Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 03:19:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472568.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_SRR3472568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472568_1.fastq.gz SRR3472568_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 03:19:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	309,681,210
Mapped reads	304,471,048 / 98.32%
Unmapped reads	5,210,162 / 1.68%
Mapped paired reads	304,471,048 / 98.32%
Mapped reads, first in pair	152,926,302 / 49.38%
Mapped reads, second in pair	151,544,746 / 48.94%
Mapped reads, both in pair	302,545,466 / 97.7%
Mapped reads, singletons	1,925,582 / 0.62%
Secondary alignments	0
Supplementary alignments	217,875 / 0.07%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	204,963,731 / 66.19%
Duplication rate	53.73%
Clipped reads	63,822,635 / 20.61%

2.2. ACGT Content

Number/percentage of A's	7,029,455,224 / 24.23%
Number/percentage of C's	7,490,060,242 / 25.81%
Number/percentage of T's	7,108,843,940 / 24.5%
Number/percentage of G's	7,381,928,407 / 25.44%
Number/percentage of N's	5,716,296 / 0.02%

GC Percentage	51.25%

2.3. Coverage

Mean	9.3747
Standard Deviation	103.2919

2.4. Mapping Quality

Mean Mapping Quality	51.64

2.5. Insert size

Mean	8,370.51
Standard Deviation	842,762.31
P25/Median/P75	113 / 167 / 253

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	308,299,985
Insertions	2,094,369
Mapped reads with at least one insertion	0.67%
Deletions	2,119,546
Mapped reads with at least one deletion	0.68%
Homopolymer indels	37.84%

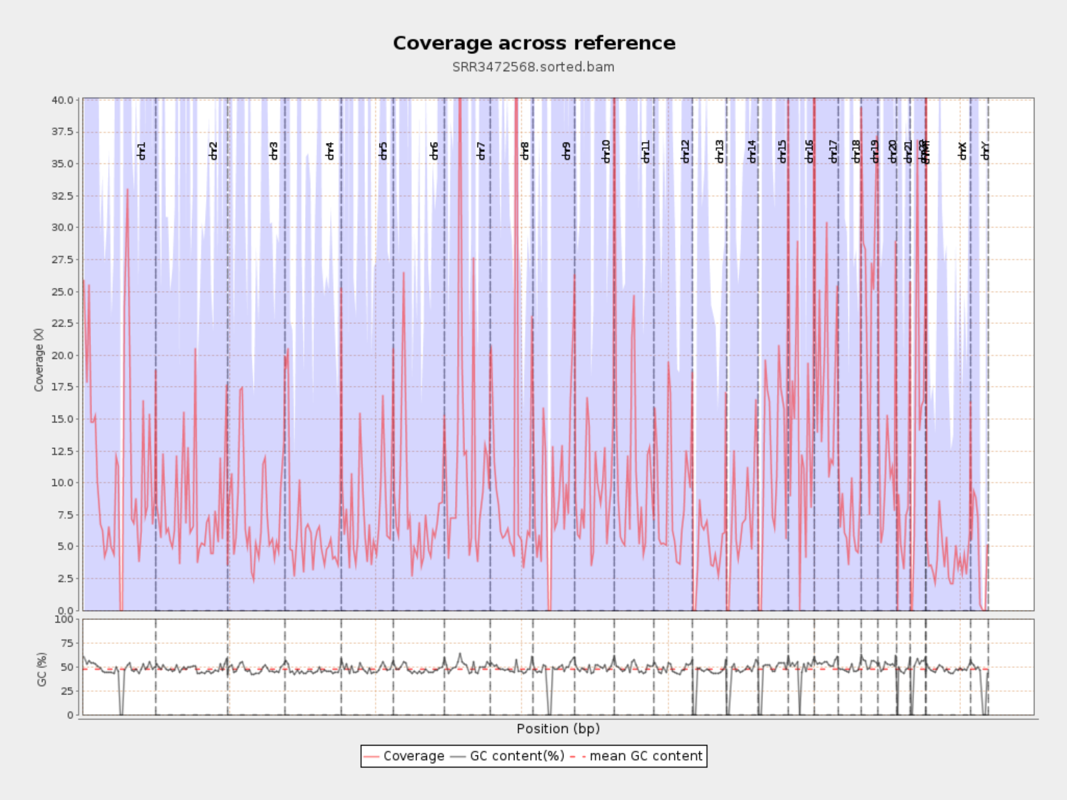
2.7. Chromosome stats

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

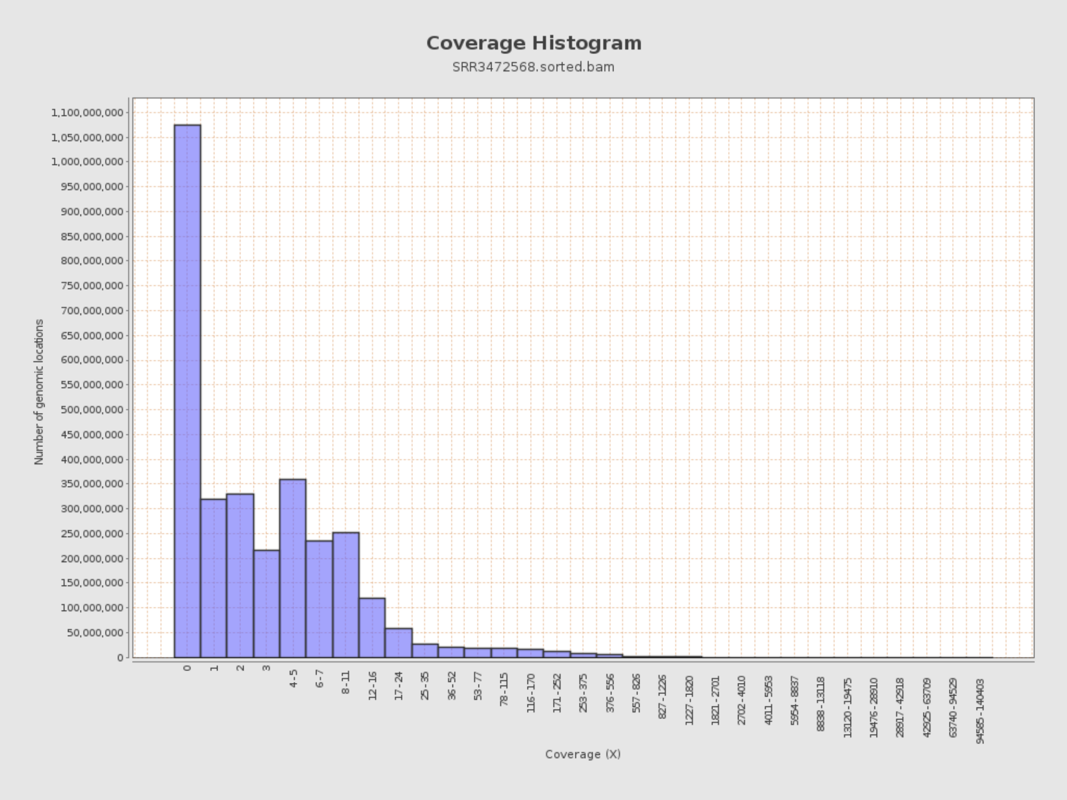
		bases	coverage	deviation
chr1	249250621	2810649939	11.2764	92.8811
chr2	243199373	1937253506	7.9657	74.0335
chr3	198022430	1517810810	7.6648	46.3812
chr4	191154276	1216049801	6.3616	55.1372
chr5	180915260	1427187128	7.8887	71.1932
chr6	171115067	1315099562	7.6855	42.7901
chr7	159138663	1943090542	12.21	327.5048
chr8	146364022	1558403638	10.6475	174.4168
chr9	141213431	1281726905	9.0765	51.7399
chr10	135534747	1229664870	9.0727	67.473
chr11	135006516	1464191958	10.8453	52.428
chr12	133851895	1227015571	9.167	39.8928
chr13	115169878	558262910	4.8473	24.7262
chr14	107349540	773919897	7.2093	37.5087
chr15	102531392	1181481661	11.5231	64.5219
chr16	90354753	1312276940	14.5236	73.6879
chr17	81195210	1476229914	18.1812	101.8522
chr18	78077248	524948214	6.7234	63.0373
chr19	59128983	1517897510	25.671	101.4501
chr20	63025520	691079510	10.9651	59.9232
chr21	48129895	382531532	7.9479	65.5371
chr22	51304566	748858754	14.5963	81.0222
chrMT	16571	2140949	129.1985	46.4374
chrX	155270560	653110982	4.2063	22.6566

chrY	59373566	270237407	4.5515	83.6462

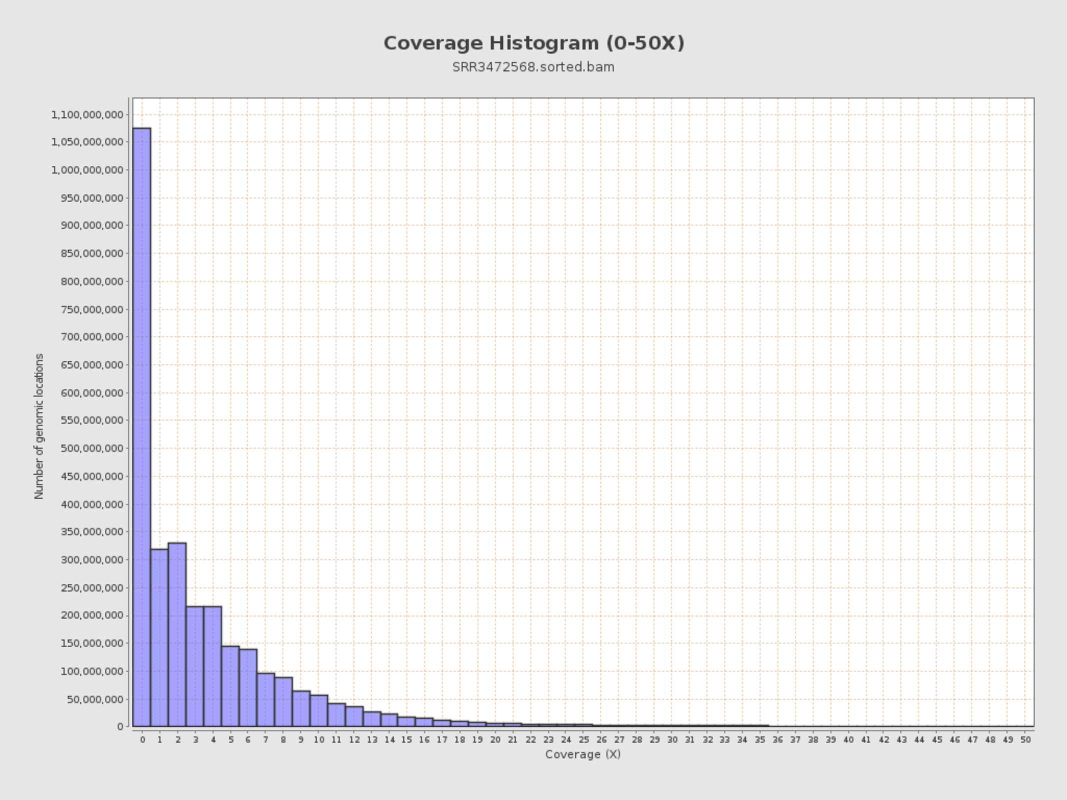
3. Results : Coverage across reference



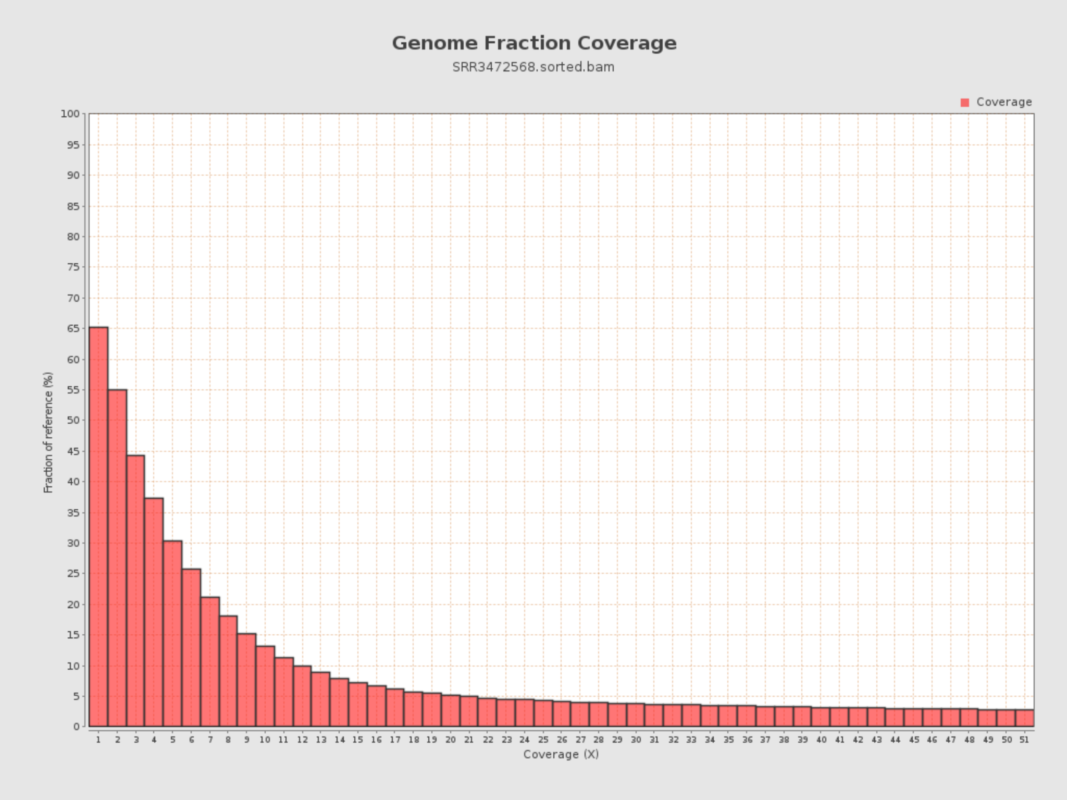
4. Results : Coverage Histogram



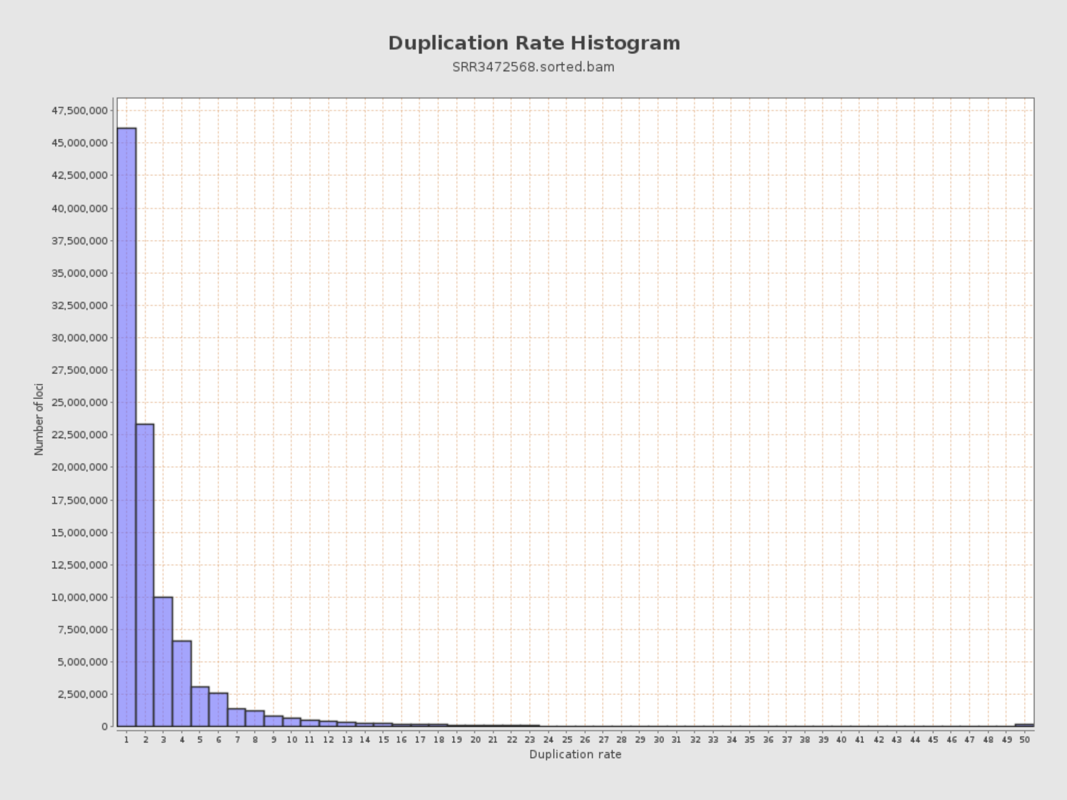
5. Results : Coverage Histogram (0-50X)



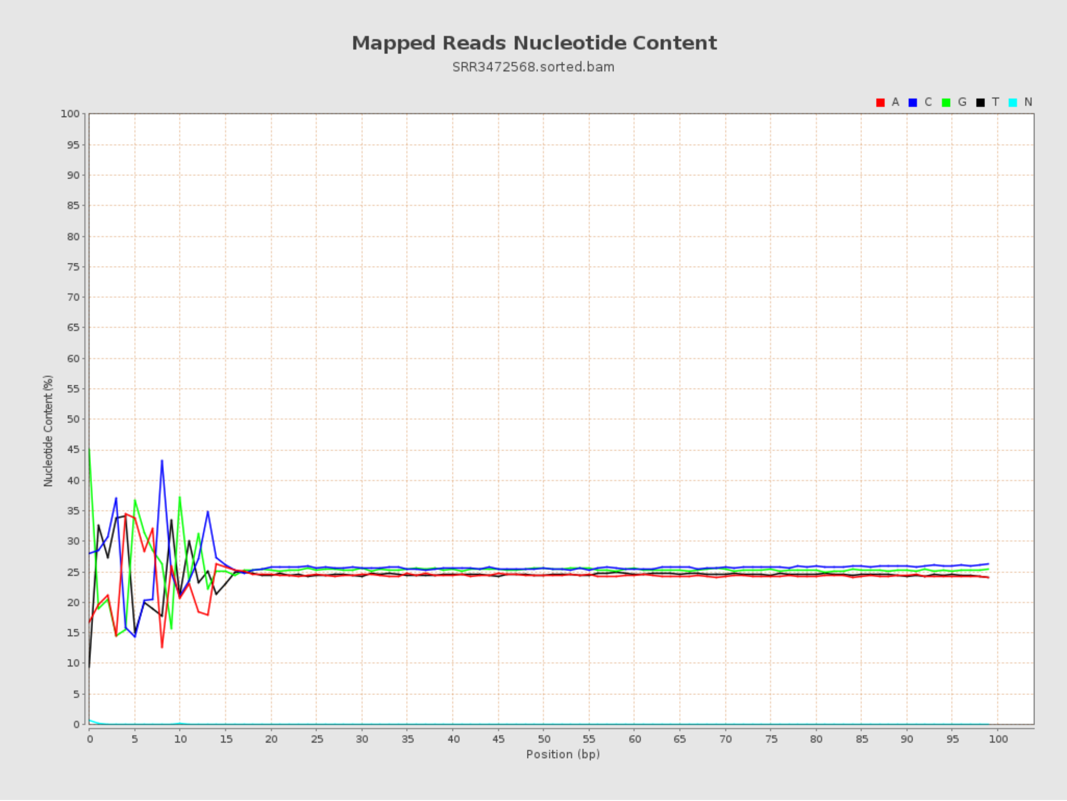
6. Results : Genome Fraction Coverage



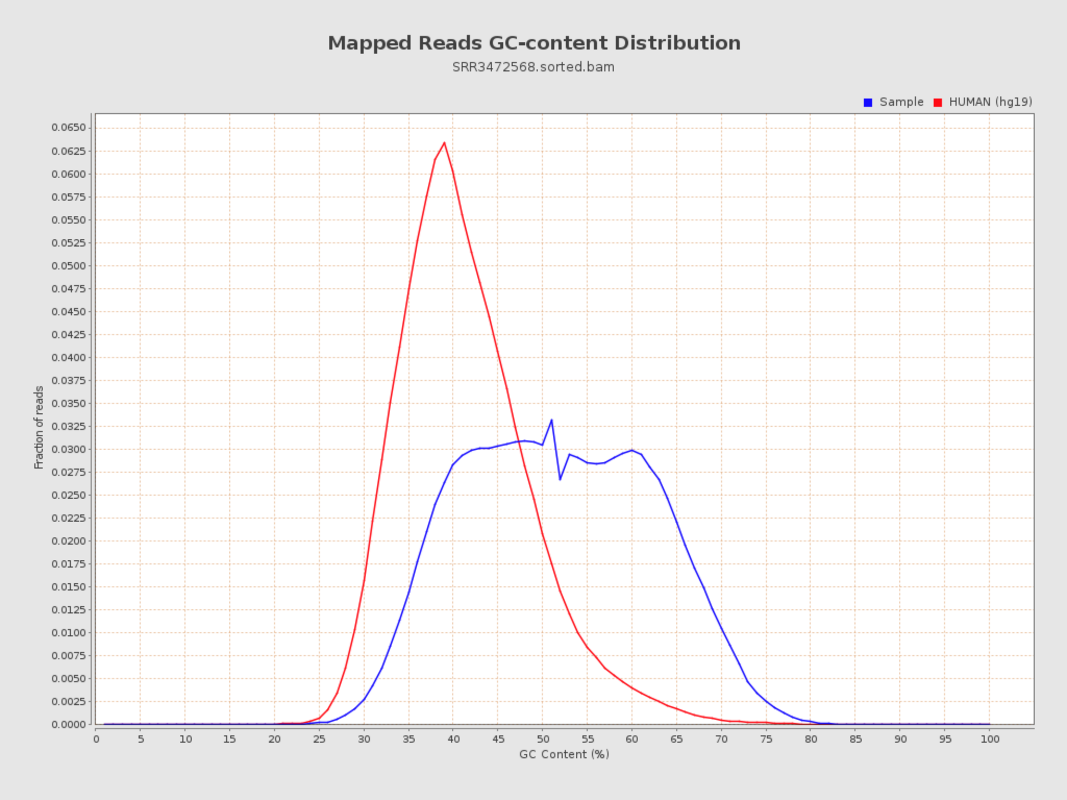
7. Results : Duplication Rate Histogram



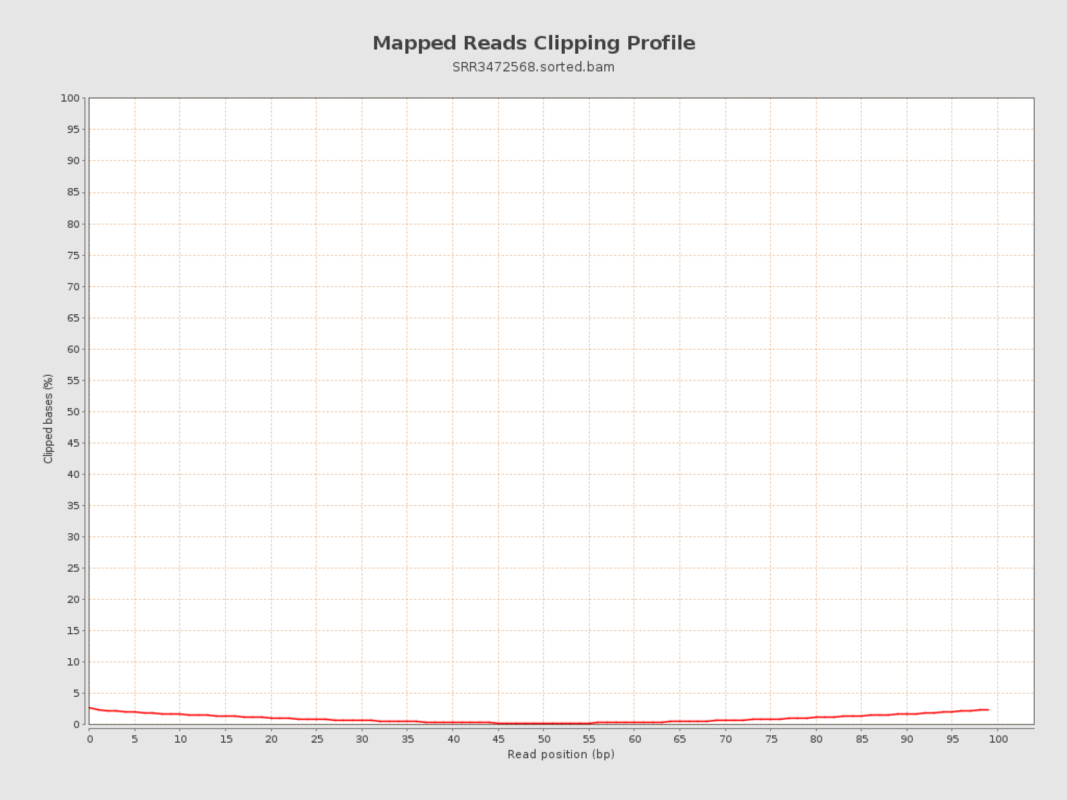
8. Results : Mapped Reads Nucleotide Content



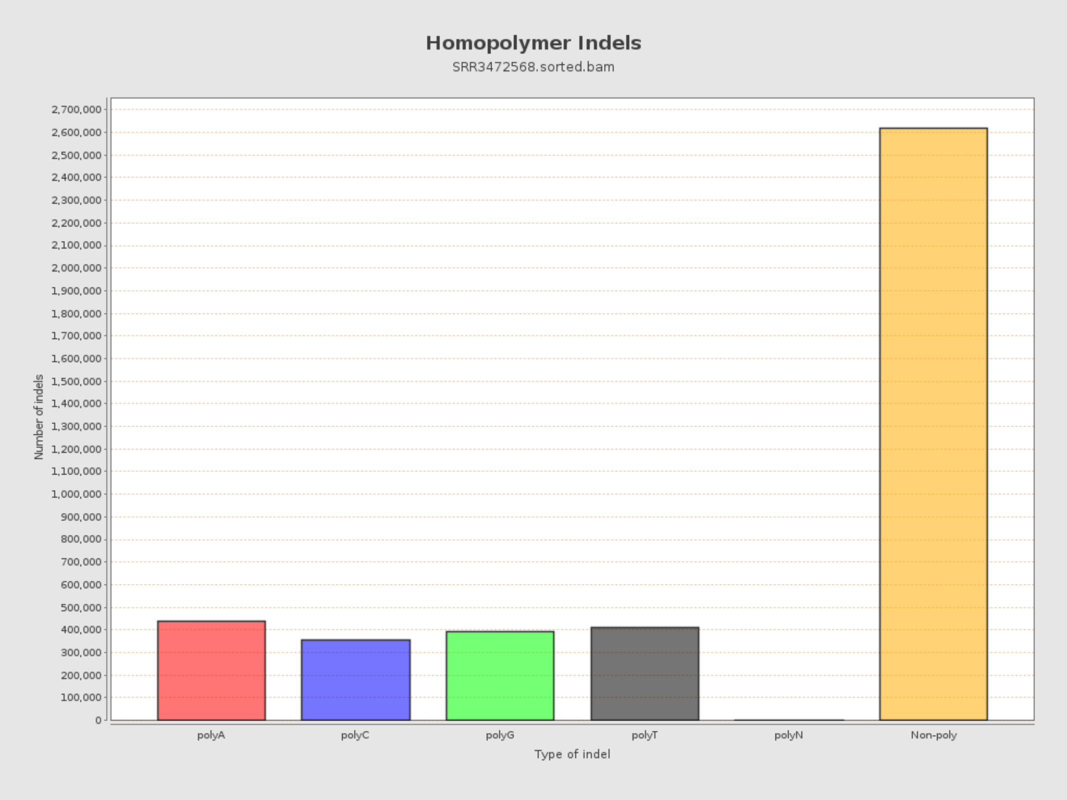
9. Results : Mapped Reads GC-content Distribution



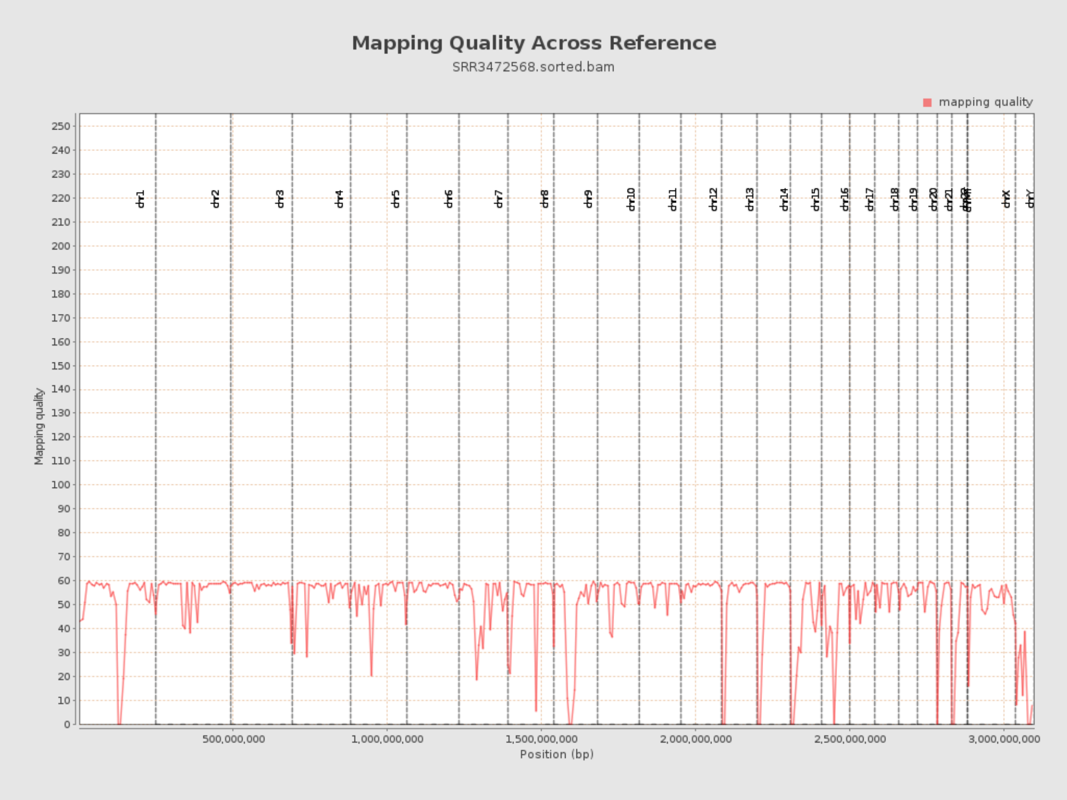
10. Results : Mapped Reads Clipping Profile



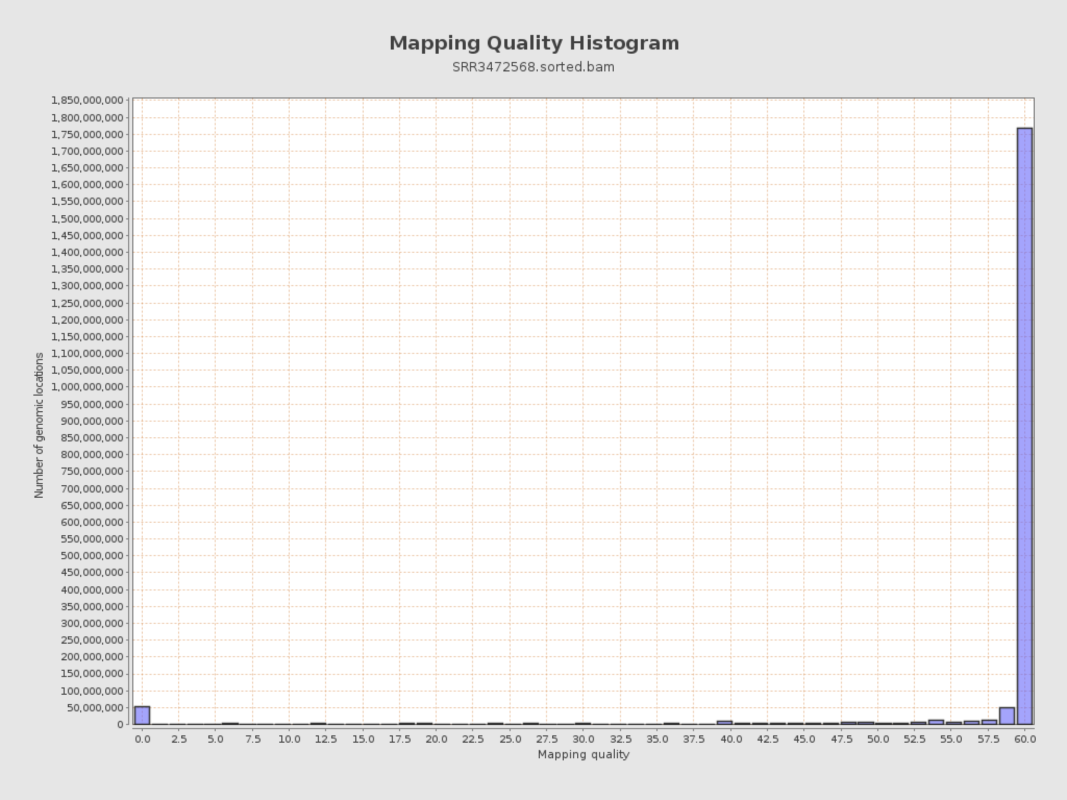
11. Results : Homopolymer Indels



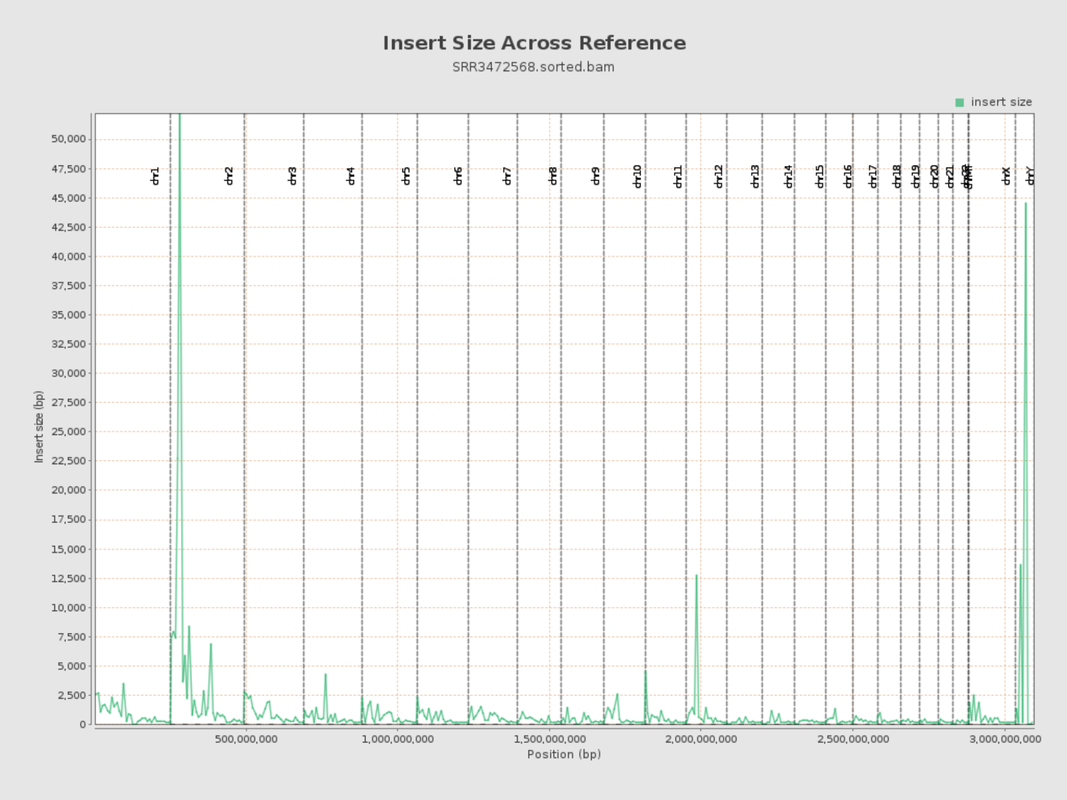
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram