



**Fig. S1. Overview of bioinformatic predictions for Nog1.**

Lines: The numbers correspond to the line shown in the figure:

- 1) Protein sequence of Nog1
- 2) Charge distribution
- 3) Disordered regions (GlobPlot) and low complexity region (CDD)
- 4) Disordered regions (Meta-Disorder)
- 5) Transmembrane topology (hmmtop)
- 6) Transmembrane topology (TMHMM)
- 7) As before, shown is the second result with a score of 544
- 8) Transmembrane topology (PHDhtm)
- 9) Transmembrane topology (BCL::Jufo9D, protein.jufo9d\_tmh)
- 10) Protein binding sites (ISIS)
- 11) Beta-turns (NetTurnP)
- 12) Secondary structure (SOPMA)
- 13) Secondary structure (PSIPRED)
- 14) Secondary structure (Pred2ary via Medor)
- 15) Secondary structure (GOR4 via NPS@)
- 16) Secondary structure (PROFseq via PredictProtein)
- 17) Secondary structure (BCL::Jufo9D)
- 18) Secondary structure (Porter)