

**Supplementary Table 5:** Average retention frequencies for each 1 Mb region analyzed via high-throughput SNP genotyping.

<b>Chromosome</b>	<b>Average RF</b>	<b>Minimum RF</b>	<b>Maximum RF</b>
<b>A1</b>	19.9%	12.8%	31.5%
<b>F2</b>	35.4%	26.7%	44.7%
<b>A2</b>	27.0%	14.7%	40.0%
<b>B3</b>	21.8%	18.0%	34.7%
<b>C2</b>	26.8%	15.3%	40.7%
<b>D1</b>	36.5%	28.0%	44.7%
<b>D2</b>	33.8%	26.7%	46.7%
<b>D4</b>	28.5%	22.0%	39.3%
<b>E2</b>	33.5%	27.3%	44.7%
<b>X</b>	26.1%	16.1%	38.3%