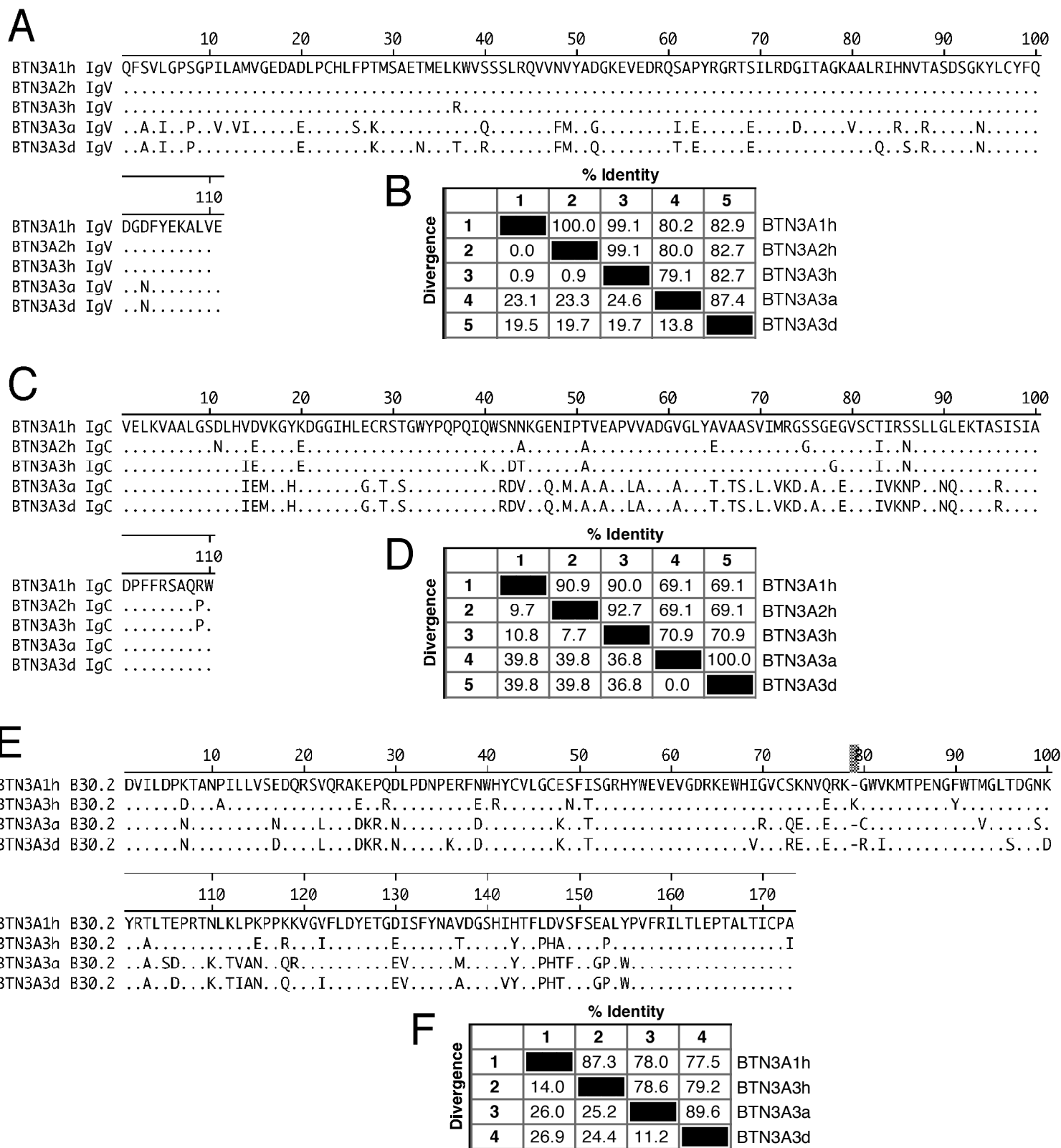


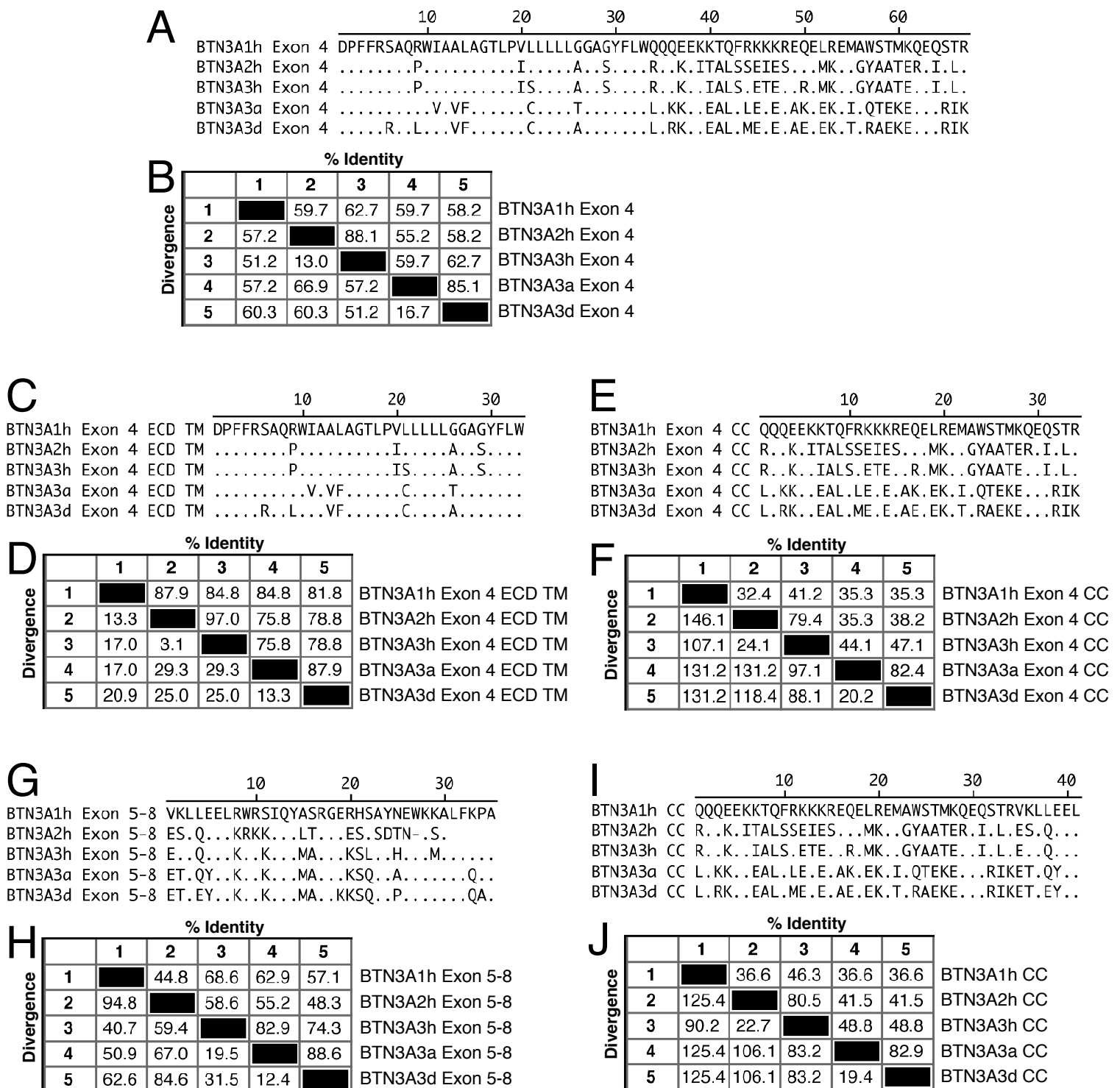
C

		% Identity					
		1	2	3	4	5	
Divergence	1	████	82.0	85.0	71.0	71.4	BTN3A1h
	2	20.6	████	90.4	66.5	68.9	BTN3A2h
	3	16.6	10.3	████	72.4	72.3	BTN3A3h
	4	36.7	44.3	32.7	████	85.5	BTN3A3a
	5	36.1	40.2	30.1	15.3	████	BTN3A3d

SUPPLEMENTAL FIGURE 2. Characteristics of BTN3A1, BTN3A2, and BTN3A3 family members. **(A)** Schematic of the domain organization of BTN3 family members for humans (h), alpacas (a), and dolphins (d). The domain lengths in the schematic are proportional to those in the proteins. **(B)** Amino acid alignments for BTN3 family members. Amino acid identity is shown as a “.” Alignment was done by the Clustal W method. **(C)** Similarity between the BTN3 family members. Identity and divergence table is shown.



SUPPLEMENTAL FIGURE 3. Characteristics of IgV, IgC, and B30.2 domains of BTN3A1, BTN3A2, and BTN3A3 family members. Amino acid alignments for IgV (A), IgC (C), and B30.2 (E) domains of BTN3 family members for humans (h), alpacas (a), and dolphins (d). Amino acid identity is shown as a “.” Alignment was done by the Clustal W method. Similarity between the IgV (B), IgC (D), and B30.2 (F) domains of BTN3 family members. Identity and divergence tables are shown.



SUPPLEMENTAL FIGURE 4. Characteristics of juxtamembrane domains of BTN3A1, BTN3A2, and BTN3A3 family members. Amino acid alignments for exon 4 (A), exon 4 extracellular and transmembrane segment (ECD TM) (C), exon 4 coiled-coil segment (CC) (E), exon 5-8 (G), and coiled-coil (CC) domain (I) of BTN3 family members for humans (h), alpacas (a), and dolphins (d). Amino acid identity is shown as a “.” Alignment was done by the Clustal W method. Similarity between the exon 4 (B), exon 4 ECD TM (D), exon 4 CC (F), exon 5-8 (H), and coiled-coil domain (J) of BTN3 family members. Identity and divergence tables are shown.