



Figure S16. Geographic distribution of *RKS1* polymorphisms. (A) Geographic distribution of the two highly divergent haplotypes located in the intergenic region between *RKS1* and *At3g57720* and at the beginning of *RKS1*, using one of the 35 SNPs in complete LD, i.e. a SNP at position 21,387,232 on chromosome 3. (B) Geographic distribution of two S susceptible alleles embedded in the R intergenic haplogroup (n = 476). The geographic distribution of the accessions with a stop codon at the beginning of *RKS1* was mapped using one of the 214,051 SNPs that is in complete LD with the stop codon; i.e. a SNP at position 21,388,948 on chromosome 3 (position 4129 in Table S8). The geographic distribution of the accessions with the additional S susceptible allele was mapped using accessions with both a 'G' base at position 21,388,849 on chromosome 3 (i.e. position 4030 in Table S8) and a 'T' base at position 21,389,085 on chromosome 3 (i.e. position 4266 in Table S8). All maps have been based on 948 natural accessions with accurate GPS coordinates and genotyped for 214,051 SNPs [64] and generated with the R packages 'maptools' and 'plotrix'. The size of the pies depends of the number of accessions genotyped for 214,051 SNPs in the sites of collection.