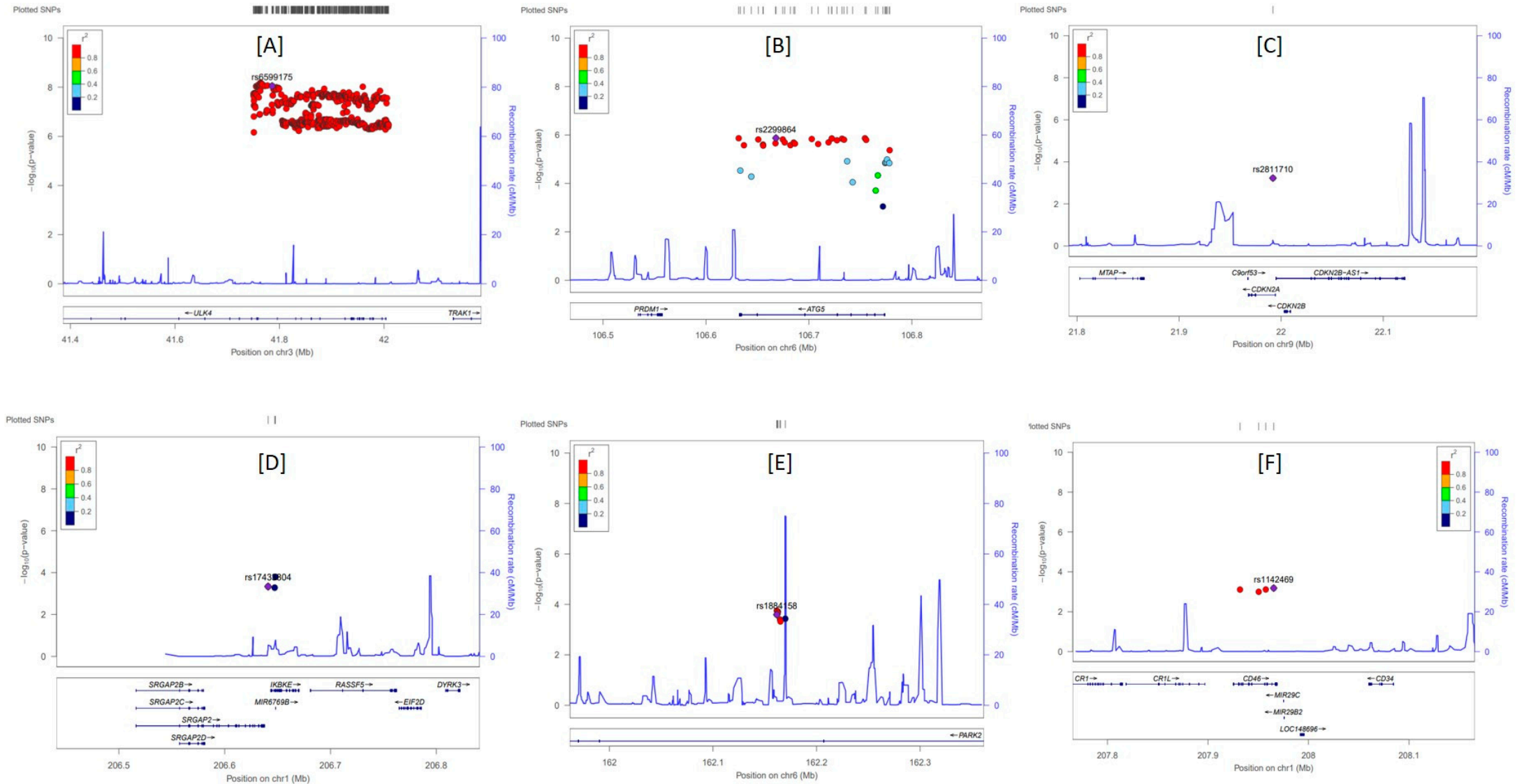


Supplementary Figure 1. Locus Zoom plots of the autophagy-related SNPs representing susceptibility regions for MM (after meta-analysis of the German and InterLymph populations).



[A] LocusZoom plot of the *ULK4* gene in chromosome 3 than includes the rs6599175 SNP ($P=8.94 \cdot 10^{-09}$) but also 501 additional SNPs associated with MM risk; **[B]** LocusZoom plot of the *ATG5* gene including the rs2299864 SNP ($P=1.35 \cdot 10^{-06}$) but also 35 additional markers associated with MM risk; **[C]** LocusZoom plot of the *CDKN2A* gene including the rs2811710 SNP ($P=5.93 \cdot 10^{-04}$). Although only this SNP in the *CDKN2A* locus was available in the GWAS datasets, this marker has been consistently associated with MM risk; **[D]** LocusZoom plot of the *IKBKE* gene encompassing the rs17433804 SNP in chromosome 1 ($p=4.62 \cdot 10^{-04}$) but also 2 neighboring SNPs showing a similar level of association. **[E]** LocusZoom plot of the *CD46* gene including the rs1142469 SNP ($p=6.55 \cdot 10^{-04}$) and 3 neighboring SNPs; **[F]** LocusZoom plot of the *PARK2* gene region [encompassing the rs1884158 SNP ($p=2.56 \cdot 10^{-04}$) and 4 additional neighboring SNPs. All the results are represented according to hg19 genome build.