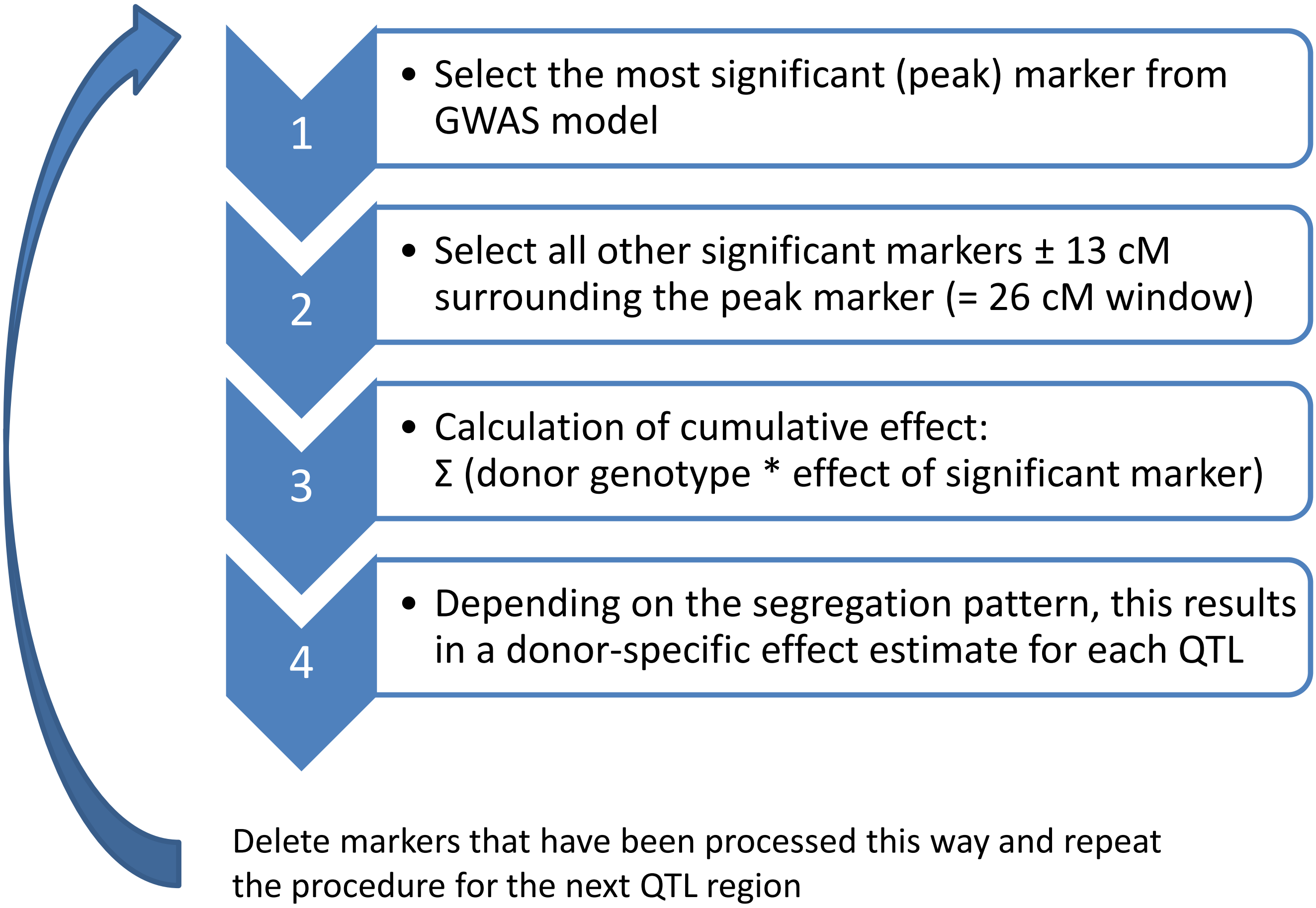
Figure S2)
QTL effect estimation for each donor allele in HEB-25

Basic pre-requisites and assumptions:

- Effect estimates from identity-by-state GWAS model ‘IBS-M’ (=Model-B, Liu et al. 2011)
- Significant markers reveal different segregation patterns across HEB donors
- Cumulation of nearby SNP effects accounts for donor-specific allelic QTL effects



1
- Select the most significant (peak) marker from GWAS model

2
- Select all other significant markers ± 13 cM surrounding the peak marker (= 26 cM window)

3
- Calculation of cumulative effect: Σ (donor genotype * effect of significant marker)

4
- Depending on the segregation pattern, this results in a donor-specific effect estimate for each QTL

Delete markers that have been processed this way and repeat the procedure for the next QTL region

Example

26 cM

Marker	SNP2	SNP1	SNP3
GWAS effect	+2	+5	-1

	Donor genotypes			Cumulation	Donor-specific QTL effect
Donor 1	0	2	2	0*2 + 2*5 + 2*(-1)	8
Donor 2	0	2	0	0*2 + 2*5 + 0*(-1)	10
Donor 3	0	0	2	0*2 + 0*5 + 2*(-1)	-2
Donor 4	2	2	2	2*2 + 2*5 + 2*(-1)	12
Donor 5	0	0	0	0*2 + 0*5 + 0*(-1)	0