Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 07:17:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960909.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_SRR960909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960909_1.fastq.gz SRR960909_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 07:17:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	137,969,456
Mapped reads	131,113,548 / 95.03%
Unmapped reads	6,855,908 / 4.97%
Mapped paired reads	131,113,548 / 95.03%
Mapped reads, first in pair	65,850,770 / 47.73%
Mapped reads, second in pair	65,262,778 / 47.3%
Mapped reads, both in pair	128,107,312 / 92.85%
Mapped reads, singletons	3,006,236 / 2.18%
Secondary alignments	0
Supplementary alignments	2,144,276 / 1.55%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	14,815,245 / 10.74%
Duplication rate	5.82%
Clipped reads	69,674,523 / 50.5%

2.2. ACGT Content

Number/percentage of A's	3,291,909,745 / 29.03%
Number/percentage of C's	2,328,636,594 / 20.54%
Number/percentage of T's	3,366,457,300 / 29.69%
Number/percentage of G's	2,351,017,336 / 20.73%
Number/percentage of N's	821,017 / 0.01%

GC Percentage	41.27%

2.3. Coverage

Mean	3.6638
Standard Deviation	50.1323

2.4. Mapping Quality

Mean Mapping Quality	52.32

2.5. Insert size

Mean	161,133.77
Standard Deviation	4,152,678.68
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	181,711,970
Insertions	1,719,331
Mapped reads with at least one insertion	1.28%
Deletions	1,455,192
Mapped reads with at least one deletion	1.08%
Homopolymer indels	36.88%

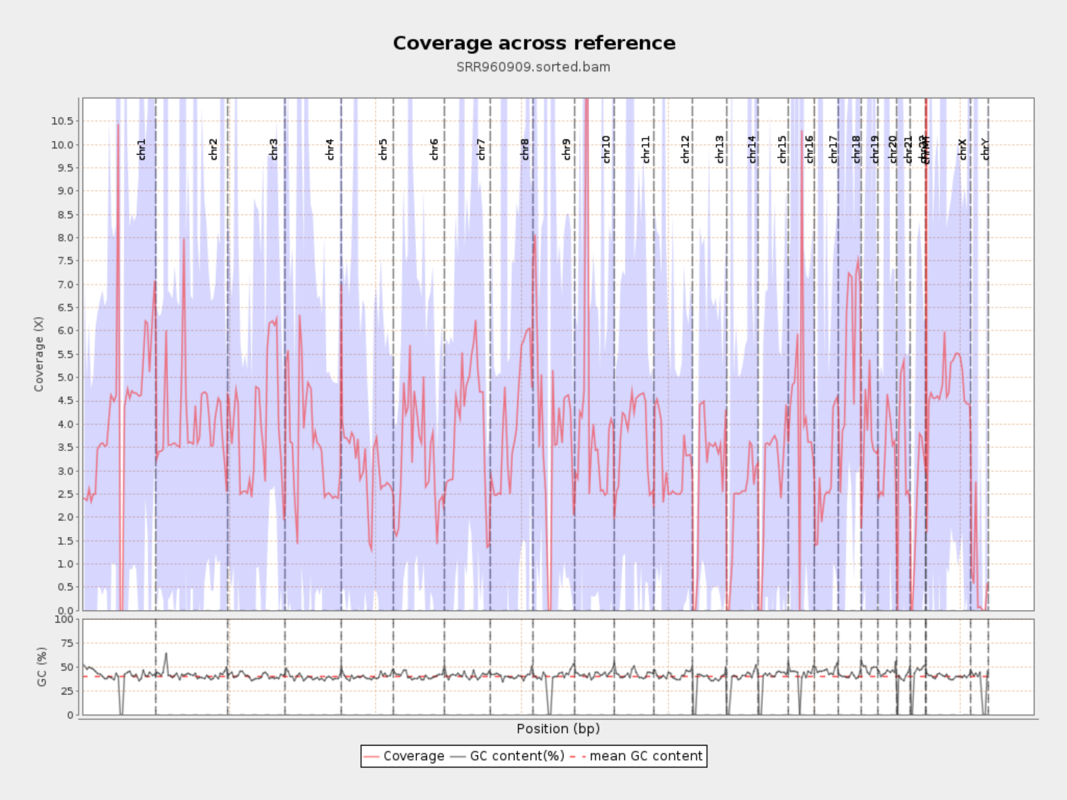
2.7. Chromosome stats

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

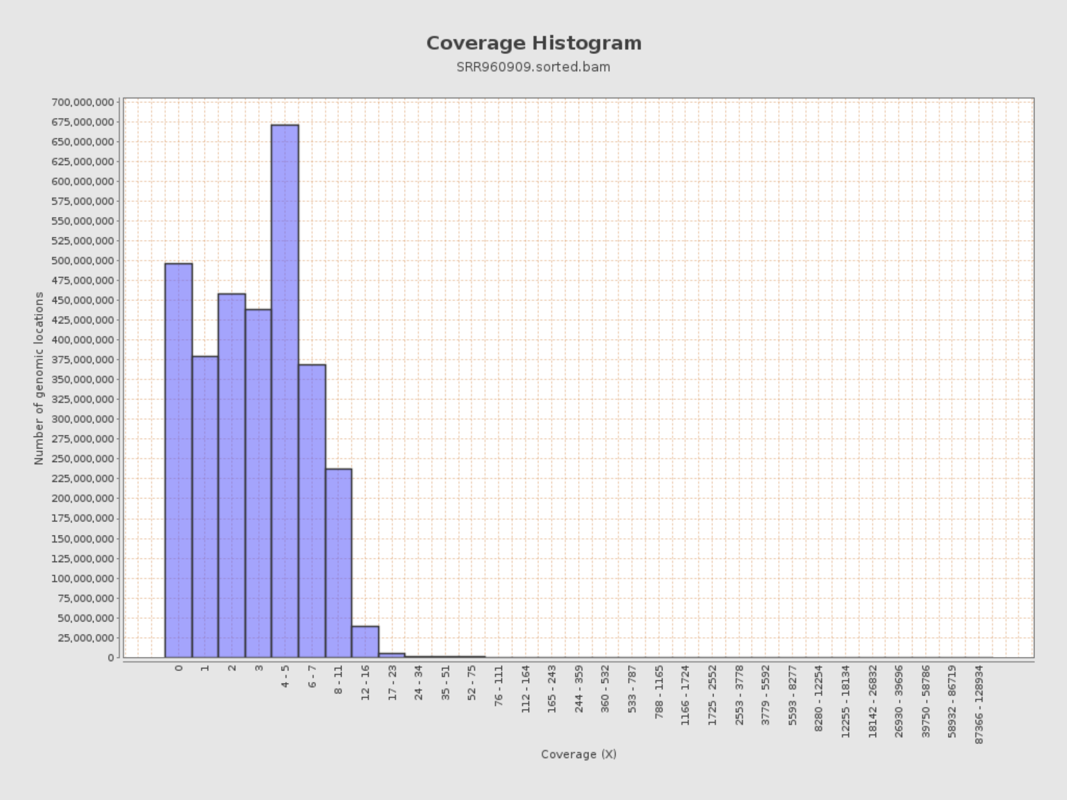
		bases	**coverage**	**deviation**
chr1	249250621	1047262950	4.2016	126.239
chr2	243199373	985022429	4.0503	74.3353
chr3	198022430	785038750	3.9644	8.1136
chr4	191154276	687814008	3.5982	21.915
chr5	180915260	554234395	3.0635	4.9646
chr6	171115067	566916066	3.3131	15.3952
chr7	159138663	642040257	4.0345	32.5968
chr8	146364022	590186305	4.0323	41.2974
chr9	141213431	541825050	3.8369	37.8991
chr10	135534747	548161492	4.0444	82.6609
chr11	135006516	513745394	3.8053	24.2458
chr12	133851895	423929627	3.1672	4.554
chr13	115169878	355075564	3.0831	3.1474
chr14	107349540	250272475	2.3314	21.0119
chr15	102531392	295222640	2.8793	3.6852
chr16	90354753	397667066	4.4012	41.9407
chr17	81195210	224478824	2.7647	12.4375
chr18	78077248	439062607	5.6234	46.6069
chr19	59128983	225340649	3.811	56.4946
chr20	63025520	211607508	3.3575	10.2705
chr21	48129895	160420318	3.3331	15.0642
chr22	51304566	118315676	2.3061	3.5071
chrMT	16571	2328684	140.5277	30.8719
chrX	155270560	740427541	4.7686	16.4486

chrY	59373566	35525473	0.5983	26.7449

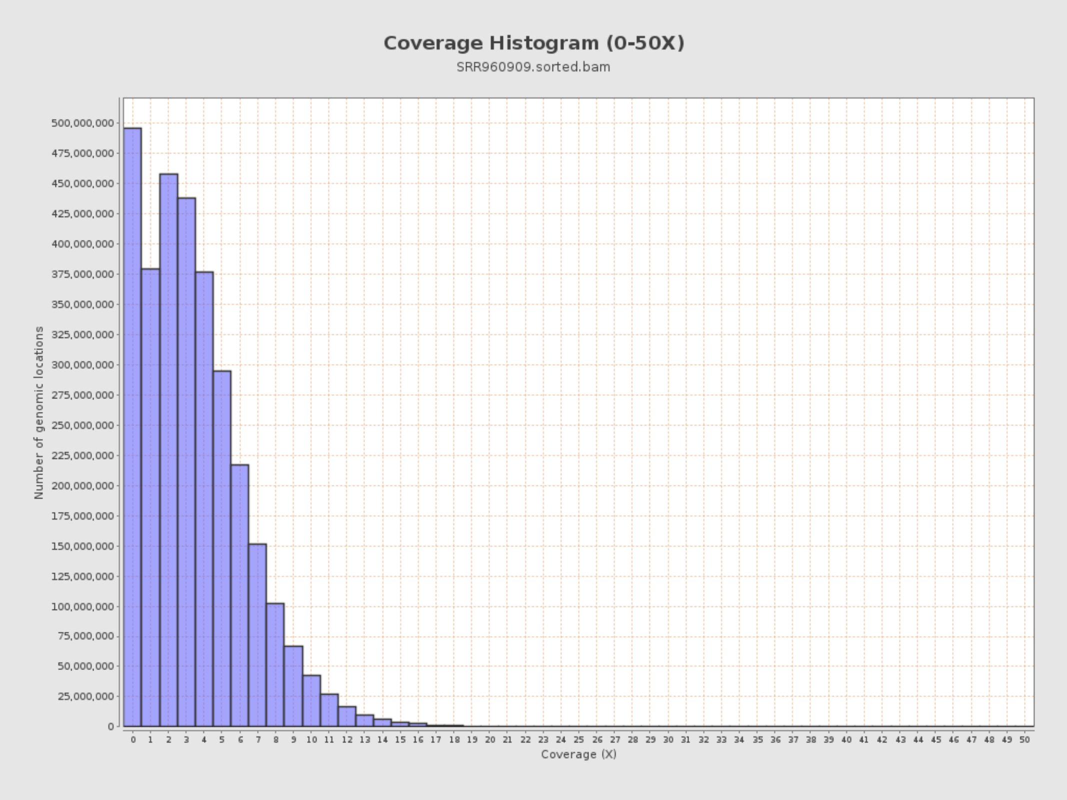
3. Results : Coverage across reference



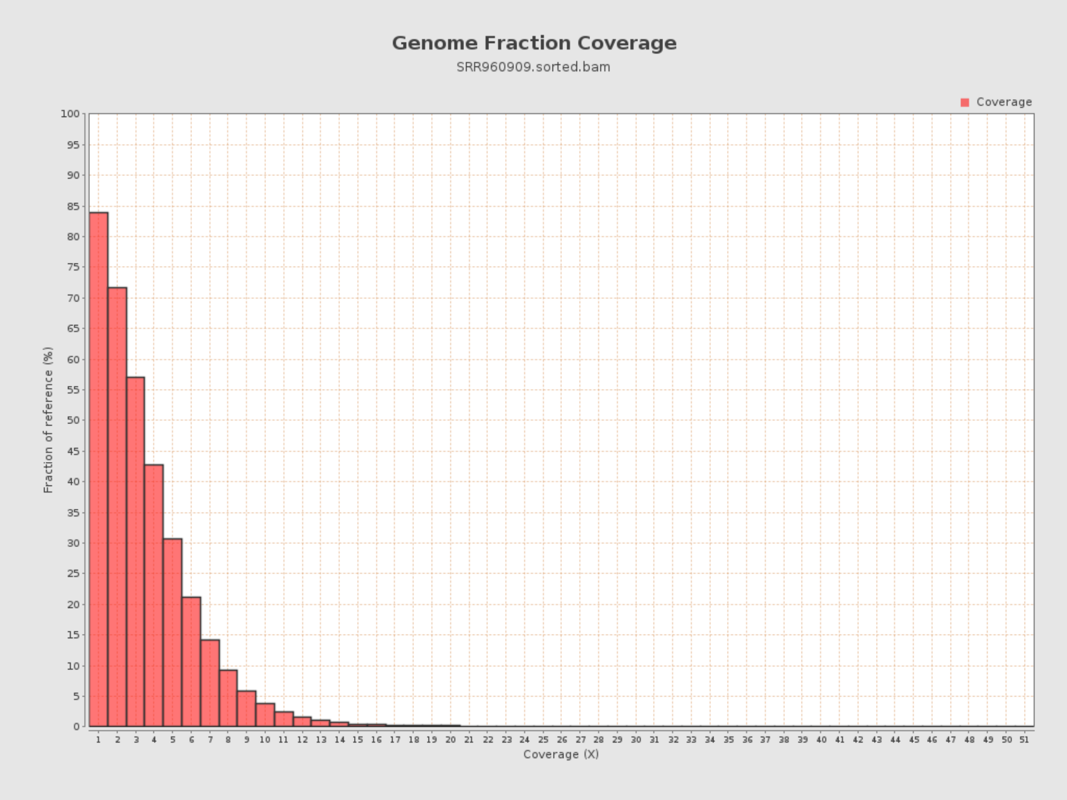
4. Results : Coverage Histogram



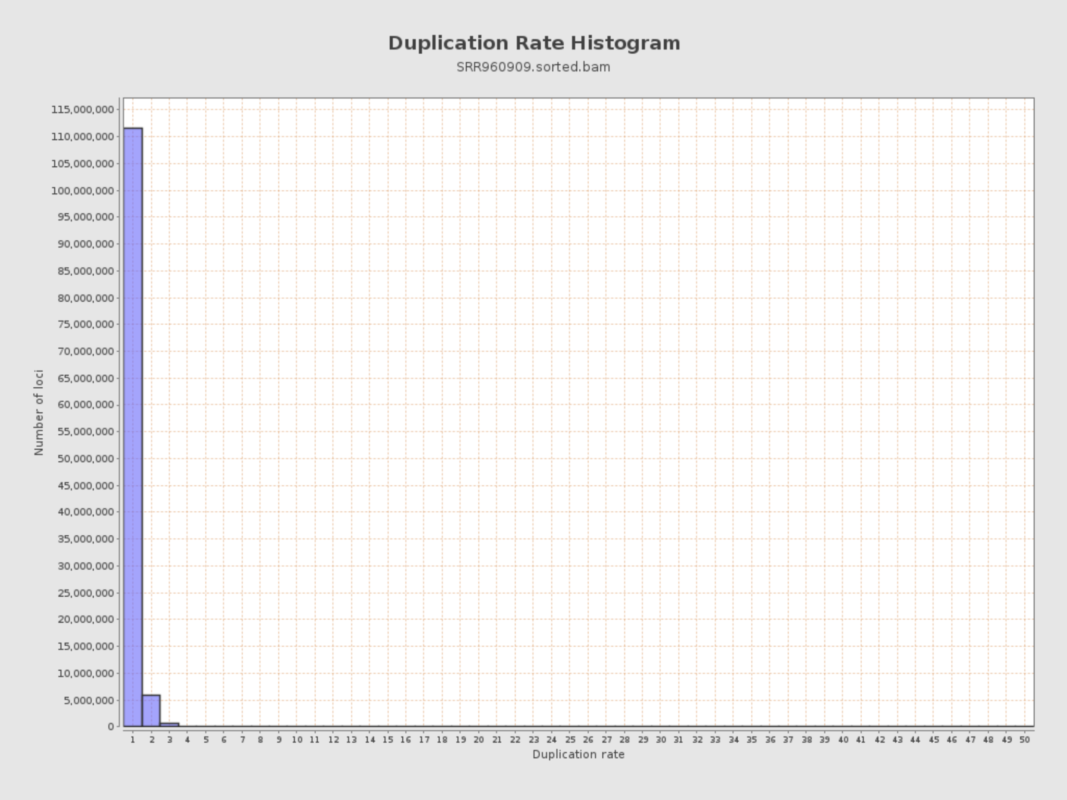
5. Results : Coverage Histogram (0-50X)



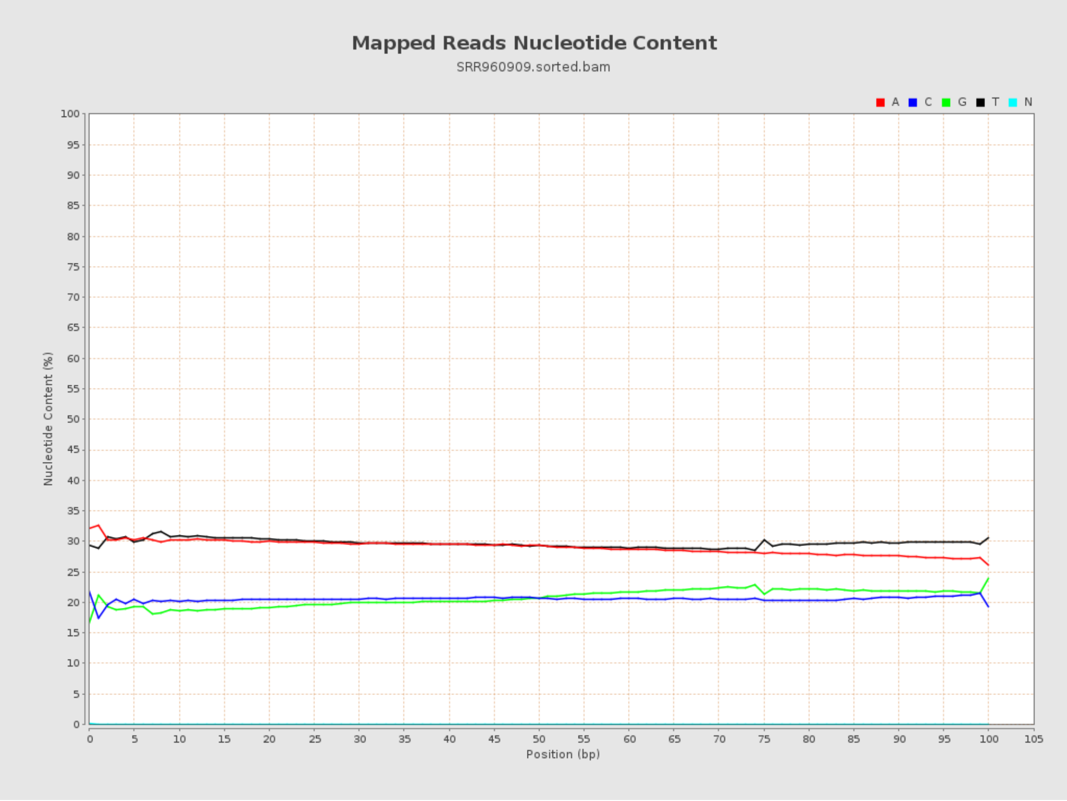
6. Results : Genome Fraction Coverage



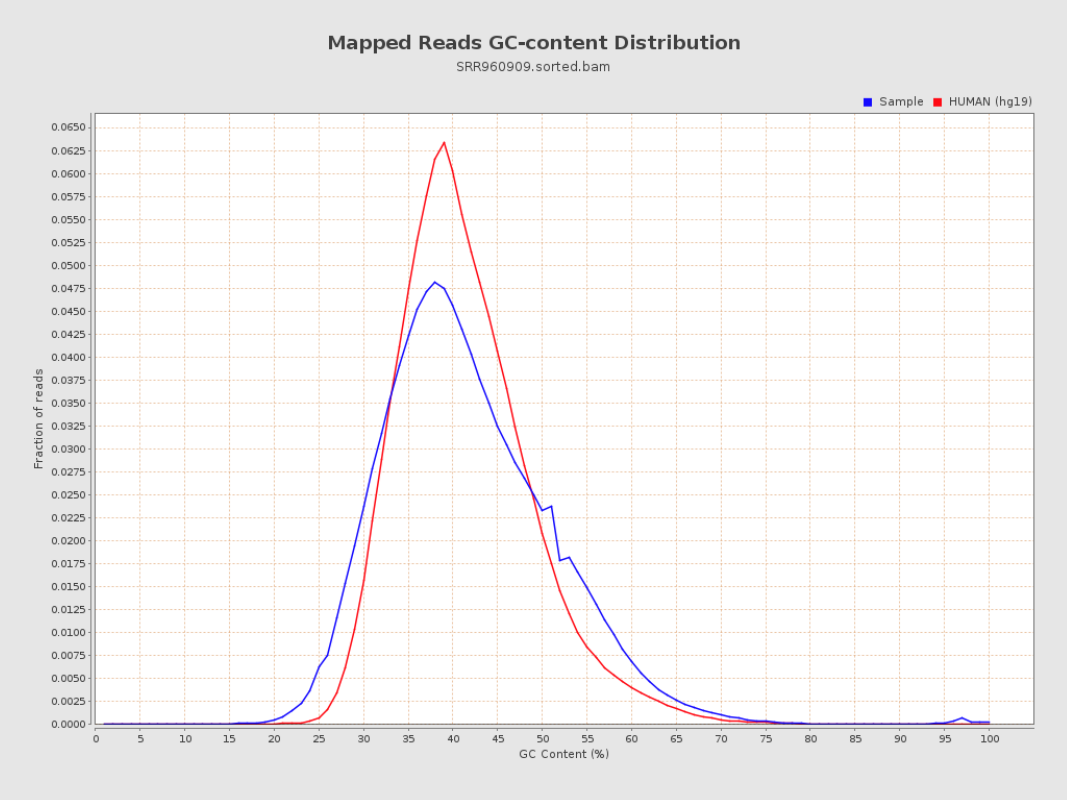
7. Results : Duplication Rate Histogram



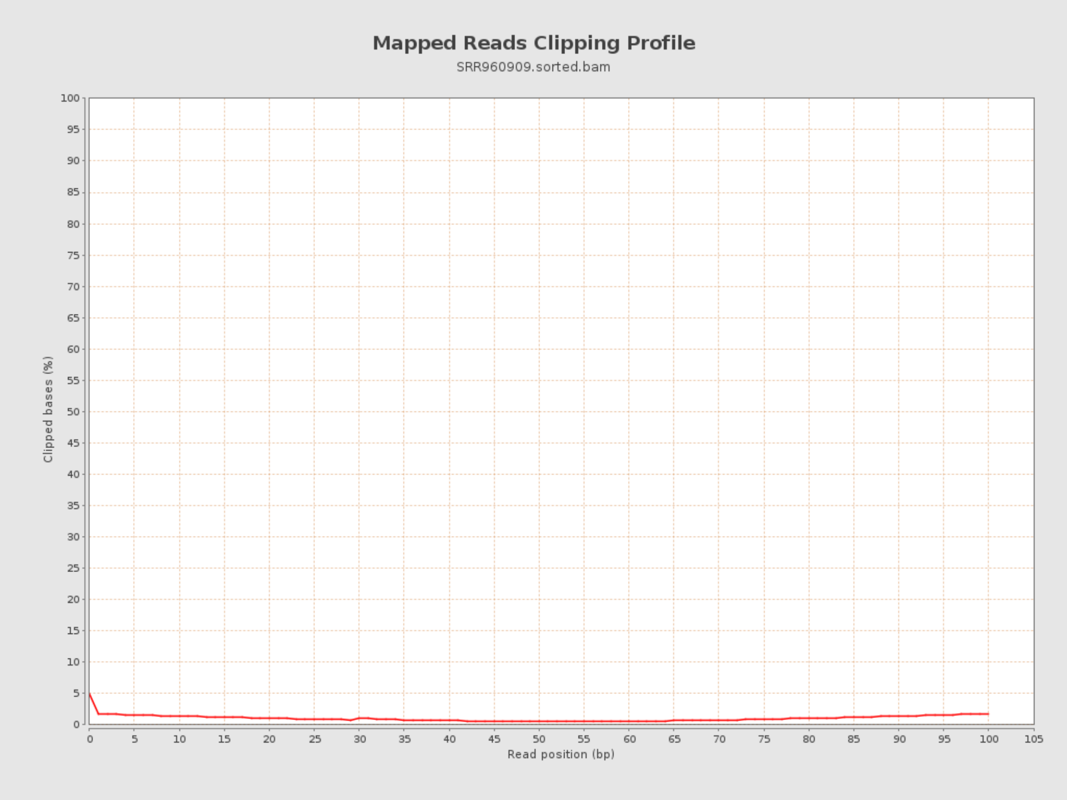
8. Results : Mapped Reads Nucleotide Content



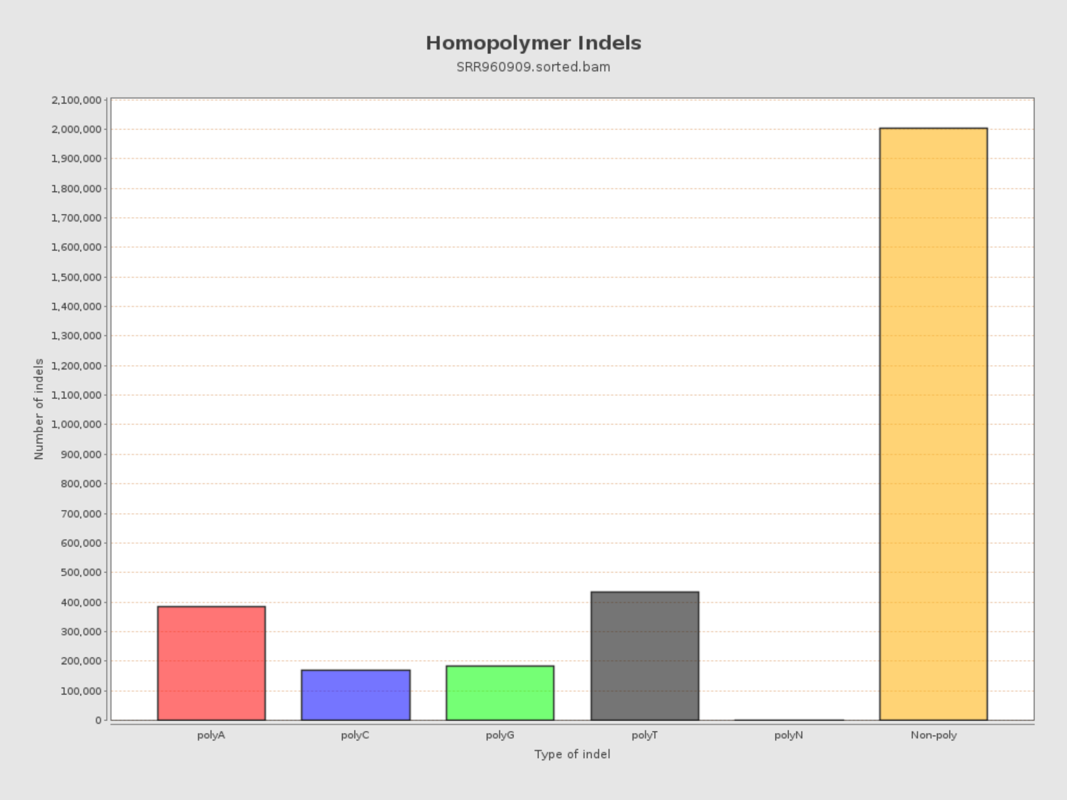
9. Results : Mapped Reads GC-content Distribution



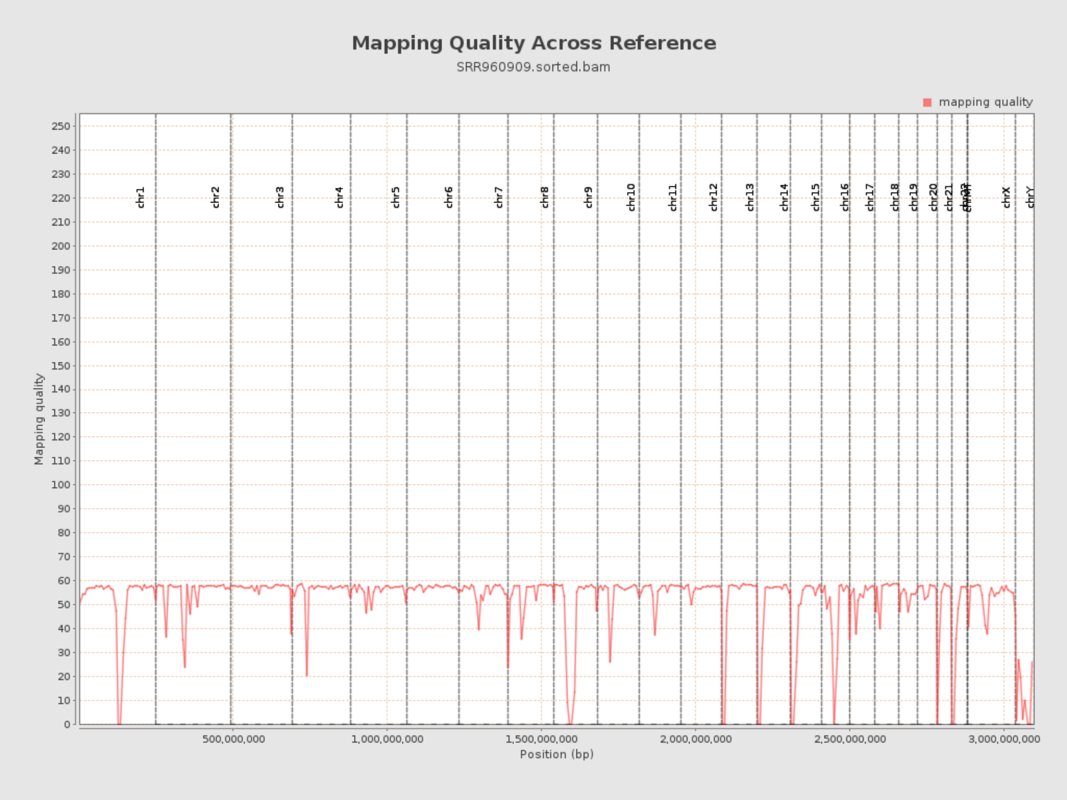
10. Results : Mapped Reads Clipping Profile



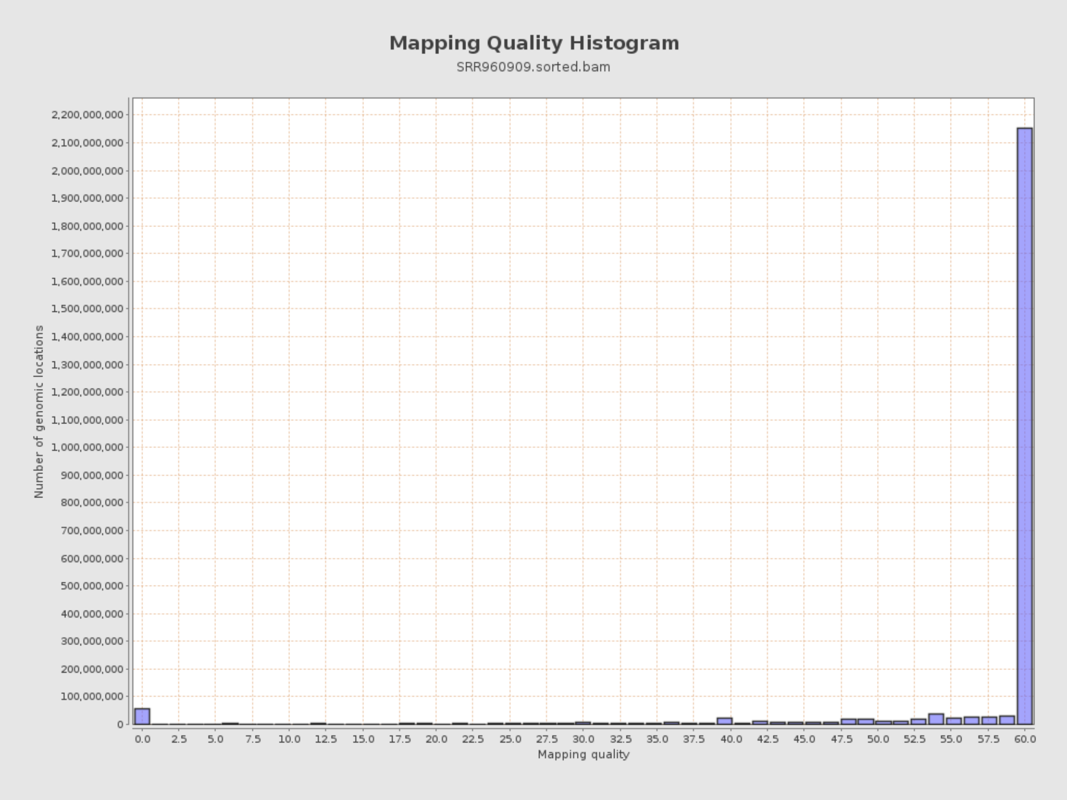
11. Results : Homopolymer Indels



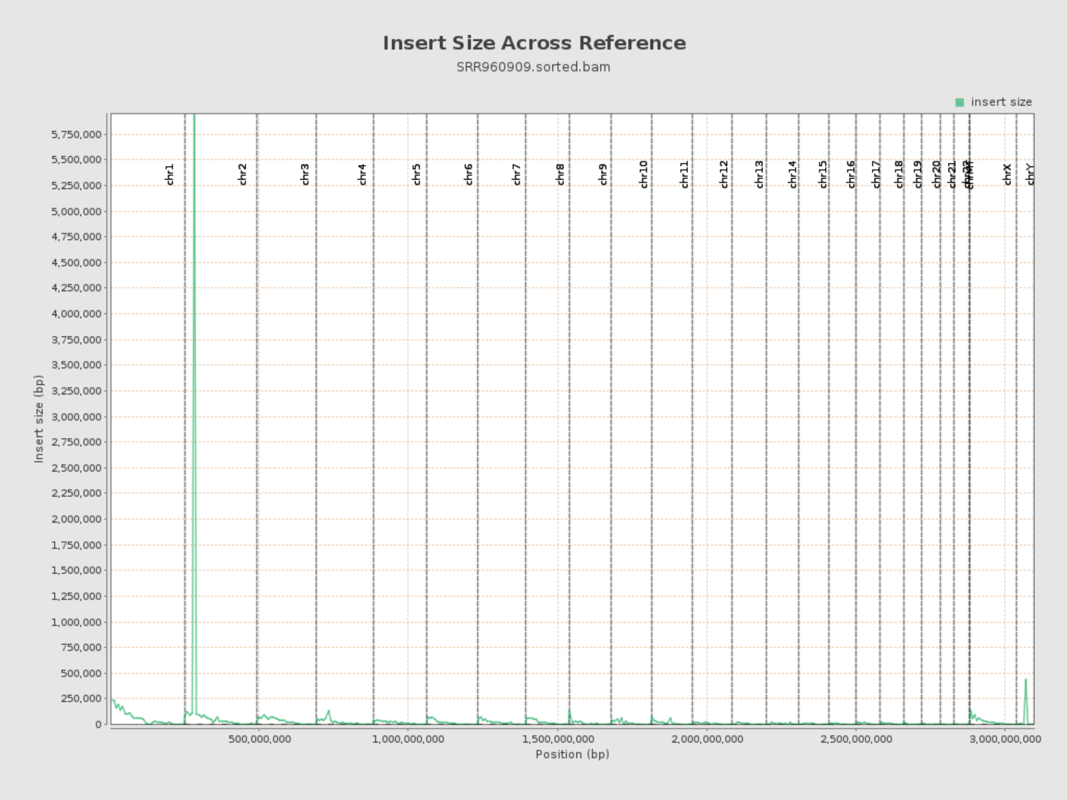
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram