

Fig S3. Detailed version of the inhibin/activin phylogeny presented in Fig. 1C. The ML analysis used the JTT+ Γ +invariant sites model, as described in the text. Support for specific groups reflects the percentage of 100 bootstrap replicates (only values $\geq 50\%$). The version in the text indicates the occurrence of indel mutations, including the indels shown to have a major functional impact.

