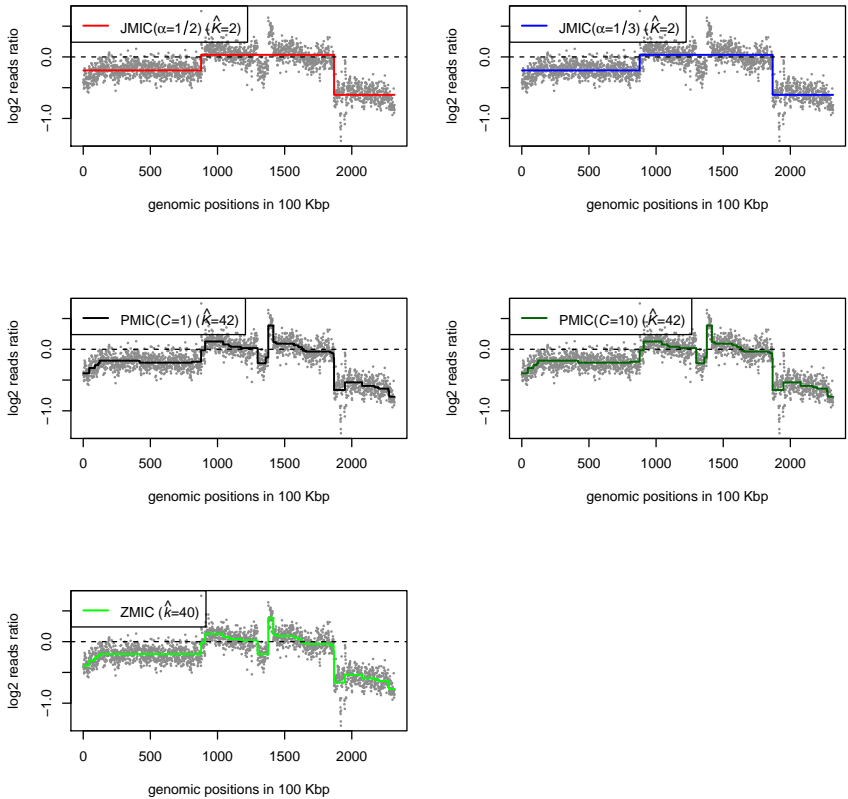
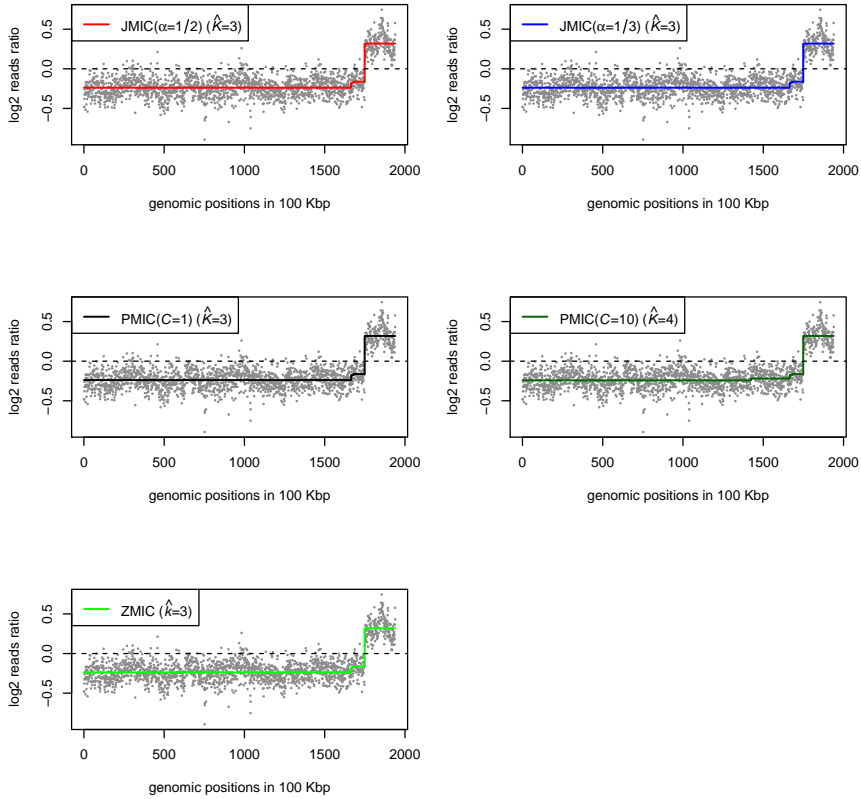


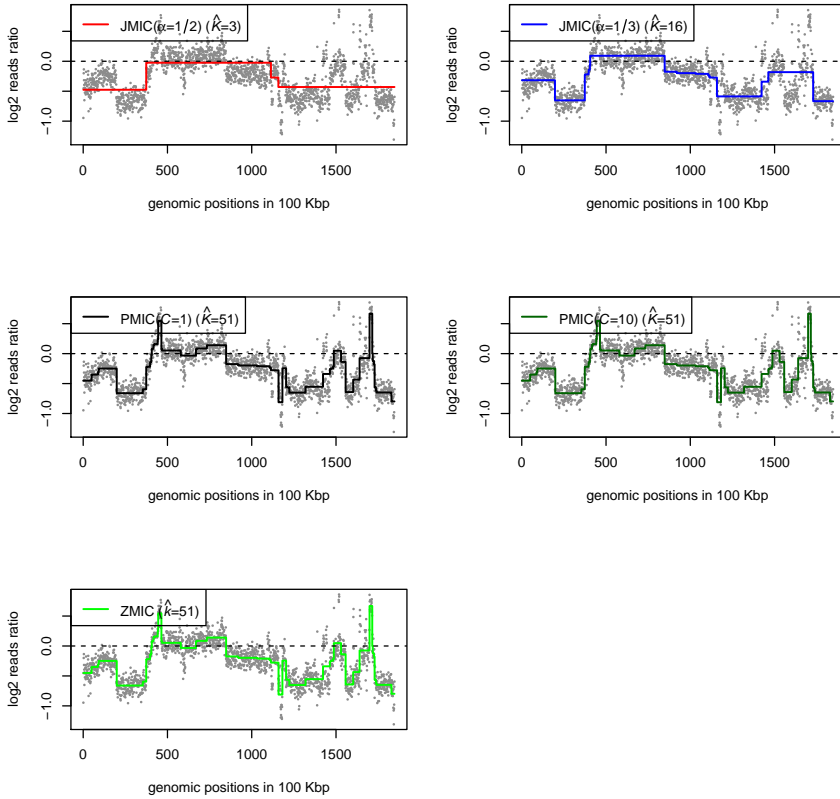
Supplemental Figures: Results on other 19 chromosomes from HCC1954



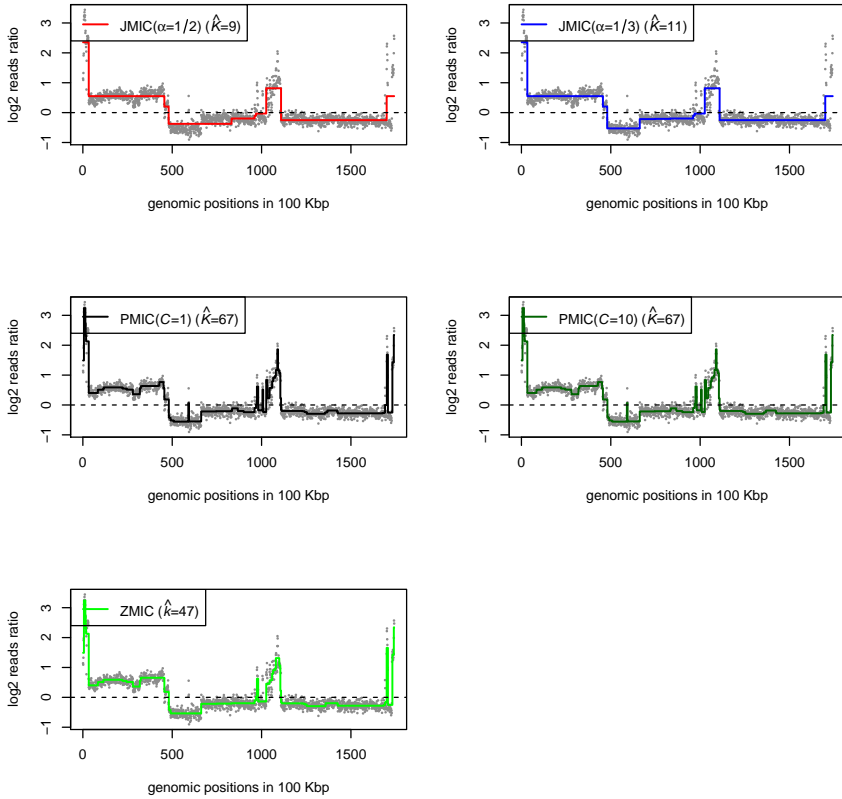
Supplemental Fig. 1: Chromosome 2 with the identified change points by the 1d fused LASSO models based on JM1C($\alpha = 1/2, 1/3$), PM1C($C = 1, 10$), ZM1C. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 2, the estimated number (or $\hat{K} + 1$) of CNV segments is 3.



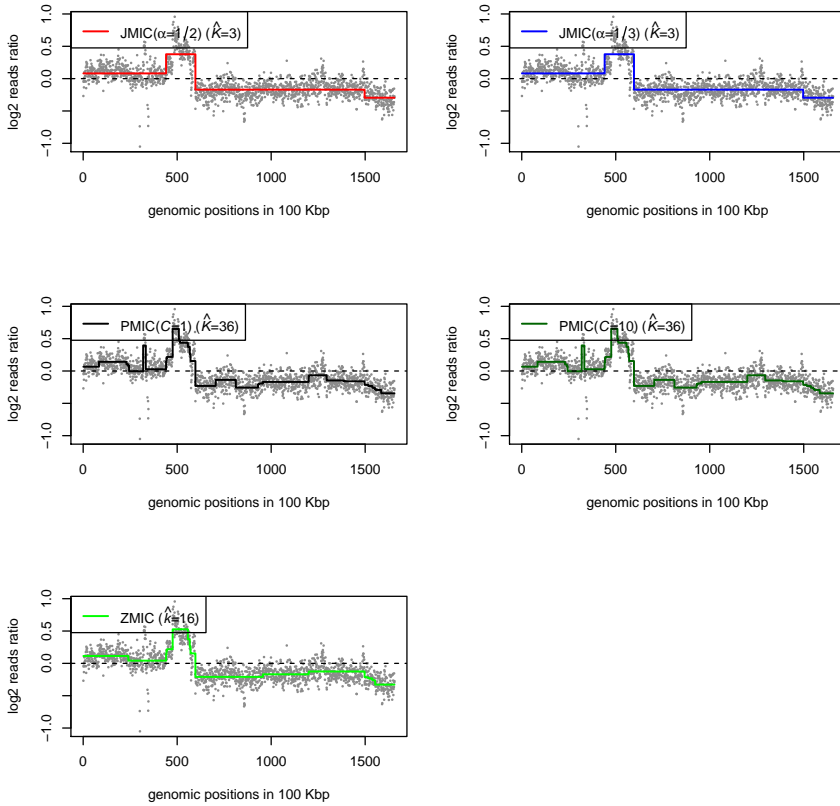
Supplemental Fig. 2: Chromosome 3 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 3, the estimated number (or $\hat{K} + 1$) of CNV segments is 4.



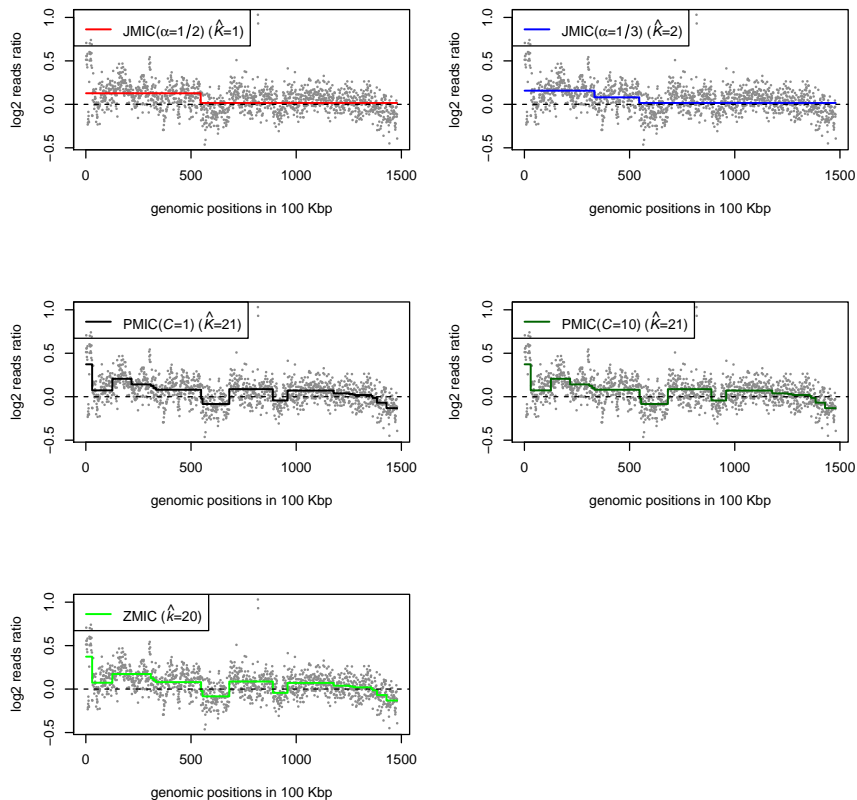
Supplemental Fig. 3: Chromosome 4 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 4, the estimated number (or $\hat{K} + 1$) of CNV segments is 17.



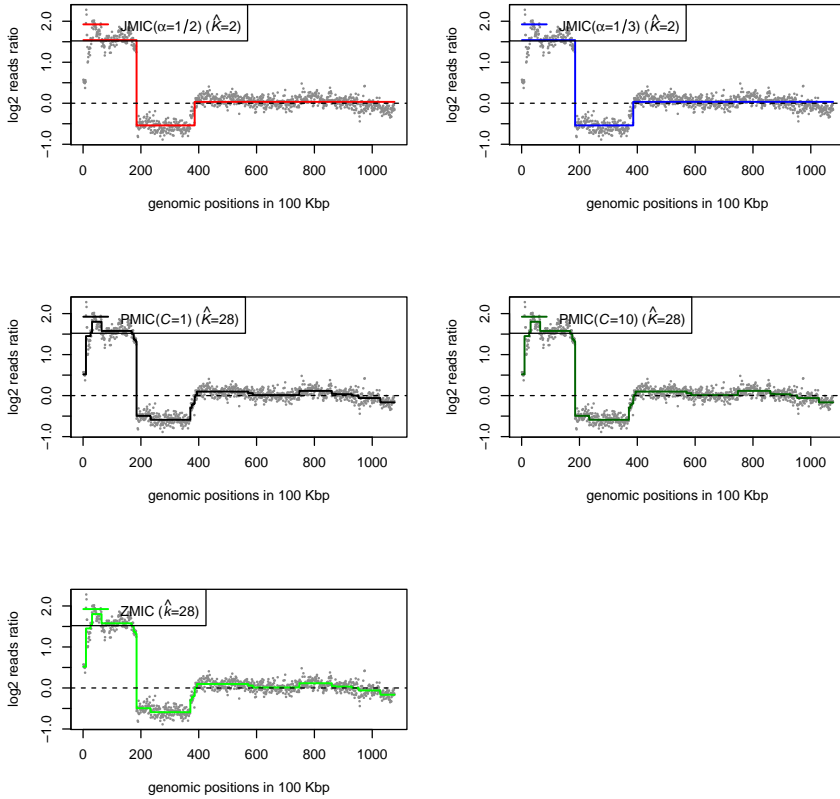
Supplemental Fig. 4: Chromosome 5 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 5, the estimated number (or $\hat{K} + 1$) of CNV segments is 10.



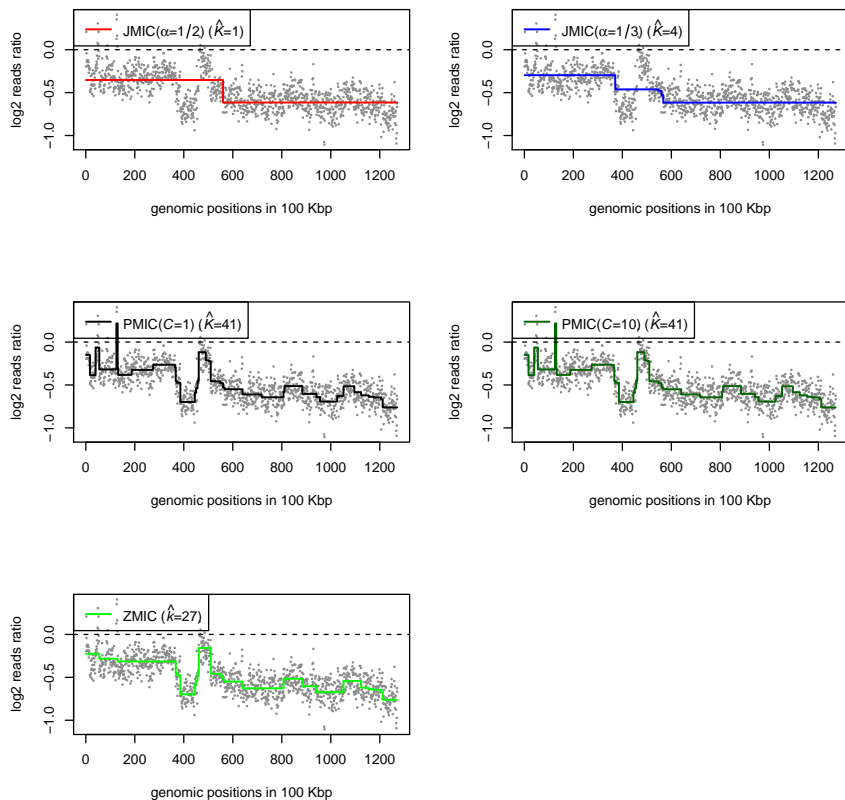
Supplemental Fig. 5: Chromosome 6 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 6, the estimated number (or $\hat{K} + 1$) of CNV segments is 4.



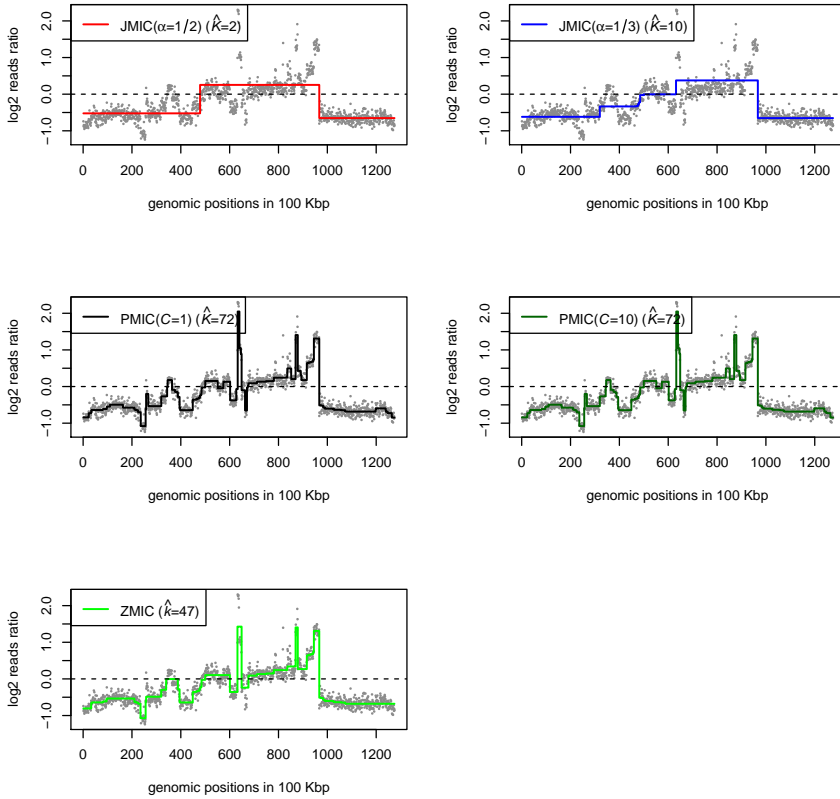
Supplemental Fig. 6: Chromosome 7 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 7, the estimated number (or $\hat{K} + 1$) of CNV segments is 3.



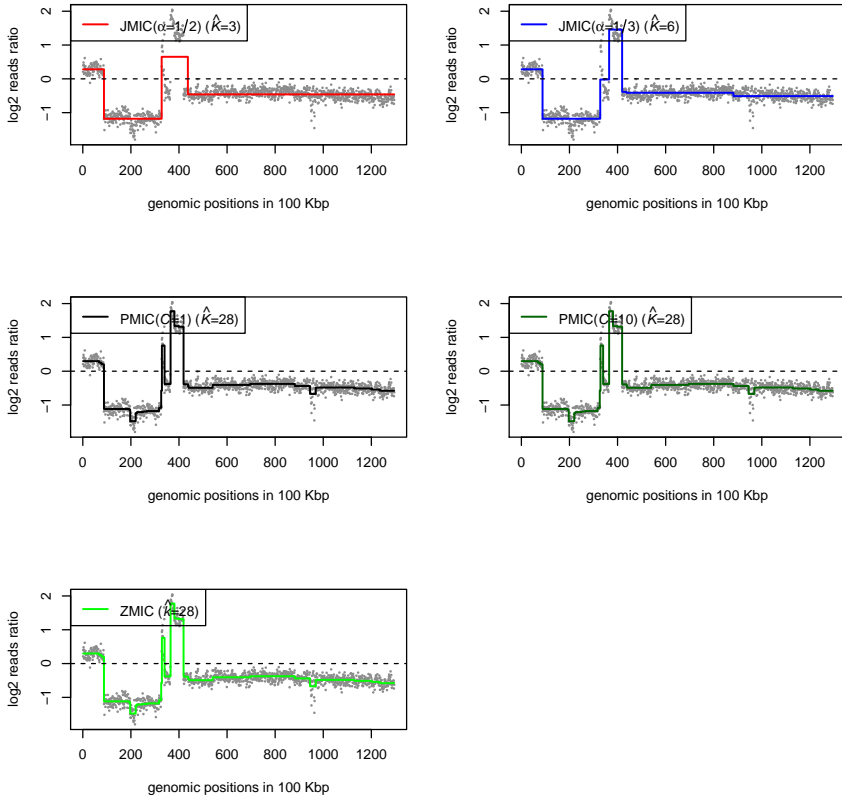
Supplemental Fig. 7: Chromosome 9 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, and ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 9, the estimated number (or $\hat{K} + 1$) of CNV segments is 3.



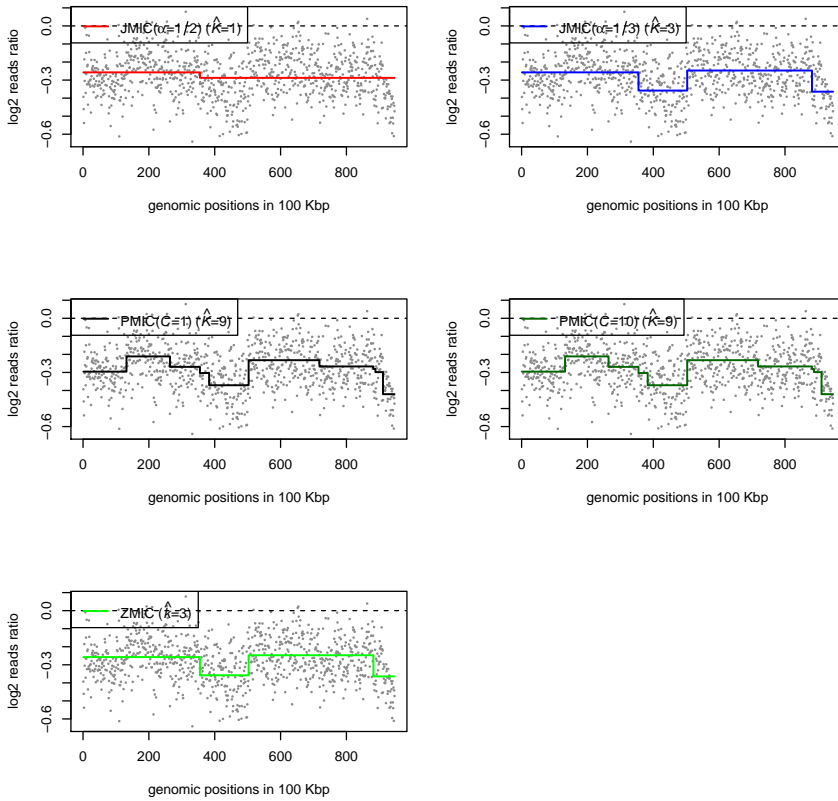
Supplemental Fig. 8: Chromosome 10 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, and ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 10, the estimated number (or $\hat{K} + 1$) of CNV segments is 5.



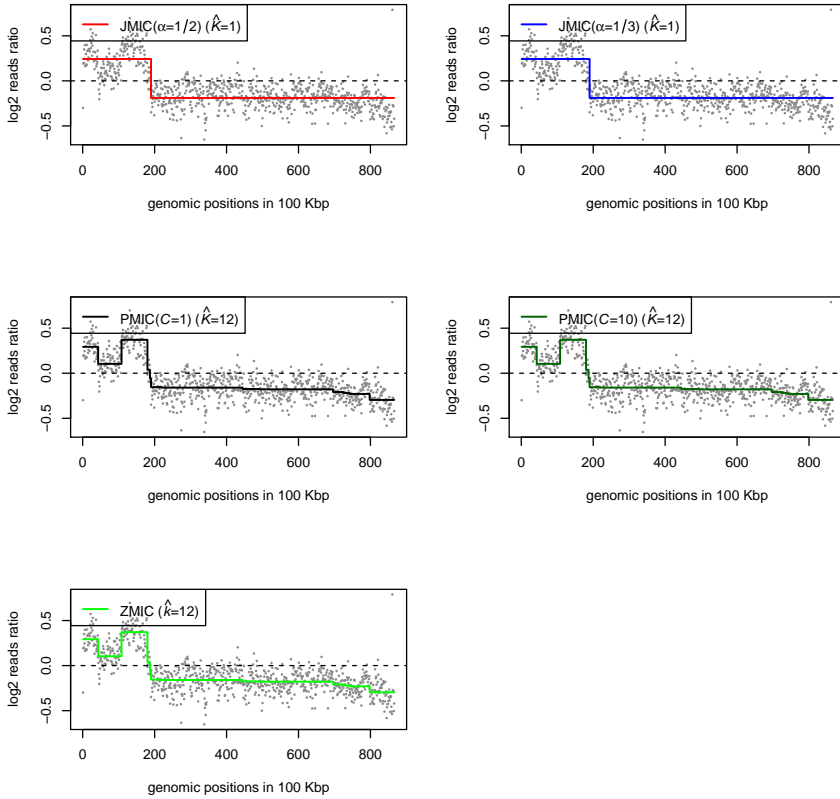
Supplemental Fig. 9: Chromosome 11 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 11, the estimated number (or $\hat{K} + 1$) of CNV segments is 11.



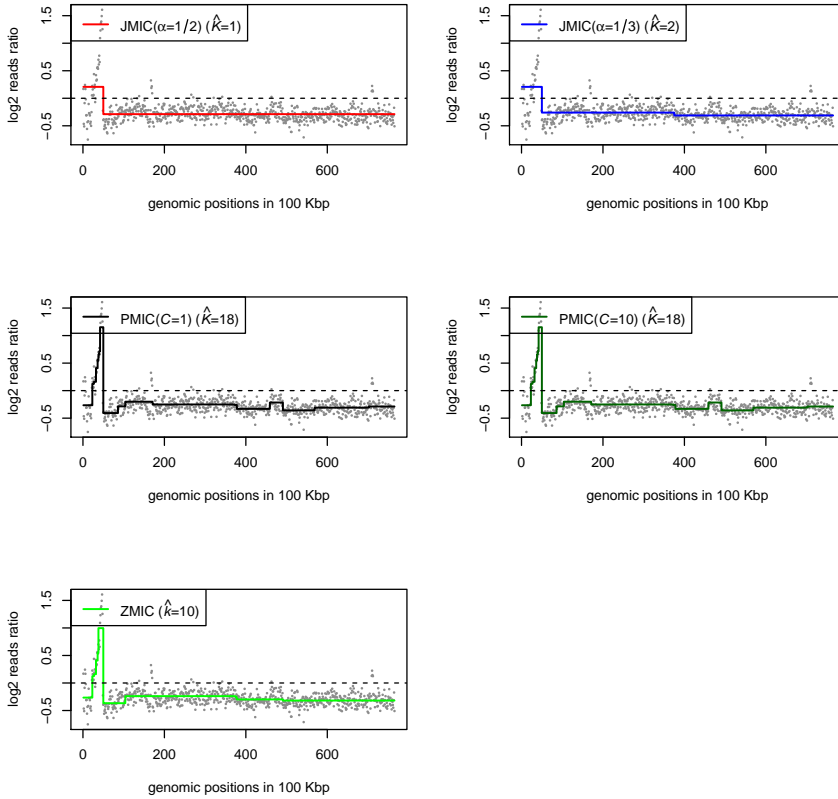
Supplemental Fig. 10: Chromosome 12 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 12, the estimated number (or $\hat{K} + 1$) of CNV segments is 7.



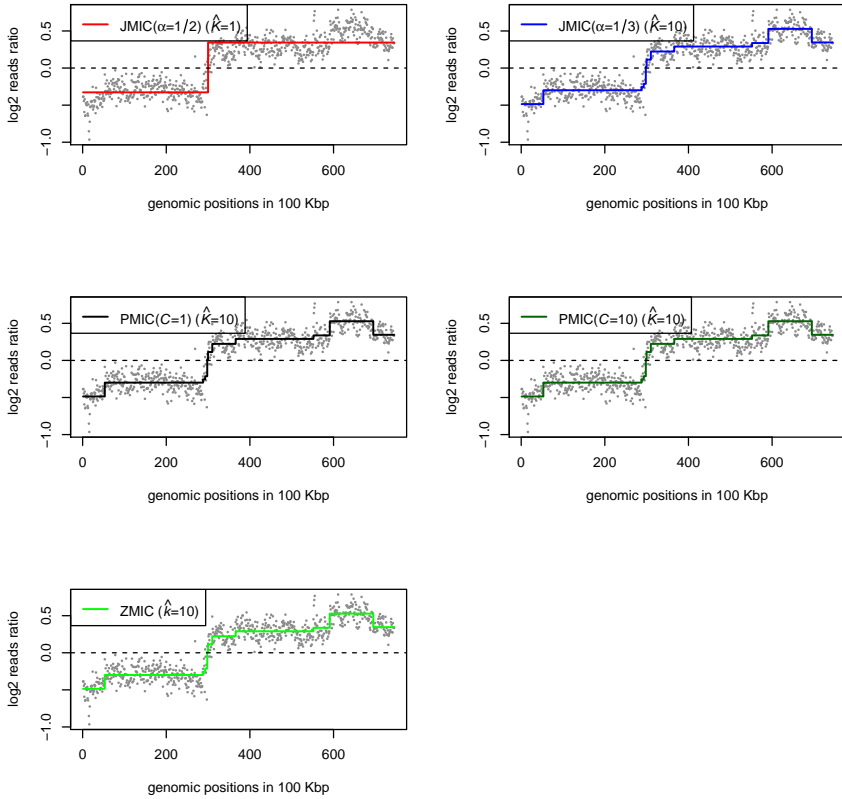
Supplemental Fig. 11: Chromosome 13 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, and ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 13, the estimated number (or $\hat{K} + 1$) of CNV segments is 4.



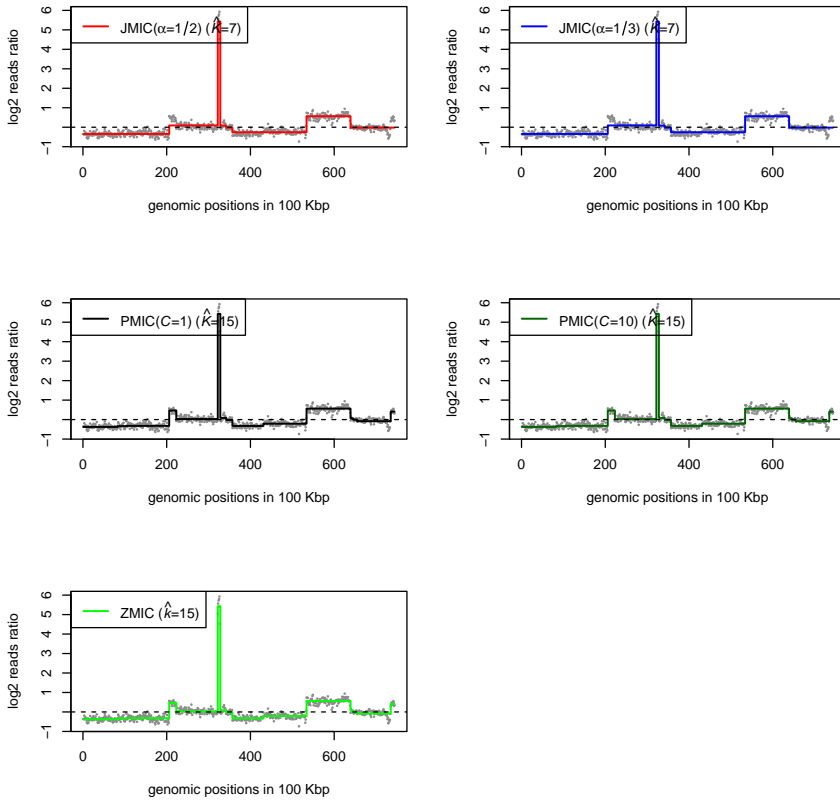
Supplemental Fig. 12: Chromosome 14 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 14, the estimated number (or $\hat{K} + 1$) of CNV segments is 2.



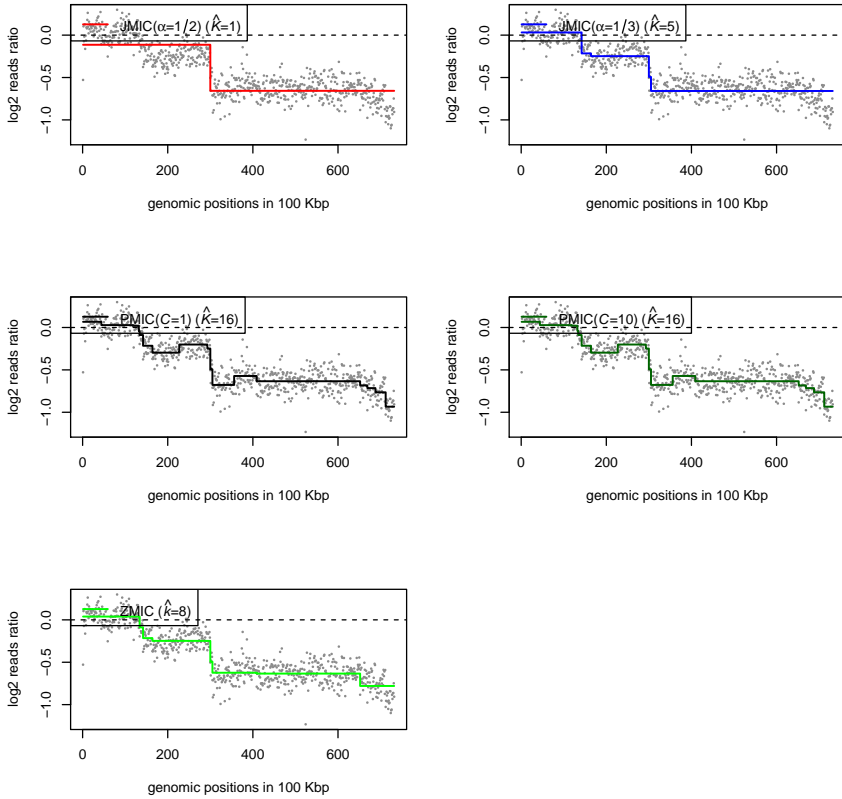
Supplemental Fig. 13: Chromosome 15 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 15, the estimated number (or $\hat{K} + 1$) of CNV segments is 3.



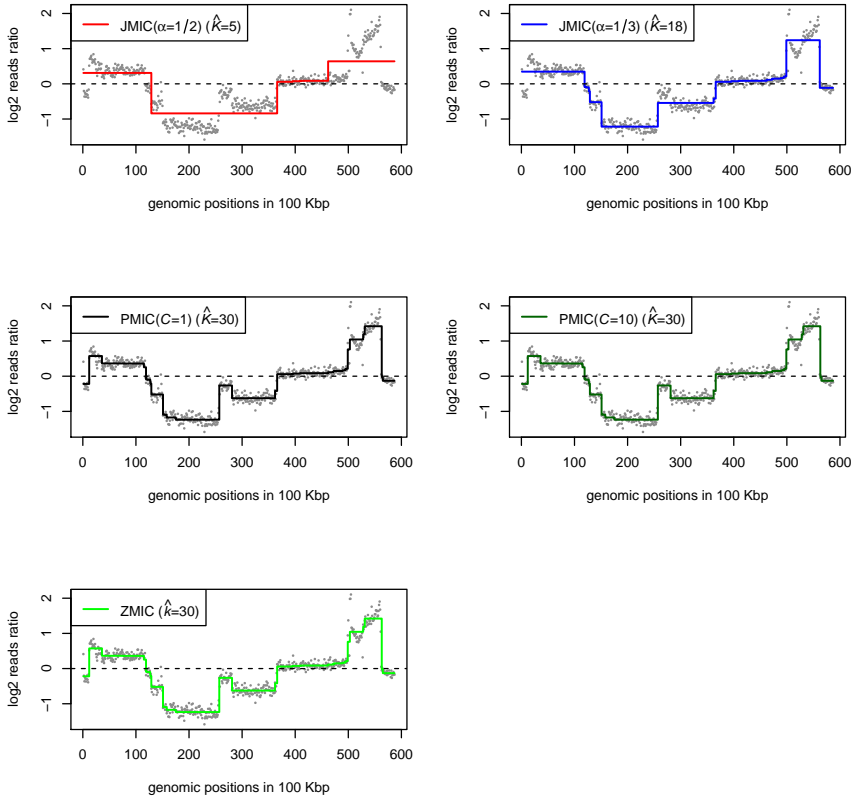
Supplemental Fig. 14: Chromosome 16 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 16, the estimated number (or $\hat{K} + 1$) of CNV segments is 11.



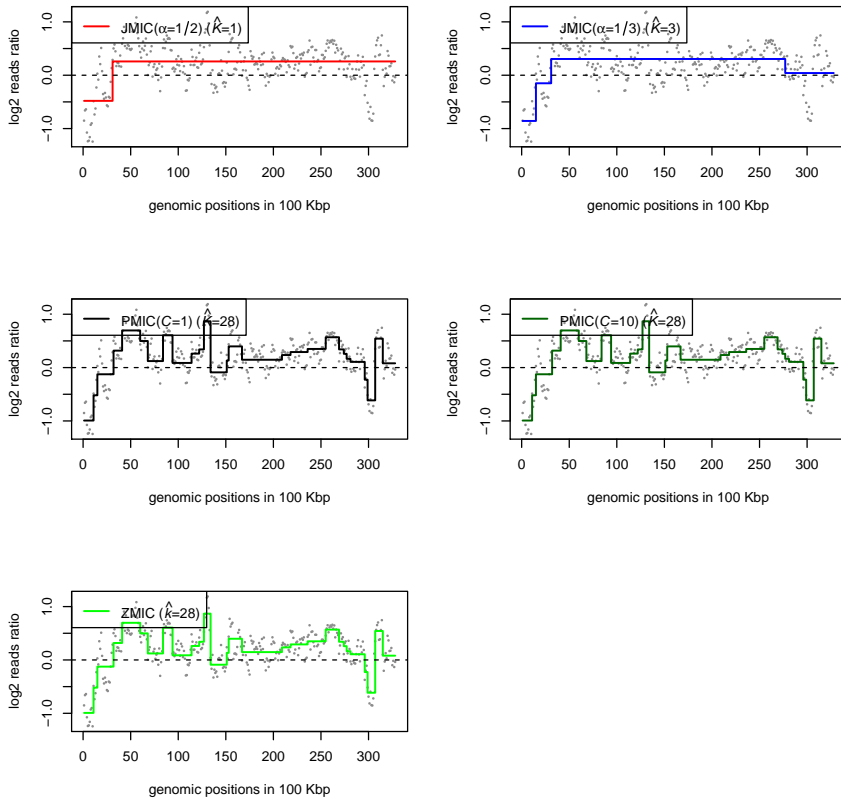
Supplemental Fig. 15: Chromosome 17 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, and ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 17, the estimated number (or $\hat{K} + 1$) of CNV segments is 8.



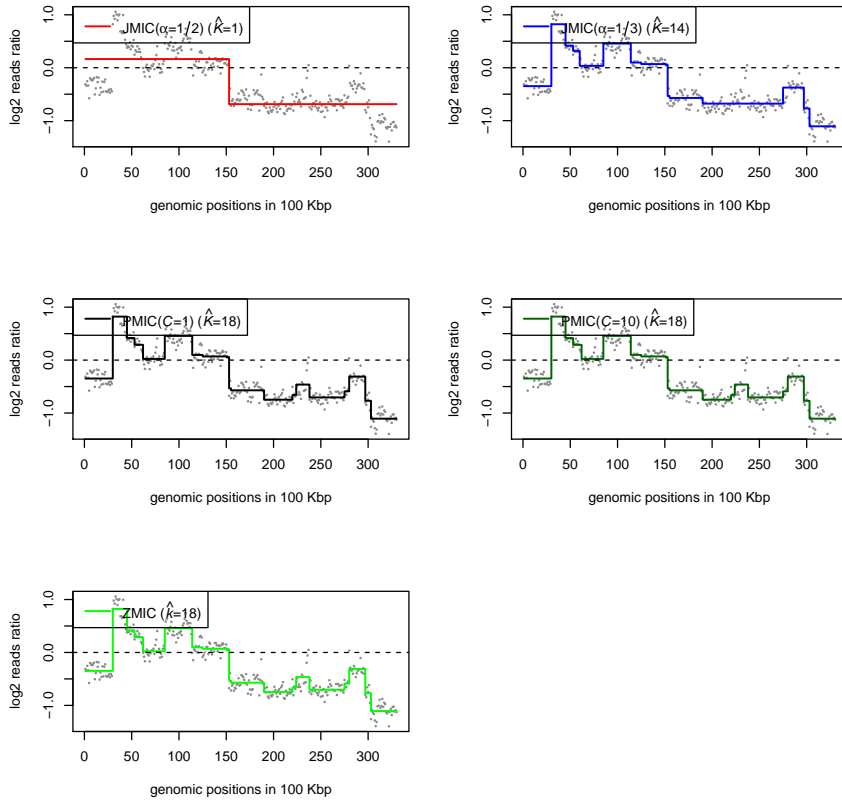
Supplemental Fig. 16: Chromosome 18 with the identified change points by the 1d fused LASSO models based on $\text{JMIC}(\alpha = 1/2, 1/3)$, $\text{PMIC}(C = 1, 10)$, and ZMIC . \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 18, the estimated number (or $\hat{K} + 1$) of CNV segments is 6.



Supplemental Fig. 17: Chromosome 20 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 20, the estimated number (or $\hat{K} + 1$) of CNV segments is 19.



Supplemental Fig. 18: Chromosome 21 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 21, the estimated number (or $\hat{K} + 1$) of CNV segments is 4.



Supplemental Fig. 19: Chromosome 22 with the identified change points by the 1d fused LASSO models based on JMIC($\alpha = 1/2, 1/3$), PMIC($C = 1, 10$), and ZMIC. \hat{K} denotes the estimated number of change points. The solid line represents the average reads ratio in each segment. The dashed line is for $\hat{y} = 0$, indicating no copy number change. For chromosome 22, the estimated number (or $\hat{K} + 1$) of CNV segments is 15.