Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 03:10:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472584.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_SRR3472584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472584_1.fastq.gz SRR3472584_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 03:10:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,520,116
Mapped reads	6,913,710 / 91.94%
Unmapped reads	606,406 / 8.06%
Mapped paired reads	6,913,710 / 91.94%
Mapped reads, first in pair	3,485,749 / 46.35%
Mapped reads, second in pair	3,427,961 / 45.58%
Mapped reads, both in pair	6,750,498 / 89.77%
Mapped reads, singletons	163,212 / 2.17%
Secondary alignments	0
Supplementary alignments	223,353 / 2.97%
Read min/max/mean length	30 / 100 / 101.16
Duplicated reads (estimated)	974,407 / 12.96%
Duplication rate	12.24%
Clipped reads	5,318,140 / 70.72%

2.2. ACGT Content

Number/percentage of A's	144,380,401 / 25.68%
Number/percentage of C's	112,357,877 / 19.98%
Number/percentage of T's	167,538,047 / 29.8%
Number/percentage of G's	137,615,567 / 24.48%
Number/percentage of N's	375,269 / 0.07%

GC Percentage	44.46%

2.3. Coverage

Mean	0.1817
Standard Deviation	1.6908

2.4. Mapping Quality

Mean Mapping Quality	50.43

2.5. Insert size

Mean	259,269.93
Standard Deviation	4,942,547.88
P25/Median/P75	92 / 131 / 180

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	6,751,373
Insertions	55,233
Mapped reads with at least one insertion	0.78%
Deletions	128,392
Mapped reads with at least one deletion	1.82%
Homopolymer indels	42.65%

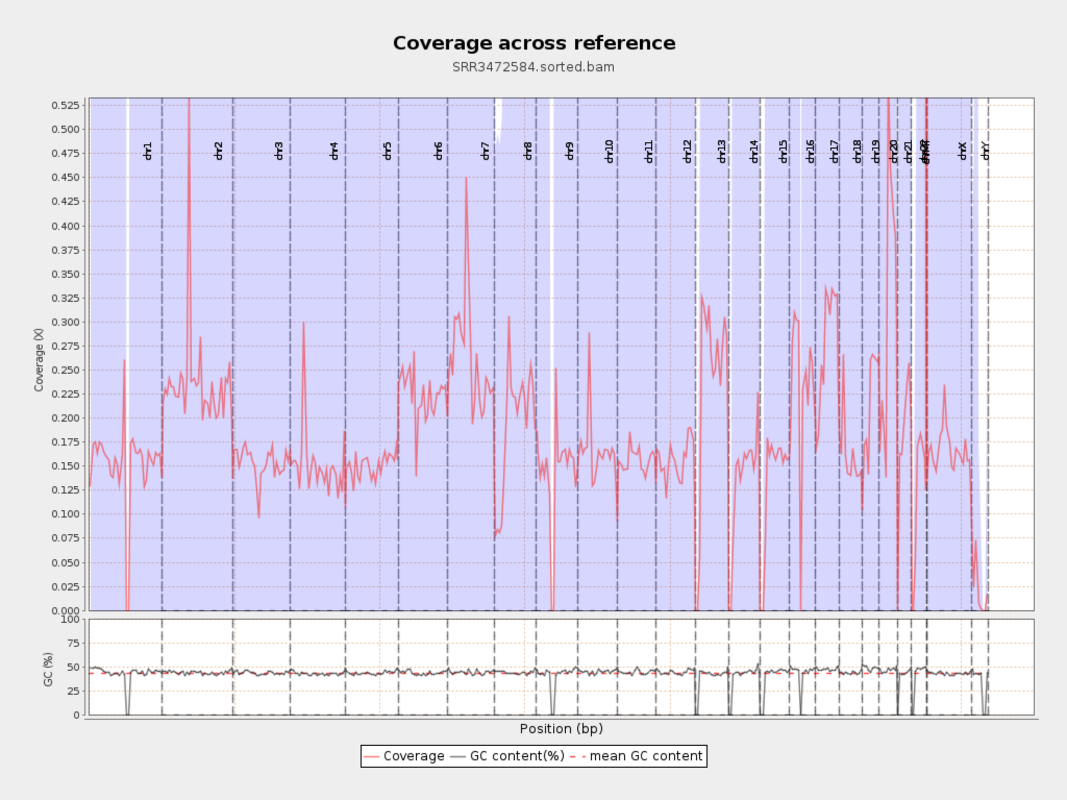
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

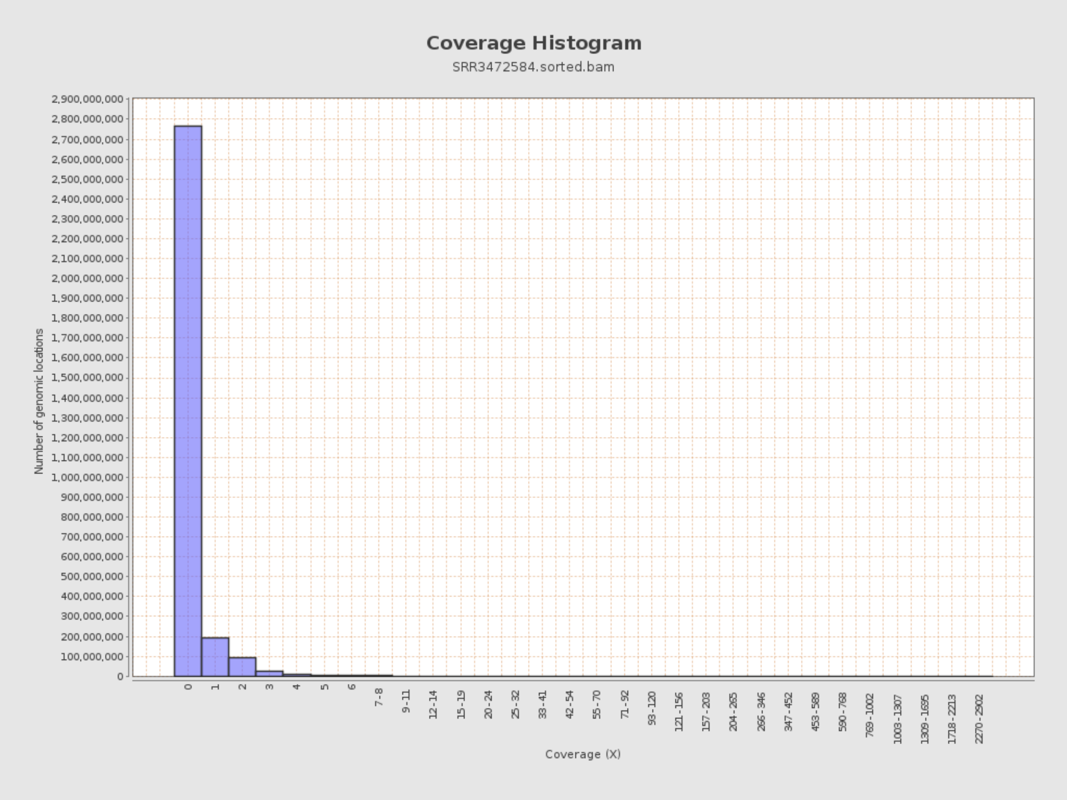
		bases	coverage	deviation
chr1	249250621	37760370	0.1515	2.0281
chr2	243199373	57879018	0.238	2.5303
chr3	198022430	30286947	0.1529	0.5621
chr4	191154276	28911101	0.1512	0.9845
chr5	180915260	27231753	0.1505	0.5945
chr6	171115067	38419882	0.2245	1.0468
chr7	159138663	42357496	0.2662	3.2679
chr8	146364022	28125584	0.1922	1.4447
chr9	141213431	19927200	0.1411	1.8662
chr10	135534747	22502591	0.166	1.4393
chr11	135006516	20941175	0.1551	1.3577
chr12	133851895	20927858	0.1564	0.5869
chr13	115169878	27096645	0.2353	0.7389
chr14	107349540	14474910	0.1348	3.2491
chr15	102531392	13706064	0.1337	0.5326
chr16	90354753	21321946	0.236	1.0174
chr17	81195210	22597656	0.2783	1.6491
chr18	78077248	12758255	0.1634	3.0891
chr19	59128983	12770062	0.216	1.4554
chr20	63025520	20172353	0.3201	1.0723
chr21	48129895	8796141	0.1828	0.8245
chr22	51304566	5969731	0.1164	0.5028
chrMT	16571	421210	25.4185	15.7966
chrX	155270560	25908002	0.1669	0.8548

chrY	59373566	1244159	0.021	0.7317

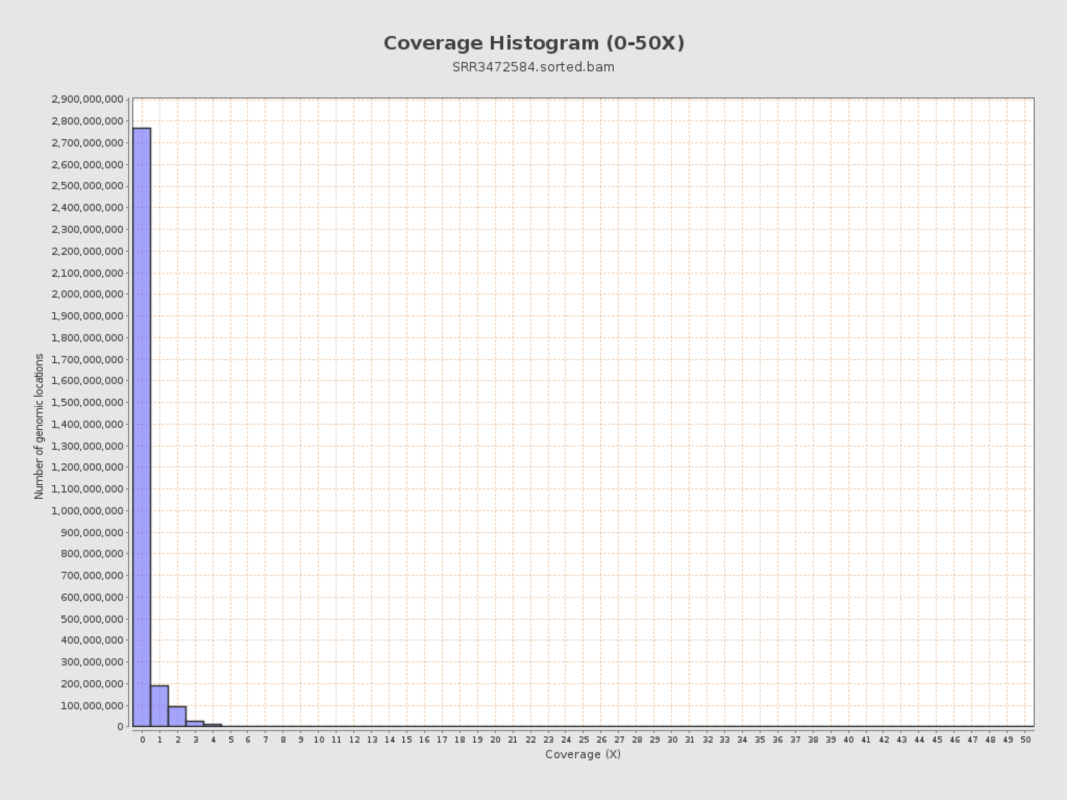
3. Results : Coverage across reference



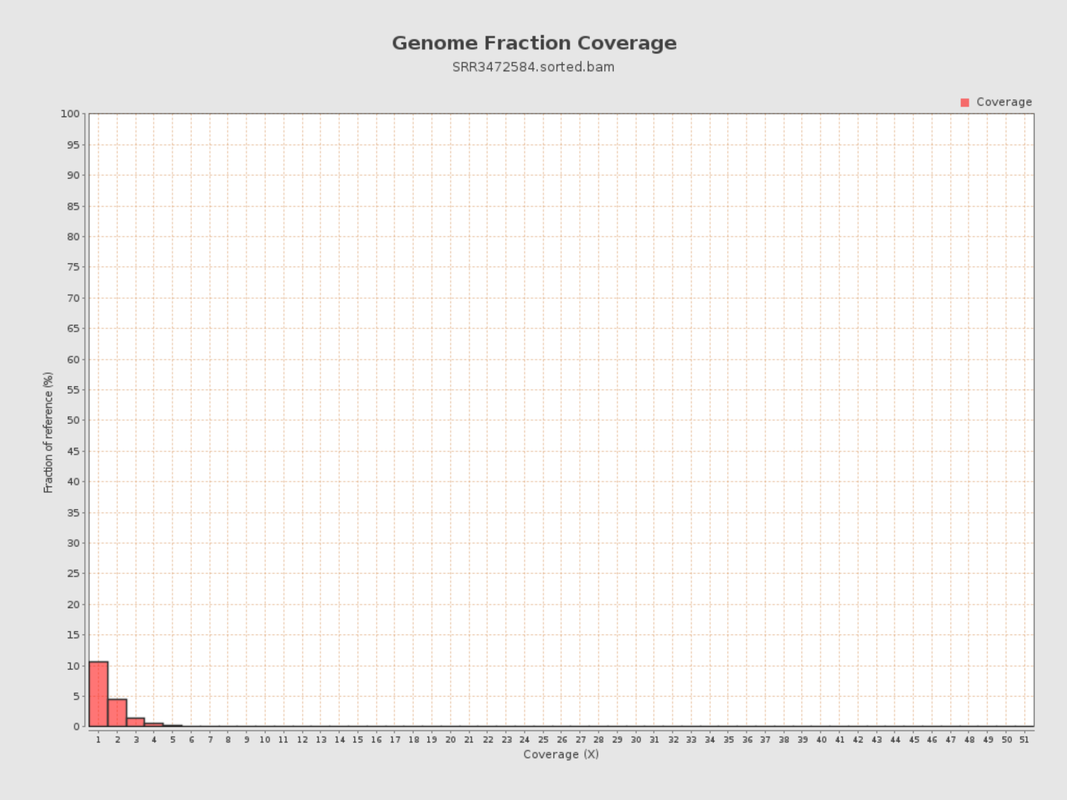
4. Results : Coverage Histogram



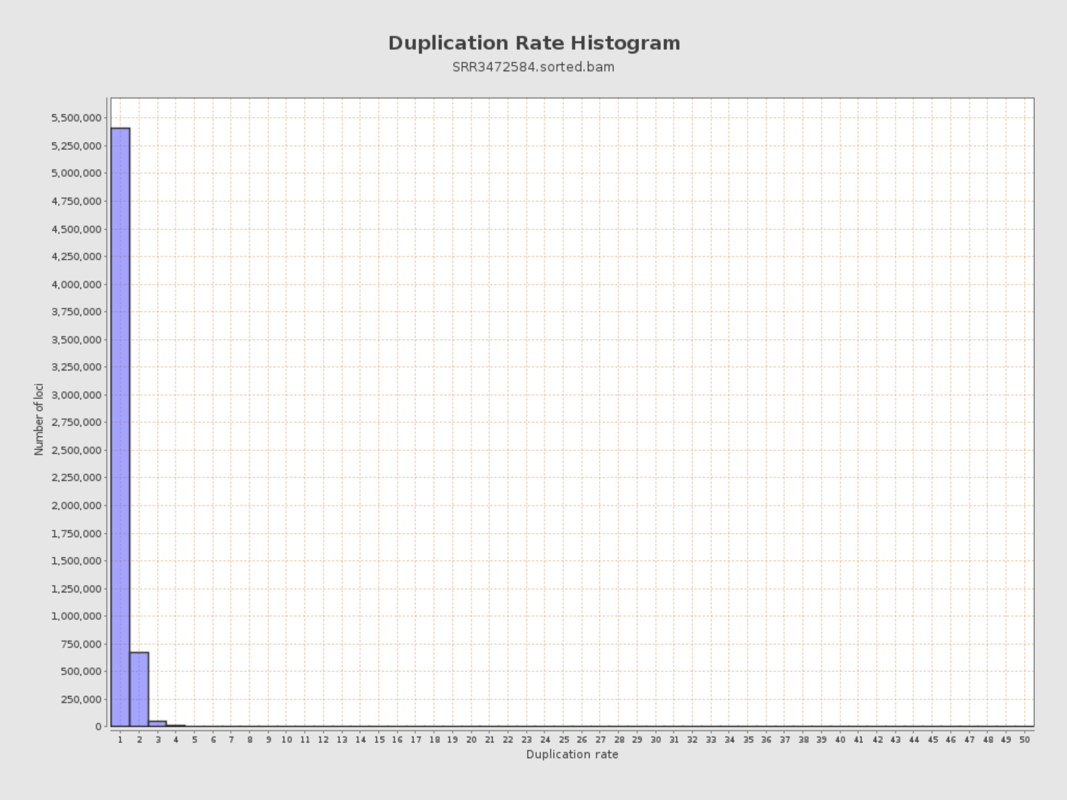
5. Results : Coverage Histogram (0-50X)



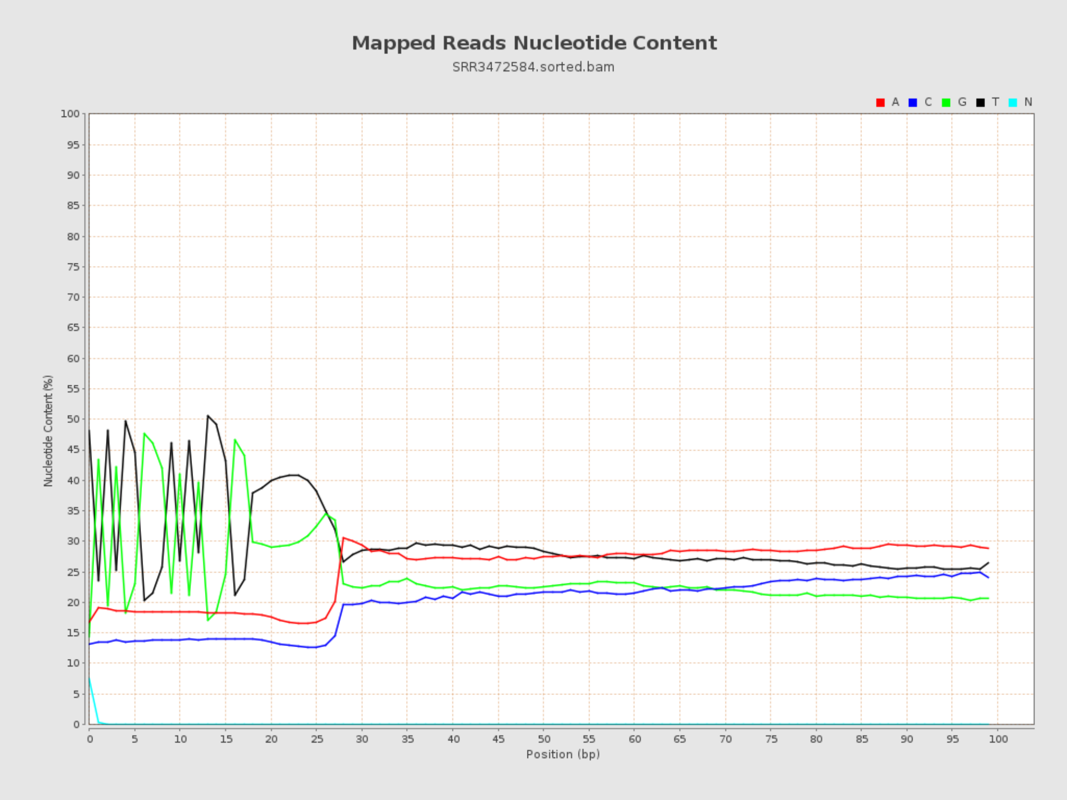
6. Results : Genome Fraction Coverage



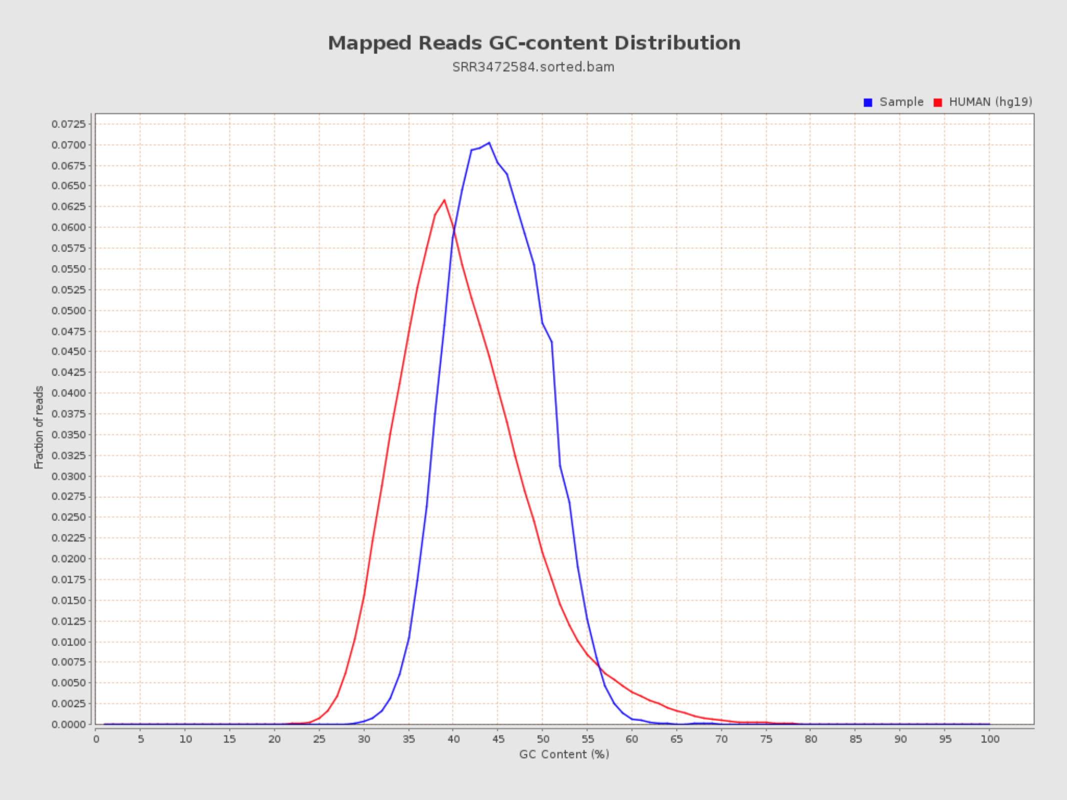
7. Results : Duplication Rate Histogram



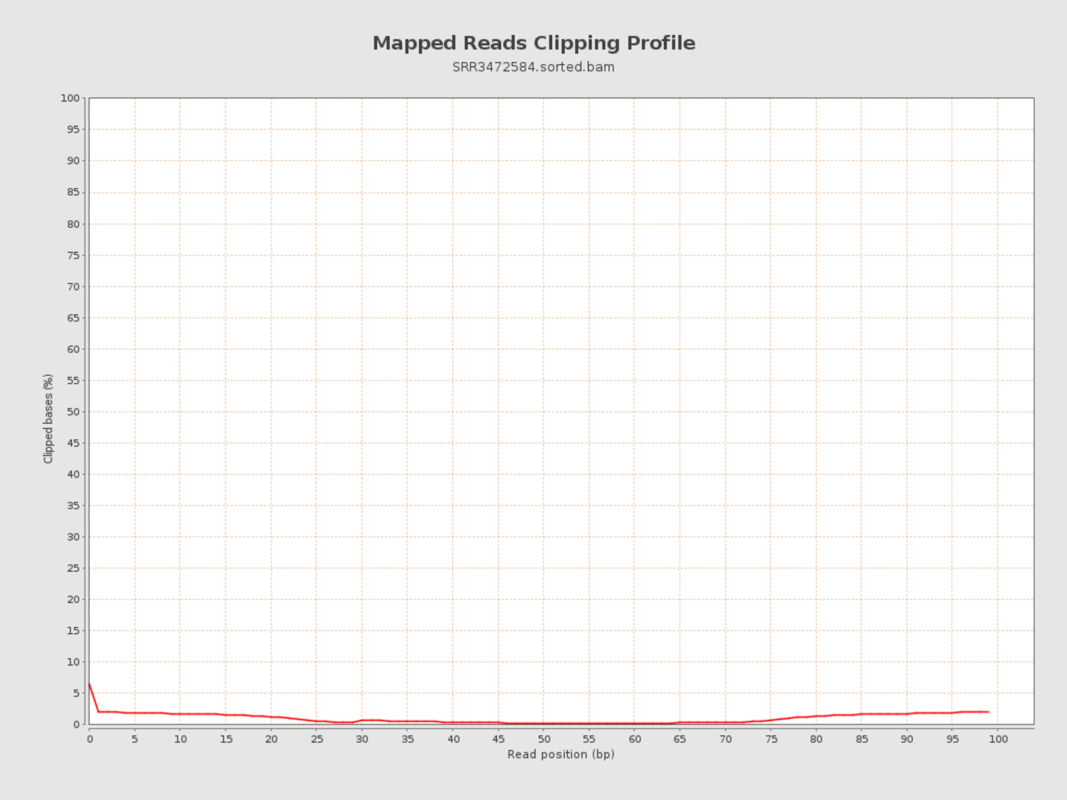
8. Results : Mapped Reads Nucleotide Content



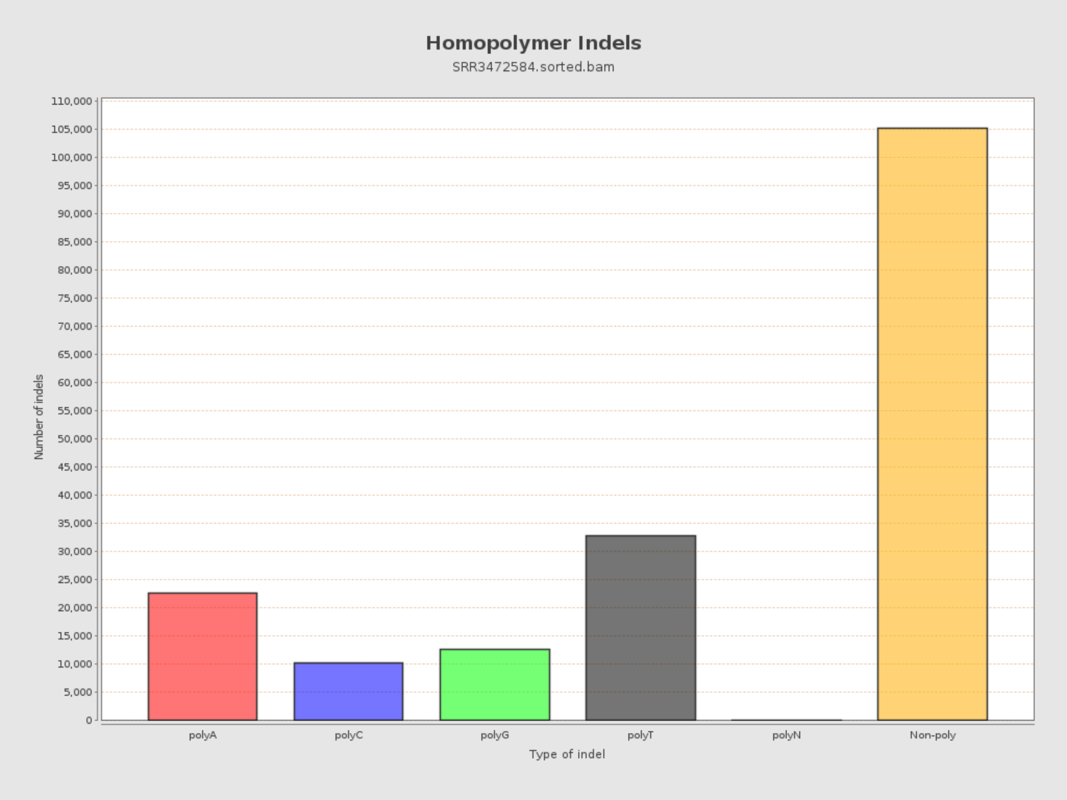
9. Results : Mapped Reads GC-content Distribution



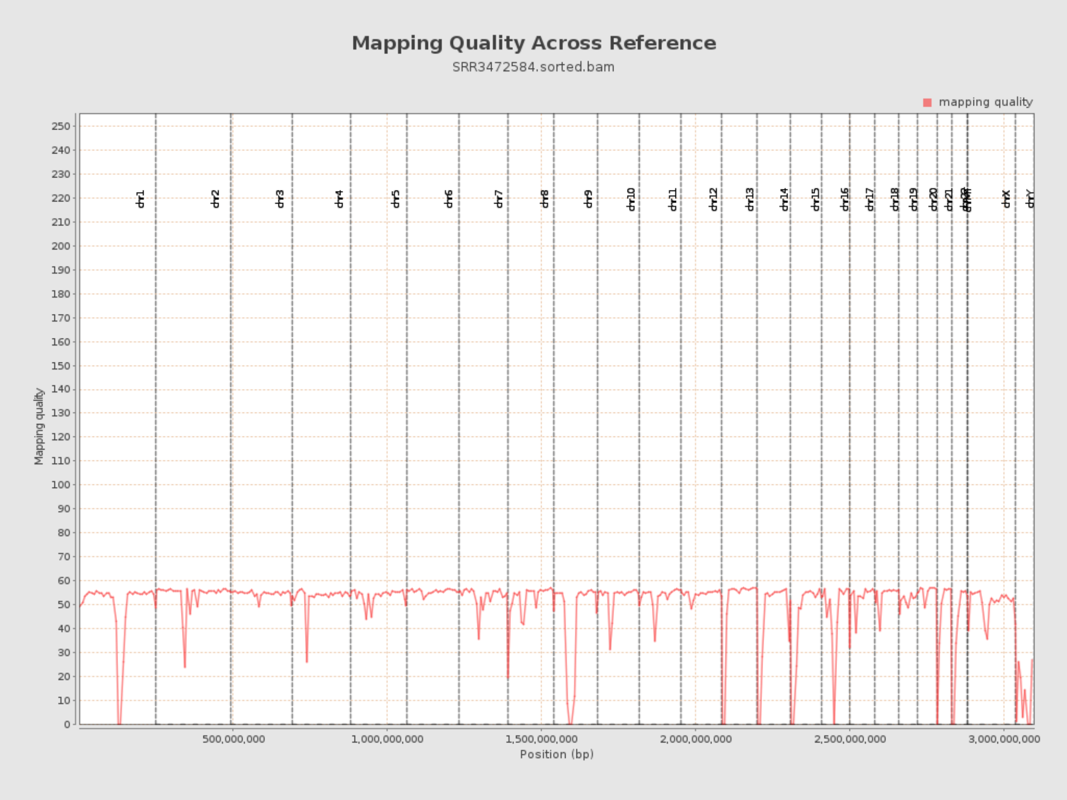
10. Results : Mapped Reads Clipping Profile



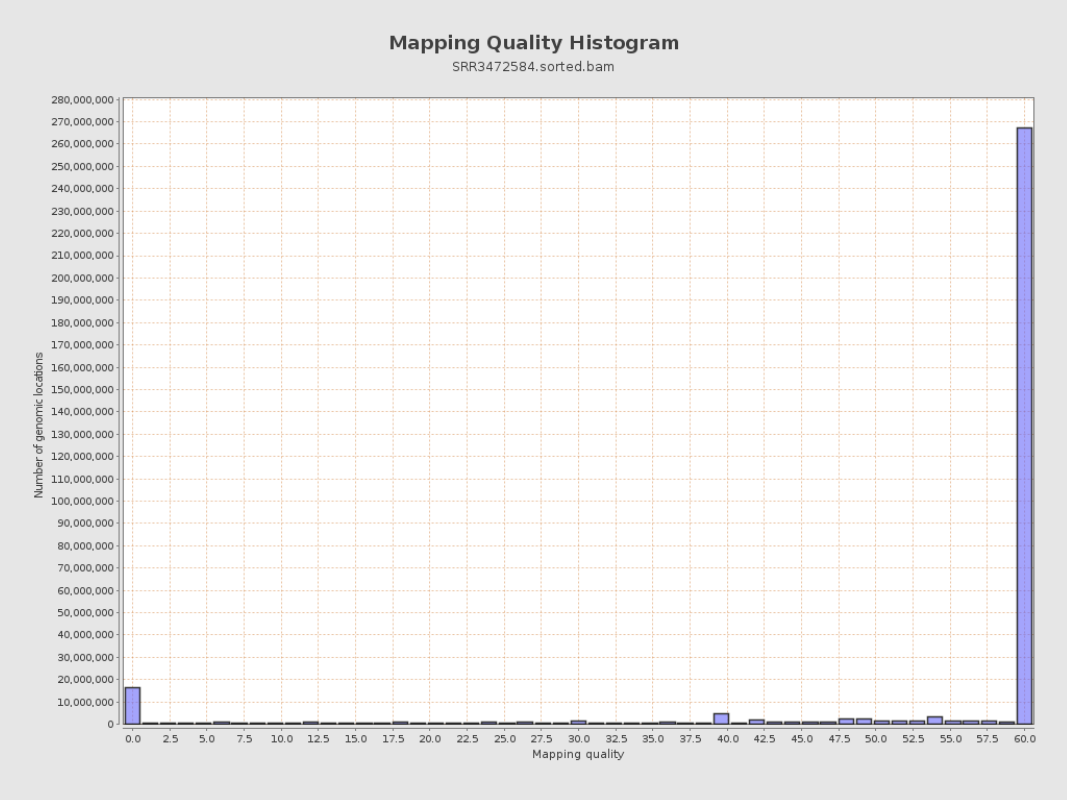
11. Results : Homopolymer Indels



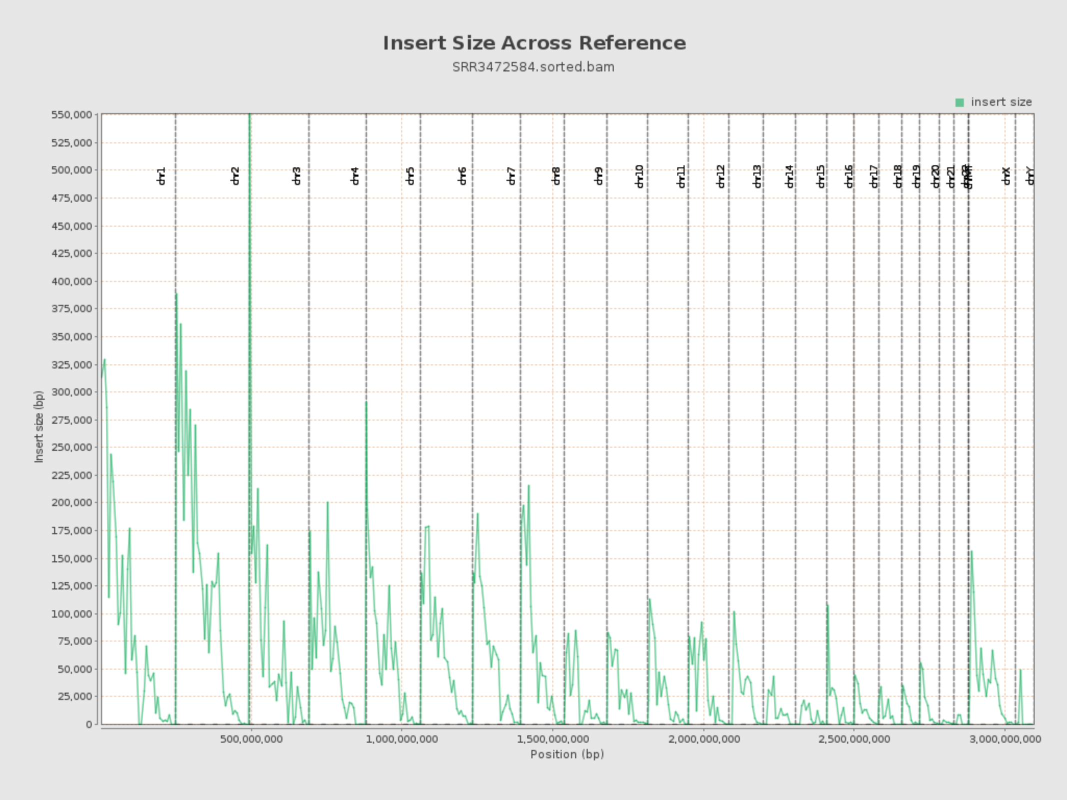
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram