

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 04:38:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618580.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_SRR618580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618580_1.fastq.gz SRR618580_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 04:38:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,080,514
Mapped reads	53,875,786 / 96.07%
Unmapped reads	2,204,728 / 3.93%
Mapped paired reads	53,875,786 / 96.07%
Mapped reads, first in pair	27,265,883 / 48.62%
Mapped reads, second in pair	26,609,903 / 47.45%
Mapped reads, both in pair	52,736,400 / 94.04%
Mapped reads, singletons	1,139,386 / 2.03%
Secondary alignments	0
Supplementary alignments	71,020 / 0.13%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	12,818,074 / 22.86%
Duplication rate	20.87%
Clipped reads	10,370,317 / 18.49%

2.2. ACGT Content

Number/percentage of A's	1,338,681,402 / 26.14%
Number/percentage of C's	1,196,226,197 / 23.36%
Number/percentage of T's	1,342,817,770 / 26.22%
Number/percentage of G's	1,243,706,502 / 24.28%
Number/percentage of N's	478,494 / 0.01%

GC Percentage	47.64%
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2.3. Coverage

Mean	1.6555
Standard Deviation	8.0126

2.4. Mapping Quality

Mean Mapping Quality	52.34
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2.5. Insert size

Mean	27,845.36
Standard Deviation	1,648,291.35
P25/Median/P75	175 / 203 / 238

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	67,673,833
Insertions	881,539
Mapped reads with at least one insertion	1.6%
Deletions	2,161,078
Mapped reads with at least one deletion	3.92%
Homopolymer indels	51.57%

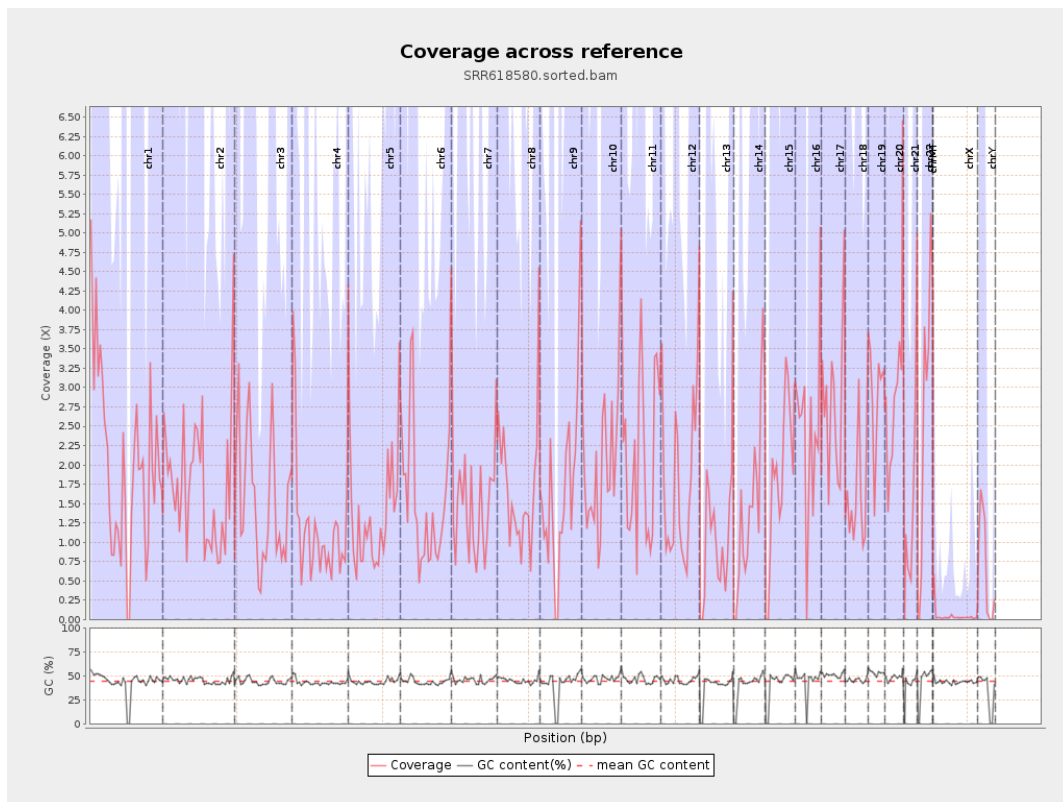
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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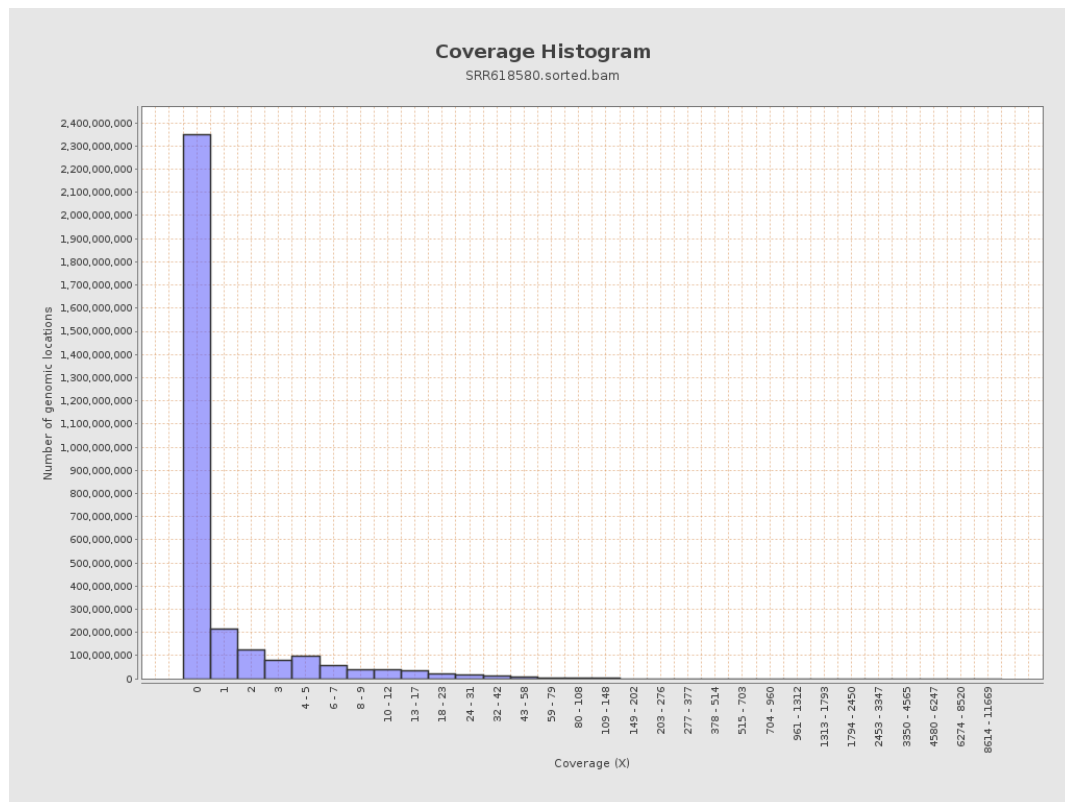
		bases	coverage	deviation
chr1	249250621	497814761	1.9972	8.1139
chr2	243199373	421664309	1.7338	9.6321
chr3	198022430	303667126	1.5335	6.0965
chr4	191154276	223975851	1.1717	5.8608
chr5	180915260	251688174	1.3912	5.7587
chr6	171115067	264443813	1.5454	6.1832
chr7	159138663	244470649	1.5362	6.0026
chr8	146364022	246201902	1.6821	7.4796
chr9	141213431	236927244	1.6778	8.0228
chr10	135534747	268147962	1.9784	7.4702
chr11	135006516	290792892	2.1539	8.1583
chr12	133851895	241274044	1.8025	8.1847
chr13	115169878	117281321	1.0183	4.6525
chr14	107349540	156313166	1.4561	6.379
chr15	102531392	187141488	1.8252	7.3536
chr16	90354753	222613333	2.4638	19.4543
chr17	81195210	223402250	2.7514	9.5335
chr18	78077248	121675160	1.5584	6.567
chr19	59128983	169161003	2.8609	10.3464
chr20	63025520	178296493	2.829	9.2795
chr21	48129895	74405776	1.5459	10.998
chr22	51304566	134222260	2.6162	10.223
chrMT	16571	4685	0.2827	1.1227
chrX	155270560	7135342	0.046	1.196

chrY	59373566	42263551	0.7118	7.3855
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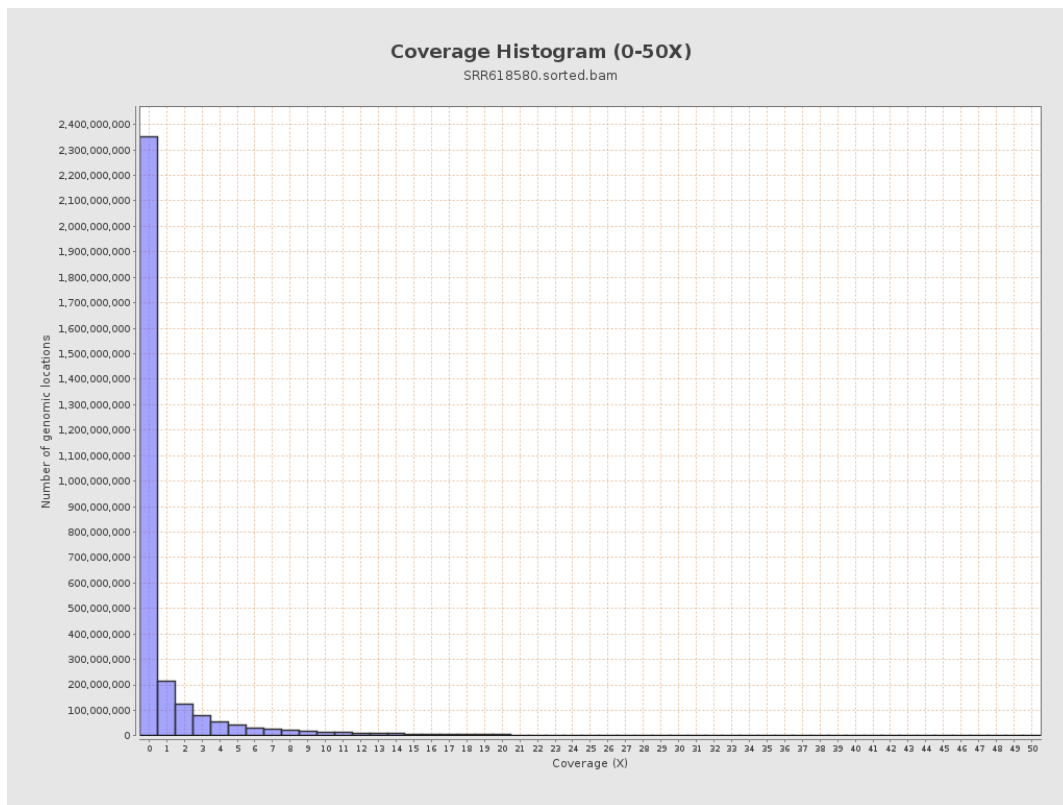
3. Results : Coverage across reference



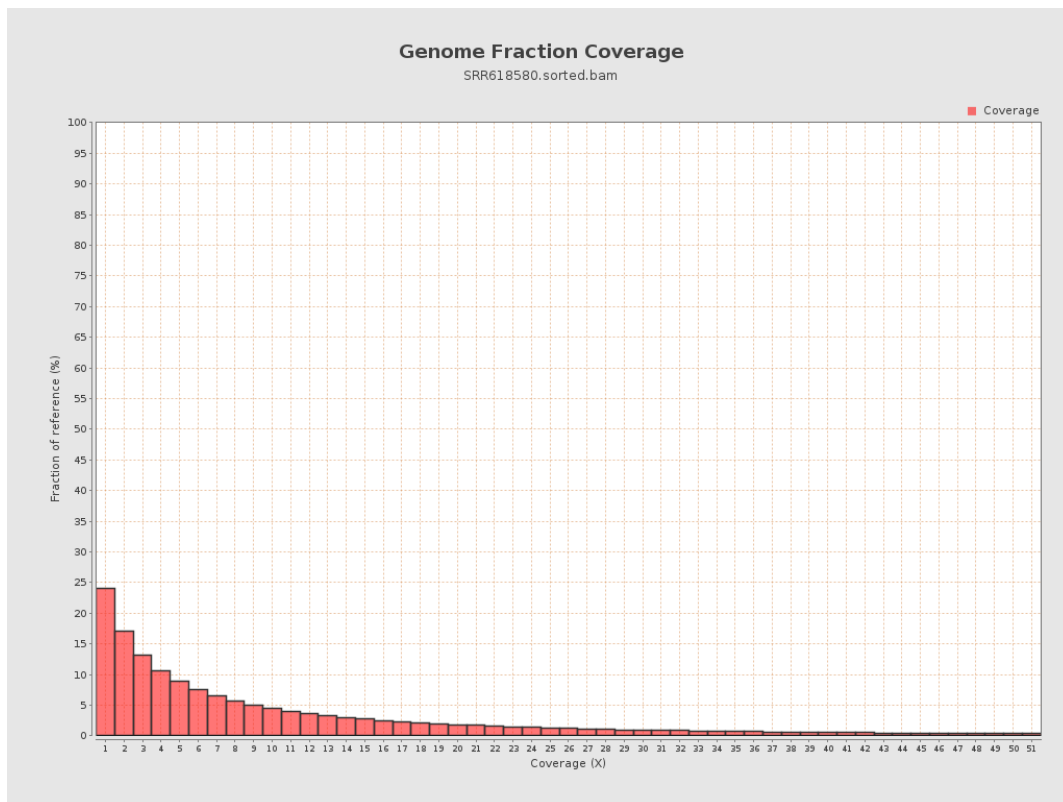
4. Results : Coverage Histogram



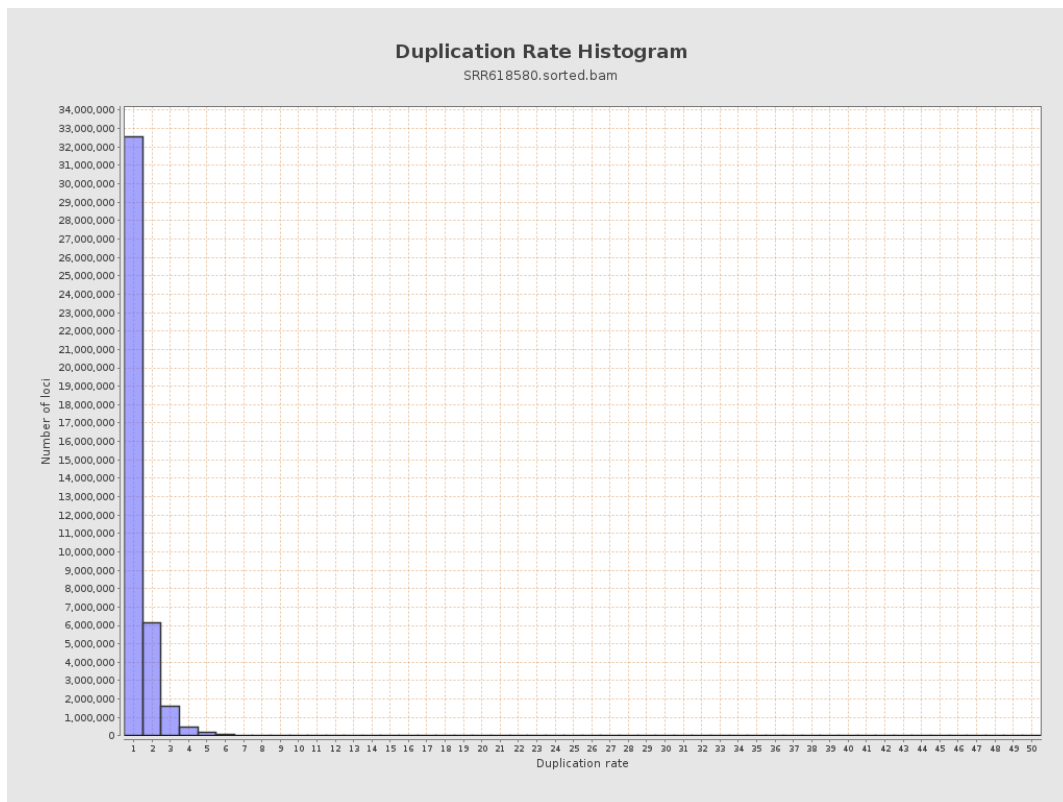
5. Results : Coverage Histogram (0-50X)



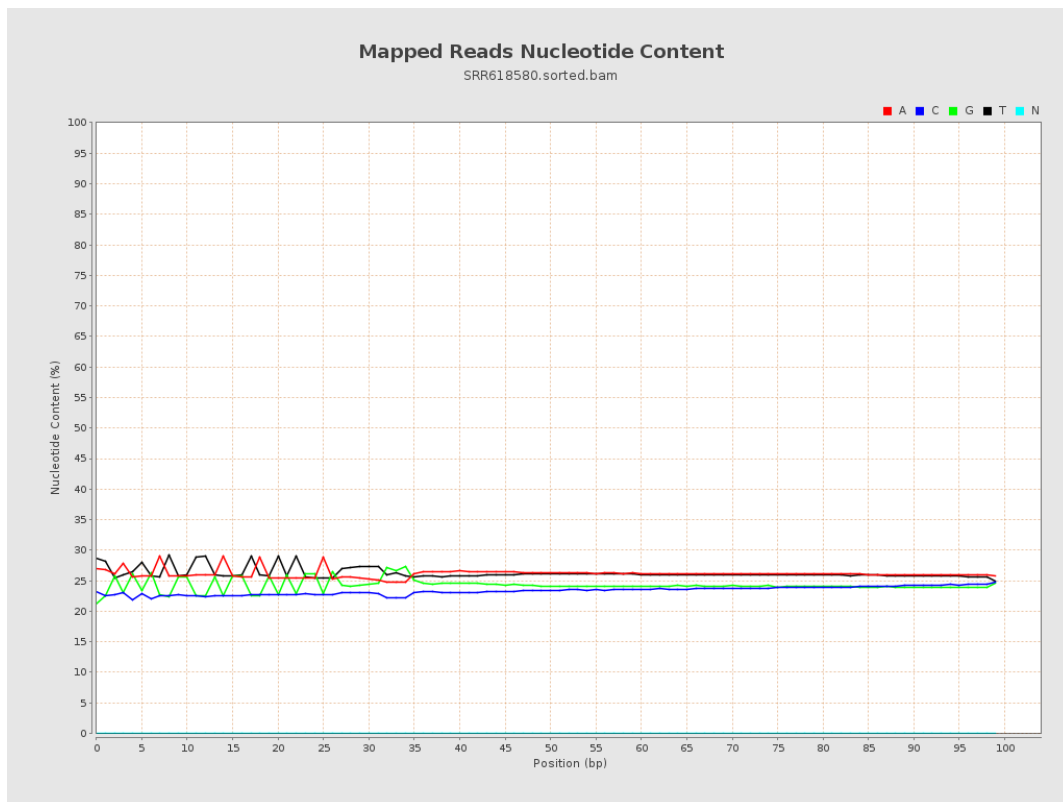
6. Results : Genome Fraction Coverage



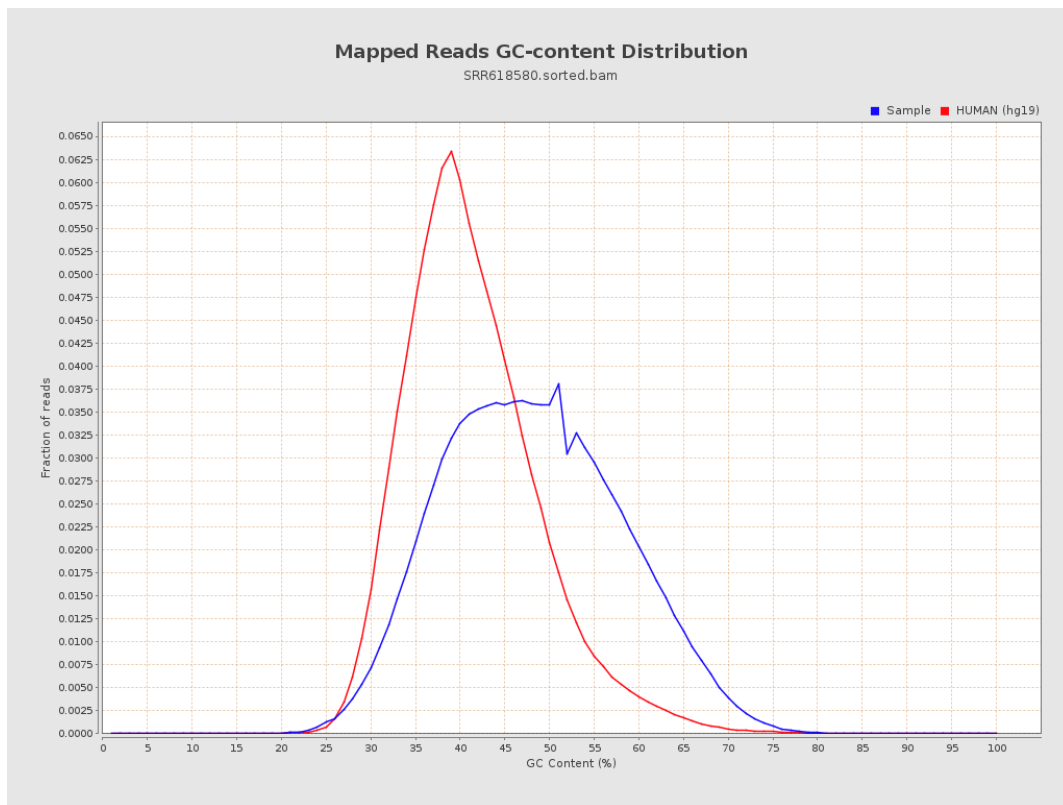
7. Results : Duplication Rate Histogram



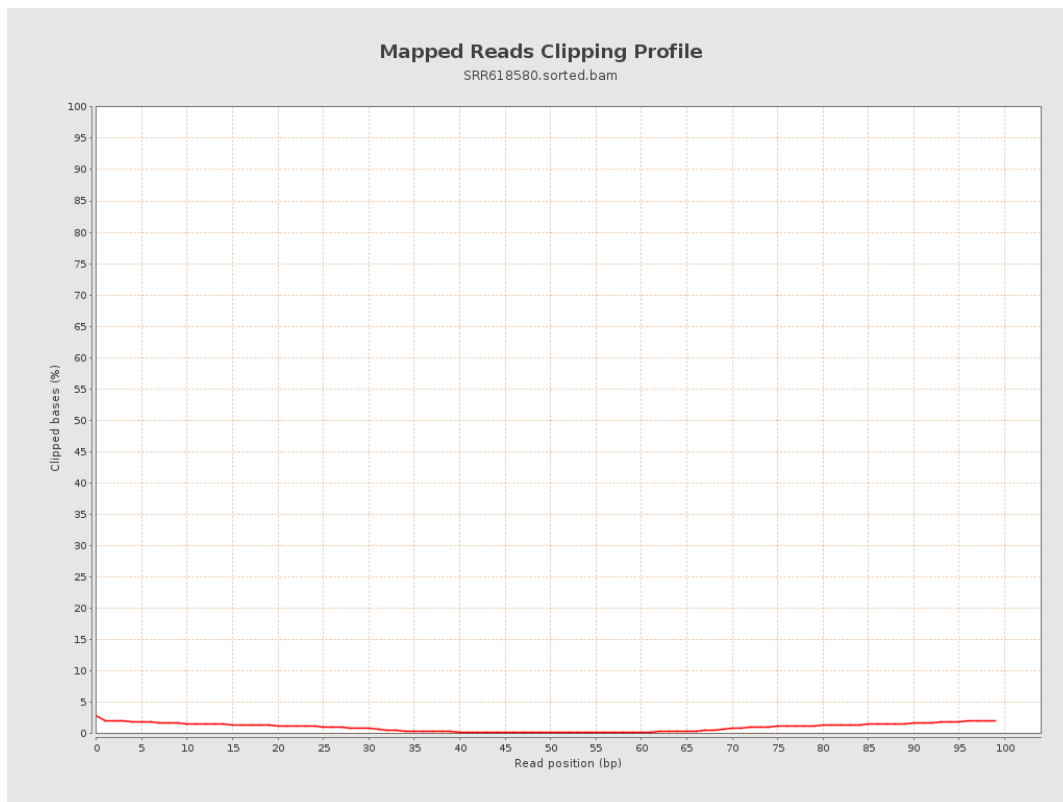
8. Results : Mapped Reads Nucleotide Content



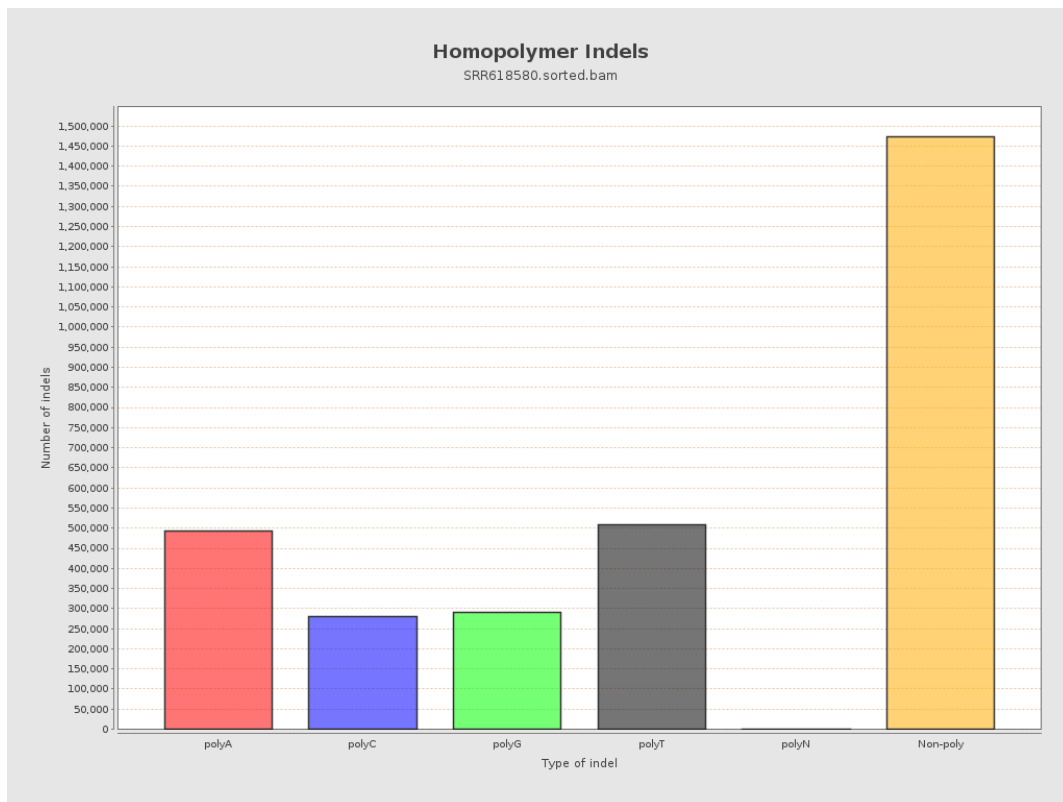
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



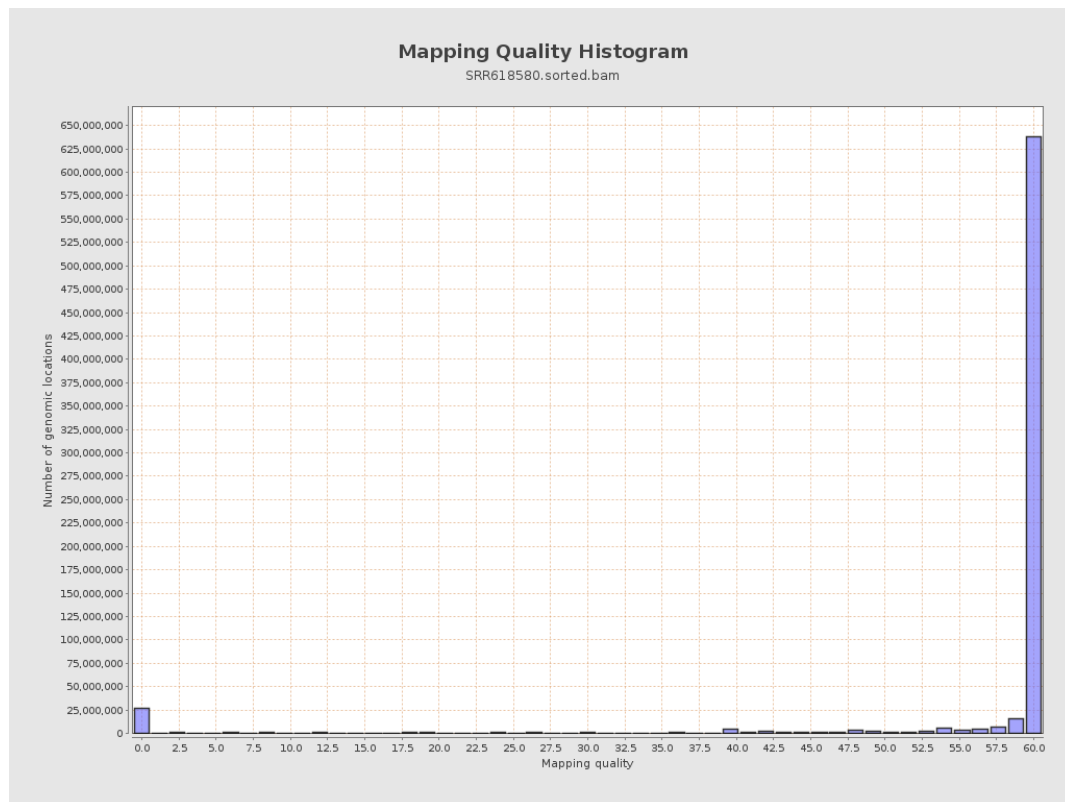
11. Results : Homopolymer Indels



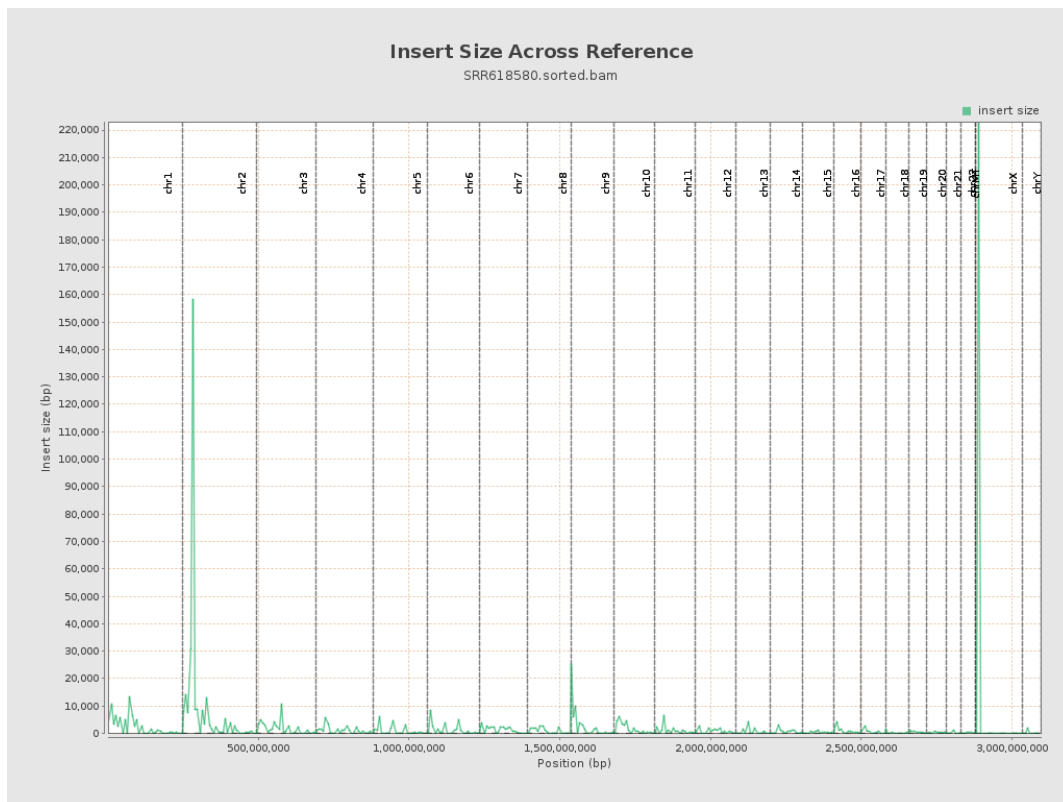
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

