

Supplemental Data

Figure S1: Conserved sequences between the human and rat *Fshr* genes. Sites of high sequence conservation (>75% identity) identified by pairwise sequence analysis between exon 21 of *Nrxn1* and exon 1 of *Lhcgr* are annotated on a segment of the (a) human and (b) rat *Fshr* gene assemblies (NT_022184 and NW_04775). Exons were assigned using the Spidey mRNA-to-genomic alignment program and displayed the expected ten exon genomic structure and are noted with raised arrows above the sequence (1, 2). Each conserved sequence is annotated with a balloon that is matched on the sequence assembly for both species. The positions of masked LINE repeats are also shown as white gaps on the sequence bar.

Table S1: Percent sequence identity between rat and human of each conserved site as calculated with pairwise BLAST analysis and the sequence of both the rat and human sites. Similarity to entries in EST or nr Genbank databases are noted by accession number.

Reference List

1. Heckert LL, Daley IJ, Griswold MD 1992 Structural organization of the follicle-stimulating hormone receptor gene. *Mol.Endocrinol.* 6:70-80
2. Gromoll, J., Pekel, E., and Nieschlag, E. The structure and organization of the human follicle-stimulating hormone receptor gene. *Genomics* 35, 308-311. 96.
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