Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 01:09:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472662.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_SRR3472662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472662_1.fastq.gz SRR3472662_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 01:09:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,631,238
Mapped reads	17,473,388 / 99.1%
Unmapped reads	157,850 / 0.9%
Mapped paired reads	17,473,388 / 99.1%
Mapped reads, first in pair	8,758,942 / 49.68%
Mapped reads, second in pair	8,714,446 / 49.43%
Mapped reads, both in pair	17,369,134 / 98.51%
Mapped reads, singletons	104,254 / 0.59%
Secondary alignments	0
Supplementary alignments	107,379 / 0.61%
Read min/max/mean length	30 / 101 / 99.77
Duplicated reads (estimated)	12,335,089 / 69.96%
Duplication rate	49.74%
Clipped reads	1,331,311 / 7.55%

2.2. ACGT Content

Number/percentage of A's	466,076,600 / 27.14%
Number/percentage of C's	394,928,644 / 22.99%
Number/percentage of T's	466,847,437 / 27.18%
Number/percentage of G's	389,342,124 / 22.67%
Number/percentage of N's	322,403 / 0.02%

GC Percentage	45.66%

2.3. Coverage

Mean	0.5549
Standard Deviation	28.4249

2.4. Mapping Quality

Mean Mapping Quality	54.56

2.5. Insert size

Mean	27,518.41
Standard Deviation	1,701,420.39
P25/Median/P75	153 / 209 / 282

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,830,319
Insertions	114,784
Mapped reads with at least one insertion	0.65%
Deletions	98,055
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.12%

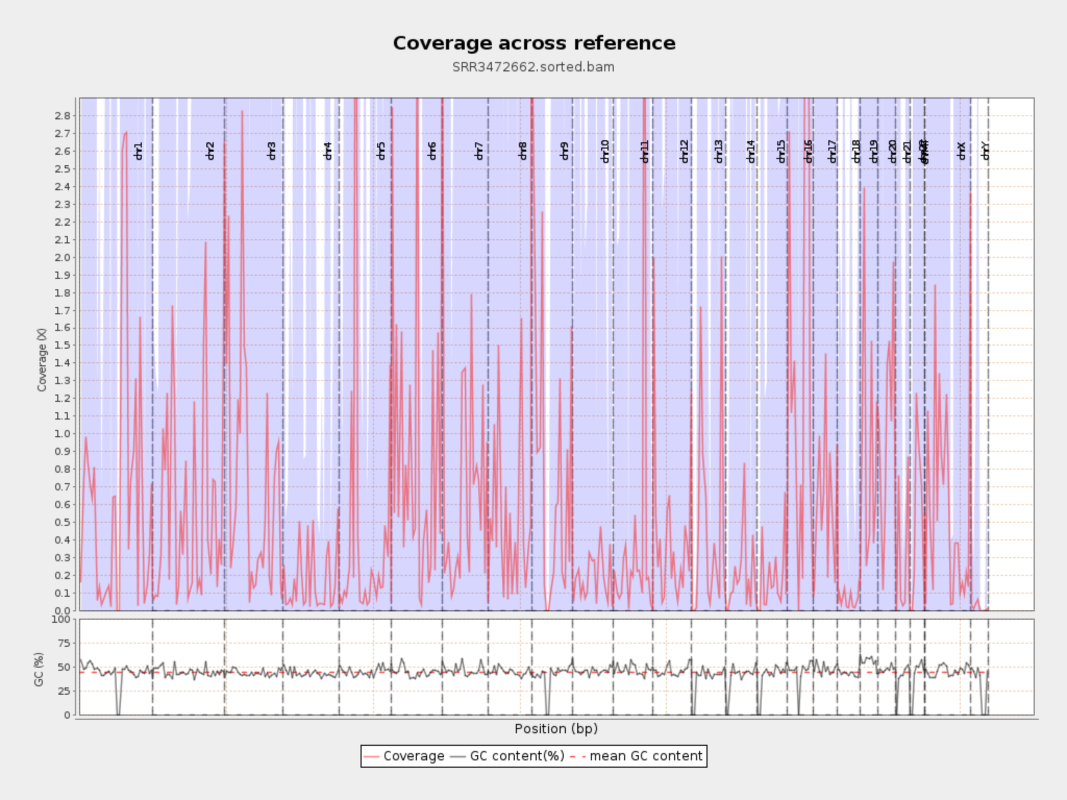
2.7. Chromosome stats

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

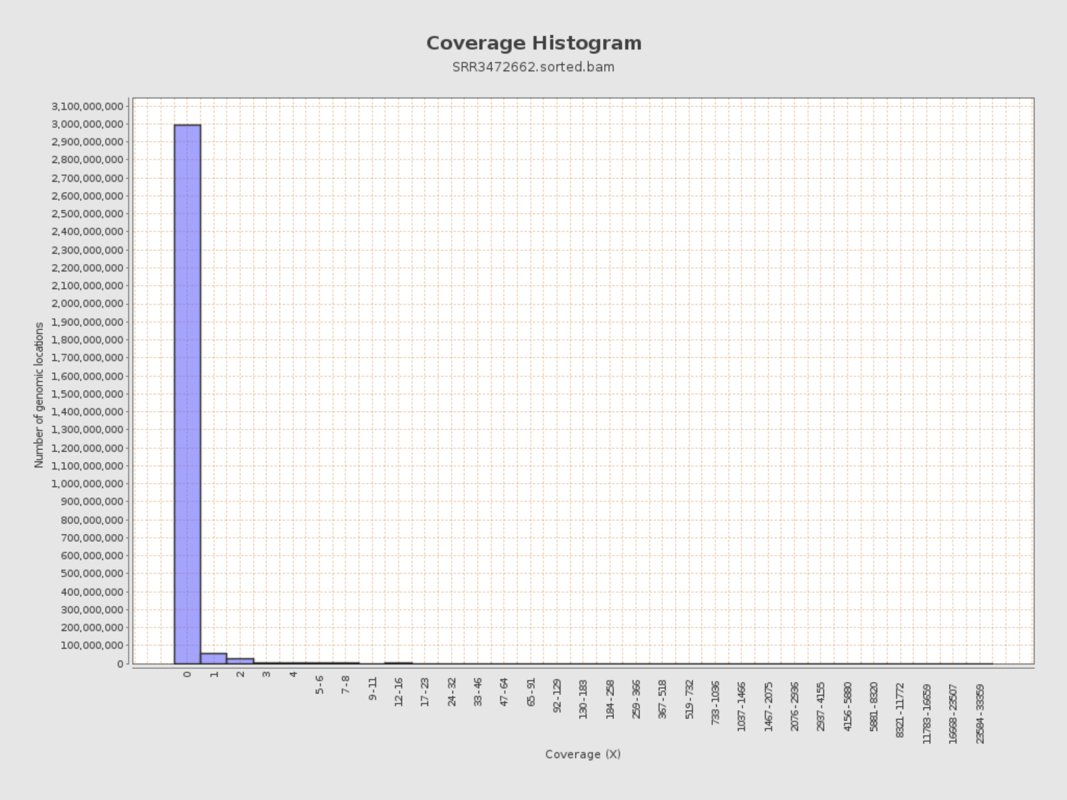
		bases	coverage	deviation
chr1	249250621	167912816	0.6737	23.9395
chr2	243199373	138857249	0.571	29.7905
chr3	198022430	153924067	0.7773	23.7197
chr4	191154276	31713832	0.1659	8.0352
chr5	180915260	84738837	0.4684	28.0888
chr6	171115067	151024981	0.8826	30.5147
chr7	159138663	110655698	0.6953	31.6129
chr8	146364022	78026094	0.5331	21.7564
chr9	141213431	124777847	0.8836	32.4179
chr10	135534747	25576656	0.1887	7.7045
chr11	135006516	60186126	0.4458	43.3709
chr12	133851895	54066596	0.4039	14.2703
chr13	115169878	54907546	0.4768	27.8097
chr14	107349540	20403393	0.1901	7.0216
chr15	102531392	19252581	0.1878	11.4271
chr16	90354753	138953423	1.5379	89.0311
chr17	81195210	49265607	0.6068	17.7182
chr18	78077248	4871746	0.0624	2.4751
chr19	59128983	54684251	0.9248	27.6142
chr20	63025520	65619851	1.0412	30.2857
chr21	48129895	14201770	0.2951	23.0641
chr22	51304566	25574552	0.4985	18.9143
chrMT	16571	9084	0.5482	1.1823
chrX	155270560	87433018	0.5631	18.5779

chrY	59373566	1111968	0.0187	1.3846

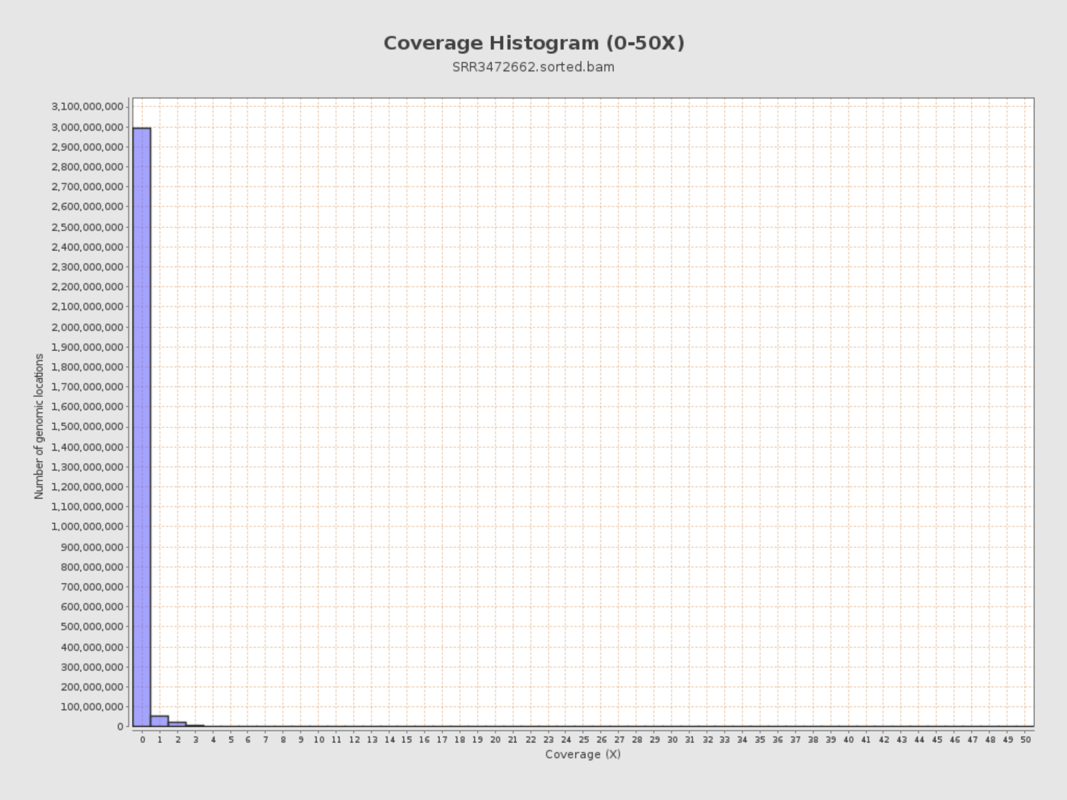
3. Results : Coverage across reference



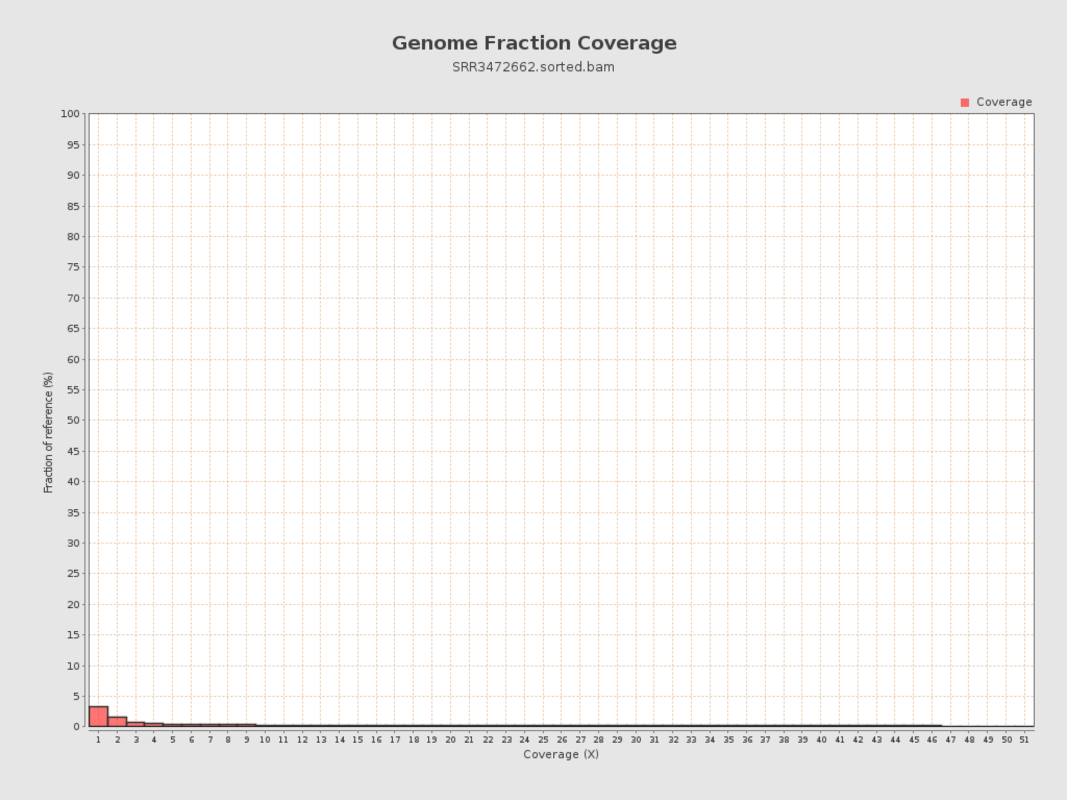
4. Results : Coverage Histogram



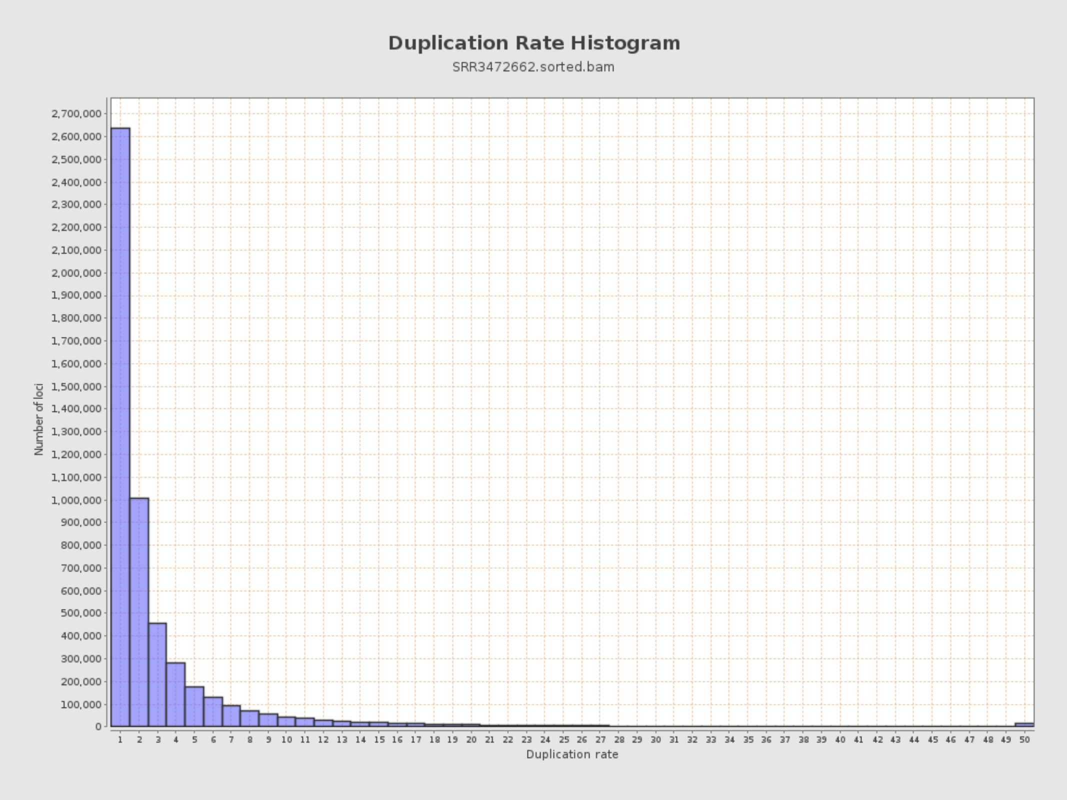
5. Results : Coverage Histogram (0-50X)



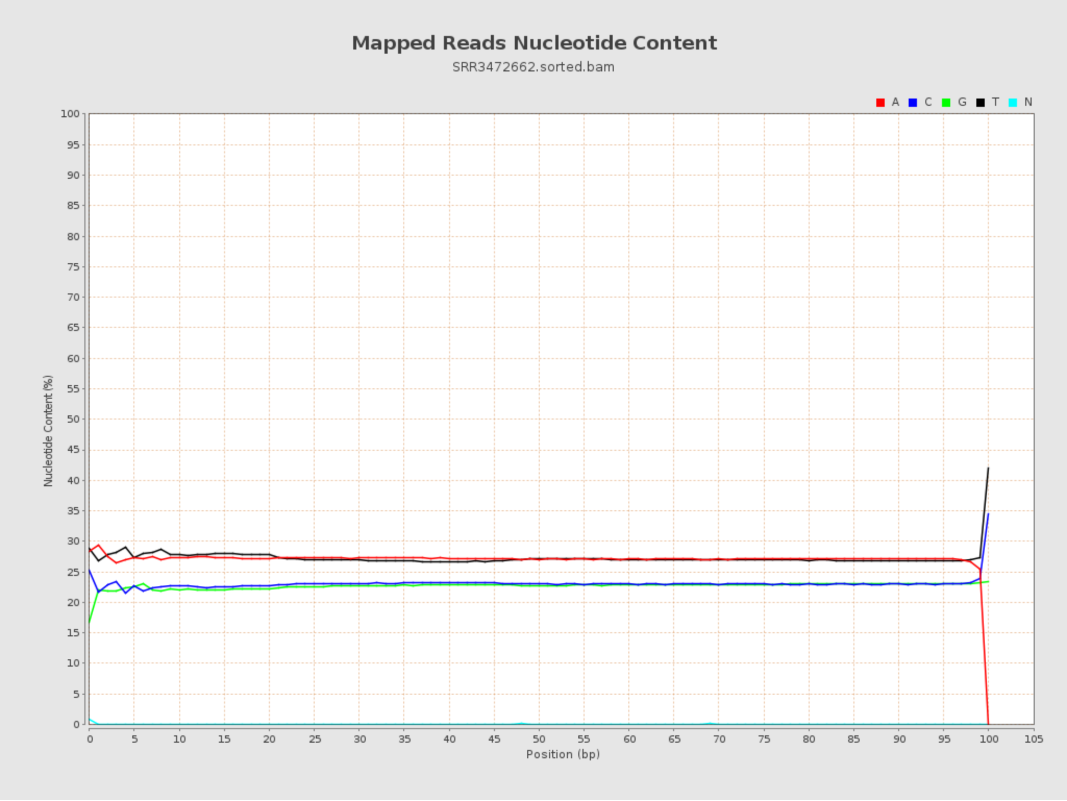
6. Results : Genome Fraction Coverage



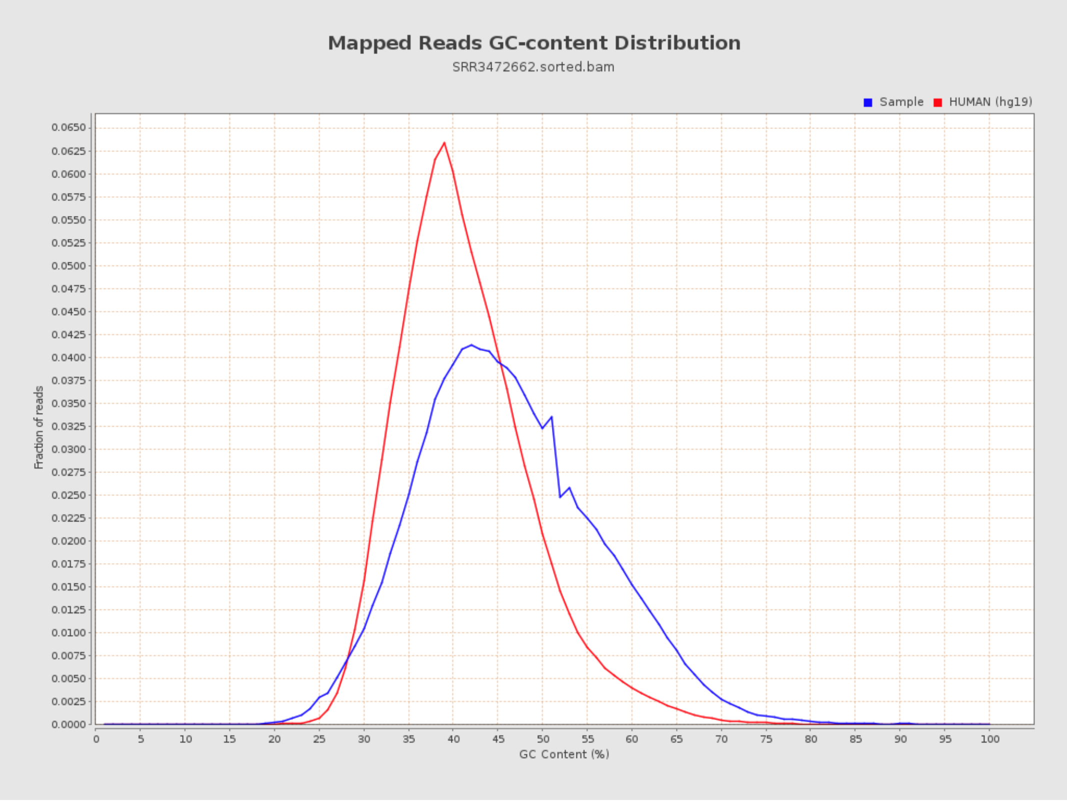
7. Results : Duplication Rate Histogram



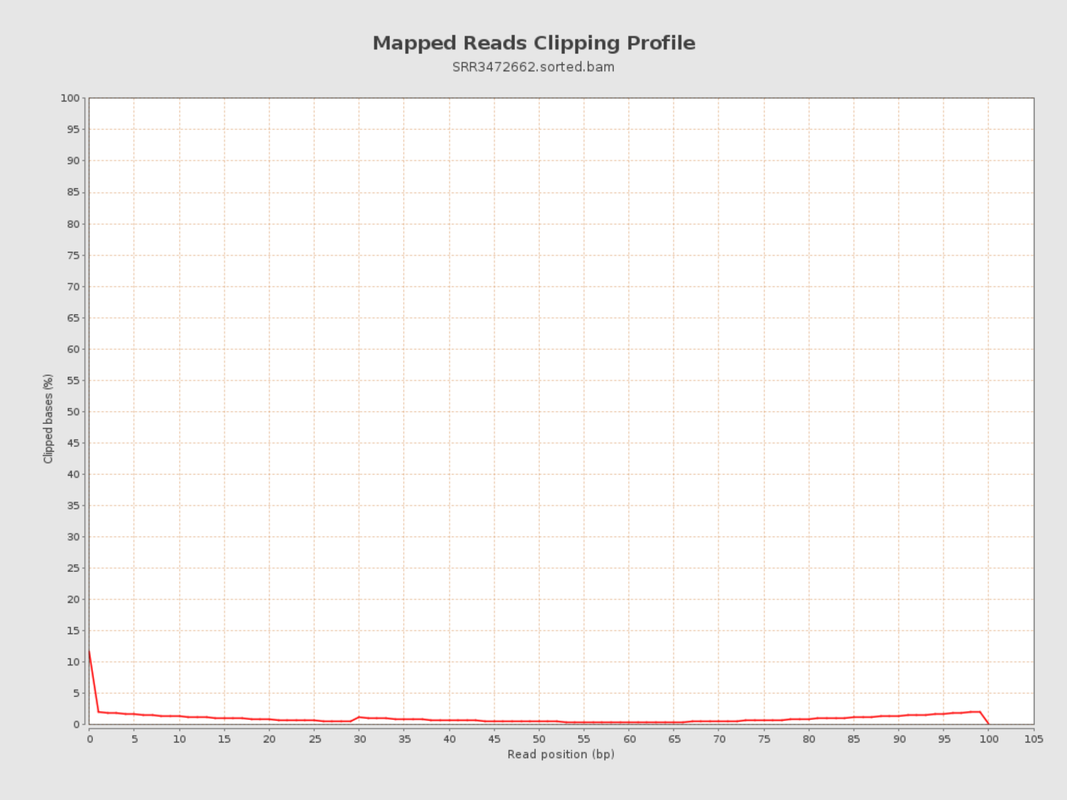
8. Results : Mapped Reads Nucleotide Content



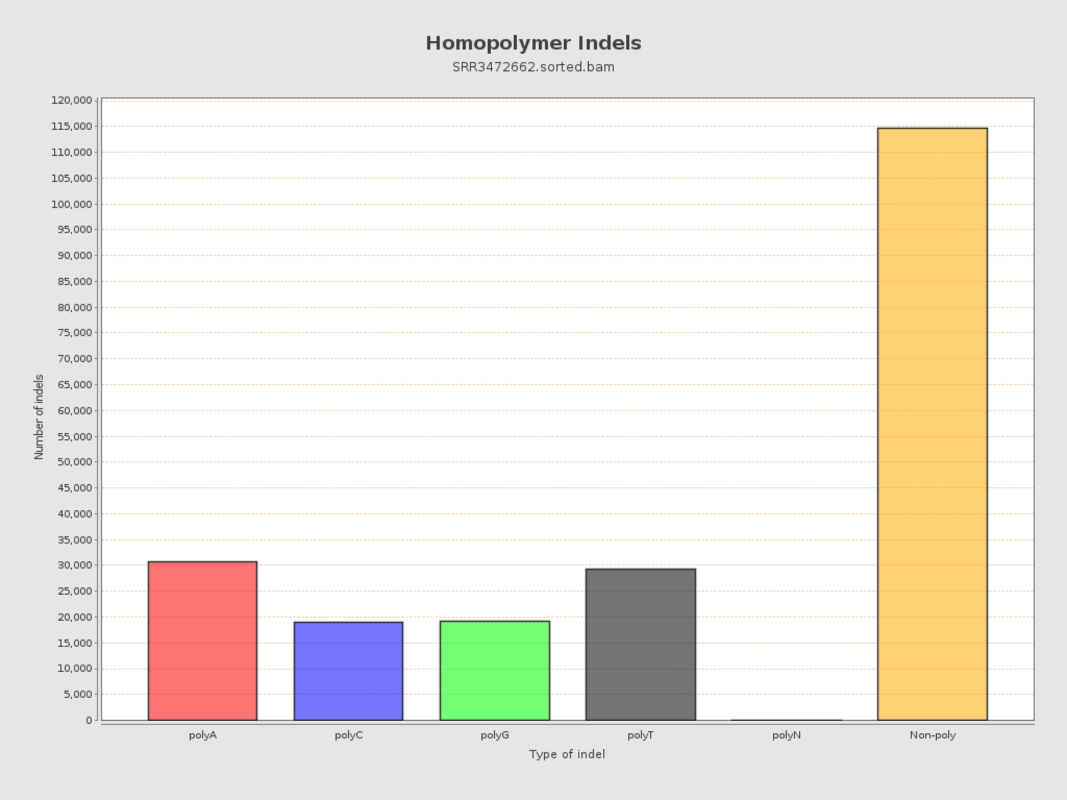
9. Results : Mapped Reads GC-content Distribution



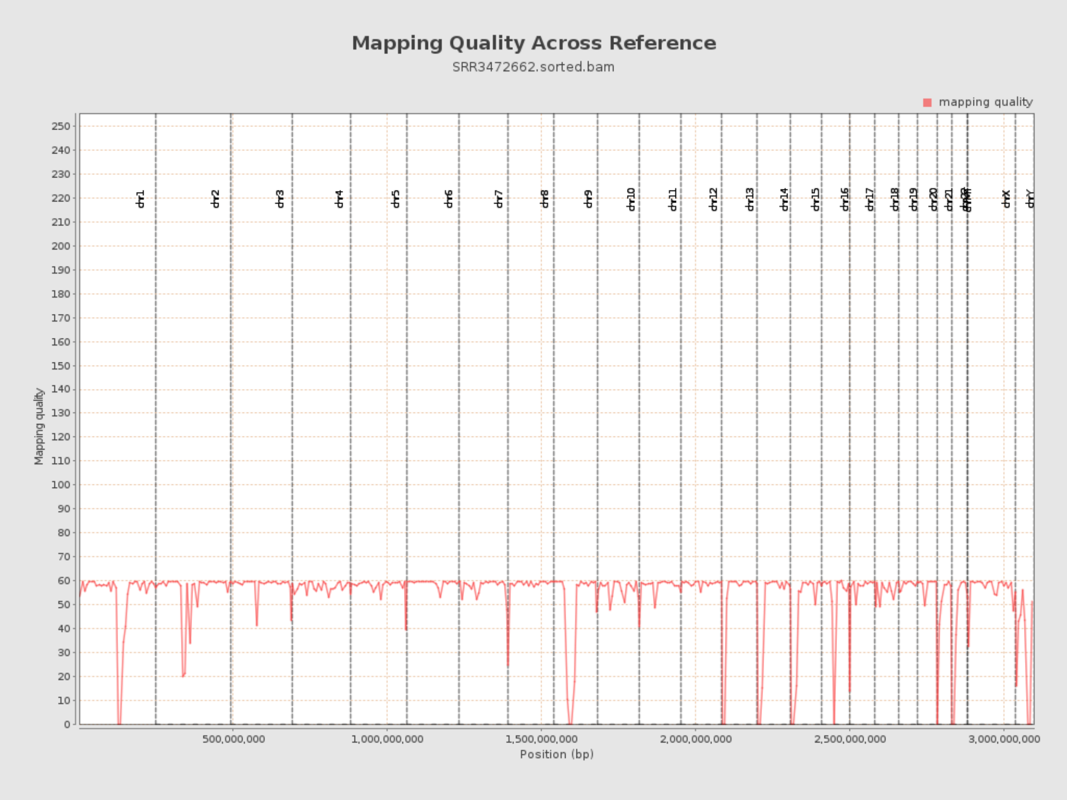
10. Results : Mapped Reads Clipping Profile



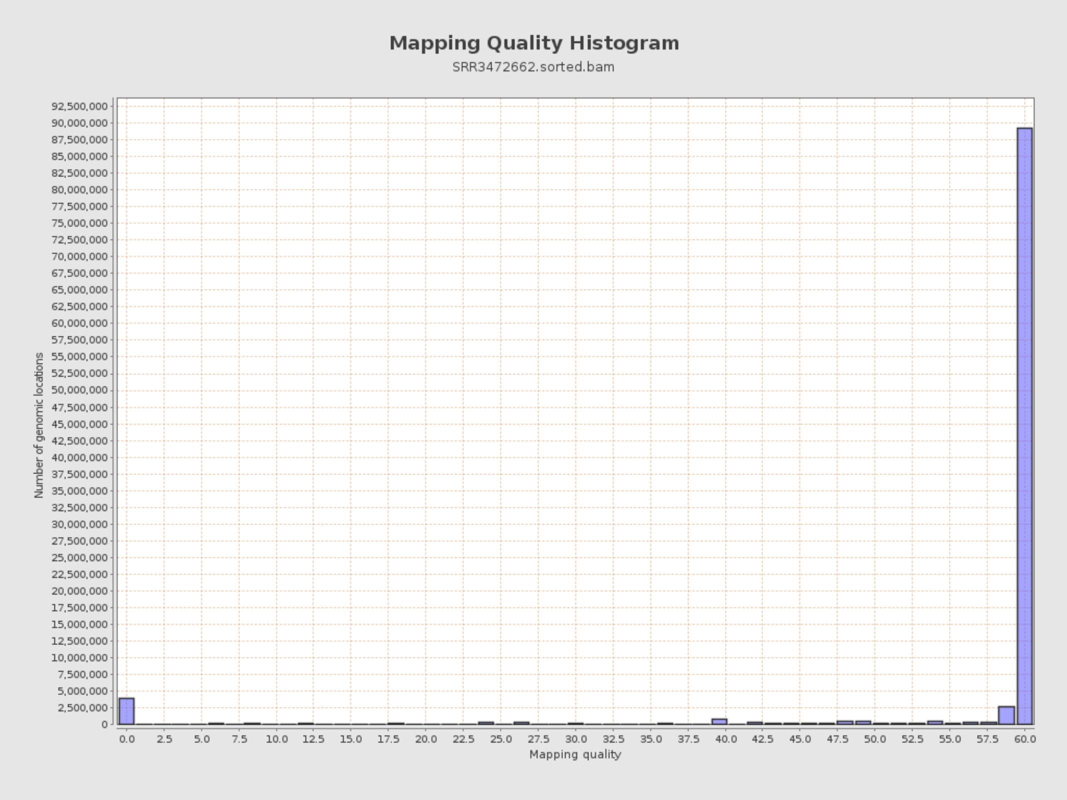
11. Results : Homopolymer Indels



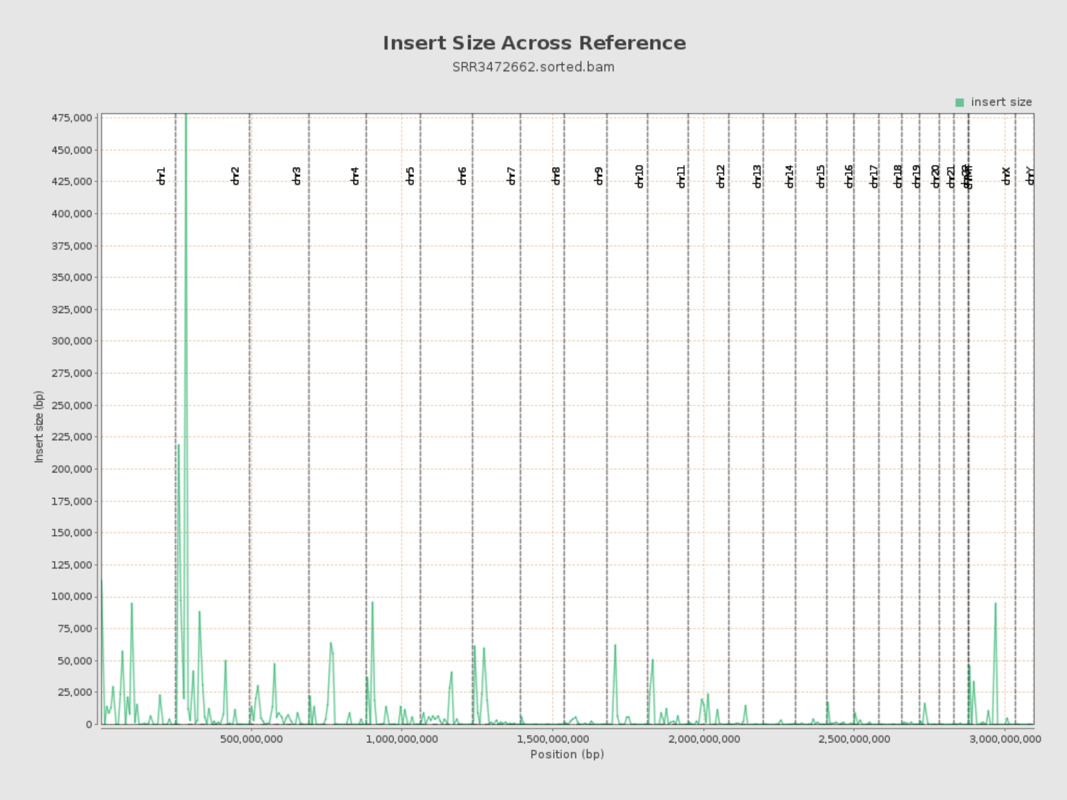
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram