Suppl. Fig. 1. Performance of chromosome aneuploidy detection by scBS-seq.

(A) Circle plots showing that the CN profiles by scBS-seq (inner) and MALBAC (outer) gave the same CN patterns for HCT116 cells. (B) Distribution of CV as a function of the mean of read numbers among different numbers of unique mapping reads.
**Suppl. Fig. 2. Classification of CN profiles by comparing SEM and TE biopsy.**

(A) The sample numbers of different CN categories and subcategories. Note that gender discordance is not considered here. (B) Representative examples of chromosome CN profiles in three major CN subcategories.
Suppl. Fig. 3. Assessment of polar body and ICM/TE origins for SEM.

(A) DNA methylation levels of O-DMRs for three SEM samples clustered with the MII oocytes and the female pronuclei compared with other samples. (B) The chromosome CN profile of the SEM sample (#S193) clustered with the female pronuclei. (C) PCA of the single-cell DNA methylation data of the EPI (n = 22) and TE (n = 25, all from day 6 embryos) using the promoter regions of the top 300 differentially expressed genes between the EPI and TE; the single-cell triple omics sequencing data were from our previous study (32). A cluster of 15 TE cells (TE cluster) was separated from a cluster of 22 EPI cells and 10 TE cells (EPI cluster). Chi square test was used for significance test. (D) PCA of the day 6 SEM samples (with no cumulus cell or polar body contamination) together with EPI and TE single cells. Eighteen SEMs were clustered with the TE cluster, and 43 SEMs were clustered with the EPI cluster. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test.
Suppl. Fig. 4. Cumulus cell and polar body ratios in SEM.

(A) Pie charts showing the numbers and percentages of the SEM samples with different cumulus (left) and polar body (right) ratios. (B) Performance characteristics of SEM,
including sensitivity, specificity, positive and negative predictive value, taking the TE biopsy as the reference. Sensitivity = [true positives]/[true positives + false negatives]; Specificity = [true negatives]/[true negatives + false positives]; positive predictive value (PPV) = [true positives]/[true positives + false positives]; negative predictive value (NPV) = [true negatives]/[true negatives + false negatives]. True positives indicated that both SEM and TE were aneuploidy; true negatives indicated that both SEM and TE were euploidy; false positives indicated that SEM was aneuploidy with TE euploidy; false negatives indicated that SEM was euploidy with TE aneuploidy. All these calculations were based on the literature of Simon's group (16). (C) Representative CN profiles for false negative SEM with nearly no maternal DNA contamination. The false negative result of the fourth case was caused by a small-segment aneuploidy of 8 Mb, which did not reach our aneuploidy calling criterion of 10 Mb. The others were all caused by aneuploid and euploid cells released into the culture medium, while no euploid cells were sampled by TE biopsy. (D)-(F) Violin plots showing D) the cumulus ratios, E) the polar body ratios, and F) the amplified DNA amount in SEM samples of day 4/5 (D5), 4/6 (D6) and 4/7 (D7). Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test. (G) Histograms showing the GDR, FNR, GCR and FPR of day 4/5 (D5) and day 4/6 (D6) SEM samples.
Suppl. Fig. 5. Impact of maternal contamination and chromosome copy number on DNA concentration in the culture medium.

(A) Violin plot showing variations in amplified DNA amounts between different contamination ratio samples. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test. (B) Violin plot showing variations in amplified DNA amounts...
between different chromosome copy number samples. Normal represented euploid; duplication represented copy number increase; deletion represented copy number decrease; both represented copy number increase and decrease. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test. (C) Correlations between the predicted and input component fractions of the simulated DNA mixing experiment. The red box indicated a total data volume of 0.5 cell; the yellow box indicated a total data volume of 1 cell; the blue box indicated a total data volume of 2 cells. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test.

Supplementary Tables

Supplementary Table 1

Sample information included quality control information, copy number variations, maternal contamination, sampling time.

Supplementary Table 2

Position of O-DMRs and C-DMRs and statistics of reads mapped on O-DMRs and C-DMRs.