Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 20:11:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960903.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_SRR960903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960903_1.fastq.gz SRR960903_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 20:11:11 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	142,486,778
Mapped reads	136,728,382 / 95.96%
Unmapped reads	5,758,396 / 4.04%
Mapped paired reads	136,728,382 / 95.96%
Mapped reads, first in pair	68,598,505 / 48.14%
Mapped reads, second in pair	68,129,877 / 47.81%
Mapped reads, both in pair	135,620,768 / 95.18%
Mapped reads, singletons	1,107,614 / 0.78%
Secondary alignments	0
Supplementary alignments	282,491 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	11,950,426 / 8.39%
Duplication rate	4.73%
Clipped reads	17,338,560 / 12.17%

2.2. ACGT Content

Number/percentage of A's	3,977,097,440 / 29.56%
Number/percentage of C's	2,739,189,823 / 20.36%
Number/percentage of T's	3,968,443,752 / 29.5%
Number/percentage of G's	2,762,908,390 / 20.54%
Number/percentage of N's	5,007,364 / 0.04%

GC Percentage	40.9%

2.3. Coverage

Mean	4.3469
Standard Deviation	46.2506

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	21,835.78
Standard Deviation	1,437,475.98
P25/Median/P75	139 / 150 / 160

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	131,650,776
Insertions	1,495,683
Mapped reads with at least one insertion	1.06%
Deletions	1,638,805
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.06%

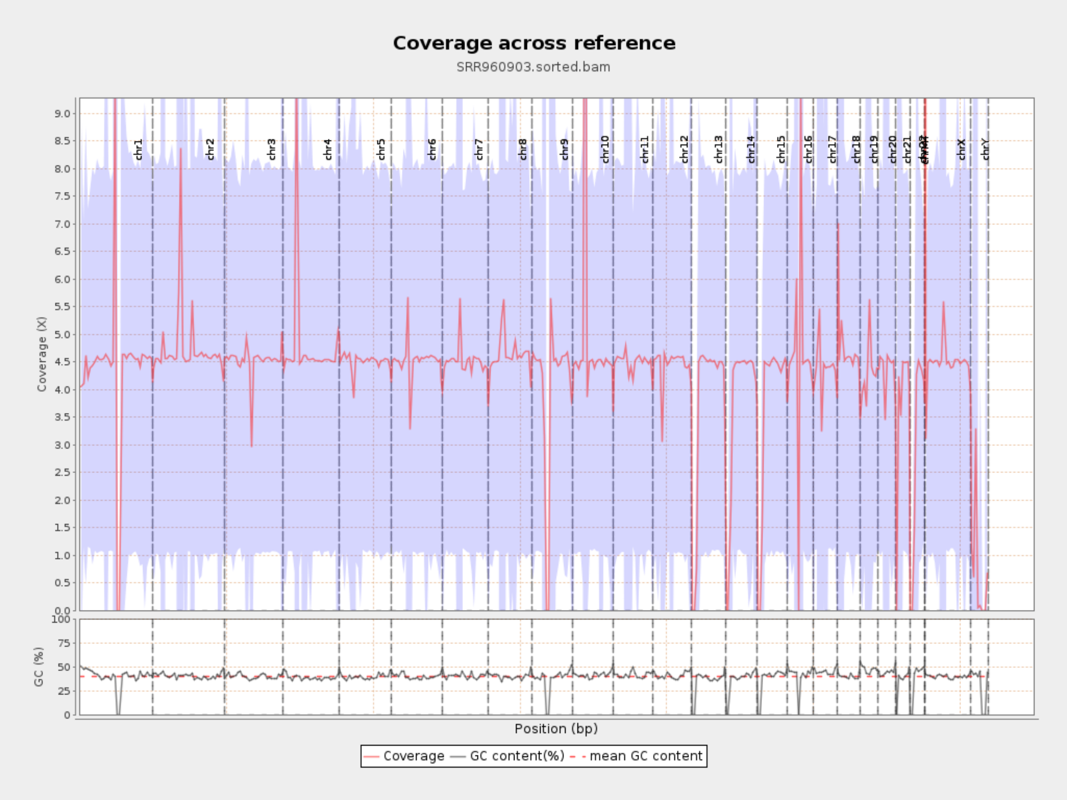
2.7. Chromosome stats

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

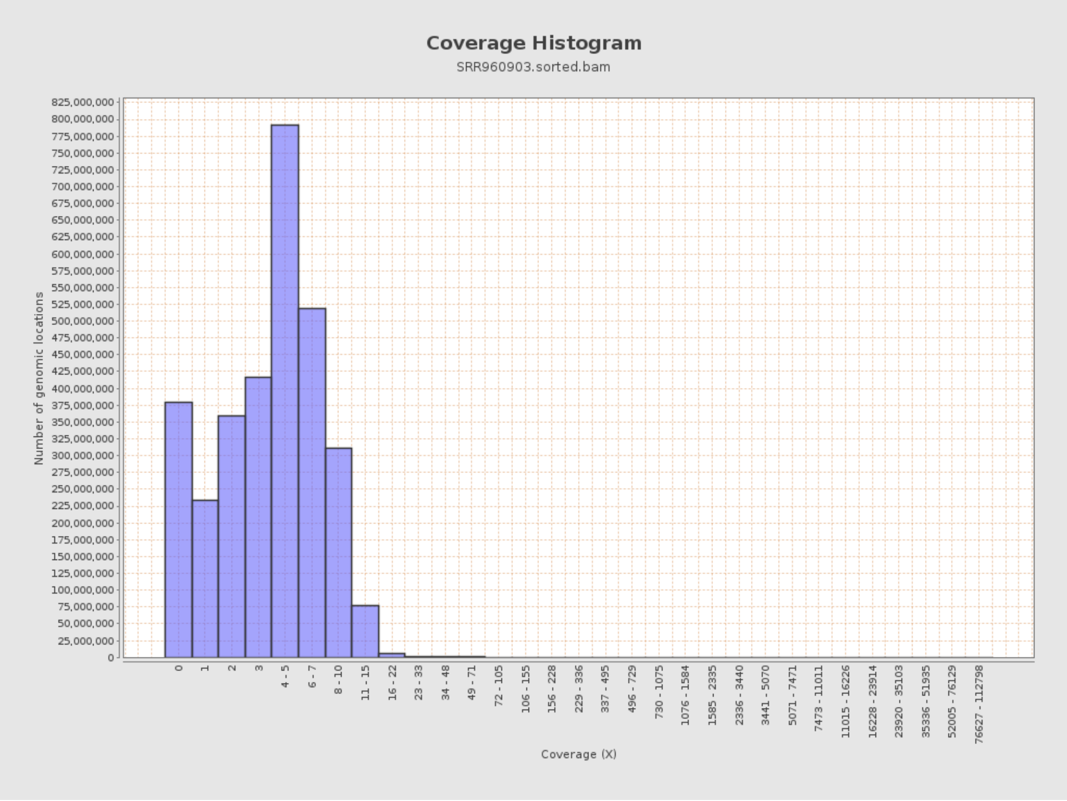
		bases	coverage	deviation
chr1	249250621	1096090377	4.3975	114.9941
chr2	243199373	1160160701	4.7704	31.944
chr3	198022430	892307558	4.5061	8.1794
chr4	191154276	909953345	4.7603	35.7232
chr5	180915260	814513489	4.5022	4.8853
chr6	171115067	776069009	4.5354	14.1472
chr7	159138663	719379732	4.5205	29.659
chr8	146364022	680921118	4.6522	51.4316
chr9	141213431	560653487	3.9703	40.6426
chr10	135534747	690953954	5.098	96.6106
chr11	135006516	605955535	4.4883	19.1789
chr12	133851895	594973840	4.445	4.4295
chr13	115169878	432200181	3.7527	3.1618
chr14	107349540	397429469	3.7022	5.8515
chr15	102531392	372041445	3.6286	3.2305
chr16	90354753	416098327	4.6052	38.6269
chr17	81195210	352926528	4.3466	17.91
chr18	78077248	369341859	4.7305	49.0814
chr19	59128983	253902901	4.2941	56.1444
chr20	63025520	274360534	4.3532	14.1461
chr21	48129895	184329139	3.8298	18.9859
chr22	51304566	152968669	2.9816	3.9323
chrMT	16571	10291928	621.0807	92.4164
chrX	155270560	696435822	4.4853	14.7997

chrY	59373566	42314740	0.7127	39.0904

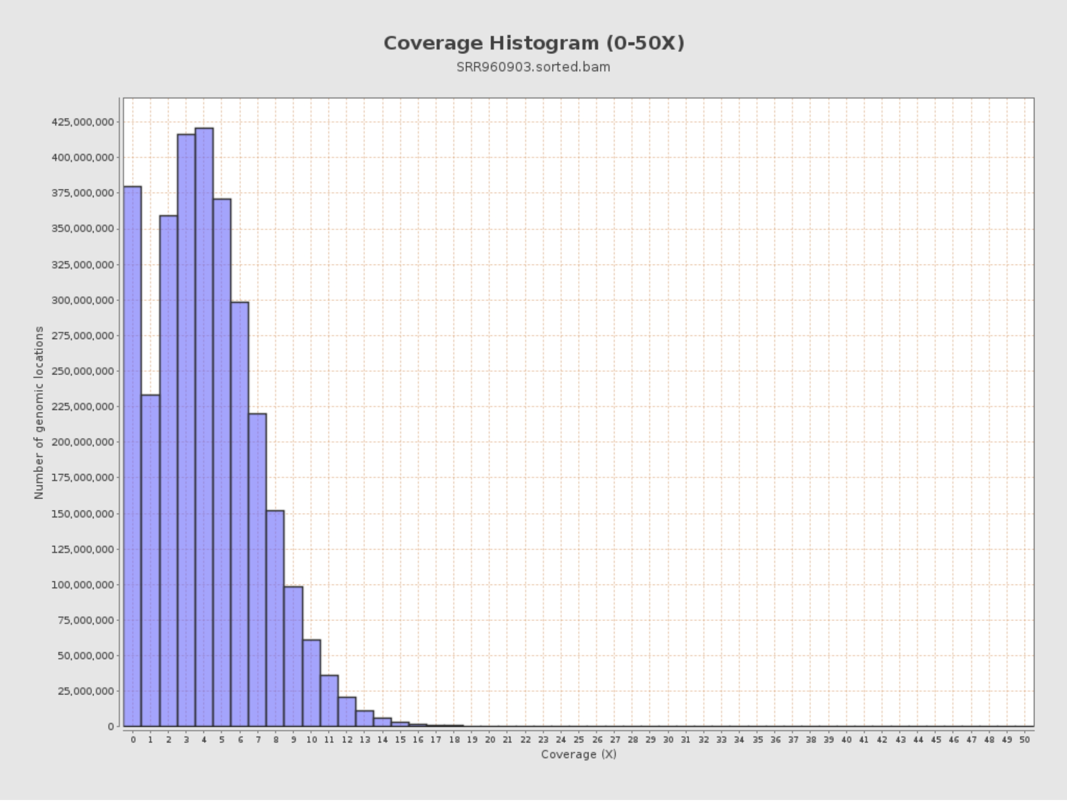
3. Results : Coverage across reference



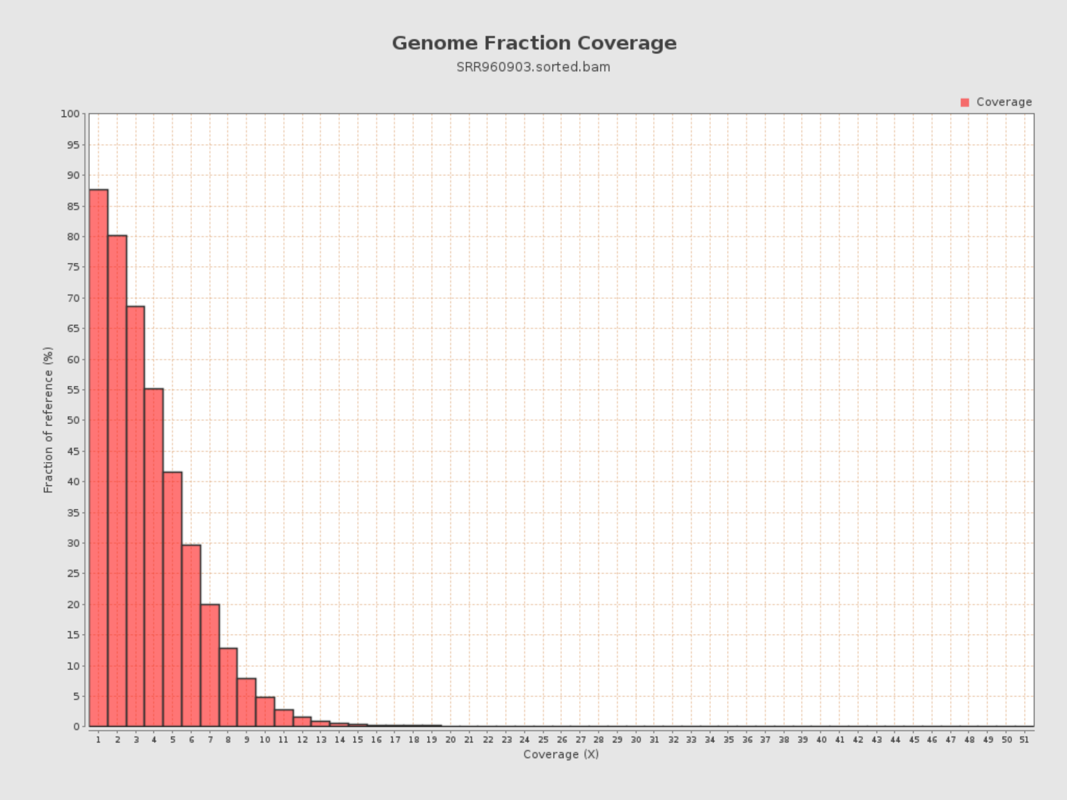
4. Results : Coverage Histogram



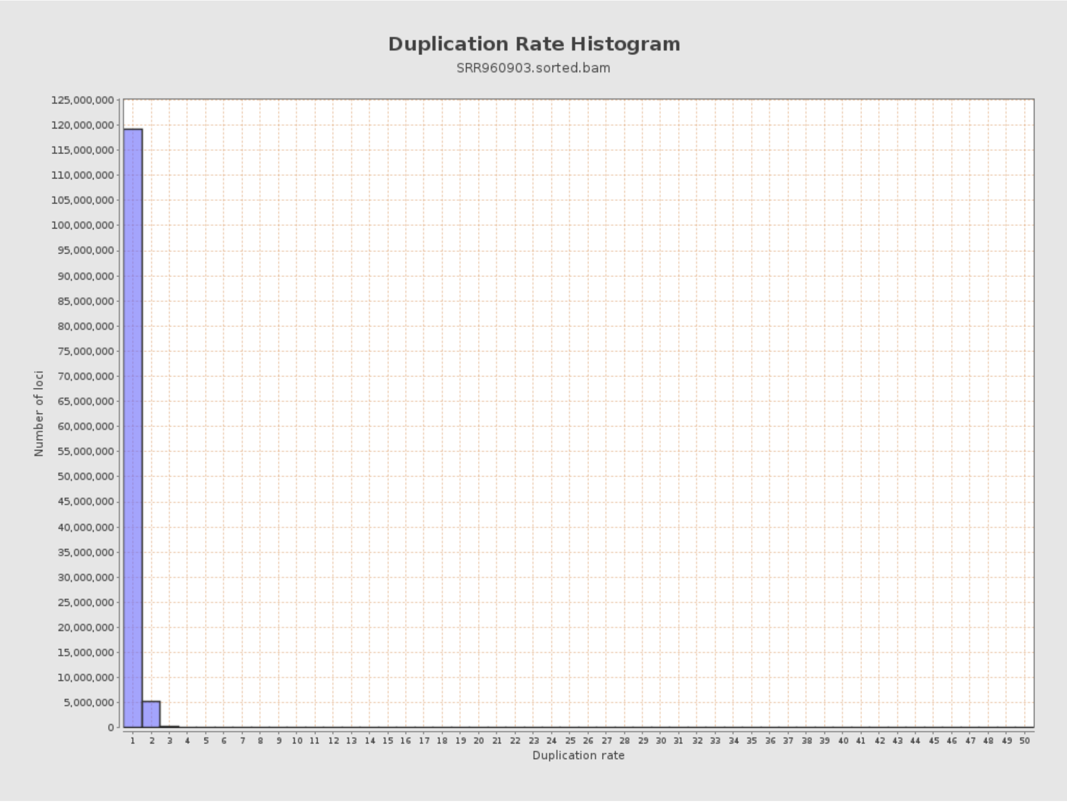
5. Results : Coverage Histogram (0-50X)



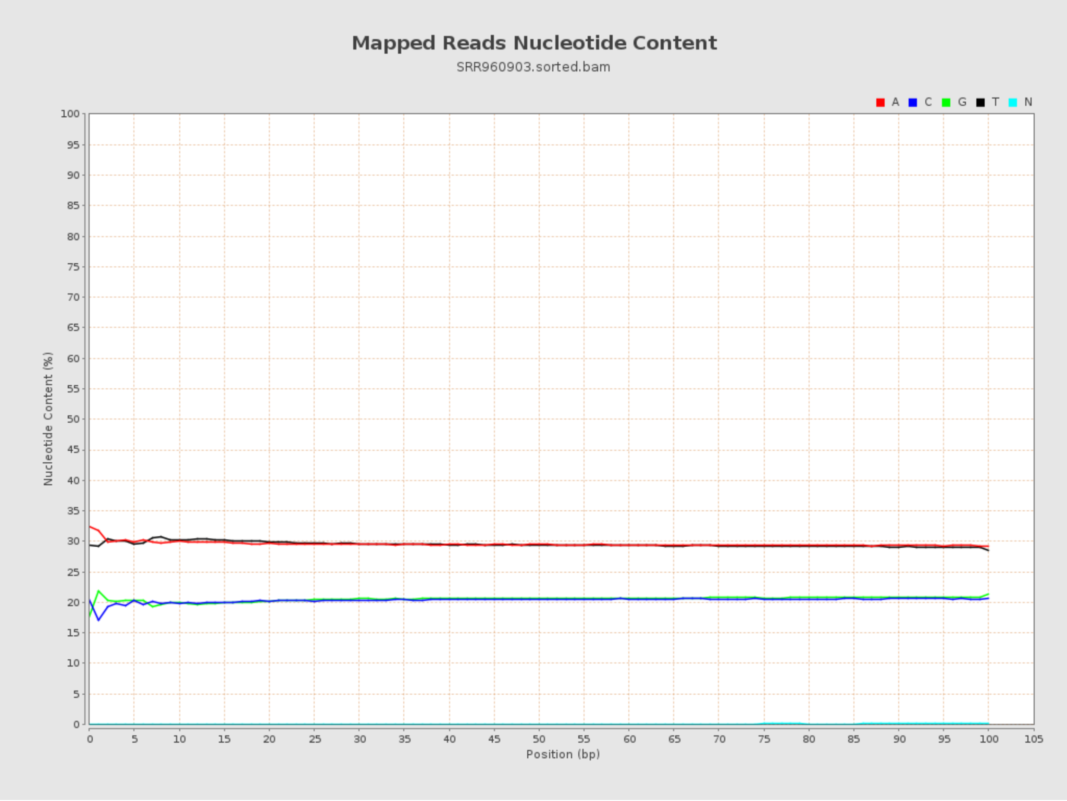
6. Results : Genome Fraction Coverage



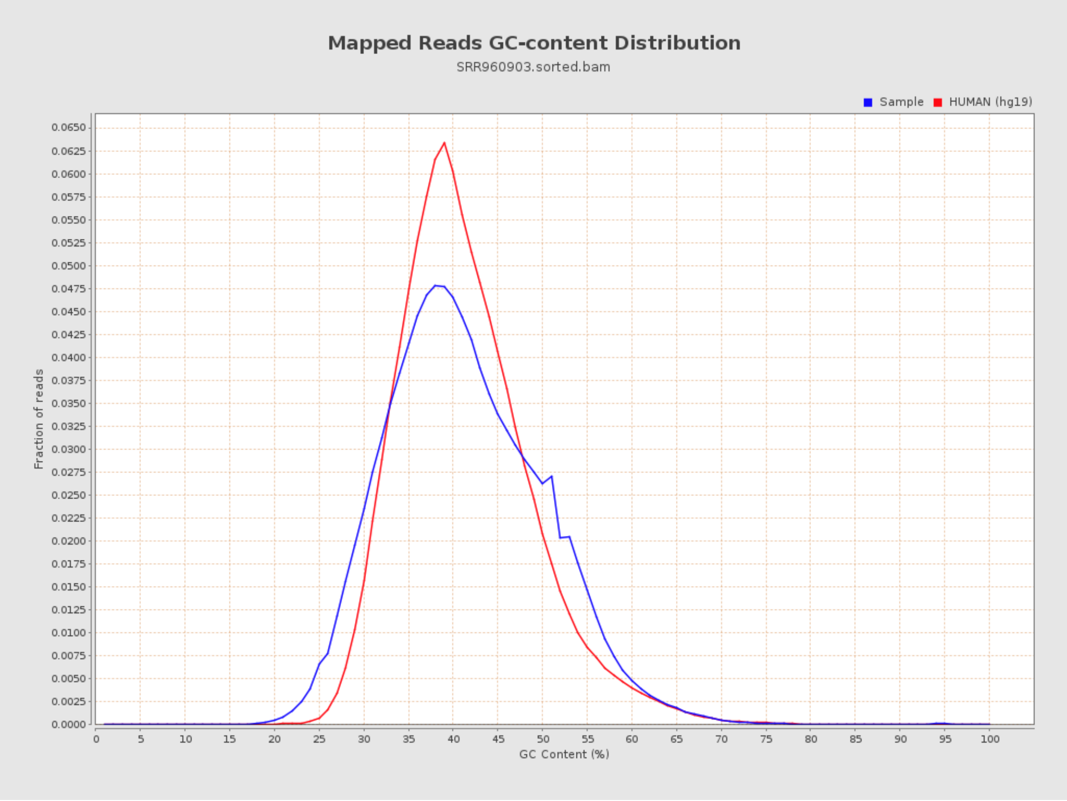
7. Results : Duplication Rate Histogram



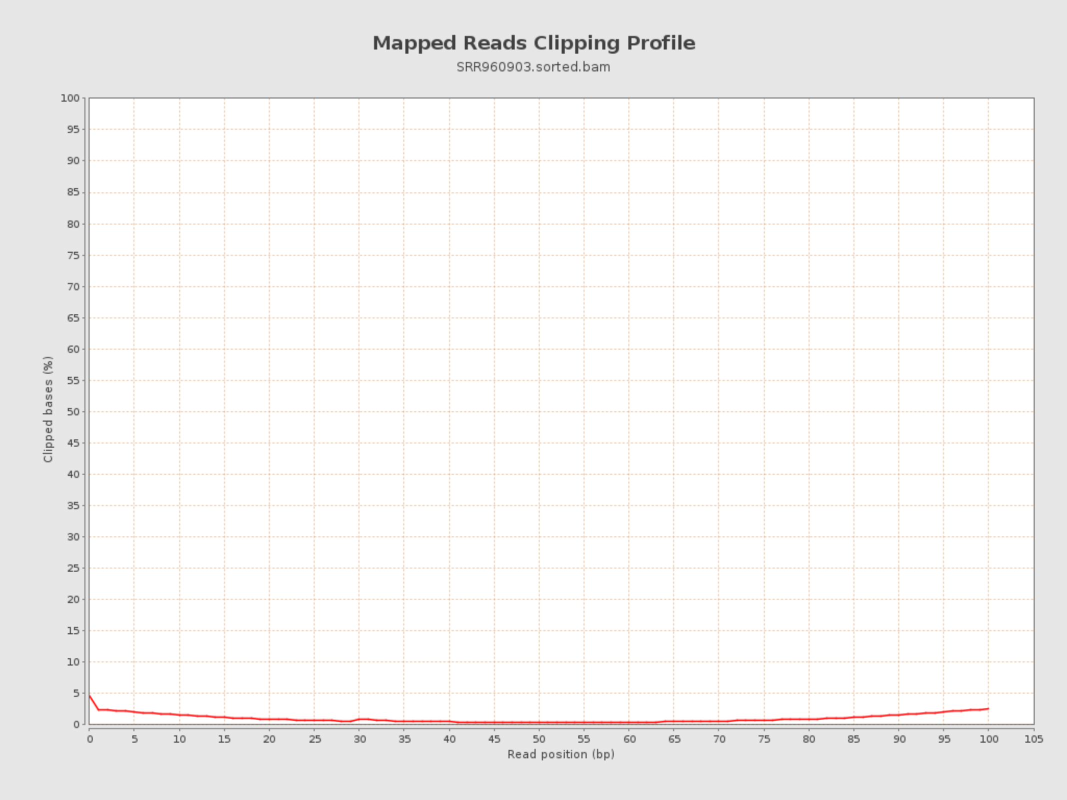
8. Results : Mapped Reads Nucleotide Content



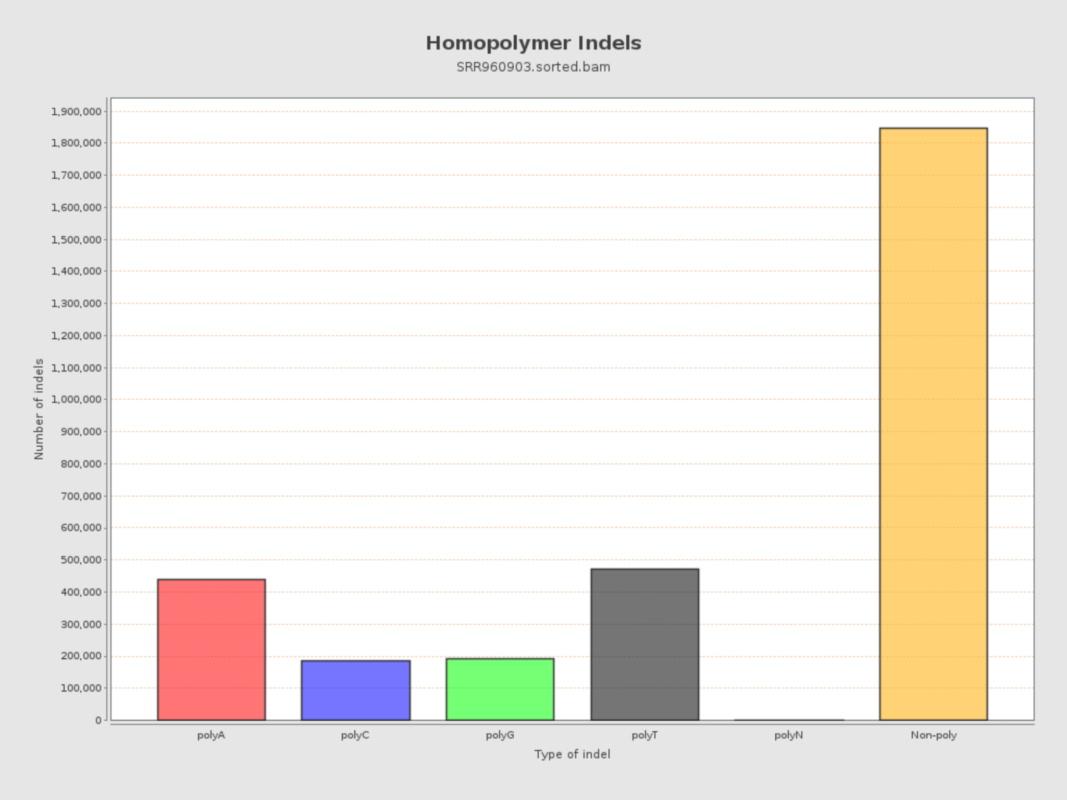
9. Results : Mapped Reads GC-content Distribution



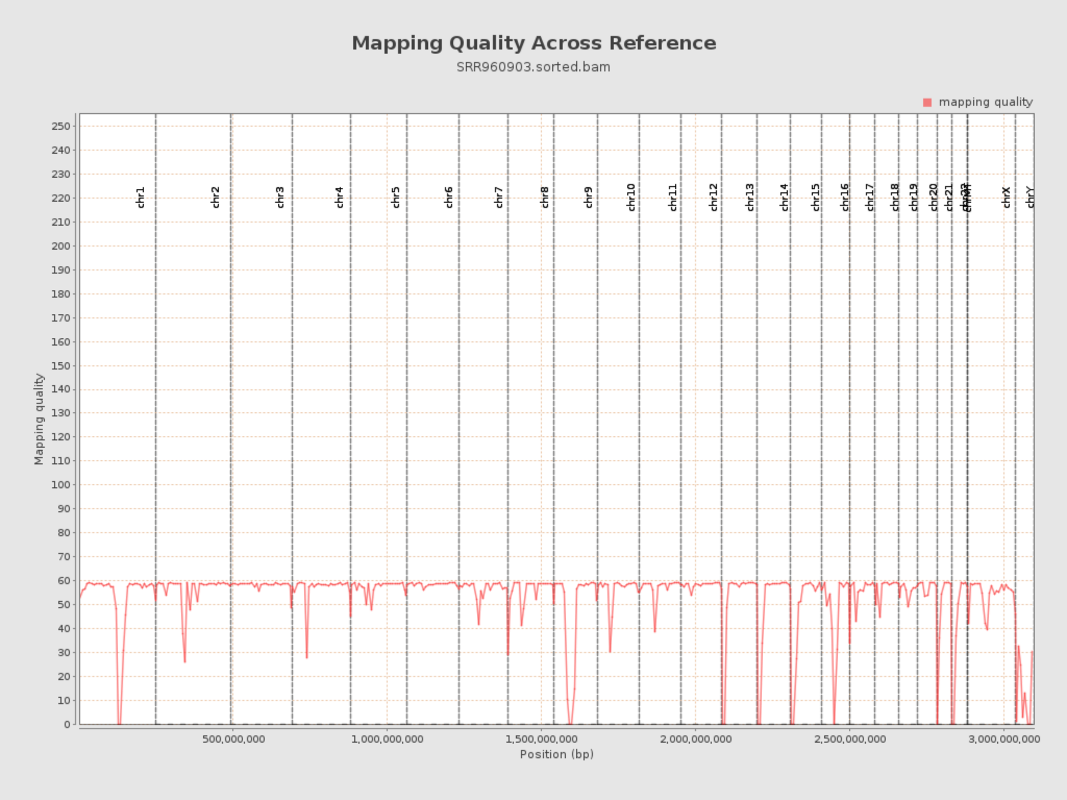
10. Results : Mapped Reads Clipping Profile



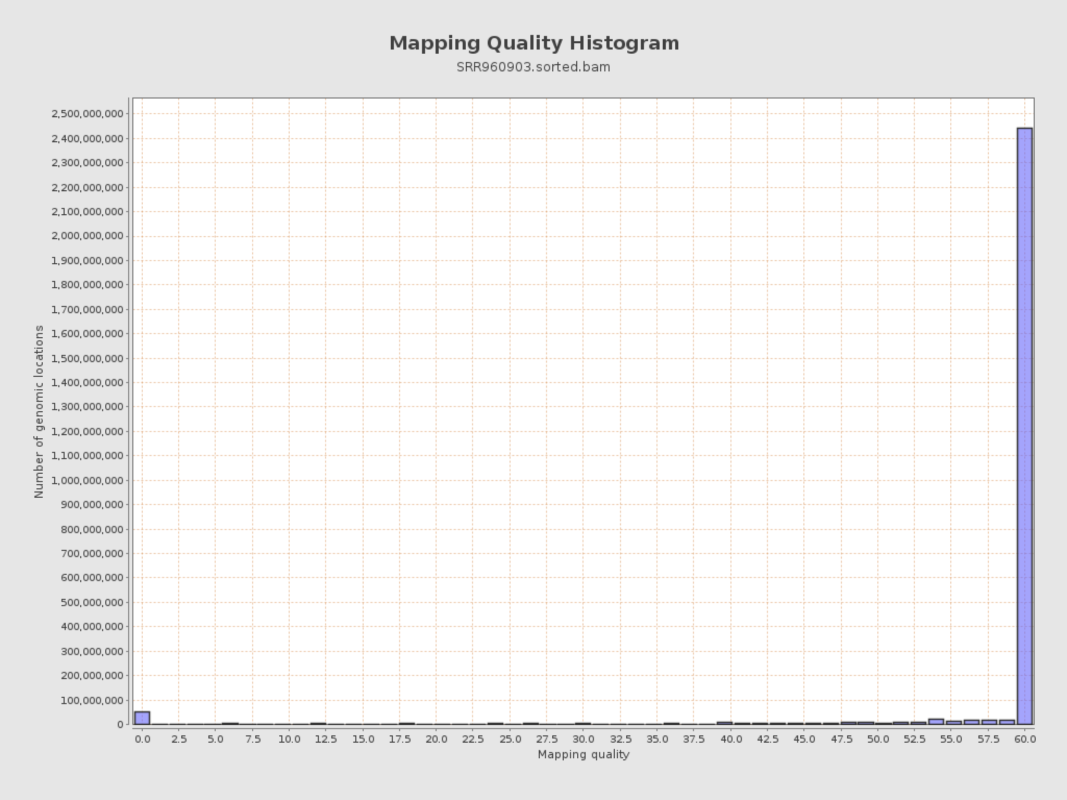
11. Results : Homopolymer Indels



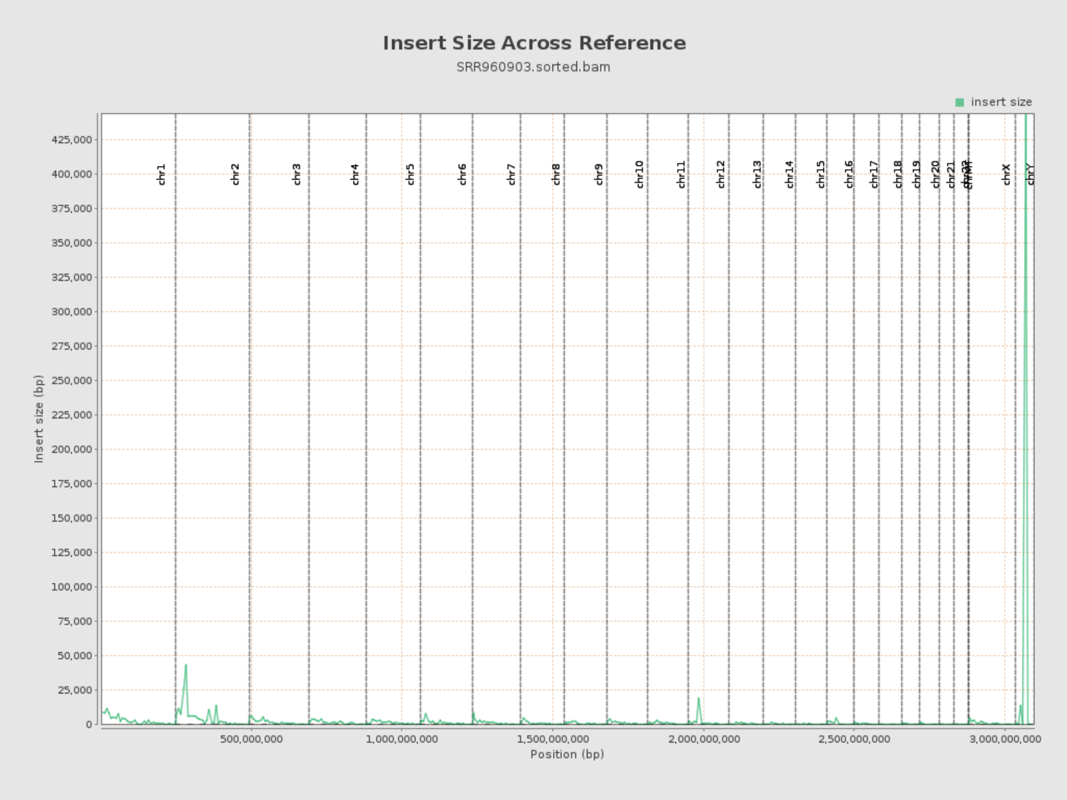
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram