Mruk et al., http://www.jgp.org/cgi/content/full/jgp.201311140/DC1

Tables S1 and S2 are available for download as Excel files.

```
                      S1
Motif Score        04AAACZZZZZZZZZZZC885
                98 ---------+---------+- 118
Residue            AFVYHVFIFLLVFSCLVLSVL
1-10                12222345566555543221
1-5-10              12222345555444432111
1-12                11112334555544443221
1-14                 1111233333333322221
1-8-14               11111111111111
1-5-8-14             11111111111111
1-16                12223333333333332111
```

```
                      S2
Motif Score        36ACCEZZZZZZZZFFFB883
               132 ---------+---------+- 152
Residue            LLILEFVMIVVFGLEYIVRVW
1-10               123333334444333333221
1-5-10              12222222221
1-12               112223445666554443221
1-14               11122233333333222111
1-8-14                11122222222222111
1-5-8-14                 11111111111111
1-16                12223333333333332111
```

```
                      S3
Motif Score        022588ACCCCBBB9960000
               173 ---------+---------+- 193
Residue            PFCVIDFIVFVASVAVIAAGT
1-10                1112234444333221
1-5-10                 1123333333221
1-12                   111111111111
1-14                  11111111111111
1-8-14                11111111111111
1-5-8-14              11111111111111
1-16                1111111111111111
```

```
                      S4
Motif Score        01111112233223333333333
               202 ---------+---------+--- 224
Residue            ALRSMRFLQILRMVRMDRRGGTW
1-10                1111111111  1111111111
1-5-10
1-12
1-14                        11111111111111
1-8-14
1-5-8-14
1-16                      1111111111111111
```

```
                      S5
Motif Score        4777CCDDFZZZFEBBBA422
               238 ---------+---------+- 258
Residue            LITAWYIGFLVLIFASFLVYL
1-10               122233334544443333211
1-5-10             1111222234333322221
1-12               122222333444322222111
1-14               111122222222221111
1-8-14                 11111111111111
1-5-8-14               11111111111111
1-16               1111111111111111
```

```
                      S6
Motif Score        036666666779776443333
               297 ---------+---------+- 317
Residue            RVLAAGFALLGISFFALPAGI
1-10                 1111111112111111111
1-5-10               1111111112111111111
1-12                 1111111222221111111
1-14                11111111111111
1-8-14              11111111111111
1-5-8-14
1-16                1111111111111111
```

Figure S1. A positive charge discriminator excludes most KCNQ4 transmembrane domains from being predicted as CaM-binding domains. Depiction of the canonical CaM-binding motifs within each transmembrane domain (S1–S6) of KCNQ4 channels. Totals (in hexadecimal) for each residue are shown. Values greater than F are scored as "Z." Yellow highlighted residues denote the meta-analysis predictions.