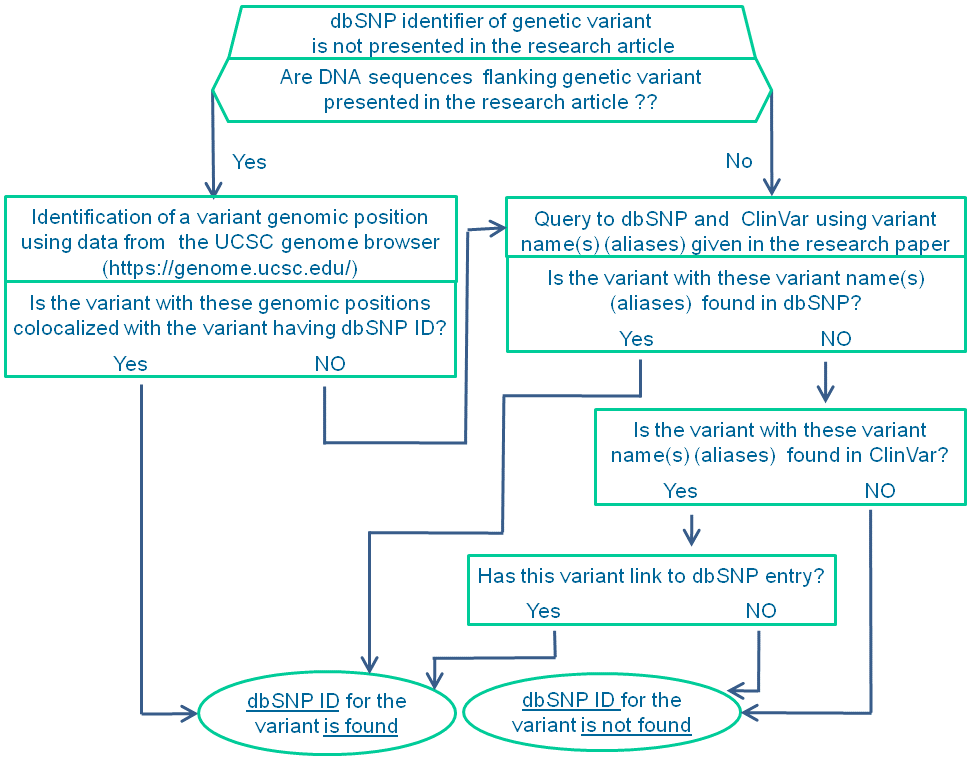
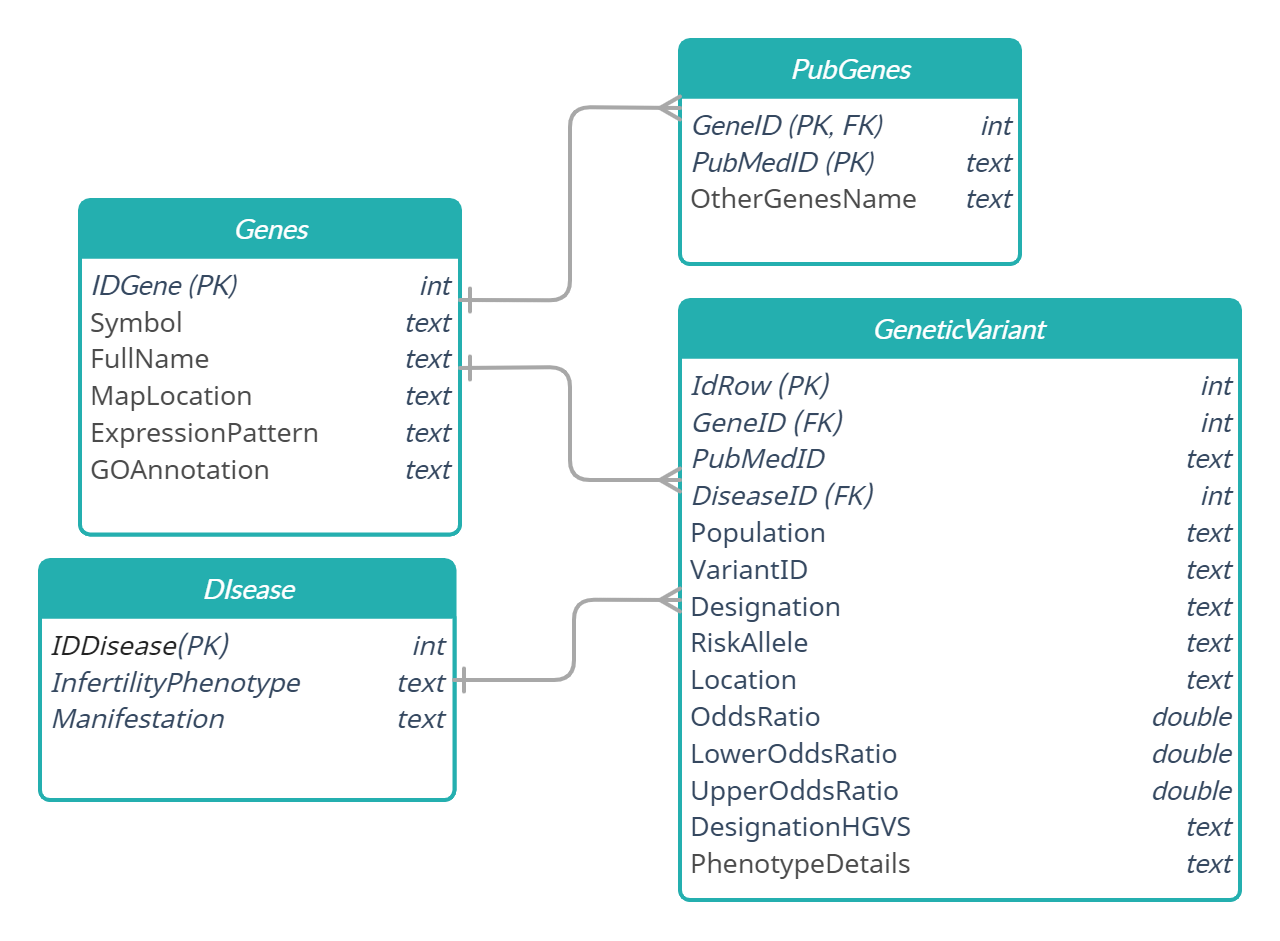


***Supplementary Material***



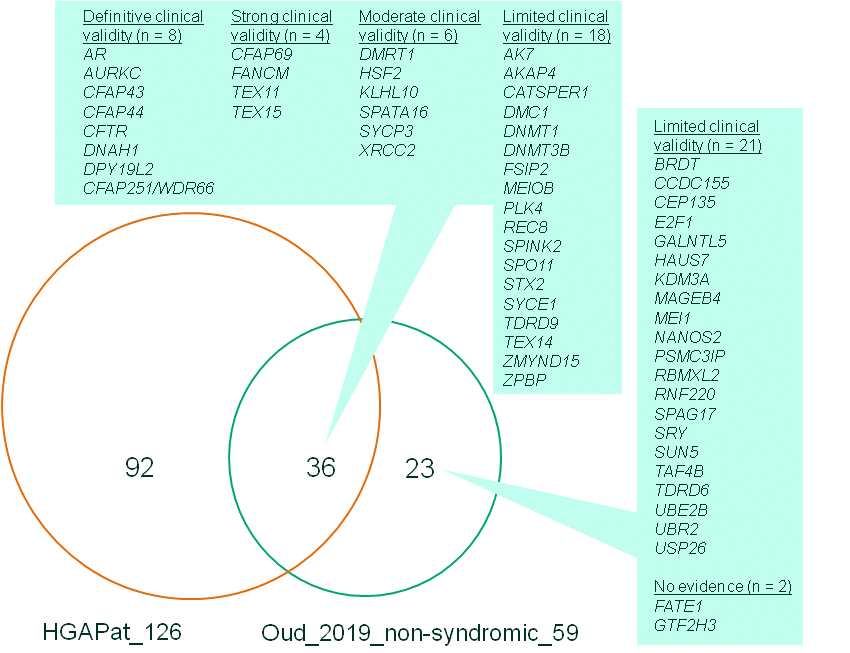
**Supplementary Figure 1.** Search for dbSNP identifiers for those genetic variants for which dbSNP identifiers were not indicated in the research articles.

Supplementary Material



**Supplementary Figure 2.** General scheme of the сatalog (ER-model of the database). The primary and foreign keys are marked PK and FK, accordingly.

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**Supplementary Figure 3.** Intersection between two lists of genes. *HGAPat\_126* designates all 126 genes from the catalog HGAPat presented in the current report. *Oud\_2019\_non-syndromic\_59* designates the list of 59 genes from [Oud et al. 2019] that have at least one potentially pathogenic variant described and had relationships with non-syndromic forms of pathologies manifested in decreased quality of semen (pathologies are listed in Table S1). These 59 genes were extracted from the TableSIV published by [Oud et al. 2019]. This figure demonstrates that (1) HGAPatcontains more genes that meet the above criteria; (2) according to [Oud et al. 2019], genes that were not found in HGAPat, but were present in the [Oud et al. 2019], have low clinical validity.

**References**

1. Oud, M.S., Volozonoka, L., Smits, R.M., Vissers, L.E., Ramos, L., Veltman, J.A. (2019). A systematic review and standardized clinical validity assessment of male infertility genes. Human Reproduction. 34(5), 932-941. doi: 10.1093/humrep/dez022.

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