

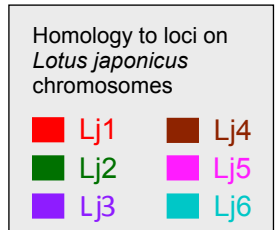
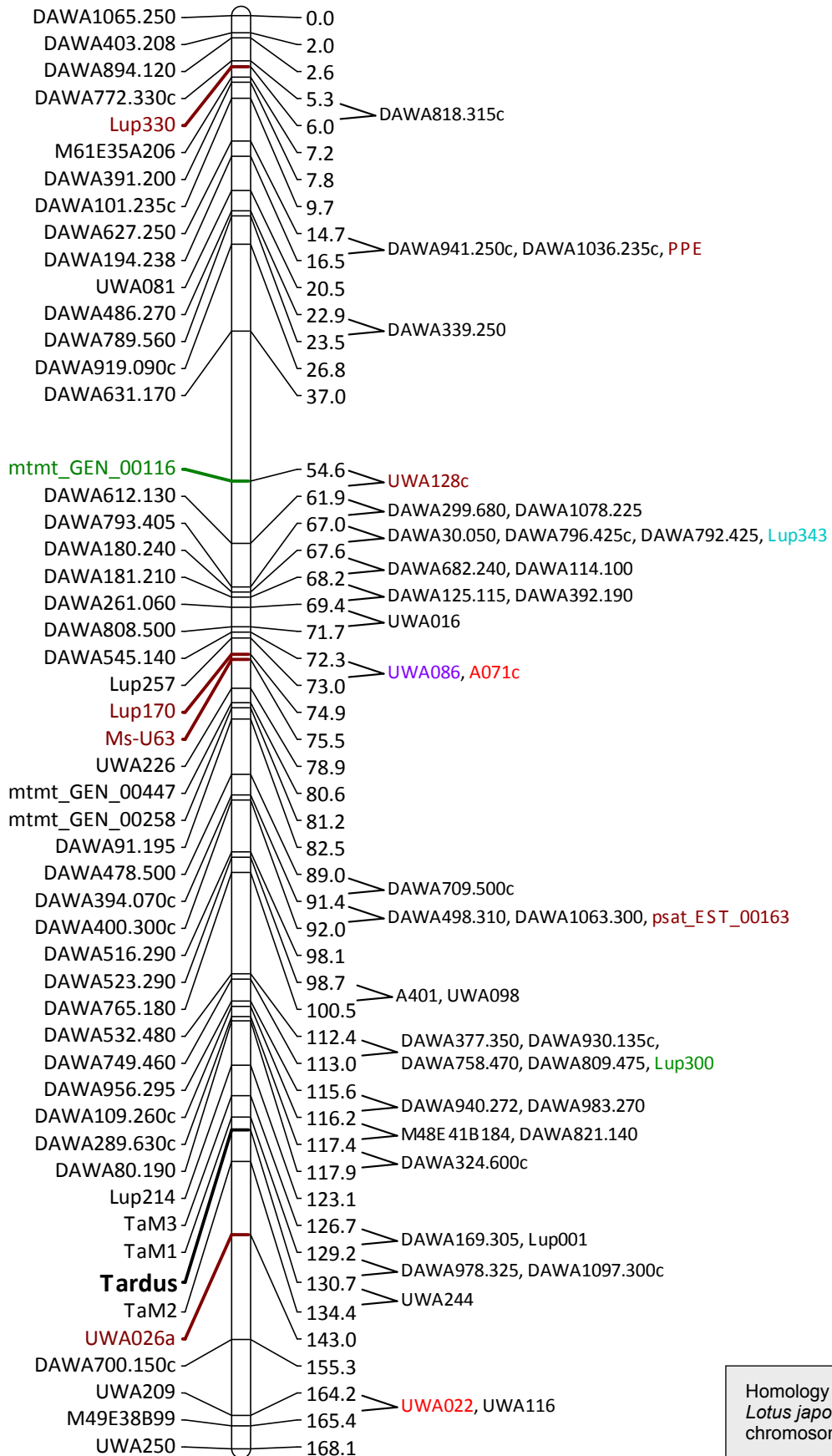
Supplementary Legends

Supplementary Table S1. Simple sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) primer combinations giving rise to microsatellite-anchored fragment length polymorphism (MFLP) markers in *Lupinus angustifolius*.

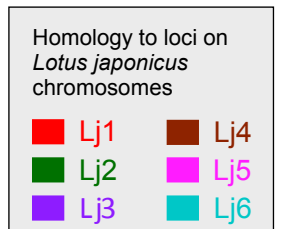
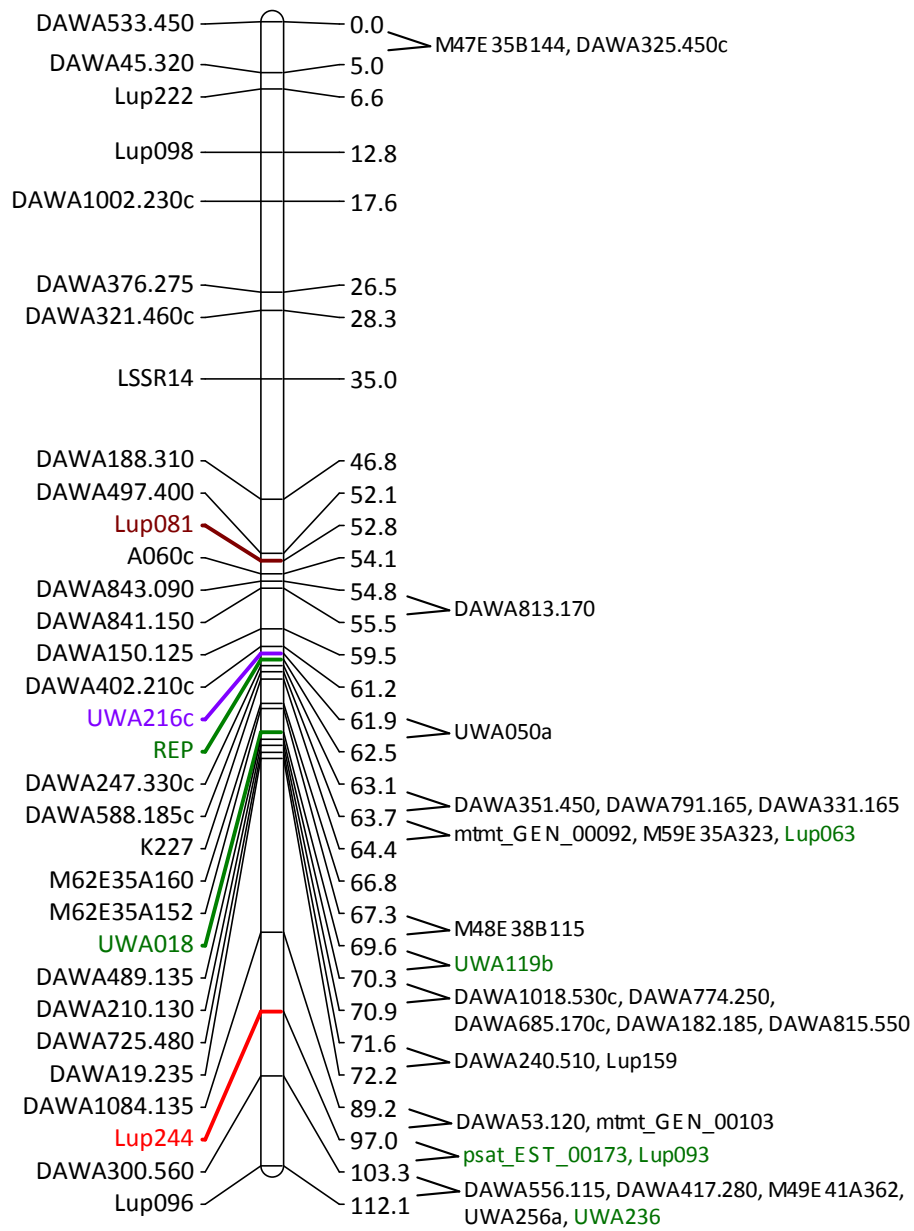
Supplementary Table S2. Data file containing linkage group locations of 1090 mapped loci and 12 unlinked markers, details of BLASTn correspondences in *Lotus japonicus* chromosomes (Lj1 to Lj6), marker assay details and genotyping in recombinant inbred lines (A018 to A135).

Supplementary Fig. S1. A dense genetic linkage map of *Lupinus angustifolius* comprising 1090 loci in 20 linkage groups (NLL-01 to NLL-20) and three small clusters (Cluster-1 to Cluster-3). Loci on the left of each linkage group are 'framework' markers used to construct the linkage group. Loci on the right of each linkage group are 'attached' markers whose approximate location between flanking markers are shown. Locus positions are in Kosambi centiMorgans. Major gene trait loci are shown in bold text. Loci with significant correspondences in the *Lotus japonicus* genome are coloured according to the chromosome containing the most significant BLASTn correspondence value (see colour key).

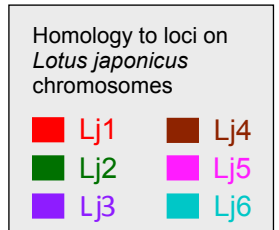
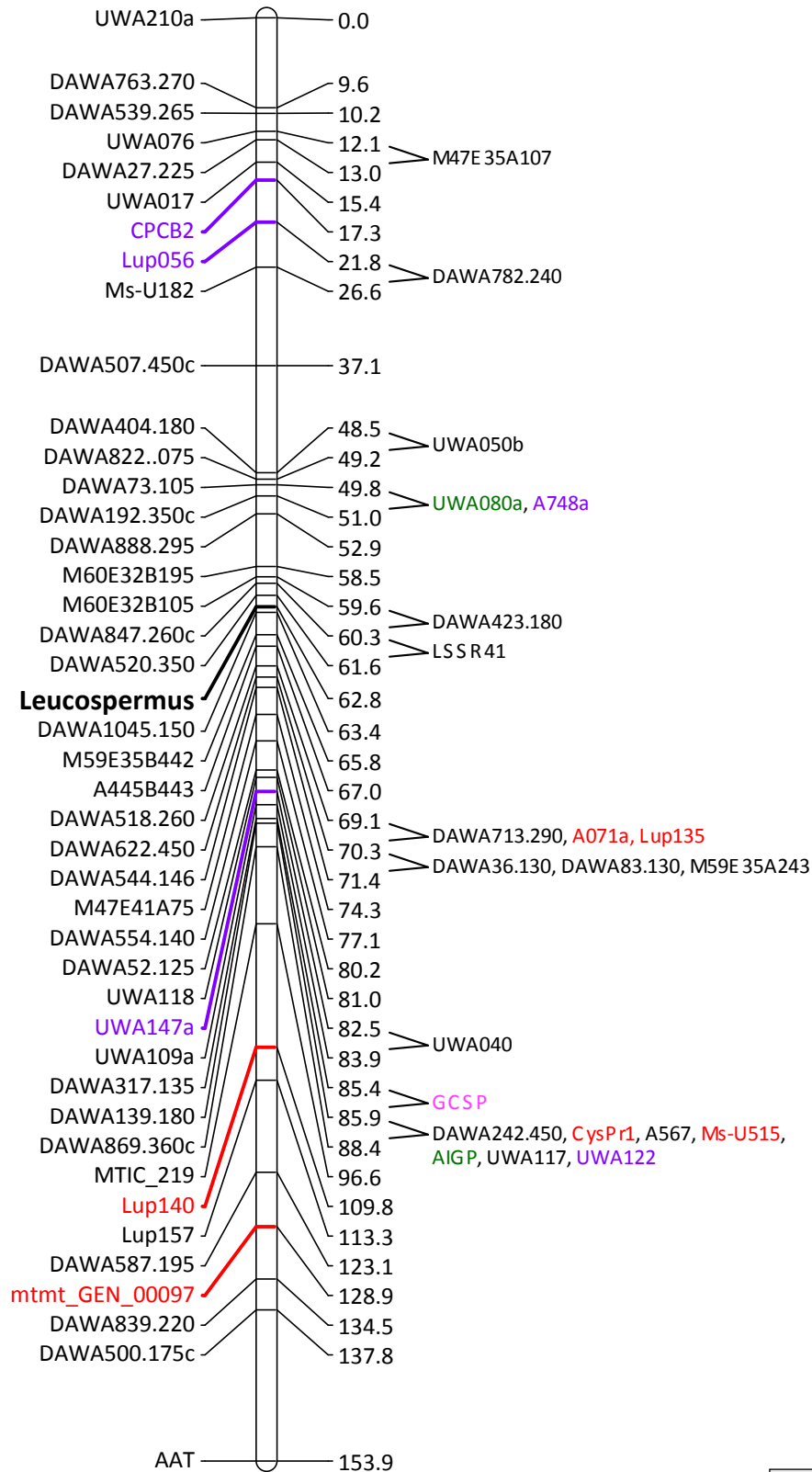
NLL-01



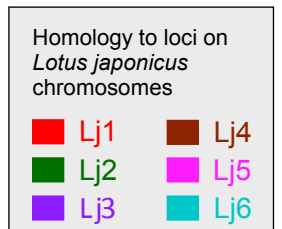
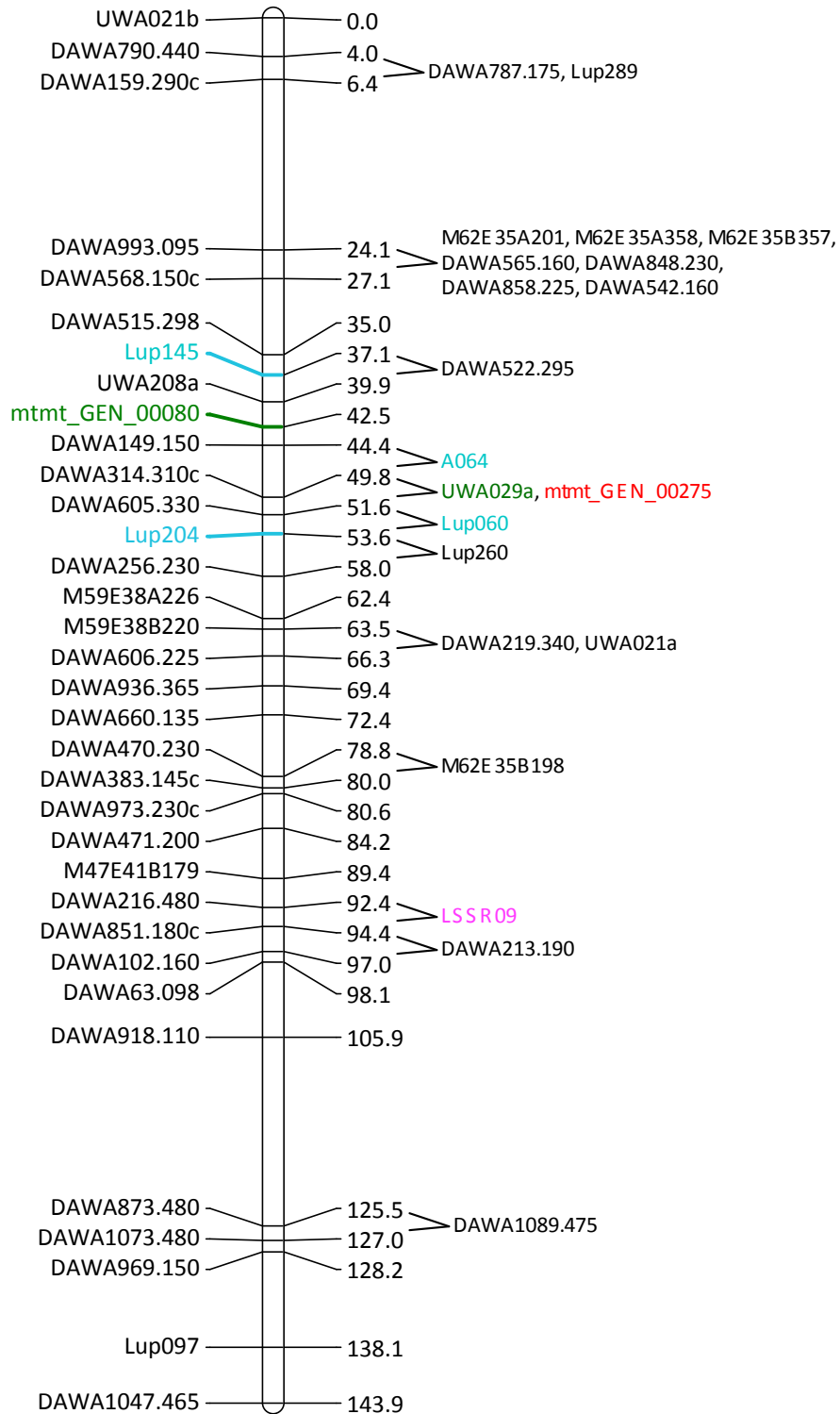
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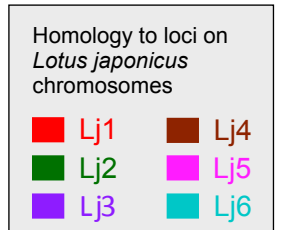
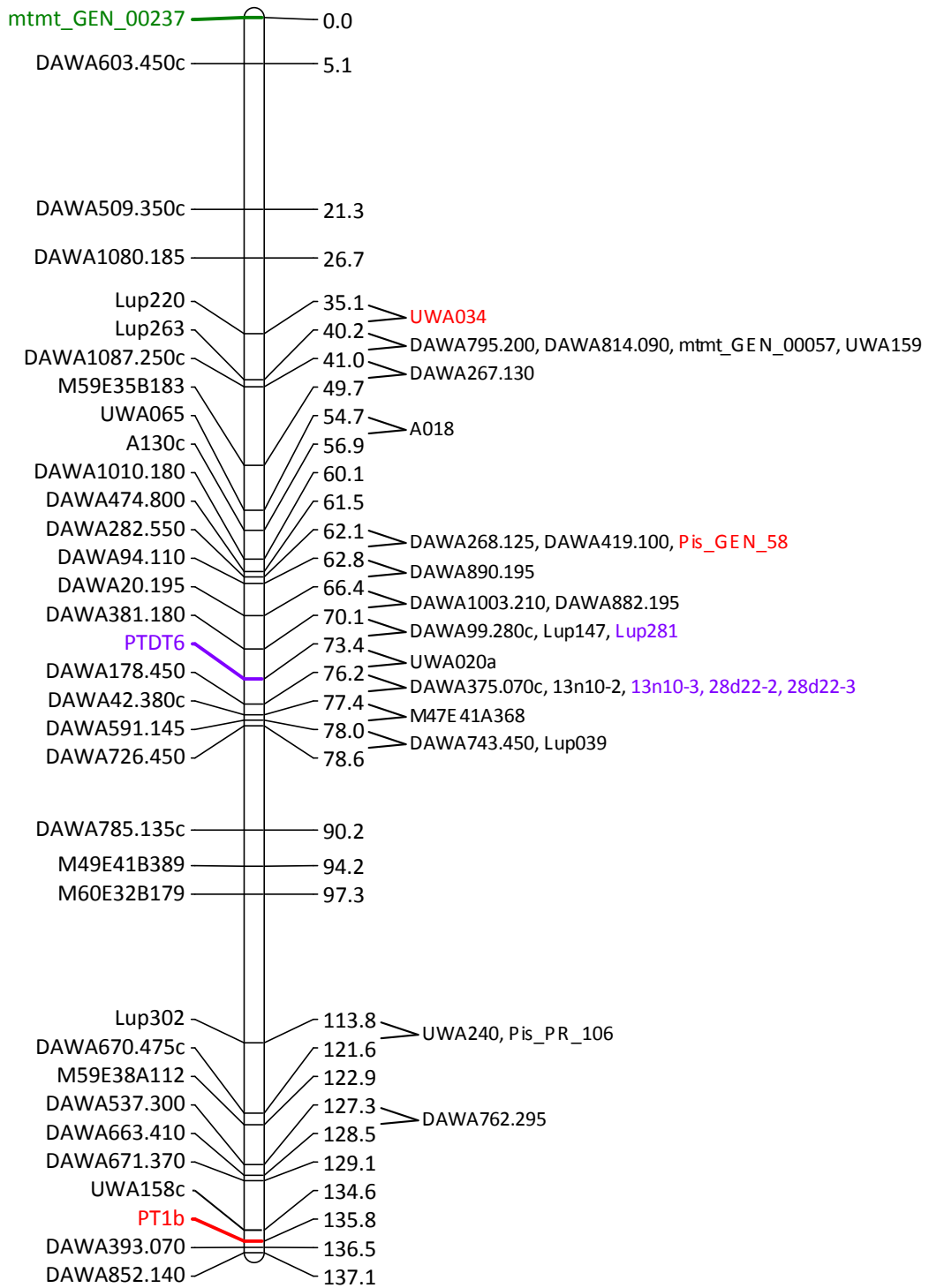
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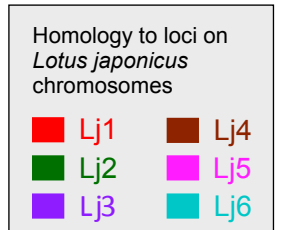
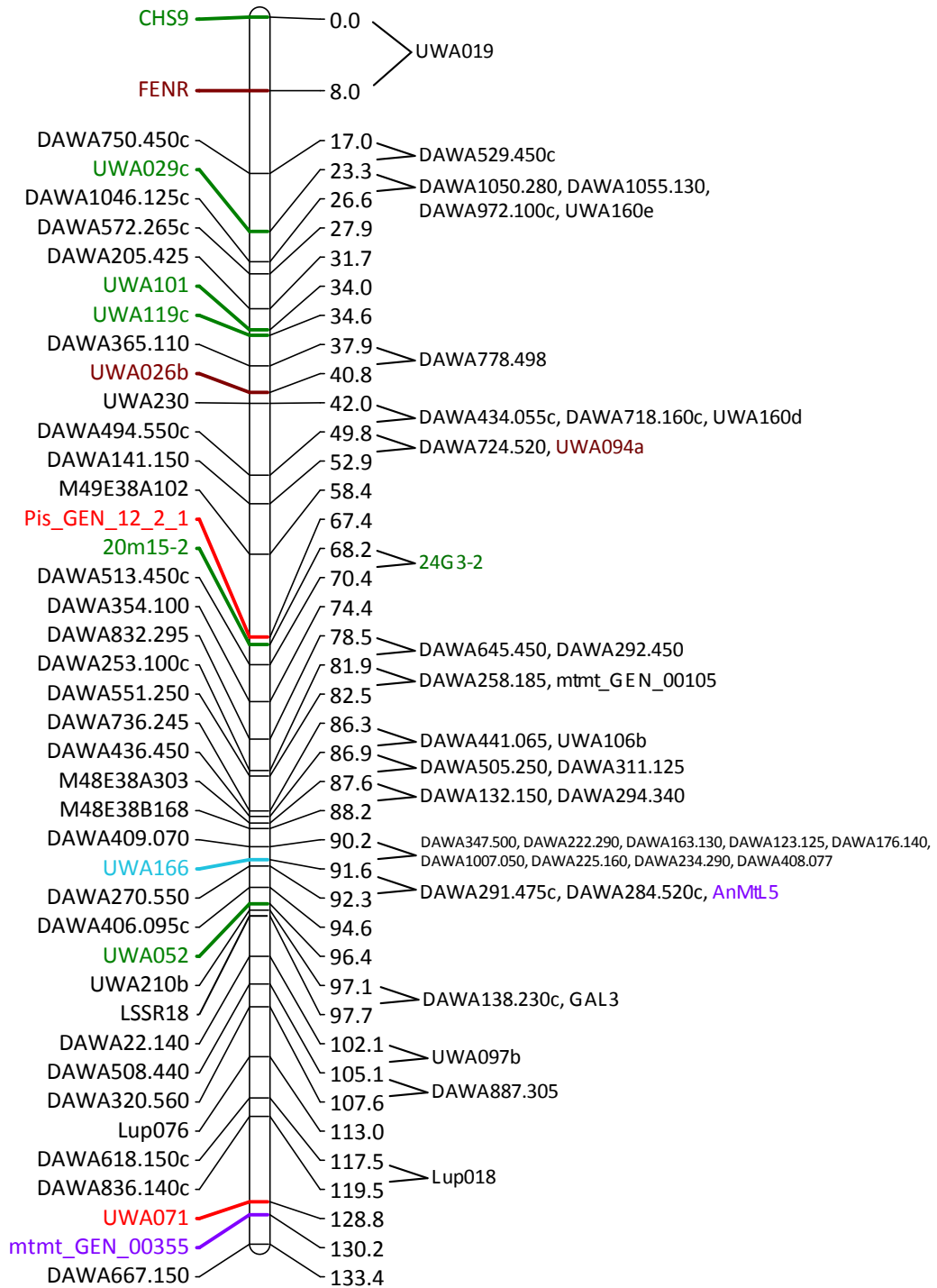
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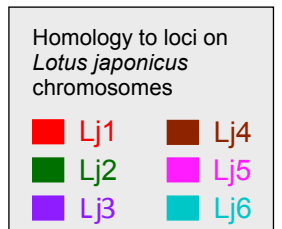
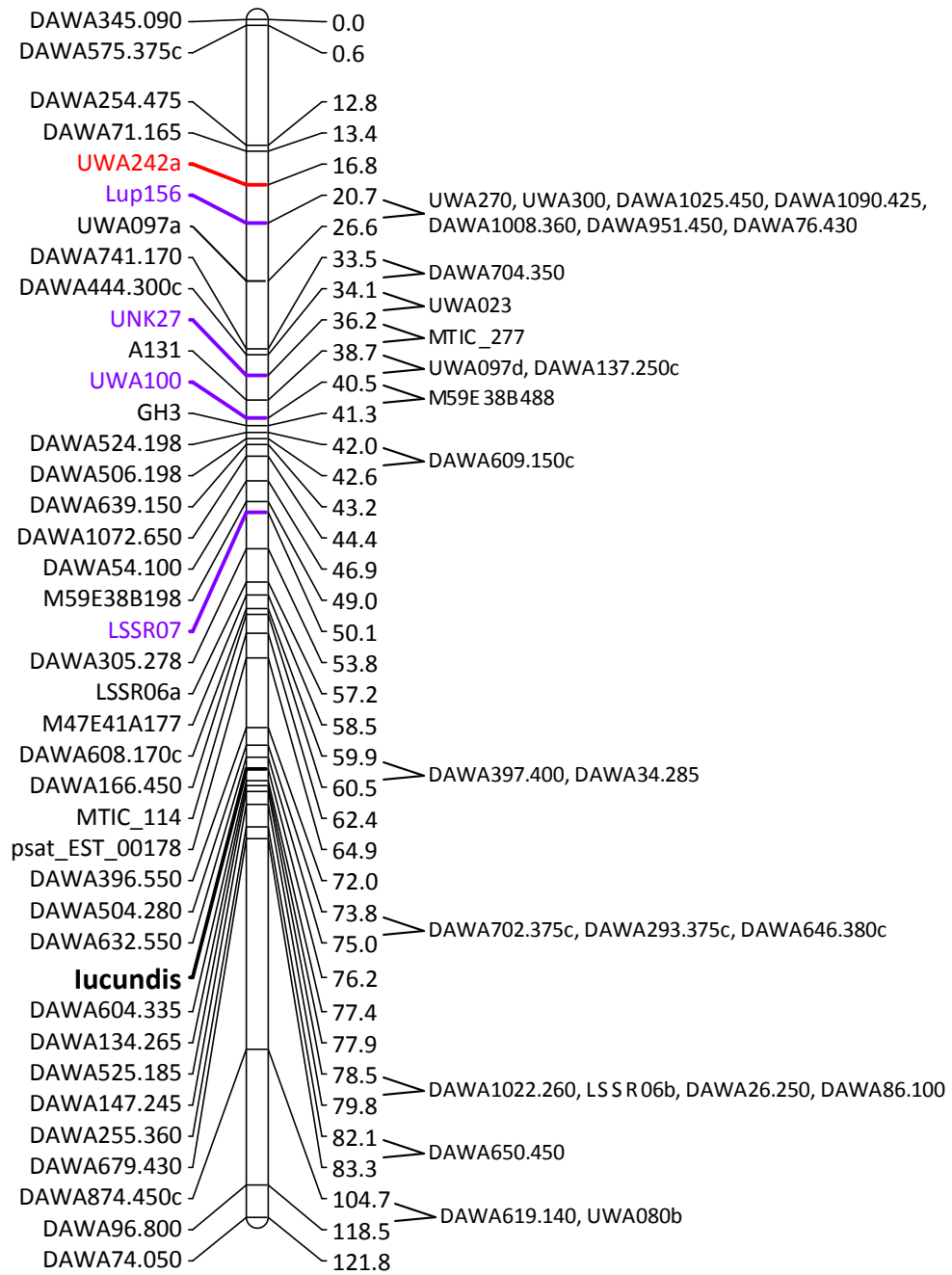
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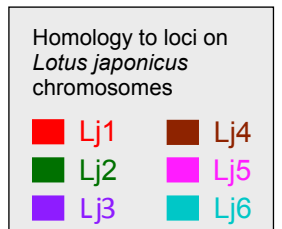
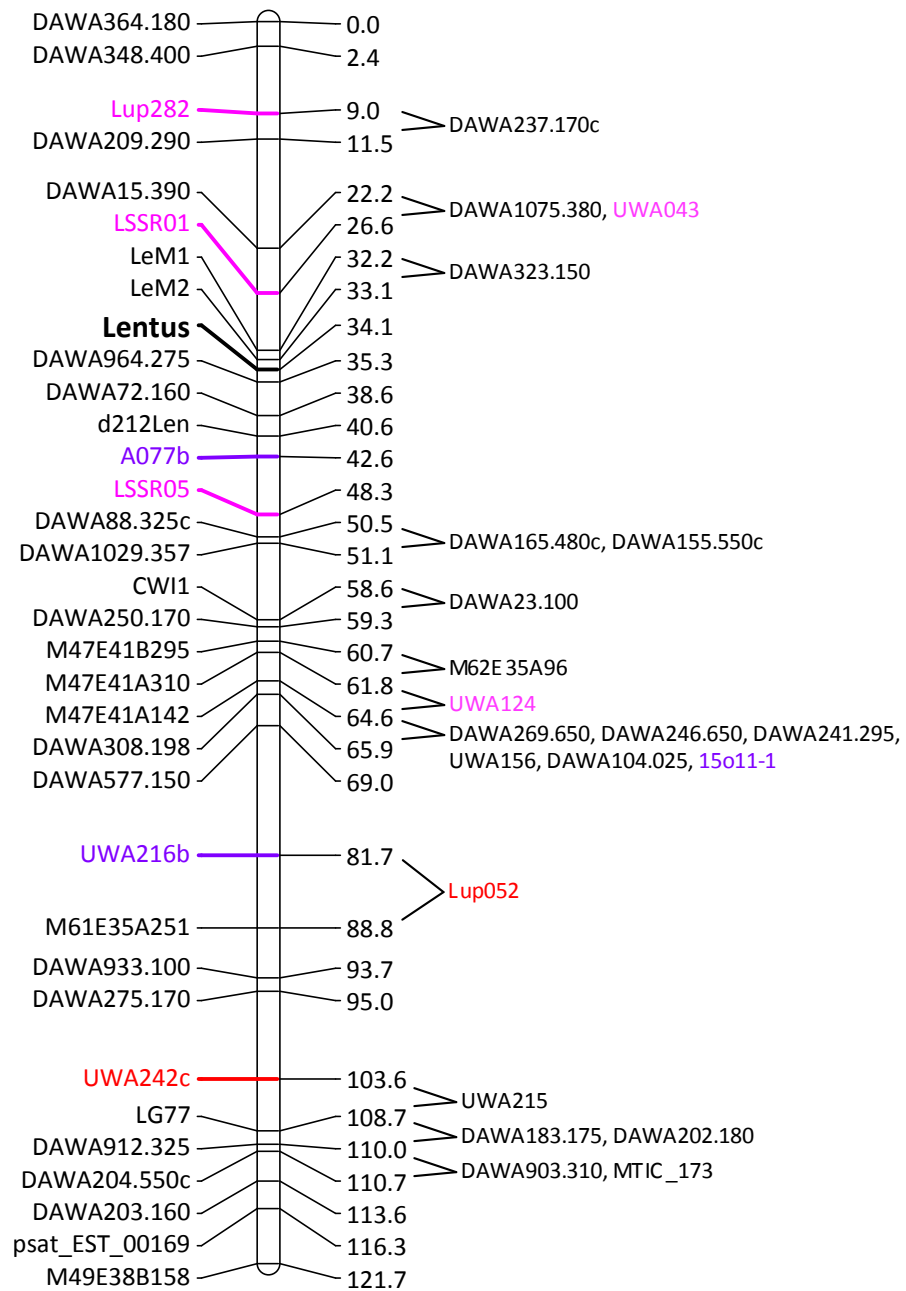
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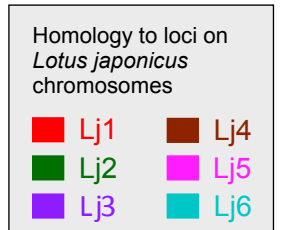
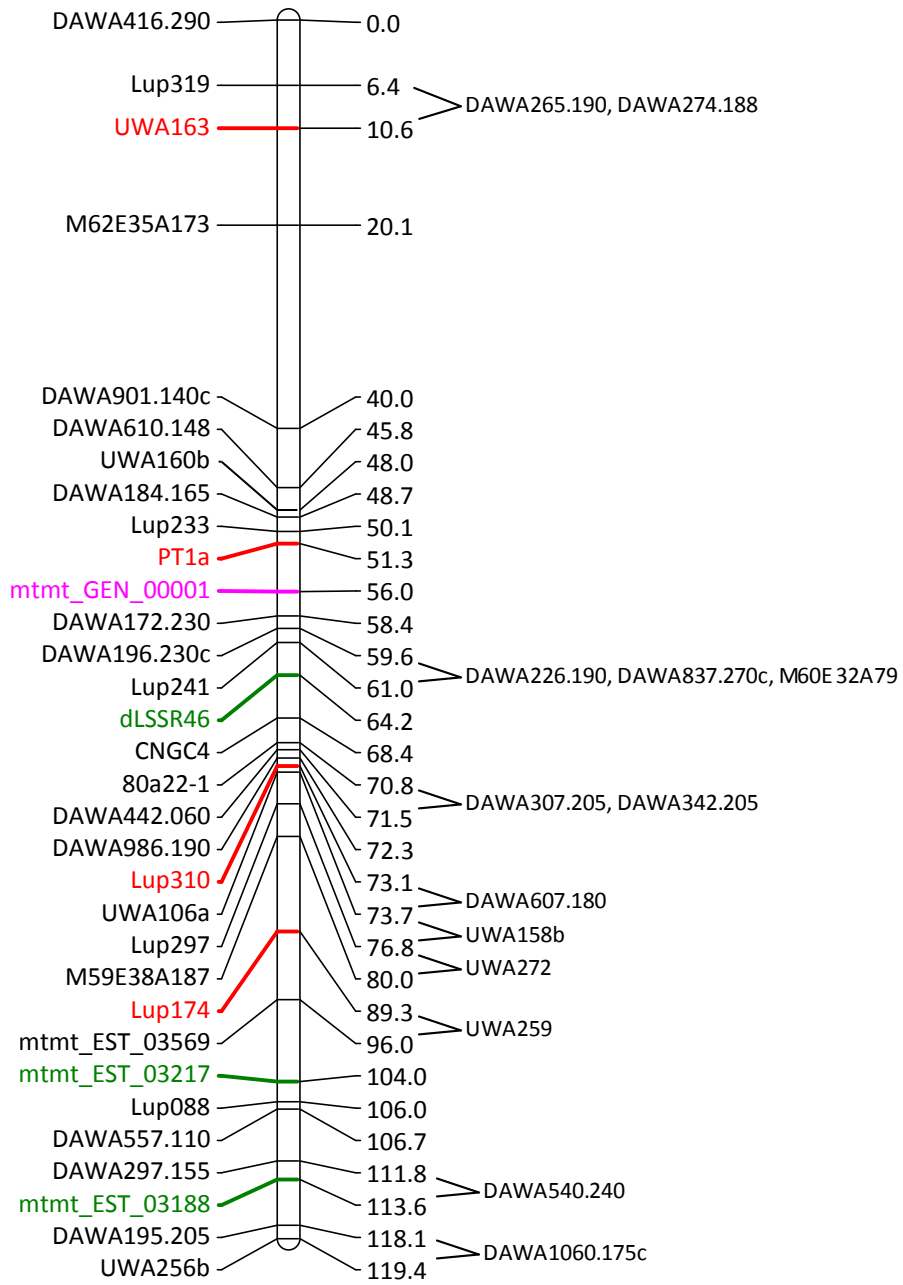
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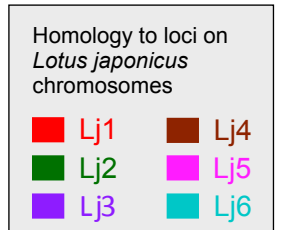
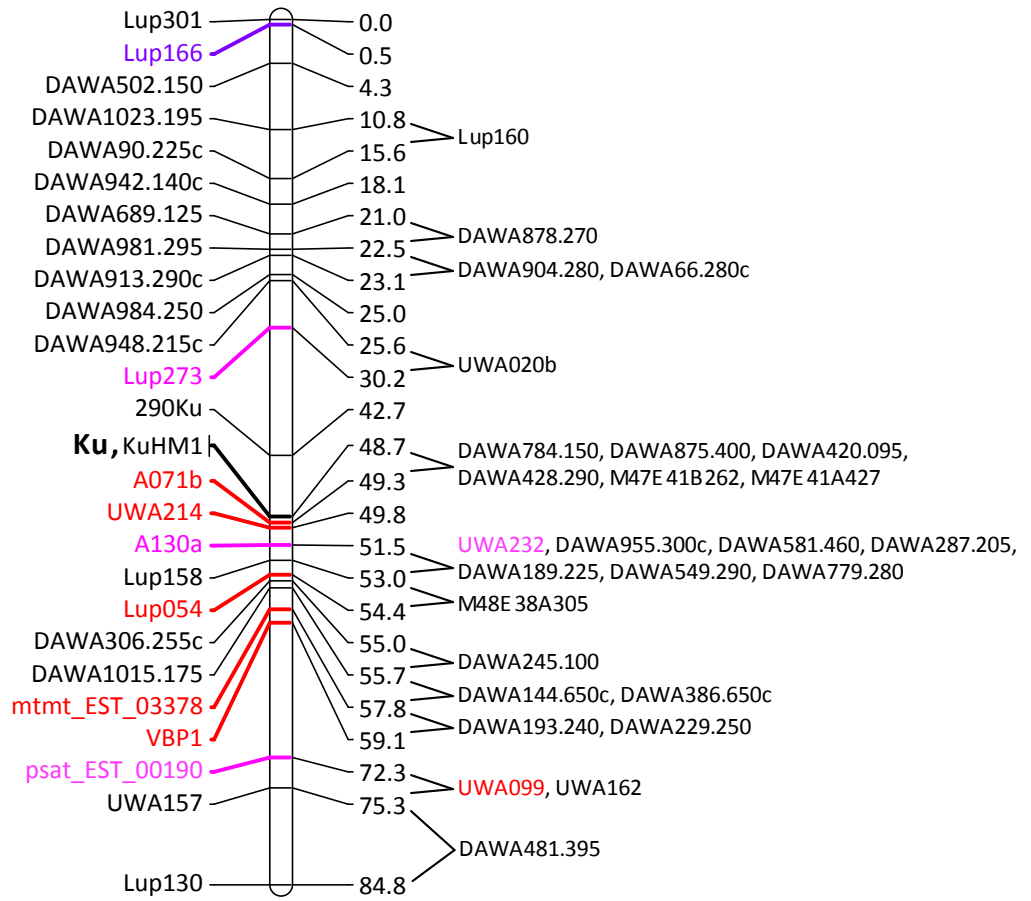
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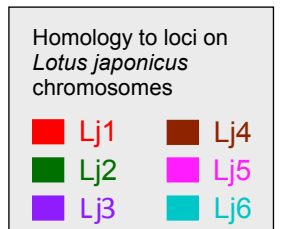
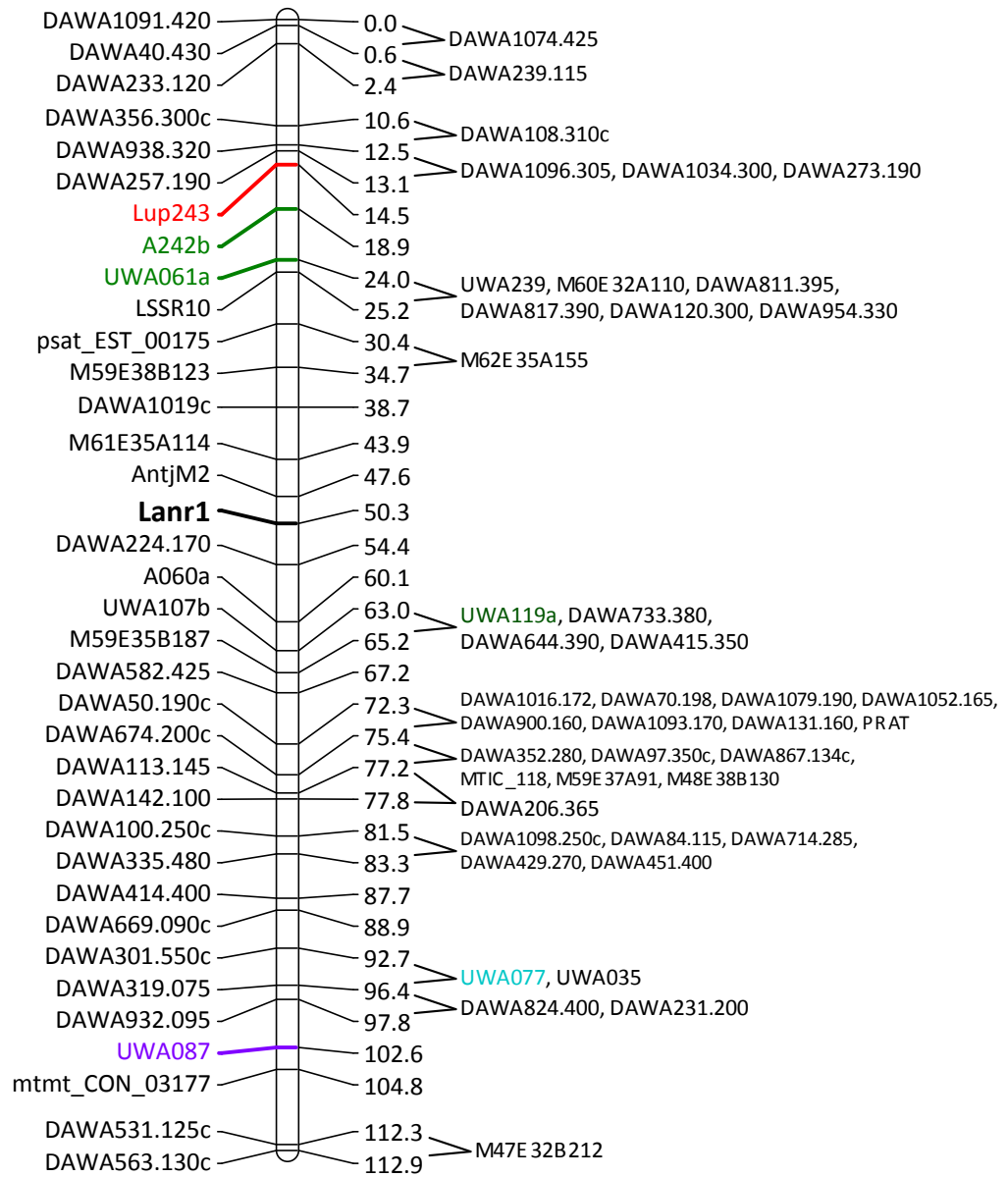
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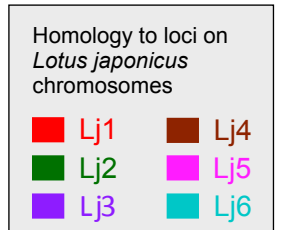
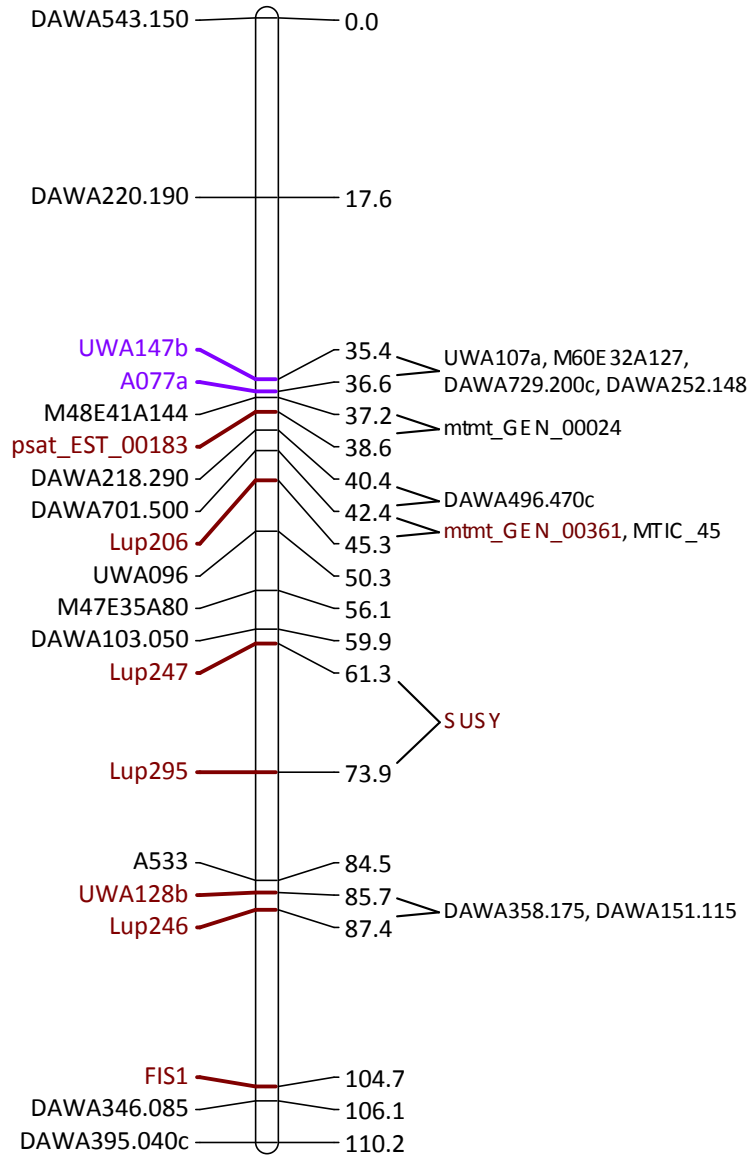
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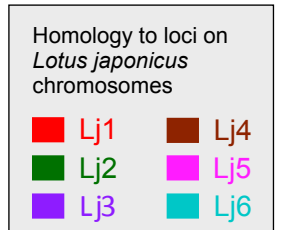
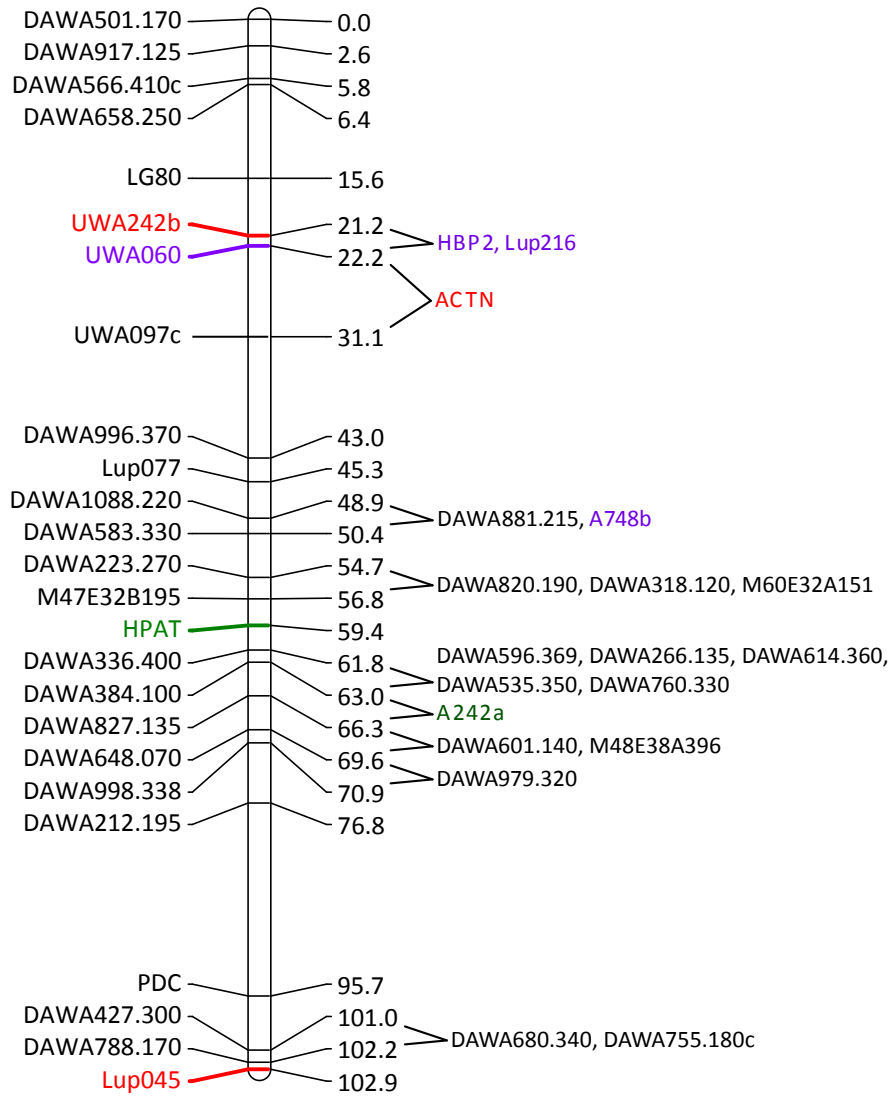
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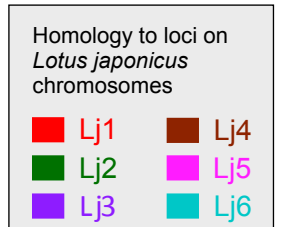
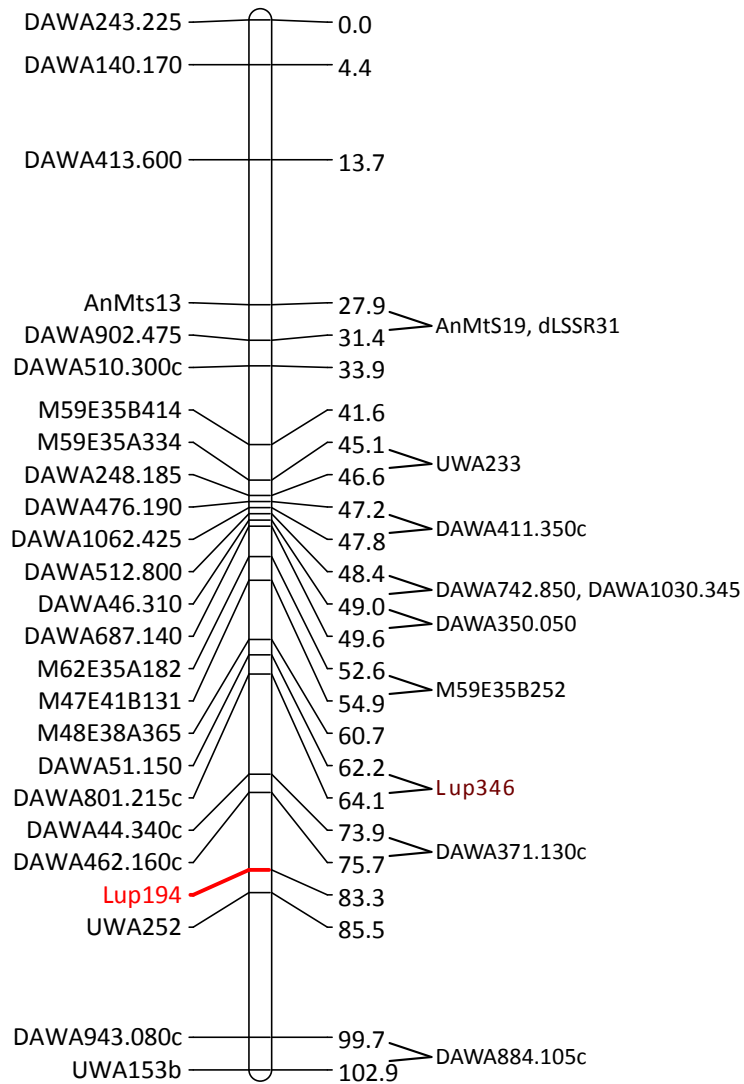
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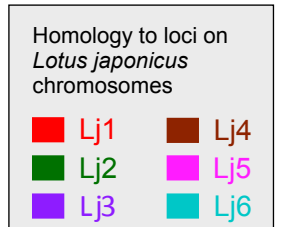
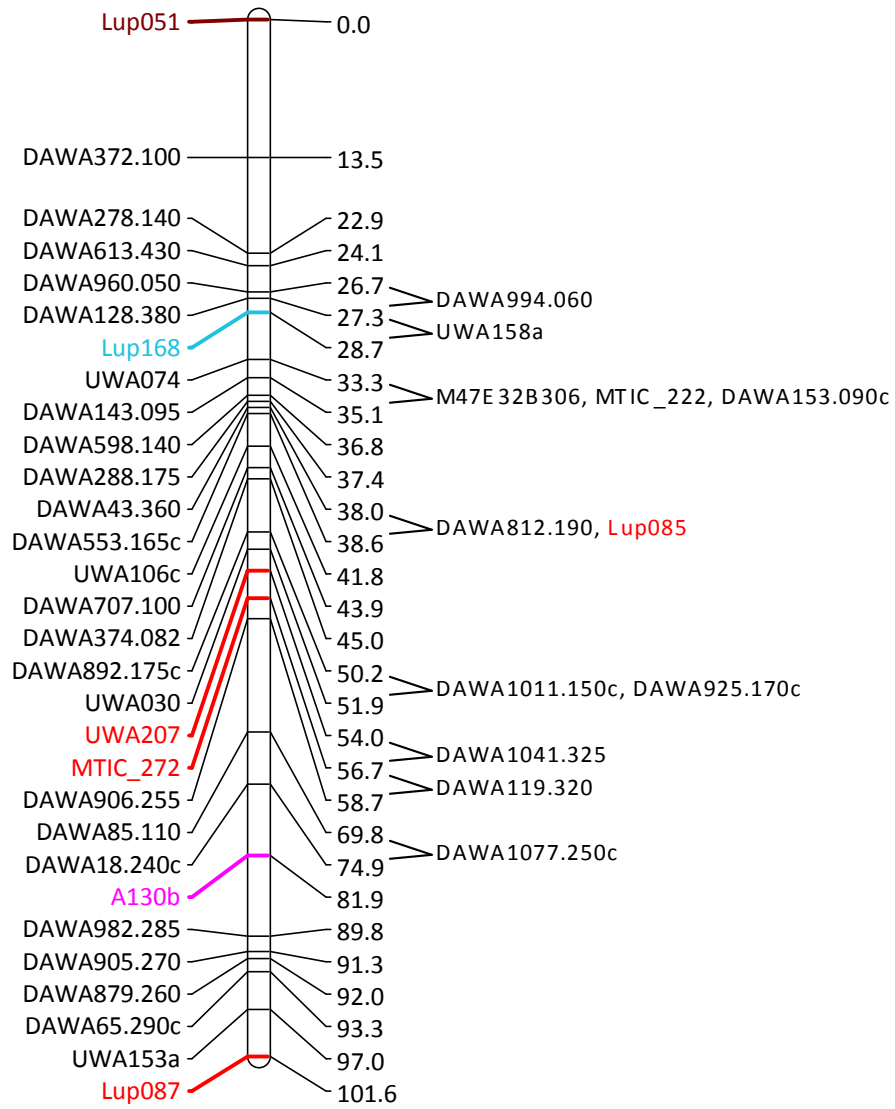
NLL-13



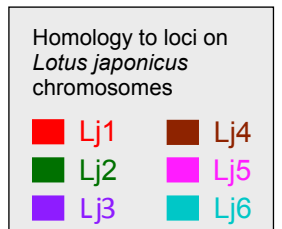
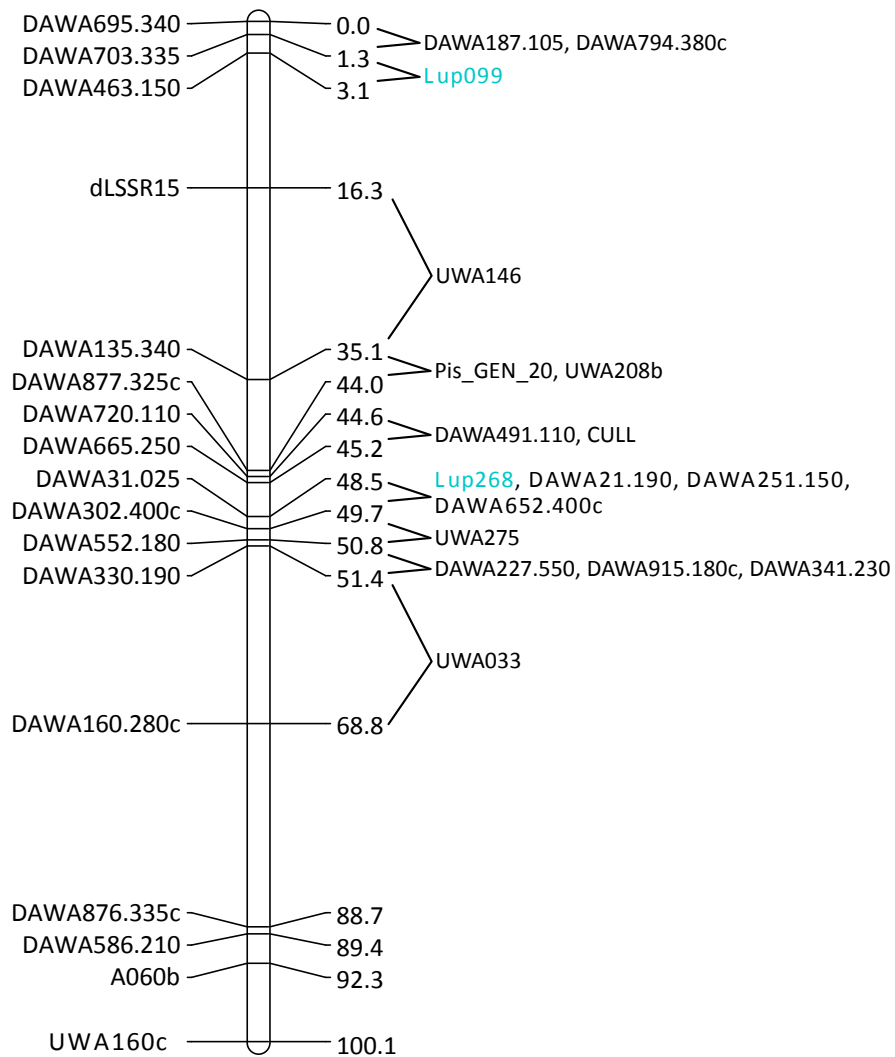
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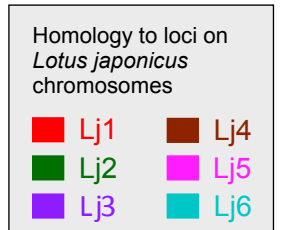
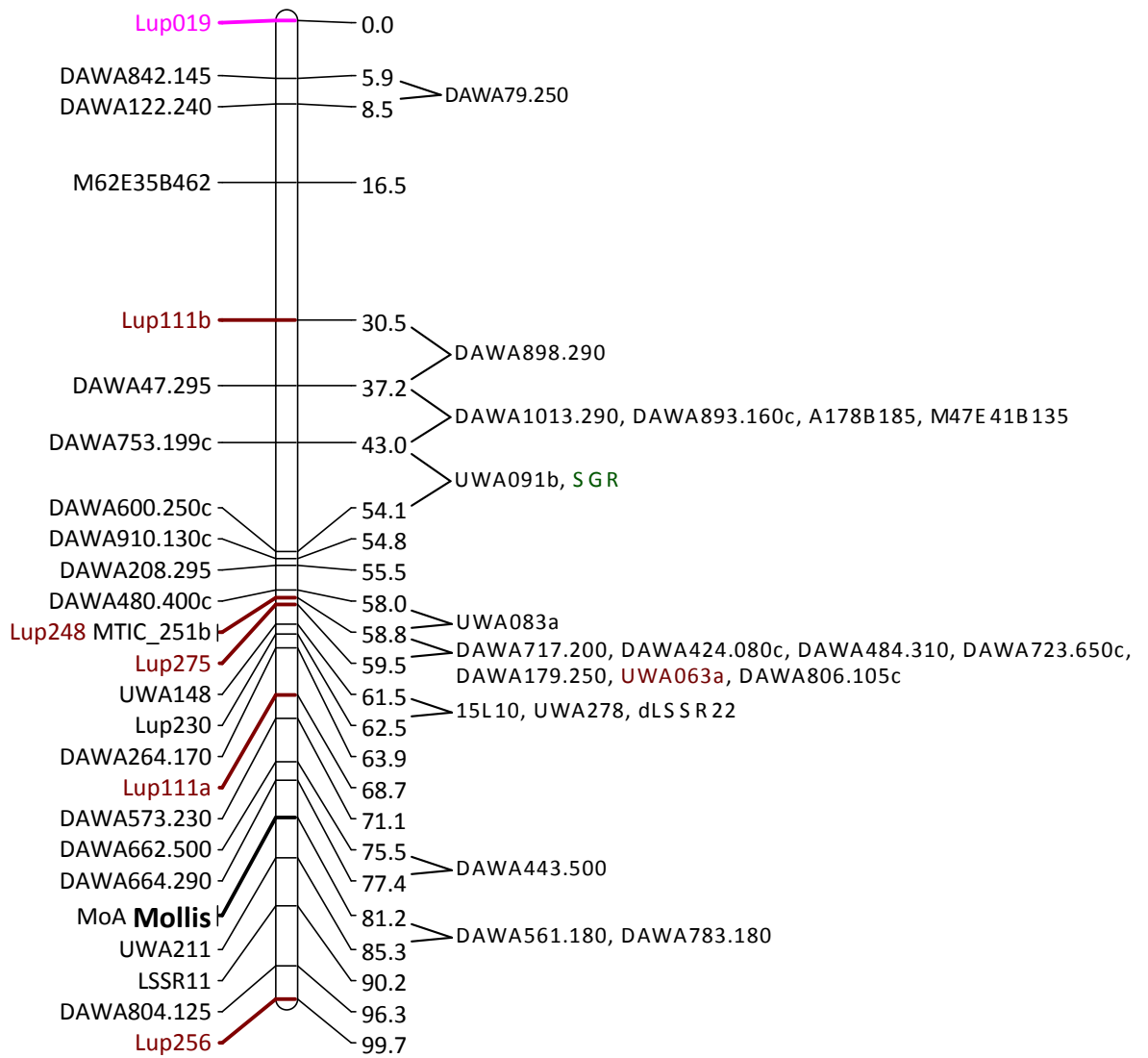
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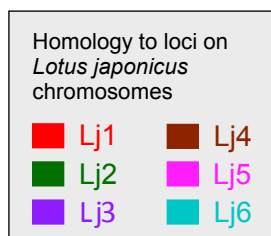
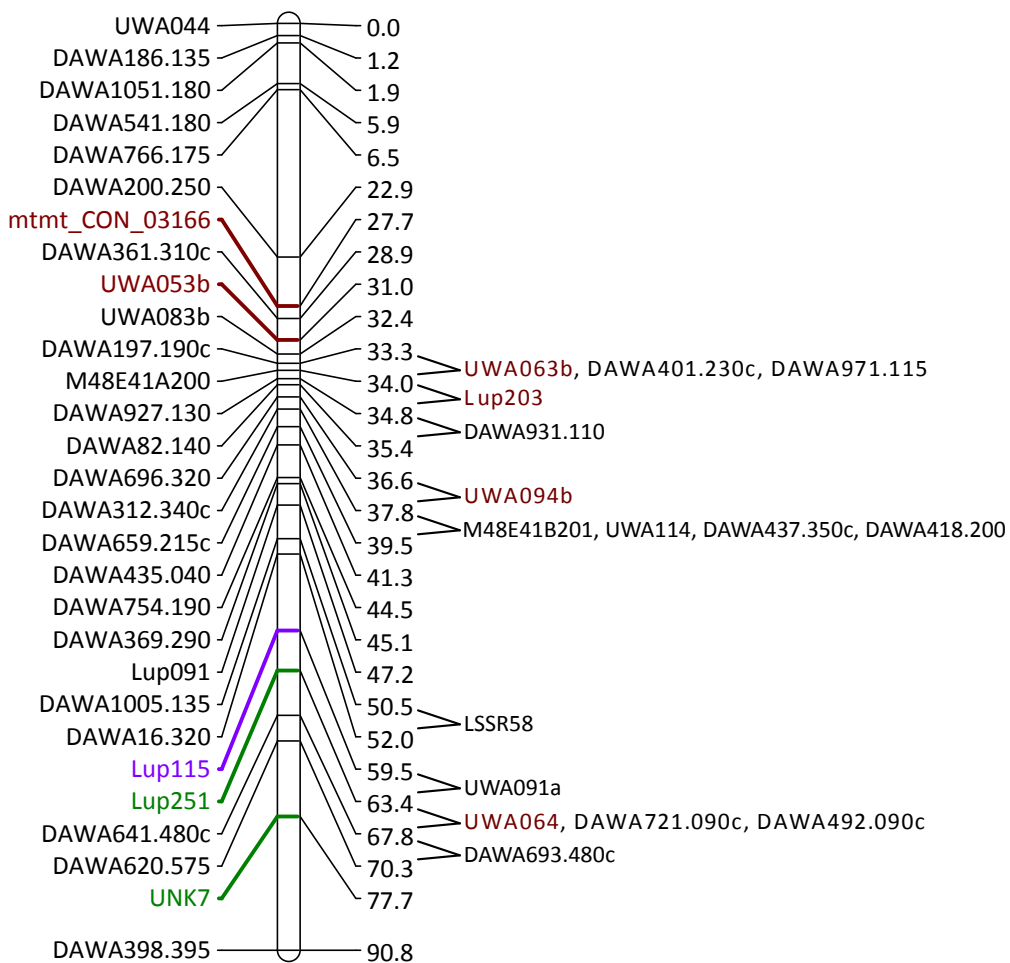
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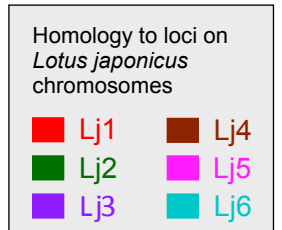
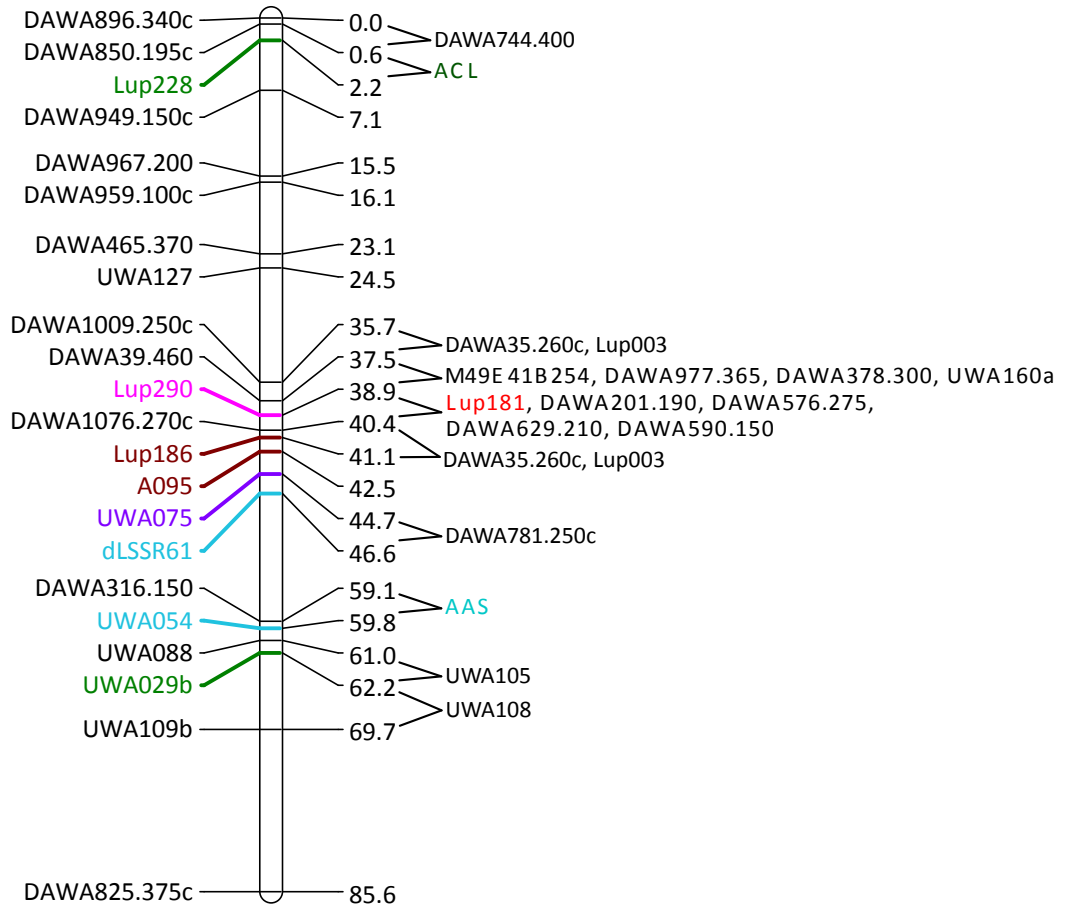
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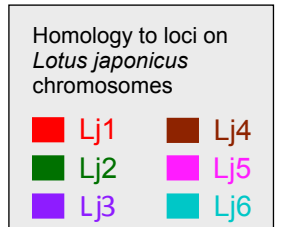
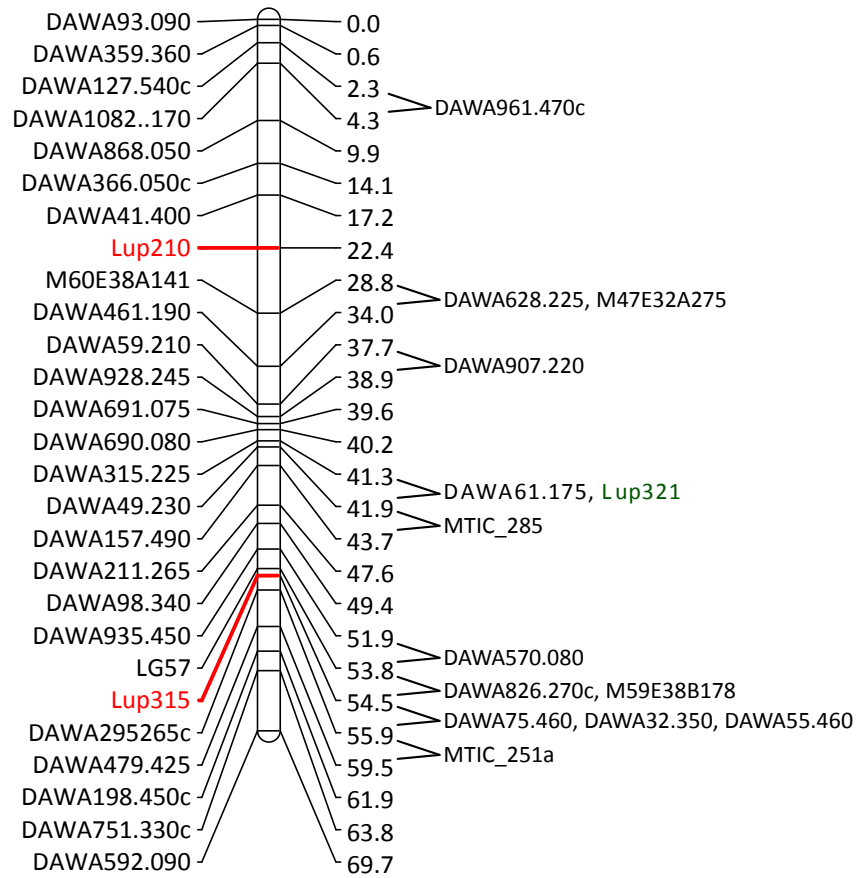
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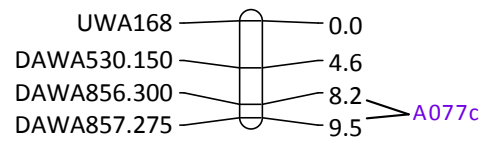
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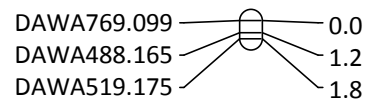
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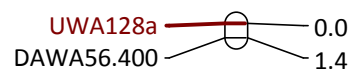
Cluster-1



Cluster-2



Cluster-3



Homology to loci on
Lotus japonicus
chromosomes



Supplementary Table S1. Simple sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) primer combinations giving rise to microsatellite-anchored fragment length polymorphism (MFLP) markers in *Lupinus angustifolius*.

SSR- anchor primers	AFLP <i>Mse</i> I-primers															
	-CAA	-CAG	-CAC	-CAT	-CGA	-CGG	-CGC	-CGT	-CCA	-CCG	-CCC	-CCT	-CTA	-CTG	-CTC	-CTT
MF128	14 ¹	25	32	39	55	64	75	87	96	106	115	127	133	144	155	164
MF129	178	188	191	198	204	211	nil	216	221	227	234	240	246	254	262	269
MF51	281	289	299	312	320	324	325	347	351	355	359	367	376	385	396	410
MF42	413	421	425	436	443	444	451	461	464	474	478	493	503	507	512	520
MF43	527	532	546	558	564	566	571	575	579	593	599	601	603	613	620	632
MF62	641	644	649	657	661	670	678	686	692	701	709	723	733	738	742	747
MF52	748	758	770	776	787	789	792	796	798	808	815	823	829	837	844	853
MF11	869	873	885	895	902	912	920	928	935	945	951	961	973	976	988	995
MF151	1002	nil	1008	1012	1018	1021	1025	1027	1032	1038	1040	1047	1056	1058	1061	1068
MF152	1072	1085	1089	1091	nil	nil	1094	nil	1095							

¹ Serial numbers denote the first scored polymorphic marker for that particular primer combination. MFLP marker names are prefixed by 'DAWA' followed by the serial numbers and amplicon sizes.