig. 4