

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 09:49:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779350.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1779350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779350_1.fastq.gz SRR1779350_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 09:49:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779350.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	312,671,364
Mapped reads	295,822,035 / 94.61%
Unmapped reads	16,849,329 / 5.39%
Mapped paired reads	295,822,035 / 94.61%
Mapped reads, first in pair	148,818,795 / 47.6%
Mapped reads, second in pair	147,003,240 / 47.02%
Mapped reads, both in pair	291,300,724 / 93.17%
Mapped reads, singletons	4,521,311 / 1.45%
Secondary alignments	0
Supplementary alignments	1,374,748 / 0.44%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	63,861,351 / 20.42%
Duplication rate	18.51%
Clipped reads	16,065,027 / 5.14%

2.2. ACGT Content

Number/percentage of A's	8,991,400,709 / 30.35%
Number/percentage of C's	5,818,410,943 / 19.64%
Number/percentage of T's	8,889,800,316 / 30%
Number/percentage of G's	5,920,864,296 / 19.98%
Number/percentage of N's	8,425,419 / 0.03%

GC Percentage	39.62%
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2.3. Coverage

Mean	9.5733
Standard Deviation	27.4127

2.4. Mapping Quality

Mean Mapping Quality	53.74
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2.5. Insert size

Mean	73,636.55
Standard Deviation	2,605,792.42
P25/Median/P75	159 / 218 / 303

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	103,064,139
Insertions	2,502,823
Mapped reads with at least one insertion	0.83%
Deletions	3,205,837
Mapped reads with at least one deletion	1.06%
Homopolymer indels	47.67%

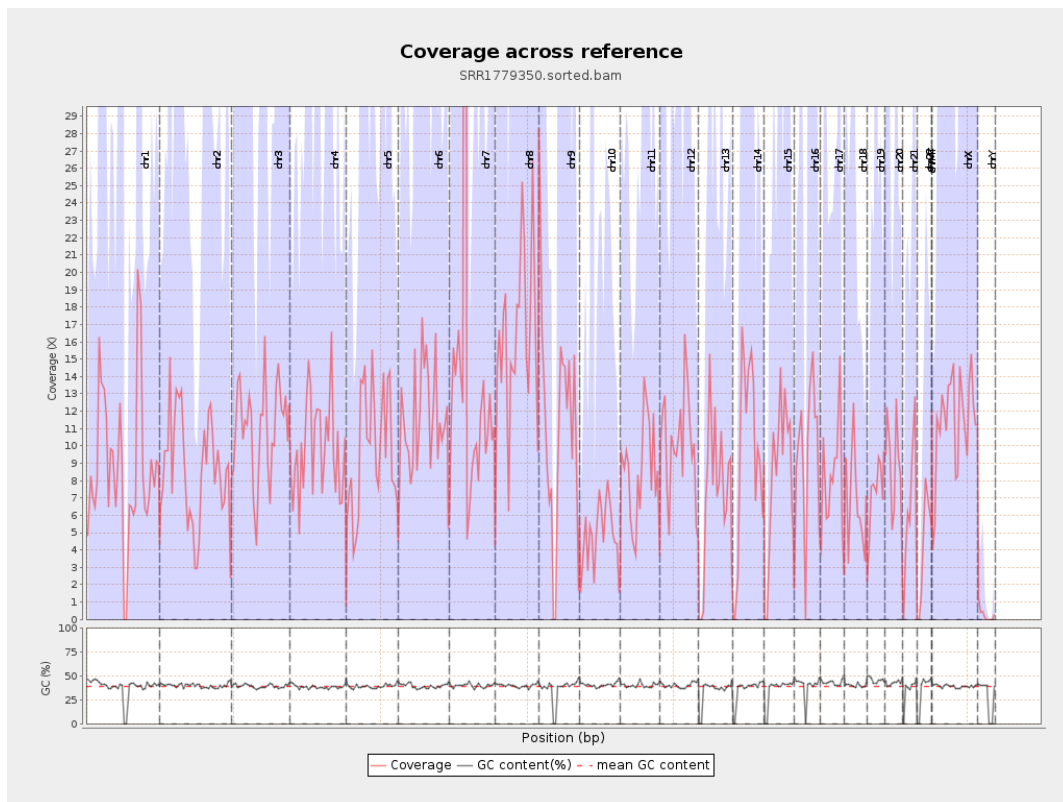
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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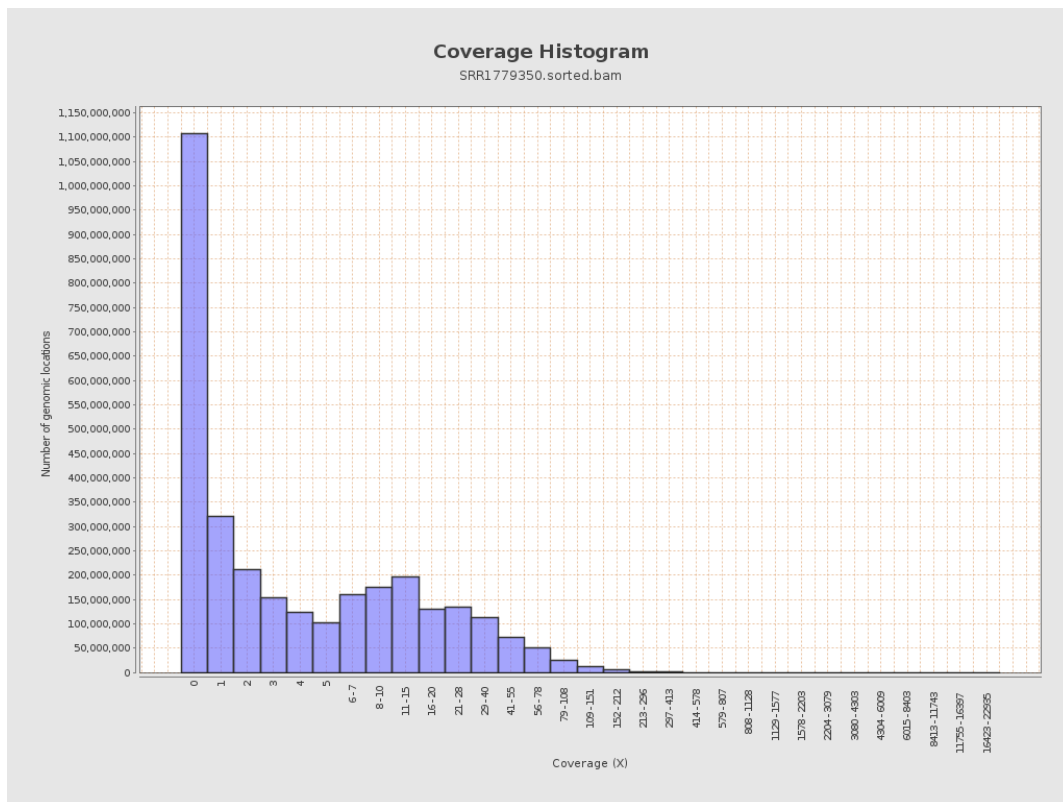
		bases	coverage	deviation
chr1	249250621	2166119234	8.6905	29.4786
chr2	243199373	2098643858	8.6293	19.8809
chr3	198022430	2179331597	11.0055	20.5136
chr4	191154276	1884339002	9.8577	19.4396
chr5	180915260	1767989256	9.7725	19.6128
chr6	171115067	2004478429	11.7142	22.3595
chr7	159138663	2391294638	15.0265	72.7344
chr8	146364022	2409236731	16.4606	27.5904
chr9	141213431	1533551359	10.8598	23.7191
chr10	135534747	653808949	4.8239	35.4637
chr11	135006516	1154339919	8.5503	18.6024
chr12	133851895	1356649615	10.1355	22.4714
chr13	115169878	837114830	7.2685	17.2081
chr14	107349540	1022412901	9.5241	20.2227
chr15	102531392	840562223	8.1981	19.231
chr16	90354753	832806597	9.2171	19.5284
chr17	81195210	639365323	7.8744	17.9193
chr18	78077248	554003550	7.0956	17.2142
chr19	59128983	431536618	7.2982	19.5341
chr20	63025520	554780160	8.8025	18.394
chr21	48129895	316821337	6.5826	16.4151
chr22	51304566	218467893	4.2583	10.5727
chrMT	16571	199333	12.029	5.4765
chrX	155270560	1772281284	11.4141	24.9329

chrY	59373566	15960251	0.2688	2.7045
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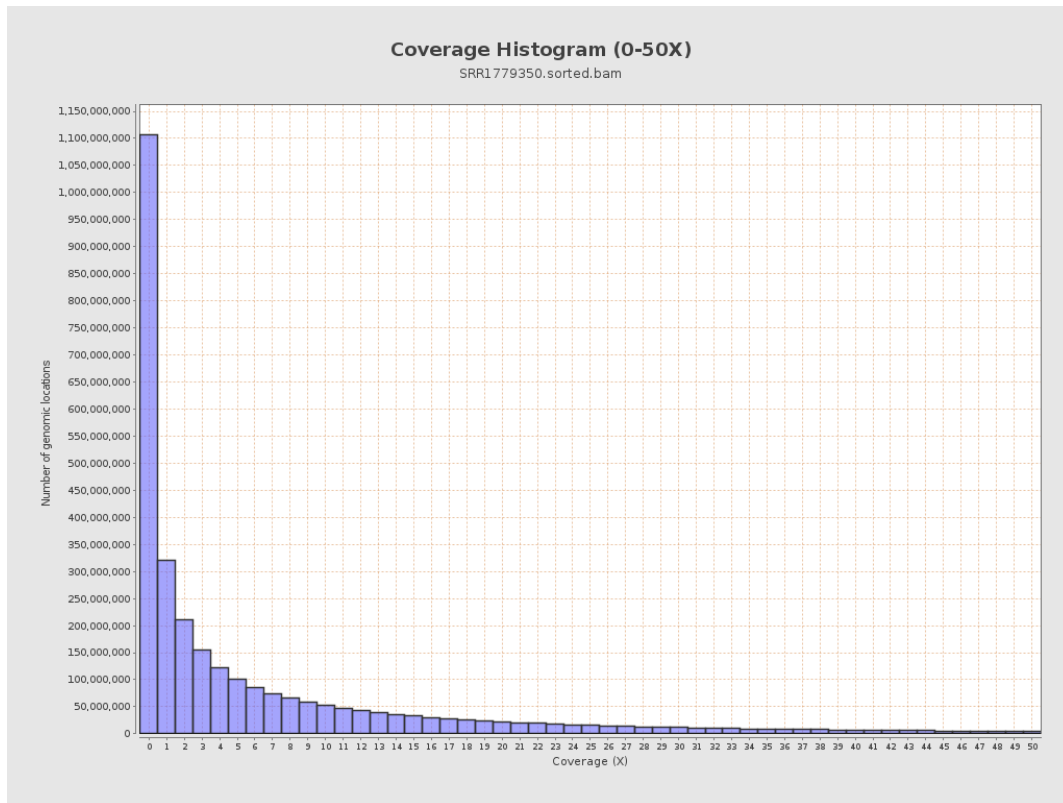
3. Results : Coverage across reference



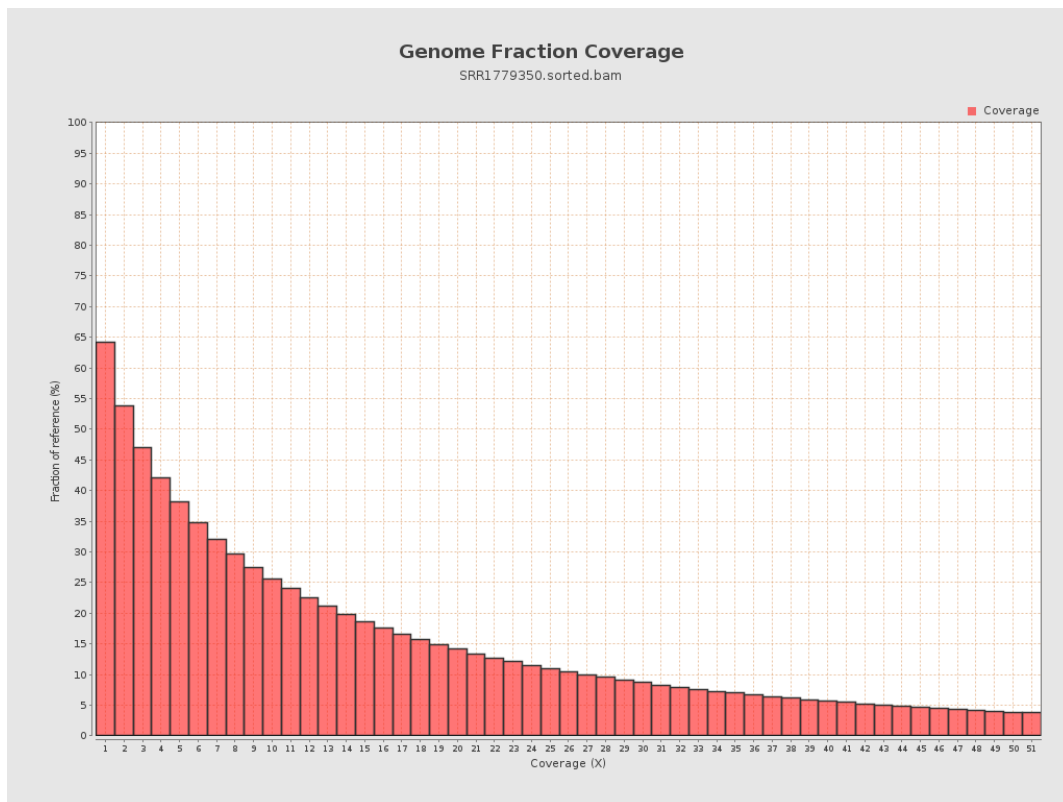
4. Results : Coverage Histogram



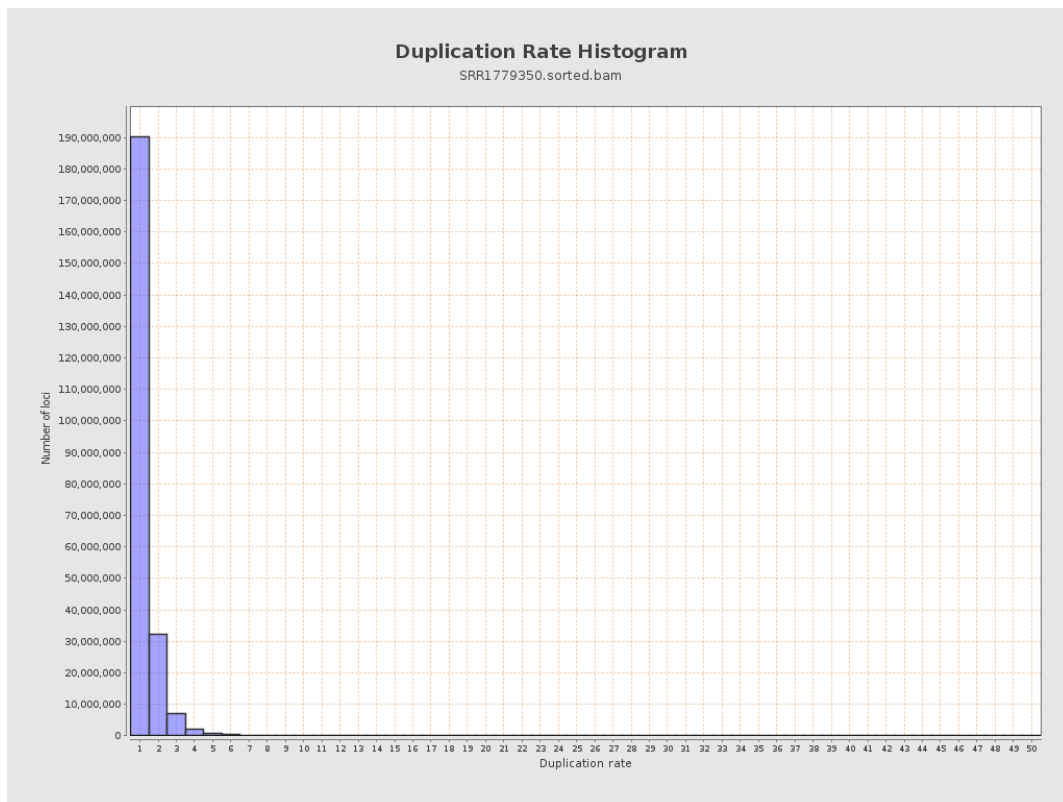
5. Results : Coverage Histogram (0-50X)



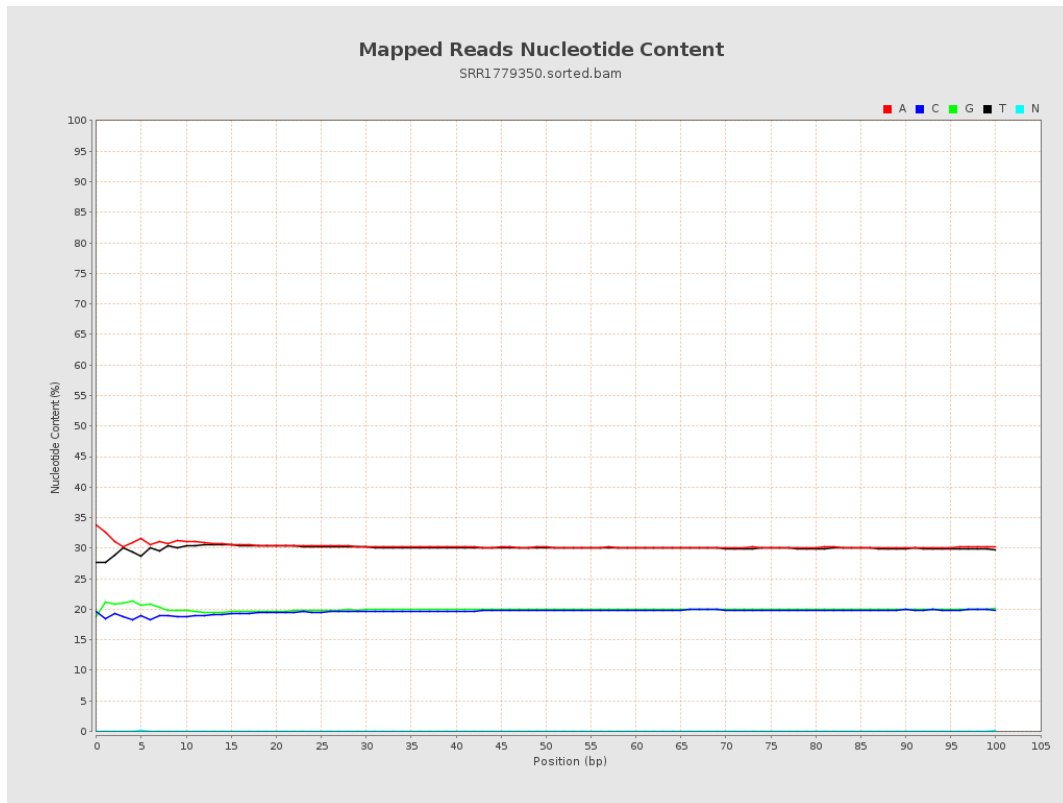
6. Results : Genome Fraction Coverage



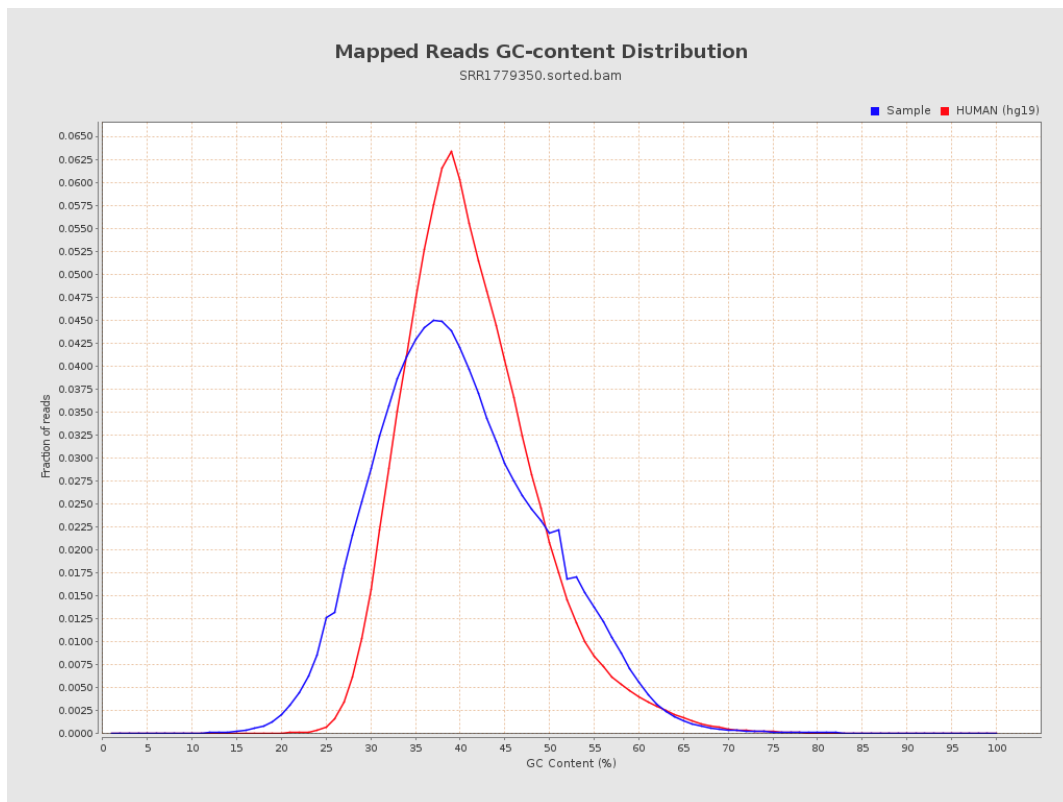
7. Results : Duplication Rate Histogram



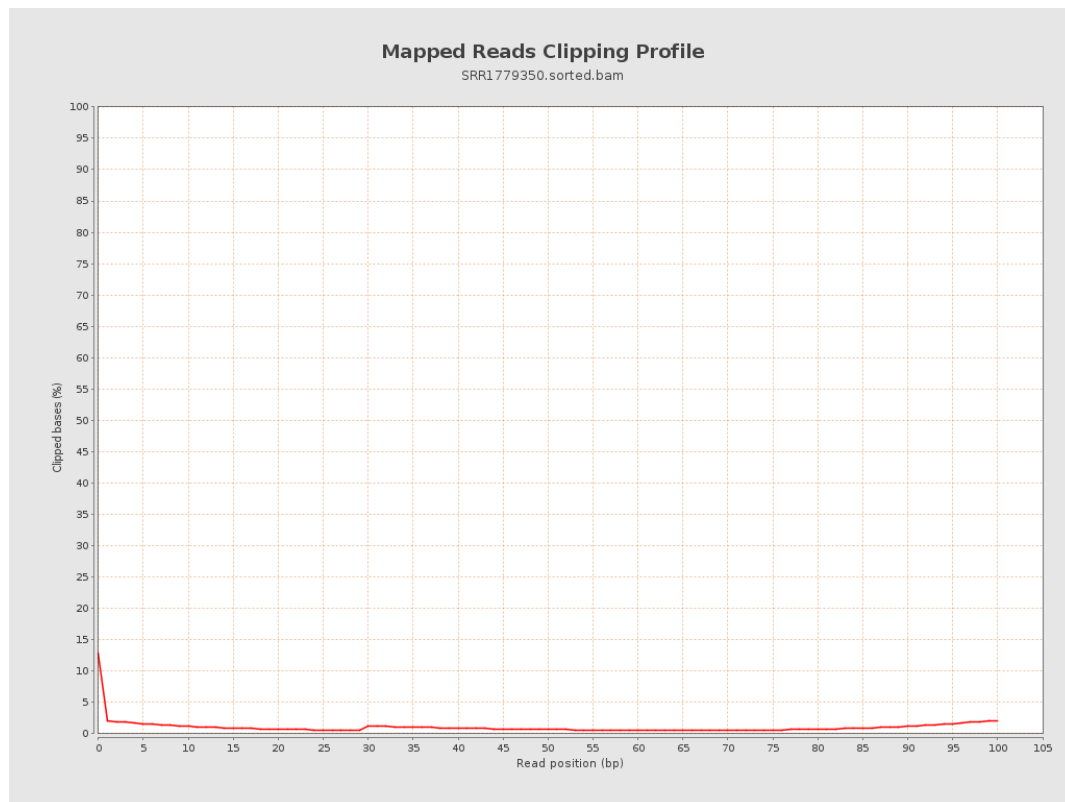
8. Results : Mapped Reads Nucleotide Content



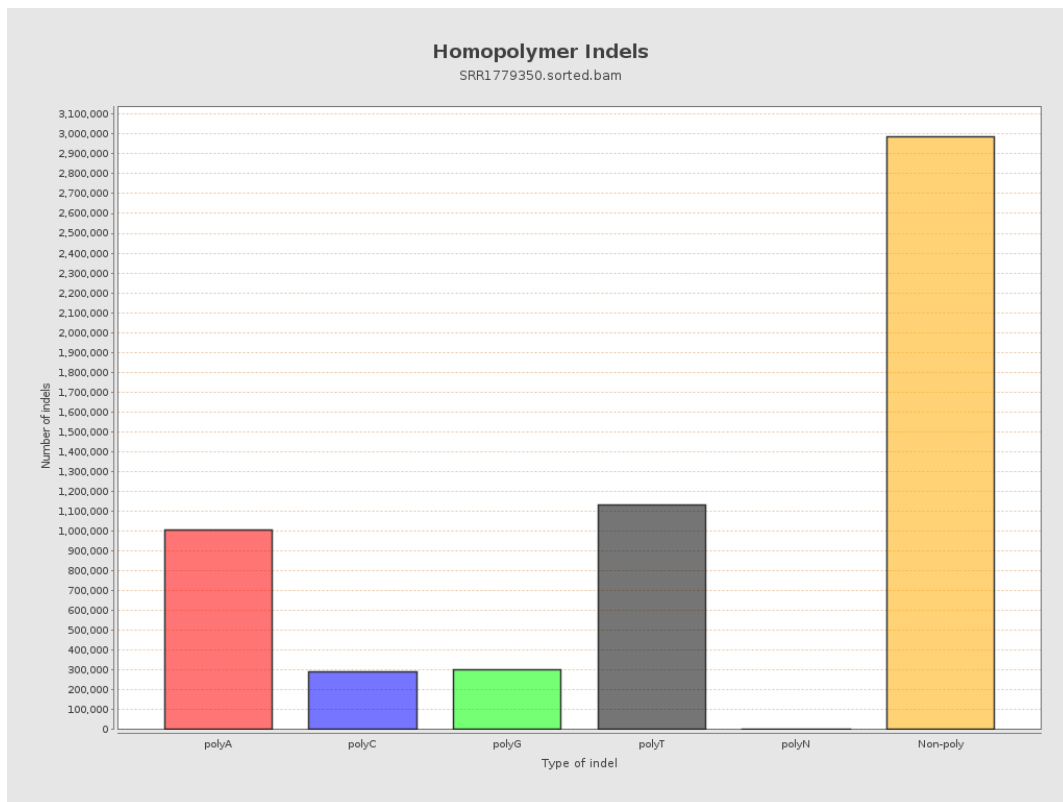
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



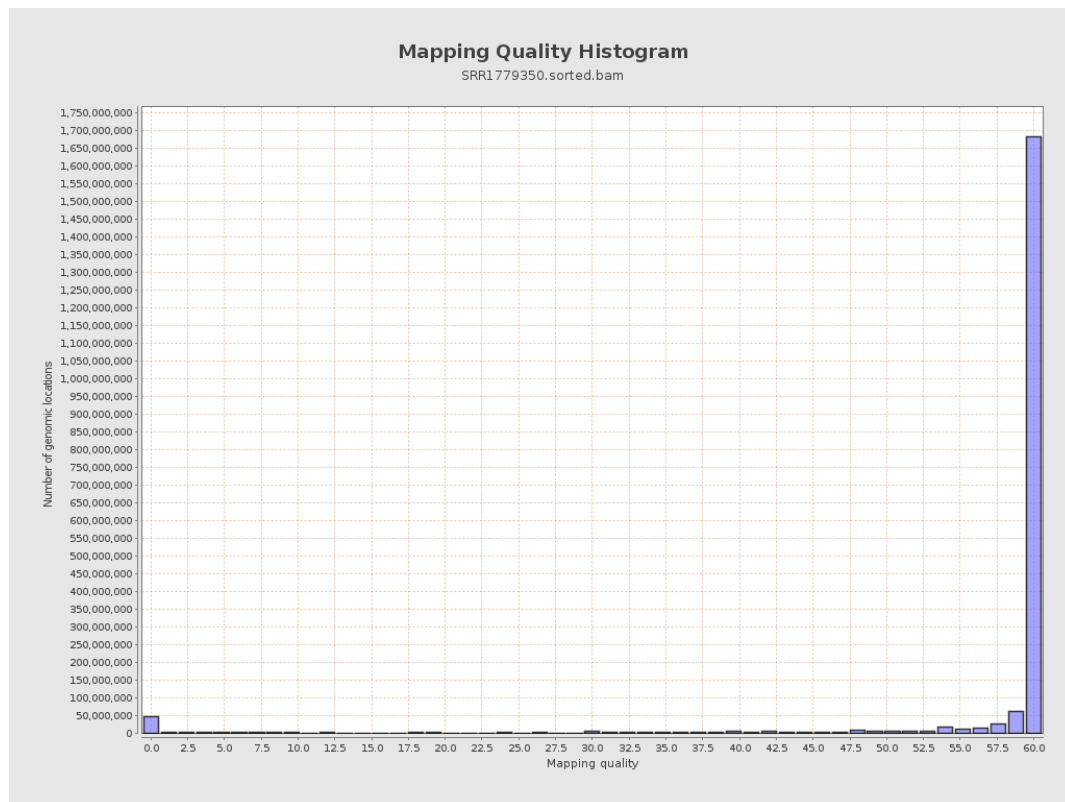
11. Results : Homopolymer Indels



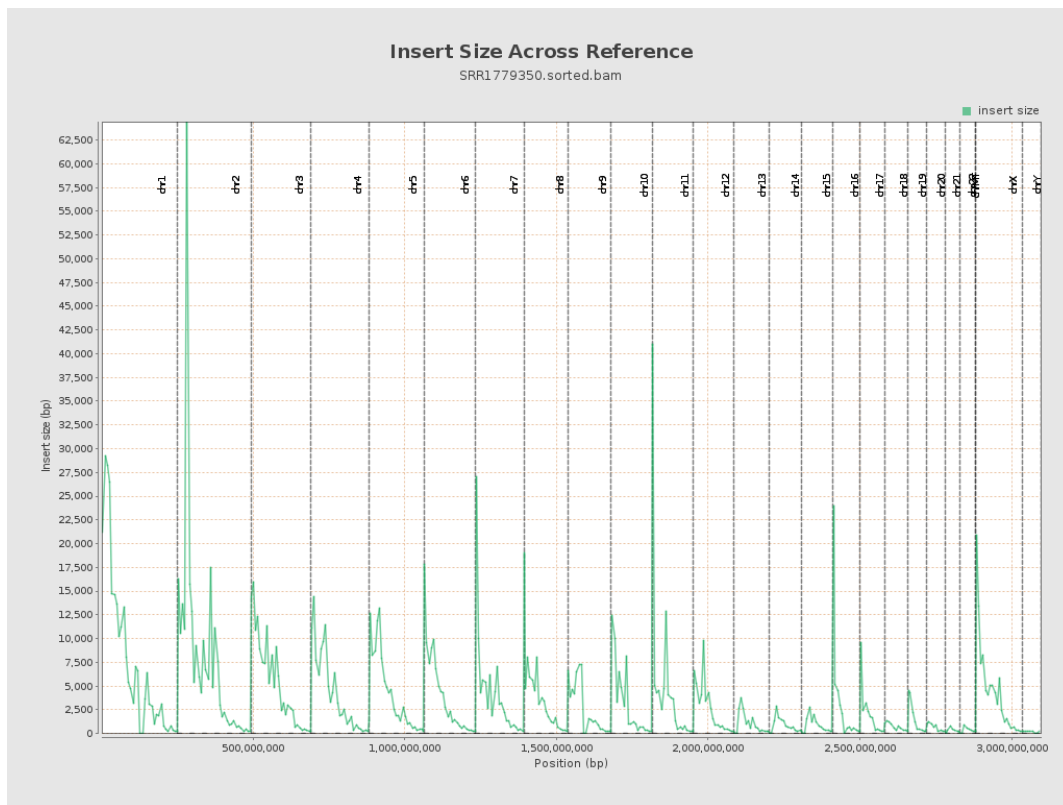
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

