Supplementary Figure Legends

Supplementary Figure 1. Fluorescence activated cell sorting to collect exhausted and non-exhausted CD8+ T cells; Exosomes identification. (A) Fluorescence activated cell sorting (FACS) was used to get PD1+TIM3+ (exhausted)/PD1-TIM3- (non-exhausted) CD8+ T cells. (B) Exosomes were identified by electron micrograph. (C) Exosomes were identified by stochastic optical reconstruction microscopy (STORM).

Supplementary Figure 2. Microarray detected the difference of IncRNA expression profile in exosomes derived from exhausted CD8+ T cells and non-exhausted CD8+ T cells. (A) The Volcano Plot of the differently expressed IncRNAs. (B) The heatmap of the differently expressed IncRNAs.

Supplementary Figure 3. Gene Ontology enrichment analysis were used to annotate the functions of the candidate IncRNAs. (A, B) Gene Ontology enrichment analysis indicated that these IncRNAs actively participated in the regulation of diverse process of CD8+ T cell activity, like metabolism, gene expression, biosynthetic process and so forth.