Supplementary figure legends

Figure S1, related to Figure 1. *Relationship between P(collision), read depth and immune status.* **(A)** P(collision) values are shown in relation to the number of unique mapped and filtered sequences for each sample (colored by sample type). **(B)** Number of unique sequences per sample, binned by sample type. Annotations to each plot show the 25^{th}-75^{th} percentiles (box), the 10^{th}-90^{th} percentiles (whiskers), and the median (horizontal line). **(C, D)** Paired values for P(collision) in acute and convalescent (*left panel*), or acute and post-convalescent (*middle panel*), or convalescent and post-convalescent (*right panel*) phase samples from individuals presenting with **(C)** primary or **(D)** secondary DENV infections. $^{**}P < 0.0001$ (acute vs. P-Conv; Wilcoxon Signed Rank), $^{*}P = 0.0046$ (Conv vs. P-Conv; Wilcoxon Signed Rank).

Figure S2, related to Figure 2. *Identification of prevalent CDR3 regions.* **(A)** Random assignment of individuals to two distinct groups for cross-validation. **(B)** Highly prevalent CDR3 regions in acute dengue cases in the training set. **(C)** Sequencing read depth in samples categorized by presence or absence of the prevalent 13-mer CDR3, 'ARLD$(Y)_5$GMDL.' Annotations to each plot show the 25^{th}-75^{th} percentiles (box), the 10^{th}-90^{th} percentiles (whiskers), and the median (horizontal line). **(D)** CDR3 regions identified as being highly prevalent in the 1^{st} Test Set. Prevalence is measured as the proportion of samples containing the CDR3 regions of interest. Each horizontal panel shows the prevalence of a CDR3 sequence in acute, convalescent and post-convalescent phase samples and in 8 non-dengue febrile cases ('febrile') and 46 healthy individuals. **(E)** BLOSUM62-like amino acid similarity scoring matrix. **(F)** Prevalent CDR3 regions that were identified using the amino acid similarity-based cross-validation. *Upper panel*: CDR3 prevalence in acute phase samples partitioned for cross-validation or by DENV serotype. *Lower panel*: prevalence in samples from 47 healthy individuals and 8 individuals with non-dengue febrile illness (Non-dengue), and in post-convalescent phase samples partitioned for cross-validation or partitioned by DENV serotype. **(G)** Ages of individuals with zero mismatch (0MM) *ARLD(Y)$_5$GMDL* CDR3 signatures and their one-mismatch derivatives (1MM) at time of sampling, compared to the ages of all individuals included in this study. Annotations to each plot show the 25^{th}-75^{th} percentiles (box), the 10^{th}-90^{th} percentiles (whiskers), and the median (horizontal line).

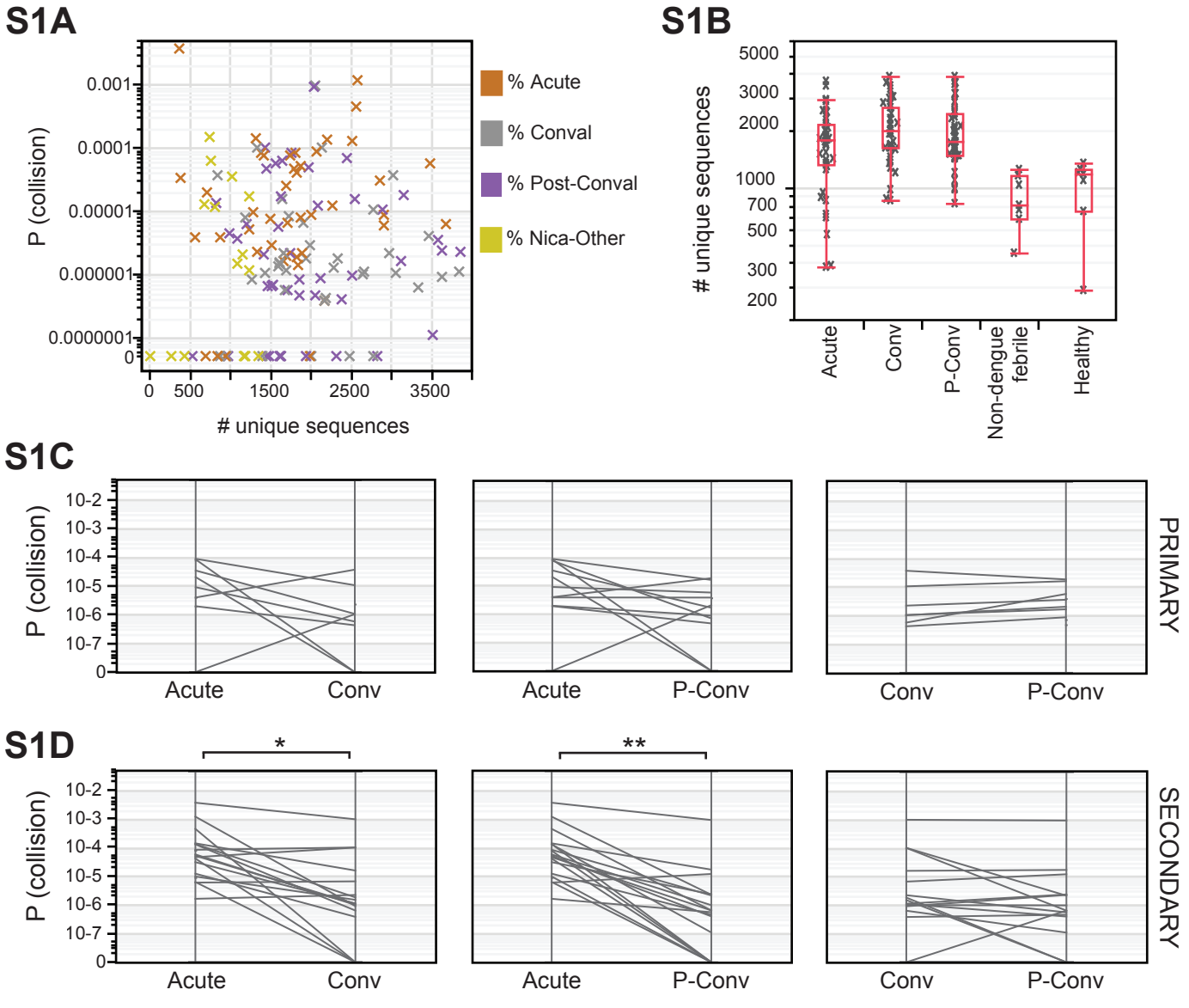
Figure S3, related to Figure 3. *Properties of prevalent CDR3 regions.* **(A)** Percent relative abundance of prevalent CDR3 regions that were identified by mismatch cross-validation. CDR3

regions are binned by the number of amino acid mismatches (0MM or 1MM) to the indicated parent sequence. Annotations to each plot show the 25^{th}-75^{th} percentiles (box), the 10^{th}-90^{th} percentiles (whiskers), and the median (horizontal line). **(B-E)** Nucleotide sequences encoding for convergent CDR3 regions. Sequences are segregated by patient identity and sample type (A, Acute; C, Convalescent; PC, Post-convalescent). #, count per sample; CON, Consensus; V, Variable region; D, Diversity region; N, non-templated additions; J, Joining region. **(F)** V genes used in encoding for the convergent CDR3 regions and their one-mismatch derivatives. Only V genes with evidence for usage in at least two samples are shown. **(G-H)** Deviations from germline nucleotide sequence in reads encoding for convergent CDR3 regions. Frequency distribution of percent mutation in V_H segments encoding for **(G)** convergent 10-mer and 13-mer CDR3 regions, compared to **(H)** baseline percent mutation distributions in similar V_H segments that encode for other CDR3 regions in these individuals. **(I)** Percent prevalence of convergent CDR3 regions in primary and secondary dengue cases. **P* < 0.05, ***P* < 0.005 for comparisons between acute primary and acute secondary (Fisher's test).

Figure S4, related to Figure 4. *Possible V_H phylogenies for B cells with convergent 13-mer CDR3 regions.* Phylogenies are shown for reads derived from (**A-B**) IGHV1-46 and IGHJ6, and (**C-E**) IGHV5-51 and IGHJ6 genes for various individuals, along with the number of nucleotide changes between any two nodes. The sizes of the circles represent the number of reads. Reads that encode for ARID$(Y)_5$GMDL and ARLD$(Y)_5$GMDL CDR3 regions and their derivatives with ≥95% similarity or 90-95% similarity are highlighted using red, orange and green boxes, respectively. *Methods:* A probabilistic generative model was used to assign a probability to each possible phylogeny. Markov Chain Monte Carlo (MCMC) was applied to sample this probability distribution over all possible phylogenies subject to the constraint that the phylogeny must generate the observed empirical heavy chain reads. Per MCMC iteration, block Gibbs sampling was performed on each of the following parameters: phylogenetic tree structure, birth and death times of individual subclones, birth and death rates, mutation rates, read error rates, subclone consensus sequences, and assignment of reads to subclones. The sampled trees were then optimized, and the most optimized sample was selected as the final representative output.

Figure S5, related to Figure 5. *Prevalence and physicochemical properties of clusters associated with convergent CDR3 regions.* **(A)** Percent prevalence of clusters associated with the convergent 10-mer and 13-mer CDR3 regions in various sample subsets. **(B, C)** Residue-specific properties of 10-mer and 13-mer clusters containing the convergent CDR3 regions and

their associated CDR2 and CDR1 regions. Scores for molecular weight (top line plot), isoelectric pH (center line plot) or hydrophilicity (bottom line plot)**.** Purple line, scores for germline CDR1 and CDR2 sequences (middle and right panels) or median scores across all CDR3 regions of length **(B)** 10 or **(C)** 13 (left panels); thick orange line, median scores across all members of the cluster; faded orange lines, scores for individual members of the cluster. Observed frequencies of association between CDR3 and CDR1 or CDR2 clusters are shown (freq), as well as the extent of amino acid conservation and consensus peptide sequences for the CDR clusters.


S1A
P (collision)
0.001
0.0001
0.00001
0.000001
0.0000001
0
0
500
1500
2500
3500
unique sequences
% Acute
% Conval
% Post-Conval
% Nica-Other
S1B
unique sequences
5000
3000
2000
1000
700
500
300
200
Acute
Conv
P-Conv
Non-dengue febrile
Healthy
S1C
P (collision)
10-2
10-3
10-4
10-5
10-6
10-7
0
Acute
Conv
Acute
P-Conv
Conv
P-Conv
PRIMARY
S1D
*
**
P (collision)
10-2
10-3
10-4
10-5
10-6
10-7
0
Acute
Conv
Acute
P-Conv
Conv
P-Conv
SECONDARY

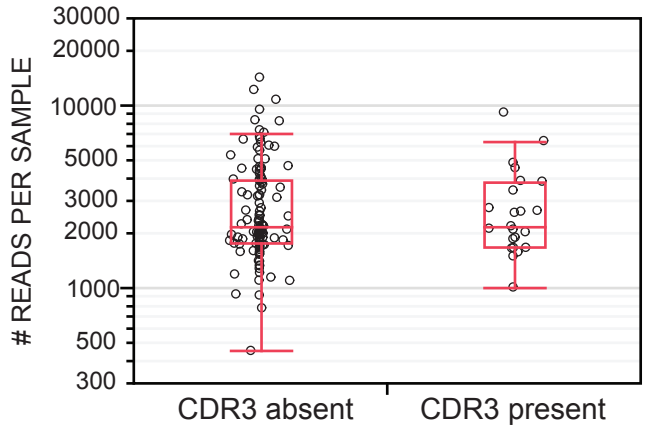
S2A

Group		Training set	Testing set
# dengue cases		22	22
Immune status	Primary	12	10
	Secondary	10	12
DENV serotype	DENV-2	14	8
	DENV-3	8	14
Diagnosis	DF	11	12
	DHF/DSS	11	10

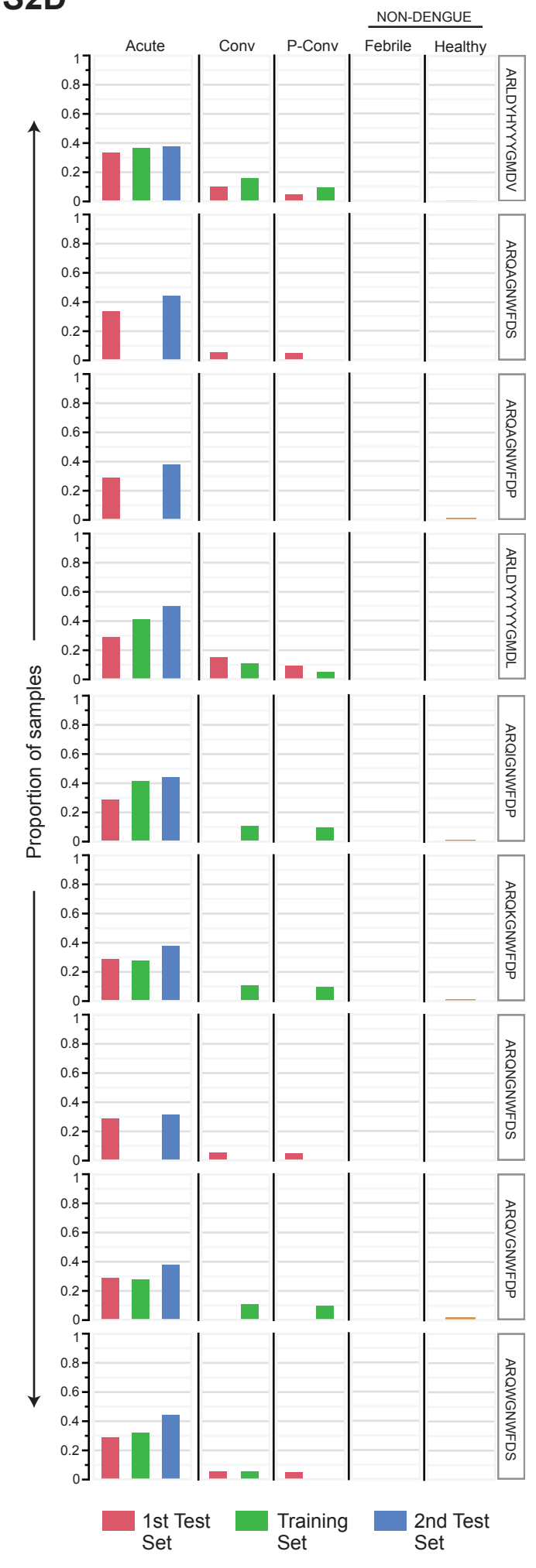
S2B

CDR3	Proportion (Acute)	Proportion (Conv)	Proportion (P-Conv)
ARIDYYYYYGMDL	0.36	0.05	0
ARLDYHNYYGMDV	0.36	0.05	0
ARLDYYYYYGMDI	0.36	0.11	0.05
ARLDYYYYYGMDL	0.41	0.11	0.05
ARQIGNWFDP	0.41	0.11	0.09
ARLDYHYYYGMDV	0.36	0.16	0.09
ARIDYYYYYGMDV	0.45	0.26	0.18
ARGGYYYGMDV	0.36	0.37	0.23
ARLDYYYYYGMDV	0.45	0.26	0.23
ARGRGMDV	0.36	0.05	0.27

S2C



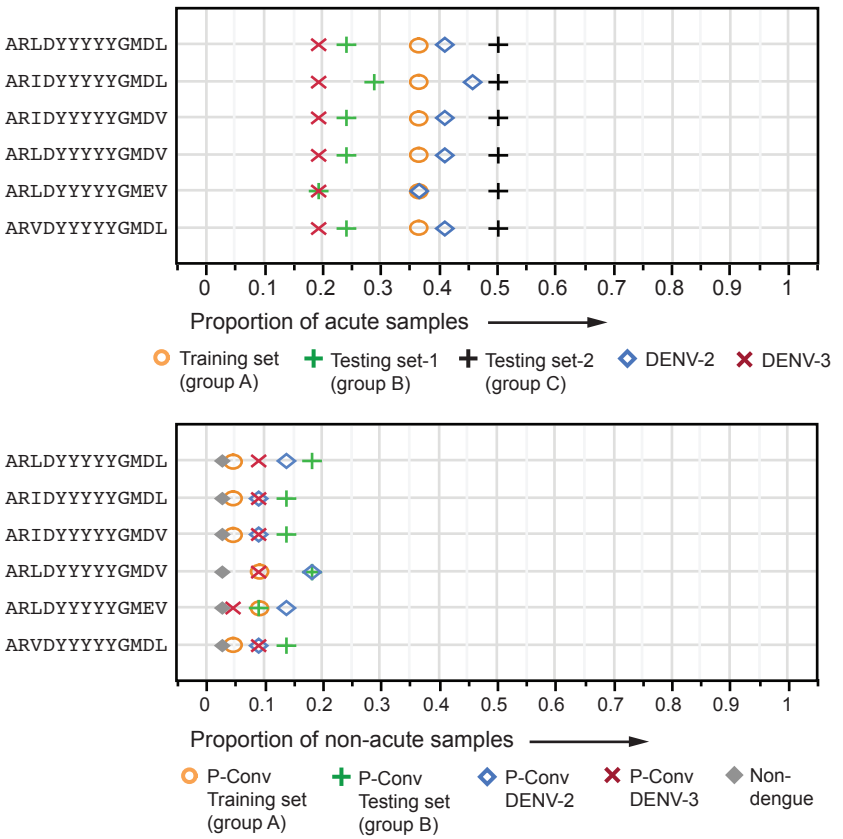
S2D



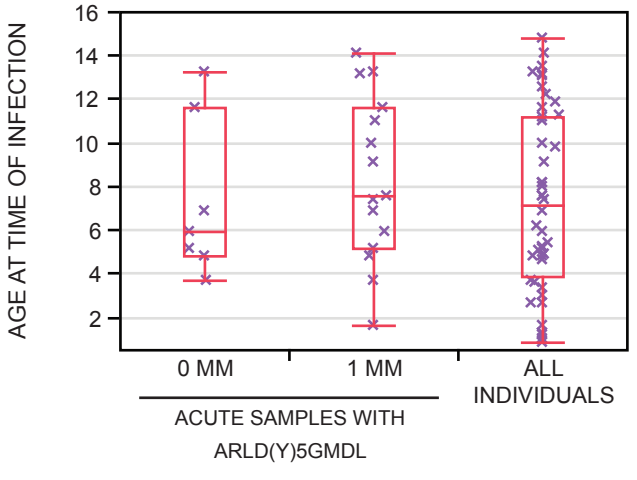
S2E

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	9																			
S	-1	4																		
T	-1	3	5																	
P	-4	-2	-1	7																
A	0	1	0	-1	4															
G	-4	0	-2	-1	0	6														
N	-3	1	1	-2	0	-1	6													
D	-3	-1	-1	-2	-2	-1	0	6												
E	-4	-1	-1	-2	-1	-1	0	3	5											
Q	-3	1	0	-1	0	-2	2	0	1	5										
H	-4	-2	-2	-2	-1	-2	0	-1	-1	0	8									
R	-4	-2	-1	-3	-1	-2	0	-2	-2	0	2	6								
K	-4	-2	-1	-2	-1	-2	0	-2	-1	0	2	4	6							
M	-1	0	-1	-1	-1	-3	-1	-2	-1	0	-2	-2	-1	5						
I	-1	-1	-1	-2	-1	-4	-2	-2	-2	-3	-3	-2	-2	2	4					
L	-1	-1	-1	-2	-1	-4	-2	-3	-2	-2	-3	-2	-2	2	2	4				
V	-1	-1	0	-1	2	-3	-2	-2	-1	-2	-3	-2	-2	2	3	3	4			
F	-2	-1	-2	-3	-2	-3	-2	-2	-4	-3	-2	-2	-3	0	1	0	-1	6		
Y	-2	-1	-2	-2	-2	-3	-1	-2	-3	-1	0	-2	-2	-1	0	-1	1	4	6	
W	-2	-2	-2	-3	-3	-4	-3	-4	-4	-2	-2	-2	-3	-1	-1	-2	0	2	3	9

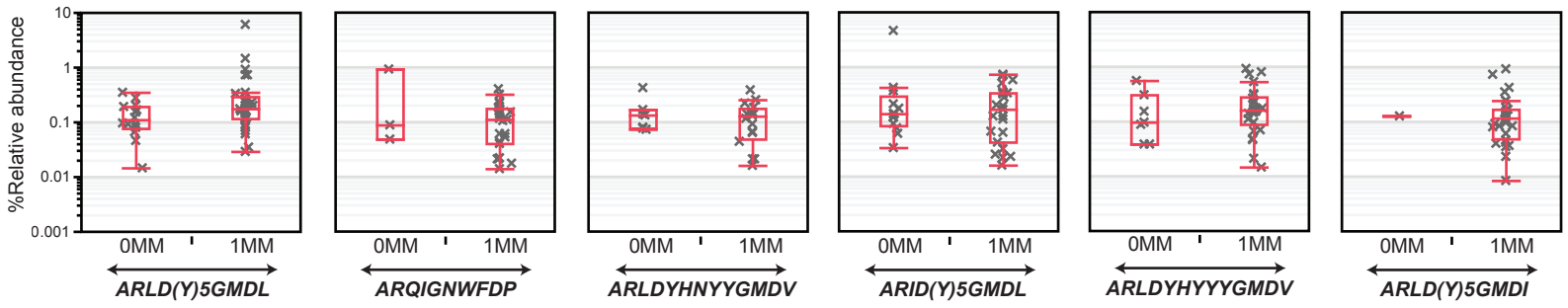
S2F



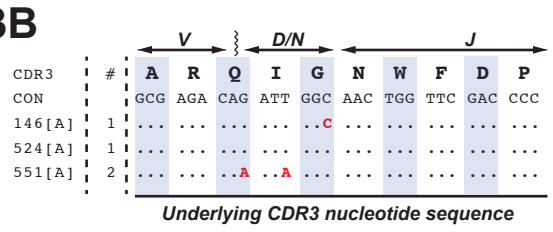
S2G



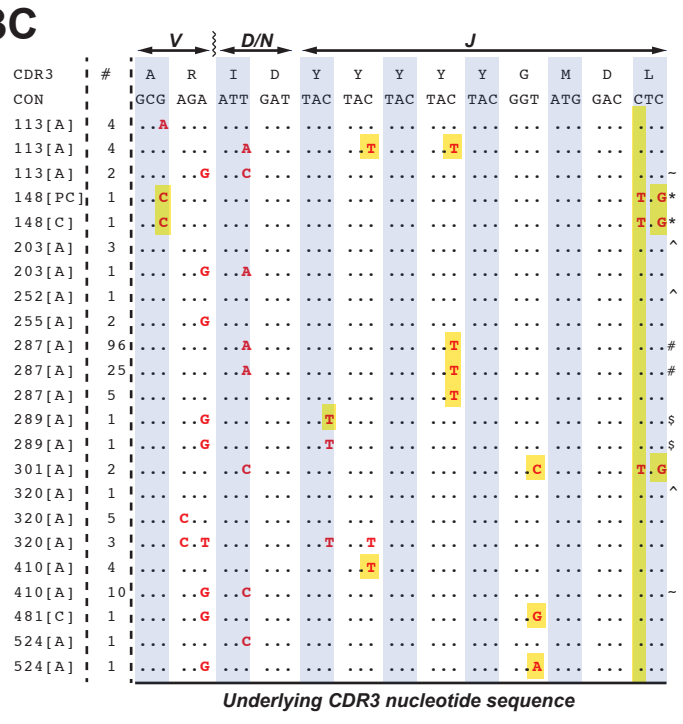
S3A



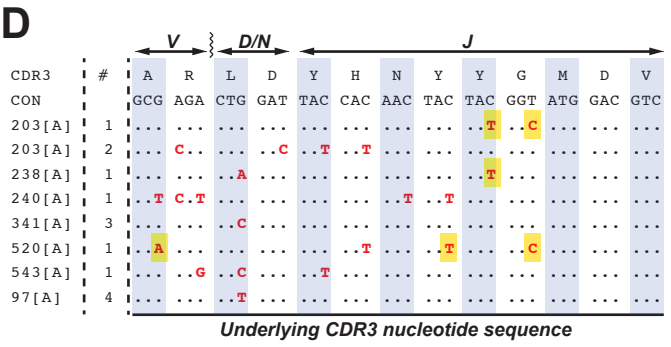
S3B



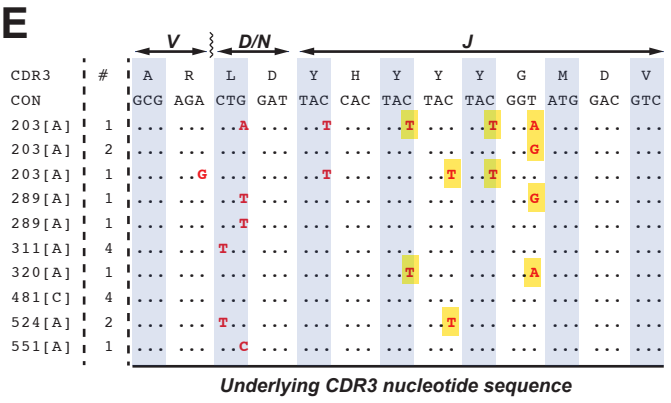
S3C



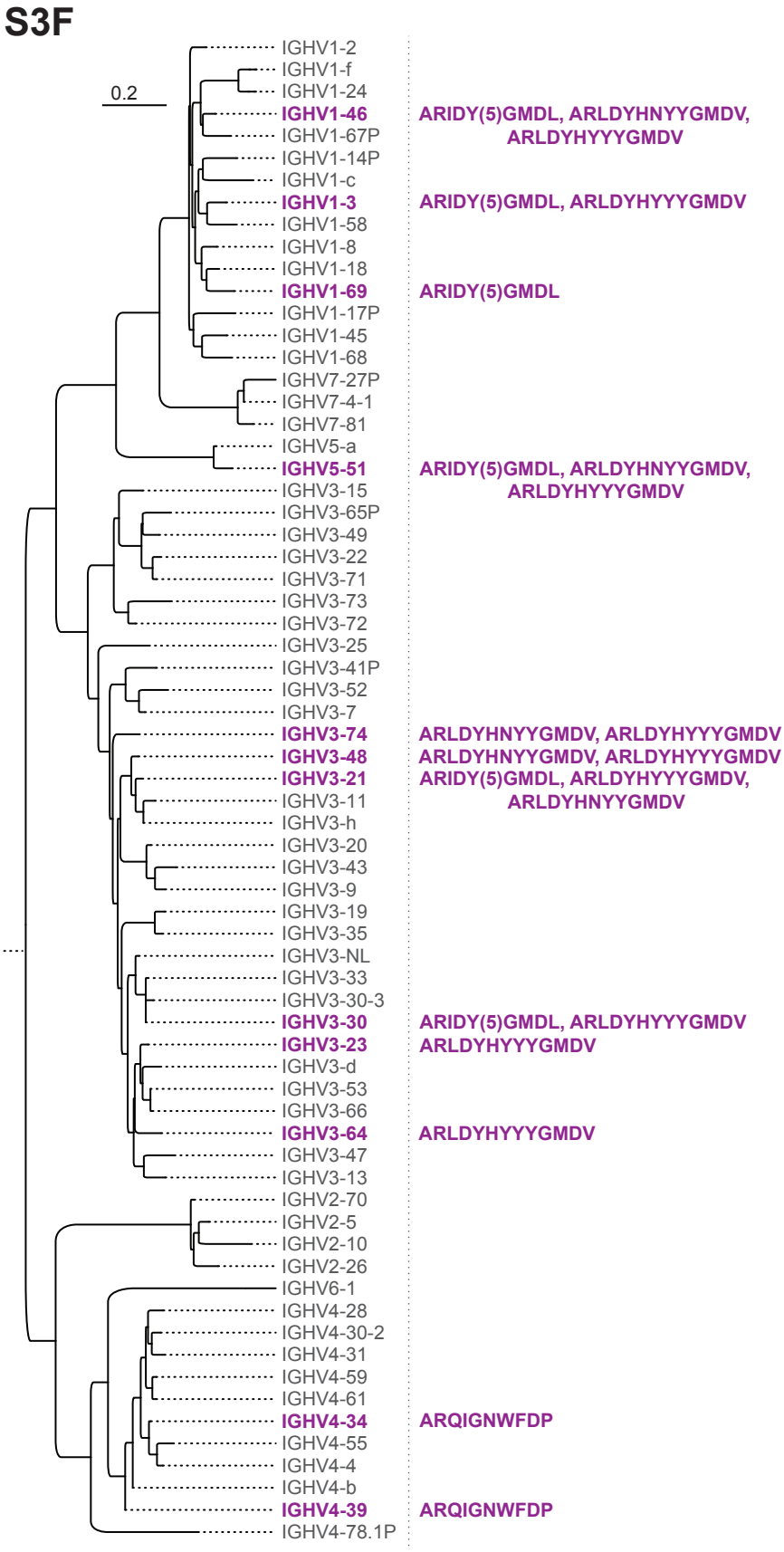
S3D



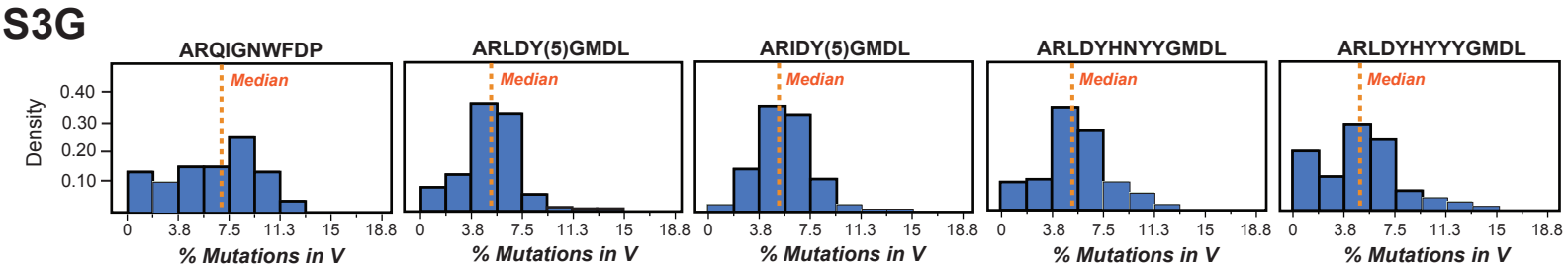
S3E



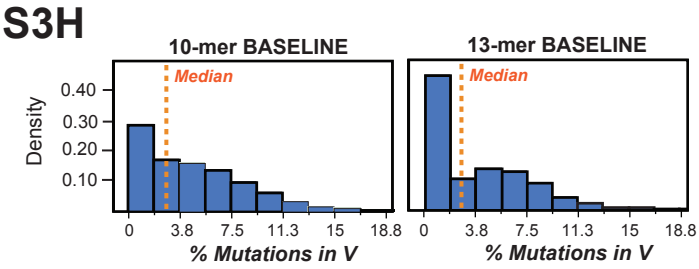
S3F



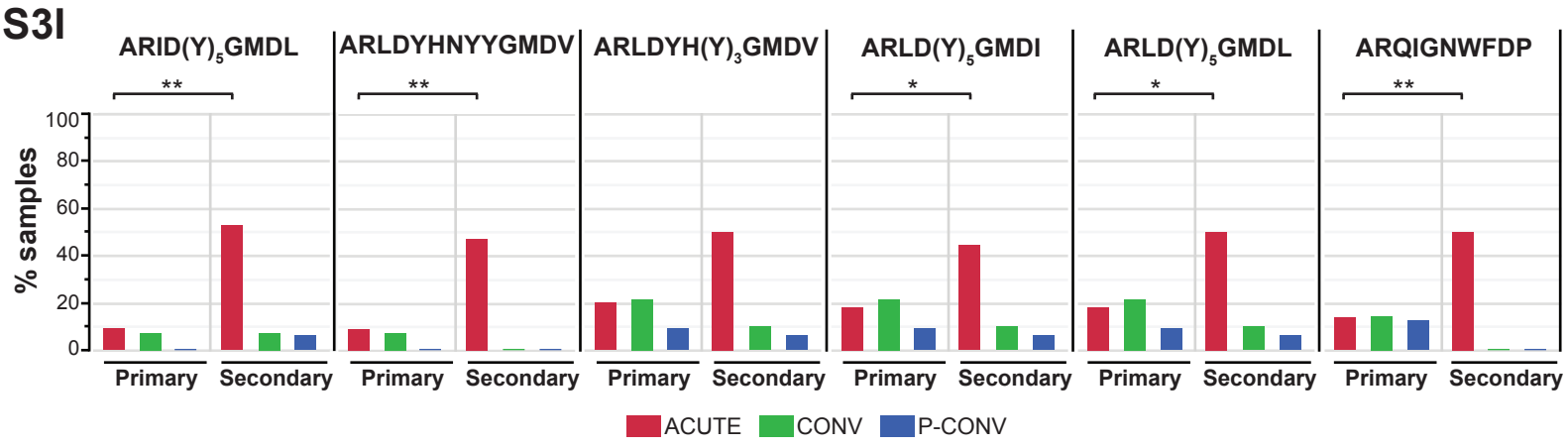
S3G



S3H

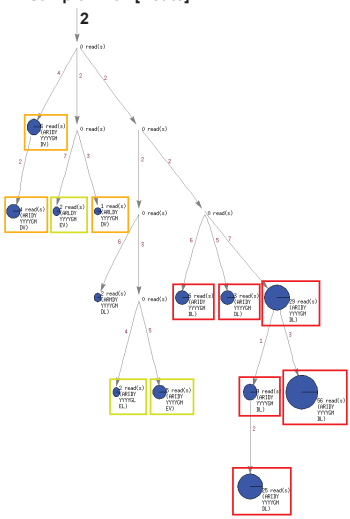


S3I



S4A

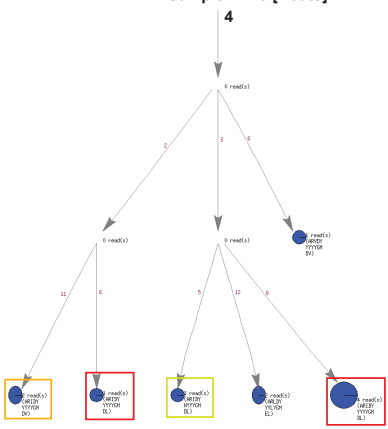
Sample # 287 [Acute]



ARIDY(5)GMDL
≥95% similar to ARIDY(5)GMDL
90-95% similar to ARIDY(5)GMDL

S4B

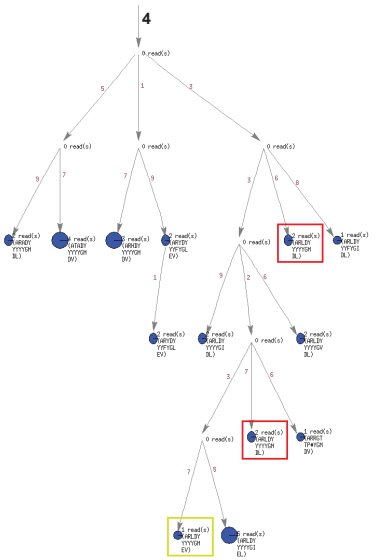
Sample # 113 [Acute]



ARIDY(5)GMDL
≥95% similar to ARIDY(5)GMDL
90-95% similar to ARIDY(5)GMDL

S4C

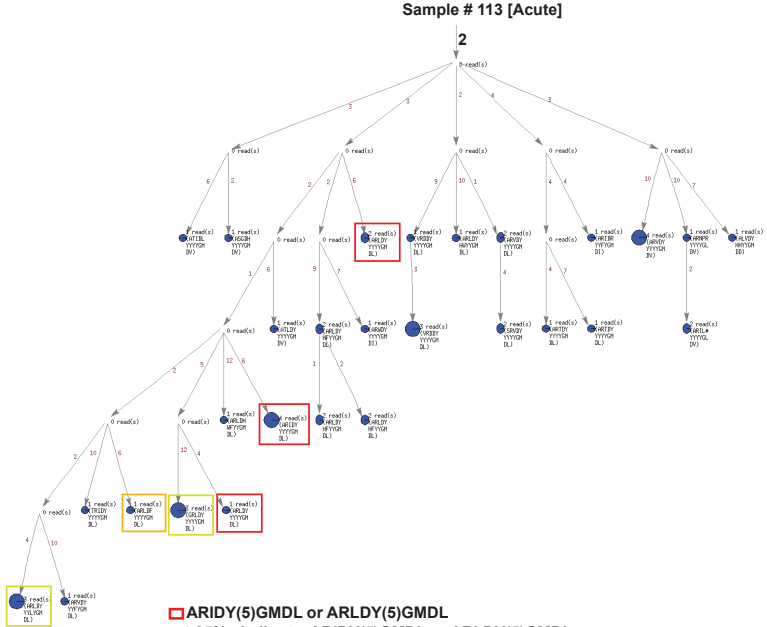
Sample # 97 [Acute]



ARLDY(5)GMDL
≥95% similar to ARLDY(5)GMDL
90-95% similar to ARLDY(5)GMDL

S4D

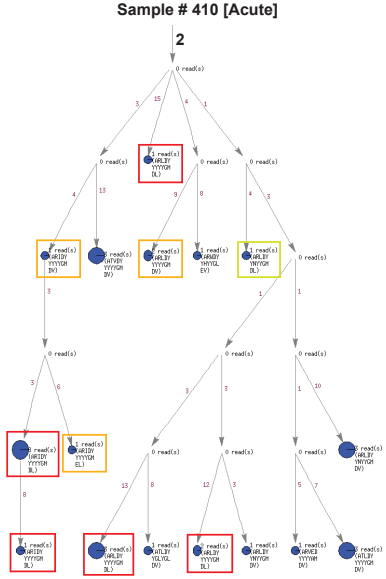
Sample # 113 [Acute]



ARIDY(5)GMDL or ARLDY(5)GMDL
≥95% similar to ARIDY(5)GMDL or ARLDY(5)GMDL
90-95% similar to ARIDY(5)GMDL or ARLDY(5)GMDL

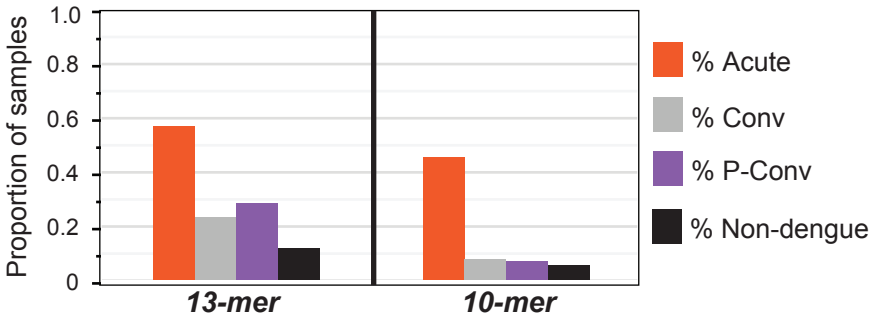
S4E

Sample # 410 [Acute]

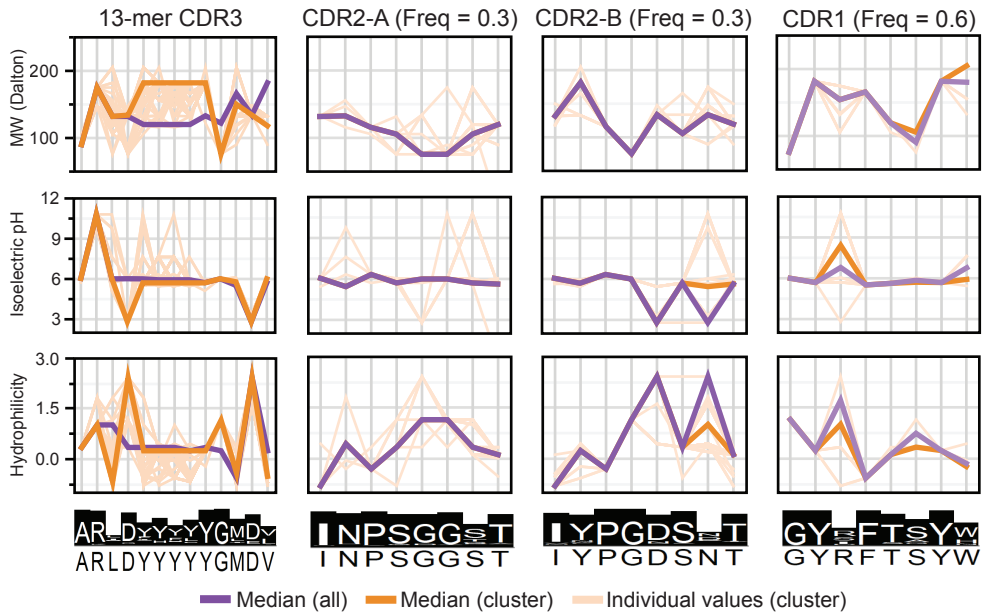


ARIDY(5)GMDL or ARLDY(5)GMDL
≥95% similar to ARIDY(5)GMDL or ARLDY(5)GMDL
90-95% similar to ARIDY(5)GMDL or ARLDY(5)GMDL

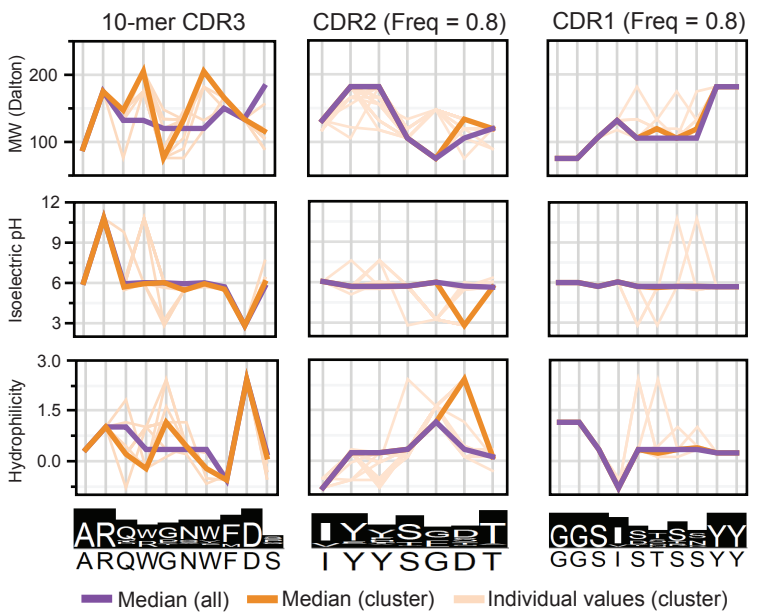
S5A


Proportion of samples
1.0
0.8
0.6
0.4
0.2
0
13-mer
10-mer
% Acute
% Conv
% P-Conv
% Non-dengue

S5B


13-mer CDR3
CDR2-A (Freq = 0.3)
CDR2-B (Freq = 0.3)
CDR1 (Freq = 0.6)
MW (Dalton)
Isoelectric pH
Hydrophilicity
ARLDYYYYYGMDV
INPSGGST
IYPGDSNT
GYRFTSYW
Median (all)
Median (cluster)
Individual values (cluster)

S5C


10-mer CDR3
CDR2 (Freq = 0.8)
CDR1 (Freq = 0.8)
MW (Dalton)
Isoelectric pH
Hydrophilicity
ARQWGNWFDS
IYYSGDT
GGSISTSSYY
Median (all)
Median (cluster)
Individual values (cluster)

Supplementary tables

Table S1, related to Table 1. *Description of samples used in this study, and read counts per sample pre- and post-filtering.*

Specimen ID	Disease severity^	Serotype	Immune status	Time-point*	# with correct barcode	# parsed by iHMMune-align	# with indels parsed by iHMMune-align	# spam reads (post-parsing)	# in-frame with at least one N1 or N2 base (final count)
148	DSS	DENV-2	Secondary	Acute	2319	1461	166	7	904
172	DHF	DENV-2	Primary	Acute	8228	5421	643	37	3585
194	DF	DENV-2	Primary	Acute	4239	2683	257	33	1993
199	DF	DENV-2	Primary	Acute	13417	8392	829	0	5620
203	DF	DENV-2	Secondary	Acute	8371	5245	664	37	3398
208	DF	DENV-3	Primary	Acute	3884	2667	235	0	2114
232	DSS	DENV-2	Secondary	Acute	8623	5289	573	26	3520
237	DF	DENV-2	Secondary	Acute	9251	5748	593	22	3829
238	DF	DENV-2	Secondary	Acute	11067	6965	784	54	4816
240	DF	DENV-2	Secondary	Acute	9468	6154	682	15	4338
249	DF	DENV-2	Secondary	Acute	9082	5451	489	11	3667
252	DF	DENV-2	Secondary	Acute	4800	3161	379	10	2165
255	DSS	DENV-2	Primary	Acute	3802	2350	263	18	1558
275	DSS	DENV-2	Secondary	Acute	3376	2026	228	5	1317
276	DHF	DENV-3	Primary	Acute	4167	2534	264	28	1663
287	DSS	DENV-2	Secondary	Acute	4648	2826	272	15	1840
289	DSS	DENV-2	Secondary	Acute	6275	3864	439	19	2630
299	DSS	DENV-2	Secondary	Acute	5796	3738	407	22	2604
301	DSS	DENV-2	Secondary	Acute	14572	9232	838	28	6341
307	DF	DENV-2	Primary	Acute	4955	3013	295	26	2011
311	DSS	DENV-2	Secondary	Acute	8051	5075	542	30	3397
320	DSS	DENV-2	Secondary	Acute	4846	3026	338	8	2099
376	DHF	DENV-3	Primary	Acute	2719	1638	186	16	1090
391	DHF	DENV-3	Primary	Acute	3947	2429	224	7	1649
422	DF	DENV-2	Primary	Acute	1936	1196	146	5	769
444	DHF	DENV-3	Secondary	Acute	4364	2674	248	20	1852
455	DF	DENV-3	Primary	Acute	5094	3303	259	32	2165
479	DF	DENV-3	Primary	Acute	4350	2816	250	16	1881
481	DF	DENV-3	Secondary	Acute	3762	2503	243	16	1645
489	DF	DENV-3	Secondary	Acute	4580	3065	280	32	2074
500	DF	DENV-3	Secondary	Acute	4658	3114	293	31	2155
514	DF	DENV-3	Secondary	Acute	3610	2364	230	13	1639
515	DF	DENV-3	Secondary	Acute	4212	2731	234	14	1811
517	DHF	DENV-3	Secondary	Acute	3623	2342	248	6	1635
520	DHF	DENV-3	Secondary	Acute	9007	6038	656	26	3904

524	DSS	DENV-2	Secondary	Acute	4071	2950	313	9	2075
529	DHF	DENV-3	Primary	Acute	9587	6032	694	74	3887
543	DHF	DENV-3	Secondary	Acute	3839	2715	235	15	1972
551	DHF	DENV-3	Secondary	Acute	1951	1409	161	9	1000
555	DF	DENV-3	Primary	Acute	9808	6448	670	19	4509
558	DF	DENV-3	Primary	Acute	2760	1823	149	6	1265
563	DF	DENV-3	Primary	Acute	4848	3277	289	30	2308
569	DF	DENV-3	Secondary	Acute	2784	1779	202	17	1307
148	DSS	DENV-2	Secondary	Conv	6502	4135	511	21	2723
172	DHF	DENV-2	Primary	Conv	10690	6854	780	21	4517
194	DF	DENV-2	Primary	Conv	12174	7942	868	29	5293
199	DF	DENV-2	Primary	Conv	9605	6171	649	45	4180
203	DF	DENV-2	Secondary	Conv	14372	8942	927	74	5905
208	DF	DENV-3	Primary	Conv	8873	5596	585	42	3799
232	DSS	DENV-2	Secondary	Conv	6542	3817	360	22	2638
237	DF	DENV-2	Secondary	Conv	9196	5807	653	37	3757
238	DF	DENV-2	Secondary	Conv	7859	4899	487	27	3201
240	DF	DENV-2	Secondary	Conv	10512	6610	743	40	4416
249	DF	DENV-2	Secondary	Conv	8591	5118	497	25	3322
252	DF	DENV-2	Secondary	Conv	3455	2180	242	21	1512
255	DSS	DENV-2	Primary	Conv	4650	3092	285	19	2065
265	DF	DENV-3	Primary	Conv	8736	5498	595	24	3835
275	DSS	DENV-2	Secondary	Conv	3941	2426	268	11	1543
276	DHF	DENV-3	Primary	Conv	5051	3068	291	21	2075
287	DSS	DENV-2	Secondary	Conv	5611	3135	277	27	2103
289	DSS	DENV-2	Secondary	Conv	5788	3730	358	23	2467
299	DSS	DENV-2	Secondary	Conv	5232	3300	333	21	2218
301	DSS	DENV-2	Secondary	Conv	7320	4658	422	28	3153
376	DHF	DENV-3	Primary	Conv	3354	2055	182	13	1396
422	DF	DENV-2	Primary	Conv	2029	1262	132	12	916
444	DHF	DENV-3	Secondary	Conv	4991	3098	258	26	2200
455	DF	DENV-3	Primary	Conv	4811	3183	302	6	2075
479	DF	DENV-3	Primary	Conv	4523	2957	326	17	1938
481	DF	DENV-3	Secondary	Conv	4016	2736	270	12	1875
489	DF	DENV-3	Secondary	Conv	5537	3678	364	14	2450
500	DF	DENV-3	Secondary	Conv	4036	2690	236	16	1835
514	DF	DENV-3	Secondary	Conv	3869	2488	225	14	1735
515	DF	DENV-3	Secondary	Conv	3588	2261	239	8	1519
517	DHF	DENV-3	Secondary	Conv	3970	2510	243	11	1738
520	DHF	DENV-3	Secondary	Conv	3036	2125	220	8	1481
524	DSS	DENV-2	Secondary	Conv	3206	2271	240	8	1565
529	DHF	DENV-3	Primary	Conv	3532	2468	216	5	1689
543	DHF	DENV-3	Secondary	Conv	3777	2709	247	20	1942

551	DHF	DENV-3	Secondary	Conv	2225	1622	143	5	1200
555	DF	DENV-3	Primary	Conv	4099	2733	279	25	1892
563	DF	DENV-3	Primary	Conv	5615	3862	375	25	2606
569	DF	DENV-3	Secondary	Conv	4785	3182	268	23	2338
148	DSS	DENV-2	Secondary	P-Conv	6165	4013	523	13	2564
172	DHF	DENV-2	Primary	P-Conv	12105	7622	843	30	5038
194	DF	DENV-2	Primary	P-Conv	11953	7452	780	40	5047
199	DF	DENV-2	Primary	P-Conv	9188	5809	598	21	3835
203	DF	DENV-2	Secondary	P-Conv	15646	9811	1022	61	6506
208	DF	DENV-3	Primary	P-Conv	9252	5739	608	41	3893
232	DSS	DENV-2	Secondary	P-Conv	7328	4303	490	24	2890
237	DF	DENV-2	Secondary	P-Conv	9909	6311	684	27	4042
238	DF	DENV-2	Secondary	P-Conv	7288	4540	498	22	3100
240	DF	DENV-2	Secondary	P-Conv	10935	6883	787	29	4563
249	DF	DENV-2	Secondary	P-Conv	7609	4606	458	27	3199
252	DF	DENV-2	Secondary	P-Conv	3664	2318	256	21	1562
255	DSS	DENV-2	Primary	P-Conv	4797	3086	323	15	1999
265	DF	DENV-3	Primary	P-Conv	11336	7062	816	30	4474
275	DSS	DENV-2	Secondary	P-Conv	3886	2418	246	11	1582
276	DHF	DENV-3	Primary	P-Conv	5084	3077	308	22	2008
287	DSS	DENV-2	Secondary	P-Conv	5204	3055	265	16	2085
289	DSS	DENV-2	Secondary	P-Conv	5938	3682	401	18	2485
299	DSS	DENV-2	Secondary	P-Conv	4802	3064	304	14	2010
301	DSS	DENV-2	Secondary	P-Conv	7289	4743	440	30	3192
307	DF	DENV-2	Primary	P-Conv	5082	3053	257	34	2003
311	DSS	DENV-2	Secondary	P-Conv	1226	768	74	7	449
320	DSS	DENV-2	Secondary	P-Conv	3435	1673	201	6	1178
376	DHF	DENV-3	Primary	P-Conv	3434	2098	210	9	1387
391	DHF	DENV-3	Primary	P-Conv	4047	2503	255	16	1708
422	DF	DENV-2	Primary	P-Conv	3782	2331	242	11	1606
444	DHF	DENV-3	Secondary	P-Conv	4481	2758	259	33	1872
455	DF	DENV-3	Primary	P-Conv	4090	2650	246	14	1720
479	DF	DENV-3	Primary	P-Conv	6249	4148	354	27	2717
481	DF	DENV-3	Secondary	P-Conv	3822	2531	239	32	1713
489	DF	DENV-3	Secondary	P-Conv	4016	2703	276	10	1805
500	DF	DENV-3	Secondary	P-Conv	4801	3211	275	16	2291
514	DF	DENV-3	Secondary	P-Conv	4345	2749	233	8	1877
515	DF	DENV-3	Secondary	P-Conv	5580	3582	392	17	2358
517	DHF	DENV-3	Secondary	P-Conv	3617	2361	216	17	1678
520	DHF	DENV-3	Secondary	P-Conv	3549	2532	266	12	1784
524	DSS	DENV-2	Secondary	P-Conv	3636	2581	264	9	1758
529	DHF	DENV-3	Primary	P-Conv	2248	1570	170	14	1087
543	DHF	DENV-3	Secondary	P-Conv	3678	2713	256	13	1953

551	DHF	DENV-3	Secondary	P-Conv	2227	1623	138	5	1133
555	DF	DENV-3	Primary	P-Conv	3765	2592	241	18	1799
558	DF	DENV-3	Primary	P-Conv	3644	2451	250	9	1706
563	DF	DENV-3	Primary	P-Conv	4584	3124	272	17	2180
569	DF	DENV-3	Secondary	P-Conv	4054	2554	204	26	1858
171	n/a	n/a	n/a	Febrile	3155	2174	234	22	1554
207	n/a	n/a	n/a	Febrile	4149	2869	245	7	1973
209	n/a	n/a	n/a	Febrile	3664	2317	254	18	1596
220	n/a	n/a	n/a	Febrile	3304	2084	183	29	1460
330	n/a	n/a	n/a	Febrile	1914	1163	107	3	807
332	n/a	n/a	n/a	Febrile	1851	1121	150	2	771
345	n/a	n/a	n/a	Febrile	2004	1232	134	14	872
1503	n/a	n/a	n/a	Healthy	2763	1849	212	10	1272
223	n/a	n/a	n/a	Healthy	2072	1250	132	7	881
2603	n/a	n/a	n/a	Healthy	2663	1700	168	11	1211
331	n/a	n/a	n/a	Healthy	649	422	61	2	311
4057	n/a	n/a	n/a	Healthy	3033	2018	173	16	1439
4431	n/a	n/a	n/a	Healthy	2560	1718	184	5	1224
4468	n/a	n/a	n/a	Healthy	2985	1870	185	5	1303
4873	n/a	n/a	n/a	Healthy	1672	1033	105	8	715
55[$]	DF	DENV-2	Primary	Acute	14522	12986	1230	87	8246
97[$]	DSS	DENV-2	Secondary	Acute	10935	9699	844	42	6461
113[$]	DF	DENV-2	Secondary	Acute	13171	11044	1118	75	7267
114[$]	DF	DENV-2	Secondary	Acute	10832	8971	933	37	5985
128[$]	DHF	DENV-2	Secondary	Acute	9254	7282	718	27	4622
146[$]	DSS	DENV-2	Secondary	Acute	10384	9131	916	31	5843
188[$]	DHF	DENV-2	Secondary	Acute	7841	6931	650	50	4431
189[$]	DSS	DENV-2	Secondary	Acute	12198	10322	1086	41	6675
212[$]	DSS	DENV-2	Secondary	Acute	28269	21941	2237	161	14118
308[$]	DSS	DENV-2	Secondary	Acute	10351	9145	855	112	6212
313[$]	DF	DENV-2	Secondary	Acute	23816	18908	1795	195	12088
314[$]	DHF	DENV-2	Secondary	Acute	16626	14413	1398	70	9417
341[$]	DHF	DENV-2	Secondary	Acute	15005	12157	1243	66	8138
364[$]	DHF	DENV-2	Secondary	Acute	13020	10670	1098	112	7040
410[$]	DF	DENV-2	Secondary	Acute	18782	15771	1632	61	10677
524[$]	DSS	DENV-2	Secondary	Acute	12908	11075	1224	63	7015

*Conv, Convalescent. P-Conv, Post-convalescent. Febrile, Non-dengue febrile
^DF, dengue fever. DHF, dengue hemorrhagic fever. DSS, dengue shock syndrome. n/a, not available
[$]2nd Test set samples

Table S2, related to Figure 1. *P(collision) scores used in Figure 1.*

Patient ID	Acute	Conv*	P-Conv	Non-dengue febrile	Healthy
148	3.67E-03	9.70E-04	9.13E-04		
172	8.62E-05	1.04E-05	1.57E-05		
194	3.89E-06	3.62E-05	1.81E-05		
203	3.10E-05	1.12E-06	2.36E-06		
232	6.00E-06	6.63E-06	1.20E-05		
237	1.29E-04	6.35E-07	1.09E-07		
238	5.76E-05	9.97E-07	9.78E-07		
240	1.20E-03	9.09E-07	2.26E-06		
249	5.19E-05	1.09E-06	3.98E-07		
252	4.13E-05	1.00E-08	1.00E-08		
255	8.20E-05	1.00E-08	1.00E-08		
275	9.77E-06	1.50E-06	1.00E-08		
287	1.41E-04	1.58E-05	1.70E-05		
289	1.33E-04	1.83E-06	1.00E-08		
299	1.23E-05	3.83E-07	4.59E-07		
301	6.29E-06	1.00E-08	1.00E-08		
307	1.88E-06	n/a	4.64E-07		
311	8.70E-06	n/a	n/a		
320	7.77E-05	n/a	1.00E-08		
422	1.99E-05	1.00E-08	1.00E-08		
524	4.63E-05	1.00E-04	6.41E-07		
208	3.38E-05	1.05E-06	1.65E-06		
265	n/a	2.22E-06	3.55E-06		
276	1.94E-06	4.23E-07	8.72E-07		
376	1.00E-08	1.03E-06	2.03E-06		
391	7.48E-05	n/a	6.97E-07		
444	8.37E-05	1.01E-04	2.14E-06		
520	4.48E-04	1.00E-08	6.42E-07		
543	1.63E-06	2.22E-06	5.56E-07		
555	8.88E-06	5.69E-07	5.65E-06		
558	3.80E-06	n/a	3.76E-06		
171				1.18E-05	
207				1.75E-05	
209				3.60E-05	
220				2.08E-06	
330				1.27E-05	
332				0.00E+00	
345				6.30E-05	
223					1.47E-04
331					0.00E+00

1503	0.00E+00
2603	1.46E-06
4057	0.00E+00
4431	0.00E+00
4468	1.16E-06
4873	0.00E+00

n/a, not available

*Only convalescent samples that were collected 7-21 days post-symptom onset were considered for this analysis.

Table S3, related to Figure 2. *P-values, q-values and L1-regularized log odds ratios associated with convergent CDR3 regions and CDR3 clusters that were significantly more prevalent in acute dengue compared to non-dengue cases.*

Fisher's exact P-values, Benjamini-Hochberg q-values and L1-regularized log odds ratios for CDR3 regions that were significantly more prevalent in acute dengue compared to non-dengue cases

CDR3	Fisher exact *P*-value	Benjamini-Hochberg q-value	Adjusted log odds ratios	Odds ratios
ARLDYYYYYGMDL	4.715e-8	0.0001572	0.59	1.805
ARIDYYYYYGMDL	0.0000001192	0.000397		
ARLDYYHYYGMDL	0.0000001192	0.000397		
ARLDYHYYYGMDV	0.0000001192	0.000397	0.182	1.199
ARLDYYYYYGMDI	0.0000002967	0.000988		
ARQWGNWFDS	0.0000007279	0.002421		
ARQAGNWFDS	0.0000007279	0.002421		
ARLDYHNYYGMDV	0.0000007279	0.002421	0.223	1.25
ARQTGNWFDS	0.0000007279	0.002421	0.29	1.336
ARQIGNWFDP	0.000001632	0.005426		
ARLDYYSYYGMDL	0.000001761	0.005841		
ARQDYYYYYGMDL	0.000001761	0.005841		
ARQAGNWFDP	0.000001761	0.005841		
ARQIGNWFDS	0.000001761	0.005841		
ARLDYYNYYGMDL	0.000001761	0.005841		
ARLDYYNYYGMDV	0.000001761	0.005841		
ARQVGNWFDS	0.000001761	0.005841		
ARQLGNWFDS	0.000001761	0.005841	0.048	1.049
ARQRGNWFDP	0.000003847	0.01276	0.703	2.019
ARLDYYQYYGMDL	0.000004202	0.01388		
AREDYYYYYGMDL	0.000004202	0.01388		
ARQRGNWFDS	0.000004202	0.01388		
ARLDYYFYYGMDL	0.000004202	0.01388		
ARIDYHYYYGMDV	0.000004202	0.01388		
ARQSGNWFDS	0.000004202	0.01388		
ARQKGNWFDS	0.000004202	0.01388		
ARQMGNWFDP	0.000004202	0.01388		
ATLDYYYYYGMDV	0.000004202	0.01388		
ARLDYHYYYGMDL	0.000004202	0.01388		
ARLDYYYLYGMDV	0.000004202	0.01388		
ARIDYYHYYGMDV	0.000004202	0.01388		
ARIDYYYYYGMDV	0.000004655	0.01537	0.577	1.781
ATIDYYYYYGMDV	0.000009896	0.03256		
ARQSGNWFDP	0.000009896	0.03256		
ARMDYYYYYGMDL	0.000009896	0.03256		
ARLDYYYLYGMDL	0.000009896	0.03256		
ARLDYYYNYGMDL	0.000009896	0.03256		
ARQMGNWFDS	0.000009896	0.03256		
ARQLGNWFDP	0.000009896	0.03256		
ARLDYHFYYGMDV	0.000009896	0.03256		

ARCDYYYYYGMDL	0.000009896	0.03256		
ARLDFYYYYGMDL	0.000009896	0.03256		
ARQNGNWFDS	0.000009896	0.03256		
ARYDYYYYYGMDL	0.000009896	0.03256		
ARADYYYYYGMDL	0.000009896	0.03256		
ARGGYSDY			0.553	1.739
ARGPTLDY			0.371	1.449
ARGGPYYFDY			0.323	1.382
ARQWGNWFDR			0.212	1.236
ARQYGNYFDY			0.149	1.161
ARDGGSYYFDY			0.098	1.102
ARGLTGFDY			0.074	1.077
ARYYFDY			0.023	1.023
ARAGSYYFDY			0.011	1.011
ARVYYYYYGMDV			0.011	1.011

L1-regularized logs odds ratios for dengue-associated CDR3 clusters identified by logistic regression

Representative CDR3 (# CDR3 regions in cluster)	Adjusted log odds ratios	Odds ratios	Cluster Members
ARIDYYHYYGMDL (20)	1.742	5.710	ARIDYYHYYGMDL, ARLDYYQYYGMDL, AREDYYYYYGMDL, ARQDYYYYYGMDL, ARVDYYYYYGMDL, ARIDYYYYYGMDL, ARMDYYYYYGMDL, ARLDYYFYYGMDL, ARLDYYNYYGMDL, ARLDYYYYYGMDL, ARCDYYYYYGMDL, ARTDYYYYYGMDL, ARIDYYSYYGMDL, ARYDYYYYYGMDL, ARLDYYHYYGMDL, ARSDYYHYYGMDL, ARDDYYSYYGMDL, ARCDYYFYYGMDL, ARIDYYQYYGMDL, ARADYYYYYGMDL
ARGYYYGGMDV (2)	1.561	4.762	ARGYYYGGMDV, VRGYYYYGMDV
AREPHFDY (2)	1.460	4.305	AREPHFDY, ARDPHFDY
ARQWENWFDS (42)	1.415	4.115	ARQWENWFDS, ARQVRNWFDS, ARQWGNWFDS, ARQLRNWFDS, ARQDRNWFDS, ARQIRNWFDS, ARQQRNWFDS, ARQEKNWFDS, ARQRKNWFDS, ARQDNNWFDS, ARQWTNWFDS, ARQWDNWFDS, ARQRDNWFDS, ARQLENWFDS, ARQVKNWFDS, ARQDENWFDS, ARQKRNWFDS, ARQDSNWFDS, ARQVSNWFDS, ARQVTNWFDS, ARQRQNWFDS, ARQQKNWFDS, ARQERNWFDS, ARQLNNWFDS, ARQSKNWFDS, ARQNQNWFDS, ARQQENWFDS, ARQNSNWFDS, ARQRTNWFDS, ARQNANWFDS, ARQFTNWFDS, ARQSTNWFDS, ARQYTNWFDS, ARQRRNWFDS, ARQTDNWFDS, ARQISNWFDS, ARQDQNWFDS, ARQNTNWFDS, ARQTQNWFDS, ARQNYNWFDS, ARQASNWFDS, ARQHTNWFDS
ARGLGRFDP (1)	1.332	3.790	ARGLGRFDP
ARAGSYYFDY (5)	1.274	3.575	ARAGSYYFDY, AREGPYYFDY, ARGGPYYFDY, ARAGPYYFDY, ARAGAYYFDY
ASLDYHFYYGMDV (11)	0.901	2.462	ASLDYHFYYGMDV, ATLDYHFYYGMDV, ARLDYHHYYGMDV, ARLDYHNYYGMDV, ARLDYHYYYGMDV, ATLDYHNYYGMDV, ARLDYHFYYGMDV, ATLDYHSYYGMDV, ARLDYHSYYGMDV, ARLDYHQYYGMDV, ARLDYHTYYGMDV

ARDTYYYDSSGYFDY (1)	0.448	1.565	ARDTYYYDSSGYFDY
AREDYMDV (2)	0.360	1.433	AREDYMDV, AREDAMDV
ARQITNWFDA (11)	0.160	1.174	ARQITNWFDA, ARQITNWFDP, ARQWTNWFDA, ARQWTNWFDP, ARQTTNWFDA, ARQVTNWFDL, ARQLTNWFDL, ARQWTNWFDL, ARQTTNWFDS, ARQVTNWFDA, ARQWTNWFDR
ARGTGTLDY (2)	0.101	1.106	ARGTGTLDY, ARGTGTSDY
ARQSGNYFDY (12)	0.056	1.057	ARQSGNYFDY, ARQSGNYFDH, ARQLGNYFDR, ARQFGNYFDA, ARQSGNYFDS, ARQSGNYFDA, ARQSGNYFDD, ARQSGNYFDN, ARQSGNYFDF, ARQLGNYFDS, ARQTGNYFDS, ARQFGNYFDN

Comparison of various measures attributed to CDR3 regions identified using the cross-validation algorithm

CDR3	Average prevalence* (mismatch)	Average prevalence* (amino acid similarity)	Benjamini-Hochberg q-value	Adjusted log odds ratio	
				Singleton	Post-clustering
ARLDYYYYYGMDL	0.398	0.367	0.000157	0.590	1.742
ARIDYYYYYGMDL	0.383	0.383	0.000397	-	1.742
ARQIGNWFDP	0.377	0.134	0.00543	-	-
ARLDYHYYYGMDV	0.357	0.170	0.000397	0.182	0.901
ARLDYHNYYGMDV	0.326	0.228	0.00242	0.223	0.901

*Average prevalence in acute dengue cases in the training, 1st test and 2nd test sets

Table S4, related to Figure 5. *10-mer and 13-mer CDR3 clusters with significant Fisher's P values (< 0.05) for prevalence comparisons between acute and post-convalescent samples, or between acute and non-dengue samples.*

CDR3 length	Cluster #	# CDR3 regions	Acute	Conv	P-Conv	Non-Dengue	Fisher's *P* (Acute / P-Conv)	Fisher's *P* (Acute / Non-Dengue)	Clusters highlighted in Figure 5**
10	386	48	17	3	4	2	2.29E-04	7.29E-07	**
10	197	27	14	1	1	2	5.70E-05	2.33E-05	
10	69	20	11	3	1	1	8.33E-04	1.12E-04	**
10	284	14	9	2	2	0	1.89E-02	1.24E-04	
10	353	8	6	1	0	0	7.42E-03	3.00E-03	
10	286	8	6	2	1	0	4.38E-02	3.00E-03	
10	193	8	5	0	1	0	8.89E-02	8.29E-03	
10	143	7	4	2	1	0	1.74E-01	2.25E-02	
10	376	5	4	0	0	0	4.08E-02	2.25E-02	
10	350	6	4	0	0	0	4.08E-02	2.25E-02	**
10	40	6	4	1	0	0	4.08E-02	2.25E-02	
10	32	7	4	1	0	1	4.08E-02	7.91E-02	
13	985	36	14	3	0	0	1.45E-05	2.80E-06	
13	2227	46	13	2	2	2	1.65E-03	4.23E-04	**
13	1254	12	7	2	0	2	5.51E-03	7.32E-02	
13	1215	21	0	4	7	9	1.21E-02	4.12E-03	
13	1050	5	5	0	0	0	2.61E-02	1.49E-02	
13	2562	11	0	1	6	4	2.61E-02	1.27E-01	
13	1111	16	10	3	3	0	3.85E-02	1.52E-04	**
13	2847	28	2	8	9	7	4.92E-02	2.91E-01	
13	2270	142	22	12	14	8	8.34E-02	1.55E-04	**
13	305	16	0	1	3	11	2.41E-01	1.02E-03	
13	1716	13	0	2	3	7	2.41E-01	1.63E-02	
13	544	20	0	4	5	6	5.54E-02	3.23E-02	
13	138	11	0	1	2	6	4.94E-01	3.23E-02	
13	1519	13	0	1	1	6	1.00E+00	3.23E-02	
13	2559	4	4	0	0	0	5.54E-02	3.56E-02	
13	815	12	1	3	0	8	4.94E-01	4.09E-02	
13	2337	13	1	1	0	8	4.94E-01	4.09E-02	
13	943	16	1	1	3	8	6.16E-01	4.09E-02	

These clusters contain 13-mer and 10-mer CDR3 regions that were identified by mismatch cross-validation (highlighted in **Figure 5, with members from other clusters faded).