

SUMMARY

[0005] Provided herein are novel CLDN6 binding domains, and anti-CLDN6 x anti-CD3 antibodies that include such CLDN6 binding domains. Also provided herein are methods of using such antibodies for the treatment of CLDN6-associated cancers.

[0006] In a first aspect, provided herein is a construct that binds CLDN6 comprising a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain (VH)/variable light domain (VL) pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221 and SEQ ID NO: 321), H1.7_L1.4 (SEQ ID NO: 225 and SEQ ID NO: 321), H1.8_L1.4 (SEQ ID NO: 229 and SEQ ID NO: 321), H1.9_L1.4 (SEQ ID NO: 233 and SEQ ID NO: 321), H1.19_L1.4 (SEQ ID NO: 237 and SEQ ID NO: 321), H1.22_L1.4 (SEQ ID NO: 241 and SEQ ID NO: 321), H1.24_L1.4 (SEQ ID NO: 245 and SEQ ID NO: 321).

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H1.2_L1.187 (SEQ ID NO: 205 and SEQ ID NO: 369), H1.3_L1.187 (SEQ ID NO: 209 and SEQ ID NO: 369), H1.4_L1.187 (SEQ ID NO: 213 and SEQ ID NO: 369), H1.5_L1.187 (SEQ ID NO: 217 and SEQ ID NO: 369), H1.6_L1.187 (SEQ ID NO: 221 and SEQ ID NO: 369), H1.7_L1.187 (SEQ ID NO: 225 and SEQ ID NO: 369), H1.8_L1.187 (SEQ ID NO: 229 and SEQ ID NO: 369), H1.19_L1.187 (SEQ ID NO: 237 and SEQ ID NO: 369), H1.22_L1.187 (SEQ ID NO: 241 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), H2_L1.187 (SEQ ID NO: 189 and SEQ ID NO: 369), H2.1_L1.187 (SEQ ID NO: 249 and SEQ ID NO: 369), H2.2_L1.187 (SEQ ID NO: 253 and SEQ ID NO: 369), H2.3_L1.187 (SEQ ID NO: 257 and SEQ ID NO: 369), H2.4_L1.187 (SEQ ID NO: 261 and SEQ ID NO: 369), H2.5_L1.187 (SEQ ID NO: 265 and SEQ ID NO: 369), H2.6_L1.187 (SEQ ID NO: 269 and SEQ ID NO: 369), H2.7_L1.187 (SEQ ID NO: 273 and SEQ ID NO: 369), H2.8_L1.187 (SEQ ID NO: 277 and SEQ ID NO: 369), H2.9_L1.187 (SEQ ID NO: 281 and SEQ ID NO: 369), H2.11_L1.187 (SEQ ID NO: 285 and SEQ ID NO: 369), H2.12_L1.187 (SEQ ID NO: 289 and SEQ ID NO: 369), H2.71_L1.187 (SEQ ID NO: 293 and SEQ ID NO: 369), H2.75_L1.187 (SEQ ID NO: 297 and SEQ ID NO: 369), H2.90_L1.187 (SEQ ID NO: 301 and SEQ ID NO: 369), H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369), H2.118_L1.187 (SEQ ID NO: 309 and SEQ ID NO: 369), H2.119_L1.187 (SEQ ID NO: 313 and SEQ ID NO: 369), H1_L1.189 (SEQ ID NO: 185 and SEQ ID NO: 373), H1.1_L1.189 (SEQ ID NO: 201 and SEQ ID NO: 373), H1.2_L1.189 (SEQ ID NO: 205 and SEQ ID NO: 373), H1.3_L1.189 (SEQ ID NO: 209 and SEQ ID NO: 373), H1.4_L1.189 (SEQ ID NO: 213 and SEQ ID NO: 373), H1.5_L1.189 (SEQ ID NO: 217 and SEQ ID NO: 373), H1.6_L1.189 (SEQ ID NO: 221 and SEQ ID NO: 373), H1.7_L1.189 (SEQ ID NO: 225 and SEQ ID NO: 373), H1.8_L1.189 (SEQ ID NO: 229 and SEQ ID NO: 373), H1.9_L1.189 (SEQ ID NO: 233 and SEQ ID NO: 373), H1.19_L1.189 (SEQ ID NO: 237 and SEQ ID NO: 373), H1.22_L1.189 (SEQ ID NO: 241 and SEQ ID NO: 373), H1.24_L1.189 (SEQ ID NO: 245 and SEQ ID NO: 373), H2_L1.189 (SEQ ID NO: 189 and SEQ ID NO: 373), H2.1_L1.189 (SEQ ID NO: 249 and SEQ ID NO: 373), H2.2_L1.189 (SEQ ID NO: 253 and SEQ ID NO: 373), H2.3_L1.189 (SEQ ID NO: 257 and SEQ ID NO: 373), H2.4_L1.189 (SEQ ID NO: 261 and SEQ ID NO: 373), H2.5_L1.189 (SEQ ID NO: 265 and SEQ ID NO: 373), H2.6_L1.189 (SEQ ID NO: 269 and SEQ ID NO: 373), H2.7_L1.189 (SEQ ID NO: 273 and SEQ ID NO: 373), H2.8_L1.189 (SEQ ID NO: 277 and SEQ ID NO: 373), H2.9_L1.189 (SEQ ID NO: 281 and SEQ ID NO: 373), H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

In one example, provided herein are compositions comprising a CLDN6 antigen binding domain. In some examples, the CLDN6 antigen binding domain comprises a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain (VH)/variable light domain (VL) pair selected from the group consisting: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1, H1.24_L1.1, H2_L1.1, H2.1_L1.1, H2.2_L1.1, H2.3_L1.1, H2.4_L1.1, H2.5_L1.1, H2.6_L1.1, H2.7_L1.1, H2.8_L1.1, H2.9_L1.1, H2.11_L1.1, H2.12_L1.1, H2.71_L1.1, H2.75_L1.1, H2.90_L1.1, H2.91_L1.1, H2.118_L1.1, H2.119_L1.1, H1_L1.4, H1.1_L1.4, H1.2_L1.4, H1.3_L1.4, H1.4_L1.4, H1.5_L1.4, H1.6_L1.4, H1.7_L1.4, H1.8_L1.4, H1.9_L1.4, H1.19_L1.4, H1.22_L1.4, H1.24_L1.4, H2_L1.4, H2.1_L1.4, H2.2_L1.4, H2.3_L1.4, H2.4_L1.4, H2.5_L1.4, H2.6_L1.4, H2.7_L1.4, H2.8_L1.4, H2.9_L1.4, H2.11_L1.4, H2.12_L1.4, H2.71_L1.4, H2.75_L1.4, H2.90_L1.4, H2.91_L1.4, H2.118_L1.4, H2.119_L1.4, H1_L1.7, H1.1_L1.7, H1.2_L1.7, H1.3_L1.7, H1.4_L1.7, H1.5_L1.7, H1.6_L1.7, H1.7_L1.7, H1.8_L1.7, H1.9_L1.7, H1.19_L1.7, H1.22_L1.7, H1.24_L1.7, H2_L1.7, H2.1_L1.7, H2.2_L1.7, H2.3_L1.7, H2.4_L1.7, H2.5_L1.7, H2.6_L1.7, H2.7_L1.7, H2.8_L1.7, H2.9_L1.7, H2.11_L1.7, H2.12_L1.7, H2.71_L1.7, H2.75_L1.7, H2.90_L1.7, H2.91_L1.7, H2.118_L1.7, H2.119_L1.7, H1_L1.16, H1.1_L1.16, H1.2_L1.16, H1.3_L1.16, H1.4_L1.16, H1.5_L1.16, H1.6_L1.16, H1.7_L1.16, H1.8_L1.16, H1.9_L1.16, H1.19_L1.16, H1.22_L1.16, H1.24_L1.16, H2_L1.16, H2.1_L1.16, H2.2_L1.16, H2.3_L1.16, H2.4_L1.16, H2.5_L1.16, H2.6_L1.16, H2.7_L1.16, H2.8_L1.16, H2.9_L1.16, H2.11_L1.16, H2.12_L1.16, H2.71_L1.16, H2.75_L1.16, H2.90_L1.16, H2.91_L1.16, H2.118_L1.16, H2.119_L1.16, H1_L1.18, H1.1_L1.18, H1.2_L1.18, H1.3_L1.18, H1.4_L1.18, H1.5_L1.18, H1.6_L1.18, H1.7_L1.18, H1.8_L1.18, H1.9_L1.18, H1.19_L1.18, H1.22_L1.18, H1.24_L1.18, H2_L1.18, H2.1_L1.18, H2.2_L1.18, H2.3_L1.18, H2.4_L1.18, H2.5_L1.18,

H2.4_L1.107, H2.5_L1.107, H2.6_L1.107, H2.7_L1.107, H2.8_L1.107, H2.9_L1.107, H2.11_L1.107, H2.12_L1.107, H2.71_L1.107, H2.75_L1.107, H2.90_L1.107, H2.91_L1.107, H2.118_L1.107, H2.119_L1.107, H1_L1.114, H1.1_L1.114, H1.2_L1.114, H1.3_L1.114, H1.4_L1.114, H1.5_L1.114, H1.6_L1.114, H1.7_L1.114, H1.8_L1.114, H1.9_L1.114, H1.19_L1.114, H1.22_L1.114, H1.24_L1.114, H2_L1.114, H2.1_L1.114, H2.2_L1.114, H2.3_L1.114, H2.4_L1.114, H2.5_L1.114, H2.6_L1.114, H2.7_L1.114, H2.8_L1.114, H2.9_L1.114, H2.11_L1.114, H2.12_L1.114, H2.71_L1.114, H2.75_L1.114, H2.90_L1.114, H2.91_L1.114, H2.118_L1.114, H2.119_L1.114, H1_L1.187, H1.1_L1.187, H1.2_L1.187, H1.3_L1.187, H1.4_L1.187, H1.5_L1.187, H1.6_L1.187, H1.7_L1.187, H1.8_L1.187, H1.9_L1.187, H1.19_L1.187, H1.22_L1.187, H1.24_L1.187, H2_L1.187, H2.1_L1.187, H2.2_L1.187, H2.3_L1.187, H2.4_L1.187, H2.5_L1.187, H2.6_L1.187, H2.7_L1.187, H2.8_L1.187, H2.9_L1.187, H2.11_L1.187, H2.12_L1.187, H2.71_L1.187, H2.75_L1.187, H2.90_L1.187, H2.91_L1.187, H2.118_L1.187, H2.119_L1.187, H1_L1.189, H1.1_L1.189, H1.2_L1.189, H1.3_L1.189, H1.4_L1.189, H1.5_L1.189, H1.6_L1.189, H1.7_L1.189, H1.8_L1.189, H1.9_L1.189, H1.19_L1.189, H1.22_L1.189, H1.24_L1.189, H2_L1.189, H2.1_L1.189, H2.2_L1.189, H2.3_L1.189, H2.4_L1.189, H2.5_L1.189, H2.6_L1.189, H2.7_L1.189, H2.8_L1.189, H2.9_L1.189, H2.11_L1.189, H2.12_L1.189, H2.71_L1.189, H2.75_L1.189, H2.90_L1.189, H2.91_L1.189, H2.118_L1.189, H2.119_L1.189, H1_L2, H1.1_L2, H1.2_L2, H1.3_L2, H1.4_L2, H1.5_L2, H1.6_L2, H1.7_L2, H1.8_L2, H1.9_L2, H1.19_L2, H1.22_L2, H1.24_L2, H2_L2, H2.1_L2, H2.2_L2, H2.3_L2, H2.4_L2, H2.5_L2, H2.6_L2, H2.7_L2, H2.8_L2, H2.9_L2, H2.11_L2, H2.12_L2, H2.71_L2, H2.75_L2, H2.90_L2, H2.91_L2, H2.118_L2 and H2.119_L2.

[0007] In some examples, the CLDN6 antigen binding domain comprises a VH/VL pair selected from the group consisting of: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1, H1.24_L1.1, H2_L1.1, H2.1_L1.1, H2.2_L1.1, H2.3_L1.1, H2.4_L1.1, H2.5_L1.1, H2.6_L1.1, H2.7_L1.1, H2.8_L1.1, H2.9_L1.1, H2.11_L1.1, H2.12_L1.1, H2.71_L1.1, H2.75_L1.1, H2.90_L1.1, H2.91_L1.1, H2.118_L1.1, H2.119_L1.1, H1_L1.4, H1.1_L1.4, H1.2_L1.4, H1.3_L1.4, H1.4_L1.4, H1.5_L1.4, H1.6_L1.4, H1.7_L1.4, H1.8_L1.4, H1.9_L1.4,

H1.6_L2, H1.7_L2, H1.8_L2, H1.9_L2, H1.19_L2, H1.22_L2, H1.24_L2, H2_L2, H2.1_L2, H2.2_L2, H2.3_L2, H2.4_L2, H2.5_L2, H2.6_L2, H2.7_L2, H2.8_L2, H2.9_L2, H2.11_L2, H2.12_L2, H2.71_L2, H2.75_L2, H2.90_L2, H2.91_L2, H2.118_L2 and H2.119_L2.

[0008] 3. In some examples, the VH/VL pair is selected from the group consisting of H1.9_L1.187, H1.24_L1.187, H2.91_L1.187 and H1.9_L1.187.

[0009] In some examples, the composition is a monoclonal antibody.

[0010] In another aspect, provided herein is a heterodimeric antibody comprising: a) a first monomer comprising: i) an anti-CD3 scFv comprising a first variable light domain, an scFv linker and a first variable heavy domain; and ii) a first Fc domain, wherein the scFv is covalently attached to the N-terminus of the first Fc domain using a domain linker; b) a second monomer comprising a VH2-CH1-hinge-CH2-CH3 monomer, wherein VH is a second variable heavy domain and CH2-CH3 is a second Fc domain; and c) a light chain comprising a second variable light domain, wherein the second variable heavy domain and the second variable light domain form a CLDN6 antigen binding domain (ABD), wherein the CLDN6 antigen binding domain comprises a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain/variable light domain pair selected from the group consisting of:

H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317),

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[illegible]

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H2.2_L1.114 (SEQ ID NO: 253 and SEQ ID NO: 365), H2.3_L1.114 (SEQ ID NO: 257 and SEQ ID NO: 365), H2.4_L1.114 (SEQ ID NO: 261 and SEQ ID NO: 365), H2.5_L1.114 (SEQ ID NO: 265 and SEQ ID NO: 365), H2.6_L1.114 (SEQ ID NO: 269 and SEQ ID NO: 365), H2.7_L1.114 (SEQ ID NO: 273 and SEQ ID NO: 365), H2.8_L1.114 (SEQ ID NO: 277 and SEQ ID NO: 365), H2.9_L1.114 (SEQ ID NO: 281 and SEQ ID NO: 365), H2.11_L1.114 (SEQ ID NO: 285 and SEQ ID NO: 365), H2.12_L1.114 (SEQ ID NO: 289 and SEQ ID NO: 365), H2.71_L1.114 (SEQ ID NO: 293 and SEQ ID NO: 365), H2.75_L1.114 (SEQ ID NO: 297 and SEQ ID NO: 365), H2.90_L1.114 (SEQ ID NO: 301 and SEQ ID NO: 365), H2.91_L1.114 (SEQ ID NO: 305 and SEQ ID NO: 365), H2.118_L1.114 (SEQ ID NO: 309 and SEQ ID NO: 365), H2.119_L1.114 (SEQ ID NO: 313 and SEQ ID NO: 365), H1_L1.187 (SEQ ID NO: 185 and SEQ ID NO: 369), H1.1_L1.187 (SEQ ID NO: 201 and SEQ ID NO: 369), H1.2_L1.187 (SEQ ID NO: 205 and SEQ ID NO: 369), H1.3_L1.187 (SEQ ID NO: 209 and SEQ ID NO: 369), H1.4_L1.187 (SEQ ID NO: 213 and SEQ ID NO: 369), H1.5_L1.187 (SEQ ID NO: 217 and SEQ ID NO: 369), H1.6_L1.187 (SEQ ID NO: 221 and SEQ ID NO: 369), H1.7_L1.187 (SEQ ID NO: 225 and SEQ ID NO: 369), H1.8_L1.187 (SEQ ID NO: 229 and SEQ ID NO: 369), H1.19_L1.187 (SEQ ID NO: 237 and SEQ ID NO: 369), H1.22_L1.187 (SEQ ID NO: 241 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), H2_L1.187 (SEQ ID NO: 189 and SEQ ID NO: 369), H2.1_L1.187 (SEQ ID NO: 249 and SEQ ID NO: 369), H2.2_L1.187 (SEQ ID NO: 253 and SEQ ID NO: 369), H2.3_L1.187 (SEQ ID NO: 257 and SEQ ID NO: 369), H2.4_L1.187 (SEQ ID NO: 261 and SEQ ID NO: 369), H2.5_L1.187 (SEQ ID NO: 265 and SEQ ID NO: 369), H2.6_L1.187 (SEQ ID NO: 269 and SEQ ID NO: 369), H2.7_L1.187 (SEQ ID NO: 273 and SEQ ID NO: 369), H2.8_L1.187 (SEQ ID NO: 277 and SEQ ID NO: 369), H2.9_L1.187 (SEQ ID NO: 281 and SEQ ID NO: 369), H2.11_L1.187 (SEQ ID NO: 285 and SEQ ID NO: 369), H2.12_L1.187 (SEQ ID NO: 289 and SEQ ID NO: 369), H2.71_L1.187 (SEQ ID NO: 293 and SEQ ID NO: 369), H2.75_L1.187 (SEQ ID NO: 297 and SEQ ID NO: 369), H2.90_L1.187 (SEQ ID NO: 301 and SEQ ID NO: 369), H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369), H2.118_L1.187 (SEQ ID NO: 309 and SEQ ID NO: 369), H2.119_L1.187 (SEQ ID NO: 313 and SEQ ID NO: 369), H1_L1.189 (SEQ ID NO: 185 and SEQ ID NO: 373), H1.1_L1.189 (SEQ ID NO: 201 and SEQ ID NO: 373), H1.2_L1.189 (SEQ ID NO: 205 and SEQ ID NO: 373), H1.3_L1.189 (SEQ ID NO: 209 and SEQ ID NO: 373), H1.4_L1.189 (SEQ ID NO: 213 and SEQ ID NO: 373), H1.5_L1.189 (SEQ ID NO: 217 and SEQ ID NO: 373), H1.6_L1.189 (SEQ ID NO: 221 and SEQ ID NO: 373), H1.7_L1.189 (SEQ ID NO: 225 and SEQ ID NO: 373), H1.8_L1.189 (SEQ ID NO: 229 and SEQ ID NO: 373), H1.9_L1.189 (SEQ ID NO: 233 and SEQ ID NO: 373), H1.19_L1.189 (SEQ ID NO: 237 and SEQ ID NO: 373), H1.22_L1.189 (SEQ ID NO: 241 and SEQ ID NO: 373), H1.24_L1.189 (SEQ ID NO: 245 and SEQ ID NO: 373), H2_L1.189 (SEQ ID NO: 189 and SEQ ID NO: 373), H2.1_L1.189 (SEQ ID NO: 249 and SEQ ID NO: 373), H2.2_L1.189 (SEQ ID NO: 253 and SEQ ID NO: 373), H2.3_L1.189 (SEQ ID NO: 257 and SEQ ID NO: 373), H2.4_L1.189 (SEQ ID NO: 261 and SEQ ID NO: 373), H2.5_L1.189 (SEQ ID NO: 265 and SEQ ID NO: 373), H2.6_L1.189 (SEQ ID NO: 269 and SEQ ID NO: 373), H2.7_L1.189 (SEQ ID NO: 273 and SEQ ID NO: 373), H2.8_L1.189 (SEQ ID NO: 277 and SEQ ID NO: 373), H2.9_L1.189 (SEQ ID NO: 281 and SEQ ID NO: 373), H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197),

H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197). In one example, provided herein is a heterodimeric antibody comprising: a) a first monomer, b) a second monomer, and c) a light chain. The first monomer comprises: i) an anti-CD3 scFv comprising a first variable light domain, an scFv linker and a first variable heavy domain; and ii) a first Fc domain, wherein the scFv is covalently attached to the N-terminus of the first Fc domain using a domain linker. The second monomer comprises a VH2-CH1-hinge-CH2-CH3 monomer, wherein VH is a second variable heavy domain and CH2-CH3 is a second Fc domain. The light chain comprises a second variable light domain. In this example, the second variable heavy domain and the second variable light domain form a CLDN6 antigen binding domain (ABD).

[0011] In some examples, the CLDN6 binding domain comprises a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain/variable light domain pair selected from the group consisting of: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1, H1.24_L1.1, H2_L1.1, H2.1_L1.1, H2.2_L1.1, H2.3_L1.1, H2.4_L1.1, H2.5_L1.1, H2.6_L1.1, H2.7_L1.1, H2.8_L1.1, H2.9_L1.1, H2.11_L1.1, H2.12_L1.1, H2.71_L1.1, H2.75_L1.1, H2.90_L1.1, H2.91_L1.1, H2.118_L1.1, H2.119_L1.1, H1_L1.4, H1.1_L1.4, H1.2_L1.4, H1.3_L1.4, H1.4_L1.4, H1.5_L1.4, H1.6_L1.4, H1.7_L1.4, H1.8_L1.4, H1.9_L1.4, H1.19_L1.4, H1.22_L1.4, H1.24_L1.4, H2_L1.4, H2.1_L1.4, H2.2_L1.4, H2.3_L1.4, H2.4_L1.4, H2.5_L1.4, H2.6_L1.4, H2.7_L1.4, H2.8_L1.4, H2.9_L1.4, H2.11_L1.4, H2.12_L1.4, H2.71_L1.4, H2.75_L1.4, H2.90_L1.4, H2.91_L1.4, H2.118_L1.4, H2.119_L1.4, H1_L1.7, H1.1_L1.7, H1.2_L1.7, H1.3_L1.7, H1.4_L1.7, H1.5_L1.7, H1.6_L1.7, H1.7_L1.7, H1.8_L1.7, H1.9_L1.7, H1.19_L1.7, H1.22_L1.7,

[0012] In some examples, the CLDN6 binding domain comprises a VH/VL pair selected from the group consisting of: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1, H1.24_L1.1, H2_L1.1, H2.1_L1.1, H2.2_L1.1, H2.3_L1.1, H2.4_L1.1, H2.5_L1.1, H2.6_L1.1, H2.7_L1.1, H2.8_L1.1, H2.9_L1.1, H2.11_L1.1, H2.12_L1.1, H2.71_L1.1, H2.75_L1.1, H2.90_L1.1, H2.91_L1.1, H2.118_L1.1, H2.119_L1.1, H1_L1.4, H1.1_L1.4, H1.2_L1.4, H1.3_L1.4, H1.4_L1.4, H1.5_L1.4, H1.6_L1.4, H1.7_L1.4, H1.8_L1.4, H1.9_L1.4, H1.19_L1.4, H1.22_L1.4, H1.24_L1.4, H2_L1.4, H2.1_L1.4, H2.2_L1.4, H2.3_L1.4, H2.4_L1.4, H2.5_L1.4, H2.6_L1.4, H2.7_L1.4, H2.8_L1.4, H2.9_L1.4, H2.11_L1.4, H2.12_L1.4, H2.71_L1.4, H2.75_L1.4, H2.90_L1.4, H2.91_L1.4, H2.118_L1.4, H2.119_L1.4, H1_L1.7, H1.1_L1.7, H1.2_L1.7, H1.3_L1.7, H1.4_L1.7, H1.5_L1.7, H1.6_L1.7, H1.7_L1.7, H1.8_L1.7, H1.9_L1.7, H1.19_L1.7, H1.22_L1.7, H1.24_L1.7, H2_L1.7, H2.1_L1.7, H2.2_L1.7, H2.3_L1.7, H2.4_L1.7, H2.5_L1.7, H2.6_L1.7, H2.7_L1.7, H2.8_L1.7, H2.9_L1.7, H2.11_L1.7, H2.12_L1.7, H2.71_L1.7, H2.75_L1.7, H2.90_L1.7, H2.91_L1.7, H2.118_L1.7, H2.119_L1.7, H1_L1.16, H1.1_L1.16, H1.2_L1.16, H1.3_L1.16, H1.4_L1.16, H1.5_L1.16, H1.6_L1.16, H1.7_L1.16, H1.8_L1.16, H1.9_L1.16, H1.19_L1.16, H1.22_L1.16, H1.24_L1.16, H2_L1.16, H2.1_L1.16, H2.2_L1.16, H2.3_L1.16, H2.4_L1.16, H2.5_L1.16, H2.6_L1.16, H2.7_L1.16, H2.8_L1.16, H2.9_L1.16, H2.11_L1.16, H2.12_L1.16, H2.71_L1.16, H2.75_L1.16, H2.90_L1.16, H2.91_L1.16, H2.118_L1.16, H2.119_L1.16, H1_L1.18, H1.1_L1.18, H1.2_L1.18, H1.3_L1.18, H1.4_L1.18, H1.5_L1.18, H1.6_L1.18, H1.7_L1.18, H1.8_L1.18, H1.9_L1.18, H1.19_L1.18, H1.22_L1.18, H1.24_L1.18, H2_L1.18, H2.1_L1.18, H2.2_L1.18, H2.3_L1.18, H2.4_L1.18, H2.5_L1.18, H2.6_L1.18, H2.7_L1.18, H2.8_L1.18, H2.9_L1.18, H2.11_L1.18, H2.12_L1.18, H2.71_L1.18, H2.75_L1.18, H2.90_L1.18, H2.91_L1.18, H2.118_L1.18, H2.119_L1.18, H1_L1.19, H1.1_L1.19, H1.2_L1.19, H1.3_L1.19, H1.4_L1.19, H1.5_L1.19, H1.6_L1.19, H1.7_L1.19, H1.8_L1.19, H1.9_L1.19, H1.19_L1.19, H1.22_L1.19, H1.24_L1.19, H2_L1.19, H2.1_L1.19, H2.2_L1.19, H2.3_L1.19, H2.4_L1.19, H2.5_L1.19, H2.6_L1.19, H2.7_L1.19, H2.8_L1.19, H2.9_L1.19, H2.11_L1.19, H2.12_L1.19, H2.71_L1.19, H2.75_L1.19, H2.90_L1.19, H2.91_L1.19, H2.118_L1.19, H2.119_L1.19, H1_L1.21, H1.1_L1.21, H1.2_L1.21, H1.3_L1.21, H1.4_L1.21, H1.5_L1.21, H1.6_L1.21,

H1.2_L1.187, H1.3_L1.187, H1.4_L1.187, H1.5_L1.187, H1.6_L1.187, H1.7_L1.187, H1.8_L1.187, H1.9_L1.187, H1.19_L1.187, H1.22_L1.187, H1.24_L1.187, H2_L1.187, H2.1_L1.187, H2.2_L1.187, H2.3_L1.187, H2.4_L1.187, H2.5_L1.187, H2.6_L1.187, H2.7_L1.187, H2.8_L1.187, H2.9_L1.187, H2.11_L1.187, H2.12_L1.187, H2.71_L1.187, H2.75_L1.187, H2.90_L1.187, H2.91_L1.187, H2.118_L1.187, H2.119_L1.187, H1_L1.189, H1.1_L1.189, H1.2_L1.189, H1.3_L1.189, H1.4_L1.189, H1.5_L1.189, H1.6_L1.189, H1.7_L1.189, H1.8_L1.189, H1.9_L1.189, H1.19_L1.189, H1.22_L1.189, H1.24_L1.189, H2_L1.189, H2.1_L1.189, H2.2_L1.189, H2.3_L1.189, H2.4_L1.189, H2.5_L1.189, H2.6_L1.189, H2.7_L1.189, H2.8_L1.189, H2.9_L1.189, H2.11_L1.189, H2.12_L1.189, H2.71_L1.189, H2.75_L1.189, H2.90_L1.189, H2.91_L1.189, H2.118_L1.189, H2.119_L1.189, H1_L2, H1.1_L2, H1.2_L2, H1.3_L2, H1.4_L2, H1.5_L2, H1.6_L2, H1.7_L2, H1.8_L2, H1.9_L2, H1.19_L2, H1.22_L2, H1.24_L2, H2_L2, H2.1_L2, H2.2_L2, H2.3_L2, H2.4_L2, H2.5_L2, H2.6_L2, H2.7_L2, H2.8_L2, H2.9_L2, H2.11_L2, H2.12_L2, H2.71_L2, H2.75_L2, H2.90_L2, H2.91_L2, H2.118_L2 and H2.119_L2.

[0013] In certain examples, the CLDN6 binding domain comprises a VH/VL pair selected from the group consisting of: H1.9_L1.187, H1.24_L1.187, H2.91_L1.187 and H1.9_L1.187.

[0014] In some examples of the heterodimeric antibody, the anti-CD3 scFv comprises a VH/VL pair selected from the group consisting of H1.30_L1.47, H1.32_L1.47, H1.89_L1.47, H1.90_L1.47, H1.33_L1.47, H1.31_L1.47, L1.47_H1.30, L1.47_H1.30, L1.47_H1.32, L1.47_H1.89, L1.47_H1.90, L1.47_H1.33, and L1.47_H1.31.

[0015] In some examples of the heterodimeric antibody, the scFv linker is a charged scFv linker.

[0016] In some examples, the first and second Fc domains are variant Fc domains. In some examples, the first and second Fc domains comprise a set of heterodimerization variants selected from the group consisting of those depicted in Figures 1A-1E. In some examples, the set of heterodimerization variants selected is from the group consisting of S364K/E357Q : L368D/K370S; S364K : L368D/K370S; S364K : L368E/K370S; D401K: T411E/K360E/Q362E; and T366W : T366S/L368A/Y407V, wherein numbering is according to EU numbering.

[0017] In some examples, the first and second monomers further comprise one or more ablation variants. In some examples, the one or more ablation variants are E233P/L234V/L235A/G236del/S267K, wherein numbering is according to EU numbering.

[0018] In exemplary examples, one of the first or second monomer comprises one or more pI variants. In some examples, the one or more pI variants are N208D/Q295E/N384D/Q418E/N421D, wherein numbering is according to EU numbering.

[0019] In exemplary examples of the heterodimeric antibody, the first monomer comprises amino acid variants S364K/E357Q/ E233P/L234V/L235A/G236del/S267K, the second monomer comprises amino acid variants L368D/K370S/N208D/Q295E/N384D/Q418E/N421D/E233P/L234V/L235A/G236del/S267K, and wherein numbering is according to EU numbering.

[0020] In some examples, the first and second monomers each further comprise amino acid variants 428/434S, wherein numbering is according to EU numbering.

[0021] In another aspect, provided herein is a heterodimeric antibody comprising: a) a first monomer comprising, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3, wherein VH1 is a first variable heavy domain, scFv is an anti-CD3 scFv, linker 1 and linker 2 are a first domain linker and second domain linker, respectively, and CH2-CH3 is a first Fc domain; b) a second monomer comprising, from N-terminal to C-terminal, a VH2-CH1-hinge-CH2-CH3, wherein VH2 is a second variable heavy domain and CH2-CH3 is a second Fc domain; c) a first common light chain comprising a variable light domain and a constant light domain; and d) a second common light chain comprising a variable light domain and a constant light domain, wherein the first variable heavy domain and the variable light domain of the first common light chain form a first CLDN6 ABD, and the second variable heavy domain and the variable light domain of the second common light chain form a second CLDN6 ABD, wherein the first and second CLDN6 antigen binding domains each comprise a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317),

H1_L1.27 (SEQ ID NO: 185 and SEQ ID NO: 353), H1.1_L1.27 (SEQ ID NO: 201 and SEQ ID NO: 353), H1.2_L1.27 (SEQ ID NO: 205 and SEQ ID NO: 353), H1.3_L1.27 (SEQ ID NO: 209 and SEQ ID NO: 353), H1.4_L1.27 (SEQ ID NO: 213 and SEQ ID NO: 353), H1.5_L1.27 (SEQ ID NO: 217 and SEQ ID NO: 353), H1.6_L1.27 (SEQ ID NO: 221 and SEQ ID NO: 353), H1.7_L1.27 (SEQ ID NO: 225 and SEQ ID NO: 353), H1.8_L1.27 (SEQ ID NO: 229 and SEQ ID NO: 353), H1.9_L1.27 (SEQ ID NO: 233 and SEQ ID NO: 353), H1.19_L1.27 (SEQ ID NO: 237 and SEQ ID NO: 353), H1.22_L1.27 (SEQ ID NO: 241 and SEQ ID NO: 353), H1.24_L1.27 (SEQ ID NO: 245 and SEQ ID NO: 353), H2_L1.27 (SEQ ID NO: 189 and SEQ ID NO: 353), H2.1_L1.27 (SEQ ID NO: 249 and SEQ ID NO: 353), H2.2_L1.27 (SEQ ID NO: 253 and SEQ ID NO: 353), H2.3_L1.27 (SEQ ID NO: 257 and SEQ ID NO: 353), H2.4_L1.27 (SEQ ID NO: 261 and SEQ ID NO: 353), H2.5_L1.27 (SEQ ID NO: 265 and SEQ ID NO: 353), H2.6_L1.27 (SEQ ID NO: 269 and SEQ ID NO: 353), H2.7_L1.27 (SEQ ID NO: 273 and SEQ ID NO: 353), H2.8_L1.27 (SEQ ID NO: 277 and SEQ ID NO: 353), H2.9_L1.27 (SEQ ID NO: 281 and SEQ ID NO: 353), H2.11_L1.27 (SEQ ID NO: 285 and SEQ ID NO: 353), H2.12_L1.27 (SEQ ID NO: 289 and SEQ ID NO: 353), H2.71_L1.27 (SEQ ID NO: 293 and SEQ ID NO: 353), H2.75_L1.27 (SEQ ID NO: 297 and SEQ ID NO: 353), H2.90_L1.27 (SEQ ID NO: 301 and SEQ ID NO: 353), H2.91_L1.27 (SEQ ID NO: 305 and SEQ ID NO: 353), H2.118_L1.27 (SEQ ID NO: 309 and SEQ ID NO: 353), H2.119_L1.27 (SEQ ID NO: 313 and SEQ ID NO: 353), H1_L1.60 (SEQ ID NO: 185 and SEQ ID NO: 357), H1.1_L1.60 (SEQ ID NO: 201 and SEQ ID NO: 357), H1.2_L1.60 (SEQ ID NO: 205 and SEQ ID NO: 357), H1.3_L1.60 (SEQ ID NO: 209 and SEQ ID NO: 357), H1.4_L1.60 (SEQ ID NO: 213 and SEQ ID NO: 357), H1.5_L1.60 (SEQ ID NO: 217 and SEQ ID NO: 357), H1.6_L1.60 (SEQ ID NO: 221 and SEQ ID NO: 357), H1.7_L1.60 (SEQ ID NO: 225 and SEQ ID NO: 357), H1.8_L1.60 (SEQ ID NO: 229 and SEQ ID NO: 357), H1.9_L1.60 (SEQ ID NO: 233 and SEQ ID NO: 357), H1.19_L1.60 (SEQ ID NO: 237 and SEQ ID NO: 357), H1.22_L1.60 (SEQ ID NO: 241 and SEQ ID NO: 357), H1.24_L1.60 (SEQ ID NO: 245 and SEQ ID NO: 357), H2_L1.60 (SEQ ID NO: 189 and SEQ ID NO: 357), H2.1_L1.60 (SEQ ID NO: 249 and SEQ ID NO: 357), H2.2_L1.60 (SEQ ID NO: 253 and SEQ ID NO: 357), H2.3_L1.60 (SEQ ID NO: 257 and SEQ ID NO: 357), H2.4_L1.60 (SEQ ID NO: 261 and SEQ ID NO: 357), H2.5_L1.60 (SEQ ID NO: 265 and SEQ ID NO: 357), H2.6_L1.60 (SEQ ID NO: 269 and SEQ ID NO: 357), H2.7_L1.60 (SEQ ID NO: 273 and SEQ ID NO: 357), H2.8_L1.60 (SEQ ID NO: 277 and SEQ ID NO: 357), H2.9_L1.60 (SEQ ID NO: 281 and SEQ ID NO: 357), H2.11_L1.60 (SEQ ID NO: 285 and SEQ ID NO: 357), H2.12_L1.60 (SEQ ID NO: 289 and SEQ ID NO: 357), H2.71_L1.60 (SEQ ID NO: 293 and SEQ ID NO: 357), H2.75_L1.60 (SEQ ID NO: 297 and SEQ ID NO: 357), H2.90_L1.60 (SEQ ID NO: 301 and SEQ ID NO: 357), H2.91_L1.60 (SEQ ID NO: 305 and SEQ ID NO: 357), H2.118_L1.60 (SEQ ID NO: 309 and SEQ ID NO: 357), H2.119_L1.60 (SEQ ID NO: 313 and SEQ ID NO: 357), H1_L1.107 (SEQ ID NO: 185 and SEQ ID NO: 361), H1.1_L1.107 (SEQ ID NO: 201 and SEQ ID NO: 361), H1.2_L1.107 (SEQ ID NO: 205 and SEQ ID NO: 361), H1.3_L1.107 (SEQ ID NO: 209 and SEQ ID NO: 361), H1.4_L1.107 (SEQ ID NO: 213 and SEQ ID NO: 361), H1.5_L1.107 (SEQ ID NO: 217 and SEQ ID NO: 361), H1.6_L1.107 (SEQ ID NO: 221 and SEQ ID NO: 361), H1.7_L1.107 (SEQ ID NO: 225 and SEQ ID NO: 361), H1.8_L1.107 (SEQ ID NO: 229 and SEQ ID NO: 361), H1.9_L1.107 (SEQ ID NO: 233 and SEQ ID NO: 361), H1.19_L1.107 (SEQ ID NO: 237 and SEQ ID NO: 361), H1.22_L1.107 (SEQ ID NO: 241 and SEQ ID NO: 361), H1.24_L1.107 (SEQ ID NO: 245 and SEQ ID NO: 361), H2_L1.107 (SEQ ID NO: 189 and SEQ ID NO: 361), H2.1_L1.107 (SEQ ID NO: 249 and SEQ ID NO: 361), H2.2_L1.107 (SEQ ID NO: 253 and SEQ ID NO: 361), H2.3_L1.107 (SEQ ID NO: 257 and SEQ ID NO: 361), H2.4_L1.107 (SEQ ID NO: 261 and SEQ ID NO: 361), H2.5_L1.107 (SEQ ID NO: 265 and SEQ ID NO: 361), H2.6_L1.107 (SEQ ID NO: 269 and SEQ ID NO: 361), H2.7_L1.107 (SEQ ID NO: 273 and SEQ ID NO: 361), H2.8_L1.107 (SEQ ID NO: 277 and SEQ ID NO: 361), H2.9_L1.107 (SEQ ID NO: 281 and SEQ ID NO: 361), H2.11_L1.107 (SEQ ID NO: 285 and SEQ ID NO: 361), H2.12_L1.107 (SEQ ID NO: 289 and SEQ ID NO: 361), H2.71_L1.107 (SEQ ID NO: 293 and SEQ ID NO: 361), H2.75_L1.107 (SEQ ID NO: 297 and SEQ ID NO: 361),

H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197). In another example, provided herein is a heterodimeric antibody comprising: a) a first monomer comprising, from N-terminal to C-terminal, a scFv-linker-CH2-CH3, wherein scFv is an anti-CD3 scFv and CH2-CH3 is a first Fc domain; b) a second monomer comprising, from N-terminal to C-terminal, a VH-CH1-hinge-CH2-CH3, wherein CH2-CH3 is a second Fc domain; and c) a light chain comprising VL-CL. The first variant Fc domain comprises amino acid variants S364K/E357Q, the second variant Fc domain comprises amino acid variants L368D/K370S, the first and second variant Fc domains each comprises amino acid variants E233P/L234V/L235A/G236del/S267K, and the CH1-hinge-CH2-CH3 of the second monomer comprises amino acid variants N208D/Q295E/N384D/Q418E/N421D (EU numbering). Further, the VH and VL form an CLDN6 binding domain comprising the variable heavy domain and the variable light domain, respectively, of an CLDN6 binding domain selected from H1.9_L1.187, H1.24_L1.187, H2.91_L1.187 and H1.9_L1.187; and the anti-CD3 scFv comprises the variable heavy domain and the variable light domain of a CD3 binding domain selected from H1.30_L1.47, H1.32_L1.47, H1.89_L1.47, H1.90_L1.47, H1.33_L1.47, H1.31_L1.47, L1.47_H1.30, L1.47_H1.30, L1.47_H1.32, L1.47_H1.89, L1.47_H1.90, L1.47_H1.33, and L1.47_H1.31.

[0022] In some examples, the first and second variant Fc domains each further comprise amino acid variants 428/434S, wherein numbering is according to EU numbering.

[0023] In another aspect, provided herein is a heterodimeric antibody comprising: a) a first monomer comprising, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3, wherein VH1 is a first variable heavy domain, scFv is an anti-CD3 scFv, linker 1 and linker 2 are a first domain linker and second domain linker, respectively, and CH2-CH3 is a first variant Fc domain; b) a second monomer comprising, from N-terminal to C-terminal, a VH2-CH1-hinge-CH2-CH3, wherein VH2 is a second variable heavy domain, and CH2-CH3 is a second variant Fc domain; and c) a first common light chain comprising a variable light domain and a constant light domain; and d) a second common light chain comprising a variable light domain and a constant light domain, wherein the first variable heavy domain and the variable light domain of the first common light chain form a first CLDN3 ABD, and the second variable heavy domain and the variable light domain of the second common light chain form a second CLDN3 ABD, wherein the first variant Fc domain comprises amino acid variants S364K/E357Q, wherein the second variant Fc domain comprises amino acid variants L368D/K370S, wherein the first and second variant Fc domains each comprises amino acid variants E233P/L234V/L235A/G236del/S267K, wherein the CH1-hinge-CH2-CH3 of the second monomer comprises amino acid variants N208D/Q295E/N384D/Q418E/N421D, wherein each of the first and second CLDN6 antigen binding domains have a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), and H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369); wherein the anti-CD3 scFv comprises a variable heavy domain and a variable light domain of a CD3 antigen binding domain selected from the group consisting of: L1.47_H1.32 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.30_L1.47 (SEQ ID NO: 100 and SEQ ID NO: 104), H1.32_L1.47 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.89_L1.47 (SEQ ID NO: 122 and SEQ ID NO: 126), H1.90_L1.47 (SEQ ID NO: 133 and SEQ ID NO: 137), H1.33_L1.47 (SEQ ID NO: 144 and SEQ ID NO: 148), H1.31_L1.47 (SEQ ID NO: 155 and SEQ ID NO: 159), L1.47_H1.30 (SEQ ID NO: 100 and SEQ ID NO: 104), L1.47_H1.89 (SEQ ID NO: 122 and SEQ ID NO: 126), L1.47_H1.90 (SEQ ID NO: 133 and SEQ ID NO: 137), L1.47_H1.33 (SEQ ID NO: 144 and SEQ ID NO: 148), and L1.47_H1.31, (SEQ ID NO: 155 and SEQ ID NO: 159), and wherein numbering is according to EU numbering.

In another example, provided herein is a heterodimeric antibody comprising: a) a first monomer, b) a second monomer, and c) a common light chain. The first monomer comprises, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3, wherein VH1 is a first variable heavy domain, scFv is an anti-CD3 scFv, linker 1 and linker 2 are a first domain linker and second domain linker, respectively, and CH2-CH3 is a first Fc domain. The second monomer comprises, from N-terminal to C-terminal, a VH2-CH1-hinge-CH2-CH3, wherein VH2 is a second variable heavy domain and CH2-CH3 is a second Fc domain; and c) a common light chain comprising a variable light domain. The first variable heavy domain and the variable light domain form a first CLDN6 ABD, and the second variable heavy domain and the variable light domain form a second CLDN6 ABD.

[0024] In some examples, the first and second CLDN6 binding domains each comprise a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a VH/VL pair selected from the group consisting of: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1, H1.24_L1.1, H2_L1.1, H2.1_L1.1, H2.2_L1.1, H2.3_L1.1, H2.4_L1.1, H2.5_L1.1, H2.6_L1.1, H2.7_L1.1, H2.8_L1.1, H2.9_L1.1, H2.11_L1.1, H2.12_L1.1, H2.71_L1.1, H2.75_L1.1, H2.90_L1.1, H2.91_L1.1, H2.118_L1.1, H2.119_L1.1, H1_L1.4, H1.1_L1.4, H1.2_L1.4, H1.3_L1.4, H1.4_L1.4, H1.5_L1.4, H1.6_L1.4, H1.7_L1.4, H1.8_L1.4, H1.9_L1.4, H1.19_L1.4, H1.22_L1.4, H1.24_L1.4, H2_L1.4, H2.1_L1.4, H2.2_L1.4, H2.3_L1.4, H2.4_L1.4, H2.5_L1.4, H2.6_L1.4, H2.7_L1.4, H2.8_L1.4, H2.9_L1.4, H2.11_L1.4, H2.12_L1.4, H2.71_L1.4, H2.75_L1.4, H2.90_L1.4, H2.91_L1.4, H2.118_L1.4, H2.119_L1.4, H1_L1.7, H1.1_L1.7, H1.2_L1.7, H1.3_L1.7, H1.4_L1.7, H1.5_L1.7, H1.6_L1.7, H1.7_L1.7, H1.8_L1.7, H1.9_L1.7, H1.19_L1.7, H1.22_L1.7, H1.24_L1.7, H2_L1.7, H2.1_L1.7, H2.2_L1.7, H2.3_L1.7, H2.4_L1.7, H2.5_L1.7, H2.6_L1.7, H2.7_L1.7, H2.8_L1.7, H2.9_L1.7, H2.11_L1.7, H2.12_L1.7, H2.71_L1.7, H2.75_L1.7, H2.90_L1.7, H2.91_L1.7, H2.118_L1.7, H2.119_L1.7, H1_L1.16, H1.1_L1.16, H1.2_L1.16, H1.3_L1.16, H1.4_L1.16, H1.5_L1.16, H1.6_L1.16, H1.7_L1.16, H1.8_L1.16, H1.9_L1.16, H1.19_L1.16, H1.22_L1.16, H1.24_L1.16, H2_L1.16, H2.1_L1.16, H2.2_L1.16, H2.3_L1.16, H2.4_L1.16, H2.5_L1.16, H2.6_L1.16, H2.7_L1.16, H2.8_L1.16,

H2.11_L1.60, H2.12_L1.60, H2.71_L1.60, H2.75_L1.60, H2.90_L1.60, H2.91_L1.60, H2.118_L1.60, H2.119_L1.60, H1_L1.107, H1.1_L1.107, H1.2_L1.107, H1.3_L1.107, H1.4_L1.107, H1.5_L1.107, H1.6_L1.107, H1.7_L1.107, H1.8_L1.107, H1.9_L1.107, H1.19_L1.107, H1.22_L1.107, H1.24_L1.107, H2_L1.107, H2.1_L1.107, H2.2_L1.107, H2.3_L1.107, H2.4_L1.107, H2.5_L1.107, H2.6_L1.107, H2.7_L1.107, H2.8_L1.107, H2.9_L1.107, H2.11_L1.107, H2.12_L1.107, H2.71_L1.107, H2.75_L1.107, H2.90_L1.107, H2.91_L1.107, H2.118_L1.107, H2.119_L1.107, H1_L1.114, H1.1_L1.114, H1.2_L1.114, H1.3_L1.114, H1.4_L1.114, H1.5_L1.114, H1.6_L1.114, H1.7_L1.114, H1.8_L1.114, H1.9_L1.114, H1.19_L1.114, H1.22_L1.114, H1.24_L1.114, H2_L1.114, H2.1_L1.114, H2.2_L1.114, H2.3_L1.114, H2.4_L1.114, H2.5_L1.114, H2.6_L1.114, H2.7_L1.114, H2.8_L1.114, H2.9_L1.114, H2.11_L1.114, H2.12_L1.114, H2.71_L1.114, H2.75_L1.114, H2.90_L1.114, H2.91_L1.114, H2.118_L1.114, H2.119_L1.114, H1_L1.187, H1.1_L1.187, H1.2_L1.187, H1.3_L1.187, H1.4_L1.187, H1.5_L1.187, H1.6_L1.187, H1.7_L1.187, H1.8_L1.187, H1.9_L1.187, H1.19_L1.187, H1.22_L1.187, H1.24_L1.187, H2_L1.187, H2.1_L1.187, H2.2_L1.187, H2.3_L1.187, H2.4_L1.187, H2.5_L1.187, H2.6_L1.187, H2.7_L1.187, H2.8_L1.187, H2.9_L1.187, H2.11_L1.187, H2.12_L1.187, H2.71_L1.187, H2.75_L1.187, H2.90_L1.187, H2.91_L1.187, H2.118_L1.187, H2.119_L1.187, H1_L1.189, H1.1_L1.189, H1.2_L1.189, H1.3_L1.189, H1.4_L1.189, H1.5_L1.189, H1.6_L1.189, H1.7_L1.189, H1.8_L1.189, H1.9_L1.189, H1.19_L1.189, H1.22_L1.189, H1.24_L1.189, H2_L1.189, H2.1_L1.189, H2.2_L1.189, H2.3_L1.189, H2.4_L1.189, H2.5_L1.189, H2.6_L1.189, H2.7_L1.189, H2.8_L1.189, H2.9_L1.189, H2.11_L1.189, H2.12_L1.189, H2.71_L1.189, H2.75_L1.189, H2.90_L1.189, H2.91_L1.189, H2.118_L1.189, H2.119_L1.189, H1_L2, H1.1_L2, H1.2_L2, H1.3_L2, H1.4_L2, H1.5_L2, H1.6_L2, H1.7_L2, H1.8_L2, H1.9_L2, H1.19_L2, H1.22_L2, H1.24_L2, H2_L2, H2.1_L2, H2.2_L2, H2.3_L2, H2.4_L2, H2.5_L2, H2.6_L2, H2.7_L2, H2.8_L2, H2.9_L2, H2.11_L2, H2.12_L2, H2.71_L2, H2.75_L2, H2.90_L2, H2.91_L2, H2.118_L2 and H2.119_L2.

[0025] In exemplary examples, each of the first and second CLDN6 binding domains comprise a VH/VL pair selected from the group consisting of: H1_L1, H1.1_L1, H1.2_L1, H1.3_L1, H1.4_L1, H1.5_L1, H1.6_L1, H1.7_L1, H1.8_L1, H1.9_L1, H1.19_L1, H1.22_L1, H1.24_L1, H2_L1, H2.1_L1, H2.2_L1, H2.3_L1, H2.4_L1, H2.5_L1, H2.6_L1, H2.7_L1, H2.8_L1, H2.9_L1, H2.11_L1, H2.12_L1, H2.71_L1, H2.75_L1, H2.90_L1, H2.91_L1, H2.118_L1, H2.119_L1, H1_L1.1, H1.1_L1.1, H1.2_L1.1, H1.3_L1.1, H1.4_L1.1, H1.5_L1.1, H1.6_L1.1, H1.7_L1.1, H1.8_L1.1, H1.9_L1.1, H1.19_L1.1, H1.22_L1.1,

H1.24_L1.189, H2_L1.189, H2.1_L1.189, H2.2_L1.189, H2.3_L1.189, H2.4_L1.189, H2.5_L1.189, H2.6_L1.189, H2.7_L1.189, H2.8_L1.189, H2.9_L1.189, H2.11_L1.189, H2.12_L1.189, H2.71_L1.189, H2.75_L1.189, H2.90_L1.189, H2.91_L1.189, H2.118_L1.189, H2.119_L1.189, H1_L2, H1.1_L2, H1.2_L2, H1.3_L2, H1.4_L2, H1.5_L2, H1.6_L2, H1.7_L2, H1.8_L2, H1.9_L2, H1.19_L2, H1.22_L2, H1.24_L2, H2_L2, H2.1_L2, H2.2_L2, H2.3_L2, H2.4_L2, H2.5_L2, H2.6_L2, H2.7_L2, H2.8_L2, H2.9_L2, H2.11_L2, H2.12_L2, H2.71_L2, H2.75_L2, H2.90_L2, H2.91_L2, H2.118_L2 and H2.119_L2.

[0026] In some examples, the VH/VL pairs are selected from the group consisting of H1.9_L1.187, H1.24_L1.187, H2.91_L1.187 and H1.9_L1.187.

[0027] In some examples, the scFv comprises a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from VH/VL pairs selected from the group consisting of: H1.30_L1.47, H1.32_L1.47, H1.89_L1.47, H1.90_L1.47, H1.33_L1.47, H1.31_L1.47, L1.47_H1.30, L1.47_H1.30, L1.47_H1.32, L1.47_H1.89, L1.47_H1.90, L1.47_H1.33, and L1.47_H1.31. In exemplary examples, the scFv comprises the variable heavy domain and variable light domain of any of the following CD3 binding domains: H1.30_L1.47, H1.32_L1.47, H1.89_L1.47, H1.90_L1.47, H1.33_L1.47, H1.31_L1.47, L1.47_H1.30, L1.47_H1.30, L1.47_H1.32, L1.47_H1.89, L1.47_H1.90, L1.47_H1.33, and L1.47_H1.31.

[0028] In some examples of the heterodimeric antibody, the scFv linker is a charged scFv linker. In some examples, the scFv linker is a charged scFv linker having the amino acid sequence (GKPGS)₄ (SEQ ID NO: 1).

[0029] In some examples, the first and second Fc domains are variant Fc domains. In some examples, the first and second Fc domains comprise a set of heterodimerization variants selected from the group consisting of those depicted in Figures 1A-1E. In some examples, the set of heterodimerization variants selected is from the group consisting of S364K/E357Q : L368D/K370S; S364K : L368D/K370S; S364K : L368E/K370S; D401K: T411E/K360E/Q362E; and T366W : T366S/L368A/Y407V, wherein numbering is according to EU numbering.

[0030] In some examples, the first and second monomers further comprise one or more ablation variants. In some examples, the one or more ablation variants are E233P/L234V/L235A/G236del/S267K, wherein numbering is according to EU numbering.

[0031] In exemplary examples, one of the first or second monomer comprises one or more pI variants. In some examples, the one or more pI variants are N208D/Q295E/N384D/Q418E/N421D, wherein numbering is according to EU numbering.

[0032] In exemplary examples of the heterodimeric antibody, the first monomer comprises amino acid variants S364K/E357Q/ E233P/L234V/L235A/G236del/S267K, the second monomer comprises amino acid variants L368D/K370S/N208D/Q295E/N384D/Q418E/N421D/E233P/L234V/L235A/G236del/S267K, and wherein numbering is according to EU numbering.

[0033] In some examples, the first and second monomers each further comprise amino acid variants 428/434S, wherein numbering is according to EU numbering.

[0034] In another aspect, provided herein is a nucleic acid composition comprising: a) a first nucleic acid encoding the first monomer as disclosed herein; b) a second nucleic acid encoding the second monomer as disclosed herein; and c) a third nucleic acid encoding the light chain as disclosed herein, respectively. In another aspect, provided herein is an expression vector composition comprising: a) a first expression vector comprising the first nucleic acid as disclosed herein; b) a second expression vector comprising the second nucleic acid as disclosed herein; and c) a third expression vector comprising the third nucleic acid as disclosed herein. In another aspect, provided herein is a host cell transformed with the expression vector composition as disclosed herein. In another aspect, provided herein is a method of making a heterodimeric antibody comprising culturing the host cell as disclosed herein under conditions wherein the antibody is expressed and recovering the antibody. In another aspect, provided herein is a heterodimeric antibody comprising: a) a first monomer having an amino acid sequence of SEQ ID NO: 567; b) a second monomer having an amino acid sequence of SEQ ID NO: 568; and c) a light chain having an amino acid sequence of SEQ ID NO: 569. In another example, provided herein is heterodimeric antibody comprising: a) a first monomer, b) a second monomer, and c) a common light chain. The first monomer comprises, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3, wherein scFv is an anti-CD3 scFv and CH2-CH3 is a first Fc domain. The second monomer comprises, from N-terminal to C-terminal, a VH1-CH1-hinge-CH2-CH3, wherein CH2-CH3 is a second Fc domain. The common light chain comprising VL-CL. The first variant Fc domain comprises amino acid variants S364K/E357Q, the second variant Fc domain comprises amino acid variants L368D/K370S, the first and second variant Fc domains each comprises amino acid variants E233P/L234V/L235A/G236del/S267K, and the CH1-hinge-CH2-CH3 of the second monomer comprises amino acid variants N208D/Q295E/N384D/Q418E/N421D (EU numbering). The VH and VL comprise the variable heavy domain and the variable light domain of a CLDN6 ABD selected from H1.9_L1.187, H1.24_L1.187, H2.91_L1.187 and H1.9_L1.187; and the anti-CD3 scFv comprises the variable heavy domain and the variable light domain of a CD3 binding domain selected from H1.30_L1.47, H1.32_L1.47, H1.89_L1.47, H1.90_L1.47, H1.33_L1.47, H1.31_L1.47, L1.47_H1.30, L1.47_H1.30, L1.47_H1.32, L1.47_H1.89, L1.47_H1.90, L1.47_H1.33, and L1.47_H1.31.

[0035] Also provided herein are nucleic acid compositions comprising nucleic acids encoding the antibodies described herein, expression vector compositions that include such nucleic acids, host cells for making the antibodies that comprise the expression vector compositions, and methods of making the antibodies.

WHAT IS CLAIMED IS:

1. A construct that binds CLDN6 comprising a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain (VH)/variable light domain (VL) pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317).

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293 and SEQ ID NO: 325), H2.75_L1.7 (SEQ ID NO: 297 and SEQ ID NO: 325), H2.90_L1.7 (SEQ ID NO: 301 and SEQ ID NO: 325), H2.91_L1.7 (SEQ ID NO: 305 and SEQ ID NO: 325), H2.118_L1.7 (SEQ ID NO: 309 and SEQ ID NO: 325), H2.119_L1.7 (SEQ ID NO: 313 and SEQ ID NO: 325), H1_L1.16 (SEQ ID NO: 185 and SEQ ID NO: 329), H1.1_L1.16 (SEQ ID NO: 201 and SEQ ID NO: 329), H1.2_L1.16 (SEQ ID NO: 205 and SEQ ID NO: 329), H1.3_L1.16 (SEQ ID NO: 209 and SEQ ID NO: 329), H1.4_L1.16 (SEQ ID NO: 213 and SEQ ID NO: 329), H1.5_L1.16 (SEQ ID NO: 217 and SEQ ID NO: 329), H1.6_L1.16 (SEQ ID NO: 221 and SEQ ID NO: 329), H1.7_L1.16 (SEQ ID NO: 225 and SEQ ID NO: 329), H1.8_L1.16 (SEQ ID NO: 229 and SEQ ID NO: 329), H1.9_L1.16 (SEQ ID NO: 233 and SEQ ID NO: 329), H1.19_L1.16 (SEQ ID NO: 237 and SEQ ID NO: 329), H1.22_L1.16 (SEQ ID NO: 241 and SEQ ID NO: 329), H1.24_L1.16 (SEQ ID NO: 245 and SEQ ID NO: 329), H2_L1.16 (SEQ ID NO: 189 and SEQ ID NO: 329), H2.1_L1.16 (SEQ ID NO: 249 and SEQ ID NO: 329), H2.2_L1.16 (SEQ ID NO: 253 and SEQ ID NO: 329), H2.3_L1.16 (SEQ ID NO: 257 and SEQ ID NO: 329), H2.4_L1.16 (SEQ ID NO: 261 and SEQ ID NO: 329), H2.5_L1.16 (SEQ ID NO: 265 and SEQ ID NO: 329), H2.6_L1.16 (SEQ ID NO: 269 and SEQ ID NO: 329), H2.7_L1.16 (SEQ ID NO: 273 and SEQ ID NO: 329), H2.8_L1.16 (SEQ ID NO: 277 and SEQ ID NO: 329), H2.9_L1.16 (SEQ ID NO: 281 and SEQ ID NO: 329), H2.11_L1.16 (SEQ ID NO: 285 and SEQ ID NO: 329), H2.12_L1.16 (SEQ ID NO: 289 and SEQ ID NO: 329), H2.71_L1.16 (SEQ ID NO: 293 and SEQ ID NO: 329), H2.75_L1.16 (SEQ ID NO: 297 and SEQ ID NO: 329), H2.90_L1.16 (SEQ ID NO: 301 and SEQ ID NO: 329), H2.91_L1.16 (SEQ ID NO: 305 and SEQ ID NO: 329), H2.118_L1.16 (SEQ ID NO: 309 and SEQ ID NO: 329), H2.119_L1.16 (SEQ ID NO: 313 and SEQ ID NO: 329), H1_L1.18 (SEQ ID NO: 185 and SEQ ID NO: 333), H1.1_L1.18 (SEQ ID NO: 201 and SEQ ID NO: 333), H1.2_L1.18 (SEQ ID NO: 205 and SEQ ID NO: 333), H1.3_L1.18 (SEQ ID NO: 209 and SEQ ID NO: 333), H1.4_L1.18 (SEQ ID NO: 213 and SEQ ID NO: 333), H1.5_L1.18 (SEQ ID NO: 217 and SEQ ID NO: 333), H1.6_L1.18 (SEQ ID NO: 221 and SEQ ID NO: 333), H1.7_L1.18 (SEQ ID NO: 225 and SEQ ID NO: 333), H1.8_L1.18 (SEQ ID NO: 229 and SEQ ID NO: 333), H1.9_L1.18 (SEQ ID NO: 233 and SEQ ID NO: 333), H1.19_L1.18 (SEQ ID NO: 237 and SEQ ID NO: 333), H1.22_L1.18 (SEQ ID NO: 241 and SEQ ID NO: 333), H1.24_L1.18 (SEQ ID NO: 245 and SEQ ID NO: 333), H2_L1.18 (SEQ ID NO: 189 and SEQ ID NO: 333), H2.1_L1.18 (SEQ ID NO: 249 and SEQ ID NO: 333), H2.2_L1.18 (SEQ ID NO: 253 and SEQ ID NO: 333), H2.3_L1.18 (SEQ ID NO: 257 and SEQ ID NO: 333), H2.4_L1.18 (SEQ ID NO: 261 and SEQ ID NO: 333), H2.5_L1.18 (SEQ ID NO: 265 and SEQ ID NO: 333), H2.6_L1.18 (SEQ ID NO: 269 and SEQ ID NO: 333), H2.7_L1.18 (SEQ ID NO: 273 and SEQ ID NO: 333), H2.8_L1.18 (SEQ ID NO: 277 and SEQ ID NO: 333), H2.9_L1.18 (SEQ ID NO: 281 and SEQ ID NO: 333), H2.11_L1.18 (SEQ ID NO: 285 and SEQ ID NO: 333), H2.12_L1.18 (SEQ ID NO: 289 and SEQ ID NO: 333), H2.71_L1.18 (SEQ ID NO: 293 and SEQ ID NO: 333), H2.75_L1.18 (SEQ ID NO: 297 and SEQ ID NO: 333), H2.90_L1.18 (SEQ ID NO: 301 and SEQ ID NO: 333), H2.91_L1.18 (SEQ ID NO: 305 and SEQ ID NO: 333), H2.118_L1.18 (SEQ ID NO: 309 and SEQ ID NO: 333), H2.119_L1.18 (SEQ ID NO: 313 and SEQ ID NO: 333).

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(SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

2. The construct according to claim 1, wherein the construct comprises a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193),

H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221 and SEQ ID NO: 321), H1.7_L1.4 (SEQ ID NO: 225 and SEQ ID NO: 321), H1.8_L1.4 (SEQ ID NO: 229 and SEQ ID NO: 321), H1.9_L1.4 (SEQ ID NO: 233 and SEQ ID NO: 321), H1.19_L1.4 (SEQ ID NO: 237 and SEQ ID NO: 321), H1.22_L1.4 (SEQ ID NO: 241 and SEQ ID NO: 321), H1.24_L1.4 (SEQ ID NO: 245 and SEQ ID NO: 321), H2_L1.4 (SEQ ID NO: 189 and SEQ ID NO: 321), H2.1_L1.4 (SEQ ID NO: 249 and SEQ ID NO: 321), H2.2_L1.4 (SEQ ID NO: 253 and SEQ ID NO: 321), H2.3_L1.4 (SEQ ID NO: 257 and SEQ ID NO: 321), H2.4_L1.4 (SEQ ID NO: 261 and SEQ ID NO: 321), H2.5_L1.4 (SEQ ID NO: 265 and SEQ ID NO: 321), H2.6_L1.4 (SEQ ID NO: 269 and SEQ ID NO: 321), H2.7_L1.4 (SEQ ID NO: 273 and SEQ ID NO: 321), H2.8_L1.4 (SEQ ID NO: 277 and SEQ ID NO: 321), H2.9_L1.4 (SEQ ID NO: 281 and SEQ ID NO: 321), H2.11_L1.4 (SEQ ID NO: 285 and SEQ ID NO: 321), H2.12_L1.4 (SEQ ID NO: 289 and SEQ ID NO: 321), H2.71_L1.4 (SEQ ID NO: 293 and SEQ ID NO: 321), H2.75_L1.4 (SEQ ID NO: 297 and SEQ ID NO: 321), H2.90_L1.4 (SEQ ID NO: 301 and SEQ ID NO: 321), H2.91_L1.4 (SEQ ID NO: 305 and SEQ ID NO: 321), H2.118_L1.4 (SEQ ID NO: 309 and SEQ ID NO: 321), H2.119_L1.4 (SEQ ID NO: 313 and SEQ ID NO: 321), H1_L1.7 (SEQ ID NO: 185 and SEQ ID NO: 325), H1.1_L1.7 (SEQ ID NO: 201 and SEQ ID NO: 325), H1.2_L1.7 (SEQ ID NO: 205 and SEQ ID NO: 325),

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and SEQ ID NO: 373), H1.19_L1.189 (SEQ ID NO: 237 and SEQ ID NO: 373), H1.22_L1.189 (SEQ ID NO: 241 and SEQ ID NO: 373), H1.24_L1.189 (SEQ ID NO: 245 and SEQ ID NO: 373), H2_L1.189 (SEQ ID NO: 189 and SEQ ID NO: 373), H2.1_L1.189 (SEQ ID NO: 249 and SEQ ID NO: 373), H2.2_L1.189 (SEQ ID NO: 253 and SEQ ID NO: 373), H2.3_L1.189 (SEQ ID NO: 257 and SEQ ID NO: 373), H2.4_L1.189 (SEQ ID NO: 261 and SEQ ID NO: 373), H2.5_L1.189 (SEQ ID NO: 265 and SEQ ID NO: 373), H2.6_L1.189 (SEQ ID NO: 269 and SEQ ID NO: 373), H2.7_L1.189 (SEQ ID NO: 273 and SEQ ID NO: 373), H2.8_L1.189 (SEQ ID NO: 277 and SEQ ID NO: 373), H2.9_L1.189 (SEQ ID NO: 281 and SEQ ID NO: 373), H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

3. The construct according to claim 2, wherein the VH/VL pair is selected from the group consisting of H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), and H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369).

4. The construct according to any of claims 1-3, wherein the construct is a monoclonal antibody.

5. A heterodimeric antibody comprising:

a) a first monomer comprising:

i) an anti-CD3 scFv comprising a first variable light domain, an scFv linker and a first variable heavy domain; and

ii) a first Fc domain, wherein the scFv is covalently attached to the N-terminus of the first Fc domain using a domain linker;

b) a second monomer comprising a VH2-CH1-hinge-CH2-CH3 monomer, wherein VH is a second variable heavy domain and CH2-CH3 is a second Fc domain; and

c) a light chain comprising a second variable light domain,

wherein the second variable heavy domain and the second variable light domain form a CLDN6 antigen binding domain (ABD),

wherein the CLDN6 antigen binding domain comprises a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a variable heavy domain/variable light domain pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317),

NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221 and SEQ ID NO: 321), H1.7_L1.4 (SEQ ID NO: 225 and SEQ ID NO: 321), H1.8_L1.4 (SEQ ID NO: 229 and SEQ ID NO: 321), H1.9_L1.4 (SEQ ID NO: 233 and SEQ ID NO: 321), H1.19_L1.4 (SEQ ID NO: 237 and SEQ ID NO: 321), H1.22_L1.4 (SEQ ID NO: 241 and SEQ ID NO: 321), H1.24_L1.4 (SEQ ID NO: 245 and SEQ ID NO: 321), H2_L1.4 (SEQ ID NO: 189 and SEQ ID NO: 321), H2.1_L1.4 (SEQ ID NO: 249 and SEQ ID NO: 321), H2.2_L1.4 (SEQ ID NO: 253 and SEQ ID NO: 321), H2.3_L1.4 (SEQ ID NO: 257 and SEQ ID NO: 321), H2.4_L1.4 (SEQ ID NO: 261 and SEQ ID NO: 321), H2.5_L1.4 (SEQ ID NO: 265 and SEQ ID NO: 321), H2.6_L1.4 (SEQ ID NO: 269 and SEQ ID NO: 321), H2.7_L1.4 (SEQ ID NO: 273 and SEQ ID NO: 321), H2.8_L1.4 (SEQ ID NO: 277 and SEQ ID NO: 321), H2.9_L1.4 (SEQ ID NO: 281 and SEQ ID NO: 321), H2.11_L1.4 (SEQ ID NO: 285 and SEQ ID NO: 321), H2.12_L1.4 (SEQ ID NO: 289 and SEQ ID NO: 321), H2.71_L1.4 (SEQ ID NO: 293 and SEQ ID NO: 321), H2.75_L1.4 (SEQ ID NO: 297 and SEQ ID NO: 321), H2.90_L1.4 (SEQ ID NO: 301 and SEQ ID NO: 321), H2.91_L1.4 (SEQ ID NO: 305 and SEQ ID NO: 321), H2.118_L1.4 (SEQ ID NO: 309 and SEQ ID NO: 321), H2.119_L1.4 (SEQ ID NO: 313 and SEQ ID NO: 321), H1_L1.7 (SEQ ID NO: 185 and SEQ ID NO: 325), H1.1_L1.7 (SEQ ID NO: 201 and SEQ ID NO: 325), H1.2_L1.7 (SEQ ID NO: 205 and SEQ ID NO: 325), H1.3_L1.7 (SEQ ID NO: 209 and SEQ ID NO: 325), H1.4_L1.7 (SEQ ID NO: 213 and SEQ ID NO: 325), H1.5_L1.7 (SEQ ID NO: 217 and SEQ ID NO: 325), H1.6_L1.7 (SEQ ID NO: 221 and SEQ ID NO: 325), H1.7_L1.7 (SEQ ID NO: 225 and SEQ ID NO: 325), H1.8_L1.7 (SEQ ID NO: 229 and SEQ ID NO: 325), H1.9_L1.7 (SEQ ID NO: 233 and SEQ ID NO: 325), H1.19_L1.7 (SEQ ID NO: 237 and SEQ ID NO: 325), H1.22_L1.7 (SEQ ID NO: 241

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6. The heterodimeric antibody according to claim 5, wherein the CLDN6 antigen binding domain comprises a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193),

193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221 and SEQ ID NO: 321), H1.7_L1.4 (SEQ ID NO: 225 and SEQ ID NO: 321), H1.8_L1.4 (SEQ ID NO: 229 and SEQ ID NO: 321), H1.9_L1.4 (SEQ ID NO: 233 and SEQ ID NO: 321), H1.19_L1.4 (SEQ ID NO: 237 and SEQ ID NO: 321), H1.22_L1.4 (SEQ ID NO: 241 and SEQ ID NO: 321), H1.24_L1.4 (SEQ ID NO: 245 and SEQ ID NO: 321), H2_L1.4 (SEQ ID NO: 189 and SEQ ID NO: 321), H2.1_L1.4 (SEQ ID NO: 249 and SEQ ID NO: 321), H2.2_L1.4 (SEQ ID NO: 253 and SEQ ID NO: 321), H2.3_L1.4 (SEQ ID NO: 257 and SEQ ID NO: 321), H2.4_L1.4 (SEQ ID NO: 261 and SEQ ID NO: 321), H2.5_L1.4 (SEQ ID NO: 265 and SEQ ID NO: 321),

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SEQ ID NO: 361), H2.90_L1.107 (SEQ ID NO: 301 and SEQ ID NO: 361), H2.91_L1.107 (SEQ ID NO: 305 and SEQ ID NO: 361), H2.118_L1.107 (SEQ ID NO: 309 and SEQ ID NO: 361), H2.119_L1.107 (SEQ ID NO: 313 and SEQ ID NO: 361), H1_L1.114 (SEQ ID NO: 185 and SEQ ID NO: 365), H1.1_L1.114 (SEQ ID NO: 201 and SEQ ID NO: 365), H1.2_L1.114 (SEQ ID NO: 205 and SEQ ID NO: 365), H1.3_L1.114 (SEQ ID NO: 209 and SEQ ID NO: 365), H1.4_L1.114 (SEQ ID NO: 213 and SEQ ID NO: 365), H1.5_L1.114 (SEQ ID NO: 217 and SEQ ID NO: 365), H1.6_L1.114 (SEQ ID NO: 221 and SEQ ID NO: 365), H1.7_L1.114 (SEQ ID NO: 225 and SEQ ID NO: 365), H1.8_L1.114 (SEQ ID NO: 229 and SEQ ID NO: 365), H1.9_L1.114 (SEQ ID NO: 233 and SEQ ID NO: 365), H1.19_L1.114 (SEQ ID NO: 237 and SEQ ID NO: 365), H1.22_L1.114 (SEQ ID NO: 241 and SEQ ID NO: 365), H1.24_L1.114 (SEQ ID NO: 245 and SEQ ID NO: 365), H2_L1.114 (SEQ ID NO: 189 and SEQ ID NO: 365), H2.1_L1.114 (SEQ ID NO: 249 and SEQ ID NO: 365), H2.2_L1.114 (SEQ ID NO: 253 and SEQ ID NO: 365), H2.3_L1.114 (SEQ ID NO: 257 and SEQ ID NO: 365), H2.4_L1.114 (SEQ ID NO: 261 and SEQ ID NO: 365), H2.5_L1.114 (SEQ ID NO: 265 and SEQ ID NO: 365), H2.6_L1.114 (SEQ ID NO: 269 and SEQ ID NO: 365), H2.7_L1.114 (SEQ ID NO: 273 and SEQ ID NO: 365), H2.8_L1.114 (SEQ ID NO: 277 and SEQ ID NO: 365), H2.9_L1.114 (SEQ ID NO: 281 and SEQ ID NO: 365), H2.11_L1.114 (SEQ ID NO: 285 and SEQ ID NO: 365), H2.12_L1.114 (SEQ ID NO: 289 and SEQ ID NO: 365), H2.71_L1.114 (SEQ ID NO: 293 and SEQ ID NO: 365), H2.75_L1.114 (SEQ ID NO: 297 and SEQ ID NO: 365), H2.90_L1.114 (SEQ ID NO: 301 and SEQ ID NO: 365), H2.91_L1.114 (SEQ ID NO: 305 and SEQ ID NO: 365), H2.118_L1.114 (SEQ ID NO: 309 and SEQ ID NO: 365), H2.119_L1.114 (SEQ ID NO: 313 and SEQ ID NO: 365), H1_L1.187 (SEQ ID NO: 185 and SEQ ID NO: 369), H1.1_L1.187 (SEQ ID NO: 201 and SEQ ID NO: 369), H1.2_L1.187 (SEQ ID NO: 205 and SEQ ID NO: 369), H1.3_L1.187 (SEQ ID NO: 209 and SEQ ID NO: 369), H1.4_L1.187 (SEQ ID NO: 213 and SEQ ID NO: 369), H1.5_L1.187 (SEQ ID NO: 217 and SEQ ID NO: 369), H1.6_L1.187 (SEQ ID NO: 221 and SEQ ID NO: 369), H1.7_L1.187 (SEQ ID NO: 225 and SEQ ID NO: 369), H1.8_L1.187 (SEQ ID NO: 229 and SEQ ID NO: 369), H1.19_L1.187 (SEQ ID NO: 237 and SEQ ID NO: 369), H1.22_L1.187 (SEQ ID NO: 241 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), H2_L1.187 (SEQ ID NO: 189 and SEQ ID NO: 369), H2.1_L1.187 (SEQ ID NO: 249 and SEQ ID NO: 369), H2.2_L1.187 (SEQ ID NO: 253 and SEQ ID NO: 369), H2.3_L1.187 (SEQ ID NO: 257 and SEQ ID NO: 369), H2.4_L1.187 (SEQ ID NO: 261 and SEQ ID NO: 369), H2.5_L1.187 (SEQ ID NO: 265 and SEQ ID NO: 369), H2.6_L1.187 (SEQ ID NO: 269 and SEQ ID NO: 369), H2.7_L1.187 (SEQ ID NO: 273 and SEQ ID NO: 369), H2.8_L1.187 (SEQ ID NO: 277 and SEQ ID NO: 369), H2.9_L1.187 (SEQ ID NO: 281 and SEQ ID NO: 369), H2.11_L1.187 (SEQ ID NO: 285 and SEQ ID NO: 369), H2.12_L1.187 (SEQ ID NO: 289 and SEQ ID NO: 369), H2.71_L1.187 (SEQ ID NO: 293 and SEQ ID NO: 369), H2.75_L1.187 (SEQ ID NO: 297 and SEQ ID NO: 369), H2.90_L1.187

(SEQ ID NO: 301 and SEQ ID NO: 369), H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369), H2.118_L1.187 (SEQ ID NO: 309 and SEQ ID NO: 369), H2.119_L1.187 (SEQ ID NO: 313 and SEQ ID NO: 369), H1_L1.189 (SEQ ID NO: 185 and SEQ ID NO: 373), H1.1_L1.189 (SEQ ID NO: 201 and SEQ ID NO: 373), H1.2_L1.189 (SEQ ID NO: 205 and SEQ ID NO: 373), H1.3_L1.189 (SEQ ID NO: 209 and SEQ ID NO: 373), H1.4_L1.189 (SEQ ID NO: 213 and SEQ ID NO: 373), H1.5_L1.189 (SEQ ID NO: 217 and SEQ ID NO: 373), H1.6_L1.189 (SEQ ID NO: 221 and SEQ ID NO: 373), H1.7_L1.189 (SEQ ID NO: 225 and SEQ ID NO: 373), H1.8_L1.189 (SEQ ID NO: 229 and SEQ ID NO: 373), H1.9_L1.189 (SEQ ID NO: 233 and SEQ ID NO: 373), H1.19_L1.189 (SEQ ID NO: 237 and SEQ ID NO: 373), H1.22_L1.189 (SEQ ID NO: 241 and SEQ ID NO: 373), H1.24_L1.189 (SEQ ID NO: 245 and SEQ ID NO: 373), H2_L1.189 (SEQ ID NO: 189 and SEQ ID NO: 373), H2.1_L1.189 (SEQ ID NO: 249 and SEQ ID NO: 373), H2.2_L1.189 (SEQ ID NO: 253 and SEQ ID NO: 373), H2.3_L1.189 (SEQ ID NO: 257 and SEQ ID NO: 373), H2.4_L1.189 (SEQ ID NO: 261 and SEQ ID NO: 373), H2.5_L1.189 (SEQ ID NO: 265 and SEQ ID NO: 373), H2.6_L1.189 (SEQ ID NO: 269 and SEQ ID NO: 373), H2.7_L1.189 (SEQ ID NO: 273 and SEQ ID NO: 373), H2.8_L1.189 (SEQ ID NO: 277 and SEQ ID NO: 373), H2.9_L1.189 (SEQ ID NO: 281 and SEQ ID NO: 373), H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301

and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

7. A heterodimeric antibody comprising:

a) a first monomer comprising, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3,

wherein VH1 is a first variable heavy domain, scFv is an anti-CD3 scFv, linker 1 and linker 2 are a first domain linker and second domain linker, respectively, and CH2-CH3 is a first Fc domain;

b) a second monomer comprising, from N-terminal to C-terminal, a VH2-CH1-hinge-CH2-CH3, wherein VH2 is a second variable heavy domain and CH2-CH3 is a second Fc domain;

c) a first common light chain comprising a variable light domain and a constant light domain; and

d) a second common light chain comprising a variable light domain and a constant light domain,

wherein the first variable heavy domain and the variable light domain of the first common light chain form a first CLDN6 ABD, and the second variable heavy domain and the variable light domain of the second common light chain form a second CLDN6 ABD,

wherein the first and second CLDN6 antigen binding domains each comprise a set of 6 CDRs (vhCDR1, vhCDR2, vhCDR3, vlCDR1, vlCDR2 and vlCDR3) from a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205 and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID

NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221 and SEQ ID NO: 321), H1.7_L1.4 (SEQ ID NO: 225 and SEQ ID NO: 321), H1.8_L1.4 (SEQ ID NO: 229 and SEQ ID NO: 321), H1.9_L1.4 (SEQ ID NO: 233 and SEQ ID NO: 321), H1.19_L1.4 (SEQ ID NO: 237 and SEQ ID NO: 321), H1.22_L1.4 (SEQ ID NO: 241 and SEQ ID NO: 321), H1.24_L1.4 (SEQ ID NO: 245 and SEQ ID NO: 321), H2_L1.4 (SEQ ID NO: 189 and SEQ ID NO: 321), H2.1_L1.4 (SEQ ID NO: 249 and SEQ ID NO: 321), H2.2_L1.4 (SEQ ID NO: 253 and SEQ ID NO: 321), H2.3_L1.4 (SEQ ID NO: 257 and SEQ ID NO: 321), H2.4_L1.4 (SEQ ID NO: 261 and SEQ ID NO: 321), H2.5_L1.4 (SEQ ID NO: 265 and SEQ ID NO: 321), H2.6_L1.4 (SEQ ID NO: 269 and SEQ ID NO: 321), H2.7_L1.4 (SEQ ID NO: 273 and SEQ ID NO: 321), H2.8_L1.4 (SEQ ID NO: 277 and SEQ ID NO: 321), H2.9_L1.4 (SEQ ID NO: 281 and SEQ ID NO: 321), H2.11_L1.4 (SEQ ID NO: 285 and SEQ ID NO: 321), H2.12_L1.4 (SEQ ID NO: 289 and SEQ ID NO: 321), H2.71_L1.4 (SEQ ID NO: 293 and SEQ ID NO: 321), H2.75_L1.4 (SEQ ID NO: 297 and SEQ ID NO: 321), H2.90_L1.4 (SEQ ID NO: 301 and SEQ ID NO: 321), H2.91_L1.4 (SEQ ID NO: 305 and SEQ ID NO: 321), H2.118_L1.4 (SEQ ID NO: 309 and SEQ ID NO: 321), H2.119_L1.4

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and SEQ ID NO: 365), H1.6_L1.114 (SEQ ID NO: 221 and SEQ ID NO: 365), H1.7_L1.114 (SEQ ID NO: 225 and SEQ ID NO: 365), H1.8_L1.114 (SEQ ID NO: 229 and SEQ ID NO: 365), H1.9_L1.114 (SEQ ID NO: 233 and SEQ ID NO: 365), H1.19_L1.114 (SEQ ID NO: 237 and SEQ ID NO: 365), H1.22_L1.114 (SEQ ID NO: 241 and SEQ ID NO: 365), H1.24_L1.114 (SEQ ID NO: 245 and SEQ ID NO: 365), H2_L1.114 (SEQ ID NO: 189 and SEQ ID NO: 365), H2.1_L1.114 (SEQ ID NO: 249 and SEQ ID NO: 365), H2.2_L1.114 (SEQ ID NO: 253 and SEQ ID NO: 365), H2.3_L1.114 (SEQ ID NO: 257 and SEQ ID NO: 365), H2.4_L1.114 (SEQ ID NO: 261 and SEQ ID NO: 365), H2.5_L1.114 (SEQ ID NO: 265 and SEQ ID NO: 365), H2.6_L1.114 (SEQ ID NO: 269 and SEQ ID NO: 365), H2.7_L1.114 (SEQ ID NO: 273 and SEQ ID NO: 365), H2.8_L1.114 (SEQ ID NO: 277 and SEQ ID NO: 365), H2.9_L1.114 (SEQ ID NO: 281 and SEQ ID NO: 365), H2.11_L1.114 (SEQ ID NO: 285 and SEQ ID NO: 365), H2.12_L1.114 (SEQ ID NO: 289 and SEQ ID NO: 365), H2.71_L1.114 (SEQ ID NO: 293 and SEQ ID NO: 365), H2.75_L1.114 (SEQ ID NO: 297 and SEQ ID NO: 365), H2.90_L1.114 (SEQ ID NO: 301 and SEQ ID NO: 365), H2.91_L1.114 (SEQ ID NO: 305 and SEQ ID NO: 365), H2.118_L1.114 (SEQ ID NO: 309 and SEQ ID NO: 365), H2.119_L1.114 (SEQ ID NO: 313 and SEQ ID NO: 365), H1_L1.187 (SEQ ID NO: 185 and SEQ ID NO: 369), H1.1_L1.187 (SEQ ID NO: 201 and SEQ ID NO: 369), H1.2_L1.187 (SEQ ID NO: 205 and SEQ ID NO: 369), H1.3_L1.187 (SEQ ID NO: 209 and SEQ ID NO: 369), H1.4_L1.187 (SEQ ID NO: 213 and SEQ ID NO: 369), H1.5_L1.187 (SEQ ID NO: 217 and SEQ ID NO: 369), H1.6_L1.187 (SEQ ID NO: 221 and SEQ ID NO: 369), H1.7_L1.187 (SEQ ID NO: 225 and SEQ ID NO: 369), H1.8_L1.187 (SEQ ID NO: 229 and SEQ ID NO: 369), H1.19_L1.187 (SEQ ID NO: 237 and SEQ ID NO: 369), H1.22_L1.187 (SEQ ID NO: 241 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), H2_L1.187 (SEQ ID NO: 189 and SEQ ID NO: 369), H2.1_L1.187 (SEQ ID NO: 249 and SEQ ID NO: 369), H2.2_L1.187 (SEQ ID NO: 253 and SEQ ID NO: 369), H2.3_L1.187 (SEQ ID NO: 257 and SEQ ID NO: 369), H2.4_L1.187 (SEQ ID NO: 261 and SEQ ID NO: 369), H2.5_L1.187 (SEQ ID NO: 265 and SEQ ID NO: 369), H2.6_L1.187 (SEQ ID NO: 269 and SEQ ID NO: 369), H2.7_L1.187 (SEQ ID NO: 273 and SEQ ID NO: 369), H2.8_L1.187 (SEQ ID NO: 277 and SEQ ID NO: 369), H2.9_L1.187 (SEQ ID NO: 281 and SEQ ID NO: 369), H2.11_L1.187 (SEQ ID NO: 285 and SEQ ID NO: 369), H2.12_L1.187 (SEQ ID NO: 289 and SEQ ID NO: 369), H2.71_L1.187 (SEQ ID NO: 293 and SEQ ID NO: 369), H2.75_L1.187 (SEQ ID NO: 297 and SEQ ID NO: 369), H2.90_L1.187 (SEQ ID NO: 301 and SEQ ID NO: 369), H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369), H2.118_L1.187 (SEQ ID NO: 309 and SEQ ID NO: 369), H2.119_L1.187 (SEQ ID NO: 313 and SEQ ID NO: 369), H1_L1.189 (SEQ ID NO: 185 and SEQ ID NO: 373), H1.1_L1.189 (SEQ ID NO: 201 and SEQ ID NO: 373), H1.2_L1.189 (SEQ ID NO: 205 and SEQ ID NO: 373), H1.3_L1.189 (SEQ ID NO: 209 and SEQ ID NO: 373), H1.4_L1.189 (SEQ ID NO: 213 and SEQ ID NO: 373), H1.5_L1.189 (SEQ ID NO: 217 and SEQ ID NO: 373), H1.6_L1.189

(SEQ ID NO: 221 and SEQ ID NO: 373), H1.7_L1.189 (SEQ ID NO: 225 and SEQ ID NO: 373), H1.8_L1.189 (SEQ ID NO: 229 and SEQ ID NO: 373), H1.9_L1.189 (SEQ ID NO: 233 and SEQ ID NO: 373), H1.19_L1.189 (SEQ ID NO: 237 and SEQ ID NO: 373), H1.22_L1.189 (SEQ ID NO: 241 and SEQ ID NO: 373), H1.24_L1.189 (SEQ ID NO: 245 and SEQ ID NO: 373), H2_L1.189 (SEQ ID NO: 189 and SEQ ID NO: 373), H2.1_L1.189 (SEQ ID NO: 249 and SEQ ID NO: 373), H2.2_L1.189 (SEQ ID NO: 253 and SEQ ID NO: 373), H2.3_L1.189 (SEQ ID NO: 257 and SEQ ID NO: 373), H2.4_L1.189 (SEQ ID NO: 261 and SEQ ID NO: 373), H2.5_L1.189 (SEQ ID NO: 265 and SEQ ID NO: 373), H2.6_L1.189 (SEQ ID NO: 269 and SEQ ID NO: 373), H2.7_L1.189 (SEQ ID NO: 273 and SEQ ID NO: 373), H2.8_L1.189 (SEQ ID NO: 277 and SEQ ID NO: 373), H2.9_L1.189 (SEQ ID NO: 281 and SEQ ID NO: 373), H2.11_L1.189 (SEQ ID NO: 285 and SEQ ID NO: 373), H2.12_L1.189 (SEQ ID NO: 289 and SEQ ID NO: 373), H2.71_L1.189 (SEQ ID NO: 293 and SEQ ID NO: 373), H2.75_L1.189 (SEQ ID NO: 297 and SEQ ID NO: 373), H2.90_L1.189 (SEQ ID NO: 301 and SEQ ID NO: 373), H2.91_L1.189 (SEQ ID NO: 305 and SEQ ID NO: 373), H2.118_L1.189 (SEQ ID NO: 309 and SEQ ID NO: 373), H2.119_L1.189 (SEQ ID NO: 313 and SEQ ID NO: 373), H1_L2 (SEQ ID NO: 185 and SEQ ID NO: 197), H1.1_L2 (SEQ ID NO: 201 and SEQ ID NO: 197), H1.2_L2 (SEQ ID NO: 205 and SEQ ID NO: 197), H1.3_L2 (SEQ ID NO: 209 and SEQ ID NO: 197), H1.4_L2 (SEQ ID NO: 213 and SEQ ID NO: 197), H1.5_L2 (SEQ ID NO: 217 and SEQ ID NO: 197), H1.6_L2 (SEQ ID NO: 221 and SEQ ID NO: 197), H1.7_L2 (SEQ ID NO: 225 and SEQ ID NO: 197), H1.8_L2 (SEQ ID NO: 229 and SEQ ID NO: 197), H1.9_L2 (SEQ ID NO: 233 and SEQ ID NO: 197), H1.19_L2 (SEQ ID NO: 237 and SEQ ID NO: 197), H1.22_L2 (SEQ ID NO: 241 and SEQ ID NO: 197), H1.24_L2 (SEQ ID NO: 245 and SEQ ID NO: 197), H2_L2 (SEQ ID NO: 189 and SEQ ID NO: 197), H2.1_L2 (SEQ ID NO: 249 and SEQ ID NO: 197), H2.2_L2 (SEQ ID NO: 253 and SEQ ID NO: 197), H2.3_L2 (SEQ ID NO: 257 and SEQ ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

8. The heterodimeric antibody according to claim 7, wherein each of the first and second CLDN6 antigen binding domains comprises a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1_L1 (SEQ ID NO: 185 and SEQ ID NO: 193), H1.1_L1 (SEQ ID NO: 201 and SEQ ID NO: 193), H1.2_L1 (SEQ ID NO: 205

and SEQ ID NO: 193), H1.3_L1 (SEQ ID NO: 209 and SEQ ID NO: 193), H1.4_L1 (SEQ ID NO: 213 and SEQ ID NO: 193), H1.5_L1 (SEQ ID NO: 217 and SEQ ID NO: 193), H1.6_L1 (SEQ ID NO: 221 and SEQ ID NO: 193), H1.7_L1 (SEQ ID NO: 225 and SEQ ID NO: 193), H1.8_L1 (SEQ ID NO: 229 and SEQ ID NO: 193), H1.9_L1 (SEQ ID NO: 233 and SEQ ID NO: 193), H1.19_L1 (SEQ ID NO: 237 and SEQ ID NO: 193), H1.22_L1 (SEQ ID NO: 241 and SEQ ID NO: 193), H1.24_L1 (SEQ ID NO: 245 and SEQ ID NO: 193), H2_L1 (SEQ ID NO: 189 and SEQ ID NO: 193), H2.1_L1 (SEQ ID NO: 249 and SEQ ID NO: 193), H2.2_L1 (SEQ ID NO: 253 and SEQ ID NO: 193), H2.3_L1 (SEQ ID NO: 257 and SEQ ID NO: 193), H2.4_L1 (SEQ ID NO: 261 and SEQ ID NO: 193), H2.5_L1 (SEQ ID NO: 265 and SEQ ID NO: 193), H2.6_L1 (SEQ ID NO: 269 and SEQ ID NO: 193), H2.7_L1 (SEQ ID NO: 273 and SEQ ID NO: 193), H2.8_L1 (SEQ ID NO: 277 and SEQ ID NO: 193), H2.9_L1 (SEQ ID NO: 281 and SEQ ID NO: 193), H2.11_L1 (SEQ ID NO: 285 and SEQ ID NO: 193), H2.12_L1 (SEQ ID NO: 289 and SEQ ID NO: 193), H2.71_L1 (SEQ ID NO: 293 and SEQ ID NO: 193), H2.75_L1 (SEQ ID NO: 297 and SEQ ID NO: 193), H2.90_L1 (SEQ ID NO: 301 and SEQ ID NO: 193), H2.91_L1 (SEQ ID NO: 305 and SEQ ID NO: 193), H2.118_L1 (SEQ ID NO: 309 and SEQ ID NO: 193), H2.119_L1 (SEQ ID NO: 313 and SEQ ID NO: 193), H1_L1.1 (SEQ ID NO: 185 and SEQ ID NO: 317), H1.1_L1.1 (SEQ ID NO: 201 and SEQ ID NO: 317), H1.2_L1.1 (SEQ ID NO: 205 and SEQ ID NO: 317), H1.3_L1.1 (SEQ ID NO: 209 and SEQ ID NO: 317), H1.4_L1.1 (SEQ ID NO: 213 and SEQ ID NO: 317), H1.5_L1.1 (SEQ ID NO: 217 and SEQ ID NO: 317), H1.6_L1.1 (SEQ ID NO: 221 and SEQ ID NO: 317), H1.7_L1.1 (SEQ ID NO: 225 and SEQ ID NO: 317), H1.8_L1.1 (SEQ ID NO: 229 and SEQ ID NO: 317), H1.9_L1.1 (SEQ ID NO: 233 and SEQ ID NO: 317), H1.19_L1.1 (SEQ ID NO: 237 and SEQ ID NO: 317), H1.22_L1.1 (SEQ ID NO: 241 and SEQ ID NO: 317), H1.24_L1.1 (SEQ ID NO: 245 and SEQ ID NO: 317), H2_L1.1 (SEQ ID NO: 189 and SEQ ID NO: 317), H2.1_L1.1 (SEQ ID NO: 249 and SEQ ID NO: 317), H2.2_L1.1 (SEQ ID NO: 253 and SEQ ID NO: 317), H2.3_L1.1 (SEQ ID NO: 257 and SEQ ID NO: 317), H2.4_L1.1 (SEQ ID NO: 261 and SEQ ID NO: 317), H2.5_L1.1 (SEQ ID NO: 265 and SEQ ID NO: 317), H2.6_L1.1 (SEQ ID NO: 269 and SEQ ID NO: 317), H2.7_L1.1 (SEQ ID NO: 273 and SEQ ID NO: 317), H2.8_L1.1 (SEQ ID NO: 277 and SEQ ID NO: 317), H2.9_L1.1 (SEQ ID NO: 281 and SEQ ID NO: 317), H2.11_L1.1 (SEQ ID NO: 285 and SEQ ID NO: 317), H2.12_L1.1 (SEQ ID NO: 289 and SEQ ID NO: 317), H2.71_L1.1 (SEQ ID NO: 293 and SEQ ID NO: 317), H2.75_L1.1 (SEQ ID NO: 297 and SEQ ID NO: 317), H2.90_L1.1 (SEQ ID NO: 301 and SEQ ID NO: 317), H2.91_L1.1 (SEQ ID NO: 305 and SEQ ID NO: 317), H2.118_L1.1 (SEQ ID NO: 309 and SEQ ID NO: 317), H2.119_L1.1 (SEQ ID NO: 313 and SEQ ID NO: 317), H1_L1.4 (SEQ ID NO: 185 and SEQ ID NO: 321), H1.1_L1.4 (SEQ ID NO: 201 and SEQ ID NO: 321), H1.2_L1.4 (SEQ ID NO: 205 and SEQ ID NO: 321), H1.3_L1.4 (SEQ ID NO: 209 and SEQ ID NO: 321), H1.4_L1.4 (SEQ ID NO: 213 and SEQ ID NO: 321), H1.5_L1.4 (SEQ ID NO: 217 and SEQ ID NO: 321), H1.6_L1.4 (SEQ ID NO: 221

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ID NO: 197), H2.4_L2 (SEQ ID NO: 261 and SEQ ID NO: 197), H2.5_L2 (SEQ ID NO: 265 and SEQ ID NO: 197), H2.6_L2 (SEQ ID NO: 269 and SEQ ID NO: 197), H2.7_L2 (SEQ ID NO: 273 and SEQ ID NO: 197), H2.8_L2 (SEQ ID NO: 277 and SEQ ID NO: 197), H2.9_L2 (SEQ ID NO: 281 and SEQ ID NO: 197), H2.11_L2 (SEQ ID NO: 285 and SEQ ID NO: 197), H2.12_L2 (SEQ ID NO: 289 and SEQ ID NO: 197), H2.71_L2 (SEQ ID NO: 293 and SEQ ID NO: 197), H2.75_L2 (SEQ ID NO: 297 and SEQ ID NO: 197), H2.90_L2 (SEQ ID NO: 301 and SEQ ID NO: 197), H2.91_L2 (SEQ ID NO: 305 and SEQ ID NO: 197), H2.118_L2 (SEQ ID NO: 309 and SEQ ID NO: 197), and H2.119_L2. (SEQ ID NO: 313 and SEQ ID NO: 197).

9. The heterodimeric antibody according to claim 7 or 8, wherein the scFv comprises a variable heavy domain and a variable light domain of any of the following CD3 antigen binding domains: L1.47_H1.32 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.30_L1.47 (SEQ ID NO: 100 and SEQ ID NO: 104), H1.32_L1.47 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.89_L1.47 (SEQ ID NO: 122 and SEQ ID NO: 126), H1.90_L1.47 (SEQ ID NO: 133 and SEQ ID NO: 137), H1.33_L1.47 (SEQ ID NO: 144 and SEQ ID NO: 148), H1.31_L1.47 (SEQ ID NO: 155 and SEQ ID NO: 159), L1.47_H1.30 (SEQ ID NO: 100 and SEQ ID NO: 104), L1.47_H1.89 (SEQ ID NO: 122 and SEQ ID NO: 126), L1.47_H1.90 (SEQ ID NO: 133 and SEQ ID NO: 137), L1.47_H1.33 (SEQ ID NO: 144 and SEQ ID NO: 148), and L1.47_H1.31, (SEQ ID NO: 155 and SEQ ID NO: 159).

10. A heterodimeric antibody according to any one of claims 7 to 9, wherein the first and second Fc domains are variant Fc domains.

11. A heterodimeric antibody according to any of claims 7 to 10, wherein the first and second Fc domains comprise a set of heterodimerization variants selected from the group consisting of those depicted in Figures 1A-1E.

12. A heterodimeric antibody according to claim 11, wherein the set of heterodimerization variants selected is from the group consisting of S364K/E357Q : L368D/K370S; S364K : L368D/K370S; S364K : L368E/K370S; D401K: T411E/K360E/Q362E; and T366W : T366S/L368A/Y407V, wherein numbering is according to EU numbering.

13. A heterodimeric antibody according to any of claims 7 to 12, wherein the first and second monomers further comprise one or more ablation variants.

14. A heterodimeric antibody according to claim 13, wherein one or more ablation variants are E233P/L234V/L235A/G236del/S267K, wherein numbering is according to EU numbering.

15. A heterodimeric antibody according to any of claims 7 to 14, wherein one of the first or second monomer further comprises one or more pl variants.

16. A heterodimeric antibody according to claim 15, wherein the pl variants are N208D/Q295E/N384D/Q418E/N421D, wherein numbering is according to EU numbering.

17. A heterodimeric antibody according to any one of claims 7 to 16, wherein the first variant Fc domain comprises amino acid variants S364K/E357Q/E233P/L234V/L235A/G236del/S267K, wherein the second variant Fc domain comprises amino acid variants L368D/K370S/N208D/Q295E/N384D/Q418E/N421D/E233P/L234V/L235A/G236del/S267K, and wherein numbering is according to EU numbering.

18. A heterodimeric antibody according to claim 17, wherein the scFv linker is a charged scFv linker having the amino acid sequence (GKPGS)₄ (SEQ ID NO: 1).

19. A heterodimeric antibody according to claim 18, wherein the first and second variant Fc domains each further comprise amino acid variants M428L/N434S, wherein numbering is according to EU numbering.

20. A heterodimeric antibody comprising:

a) a first monomer comprising, from N-terminal to C-terminal, a VH1-CH1-linker 1-scFv-linker 2-CH2-CH3,

wherein VH1 is a first variable heavy domain, scFv is an anti-CD3 scFv, linker 1 and linker 2 are a first domain linker and second domain linker, respectively, and CH2-CH3 is a first variant Fc domain;

b) a second monomer comprising, from N-terminal to C-terminal, a VH2-CH1-hinge-CH2-CH3, wherein VH2 is a second variable heavy domain, and CH2-CH3 is a second variant Fc domain; and

c) a first common light chain comprising a variable light domain and a constant light domain; and

d) a second common light chain comprising a variable light domain and a constant light domain,

wherein the first variable heavy domain and the variable light domain of the first common light chain form a first CLDN3 ABD, and the second variable heavy domain and the variable light domain of the second common light chain form a second CLDN3 ABD,

wherein the first variant Fc domain comprises amino acid variants S364K/E357Q,
wherein the second variant Fc domain comprises amino acid variants L368D/K370S,
wherein the first and second variant Fc domains each comprises amino acid variants E233P/L234V/L235A/G236del/S267K,

wherein the CH1-hinge-CH2-CH3 of the second monomer comprises amino acid variants N208D/Q295E/N384D/Q418E/N421D,

wherein each of the first and second CLDN6 antigen binding domains have a VH/VL pair selected from the group consisting of: H1.9_L1.187 (SEQ ID NO: 233 and SEQ ID NO: 369), H1.24_L1.187 (SEQ ID NO: 245 and SEQ ID NO: 369), and H2.91_L1.187 (SEQ ID NO: 305 and SEQ ID NO: 369);

wherein the anti-CD3 scFv comprises a variable heavy domain and a variable light domain of a CD3 antigen binding domain selected from the group consisting of: L1.47_H1.32 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.30_L1.47 (SEQ ID NO: 100 and SEQ ID NO: 104), H1.32_L1.47 (SEQ ID NO: 111 and SEQ ID NO: 115), H1.89_L1.47 (SEQ ID NO: 122 and SEQ ID NO: 126), H1.90_L1.47 (SEQ ID NO: 133 and SEQ ID NO: 137), H1.33_L1.47 (SEQ ID NO: 144 and SEQ ID NO: 148), H1.31_L1.47 (SEQ ID NO: 155 and SEQ ID NO: 159), L1.47_H1.30 (SEQ ID NO: 100 and SEQ ID NO: 104), L1.47_H1.89 (SEQ ID NO: 122 and SEQ ID NO: 126), L1.47_H1.90 (SEQ ID NO: 133 and SEQ ID NO: 137), L1.47_H1.33 (SEQ ID NO: 144 and SEQ ID NO: 148), and L1.47_H1.31, (SEQ ID NO: 155 and SEQ ID NO: 159), and

wherein numbering is according to EU numbering.

21. A heterodimeric antibody according to claim 20, wherein the first and second variant Fc domains each further comprise amino acid variants M428L/N434S.

22. A nucleic acid composition comprising:

- a) a first nucleic acid encoding the first monomer of any of claims 7 to 21;
- b) a second nucleic acid encoding the second monomer of any of claims 7 to 21; and
- c) a third nucleic acid encoding the light chain of any of claims 7 to 21, respectively.

23. An expression vector composition comprising:

- a) a first expression vector comprising the first nucleic acid of claim 22;
- b) a second expression vector comprising the second nucleic acid of claim 22; and
- c) a third expression vector comprising the third nucleic acid of claim 22.

24. A host cell transformed with the expression vector composition of claim 23.

25. A method of making a heterodimeric antibody comprising culturing the host cell of claim 24 under conditions wherein the antibody is expressed and recovering the antibody.

26. A heterodimeric antibody comprising:

- a) a first monomer having an amino acid sequence of SEQ ID NO: 567;
- b) a second monomer having an amino acid sequence of SEQ ID NO: 568; and
- c) a light chain having an amino acid sequence of SEQ ID NO: 569.