

Detection of novel QTLs for late blight resistance derived 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

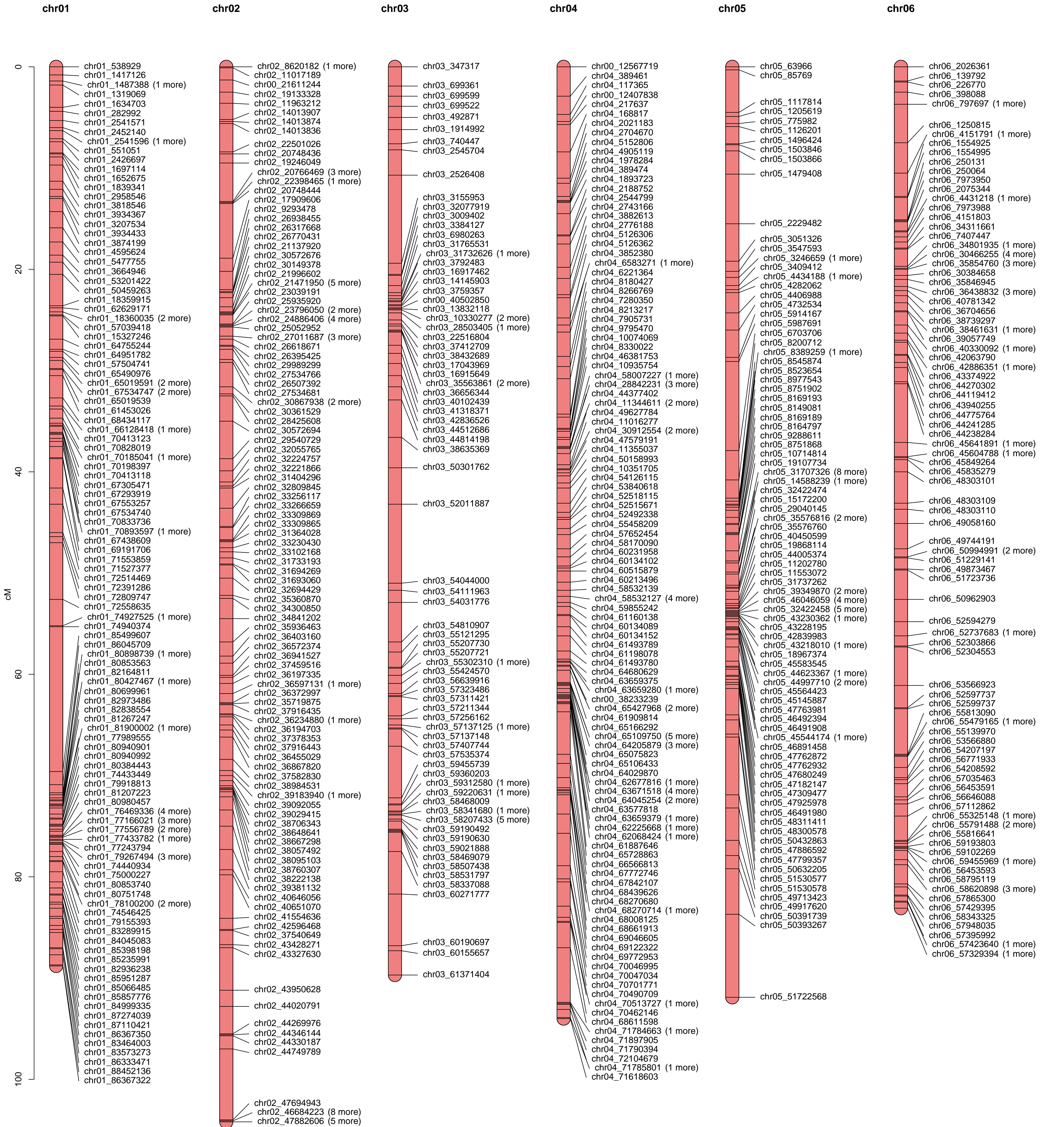
Page 1-2: Genetic map created using 1431 SNP markers of all types (segregating in the female parent <lmxll>; segregating in both parents <hkxhk>; segregating in the male parent <nnxnp>) of the MCD diploid population.

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

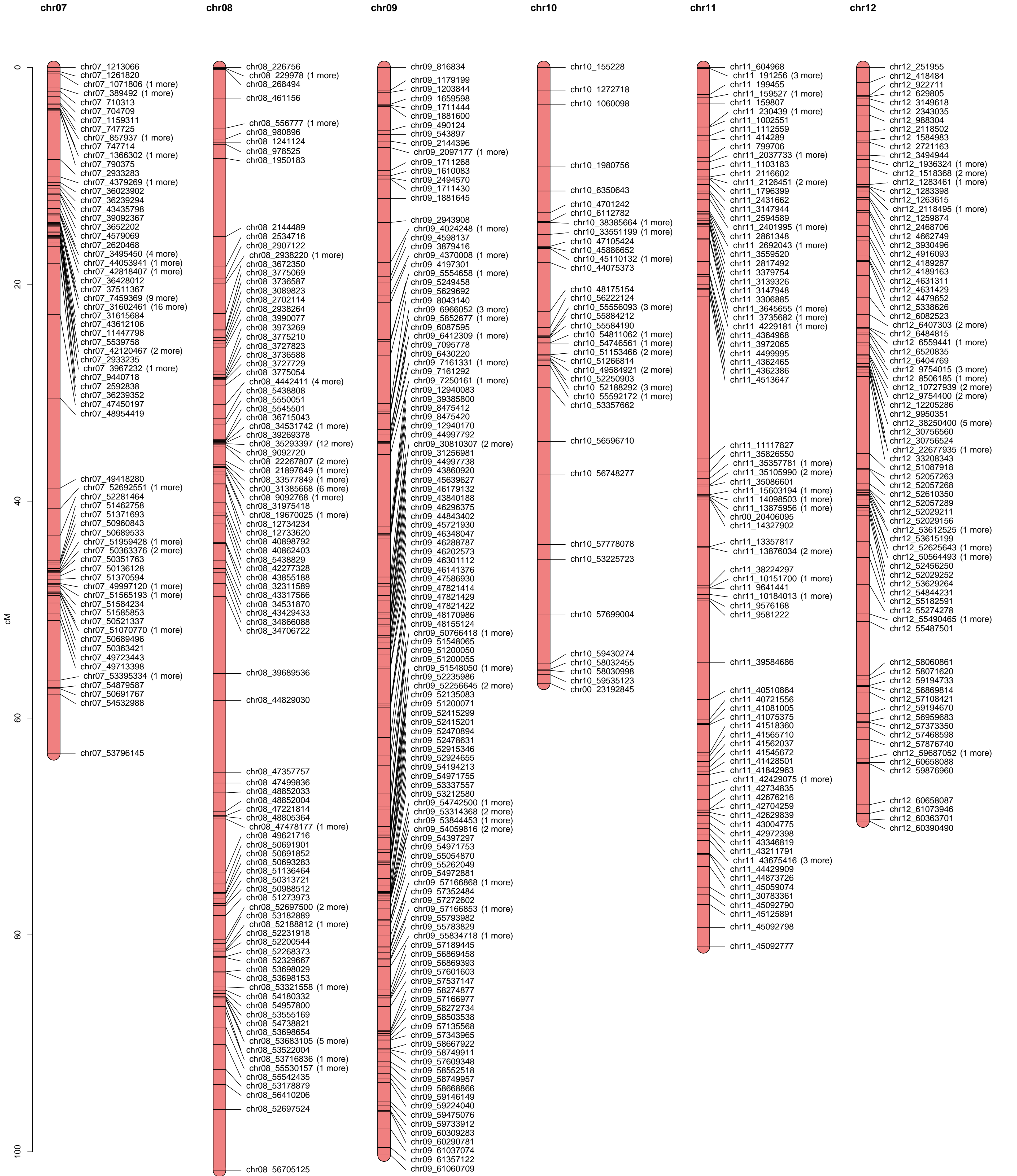
Page 5-16: Genetic map created using 967 SNP markers unique to the female parent of the PAM tetraploid population.

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

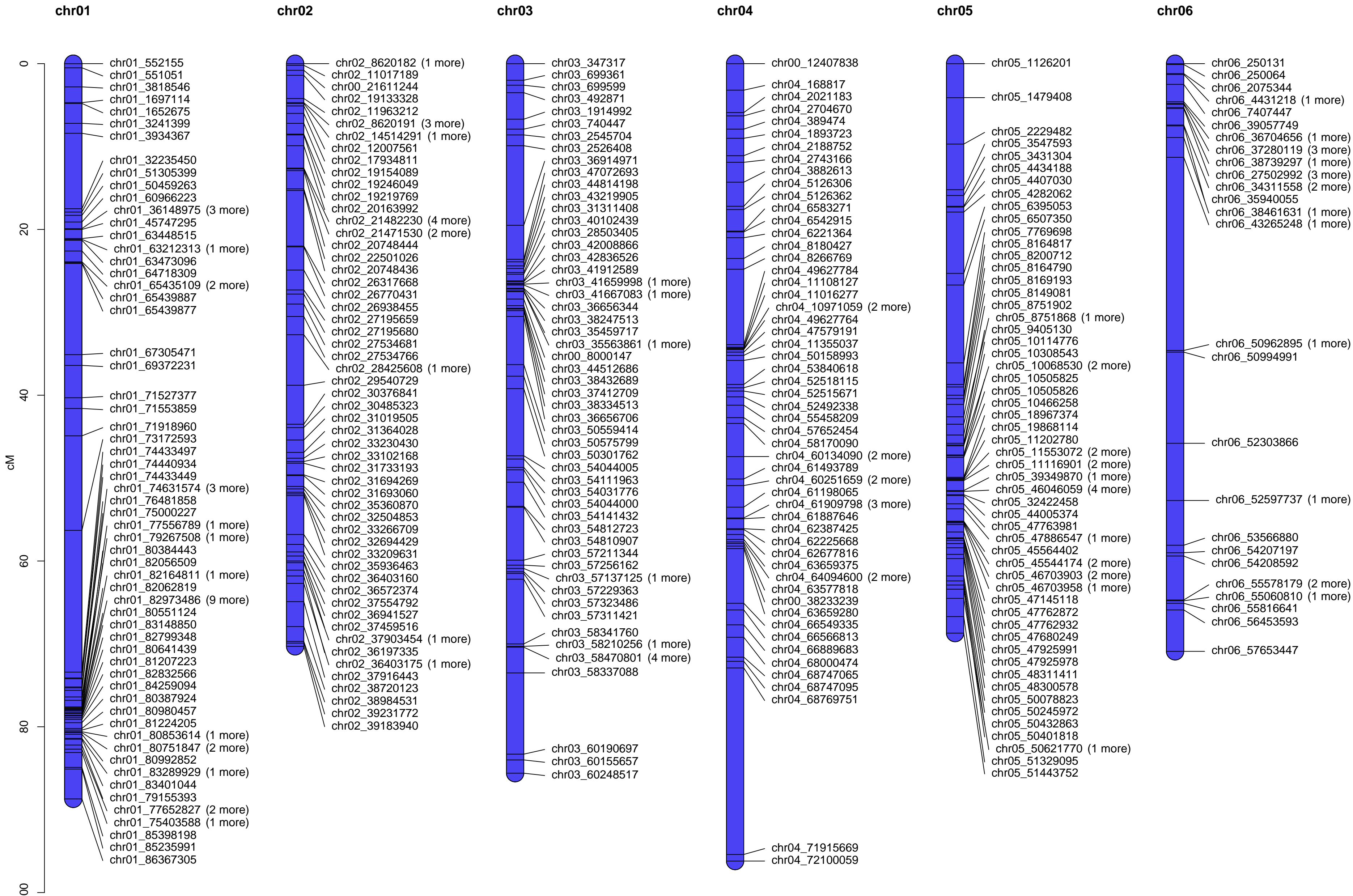
MCD genetic map (All marker types, chr01–chr06)



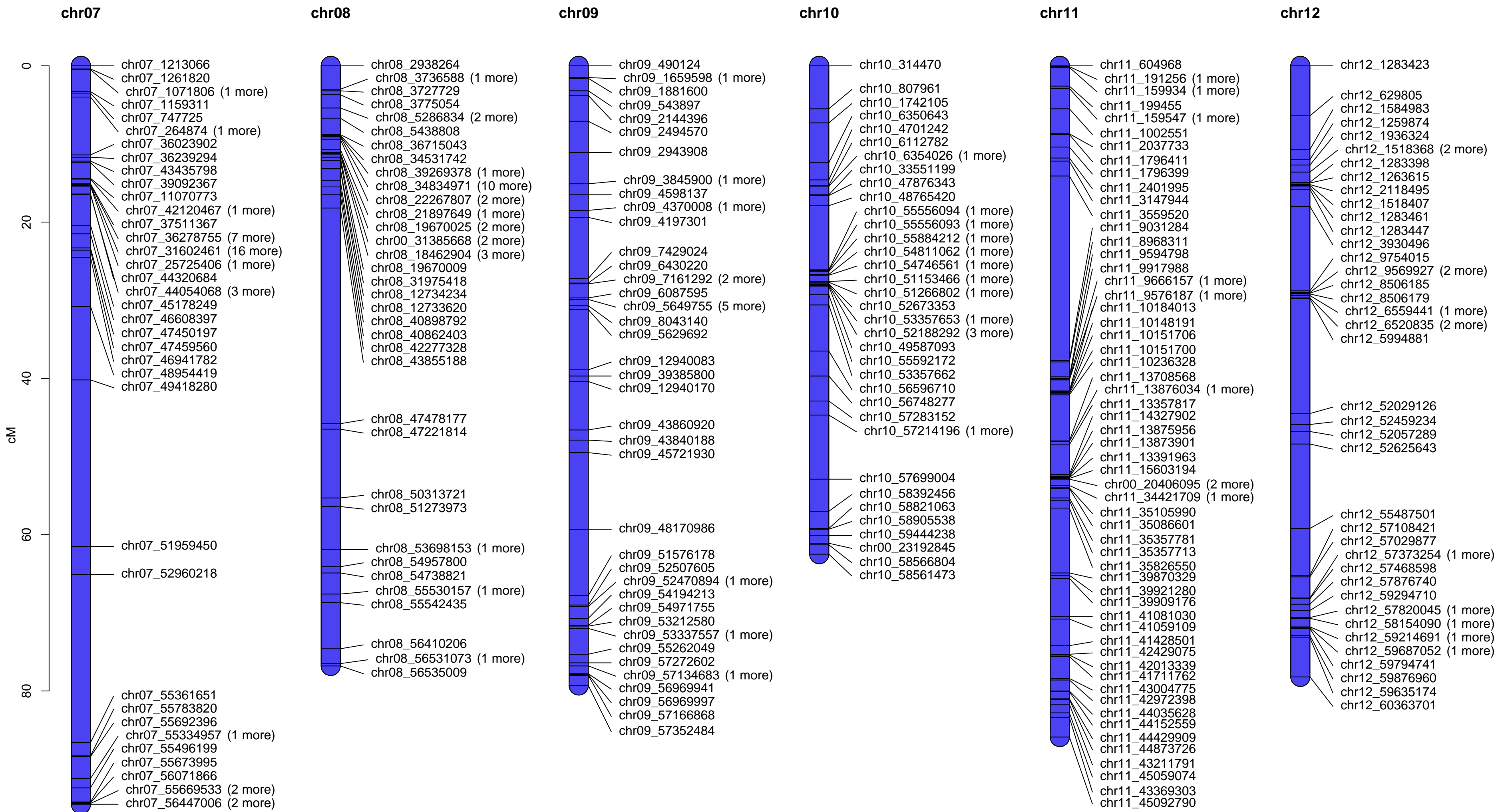
MCD genetic map (All marker types, chr07–chr12)



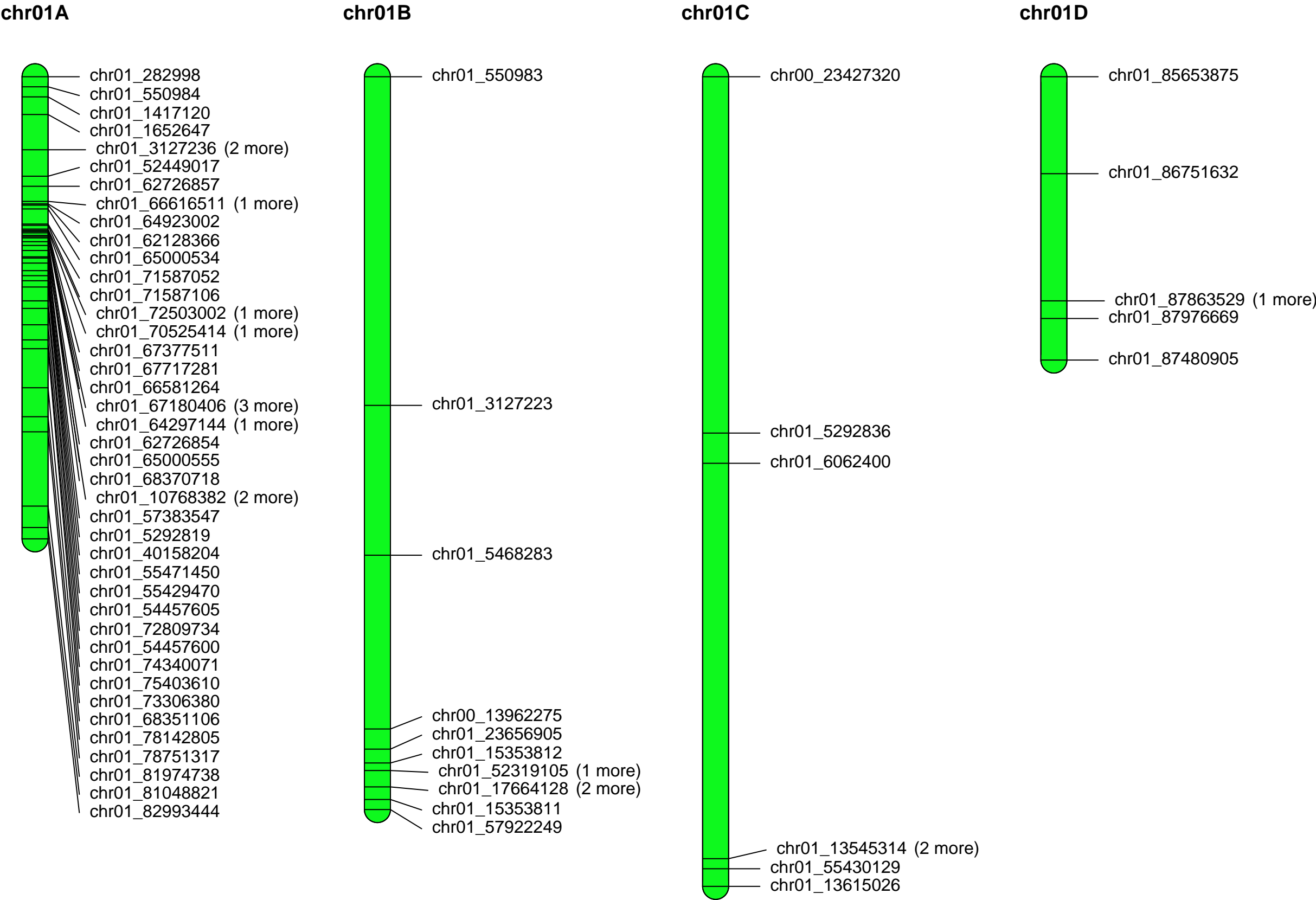
MCD MALE genetic map (markers unique to IVP10–281–1, chr01–chr06)



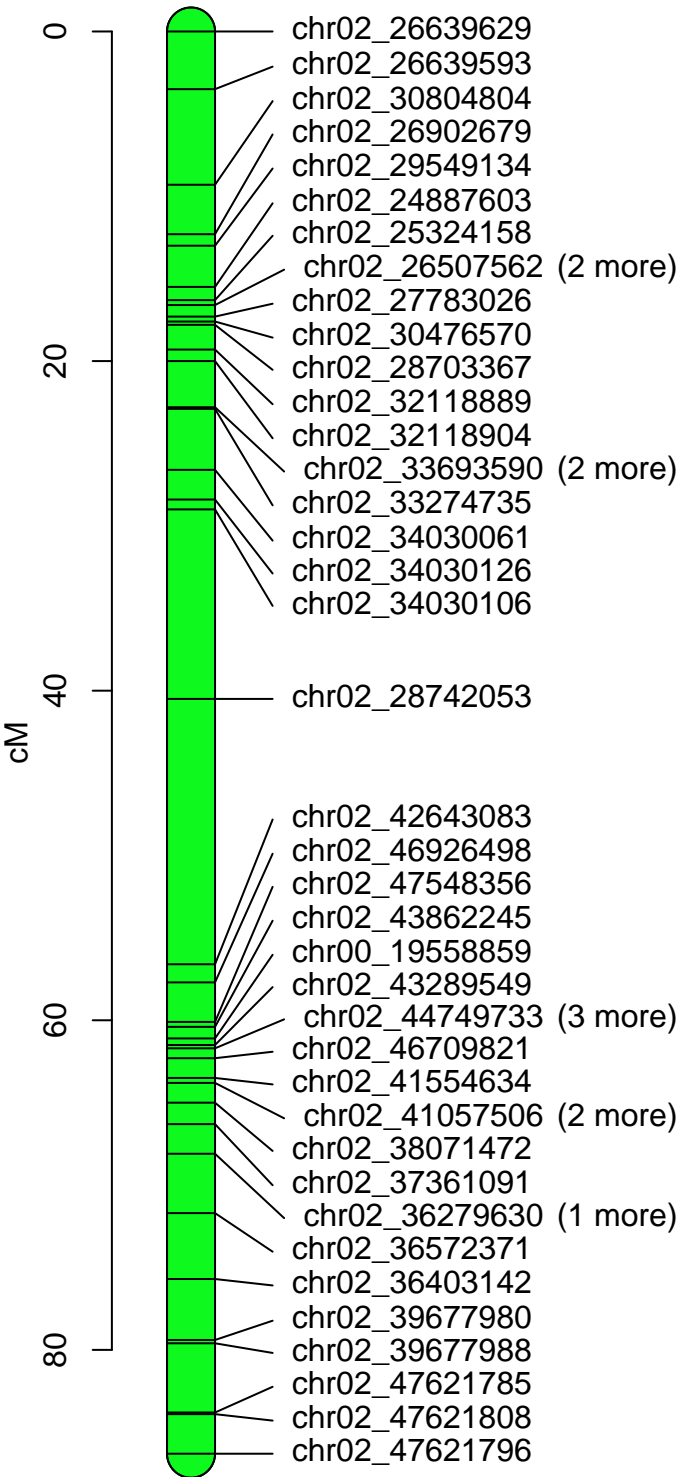
MCD MALE genetic map (markers unique to IVP10-281-1, chr07-chr12)



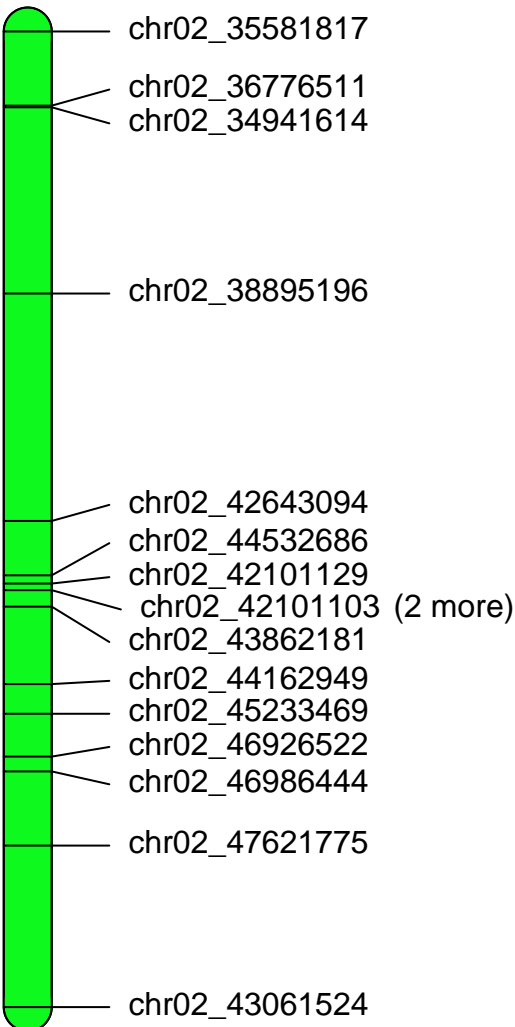
PAM genetic map



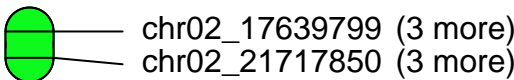
chr02A



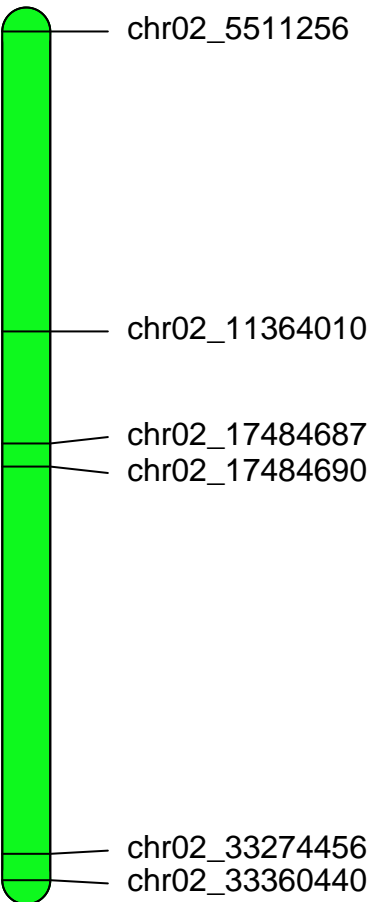
chr02B



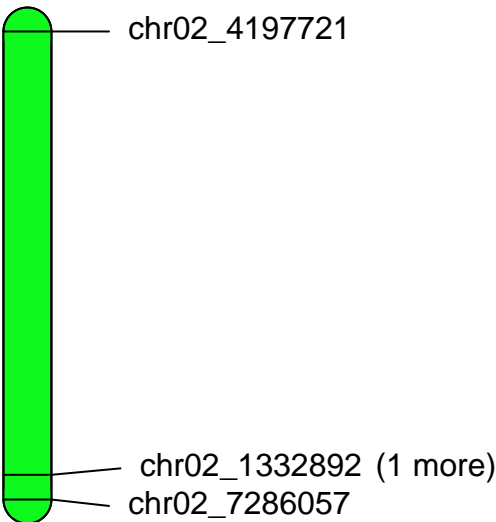
chr02C



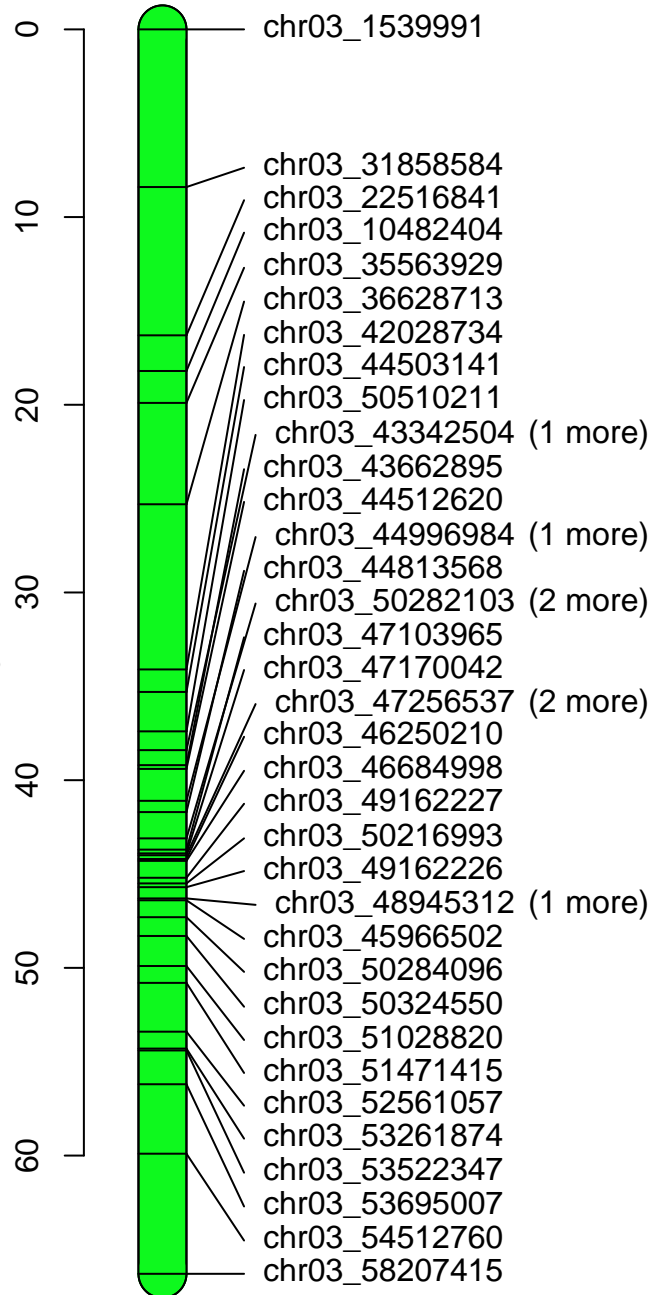
chr02D



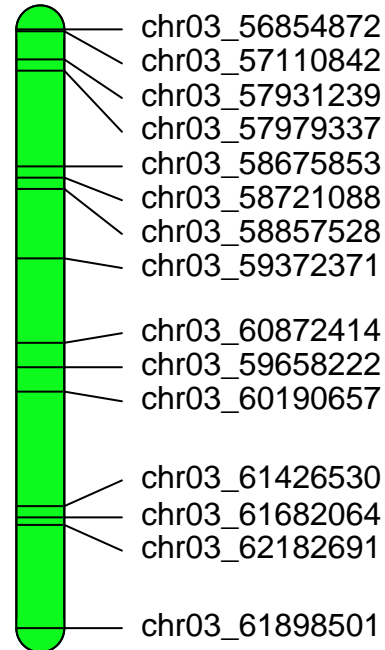
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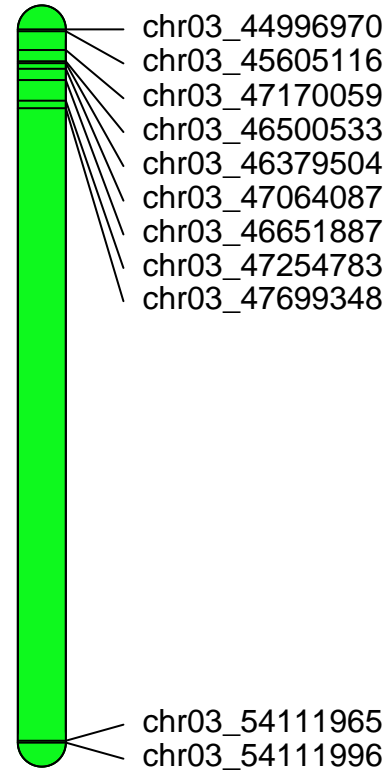
chr03A



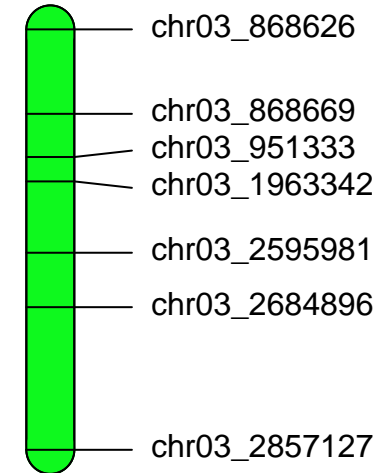
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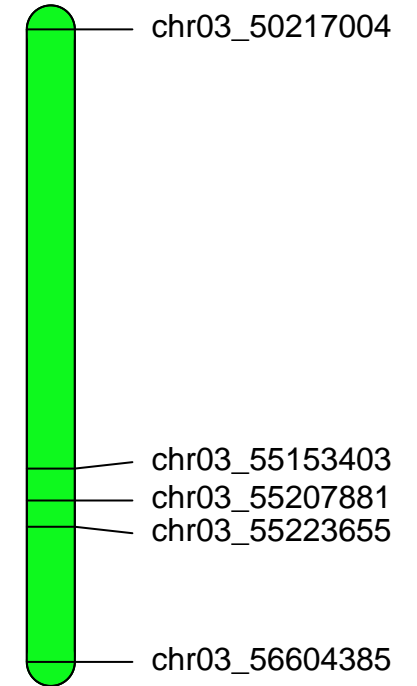
chr03C



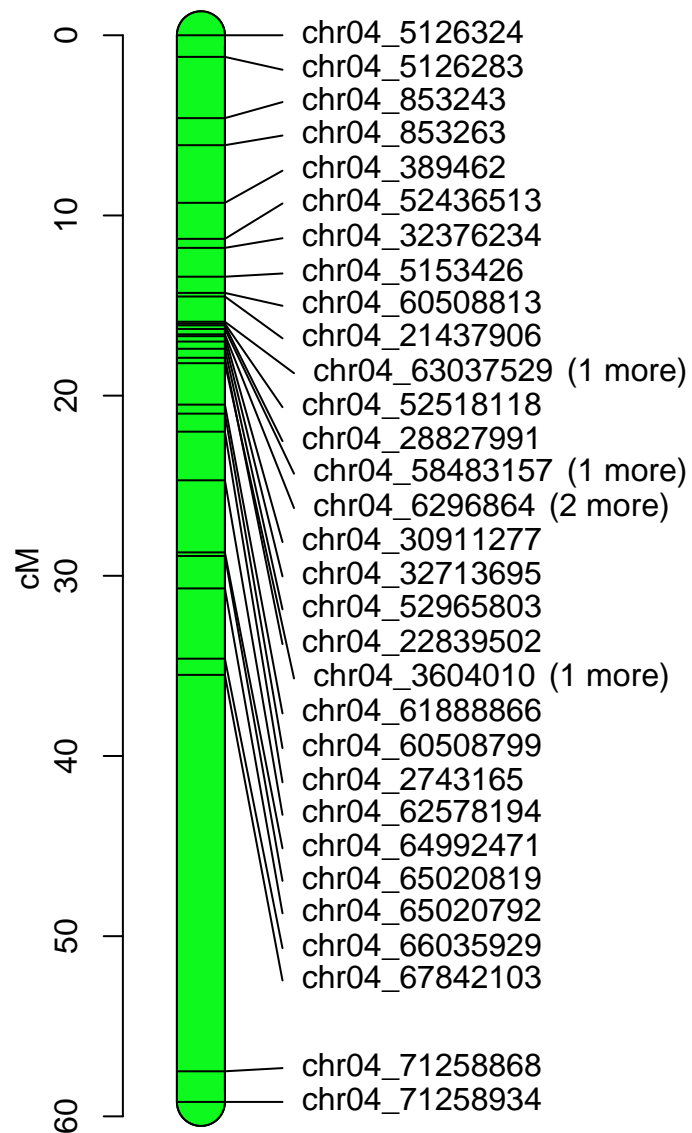
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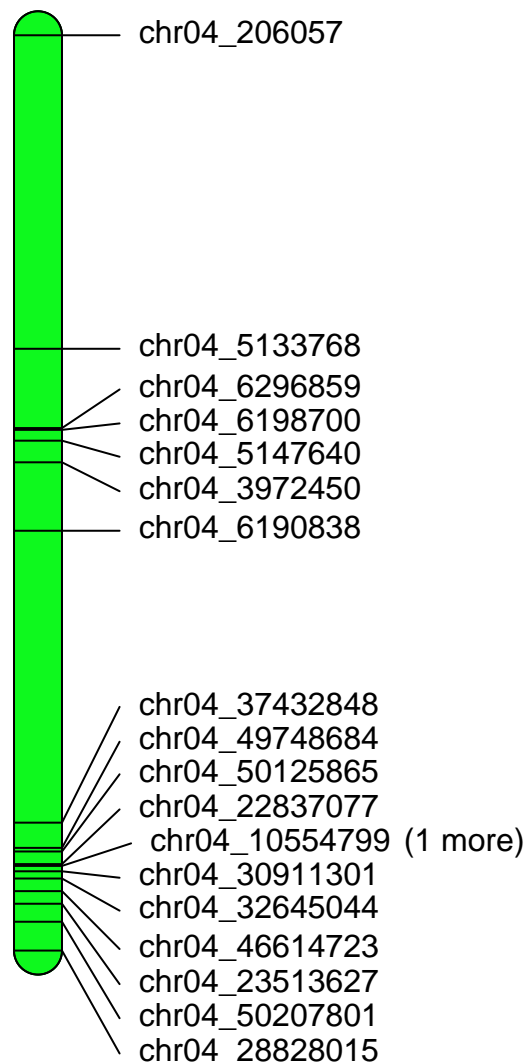
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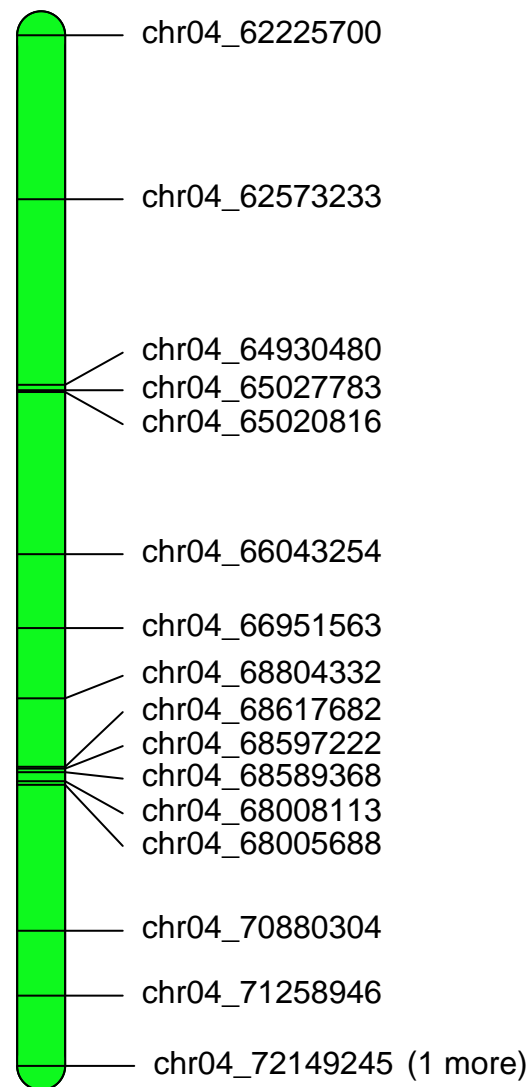
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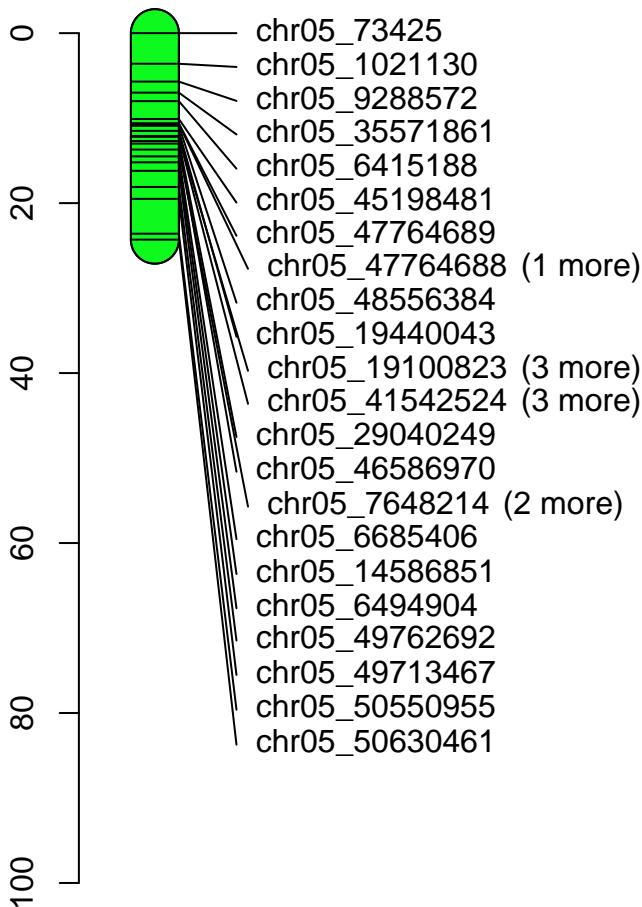
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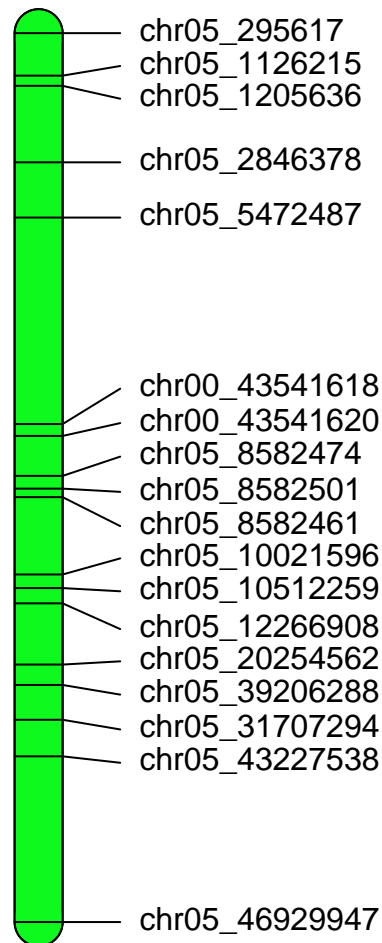
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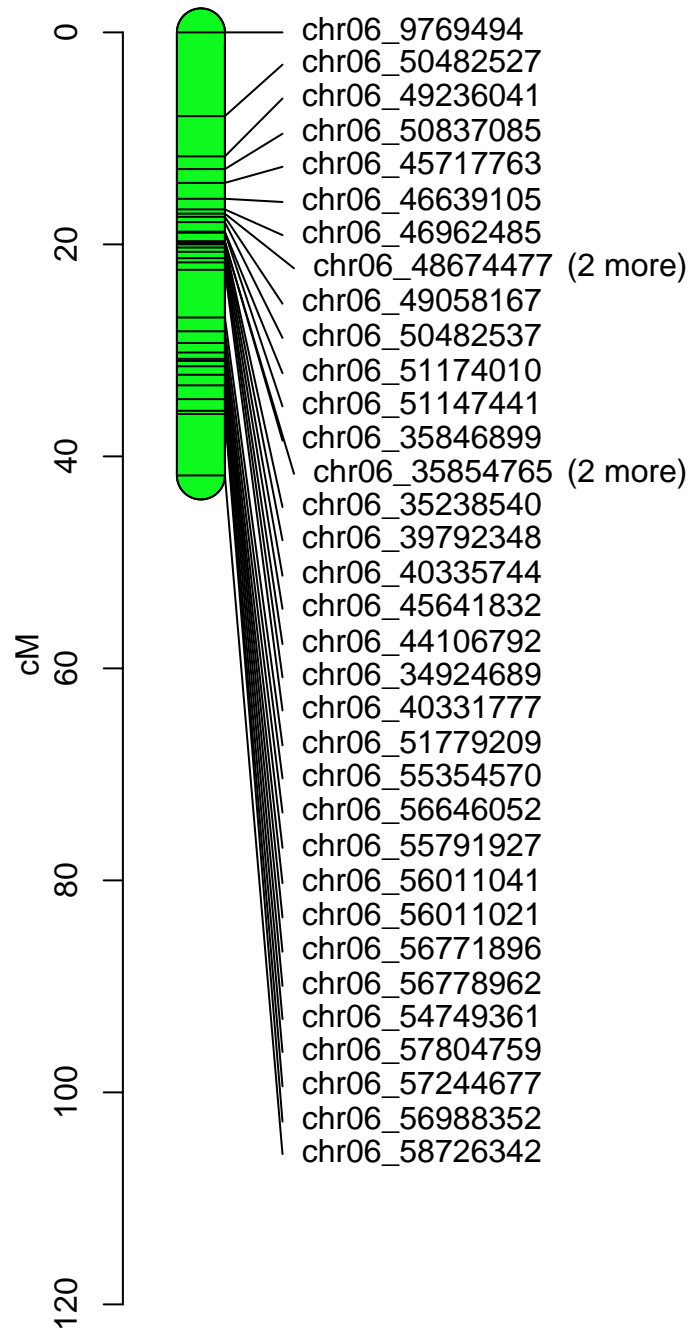
chr05A



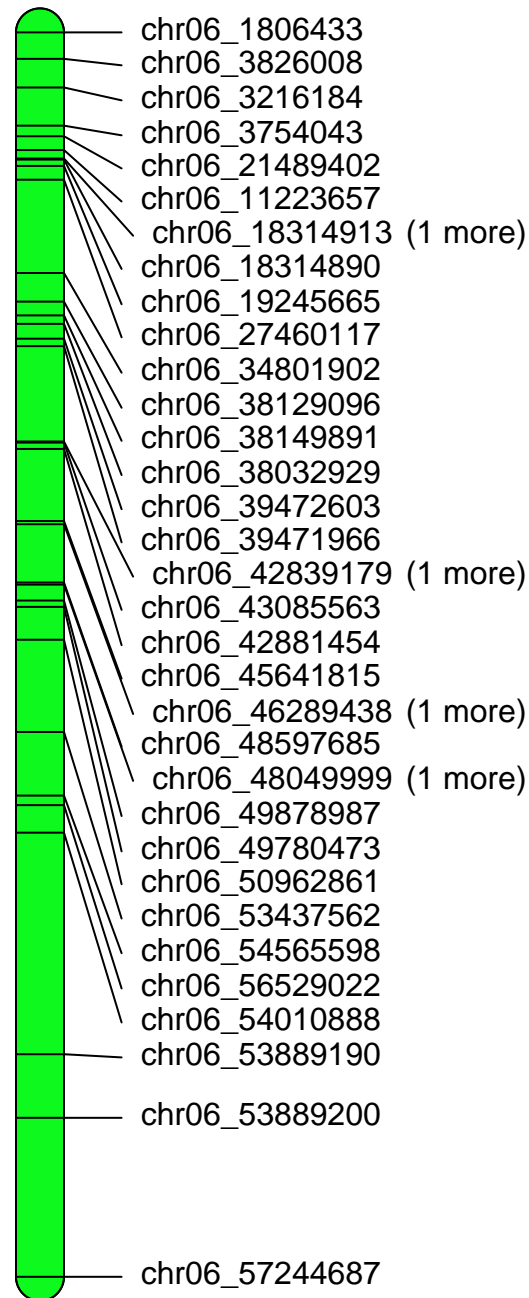
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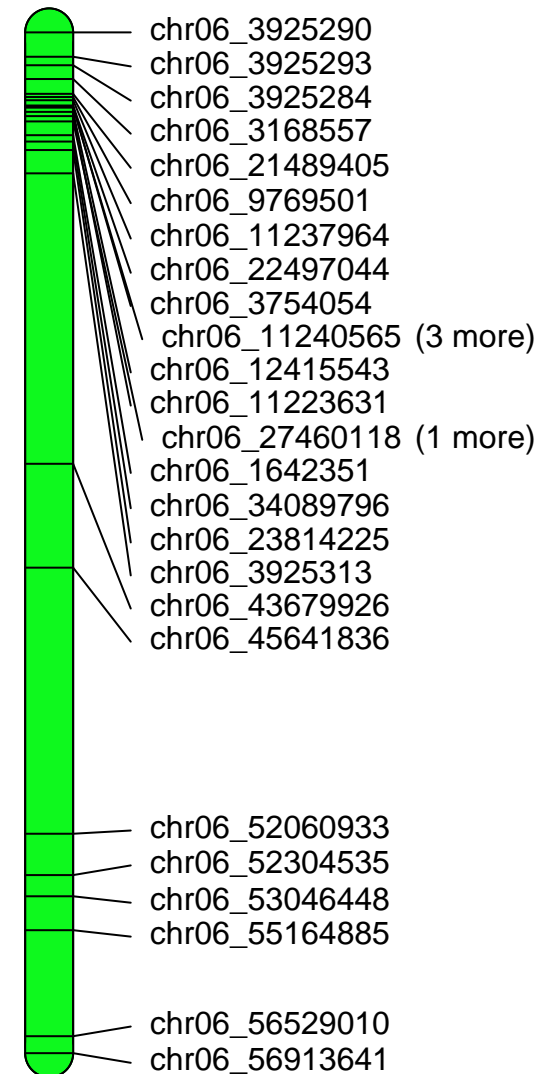
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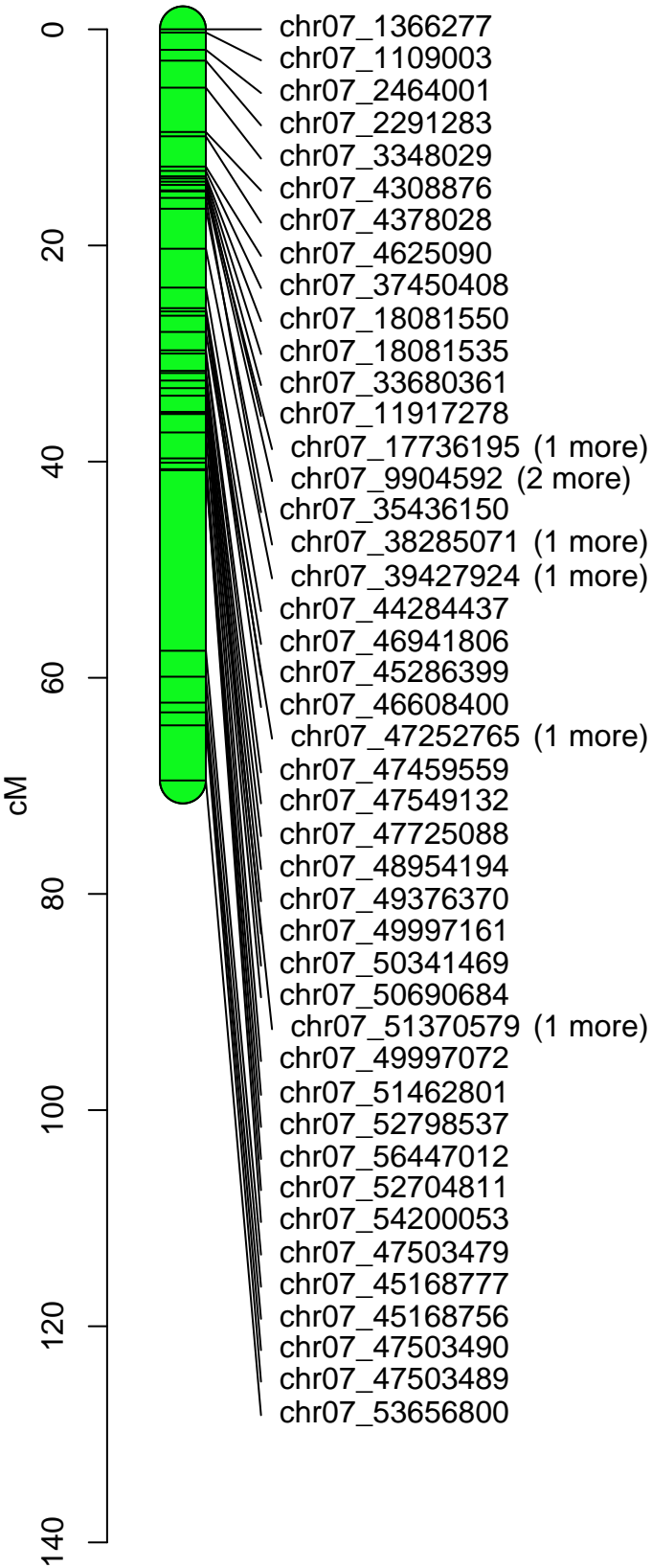
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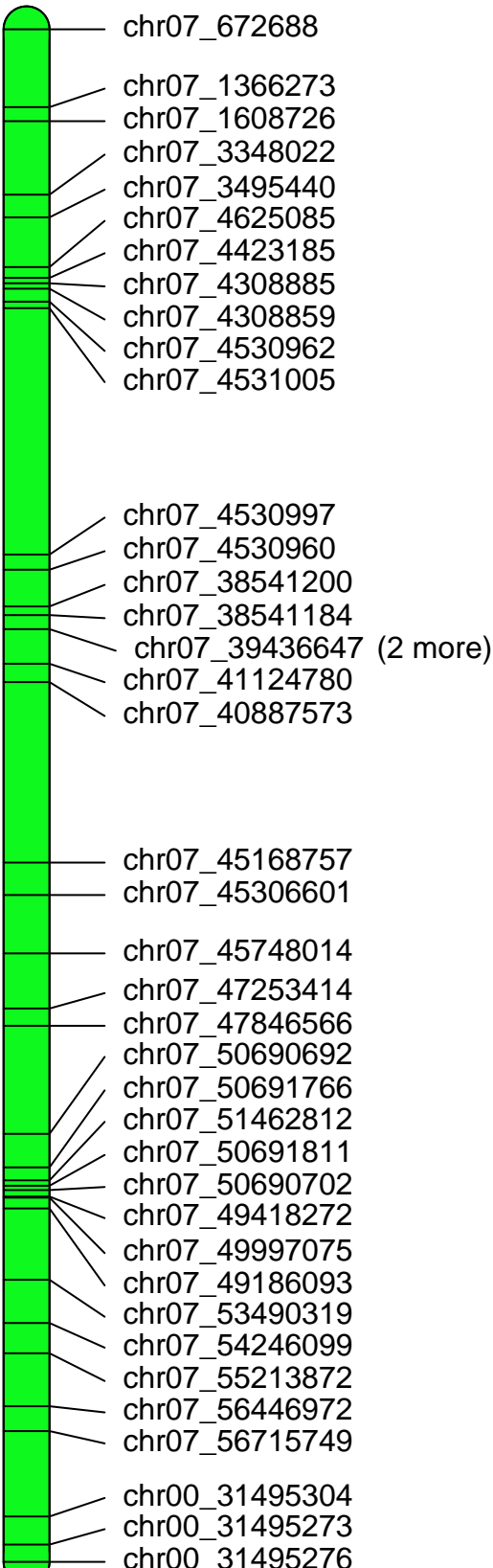
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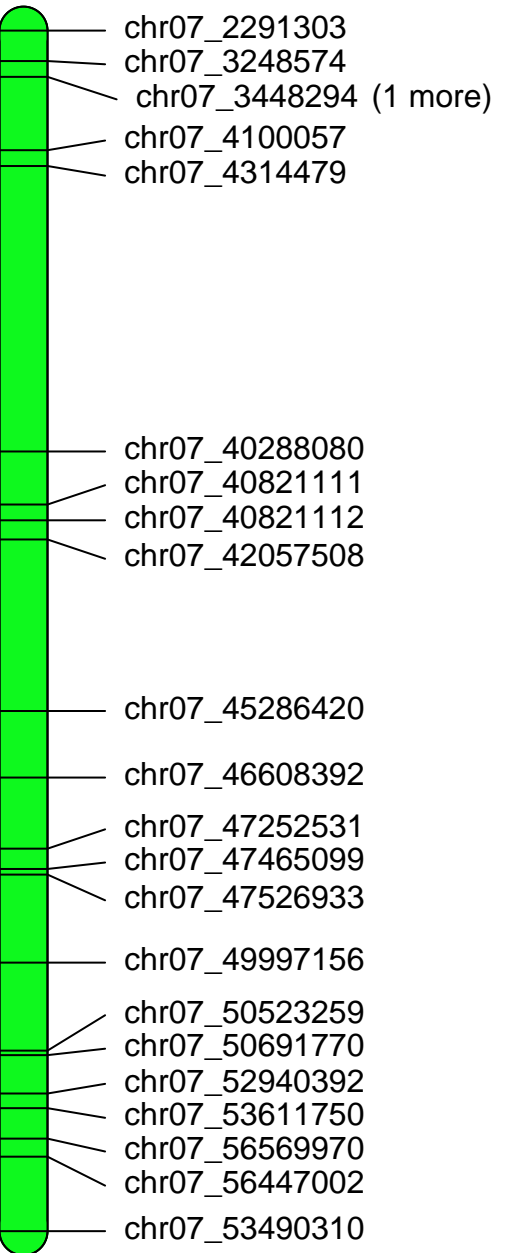
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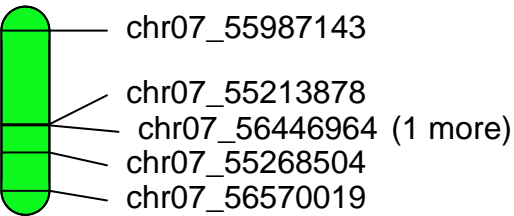
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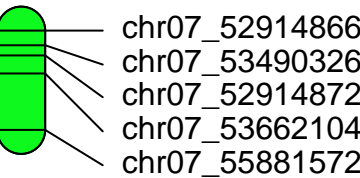
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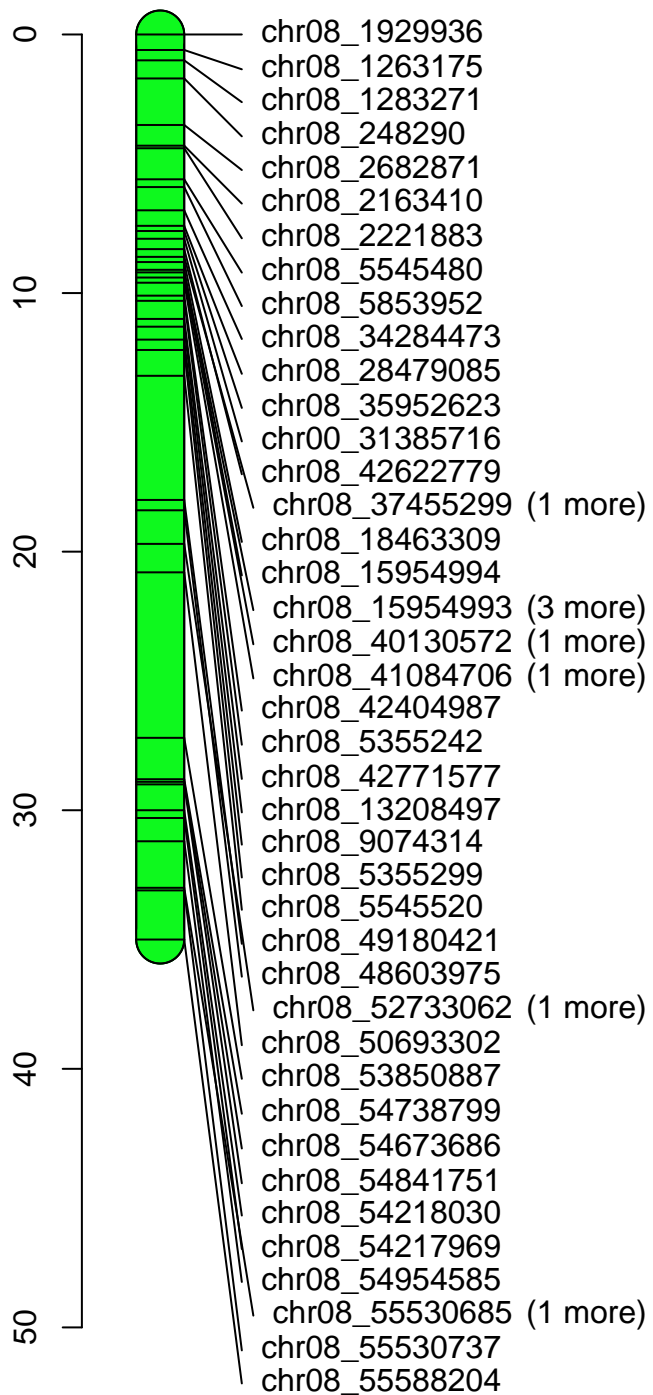
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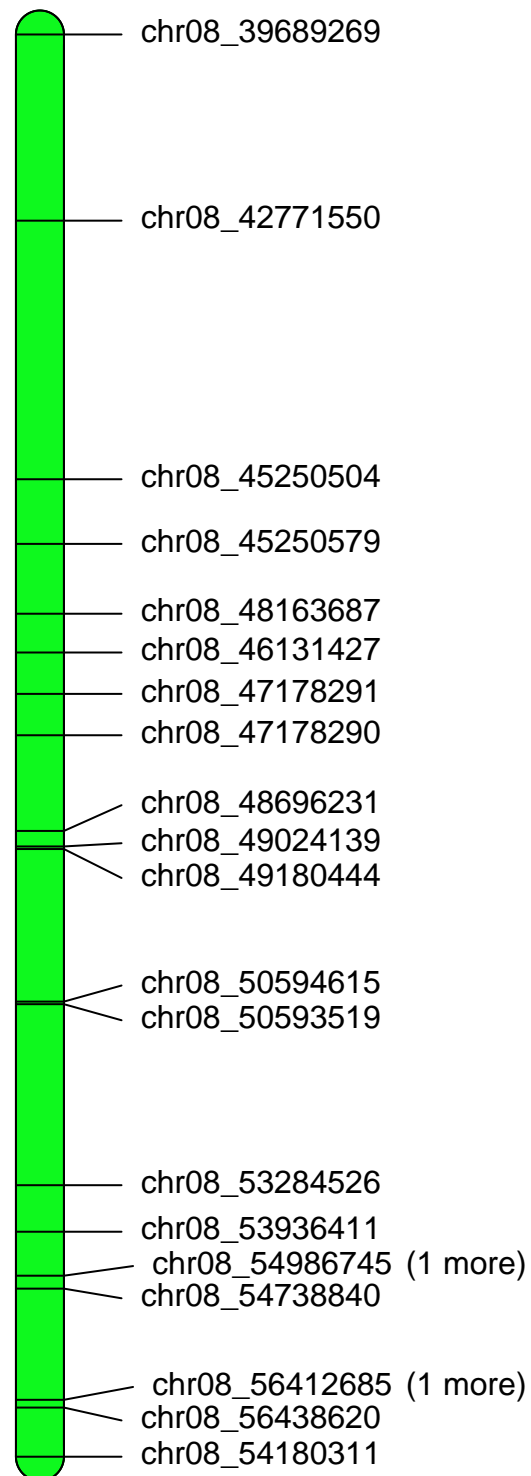
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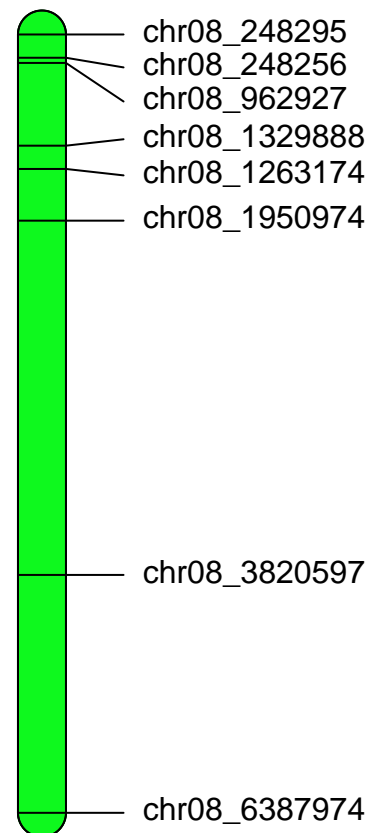
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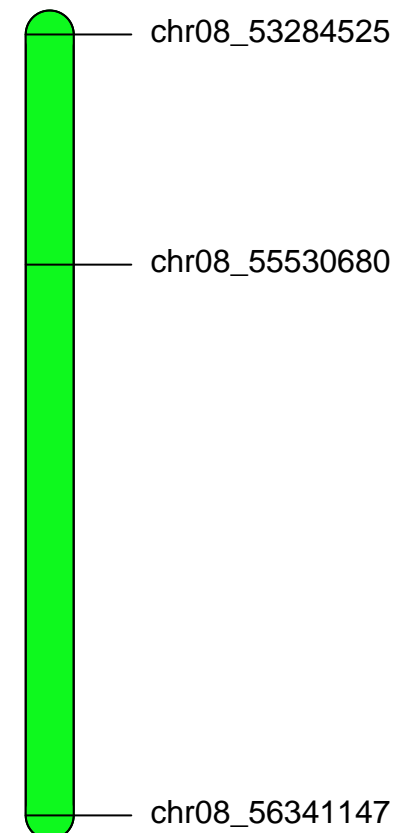
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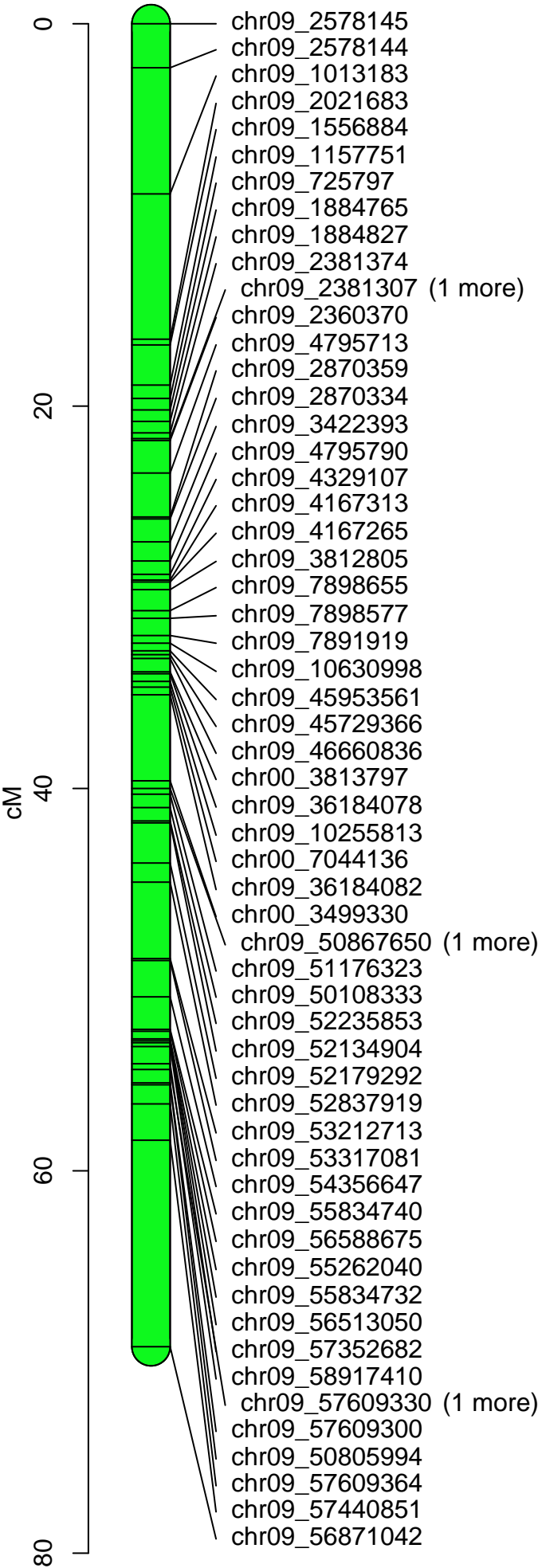
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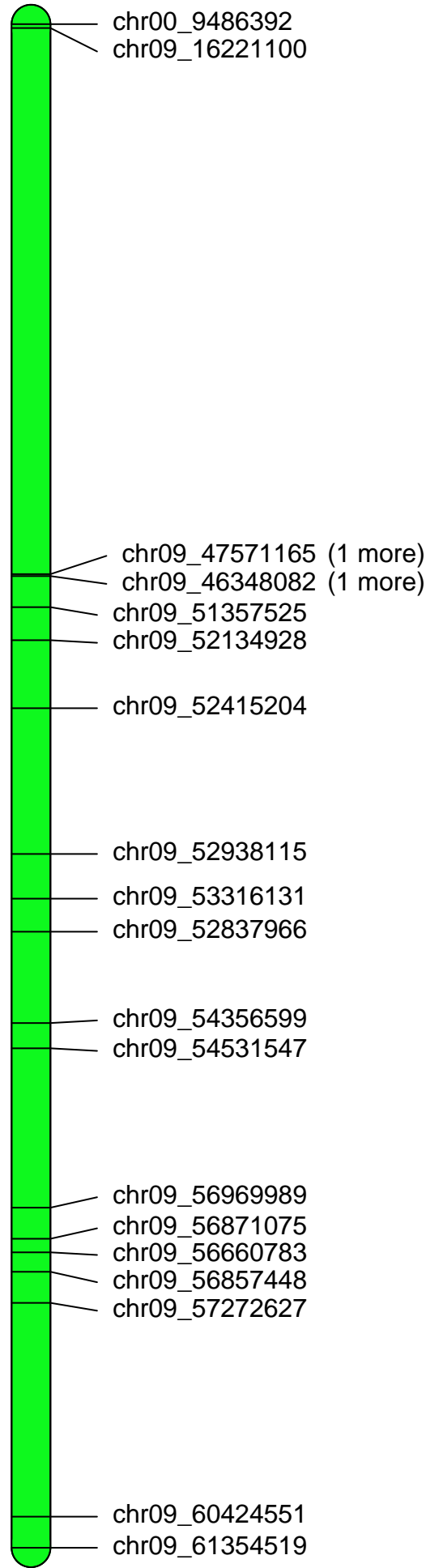
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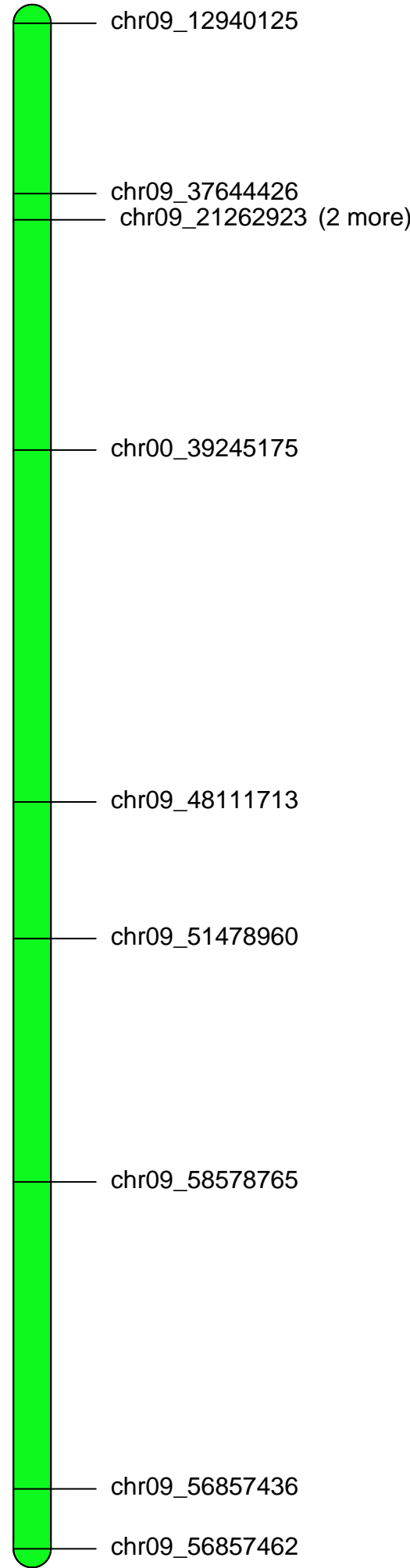
chr09A



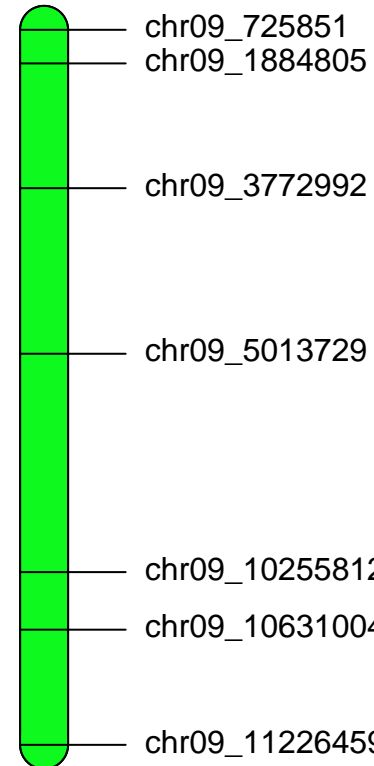
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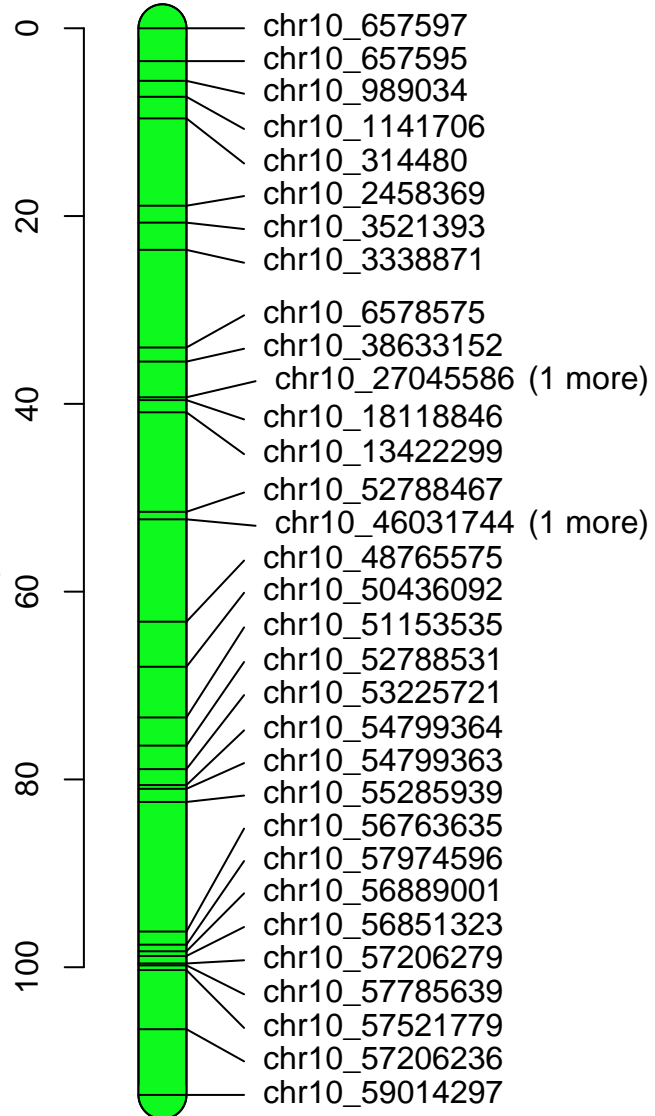
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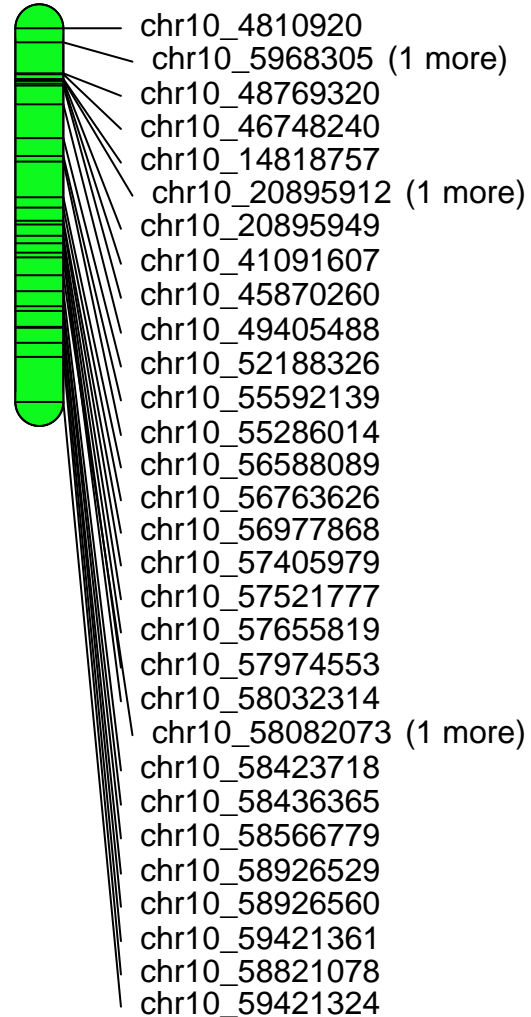
chr09D



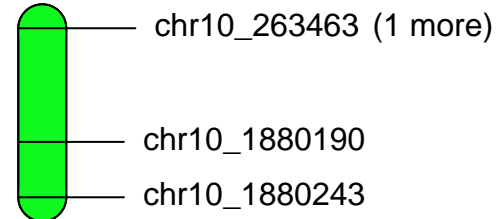
chr10A



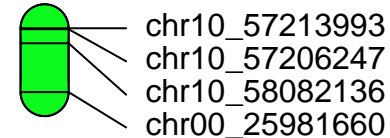
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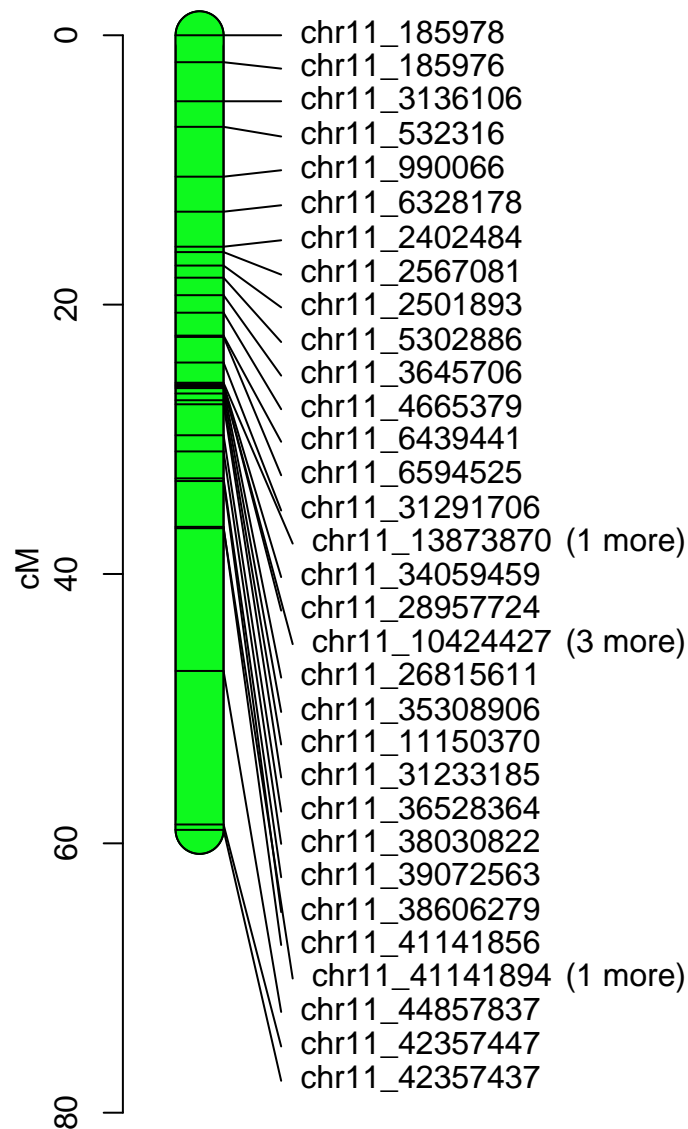
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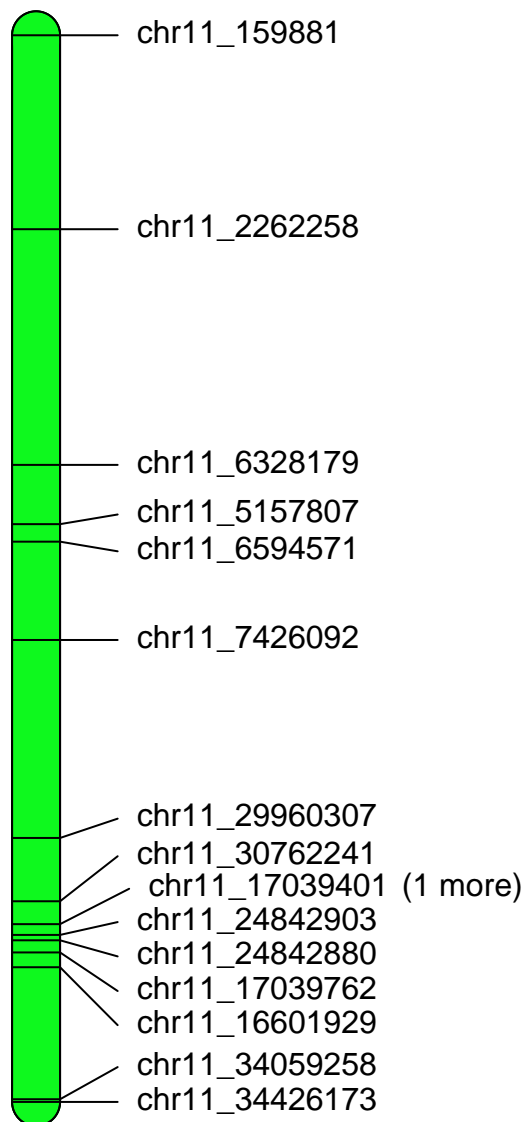
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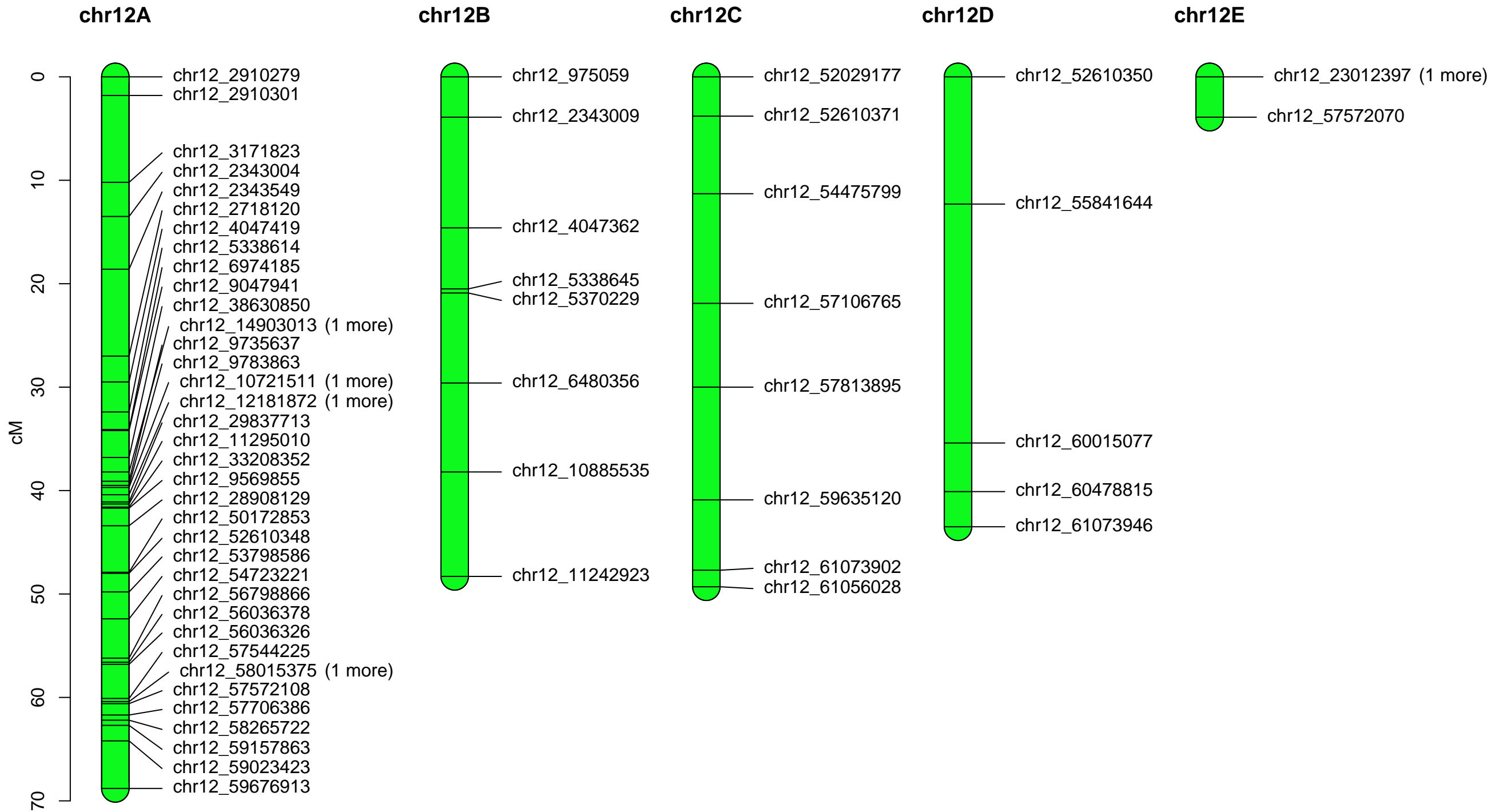


chr11A



chr11B





Map	LG	Position (cM)	Locus	chr00 contig	PGSC Pseudomolecule Tiling Path
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	chr02	1.339	chr00_21611244	chr00:21579816..21728535	PGSC0003DMB000000756
	chr03	23.829	chr00_40502850	chr00:40502447..40504311	PGSC0003DMB0000002378
	chr03	23.986	chr00_8000147	chr00:7515800..8485525	PGSC0003DMB0000000254
	chr04	0	chr00_12567719	chr00:12173931..12667864	PGSC0003DMB0000000431
	chr04	5.365	chr00_12407838	chr00:12173931..12667864	PGSC0003DMB0000000431
	chr04	59.086	chr00_38233239	chr00:38228241..38233666	PGSC0003DMB0000001643
	chr08	36.763	chr00_31385668	chr00:31364510..31394384	PGSC0003DMB0000001091
	chr10	56.754	chr00_23192845	chr00:23101765..23217759	PGSC0003DMB0000000798
	chr11	39.652	chr00_20406095	chr00:20257527..20437853	PGSC0003DMB0000000715
MCD MALE	chr01	19.942	chr00_28505932	chr00:28466967..28514885	PGSC0003DMB0000000979
	chr02	0.782	chr00_21611244	chr00:21579816..21728535	PGSC0003DMB000000756
	chr03	28.384	chr00_8000147	chr00:7515800..8485525	PGSC0003DMB0000000254
	chr04	0	chr00_12407838	chr00:12173931..12667864	PGSC0003DMB0000000431
	chr04	58.24	chr00_38233239	chr00:38228241..38233666	PGSC0003DMB0000001643
	chr08	11.205	chr00_31385668	chr00:31364510..31394384	PGSC0003DMB0000001091
	chr10	61.118	chr00_23192845	chr00:23101765..23217759	PGSC0003DMB0000000798
	chr11	52.861	chr00_20406095	chr00:20257527..20437853	PGSC0003DMB0000000715
PAM FEMALE	chr01B	51.832	chr00_13962275	chr00:13530242..13971654	PGSC0003DMB0000000464
	chr01C	0	chr00_23427320	chr00:23333778..23446661	PGSC0003DMB0000000805
	chr02A	61.108	chr00_19558859	chr00:19450431..19661773	PGSC0003DMB0000000670
	chr05A	12.092	chr00_37599899	chr00:37597868..37605383	PGSC0003DMB0000001545
	chr05B	45.958	chr00_43541618	chr00:43541215..43541950	PGSC0003DMB0000004984
	chr05B	47.434	chr00_43541620	chr00:43541215..43541950	PGSC0003DMB0000004984
	chr07B	140.205	chr00_31495273	chr00:31483820..31513220	PGSC0003DMB0000001096
	chr07B	141.778	chr00_31495276	chr00:31483820..31513220	PGSC0003DMB0000001096
	chr07B	137.612	chr00_31495304	chr00:31483820..31513220	PGSC0003DMB0000001096
	chr08A	7.861	chr00_31385716	chr00:31364510..31394384	PGSC0003DMB0000001091
	chr09A	33.917	chr00_3813797	chr00:1708939..3871400	PGSC0003DMB0000000064
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	chr09C	22.756	chr00_39245175	chr00:39242151..39245446	PGSC0003DMB0000001879
	chr09C	10.507	chr00_5896866	chr00:6457363..7515699	PGSC0003DMB0000000230
	chr09C	10.521	chr00_7044118	chr00:5010086..6318492	PGSC0003DMB0000000170
	chr10D	6.82	chr00_25981660	chr00:25967526..26033986	PGSC0003DMB0000000896