

Table S5 Full-length cDNA sequence information. Differences between our full-length cDNA sequence and the Ensembl transcript are listed below.

Gene Reference transcript	Location of Base Change	Consequence
<i>irs2</i> ENSDART00000053924	NA	NA
<i>btr01</i> ENSDART00000073689	1129, insertion (45 nucleotides)	retention of 45 nucleotides of predicted intronic sequence at the exon-intron 11 boundary, with a resulting in-frame addition of 15 amino acids: GTTTGCACCCTTCCACAGAA AGATCGCTGGGAGTGTATCA ACAAA
<i>crtc3</i> ENSDART00000073903	435-440, deletion (6 nucleotides)	splicing-mediated exclusion of the first 6 bases of predicted exon 5, with a resulting in-frame deletion of two amino acids: CCACAG
<i>crtc3</i> ENSDART00000073903	G1098A	synonymous variant (proline)
<i>crtc3</i> ENSDART00000073903	1347, insertion (45 nucleotides)	addition of 45 nucleotides from a small exon within intron 4 of the Ensembl gene structure for which there is established EST evidence (AL913705), resulting in the addition of 15 amino acids: GCAGGTGGACAACAACAACA ACAACAGCAGCAACAGCAGC ACCAC