Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 03:49:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472587.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_SRR3472587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472587_1.fastq.gz SRR3472587_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 03:49:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472587.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,727,014
Mapped reads	7,046,243 / 91.19%
Unmapped reads	680,771 / 8.81%
Mapped paired reads	7,046,243 / 91.19%
Mapped reads, first in pair	3,550,883 / 45.95%
Mapped reads, second in pair	3,495,360 / 45.24%
Mapped reads, both in pair	6,894,858 / 89.23%
Mapped reads, singletons	151,385 / 1.96%
Secondary alignments	0
Supplementary alignments	191,453 / 2.48%
Read min/max/mean length	30 / 100 / 100.97
Duplicated reads (estimated)	1,071,523 / 13.87%
Duplication rate	13.89%
Clipped reads	5,385,463 / 69.7%

2.2. ACGT Content

Number/percentage of A's	145,987,165 / 25.55%
Number/percentage of C's	115,858,264 / 20.28%
Number/percentage of T's	168,353,663 / 29.47%
Number/percentage of G's	140,766,518 / 24.64%
Number/percentage of N's	386,241 / 0.07%

GC Percentage	44.92%

2.3. Coverage

Mean	0.1846
Standard Deviation	1.6239

2.4. Mapping Quality

Mean Mapping Quality	50.8

2.5. Insert size

Mean	205,844.42
Standard Deviation	4,465,227.88
P25/Median/P75	88 / 124 / 171

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	6,529,370
Insertions	51,172
Mapped reads with at least one insertion	0.71%
Deletions	124,089
Mapped reads with at least one deletion	1.73%
Homopolymer indels	43.12%

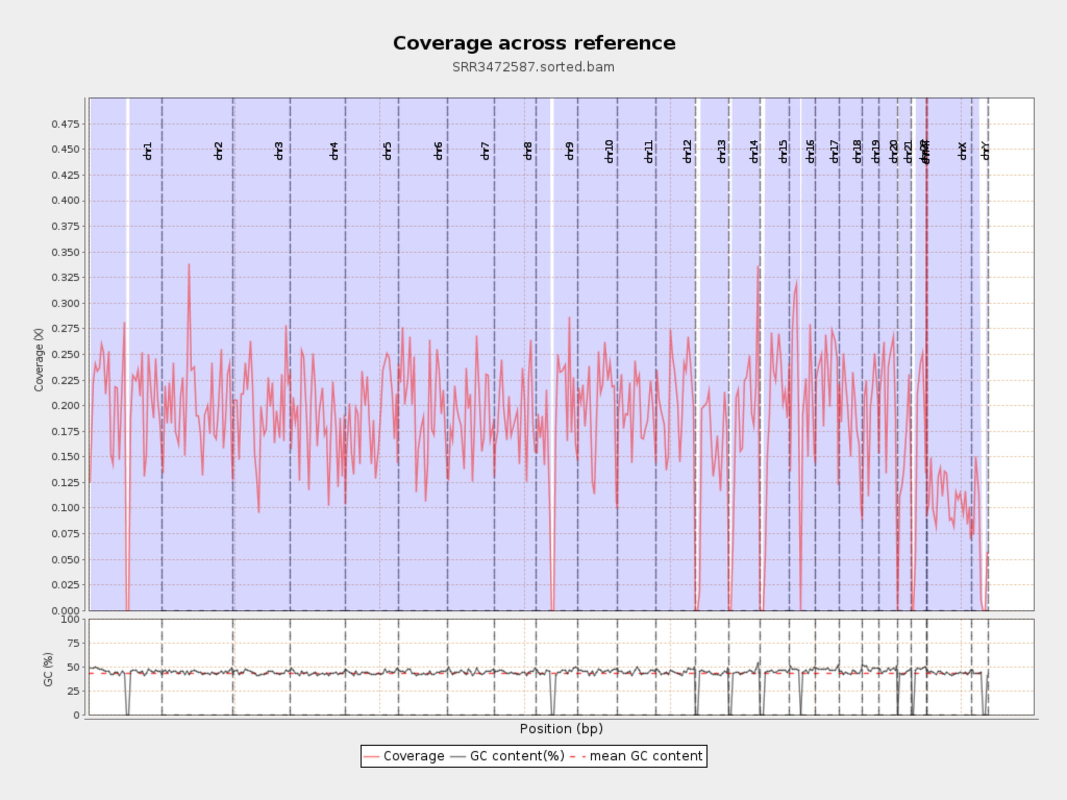
2.7. Chromosome stats

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

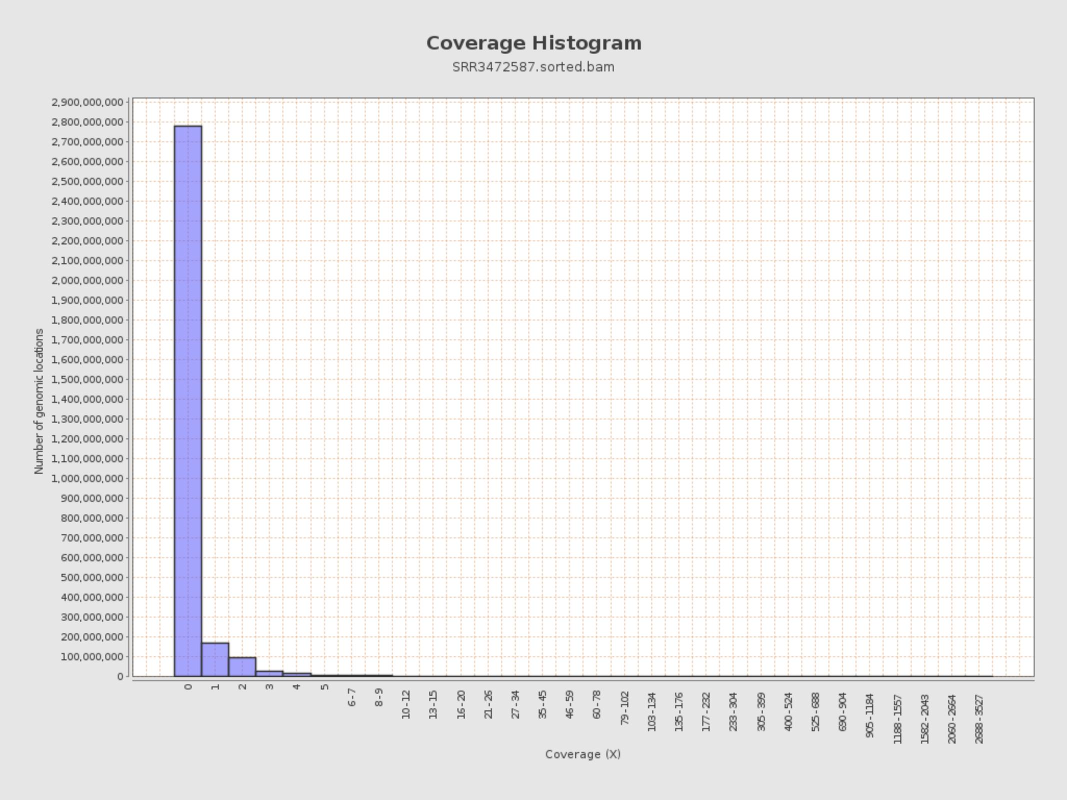
		bases	coverage	deviation
chr1	249250621	49177615	0.1973	1.9856
chr2	243199373	48799516	0.2007	1.3808
chr3	198022430	38805488	0.196	0.6891
chr4	191154276	35119678	0.1837	0.8532
chr5	180915260	34415871	0.1902	0.6931
chr6	171115067	34340582	0.2007	0.9402
chr7	159138663	30154691	0.1895	1.8517
chr8	146364022	28096838	0.192	1.1145
chr9	141213431	24776964	0.1755	1.5116
chr10	135534747	27727912	0.2046	1.3027
chr11	135006516	26161753	0.1938	1.2006
chr12	133851895	27869159	0.2082	0.7271
chr13	115169878	16660294	0.1447	0.5873
chr14	107349540	18968574	0.1767	5.7611
chr15	102531392	18066263	0.1762	0.6652
chr16	90354753	18605466	0.2059	0.866
chr17	81195210	18883710	0.2326	1.0434
chr18	78077248	15094366	0.1933	2.6296
chr19	59128983	11558507	0.1955	1.378
chr20	63025520	13670885	0.2169	1.2113
chr21	48129895	6685694	0.1389	0.7058
chr22	51304566	7551155	0.1472	0.7474
chrMT	16571	8711	0.5257	1.2714
chrX	155270560	16817107	0.1083	0.6756

chrY	59373566	3566496	0.0601	0.6426

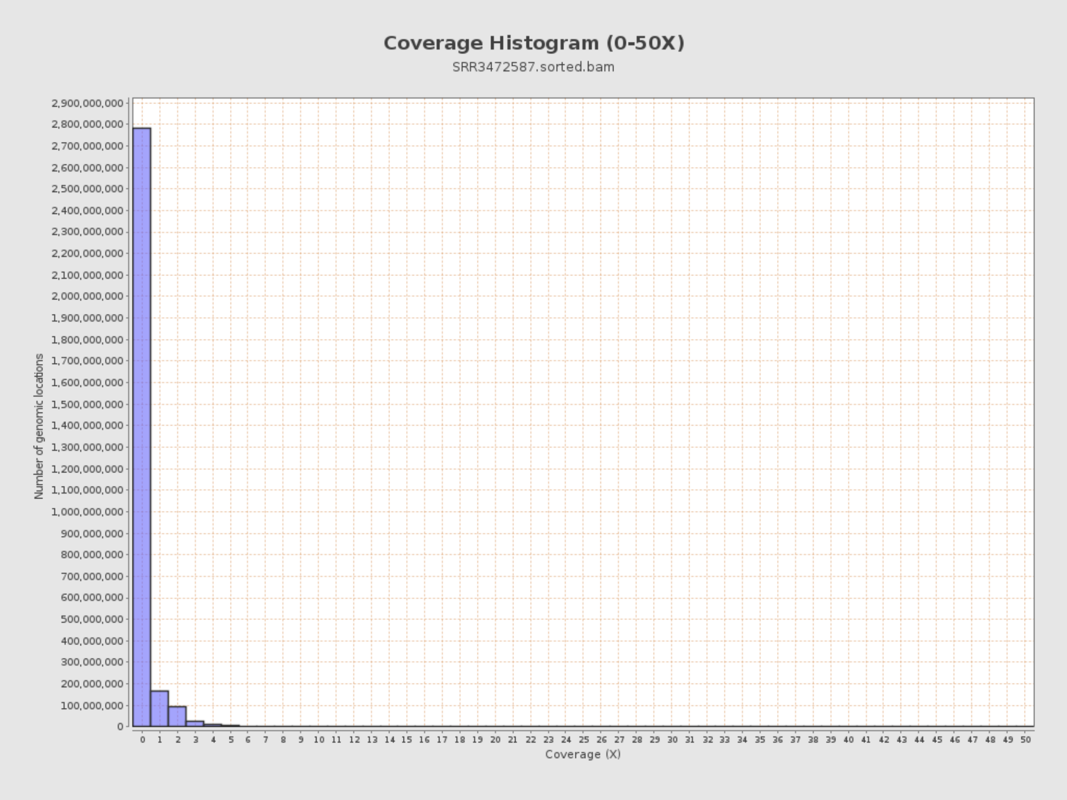
3. Results : Coverage across reference



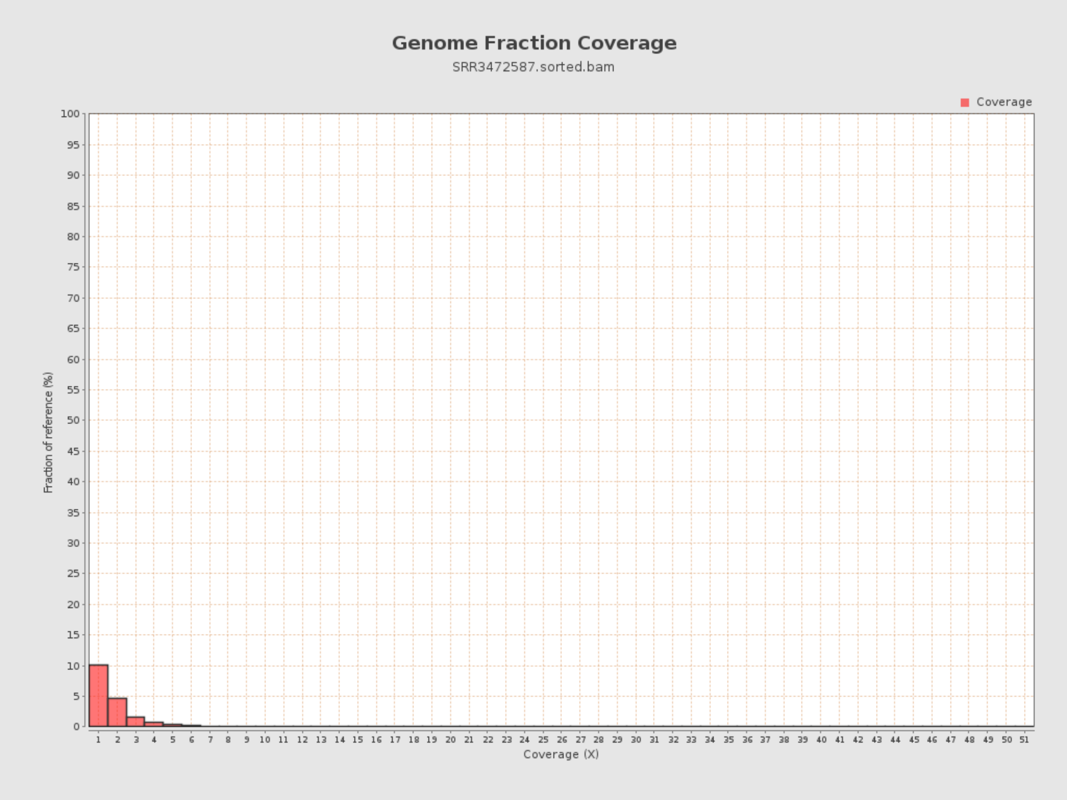
4. Results : Coverage Histogram



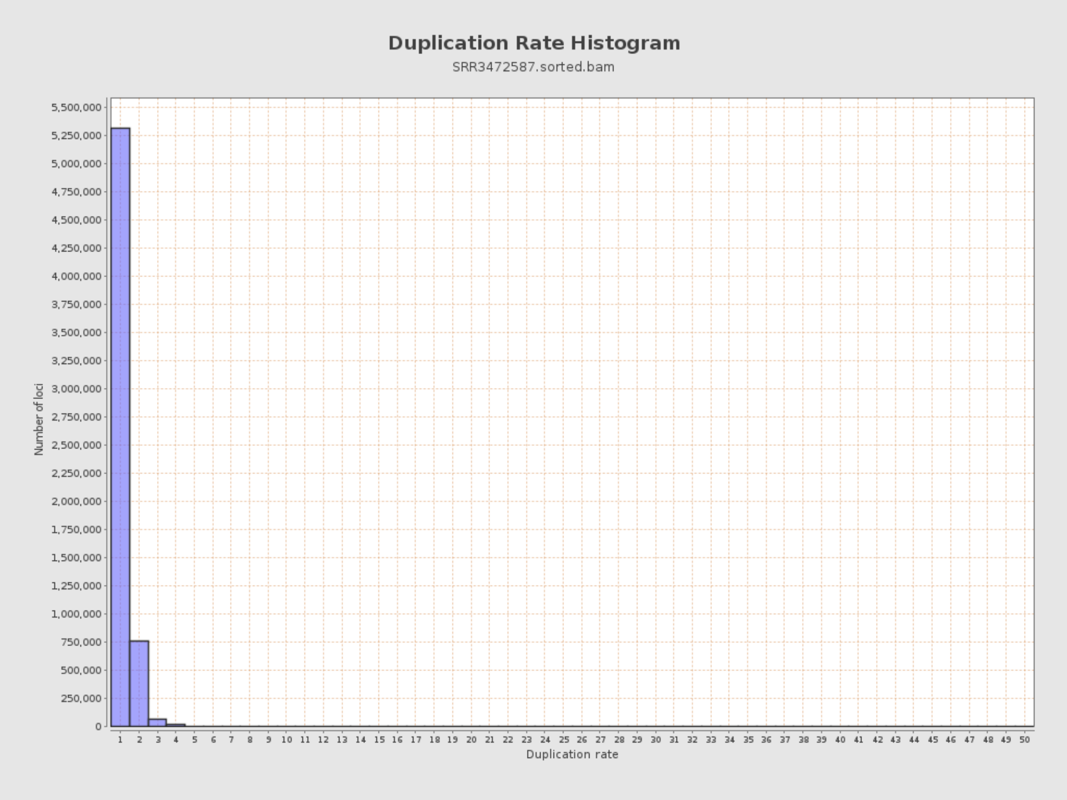
5. Results : Coverage Histogram (0-50X)



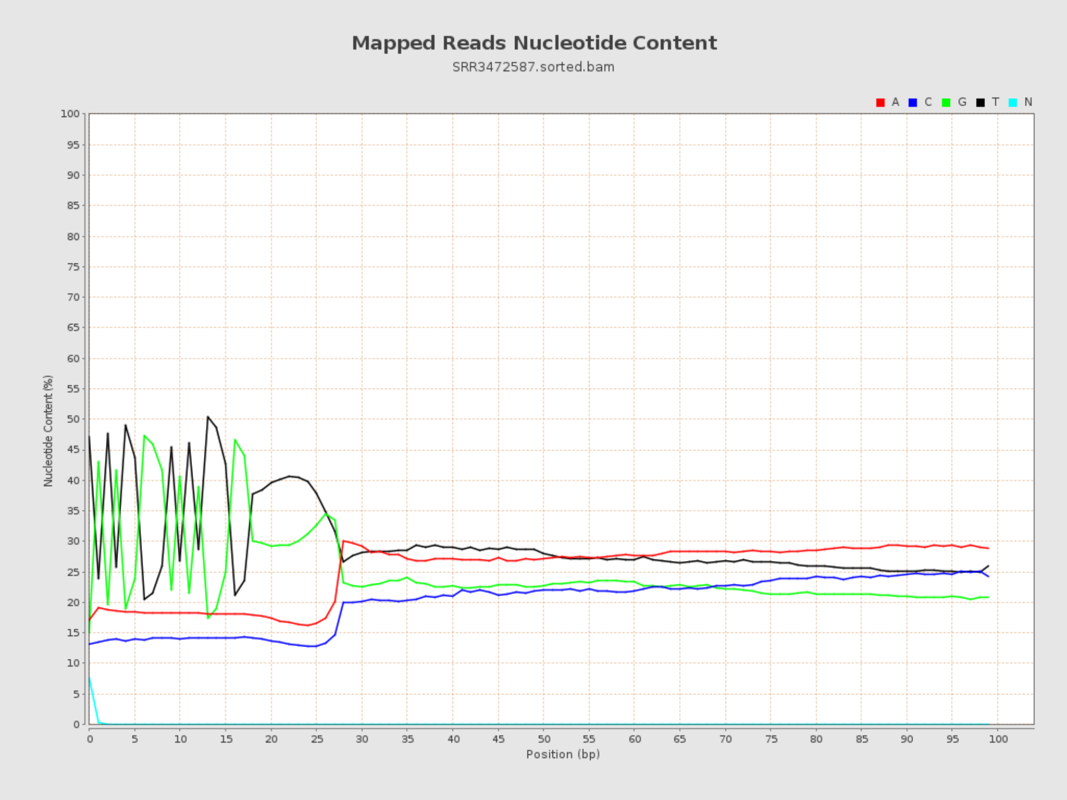
6. Results : Genome Fraction Coverage



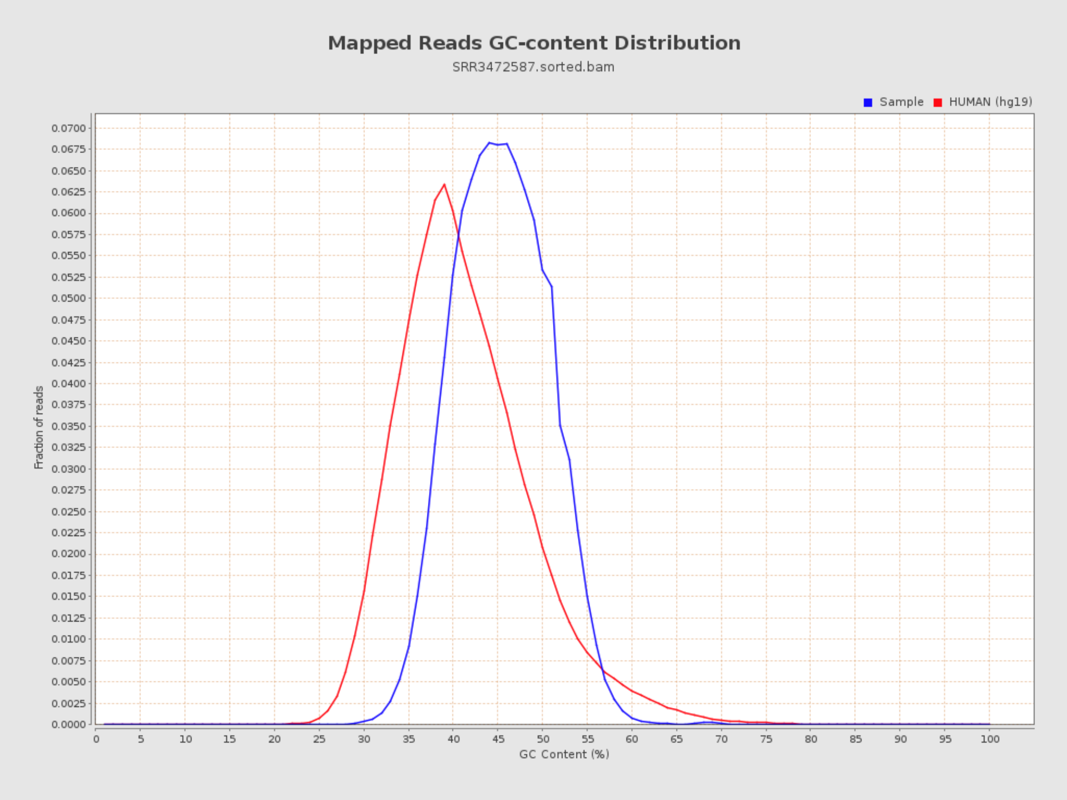
7. Results : Duplication Rate Histogram



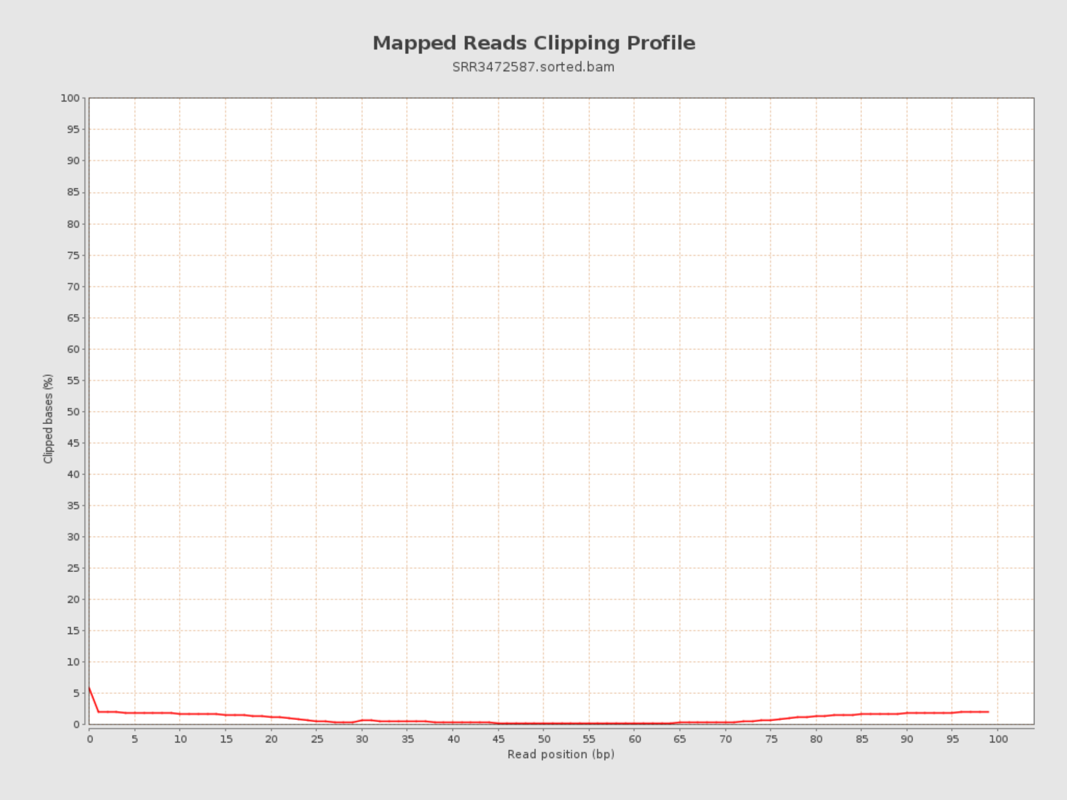
8. Results : Mapped Reads Nucleotide Content



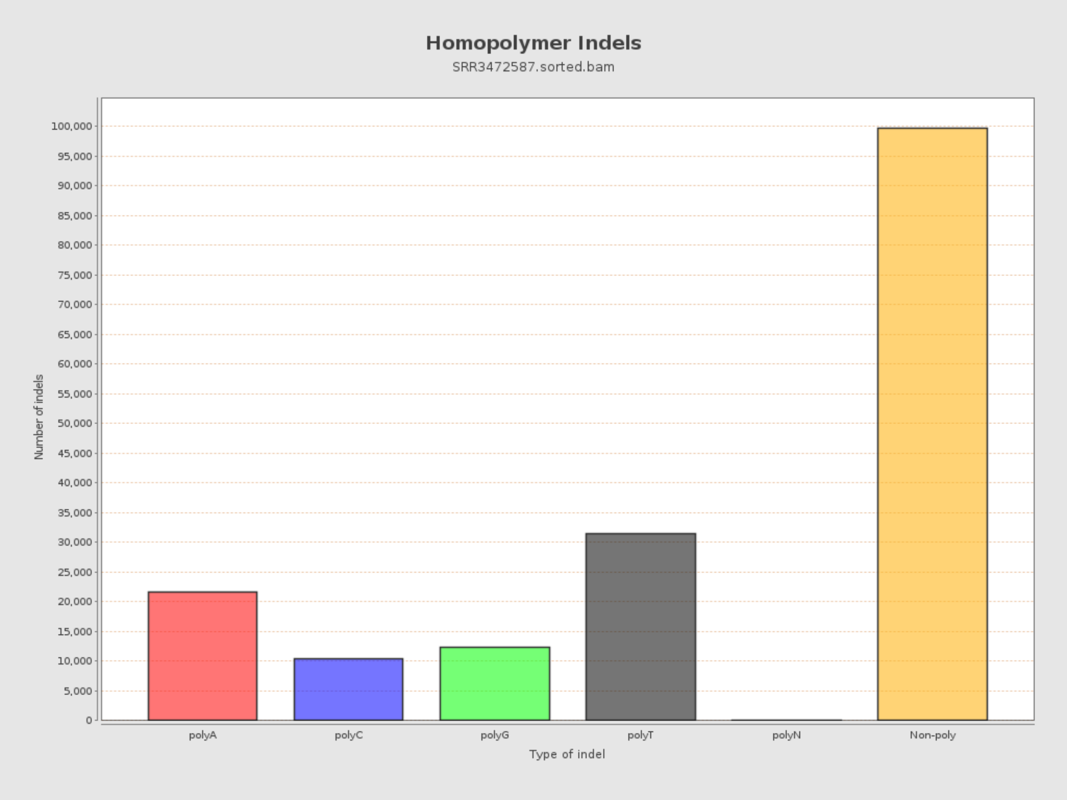
9. Results : Mapped Reads GC-content Distribution



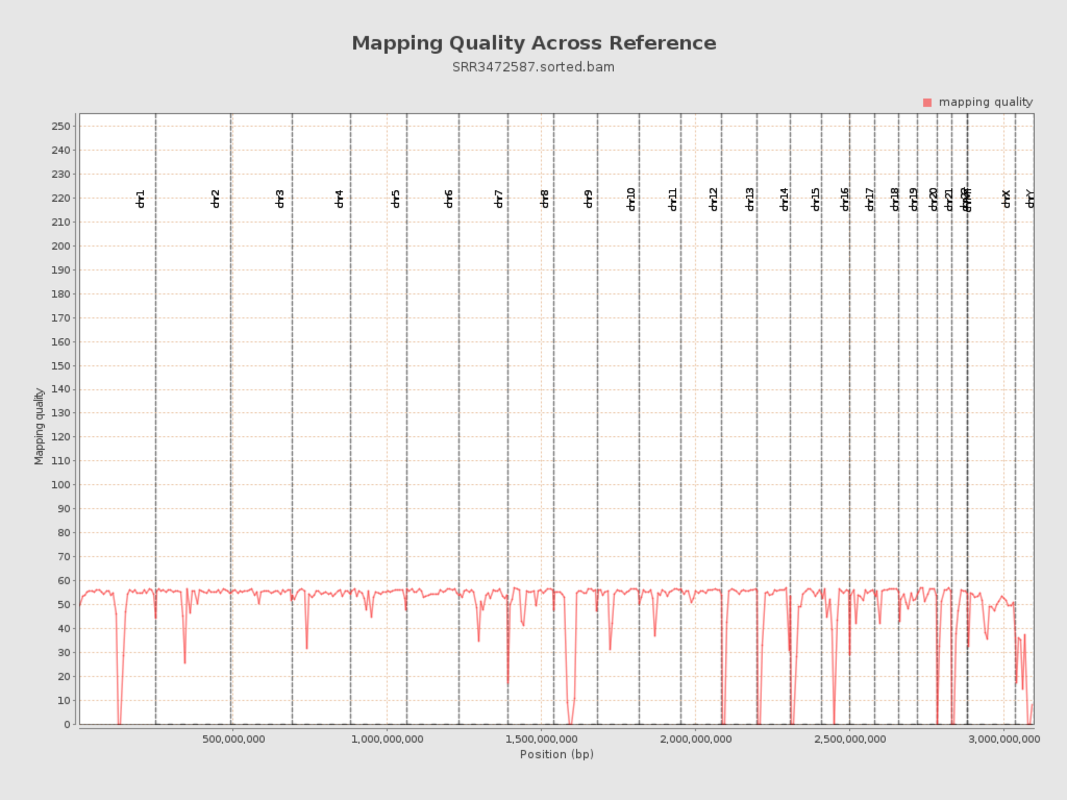
10. Results : Mapped Reads Clipping Profile



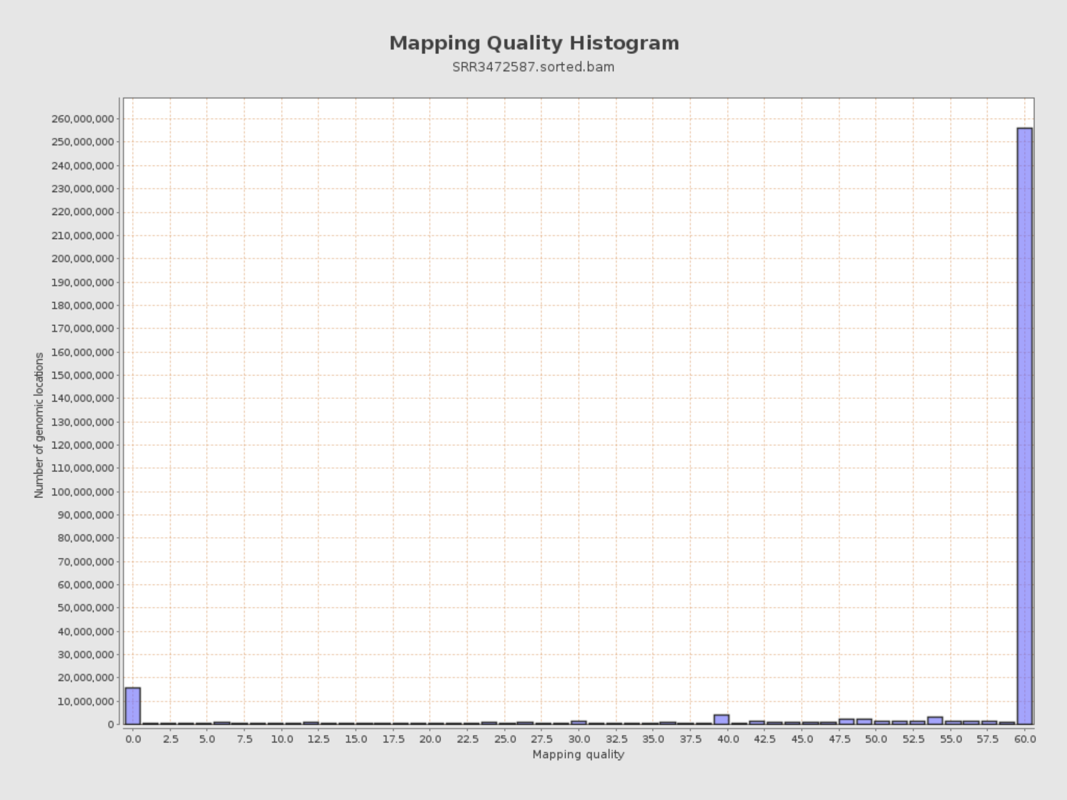
11. Results : Homopolymer Indels



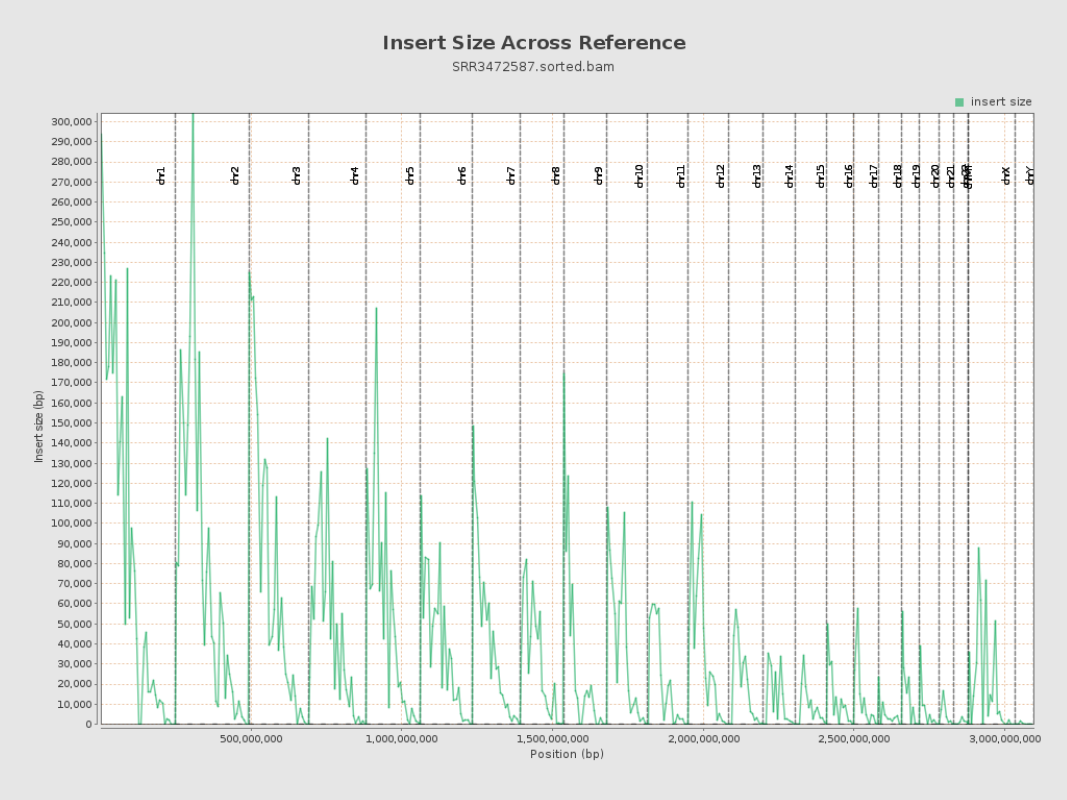
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram