Supplementary file 3. Methodological specifications of the two approaches used to link genotypes and phenotypes

	Linkage analysis	**Linkage disequilibrium mapping**
Population type	Biparental cross with known pedigree: $Y=\mu+M+e$	Population with unknown pedigree/structure: $Y=\mu+M+Q+K+e$
Nb of segregating alleles	LOW	HIGH
Resolution (i.e. nb of meiotic recombination events that have occurred between a DNA marker and a QTL)	LOW Few recombination between markers within the studied pedigree	HIGH Historical recombination within the unobserved pedigree from which the studied population was derived
Nb of markers needed to detect a QTL	LOW (low-density linkage maps)	- Extremely HIGH for genome-wide investigations - Targeted candidate genes
QTL confidence interval	LARGE (cM) Loose marker-trait association	NARROW (depends on LD window) Tight marker-trait association down to the causal variant