

# **Detection of novel QTLs for late blight resistance derived from the wild potato species *Solanum microdontum* and *Solanum pampasense***

## ***Genes***

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## **Genetic maps created using SNP markers identified using Genotyping-by-Sequencing of each population**

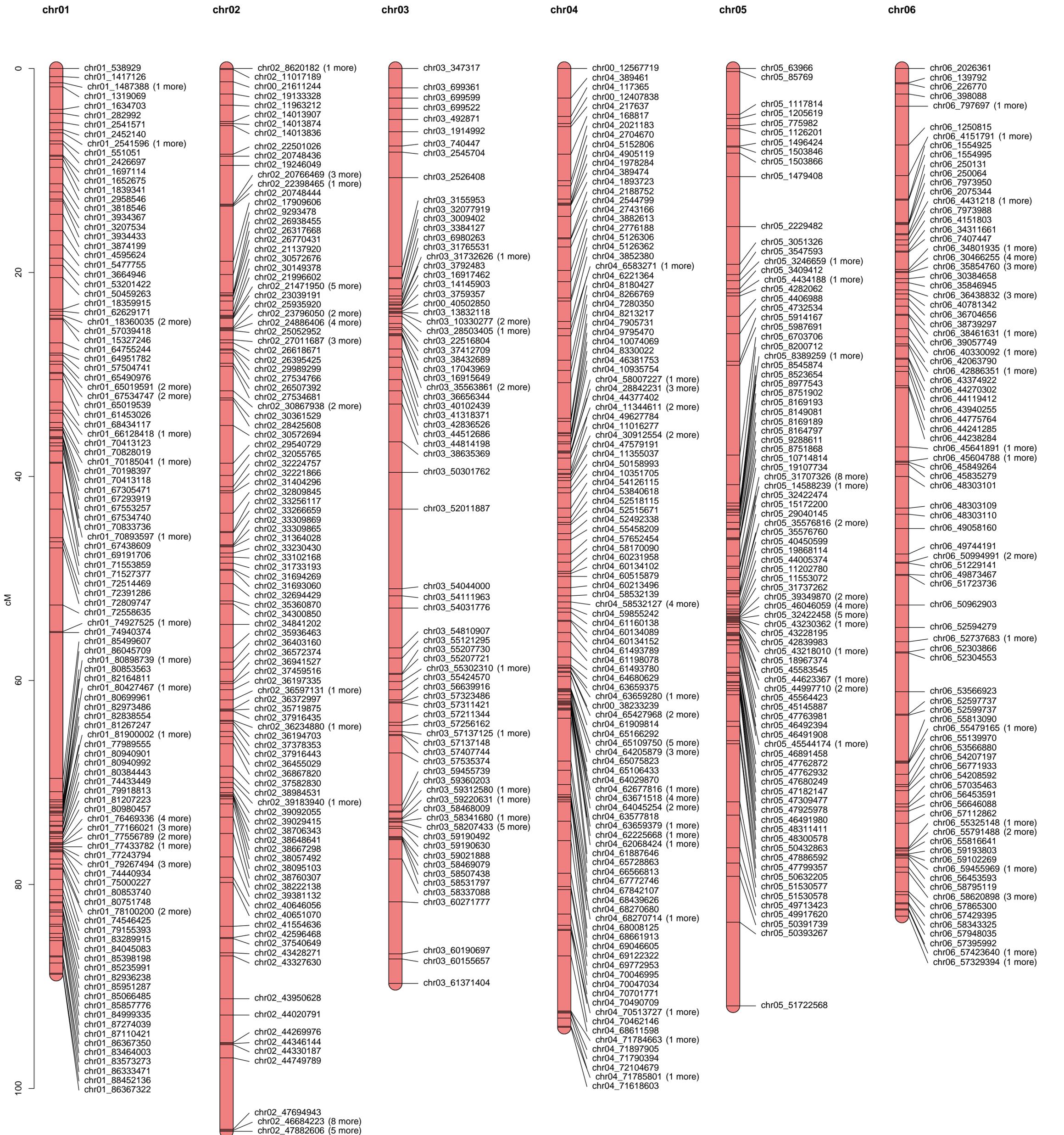
Page 1-2: Genetic map created using 1431 SNP markers of all types (segregating in the female parent <lmxll>; segregating in both parents <hkxhk>; segregating in the male parent <nnxnp>) of the MCD diploid population.

Page 3-4: Genetic map created using 752 SNP markers unique to the male parent of the MCD diploid population.

Page 5-16: Genetic map created using 967 SNP markers unique to the female parent of the PAM tetraploid population.

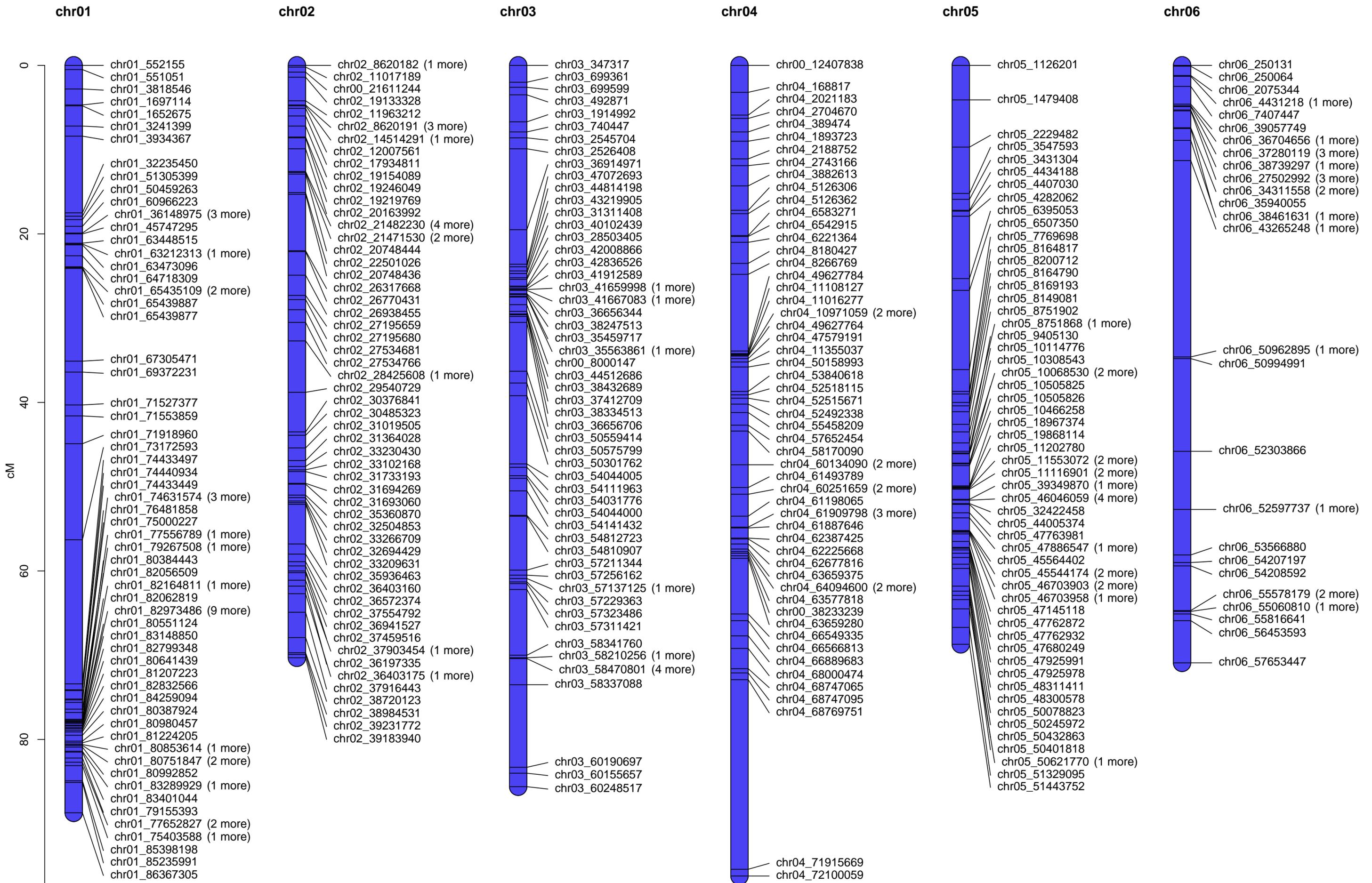
Page 17: Assignment of chr00 contigs to chromosomes based on MCD and PAM genetic maps.

# MCD genetic map (All marker types, chr01–chr06)





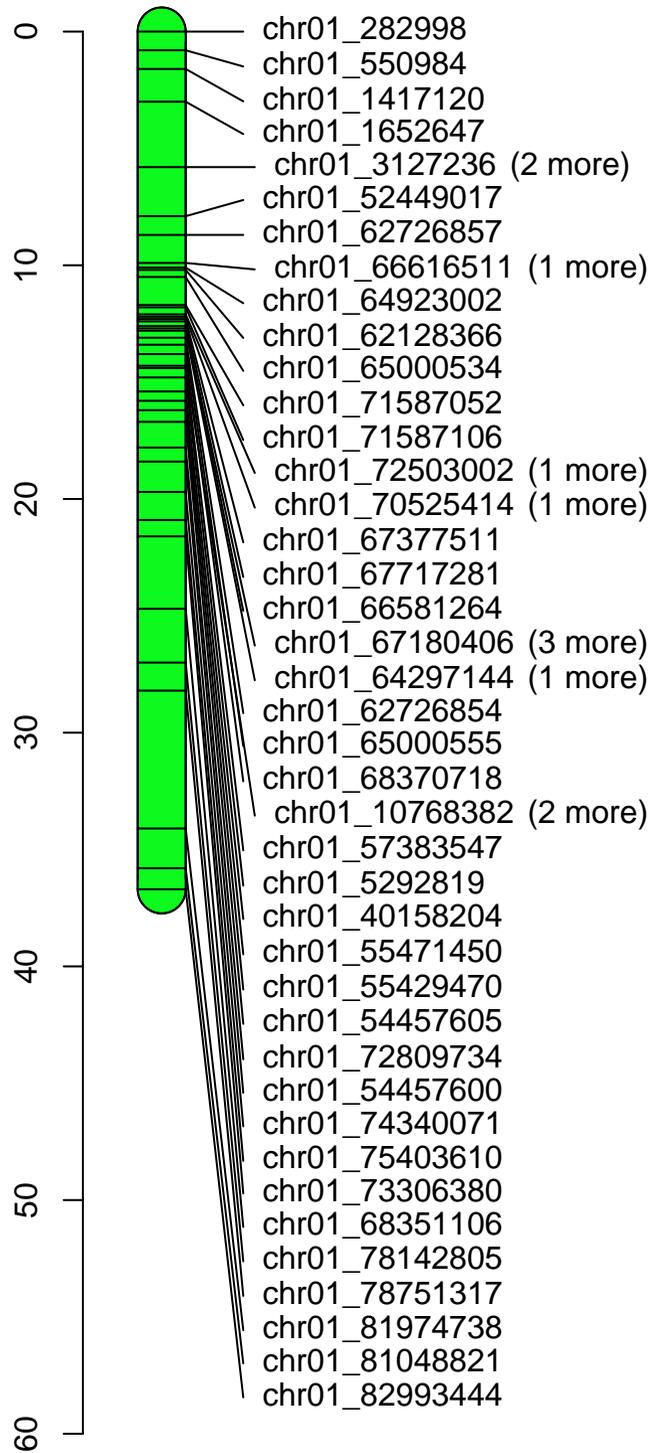
# MCD MALE genetic map (markers unique to IVP10-281-1, chr01-chr06)



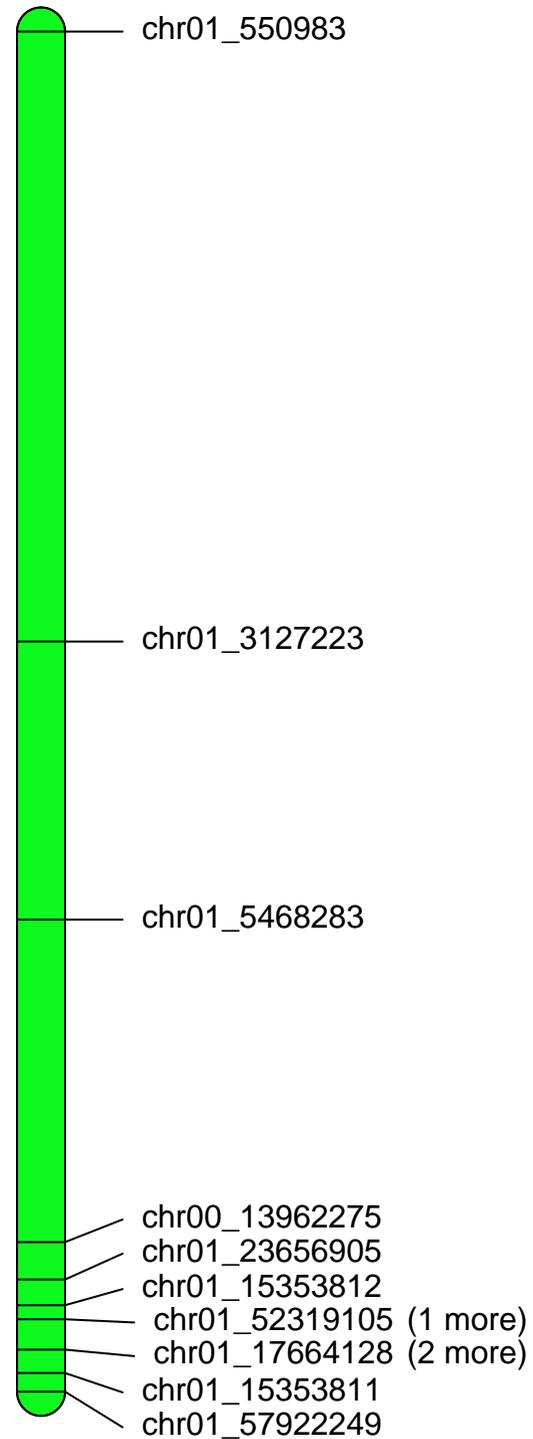


# PAM genetic map

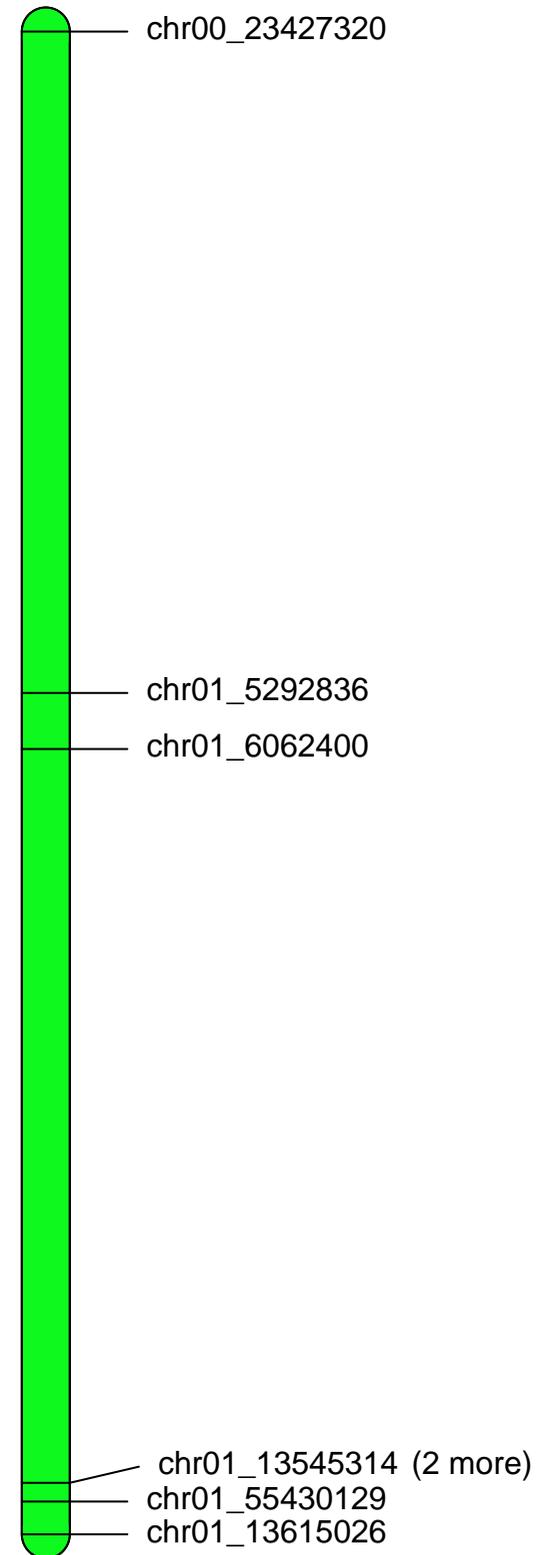
chr01A



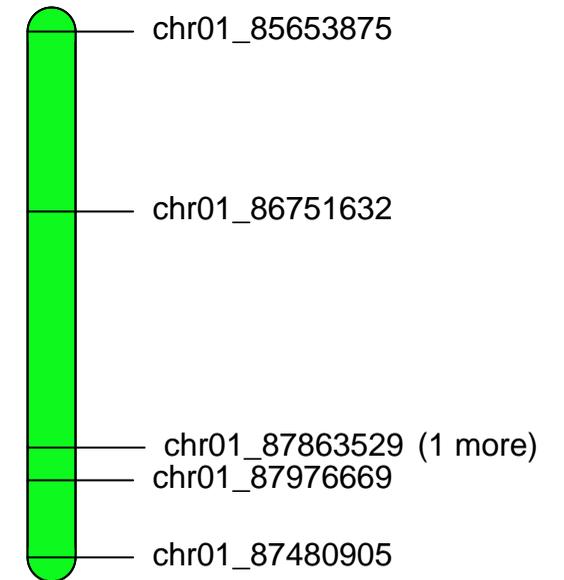
chr01B



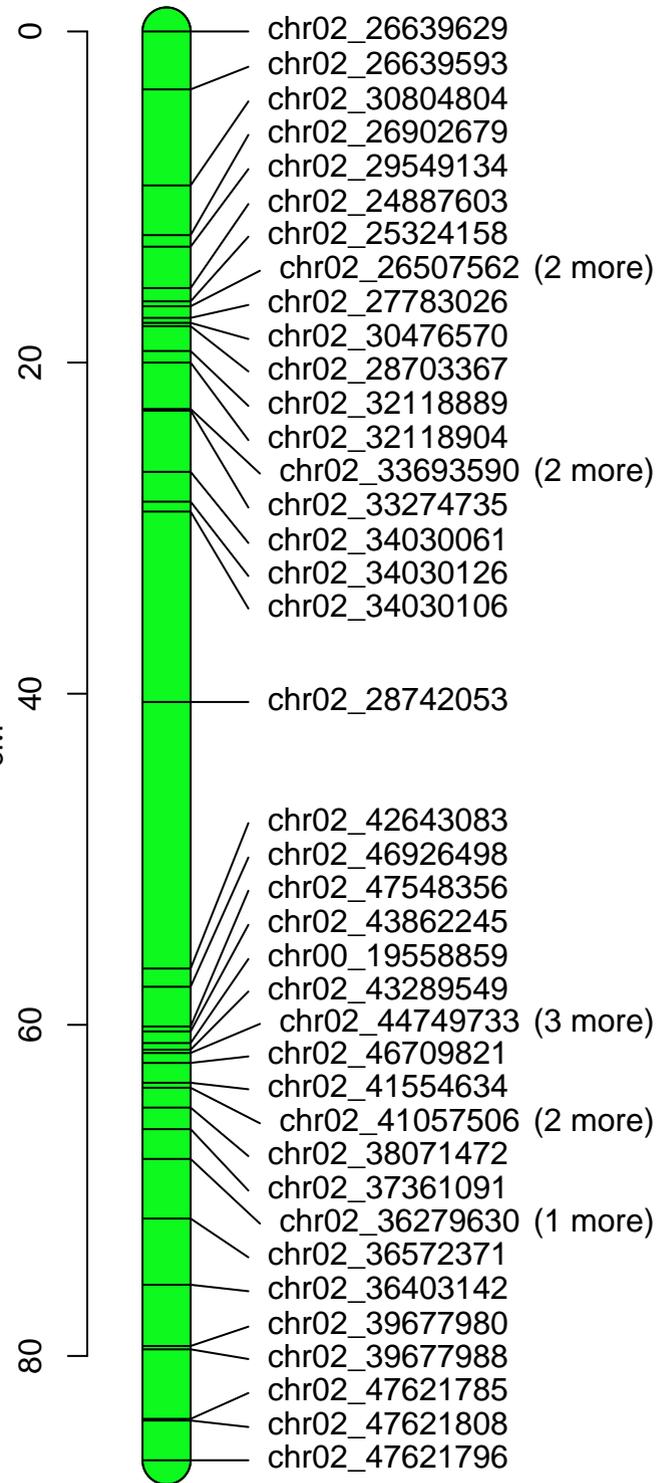
chr01C



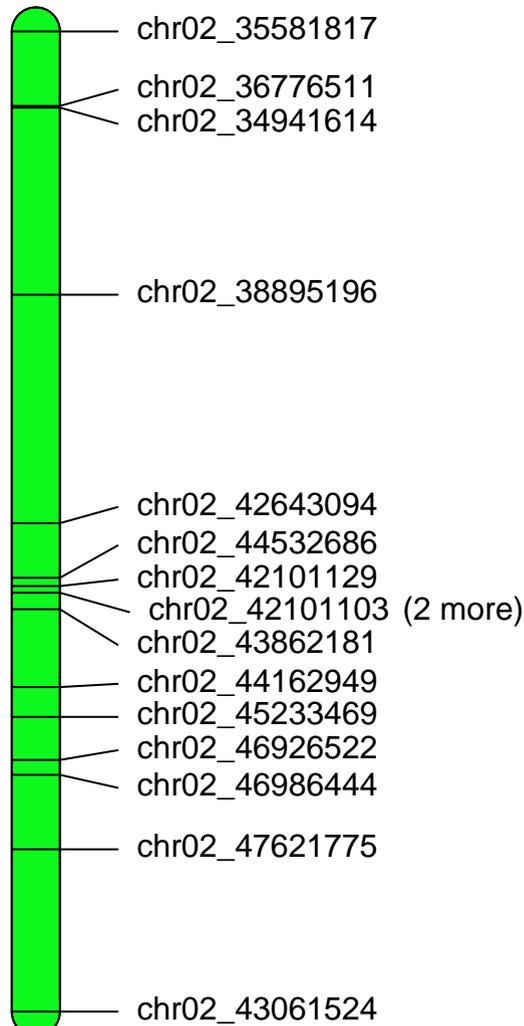
chr01D



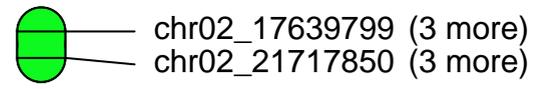
chr02A



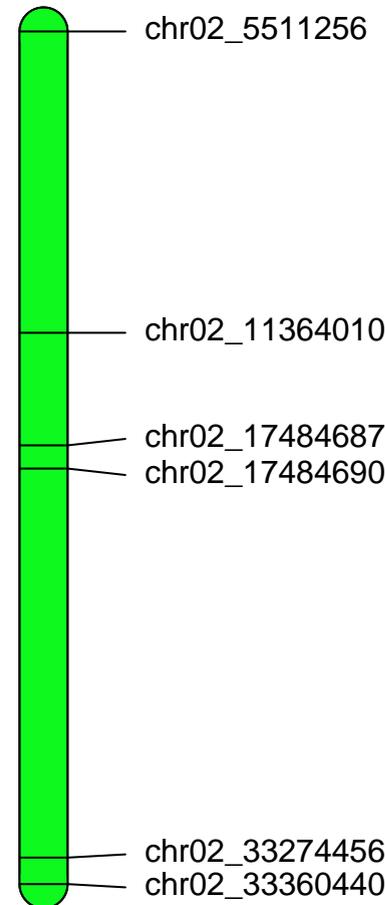
chr02B



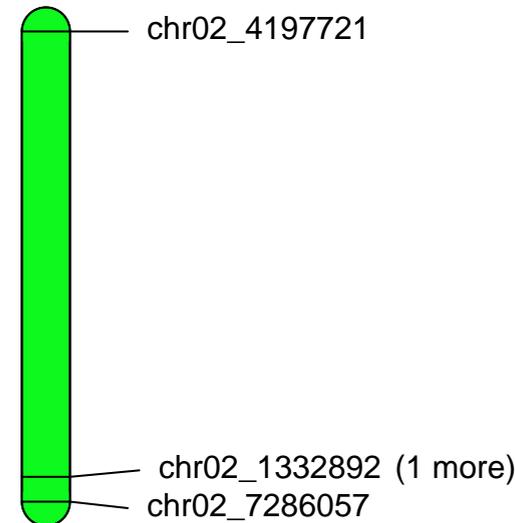
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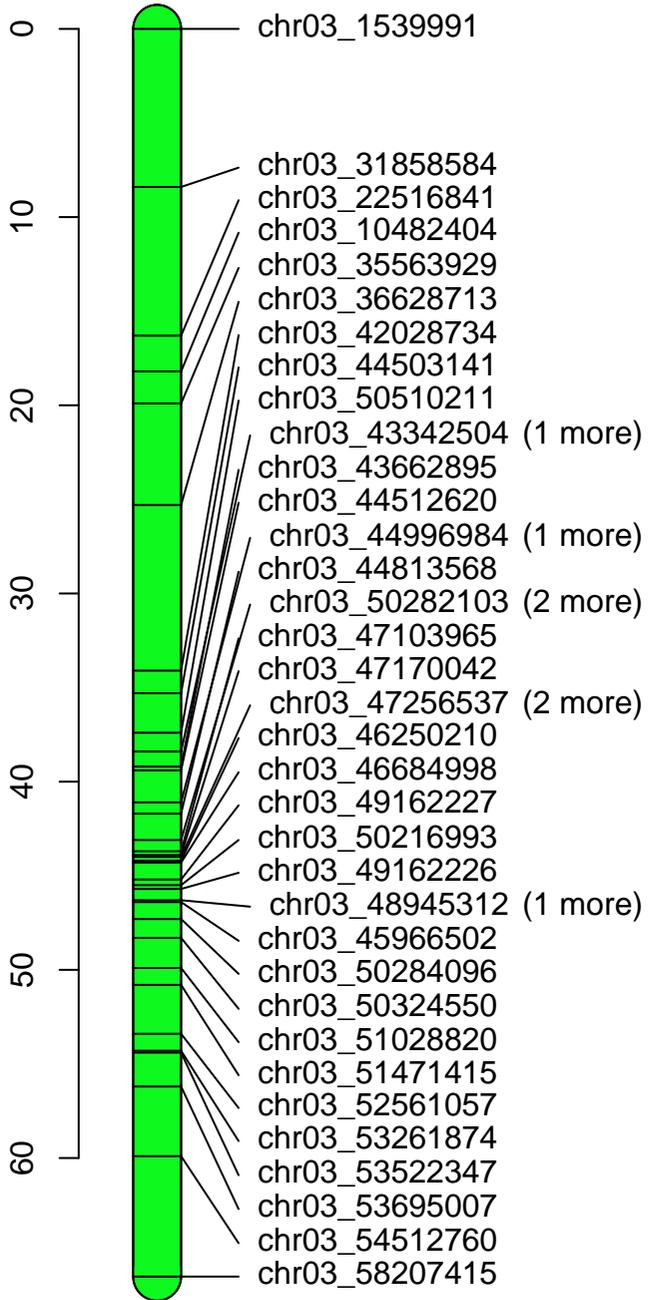
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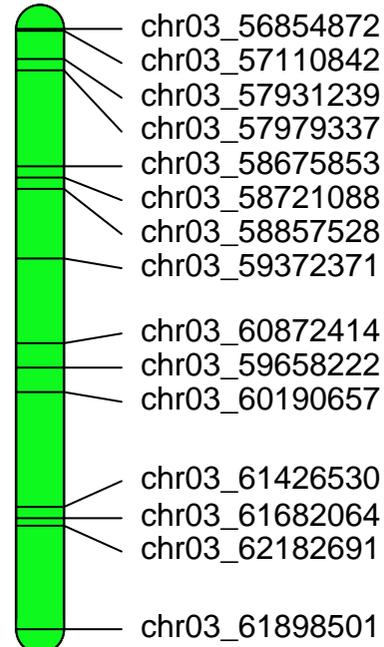
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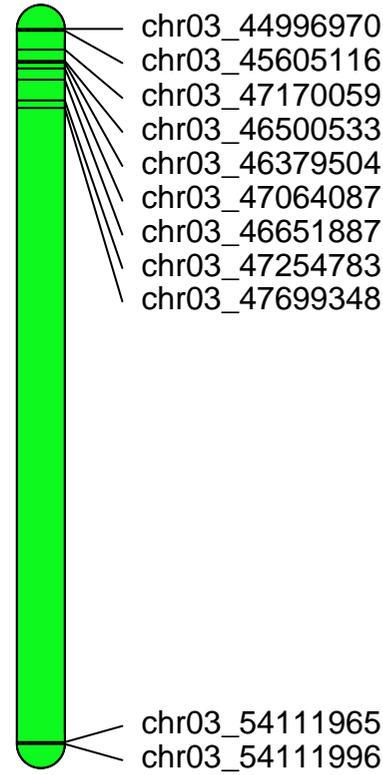
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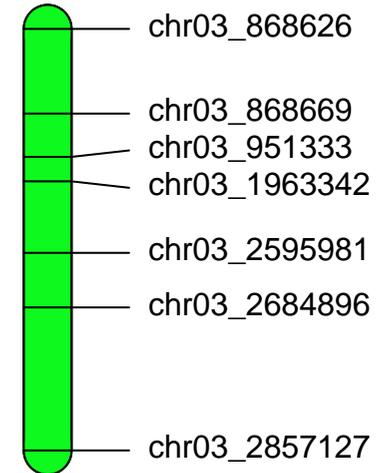
chr03B



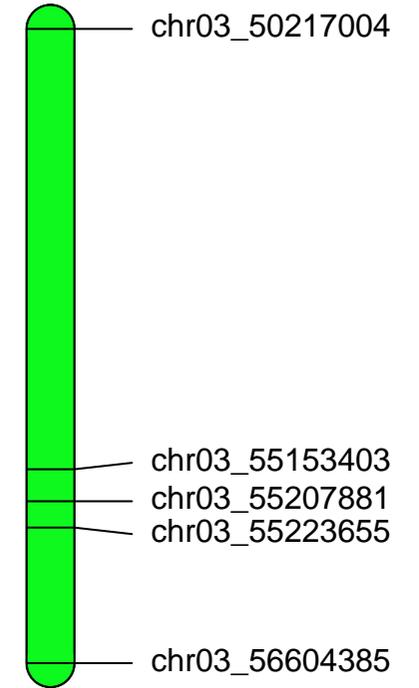
chr03C



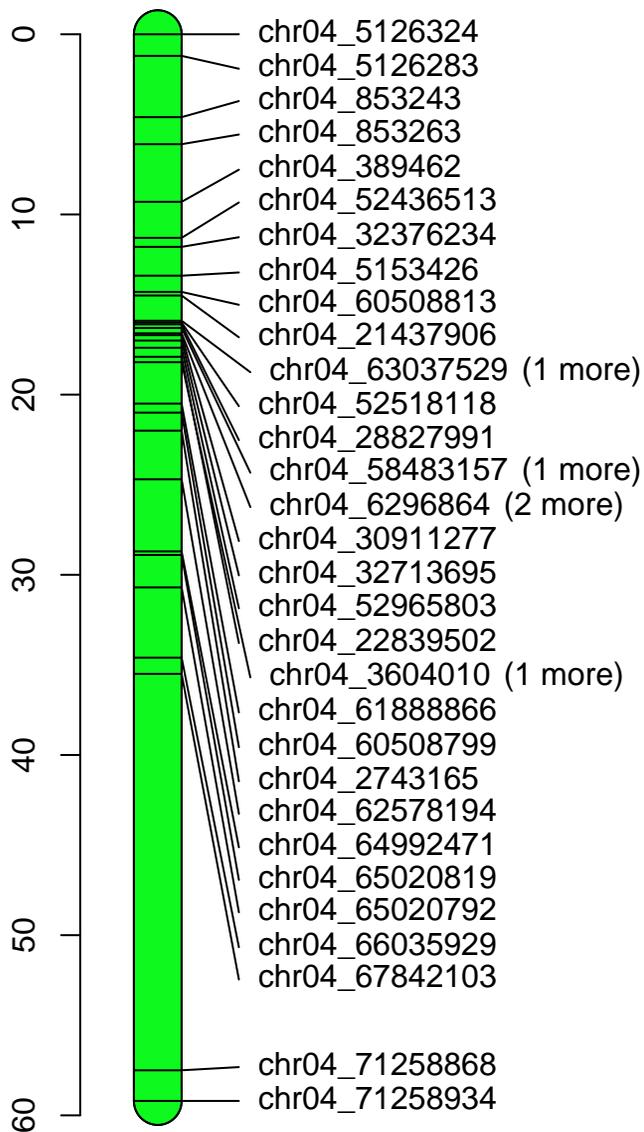
chr03D



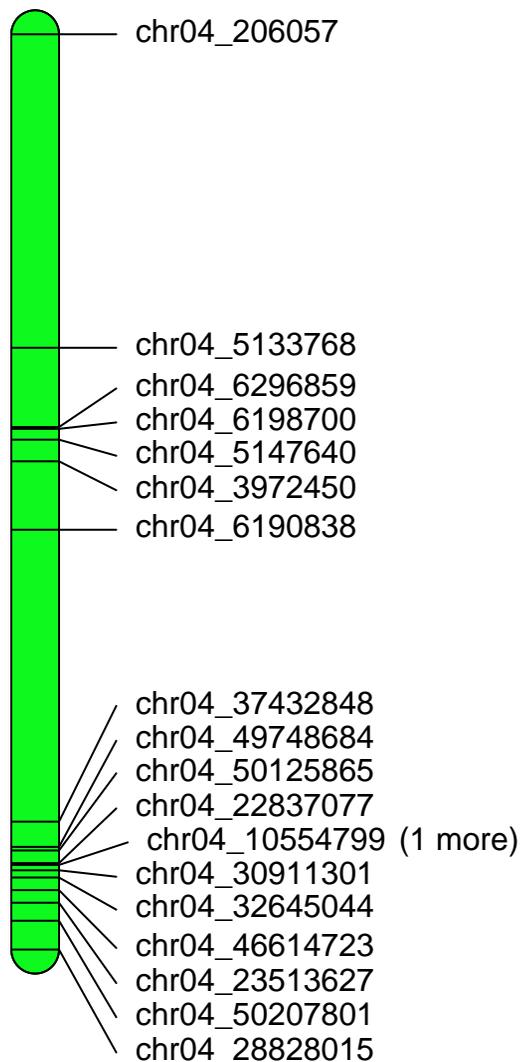
chr03E



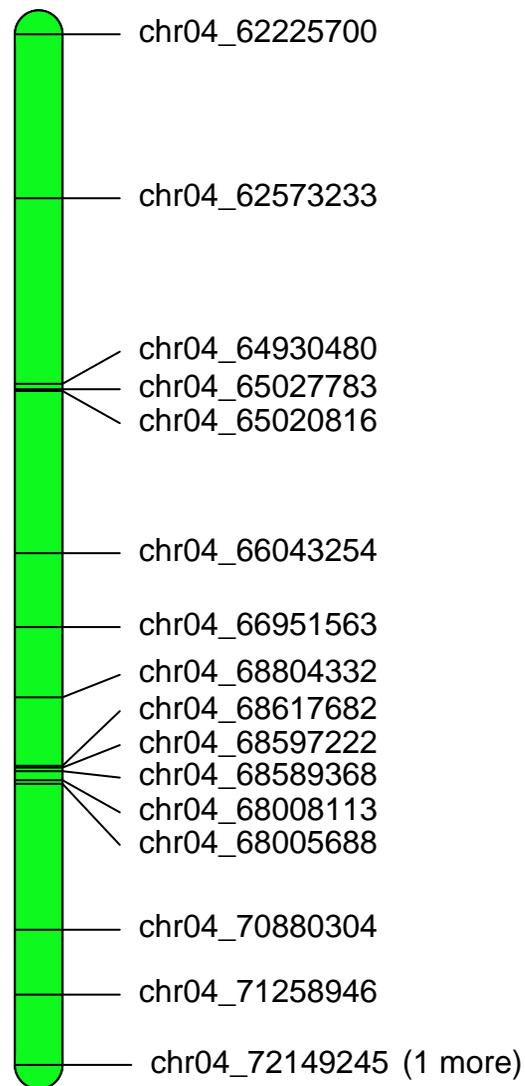
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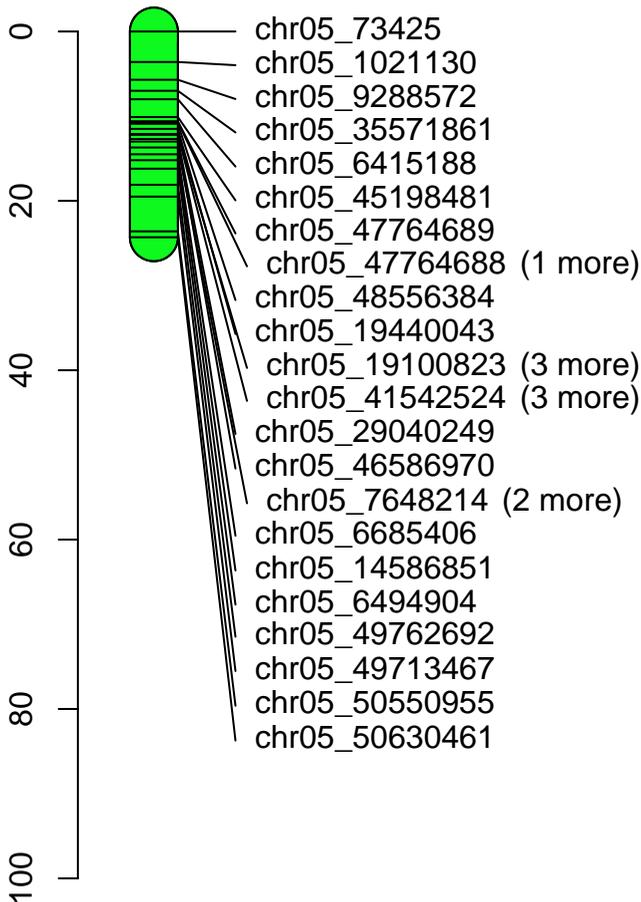
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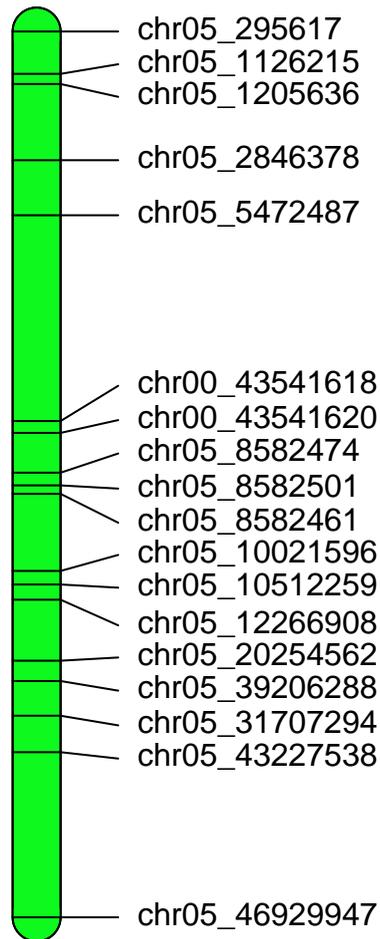
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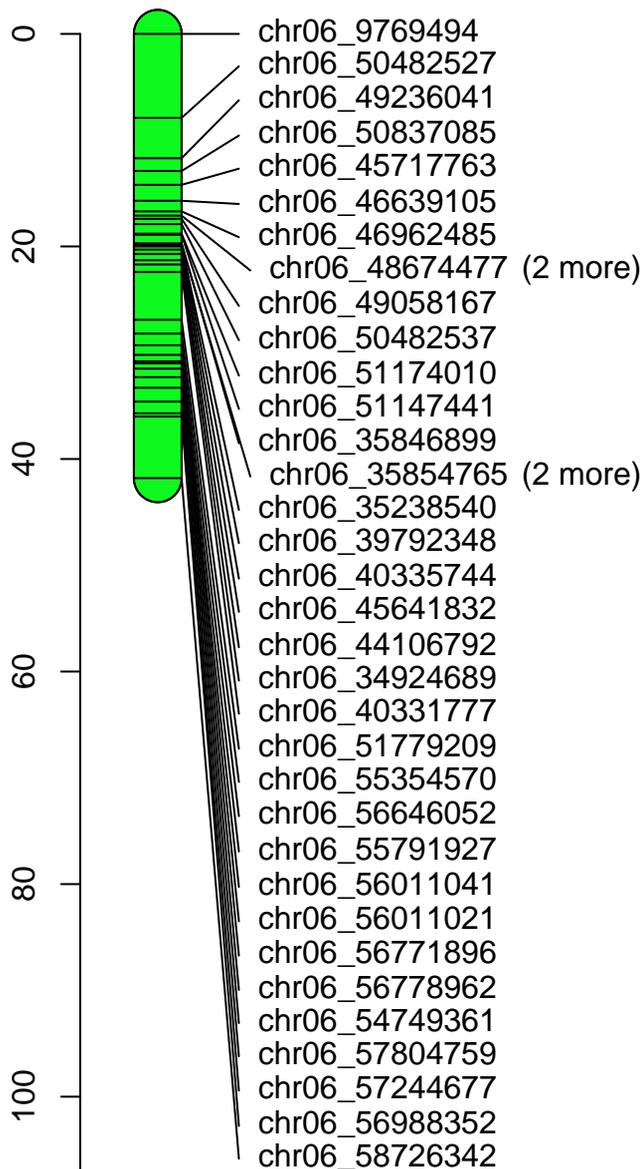
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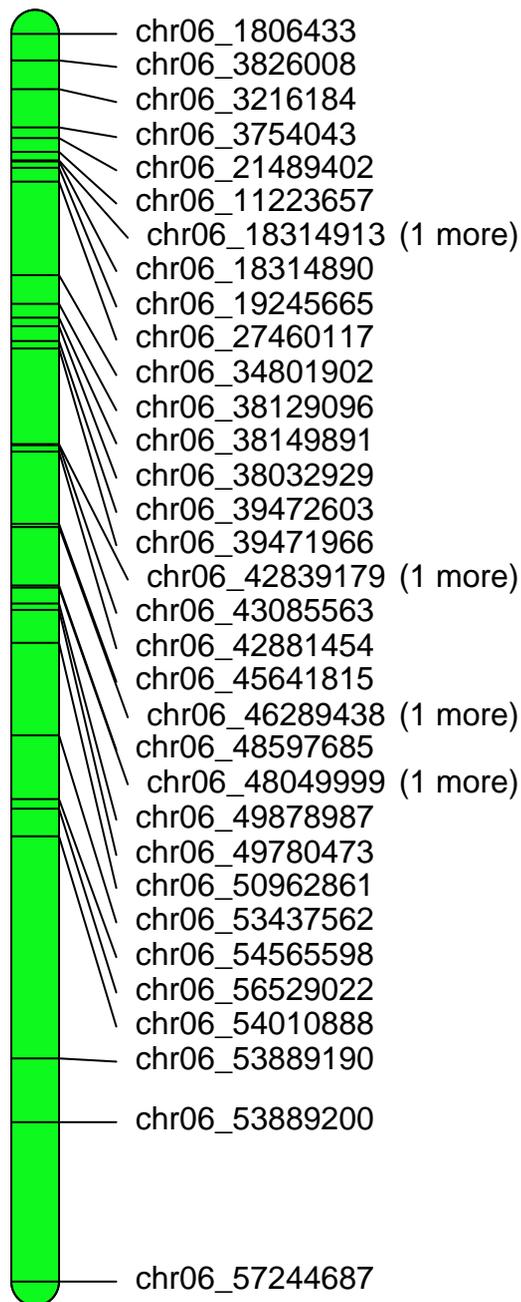
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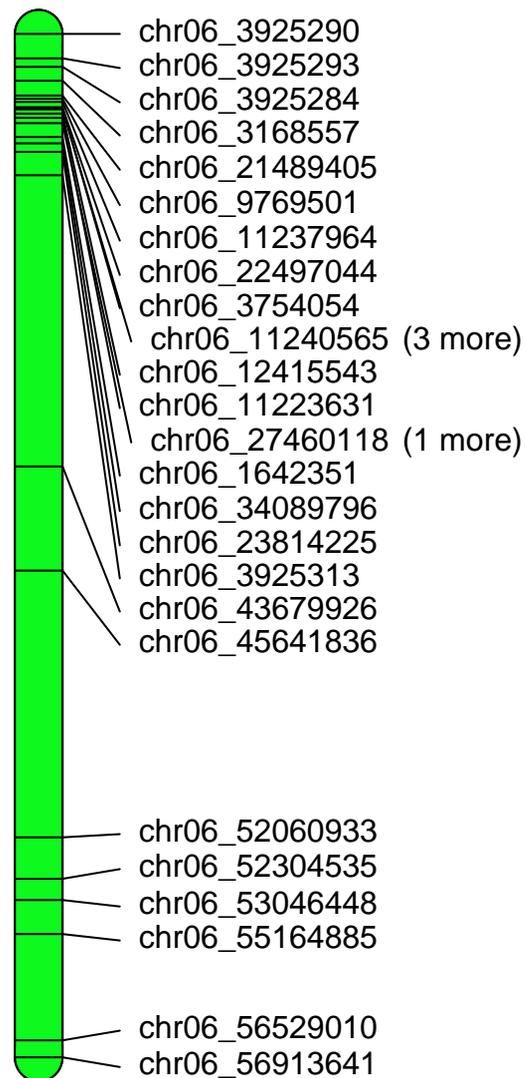
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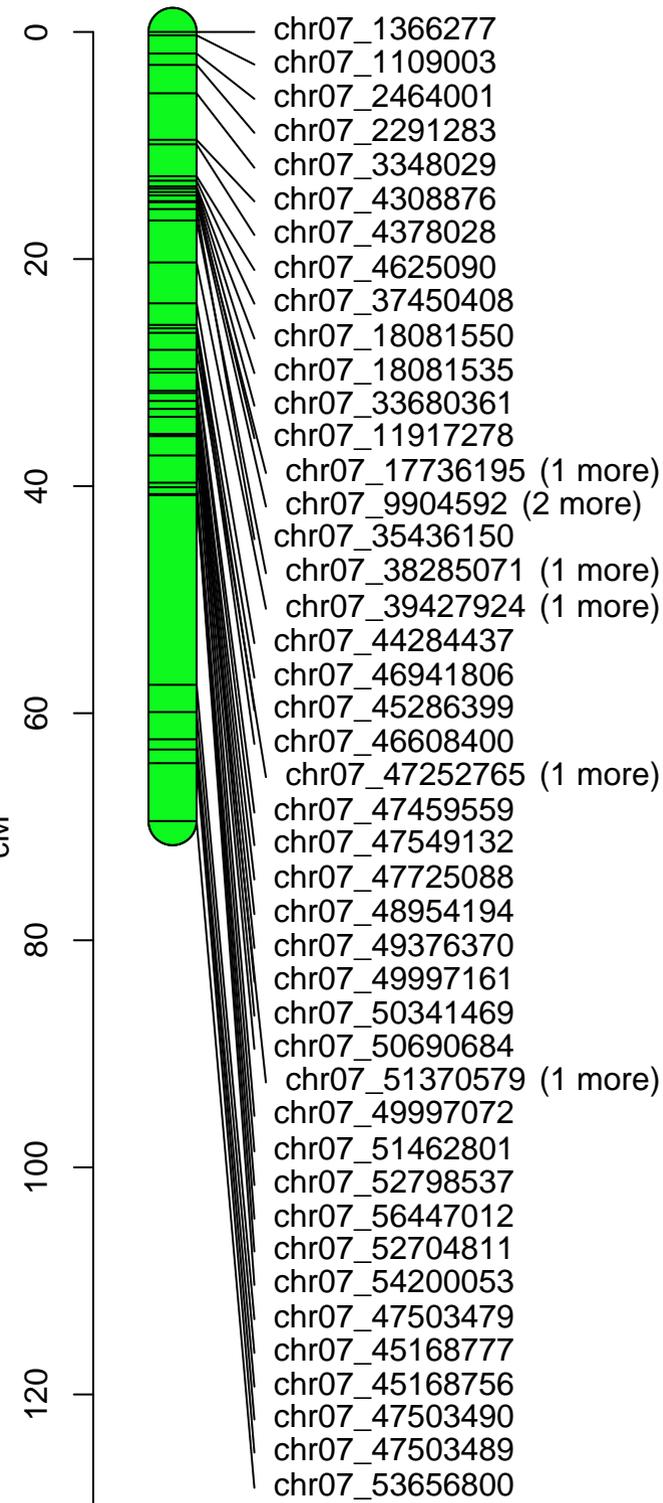
### chr06B



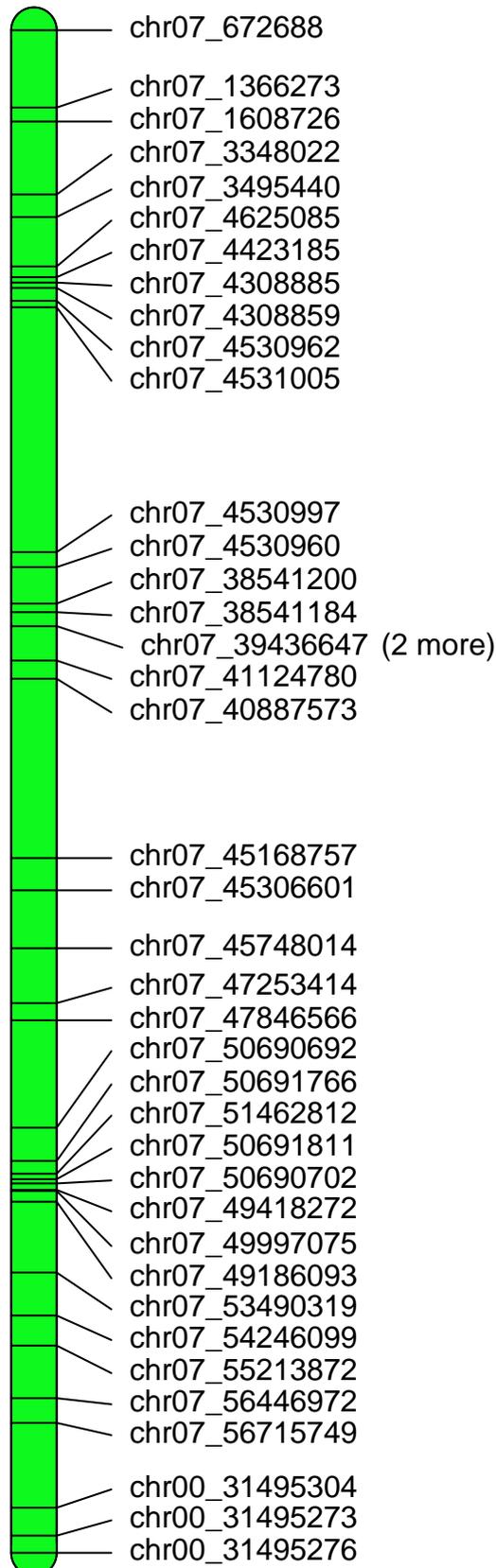
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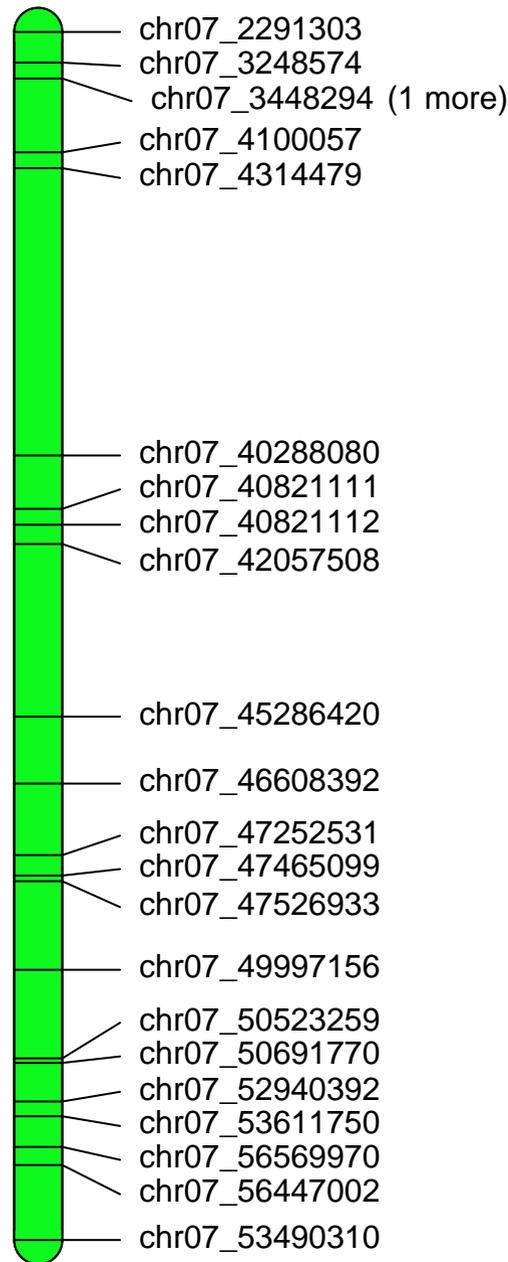
chr07A



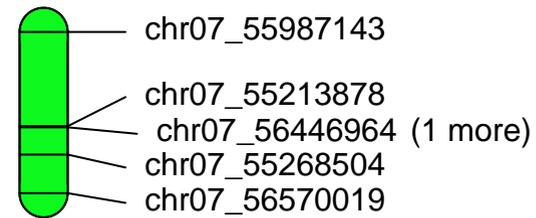
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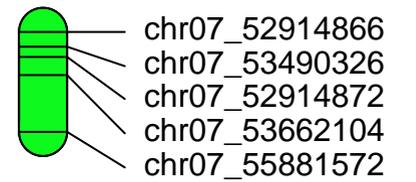
chr07C



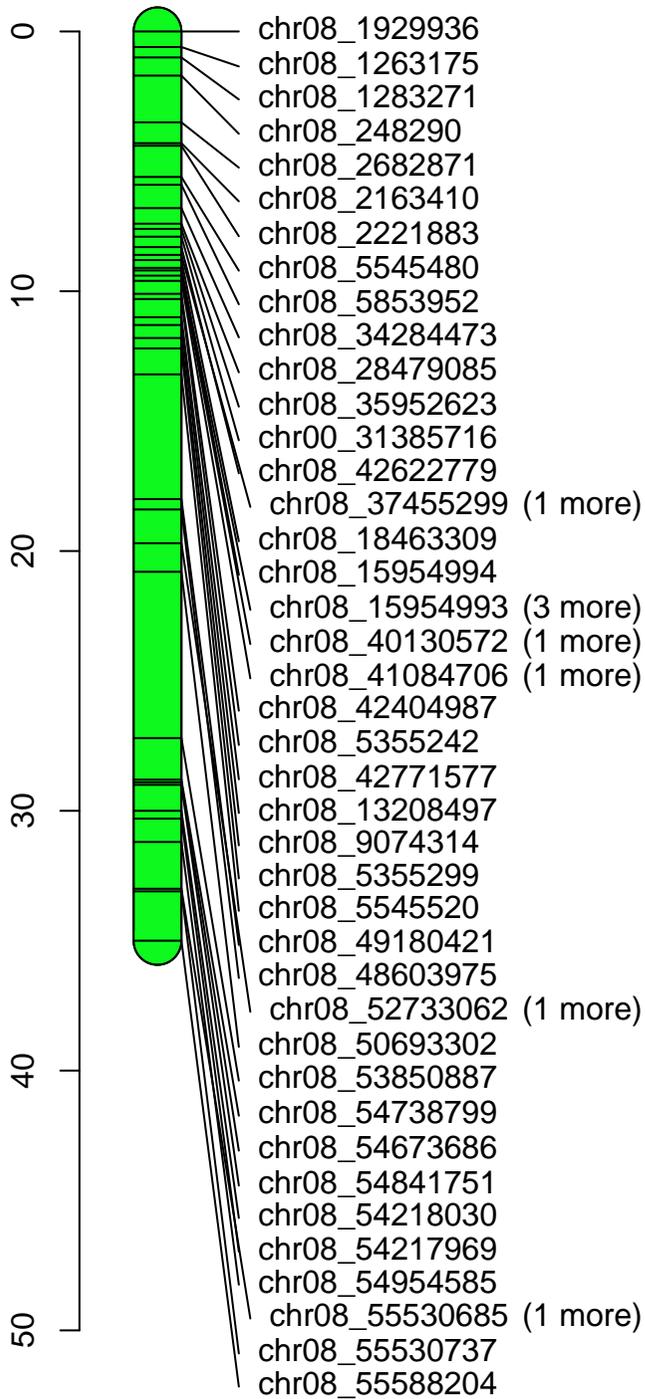
chr07D



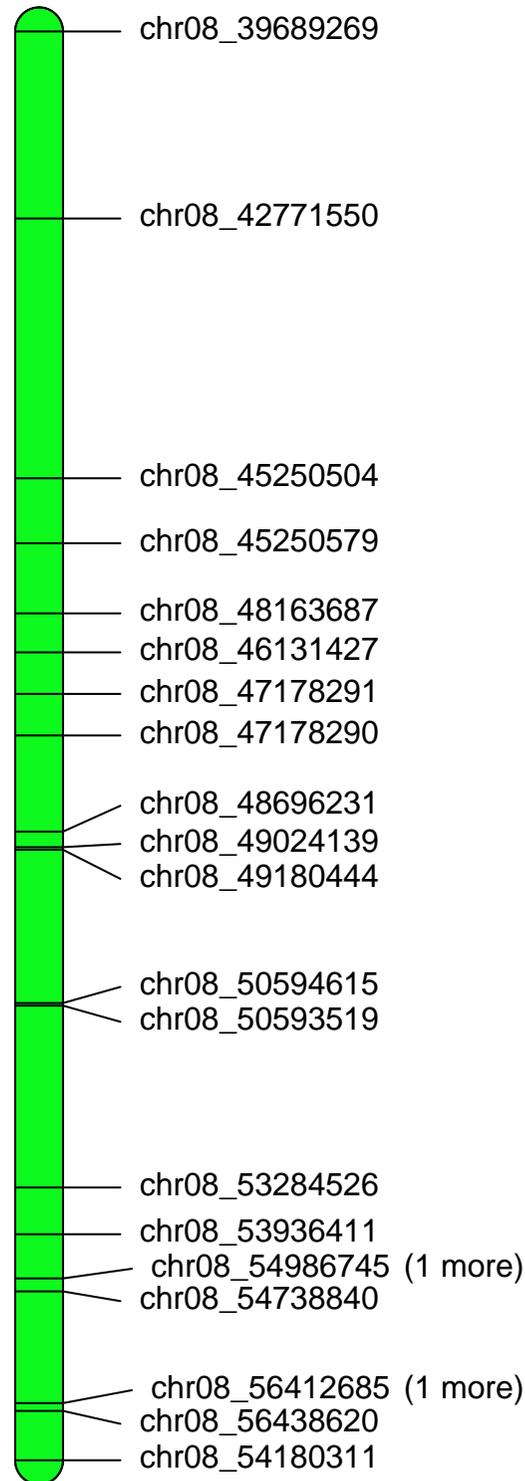
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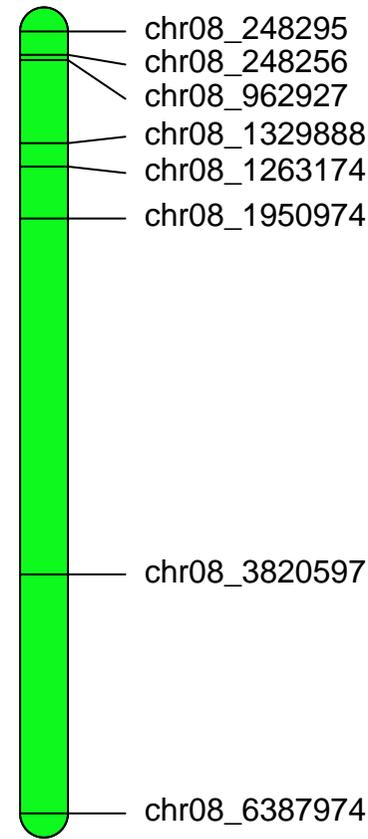
chr08A



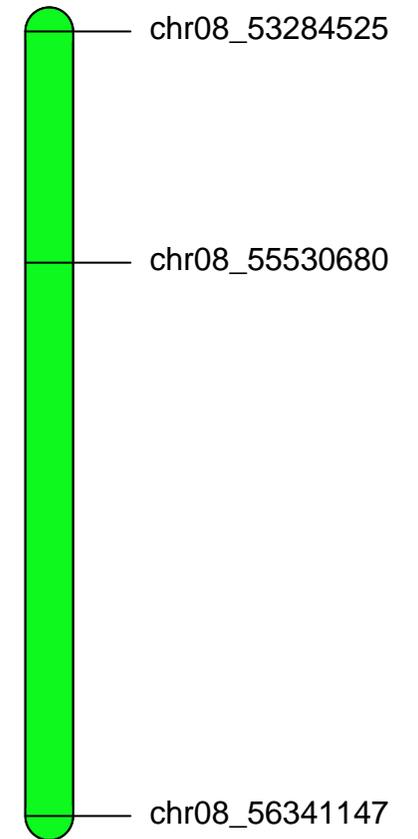
chr08B



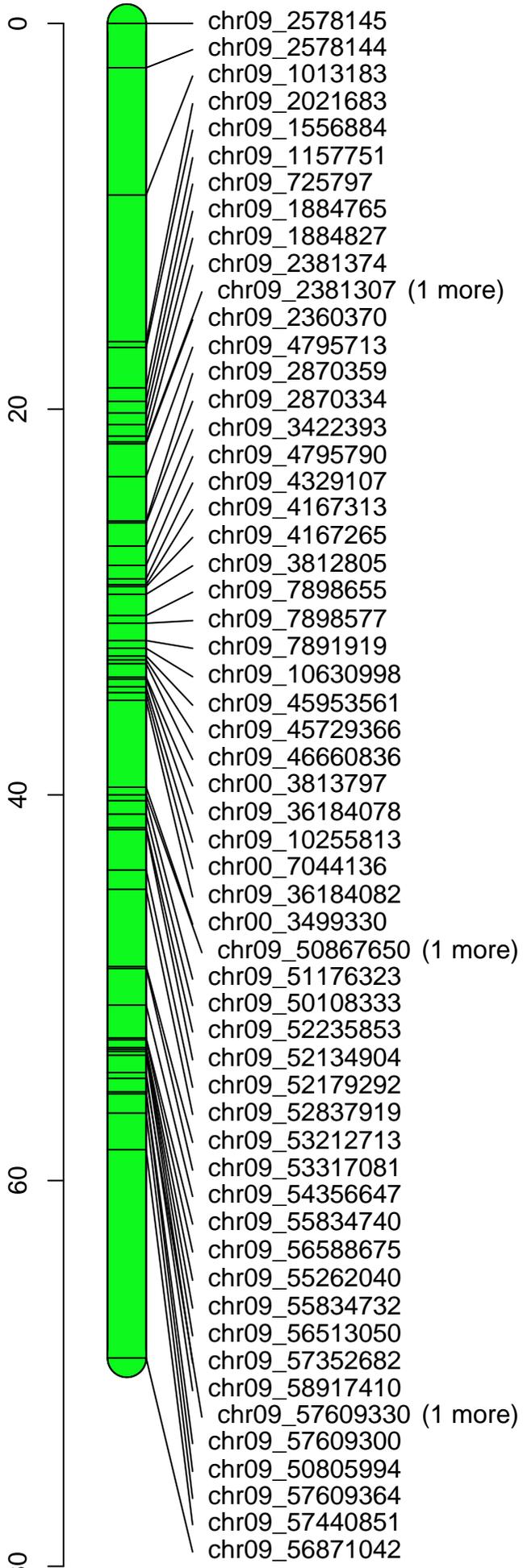
chr08C



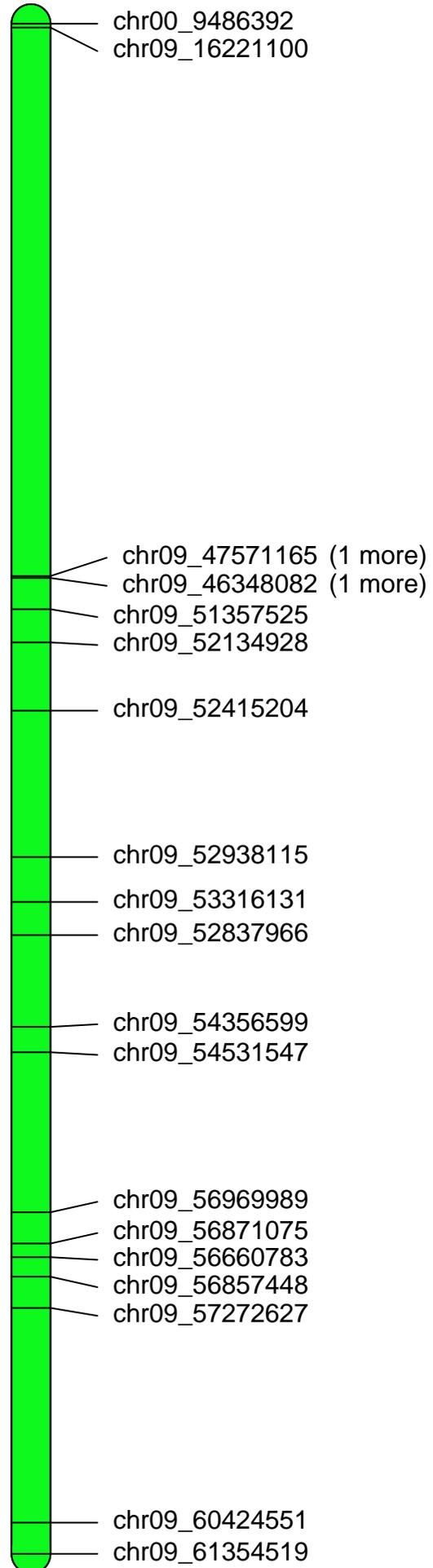
chr08D



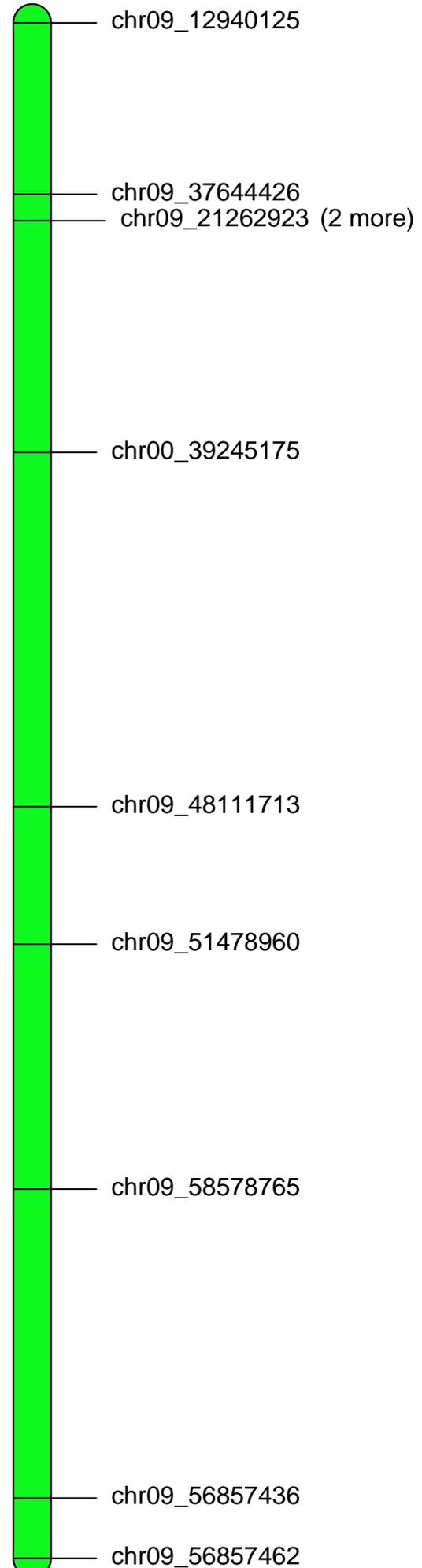
chr09A



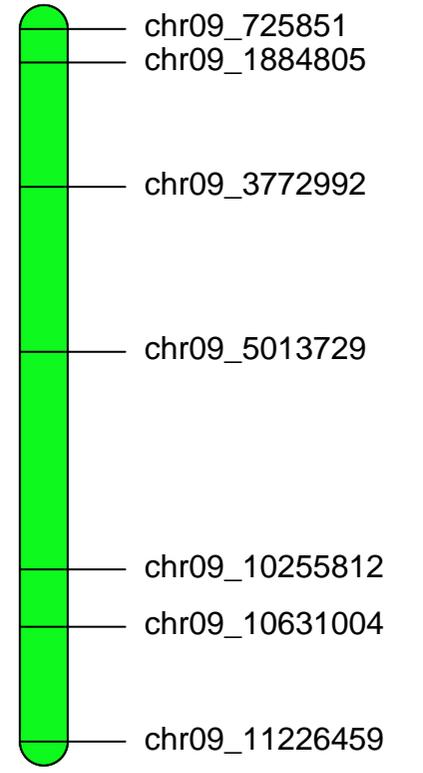
chr09B



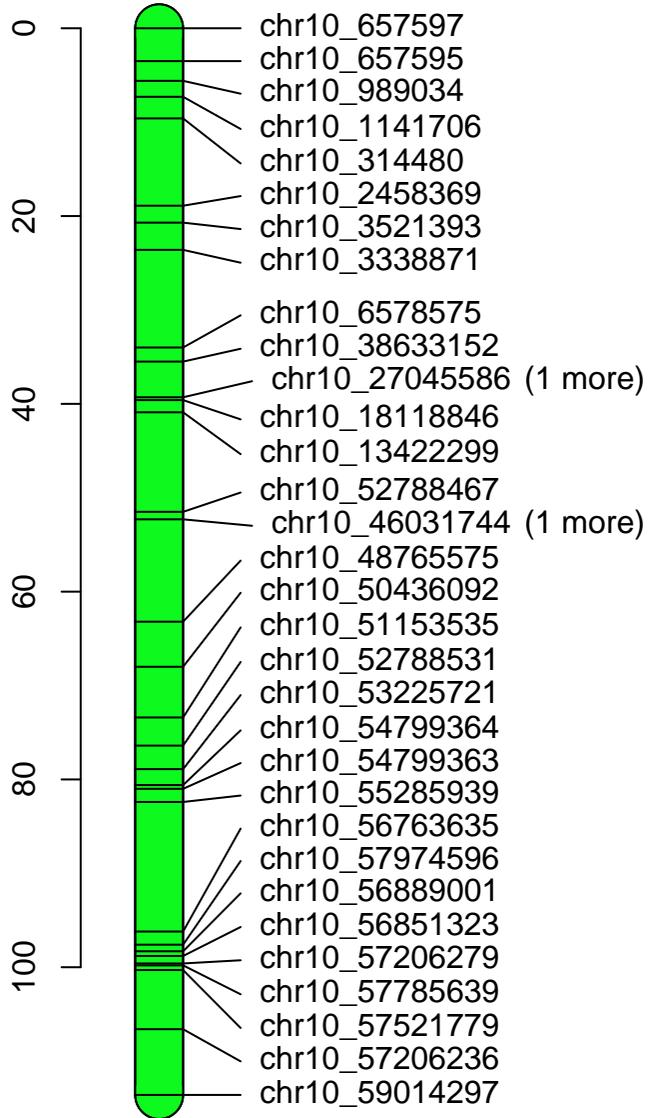
chr09C



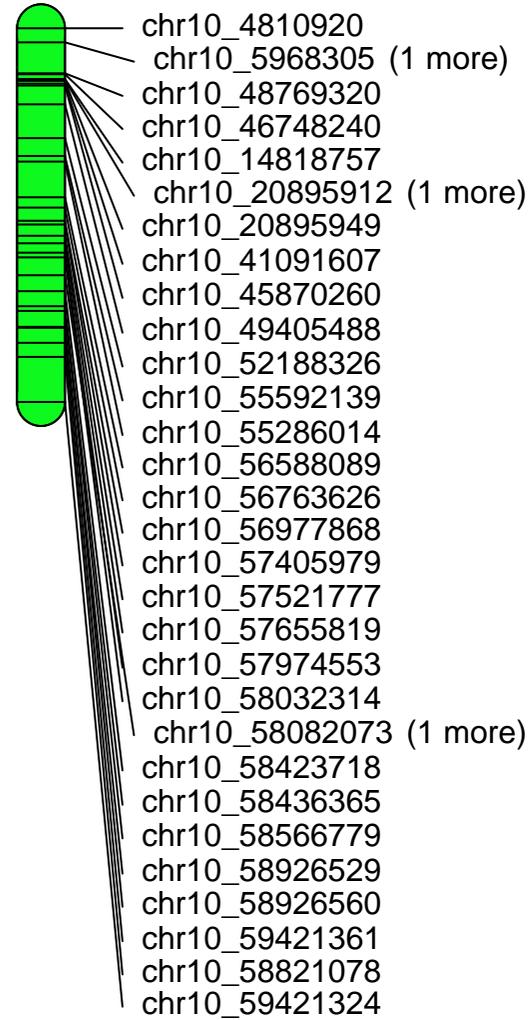
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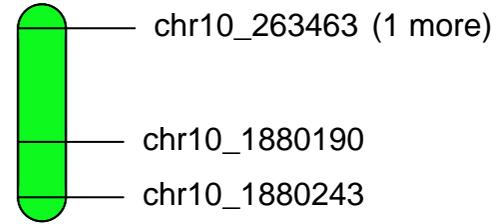
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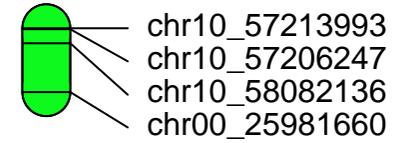
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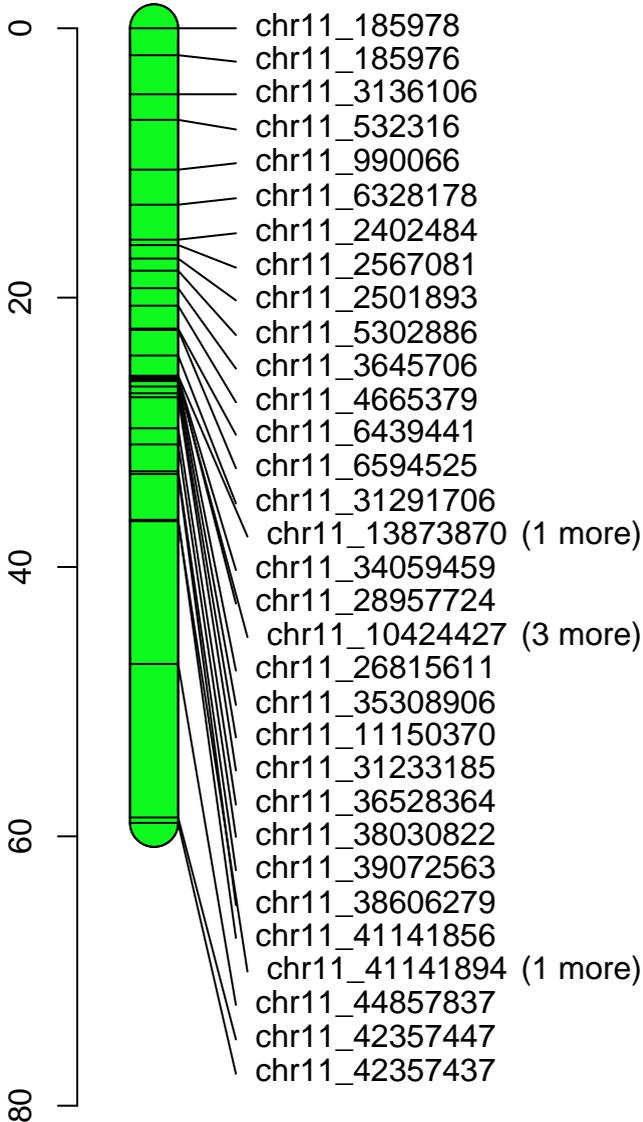
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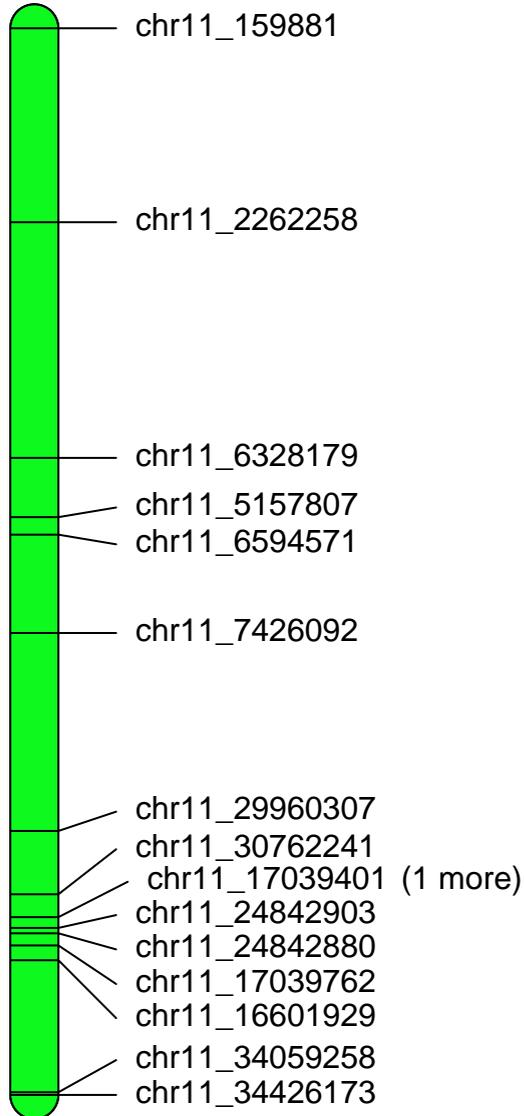
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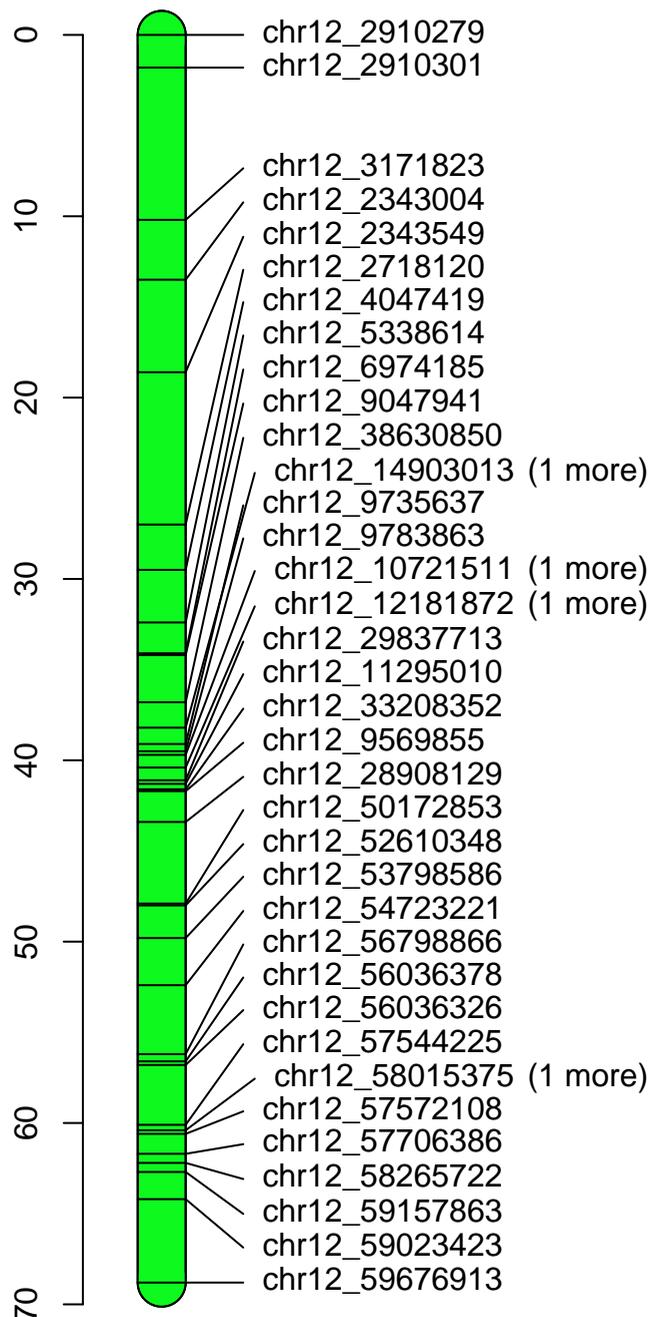
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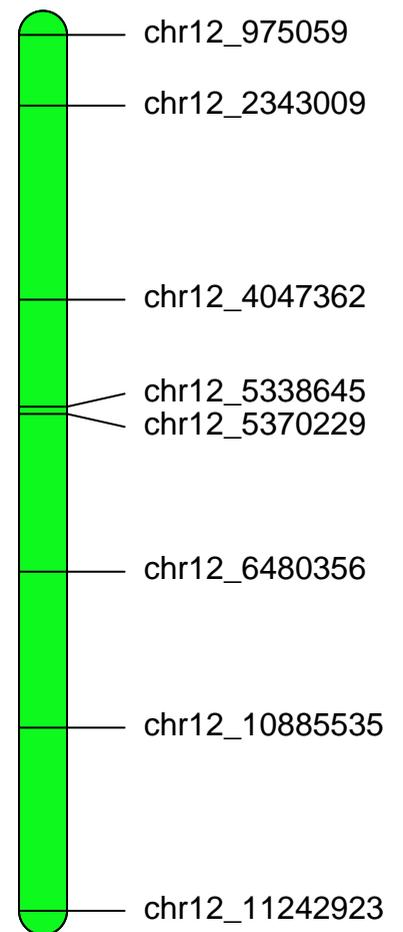
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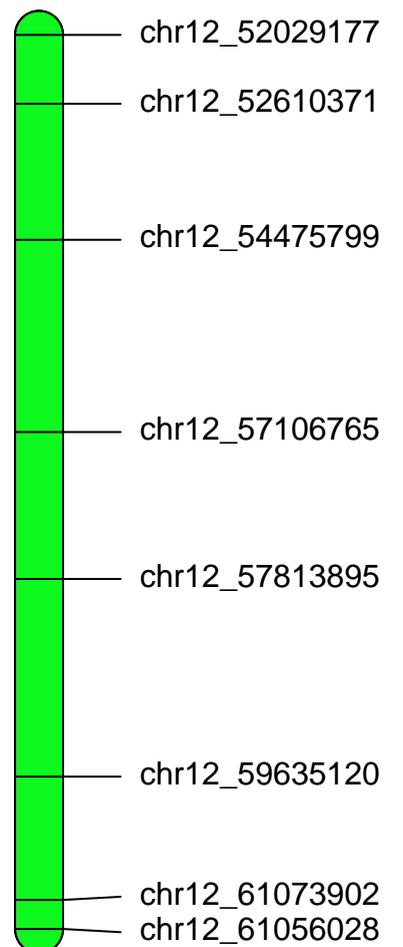
**chr12A**



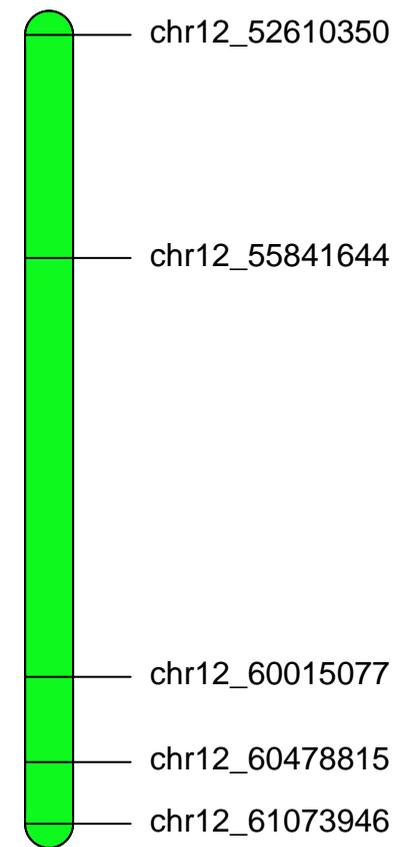
**chr12B**



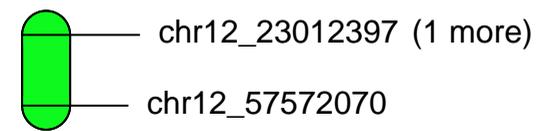
**chr12C**



**chr12D**



**chr12E**



Sheet1

Map	LG	Position (cM)	Locus	chr00 contig	PGSC Pseudomolecule Tiling Path
MCD ALL	chr01	24.237	chr00_13544987	chr00:13530242..13971654	PGSC0003DMB000000464
	chr02	1.339	chr00_21611244	chr00:21579816..21728535	PGSC0003DMB000000756
	chr03	23.829	chr00_40502850	chr00:40502447..40504311	PGSC0003DMB000002378
	chr03	23.986	chr00_8000147	chr00:7515800..8485525	PGSC0003DMB000000254
	chr04	0	chr00_12567719	chr00:12173931..12667864	PGSC0003DMB000000431
	chr04	5.365	chr00_12407838	chr00:12173931..12667864	PGSC0003DMB000000431
	chr04	59.086	chr00_38233239	chr00:38228241..38233666	PGSC0003DMB000001643
	chr08	36.763	chr00_31385668	chr00:31364510..31394384	PGSC0003DMB000001091
	chr10	56.754	chr00_23192845	chr00:23101765..23217759	PGSC0003DMB000000798
	chr11	39.652	chr00_20406095	chr00:20257527..20437853	PGSC0003DMB000000715
	MCD MALE	chr01	19.942	chr00_28505932	chr00:28466967..28514885
chr02		0.782	chr00_21611244	chr00:21579816..21728535	PGSC0003DMB000000756
chr03		28.384	chr00_8000147	chr00:7515800..8485525	PGSC0003DMB000000254
chr04		0	chr00_12407838	chr00:12173931..12667864	PGSC0003DMB000000431
chr04		58.24	chr00_38233239	chr00:38228241..38233666	PGSC0003DMB000001643
chr08		11.205	chr00_31385668	chr00:31364510..31394384	PGSC0003DMB000001091
chr10		61.118	chr00_23192845	chr00:23101765..23217759	PGSC0003DMB000000798
chr11		52.861	chr00_20406095	chr00:20257527..20437853	PGSC0003DMB000000715
PAM FEMALE	chr01B	51.832	chr00_13962275	chr00:13530242..13971654	PGSC0003DMB000000464
	chr01C	0	chr00_23427320	chr00:23333778..23446661	PGSC0003DMB000000805
	chr02A	61.108	chr00_19558859	chr00:19450431..19661773	PGSC0003DMB000000670
	chr05A	12.092	chr00_37599899	chr00:37597868..37605383	PGSC0003DMB000001545
	chr05B	45.958	chr00_43541618	chr00:43541215..43541950	PGSC0003DMB000004984
	chr05B	47.434	chr00_43541620	chr00:43541215..43541950	PGSC0003DMB000004984
	chr07B	140.205	chr00_31495273	chr00:31483820..31513220	PGSC0003DMB000001096
	chr07B	141.778	chr00_31495276	chr00:31483820..31513220	PGSC0003DMB000001096
	chr07B	137.612	chr00_31495304	chr00:31483820..31513220	PGSC0003DMB000001096
	chr08A	7.861	chr00_31385716	chr00:31364510..31394384	PGSC0003DMB000001091
	chr09A	33.917	chr00_3813797	chr00:1708939..3871400	PGSC0003DMB000000064
	chr09A	34.708	chr00_7044136	chr00:6457363..7515699	PGSC0003DMB000000230
	chr09A	39.603	chr00_3499330	chr00:1708939..3871400	PGSC0003DMB000000064
	chr09B	0	chr00_9486392	chr00:9335487..10101367	PGSC0003DMB000000311
	chr09C	22.756	chr00_39245175	chr00:39242151..39245446	PGSC0003DMB000001879
	chr09C	10.507	chr00_5896866	chr00:6457363..7515699	PGSC0003DMB000000230
	chr09C	10.521	chr00_7044118	chr00:5010086..6318492	PGSC0003DMB000000170
chr10D	6.82	chr00_25981660	chr00:25967526..26033986	PGSC0003DMB000000896	