

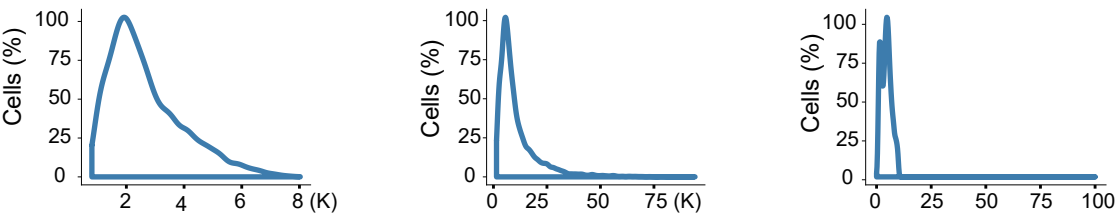
Supplementary Fig.1

a

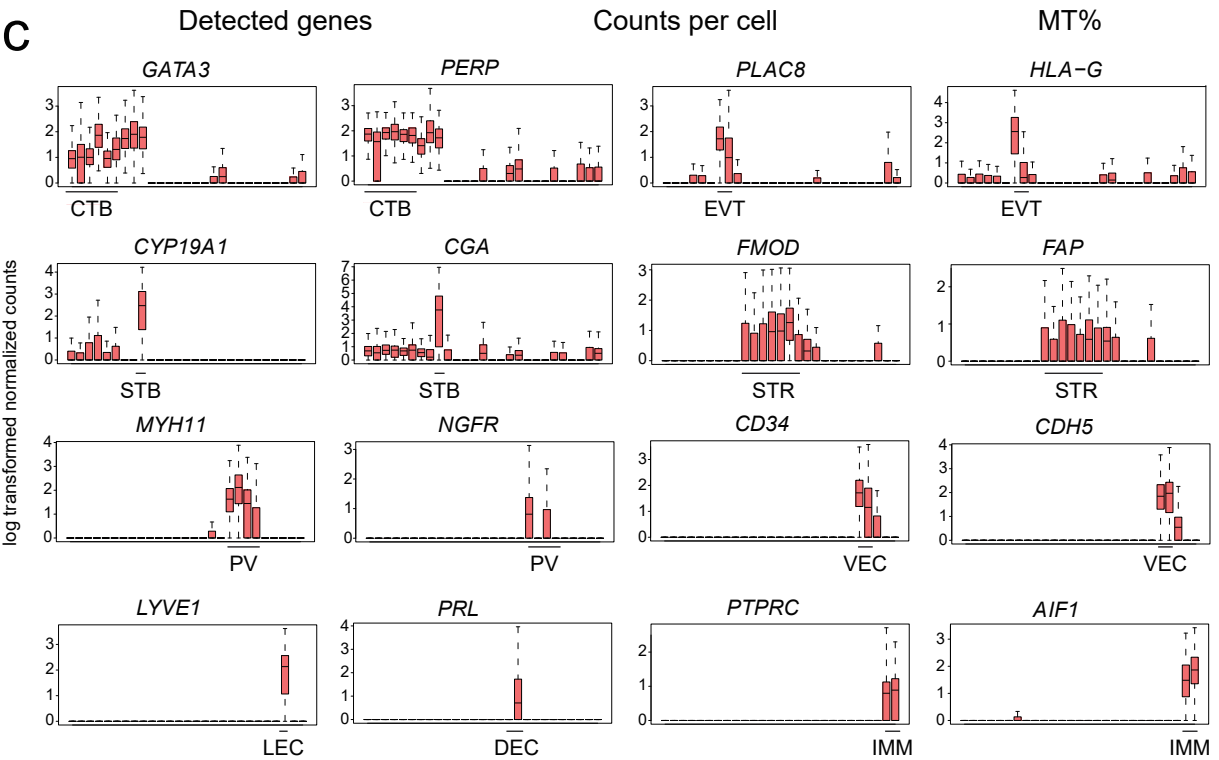
Sample information	Raw data information					Clean data information			
Sample ID	Total cells	Mean Reads per Cell(K)	Number of Reads(M)	Median Genes per Cell	Filtered cells	Remained total cells	Total cells	Rate of passed cells (%)	Sequencing saturation (%)
FS_a	797	1435	1100	1753	111	686	3138	86.1	97.0
Mid_S_a	3260	585	1900	1686	808	2452		75.2	97.1
FS_b	1740	381	660	2019	109	1631	4030	93.7	95.7
Mid_S_b	936	1730	1600	1666	288	648		69.2	98.2
Mat_S_b	1889	643	1200	2554	138	1751	4270	92.7	94.8
FS_c	1391	829	1200	2817	218	1173		84.3	93.7
Mid_S_c	2709	378	1020	3561	505	2204		81.4	88.0
Mat_S_c	1025	966	990	2616	132	893		87.1	92.7
total	13747					11438		83.2	94.7

FS: Fetal section, Mid_S: Middle section, Mat_S: Maternal section; a,b,c representing three individuals respectively

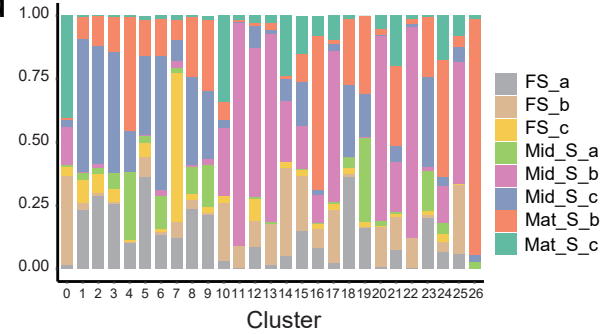
b



c



d



e

Section	Origin	Sensitivity (%)	Specificity (%)	Accuracy (%)
FS	Fetal	90.8	92.1	91.1
	Maternal	96.8	89.5	91.3
Mid_S	Fetal	92.0	86.6	91.3
	Maternal	91.9	91.1	95.7
Mat_S	Fetal	95.2	93.7	94.5
	Maternal	99.2	93.5	91.2