**Supplementary data**

Supplementary\_data\_I\_ Report\_FERTILITYvsSIMPLE\_INFERTILITY: This document presents the DECO (Differential Expression and Correlation Optimisation) analysis of differential gene expression between patients with fertility and those with simple infertility. The results of the subclass analysis using NSCA and the main differential characteristics detected between the two groups are included. The key genes identified show significant variations in expression, providing valuable information on the molecular differences between fertility and simple infertility states. The report highlights the most relevant genes according to the variability and repeatability metrics applied in the analysis. Key metrics, such as LIMMA q-values, NSCA statistics and Huber gamma, are reported to assess the variability and reliability of the detected signals.

Supplementary\_data\_II\_ Report\_FERTILITYvsCOMBINED\_INFERTILITY: This document presents the DECO (Differential Expression and Correlation Optimisation) analysis of differential gene expression between patients with fertility and those with combined infertility. The analysis includes the identification of subclasses by NSCA and the main genetic characteristics that distinguish the groups. The results reveal key differences in gene expression between the groups, highlighting the molecular pathways involved in combined infertility. The report provides details on the most relevant genes according to the variability and repeatability metrics used in the analysis. Key metrics, such as LIMMA q-values, NSCA statistics and Huber gamma, are reported to assess the variability and reliability of the detected signals.

Supplementary\_data\_III\_ Report\_SIMPLE\_INFERTILITYvsCOMBINED\_INFERTILITY: This document presents the DECO (Differential Expression and Correlation Optimisation) analysis of differential gene expression between patients with simple infertility and those with combined infertility. The results include subclass analysis through NSCA and the main differential features separating the two groups. The genes identified show divergent expression patterns between simple and combined infertility conditions, providing crucial information on the molecular differences between these states. The report highlights the most important genes according to the variability and repeatability metrics applied in the analysis. Key metrics, such as LIMMA q-values, NSCA statistics and Huber gamma, are reported to assess the variability and reliability of the detected signals.

Supplementary\_Table\_I\_Enrichment\_GO\_BP\_enrichment\_FERTILE\_vs\_SIMPLE\_INFERTILITY: This table shows the results of the GO BP enrichment analysis performed with clusterProfiler in the context of fertility versus simple infertility. Differentially expressed genes (DEGs) were identified using limma-voom as recommended by Law et al. (2014) and Ritchie et al. (2015), with a p-value < 0.05 and a log2FC greater than 1.5 or less than -1.5. Significantly enriched biological processes provide information on molecular pathways that could distinguish fertile patients from those with simple infertility.

Supplementary\_Table\_II\_Enrichment\_GO\_BP\_enrichment\_FERTILE\_vs\_COMBINED\_INFERTILITY: This table contains the results of the GO BP enrichment analysis using clusterProfiler to compare fertile patients to those with combined infertility. Differentially expressed genes (DEGs) were identified by limma-voom following the recommendations of Law et al. (2014) and Ritchie et al. (2015), with a p-value < 0.05 and a log2FC greater than 1.5 or less than -1.5. The analysis reveals enriched biological processes that show molecular differences between the two groups, providing information on the possible pathways involved in combined infertility.

Supplementary\_Table\_III\_Enrichment\_GO\_BP\_enrichment\_SIMPLE\_INFERTILITY\_vs\_COMBINED\_INFERTILITY: This table presents the results of the GO BP enrichment analysis performed with clusterProfiler, comparing single infertility with combined infertility. Differentially expressed genes (DEGs) were identified using limma-voom according to the recommendations of Law et al. (2014) and Ritchie et al. (2015), with a p-value < 0.05 and a log2FC greater than 1.5 or less than -1.5. The enriched biological processes reveal molecular differences between the two groups, providing a better understanding of the mechanisms underlying infertility progression.

Supplementary\_Table\_IV\_Enrichment\_GO\_BP\_enrichment\_FERTILE\_vs\_SIMPLE\_INFERTILITY\_DECO: This table presents the results of the GO BP enrichment analysis performed with clusterProfiler in the context of fertility versus simple infertility. Differentially expressed genes (DEGs) were selected using DECO, which identifies relevant genes based on an iterative analysis, integrating differential signals and consistent expression patterns in most samples. The analysis reveals enriched biological processes that could point to molecular differences between fertile patients and those with simple infertility.

Supplementary\_Table\_V\_Enrichment\_GO\_BP\_enrichment\_FERTILE\_vs\_COMBINED\_INFERTILITY\_DECO: This table contains the results of the GO BP enrichment analysis performed with clusterProfiler to compare fertile patients to those with combined infertility. Differentially expressed genes (DEGs) were identified using DECO, which selects genes with differential expression profiles based on a combination of recurrent signals and patterns across multiple iterations. The enriched biological processes reveal molecular differences between the two groups, providing insights into the pathways involved in combined infertility.

Supplementary\_Table\_VI\_Enrichment\_GO\_BP\_enrichment\_SIMPLE\_INFERTILITY\_vs\_COMBINED\_INFERTILITY\_DECO: This table shows the results of the GO BP enrichment analysis performed with clusterProfiler, comparing single infertility with combined infertility. Differentially expressed genes (DEGs) were selected by DECO through an iterative approach that detects recurrent genes in subsets of samples, highlighting the most consistent molecular signals. Enrichment analysis reveals biological processes that could distinguish patients with simple infertility from those with combined infertility.

Supplementary\_Table\_VII\_Enrichment\_GO\_BP\_enrichment\_FERTILE\_vs\_COMBINED\_INFERTILITY\_DEG&DECO: This table presents the results of the GO BP enrichment analysis performed with clusterProfiler in the context of fertility versus combined infertility. The differentially expressed genes (DEGs) included in this analysis are those identified by both LIMMA and DECO, reflecting shared genes that show consistent signals in both approaches. The enrichment analysis highlights biological processes potentially related to fertility and combined infertility.

Supplementary\_Table\_VIII\_Enrichment\_GO\_BP\_enrichment\_SIMPLE\_INFERTILITY\_vs\_COMBINED\_INFERTILITY\_DEG&DECO: This table contains the results of the GO BP enrichment analysis performed with clusterProfiler, comparing single infertility with combined infertility. Differentially expressed genes (DEGs) included in this analysis were identified by both LIMMA and DECO, highlighting genes shared between both methods that show consistent expression patterns. The enrichment analysis provides information on the biological processes that could explain the molecular differences between these two types of infertility.