

**Figure 2**

Summary of PAML β -distribution ω ratio variation models. The plots are derived from the estimated β -distribution parameters for the M7 (or M8, if statistically superior to M7) models for the NR genes and show for a particular gene how many codons have estimated ω ratios equal to or less than a particular ω ratio on the abscissa. In contrast to Figure 1, only data derived from analyses of all available species are included in Figure 2 (i.e., mammals-only comparisons are not included). **(A)**, **(B)**, and **(C)** apply to analyses of full-length sequences, DBD only, and LBD only, respectively. For part **(C)**, the red curve represents data for the LBD of the AHR gene. Analysis in part **(A)** is for NR1A1, IBI, ICI, IF2, IH3, III, II2, II3, 2A1, 2B1, 3A1, 3A2, 3B1, 3C1, 3C3, 4A1, 5A1, 6A1, 0B1, and 0B2; for part **(B)**, analysis is for NR1A1, IBI, ICI, IH3, III, II2, II3, 2A1, 2B1, 3A1, 3A2, 3B1, 3C1, 3C3, 4A1, 5A1, and 6A1; and for part **(C)**, analysis is for NR1A1, IBI, IF2, IH3, III, II2, II3, 2A1, 2B1, 3A1, 3A2, 3B1, 3C1, 3C3, 4A1, 5A1, 6A1, 0B1, 0B2, and AHR.