

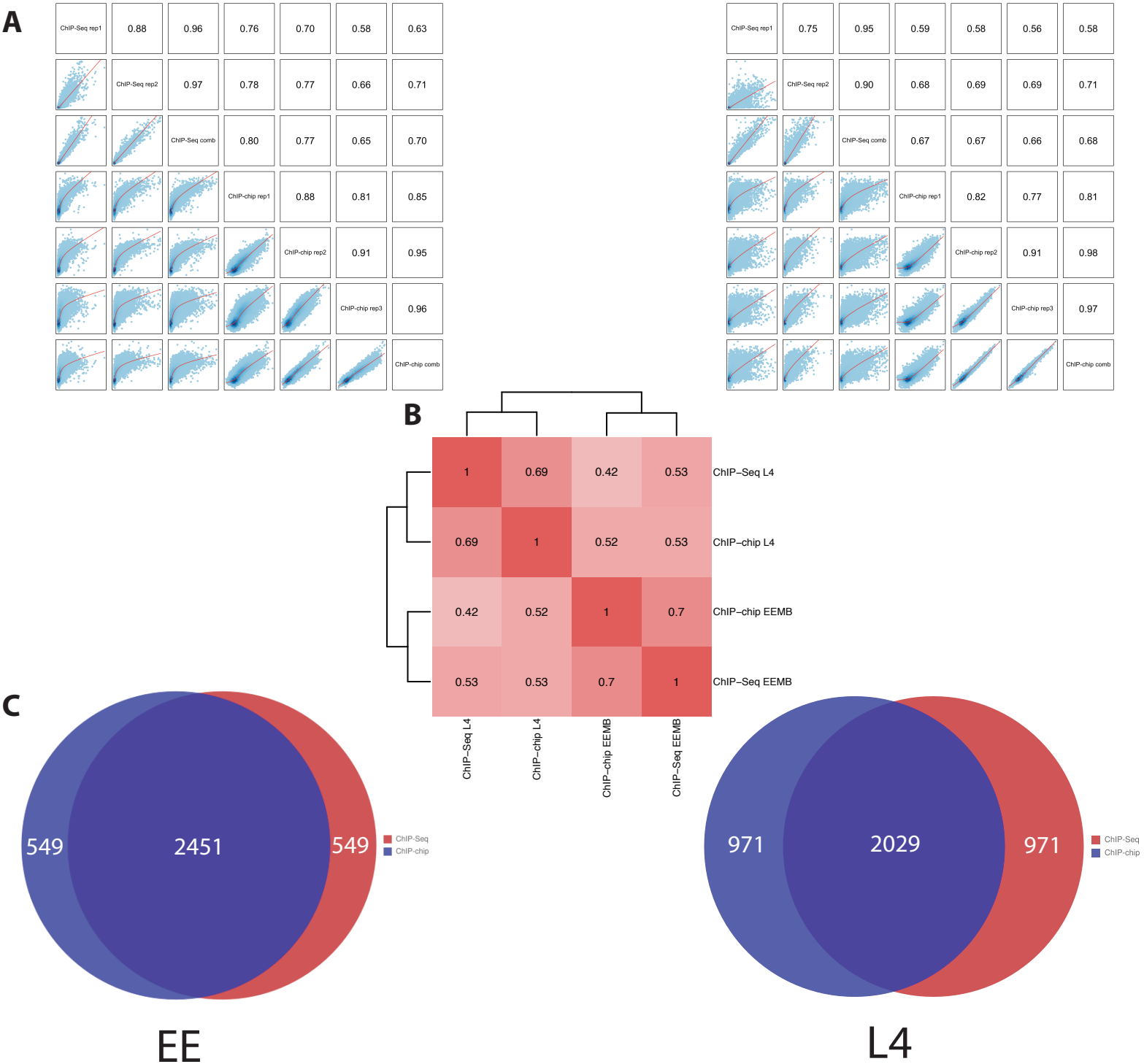


Fig. S1
[[21]ulpdf_supplex #2]]

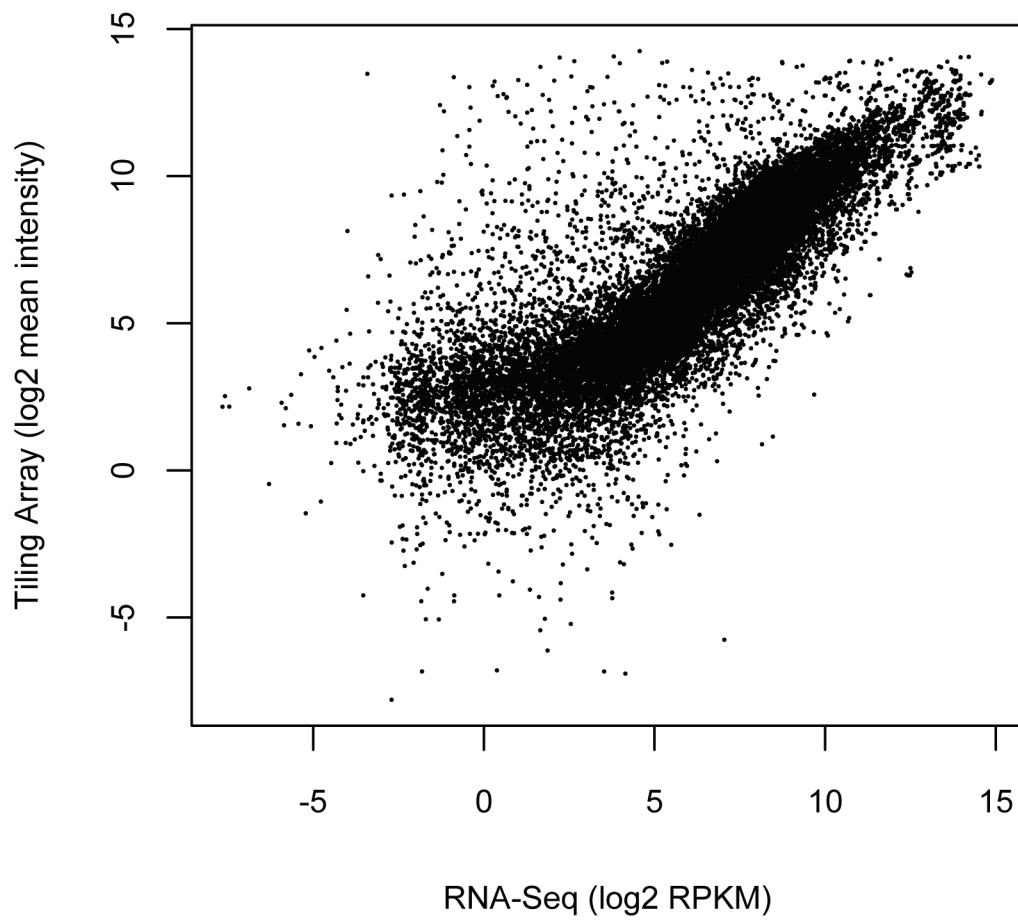


Fig. S2

[[21]julpdf_supplex #3]]

C. elegans RNAseq reads per stage/condition

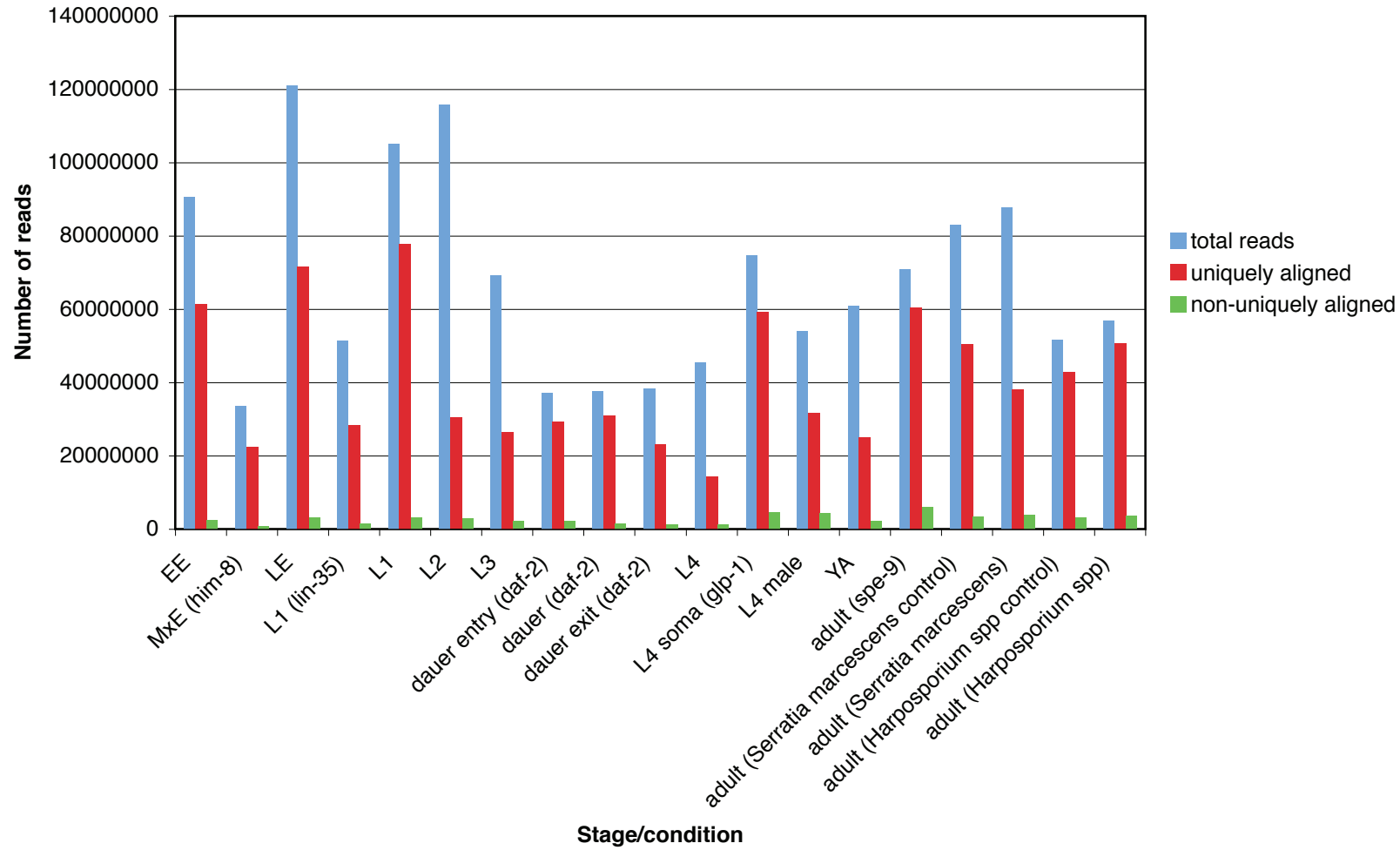


Fig. S3

[[21julpdf_supplex #11]]

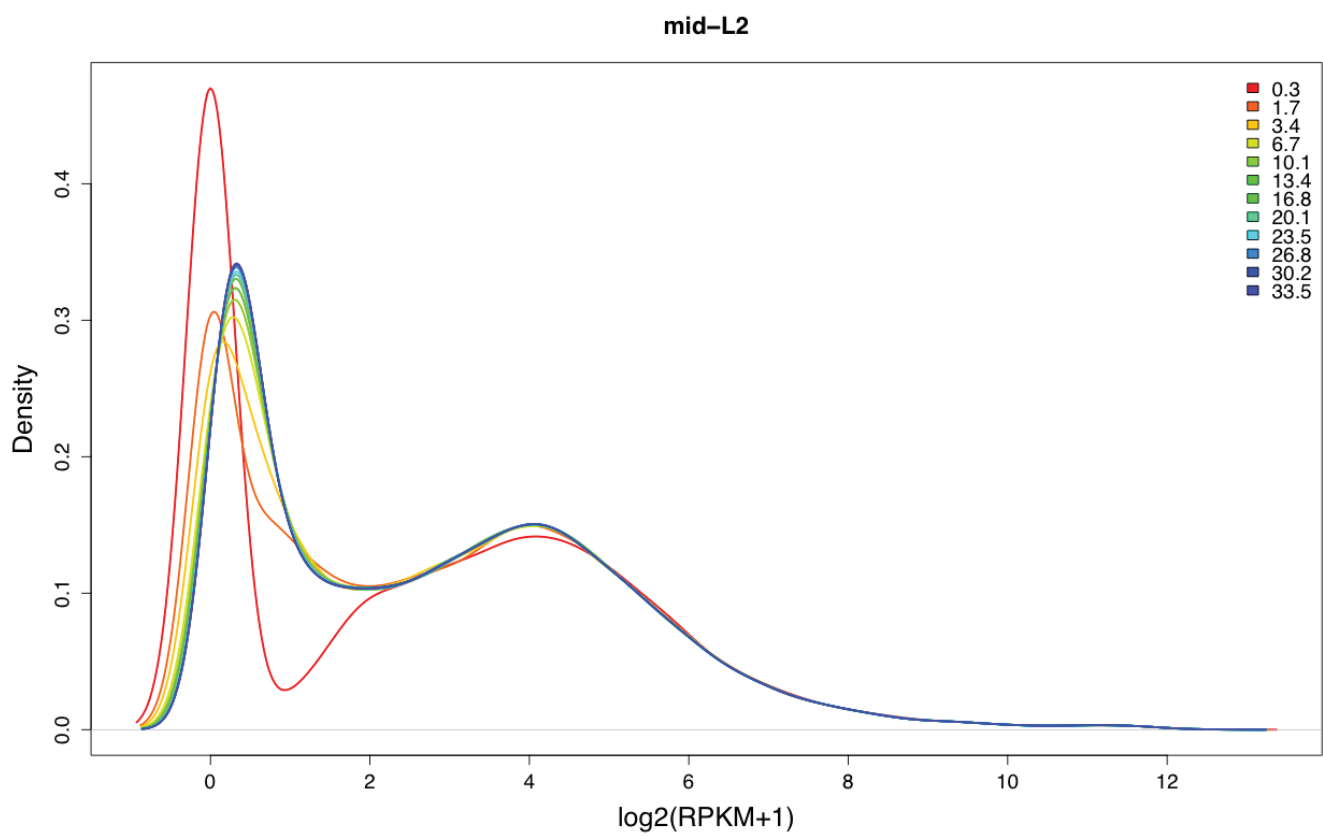


Fig. S4

[[21]ulpdf_suppex #4]]

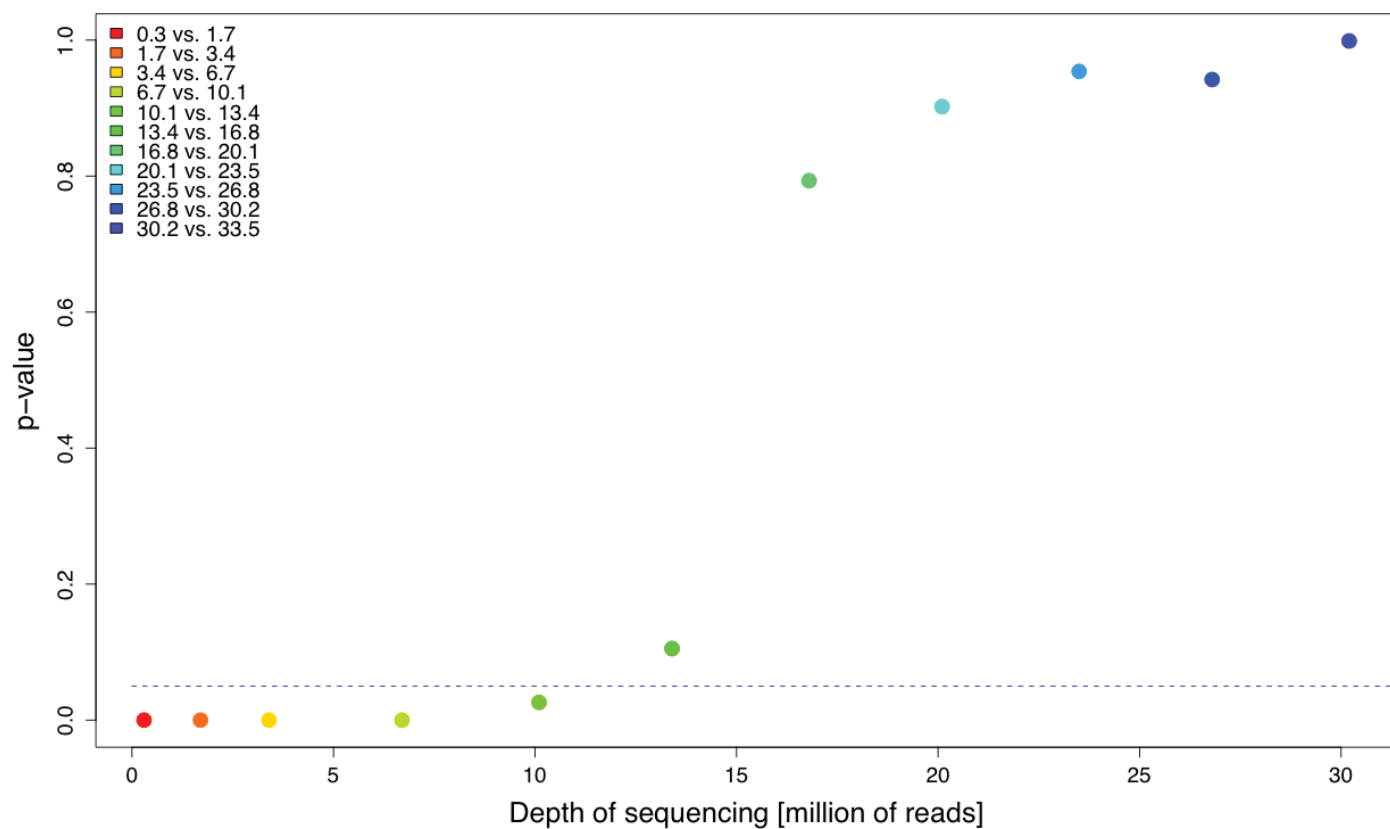


Fig. S5

[[21]julpdf_supplex #5]]

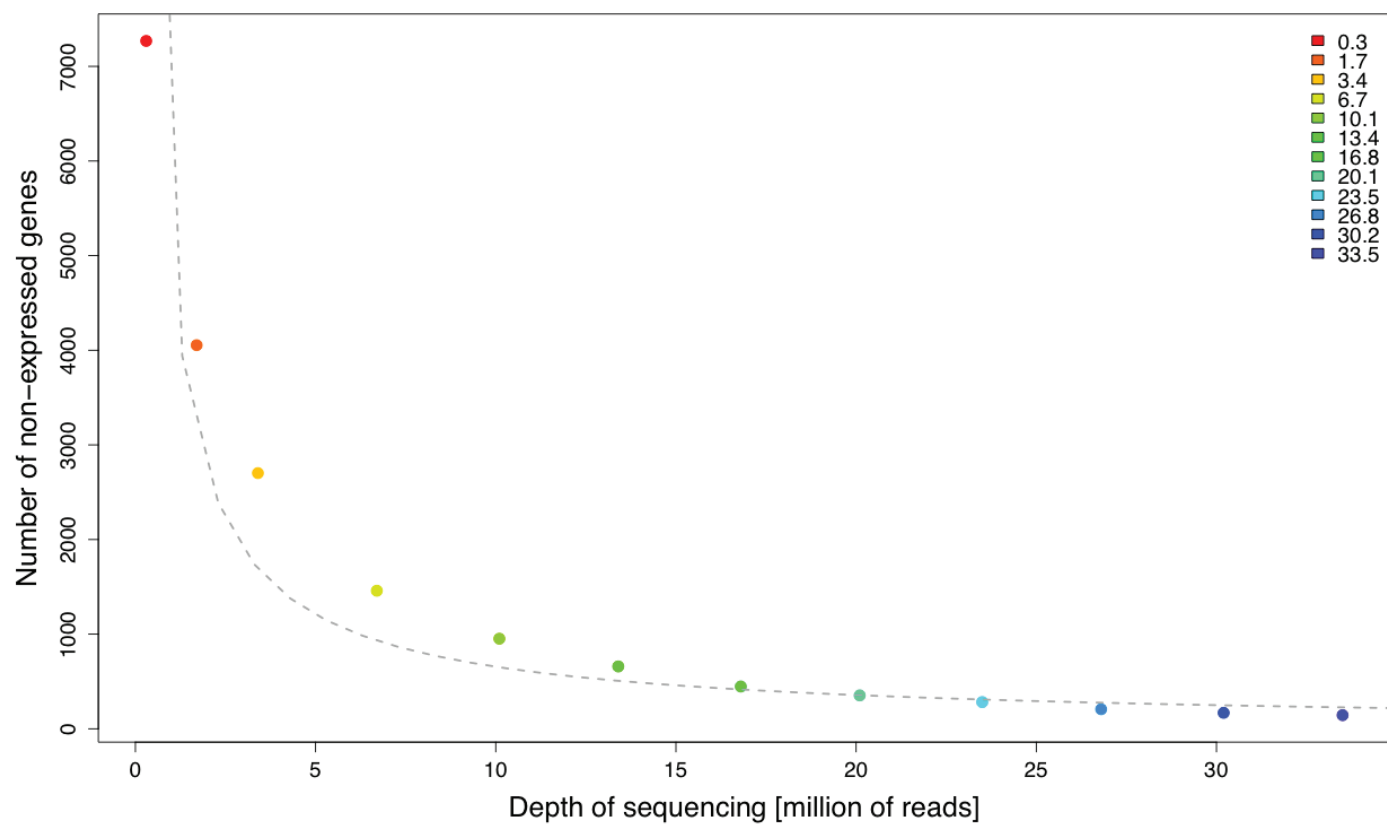


Fig. S6

[[21]julpdf_supplex #50]]

Features defined by RNAseq as compared to WormBase as of January, 2007 (WS170)

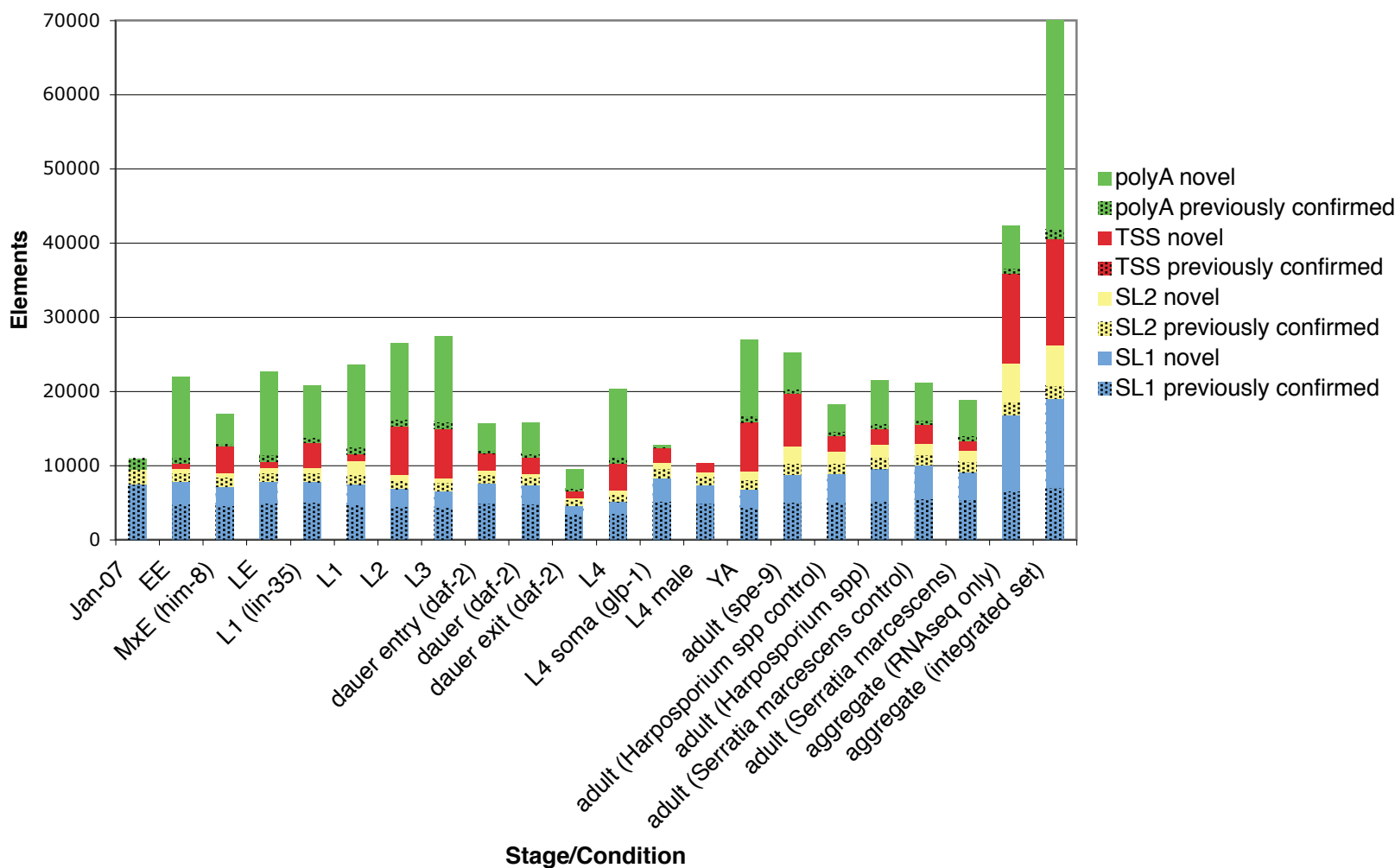


Fig. S7

[[21julpdf_supplex #7]]

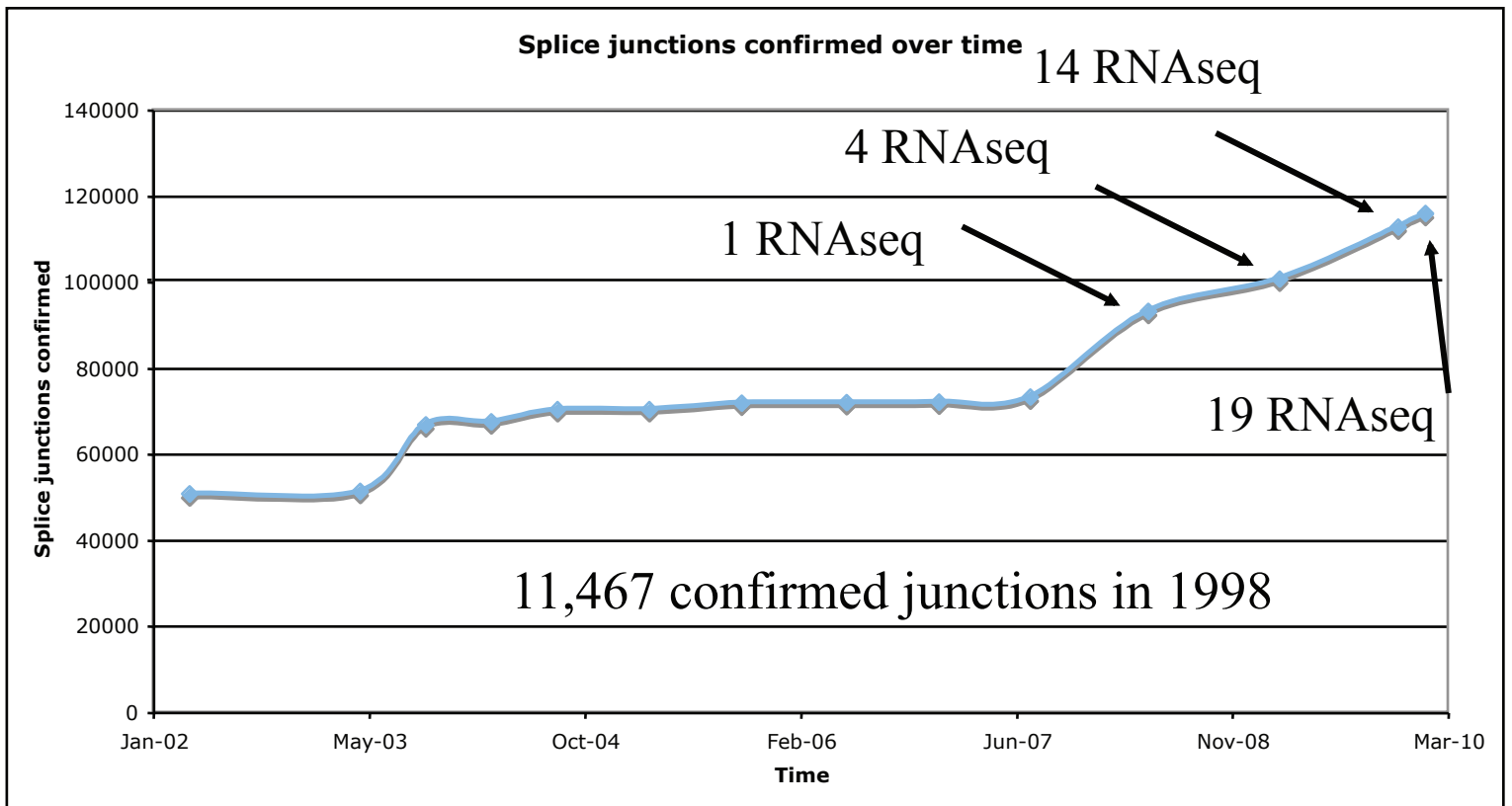


Fig. S8

[[21julpdf_supplex #6]]

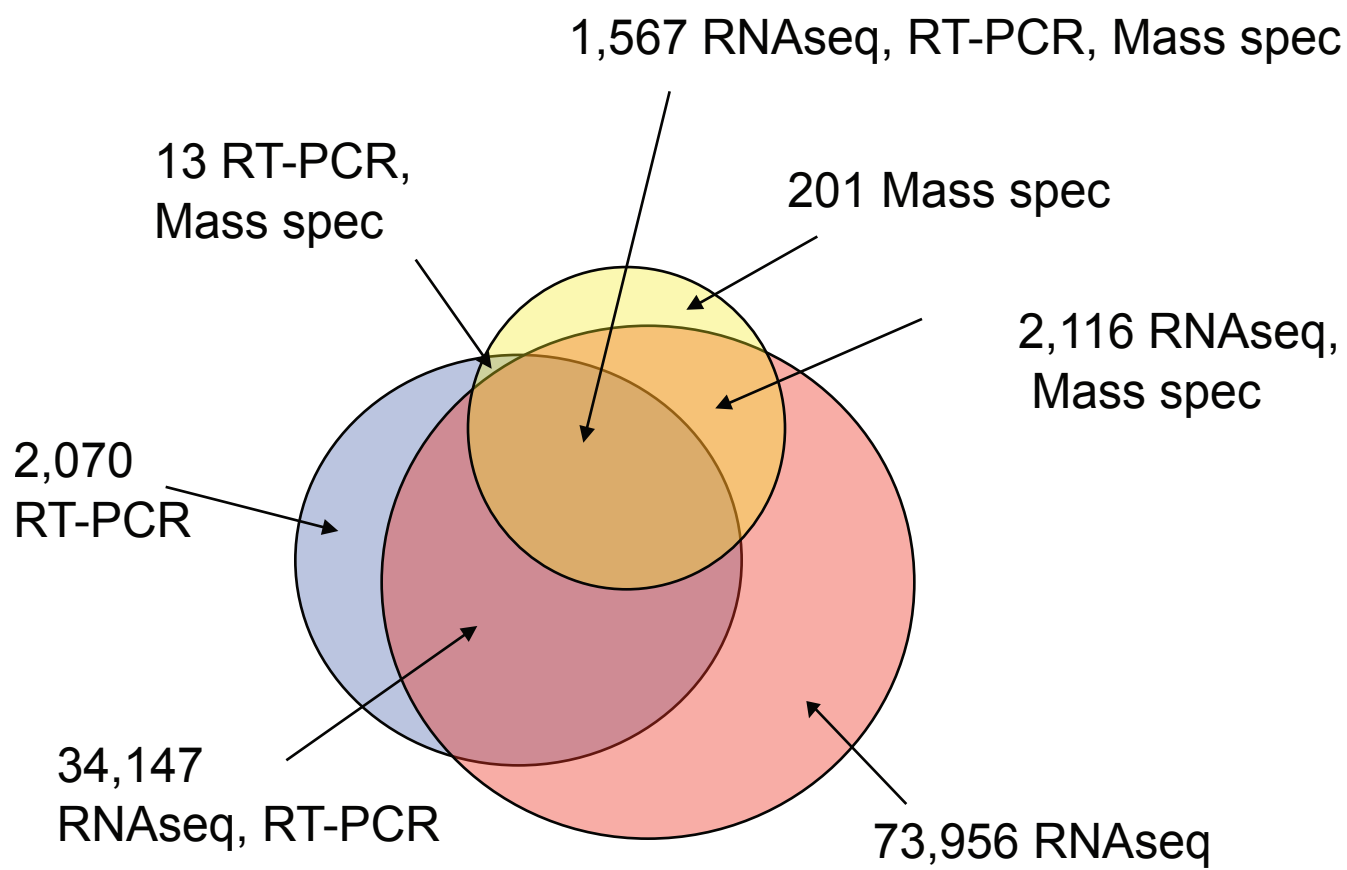
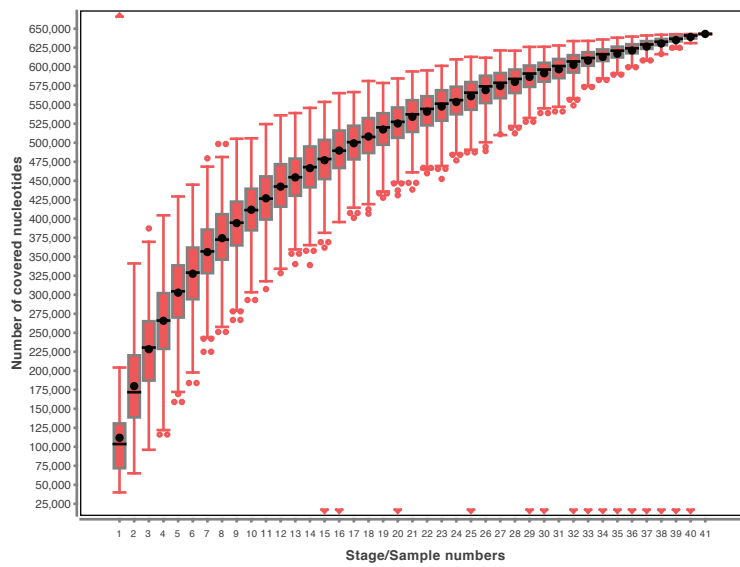


Fig. S9

[[21]julpdf_suppex #10]]

non-coding RNAs



coding exonic regions

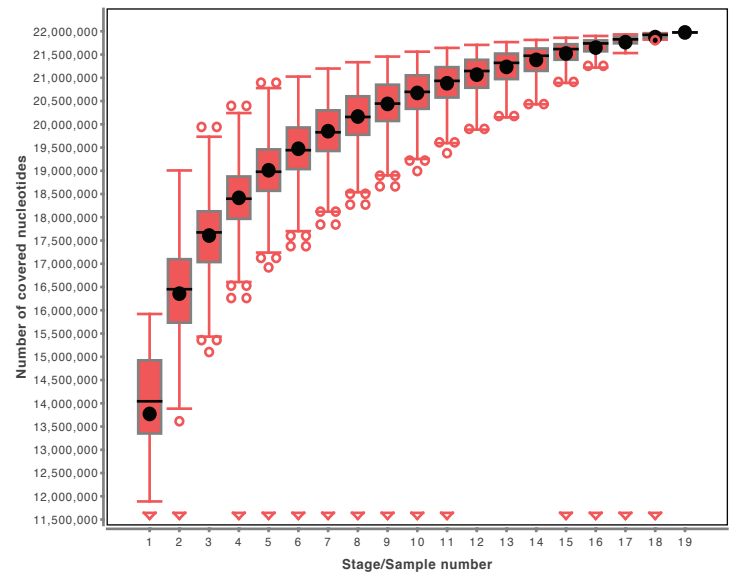


Fig. S10
[[21julpdf_supplex #19]]

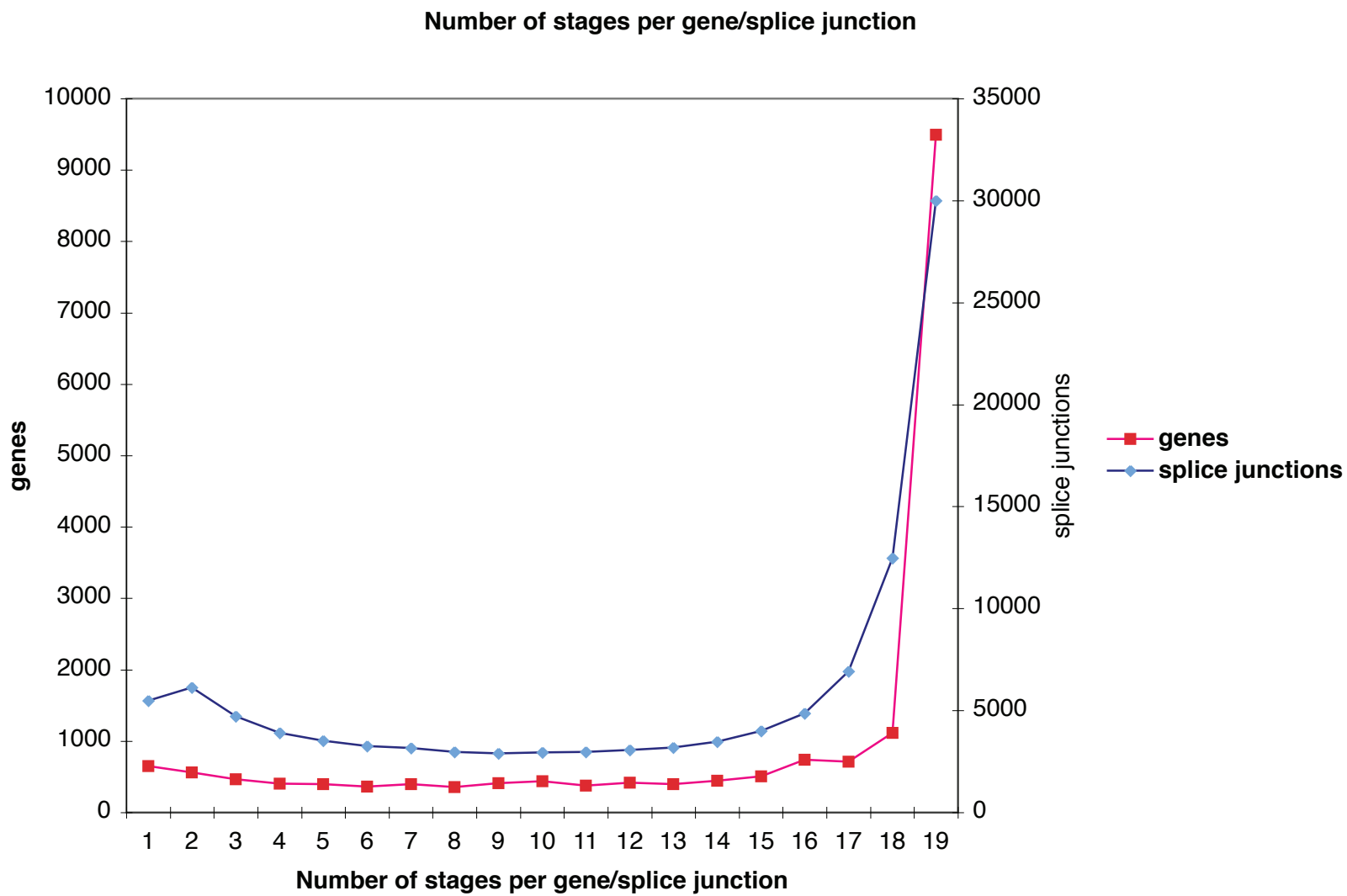


Fig. S11

[[21]julpdf_supplex #9]]

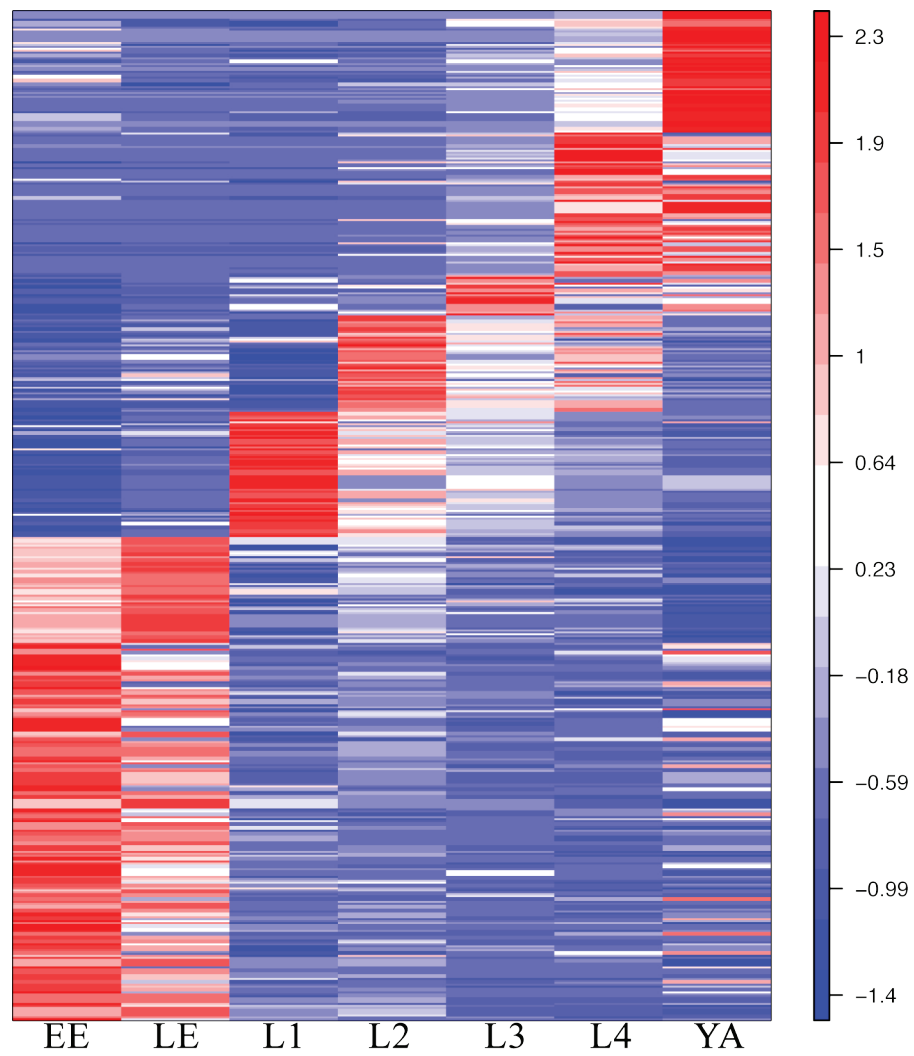


Fig. S12
[[21julpdf_suppex #13]]

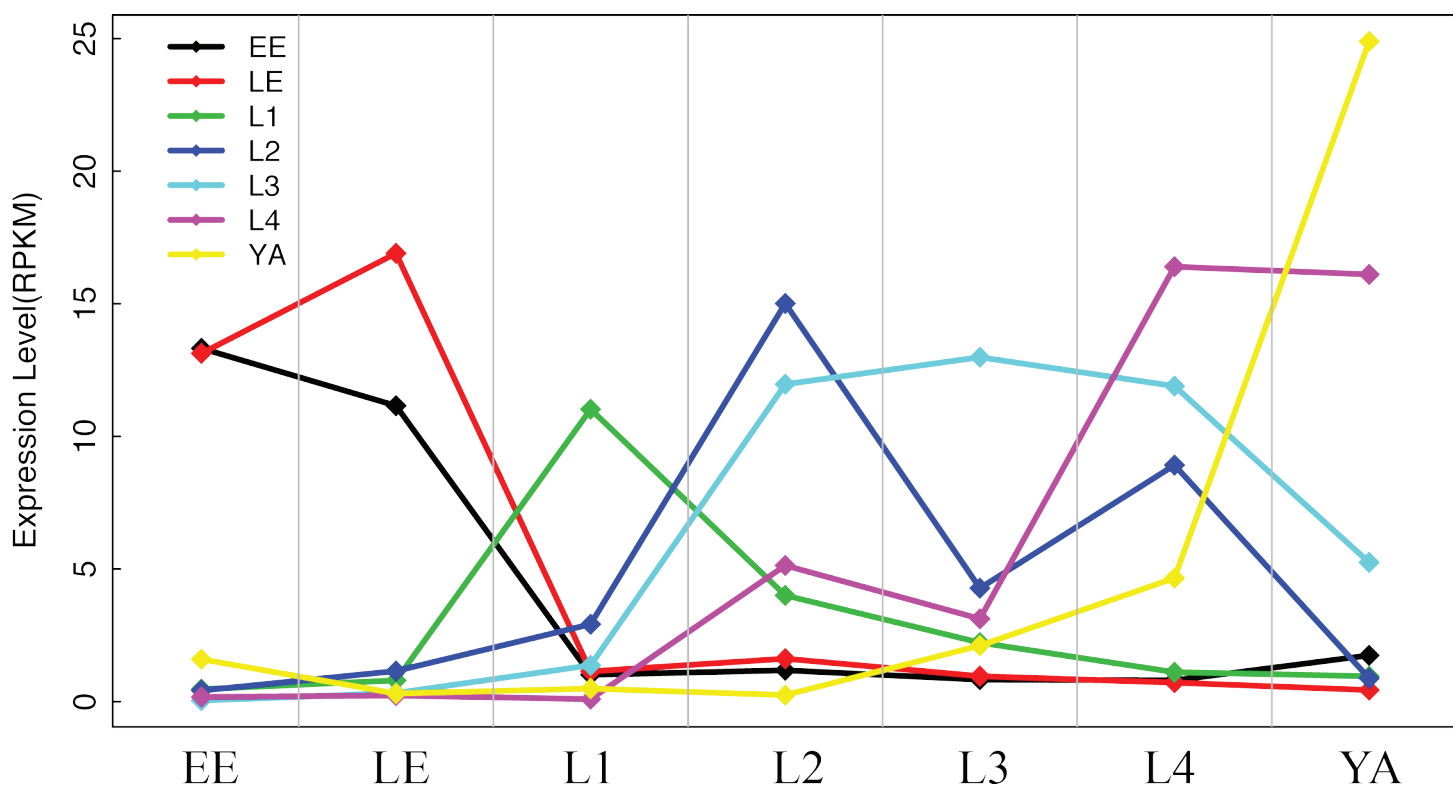


Fig. S13

[[21]ulpdf_suppex #14]]

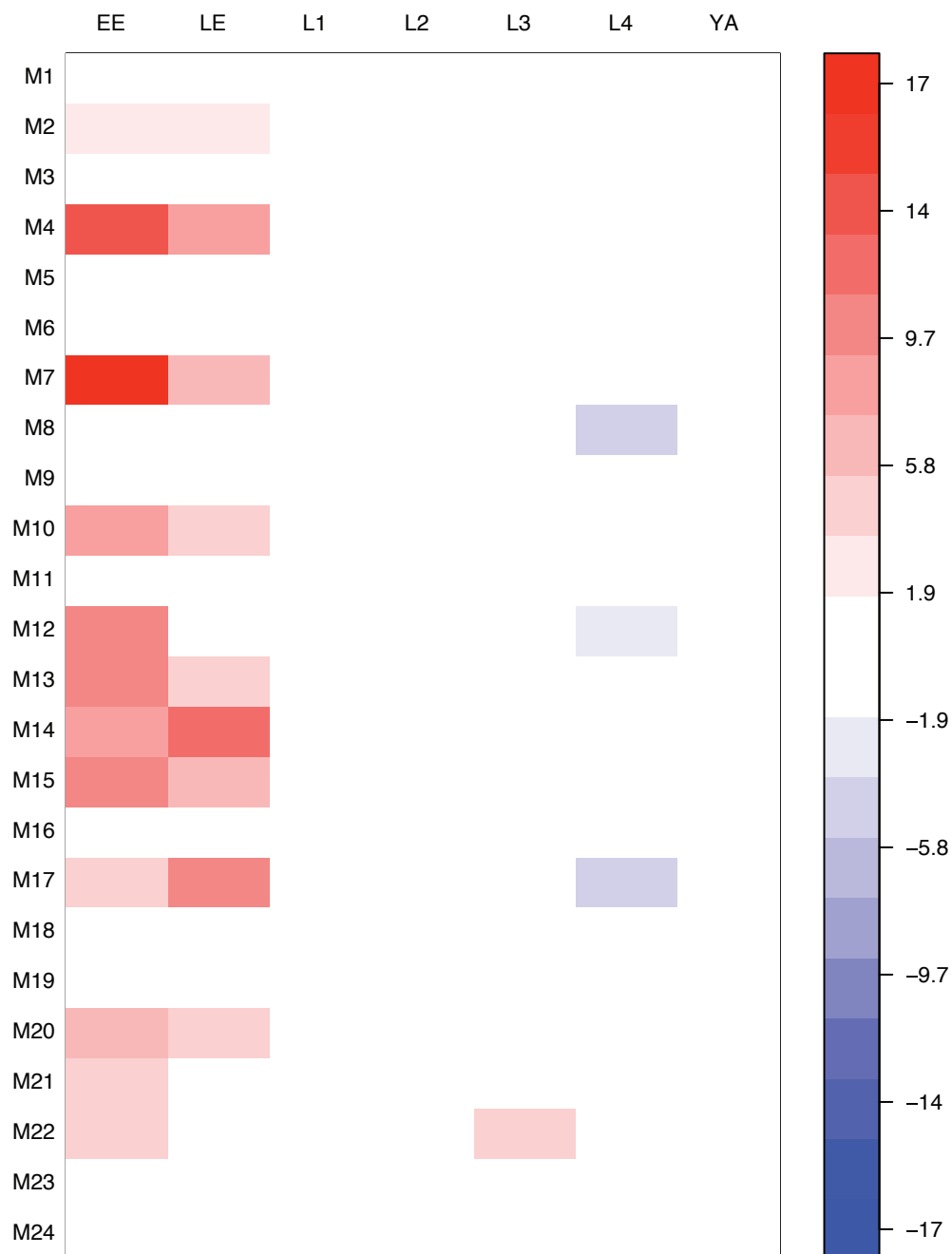


Fig. S14

[[21julpdf_suppex #15]]

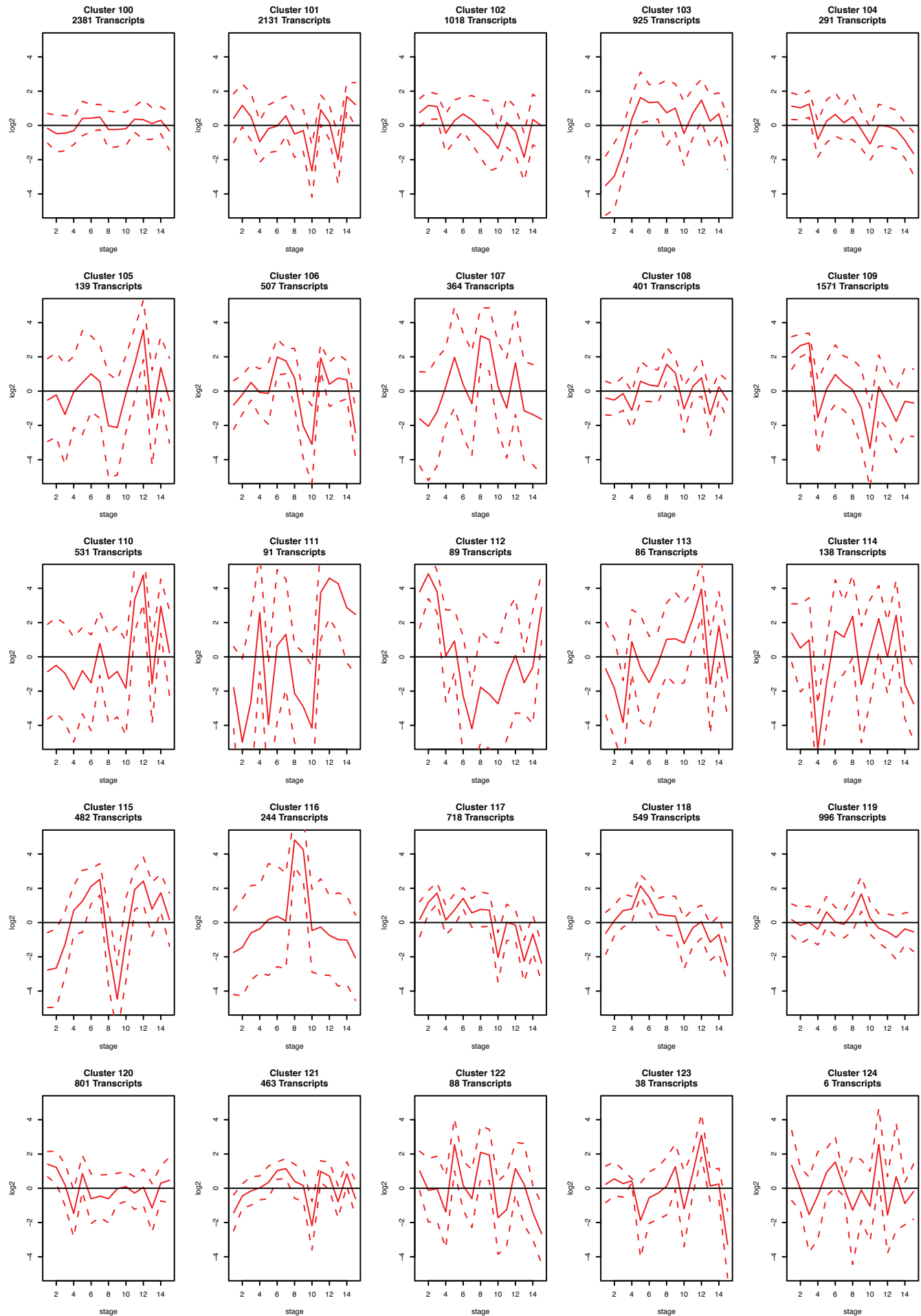


Fig. S15
 [[21julpdf_supplex #51]]

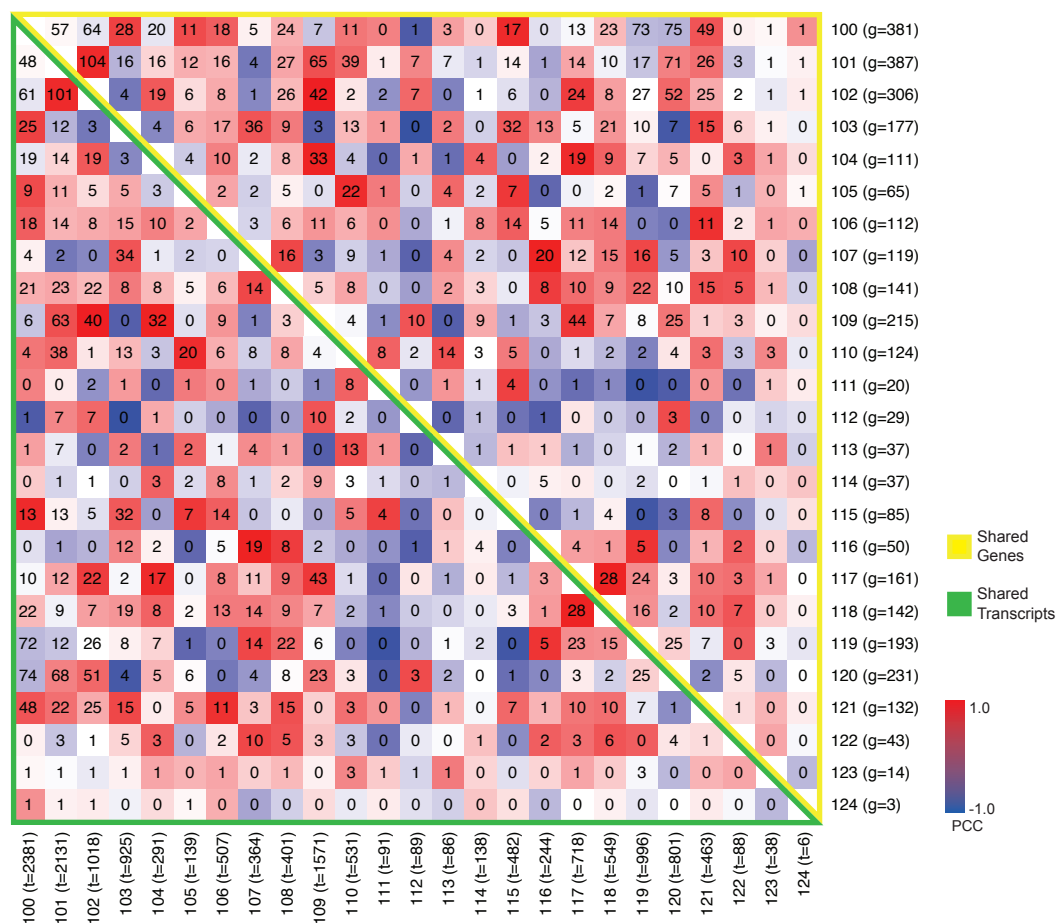


Fig. S16

[[21]julpdf_supplex #60]]

Type	# Genes	Transcript Model
Overlapping 5' UTR	492	Multiple TSS Single ATG 
Distinct 5' UTR	415	Multiple TSS Multiple ATG 
Alternative CDS Exon	792	Alternate Exon 
Extended CDS Exon	738	Extended Exon 
Overlapping 3' UTR	786	Multiple TTS Single STOP 
Distinct 3' UTR	295	Multiple TTS Multiple STOP 

Fig. S17

[[21]julpdf_supplex #52]]

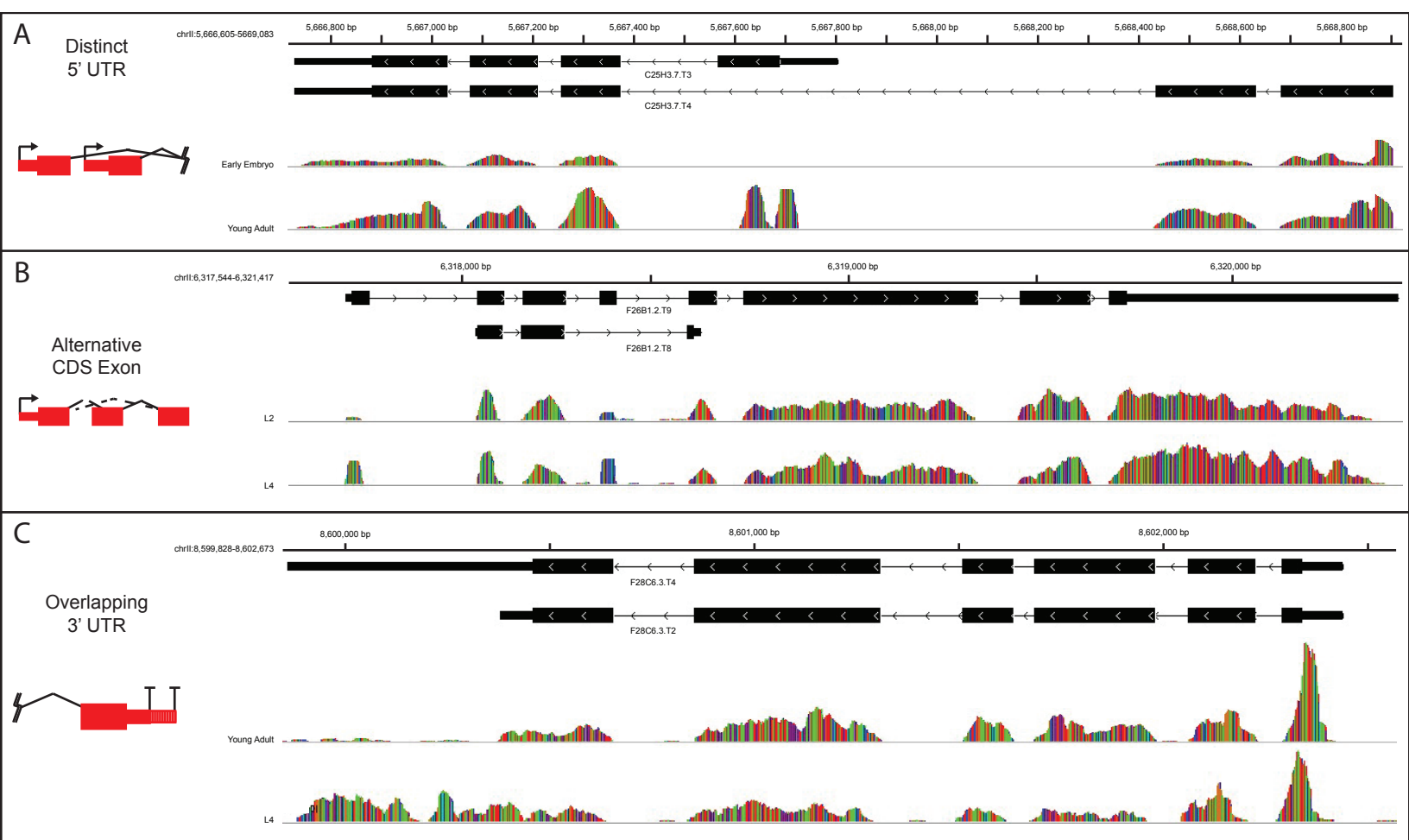


Fig. S18
[[21julpdf_supplex #59]]

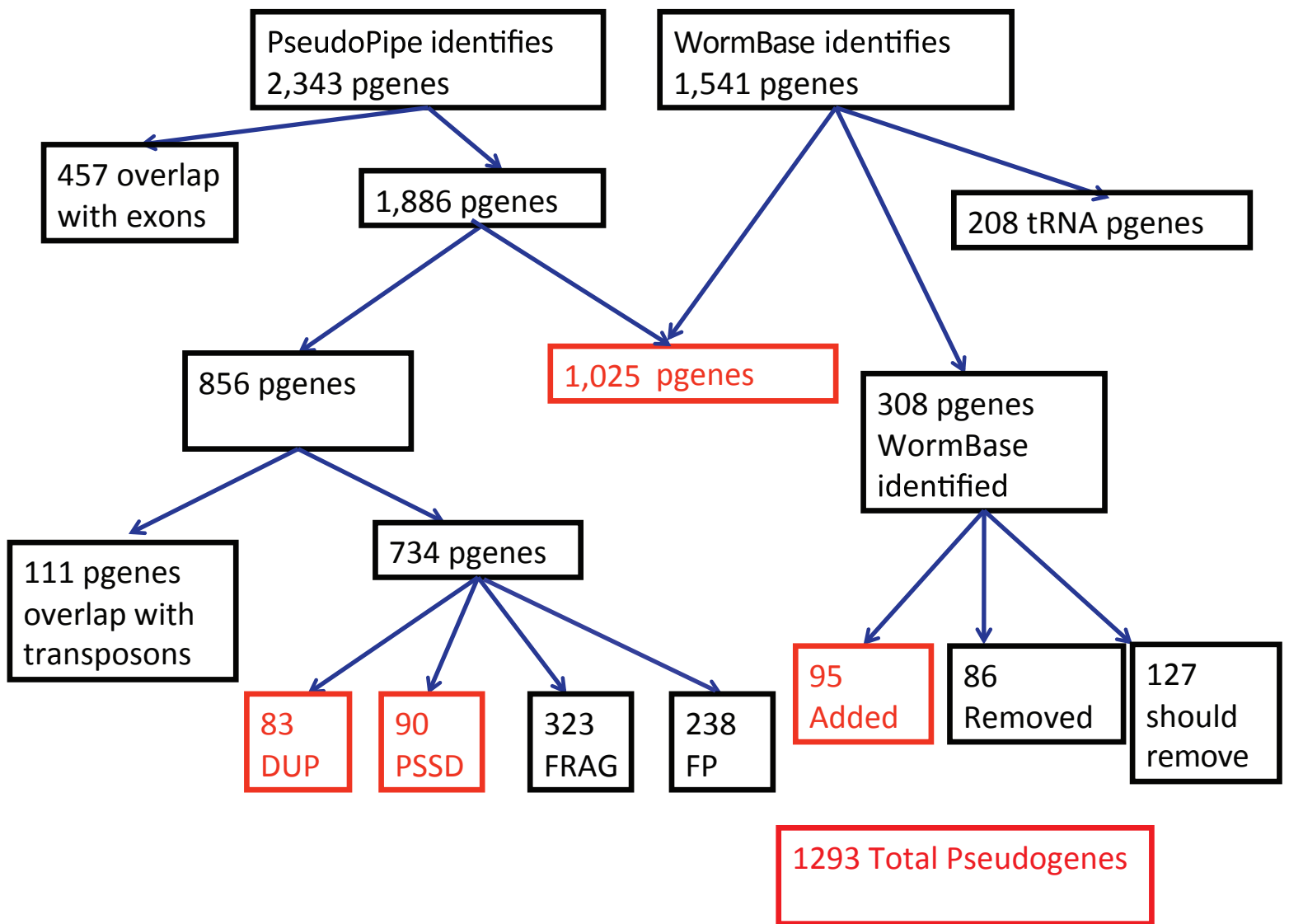


Fig. S19

[[21julpdf_supplex #58]]

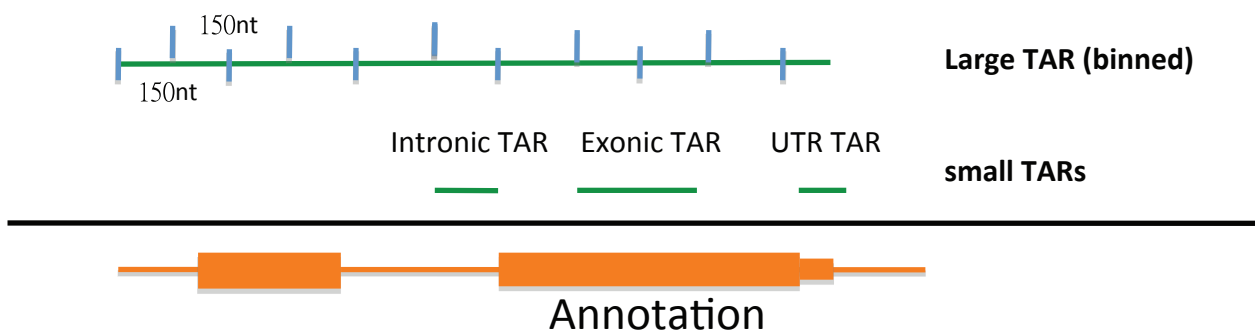
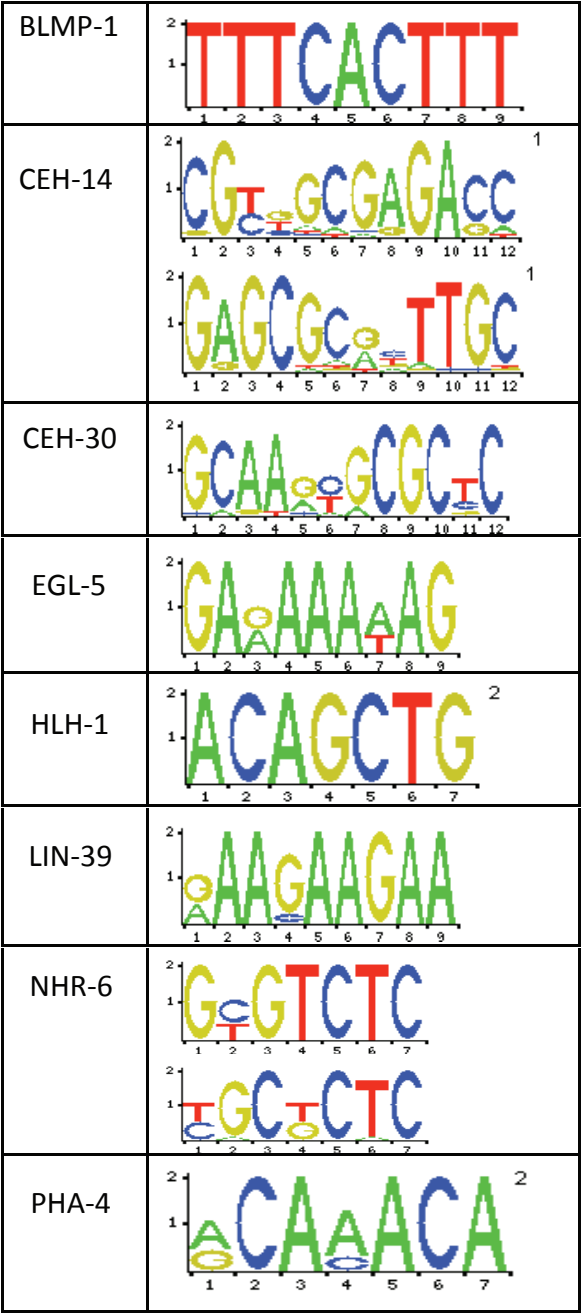


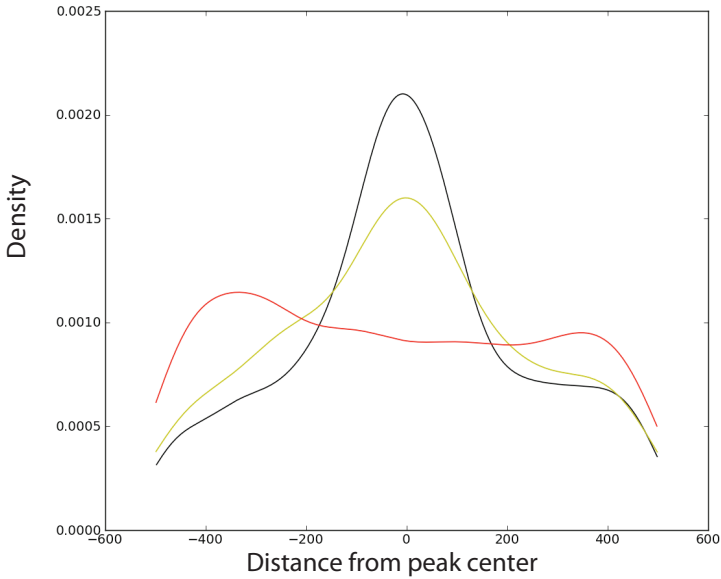
Fig. S20

[[21julpdf_supplex #18]]

A



B



C

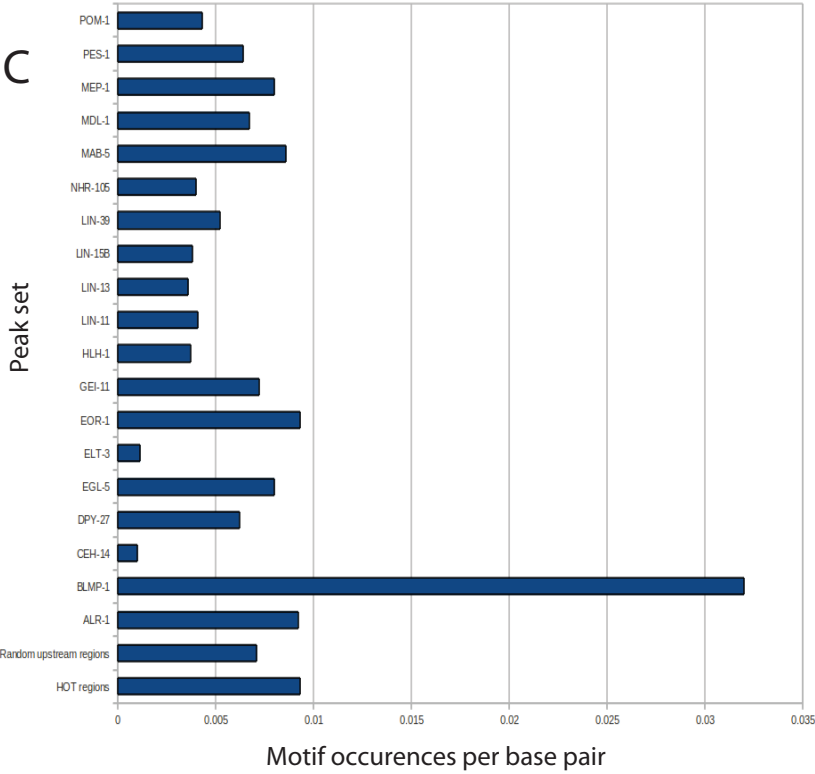


Fig. S21
[[21]ulpdf_supplex #53]]

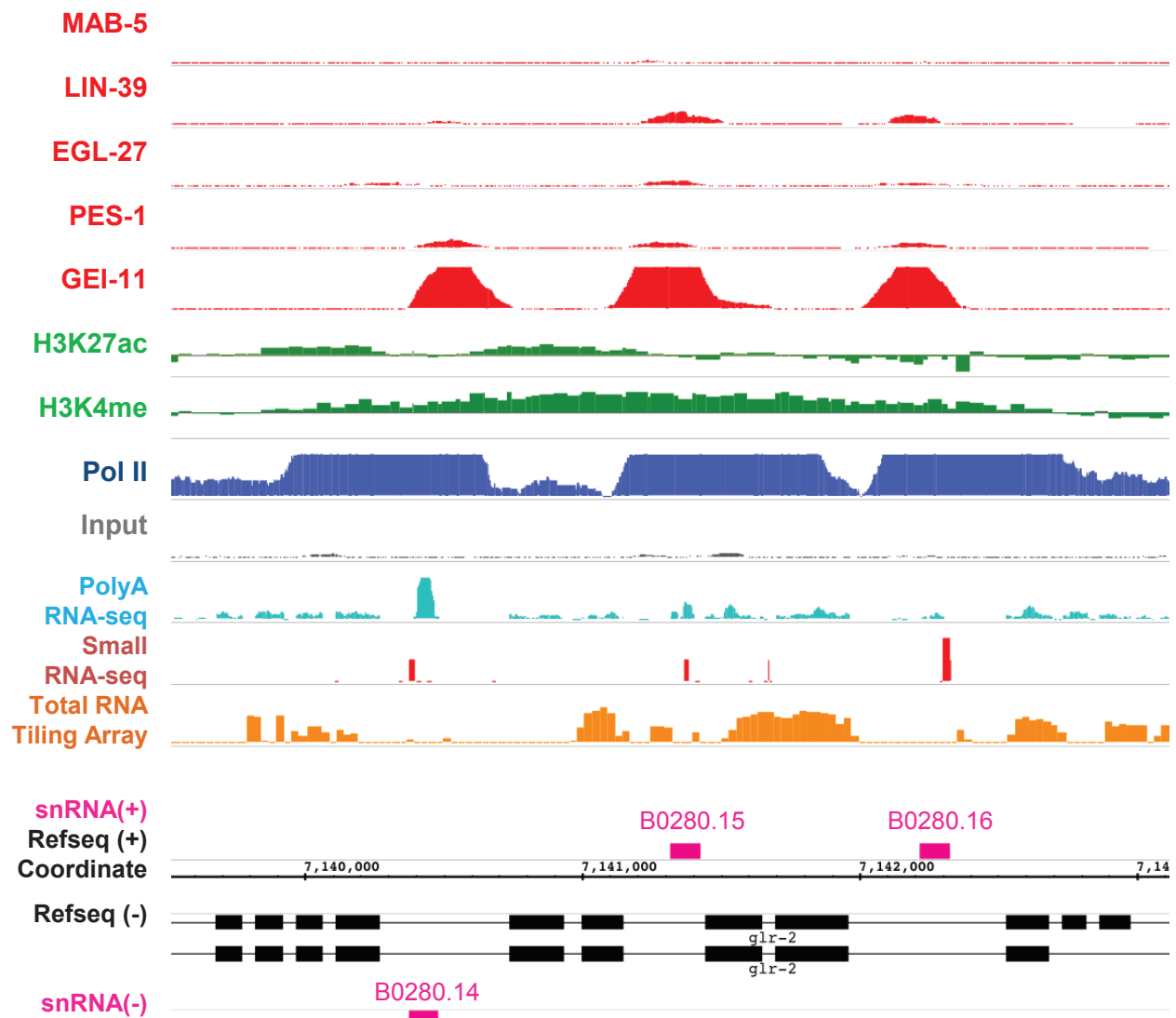
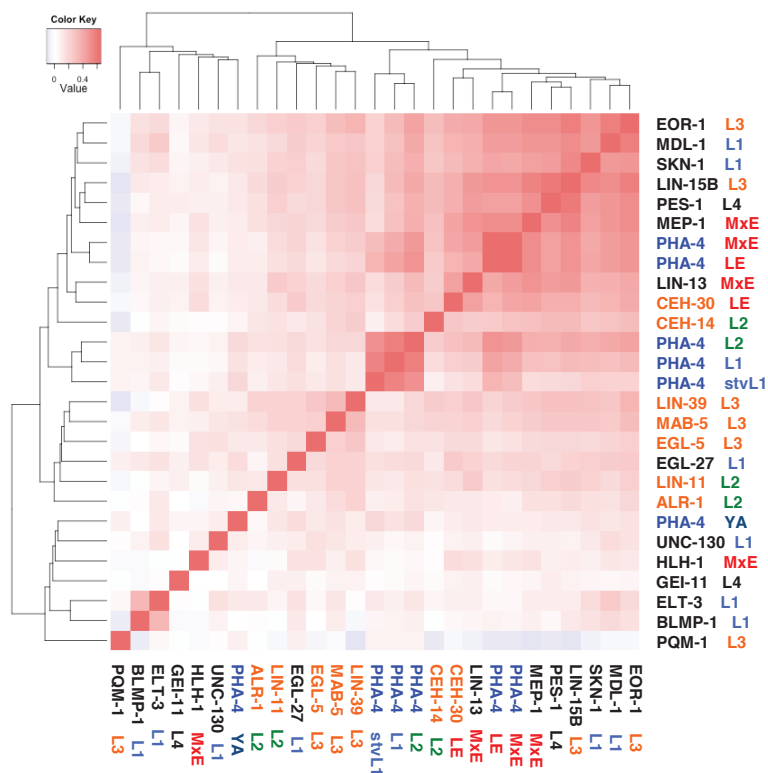


Fig. S22

[[21julpdf_supplex #25]]

A



B

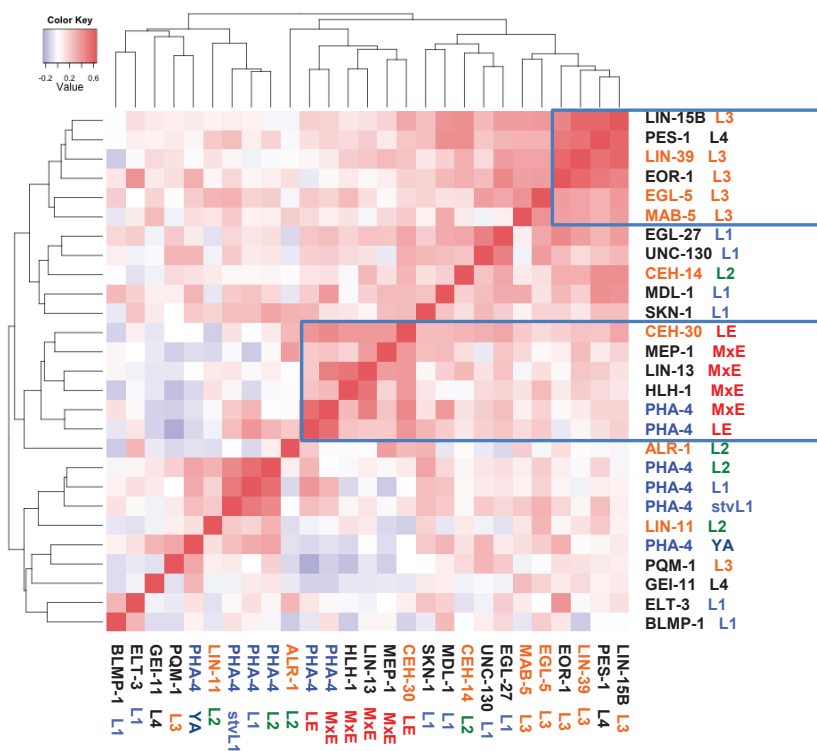


Fig. S23

[[21]julpdf_supplex #22 and #23]]

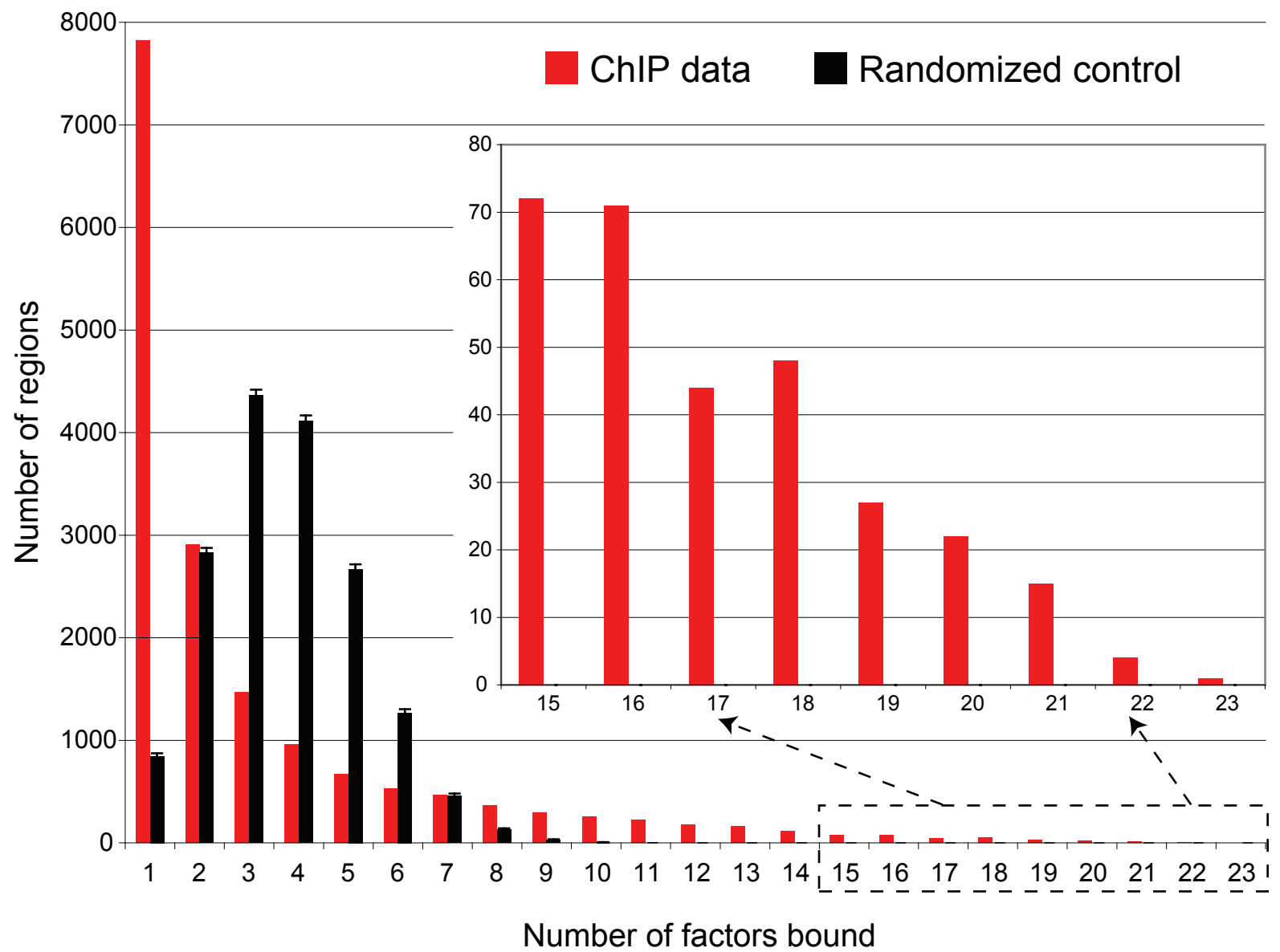


Fig. S24

[[21julpdf_supplex #27]]

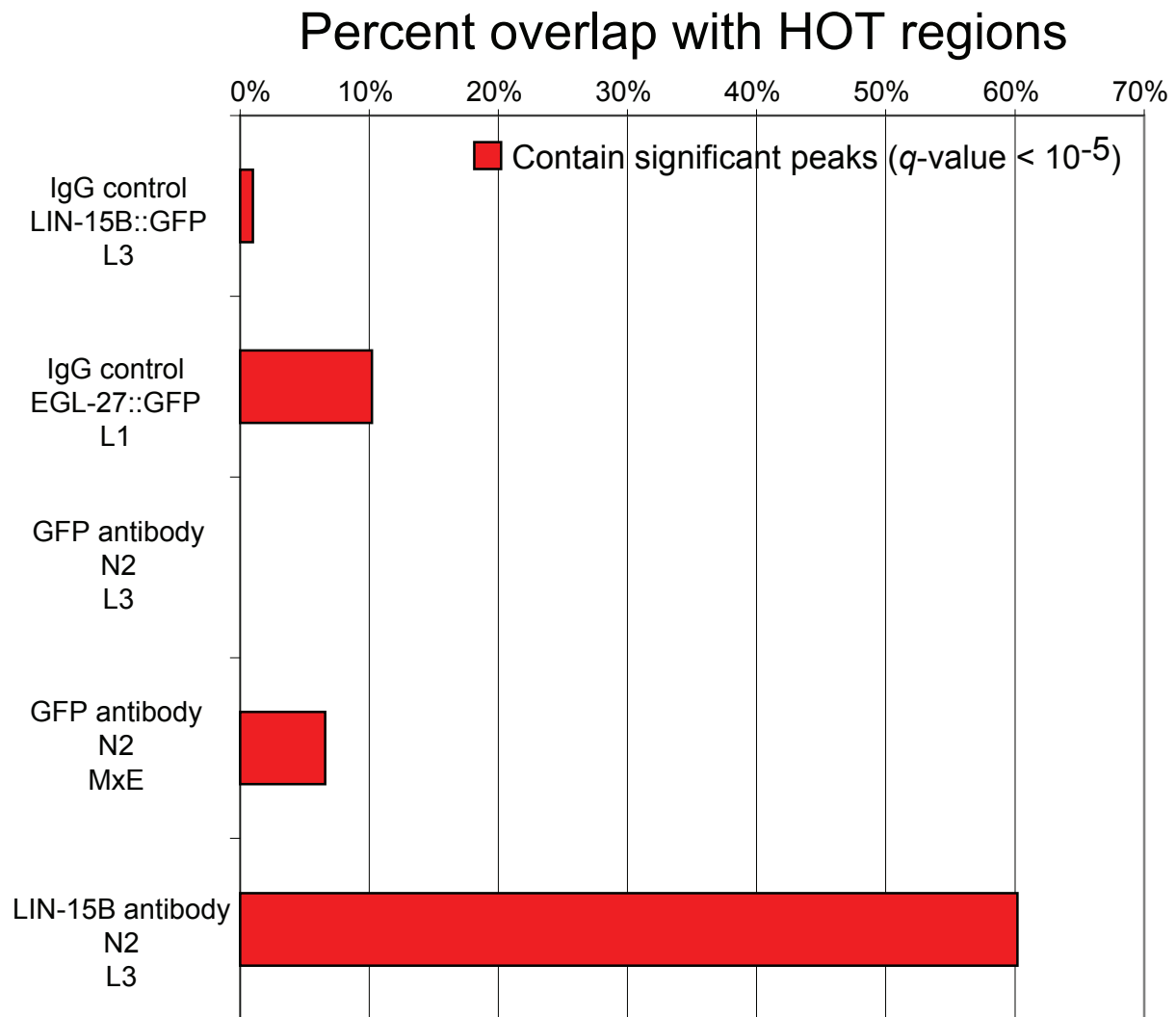


Fig. S25

[[21]ulpdf_supplex #28]]

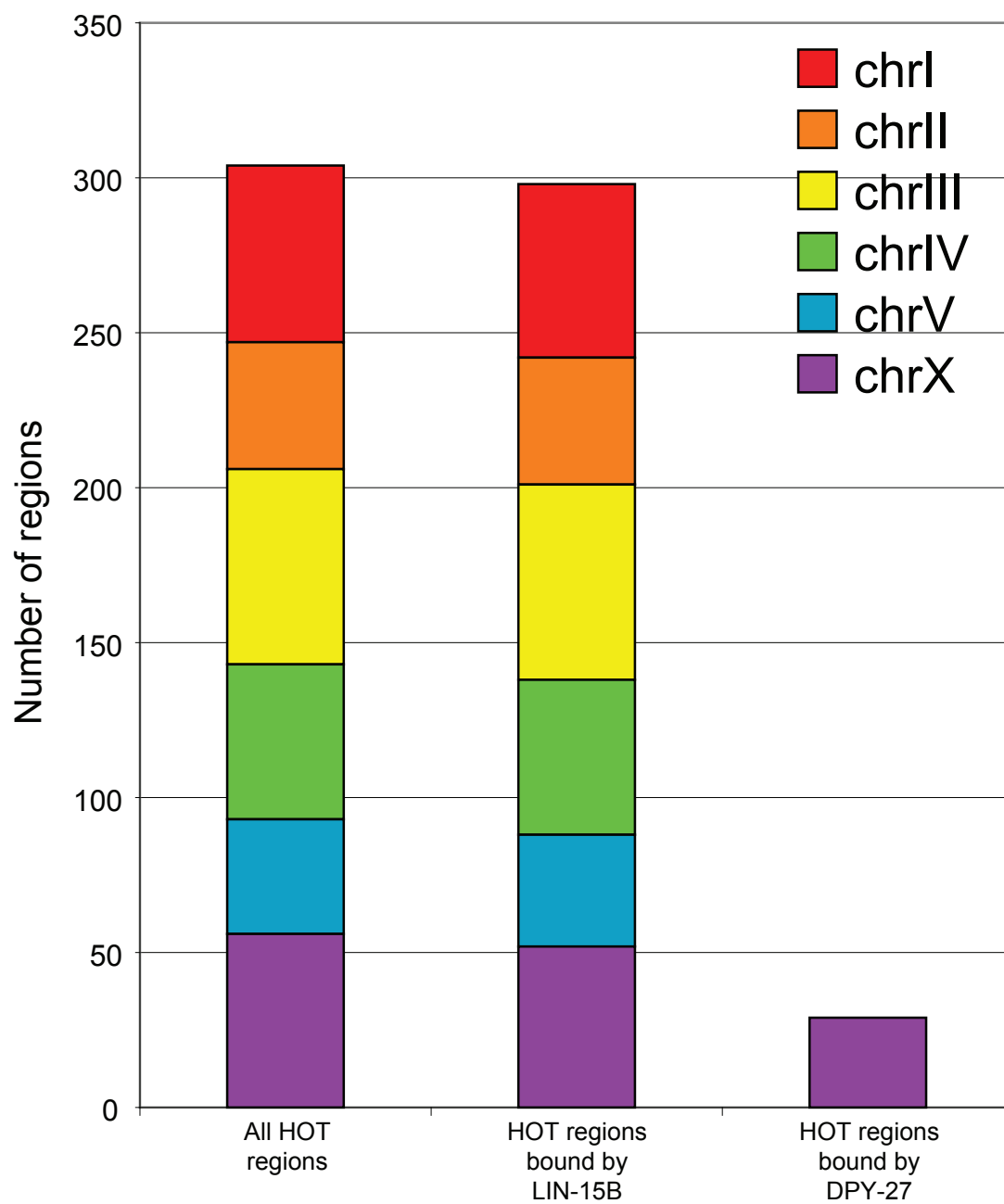


Fig. S26

[[21julpdf_supplex #29]]

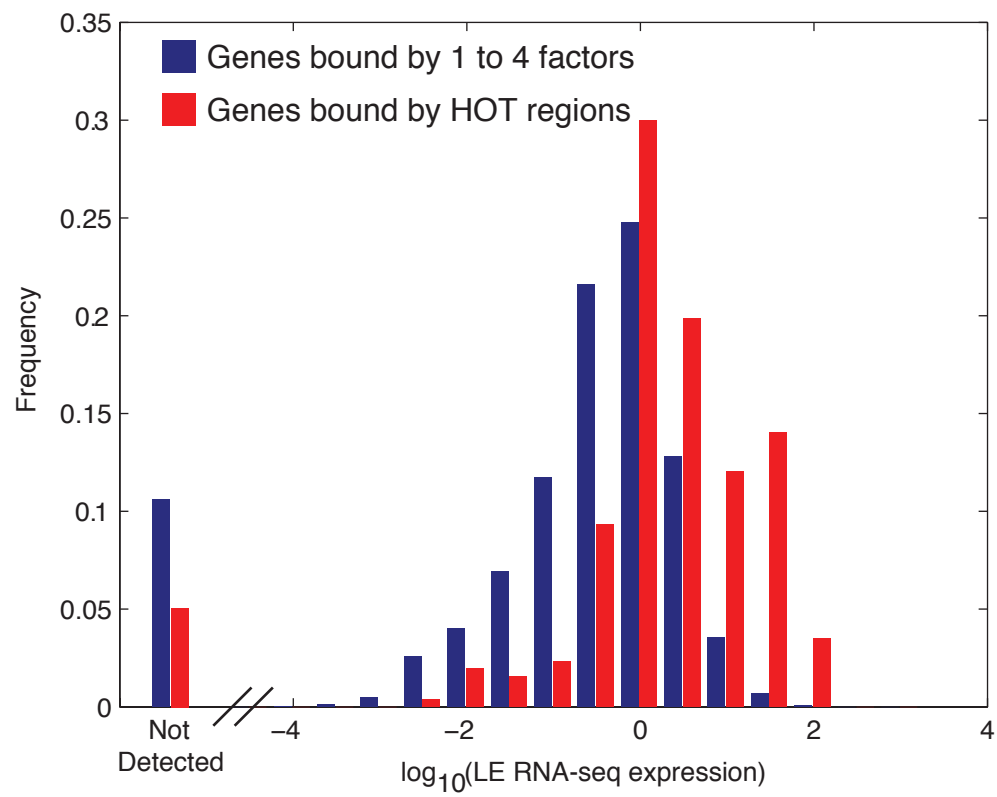


Fig. S27

[[21]julpdf_supplex #30]]

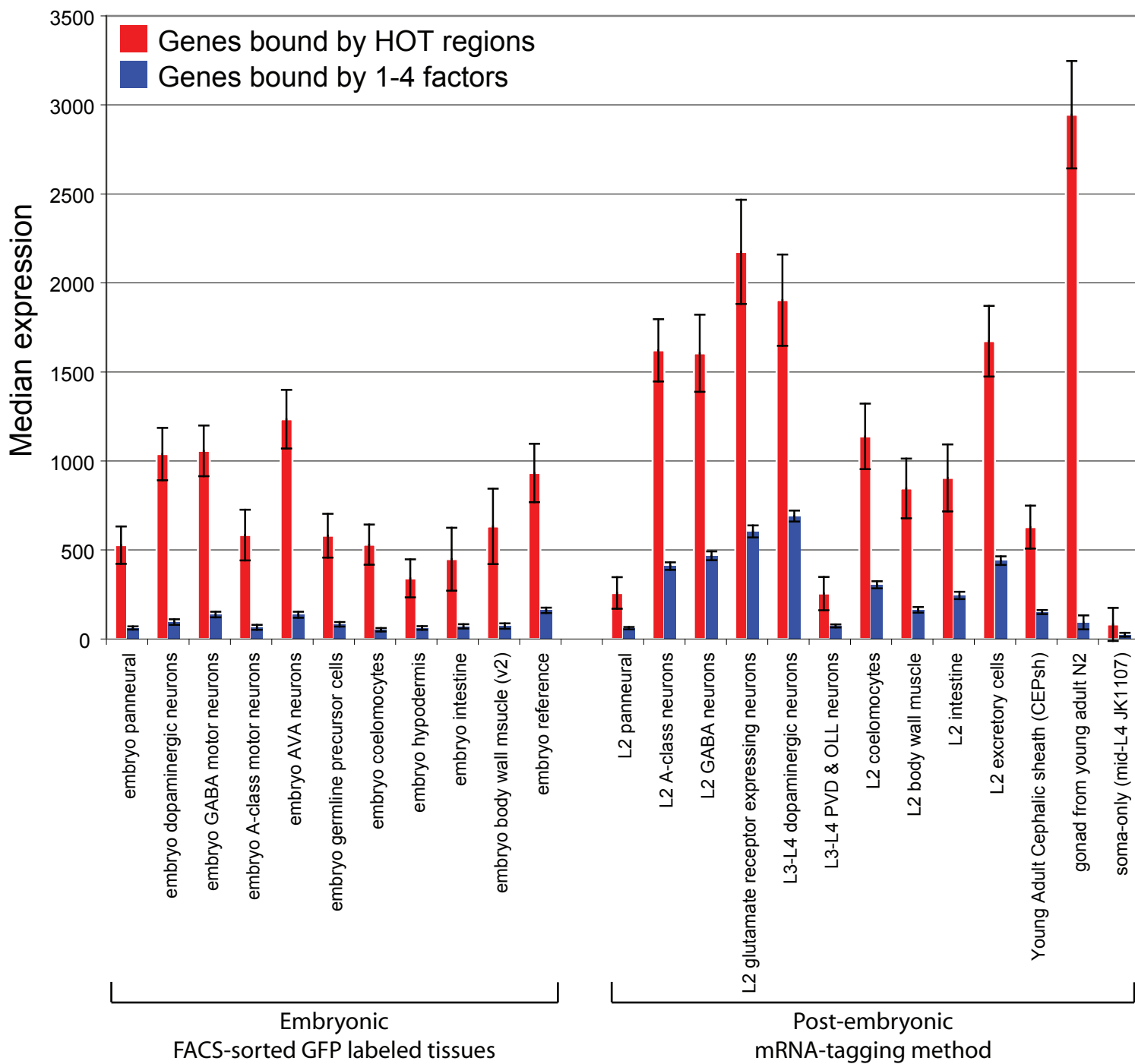


Fig. S28

[[21]julpdf_supplex 31]]

363 cells

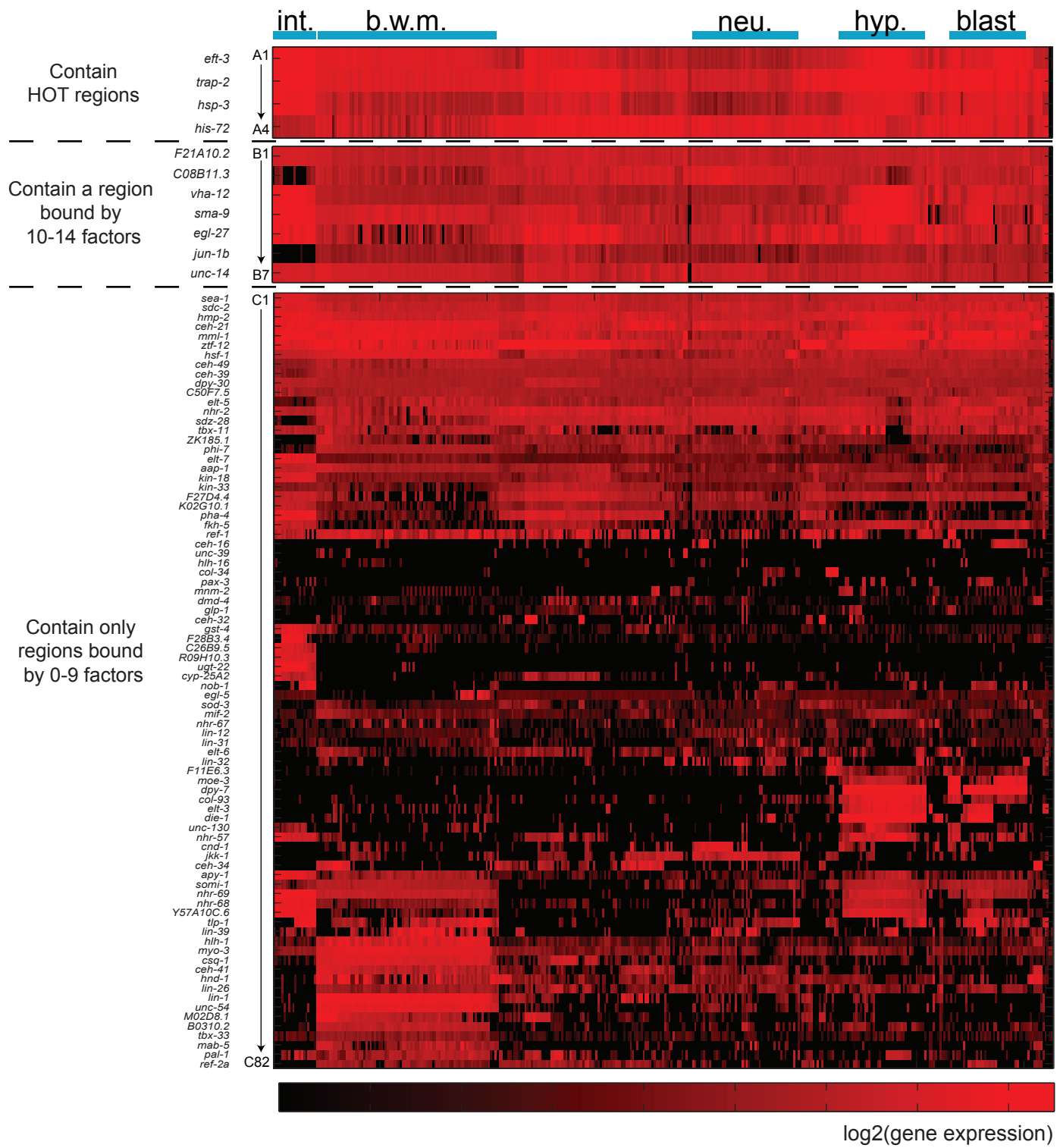


Fig. S29

[[21julpdf_supplex #26]]

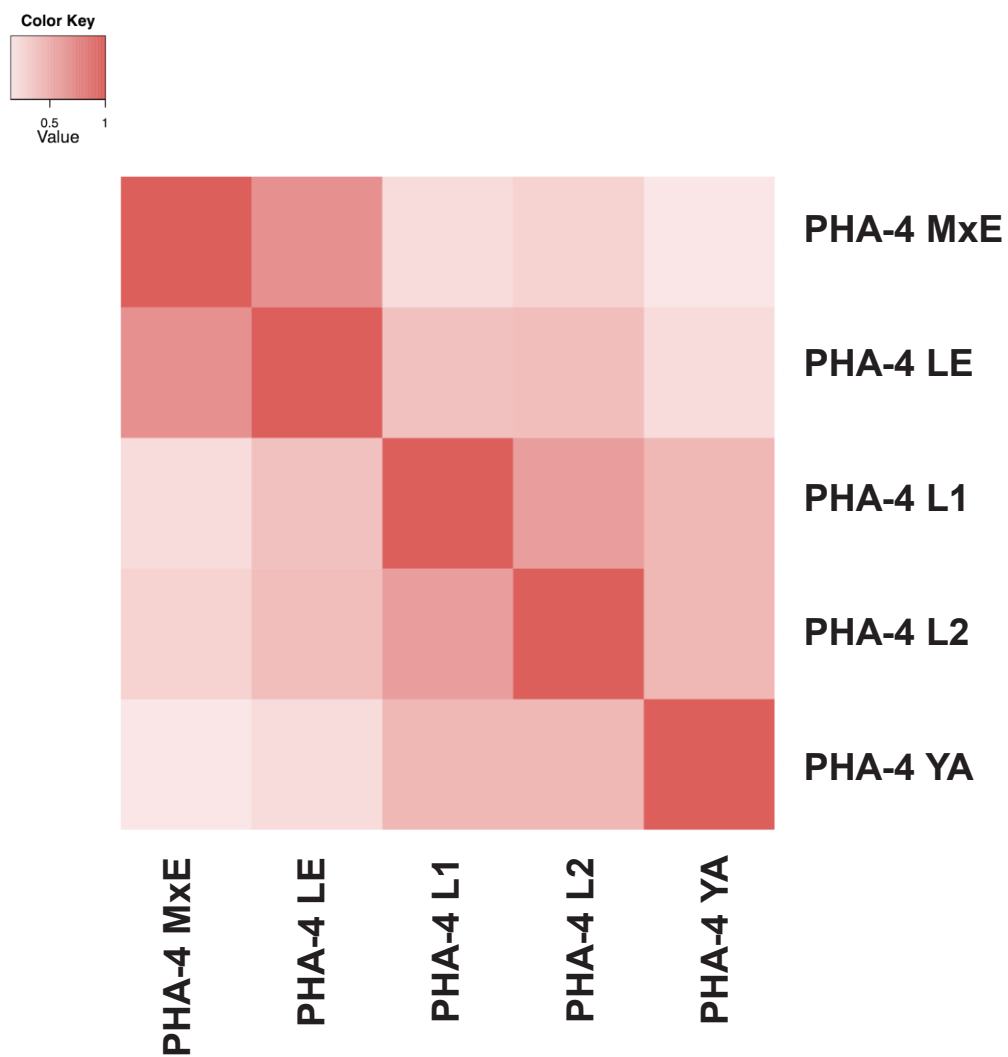


Fig. S30

[[21]julpdf_supplex #24]]

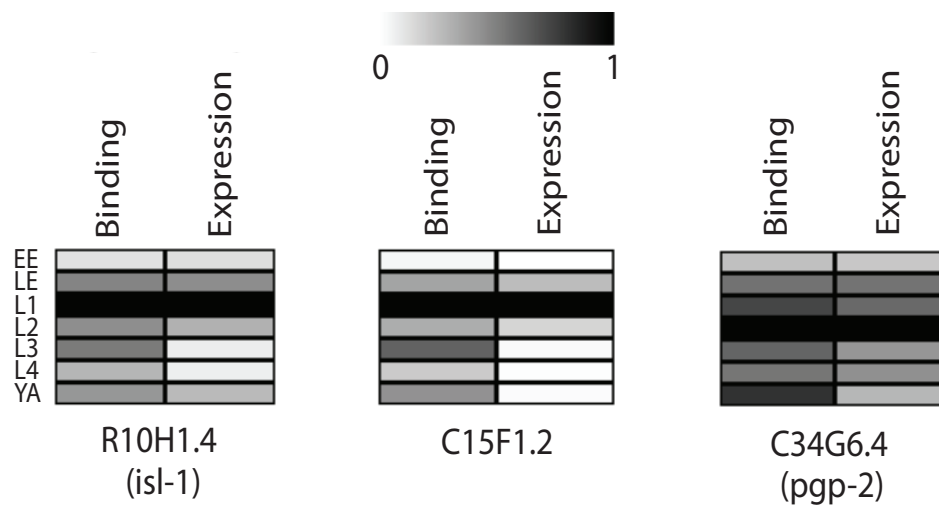


Fig. S31

[[21]ulpdf_suppex #57]]

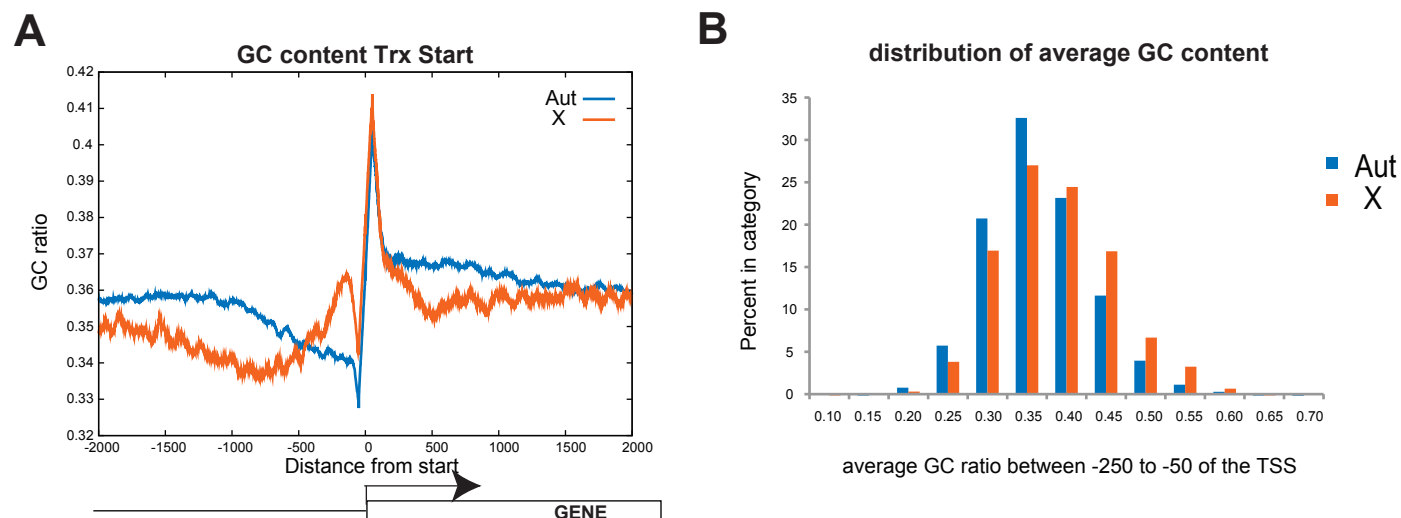


Fig. S33

[[GC_TSS]]

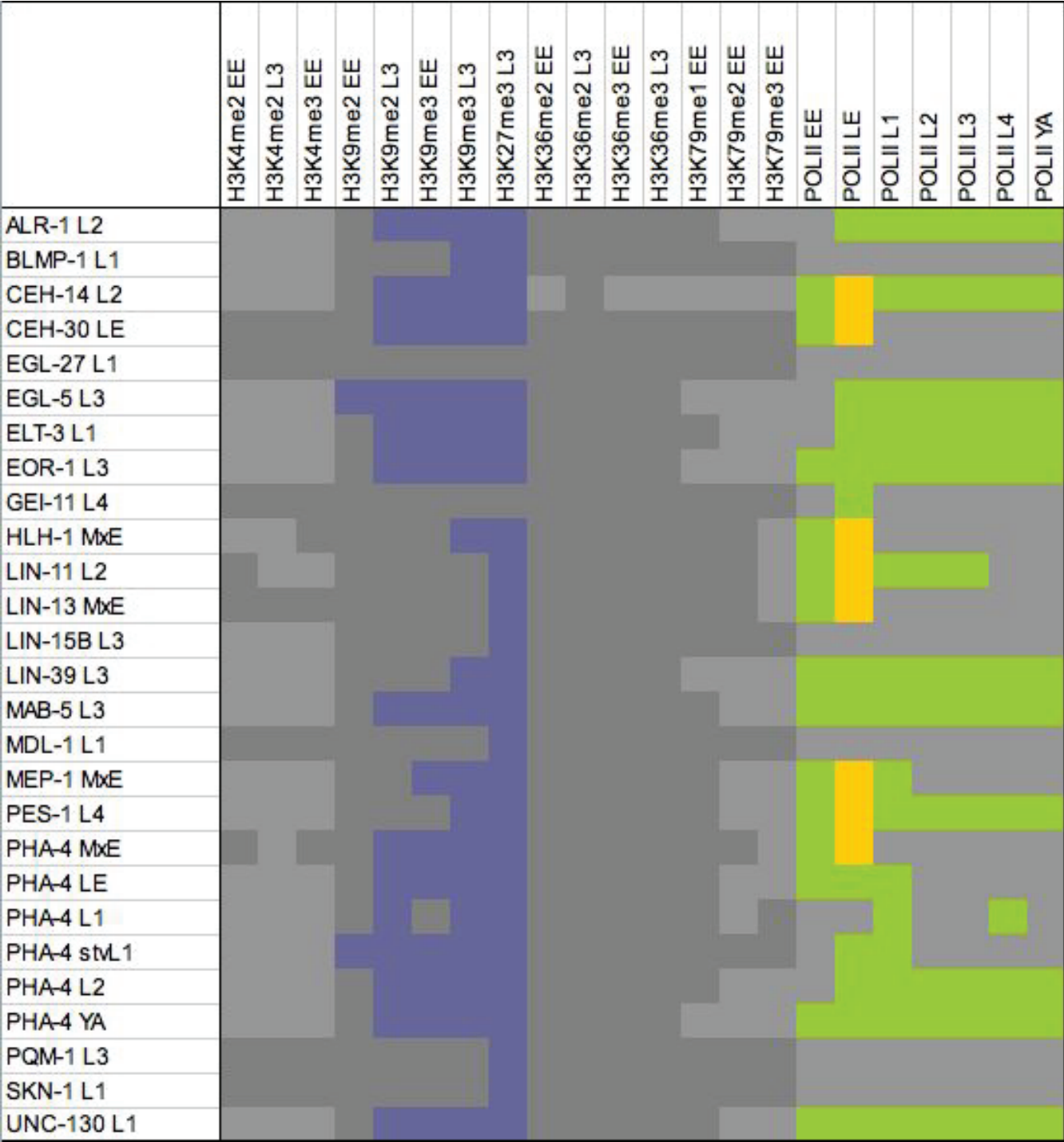


Fig. S34
[[21julpdf_supplex #37]]

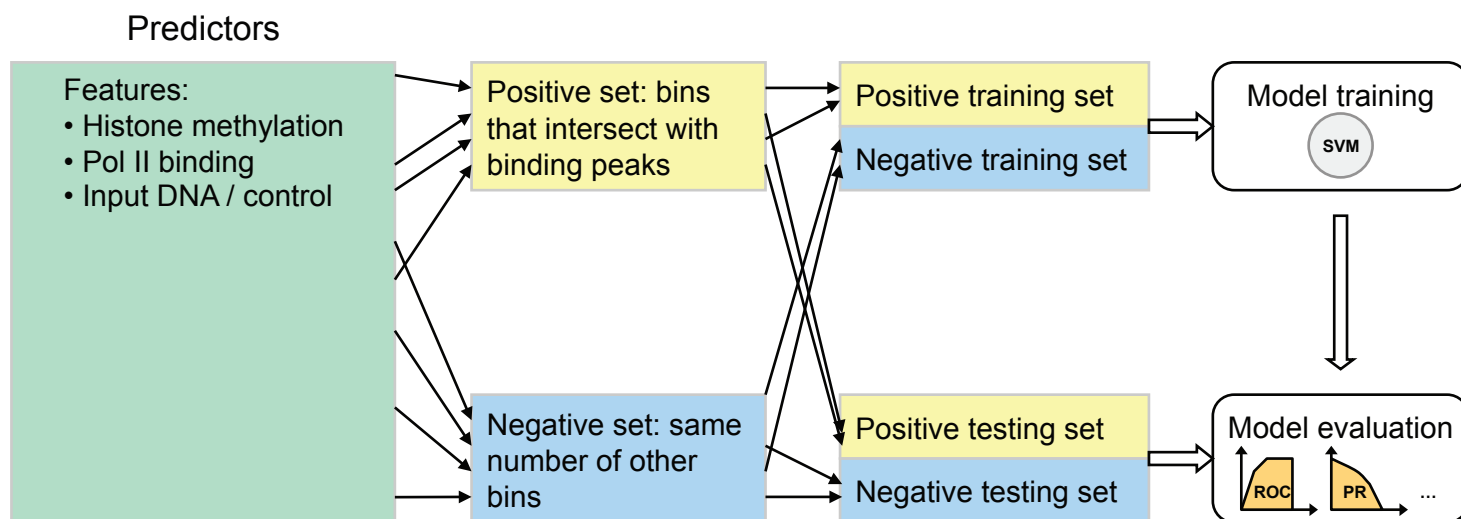


Fig. S35

[[21]ulpdf_supplex #38]]

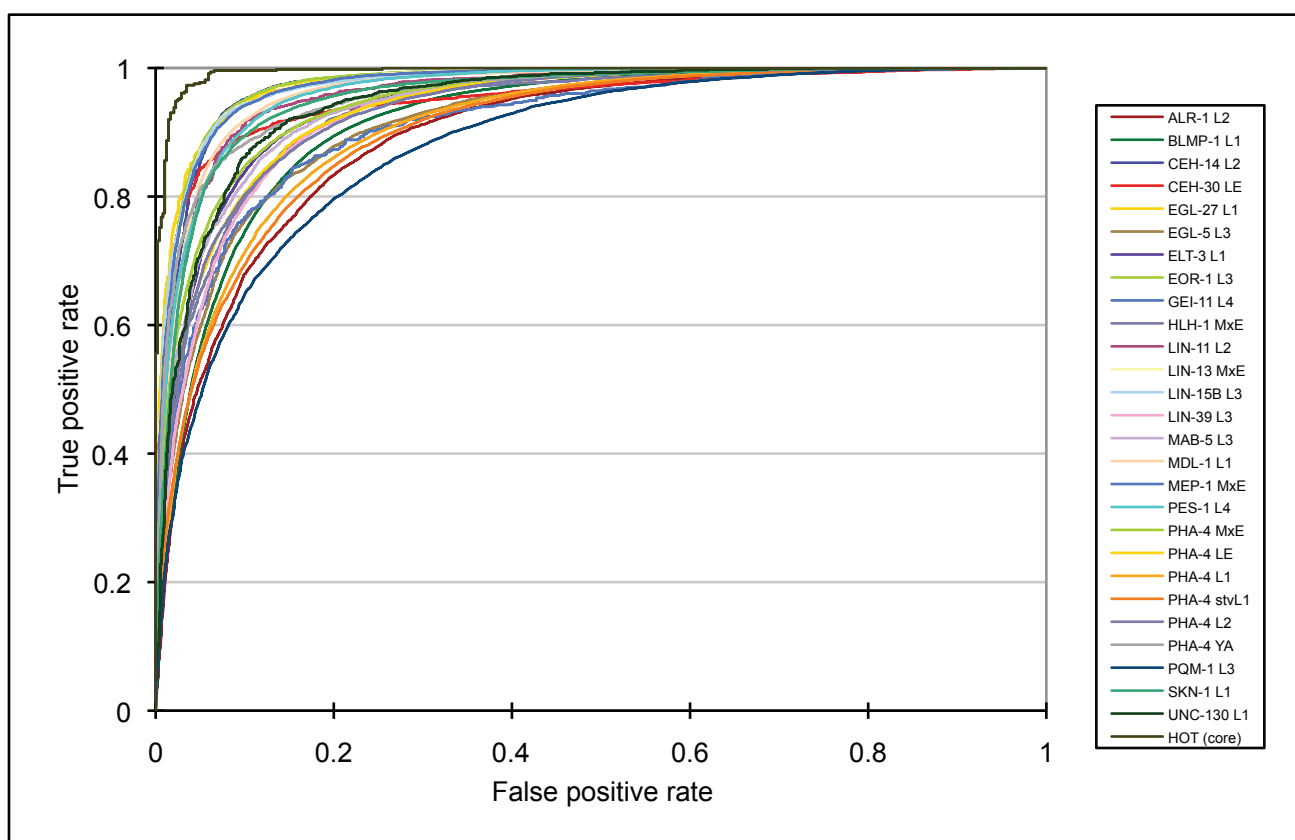


Fig. S36

[[21]julpdf_suppex #39]]

Binding experiments	Predictors																						
	All features	H3K4me2 EE	H3K4me2 L3	H3K4me3 EE	H3K9me2 EE	H3K9me2 L3	H3K9me3 EE	H3K9me3 L3	H3K27me3 L3	H3K36me2 EE	H3K36me2 L3	H3K36me3 EE	H3K36me3 L3	H3K79me1 EE	H3K79me2 EE	H3K79me3 EE	POL II EE	POL II LE	POL II L1	POL II L2	POL II L3	POL II L4	POL II YA
ALR-1 L2	0.90	0.68	0.73	0.61	0.61	0.54	0.62	0.70	0.65	0.55	0.58	0.54	0.50	0.59	0.60	0.61	0.66	0.72	0.82	0.82	0.80	0.80	0.81
BLMP-1 L1	0.92	0.67	0.80	0.66	0.52	0.62	0.62	0.68	0.67	0.48	0.55	0.54	0.62	0.59	0.64	0.62	0.67	0.71	0.85	0.87	0.85	0.82	0.85
CEH-14 L2	0.97	0.89	0.92	0.87	0.57	0.60	0.60	0.74	0.89	0.72	0.67	0.70	0.63	0.75	0.85	0.81	0.82	0.86	0.91	0.93	0.92	0.91	0.91
CEH-30 LE	0.95	0.70	0.80	0.77	0.58	0.60	0.60	0.70	0.84	0.58	0.60	0.54	0.62	0.65	0.75	0.72	0.81	0.89	0.90	0.90	0.90	0.86	0.88
EGL-27 L1	0.98	0.84	0.82	0.75	0.54	0.70	0.63	0.78	0.84	0.50	0.66	0.58	0.67	0.60	0.71	0.73	0.81	0.91	0.96	0.94	0.95	0.94	0.91
EGL-5 L3	0.92	0.75	0.82	0.68	0.58	0.65	0.63	0.74	0.77	0.56	0.57	0.52	0.60	0.61	0.66	0.67	0.74	0.82	0.87	0.89	0.87	0.86	0.86
ELT-3 L1	0.94	0.71	0.76	0.64	0.59	0.63	0.61	0.68	0.70	0.52	0.55	0.54	0.60	0.60	0.63	0.63	0.64	0.73	0.90	0.91	0.88	0.88	0.90
EOR-1 L3	0.98	0.82	0.88	0.75	0.50	0.58	0.48	0.74	0.84	0.59	0.60	0.59	0.56	0.53	0.75	0.74	0.76	0.84	0.94	0.95	0.95	0.93	0.94
GEI-11 L4	0.91	0.70	0.71	0.63	0.55	0.58	0.55	0.63	0.66	0.53	0.56	0.53	0.59	0.53	0.58	0.59	0.75	0.77	0.77	0.83	0.85	0.81	0.82
HLH-1 MxE	0.93	0.84	0.80	0.75	0.56	0.55	0.63	0.73	0.57	0.58	0.58	0.58	0.64	0.64	0.71	0.71	0.79	0.82	0.86	0.85	0.86	0.82	0.83
LIN-11 L2	0.96	0.73	0.85	0.80	0.57	0.65	0.55	0.70	0.80	0.64	0.59	0.64	0.59	0.71	0.77	0.77	0.82	0.87	0.93	0.94	0.93	0.93	0.92
LIN-13 MxE	0.97	0.88	0.87	0.87	0.58	0.63	0.56	0.55	0.84	0.52	0.52	0.58	0.59	0.66	0.80	0.77	0.81	0.90	0.91	0.91	0.91	0.90	0.90
LIN-15B L3	0.97	0.86	0.88	0.85	0.56	0.57	0.61	0.62	0.86	0.69	0.61	0.65	0.54	0.68	0.78	0.70	0.72	0.84	0.91	0.92	0.90	0.90	0.87
LIN-39 L3	0.93	0.74	0.84	0.67	0.54	0.63	0.62	0.74	0.72	0.58	0.60	0.53	0.58	0.65	0.67	0.69	0.76	0.83	0.87	0.88	0.89	0.85	0.86
MAB-5 L3	0.94	0.79	0.84	0.73	0.54	0.59	0.61	0.73	0.80	0.57	0.53	0.55	0.61	0.63	0.71	0.71	0.75	0.83	0.92	0.91	0.92	0.89	0.90
MDL-1 L1	0.97	0.80	0.84	0.74	0.56	0.61	0.62	0.72	0.80	0.61	0.59	0.48	0.60	0.57	0.67	0.68	0.72	0.84	0.94	0.94	0.94	0.90	0.91
MEP-1 MxE	0.97	0.89	0.88	0.84	0.57	0.63	0.63	0.73	0.78	0.64	0.53	0.55	0.58	0.68	0.78	0.76	0.81	0.89	0.92	0.93	0.91	0.88	0.90
PES-1 L4	0.96	0.82	0.86	0.79	0.61	0.61	0.54	0.56	0.80	0.65	0.57	0.60	0.58	0.65	0.74	0.69	0.77	0.84	0.91	0.90	0.89	0.90	0.88
PHA-4 MxE	0.95	0.80	0.84	0.77	0.57	0.64	0.60	0.73	0.79	0.54	0.58	0.56	0.60	0.66	0.74	0.73	0.78	0.88	0.88	0.88	0.87	0.83	0.85
PHA-4 LE	0.94	0.82	0.86	0.75	0.56	0.64	0.64	0.72	0.78	0.50	0.58	0.56	0.61	0.66	0.72	0.70	0.76	0.68	0.87	0.88	0.86	0.81	0.83
PHA-4 L1	0.91	0.70	0.75	0.68	0.58	0.61	0.60	0.69	0.74	0.56	0.51	0.54	0.60	0.59	0.64	0.64	0.65	0.72	0.85	0.85	0.81	0.82	0.80
PHA-4 stvL1	0.90	0.69	0.81	0.64	0.58	0.62	0.60	0.68	0.73	0.52	0.56	0.54	0.61	0.61	0.64	0.61	0.63	0.74	0.83	0.84	0.82	0.81	0.79
PHA-4 L2	0.94	0.76	0.83	0.68	0.55	0.65	0.61	0.51	0.70	0.60	0.54	0.57	0.60	0.58	0.68	0.67	0.72	0.79	0.89	0.88	0.88	0.88	0.85
PHA-4 YA	0.96	0.75	0.83	0.68	0.53	0.57	0.50	0.70	0.75	0.59	0.53	0.55	0.57	0.51	0.70	0.69	0.75	0.83	0.93	0.94	0.94	0.94	0.94
PQM-1 L3	0.88	0.62	0.66	0.60	0.59	0.62	0.54	0.64	0.51	0.53	0.62	0.58	0.66	0.51	0.58	0.56	0.60	0.67	0.81	0.81	0.77	0.81	0.75
SKN-1 L1	0.96	0.81	0.87	0.76	0.56	0.62	0.58	0.70	0.83	0.64	0.58	0.60	0.57	0.67	0.65	0.72	0.74	0.80	0.91	0.93	0.89	0.90	0.89
UNC-130 L1	0.95	0.66	0.77	0.70	0.54	0.63	0.61	0.70	0.68	0.59	0.59	0.58	0.55	0.62	0.65	0.66	0.74	0.82	0.92	0.92	0.91	0.90	0.91
HOT (core)	0.99	0.84	0.77	0.90	0.61	0.73	0.49	0.79	0.86	0.62	0.63	0.58	0.71	0.63	0.84	0.73	0.85	0.97	0.98	0.99	0.97	0.97	0.96

Fig. S37

[[21julpdf_supplex #40]]

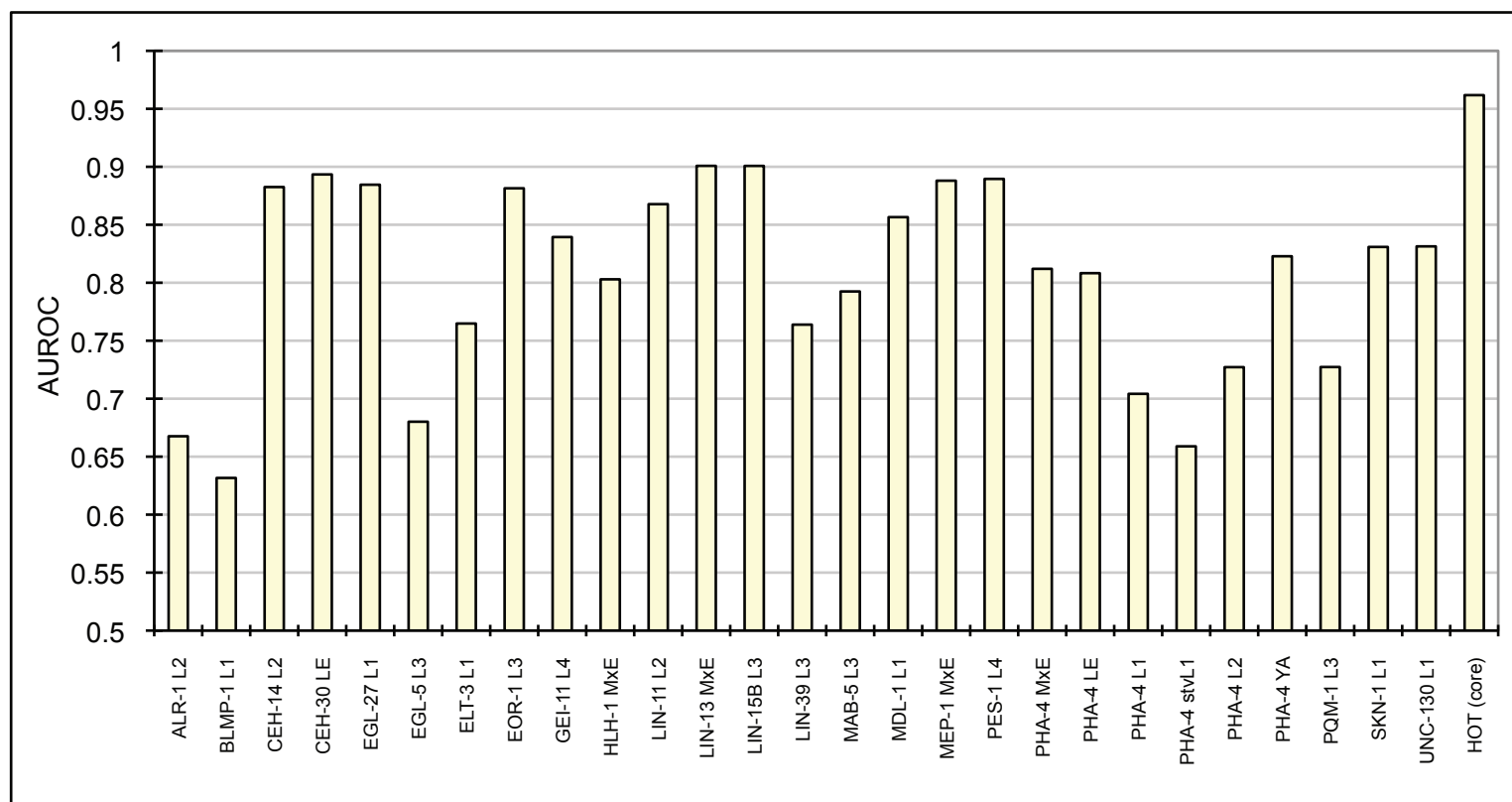


Fig. S38

[[21julpdf_supplex #41]]

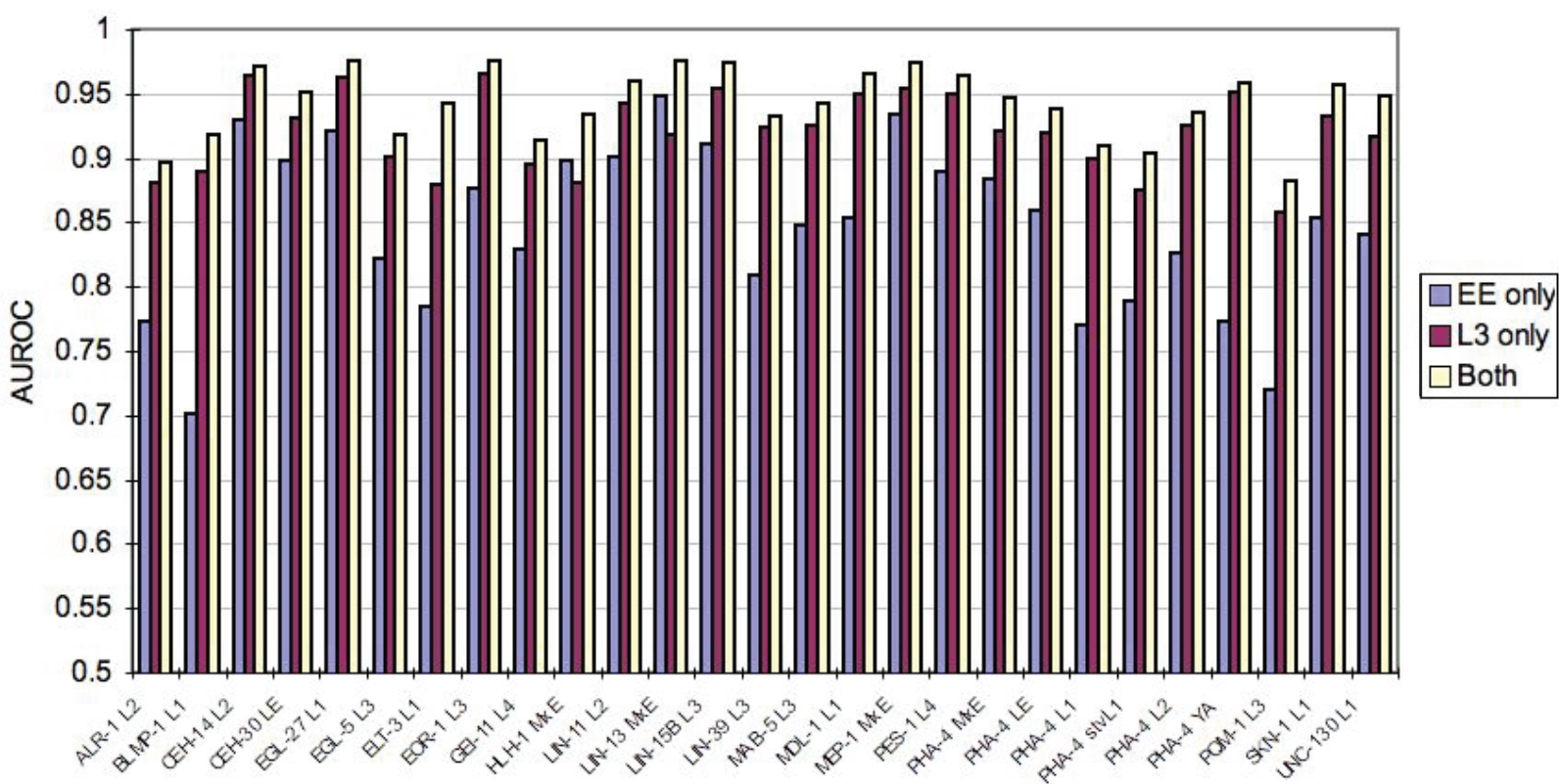


Fig. S39

[[21]julpdf_supplex #45]]

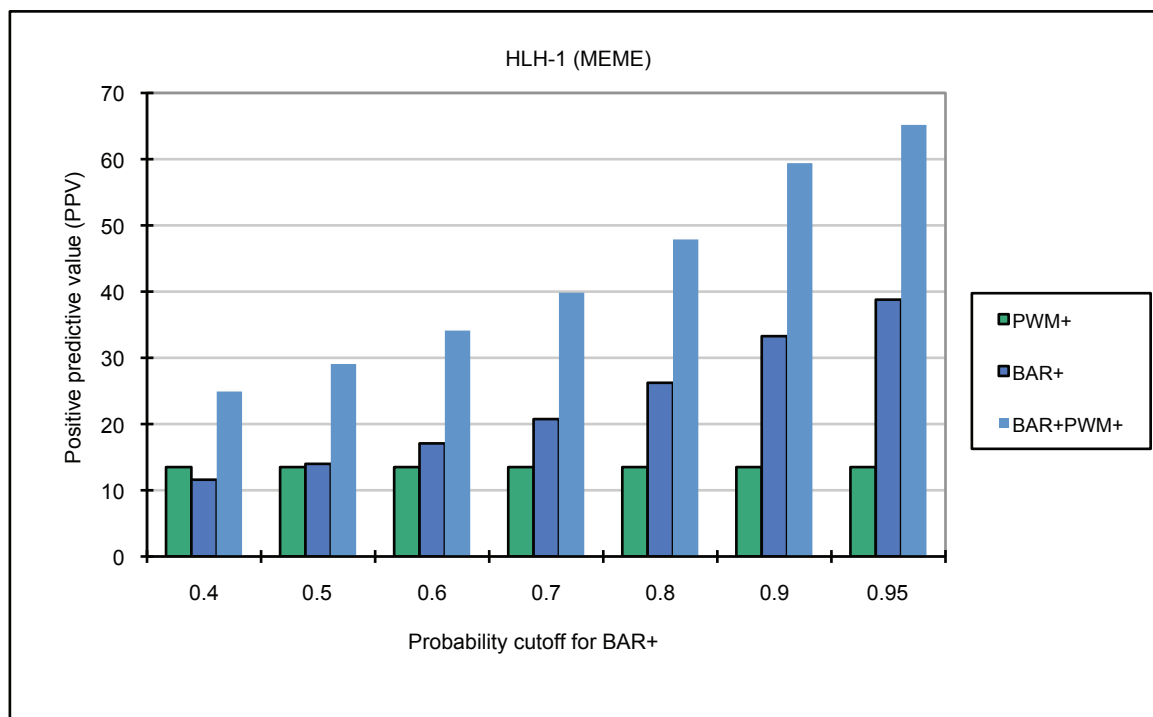
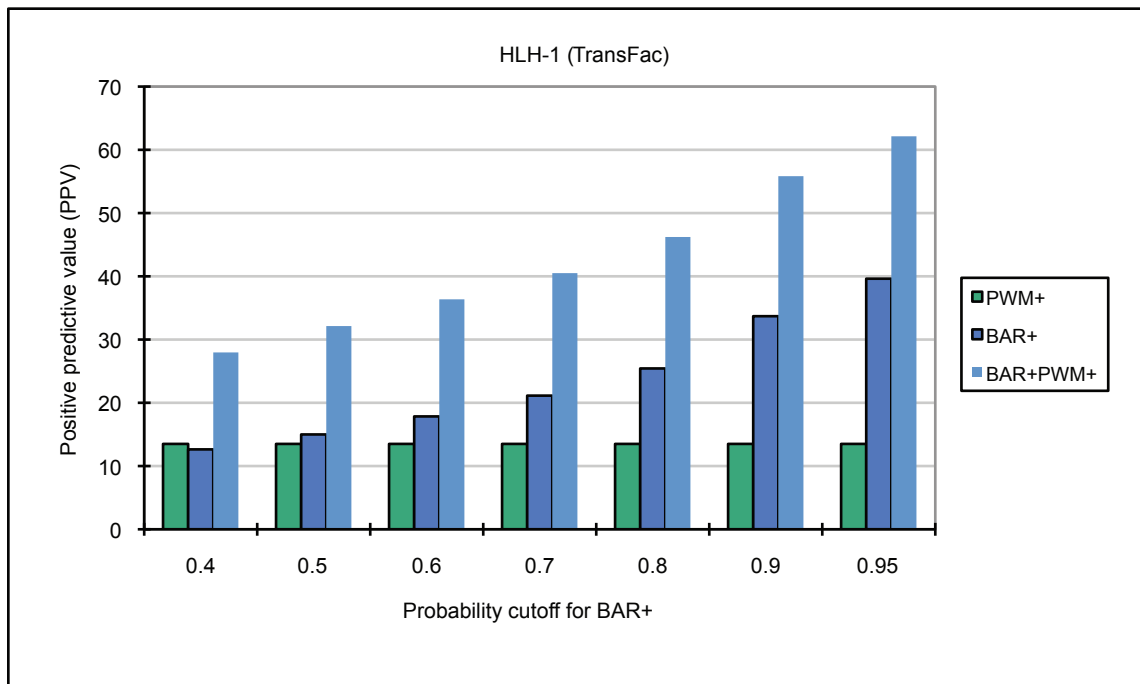


Fig. S40

[[21]julpdf_supplex #43]]

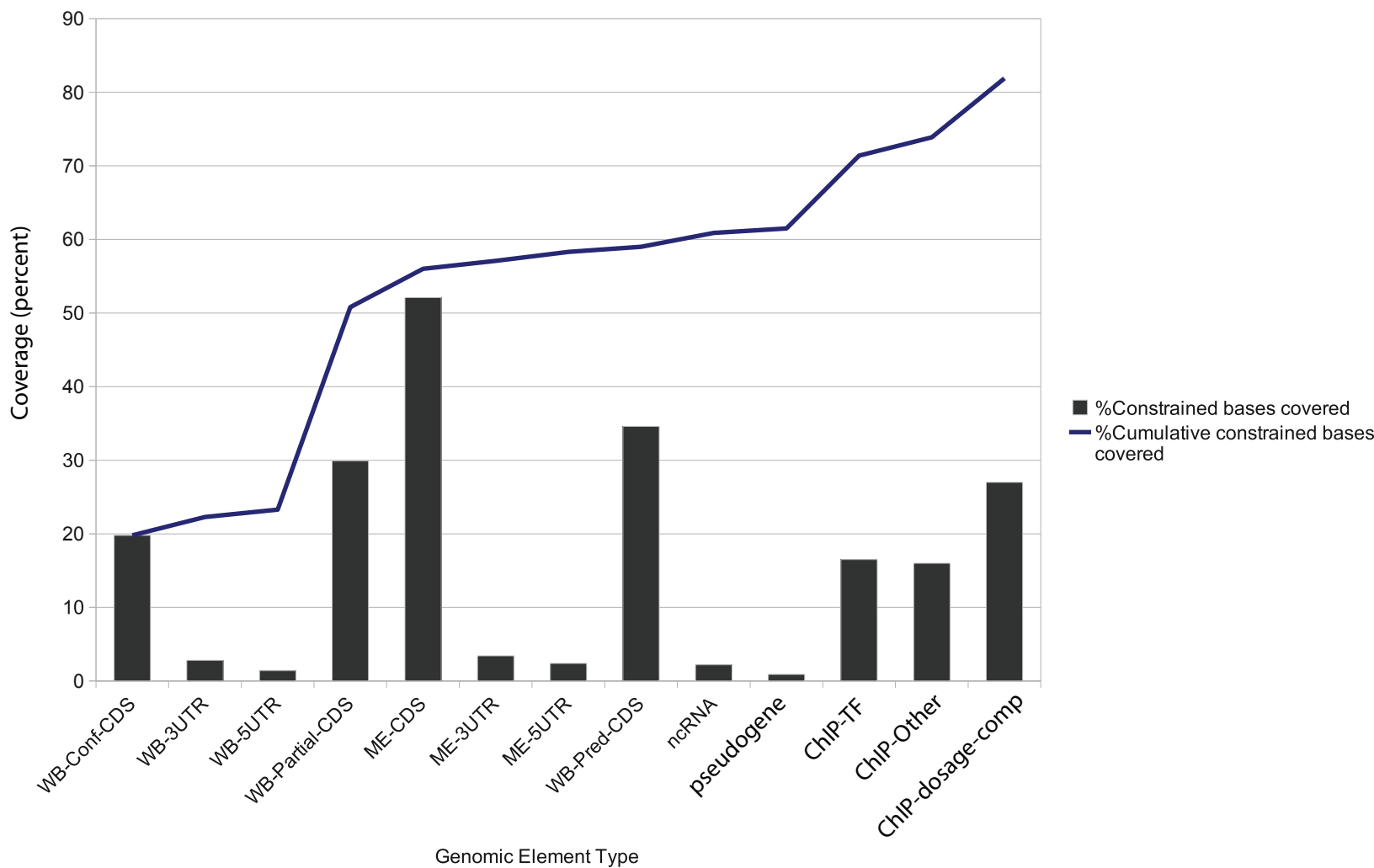


Fig. S41

[[21julpdf_supplex #54]]

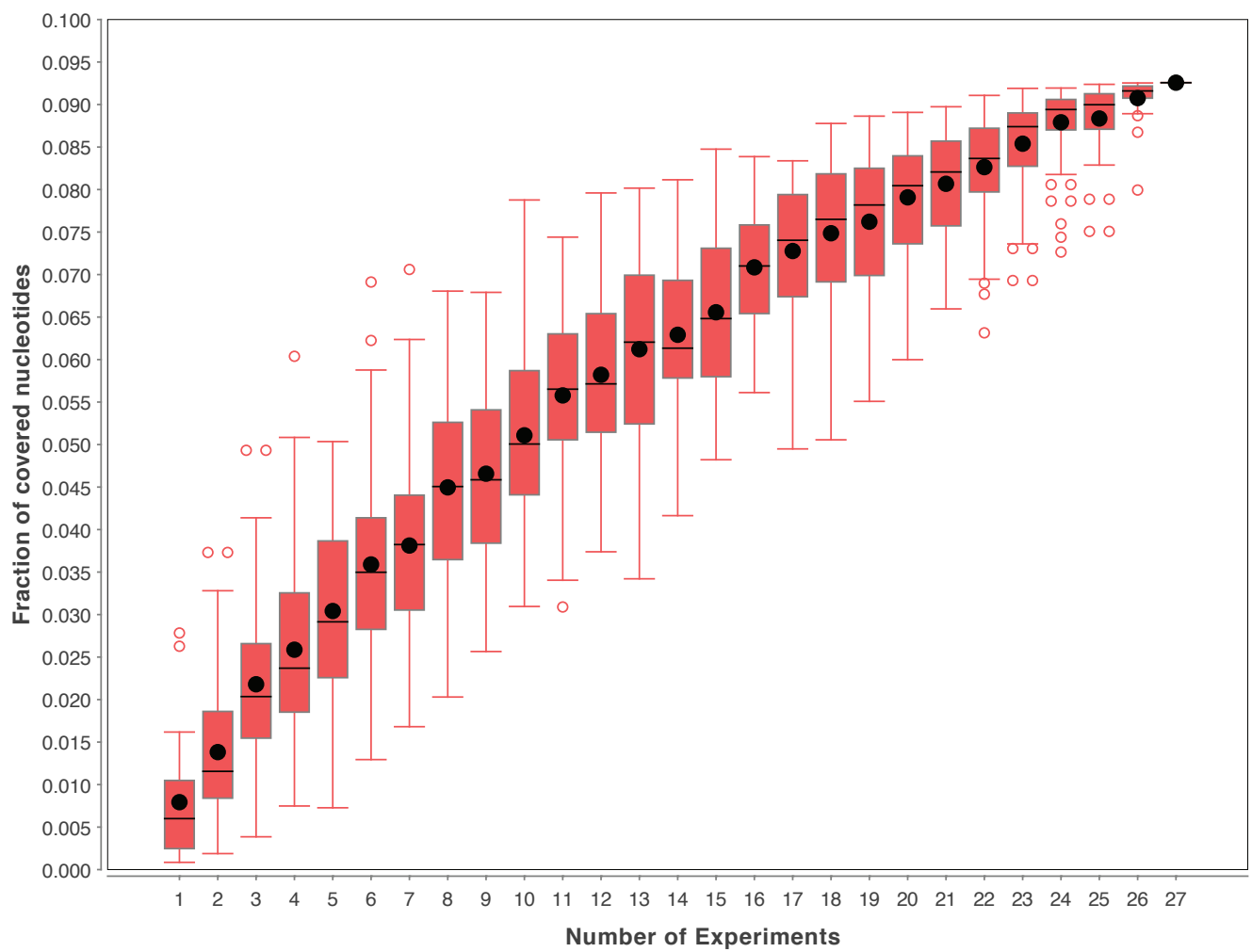


Fig. S42

[[21julpdf_supplex #20]]