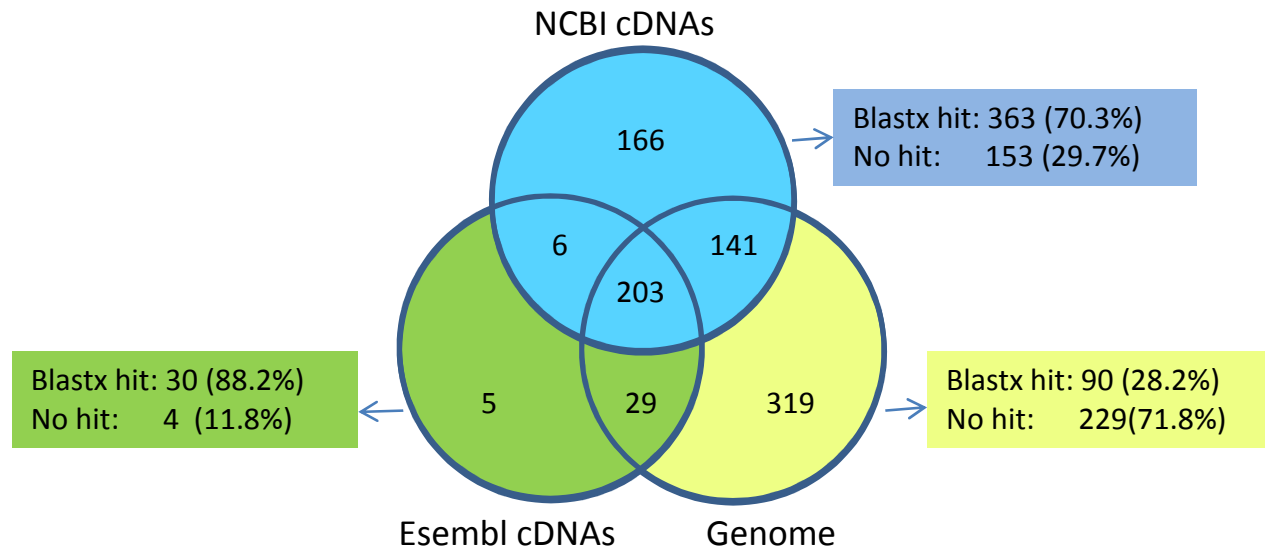


## Pinto *et al*, Additional file S1



**Additional figure S1.** Venn diagram summarizing the mapping of differentially expressed tag sequences to the three different available datasets containing *T. nigroviridis* DNA sequences. Numbers inside each area (non-proportional) indicate the number of common or specific tags showing perfect matches (26/26 identical nucleotides) to NCBI cDNAs, Ensembl cDNAs or to the *T. nigroviridis* genome, while blocks indicate the number and percentage (in brackets) of these DNA sequences that significantly matched ( $E$  value  $< 10^{-5}$ ) Swiss-Prot protein entries by BlastX (2-step procedure for tag annotation). Colors indicate the preference order given to the BlastX results of DNA matches from the different datasets when annotating the tags: matches to NCBI cDNAs (blue) used preferably, followed by Ensembl cDNAs (green) and genomic matches (yellow).