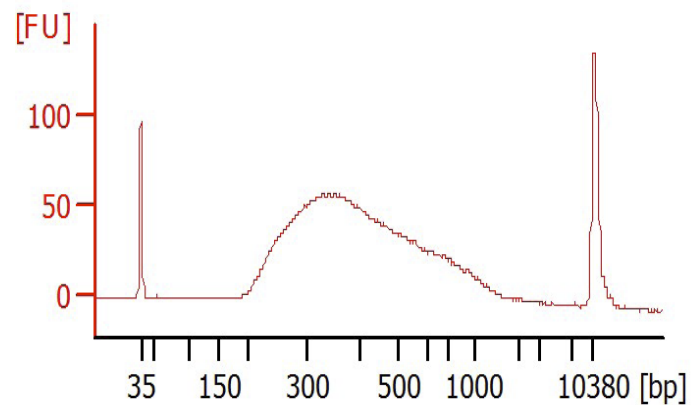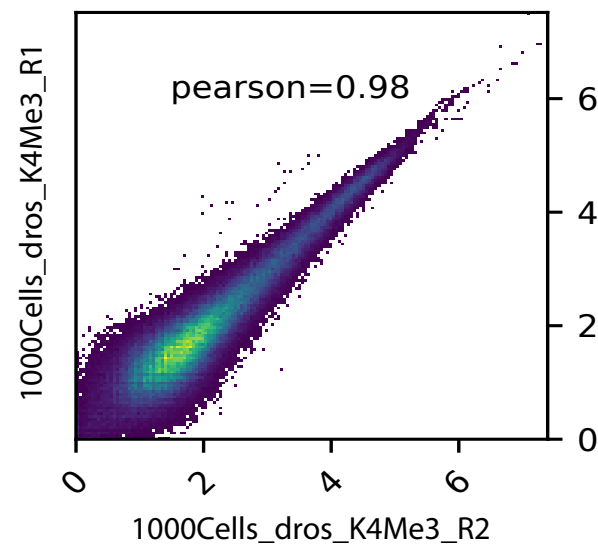# Supplementary Figure 1

A

B
pearson=0.98
1000Cells_dros_K4Me3_R1
1000Cells_dros_K4Me3_R2

C
pearson=0.95
1000Cells_dros_K9Me3_R1
1000Cells_dros_K9Me3_R2

D
pearson=0.98
100Cells_K562_K4Me3_R1
100Cells_K562_K4Me3_R2

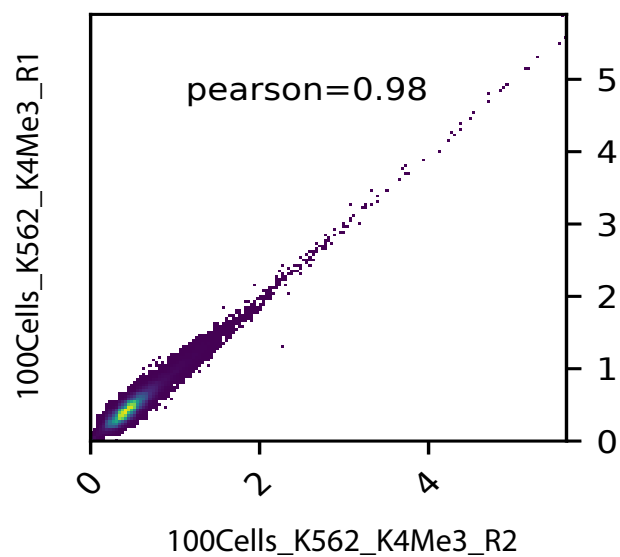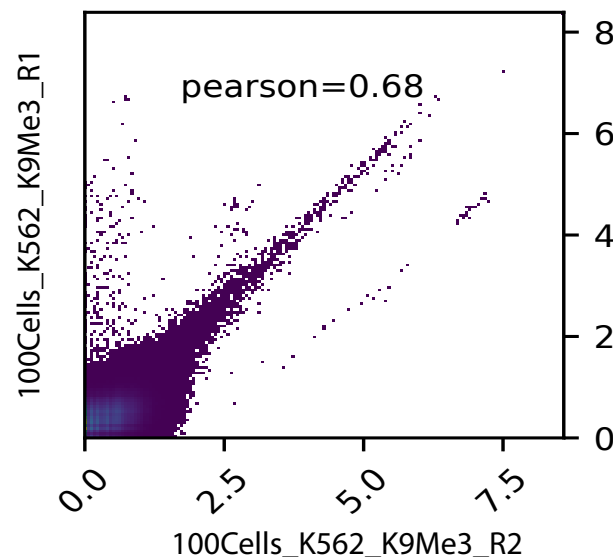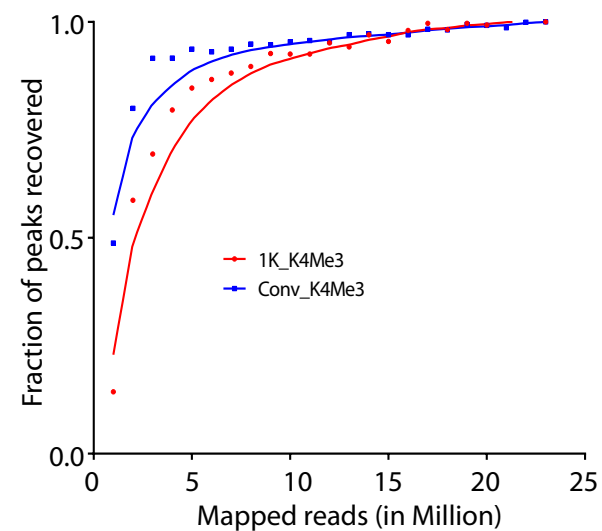**E**
pearson=0.68
100Cells_K562_K9Me3_R1
100Cells_K562_K9Me3_R2

G
Fraction of peaks recovered
Mapped reads (in Million)
1K_K4Me3
Conv_K4Me3

1K_K9Me3
Conv_K9Me3

F

Library	Overall Alignment (%)	Uniquely Mapped (%)	Multiple Mapped (%)	Duplicates (%)
K4Me3_100cells_K562_1	99.12	83.06	14.19	0.091632
K4Me3_100cells_K562_2	98.67	82.78	10.5	0.095607
K9Me3_100cells_K562_1	99.09	79.38	18.07	0.186757
K9Me3_100cells_K562_2	99.08	78.98	18.21	0.076646
K4Me3_1K_dros_1	97.1	82.67	11.57	0.481414
K4Me3_1K_dros_2	97.61	83.55	11.13	0.453763
K9Me3_1K_dros_1	96.81	60.77	32.91	0.149321
K9Me3_1K_dros_2	97.25	63.86	30.09	0.166462