

```

          FR1          CDR1          FR2          CDR2          FR3
DH840.1H QVQLKESGPGLVLPSETLSLTCAVSGTSINSAYAWGWVRLPPGKGLEWIMTVYTSTGNTYSDPSLKSRVT
DH846.1H .L..Q.....K.....D...V..S.N.G...I.Q.....D..V.I.GG.....YA...EG...A

          FR3          CDR3          FR4
DH840.1H ISKDTSKNQFSLRLSSVTVEDTAVYFCARADGSDSGWPHFDNWGQGLLVTVSS 123
DH846.1H ....A.....N...AA.....Y...KITYS...YY..Y....V..A...

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```

          FR1          CDR1          FR2          CDR2          FR3
DH840.1L EIMVTQSPATLSVSPGERATLSCRASQSVRNRIAWYQQKPGQSPRLLIYDASIRAPGIPDRLSGSGSGTEFTLTINSLEP
DH846.1L ..VM.....L.....SS.L.....A.....N..T.....F.....SG...

          FR3          CDR3          FR4
DH840.1L SDVAVYFCQLEANWLTFGGGTKVEIK
DH846.1L E.....EDH..S...Q.....

```

S13 Fig. Amino acid alignment of DH840.1 and DH846.1 variable regions.

Complementarity determining regions (CDR) and framework regions (FR) are designated using the Kabat definitions for the heavy chain (H, top) and light chain (L, bottom) variable regions. Periods indicate identical amino acids.