



Figure S5. Paralogous clusters containing *CTNNA* genes in the human genome. An example of automatic output from the Synteny Database using *EGR2* as a query, sliding window size = 50 and *Ciona intestinalis* as outgroup. The result shows that a few genes (including *EGR1-4* and *REEP1-4*) that are near *CTNNA* genes have four paralogs in the human genome consistent with the idea that the three *CTNNAs* may have originated by two rounds of whole genome duplications.