Supplementary Table 1 Sources of RPGR orthologues from 37 vertebrate and 22 invertebrate species.

Supplementary Table 2 Orthologue sequence comparison for RLD domain, and individual repeats. All-against-all pairwise percentage sequence identity for the RPGR RLD orthologues is presented based upon the multiple sequence alignment in Figure 3, for the entire domain and for each of the seven individual repeats. Vertebrates are highlighted in blue, and invertebrates in green. Each individual repeat was defined according to the blade structural length and encompassed all four beta-strands within it (A-D) starting from two residues before beta-strand A and extended up until two residues before the subsequent blade’s first beta-strand A.