Supplementary files

Figures showing the assembly of own results and published results across all autosomes (chromosome 1-18, SSC1-18) and the X chromosome.

Shown are results for expression studies for inverted teats (green), QTL studies for inverted/ functional teats (red), association studies for inverted/ functional teats (dark red), QTL studies for number of teats (blue) as well as association studies for number of teats (black). If multiple loci were reported from the same study, loci were combined; the number of combined loci is shown in parenthesis behind the reference. It is indicated if results were significant (**, P>0.05), suggestive (*, P>0.1), or if no information given. Positions are given in approximations and information were taken from the literature and the Pig QTLDB (*Hu Z-L, Park CA, Reecy JM (2016) Developmental progress and current status of the Animal QTLdb Nucleic Acids Research 44:D827-D833 doi:10.1093/nar/gkv1233*). Charts were designed using MapChart (*Voorrips RE (2002) MapChart: Software for the Graphical Presentation of Linkage Maps and QTLs Journal of Heredity 93:77-78 doi:10.1093/jhered/93.1.77*). References used are the following:

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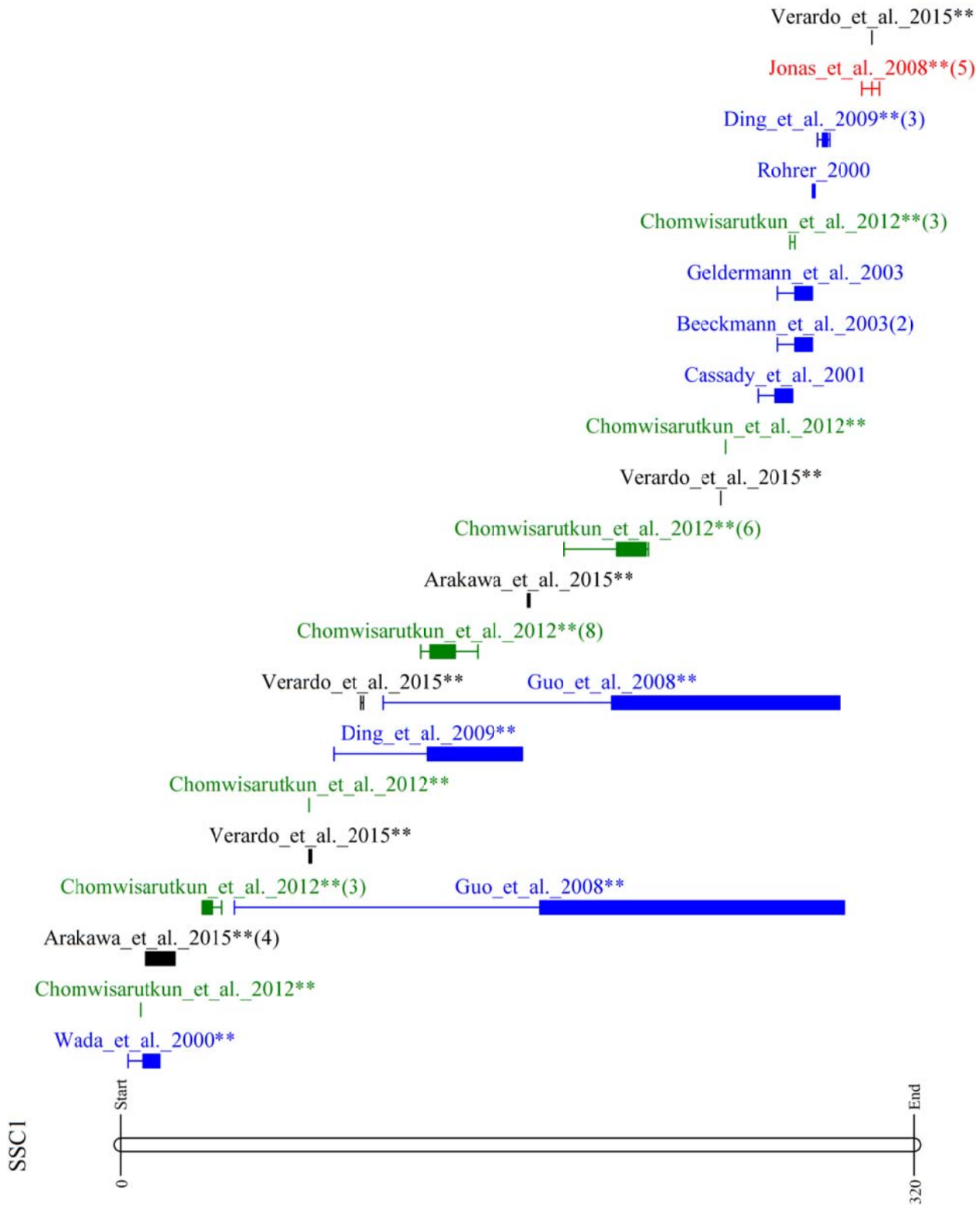
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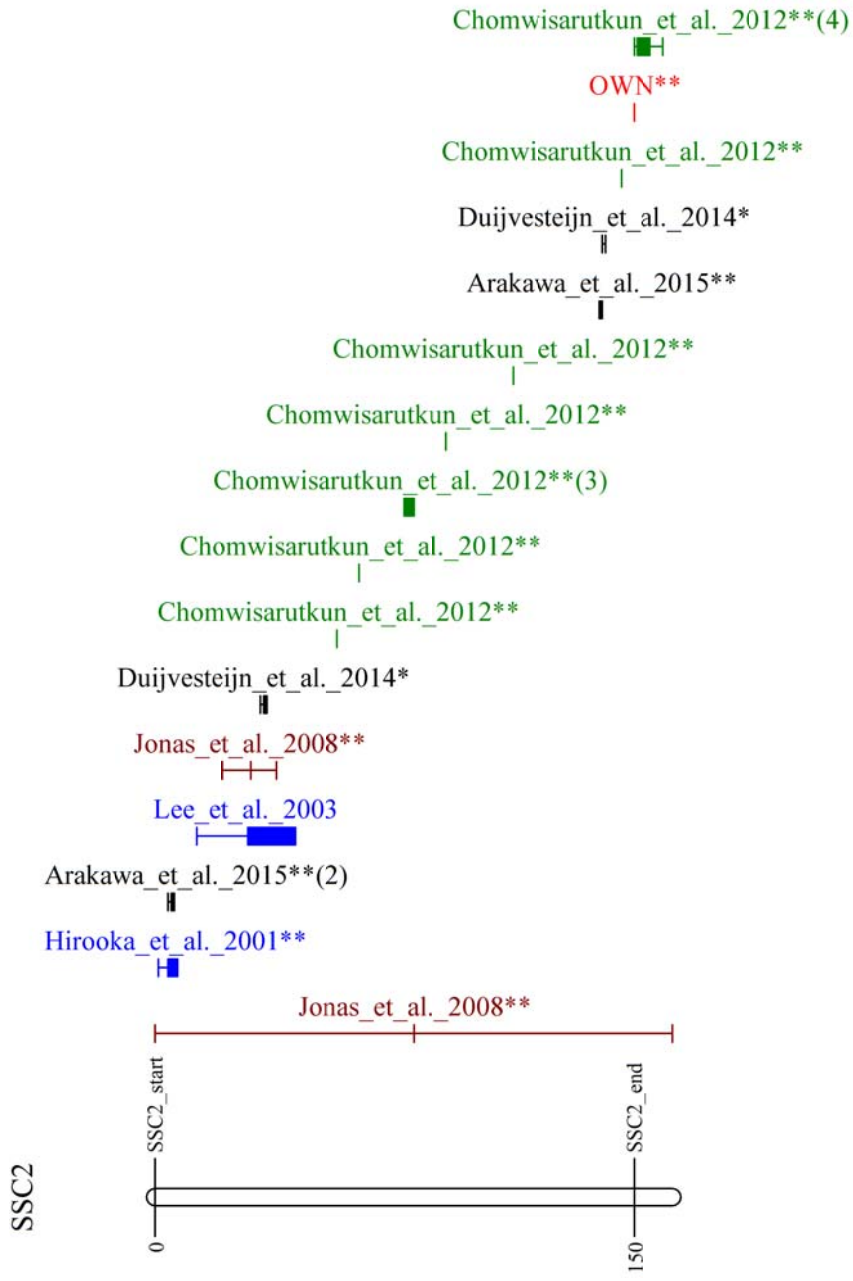
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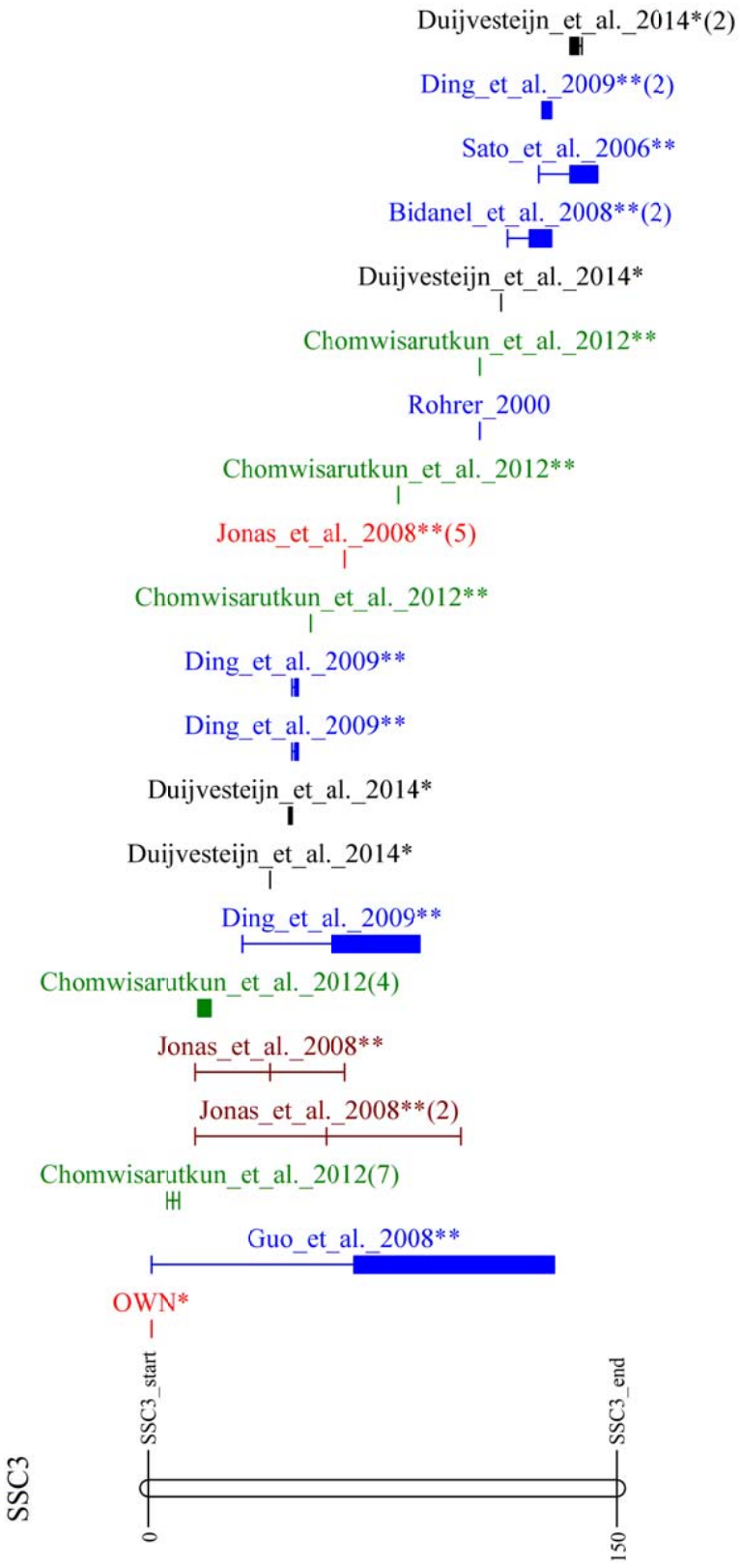
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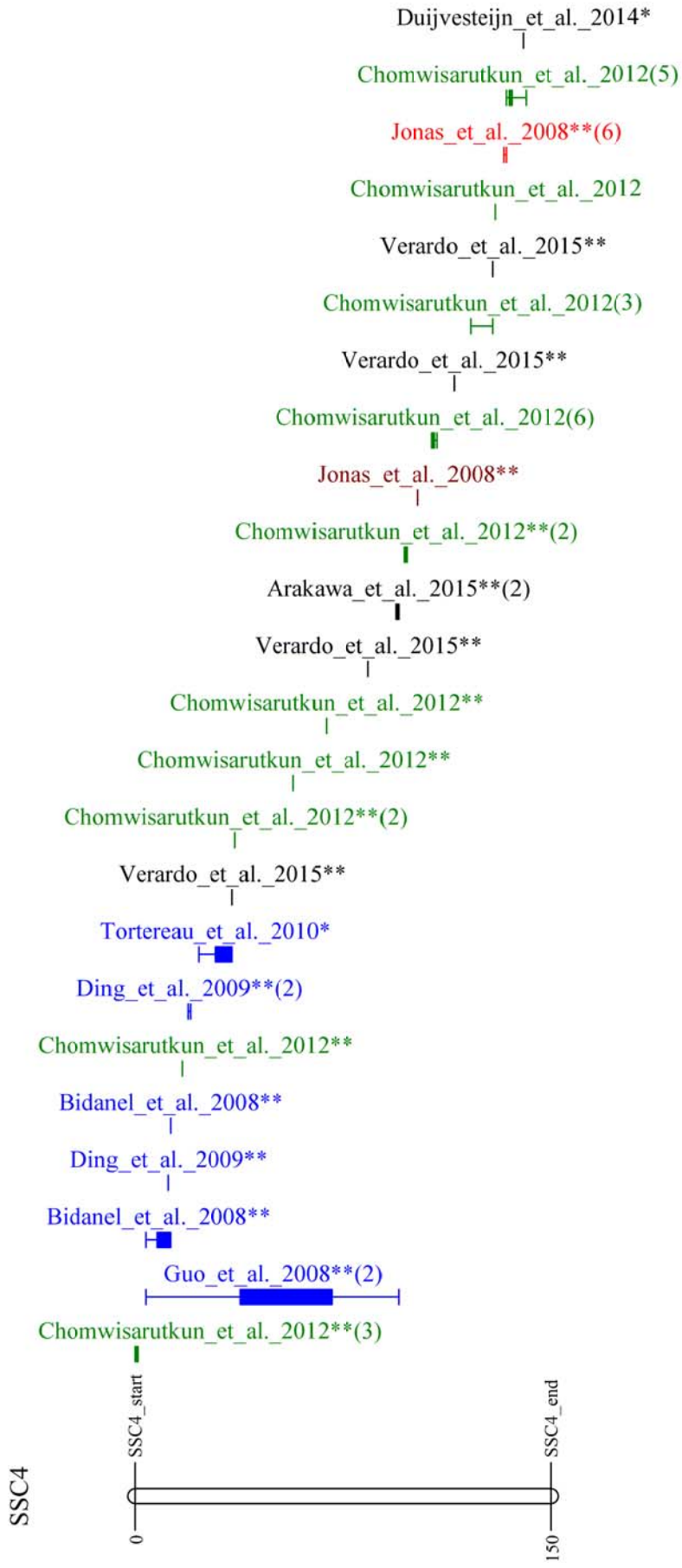
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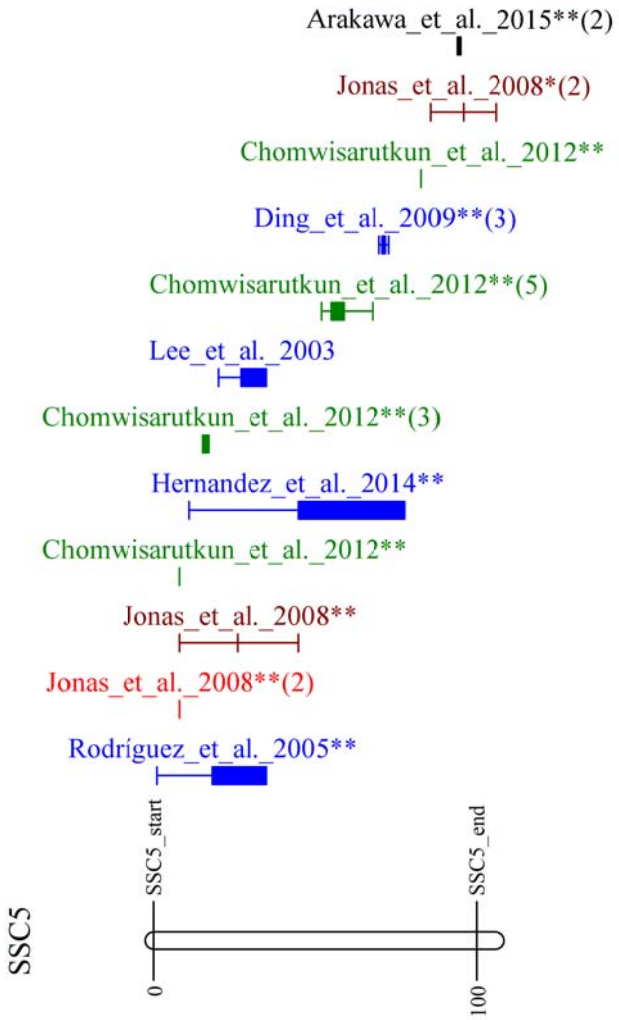
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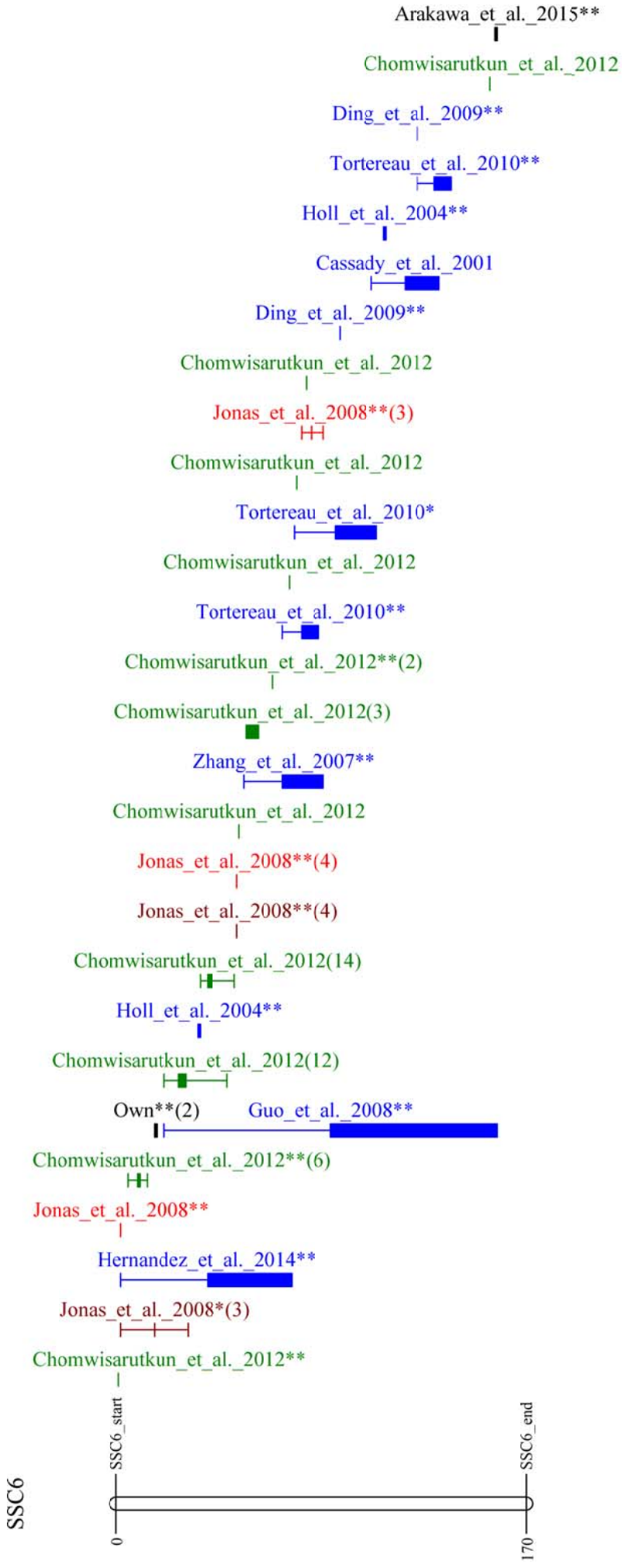
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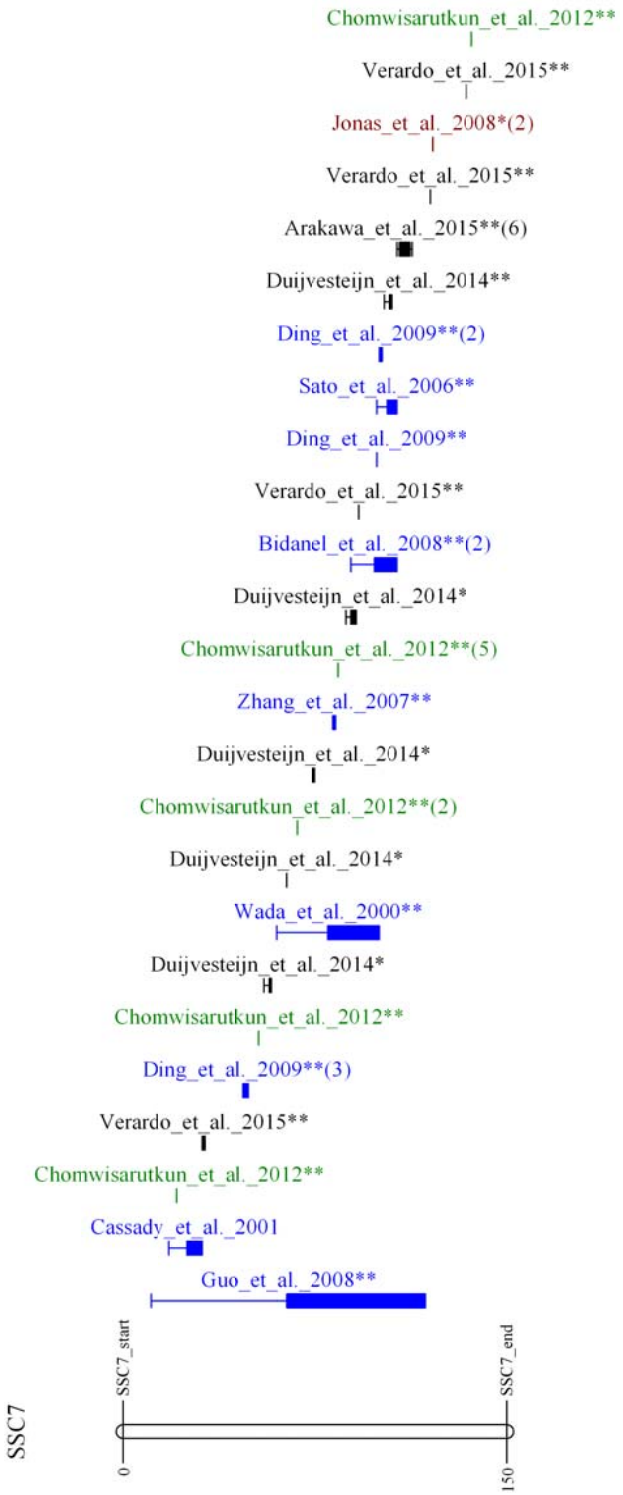
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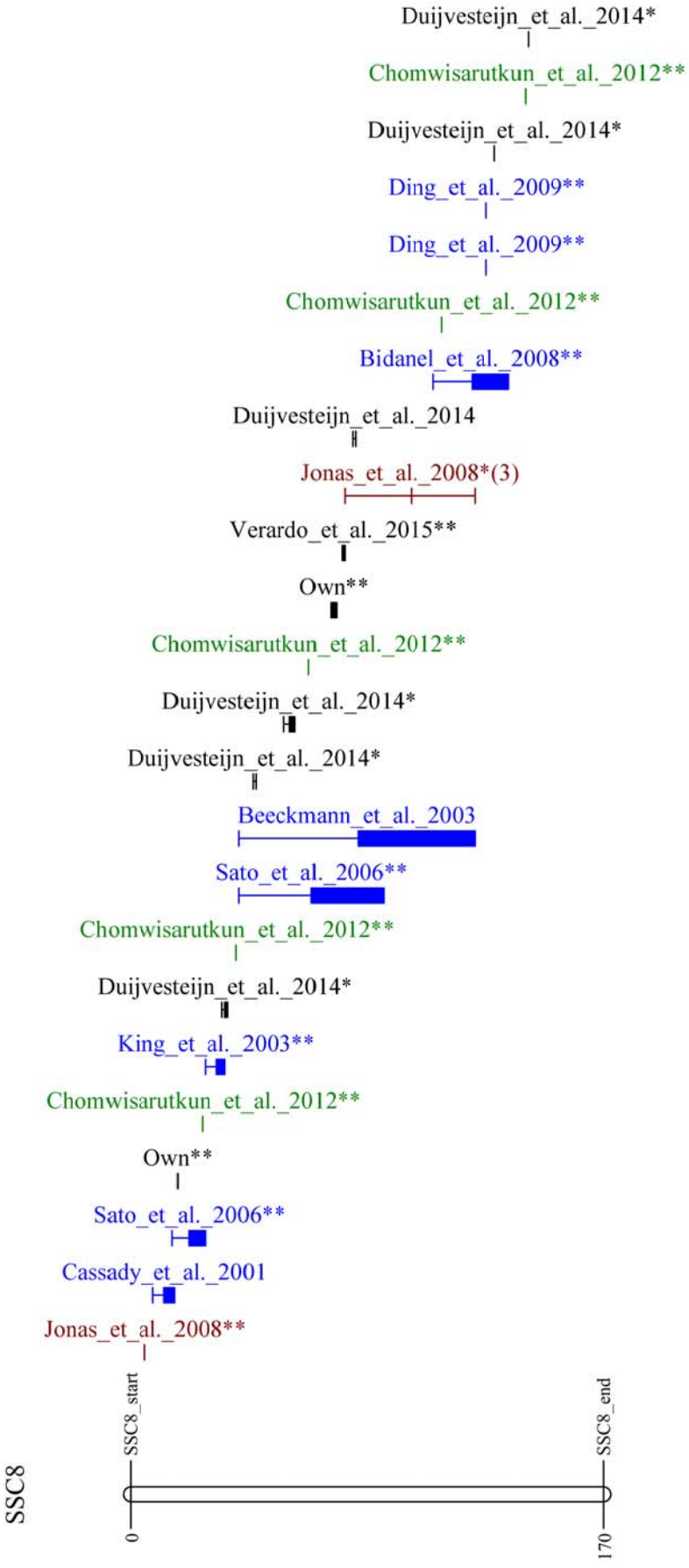
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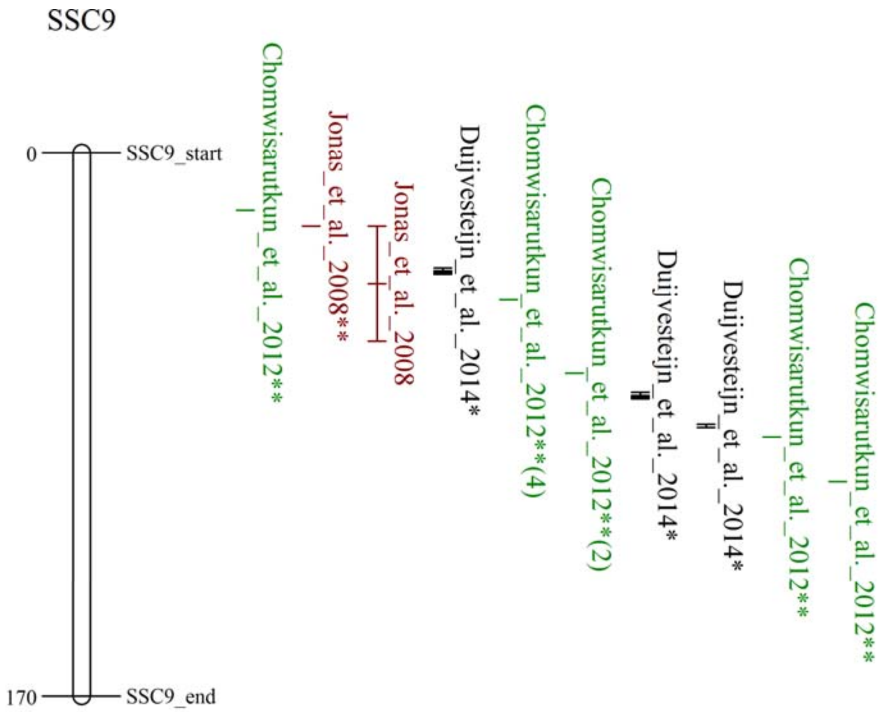
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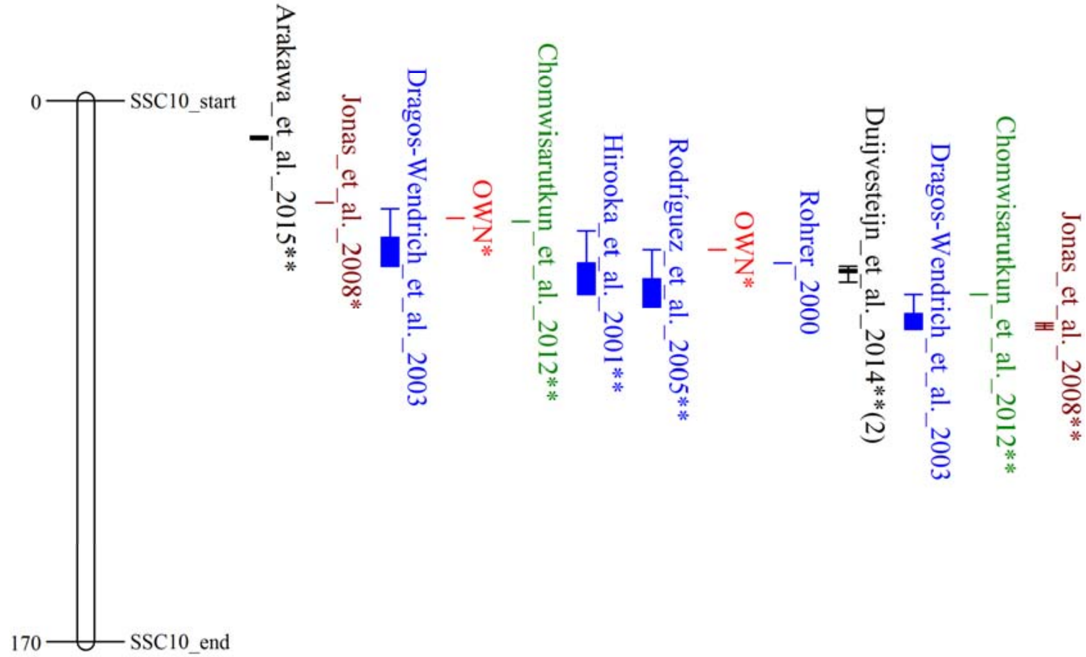

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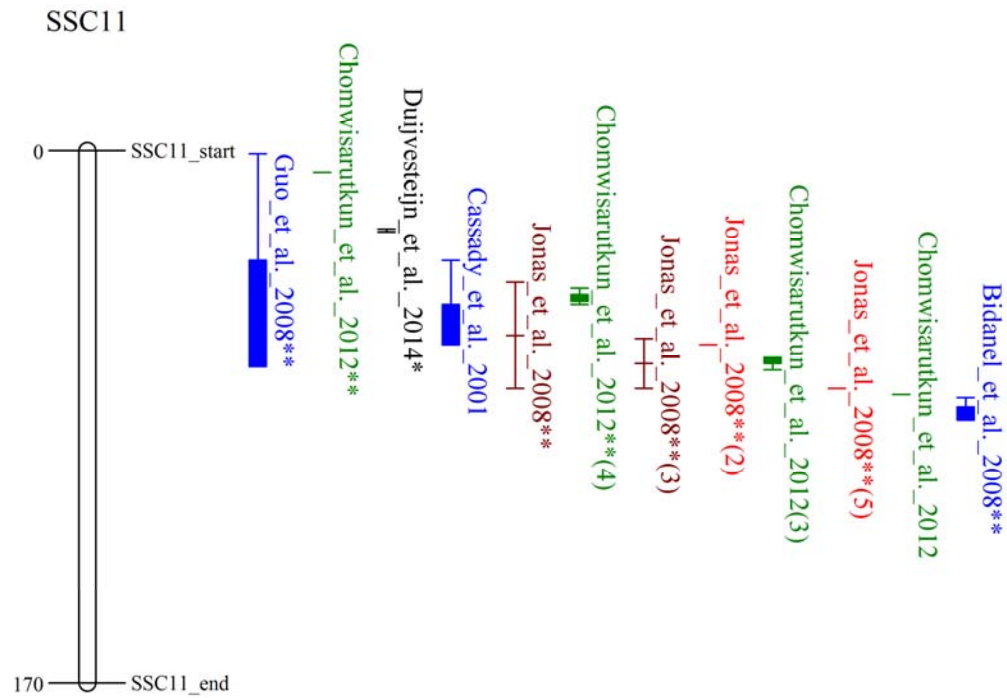

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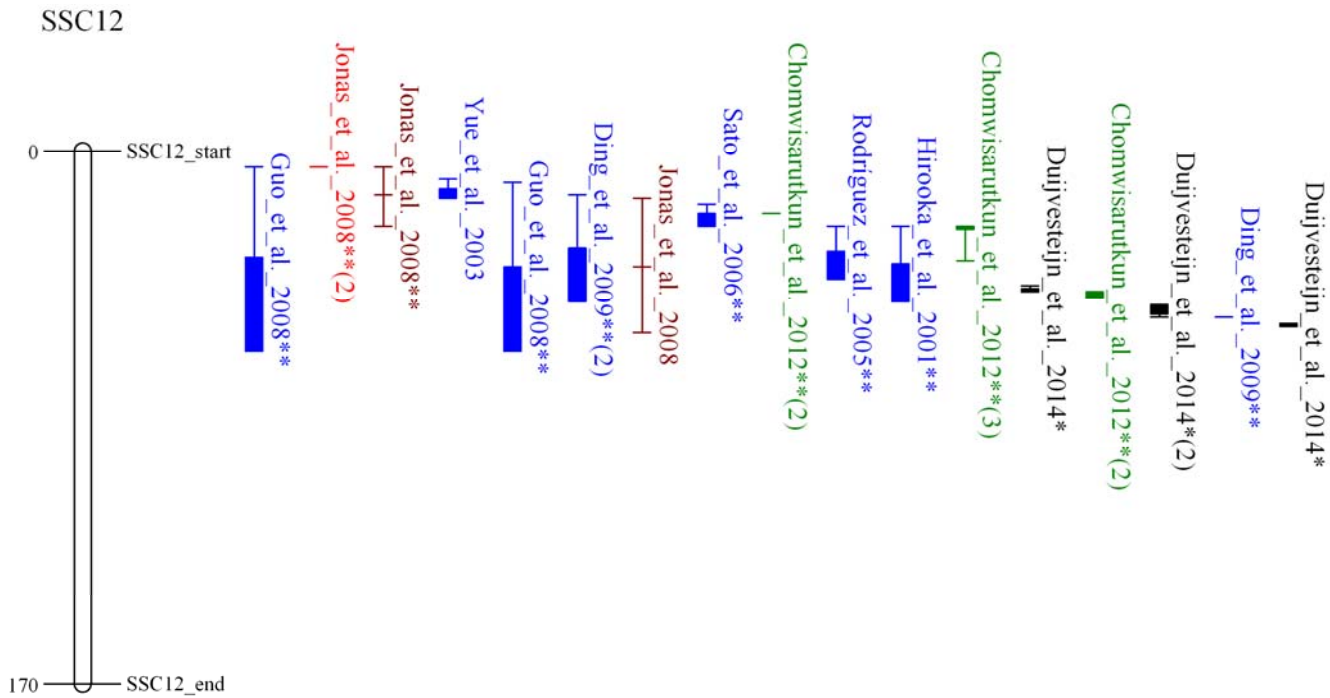
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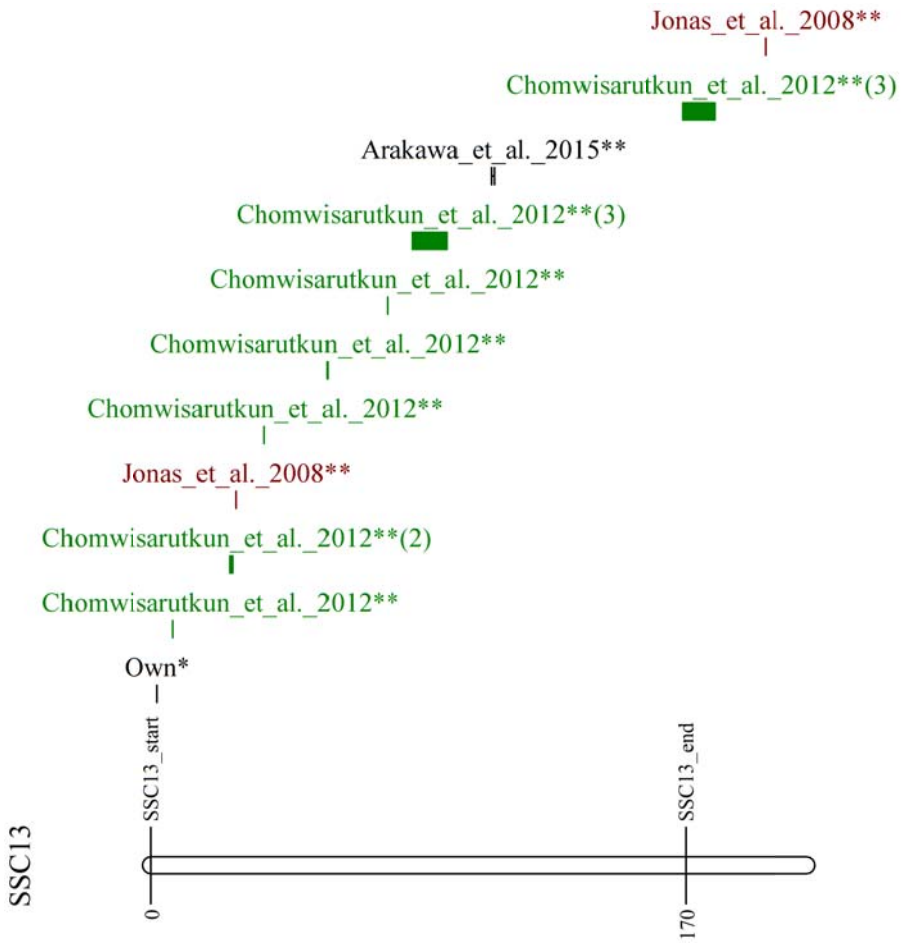
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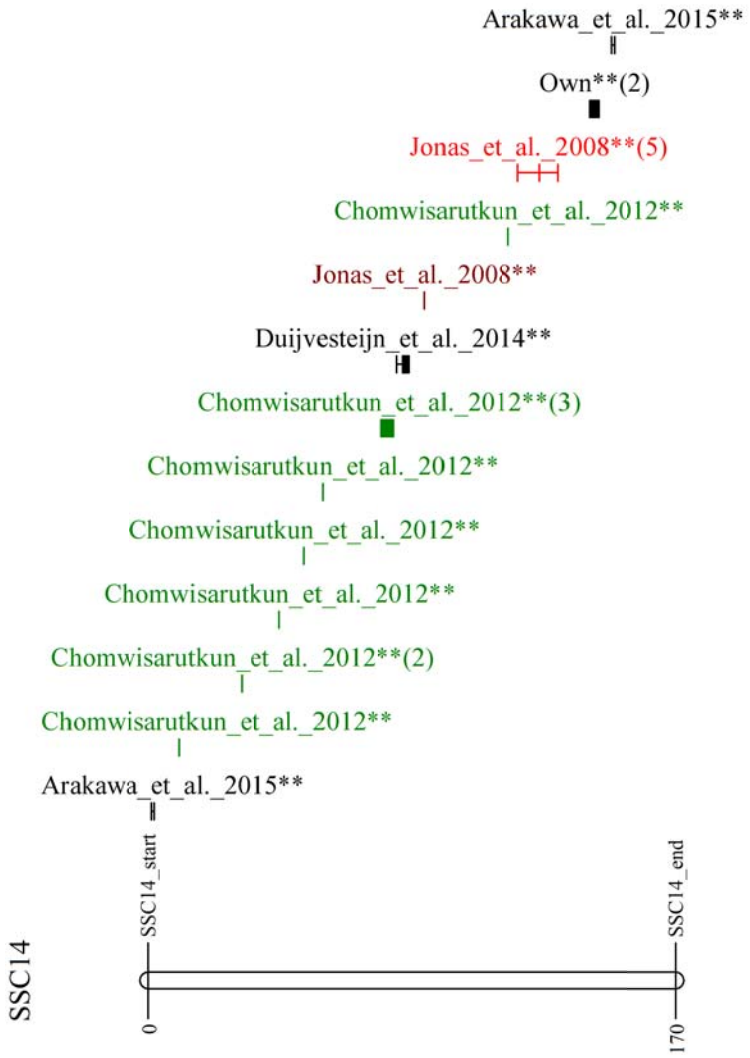
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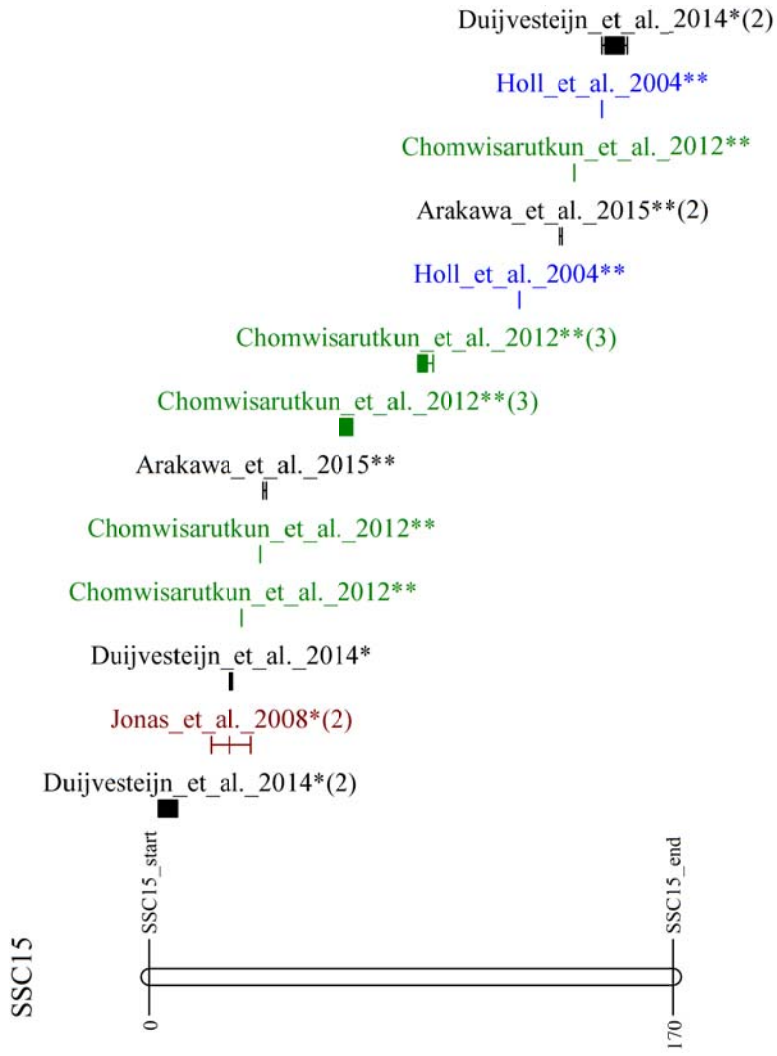
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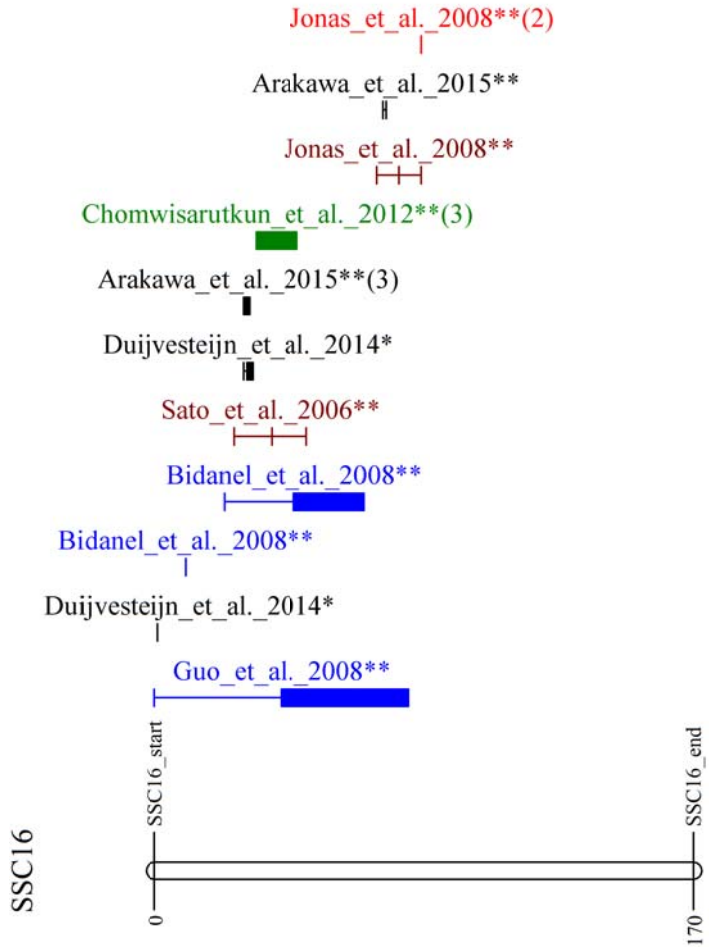
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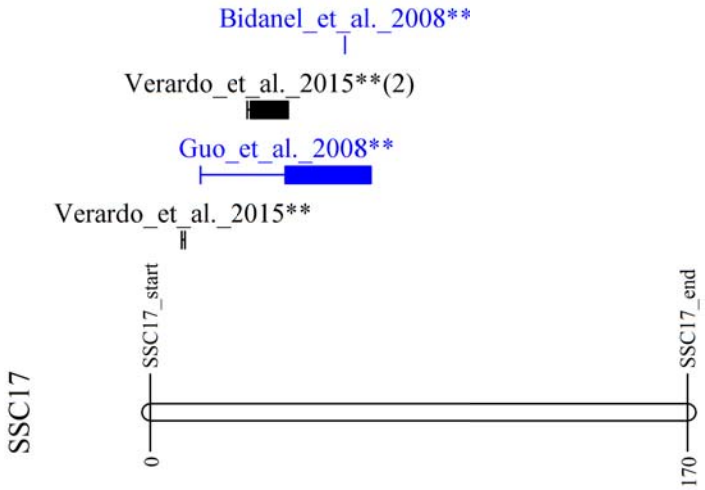
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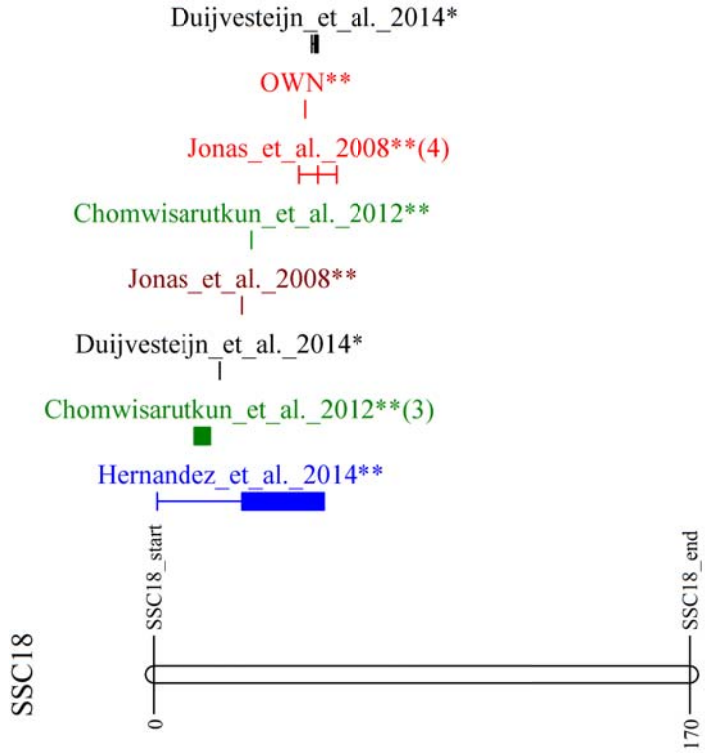
Duijvesteijn_et_al._2014*
OWN**
Jonas_et_al._2008**(4)
Chomwisarutkun_et_al._2012**
Jonas_et_al._2008**
Duijvesteijn_et_al._2014*
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Hernandez_et_al._2014**
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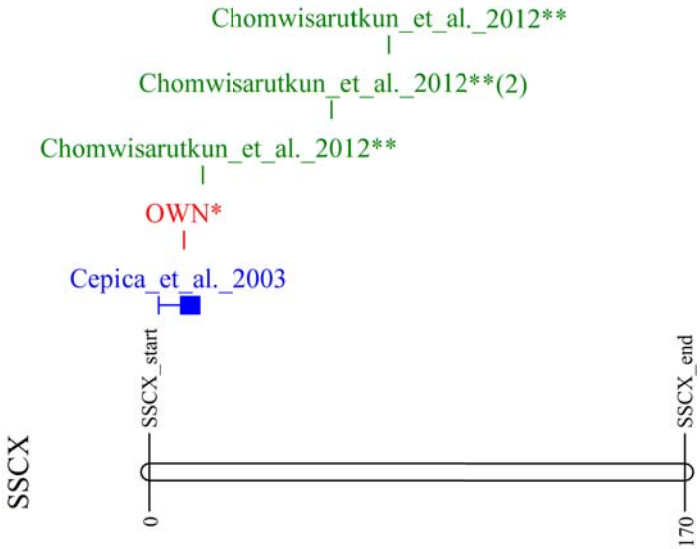
170


Chomwisarutkun_et_al._2012**
Chomwisarutkun_et_al._2012**(2)
Chomwisarutkun_et_al._2012**
OWN*
Cepica_et_al._2003
SSCX
SSCX_start
SSCX_end
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170