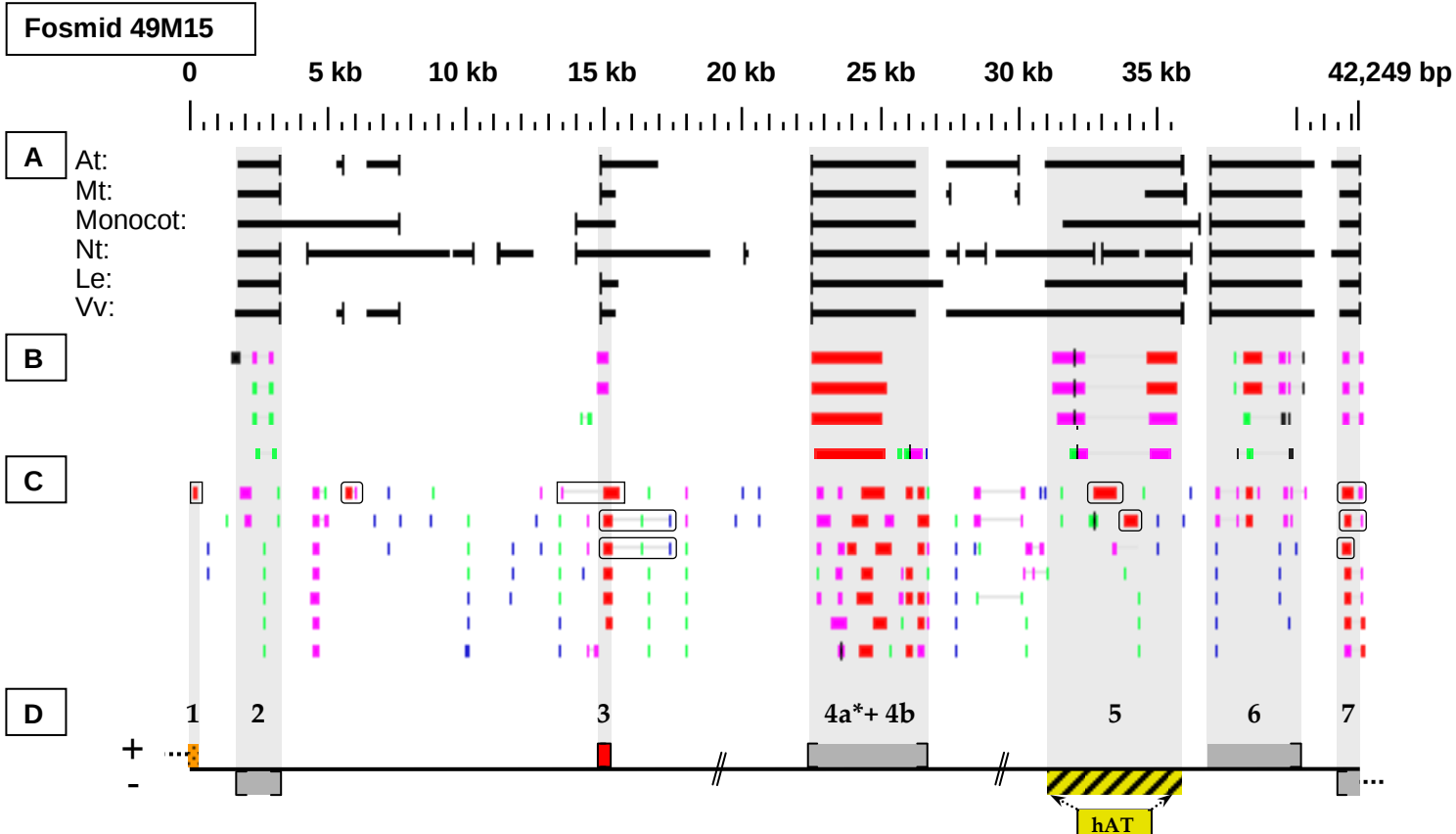




E

Motif	TC	AGT	TC	AT	CT	AG	AG	CT	CT	TC	TA	TA	TG	AT	AT	TA	AT	TC	CTT
Repeat No.	5	5	24	5	7	26	6	24	12	11	7	9	23	5	11	6	8	29	5
SSR start	1433	2353	8604	9271	10766	12563	14796	16459	16542	25286	28274	29918	30353	30707	30814	35809	36293	39658	41112

Fosmid 49M15= EU024859 (gLRR) 42,209 bp									
Putative gene location					Blastx Results				
Feature	Strand	Putative start	Putative stop	Putative identity	Feature	Strand	Putative start	Putative stop	Putative identity
1	Plus	excluded	excluded	na (EST = regulator of chromosome condensation (RCC1) family protein / UVB-resistance	4b	Plus	nd	26611	XF1 (SQUALENE EPOXIDASE 1); oxidoreductase
2	Minus	3240	1668	DUO1 (DUO POLLEN 1); DNA binding / transcription factor	CONTIG BREAK		29635	29735	
3	Plus	14811	15269	unknown protein	5	Minus	nd	nd	possible transposase
CONTIG BREAK		19100	19200		6	Plus	36823(?)	40136	hydrolase, alpha/beta fold family protein
4a*	Plus	22399	25590(?)	disease resistance family protein	7	Minus	excluded	41485	ACD1-LIKE; electron carrier