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.