What is claimed is:

1. A method for assessing whether a genetic region is associated with infertility, the method comprising:

producing a genetically modified mouse by introducing an exogenous sequence into a mouse, the exogenous sequence comprising one or more genetic regions suspected of being associated with infertility, wherein the genetic regions suspected of being associated with infertility are determined by performing a clustering analysis on a set of reference data to identify genetic regions that have no prior association with infertility that cluster with one or more genetic regions known to be associated with infertility; and

assessing the mouse for presence of an infertility-associated phenotype, wherein the presence of the phenotype is indicative of the genetic region being associated with infertility.

2. The method according to claim 1, wherein the genetic region comprises a gene.

3. The method according to claim 1, wherein data is selected from the group consisting of: gene expression data, phenotype, knowledge of gene pathway, and any combination thereof.

4. The method according to claim 1, wherein presence of the infertility-associated phenotype is used as a factor in ranking the importance of the gene in a database of genetic loci associated with infertility in humans.

5. The method according to claim 4, wherein presence of the phenotype increases the rank of the gene in the database.

6. The method according to claim 4, wherein absence of the phenotype decreases the rank of the gene in the database.

7. The method according to claim 1, wherein the alteration to the genetic region is a mutation.

8. The method according to claim 7, wherein the mutation is selected from the group consisting of: a single nucleotide polymorphism, a deletion, an insertion, a rearrangement, a copy number variation, and a combination thereof.