**Table S1. Expression yields and purification summary for all 15 antibodies**

| Samples | Targets | Total expression amount (mg/L) | Concentration (mg/mL) |
|---|---|---|---|
| 4A7 $Fc_{WT}$ | Claudin 18.2 | 118.6 | 3.56 |
| 4A7 $Fc_{3A}$ | | 240.0 | 11.24 |
| 4A7 $Fc_{95}$ | | 962.2 | 7.76 |
| GAZY $Fc_{WT}$ | CD20 | 396.3 | 3.17 |
| GAZY $Fc_{3A}$ | | 368.0 | 3.20 |
| GAZY $Fc_{95}$ | | 334.7 | 2.91 |
| MARV $Fc_{WT}$ | Marburg G Protein | 438.8 | 3.10 |
| MARV $Fc_{3A}$ | | 363.0 | 3.51 |
| MARV $Fc_{95}$ | | 353.4 | 3.30 |
| 13H8 $Fc_{WT}$ | Influenza hemagglutinin stem (H1N1) | 438.6 | 2.46 |
| 13H8 $Fc_{3A}$ | | 527.6 | 3.38 |
| 13H8 $Fc_{95}$ | | 475.9 | 2.95 |
| FD164 $Fc_{WT}$ | CD47 | 624.1 | 4.09 |
| FD164 $Fc_{3A}$ | | 742.3 | 4.03 |
| FD164 $Fc_{95}$ | | 679.0 | 4.56 |

**Table S2**

| KD for FcγR of Fc variants | | | | | | |
|---|---|---|---|---|---|---|
| Fc variants | $K_D$ for FcγRIIIa$^{158V}$ (mol/L) | $K_D$ for FcγRIIIa$^{158F}$ (mol/L) | $K_D$ for FcγRIIa (mol/L) | $K_D$ for FcγRIIb (mol/L) | $K_D$ for FcγRI (mol/L) | $K_D$ for hFcRn (mol/L) |
| 4A7 $Fc_{WT}$ | 7.890E-08 | 1.763E-07 | 1.926E-09 | 3.907E-06 | 4.398E-11 | 2.3E-08 |
| 4A7 $Fc_{3A}$ | 1.202E-08 | 1.122E-07 | 5.558E-09 | 2.719E-06 | 3.960E-11 | 2.3E-08 |
| 4A7 $Fc_{95}$ | 2.692E-09 | 7.762E-09 | 3.991E-09 | 3.676E-06 | 1.000E-12 | 2.5E-08 |
| GAZY $Fc_{WT}$ | 6.164E-08 | 1.441E-07 | 7.065E-07 | 2.200E-06 | 1.444E-10 | 2.3E-08 |
| GAZY $Fc_{3A}$ | 1.172E-08 | 3.852E-08 | 1.087E-06 | 2.493E-06 | 1.498E-10 | 1.5E-08 |
| GAZY $Fc_{95}$ | 1.254E-09 | 2.723E-09 | 5.636E-07 | 1.314E-06 | 8.569E-11 | 1.4E-08 |
| MARV $Fc_{WT}$ | 7.915E-08 | 6.122E-08 | 1.956E-07 | 9.681E-07 | 3.771E-11 | 2.0E-08 |
| MARV $Fc_{3A}$ | 6.737E-09 | 1.632E-08 | 1.745E-07 | 1.286E-06 | 5.204E-11 | 1.6E-08 |
| MARV $Fc_{95}$ | 7.572E-10 | 2.009E-09 | 8.651E-08 | 5.674E-06 | 9.080E-12 | 2.2E-08 |
| 13H8 $Fc_{WT}$ | 6.547E-07 | 1.145E-06 | 2.828E-07 | 6.285E-07 | 7.622E-10 | 6.6E-08 |
| 13H8 $Fc_{3A}$ | 1.347E-08 | 1.359E-08 | 7.041E-07 | 3.985E-07 | 5.512E-10 | 1.4E-07 |
| 13H8 $Fc_{95}$ | 3.700E-09 | 6.009E-09 | 3.928E-07 | 1.526E-07 | 3.718E-10 | 2.3E-07 |
| FD164 $Fc_{WT}$ | 1.838E-08 | 1.525E-08 | 9.992E-07 | 1.581E-06 | 1.056E-09 | 1.4E-06 |
| FD164 $Fc_{3A}$ | 1.064E-08 | 1.024E-08 | 5.524E-05 | 1.336E-06 | 1.004E-09 | 2.9E-06 |
| FD164 $Fc_{95}$ | 2.256E-09 | 4.052E-09 | 1.279E-06 | 5.377E-06 | 9.153E-10 | 3.0E-06 |
| Gazyva | 8.146E-09 | 7.536E-09 | 4.668E-07 | 9.606E-07 | 5.771E-10 | 1.5E-07 |
| MARV $Fc_{LZ01}$ | 1.395E-08 | 4.817E-08 | 8.017E-08 | 2.688E-06 | 2.039E-10 | 1.5E-08 |

**Table S3. Quantitative histopathological scores of organ lesions.**

Tissues (liver, spleen, kidney) were collected from mice at the study endpoint (as described in Figure 8D), fixed in 10% neutral buffered formalin, and embedded in paraffin. Sections were stained with Hematoxylin and Eosin (H&E) for histopathological evaluation. A board-certified pathologist, who was blinded to the experimental groups, performed the scoring.

**Scoring Criteria:**

| **Score** | **Grade** | **Pathological Description** | **Tissue Area Affected** |
|---|---|---|---|
| 0 | Normal | No observable pathological changes. | N/A |
| 1 | Minimal (+) | Focal and minimal inflammatory cell infiltration. | <5% |
| 2 | Mild (++) | Multifocal inflammation and occasional necrosis. | 5−25% |
| 3 | Moderate (+++) | Diffuse, significant inflammatory damage with noticeable necrosis. | 25−50% |
| 4 | Severe (++++) | Extensive damage with confluent necrosis or architectural distortion. | >50% |

**Table Content:** The table displays the individual scores for each animal (n=3 per group).

| Liver | | | |
|---|---|---|---|
| | Pathological changes | | |
| Samples | Hepatocyte edema | Inflammatory cell infiltration | Congestion |
| PBS | + | - | - |
| GAZY $Fc_{WT}$ | ++ | - | +++ |
| GAZY $Fc_{3A}$ | ++ | - | ++ |
| GAZY $Fc_{95}$ | ++ | - | + |

| Spleen | | |
|---|---|---|
| | Pathological changes | |
| Samples | Inflammatory cell infiltration | Congestion |
| PBS | + | - |
| GAZY $Fc_{WT}$ | ++ | - |
| GAZY $Fc_{3A}$ | +++ | + |
| GAZY $Fc_{95}$ | ++ | - |

| **Kidney** | | | |
|---|---|---|---|
| | Pathological changes | | |
| Samples | Inflammatory cell infiltration | Renal tubular atrophy | Congestion |
| PBS | - | - | - |
| GAZY $Fc_{WT}$ | + | - | - |
| GAZY $Fc_{3A}$ | + | + | - |
| GAZY $Fc_{95}$ | - | - | - |

**Table S4 Quantitative analysis of N-glycan species for Fc-engineered constructs.**

| Antibody variants | Core fucose (%) | Terminal galactose (%) | High mannose (%) | Total sialic acid (%) |
|---|---|---|---|---|
| $Fc_{WT}$ | 85.47 | 20.36 | 7.18 | 0.63 |
| $Fc_{3A}$ | 64.53 | 8.19 | 15.52 | 0.28 |
| $Fc_{95}$ | 13.85 | 9.61 | 81.2 | 0.69 |
| Gazyva | 41.3 | 30.33 | 4.75 | 0.7 |
| MARV $Fc_{LZ01}$ | 3.78 | 5.03 | 3.48 | 0.35 |
| $Fc_{3A+S239D}$ | 77.13 | 10.48 | 10.58 | 0.35 |
| $Fc_{3A+F243L}$ | 18.52 | 10.66 | 75.11 | 0.87 |
| $Fc_{3A+R292A}$ | 39.2 | 11.64 | 49.43 | 0.56 |
| $Fc_{3A+Y300L}$ | 70.4 | 8.73 | 17.18 | 0.37 |

**Note on Fc variants:** $Fc_{WT}$ and $Fc_{3A}$ are fully fucosylated IgG1 (produced in standard CHO-S cells). Gazyva and MARV $Fc_{LZ01}$ serve as afucosylated benchmarks (produced in FUT8-KO CHO-S cells). $Fc_{95}$ is a sequence-engineered variant with an intrinsically low-fucose profile (~13.85%).