

File S8

Explanation of Chromosome V QTLs by common segment and sequential minimum spanning tree methods.

Lists introgression lines that define each QTL by common segment and sequential MST method.

Method	QTL (Mb)	NILs that define QTLs
Common segment method	QTL9 (~10.91 – ~13.95)	Common HW sequence present in HW-phenotype strains (<i>ewIR69</i> and <i>ewIR71</i>). All other tested strains have N2-like phenotype.
Common segment method	Suppressor QTL10 (~10.38 - ~end)	Strain <i>ewIR70</i> contains QTL9, but has an N2-like phenotype.
Sequential MST method	QTL m9 (~4.55 – ~10.91)	Strain (<i>ewIR69</i>) has a significantly more HW-like phenotype than strain (<i>kyIR70</i>). QTL m9 is defined by the additional HW-sequence present in strain <i>ewIR69</i> and absent in <i>ewIR70</i> .