

**Table S1: properties of EM-seq libraries sequenced in this study**

<b>Sample</b>	<b>Tissue</b>	<b>Cycles</b>	<b>Total reads</b>	<b>Total reads after QC</b>	<b>Uniquely mapping reads after deduplication</b>	<b>% Reads uniquely mapping</b>	<b>Conversion rate</b>
<i>met1-3</i> heterozygote	leaf	150x150	60,407,565	57,704,567	30,318,827	52.6	99.998
<i>met1-3</i> WT segregant, line 1 F2	leaf	150x150	59,741,235	56,772,575	32,355,357	57.1	99.9978
<i>met1-3</i> WT segregant, line 1 F3	leaf	150x150	53,407,468	53,362,670	22,649,572	42.4	99.999
<i>met1-3</i> WT segregant, line 2 F2	leaf	150x150	50,522,623	50,465,956	25,117,695	40	99.9989
<i>met1-3</i> WT segregant, line 2 F3	leaf	150x150	57,417,384	55,601,549	32,596,017	58.6	99.9978
<i>met1-3</i> WT segregant, line 3 F2	leaf	150x150	54,398,483	54,337,350	24,958,077	45.9	99.999
<i>met1-3</i> WT segregant, line 3 F3	leaf	150x150	55,237,611	55,193,429	26,779,936	48.5	99.9989