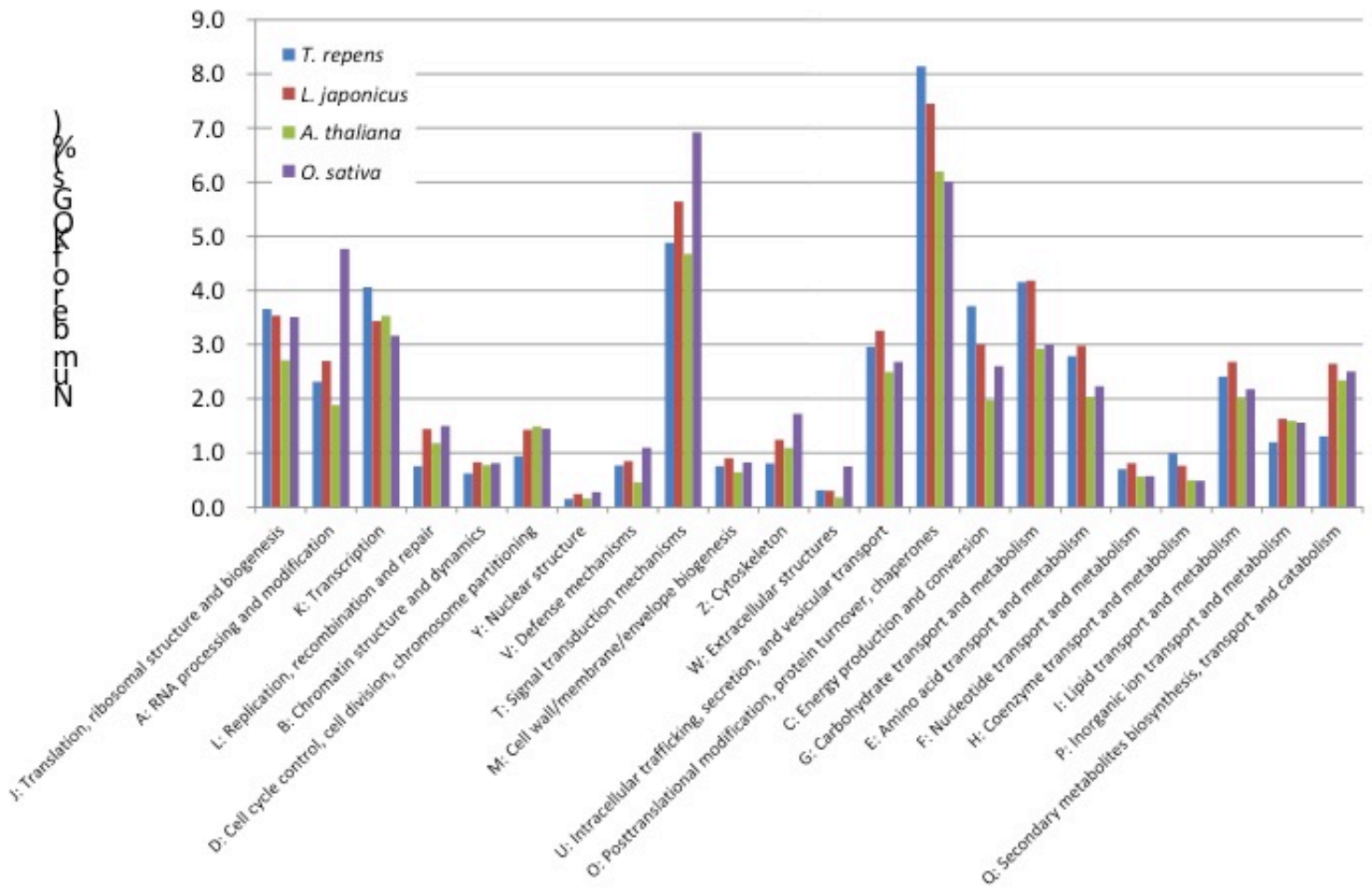
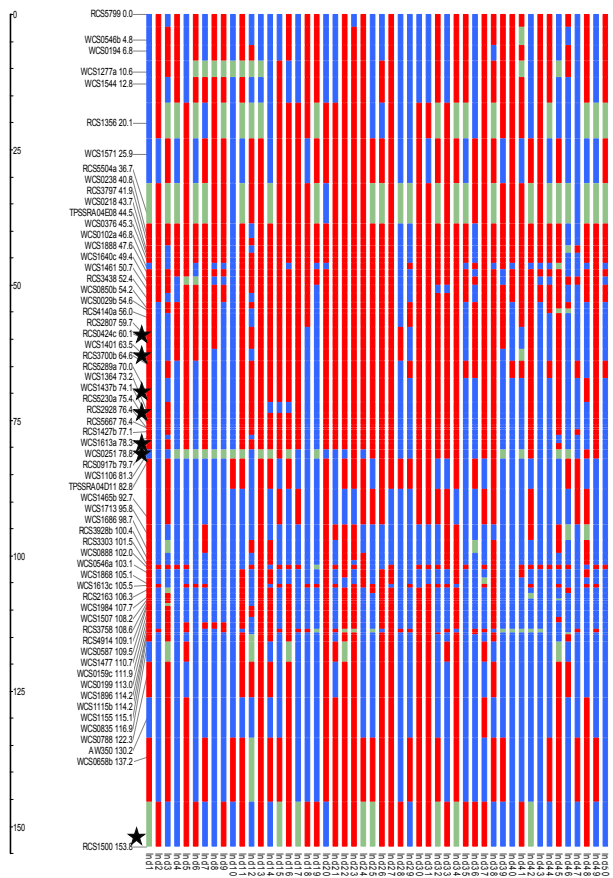


**Figure S1** Graphical genotypes of the largest linkage groups of the 'T17-349'-specific map constructed before disassembling the locus data. The linkage group consisted of a total of 296 loci. Graphical genotypes are shown for 50 of the 188  $F_1$  mapping population. Red and blue colors show the two haplotypes of 'T17-349'. Light green color shows missing data.

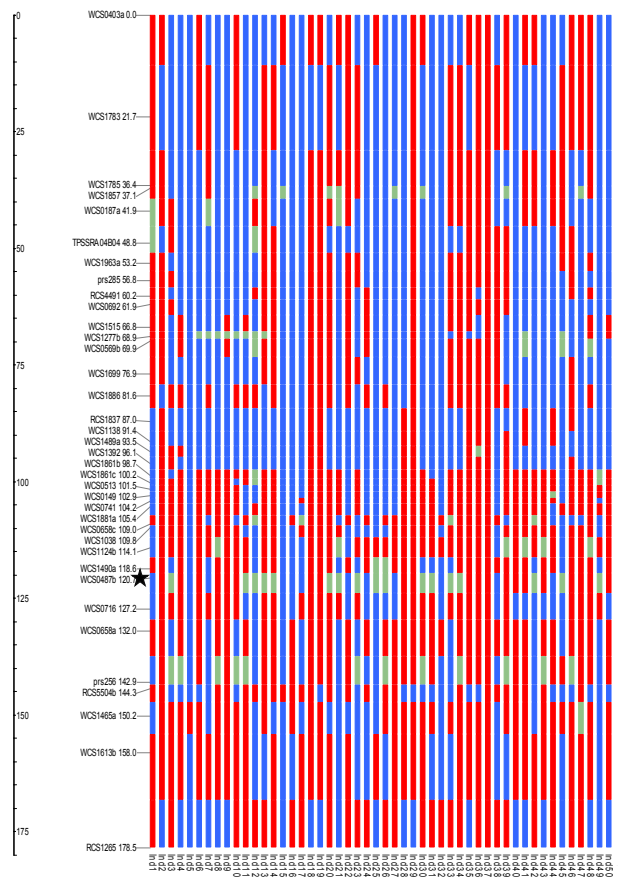


**Figure S2** Functional classification of non-redundant EST sequences of *T. repens* and unigene sequences of *L. japonicus*, *A. thaliana*, and *O. sativa* based on KOG categories. BLASTX was used to compare the non-redundant EST sequences with the sequences in the KOG database. EST sequences were then classified into the KOG categories with the most similar sequences. The total number of KOG associated ESTs sequences and non-associated were 5193 and 2789, respectively.



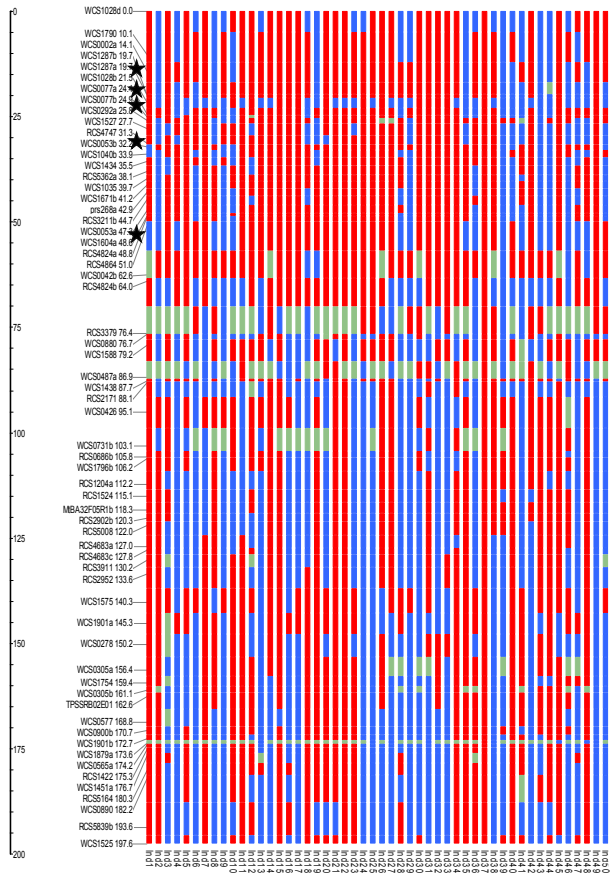
LG1a

cM

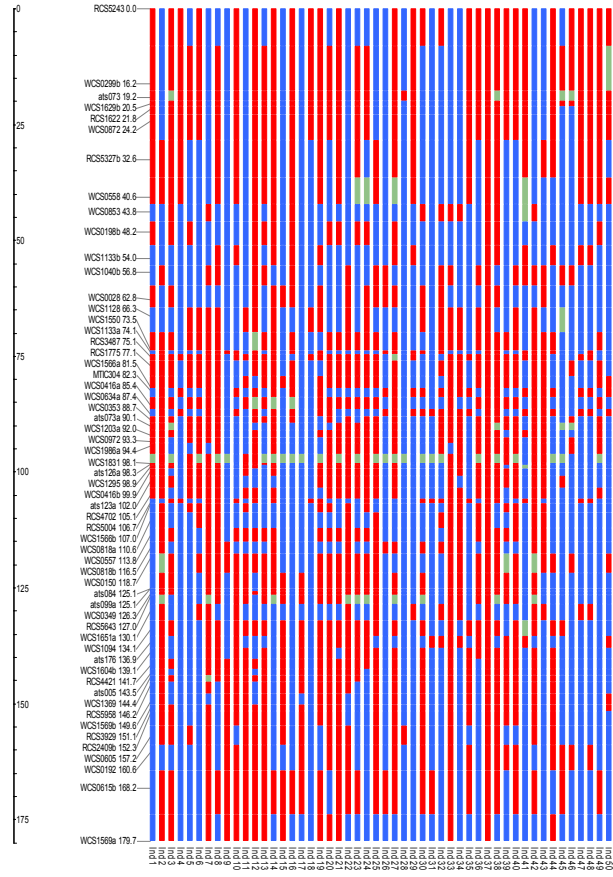


LG1b

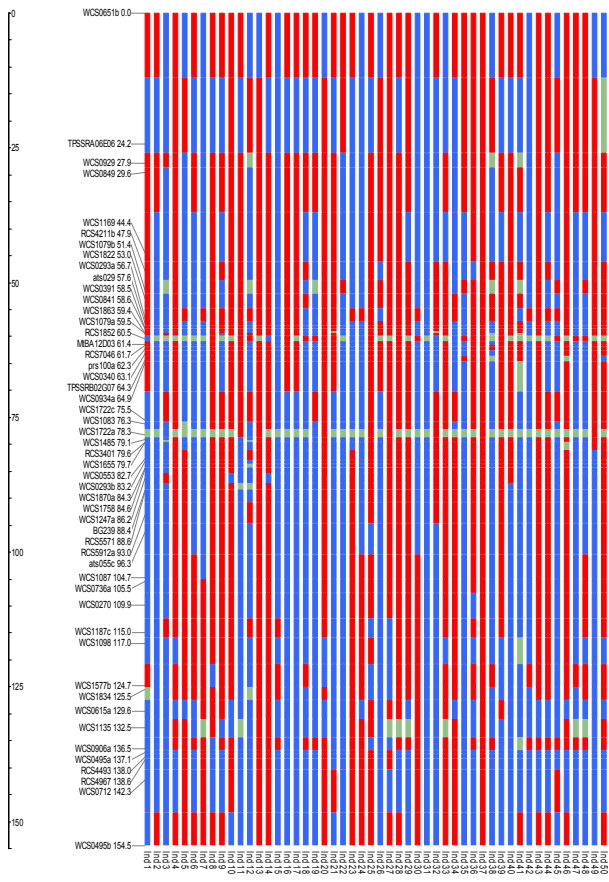
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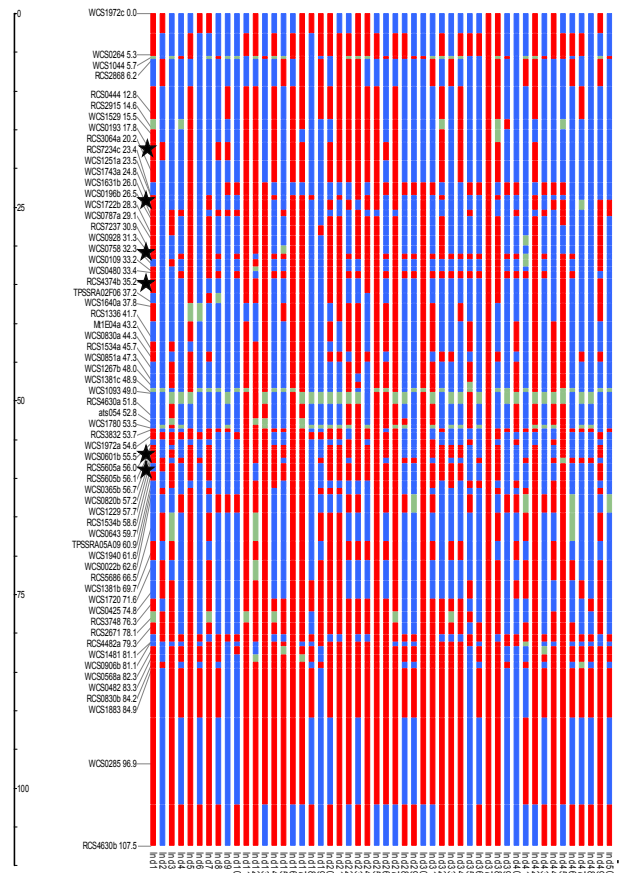
LG2a



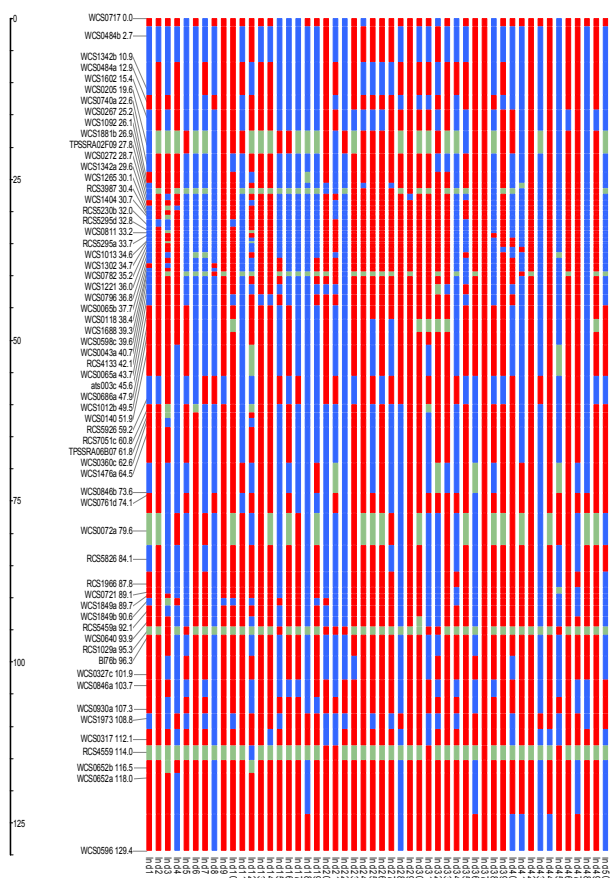
LG2b



LG3a

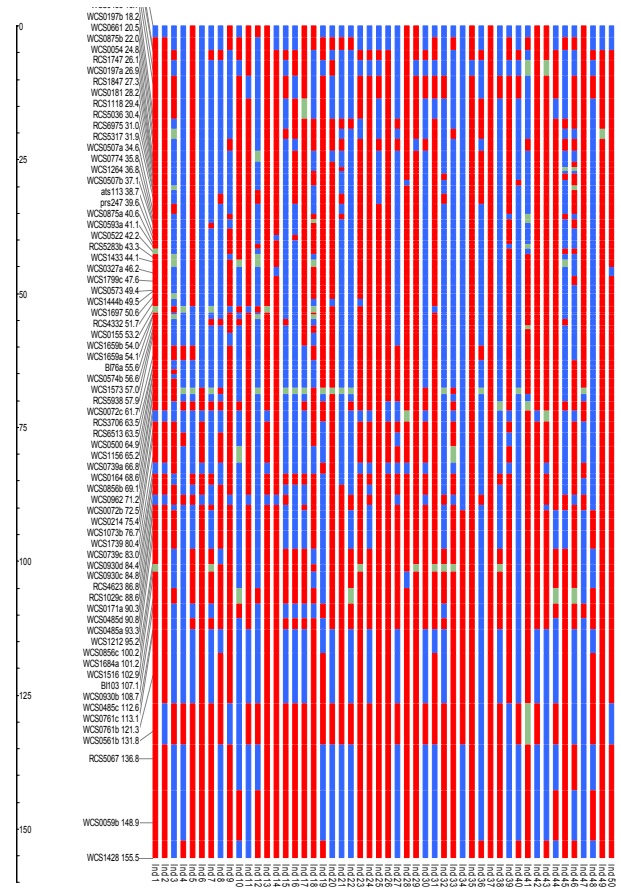


LG3b



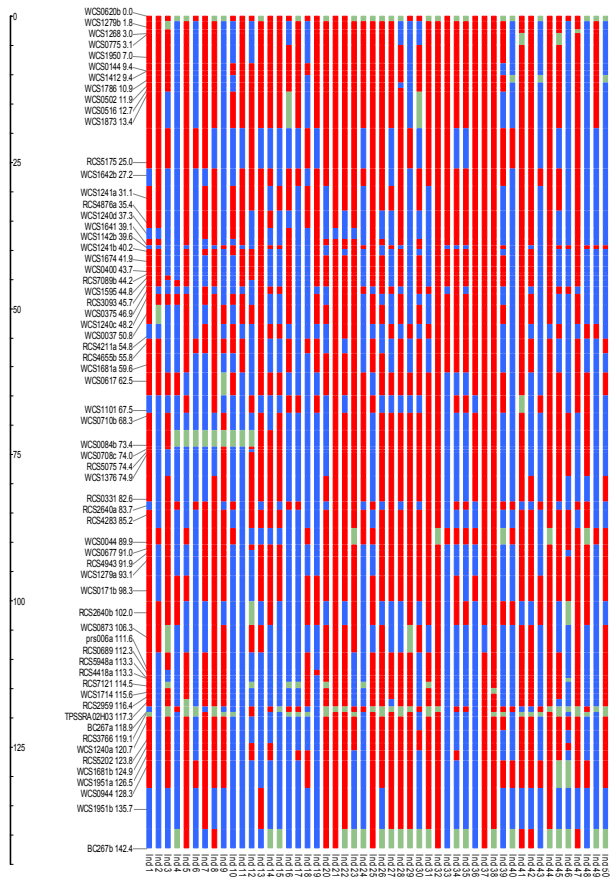
LG4a

cM



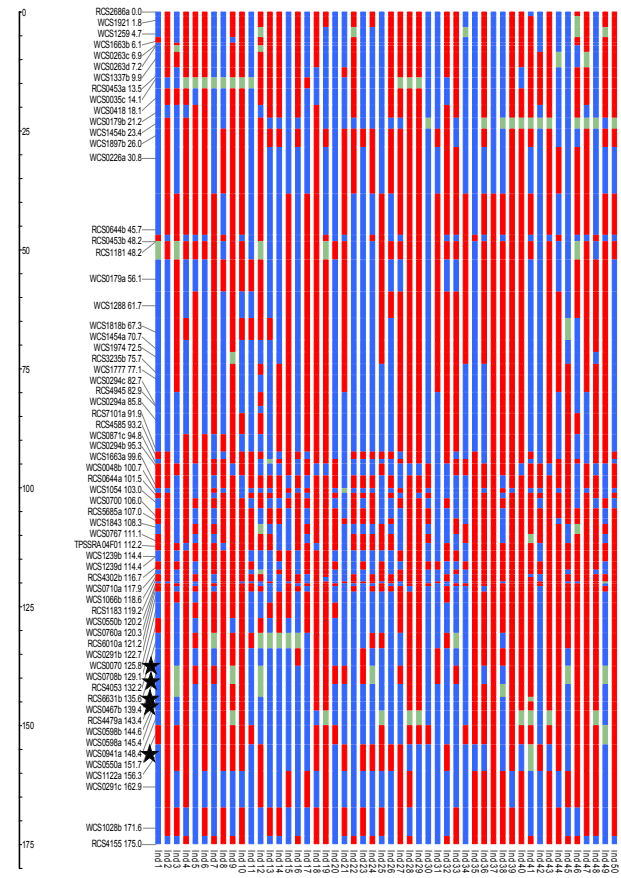
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cM



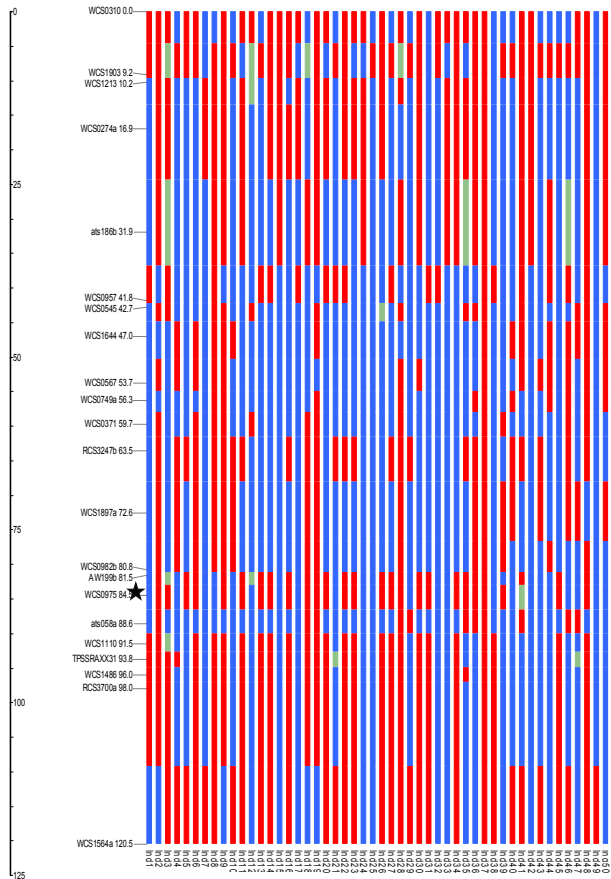
LG5a

cM

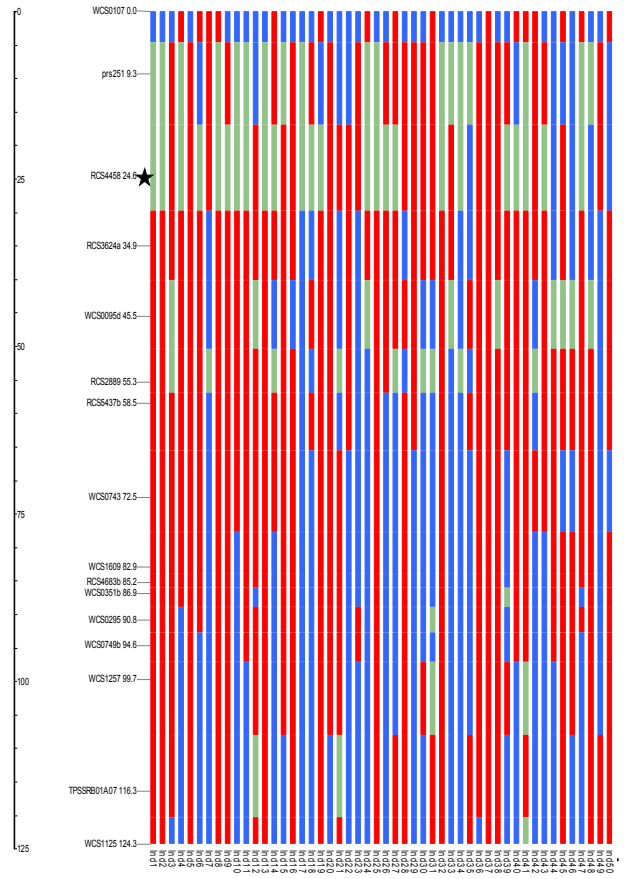


LG5b

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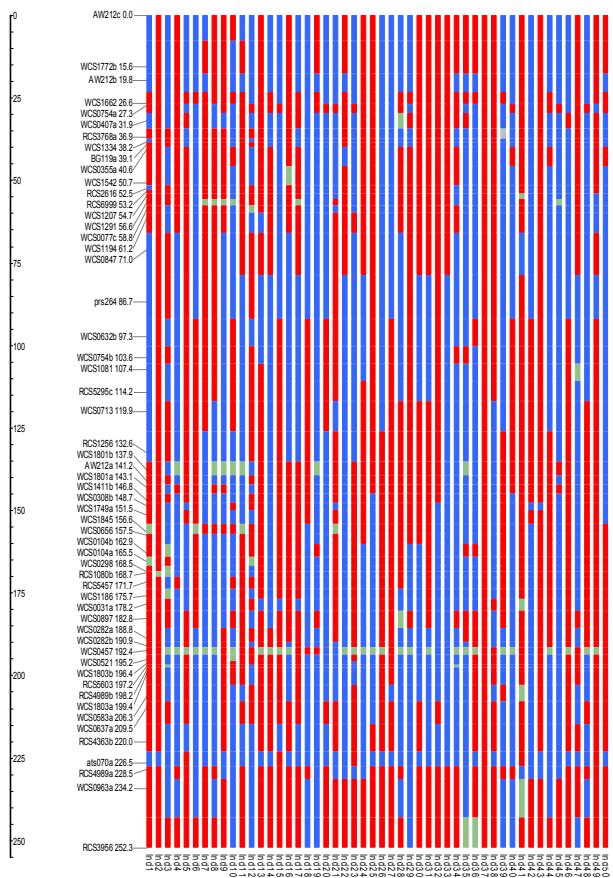


LG6a



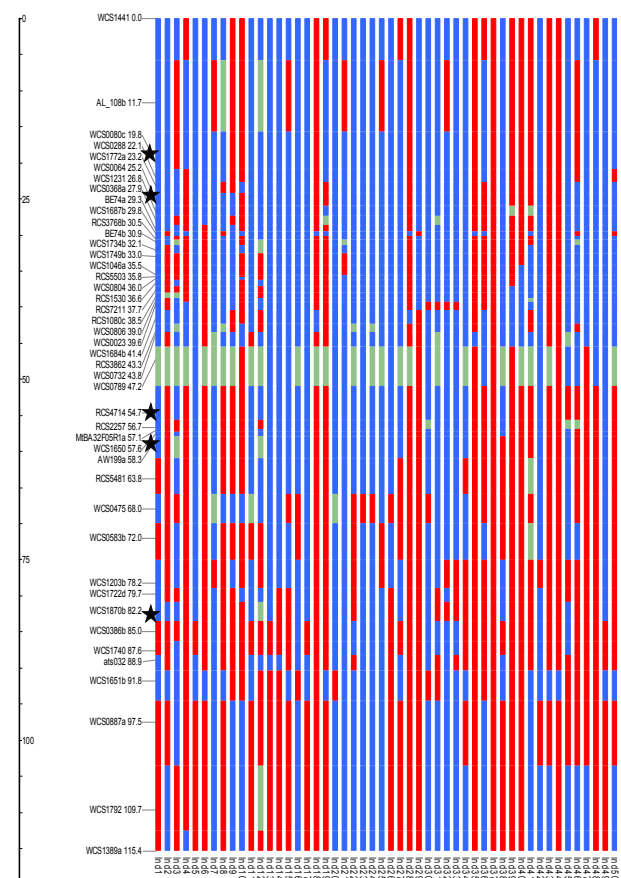
LG6b





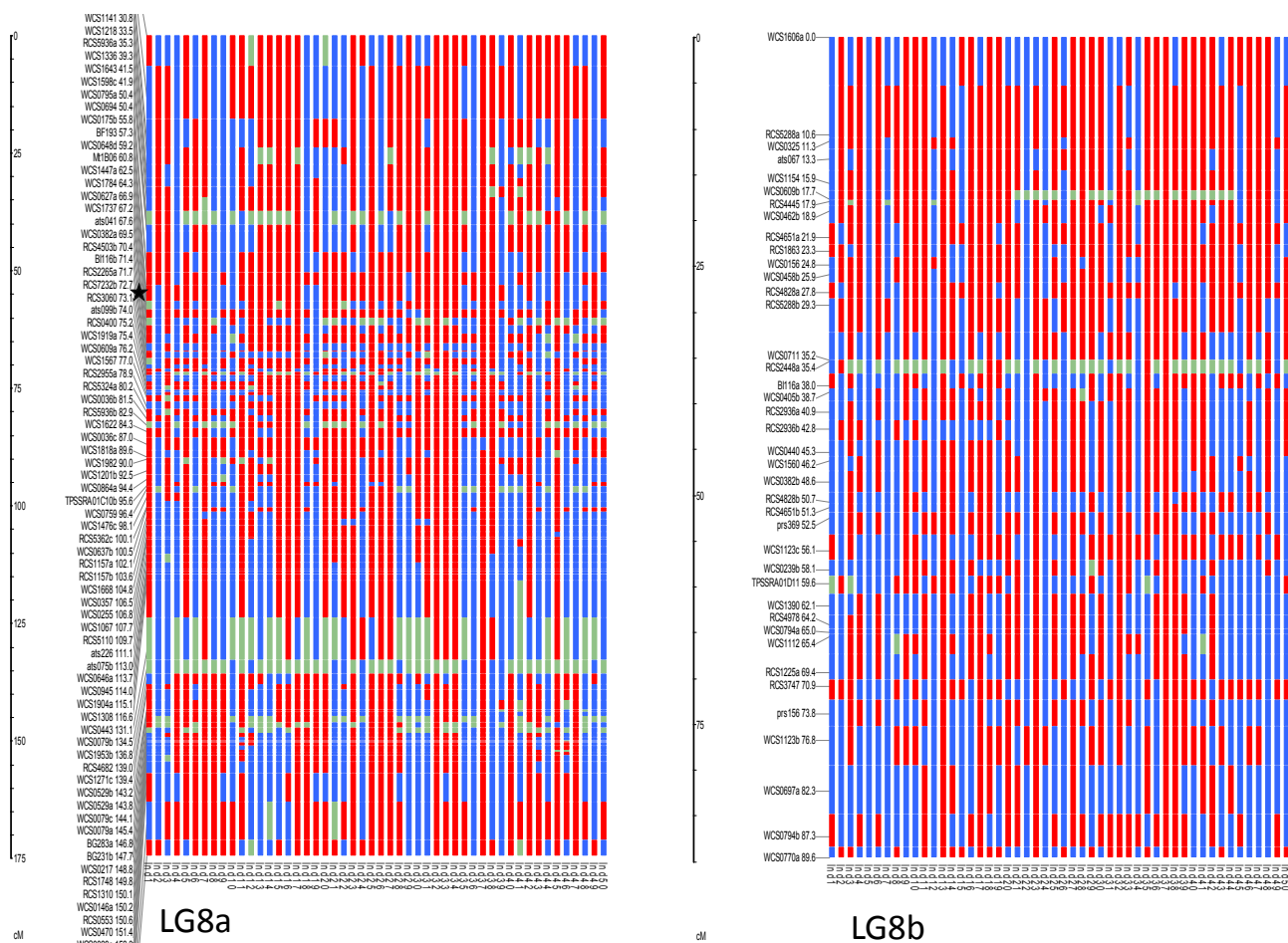
LG7a

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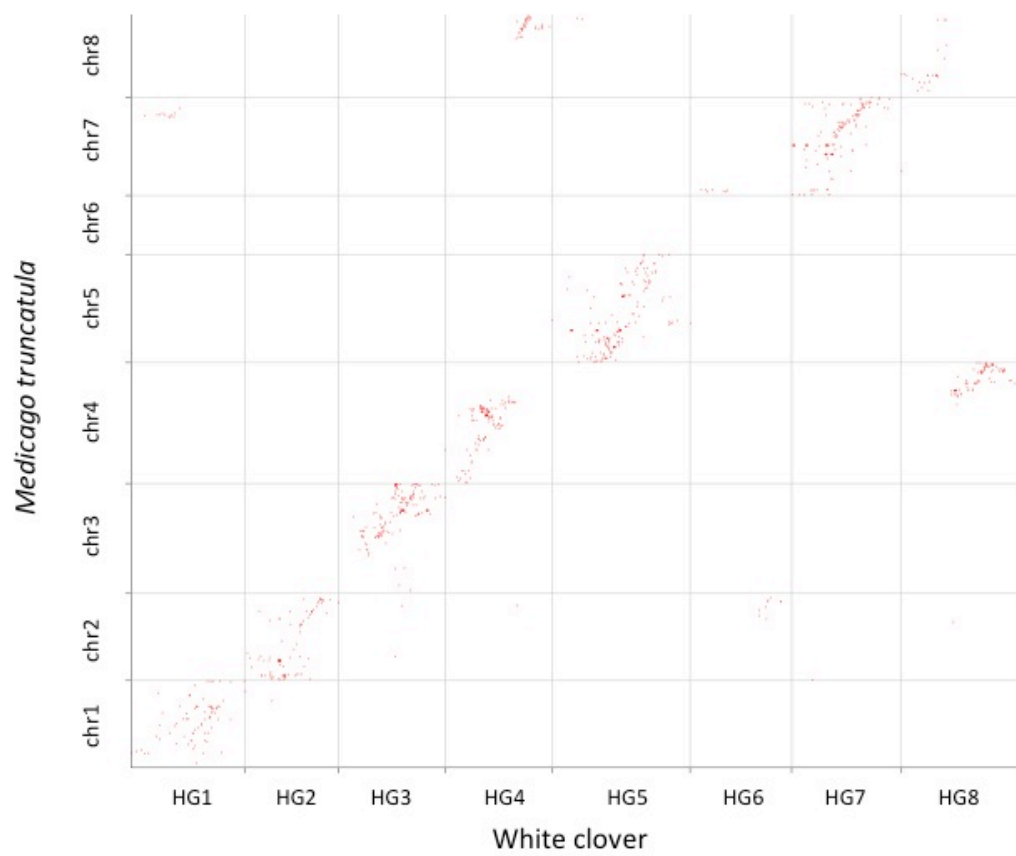


LG7b

cM



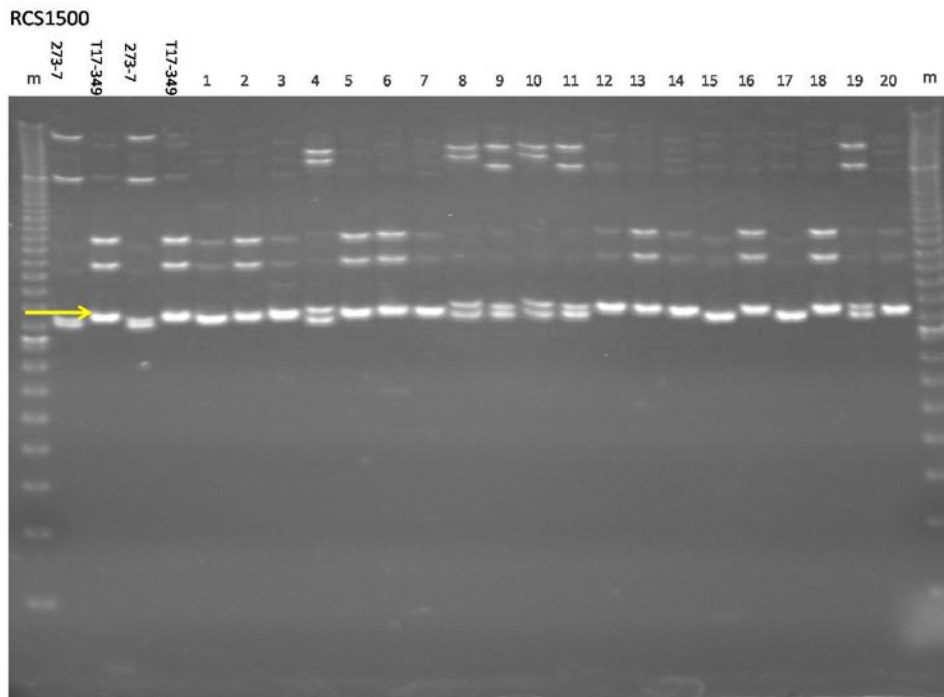
**Figure S3** Graphical genotypes of 50 of the 188 F<sub>1</sub> populations mapped onto the largest linkage group shown in Figure S1. The red and blue colors show the two haplotypes of 'T17-349'. The light green color shows missing data. Black stars indicate loci showing a high LD ( $r^2 > 0.5$ ) between loci mapped onto different linkage groups.



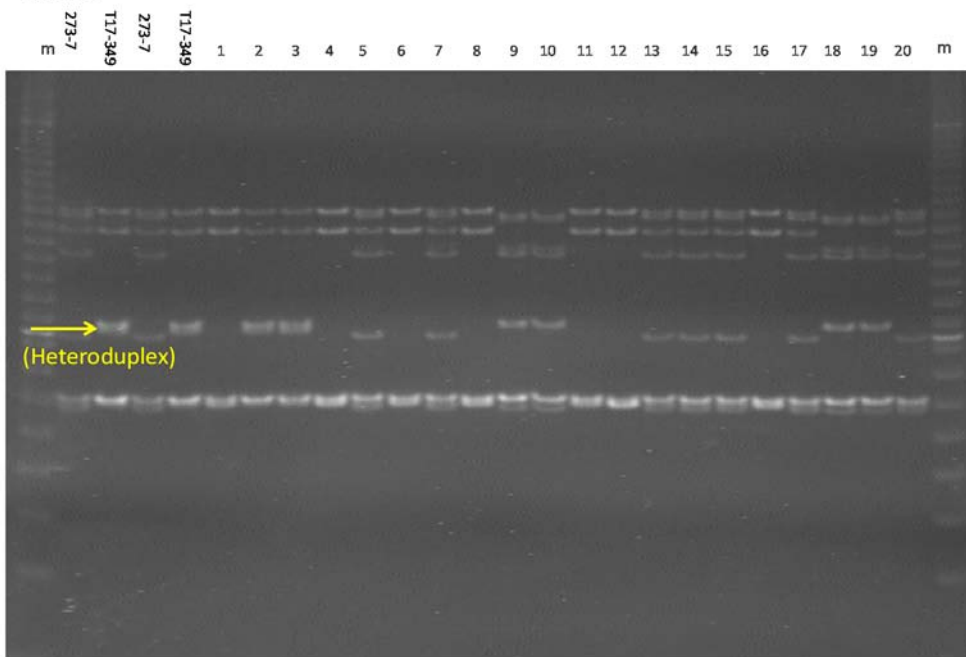
**Figure S4** Graphical view of syntenic blocks between white clover and *M. truncatula*. X and Y axis show position on mapped markers on an white clover linkage map and chromosomes of *M. truncatula* genome, respectively.

List of loci identified LD showing  $r^2 > 0.5$  between loci mapped onto different linkage groups.

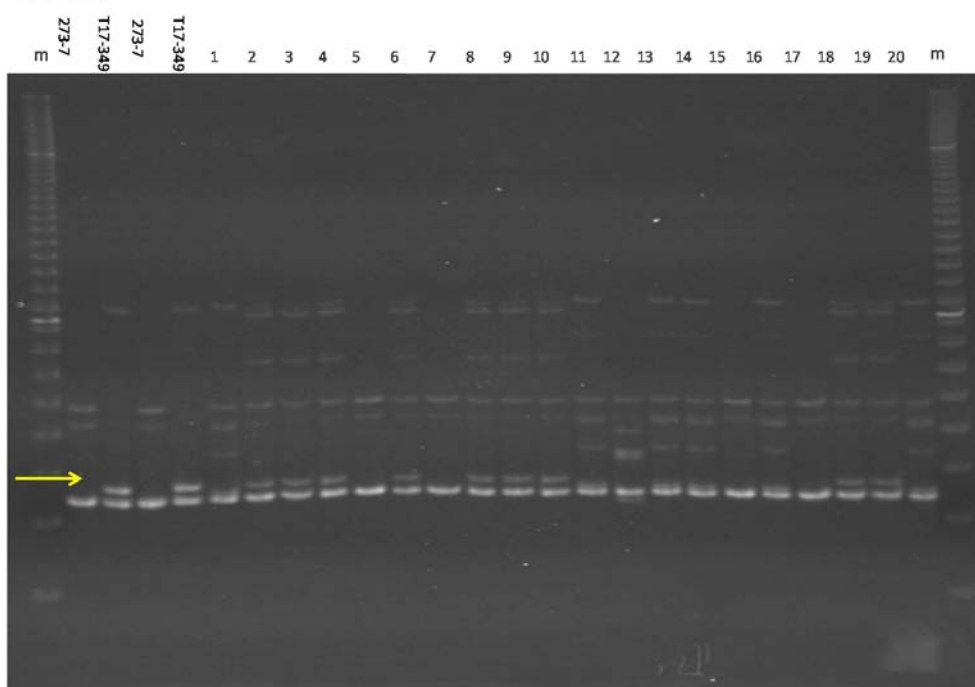
Mapped LG	Locus name	Mapped LG	Locus name
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1a	RCS2807	3b	WCS1743a
1a	RCS5289a	5b	RCS6631b
1a	WCS0251	5b	WCS0467b
1a	WCS1106	5b	WCS0598a
1a	WCS1364	5b	WCS0598b
1a	WCS1401	5b	WCS1122a
1b	WCS0487b	6a	WCS0975
2a	RCS4747	6b	RCS4458
2a	RCS4864	7b	ats032
2a	WCS0002a	7b	AW199a
2a	WCS0077a	7b	RCS4714
2a	WCS1287b	7b	WCS0064
3b	RCS3064a	7b	WCS0080c
3b	RCS4374b	7b	WCS1870b
3b	RCS5605a	8a	WCS0175b
3b	RCS7237		



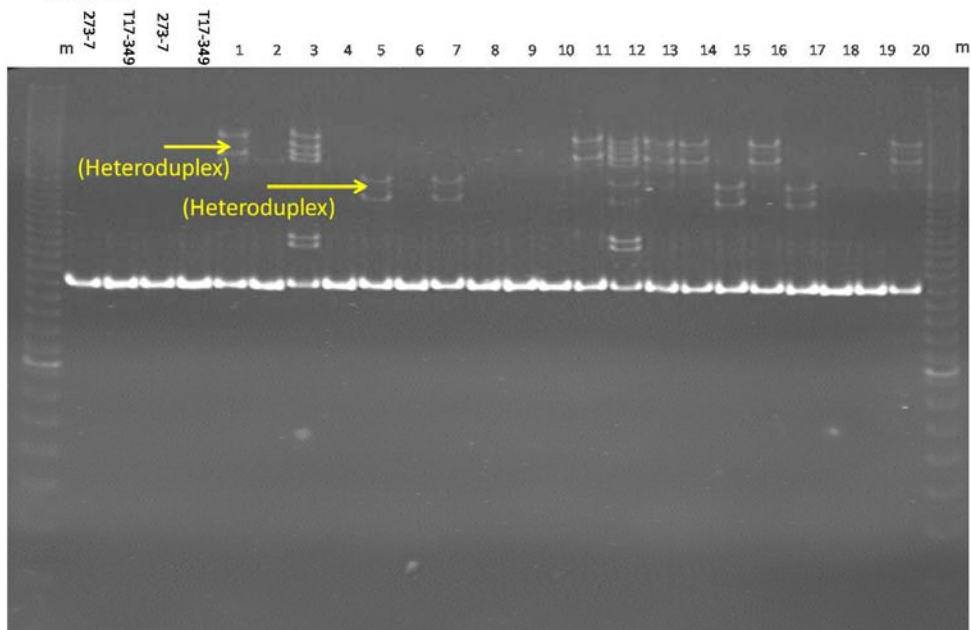
RCS2807



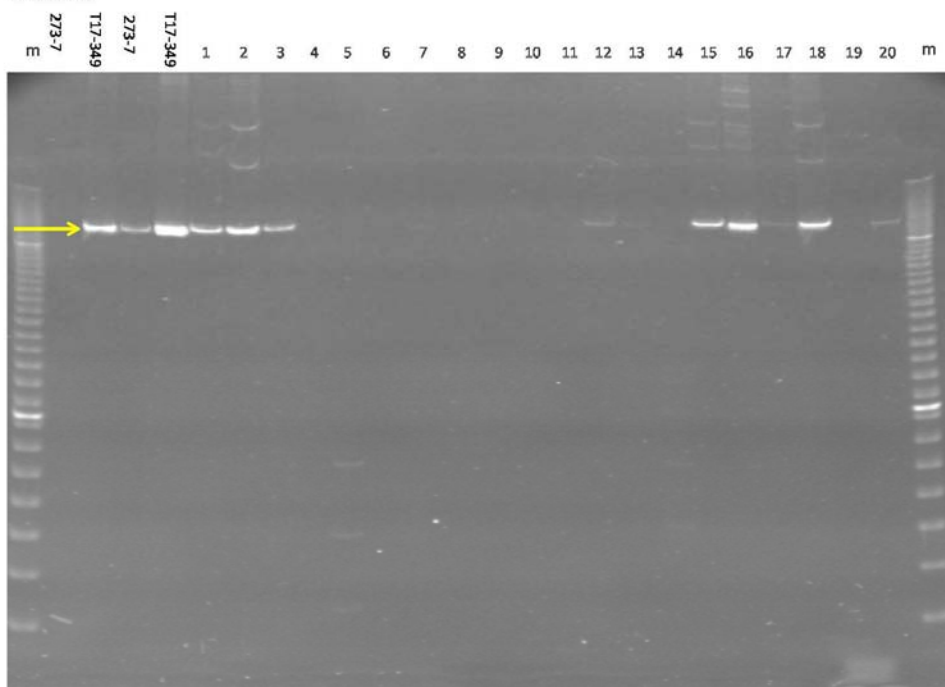
RCS5289a



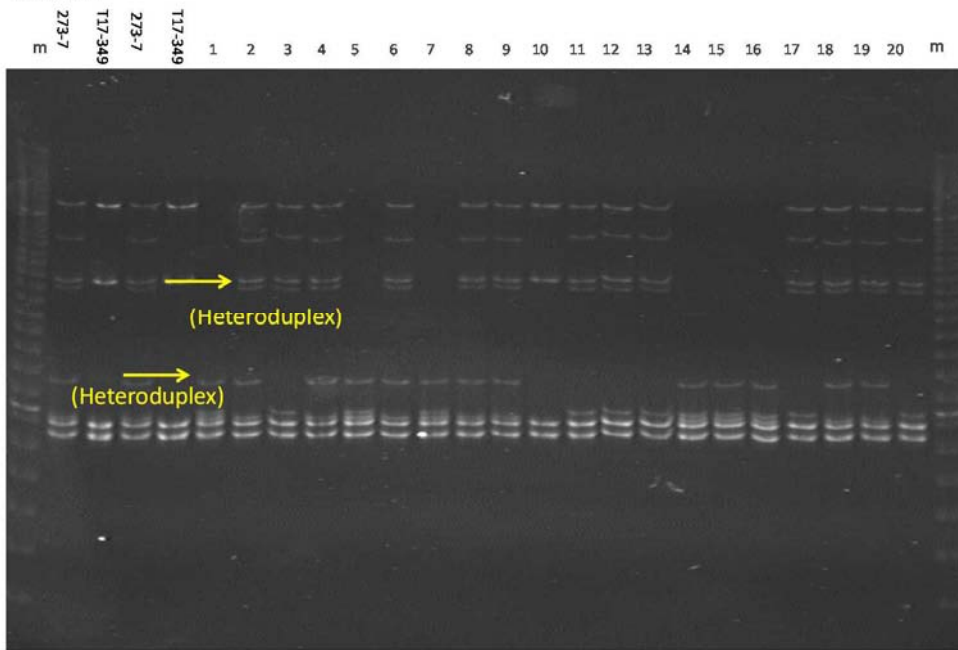
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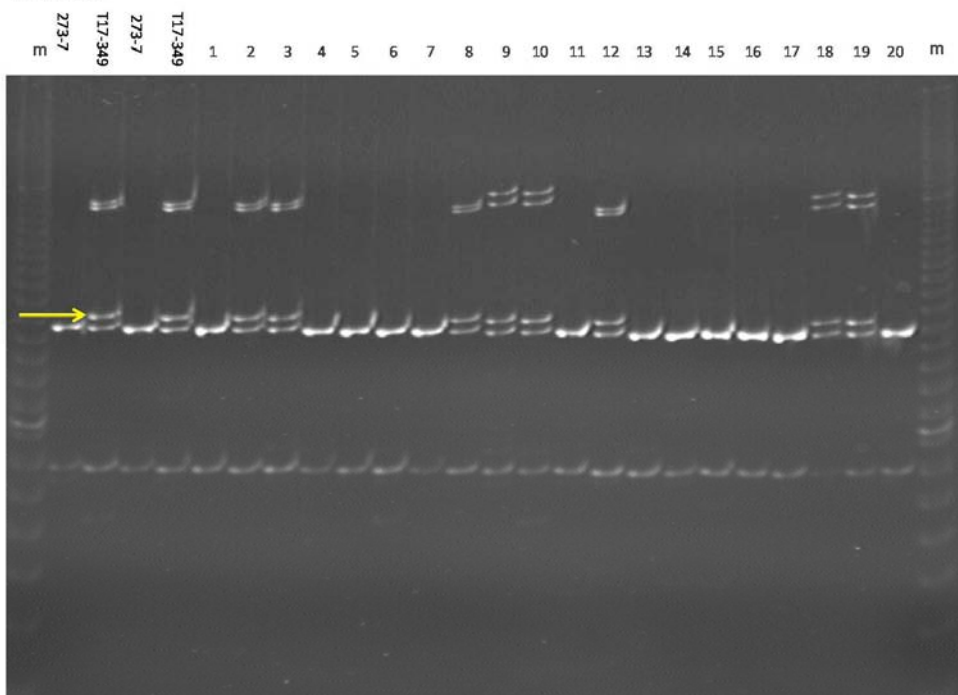
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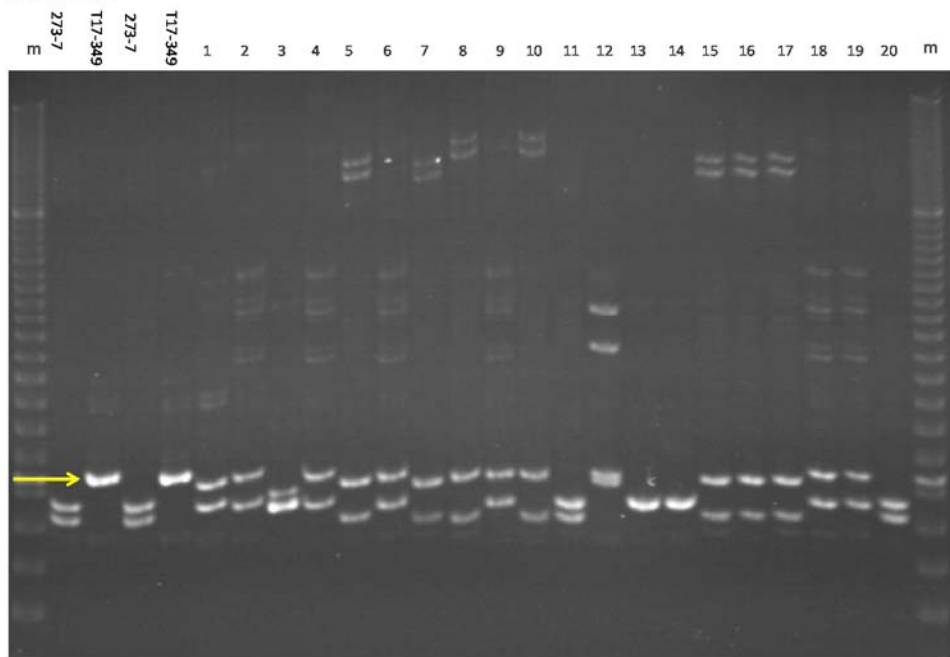
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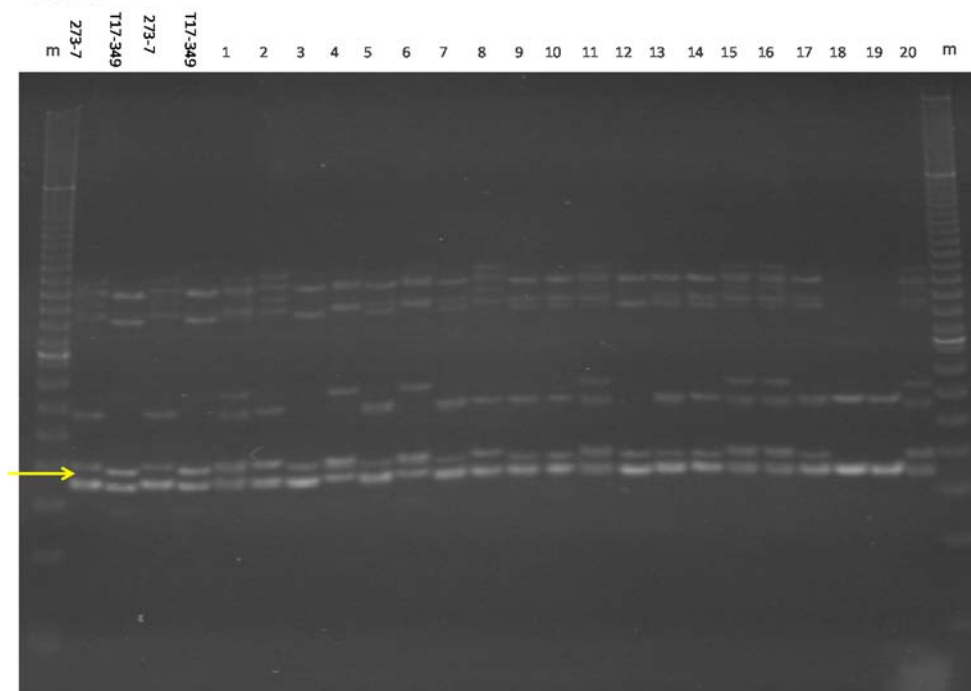
WCS1401



WCS0487b

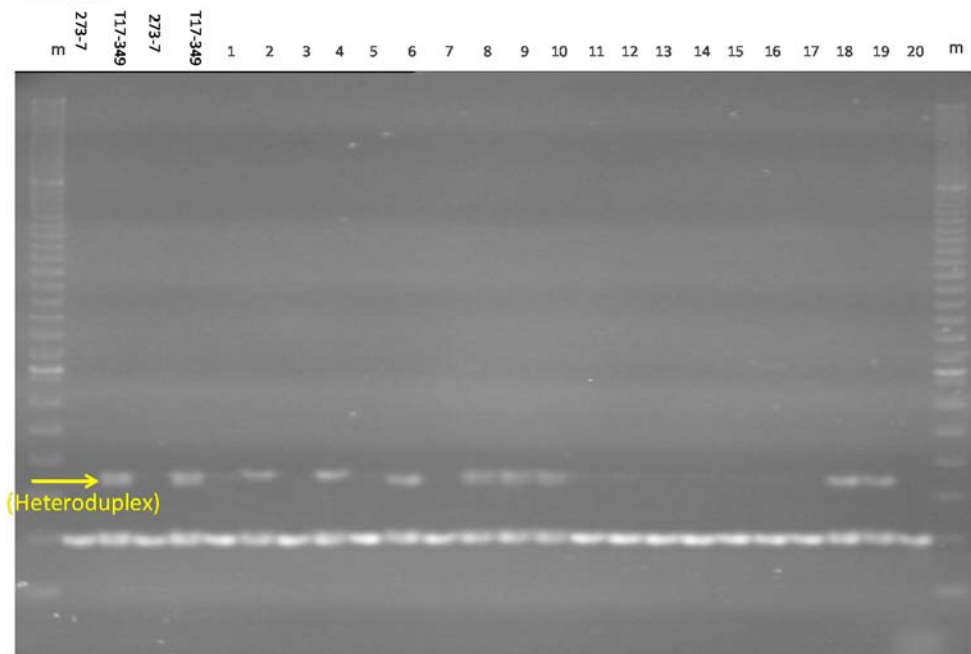


RCS4747

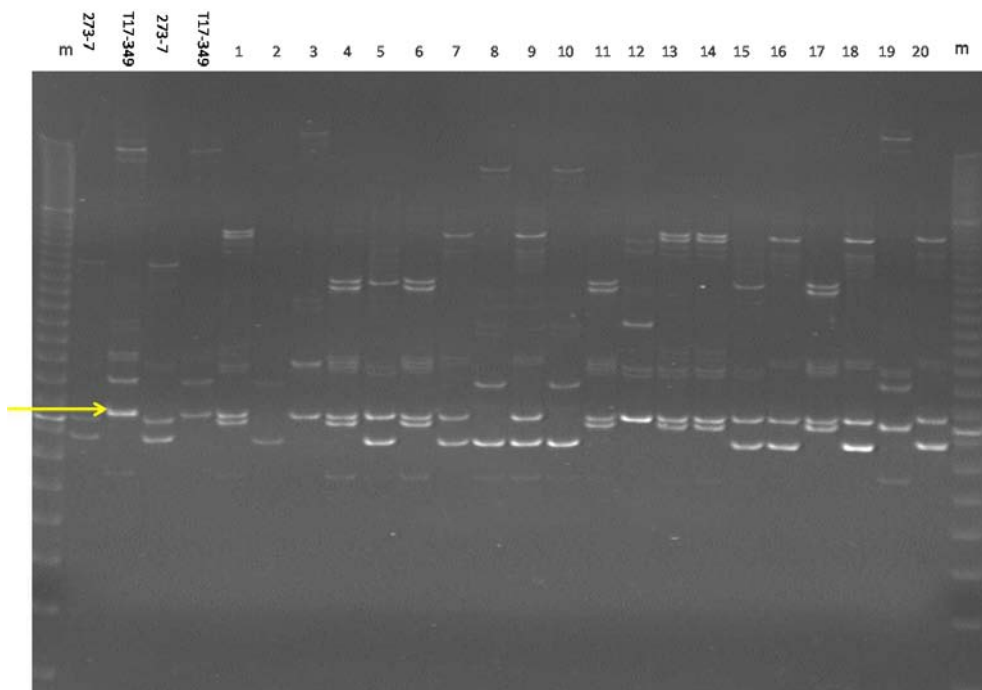




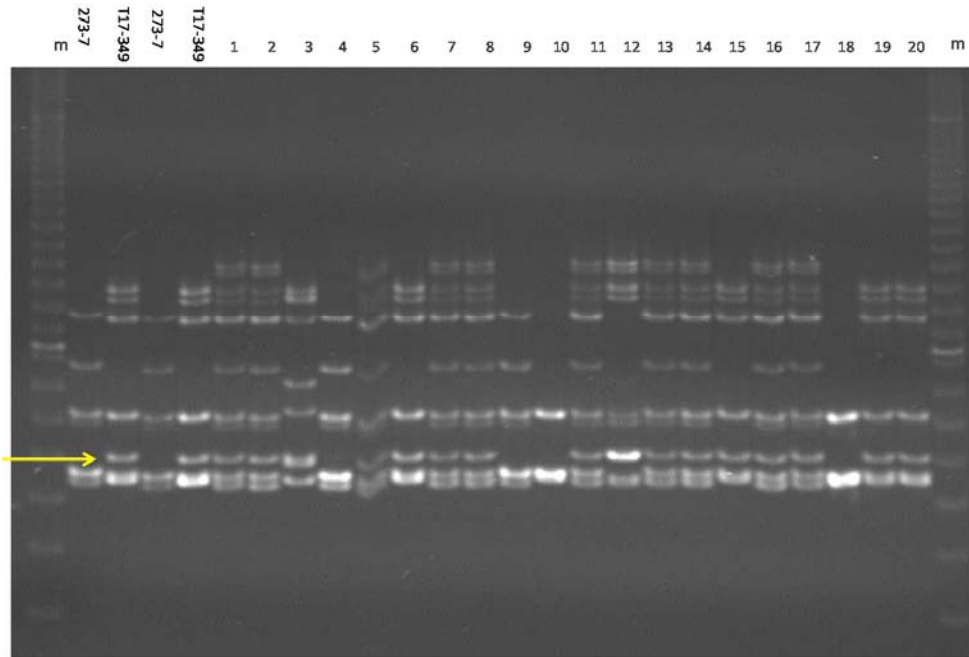
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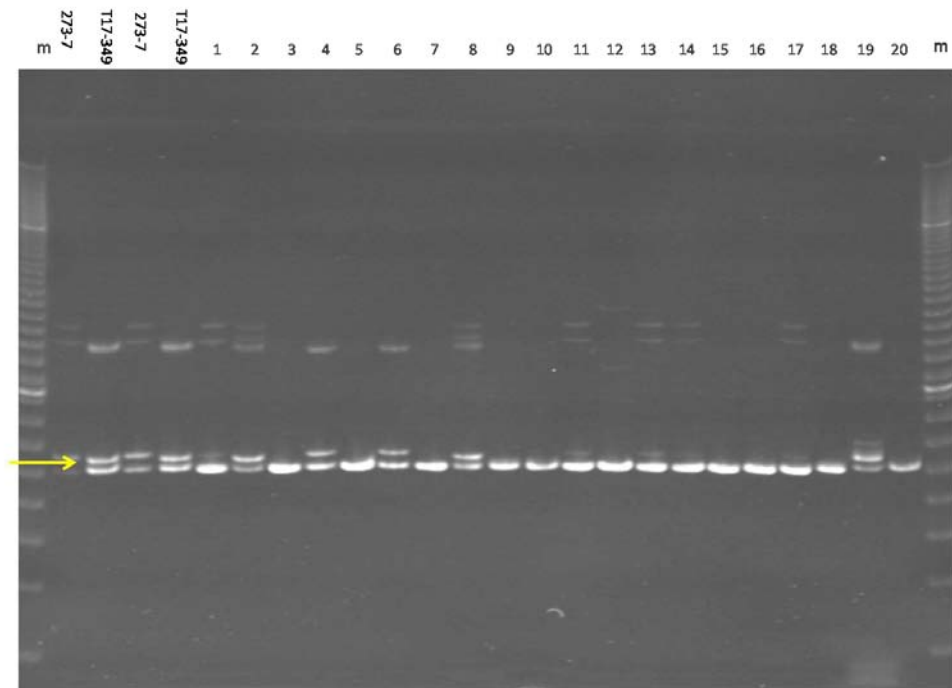
WCS0002a



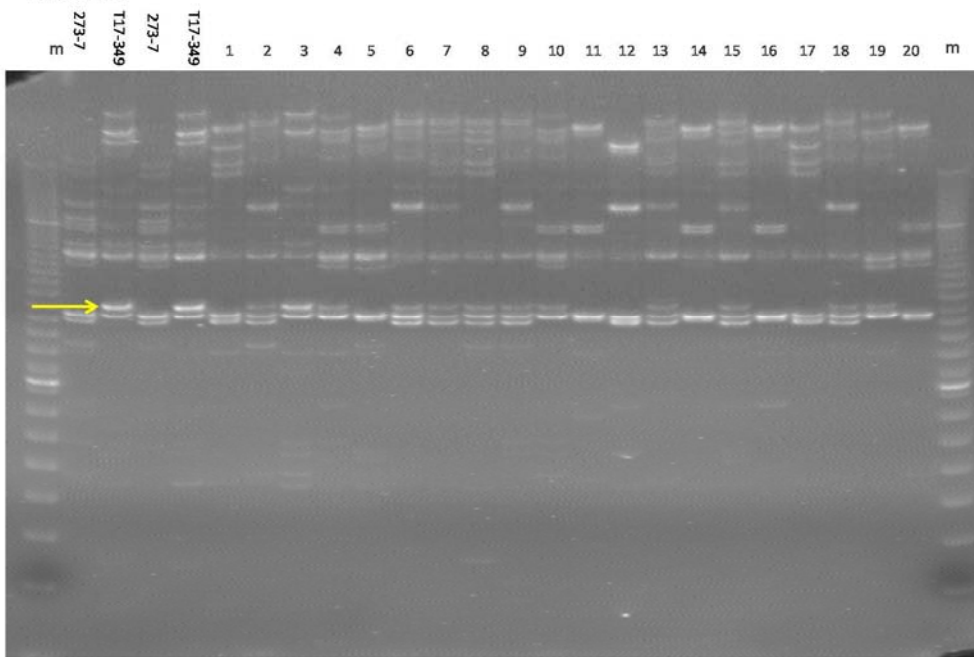
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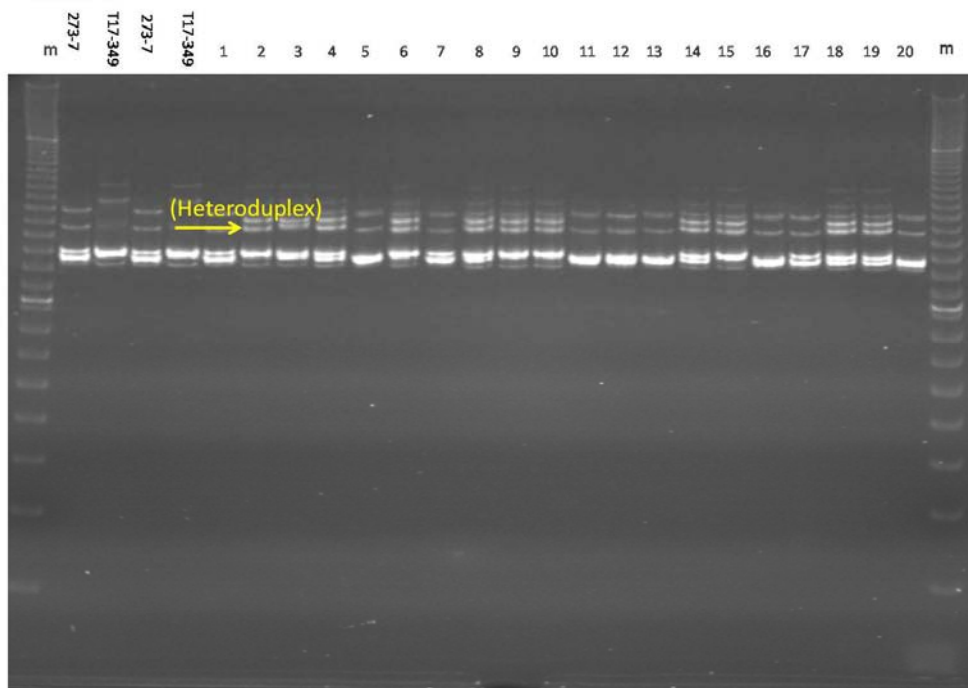
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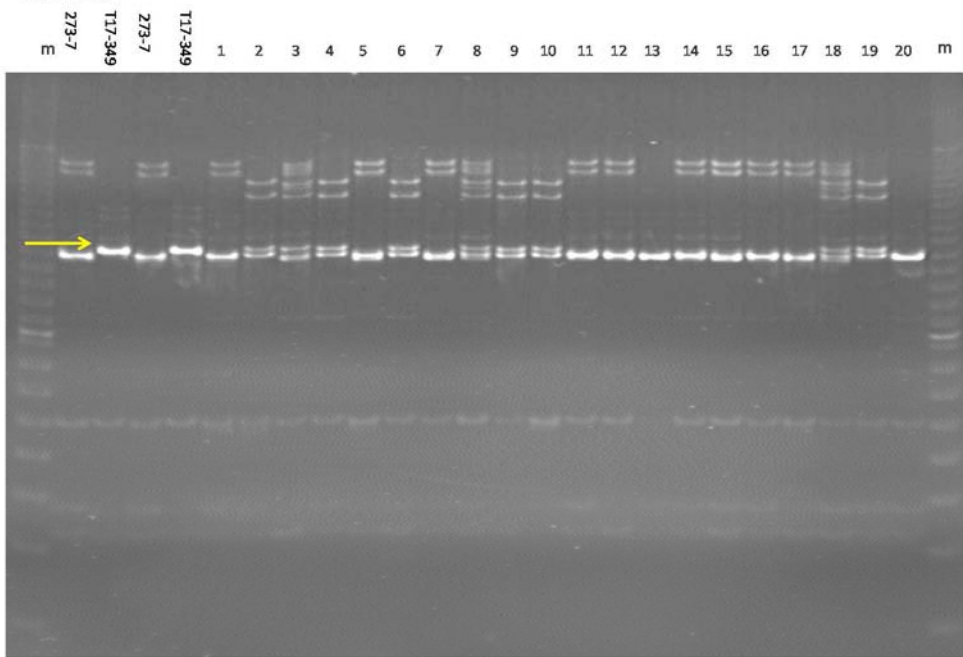
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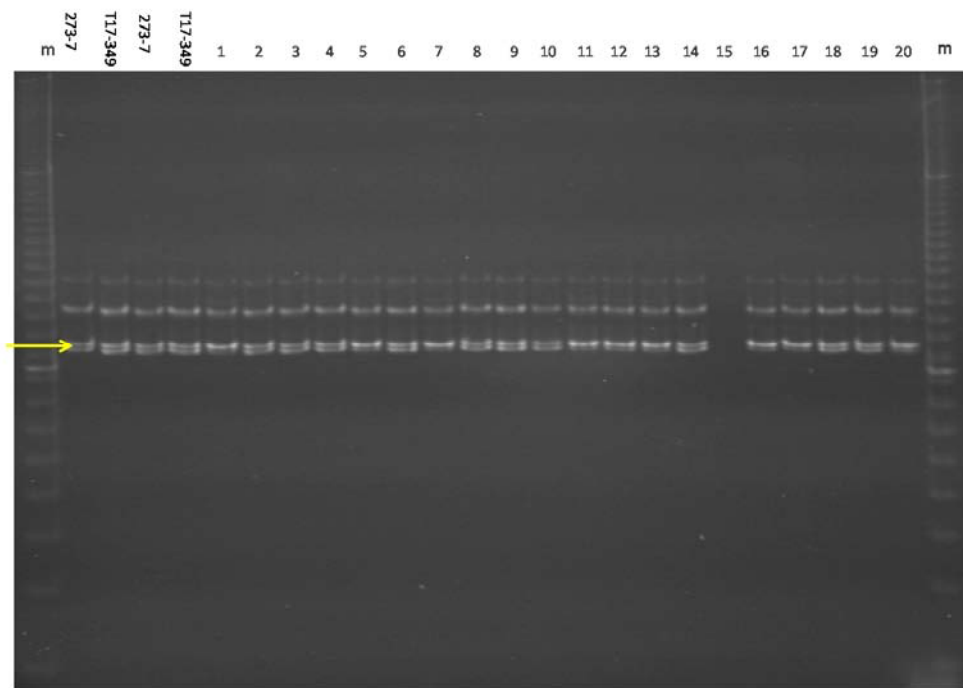
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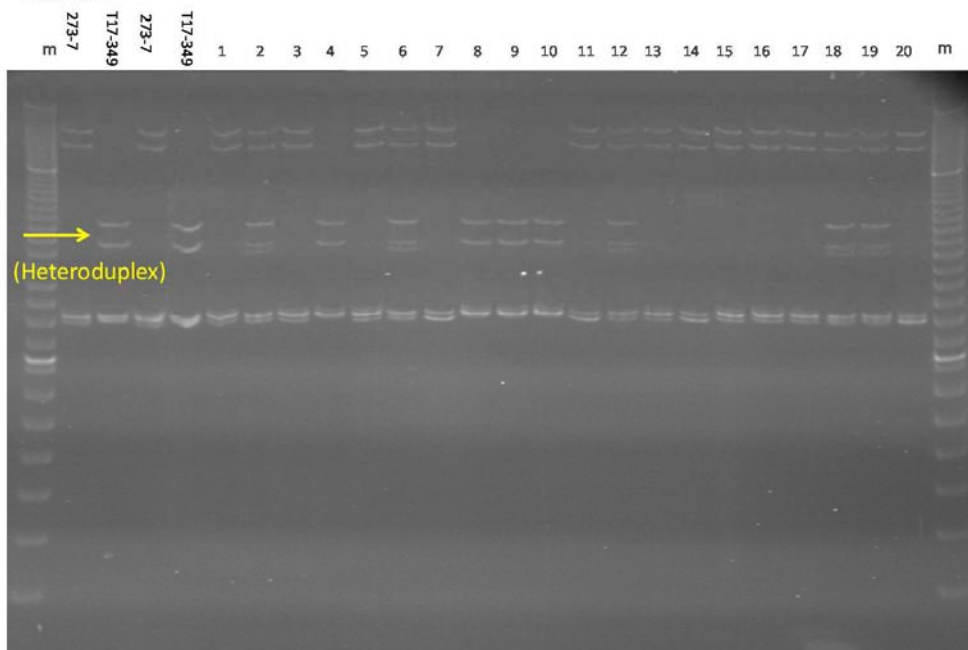
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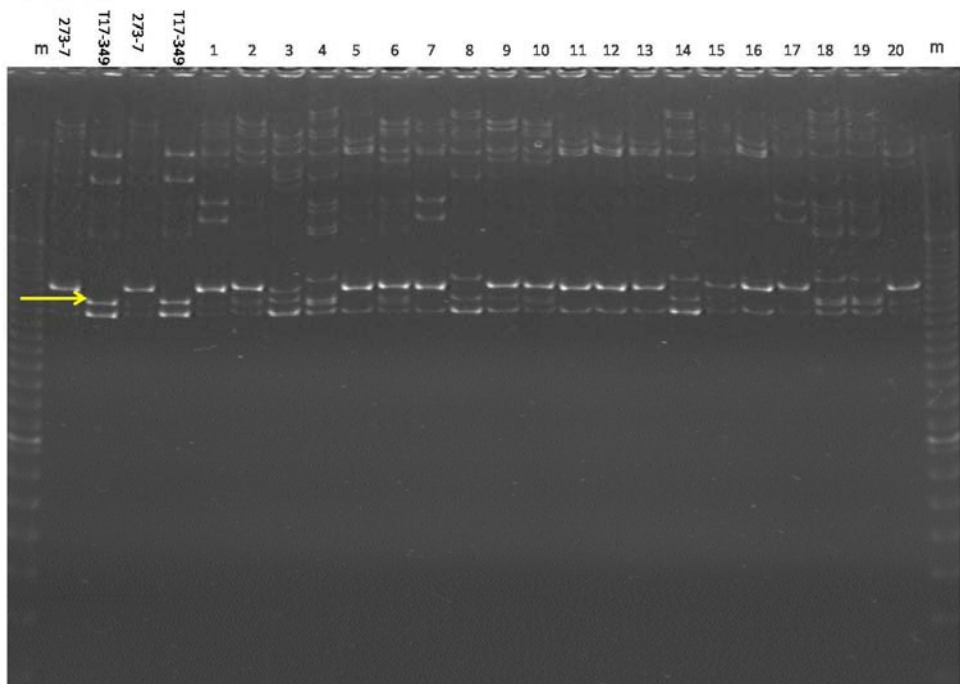
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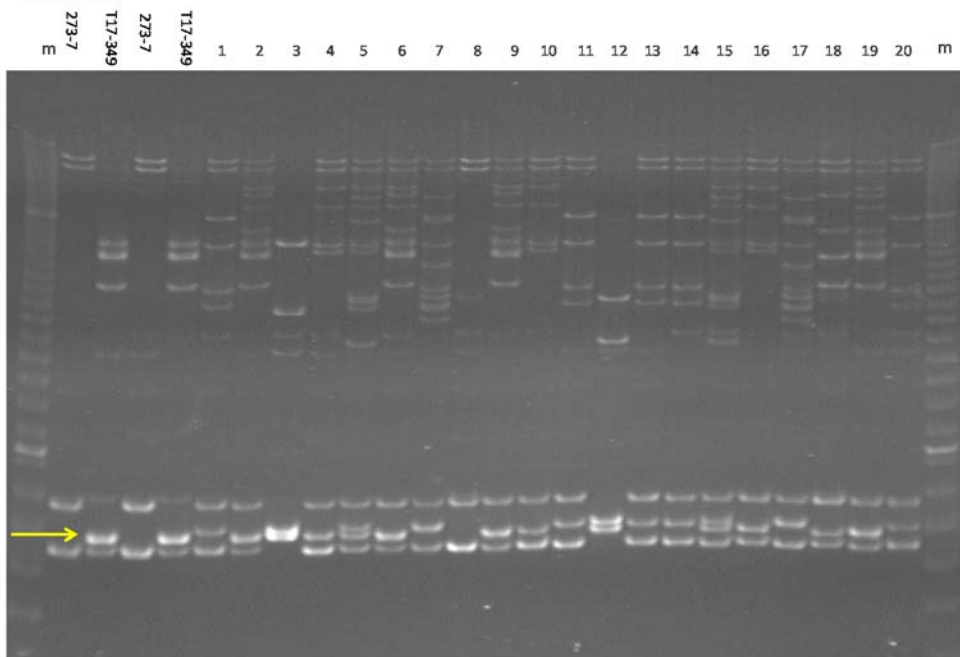
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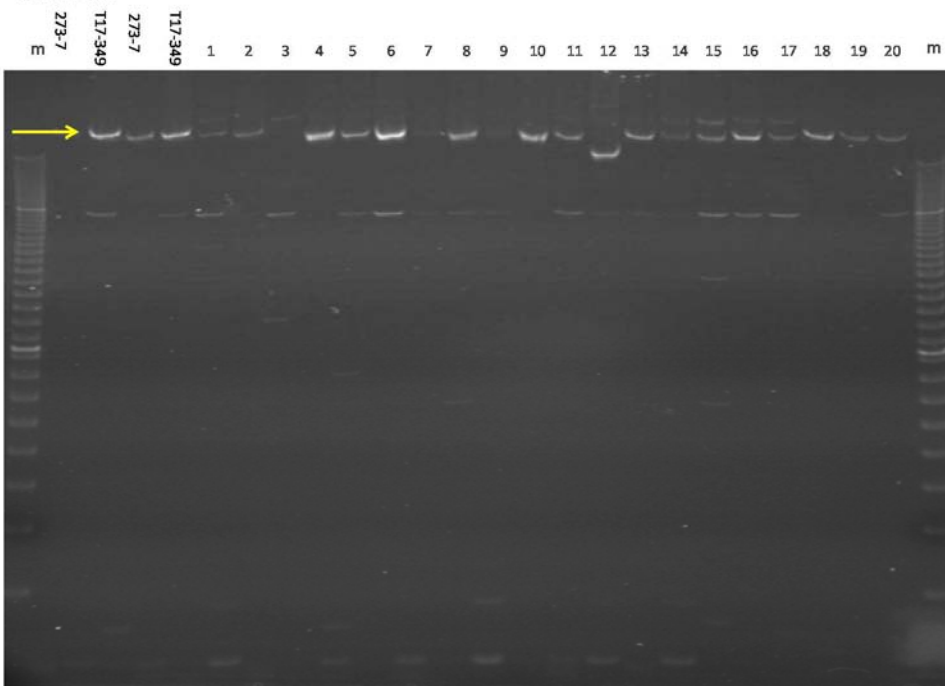
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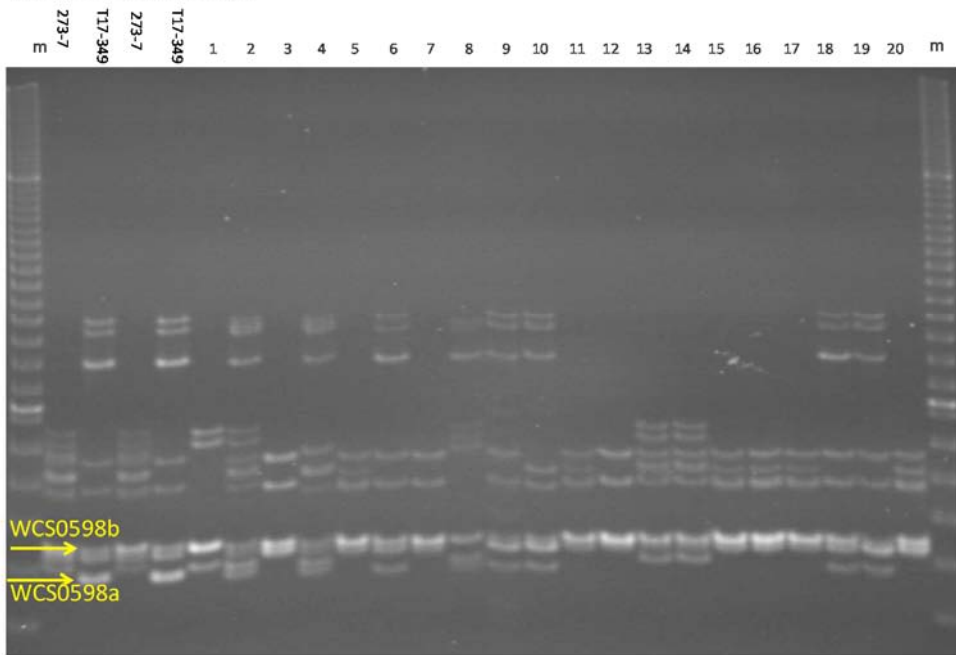
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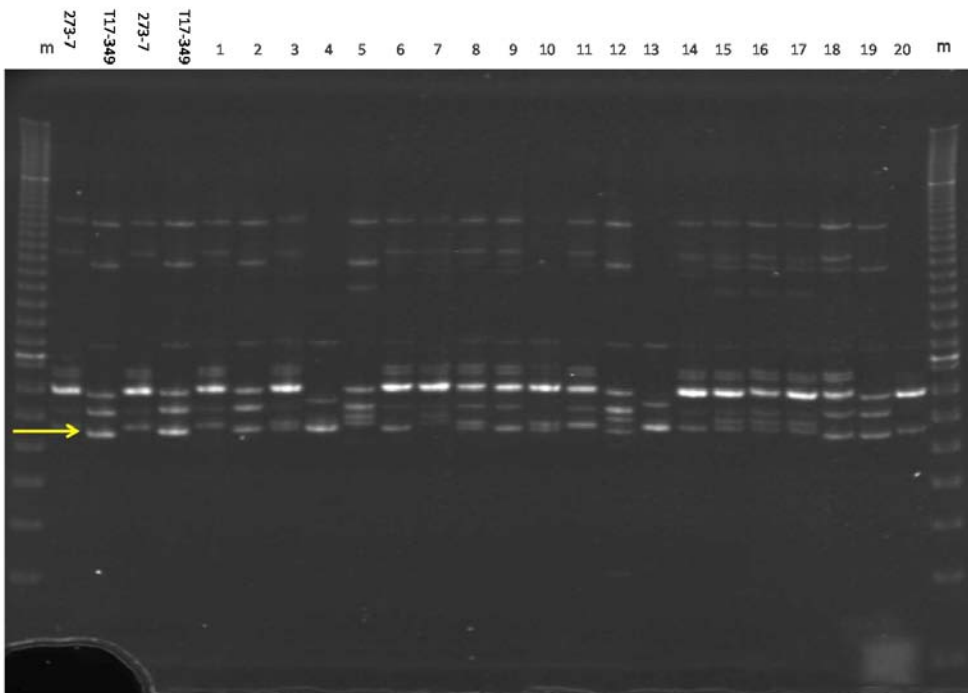
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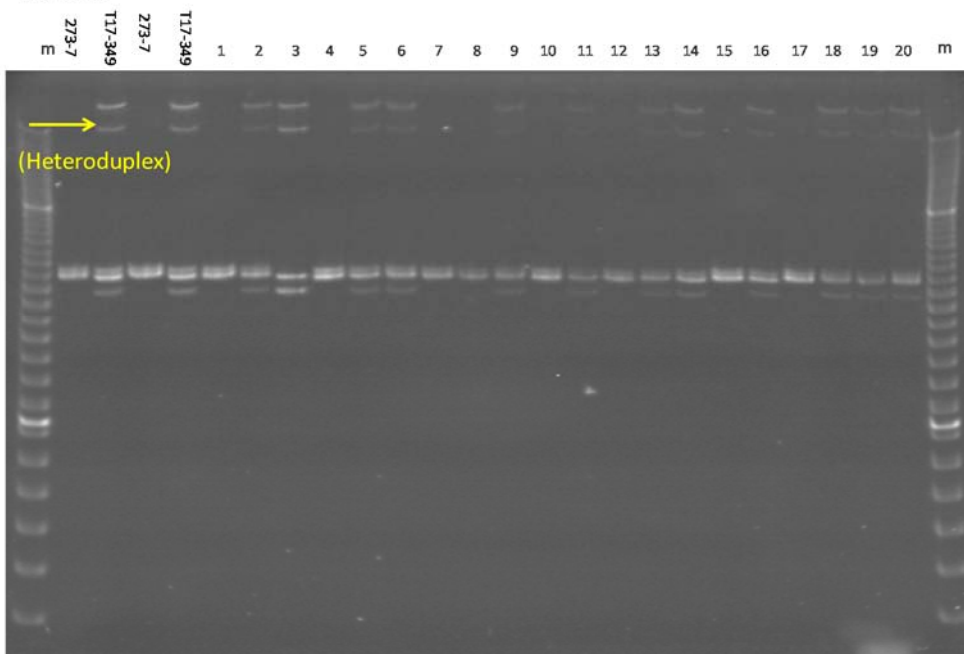
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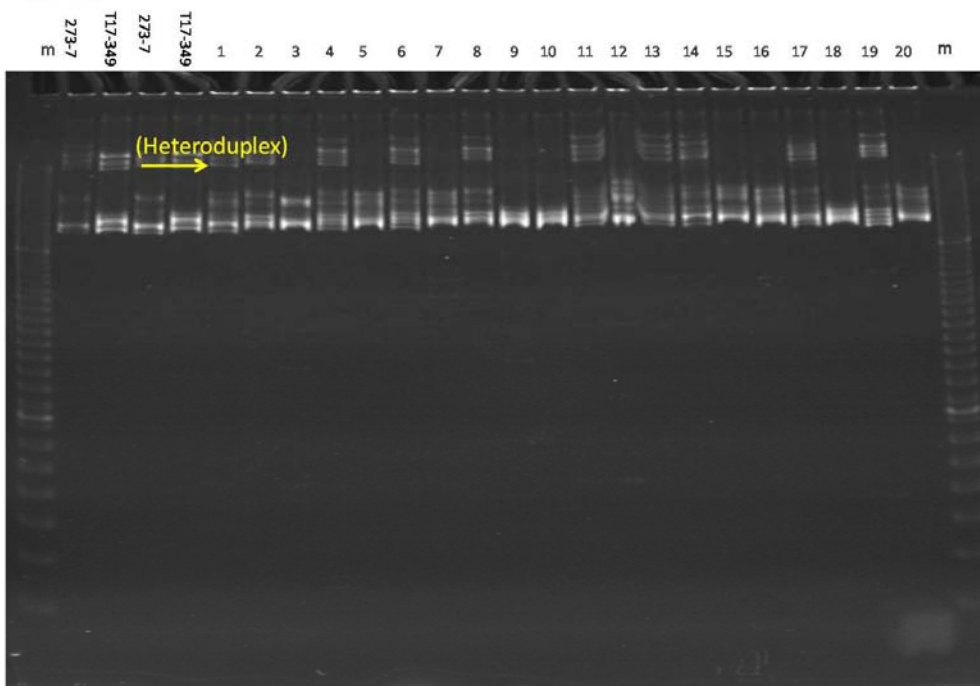
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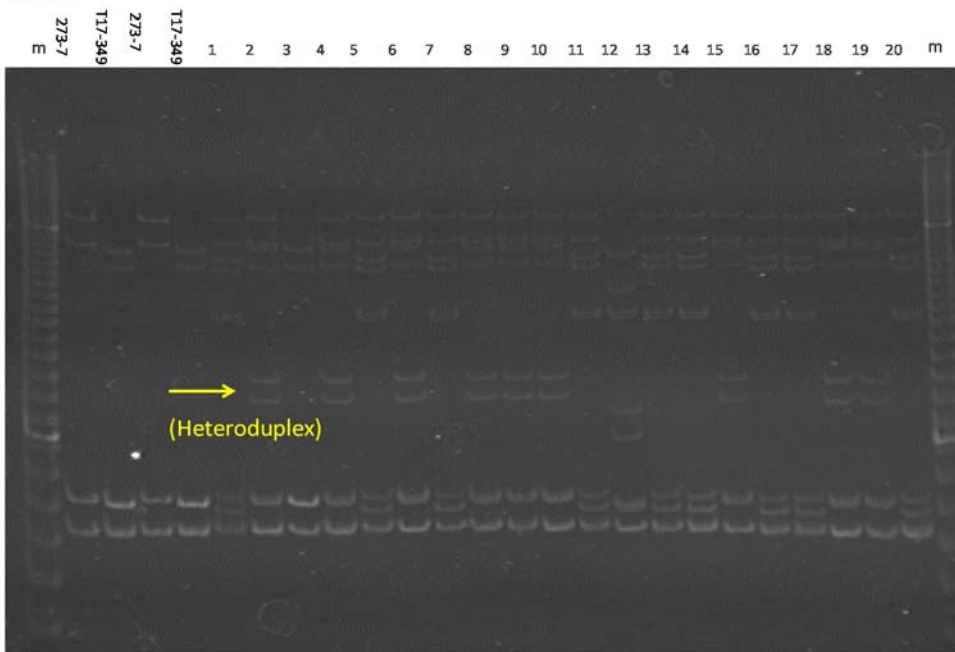


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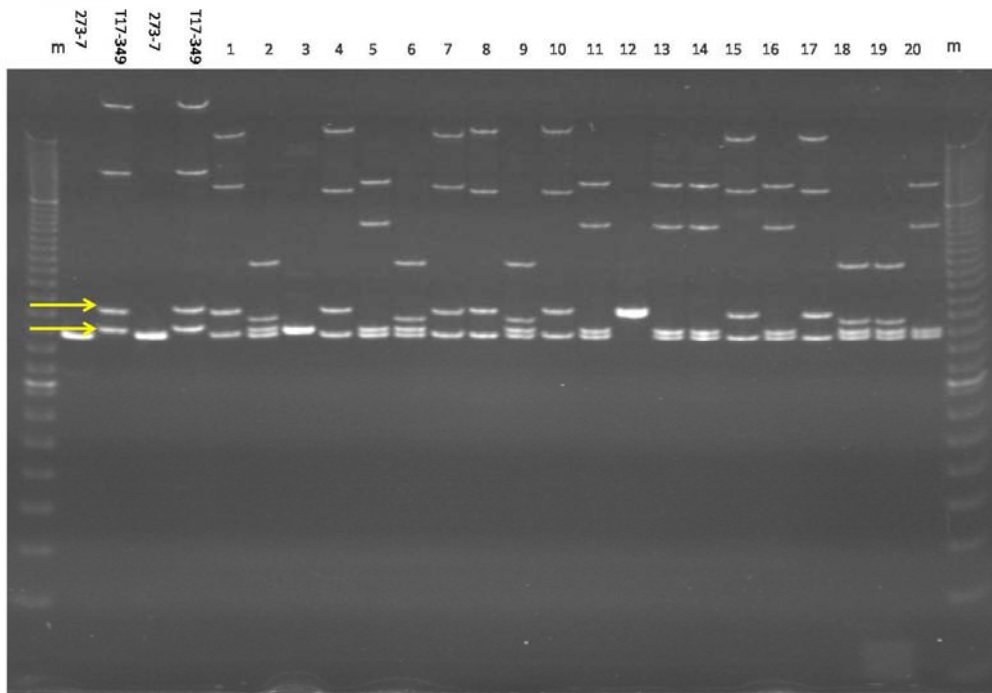




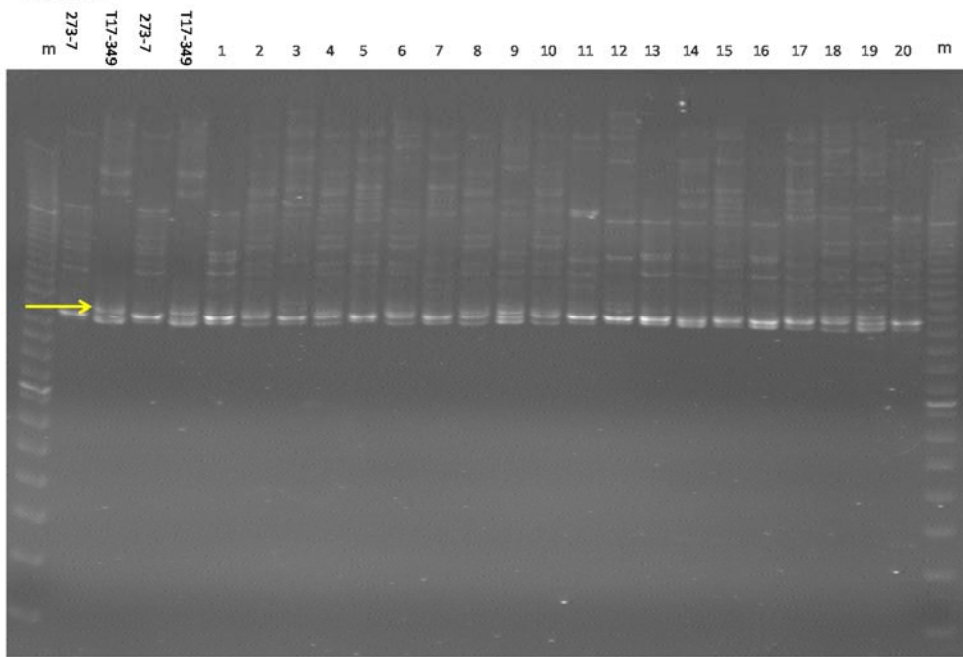
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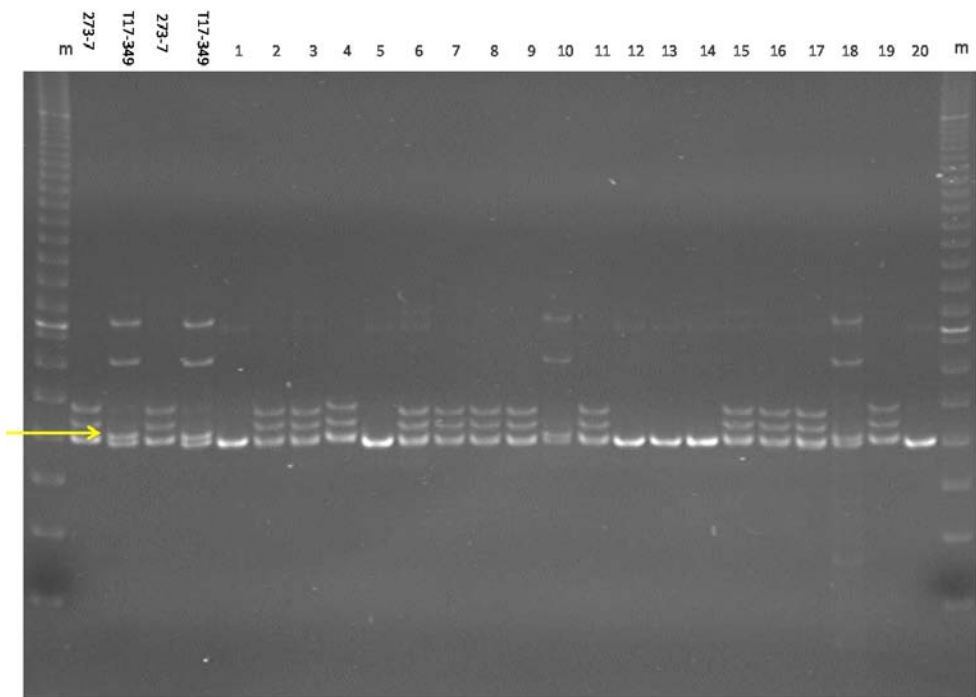
AW199a



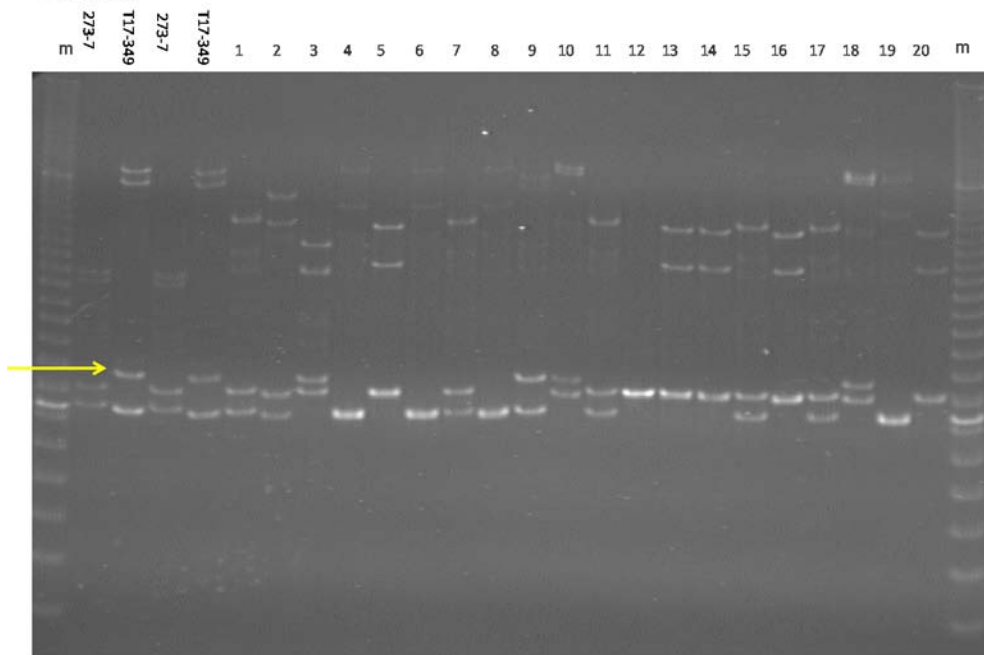
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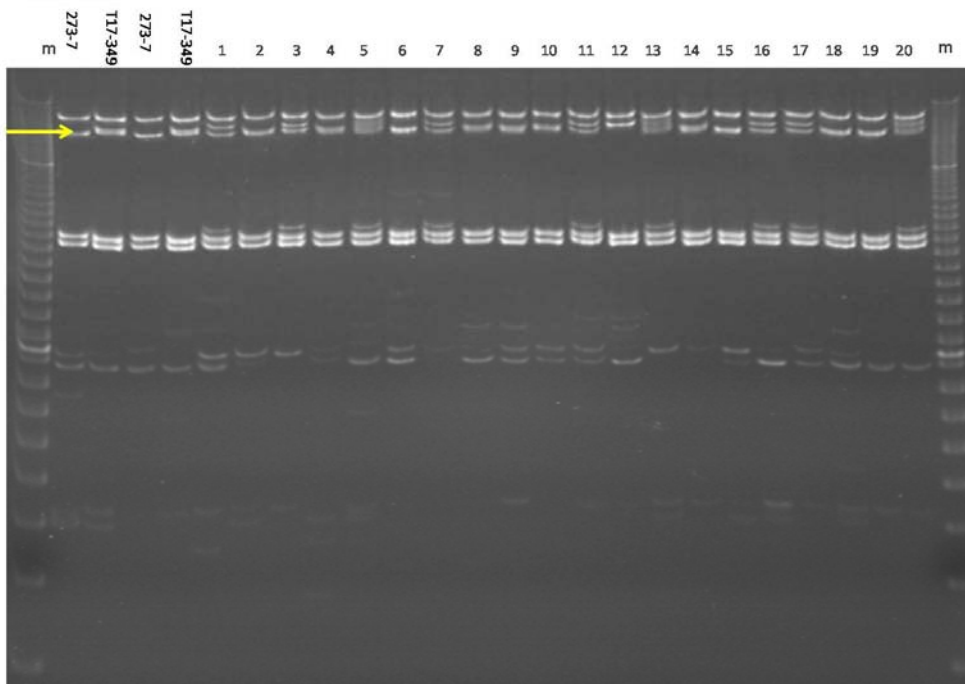
WCS0064

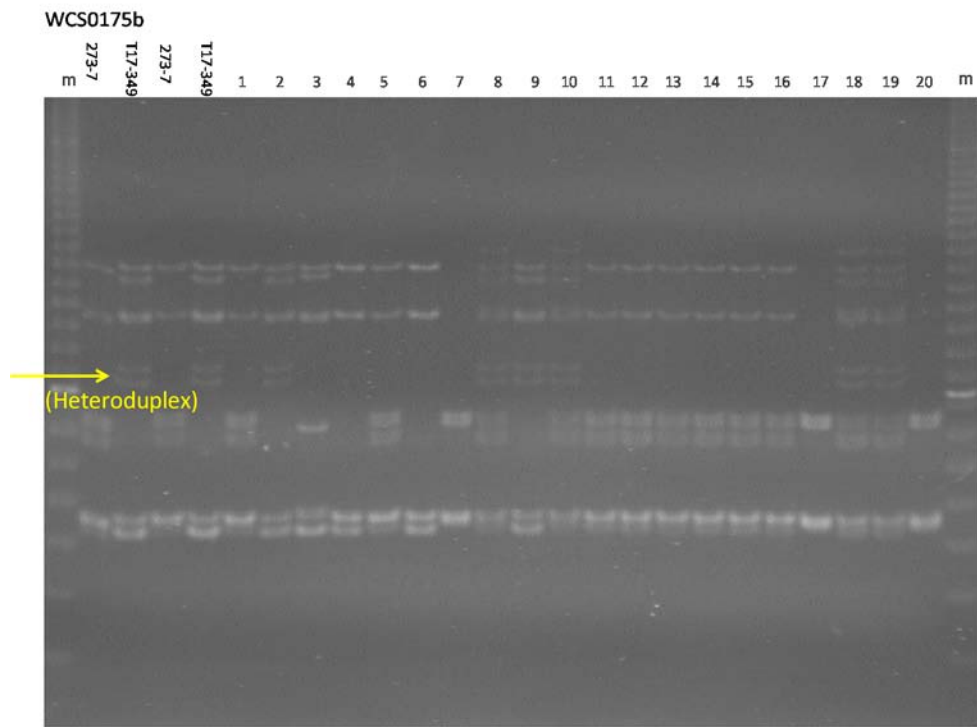


WCS0080c



WCS1870b





**Figure S5** List of loci with identified LD showing  $r^2 > 0.5$  between loci mapped onto different linkage groups, and photographs of acrylamide gel electrophoresis of PCR amplicons of the listed loci. The numbers above the acrylamide gel lanes represent IDs of  $F_1$  individuals; m represents 20 bp ladder markers. Yellow arrows indicate scored bands for locus genotyping. 'Heteroduplex' shows bands used for scoring loci but predicted as heteroduplex bands.

### Supporting Tables

These supporting tables are available for download at  
<http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.002600/-/DC1>.

**Table S1** Primer sequences, SSR motifs, and expected sizes of amplicons of white clover EST-SSR markers.

**Table S2** Locus name, position, and segregation distortion of the integrated and parental-specific maps.

**Table S3** List of the non-redundant white clover ESTs.

**Table S4** Number of mapped multiple loci and loci exhibiting parental-specific polymorphisms.

**Table S5** Locus name and position of an integrated linkage map of red clover developed from a cross between HR and R130.