Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:08:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124966.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_SRR3124966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124966_1.fastq.gz SRR3124966_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:08:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,871,382
Mapped reads	3,730,796 / 96.37%
Unmapped reads	140,586 / 3.63%
Mapped paired reads	3,730,796 / 96.37%
Mapped reads, first in pair	1,896,152 / 48.98%
Mapped reads, second in pair	1,834,644 / 47.39%
Mapped reads, both in pair	3,647,660 / 94.22%
Mapped reads, singletons	83,136 / 2.15%
Secondary alignments	0
Supplementary alignments	13,739 / 0.35%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	210,437 / 5.44%
Duplication rate	3.28%
Clipped reads	1,938,510 / 50.07%

2.2. ACGT Content

Number/percentage of A's	63,198,048 / 27.73%
Number/percentage of C's	40,097,434 / 17.6%
Number/percentage of T's	68,688,447 / 30.14%
Number/percentage of G's	55,890,578 / 24.53%
Number/percentage of N's	1 / 0%

GC Percentage	42.12%

2.3. Coverage

Mean	0.0736
Standard Deviation	0.8157

2.4. Mapping Quality

Mean Mapping Quality	51.5

2.5. Insert size

Mean	87,675.2
Standard Deviation	2,841,140.13
P25/Median/P75	128 / 171 / 233

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	1,636,053
Insertions	29,012
Mapped reads with at least one insertion	0.77%
Deletions	68,876
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.1%

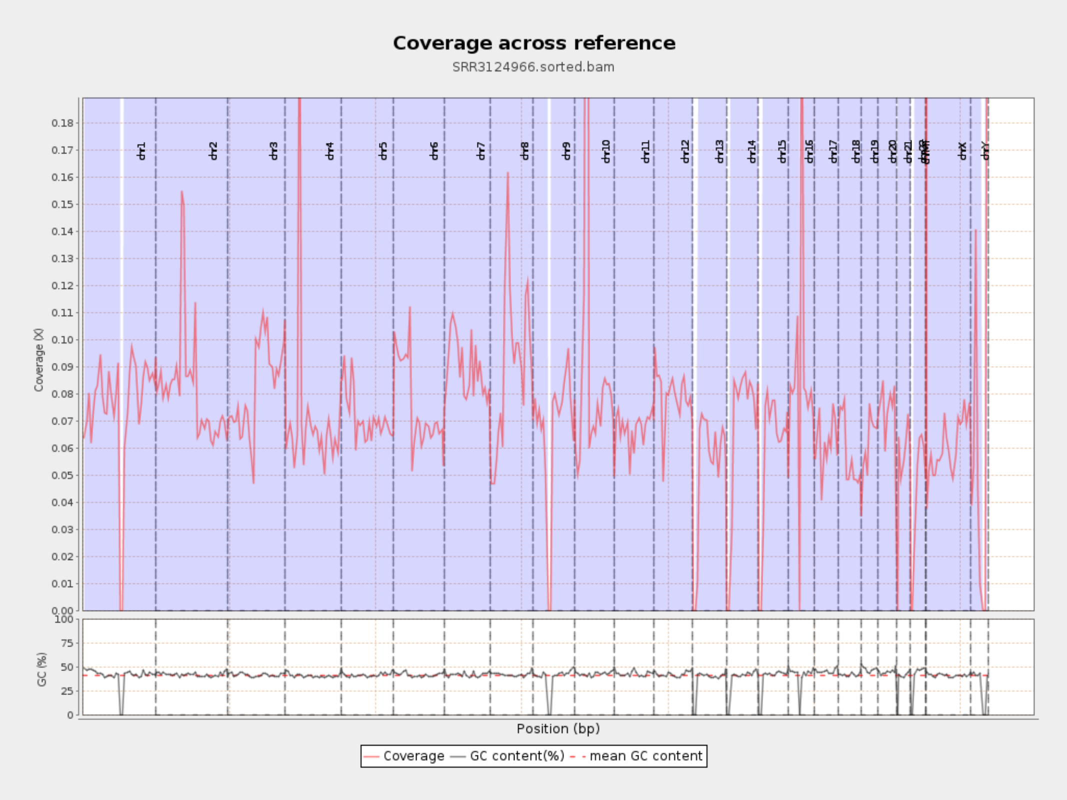
2.7. Chromosome stats

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

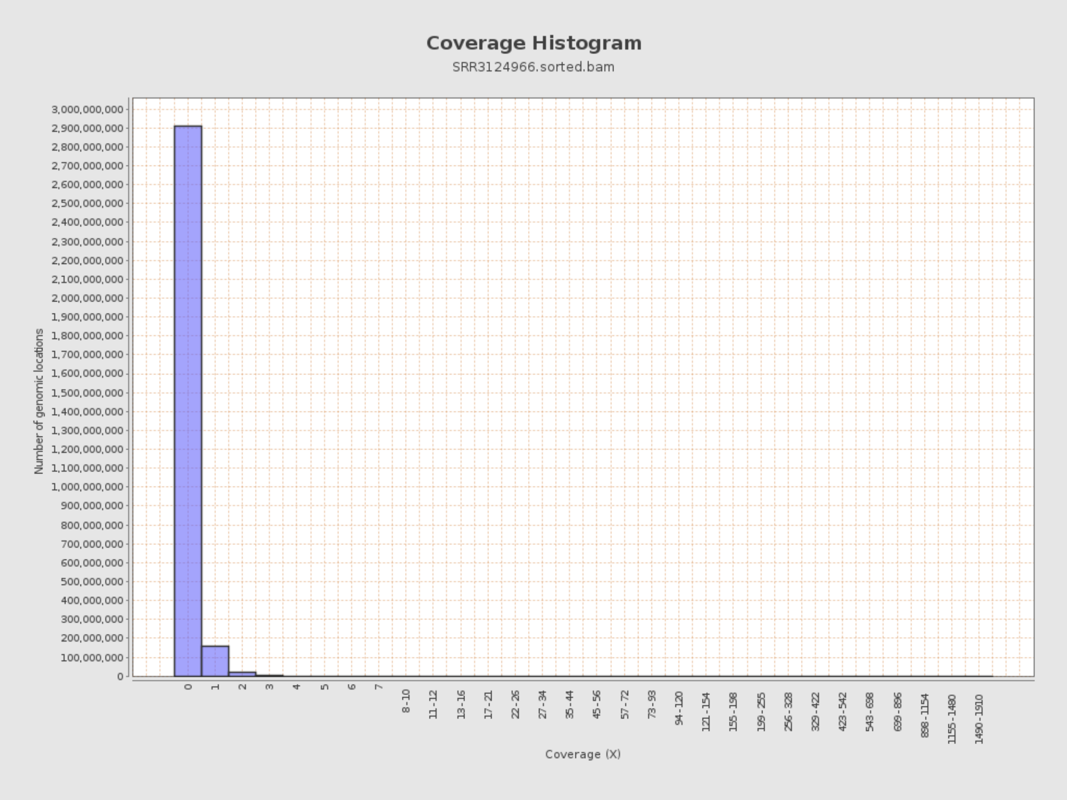
		bases	coverage	deviation
chr1	249250621	18839269	0.0756	0.4706
chr2	243199373	19925015	0.0819	0.9243
chr3	198022430	16255522	0.0821	0.3559
chr4	191154276	13662063	0.0715	0.8615
chr5	180915260	12944766	0.0716	0.3129
chr6	171115067	13040194	0.0762	0.3706
chr7	159138663	14234241	0.0894	0.5217
chr8	146364022	13312509	0.091	0.3768
chr9	141213431	9457550	0.067	0.4871
chr10	135534747	12849018	0.0948	2.7297
chr11	135006516	9046113	0.067	0.3453
chr12	133851895	10688248	0.0799	0.3256
chr13	115169878	6049323	0.0525	0.2578
chr14	107349540	7220435	0.0673	0.3254
chr15	102531392	5899644	0.0575	0.2791
chr16	90354753	8086078	0.0895	1.3558
chr17	81195210	5065970	0.0624	0.4468
chr18	78077248	4541058	0.0582	0.6359
chr19	59128983	3684683	0.0623	0.4265
chr20	63025520	4696757	0.0745	0.4145
chr21	48129895	2630916	0.0547	0.4805
chr22	51304566	2153189	0.042	0.2658
chrMT	16571	100364	6.0566	4.2432
chrX	155270560	9414174	0.0606	0.3311

chrY	59373566	4189917	0.0706	1.6176

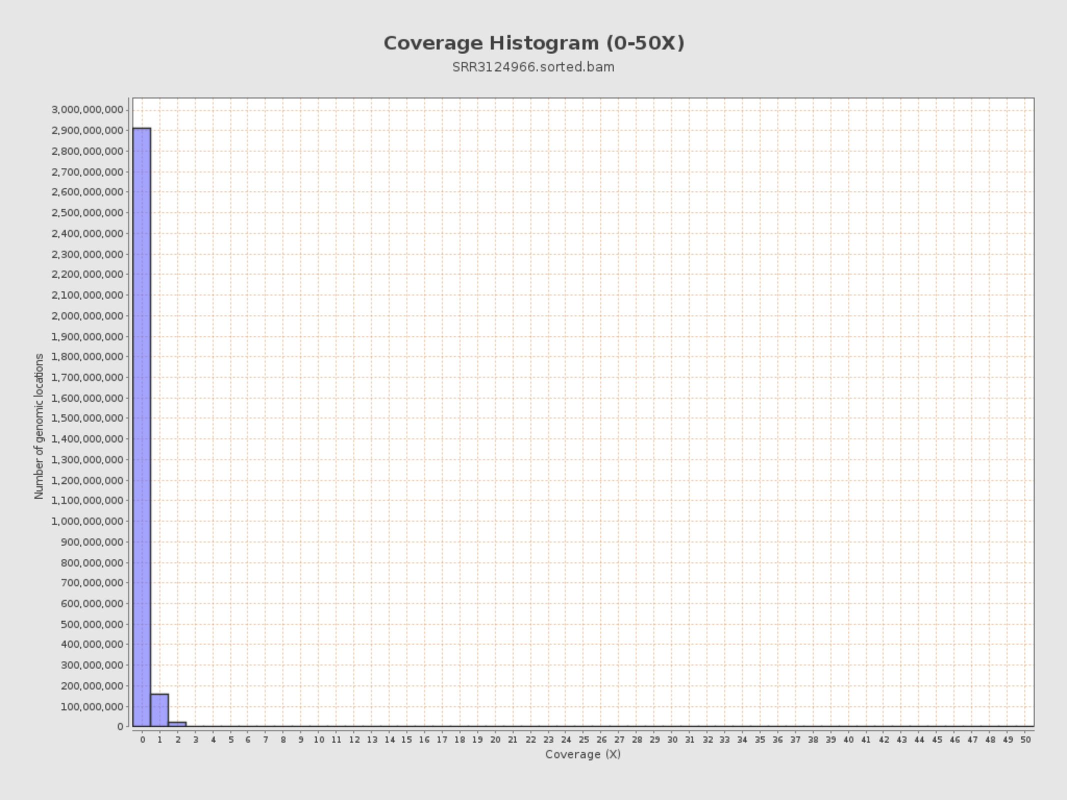
3. Results : Coverage across reference



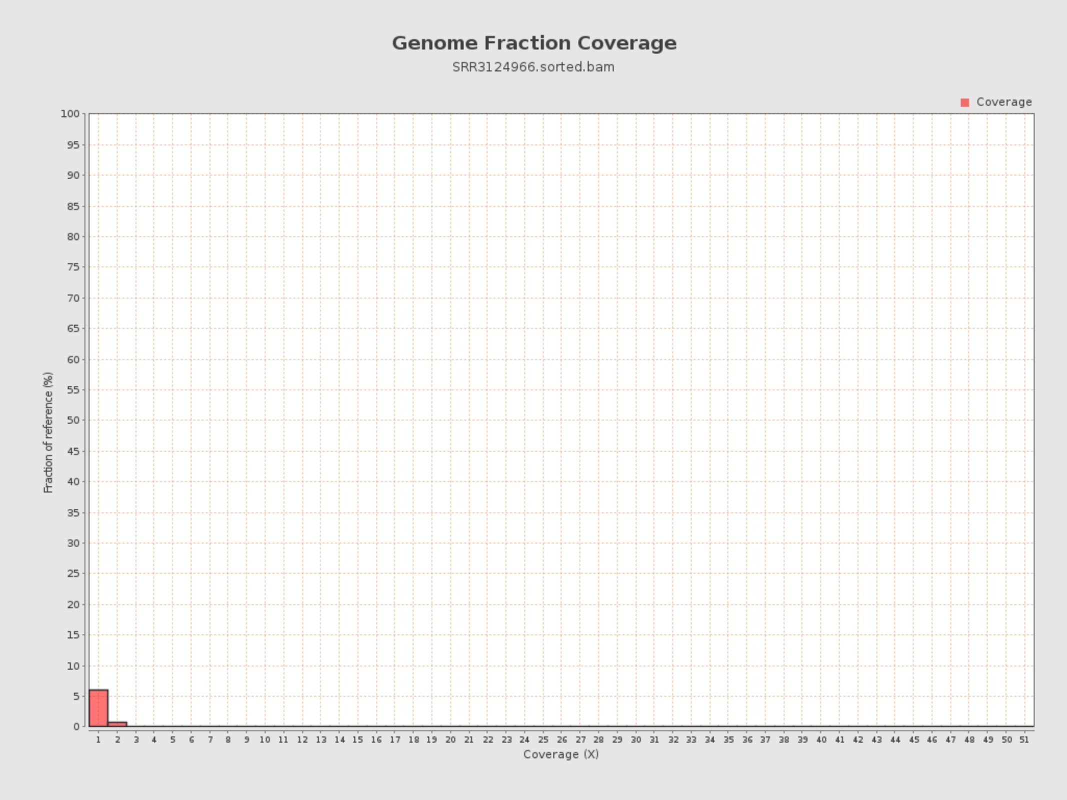
4. Results : Coverage Histogram



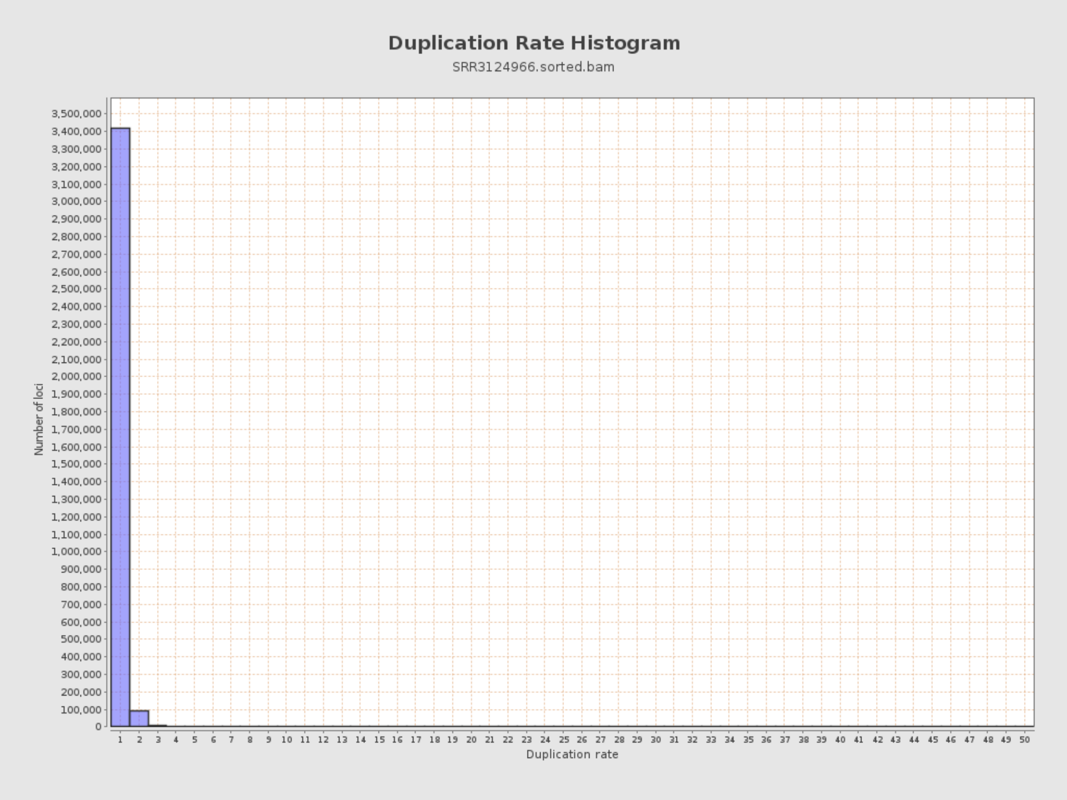
5. Results : Coverage Histogram (0-50X)



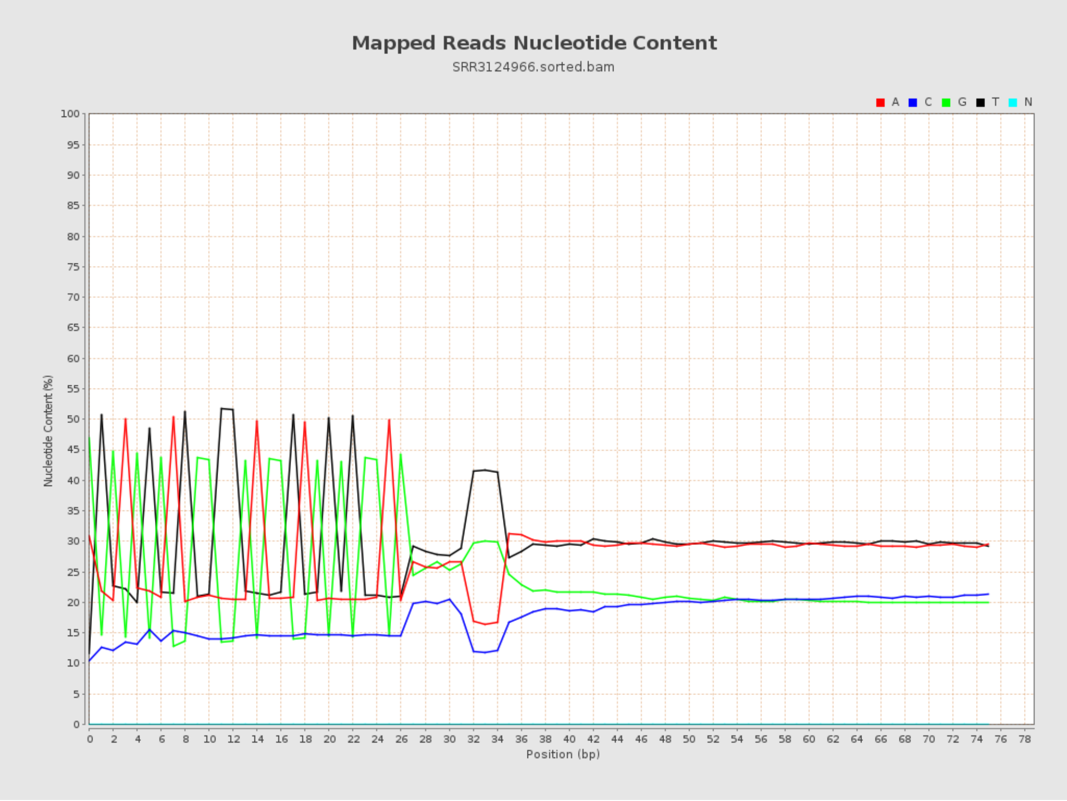
6. Results : Genome Fraction Coverage



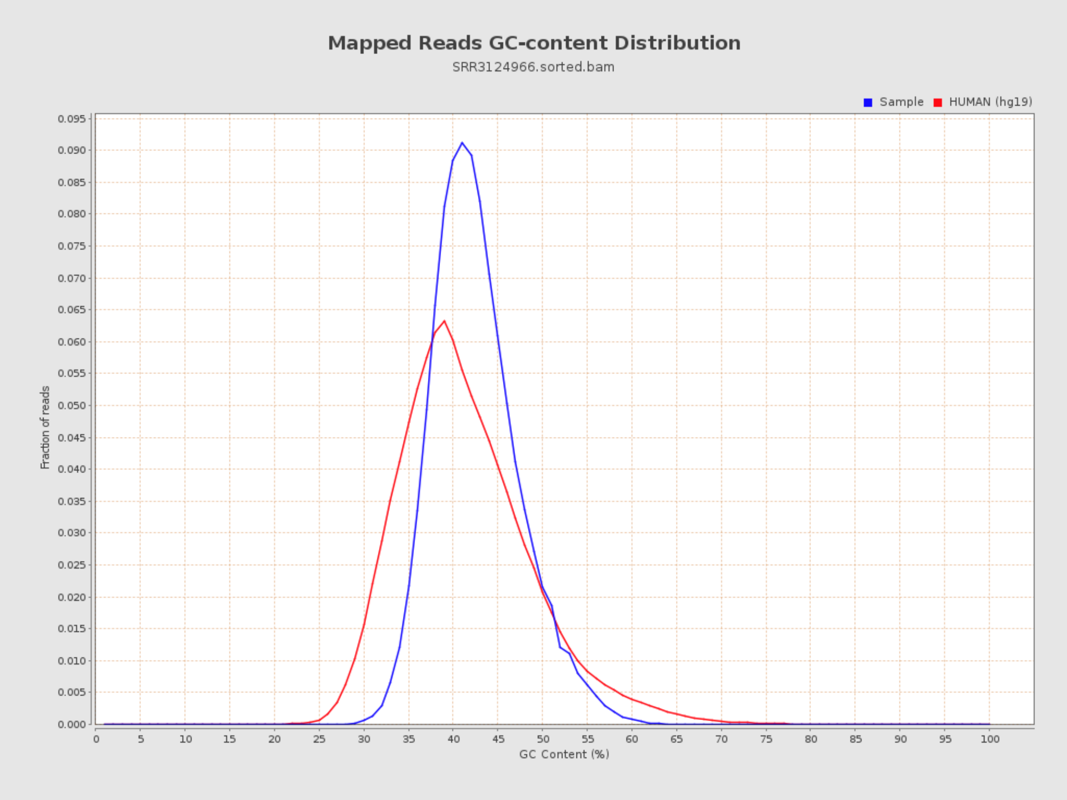
7. Results : Duplication Rate Histogram



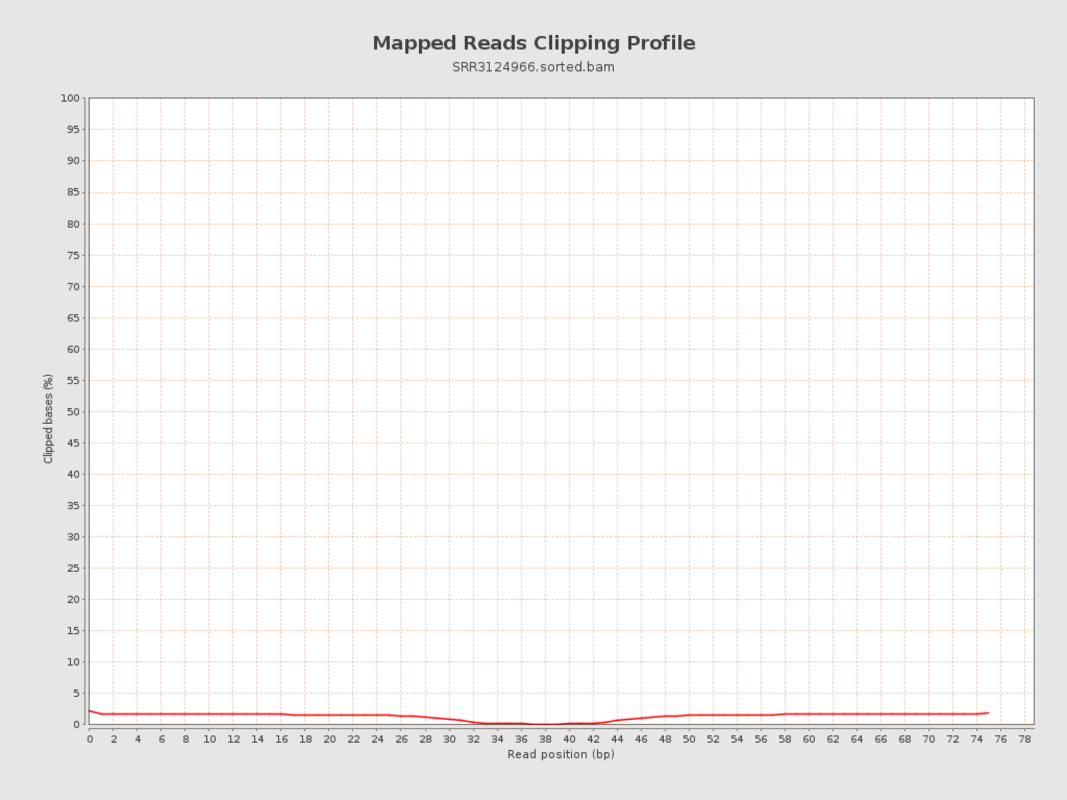
8. Results : Mapped Reads Nucleotide Content



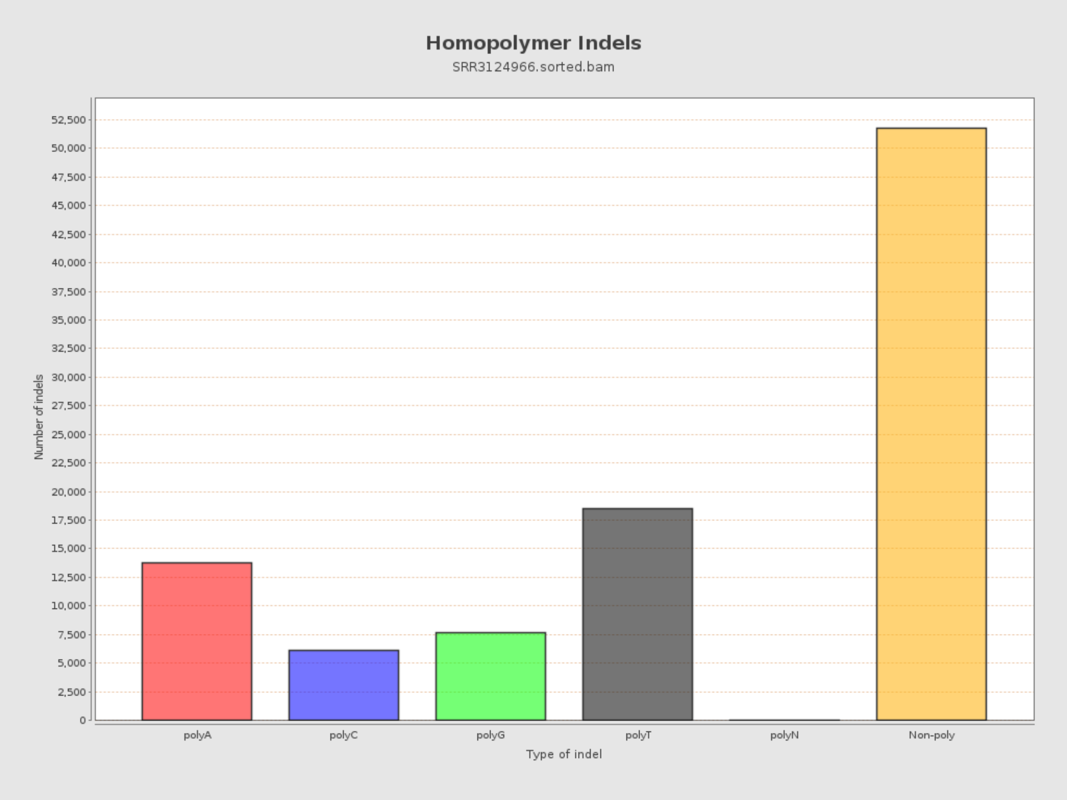
9. Results : Mapped Reads GC-content Distribution



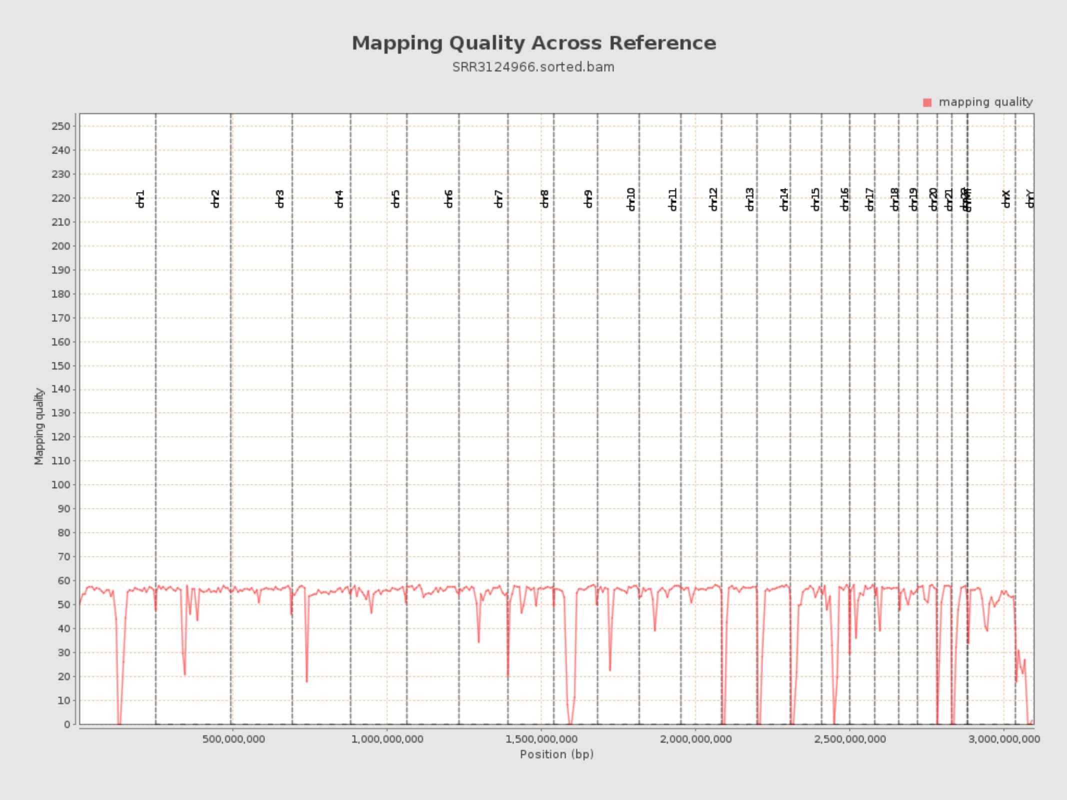
10. Results : Mapped Reads Clipping Profile



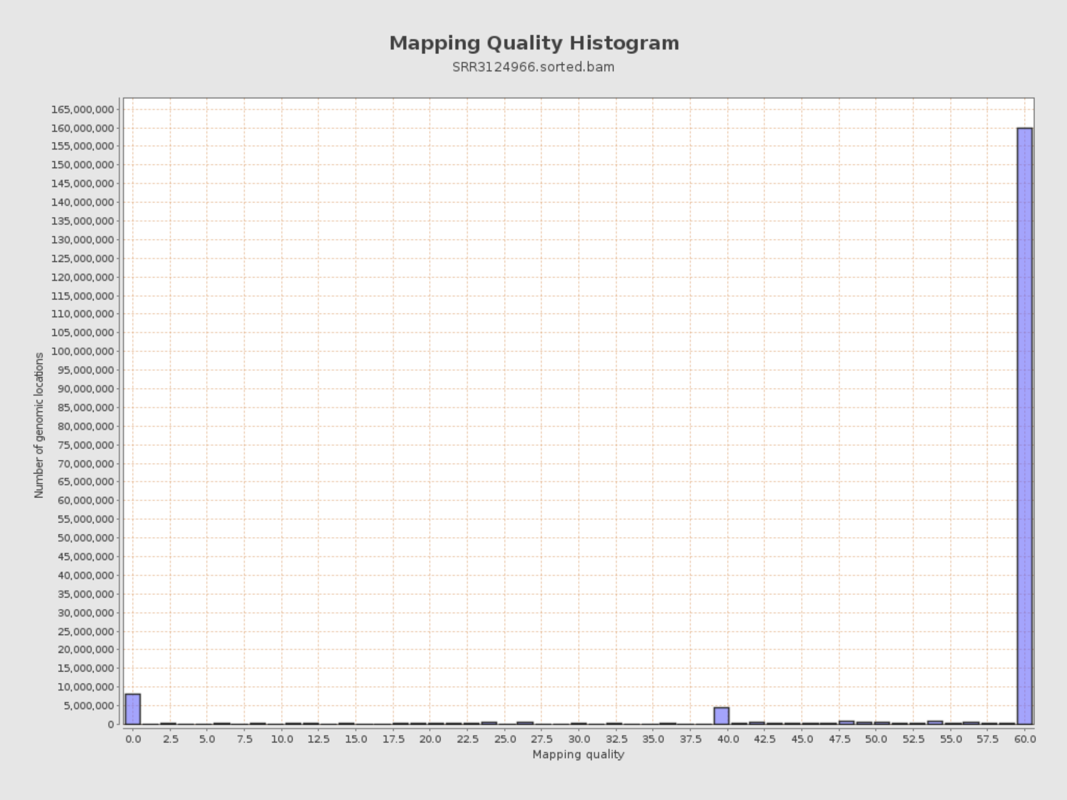
11. Results : Homopolymer Indels



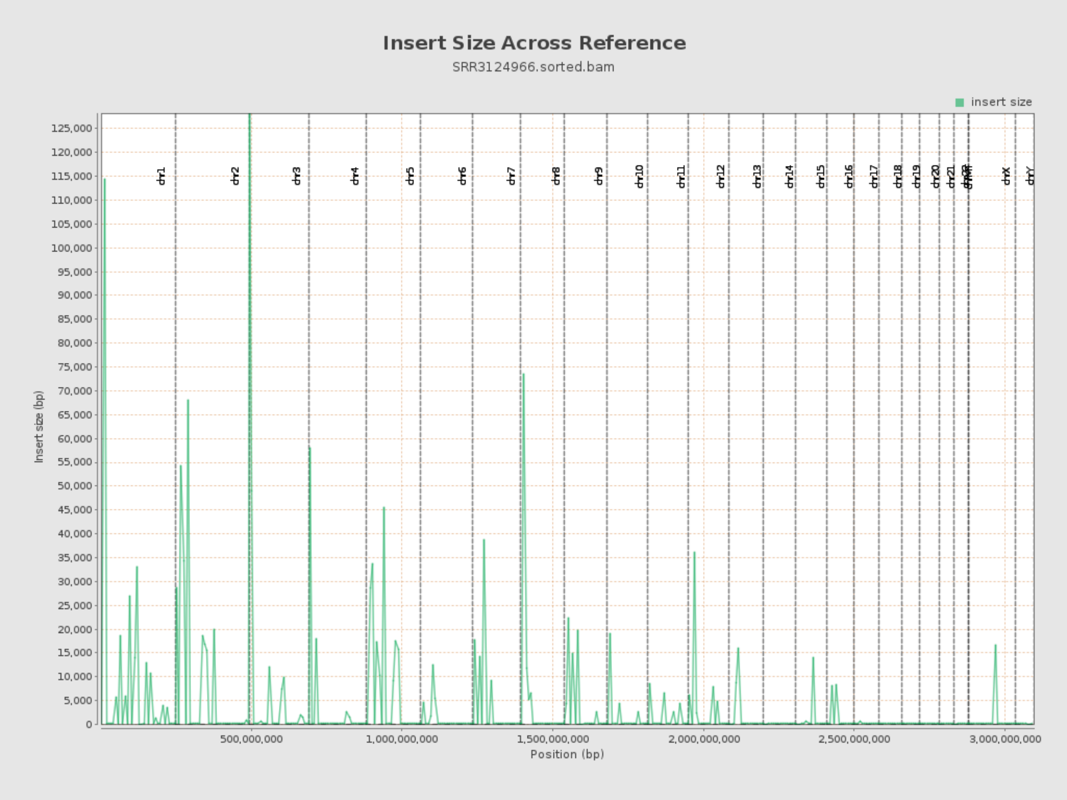
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram