

Supplementary Figure Legends

Supplementary Figure 1. Fluorescenceactivated cell sorting to collect exhausted and non-exhausted CD8+ T cells; Exosomes identification. (A)

Fluorescenceactivated 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 lncRNA expression profile in exosomes derived from exhausted CD8+ T cells and non-exhausted CD8+ T cells. (A) The Volcano Plot of the differently expressed lncRNAs.

(B) The heatmap of the differently expressed lncRNAs.

Supplementary Figure 3. Gene Ontology enrichment analysis were used to annotate the functions of the candidate lncRNAs. (A, B) Gene Ontology enrichment

analysis indicated that these lncRNAs actively participated in the regulation of diverse process of CD8+ T cell activity, like metabolism, gene expression, biosynthetic process and so forth.