## Supplemental Table 1. Genetic and functional characteristics of human mAbs

| Type of infection | Subject # | mAb | IgG subclass | λ or κ | Binding to whole virus in ELISA, for indicated serotype at 1 μg/mL | | | | Binding to rE-protein (ELISA) | Binding to rE-protein DIII fragment (ELISA) | Binding to rE-protein DI/II fragment (ELISA) | Binding to rPr-protein (ELISA) | 50% neutralization concentration (μg/mL), against indicated serotype | | | | Fold enhancement of infection, for indicated serotype at 1 μg/mL | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | D1 | D2 | D3 | D4 | | | | | D1 | D2 | D3 | D4 | D1 | D2 | D3 | D4 |
| rDENV1 Delta30 | 32 | **1K12** | IgG1 | λ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | **56** | 1 | 1 | 1 |
| | 33 | **1C8** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 13 | **31** | **130** | 15 |
| | | **1O21.2** | IgG1 | κ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 1 | 0 | 1 | 1 |
| | 35 | **1D7.3** | IgG1 | λ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | **27** | 9 | 20 | 1 |
| | | **1N23** | IgG3 | κ | + | + | + | - | + | + | - | - | >10 | >10 | >10 | >10 | 3 | 18 | 6 | 1 |
| | | **1C9** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 15 | **40** | **54** | 13 |
| | 38 | **1I23** | IgG1 | κ | + | + | + | - | + | + | - | - | >10 | >10 | >10 | >10 | 4 | 18 | **28** | 1 |
| | 39 | **1O6** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | **119** | **67** | **54** | 15 |
| | | **1I15** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | **92** | **74** | **37** | 4 |
| | 40 | **1C19.2** | IgG1 | κ | + | + | + | + | + | + | - | - | **0.22** | >10 | >10 | >10 | 5 | 1 | 1 | 1 |
| | | **1O10** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | **146** | **166** | **40** | 6 |
| | 44 | **1J16.2** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | **97** | **88** | **26** | 3 |
| | 45 | **1D7.2** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | **65** | **53** | 17 | 2 |
| | | **1L18** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | **81** | **60** | **30** | 6 |
| | | **1E8** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 6 | 3 | 24 | 4 |
| | 47 | **1C22** | IgG1 | λ | + | + | + | - | + | + | - | - | 2.5 | >10 | >10 | >10 | 3 | 11 | 10 | 2 |
| | | **1I14** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 5 | 10 | 7 | 2 |
| | | **1E1** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 8 | 8 | **26** | 4 |
| | 49 | **1M12.2** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 8 | 8 | **30** | 1 |
| | | **1H7** | IgG1 | κ | + | - | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 13 | 1 | 13 | 5 |
| | 53 | **1L13** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | **0.24** | >10 | 9 | 15 | 15 | 9 |
| | | **1I7** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 8 | **28** | 10 | 2 |
| | 55 | **1P11** | IgG3 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | **26** | 23 | **213** | 4 |
| | 57 | **1I6** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 11 | 11 | **56** | 5 |
| | | **1D3** | IgG1 | κ | + | + | + | - | - | - | - | + | >10 | >10 | >10 | >10 | 11 | 11 | **56** | 5 |
| | 58 | **1M18** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 8 | 7 | **35** | 1 |
| 1º DENV1 | 006 | **1B17.2** | IgG1 | κ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 3 | 3 | 4 | 3 |
| | | **1O12** | IgG1 | κ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 1 | 1 | 12 | 1 |
| | 106 | **1E23** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 8 | 6 | **55** | 3 |
| | | **2F13** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 5 | 5 | 3 | 1 |
| | | **1L21** | IgG1 | κ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 5 | 7 | 1 | 1 |
| | | **1M6.2** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | 8.2 | >10 | >10 | 4 | 3 | **29** | 1 |
| | | **1H7.2** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 11 | 9 | **30** | 4 |
| | | **2E14** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | **31** | 13 | 10 | 4 |

Immunoglobulin isotype, subtype and light chain utilization where determined by ELISA. Binding to each DENV serotype and recombinant E and prM protein constructs are shown. The concentration ($\mu$g/mL) at which 50% of virus was neutralized ($neut_{50}$) is shown for each dengue serotype: a dash indicates $neut_{50}$ value > 10 $\mu$g/mL, $neut_{50}$ values between 1.0-10.0 $\mu$g/mL are shown, $neut_{50}$ values < 0.5 $\mu$g/mL are bold. ADE assays were performed for each human antibody (at a concentration of 1 $\mu$g/mL) against each dengue serotype and shown as fold enhancement: > 25 fold enhancement values are bold.

**Supplemental Table 1. Genetic and functional characteristics of human mAbs (continued)**

| Type of infection | Subject # | mAb | IgG subclass | λ or κ | Binding to whole virus in ELISA, for indicated serotype at 1 μg/mL | | | | Binding to rE-protein (ELISA) | Binding to rE-protein DIII fragment (ELISA) | Binding to rE-protein DI/II fragment (ELISA) | Binding to rPr-protein (ELISA) | 50% neutralization concentration (μg/mL), against indicated serotype | | | | Fold enhancement of infection, for indicated serotype at 1 μg/mL | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | D1 | D2 | D3 | D4 | | | | | D1 | D2 | D3 | D4 | D1 | D2 | D3 | D4 |
| 1° DENV1 | 106 | **1K16.2** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 8 | **35** | 19 | 3 |
| | | **1K4.2** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 5 | 15 | 6 | 2 |
| | | **2H21** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 21 | 4 | 18 | 4 |
| | | **2B17** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 3 | 3 | 4 | 3 |
| | | **2G3** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 22 | 4 | **47** | 8 |
| | | **2J9** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 9 | 8 | **25** | 11 |
| | | **1G19** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 4 | 10 | 4 | 2 |
| | | **1N21** | IgG1 | κ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 10 | 7 | **44** | 2 |
| | | **1I13.2** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 8 | 15 | 16 | 8 |
| | | **1D8** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 5 | 9 | 8 | 6 |
| | | **1A17** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | **118** | **60** | **47** | 4 |
| | | **1D6** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 3 | 6 | 4 | 4 |
| | | **1N6** | IgG1 | κ | + | - | - | - | + | + | - | - | >10 | >10 | >10 | >10 | 5 | 0 | 1 | 1 |
| | | **2M23** | IgG1 | λ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 15 | 5 | **34** | 4 |
| | | **2I11** | IgG1 | λ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 24 | 6 | **26** | 5 |
| | | **2J21** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 18 | 7 | **28** | 1 |
| | | **2I21** | IgG1 | λ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 14 | 7 | 4 | 1 |
| | | **2E19** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 1 | 3 | 2 | 2 |
| | | **2I23** | IgG3 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 5 | 1 | 1 | 1 |
| | | **2O19** | IgG1 | λ | + | + | + | + | + | + | - | - | >10 | >10 | >10 | >10 | 2 | 2 | 2 | 1 |
| | | **2J23** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | **25** | 6 | 7 | 3 |
| | | **2B20** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 19 | 5 | 0 | 1 |
| | | **2D22.2** | IgG1 | **λ** | + | + | + | + | + | - | + | **-** | >10 | >10 | >10 | >10 | 10 | 6 | 1 | 2 |
| | GL10 | **2F17.2** | IgG1 | λ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 2 | 3 | 2 | 1 |
| | | **1H16.2** | IgG1 | κ | + | + | + | - | - | - | - | + | >10 | >10 | >10 | >10 | 1 | 5 | 3 | 2 |
| | | **1M4** | IgG1 | κ | + | + | + | + | + | - | + | - | 0.56 | **0.27** | 5.4 | 2.3 | 6 | 1 | **56** | 1 |
| | | **1I3.2** | IgG1 | κ | + | + | + | + | + | - | + | - | >10 | >10 | >10 | >10 | 9 | 5 | 18 | 8 |
| | | **2H2** | IgG1 | κ | + | + | + | + | - | - | - | + | >10 | >10 | >10 | >10 | 6 | 9 | 15 | 1 |
| | GL24 | **2G19** | IgG2 | λ | + | + | + | - | - | - | - | + | >10 | >10 | >10 | >10 | 14 | 13 | **53** | 7 |

Immunoglobulin isotype, subtype and light chain utilization where determined by ELISA. Binding to each DENV serotype and recombinant E and prM protein constructs are shown. The concentration ($\mu$g/mL) at which 50% of virus was neutralized ($neut_{50}$) is shown for each dengue serotype: a dash indicates $neut_{50}$ value > 10 $\mu$g/mL, $neut_{50}$ values between 1.0-10.0 $\mu$g/mL are shown, $neut_{50}$ values < 0.5 $\mu$g/mL are bold. ADE assays were performed for each human antibody (at a concentration of 1 $\mu$g/mL) against each dengue serotype and shown as fold enhancement: > 25 fold enhancement values are bold.

## SUPPLEMENTAL MATERIALS AND METHODS

### Recombinant DENV Proteins

Recombinant proteins representing fragments of E or prM-protein were used to determine antigens and domains recognized by human monoclonal antibodies. Recombinant DENV proteins were constructed using sequences of the above strains. Sequence optimization, gene synthesis and molecular cloning of all recombinant DENV protein constructs for expression in baculovirus was performed by GenScript USA Inc. The amino acid residues for E-protein constructs (rE) were as follows: DENV1 E80% (1-397), DENV2 E80% (1-397), DENV3 E80% (1-395), DENV4 E80% (1-397); DENV1 EI/II (1-291), DENV2 EI/II (1-291), DENV3 EI/II (1-289), DENV4 EI/II (1-291); DENV1 EIII (290-332), DENV2 EIII (290-332), DENV3 EIII (290-332), DENV4 EIII (290-332). The amino acid residues for full-length prM-protein constructs were as follows: DENV1 prM (1-166), DENV2 prM (1-166), DENV3 prM (1-166), DENV4 prM (1-166). The amino acid residues representing the soluble furin-cleaved portion of the prM-protein (rPr) were as follows: DENV1 pr (1-86), DENV2 pr (1-86), DENV3 pr (1-86), DENV4 pr (1-86). Recombinant E and prM-proteins were designed to include a StrepII tag at their C-terminal end to aid in purification and use in capture ELISA. Recombinant prM-proteins were constructed to include a glutathione *S*-transferase (GST) tag at their N-terminal end to aid with purification and solubility. Recombinant protein-containing supernatant used in capture ELISA was prepared in Sf21 insect cells grown in Grace's insect medium (GIBCO, 11605-094). Briefly, cells were grown in 150 $cm^2$ flasks (Corning, 431082) until 80% confluent prior to inoculating with baculovirus at an MOI of 1. After 5 days of incubation, cell supernatant containing recombinant DENV protein was harvested by centrifugation and frozen for later use.