Figure S1. Nucleotides sequences of RT-PCR after yap-MO(S) injection and difference between two transcript variants. yap-MO(S) targeted site is underlined by a red line. Primers used in RT-PCR are underline by two green arrows. After yap-MO(S) injection, the large fragment contains parts of intron 2 which is wrote in blue and the small fragment omits exon 2. The YAP transcript variant YAP2 loses the forth exon which is underlined by a black line.
Figure S2. BLAST result and schematic diagrams of YAP amino Acids sequences from different organisms

A) Protein sequence comparison among chicken YAP (NCBI Reference Sequence NP_990574), two mouse transcriptional variants (NCBI Reference Sequence: NP_001164618 and NP_033560), two human transcriptional variants (NCBI Reference Sequence: NP_001123617 and NP_006097), zebrafish YAP with only one WW domain and zebrafish YAP with two WW domains (NCBI Reference Sequence: NP_001132952). These amino acid sequences were analyzed using T-coffee (http://tcoffee.vital-it.ch/cgi-bin/Tcoffee/tcoffee_cgi/index.cgi). In the alignment, spaces are introduced arbitrarily and are indicated with dots. WW domain is underlined (blue), each with two featured tryptophan (W) residues denoted by blue dots. TEA/TEAD-binding domain is underlined (green). The 14-3-3 binding site is indicated by a green dashed line. HXRXXS motifs are underlined (black). proline-rich regions are indicated by a black dashed line. B) A schematic diagram shows the structures of these different YAPs. Green rectangles represent the TEA/TEAD-binding domain. Green rectangular dashed lines represent the 14-3-3 binding site. WW domains are indicated by blue blocks. Black rectangular dashed lines represent the proline-rich regions. The red blocks represent the sequence of AXRNINPSTANXP. For the purpose of clarity, some of the proteins and domains were not drawn to scale.