Supplementary Figure 1 – The expression of SSTR2 and SSTR5 on NET cells is specific. (A) WB of membrane extracts from CM and HAP1 cells. Na^+/K^+ATPase membrane expression was used as loading control. (B) Representative confocal microscopy assessment of SSTR2 and SSTR5 expression in CM and HAP1 cells.

Supplementary Figure 2 – UT T cells do not exert antigen-specific tumoricidal activity. (A) By *in vitro* BLI assay, UT T cells induced cell death in up to 10% of Luc^+ NET cell lines as compared with control preparations lacking T cells (E:T ratio 1:1). The percentage of specific tumor cell lysis was calculated using the formula: % lysis = 1-(mean BLI signal in the presence of UT T cells/mean BLI signal in the absence of T cells) x 100%. (B) The cytolytic activity of UT T cells after 24 hrs of coculture with NET cells is not dependent on E:T ratios. (C) The degree of cytotoxicity exerted by UT T cells is not dependent on the presence or absence of SSTR2 and/or SSTR5 in CM cells. (D) Assessment of the cytotoxic activity of UT cells against CM cells harboring wild-type or mutated SSTR2 and/or SSTR5 according to increasing E:T ratios after 24 hrs of coculture. (E) UT T cells induce negligible levels of cell death when co-cultured with MIN6 cells at an E:T ratio of 1:1.

Supplementary Figure 3 – Generation of $SSTR^{mut}$ CM cell lines. (A) FISH analysis reveals the presence of three copies of *SSTR2* and *SSTR5* in CM cells. (B) Representative Sanger sequencing electropherograms showing the *SSTR2* and *SSTR5* sequence in the CRISPR/Cas9 mutated CM cell lines as well as in the parental cell line. The ribbon diagram schematically shows the conformation of the wild-type and mutated SSTRs. (C) Evaluation of the SSTR2 and SSTR5 mRNA transcript by RT-PCR in the CM-SSTR2/5^{mut} cell line as compared with the parental cell line (dotted line). (D) Evaluation of the membrane expression of SSTR2 and SSTR5 by flow cytometry in the CM-SSTR2/5^{mut} cell line.

Supplementary Figure 4 – Anti-SSTR CAR T cells do not exert fratricide activity. Percentage of $SSTR2^+$ or $SSTR5^+$ UT (A) or CAR T cells (B) during the *ex vivo* expansion phase. Parallel experiments were carried out in the presence of CD3/CD28 stimulation. Data represent results

from three healthy donors. Mean values and standard errors are represented in bar charts. (C) Representative flow cytometry analysis of the membrane expression of SSTR2 and SSTR5 in freshly isolated T cells. (D) Overlay of the expression of SSTR2 and SSTR5 in lymphocytes (red) and NET cells (green). T cells express substantially lower levels of SSTRs as compared with NET cells.

Supplementary Figure 5 – Gating strategy for T cell differentiation evaluation. CD45RA, CD45RO, CD62L and CD95 were labeled through specific mAbs to distinguish between T_N, T_{SCM}, T_{CM}, T_{EM} and T_E cells.

Supplementary Figure 6 – Anti-SSTR CAR T cells inhibit the growth of BON1 xenografts. Tumor burden of BON1 xenografts measured by *in vivo* BLI at indicated days since treatment. Color scale for all images: min = 5×10^7, max 7.7×10^8.

Supplementary Figure 7 – SSTR negativity in remaining tumors after CAR T cell treatment is linked to modest tumor growth. (A) Representative microphotographs showing SSTR2 and SSTR5 negativity by IHC in a CM xenograft after CAR T cell treatment. Magnification: x20. Scale bar: 100 µm. (B) Individual CM and BON1 xenograft growth rate according to SSTR2/5 expression status by IHC. (C) Percentage of tumor necrosis as detected by blinded pathologic evaluation for CM and BON1 xenografts.