Supplementary Table SVII **Recommendations for reporting of sequencing variants.**

Topic	Recommendation
Variant calling	To ensure reliable results, establish the variant calling accuracy of the technique used and only report variants that meet a minimal level of accuracy
Variant discovery	All relevant variants should be validated in an independent sequencing reaction to prevent reporting of false-positive results
Gene nomenclature	Use the standard HGNC nomenclature: https://www.genenames.org/about/guidelines
Variant nomenclature	Use the standard HGVS nomenclature: http://varnomen.hgvs.org/
Provide sequence reference	All reported variants should include: • Genome build (e.g. GRCh37/hg19) • Transcript ID (e.g. NM_198393.3)
Inheritance pattern	Report the expected or proven inheritance pattern. Note that the inheritance pattern between mice and human may be discordant Public databases containing inheritance information: OMIM (Human): https://www.omim.org/ MGI (Mouse): http://www.informatics.jax.org/ ClinGen (Human): https://search.clinicalgenome.org/kb/gene-validity/ Prediction of inheritance pattern: Domino: https://wwwfbm.unil.ch/domino/index.html
Classification of sequencing variants	If a gene has been linked to male infertility, apply the ACMG guidelines to classify the sequencing variants. ACMG guidelines: https://www.acmg.net/docs/ACMG%20SG%20Interpretation%20of%20Sequence%20Variants%20GIM%20May%202015%20(3).pdf