Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:31:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124969.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_SRR3124969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124969_1.fastq.gz SRR3124969_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:31:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,239,730
Mapped reads	4,961,762 / 94.69%
Unmapped reads	277,968 / 5.31%
Mapped paired reads	4,961,762 / 94.69%
Mapped reads, first in pair	2,524,091 / 48.17%
Mapped reads, second in pair	2,437,671 / 46.52%
Mapped reads, both in pair	4,847,574 / 92.52%
Mapped reads, singletons	114,188 / 2.18%
Secondary alignments	0
Supplementary alignments	16,252 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	449,113 / 8.57%
Duplication rate	6.04%
Clipped reads	2,514,756 / 47.99%

2.2. ACGT Content

Number/percentage of A's	83,860,662 / 27.55%
Number/percentage of C's	54,522,561 / 17.91%
Number/percentage of T's	90,558,604 / 29.75%
Number/percentage of G's	75,407,682 / 24.78%
Number/percentage of N's	3 / 0%

GC Percentage	42.69%

2.3. Coverage

Mean	0.0984
Standard Deviation	1.1792

2.4. Mapping Quality

Mean Mapping Quality	51.5

2.5. Insert size

Mean	78,816.47
Standard Deviation	2,700,703.86
P25/Median/P75	127 / 170 / 235

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	2,186,489
Insertions	38,165
Mapped reads with at least one insertion	0.76%
Deletions	85,139
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.43%

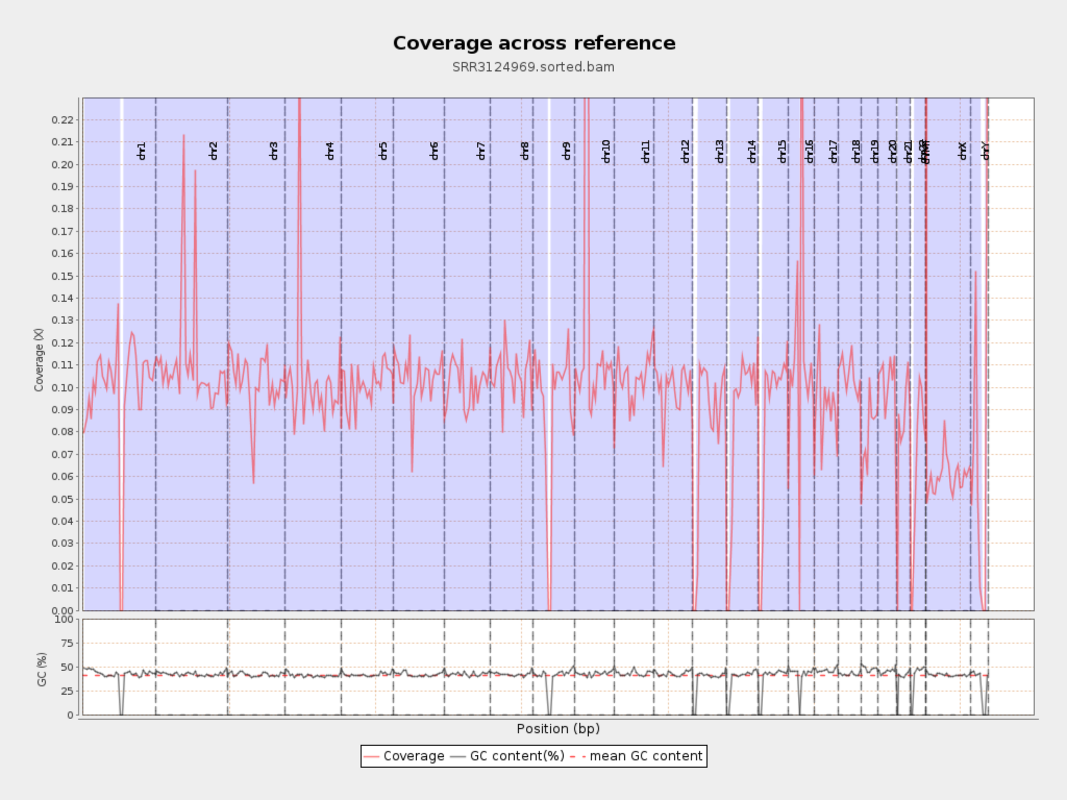
2.7. Chromosome stats

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

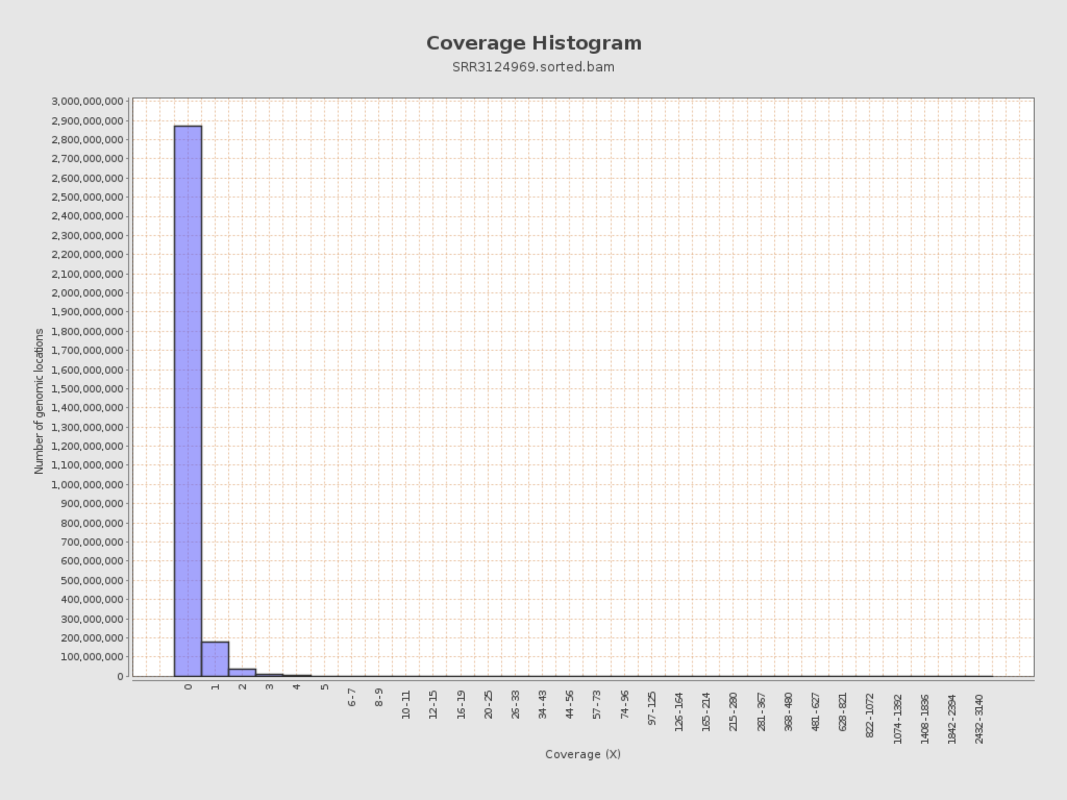
		bases	coverage	deviation
chr1	249250621	24646219	0.0989	0.6995
chr2	243199373	27262248	0.1121	1.4033
chr3	198022430	20208530	0.1021	0.4718
chr4	191154276	20128262	0.1053	0.8926
chr5	180915260	18359059	0.1015	0.4265
chr6	171115067	17871974	0.1044	0.5205
chr7	159138663	16161424	0.1016	0.6888
chr8	146364022	15462930	0.1056	0.4712
chr9	141213431	12808996	0.0907	0.7756
chr10	135534747	18042312	0.1331	4.2411
chr11	135006516	14057749	0.1041	0.5417
chr12	133851895	13384127	0.1	0.4063
chr13	115169878	9348587	0.0812	0.3563
chr14	107349540	9175263	0.0855	0.445
chr15	102531392	8786565	0.0857	0.3759
chr16	90354753	10598939	0.1173	1.7571
chr17	81195210	7581190	0.0934	0.6999
chr18	78077248	8255084	0.1057	1.1153
chr19	59128983	4706548	0.0796	0.6103
chr20	63025520	6486039	0.1029	0.5731
chr21	48129895	3959971	0.0823	0.5364
chr22	51304566	3296723	0.0643	0.3867
chrMT	16571	152667	9.2129	6.7972
chrX	155270560	9375987	0.0604	0.4054

chrY	59373566	4371410	0.0736	1.7266

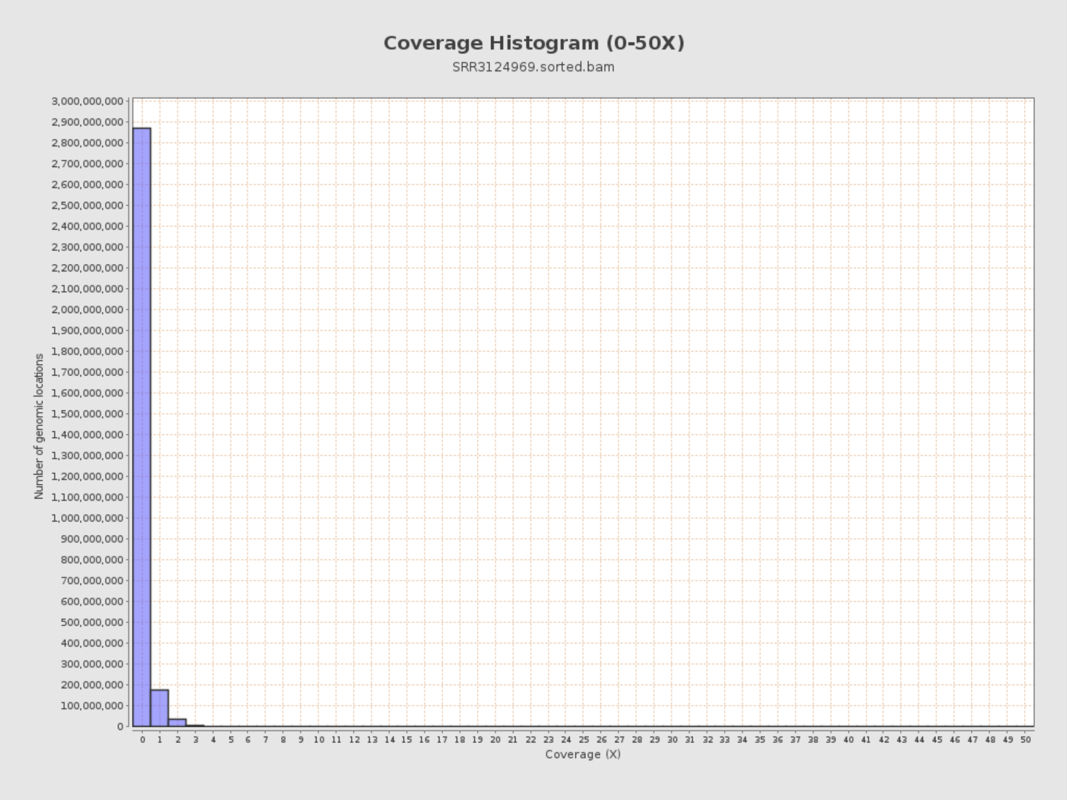
3. Results : Coverage across reference



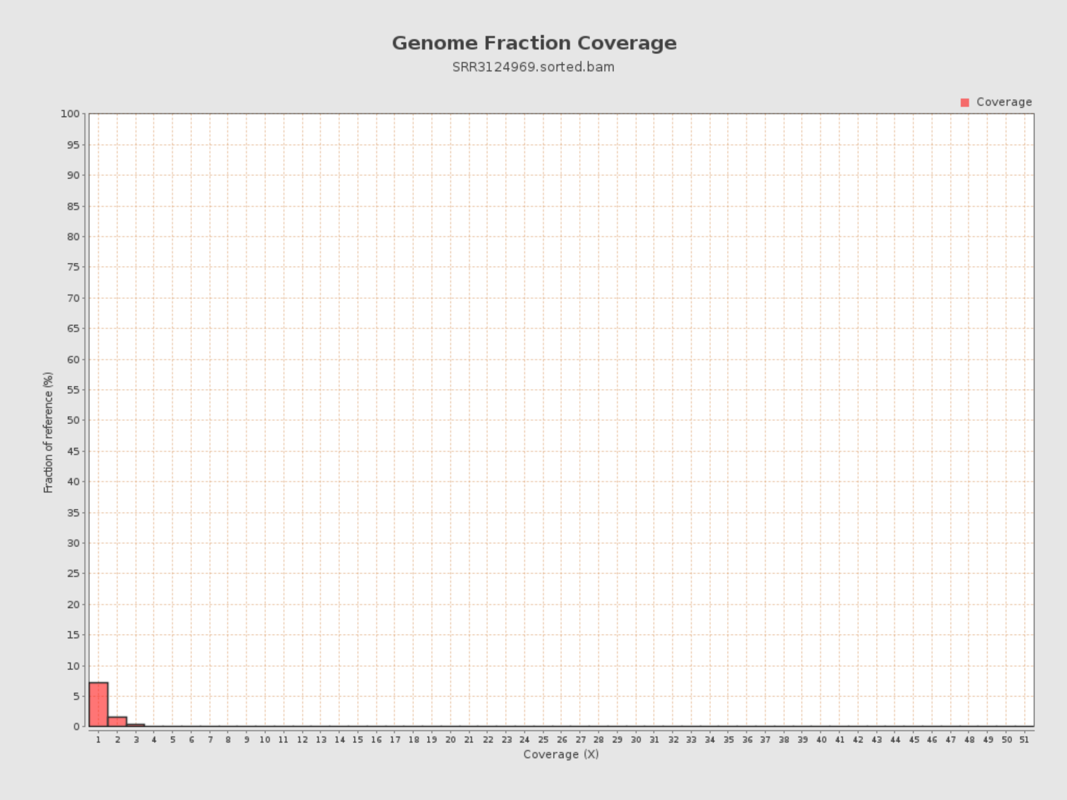
4. Results : Coverage Histogram



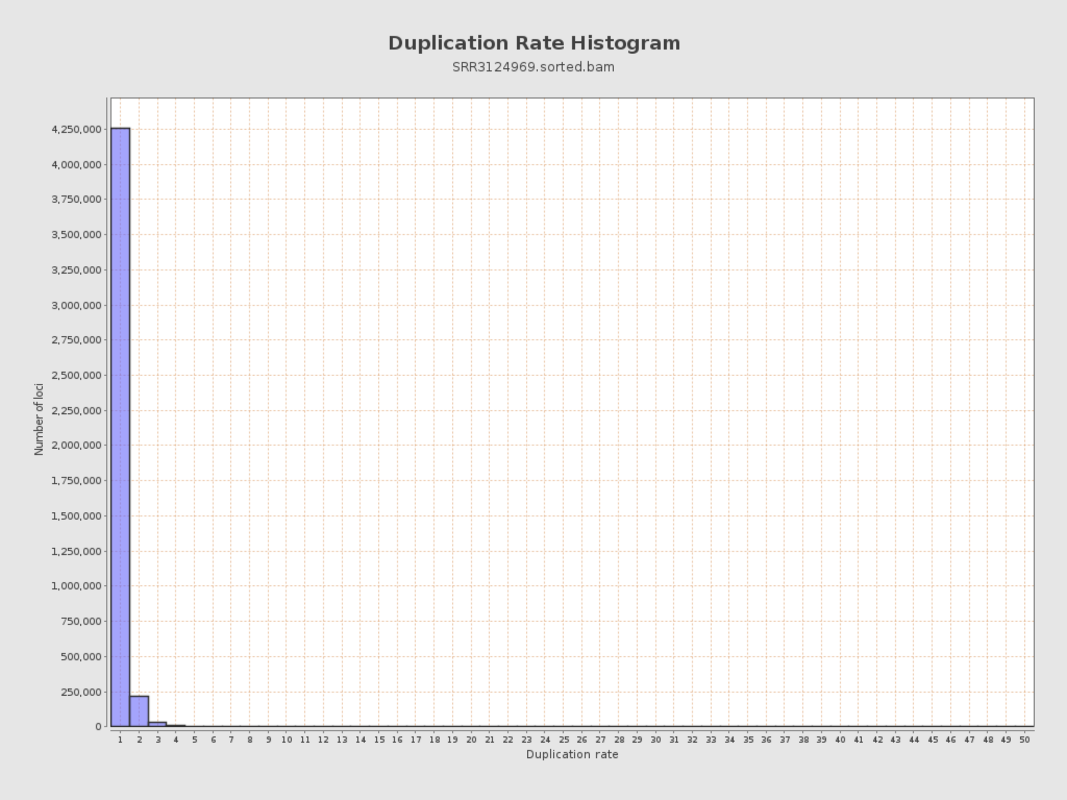
5. Results : Coverage Histogram (0-50X)



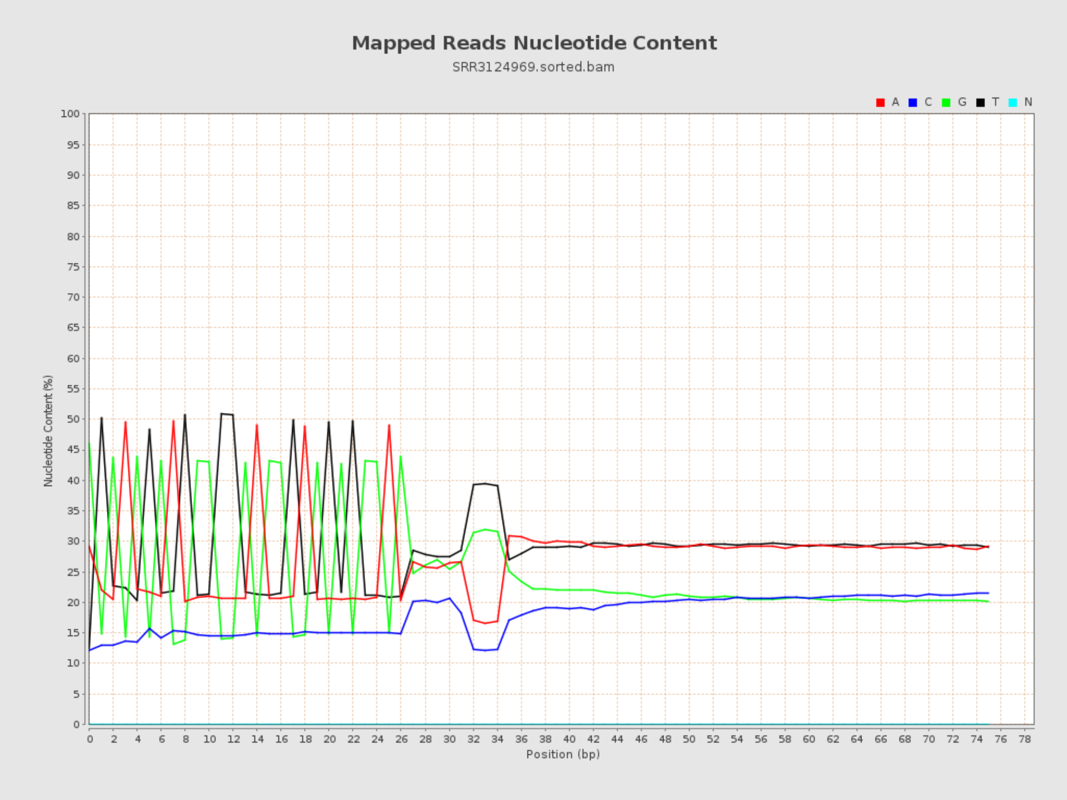
6. Results : Genome Fraction Coverage



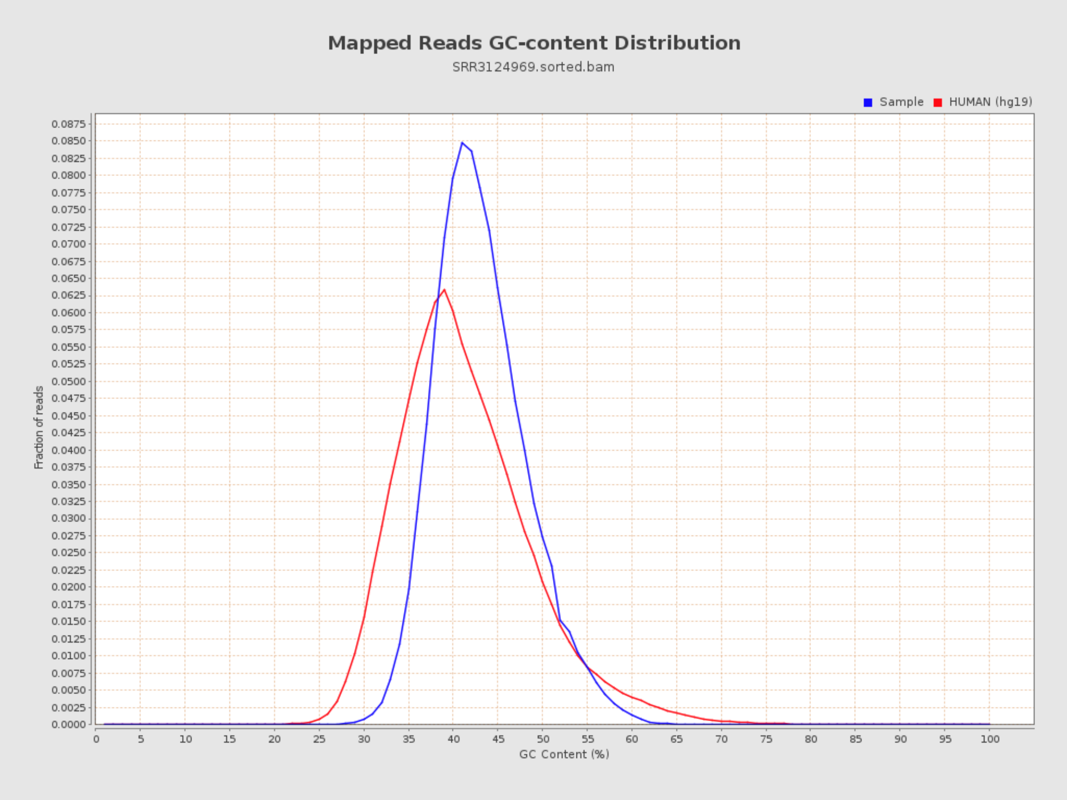
7. Results : Duplication Rate Histogram



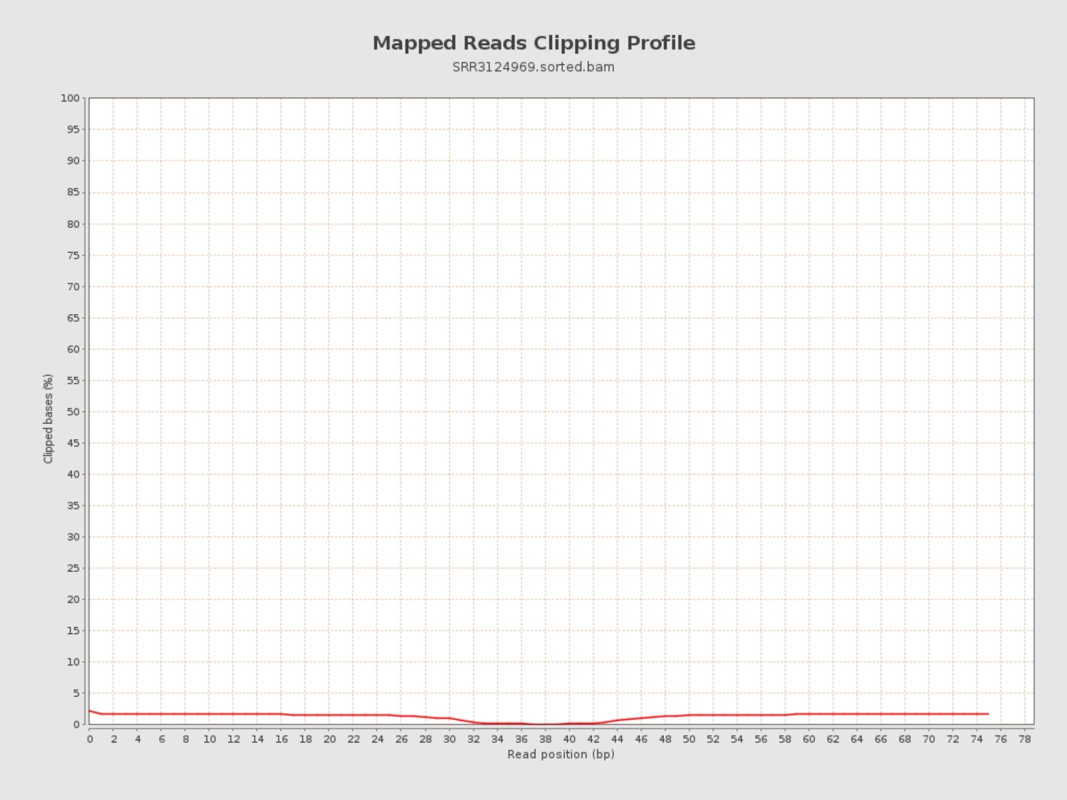
8. Results : Mapped Reads Nucleotide Content



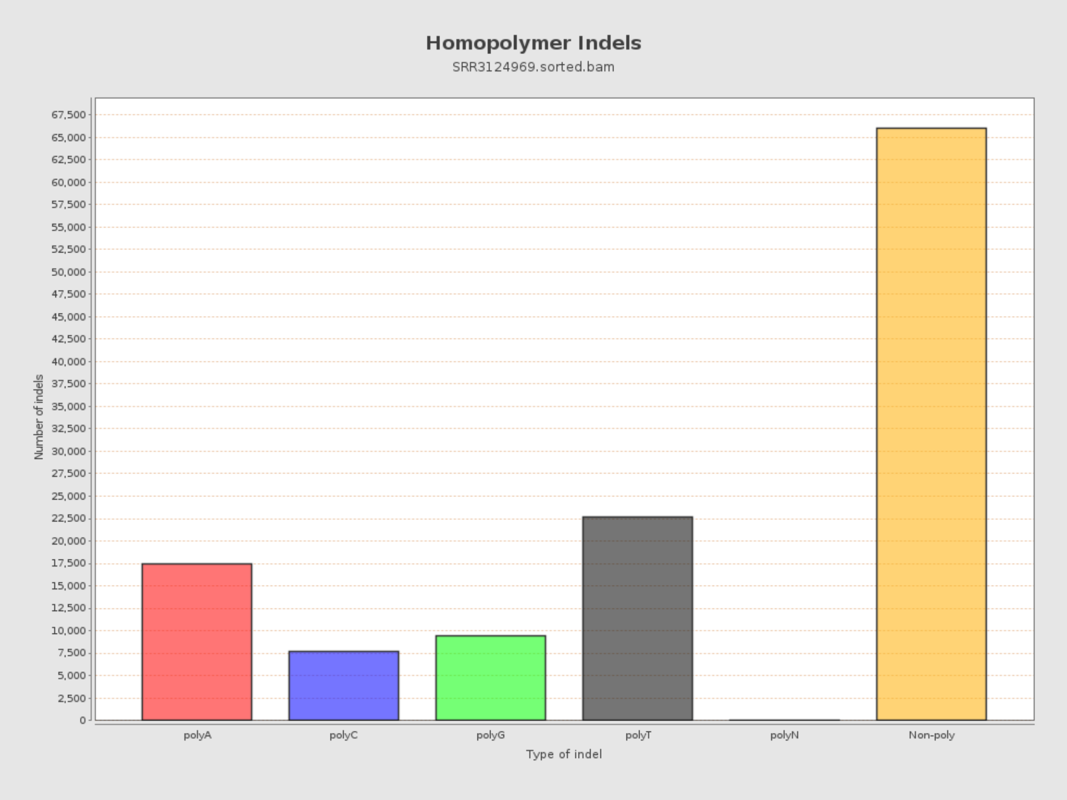
9. Results : Mapped Reads GC-content Distribution



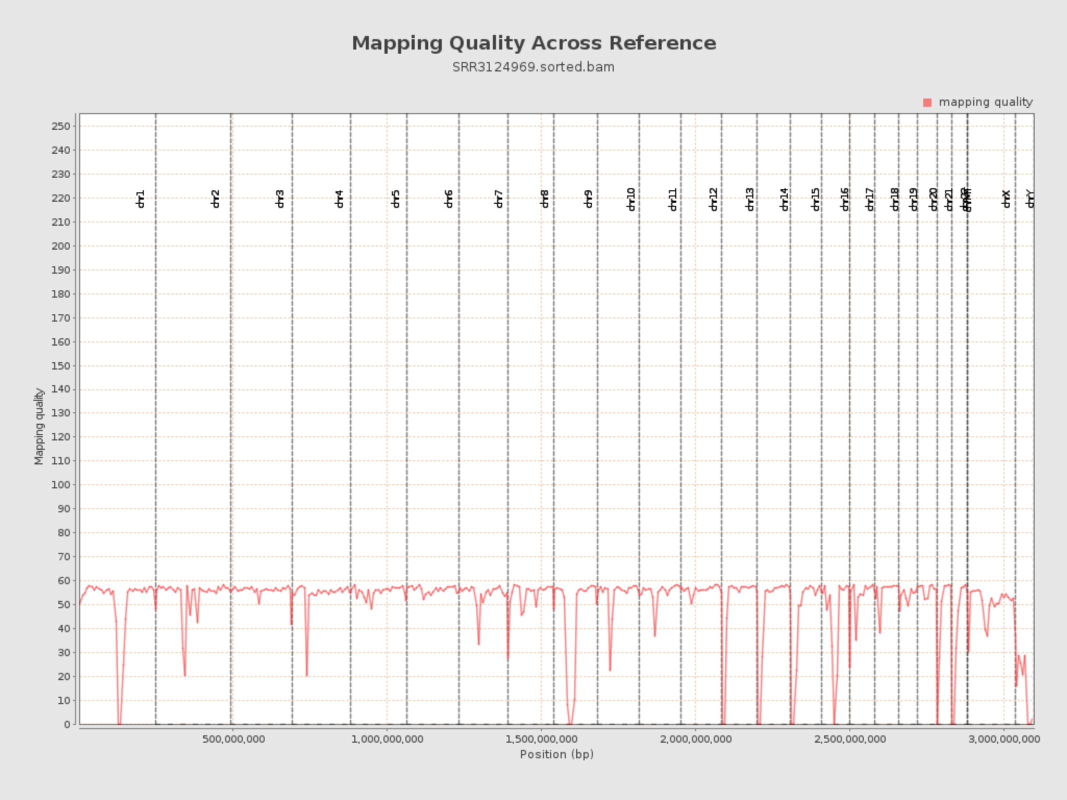
10. Results : Mapped Reads Clipping Profile



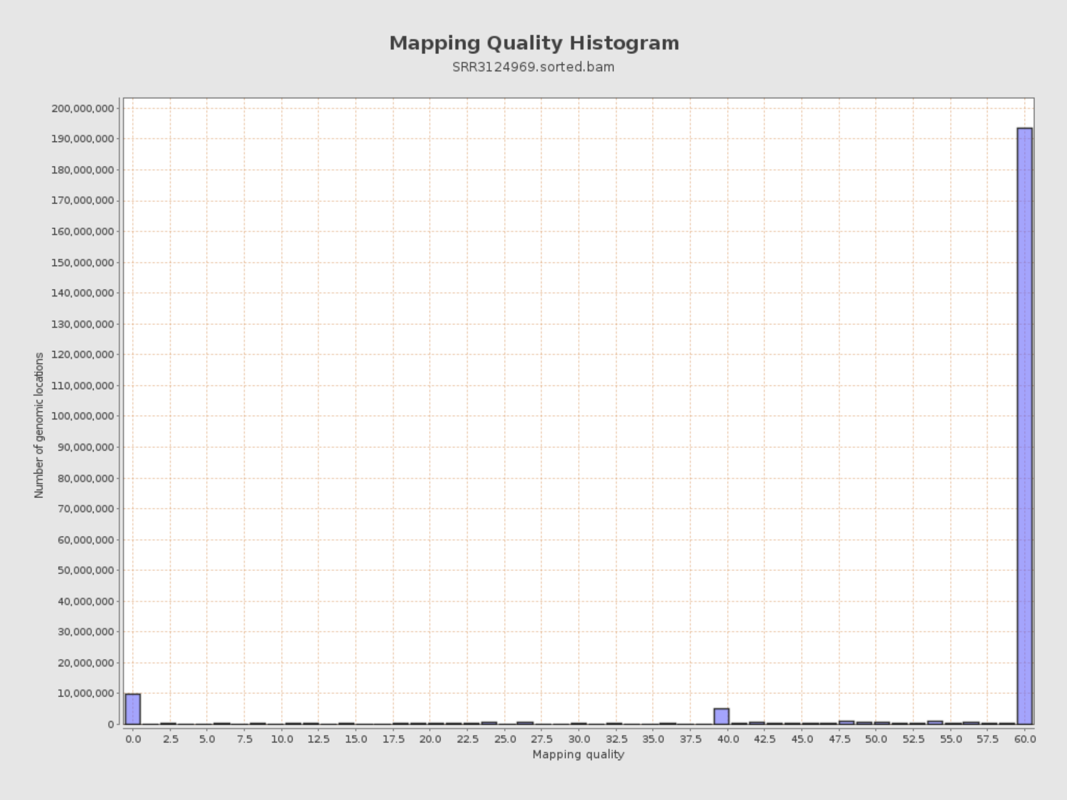
11. Results : Homopolymer Indels



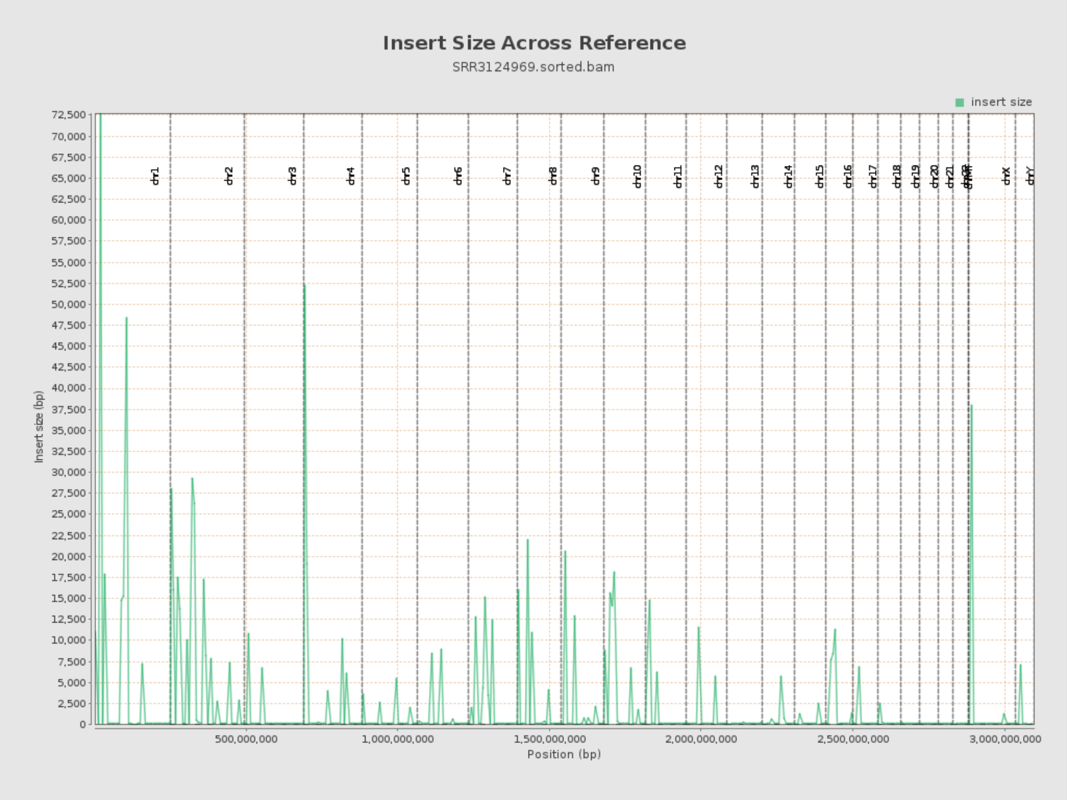
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram