Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 21:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960915.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_SRR960915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960915_1.fastq.gz SRR960915_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 21:47:45 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	225,503,192
Mapped reads	220,375,591 / 97.73%
Unmapped reads	5,127,601 / 2.27%
Mapped paired reads	220,375,591 / 97.73%
Mapped reads, first in pair	110,744,326 / 49.11%
Mapped reads, second in pair	109,631,265 / 48.62%
Mapped reads, both in pair	218,301,890 / 96.81%
Mapped reads, singletons	2,073,701 / 0.92%
Secondary alignments	0
Supplementary alignments	468,023 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	37,181,096 / 16.49%
Duplication rate	12.1%
Clipped reads	37,586,241 / 16.67%

2.2. ACGT Content

Number/percentage of A's	6,588,518,570 / 30.6%
Number/percentage of C's	4,184,806,029 / 19.44%
Number/percentage of T's	6,585,955,900 / 30.59%
Number/percentage of G's	4,163,485,511 / 19.34%
Number/percentage of N's	4,887,963 / 0.02%

GC Percentage	38.78%

2.3. Coverage

Mean	6.9561
Standard Deviation	103.2723

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	18,698.35
Standard Deviation	1,270,799.54
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	298,134,479
Insertions	2,589,668
Mapped reads with at least one insertion	1.15%
Deletions	2,862,945
Mapped reads with at least one deletion	1.26%
Homopolymer indels	40.48%

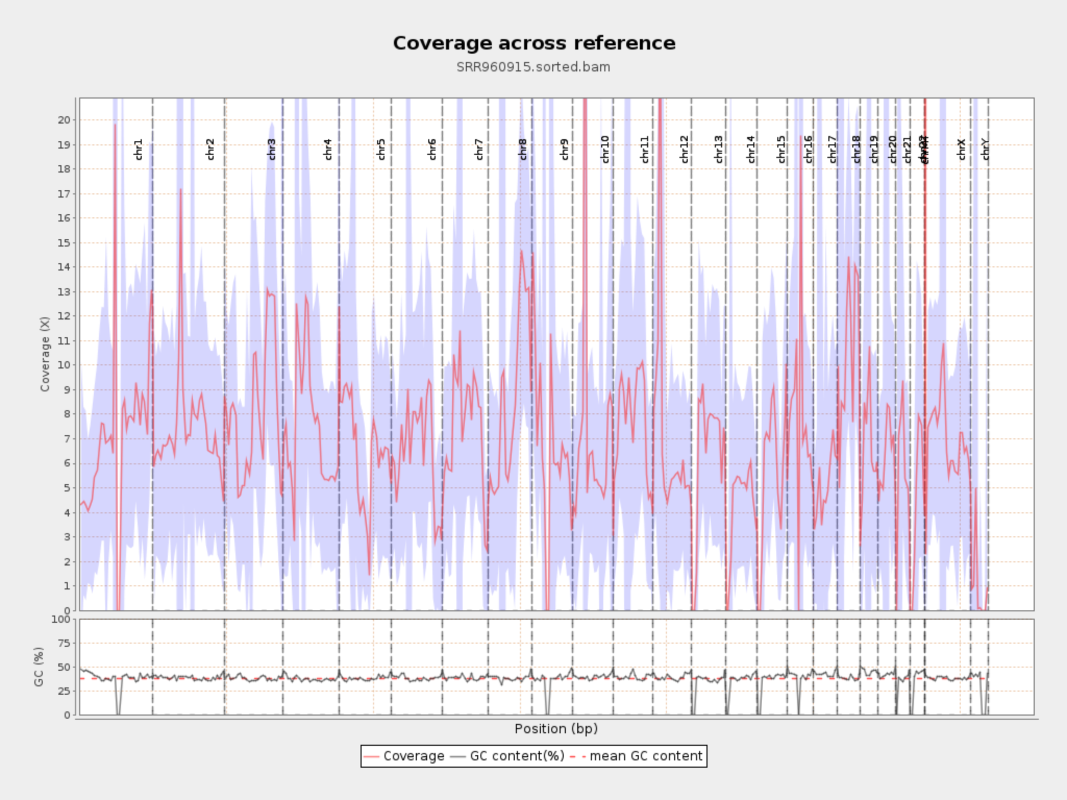
2.7. Chromosome stats

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

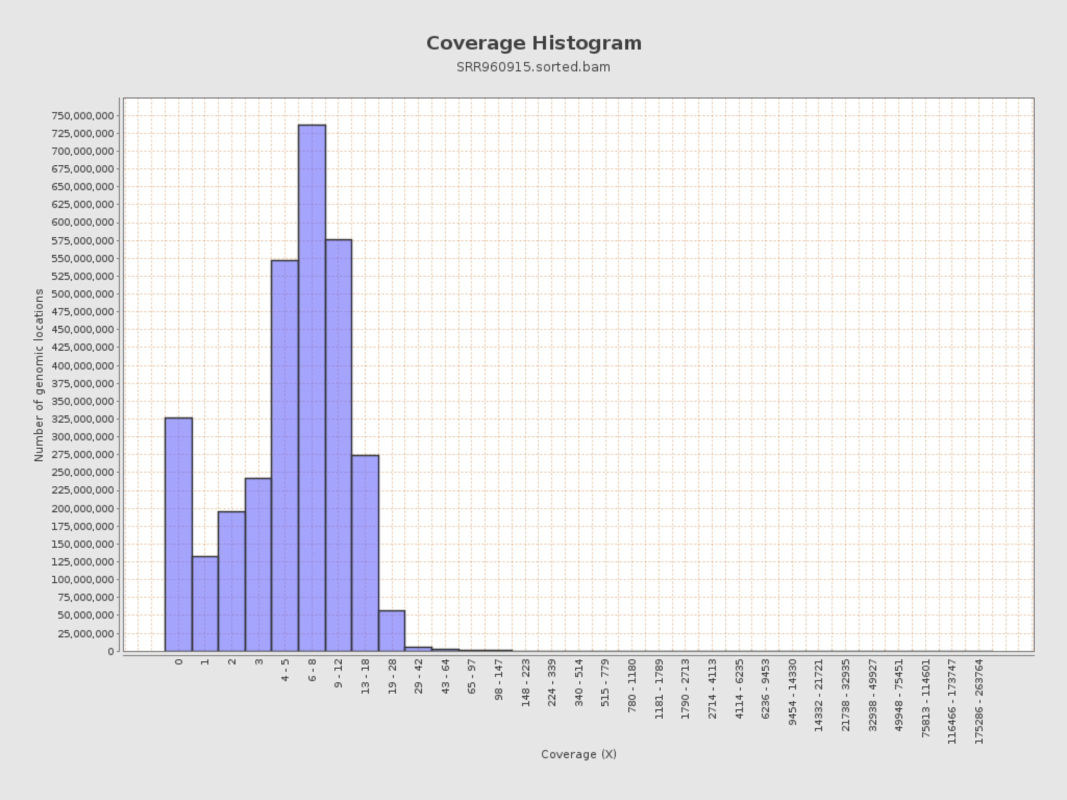
		bases	**coverage**	**deviation**
chr1	249250621	1788851154	7.1769	272.9693
chr2	243199373	1813259435	7.4559	55.0984
chr3	198022430	1600880078	8.0843	9.4299
chr4	191154276	1420875945	7.4331	56.6598
chr5	180915260	1169998058	6.4671	9.2574
chr6	171115067	1131810666	6.6143	27.0095
chr7	159138663	1184806150	7.4451	67.9006
chr8	146364022	1262748272	8.6274	132.8657
chr9	141213431	919332446	6.5102	98.0129
chr10	135534747	1026289145	7.5721	198.8576
chr11	135006516	1049967836	7.7772	43.2371
chr12	133851895	973150964	7.2704	11.4636
chr13	115169878	743142277	6.4526	4.8417
chr14	107349540	457931371	4.2658	7.2696
chr15	102531392	578870796	5.6458	5.1065
chr16	90354753	707403881	7.8292	84.8616
chr17	81195210	411093823	5.063	26.0873
chr18	78077248	828188232	10.6073	100.4692
chr19	59128983	398717546	6.7432	114.5639
chr20	63025520	405020998	6.4263	18.4981
chr21	48129895	286854525	5.96	22.3391
chr22	51304566	221983883	4.3268	5.6407
chrMT	16571	4882317	294.6302	57.7032
chrX	155270560	1088555448	7.0107	28.9851

chrY	59373566	59284278	0.9985	52.5588

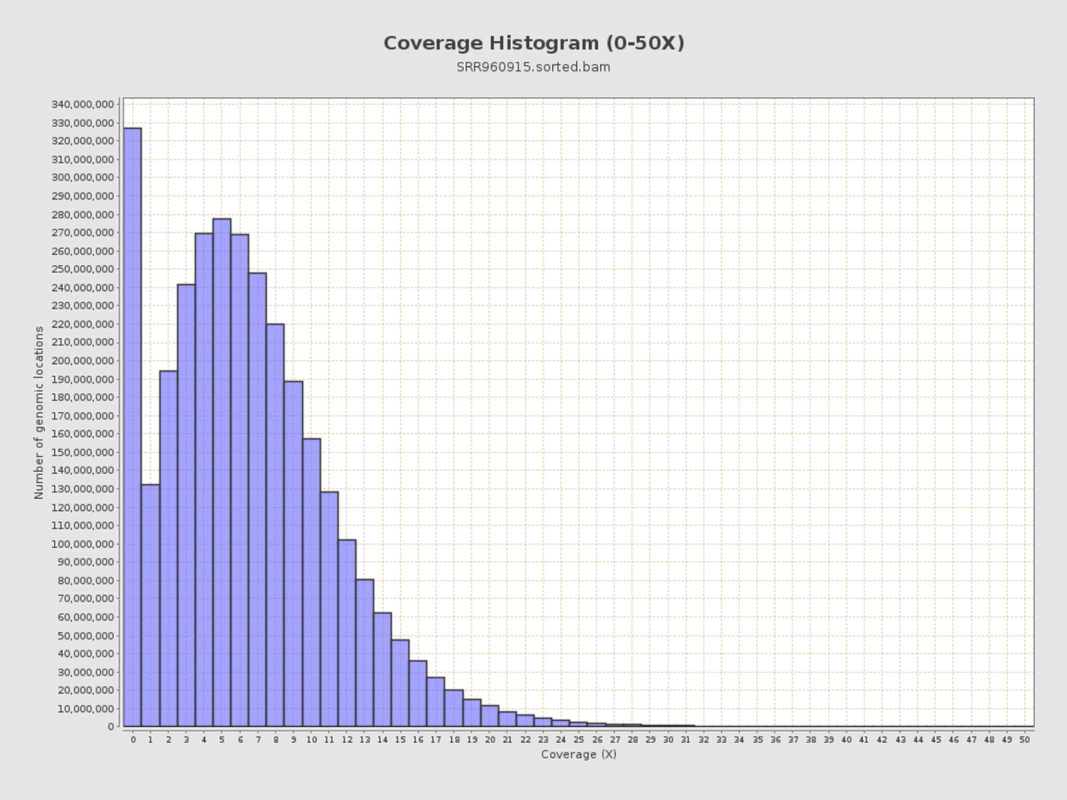
3. Results : Coverage across reference



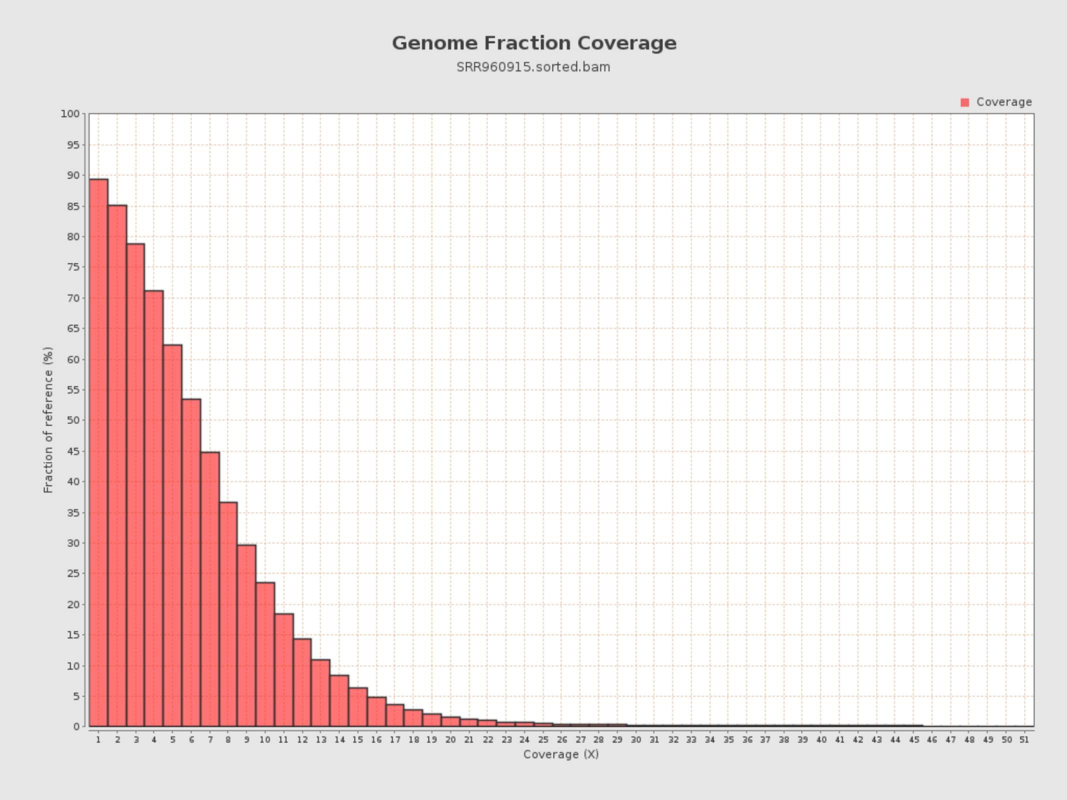
4. Results : Coverage Histogram



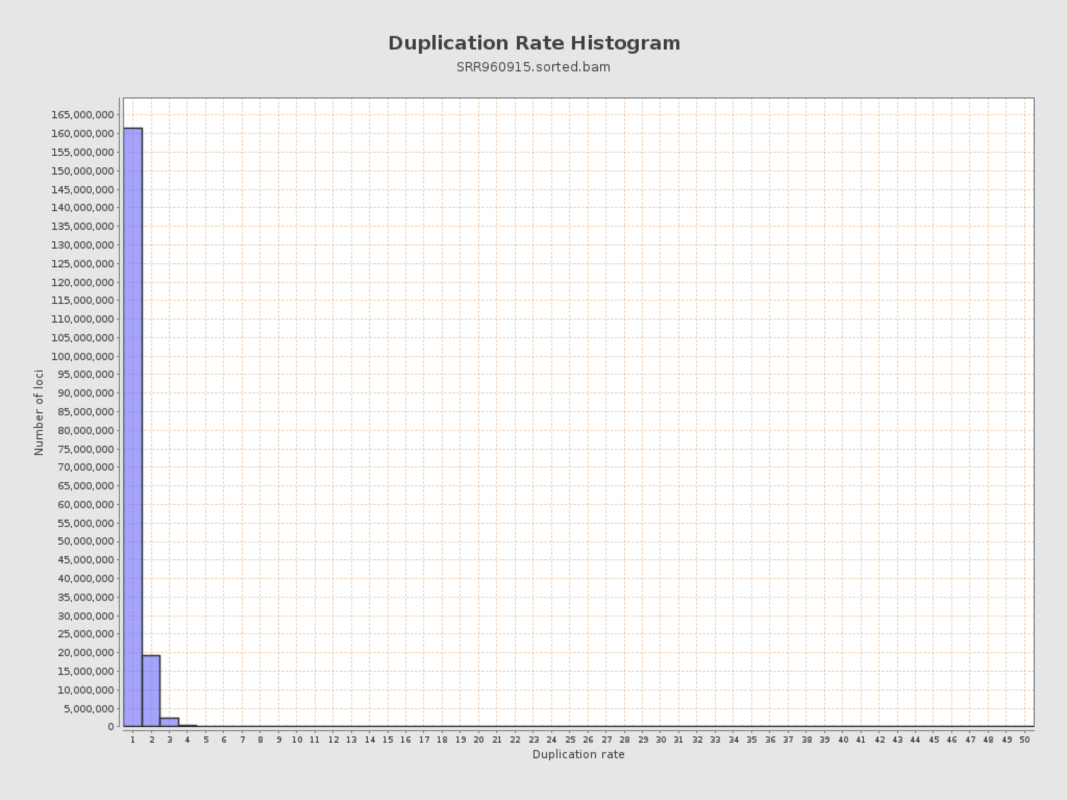
5. Results : Coverage Histogram (0-50X)



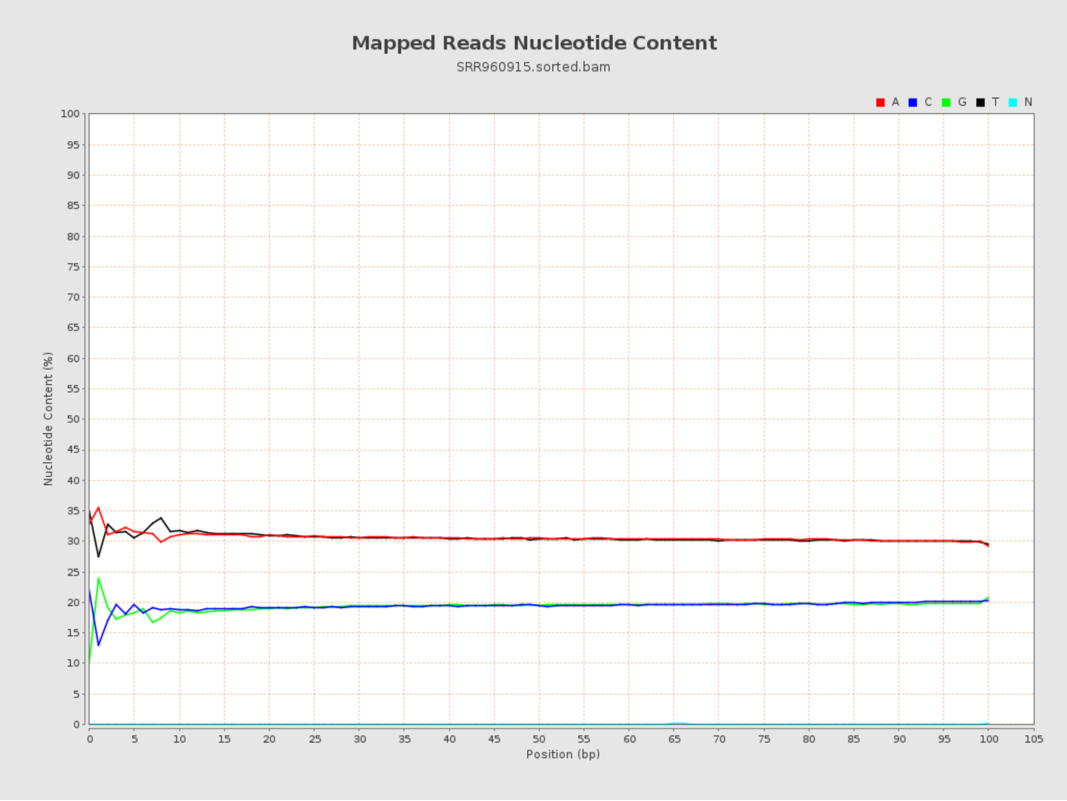
6. Results : Genome Fraction Coverage



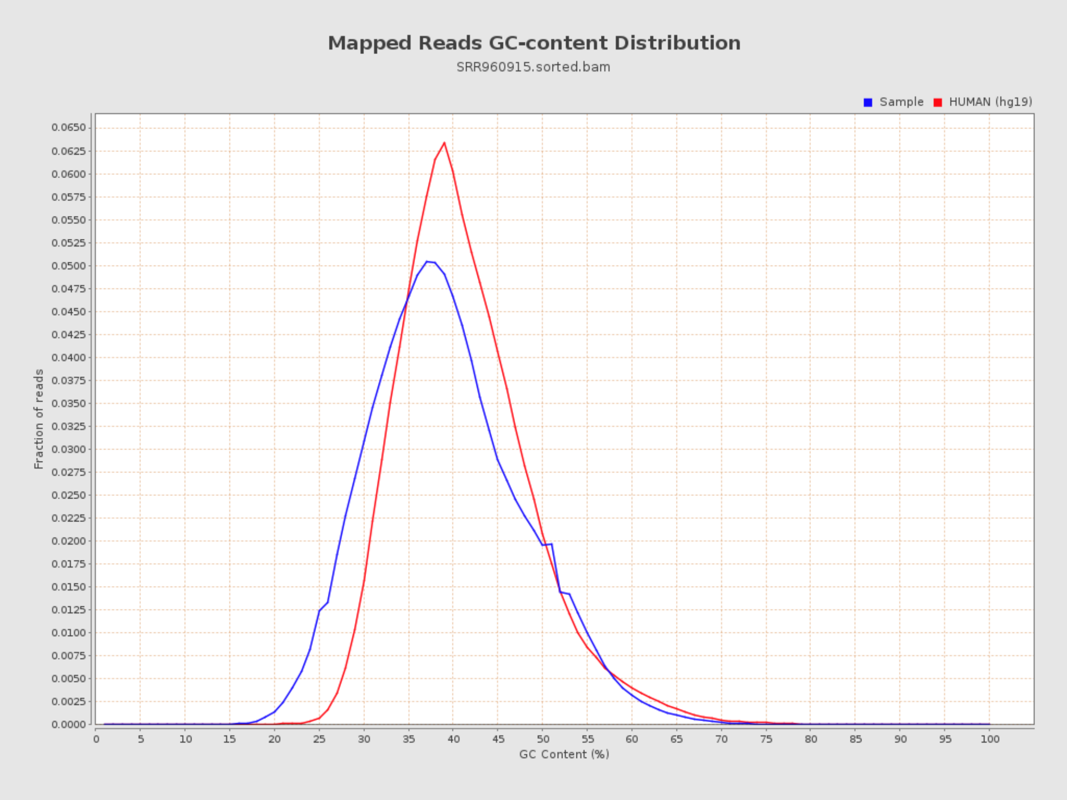
7. Results : Duplication Rate Histogram



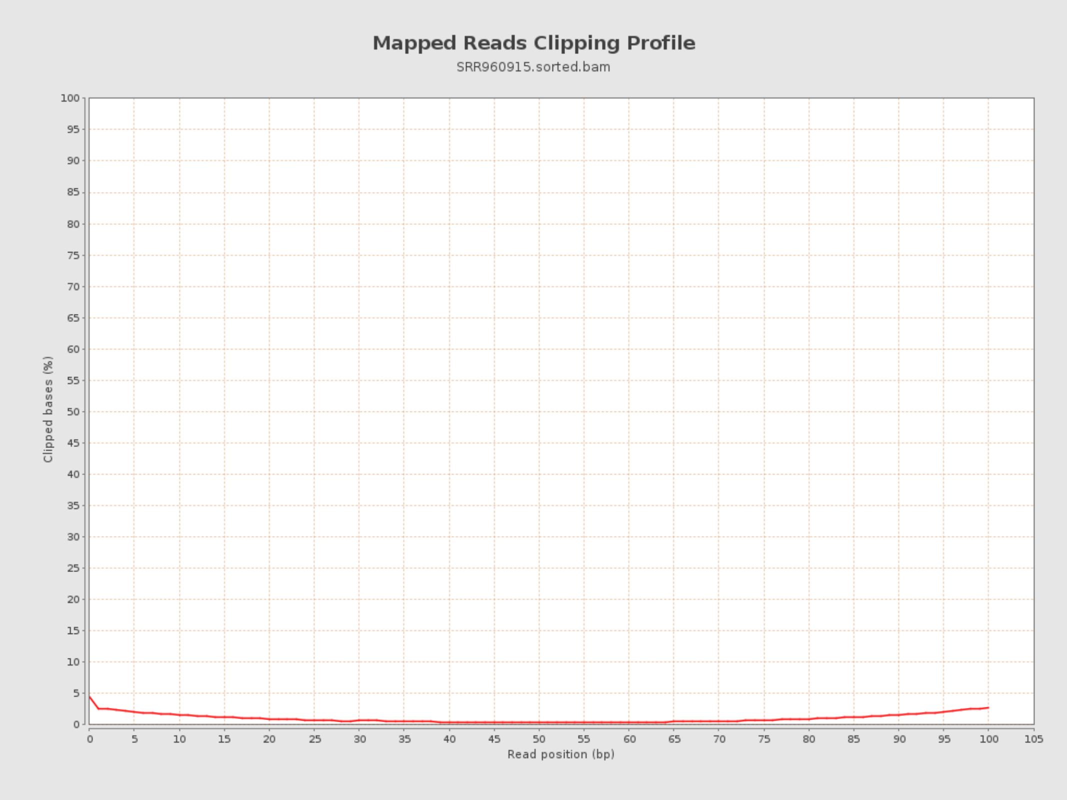
8. Results : Mapped Reads Nucleotide Content



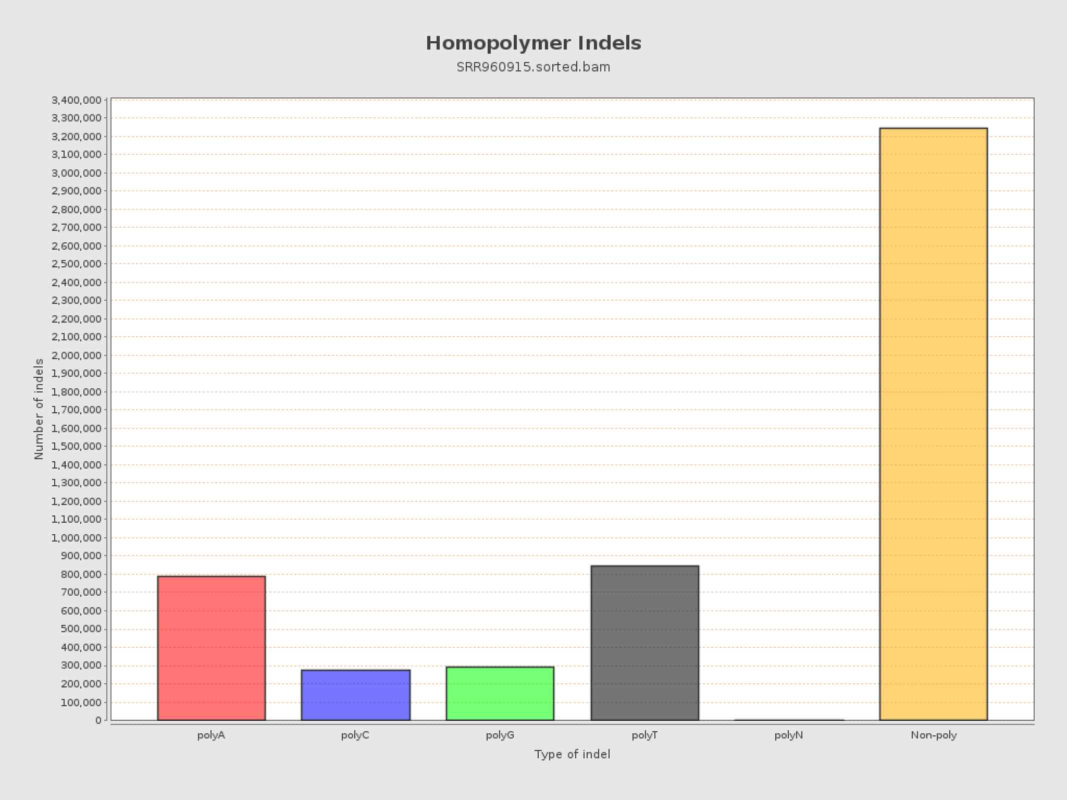
9. Results : Mapped Reads GC-content Distribution



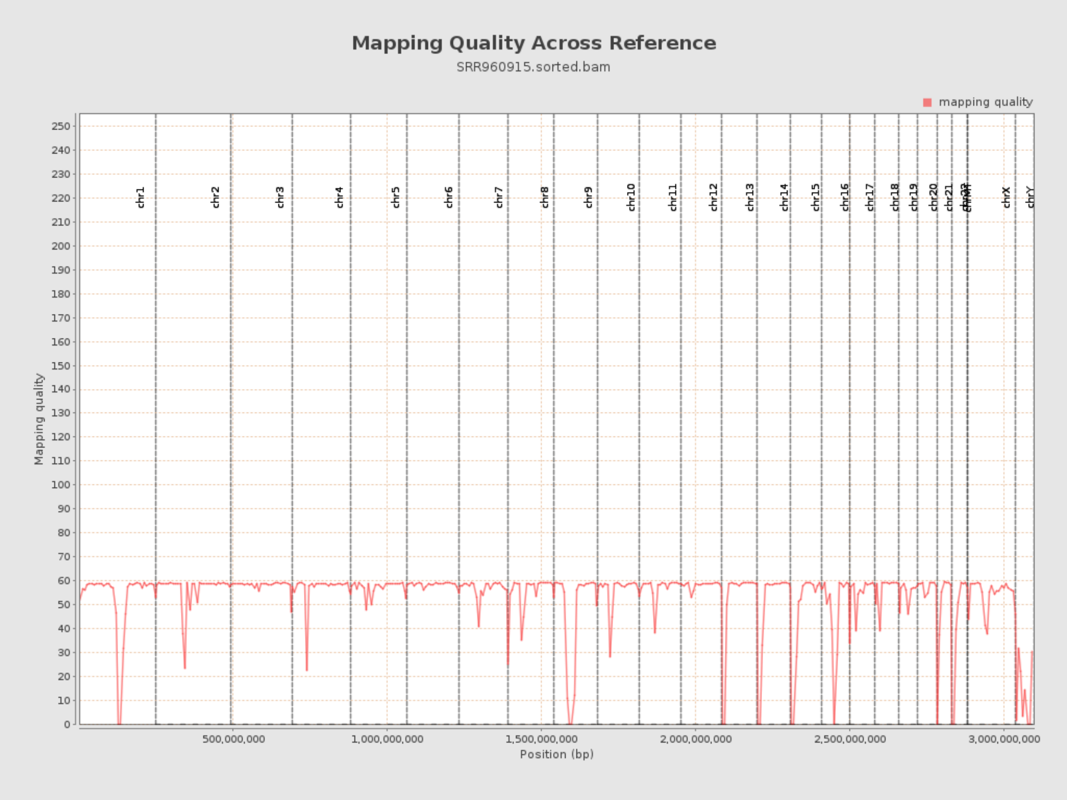
10. Results : Mapped Reads Clipping Profile



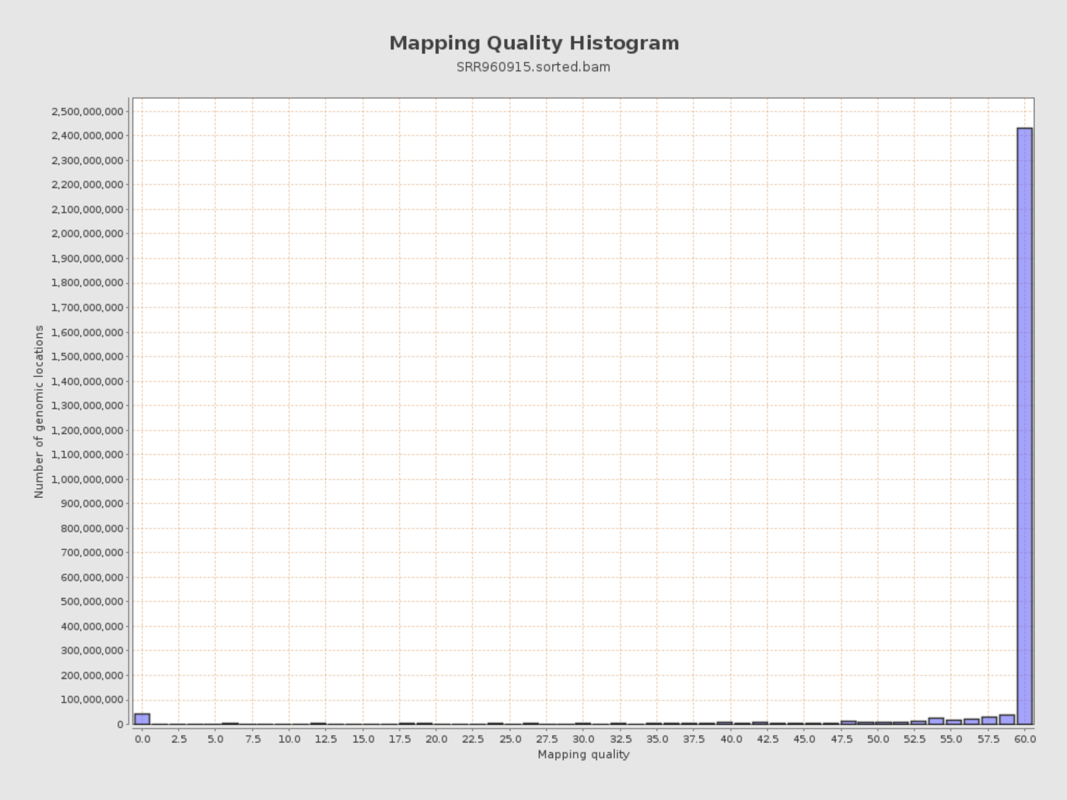
11. Results : Homopolymer Indels



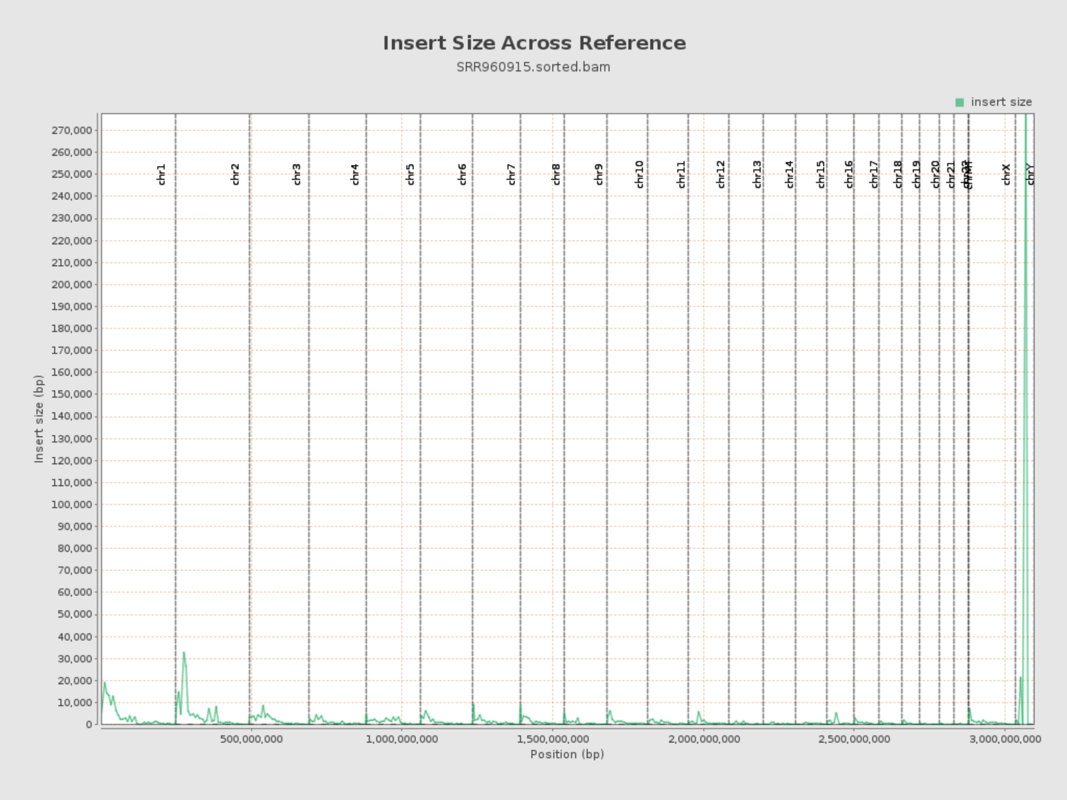
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram