ABSTRACT
GCNF's protein-coding region is located at 11 exons and the genomic structure of this nuclear receptor gene will be advantageous for future research.

INTRODUCTION
Genome sequencing is a powerful tool for understanding the structure of the human genome. This is especially true for humans with inherited diseases such as cancer and Alzheimer's. However, the methods of genome sequencing are not always reliable. The current generation of sequencing protocols are subject to a number of unknowns, which can lead to inaccurate results and, where necessary, even false positives. The aim of this study was to perform a comprehensive genotyping of mouse germ cells, using the high-throughput method (HiSeq) to identify genomic regions that could be used as a biomarker for cancer in humans.

Materials and Methods:

The experiments were carried out at the University of Oxford. The HiSeq project was funded by the Genome Institute (NIH) (ERC/EOS/14/ NR6A1, the germ cell nuclear factor, is a member of the nuclear receptor superfamily. It was originally isolated from mouse cDNA libraries, but homologs of GCNF have been identified in humans, frogs, and fish. As no ligand has been discovered, it is classified as an orphan receptor. RTR (retinoid acid receptor-related testis-associated receptor) or NCNF is the only known member within gcnf. The mouse GcNf gene is highly expressed in the same appears in various embryonic cells

CONCLUSION
Remarkable conclusions The protein-coding region of GCNF is located in 11 exons and requires further research to define the regulatory/promoter region. The genomic structure of this particular nuclear receptor, which belongs to the sixth subfamily, will be crucial for future research on this distinct receptor.