

## Expression of cilia and centrosome related genes during spermatogenesis

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**Background.** Spermatogenesis is a complex process where undifferentiated spermatogonia develop into highly differentiated spermatozoa. During the last phase of sperm development, spermiogenesis, the haploid spermatid is remodeled by condensation of the nucleus and formation of the flagellum and acrosome. The axonemal structure of the flagellum is identical to the ciliary axoneme. In addition, the sperm tail contains accessory structures; mitochondrial sheath, outer dense fibers and fibrous sheath. In this study we used SOLiD 4 next-generation sequencing platform for analysis of gene expression and isoform content of cilia and centrosome related genes at five different time points during the first wave of spermatogenesis.

**Results.** Differential gene and isoform level expression was analyzed with the Cufflinks pipeline. In total over 26 000 genes were expressed in the testis and isoforms were detected for 57% of expressed genes. Differential promoter and transcription start site usage appeared also to play a role in regulation of gene expression during spermatogenesis. Centrosomal and cilia related genes showed differential expression pattern during spermatogenesis based on their biological function. Peak expression for cilia formation specific genes was identified at PND 17 and for motility related genes at PND 21. Gene expression for centrosomal genes mainly increased throughout the progression of spermatogenesis. However, e.g. basal body related genes showed increase in expression at PND 17. We also identified differential expression of gene isoforms highlighting the role of gene splicing and differential transcription initiation.

**Conclusions.** Transcriptomic analysis of testis tissue samples is highly informative due to the large number of expressed genes and identified isoforms. Thus, this dataset can be used for identification of novel gene isoforms and investigation of differential expression at gene and isoform level. Analysis of centrosome and cilia associated genes during spermatogenesis underlined the specific expression patterns of these genes based on their role in the cilia formation.