Figure S6   Bürstenbinder et al.
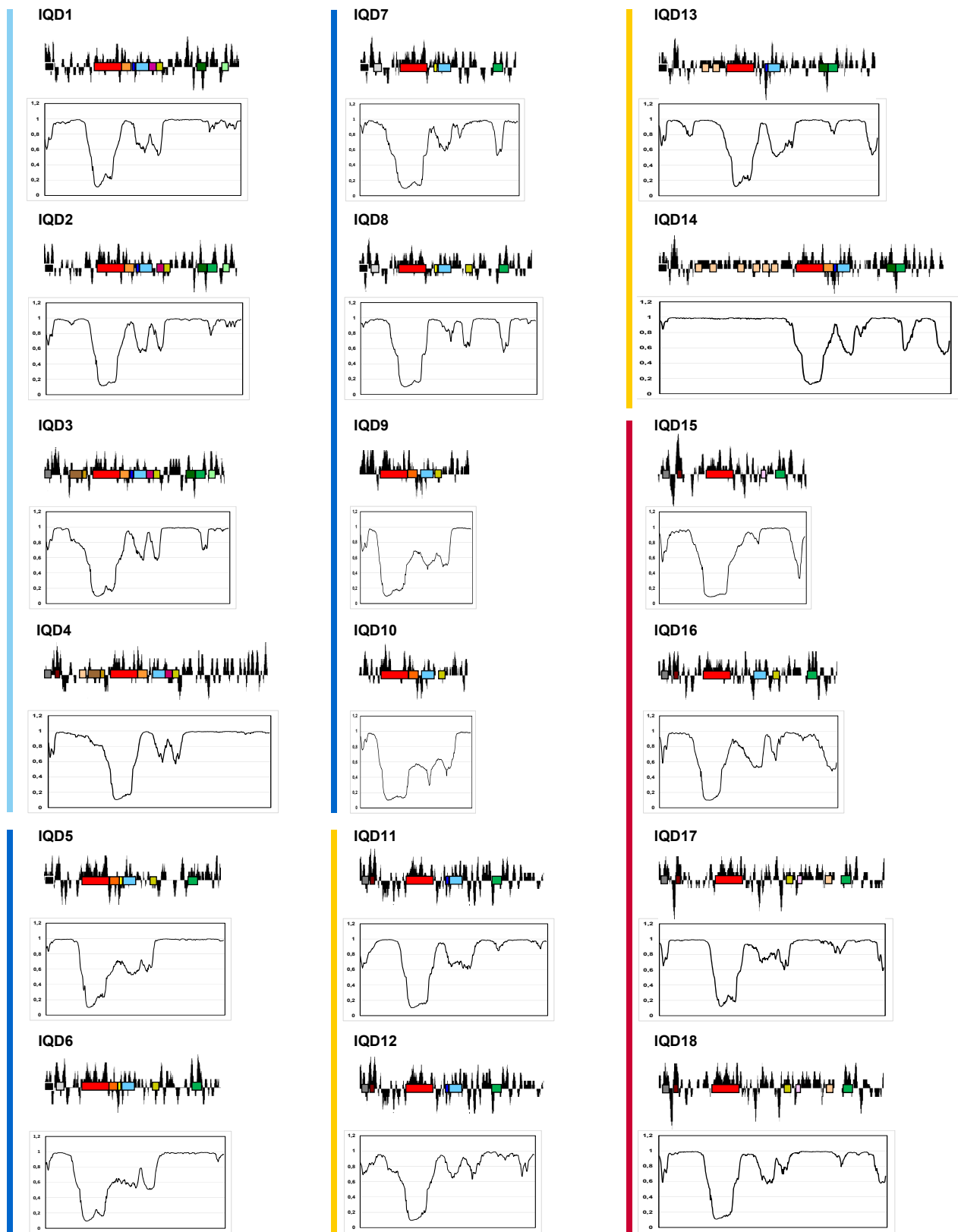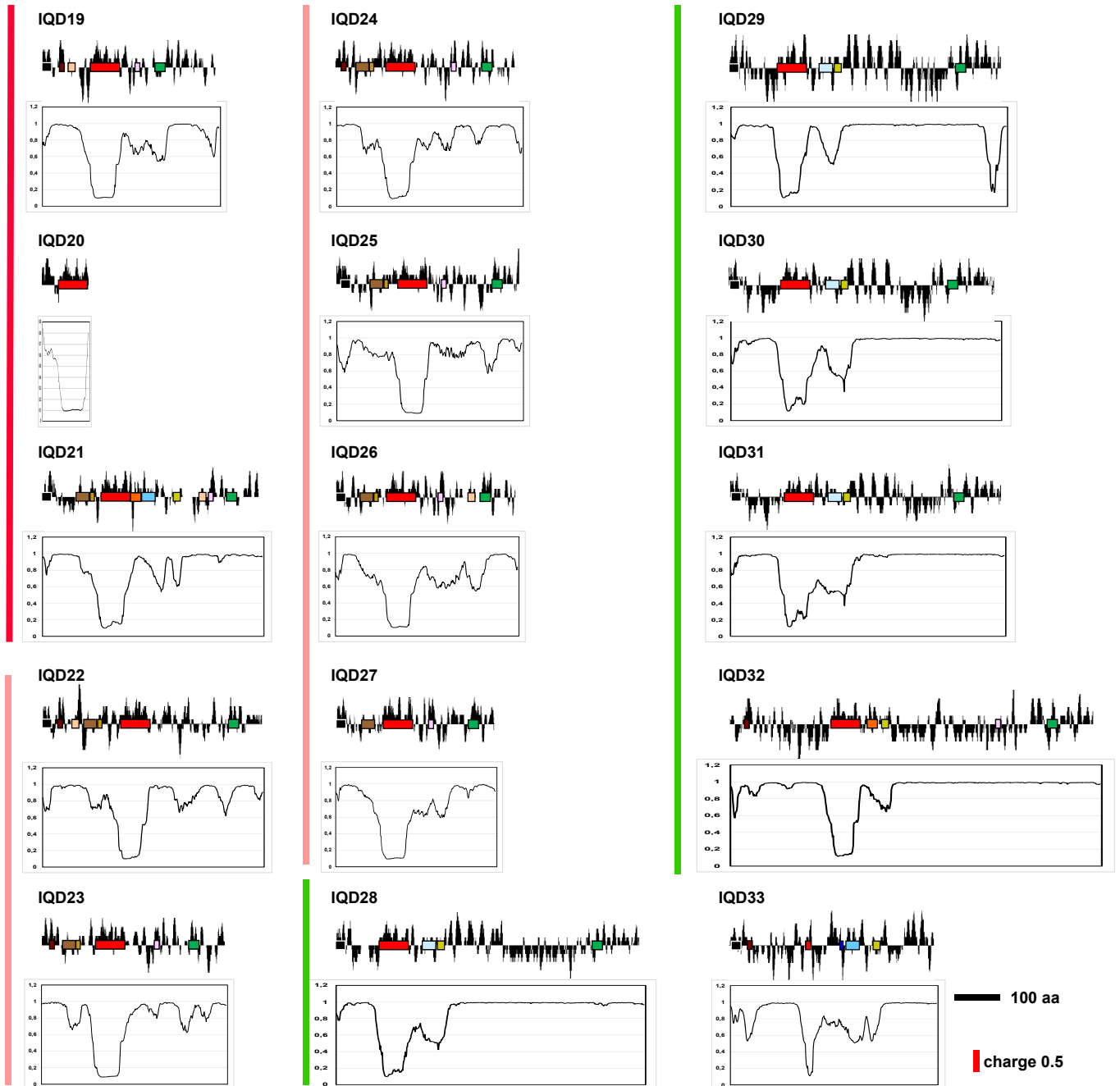
IQD1

IQD2

IQD3

IQD4

IQD5

IQD6

IQD7

IQD8

IQD9

IQD10

IQD11

IQD12

IQD13

IQD14

IQD15

IQD16

IQD17

IQD18

Supplemental Figure 6. Predicted Properties of *A. thaliana* IQD Proteins.
The predicted amino acid sequences of the 33 *Arabidopsis* IQD proteins were analyzed for charge distribution (top) and intrinsic disorder (bottom) using the EMBOSS charge tool (http://emboss.bioinformatics.nl/cgi-bin/emboss/charge) and SPINE-D (Zhang et al., 2012) neural networks (http://sparks-lab.org/SPINE-D/), respectively. The plots (length of IQD proteins) are drawn to scale, and shown according to the position of motifs and domains (red, IQ67 domain) and phylogenetic groups (vertical bars). Mean charges were computed across a window of 5 amino acid residues using the following values: -1 (Asp, Glu), +0.5 (His), +1 (Lys, Arg). The IQ67 domain is likely highly ordered (scores < 0.4), whereas the flanking regions are predicted to be largely disordered. Scores of 0.4-0.7 indicate semi-disorder (semi-collapsed with some secondary structure), and scores of 0.7-1.0 indicate full disorder.