

Supplementary information

Engineering tumor-specific gene nanomedicine to recruit and activate T cells for enhanced immunotherapy

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Content

Supplementary Fig. 1 Construction of pTyr-C9AP, pSur-C9AP and other control plasmids.

Supplementary Fig. 2 Stability test of NP_{Tyr-C9AP}.

Supplementary Fig. 3 mRNA expression of CXCL9 in NP_{Tyr-C9AP}-transfected B16-F10 cells.

Supplementary Fig. 4 Representative flow cytometry plots of CD8⁺ T cells recruited into the lower chamber of the transwell plates.

Supplementary Fig. 5 mRNA expression of α PD-L1 in NP_{Tyr-C9AP}-transfected B16-F10 cells.

Supplementary Fig. 6 Representative flow cytometry plots of PD-L1 expression of IFN- γ -stimulated-B16-F10 cells.

Supplementary Fig. 7 ELISA analysis of the capability of α PD-L1 to bind PD-L1.

Supplementary Fig. 8 mRNA expression of CXCL9 and α PD-L1 in melanoma after different treatments.

Supplementary Fig. 9 Serum concentrations of CXCL9 after different treatments.

Supplementary Fig. 10 Body weights of mice bearing B16-F10 melanoma treated with NP_{Tyr-C9AP} or other controls.

Supplementary Fig. 11 Representative H&E staining of major organs after different treatments.

Supplementary Fig. 12 Gating strategies of flow cytometry analysis of immune cells in melanoma.

Supplementary Fig. 13 Percentages of CD3⁺ T cells in melanoma after different treatments.

Supplementary Fig. 14 Percentages of granzyme B⁺, perforin⁺, IFN- γ ⁺ T cells in melanoma after different treatments.

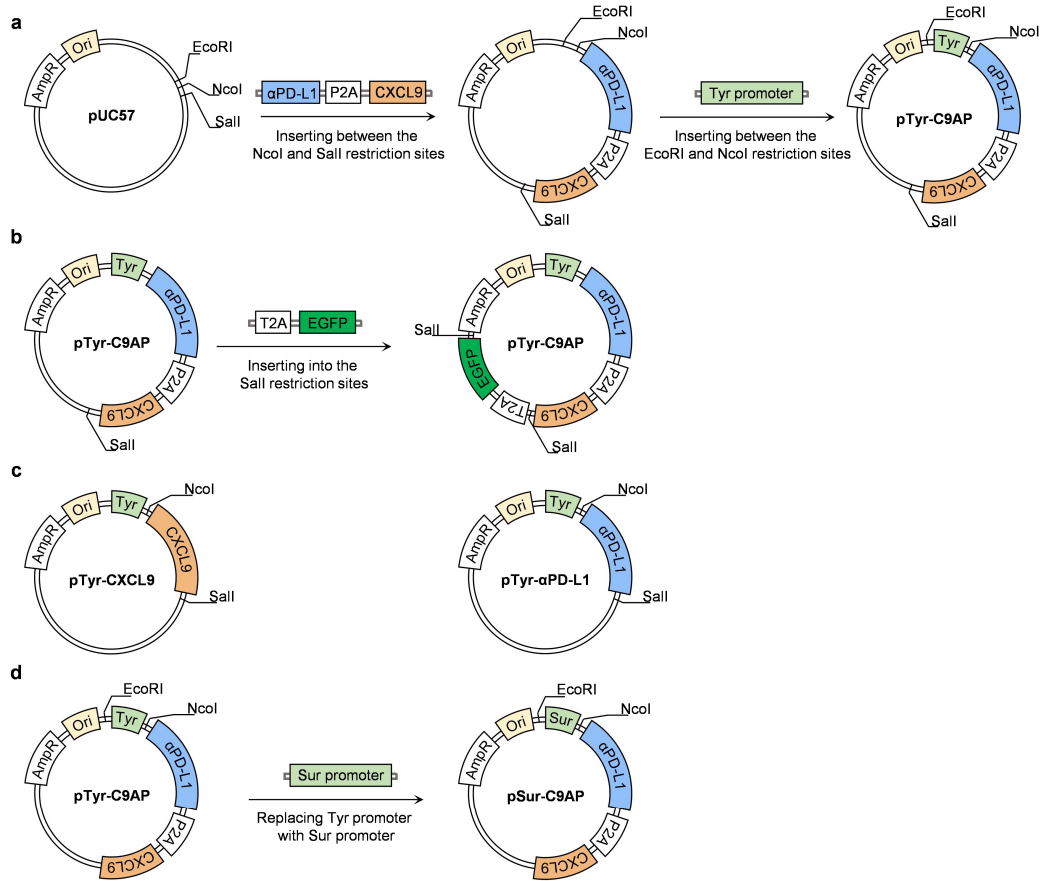
Supplementary Fig. 15 Percentages of CD3⁺ T cells in melanoma after NP_{Sur-C9AP} treatment.

Supplementary Fig. 16 Percentages of CD3⁺ T cells in CT26, Panc02 and 4T1 tumors after NP_{Sur-C9AP} treatment.

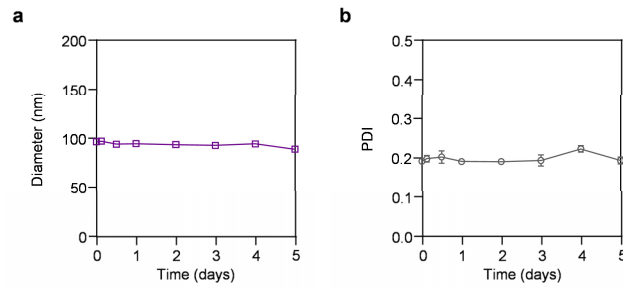
Supplementary Fig. 17 Percentages of NK cells in CT26, Panc02 and 4T1 tumors after NP_{Sur-C9AP} treatment.

Supplementary Table. 1 Primer sequences of qRT-PCR analysis.

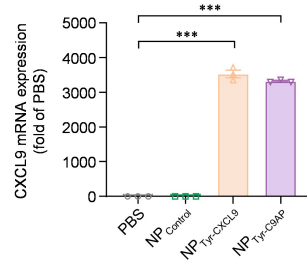
Supplementary Table. 2 Sequences of Tyrosinase (Tyr) promoter and Survivin (Sur) promoter.



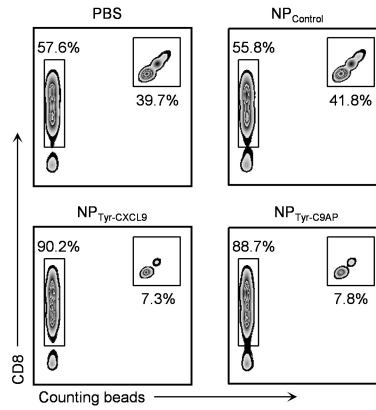
Supplementary Fig. 1 Construction of pTyr-C9AP, pSur-C9AP and other control plasmids. a Construction of pTyr-C9AP by inserting α PD-L1-P2A-CXCL9 fragment and Tyr promoter into pUC57 backbone plasmid. pTyr-C9AP was used to co-express CXCL9 and α PD-L1 specifically in melanoma cells. **b** Construction of pTyr-C9AP containing EGFP reporter gene by inserting T2A-EGFP fragment into SalI site. pTyr-C9AP containing EGFP reporter gene was used to analyze the melanoma-specificity of NP_{Tyr-C9AP}. **c** Maps of pTyr-CXCL9 and pTyr- α PD-L1, which specifically express CXCL9 or α PD-L1 alone in melanoma cells, were used as the controls of pTyr-C9AP. **d** Construction of pSur-C9AP by replacing the Tyr promoter of pTyr-C9AP with Sur promoter. pSur-C9AP was used to co-express CXCL9 and α PD-L1 specifically in different tumor cells.



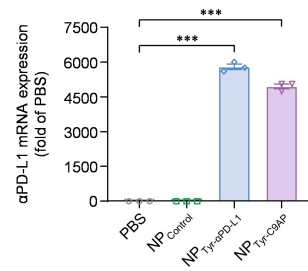
Supplementary Fig. 2 Stability test of NP_{Tyr-C9AP}. **a, b** Diameter (**a**) and polydispersity index (PDI) (**b**) of NP_{Tyr-C9AP} after being incubated in DMEM medium containing 10% FBS. The diameter and PDI were detected by Zetasizer Nano ZS90 at different time periods. The data are shown as the means $\pm$ SEM of $n = 3$.



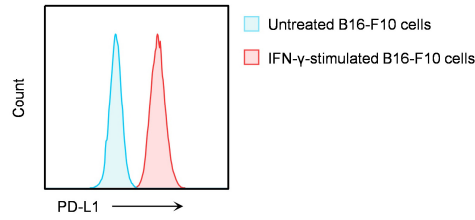
Supplementary Fig. 3 mRNA expression of CXCL9 in NP_{Tyr-C9AP}-transfected B16-F10 cells. B16-F10 cells were incubated with PBS, NP_{Control}, NP_{Tyr-CXCL9} or NP_{Tyr-C9AP} for 6 h, and CXCL9 mRNA expression was detected by qRT-PCR at 48 h after different transfections. The data are shown as the means $\pm$ SEM of $n = 3$. One-way ANOVA with Tukey's multiple comparison test. *** $P < 0.001$.



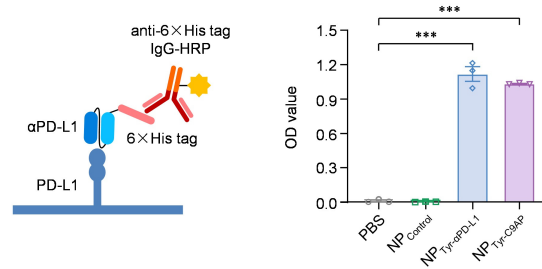
Supplementary Fig. 4 Representative flow cytometry plots of CD8⁺ T cells recruited into the lower chamber of the transwell plates. Activated CD8⁺ T cells were labeled with DiI dye, and were cultured in the upper chamber of transwell plates at the density of 1×10^6 cells per well. Then, the culture supernatants of PBS, NP_{Control}, NP_{Tyr-CXCL9} or NP_{Tyr-C9AP}-transfected B16-F10 cells were placed in the lower chamber. Three hours after incubation, CD8⁺ T cells recruited in the lower chamber were collected and were labeled with FITC anti-mouse CD8a antibody. Then, 10 μ l of Precision Count Beads were added into each sample before being analyzed by flow cytometry. The numbers of recruited CD8⁺ T cells were calculated using the formula: Absolute Count of CD8⁺ T Cells = Ratio of CD8⁺ T Cells/Counting Beads $\times$ Absolute Count of Counting Beads.



Supplementary Fig. 5 mRNA expression of α PD-L1 in NP_{Tyr-C9AP}-transfected B16-F10 cells. B16-F10 cells were incubated with PBS, NP_{Control}, NP_{Tyr- α PD-L1} or NP_{Tyr-C9AP} for 6 h, and α PD-L1 mRNA expression was detected by qRT-PCR at 48 h after different transfections. The data are shown as the means $\pm$ SEM of $n = 3$. One-way ANOVA with Tukey's multiple comparison test. *** $P < 0.001$.

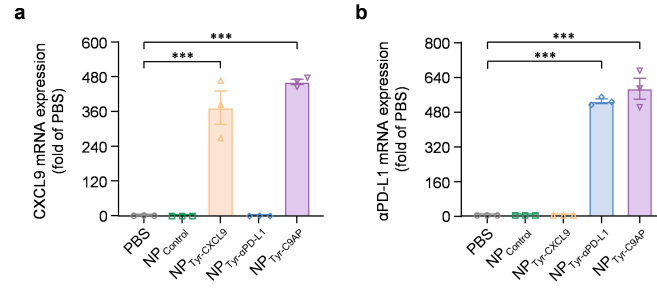


Supplementary Fig. 6 Representative flow cytometry plots of PD-L1 expression of IFN- γ -stimulated-B16-F10 cells. B16-F10 cells were stimulated with IFN- γ (20 ng ml⁻¹) for 48 h. Then, the IFN- γ -stimulated B16-F10 cells were stained with PE anti-mouse PD-L1 antibody (clone: 10F.9G2, BioLegend), and the expression of PD-L1 was analyzed by flow cytometry. The data are representative of three independent experiments

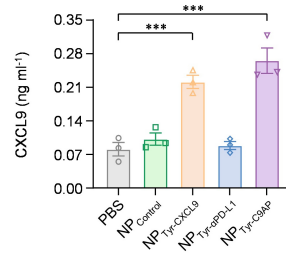


Supplementary Fig. 7 ELISA analysis of the capability of α PD-L1 to bind PD-L1.

The culture supernatants of B16-F10 cells transfected with PBS, NP_{Control}, NP_{Tyr- α PD-L1} or NP_{Tyr-C9AP} were collected at 72 h after different transfections. Then, the culture supernatants were added into the ELISA plates coated with PD-L1 molecule (SinoBiological, Beijing, China). One hour after incubation, the quantity of α PD-L1 that bound to PD-L1 molecule was detected using anti-6 $\times$ His tag IgG-HRP (SinoBiological) to label 6 $\times$ His tag of α PD-L1. The data are shown as the means $\pm$ SEM of n = 3. One-way ANOVA with Tukey's multiple comparison test. *** P <0.001.



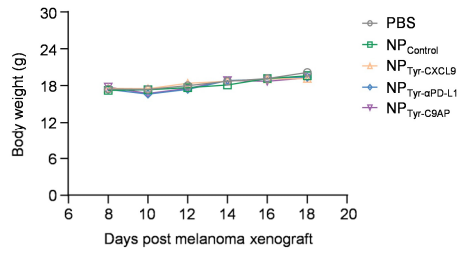
Supplementary Fig. 8 mRNA expression of CXCL9 (a) and αPD-L1 (b) in melanoma after different treatments. Mice bearing B16-F10 melanoma were intravenously injected with PBS, NP_{Control}, NP_{Tyr}-CXCL9, NP_{Tyr}-αPD-L1 or NP_{Tyr}-C9AP ($n = 3$ mice per group). Seventy-two hours after injection, the mRNA expression of CXCL9 and αPD-L1 in melanoma tissues were detected by qRT-PCR. The data are shown as the means $\pm$ SEM of $n = 3$. One-way ANOVA with Tukey's multiple comparison test. *** $P < 0.001$.



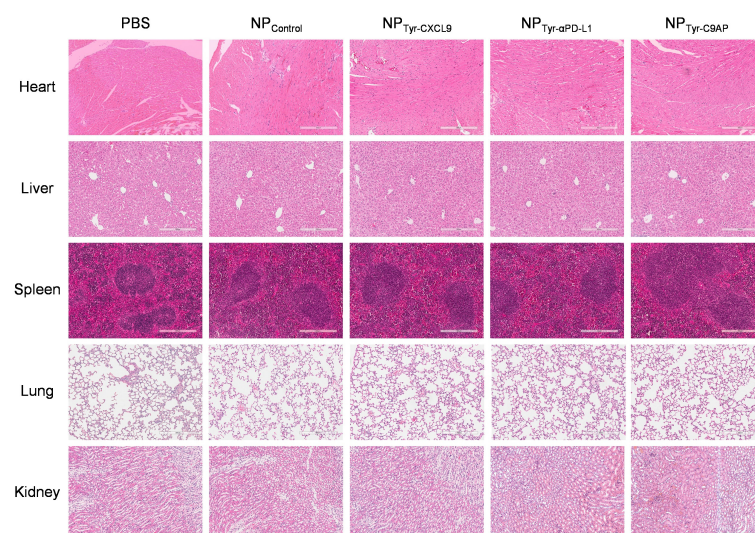
Supplementary Fig. 9 Serum concentrations of CXCL9 after different treatments.

Mice bearing B16-F10 melanoma were intravenously injected with PBS, NP_{Control}, NP_{Tyr-CXCL9}, NP_{Tyr-αPD-L1} or NP_{Tyr-C9AP} ($n = 3$ mice per group). Seventy-two hours after injection, the serum samples were collected, and the concentrations of CXCL9 in the serum were detected by ELISA. The data are shown as the means $\pm$ SEM of $n = 3$.

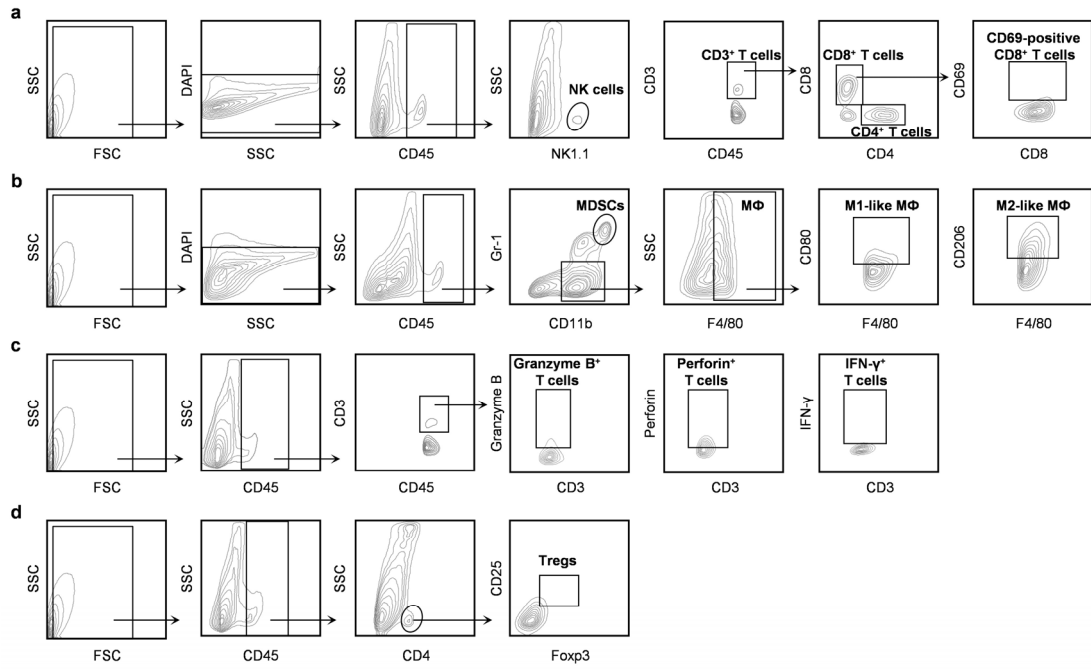
One-way ANOVA with Tukey's multiple comparison test. *** $P < 0.001$.



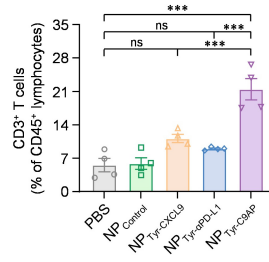
Supplementary Fig. 10 Body weights of mice bearing B16-F10 melanoma treated with NP_{Tyr-C9AP} or other controls. Mice bearing B16-F10 melanoma were intravenously injected with PBS, NP_{Control}, NP_{Tyr-CXCL9}, NP_{Tyr-αPD-L1} or NP_{Tyr-C9AP} every other day for five injections (n = 10 mice per group), as illustrated in Fig. 4c. The body weights of the mice were monitored every other day since the first injection. The data are shown as the means ± SEM of n = 10.



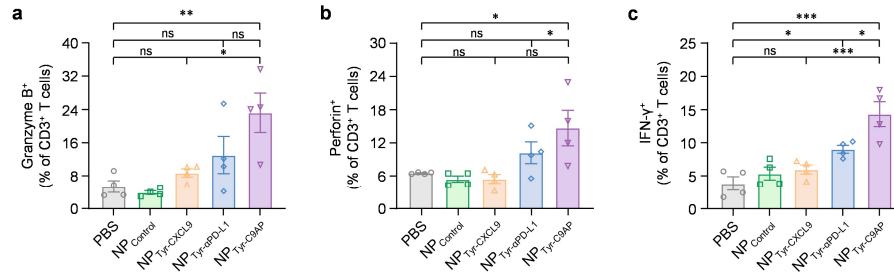
Supplementary Fig. 11 Representative H&E staining of major organs after different treatments. The major organs (including heart, liver, spleen, lung and kidney) of mice bearing B16-F10 melanoma were collected at the end of different treatments, and the histopathology of each organ was analyzed by haemotoxylin & eosin (H&E) staining. Scale bar = 300 μm.



Supplementary Fig. 12 Gating strategies of flow cytometry analysis of immune cells in melanoma. a Gating strategies of CD3⁺, CD4⁺, CD8⁺, CD69-positive CD8⁺ T cells and natural killer (NK) cells. **b** Gating strategies of myeloid-derived suppressor cells (MDSCs), M1-like and M2-like macrophages (MΦ). **c** Gating strategies of granzyme B⁺, perforin⁺ and IFN-γ⁺ T cells. **d** Gating strategies of regulatory T cells (Tregs).

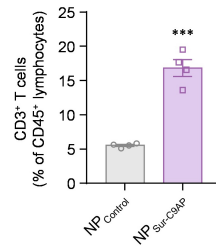


Supplementary Fig. 13 Percentages of CD3⁺ T cells in melanoma after different treatments. The representative flow cytometry plots were correspondingly shown in Fig. 5a. The data are shown as the means $\pm$ SEM of $n = 4$. One-way ANOVA with Tukey's multiple comparison test. *** $P < 0.001$; ns indicates no significant difference.

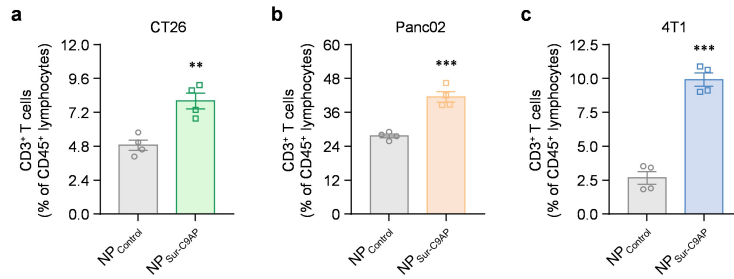


Supplementary Fig. 14 Percentages of granzyme B⁺ (a), perforin⁺ (b), IFN-γ⁺ (c)

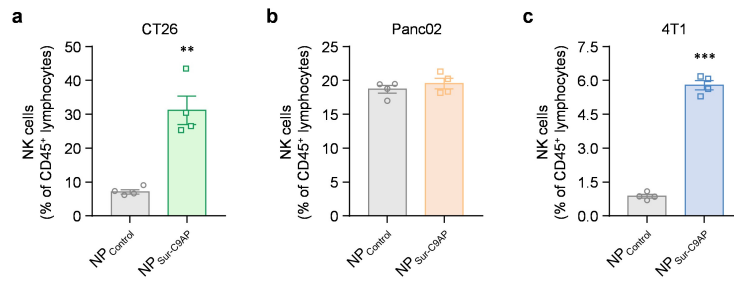
T cells in melanoma after different treatments. The representative flow cytometry plots were correspondingly shown in Fig. 5h. The data are shown as the means $\pm$ SEM of $n = 4$. One-way ANOVA with Tukey's multiple comparison test. $*P < 0.05$; $**P < 0.01$; $***P < 0.001$; ns indicates no significant difference.



Supplementary Fig. 15 Percentages of CD3⁺ T cells in melanoma after NP_{Sur-C9AP} treatment. Mice bearing B16-F10 melanoma were intravenously injected with NP_{Control} or NP_{Sur-C9AP} every other day for five injections. At the end of the treatments, the melanoma tissues were isolated, and the percentages of CD3⁺ T cells were analyzed by flow cytometry. The representative flow cytometry plots were correspondingly shown in Fig. 6e. The data are shown as the means $\pm$ SEM of $n = 4$. Student's t -test. *** $P < 0.001$.



Supplementary Fig. 16 Percentages of CD3⁺ T cells in CT26 (a), Panc02 (b) and 4T1 (c) tumors after NP_{Sur-C9AP} treatment. Mice bearing CT26, Panc02 and 4T1 tumors were intravenously injected with NP_{Control} or NP_{Sur-C9AP} every other day. At the end of the treatments, the tumor tissues were isolated, and the percentages of CD3⁺ T cells were analyzed by flow cytometry. The representative flow cytometry plots were correspondingly shown in Fig. 6o to q. The data are shown as the means $\pm$ SEM of $n = 4$. Student's t -test. ** $P < 0.01$; *** $P < 0.001$.



Supplementary Fig. 17 Percentages of NK cells in CT26 (a), Panc02 (b) and 4T1 (c) tumors after NP_{Sur-C9AP} treatment. The data are shown as the means $\pm$ SEM of $n = 4$. Student's t -test. ** $P < 0.01$; *** $P < 0.001$.

Supplementary Table. 1 Primer sequences of qRT-PCR analysis.

CXCL9	Forward: 5'-TCCTCTTGGGCATCATCTTCC-3' Reverse: 5'-TTTGTAGTGGATCGTGCCTCG-3'
α PD-L1	Forward: 5'-GAATGGGTGGCGTGGATTAG-3' Reverse: 5'-GGCTGTTCATCTGCAGATACG-3'
GAPDH	Forward: 5'-AGGTCGGTGTGAACGGATTTG-3' Reverse: 5'-TGTAGACCATGTAGTTGAGGTCA-3'

Supplementary Table. 2 Sequences of Tyrosinase (Tyr) promoter and Survivin (Sur) promoter.

Tyr promoter	5'-CCTGCAGGTCATAGTTCCTGCCAGCTGACTTTGTCAAGA CAGTGATGTCTGTGTTCCAGCAGTTGTTCTGAGTATCCTTT TCATTATCCACTGTCCTTTCTTCTTAAATTCCACCCCCAACA TTGTAAATAGCTTCTTTCTTAAACTCTGTTCAAAGAACCAG CTTGAGTGTGTCAGCTGCTTCCTGCTGGGGTCCTGGCAAA CCACTAGTGACCTTTATTCATAAGAGATGATGTATTCTTGAT ACTACTTCTCATTTGCAAATTCCAATTATTATTAATTCATAT CAATTAGAATAATATATCTTCCTTCAATTTAGTTACCTCACTA TGGGCTATGTACAAACTCCAAGAAAAAGTTAGTCATGTGC TTTGCAGAAGATAAAAGCTTAGTGTAACAGGCTGAGAG TATTTGATGTAAGAAGGGGAGTGGTTATATAGGTCTTAGCC AAAACATGTGATAGTCACTCCAGGGGTTGCTGGAAAAGAA GTCTGTGACACTCATTAACCTATTGGTGCAGATTTTGTATGA TCTAAAGGAGAC-3'
Sur promoter	5'-GGCAGGGACGAGCTGGCGCGGCGTCGCTGGGTGCACC GCGACCACGGGCAGAGCCACGCGGCGGGAGGACTACAAC TCCCGGCACACCCCGCGCCGCCCGCCTCTACTCCCAGAA GGCCGCGGGGGGTGGACCGCCTAAGAGGGCGTGCGCTCC CGACATGCCCCGCGGCGCGCCATTAACCGCCAGATTTGAAT CGCGGGACCCGTTGGCAGAGGTGGCGGCGGCGGCATGGG TGCCCCGACGTTGCCCCCTGCCTGG-3'