Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:26:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472529.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_SRR3472529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472529_1.fastq.gz SRR3472529_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:26:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,543,836
Mapped reads	6,450,875 / 98.58%
Unmapped reads	92,961 / 1.42%
Mapped paired reads	6,450,875 / 98.58%
Mapped reads, first in pair	3,236,372 / 49.46%
Mapped reads, second in pair	3,214,503 / 49.12%
Mapped reads, both in pair	6,405,904 / 97.89%
Mapped reads, singletons	44,971 / 0.69%
Secondary alignments	0
Supplementary alignments	25,559 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	3,331,003 / 50.9%
Duplication rate	41.41%
Clipped reads	548,866 / 8.39%

2.2. ACGT Content

Number/percentage of A's	172,558,131 / 27.21%
Number/percentage of C's	145,600,133 / 22.96%
Number/percentage of T's	171,547,889 / 27.05%
Number/percentage of G's	144,453,731 / 22.78%
Number/percentage of N's	100,556 / 0.02%

GC Percentage	45.73%

2.3. Coverage

Mean	0.2049
Standard Deviation	7.4869

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	28,735.26
Standard Deviation	1,661,549.1
P25/Median/P75	161 / 222 / 298

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	3,646,030
Insertions	33,023
Mapped reads with at least one insertion	0.51%
Deletions	32,400
Mapped reads with at least one deletion	0.5%
Homopolymer indels	42.49%

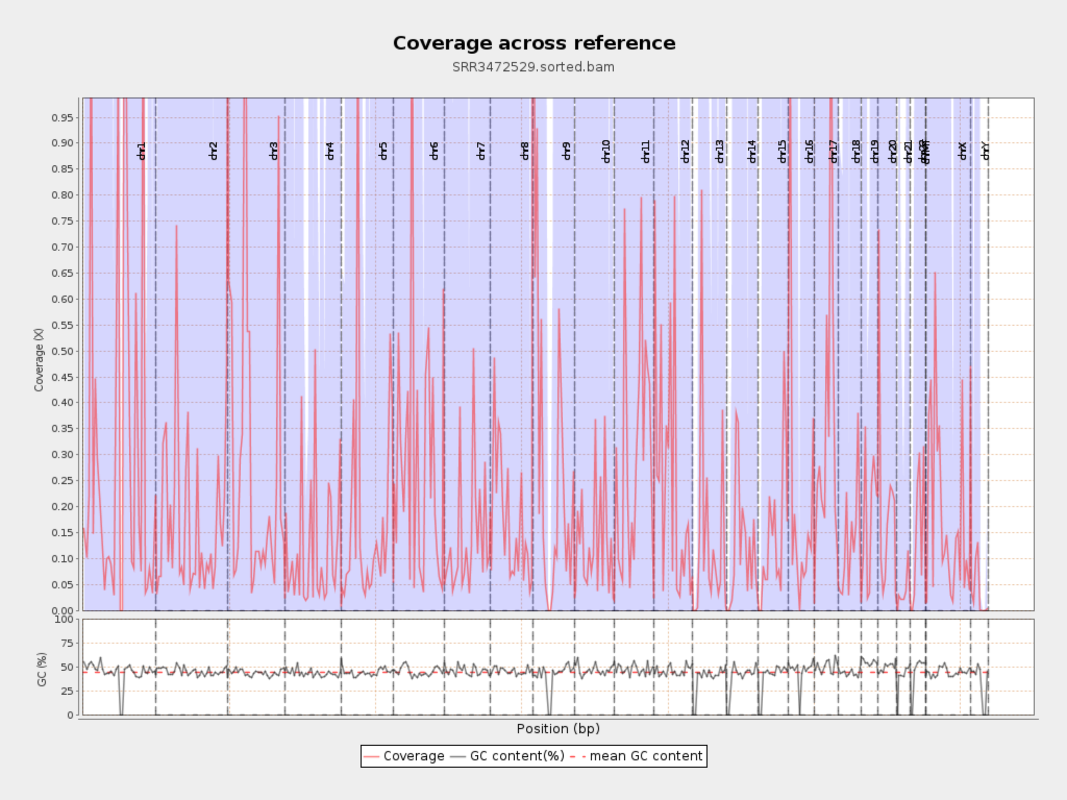
2.7. Chromosome stats

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

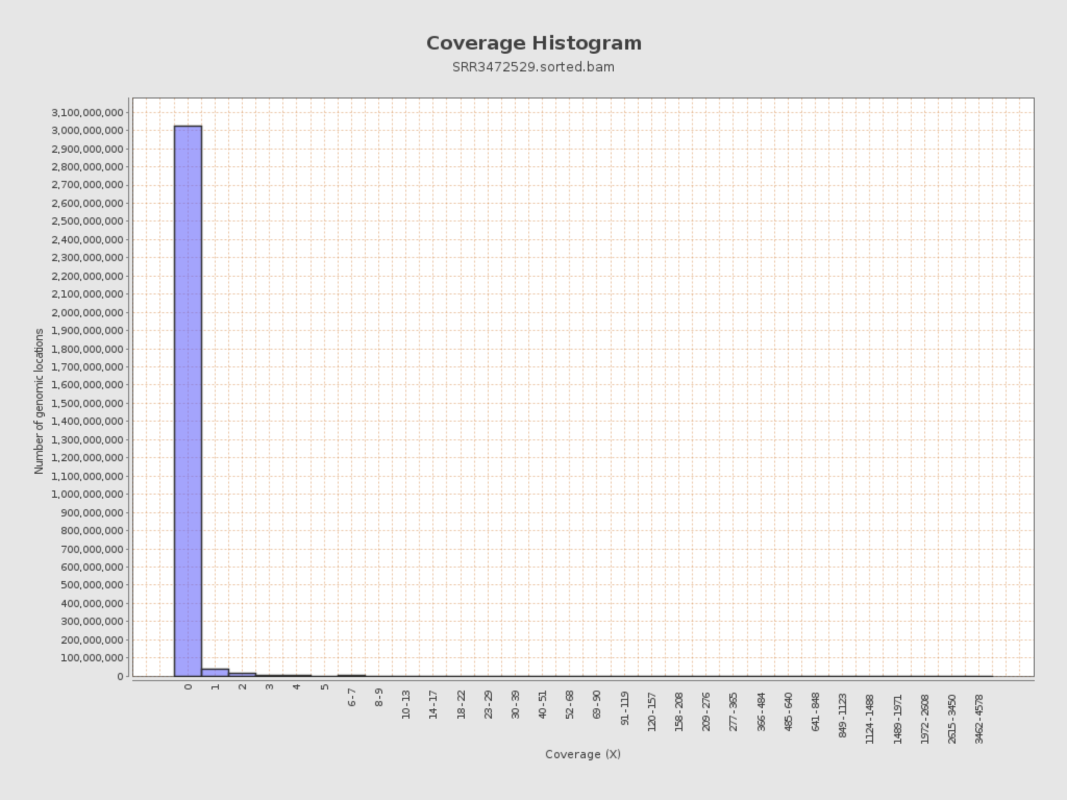
		bases	coverage	deviation
chr1	249250621	78893921	0.3165	11.9272
chr2	243199373	40647784	0.1671	5.9601
chr3	198022430	58952065	0.2977	7.9324
chr4	191154276	23522859	0.1231	4.9387
chr5	180915260	33181422	0.1834	6.0638
chr6	171115067	50629153	0.2959	9.9902
chr7	159138663	22494136	0.1413	4.1742
chr8	146364022	24469401	0.1672	5.4655
chr9	141213431	36679853	0.2597	7.3475
chr10	135534747	18751203	0.1383	5.7058
chr11	135006516	40388957	0.2992	11.2672
chr12	133851895	35490312	0.2651	8.2864
chr13	115169878	16610597	0.1442	7.1197
chr14	107349540	13409687	0.1249	5.4476
chr15	102531392	14407854	0.1405	4.2281
chr16	90354753	20263804	0.2243	8.1906
chr17	81195210	31555290	0.3886	10.9165
chr18	78077248	10298133	0.1319	4.9898
chr19	59128983	10412227	0.1761	4.5089
chr20	63025520	12308897	0.1953	8.8454
chr21	48129895	1841425	0.0383	1.1791
chr22	51304566	7496750	0.1461	5.3037
chrMT	16571	873	0.0527	0.2633
chrX	155270560	29494606	0.19	6.5004

chrY	59373566	2137231	0.036	2.256

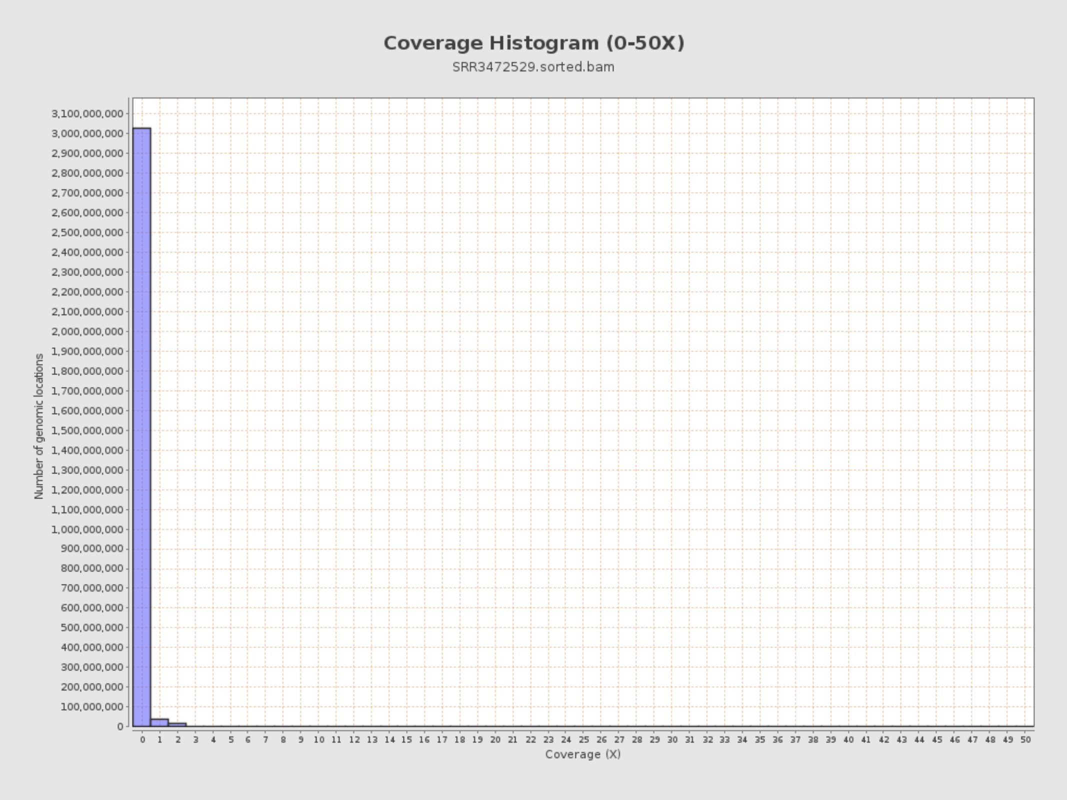
3. Results : Coverage across reference



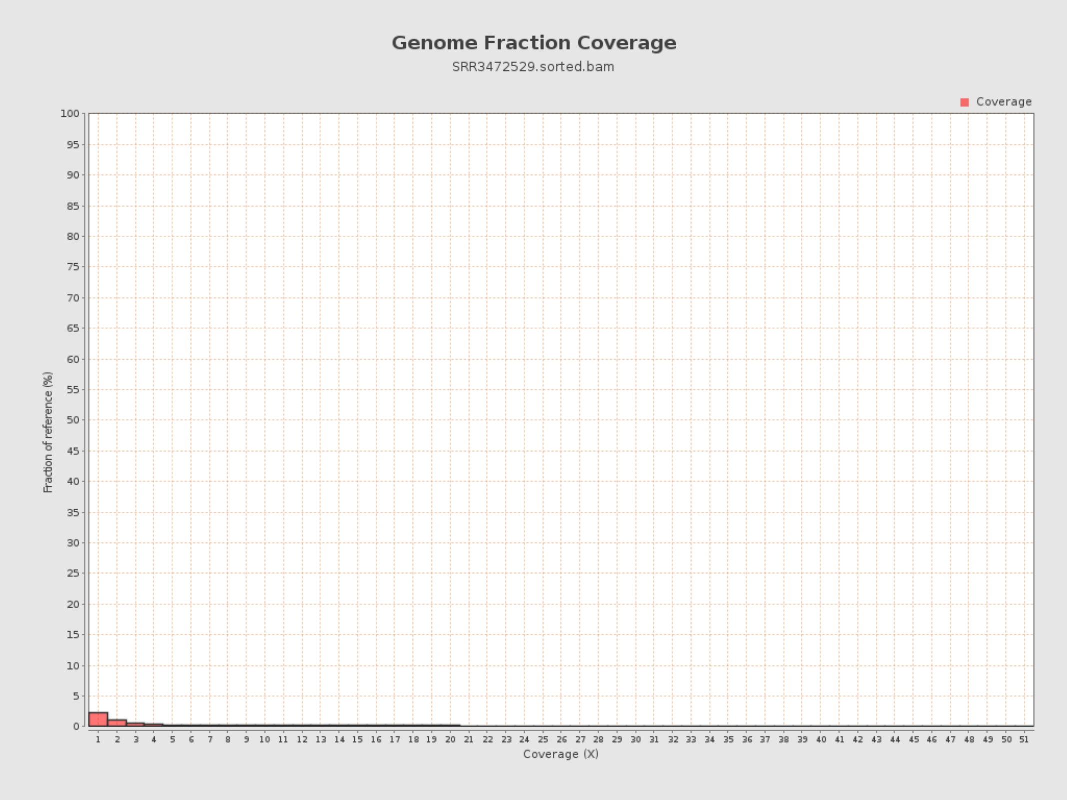
4. Results : Coverage Histogram



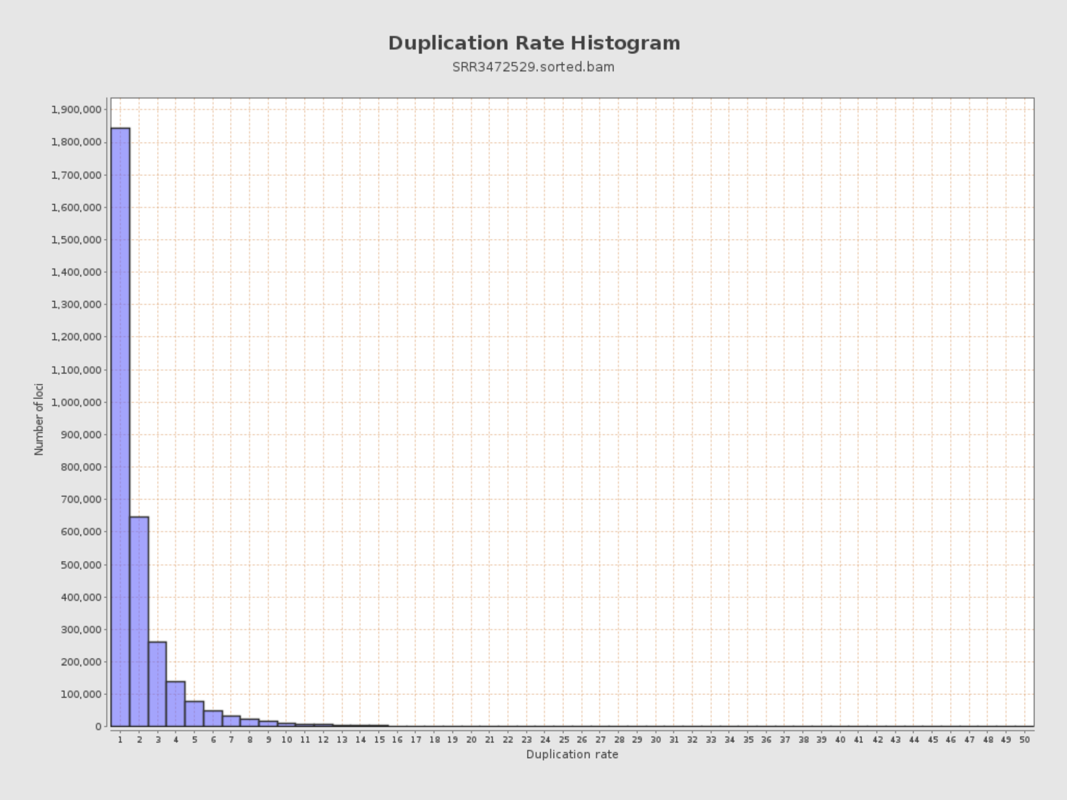
5. Results : Coverage Histogram (0-50X)



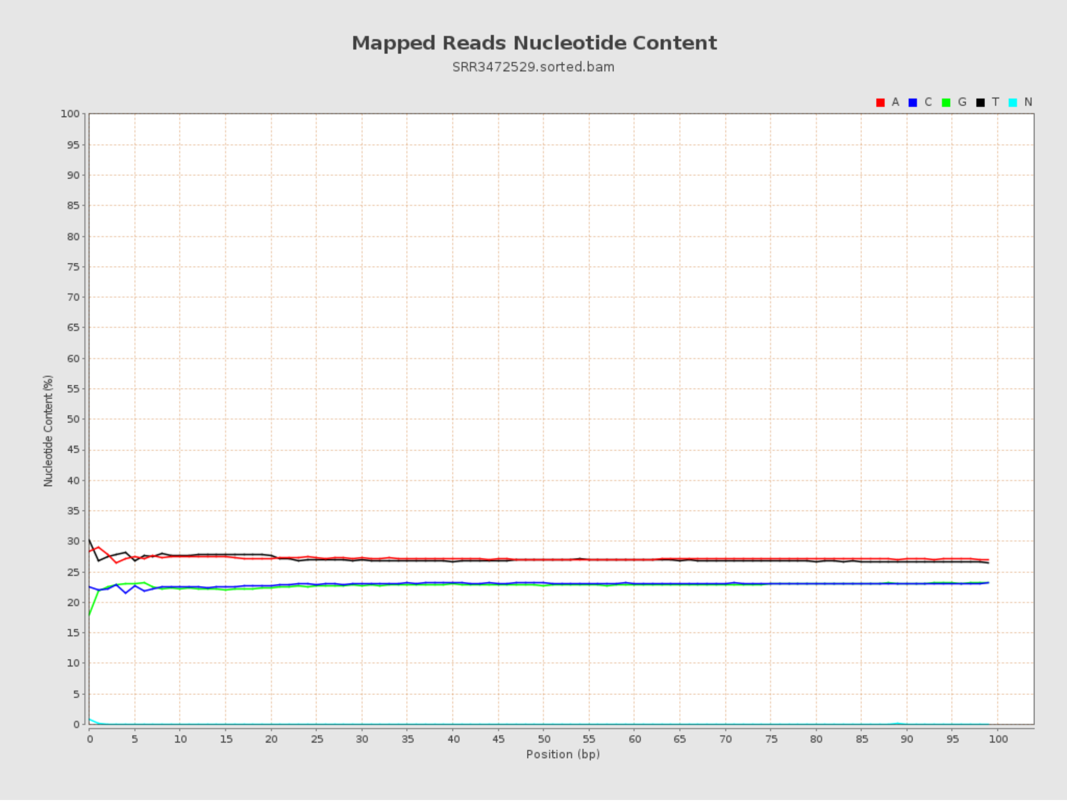
6. Results : Genome Fraction Coverage



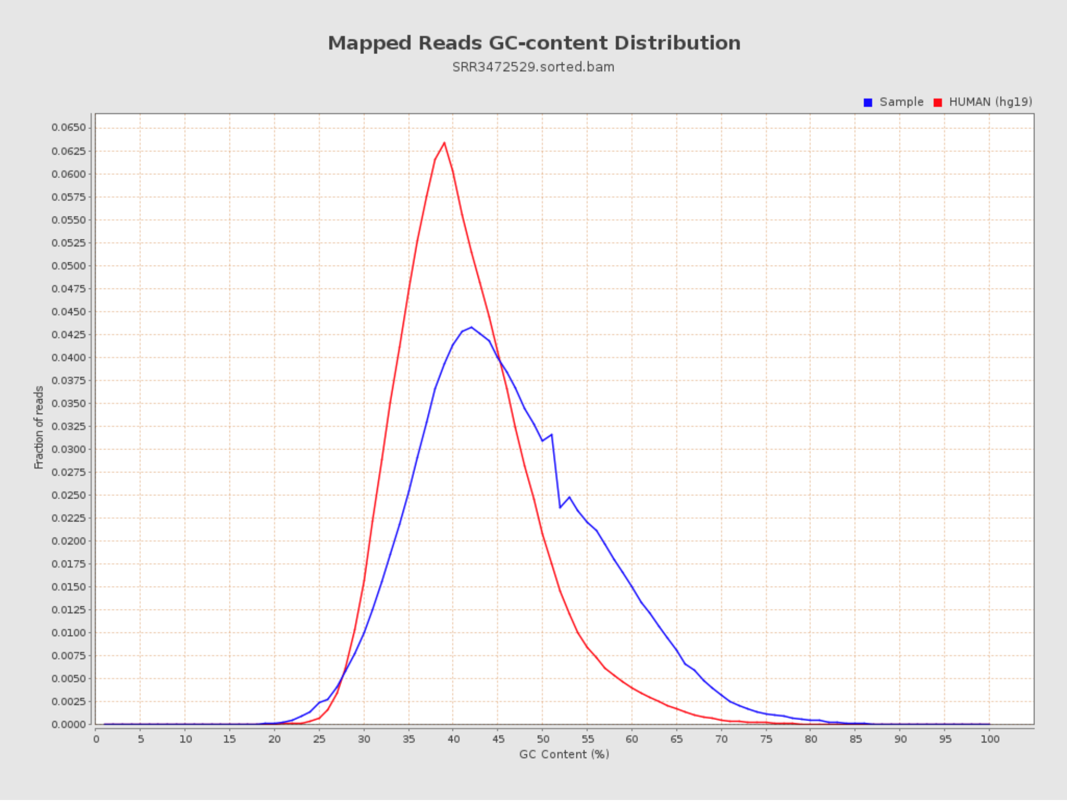
7. Results : Duplication Rate Histogram



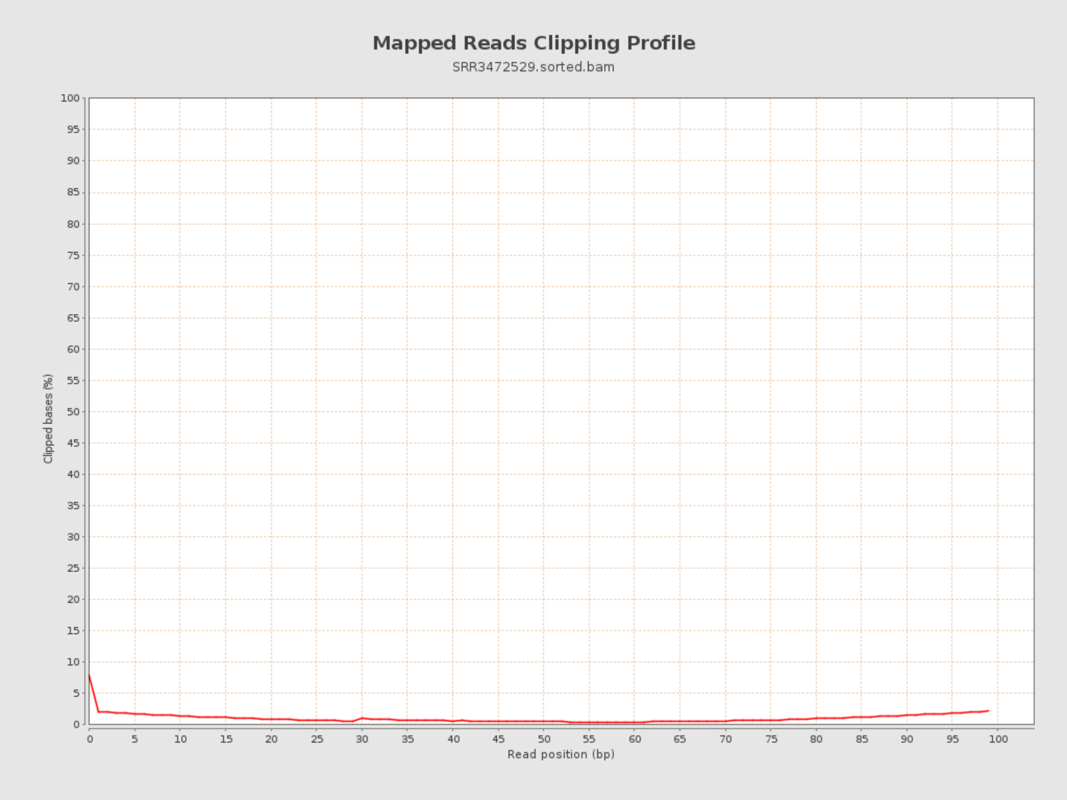
8. Results : Mapped Reads Nucleotide Content



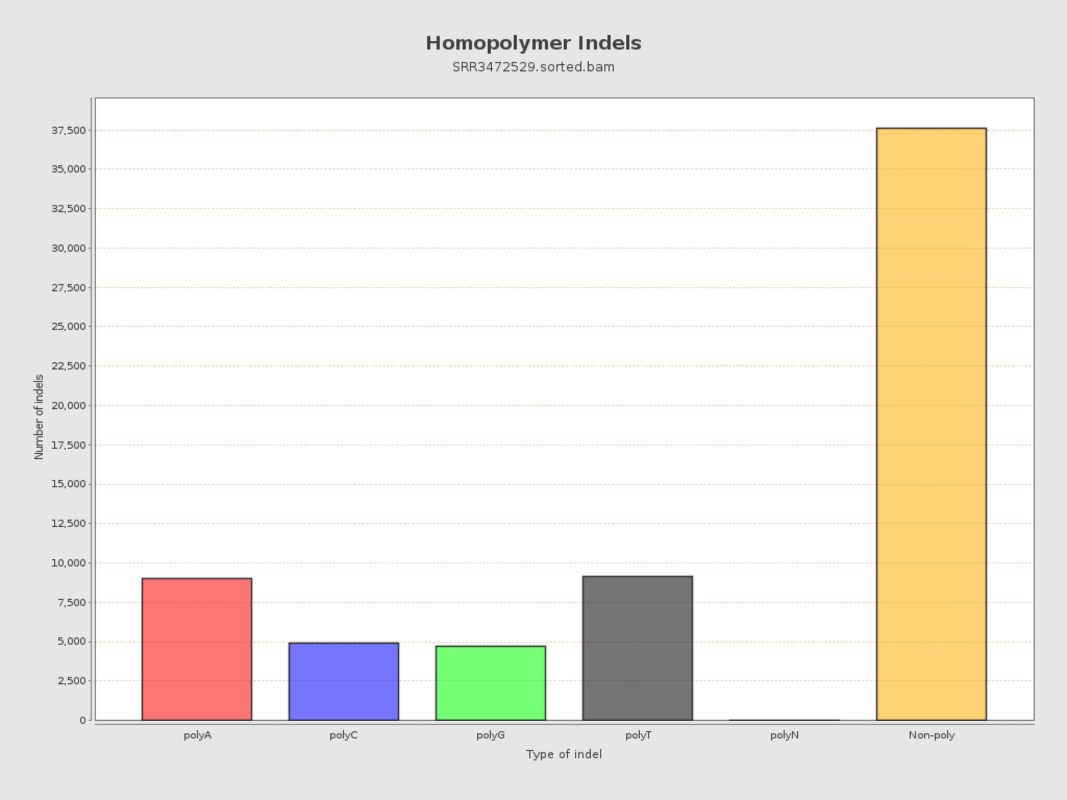
9. Results : Mapped Reads GC-content Distribution



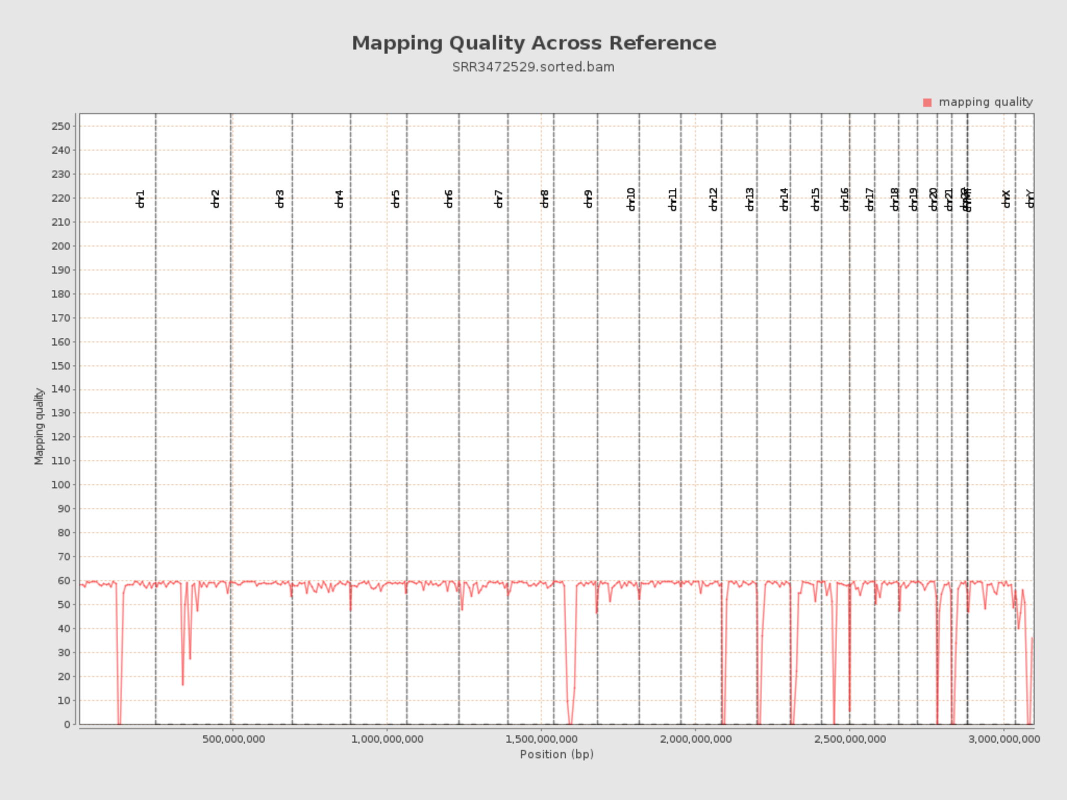
10. Results : Mapped Reads Clipping Profile



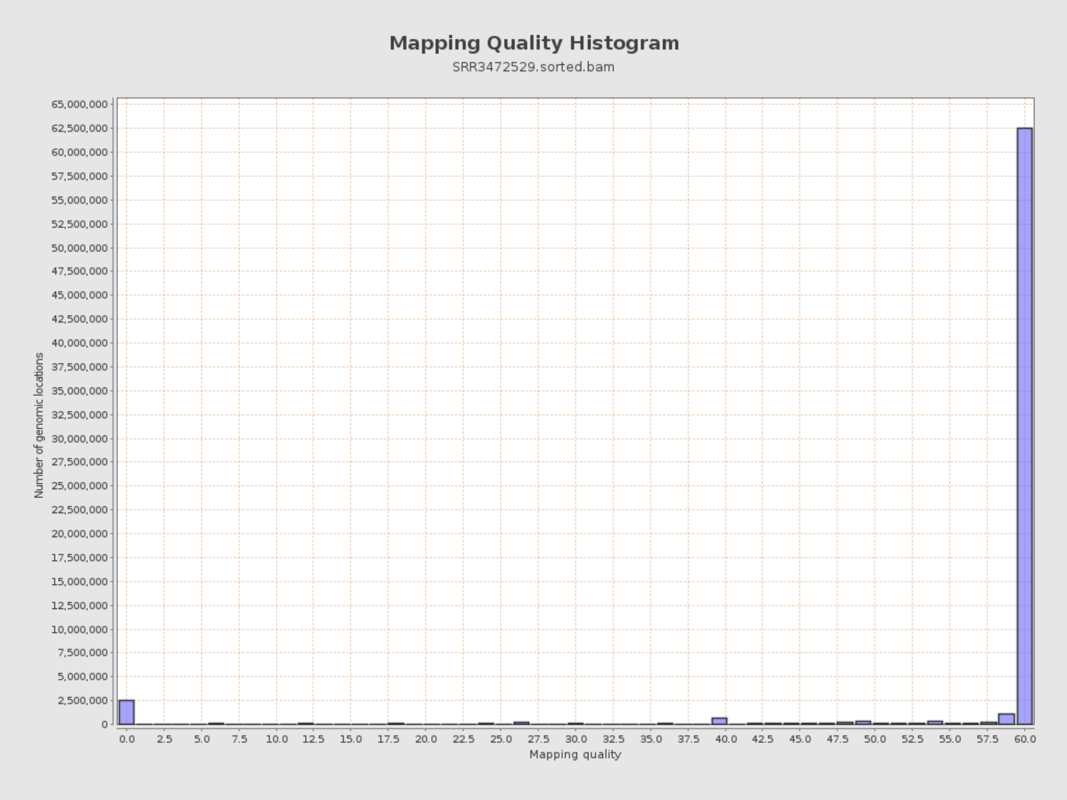
11. Results : Homopolymer Indels



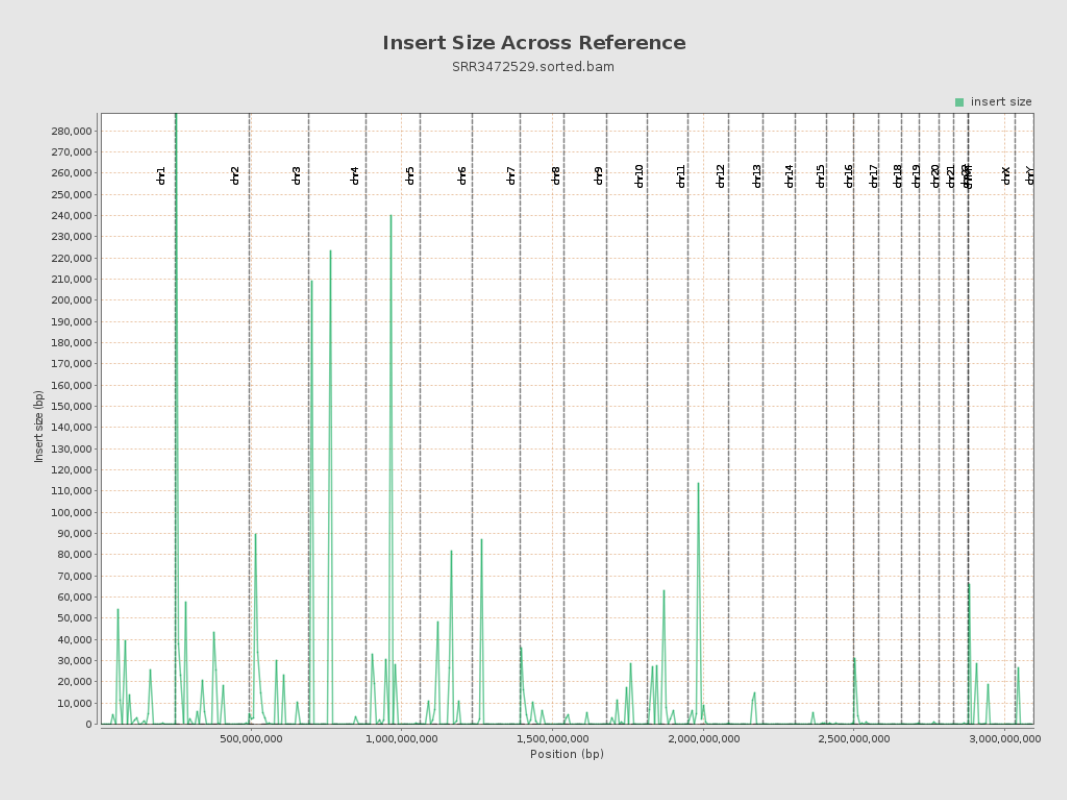
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram