

a3-F		5' -GGCTGCCAARAAYYTNATGAAYGC-3'
<i>ctnna</i>	lamprey	GGCAGCCAAGAACCTGATGAACGC
<i>ctnna3</i>	coelaca	GGCTGCCAAGAACTTGATGAATGC
<i>ctnna3</i>	chicken	GGCTGCCAAAAATTTAATGAACGC
<i>Ctnna3</i>	mouse	GGCAGCCAAGAATTTAATGAATGC
<i>ctnna1</i>	xenopus	AGCTGCGAAAAATCTGATGAATGC
<i>ctnna2</i>	xenopus	GGCAGCTAAGAATTTGATGAATGC
<i>ctnna1</i>	chicken	GGCGCCAAGAACCTGATGAACGC
<i>ctnna2</i>	chicken	GGCAGCTAAAAATCTGATGAACGC

a3-R		5' -GGCTTCTTTKCNNGGNGCYTTCAT-3'
<i>ctnna</i>	lamprey	GGCTTCTTCTCGGGTGCTTTCAT
<i>ctnna3</i>	coelaca	GGCTTTTTTTCTGGAGCCTTCAT
<i>ctnna3</i>	chicken	GGCTTCTTTTCTGGAGCCTTCAT
<i>Ctnna3</i>	mouse	GGCTTCTTAGCCGGAGCCTTCAT
<i>ctnna1</i>	frog	GGTTTCTTTTCTGGAGCCTTCAT
<i>ctnna2</i>	frog	GGTTTCTTTTCAGGTGCTTTCAT
<i>ctnna1</i>	chicken	GGCTTCTTCTCCGGAGCCTTCAT
<i>ctnna2</i>	chicken	GGTTTCTTCTCAGGTGCCTTCAT

Figure S3. Alignment shows that the degenerate *ctnna3* forward (a3-F) and reverse (a3-R) primers have no mismatches with chicken *ctnna3* genomic sequence. Both primers have one mismatch (yellow) with the corresponding region of chicken *ctnna1* and two mismatches with chicken *ctnna2*, suggesting that the primers preferentially amplify *ctnna3*, and *ctnna1* with a higher efficiency than *ctnna2* from chicken genomic DNA.