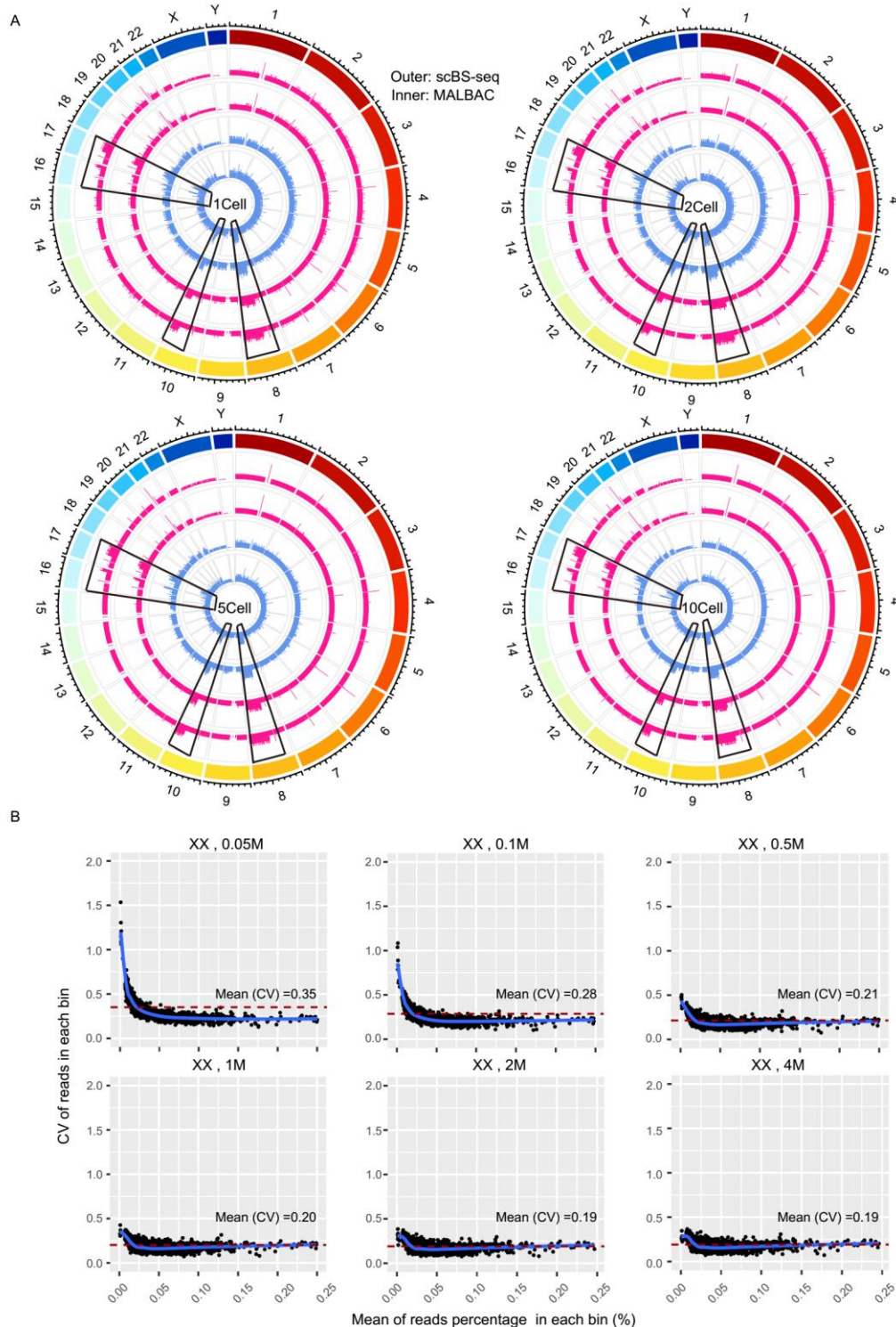


618 **Suppl. Fig. 1. Performance of chromosome aneuploidy detection by scBS-seq.**



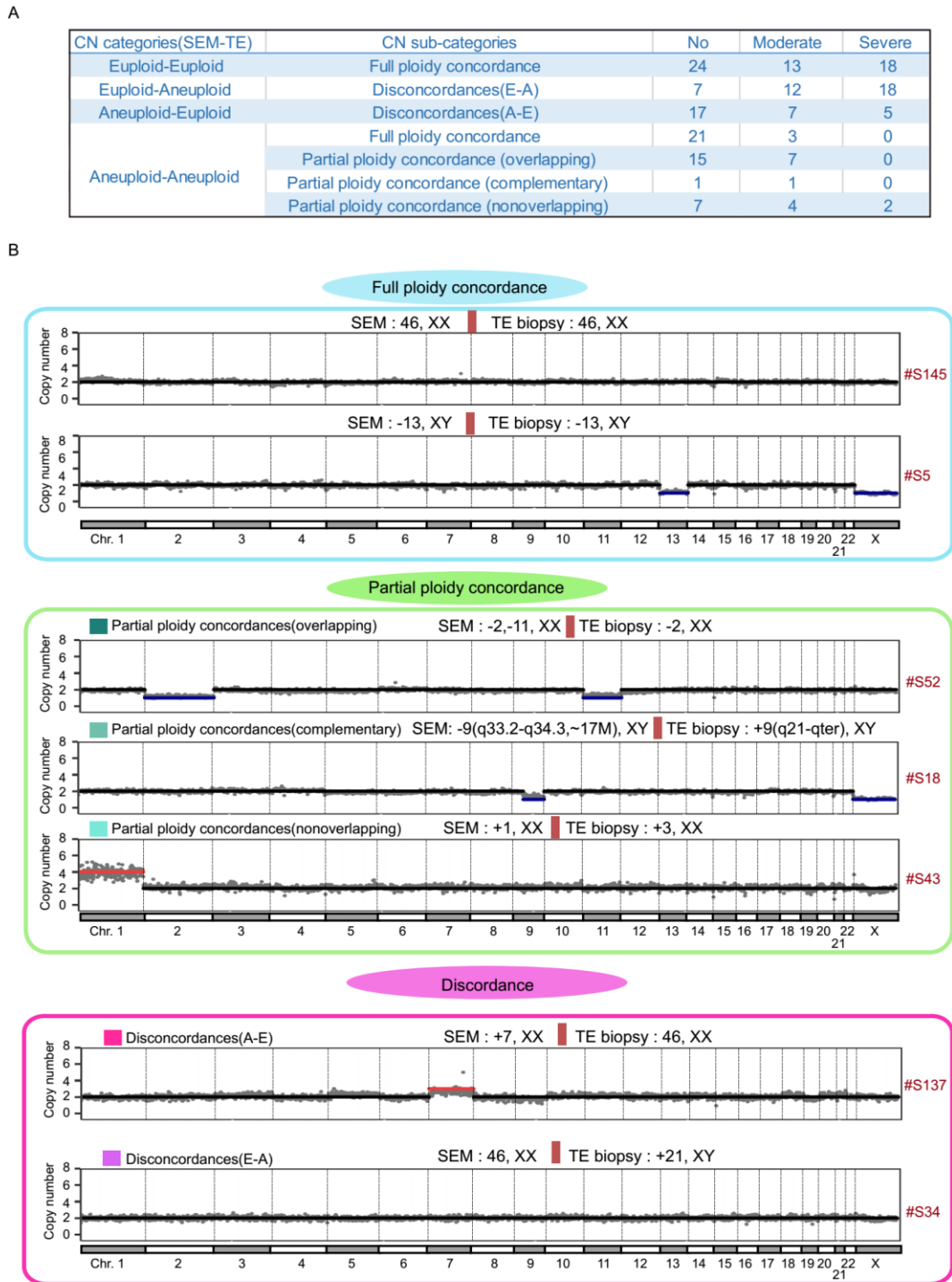
619

620 (A) Circle plots showing that the CN profiles by scBS-seq (inner) and MALBAC (outer)

621 gave the same CN patterns for HCT116 cells. (B) Distribution of CV as a function of

622 the mean of read numbers among different numbers of unique mapping reads.

623 **Suppl. Fig. 2. Classification of CN profiles by comparing SEM and TE biopsy.**



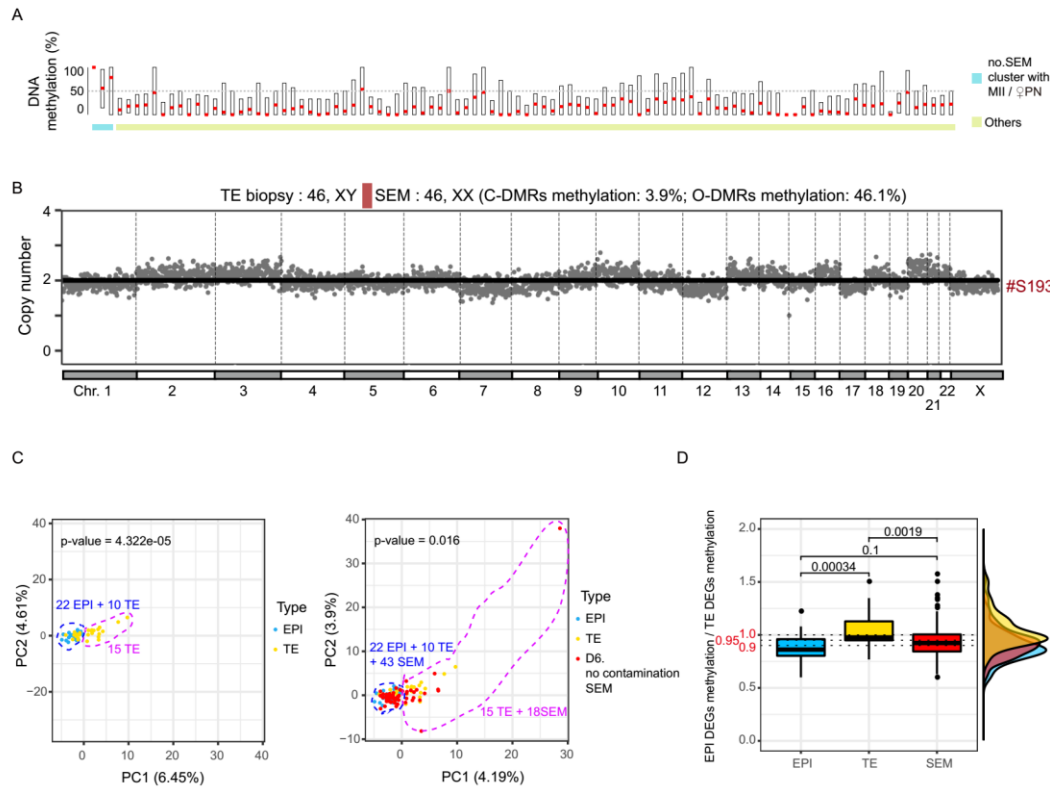
624

625 (A) The sample numbers of different CN categories and subcategories. Note that gender

626 discordance is not considered here. (B) Representative examples of chromosome CN

627 profiles in three major CN subcategories.

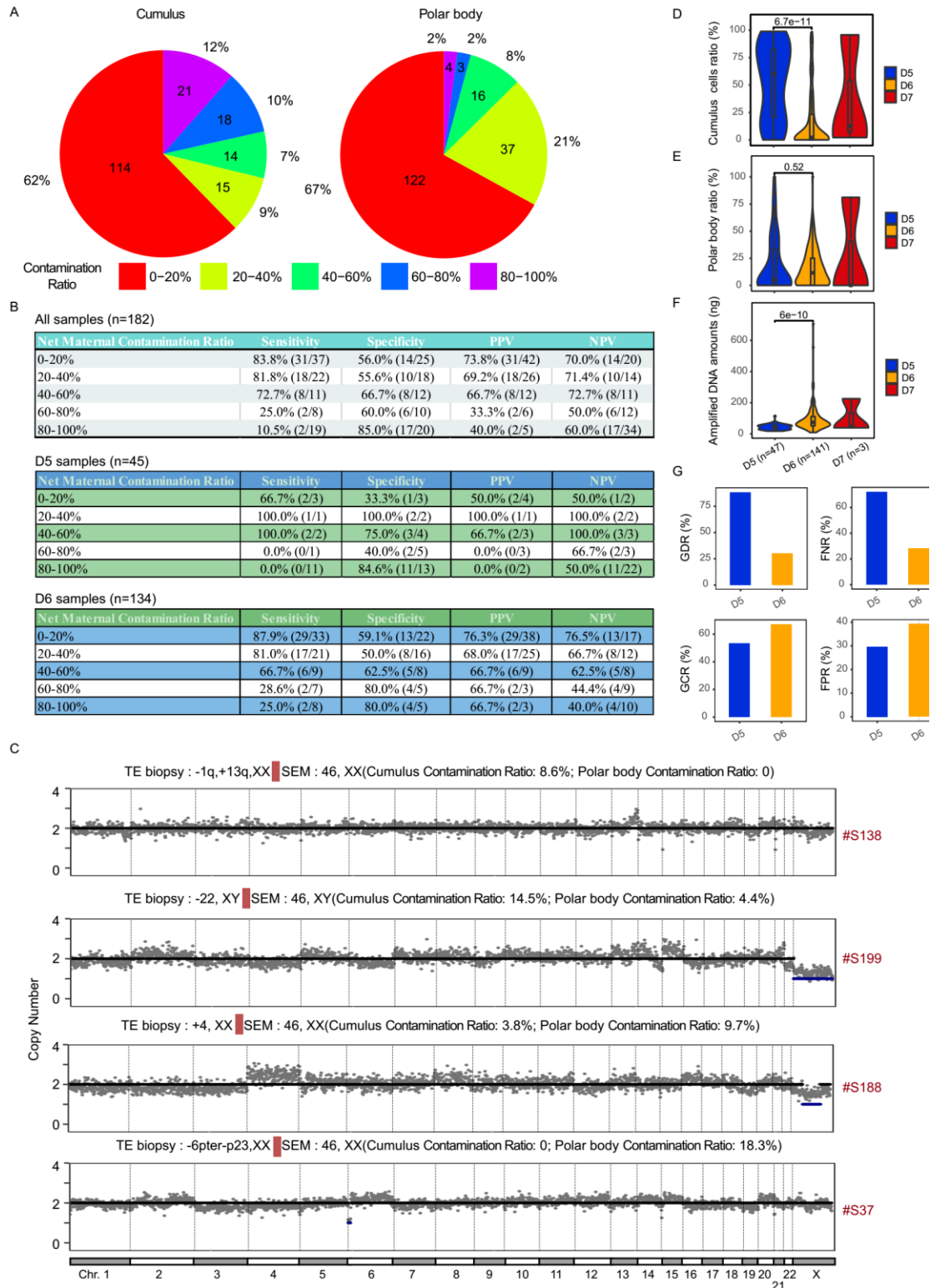
628 **Suppl. Fig. 3. Assessment of polar body and ICM/TE origins for SEM.**



629

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

642 **Suppl. Fig. 4. Cumulus cell and polar body ratios in SEM.**



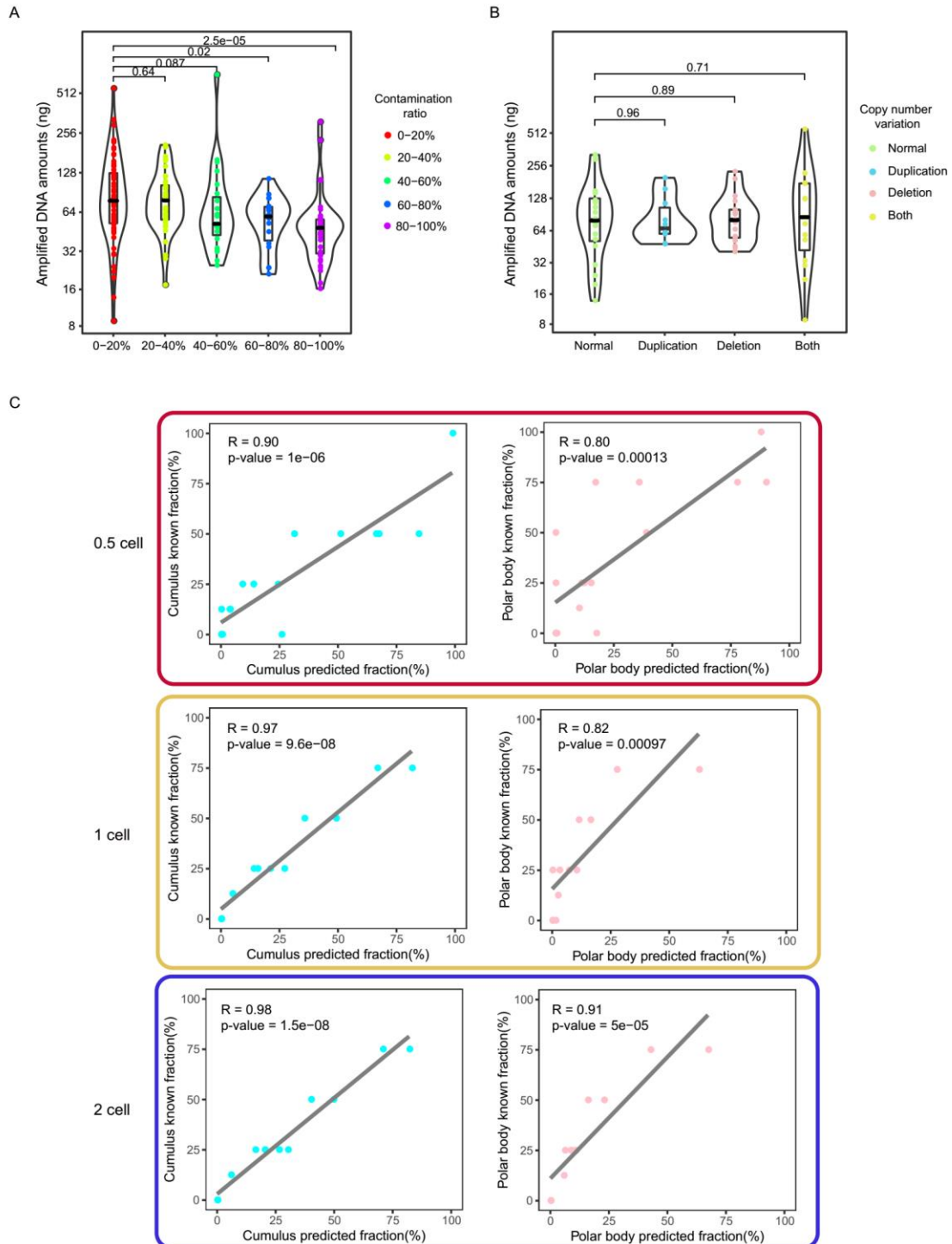
643

644 (A) Pie charts showing the numbers and percentages of the SEM samples with different

645 cumulus (left) and polar body (right) ratios. (B) Performance characteristics of SEM,

646 including sensitivity, specificity, positive and negative predictive value, taking the TE
647 biopsy as the reference. Sensitivity = [true positives]/[true positives + false negatives];
648 Specificity = [true negatives]/[true negatives + false positives]; positive predictive
649 value (PPV) = [true positives]/[true positives + false positives]; negative predictive
650 value (NPV) = [true negatives]/[true negatives + false negatives]. True positives
651 indicated that both SEM and TE were aneuploidy; true negatives indicated that both
652 SEM and TE were euploidy; false positives indicated that SEM was aneuploidy with
653 TE euploidy; false negatives indicated that SEM was euploidy with TE aneuploidy. All
654 these calculations were based on the literature of Simon's group (16). (C)
655 Representative CN profiles for false negative SEM with nearly no maternal DNA
656 contamination. The false negative result of the fourth case was caused by a small-
657 segment aneuploidy of 8 Mb, which did not reach our aneuploidy calling criterion of
658 10 Mb. The others were all caused by aneuploid and euploid cells released into the
659 culture medium, while no euploid cells were sampled by TE biopsy. (D)- (F) Violin
660 plots showing D) the cumulus ratios, E) the polar body ratios, and F) the amplified DNA
661 amount in SEM samples of day 4/5 (D5), 4/6 (D6) and 4/7 (D7). Two-tailed Mann-
662 Whitney-Wilcoxon (MWW) test was used for significance test. (G) Histograms
663 showing the GDR, FNR, GCR and FPR of day 4/5 (D5) and day 4/6 (D6) SEM samples.

664 **Suppl. Fig. 5. Impact of maternal contamination and chromosome copy number**
 665 **on DNA concentration in the culture medium.**



666
 667 **(A)** Violin plot showing variations in amplified DNA amounts between different
 668 contamination ratio samples. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was
 669 used for significance test. **(B)** Violin plot showing variations in amplified DNA amounts

670 between different chromosome copy number samples. Normal represented euploid;
671 duplication represented copy number increase; deletion represented copy number
672 decrease; both represented copy number increase and decrease. Two-tailed Mann-
673 Whitney-Wilcoxon (MWW) test was used for significance test. (C) Correlations
674 between the predicted and input component fractions of the simulated DNA mixing
675 experiment. The red box indicated a total data volume of 0.5 cell; the yellow box
676 indicated a total data volume of 1 cell; the blue box indicated a total data volume of 2
677 cells. Two-tailed Mann-Whitney-Wilcoxon (MWW) test was used for significance test.

678 **Supplementary Tables**

679 **Supplementary Table 1**

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

682 **Supplementary Table 2**

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