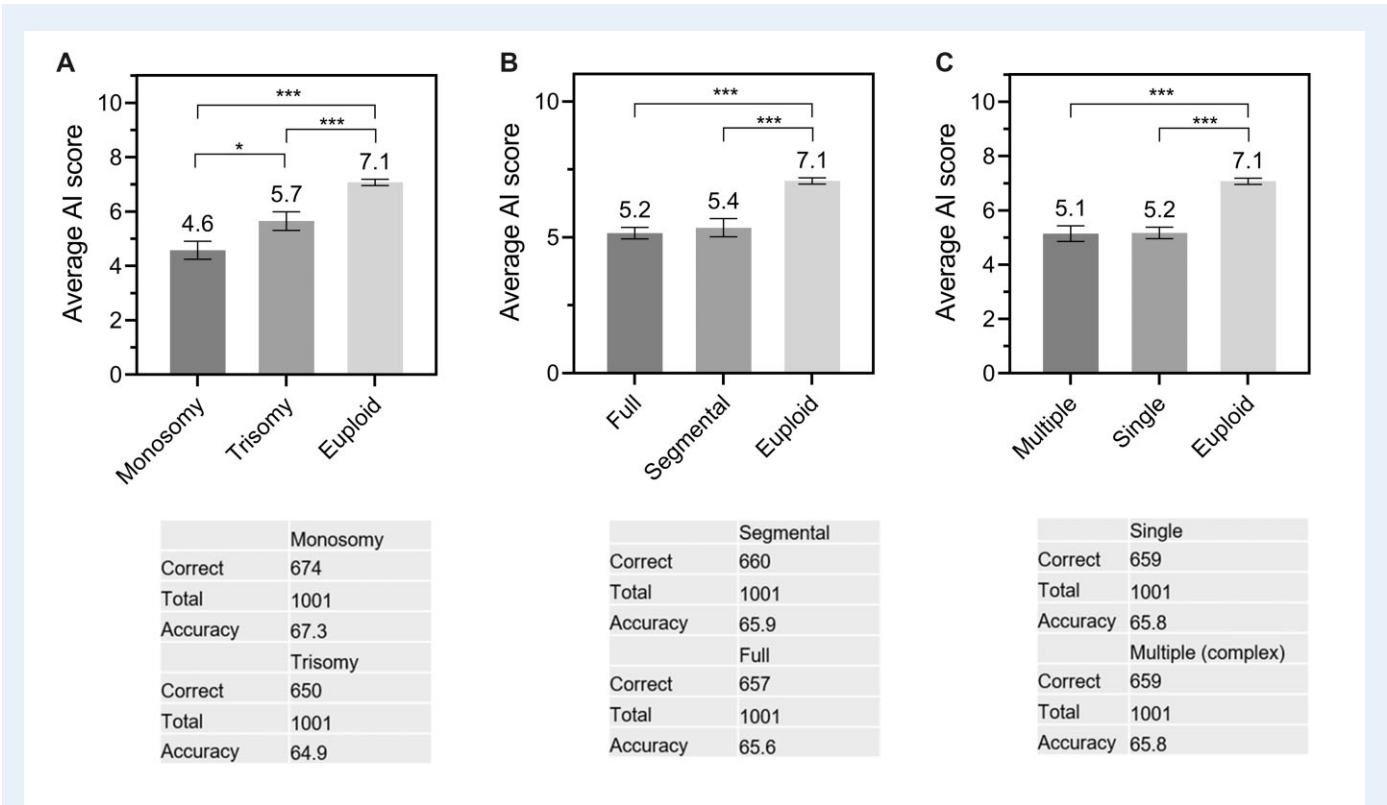


human  
reproduction

SUPPLEMENTARY DATA



**Supplementary Figure S2. Performance of the Day 5 artificial intelligence (AI) model for predicting different types of chromosomal abnormalities.** Top panel: Average genetics AI scores for human embryos with different abnormality types compared to euploid embryos on the original retrospective Day 5 blind test dataset. Bottom panel: Accuracy for predicting the specific abnormality when compared to all other embryos (euploid and embryos with other abnormalities). **(A)** Embryos with monosomic versus trisomic changes (single abnormalities only). **(B)** Embryos with full chromosomal gains or losses versus segmental duplications or deletions (single or multiple abnormalities of the same type). **(C)** Embryos with single versus multiple abnormalities (multiple abnormalities were deemed a complex karyotype). Average AI scores were compared using one-way ANOVA with Tukey's multiple comparisons post-test, *P*-values are represented as follows: \**P* < 0.05, \*\*\**P* < 0.001.