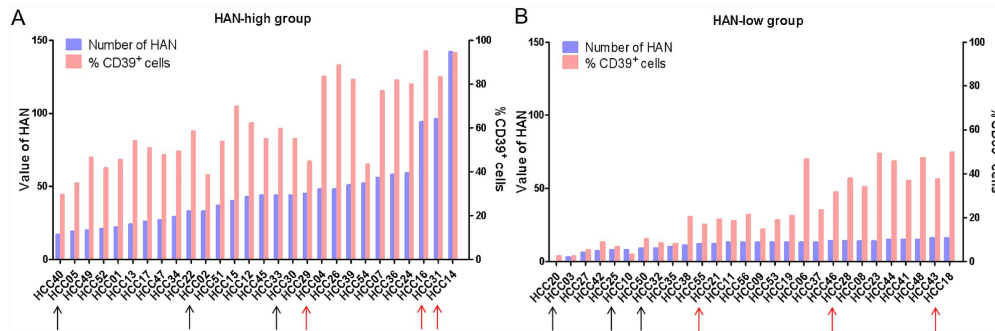


1

Supplemental Figures and legends



2

3 Supplemental Figure 1

4 Summary of the frequency of CD39⁺CD8⁺ TILs and value of HAN for all the 56 HCC5 patients. (A-B) Red bars represented the frequency of CD39⁺CD8⁺ TILs and blue bars

6 represented the value of HAN. Arrows indicated the six representative patients

7 selected for TILs and autologous tumors organoids killing assay. Red arrows indicated

8 three candidate patients selected for specific high affinity peptide identification assay.



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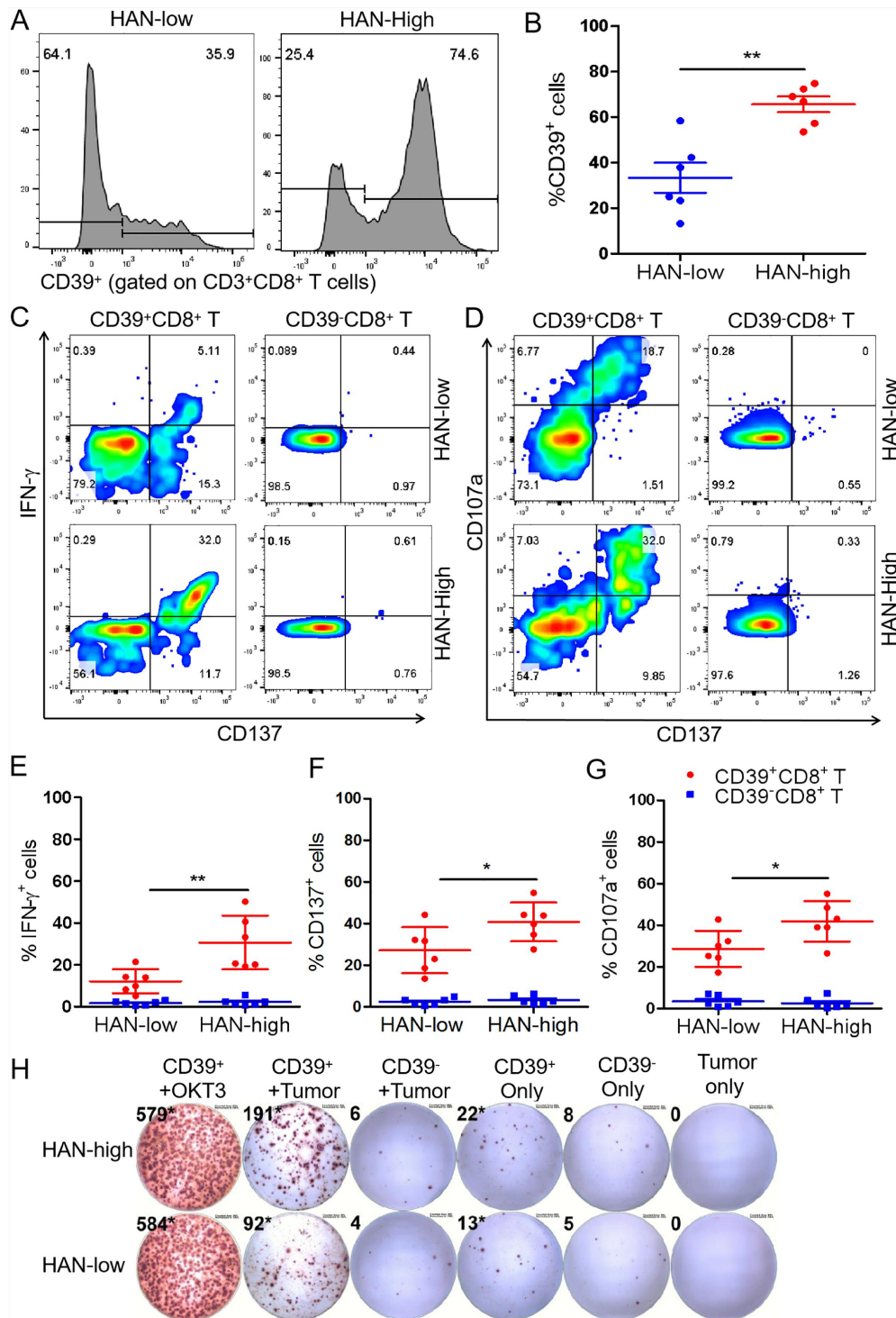
10 **Supplemental Figure 2**

11 HLA alleles Analysis by OptiType(v1.3.3) were shown for six candidate patients. (A)

12 The coverage plot of the HLA alleles for representative patient HCC14 analyzed by

13 OptiType were shown. Listed HLA alleles were with high expression abundance.

14 (B) Summary HLA alleles of all the six candidate patients were shown in this table.

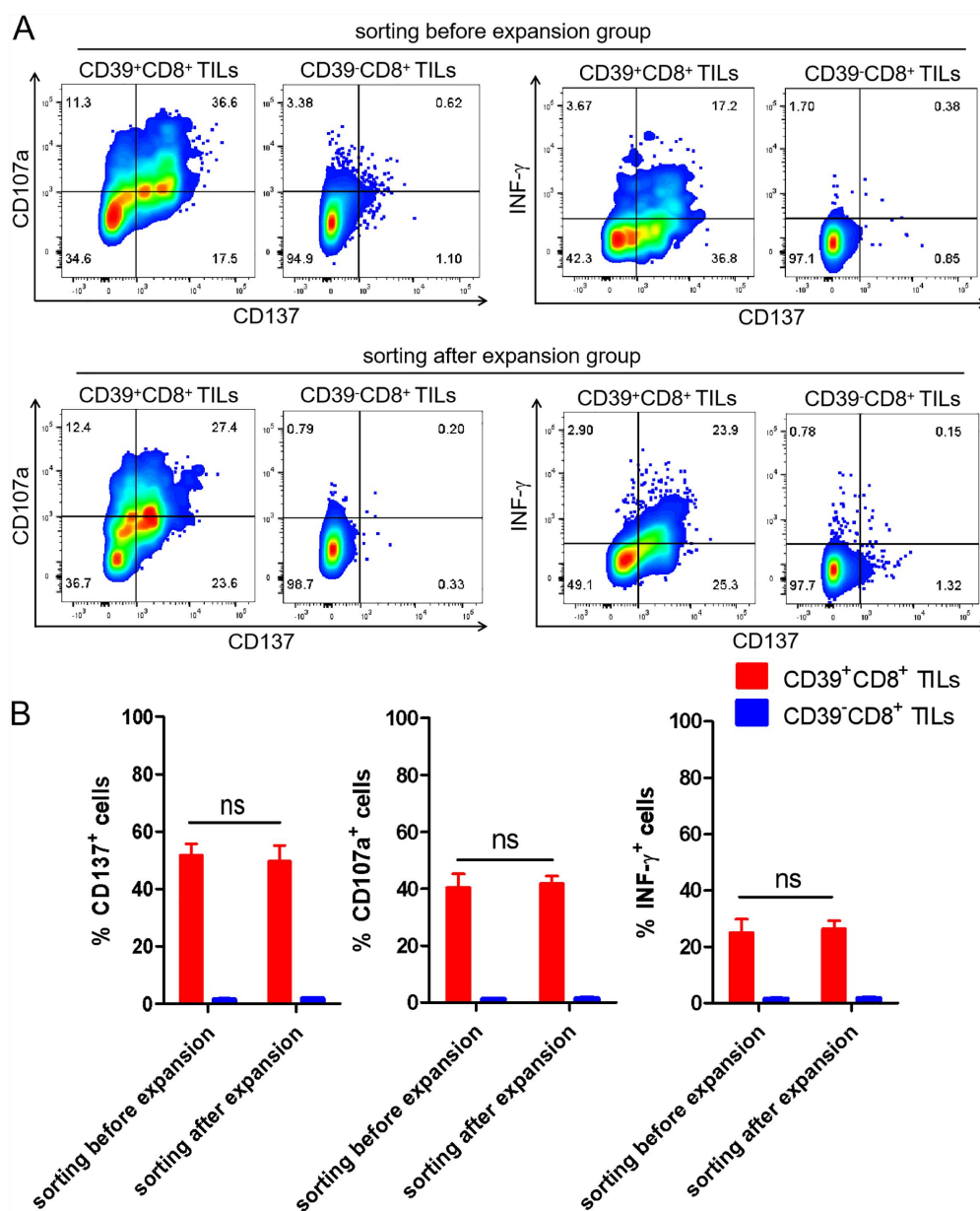


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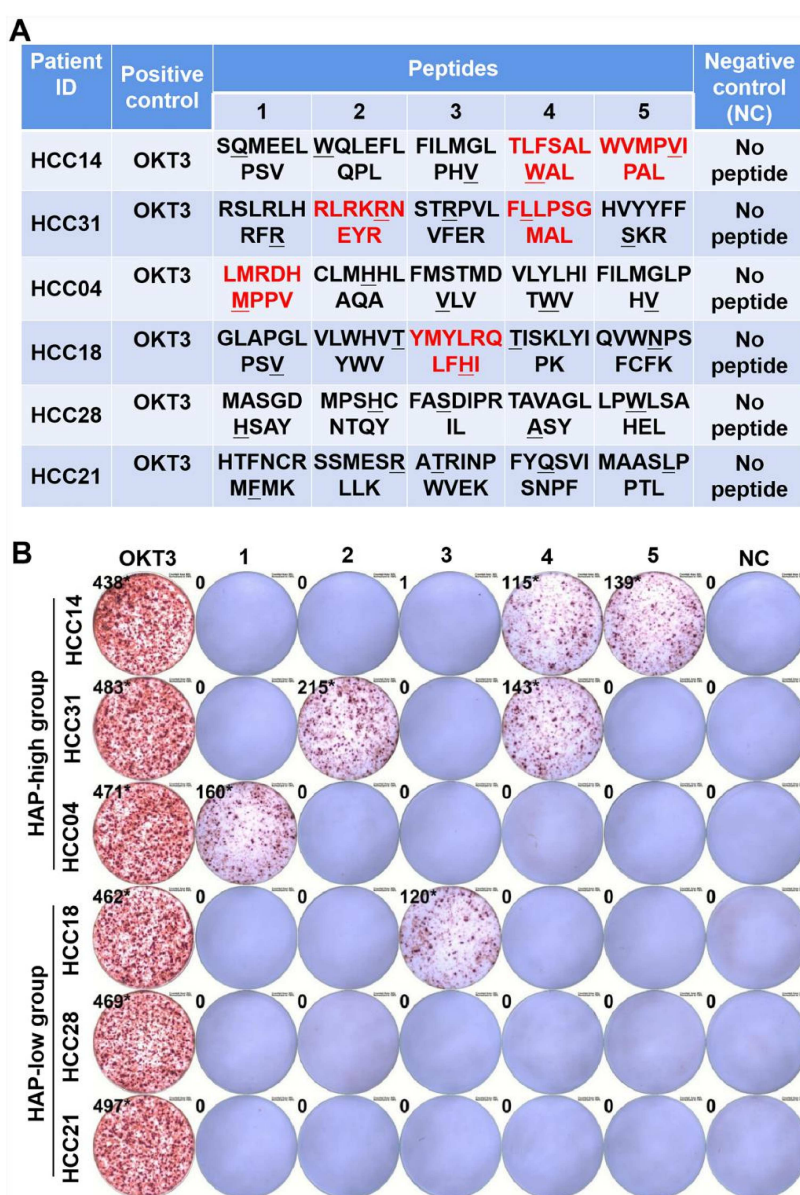
16 **Supplemental Figure 3**

17 CD39 and effector molecules expressed on TILs from surgically removed HCC fresh

18 tumor samples. (A-B) The frequency of CD39⁺CD8⁺ T cells in each group was
19 detected by flow cytometry. (C-G)The expression of IFN- γ , CD107a and CD137 on
20 CD39⁺CD8⁺ T cells was detected by flow cytometry. The dots represent different
21 patients. Data are presented as mean \pm SEM (n=6), * P < 0.05, ** P < 0.01.(H) CD39⁺/
22 CD8⁺ TILs were respectively sorted from surgically removed fresh tumor sample and
23 co-cultured with or without (TILs only) autologous tumor cells, then the IFN- γ
24 secretion was investigated by ELISPOT after 24 hours. OKT3 was used as positive
25 control.



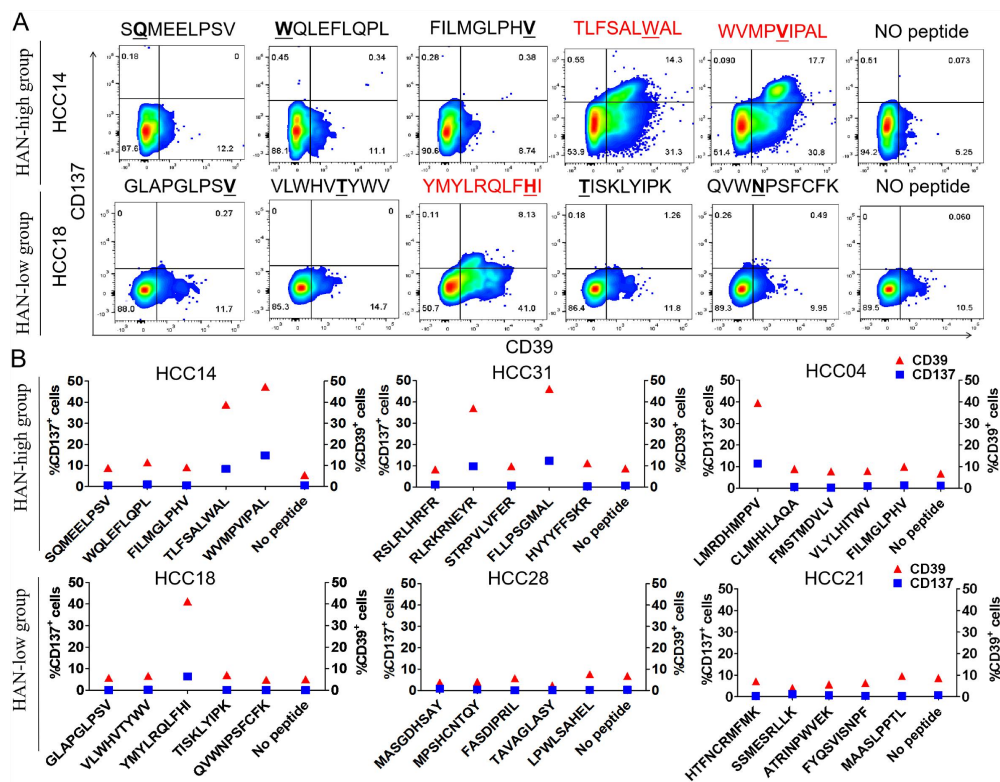
33 one was the sorting after expansion group which TILs were expanded first for 14 days
 34 and then sorted by the marker of CD39. At day 14, TILs of each group was
 35 co-cultured with tumor cells, and then the function of CD39[±] subsets was assessed by
 36 flow cytometry with intracellular staining of IFN- γ , CD107a and CD137. (B)
 37 Summary of the frequency of IFN- γ , CD107a and CD137 positive was shown.



38

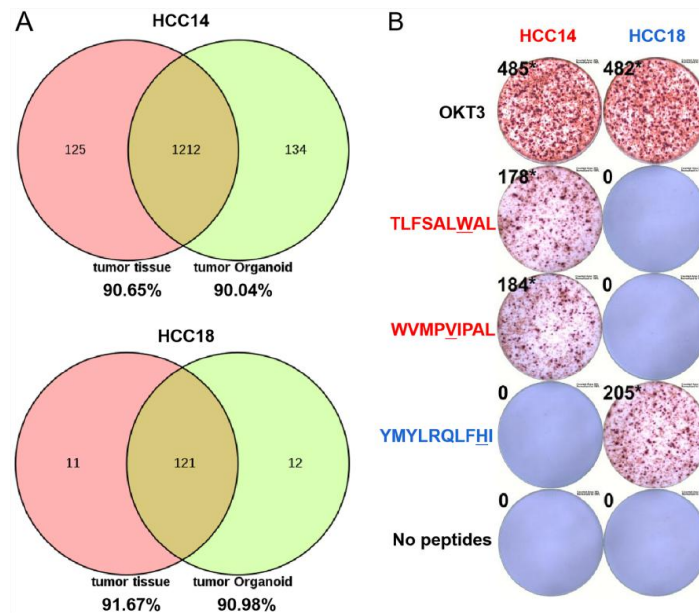
39 **Supplemental Figure 5**

40 Identification of personalized neoantigens for 6 patients. (A-B) Autologous PBMCs
 41 were stimulated with top five candidate peptides for 10 days, after which autologous
 42 tumor organoid from candidate patient was added to activate T-cell specific antigen
 43 response 24h before IFN- γ detection by ELISPOT assays. OKT3 was used as positive
 44 control, and no-peptide stimulation was tested as negative control.

45 **Supplemental Figure 6**

46 Expression of CD137 and CD39 of tumor-reactive CD39⁺CD8⁺ T cells by stimulation
 47 with candidate HANs from PBMCs. (A) Flow cytometry plots gated on CD8⁺ T cells
 48 to analyze T cell effector sensitivity against tumor organoids by CD137 and CD39
 49 up-regulation. (B) Summary of the frequency of CD39⁺ or CD137⁺ T cells was shown
 50

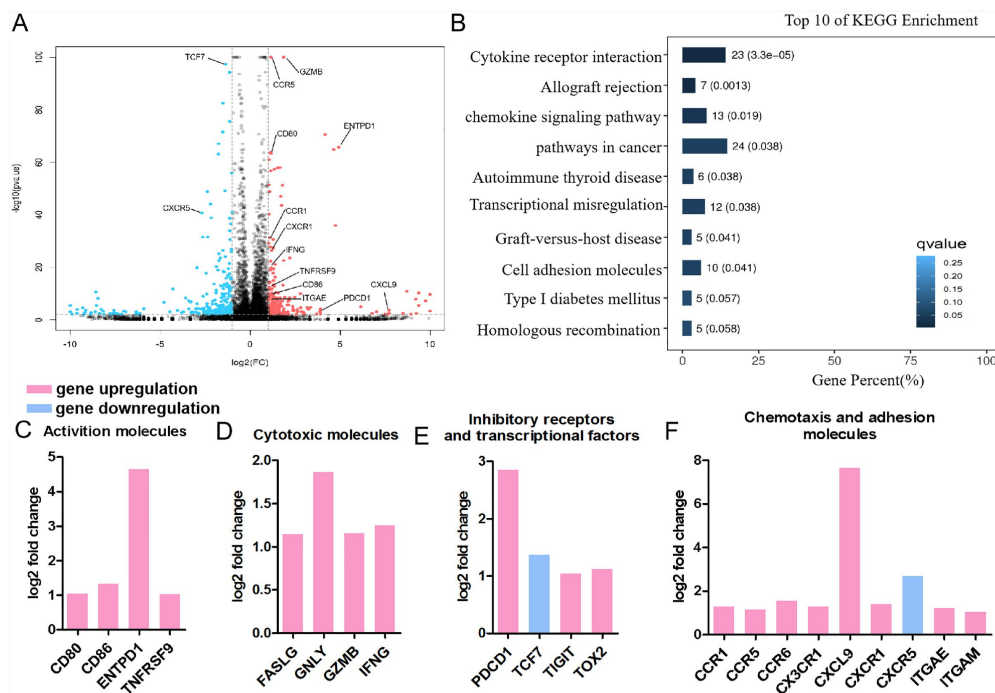
51 for all the six representative patients.



52

53 Supplemental Figure 7

54 Allogeneic positive peptides couldn't induce IFN- γ release for autologous tumor
 55 organoid killing. (A) Venn diagrams illustrate the number of somatic non-synonymous
 56 mutations present in each tumor tissue and their derivative HCC organoids. The
 57 similarity of mutation from tumor tissue and organoid was greater than 90%. (B)
 58 Autologous PBMCs from candidate patients were stimulated with autologous peptides
 59 (marked by the same color) and allogeneic peptides (marked by the different color)
 60 for 10 days, after which autologous tumor organoids from candidate patient was
 61 added to activate T-cell specific antigen response 24h before IFN- γ detection by
 62 ELISPOT assays. OKT3 was used as positive control, and no-peptide stimulation was
 63 tested as negative control.



64

65 **Supplemental Figure 8**

66 RNA-seq data of CD39⁺-CD8⁺ T cells stimulated by HAN peptide. PBMCs were
 67 stimulated by autologous HANs for 10 days and then co-cultured with autologous
 68 tumor organoids for 24h. After which CD39⁺-CD8⁺ T cells were sorted by FACS for
 69 following RNA-seq assay. (A) Volcano graph revealed the difference of genes
 70 expression analyzed by RNA-seq between CD39⁺-CD8⁺ T cells after stimulation by
 71 HAN peptide (log₂-transformed). The dashed line identified the differently expressed
 72 genes when using a P value <0.05. (B) KEGG enrichment demonstrated the
 73 significant enrichment of top 10 pathways using a P/Q value. (C-F) Bar plots
 74 indicated the RNA-seq expression of log₂ fold change of major up-regulated and
 75 down-regulated genes in CD39⁺CD8⁺ T cells compared to CD39⁻CD8⁺ T cells (P
 76 <0.05). Pink bars represented up-regulation and blue bars represented
 77 down-regulation.