**Fig. 4. Evaluation of Challenge 3: transcript identification without a reference annotation. a)** Number of detected transcripts and distribution of SQANTI structural categories, Mouse ES sample. **b)** Number of detected transcripts and distribution of transcripts per loci, Manatee sample. **c)** Length distribution of Mouse ES transcripts predictions . **d)** Length distribution of Manatee transcripts predictions. **e)** Support by orthogonal data. **f)** BUSCO metrics. **g)** Performance metrics based on SIRVs. Sen: Sensitivity, PDR: Positive Detection Rate, Pre: Precision, nrPred: non-redundant Precision, FDR: False Discovery Rate, 1/Red: Inverse of Redundancy.