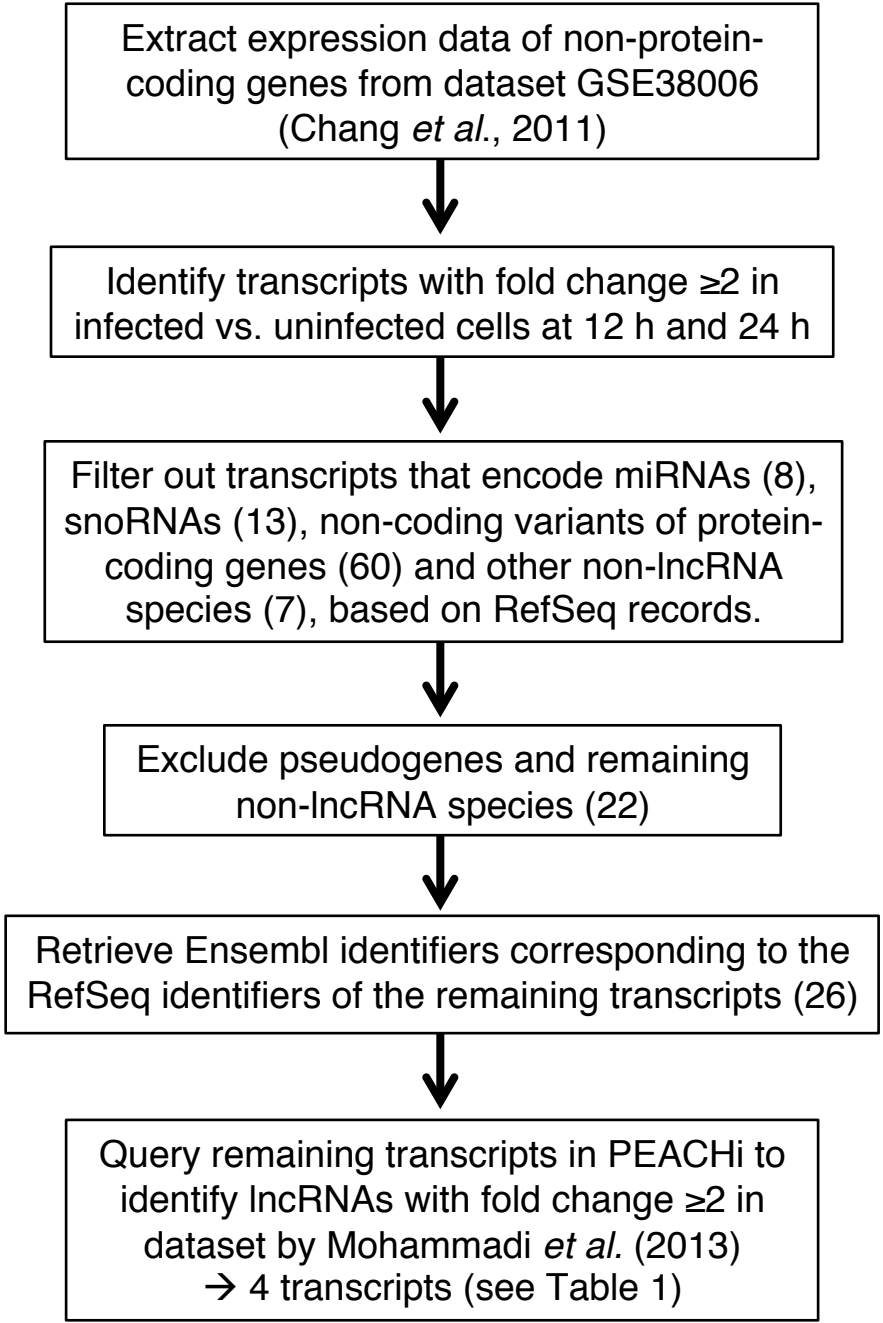
Fig. S1


Extract expression data of non-protein-coding genes from dataset GSE38006 (Chang *et al.*, 2011)
Identify transcripts with fold change ≥2 in infected vs. uninfected cells at 12 h and 24 h
Filter out transcripts that encode miRNAs (8), snoRNAs (13), non-coding variants of protein-coding genes (60) and other non-lncRNA species (7), based on RefSeq records.
Exclude pseudogenes and remaining non-lncRNA species (22)
Retrieve Ensembl identifiers corresponding to the RefSeq identifiers of the remaining transcripts (26)
Query remaining transcripts in PEACHi to identify lncRNAs with fold change ≥2 in dataset by Mohammadi *et al.* (2013)
→ 4 transcripts (see Table 1)