

## **Supplementary Material**

**Affinity maturation of a T-cell-receptor-like antibody specific for a cytomegalovirus pp65-derived peptide presented by HLA-A\*02:01**

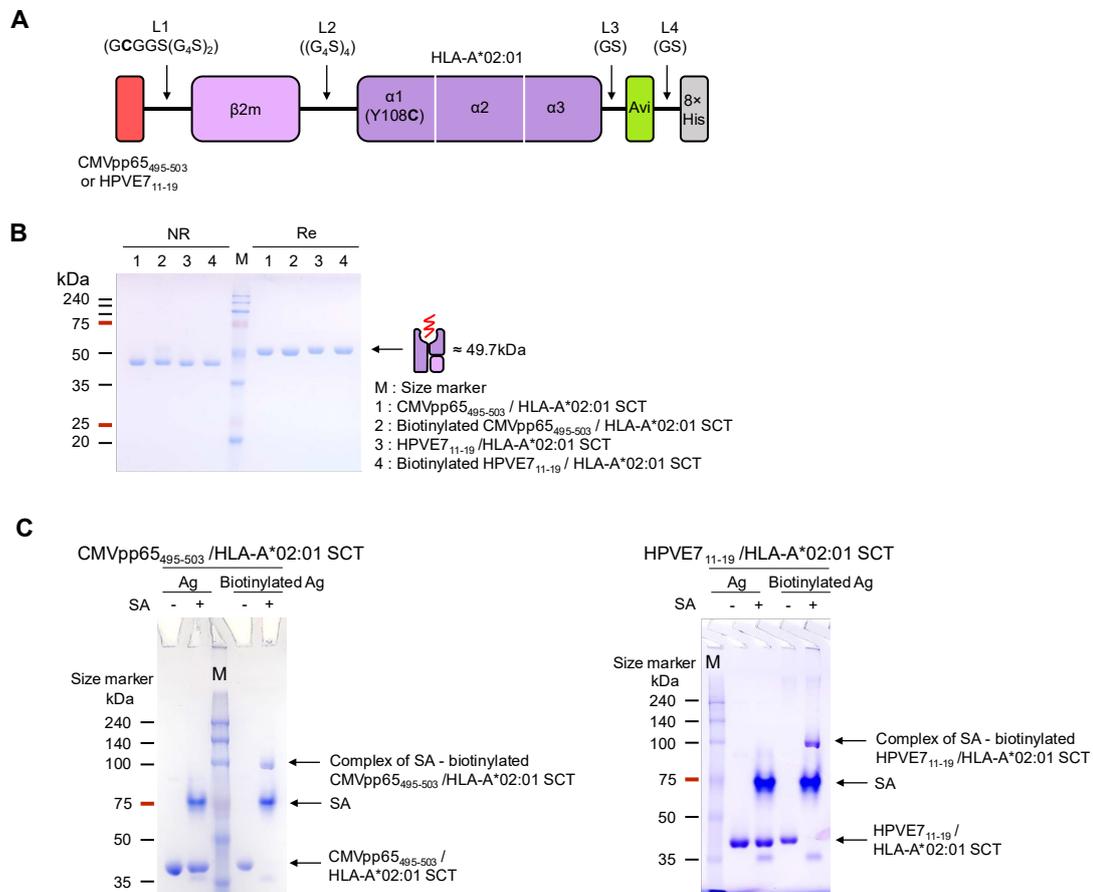
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### **Inventory of Supplementary Information**

Supplementary Figure 1

Supplementary Figure 2

## Supplementary Figure 1



### Supplementary Figure S1. Preparation of the target and off-target pMHC proteins.

(A) The expression scheme for the CMVpp65<sub>495-503</sub>/HLA-A\*02:01 SCT protein. An artificial disulfide bridge was introduced between the HLA α1 domain (Tyr108Cys) and linker L1 (position 2 of L1) to maintain stable binding of the CMVpp65<sub>495-503</sub> into the groove of the MHC-I complex.

(B) The purified CMVpp65<sub>495-503</sub>/HLA-A\*02:01 and HPVE7<sub>11-19</sub>/HLA-A\*02:01 SCT proteins (biotinylated or nonbiotinylated, 3 μg each) were analyzed by 12% SDS-PAGE under reducing (“Re”) or nonreducing (“NR”) conditions and then stained with Coomassie Brilliant Blue.

(C) Detection of biotinylated SCT proteins by streptavidin (SA)-induced band-shift analysis using SDS-PAGE under reducing conditions. Biotinylation of SCT proteins with the Avi tag (2 mg) was performed using a BirA500 kit (Avidity) following the manufacturer’s instructions.

Then, the biotinylated SCT proteins (3  $\mu$ g, 20 mol) were incubated with SA (80 mol) for 30 min at room temperature and subjected to 8% SDS-PAGE followed by Coomassie Brilliant Blue staining to determine biotinylation extent. Compared with nonbiotinylated SCT proteins, biotinylated SCT proteins in complex with SA featured a dramatic change in migration, thereby confirming biotinylation. The positions of the biotinylated or nonbiotinylated SCT proteins, SA, and the complex of a biotinylated SCT with SA are indicated with arrows.

## Supplementary Figure 2

		<u>[VH-CDR1]</u>	<u>[VH-CDR2]</u>	<u>[VH-CDR3]</u>
H9	VH	SYAISW	GIIPIFGTANYAQKFQG	GDLYYYDSSGYPRYYFDY
C1	VH	SYAISW	GIIPIFGTANYAQKFQG	GDLYYYDSSGY <b>PLWYMDY</b>
C38	VH	SYAISW	GIIPIFGTANYAQKFQG	GDLYYYDSSGY <b>PWYYMDY</b>
C1-17	VH	SYAISW	<b>SI</b> IPIF <b>GVAEYAH</b> KFQG	GDLYYYDSSGYPLWYMDY
C1-30	VH	SYAISW	<b>SI</b> IPIF <b>GAAEY</b> AQKFQG	GDLYYYDSSGYPLWYMDY

		<u>[VL-CDR1]</u>	<u>[VL-CDR2]</u>	<u>[VL-CDR3]</u>
H9	VL	RASQSVSSSYLA	GASSRAT	QHYSTSPGFT
C1	VL	RASQSVSSSYLA	GASSRAT	<b>QDYSTYPAFT</b>
C38	VL	RASQSVSSSYLA	GASSRAT	QH <b>SYAF</b> PGFT
C1-17	VL	RASQSVSSSYLA	GAS <b>TRPT</b>	<b>QDYSTYPAFT</b>
C1-30	VL	RASQSVSSSYLA	GASSR <b>PR</b>	<b>QDYSTYPAFT</b>

**Supplementary Figure S2.** Amino acid sequence alignment of the isolated clones from the first and second round of affinity maturation focusing on VH-/VL-CDRs.

The mutated residues are highlighted in bold. Clones C1 and C38 were isolated from the VH-CDR3 and VL-CDR3 library of H9 scFab, as presented in Fig. 2A. Clones C1-17 and C1-30 were isolated from the VH-CDR2 and VL-CDR2 library of C1 scFab, as shown in Fig. 3A.