



**Figure S6. Phylogeny of vertebrate Insulin receptor substrate (*Irs*) gene family sequences.** Phylogeny of *Irs* sequences from diverse vertebrate species generated by the Bayesian method. A similar phylogeny was generated by Maximum likelihood (see Figure 1). Phylogeny was rooted with sequences from acorn worm, sea urchin and lancelets (labeled as outgroups). Selected *Irs* sequences were chosen to represent the diversity of vertebrates, with different vertebrate *Irs* genes identified on the right. Similar results were obtained if other *Irs* sequences were used. Numbers at the nodes indicate posterior probabilities. Branch lengths are proportional to the inferred amount of change, with the scale bar at the bottom right. Diamonds indicate gene duplication events.