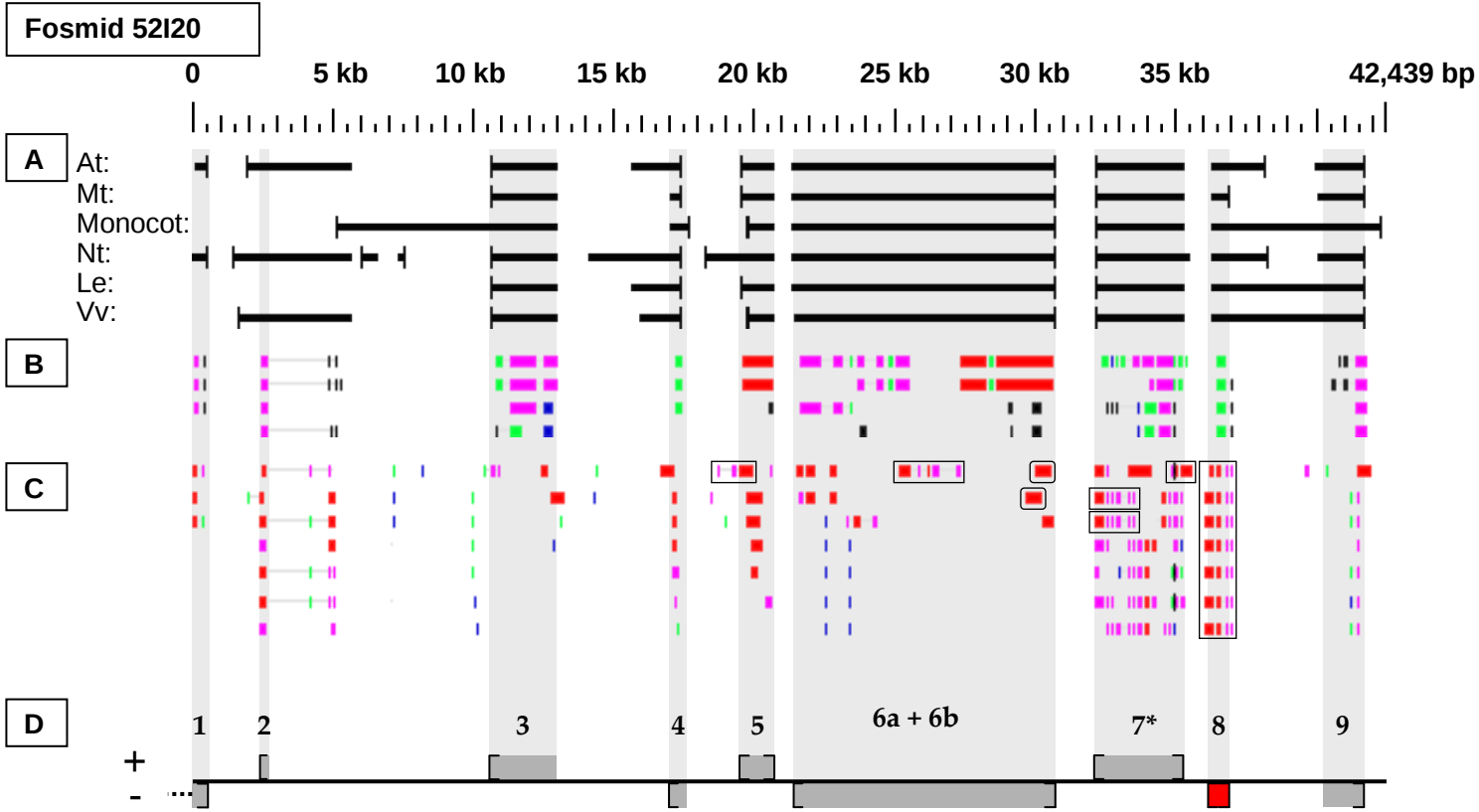




E

Motif	CT	GA	AG	AG	GA	CT	AAG					AAT						ATG	AG
Repeat No.	8	28	5	5	5	38	5					5						6	5
SSR start	8171	9982	10268	10654	12992	14369	14637					25629						39844	41115

Fosmid 52I20= EU024863 (GBSS-I) 42,439 bp

Putative gene location					Blastx Results					Putative gene location					Blastx Results				
Feature	Strand	Putative start	Putative stop	Putative identity						Feature	Strand	Putative start	Putative stop	Putative identity					
1	Minus	461	excluded	oxidoreductase						6a	Minus	nd	21408	DNA binding / binding / protein binding / zinc ion binding					
2	Plus	2418	nd	AGL42 (AGAMOUS LIKE 42); transcription factor						6b	Minus	30583 or 30622	nd	unknown protein					
3	Plus	10603	12940(?)	unknown protein						7*	Plus	32121	35247	granule-bound starch synthase I (GBSS-I)					
4	Minus	17552(?)	17046	unknown protein						8	Minus	36834	36233	60S acidic ribosomal protein P1 (RPP1C)					
5	Plus	19451	20635	hydroxyproline-rich glycoprotein family protein						9	Minus	41612	nd	RNA recognition motif (RRM)-containing protein					