**Supplementary Figure 1. Splice site prediction scores for the *ABCA4* c.6385A and c.6385G variants according to five algorithms in Alamut Visual.** The splice donor site predictions (in blue; 5’) show a decrease from 91.8 to 80.3 for SpliceSiteFinder-like. There are no scores for the other programs as the ‘GC’ canonical splice site sequence only is recognized by SpliceSiteFinder-like. A strong cryptic splice donor site at c.6386+27 in intron 47 possibly could be activated in the *ABCA4* gene carrying c.6385A>G.

