

Identification of maturation-specific proteins in human oocytes by single-cell proteomic

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Exploiting SP3, a novel technology for proteomic sample preparation using magnetic beads, we scaled down proteome analysis to single human oocytes from the in vitro fertilization program. Despite the low protein content of only ~100 ng per cell, we consistently identified ~450 proteins from individual oocytes. When comparing individual oocytes at different maturation stages, we found that the protein TDRKH is preferentially expressed in immature oocytes, while Wee2, PCNA, and DNMT1 were enriched in mature oocytes, thus indicating that the maintenance of genome integrity is crucial during oocyte maturation. The protein expression profile of oocytes was studied regarding the maturation in vitro. An innovative proteomics workflow facilitates the analysis of single human oocytes to investigate their biology.