

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 01:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472577.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_SRR3472577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472577_1.fastq.gz SRR3472577_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 01:27:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,933,710
Mapped reads	5,359,831 / 90.33%
Unmapped reads	573,879 / 9.67%
Mapped paired reads	5,359,831 / 90.33%
Mapped reads, first in pair	2,707,042 / 45.62%
Mapped reads, second in pair	2,652,789 / 44.71%
Mapped reads, both in pair	5,208,694 / 87.78%
Mapped reads, singletons	151,137 / 2.55%
Secondary alignments	0
Supplementary alignments	187,032 / 3.15%
Read min/max/mean length	30 / 100 / 101.23
Duplicated reads (estimated)	740,961 / 12.49%
Duplication rate	12.14%
Clipped reads	4,234,763 / 71.37%

2.2. ACGT Content

Number/percentage of A's	111,374,765 / 25.83%
Number/percentage of C's	84,924,427 / 19.7%
Number/percentage of T's	129,967,984 / 30.15%
Number/percentage of G's	104,563,139 / 24.25%
Number/percentage of N's	284,723 / 0.07%

GC Percentage	43.95%
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2.3. Coverage

Mean	0.1393
Standard Deviation	1.4189

2.4. Mapping Quality

Mean Mapping Quality	50.36
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2.5. Insert size

Mean	277,562.41
Standard Deviation	5,089,807.61
P25/Median/P75	90 / 129 / 184

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	5,258,011
Insertions	41,553
Mapped reads with at least one insertion	0.76%
Deletions	96,958
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.56%

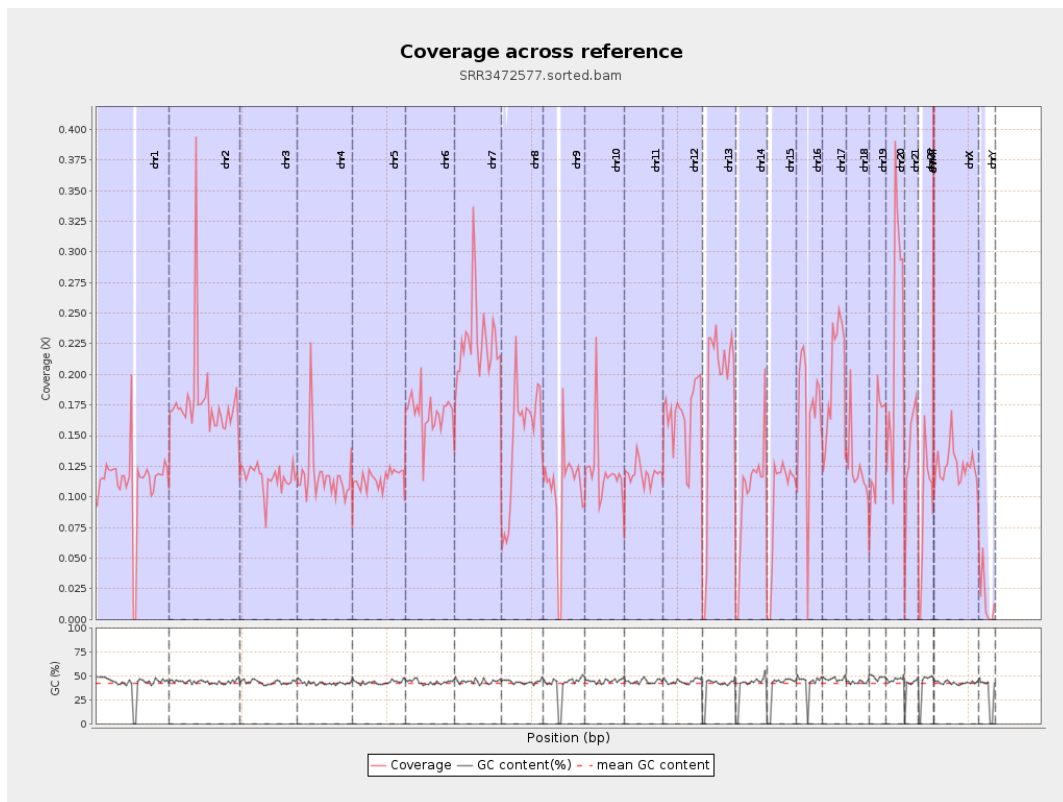
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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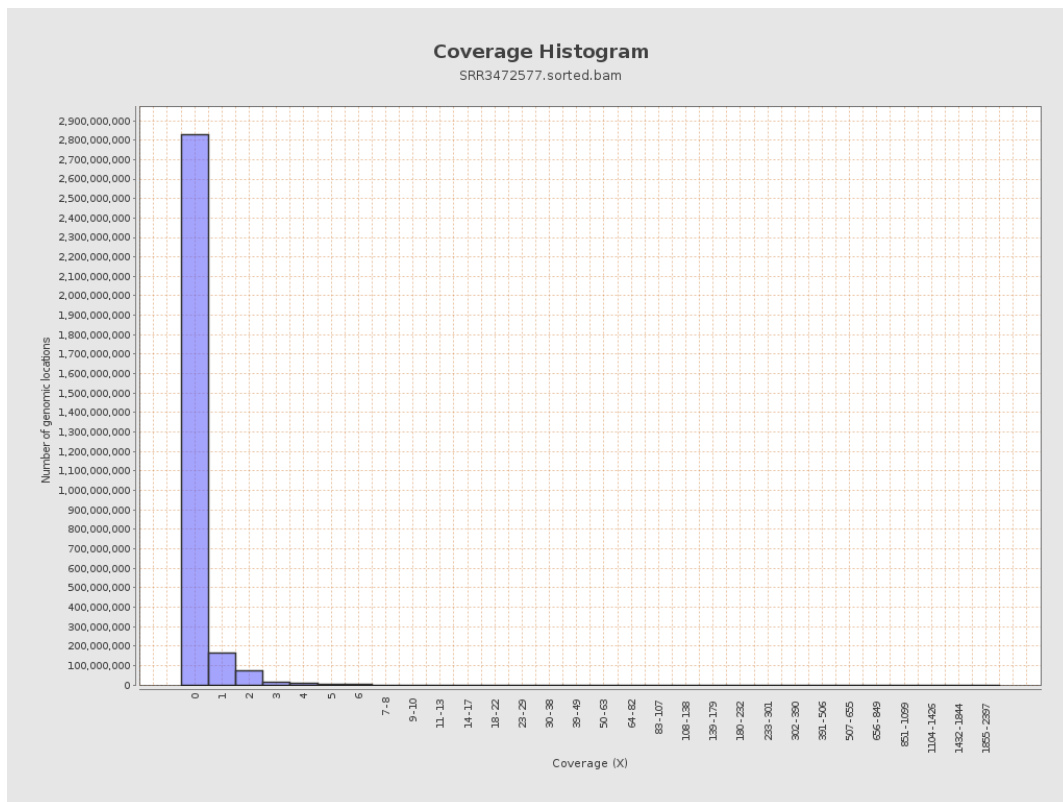
		bases	coverage	deviation
chr1	249250621	27821251	0.1116	1.6114
chr2	243199373	43270911	0.1779	1.874
chr3	198022430	22924253	0.1158	0.4686
chr4	191154276	22383496	0.1171	0.7694
chr5	180915260	20784693	0.1149	0.4956
chr6	171115067	28861692	0.1687	0.8258
chr7	159138663	36382630	0.2286	2.4664
chr8	146364022	21462276	0.1466	1.3102
chr9	141213431	14956822	0.1059	1.441
chr10	135534747	16438948	0.1213	1.2542
chr11	135006516	15929372	0.118	1.074
chr12	133851895	22289162	0.1665	0.5887
chr13	115169878	20767290	0.1803	0.6115
chr14	107349540	11072030	0.1031	3.7772
chr15	102531392	9963383	0.0972	0.4356
chr16	90354753	15276189	0.1691	0.7703
chr17	81195210	16162040	0.1991	1.1119
chr18	78077248	9771404	0.1252	2.4773
chr19	59128983	8604019	0.1455	1.1445
chr20	63025520	14595920	0.2316	0.9112
chr21	48129895	6537375	0.1358	0.6436
chr22	51304566	4566219	0.089	0.4245
chrMT	16571	12773	0.7708	1.219
chrX	155270560	19504173	0.1256	0.6832

chrY	59373566	957579	0.0161	0.6044
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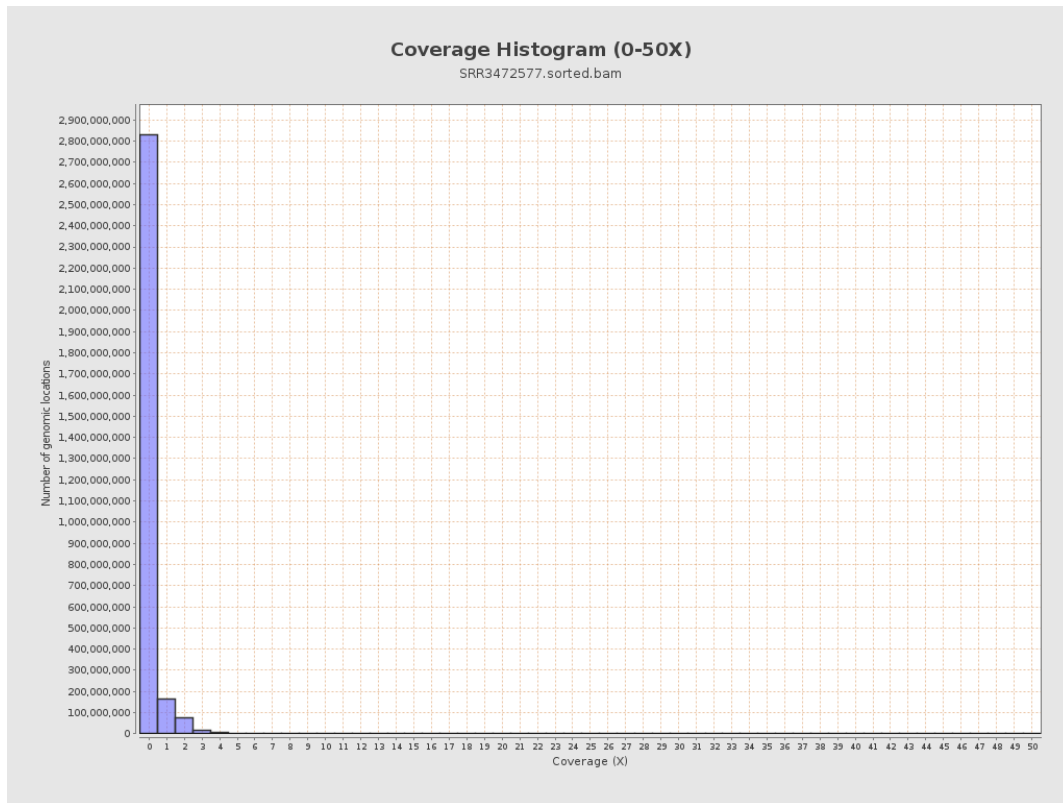
3. Results : Coverage across reference



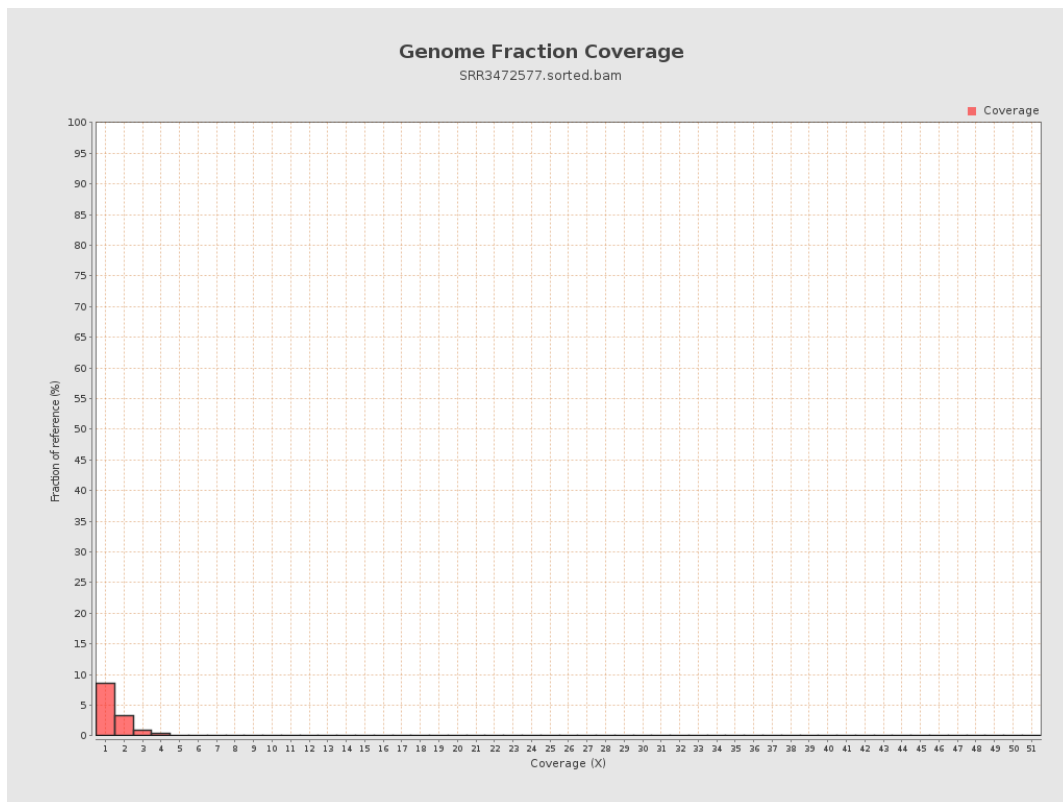
4. Results : Coverage Histogram



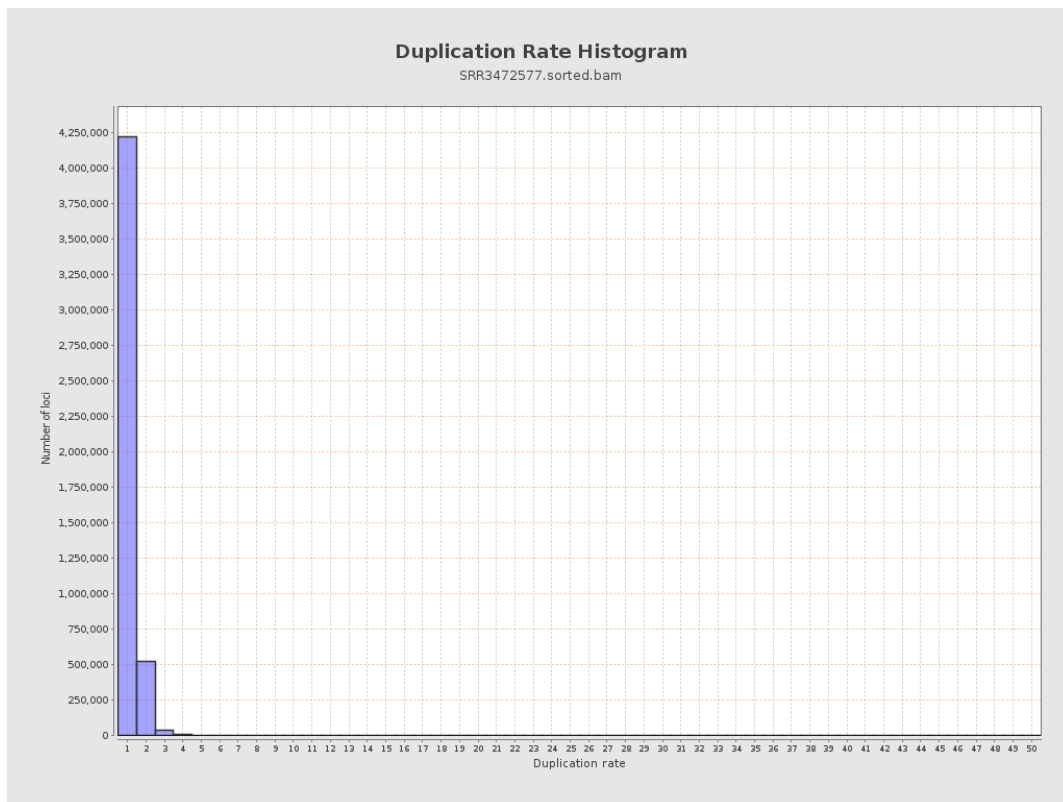
5. Results : Coverage Histogram (0-50X)



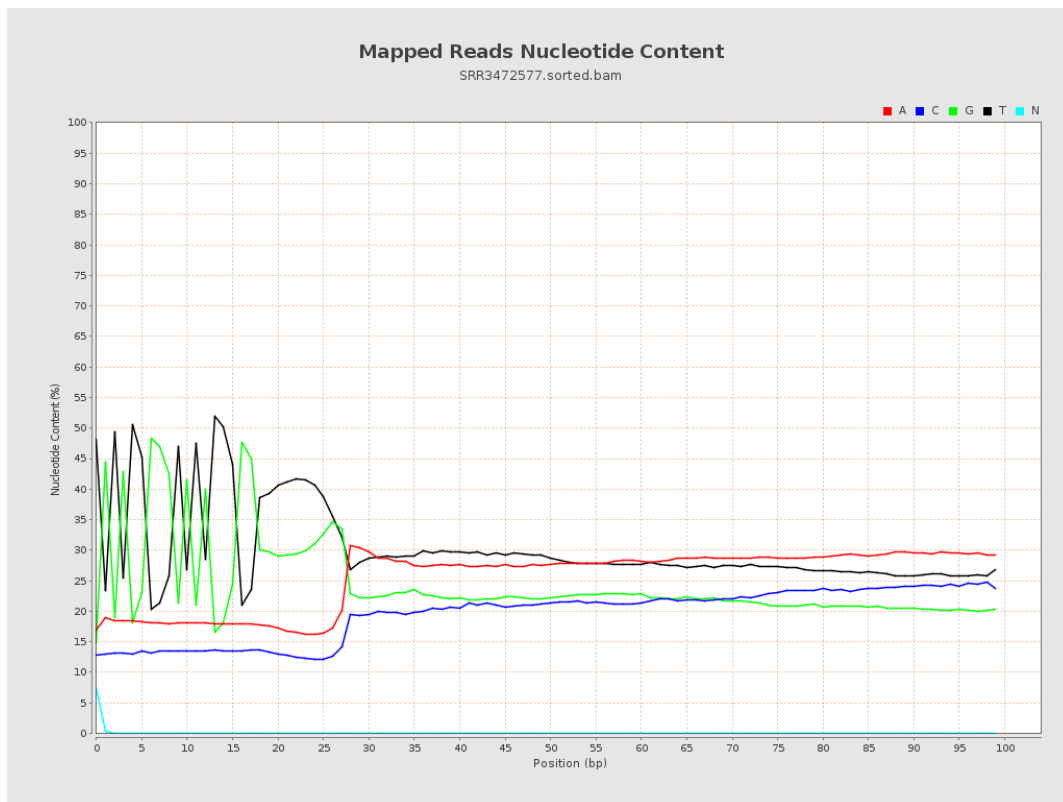
6. Results : Genome Fraction Coverage



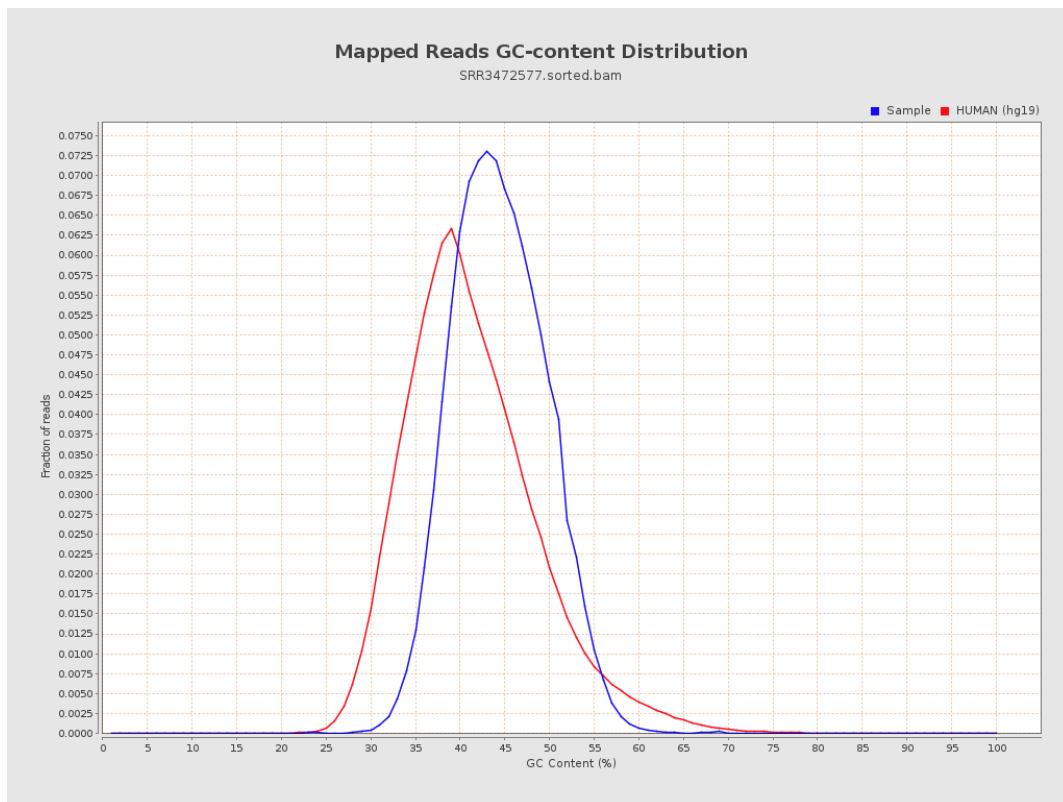
7. Results : Duplication Rate Histogram



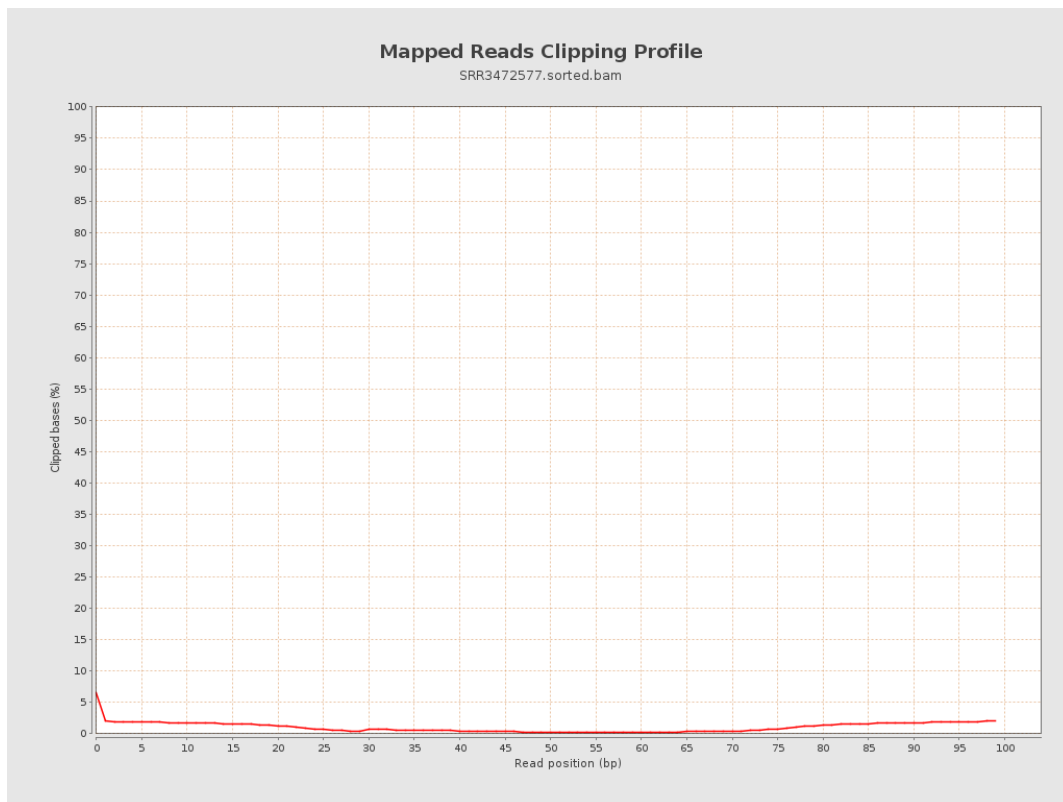
8. Results : Mapped Reads Nucleotide Content



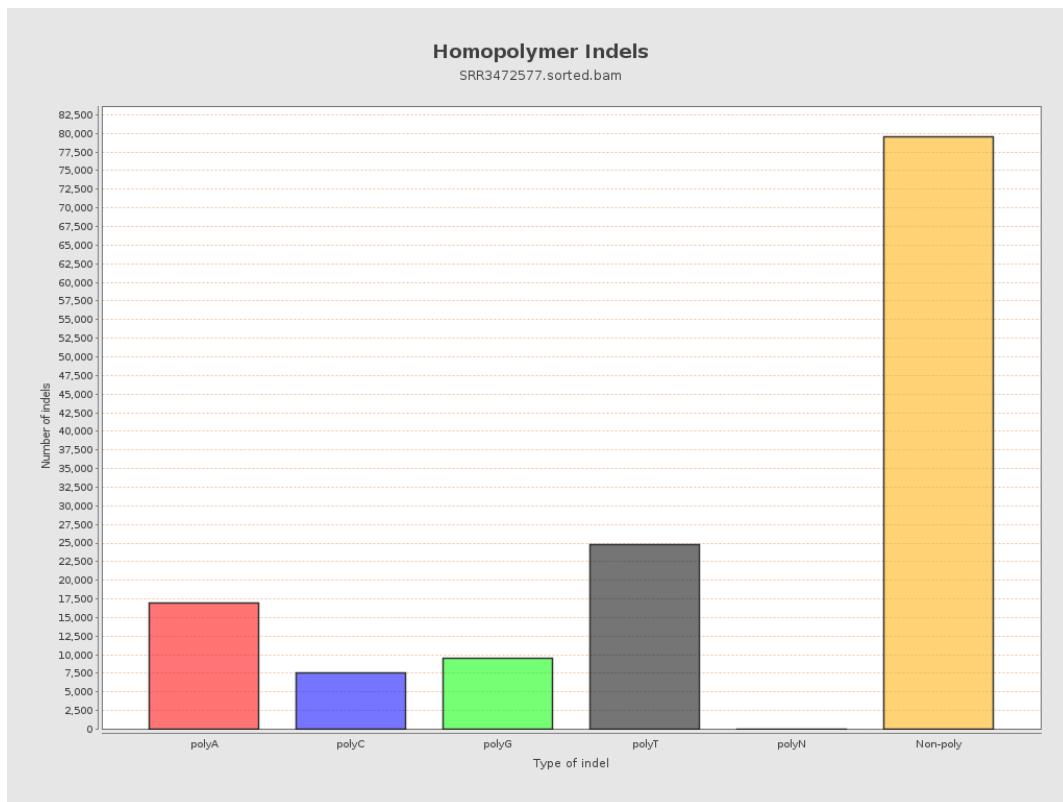
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



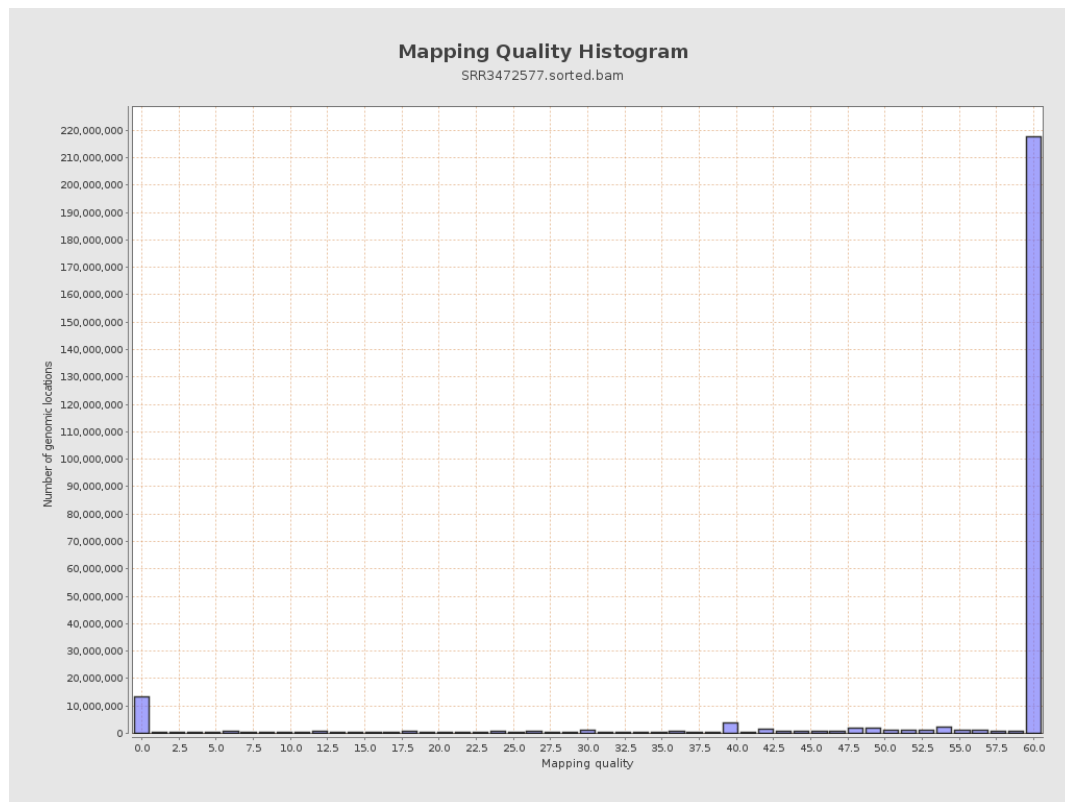
11. Results : Homopolymer Indels



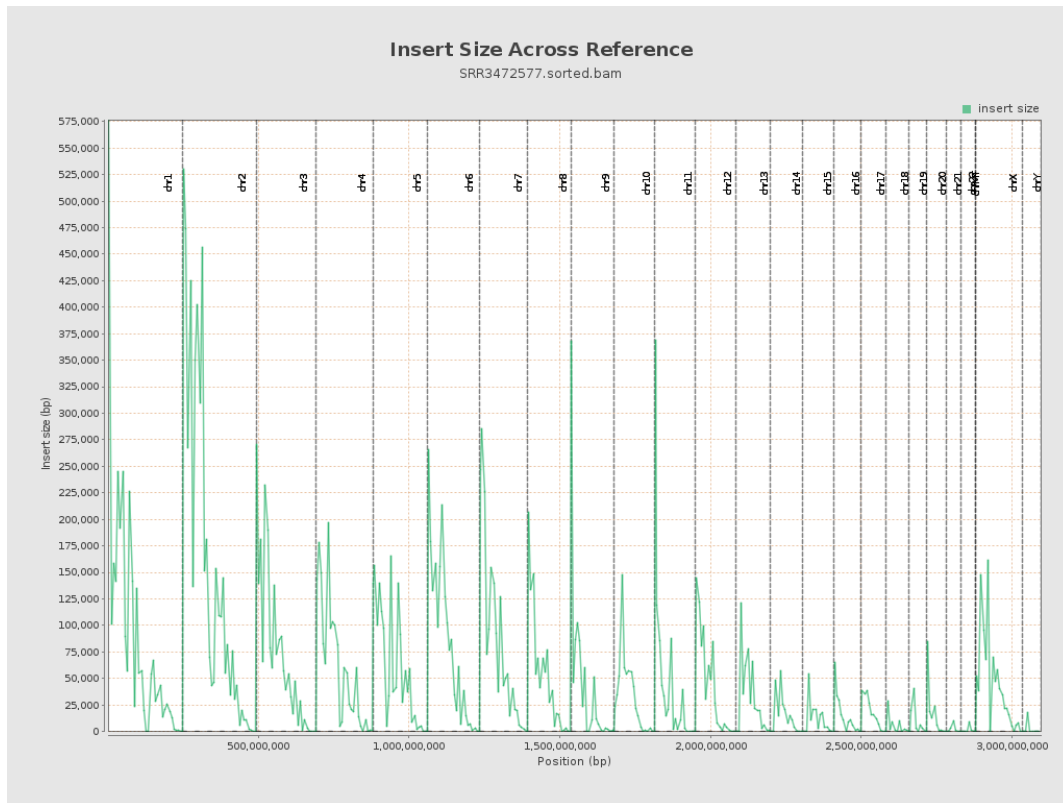
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

