Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:12:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472543.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_SRR3472543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472543_1.fastq.gz SRR3472543_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:12:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,467,332
Mapped reads	20,244,850 / 98.91%
Unmapped reads	222,482 / 1.09%
Mapped paired reads	20,244,850 / 98.91%
Mapped reads, first in pair	10,146,181 / 49.57%
Mapped reads, second in pair	10,098,669 / 49.34%
Mapped reads, both in pair	20,139,176 / 98.4%
Mapped reads, singletons	105,674 / 0.52%
Secondary alignments	0
Supplementary alignments	81,280 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	13,339,862 / 65.18%
Duplication rate	46.82%
Clipped reads	1,655,746 / 8.09%

2.2. ACGT Content

Number/percentage of A's	539,920,810 / 27.09%
Number/percentage of C's	459,403,203 / 23.05%
Number/percentage of T's	536,286,689 / 26.91%
Number/percentage of G's	456,792,335 / 22.92%
Number/percentage of N's	308,808 / 0.02%

GC Percentage	45.98%

2.3. Coverage

Mean	0.6438
Standard Deviation	23.8952

2.4. Mapping Quality

Mean Mapping Quality	55.08

2.5. Insert size

Mean	28,044.9
Standard Deviation	1,643,657.39
P25/Median/P75	167 / 231 / 308

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,653,905
Insertions	105,581
Mapped reads with at least one insertion	0.52%
Deletions	98,428
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.95%

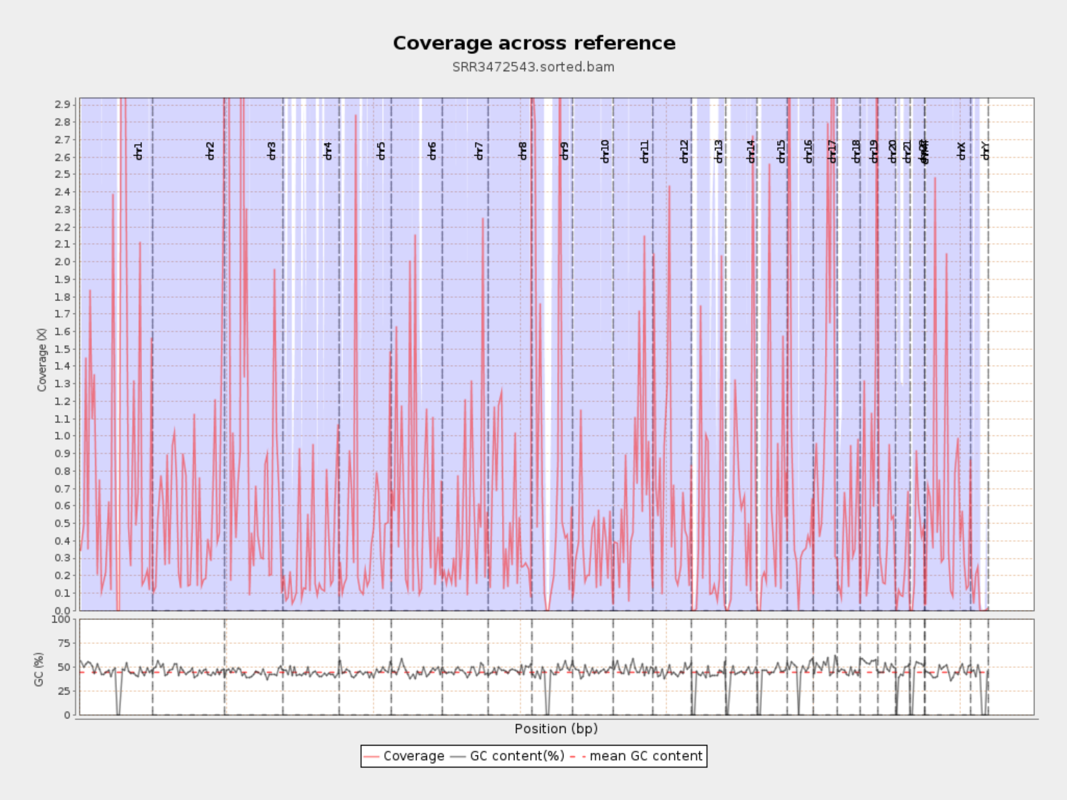
2.7. Chromosome stats

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

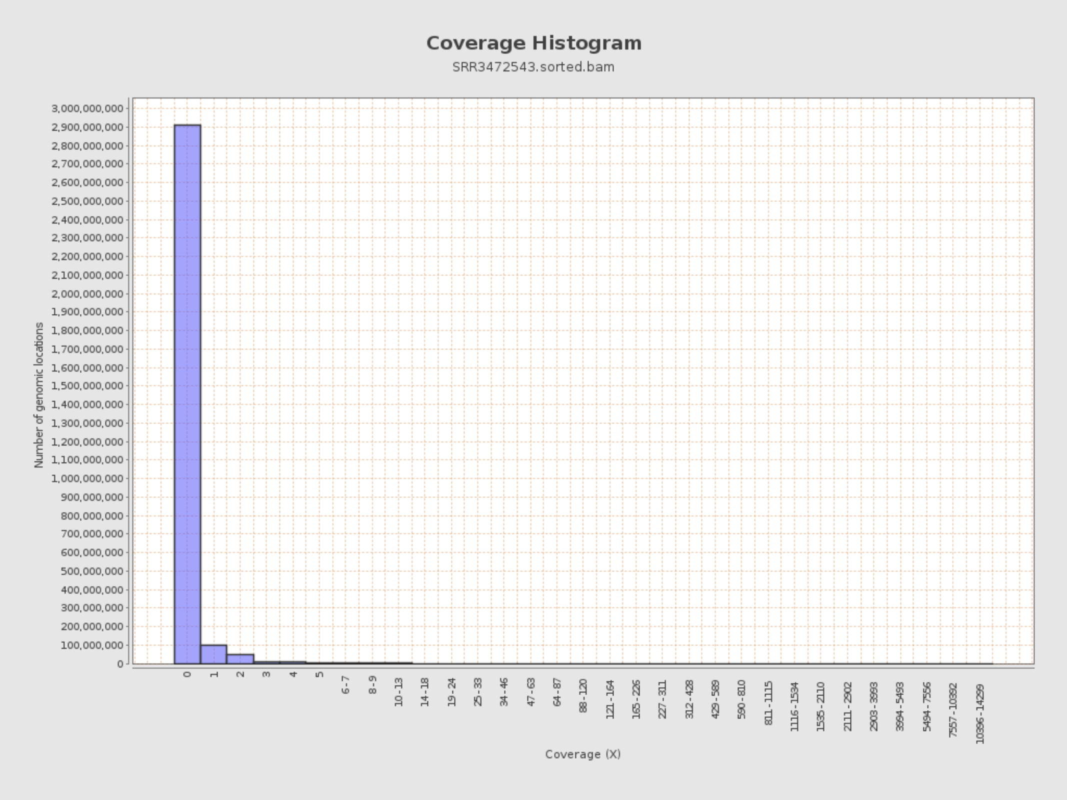
		bases	coverage	deviation
chr1	249250621	243162095	0.9756	33.7147
chr2	243199373	138030020	0.5676	17.6412
chr3	198022430	235172330	1.1876	30.8227
chr4	191154276	57260617	0.2996	10.5662
chr5	180915260	90393972	0.4996	16.2479
chr6	171115067	114104041	0.6668	22.6731
chr7	159138663	82067887	0.5157	17.1172
chr8	146364022	72202313	0.4933	17.4986
chr9	141213431	131081326	0.9282	29.1159
chr10	135534747	50354915	0.3715	15.3443
chr11	135006516	91662165	0.6789	32.8165
chr12	133851895	96611227	0.7218	22.9841
chr13	115169878	54664935	0.4746	22.097
chr14	107349540	68592420	0.639	22.7631
chr15	102531392	59762966	0.5829	32.4888
chr16	90354753	61796537	0.6839	18.2622
chr17	81195210	106916750	1.3168	53.9647
chr18	78077248	34225980	0.4384	14.8226
chr19	59128983	48488478	0.82	22.5809
chr20	63025520	27428817	0.4352	11.5277
chr21	48129895	9899044	0.2057	7.2599
chr22	51304566	20037968	0.3906	11.1231
chrMT	16571	4117	0.2484	0.6136
chrX	155270560	94008570	0.6055	18.0045

chrY	59373566	5044138	0.085	6.3803

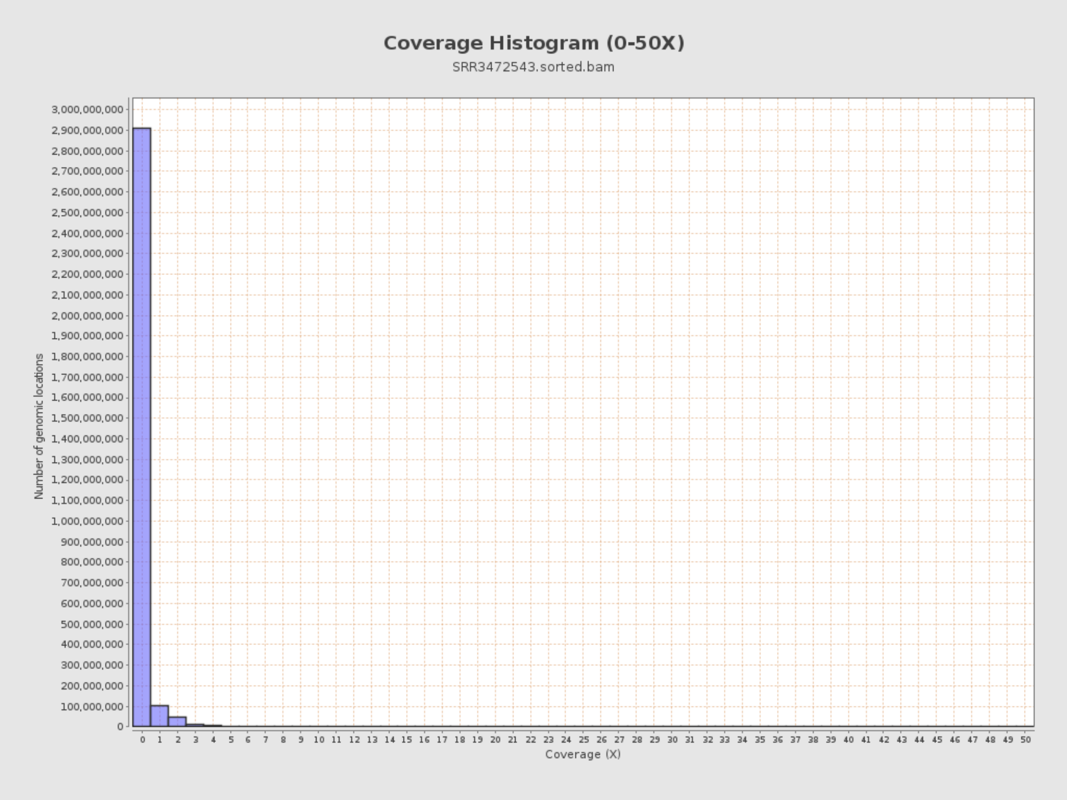
3. Results : Coverage across reference



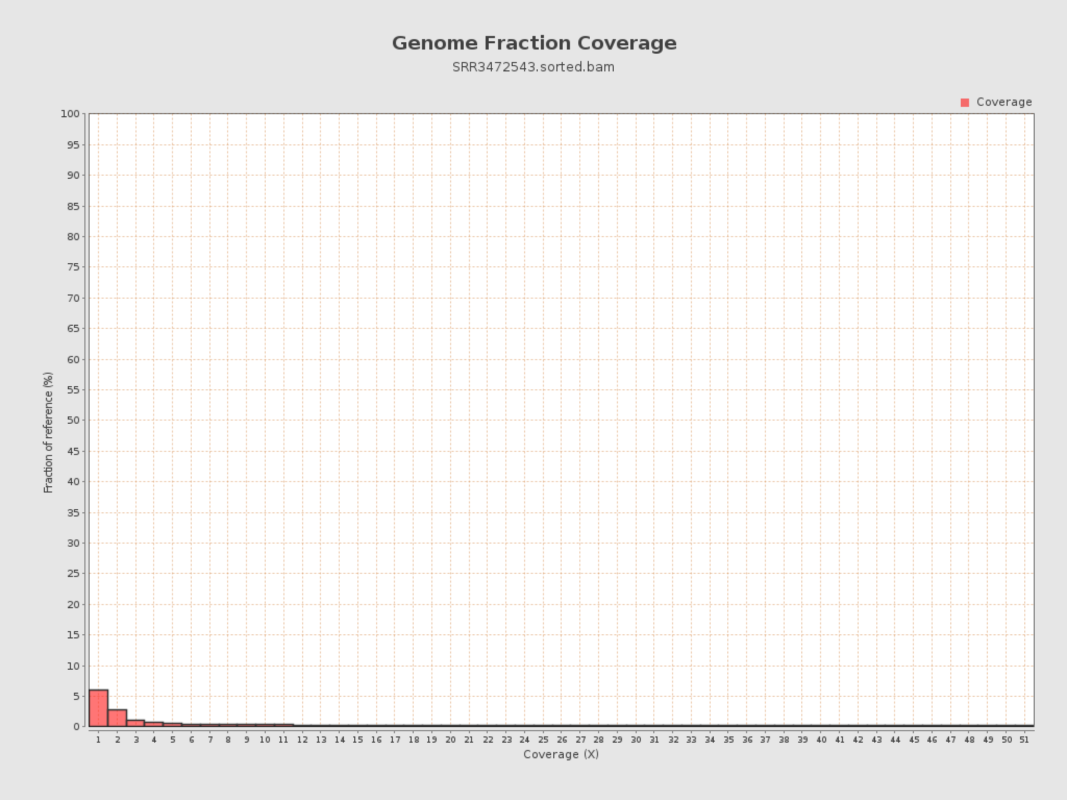
4. Results : Coverage Histogram



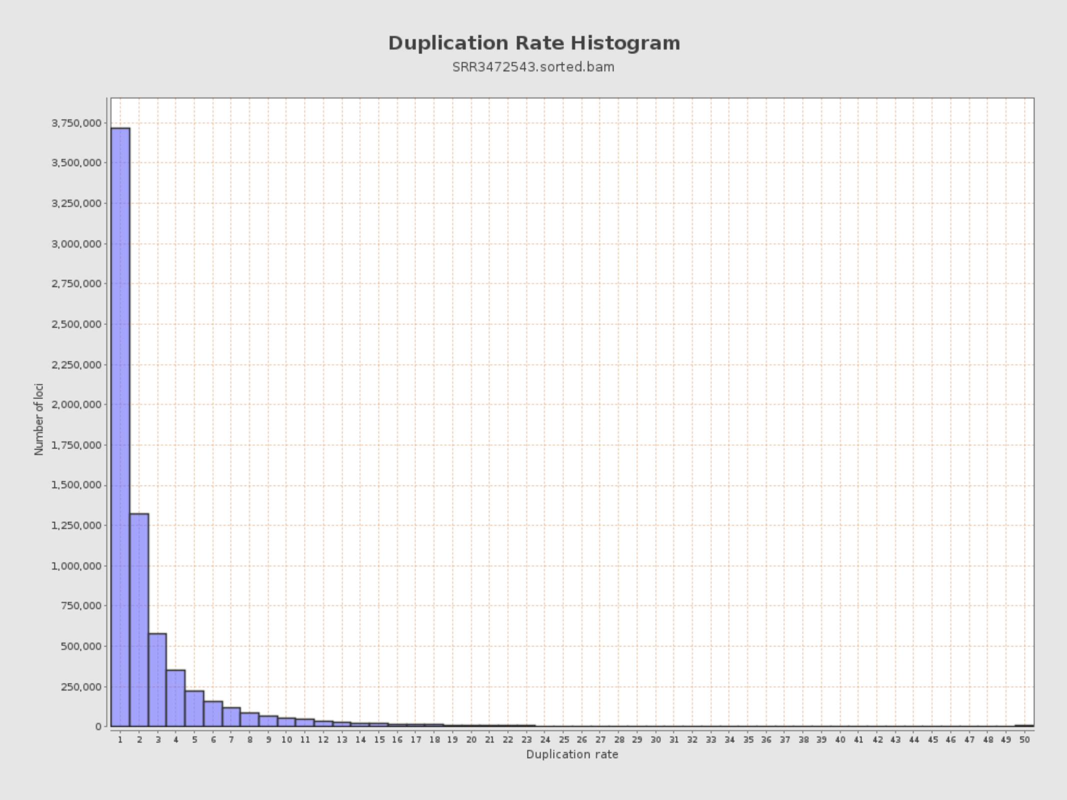
5. Results : Coverage Histogram (0-50X)



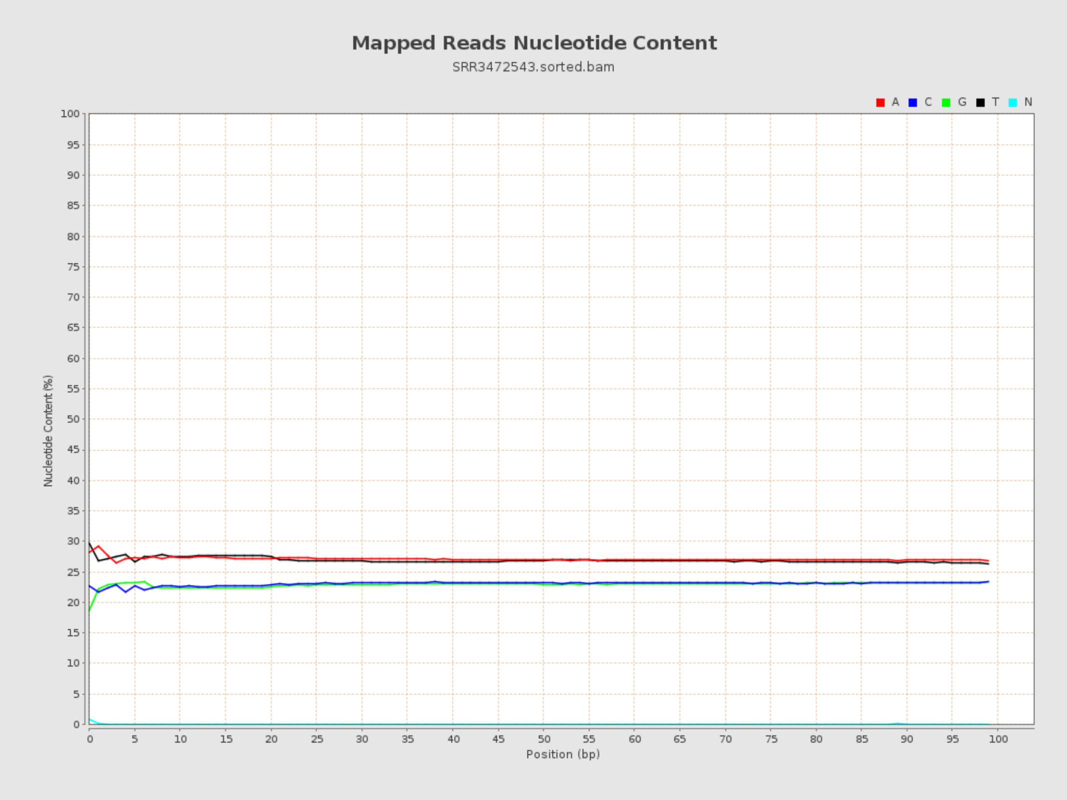
6. Results : Genome Fraction Coverage



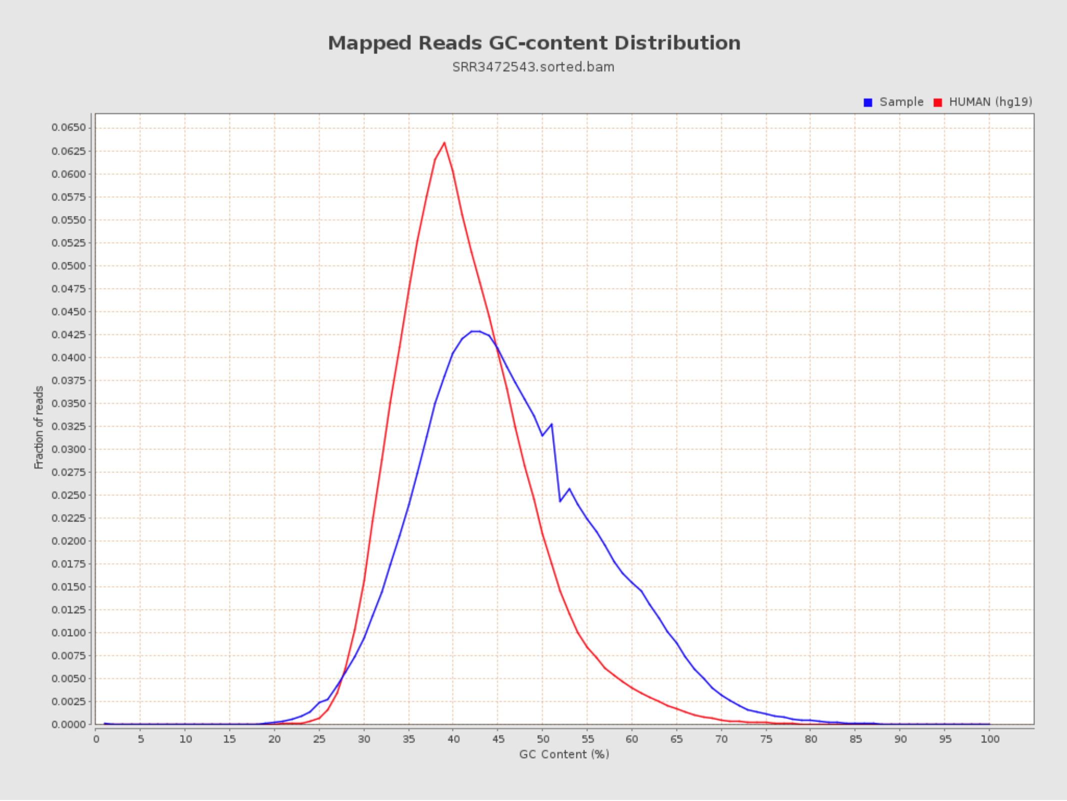
7. Results : Duplication Rate Histogram



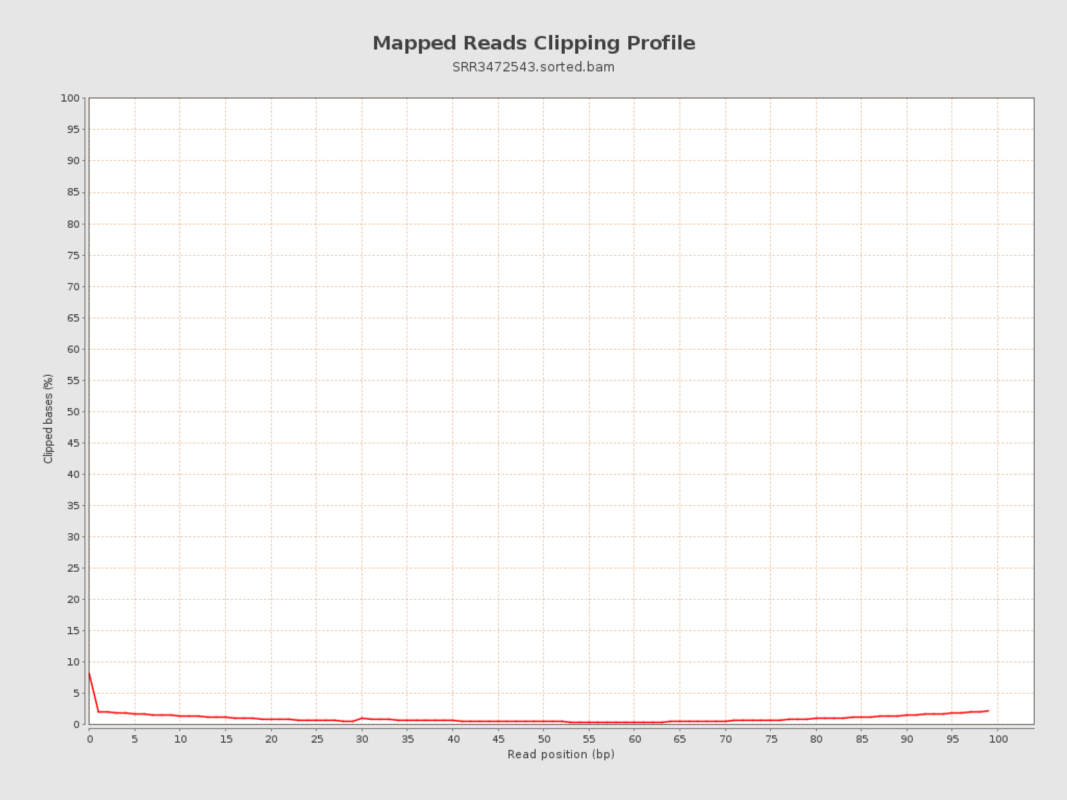
8. Results : Mapped Reads Nucleotide Content



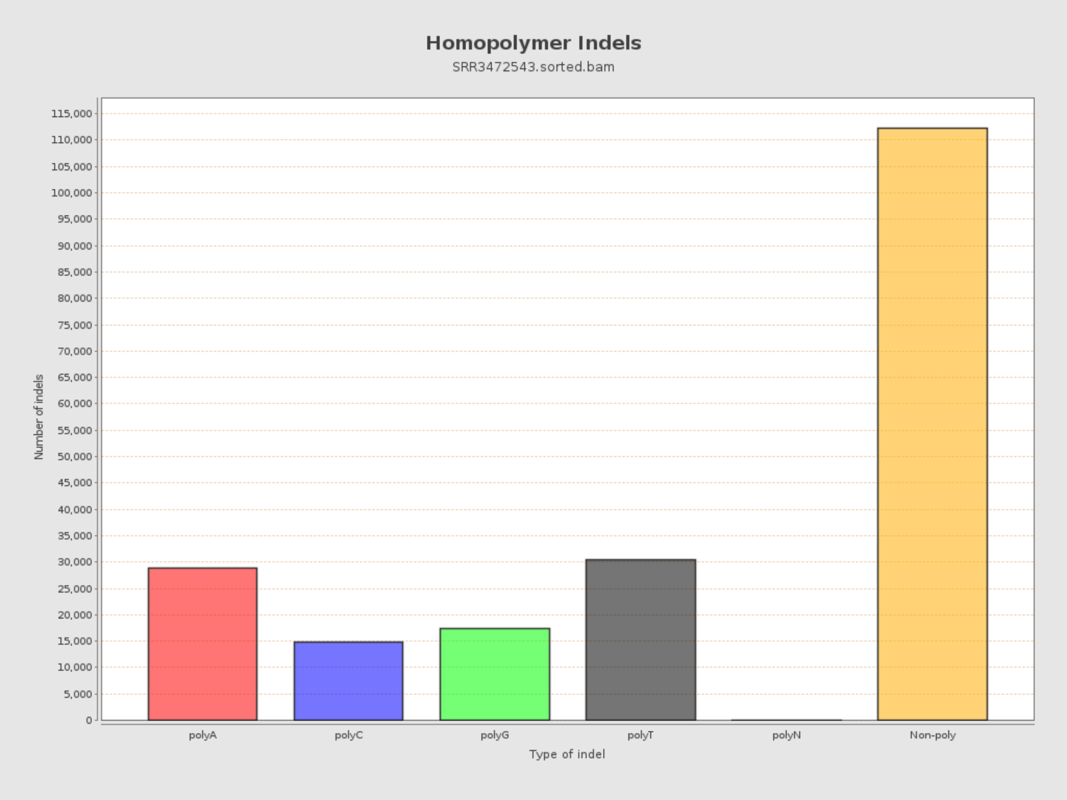
9. Results : Mapped Reads GC-content Distribution



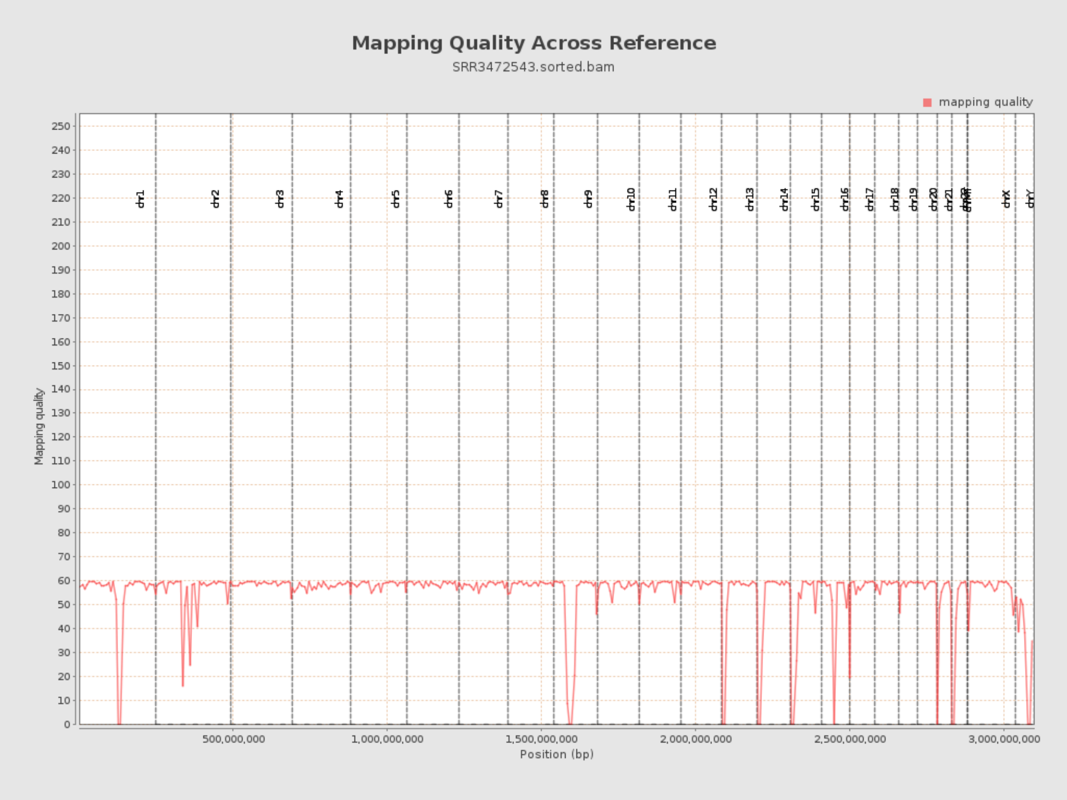
10. Results : Mapped Reads Clipping Profile



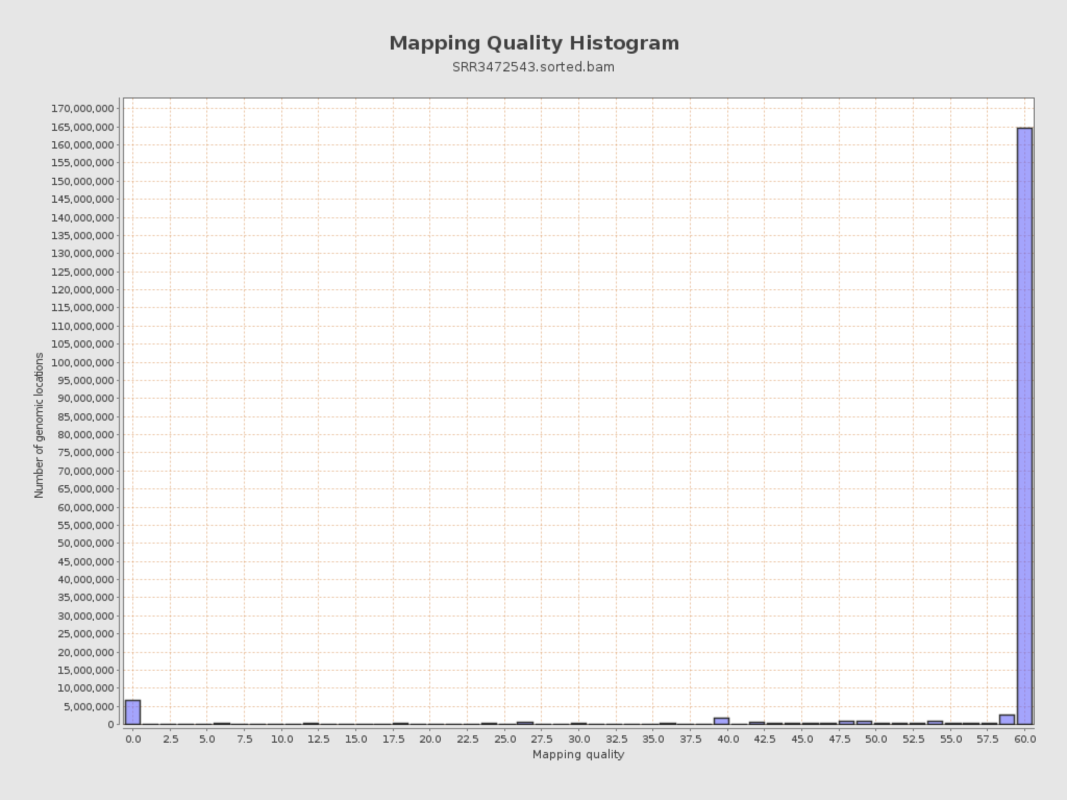
11. Results : Homopolymer Indels



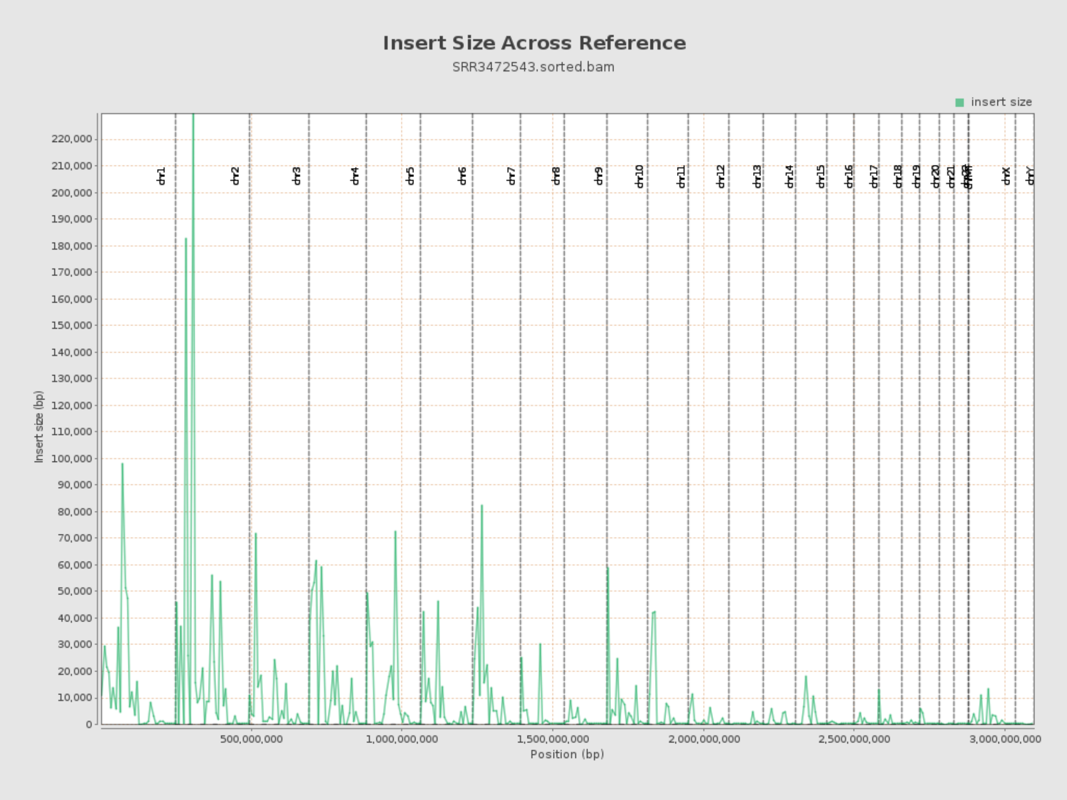
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram