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	Sample ID	**Day**[a]	**Previous infection**[b]	**Recent infection**[c]	**DF/DHF**	**% GTS**[d]					
						1	**2**	**3/4**	**1&2**	**1&3/4**	**2&3/4**
Primary cases	1-1166-6	8	N/A	DENV1	DHFII	0.161					
	1-2368-2	15	N/A	DENV1	DF	0.652					
	1-2528-9	8	N/A	DENV1	DF	0.097					
	2-0600-8	15	N/A	DENV1	DF	0.242					
	2-2781-2	17	N/A	DENV1	DF	1.05					
Secondary cases	2-1452-5	12	DENV1	DENV2	DHFI	0.258	0.054		0.045		
	2-1629-2	16	DENV1	DENV4	DF	0.358		0.346		0.685	
	2-1630-3	16	DENV1	DENV4	DF	0.079		0.185		0.435	
	2-0573-8	14	DENV1	DENV4	DF	0.57		0.426		4.56	
	2-1710-2	15	DENV3	DENV1	DHFII	0.072		0.055		0.219	
	2-0664-9	12	DENV3	DENV1	DHFII	0.497		0.258		0.942	
	2-1680-8	9	DENV2	DENV4	DF		0.546	0.083			0.119
	2-0885-5	12	DENV3	DENV2	DHFII		0.898	0.838			1.15
	2-1672-9	18	DENV4	DENV2	DF		0.575	2.09			0.6

Supplementary Table 1 Patient samples used to determine the TCRβ repertoire of CD8$^+$ HLA-A*11:01p tetramer$^+$ cells. [a]Day post-defervescence. [b]Previous infection determined by micro-FRNTs. [c]Recent infection determined by RT-PCR. [d]Frequency (%) of CD8$^+$ HLA-A*11:01p tetramer$^+$ cells. DF, dengue fever; DHF, dengue haemorrhagic fever.

TRBV	CDR3	TRBJ	Sample	Infection history	Sorted population	Freq. (%)
12-3/4	CASSLGAGELF	2-2	1-1166	Primary DENV1	1 SP	1.41
			2-1710	Secondary DENV3/DENV1	1&3/4 DP	1.82
11-2	CASSLGPDNEQF	2-1	2-2781	Primary DENV1	1 SP	10.45
			2-6449	Secondary DENV3/DENV1	1&3/4 DP	1.37
11-2	CASSLGQGAYEQY	2-7	2-2781	Primary DENV1	1 SP	2.99
			2-1629	Secondary DENV1/DENV4	1&3/4 DP	20.73
11-2	CASSLGGTDNEQF	2-1	2-1629	Secondary DENV1/DENV4	1&3/4 DP	14.63
			2-6449	Secondary DENV3/DENV1	1&3/4 DP	1.37
11-2	CASSLGPDYEQY	2-7	2-1629	Secondary DENV1/DENV4	3/4 SP, 1&3/4 DP	2.63, 2.44
			2-0573	Secondary DENV1/DENV4	3/3 SP	2.17
11-2	CASSLGGDTYEQY	2-7	2-1629	Secondary DENV1/DENV4	1&3/4 DP	13.41
			2-6449	Secondary DENV3/DENV1	1&3/4 DP	4.11
11-2	CASSLGPDSPLH	1-6	2-1672	Secondary DENV4/DENV2	3/4 SP	3.17
			2-6649	Secondary DENV3/DENV1	1&3/4 DP	1.37
6-5	CASSYRGGRAGETQY	2-5	2-0885	Secondary DENV3/DENV2	2&3/4 DP	2.5
			2-1710	Secondary DENV3/DENV1	1&3/4 DP	3.64

Supplementary Table 2 Public $NS3_{133}$ DENV-specific TCRβ sequences isolated from patients with primary or secondary DENV infection. SP, single positive; DP, double positive.

Lab no.	Day[a]	Previous infection[b]	Recent infection[c]	DF/DHF	% GTS[d]	% TRBV11-2[e]
02-0095	15	ND	DV1	DHF II	3.45	35.07
02-0608-7	12	INC	DV1	DF	0.383	6.27
02-0835-9	12	INC	DV1	DF	1.344	26.79
02-0921-5	15	INC	DV1	DF	0.92	25.98
02-1034-1	20	INC	DV1	DF	0.886	23.7
02-1092-5	13	INC	DV1	DHF II	0.211	19.43
02-1180-3	18	INC	DV1	DHF II	1.63	43.31
03-0598	23	ND	DV1	DHF II	10.53	26.12
03-0685	18	ND	DV1	DHF I	1.664	24.82
03-0686	18	ND	DV1	DHF II	0.243	32.51
03-0681	18	ND	DV4	DF	1.306	47.63
01-0019-2	23	ND	DV2	DHF I	0.17	5.29
02-0192	14	ND	DV2	DHF III	0.438	1.37
02-0285	21	ND	DV2	DHF I	0.254	3.54
02-1628-1	17	INC	DV2	DF	0.112	14.29
02-1652-7	16	INC	DV2	DF	0.922	34.16
03-0007	18	ND	DV2	DHF I	0.14	5
03-0214	16	ND	DV2	DHF I	2.259	74.81
03-0252	20	ND	DV2	DHF III	0.923	3.36
03-0407	24	ND	DV2	DHF I	0.131	5.34
03-0488	15	ND	DV2	DHF I	0.207	35.75
03-0524	23	ND	DV2	DHF III	0.156	6.41
03-0614	33	ND	DV2	DHF III	0.182	16.48

Supplementary Table 3 Patient samples used to determine the frequency (%) of CD8$^+$ HLA-A*11:01p tetramer$^+$ cells expressing TRBV11-2 (Fig. 1a,b). [a]Day post-defervescence. [b]Previous infection determined by micro-FRNTs. [c]Recent infection determined by RT-PCR. [d]Frequency (%) of CD8$^+$ HLA-A*11:01p tetramer$^+$ cells. [e]Frequency (%) of CD8$^+$ HLA-A*11:01p tetramer$^+$ cells expressing TRBV11-2. DF, dengue fever; DHF, dengue haemorrhagic fever; INC, inconclusive; ND, not determined.

TCR	D30	HLA-A*11:01	HLA-A*11:01	Bond type
CDR1α	Ala28-O	Arg163-NH2	Arg163	VDW, HB
CDR1α	Leu29	-	Arg163	VDW
CDR1α	Tyr30-OH	Arg163	Arg163-Nε	VDW, HB
CDR2α	Lys58	Ala158	-	VDW
CDR3α	Asp109-Oδ1-Oδ2	Gln62-Nε2-Oε1 Arg65-NH1	Gln62-Oε1-Nε2 Arg65-NH1	VDW, HB, SB
CDR3α	Ala110	Gln62, Asn66	Gln62, Asn66	VDW
CDR3α	Gly111	-	Asn66	VDW
CDR3α	Met113	Arg65	Arg65	VDW
CDR2β	Gln57-Nε2	Ala69, Gln72 Thr73-Oγ1	Ala69, Gln72, Thr73-Oγ1	VDW, HB
CDR2β	Asn58-Oδ1	Val76, Gln72-O Thr73	Val76, Gln72, Thr73	VDW, HB
CDR2β	Asn59	Gln72	Val76	VDW
CDR2β	Gly60-N	Gln72-Oε1	Gln72-Oε1	VDW, HB
CDR2β	Val61	-	Lys68	VDW
FWβ	Val66	Arg65, Lys68, Ala69	Arg65, Lys68, Ala69	VDW
FWβ	Asp67-Oδ2	Arg65-Nε	Arg65-Nε	VDW, SB
CDR3β	Leu108	Ala150	Ala150	VDW
CDR3β	Gln110	Ala69	Ala69	VDW
CDR3β	Gly111-O	Gln155-Nε2	Gln155	VDW, HB
CDR3β	Leu112-O	Gln155-Nε2	Gln155	VDW, HB
CDR3β	Leu113	Glu154, Gln155	Gln155, His151	VDW
CDR3β	Tyr114-OH	Ala150-O, Gln155-Oε1	Ala150-O, Gln155-Oε1	VDW, HB

VDW, van der Waals (cut-off, 4Å); HB, hydrogen bond (cut-off, 3.5Å); SB, salt bridge (cut-off, 5Å).

TCR	D30	GTS1	GTS3/4	Bond type
CDR3α	Ala110-O	Gly4, Ser5-N	Gly4, Ser5-N	VDW, HB
CDR3α	Gly111	Gly4	Gly4	VDW
CDR1β	Ala30	Asn9	Asn9	VDW
CDR2β	Gln57-Oε1	Ile7-O	Ile7-O	VDW, HB
CDR2β	Asn58-Oδ1-Nδ2	Asn9-Nδ2-Oδ1	Asn9-Nδ2-Oδ1	VDW, HB
CDR3β	Gly109	Val8	Ile7, Val8	VDW
CDR3β	Gln110-Oε1-O	Gly4-O, Ser5, Pro6 Ile7-O-N	Gly4-O, Ser5, Pro6, Ile7-O	VDW, HB
CDR3β	Gly111-O	Ser5-Oγ	Ser5	VDW, HB
CDR3β	Leu112	Ser5	Ser5	VDW
CDR3β	Tyr114	Val8	Ile8	VDW

VDW, van der Waals (cut-off, 4Å); HB, hydrogen bond (cut-off, 3.5Å); SB, salt bridge (cut-off, 5Å).

Supplementary Table 4 Contacts between the D30 TCR and HLA-A*11:01 presenting GTS1 or GTS3/4.

TCR segment	D30 TCRβ mutants	K_{Deq} (μM)	Impact
	WT	136.0 ± 7.0	
CDR1β	G28A	251.9 ± 6.7	∗
CDR1β	A30G	190.0 ± 18.9	∗
CDR2β	Q57A	NB	∗∗∗
CDR2β	N58A	>> 400	∗∗∗
CDR2β	N59A	28.51 ± 1.2	#
FWβ (control)	L81A	103.3 ± 8.3	∗
CDR3β	L108A	NB	∗∗∗
CDR3β	G109A	NB	∗∗∗
CDR3β	Q110A	>> 400	∗∗∗
CDR3β	G111A	>> 400	∗∗∗
CDR3β	L112A	>> 400	∗∗∗
CDR3β	L113A	158.5 ± 8.9	∗

Supplementary Table 5 Equilibrium binding affinities of soluble HLA-A*11:01-GTS1 complexes for wild-type and mutant D30 TCRs. NB, no binding at 400 μM HLA-A*11:01-GTS1; WT, wild-type; ∗, minimal impact (< 3-fold change in affinity); ∗∗∗, critical impact (> 5-fold decrease in affinity); #, positive impact (> 3-fold increase in affinity).

HLA-A*11:01	**D2H TCR**	**Impact**	**D13 TCR**	**Impact**	**D30 TCR**	**Impact**
WT	7.3 ± 0.9		> 400		136.0 ± 7.0	
R65A	15.8 ± 1.1	*	NB	***	NB	***
K68A	29.3 ± 1.4	**	NB	***	> 400	**
Q72A	6.3 ± 0.6	*	106.8 ± 2.0	#	23.5 ± 0.8	#
V76A	41.4 ± 3.0	***	> 400	*	106.3 ± 2.9	*
R145A (control)	10.1 ± 0.8	*	> 400	*	186.4 ± 4.1	*
E154A	10.5 ± 0.8	*	> 400	*	186.7 ± 4.3	*
Q155A	82.4 ± 7.8	***	> 400	*	>> 400	***

NB, no binding at 400 μM HLA-A*11:01-GTS1; WT, wild-type; *, minimal impact (< 3-fold change in affinity); **, moderate impact (3–5-fold decrease in affinity); ***, critical impact (> 5-fold decrease in affinity); #, positive impact (> 3-fold increase in affinity). Numbers indicate K_{Deq} values (μM).!

GTS1	**D2H TCR**	**Impact**	**D13 TCR**	**Impact**	**D30 TCR**	**Impact**
S5A	12.7 ± 1.3	*	289.6 ± 4.6	*	>> 400	***
N9D	216.4 ± 24.2	***	NB	***	>> 400	***
N9A	79.4 ± 10.8	***	>> 400	***	375.8 ± 7.6	**

NB, no binding at 400 μM HLA-A*11:01-GTS1; *, minimal impact (< 3-fold change in affinity); **, moderate impact (3–5-fold decrease in affinity); ***, critical impact (> 5-fold decrease in affinity). Numbers indicate K_{Deq} values (μM).

Supplementary Table 6 Equilibrium binding affinities of soluble wild-type and mutant HLA-A*11:01-GTS1 complexes for the D2H, D13, and D30 TCRs.

GTS1	**T_M (°C)**
GTSG**A**PIVNR (GTS1)	61.6 ± 0.8
GTSG**A**PIVNR (GTS1-A5)	61.7 ± 1.0
GTSGSPIV**A**R (GTS1-A9)	55.8 ± 1.3
GTSGSPIV**D**R (GTS1-D9)	60.5 ± 1.0

HLA-A*11:01	**T_M (°C)**
R65A	60.1 ± 0.5
K68A	58.7 ± 0.6
Q72A	62.8 ± 0.4
V76A	58.3 ± 1.4
R145A (control)	61.0 ± 0.9
E154A	61.5 ± 0.3
Q155A	61.0 ± 0.6

Supplementary Table 7 Thermal stability measurements of wild-type and mutant HLA-A*11:01-GTS1 complexes.