

File S7

Explanation of Chromosome IV QTLs defined by sequential minimum spanning tree method.

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

Introgression lines	QTL (Mb)	NILs that define QTLs
<b>First set of <i>kyIR</i> lines</b>	None	No significant differences detected.
<b>Nested <i>kyIR</i> lines</b>	QTL m2 (~0.79 - ~1.03)	HW sequence present in HW-phenotype strain <i>kyIR76</i> and absent in N2-phenotype strain <i>kyIR54</i> .
<b><i>ewIR</i> lines</b>	QTL m7 (~2.76 - ~3.35)	HW sequence present in HW-phenotype strain <i>ewIR53</i> and absent in N2.
	QTL m8 (~10.12 - ~12.75)	Defined by HW sequence present in HW phenotype strain <i>ewIR58</i> and absent in N2-phenotype strain <i>ewIR60</i>
<b>All lines</b>	QTL m2 (~0.79 - ~1.03)	HW sequence present in HW-phenotype strain <i>kyIR76</i> and absent in N2-phenotype strain <i>kyIR54</i> .
	QTL m7 (~2.76 - ~3.35)	HW sequence present in HW-phenotype strain <i>ewIR53</i> and absent in N2.
	Suppressor QTL m6 (~2.76 - ~3.92 Mb).	Additional HW sequence present in N2-phenotype strain <i>ewIR47</i> and absent in HW-phenotype strain <i>kyIR65</i> .