Supplementary Figure 1. Nucleotide sequence of the GSL1 gene with 5’upstream regulatory and terminator regions from potato DM; derived from The Potato Genome Sequencing Consortium [33]. Numbering is defined by the putative transcription start site (TSS, +1) predicted at 33 nt from the first base of the translation start site (ATG), based on a plant dimer motif YR Rule (TG, -1/+1). Putative cis-elements TATA-box (-32 to -27, highlighted violet), a pyrimidine patch (Y Patch, -26 to -20, highlighted pink) and CAAT-box (-48 to -44, highlighted red) were also identified. Other nucleotide sequences highlighted are: positions of promoter motifs annotated as numbered ovals on Figure 1A and listed in Table 2 (blue); 5’UTR (grey); exons (yellow); and intron (green). The start and stop codons are marked in red font.