**Supplemental Materials and Methods.**

*Selection of Variables.* While we initially considered including some clinical characteristics such as number of oocytes retrieved, fertilization method, number of fertilized oocytes, and use of preimplantation genetic testing (PGT), these variables were eventually dropped because the information was missing in all cycles that failed prior to oocyte retrieval and the parameters would be unknown to patients who have yet to start their assisted reproductive technology (ART) treatment. Due to a large amount of missing data on anti-mullerian hormone (AMH) (~36%) and due to the fact that it is often unknown to patients prior to an infertility workup, this variable was not considered further. Since smoking status was only weakly associated with cumulative chance of live birth, this variable was also removed. A variable encompassing sperm source and paternal age was also eventually dropped from consideration because, while the proportion of missing data was small (~8%), the group missing this information was highly informative, suggesting that excluding these cycles or conducting multiple imputation would not be appropriate. Although race/ethnicity had a significant impact on cumulative chance of live birth and has been successfully imputed in the NASS dataset,30,31 we decided not to move forward with the addition of this variable to the model given the heterogeneity of this classification and to avoid potential harm such as reinforcing disproven notions of race as a biological construct and contributing to ongoing racial disparities in health and health care.28

*Multiple Imputation of Missing Data*. Using the SUDAAN HOTDECK procedure, under the assumption of missing at random (MAR), we derived the missing BMI, race/ethnicity, sperm source, number of oocytes retrieved, and PGT data. The MAR assumption appears reasonable because, although reporting of these variables likely varies from clinic to clinic, there is no evidence to support that missingness of the data varies systematically within a specific clinic. Five multiply imputed datasets were created to compute within- and between-variations of imputed datasets in parameter estimates of models. Variables used in the imputation model included state where the cycle was performed, reporting year, patient age, gravidity, infertility diagnoses, patient race, BMI, sperm source, number of oocytes retrieved, and PGT.

*Statistical Modelling.* To obtain the CLBR after two retrievals and one, two, and three or more embryo transfer cycles, we applied the following equations proposed by Luke et al.7 and modified for use in our study. The Luke et al. paper used these equations to estimate CLBR following 1, 2, and 3 fresh ART cycles. We expanded on this to not only estimate CLBR following 1, 2, and ≥3 embryo transfer cycles (fresh or frozen) but also CLBR following 1, 2, and 3 oocyte retrievals and all embryo transfer cycles within 12 months of retrieval. Specifically, the equations we used were:

PROB2,1 = P1,3 + P2,1 (1-P1,3)

PROB2,2 = P1,3 + P2,2 (1- P1,3)

PROB2,3 = P1,3 + P2,3 (1- P1,3)

where PROB2,1 is the CLBR after two oocyte retrievals and the first embryo transfer, P1,3 is the probability of live birth after the first oocyte retrieval and three or more embryo transfer cycles within 12 months, P2,1 is the probability of live birth after the second oocyte retrieval and one embryo transfer, PROB2,2 is the CLBR after two retrievals and the second embryo transfer, P2,2 is the probability of live birth after two oocyte retrievals and the second embryo transfer, PROB2,3 is CLBR after two oocyte retrievals and three or more embryo transfers, P2,3 is the probability of live birth after two oocyte retrievals and three or more embryo transfers.

The P1,3 parameter was estimated for a given patient by taking the sum of the intercept plus the product of the beta coefficients (shown in Supplemental Table 1) x the value for each input parameter. This sum of was then back-transformed {exp(SUM)/(1+exp(SUM))} to obtain the predicted probability. The predicted probabilities, P2,1, P2,2, and P2,3, were estimated likewise.

Among return IVF patients, we used similar methodology, running three separate multinomial regression models to estimate the probability of live birth following one, two, and three additional oocyte retrievals and one, two, and three or more embryo transfer cycles that occurred within 12 months of each retrieval. The CLBR following each additional oocyte retrieval was calculated using the Luke et al. equation as described above.

To obtain the CLBR after the 2nd and 3rd embryo transfer cycles in donor oocyte recipient models, we applied the equations proposed by Luke et al: PROB2 = P1 + P2 (1-P1)) and PROB3 = PROB2 + P3 (1-PROB2)) where P1, P2 and P3 are the probability of live birth after the first, second, and third embryo transfer cycles and PROB2 and PROB3 are the CLBRs after two and three embryo transfer cycles.