

**Table 6.** Frequent haplotypes (>2%) formed by markers in the genomic segments spanned by trait-associated block 2. The trait-associated block consists of all markers in the study that were concordant on frequent haplotypes (i.e. in complete linkage disequilibrium) with rs9399137, the marker obtained in the stepwise selection procedure. The block extremities coincide with the positions of the most proximal and distal markers within each block. The haplotypes include other markers that are situated between the block extremities but are not in complete linkage disequilibrium with the block markers, which are shown in bold.

Marker ID																									
<b>rs9376090</b>	rs9389266	rs52090905	rs52090906	rs52090907	<b>rs9399137</b>	rs52090908	rs9402684	<b>rs9402685</b>	rs7743042	<b>rs11759553</b>	rs1074849	<b>rs52090909</b>	rs6930223	<b>rs4895440</b>	<b>rs4895441</b>	<b>rs9376092</b>	<b>rs9389269</b>	<b>rs9402686</b>	rs10484494	<b>rs11154792</b>	rs1411919	rs7766963	rs2223385	<b>rs9483788</b>	Hap freq
T	G	C	T	C	T	T	T	T	A	<b>A</b>	G	<b>C</b>	G	<b>A</b>	<b>A</b>	<b>C</b>	<b>T</b>	<b>G</b>	G	<b>T</b>	A	T	G	<b>T</b>	0.45
<b>C</b>	G	C	T	C	<b>C</b>	T	C	<b>C</b>	G	<b>T</b>	G	<b>G</b>	T	<b>T</b>	<b>G</b>	<b>A</b>	<b>C</b>	<b>A</b>	G	<b>C</b>	A	C	G	<b>C</b>	0.18
<b>T</b>	T	C	T	C	<b>T</b>	T	C	<b>T</b>	G	<b>A</b>	A	<b>C</b>	T	<b>A</b>	<b>A</b>	<b>C</b>	<b>T</b>	<b>G</b>	G	<b>T</b>	G	C	A	<b>T</b>	0.13
<b>T</b>	G	T	C	G	<b>T</b>	C	C	<b>T</b>	G	<b>A</b>	A	<b>C</b>	T	<b>A</b>	<b>A</b>	<b>C</b>	<b>T</b>	<b>G</b>	G	<b>T</b>	G	C	A	<b>T</b>	0.06
<b>C</b>	G	C	T	C	<b>C</b>	T	C	<b>C</b>	G	<b>T</b>	G	<b>G</b>	T	<b>T</b>	<b>G</b>	<b>A</b>	<b>C</b>	<b>A</b>	A	<b>C</b>	A	C	G	<b>C</b>	0.05
<b>T</b>	G	T	C	G	<b>T</b>	T	C	<b>T</b>	G	<b>A</b>	A	<b>C</b>	T	<b>A</b>	<b>A</b>	<b>C</b>	<b>T</b>	<b>G</b>	G	<b>T</b>	G	C	A	<b>T</b>	0.04