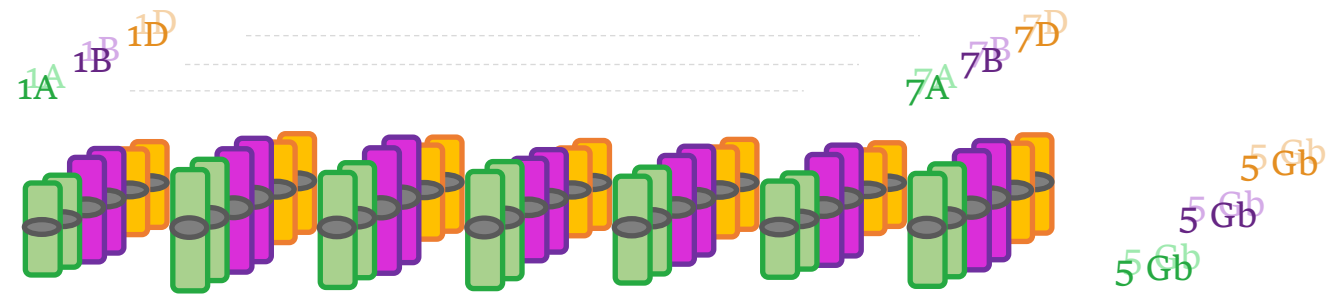
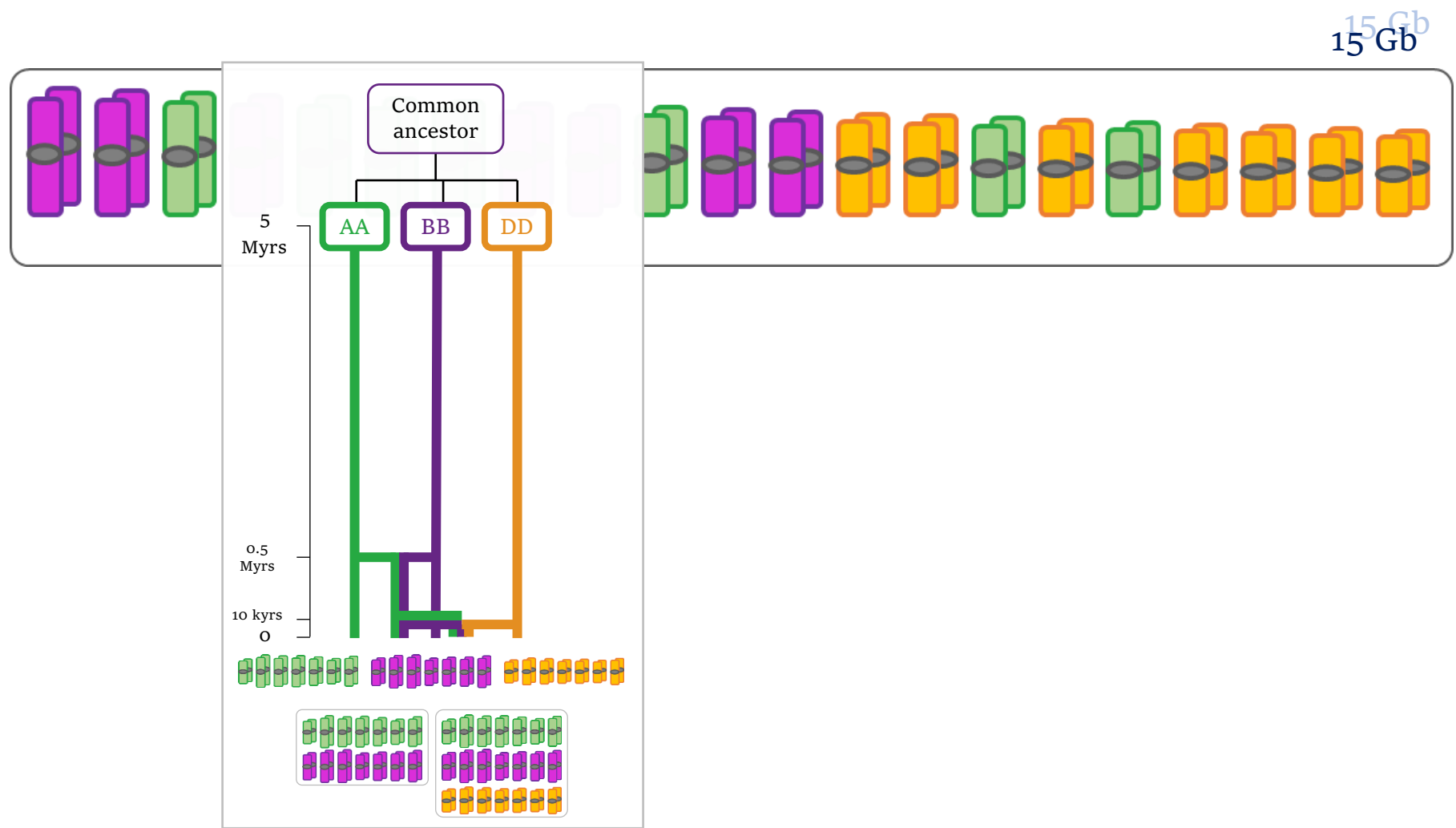
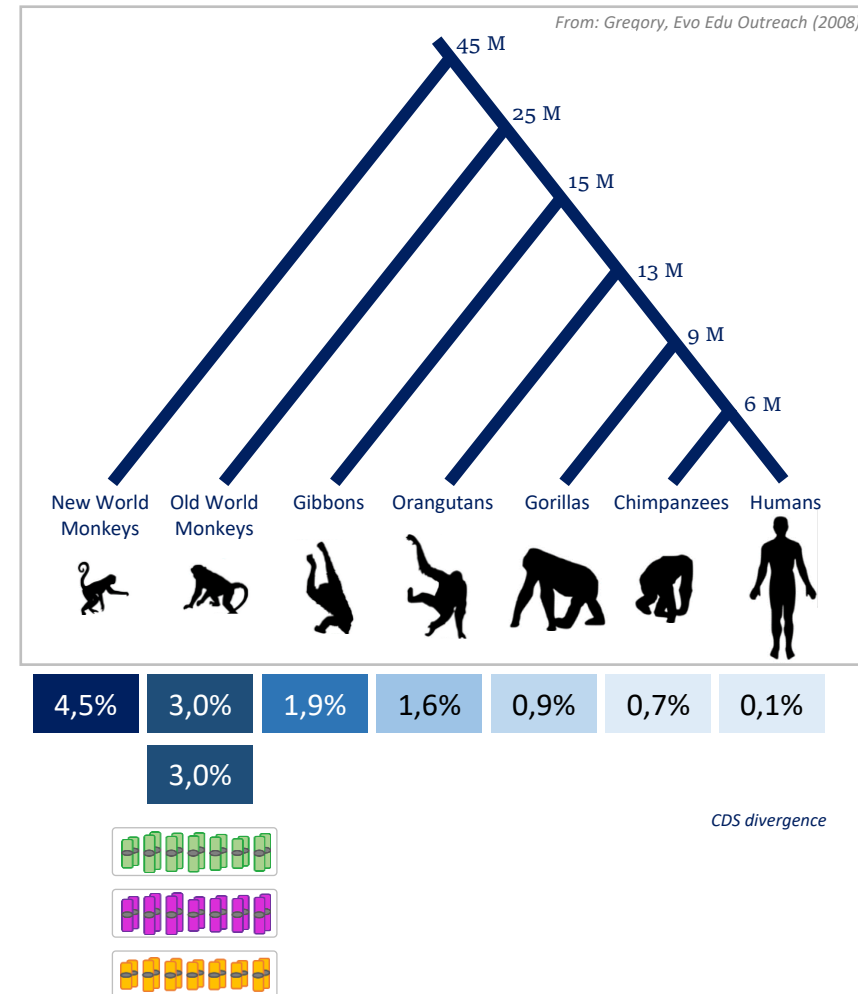
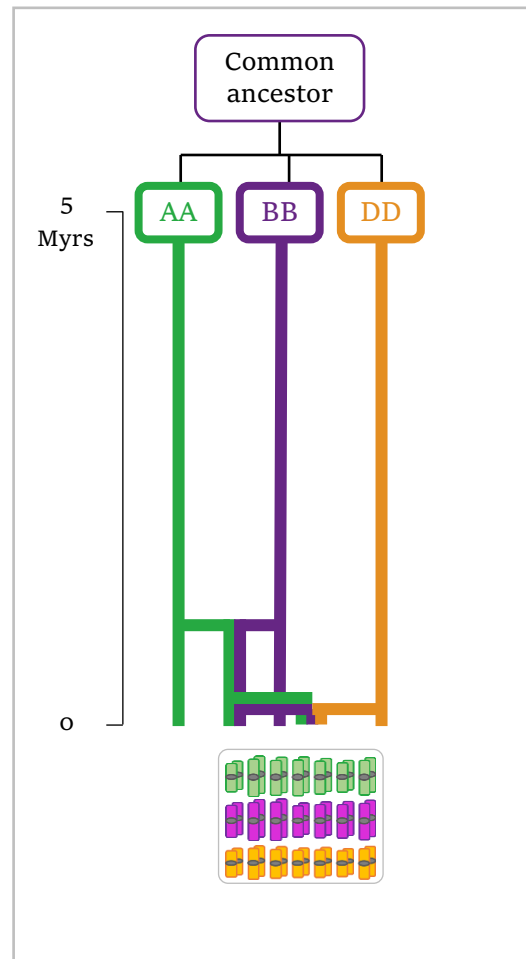


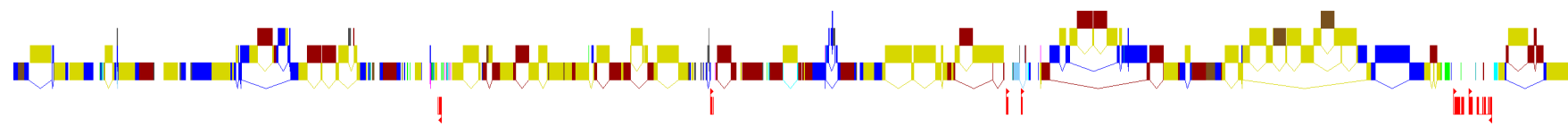
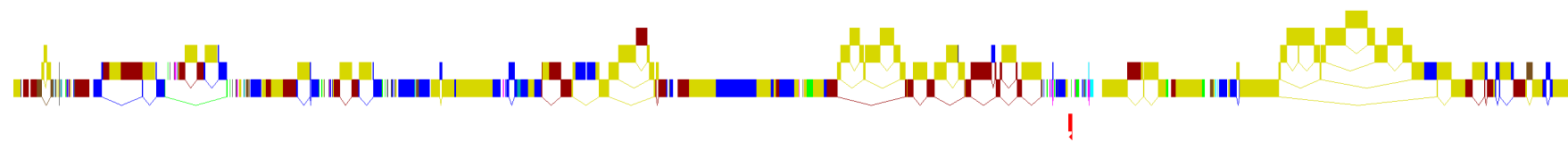
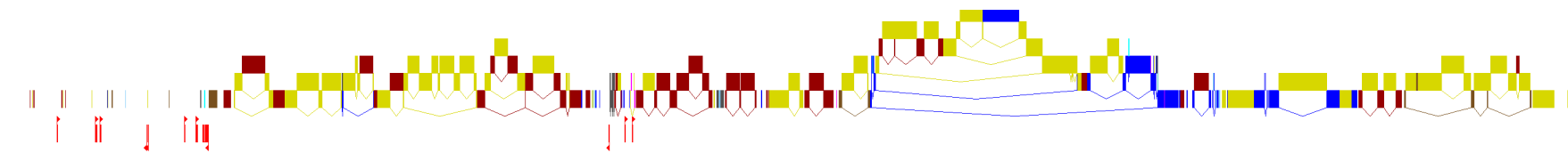
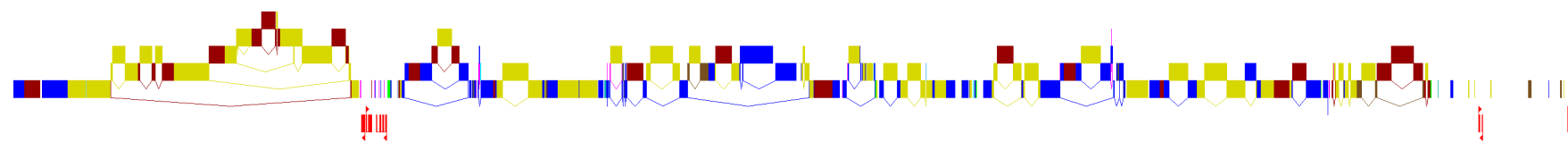
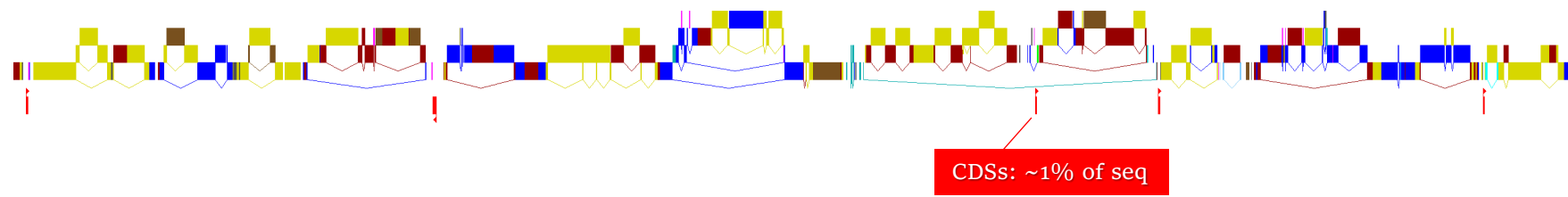
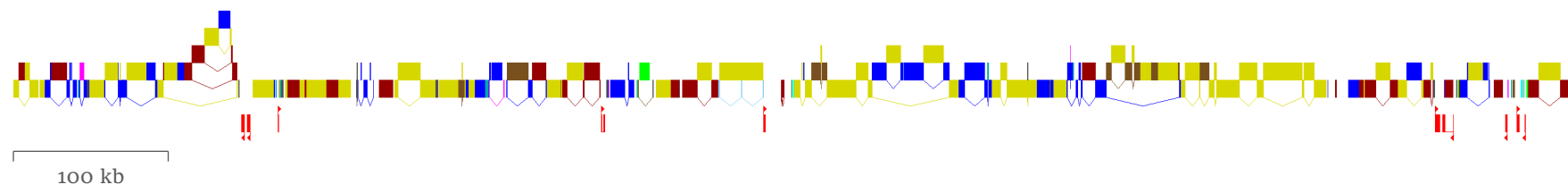
Dynamics of transposable elements in the hexaploid wheat genome

Conference Jacques Monod
Evolutionary and ecological genomics of polyploidy in plants
Sept 15th 2025 – Roscoff

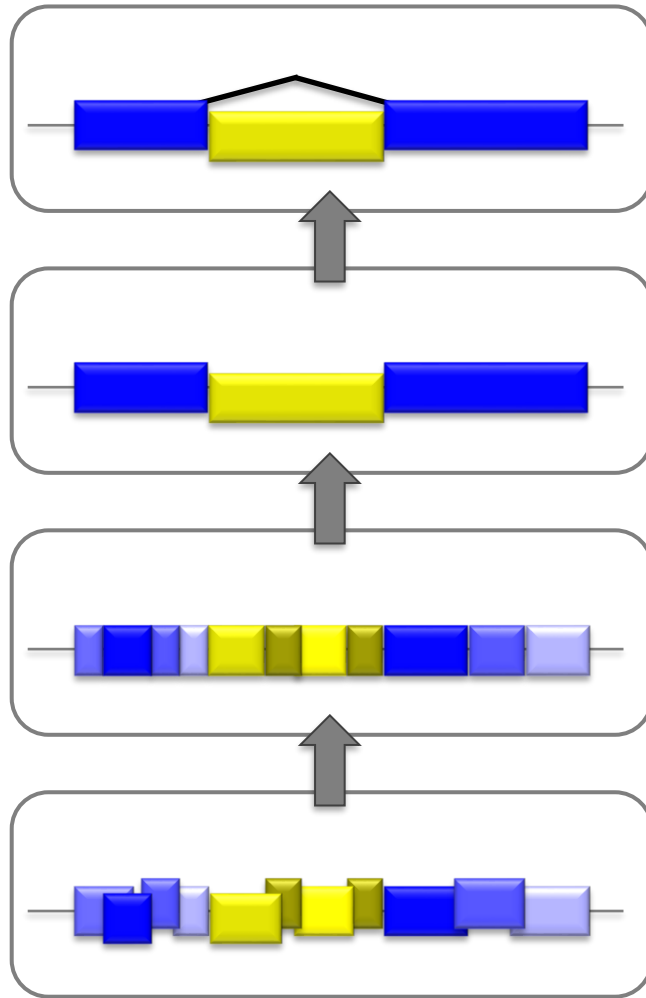








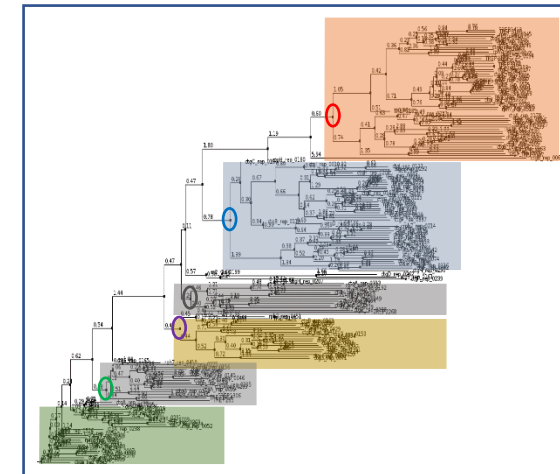
CLARITE



~5000 wheat
TE sequences

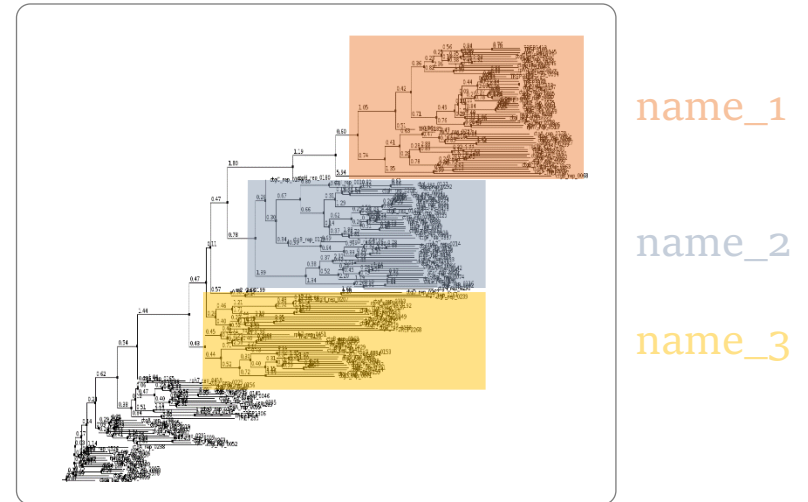
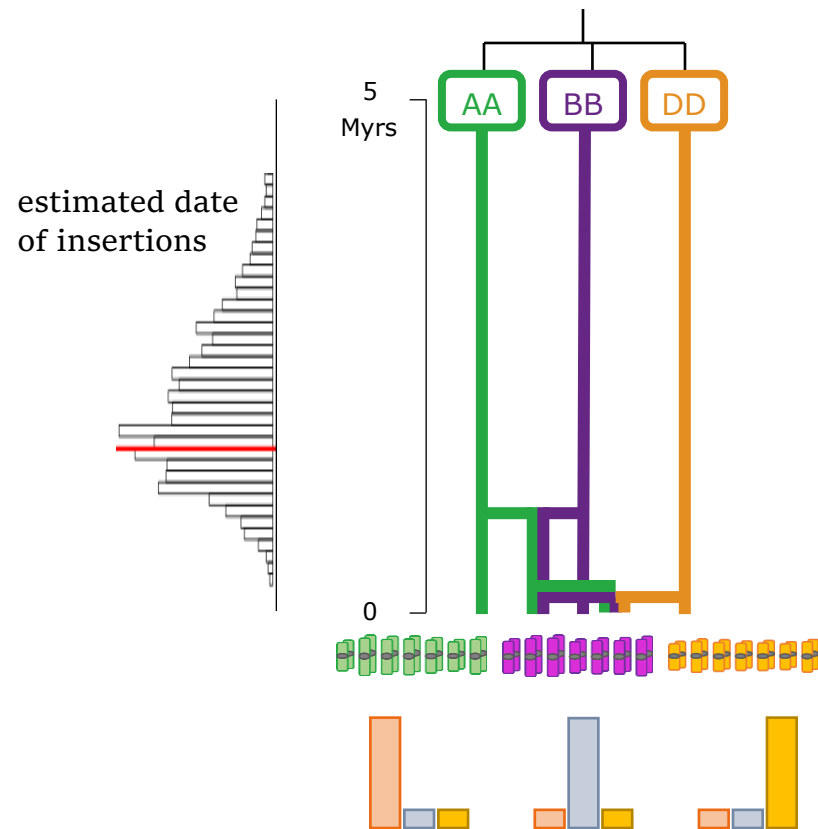


classification

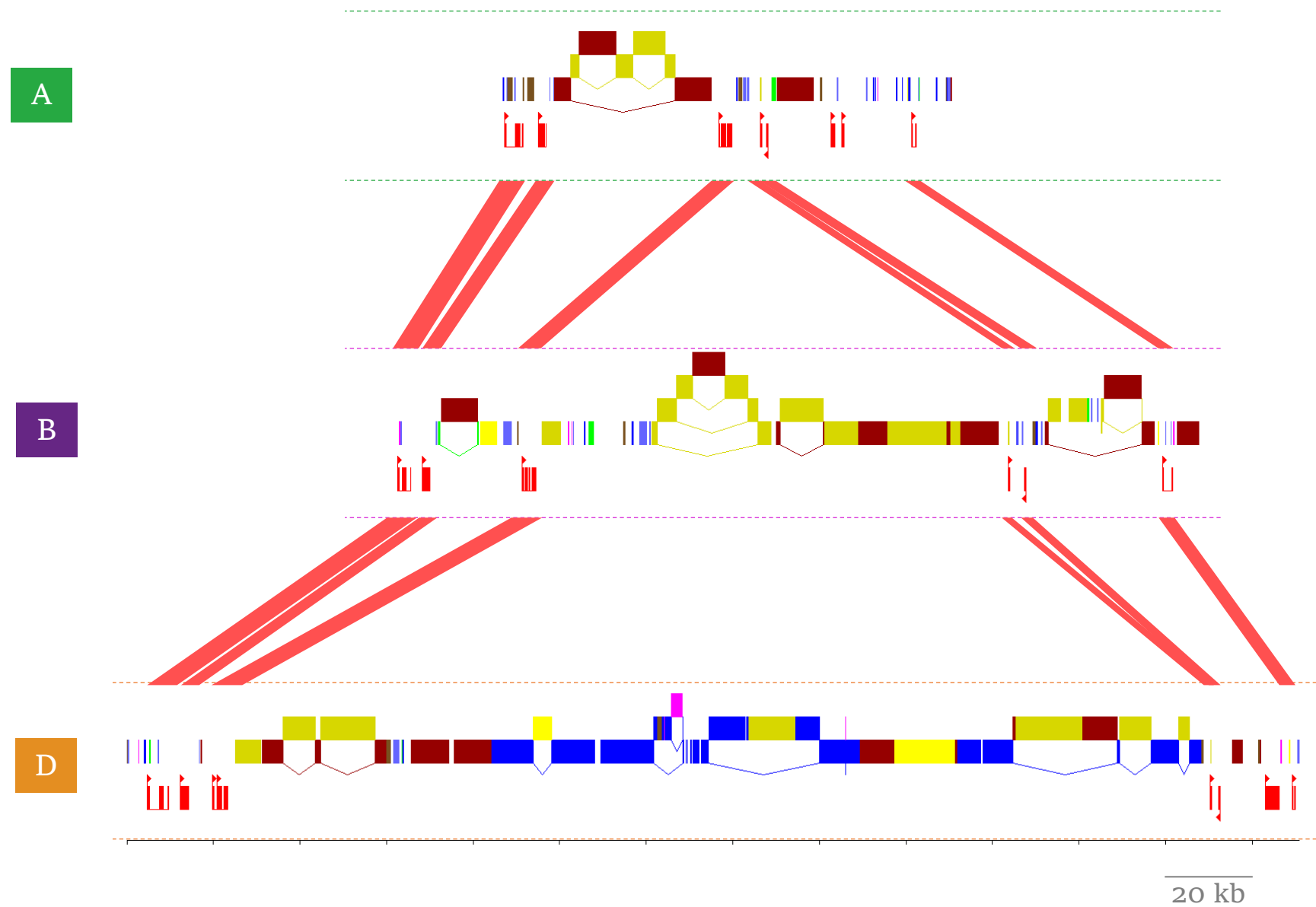


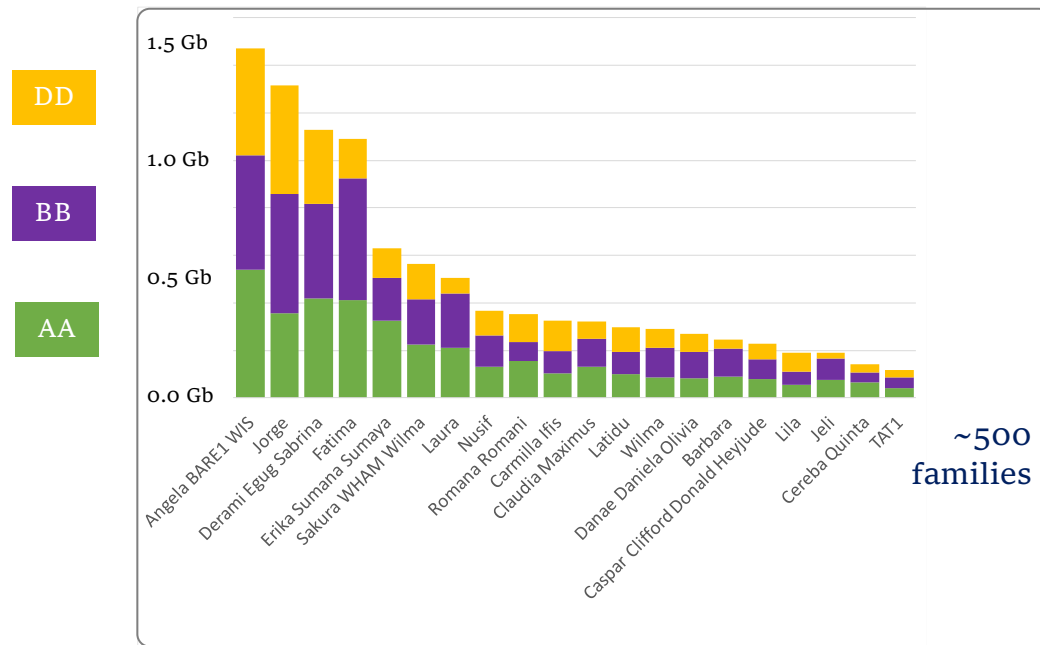
~500 (sub)families
with classification

Importance of TE classification...

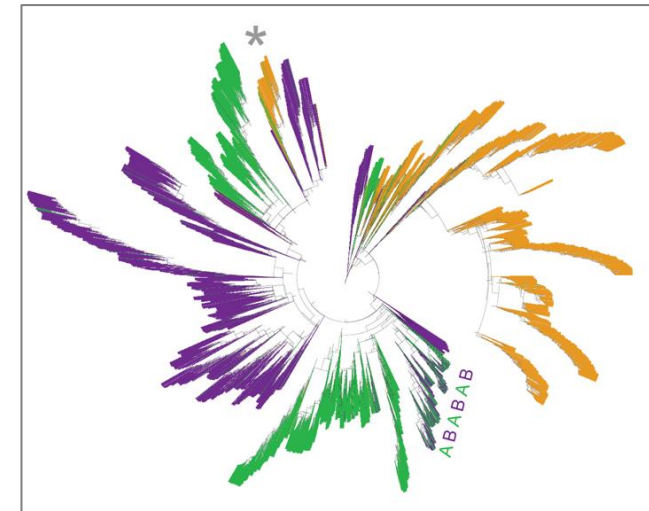


The TE turnover

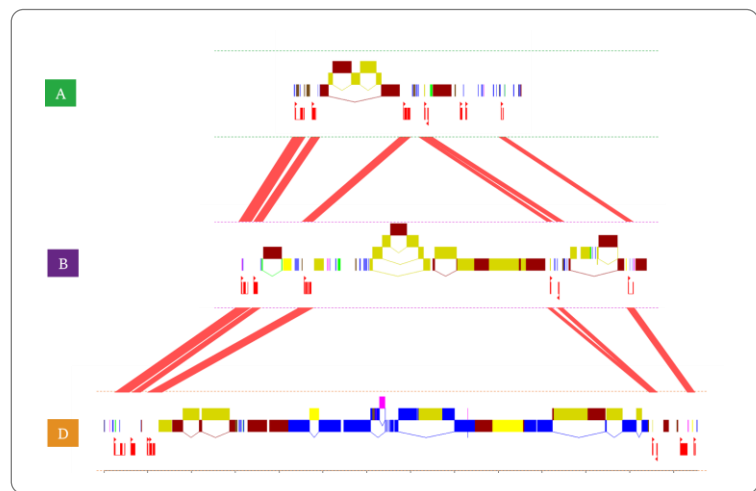
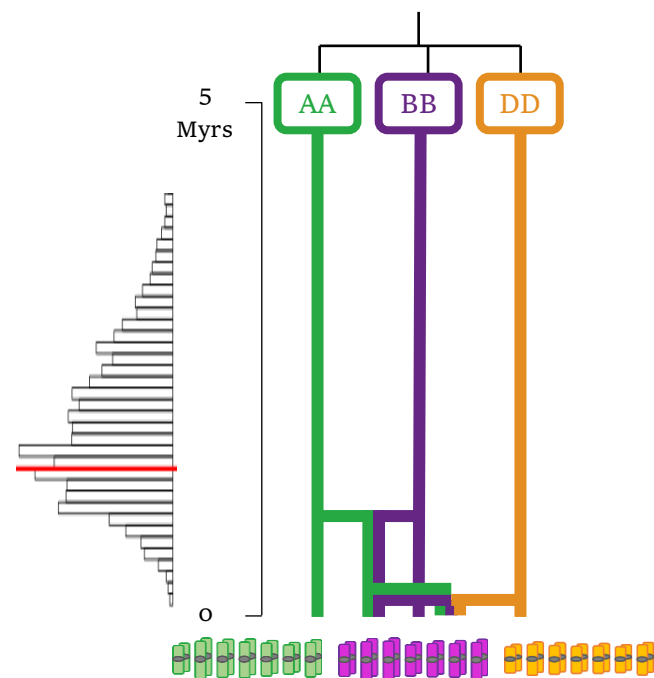




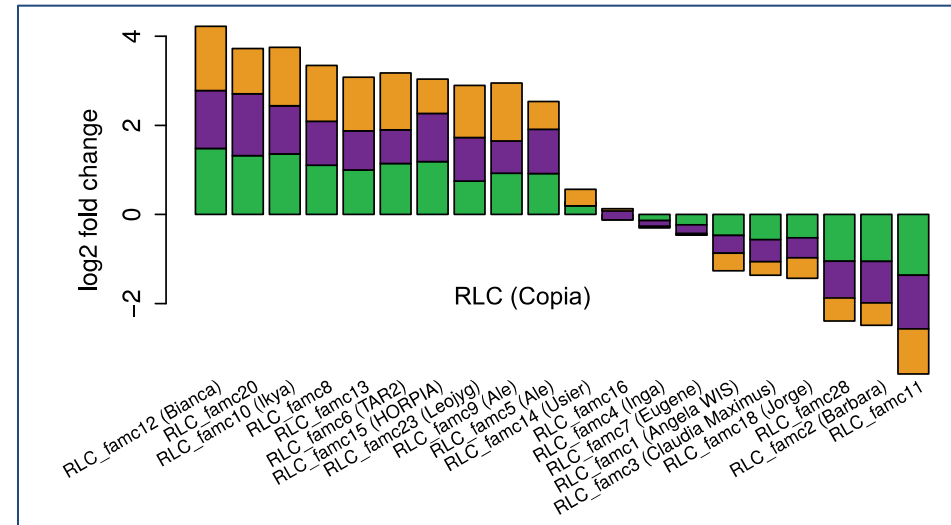
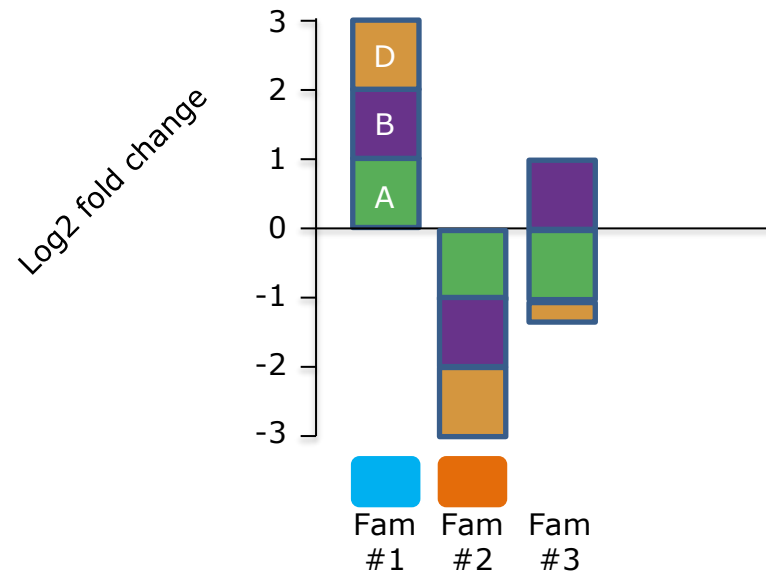
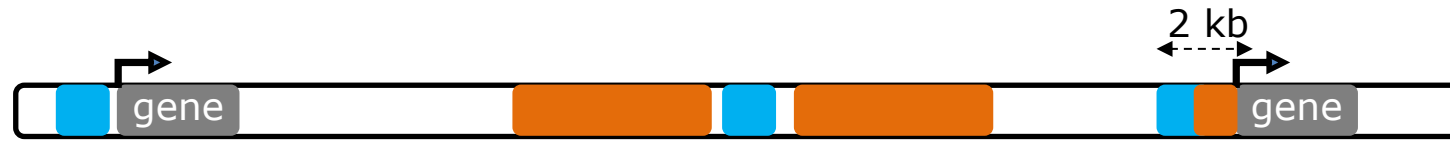
- Abundant families are the same on A-B-D
- o family specific to 1 subgenome
- Similar copy numbers of each family betw A-B-D



- TE inserted in the diploids
- rare insertions in tetraploid AABB

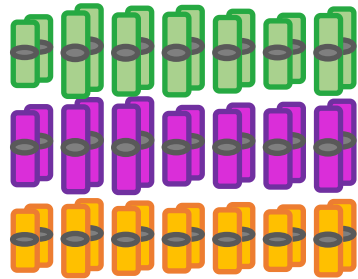
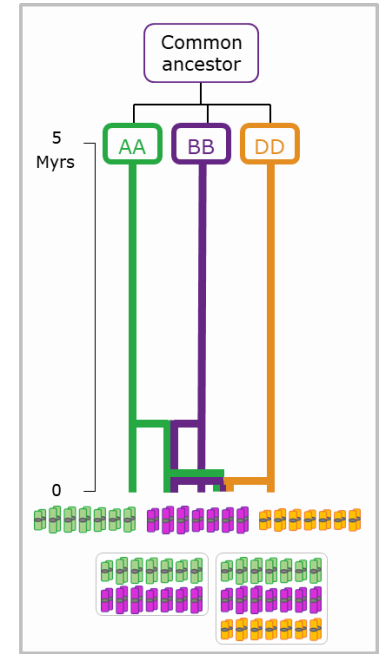


FAMILY	copy number		
	A	B	D
RLG_famc5	50991	45056	36241
RLG_famc6	25026	30352	22616
RLG_famc7	54675	31771	23264
RLG_famc8	18021	13226	14734
RLG_famc9	14913	19001	15596
RLG_famc10	12995	12470	14311
RLG_famc11	29185	18187	22347
RLG_famc12	9009	9459	11960
RLG_famc13	19810	18342	19276
RLG_famc14	6942	7710	9611
RLG_famc15	9645	11705	4173
RLG_famc16	1360	950	1543
RLG_famc17	6439	6835	6153
RLG_famc18	426	533	414
RLG_famc19	6281	6756	8100
RLG_famc20	4724	3747	3393
RLG_famc21	698	1128	860
RLG_famc22	641	712	626
RLG_famc23	834	1025	761
RLG_famc24	553	1860	985
RLG_famc25	1295	3247	1600
RLG_famc26	653	830	511
RLG_famc27	179	935	169
RLG_famc28	21	20	25
RLG_famc29	669	804	686
RLG_famc30	1562	2121	4439
RLG_famc31	260	358	375
RLG_famc32	2001	1951	962
RLG_famc33	654	677	474
RLG_famc34	101	119	133
RLG_famc35	919	1359	708
RLG_famc36	661	1095	339
RLG_famc37	1189	1092	1072
RLG_famc38	18	41	22

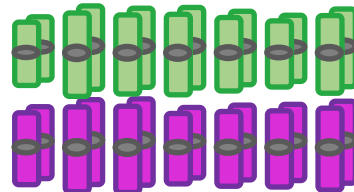


➤ Enrichment in gene promoters is conserved betw A-B-D

❖ Whole Genome Alignments



- *T. aestivum*
- 13 assembled genome seqs



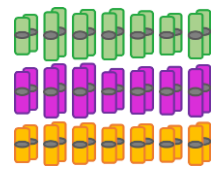
- *T. durum*
- *T. dicoccoides*



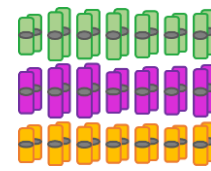
- *T. urartu*



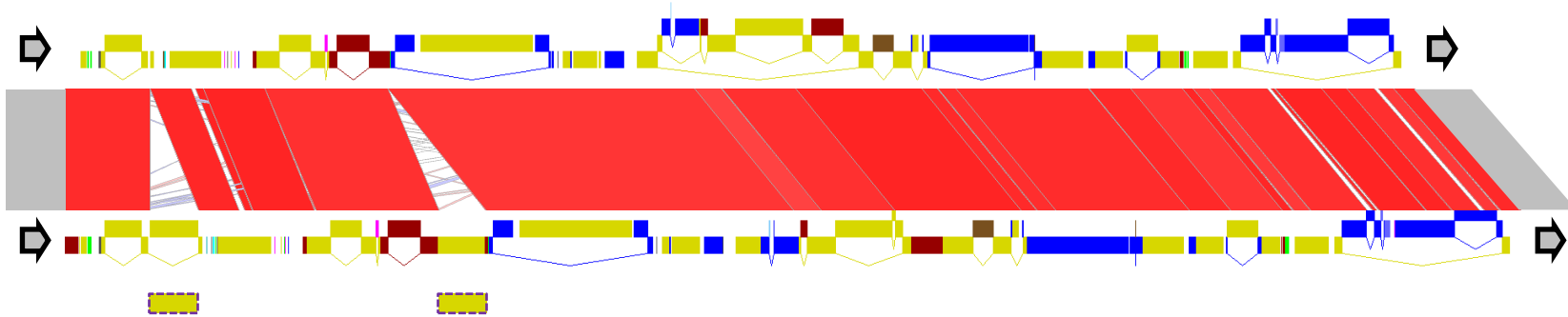
- *Ae. tauschii*



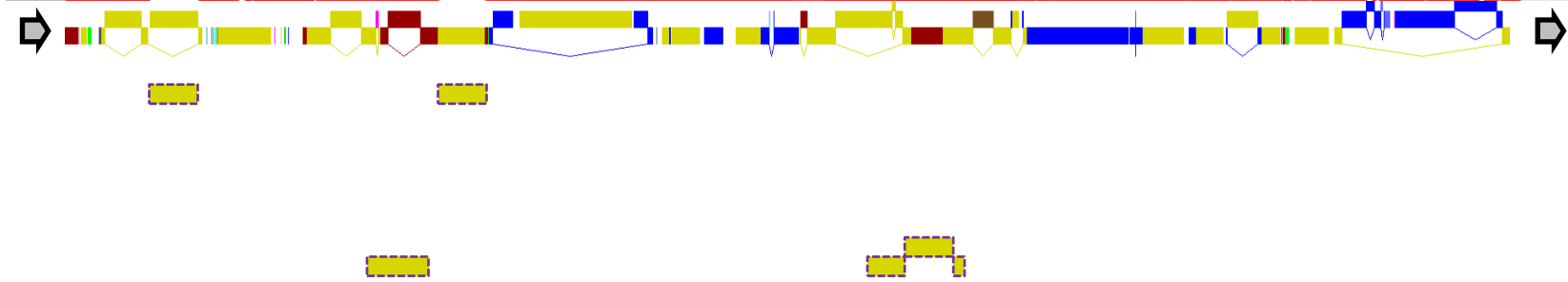
versus



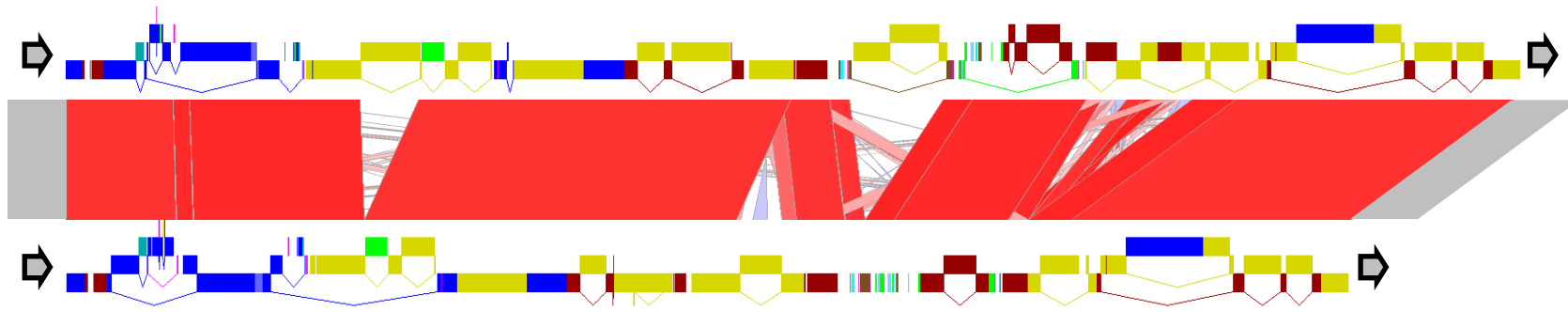
3B



3B

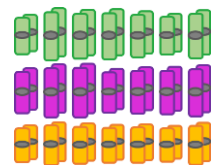


1A

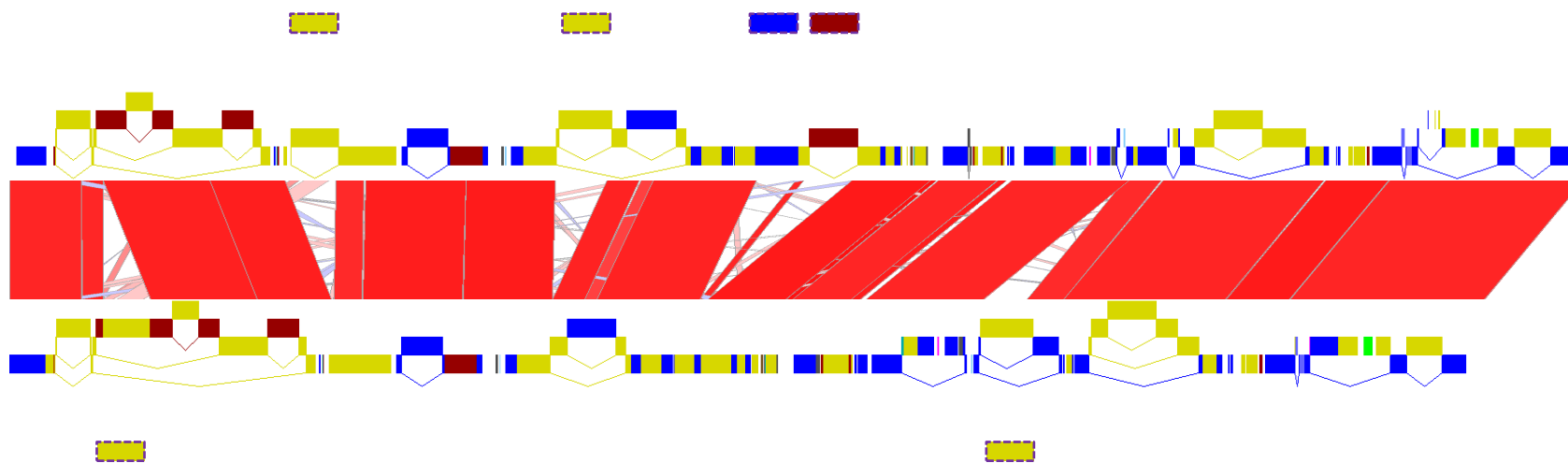
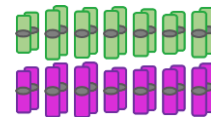


1A

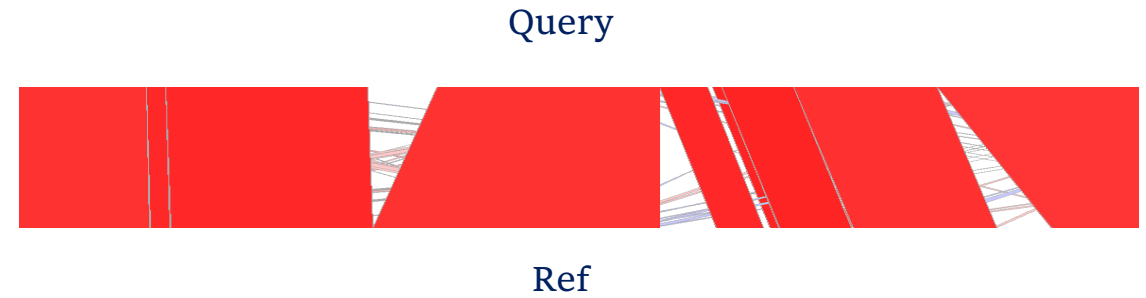




versus



❖ Counting novel insertions
~4,000–13,000 / subgenome

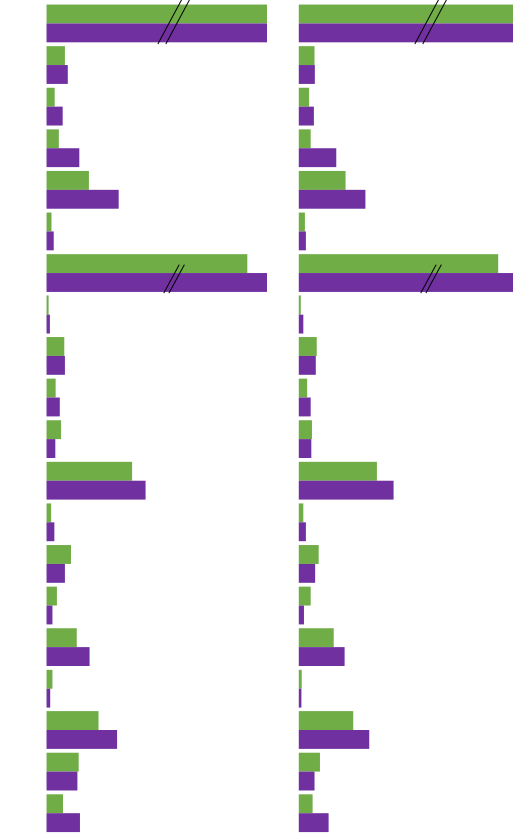
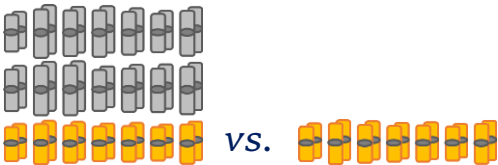
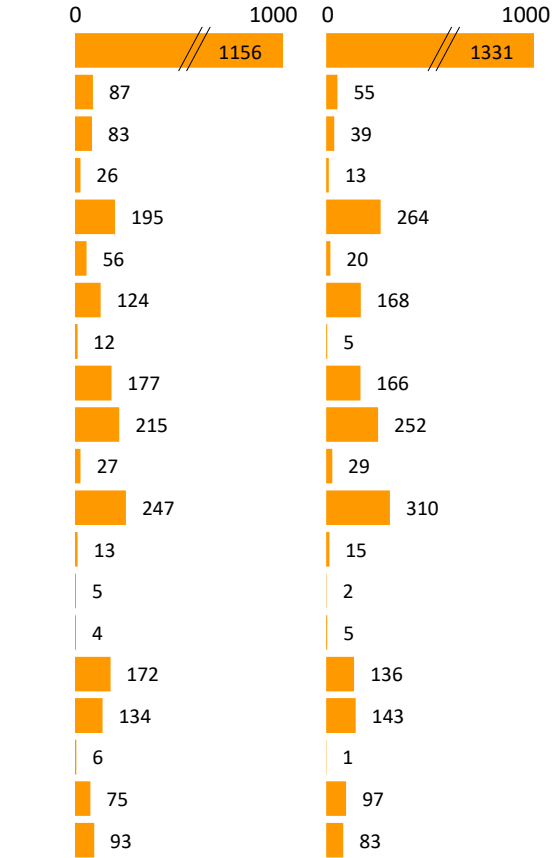
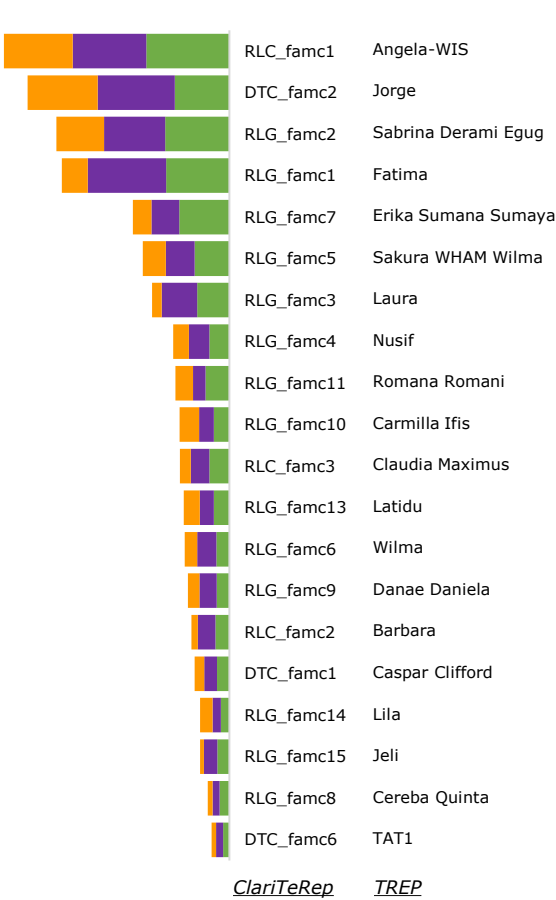


AA		# novel insertions		% variable	
		Query	Ref	Query	Ref
A	<i>T. urartu</i> ^{AA}	8 k	10 k	34	32%
	<i>T. dicoccoides</i> ^{AAB}	11 k	11 k	13	10%
	<i>T. durum</i> ^{AAB}	6 k	6 k	7	7%
	<i>T. aestivum</i> ^{AABDD}	4 k	4 k	6	6%

- No genome contraction/expansion
- No impact of polyploidy on TE activity
- ~ All families were active recently

#novel TE insertions

20 most abundant families



□ Conclusions

- TE turnover without expansion/contraction
- ~All families were active recently
- Constant transposition rate
- No impact of polyploidy
- Transposition not a response to stress...
- ...rather, a highly regulated process
- Equilibrium model of evolution (as opposed to the TE-burst model)
- Structural function of TEs under constraint?

❖ Acknowledgments

❖ GDEC

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