Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 00:13:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960905.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_SRR960905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960905_1.fastq.gz SRR960905_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 00:13:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	156,845,918
Mapped reads	153,717,147 / 98.01%
Unmapped reads	3,128,771 / 1.99%
Mapped paired reads	153,717,147 / 98.01%
Mapped reads, first in pair	77,188,369 / 49.21%
Mapped reads, second in pair	76,528,778 / 48.79%
Mapped reads, both in pair	152,561,020 / 97.27%
Mapped reads, singletons	1,156,127 / 0.74%
Secondary alignments	0
Supplementary alignments	314,641 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	14,015,824 / 8.94%
Duplication rate	5.13%
Clipped reads	18,872,882 / 12.03%

2.2. ACGT Content

Number/percentage of A's	4,473,858,561 / 29.56%
Number/percentage of C's	3,083,193,047 / 20.37%
Number/percentage of T's	4,461,628,182 / 29.48%
Number/percentage of G's	3,107,263,403 / 20.53%
Number/percentage of N's	7,462,248 / 0.05%

GC Percentage	40.91%

2.3. Coverage

Mean	4.89
Standard Deviation	51.8266

2.4. Mapping Quality

Mean Mapping Quality	53.64

2.5. Insert size

Mean	20,257.87
Standard Deviation	1,335,004.35
P25/Median/P75	139 / 150 / 160

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	148,160,518
Insertions	1,698,125
Mapped reads with at least one insertion	1.07%
Deletions	1,855,807
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.92%

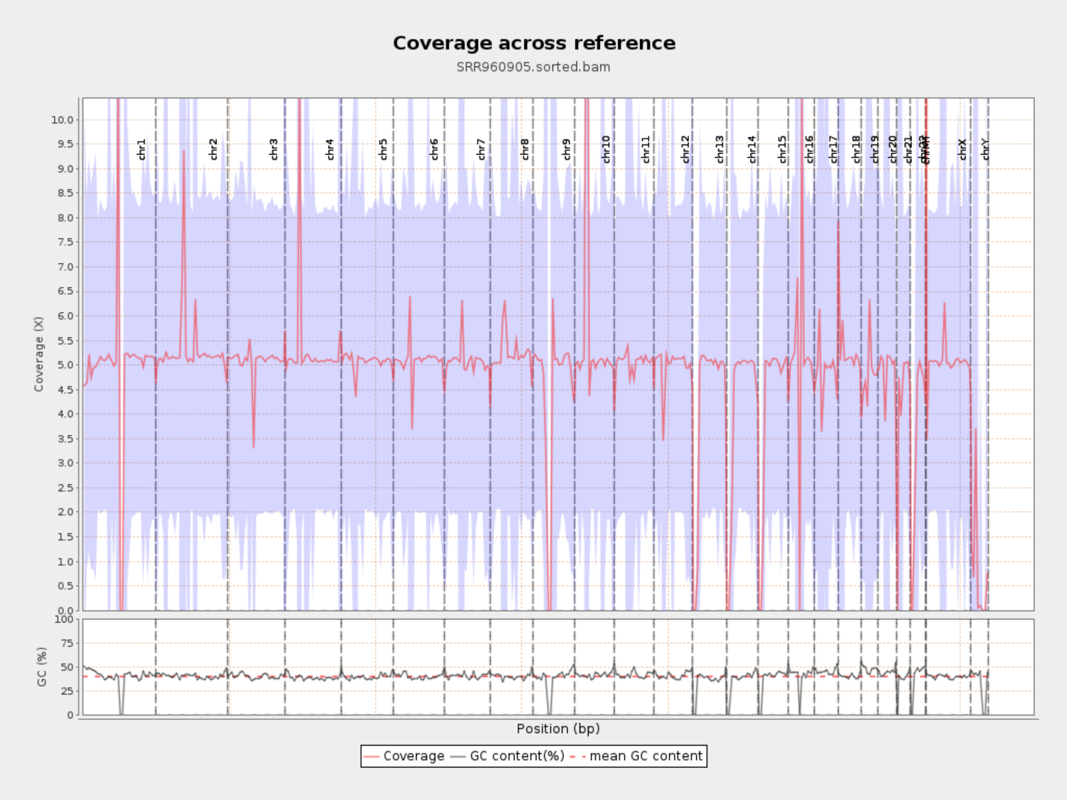
2.7. Chromosome stats

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

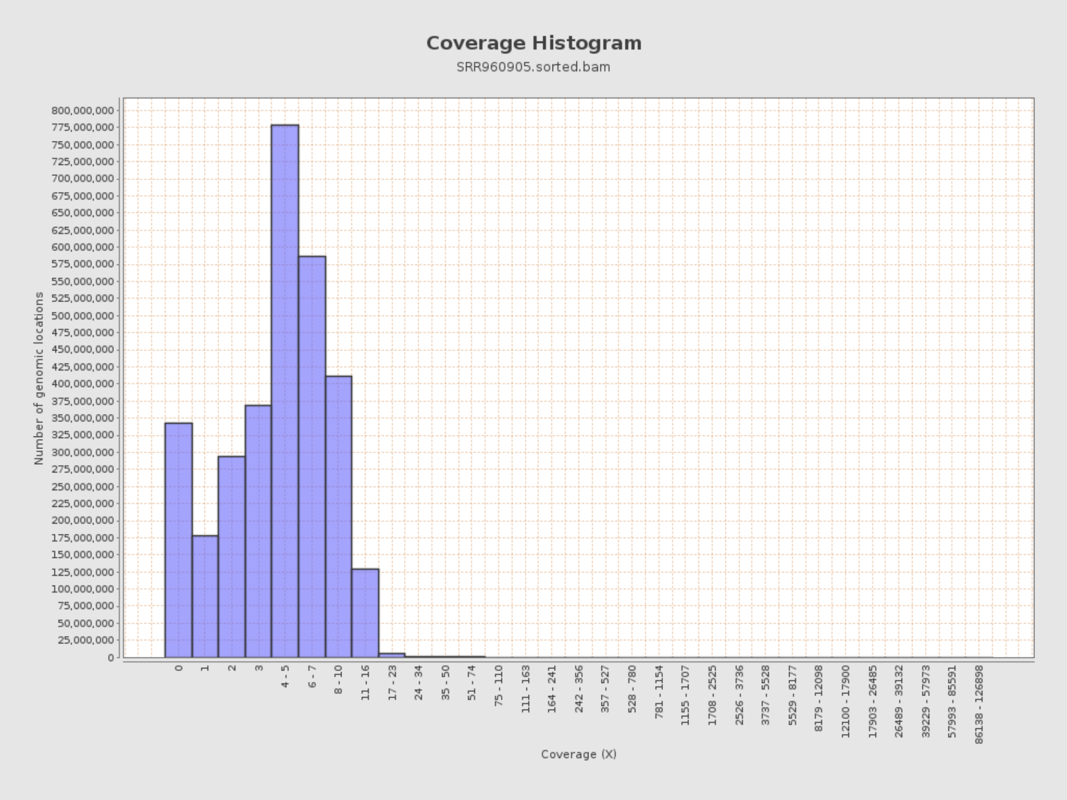
		bases	coverage	deviation
chr1	249250621	1232932603	4.9466	129.1679
chr2	243199373	1301657097	5.3522	32.8405
chr3	198022430	1004723293	5.0738	9.0844
chr4	191154276	1022321585	5.3481	40.1432
chr5	180915260	916099370	5.0637	5.3759
chr6	171115067	872652337	5.0998	15.9257
chr7	159138663	809705246	5.088	33.2869
chr8	146364022	766268347	5.2354	57.7933
chr9	141213431	631743147	4.4737	46.0175
chr10	135534747	776865122	5.7319	108.7567
chr11	135006516	682272886	5.0536	21.3606
chr12	133851895	669370860	5.0008	4.5266
chr13	115169878	486187177	4.2215	3.4491
chr14	107349540	447357673	4.1673	4.8995
chr15	102531392	419318297	4.0897	3.518
chr16	90354753	468630196	5.1866	43.422
chr17	81195210	397318631	4.8934	20.0425
chr18	78077248	414895730	5.3139	55.512
chr19	59128983	286252011	4.8411	62.9567
chr20	63025520	308829105	4.9001	15.7956
chr21	48129895	207253742	4.3061	21.0742
chr22	51304566	172430210	3.3609	4.3287
chrMT	16571	11562023	697.7263	103.8049
chrX	155270560	783646129	5.047	16.596

chrY	59373566	47550959	0.8009	44.1569

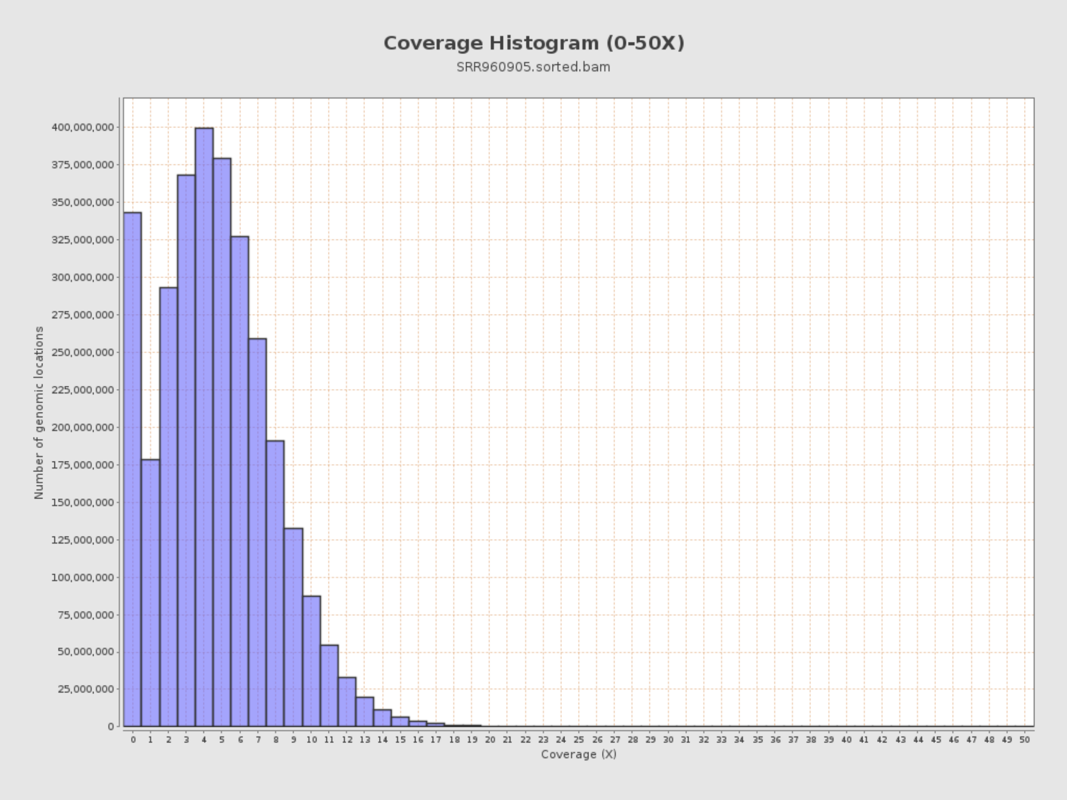
3. Results : Coverage across reference



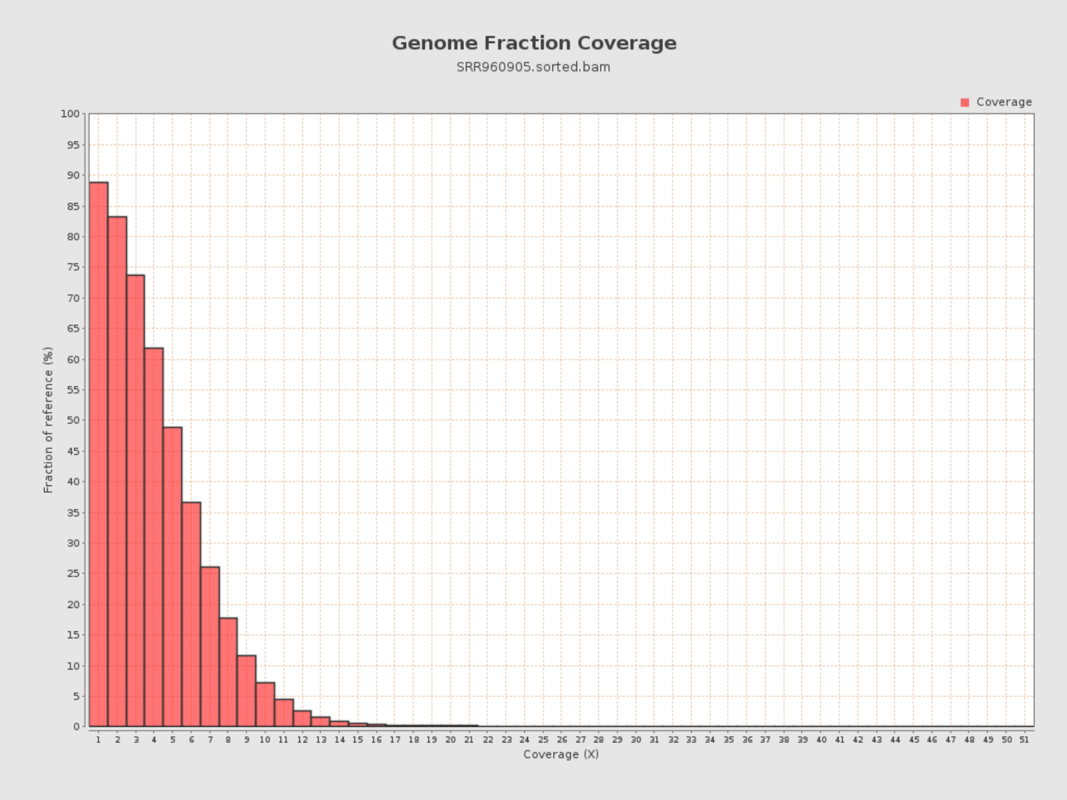
4. Results : Coverage Histogram



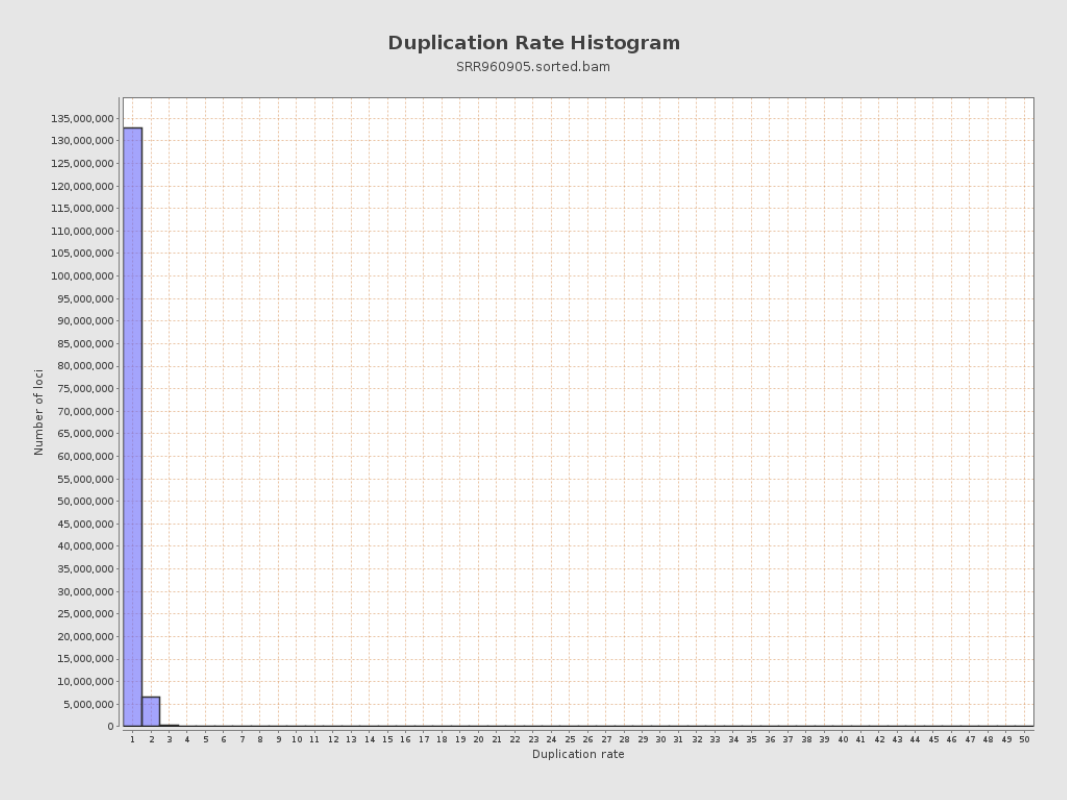
5. Results : Coverage Histogram (0-50X)



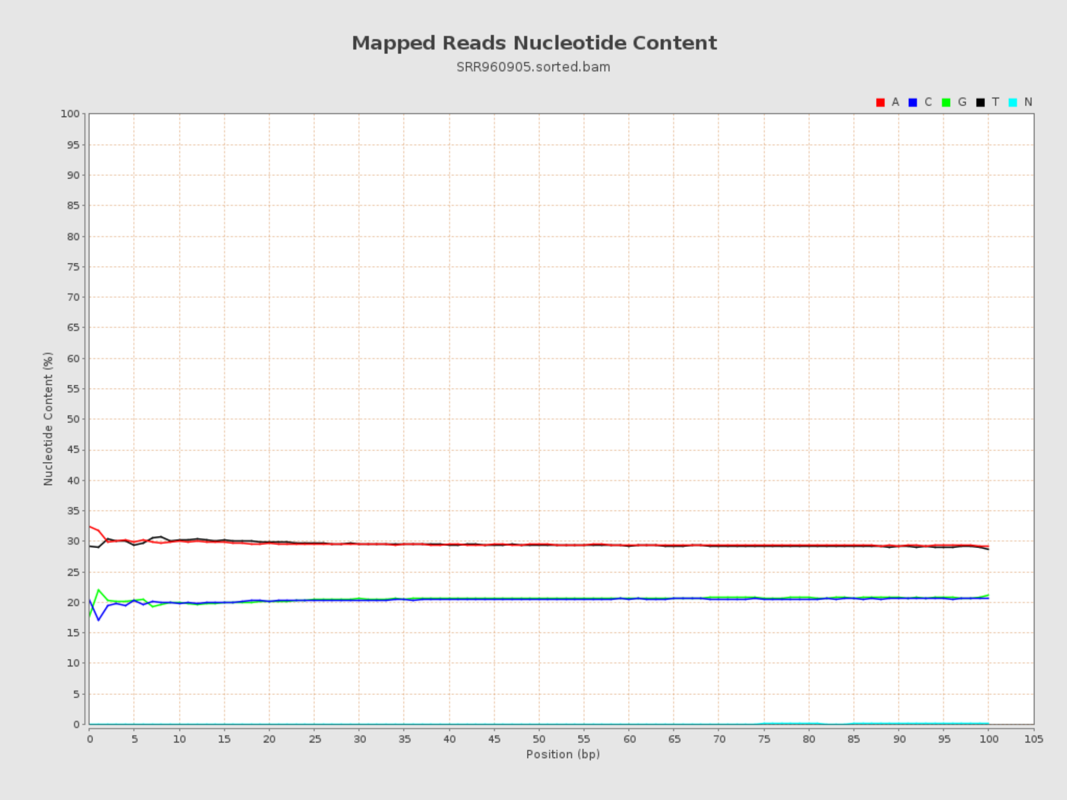
6. Results : Genome Fraction Coverage



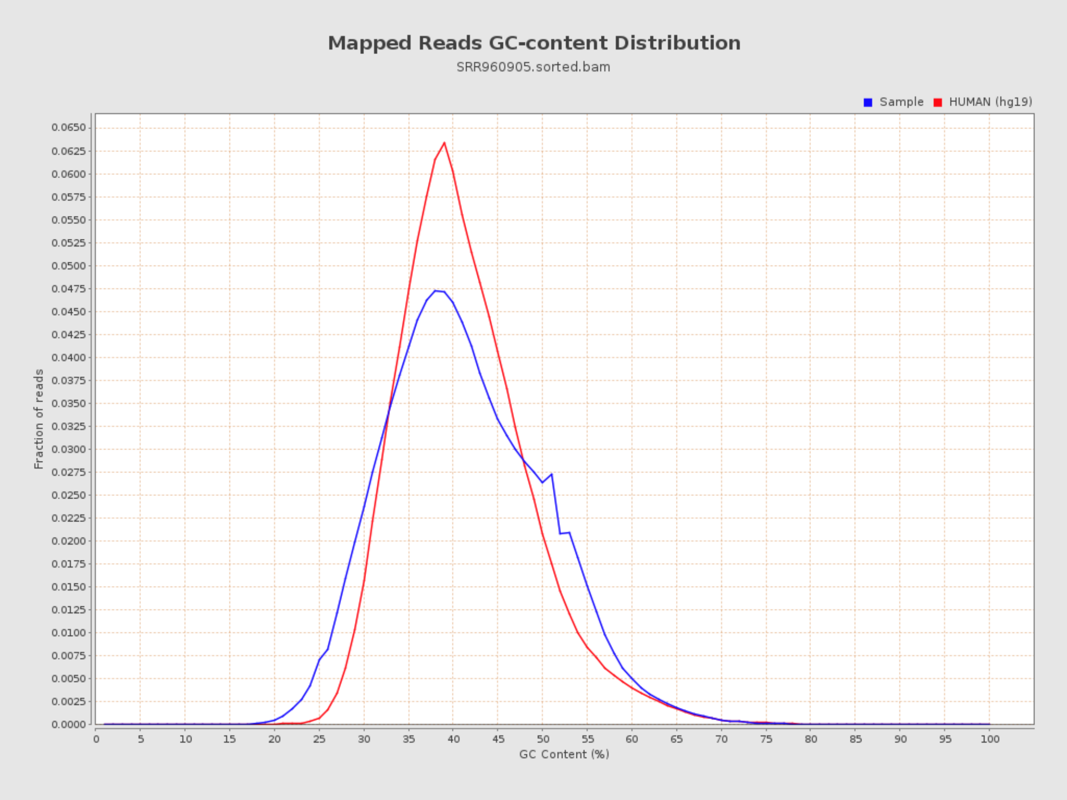
7. Results : Duplication Rate Histogram



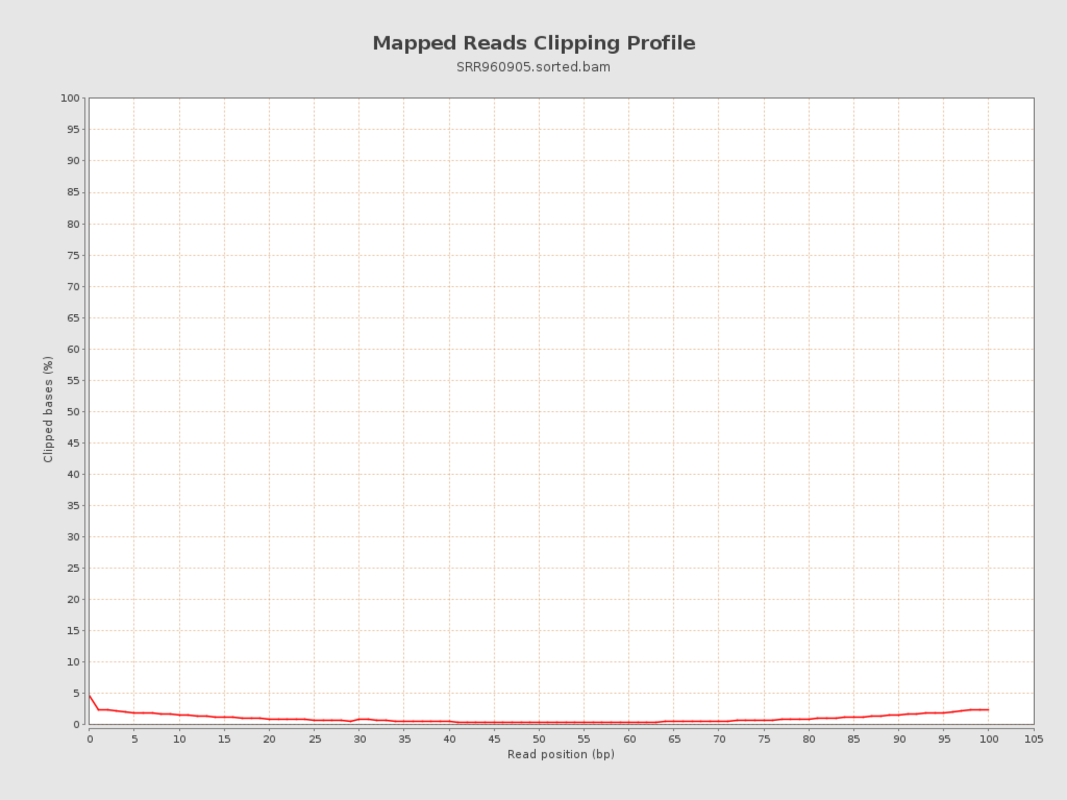
8. Results : Mapped Reads Nucleotide Content



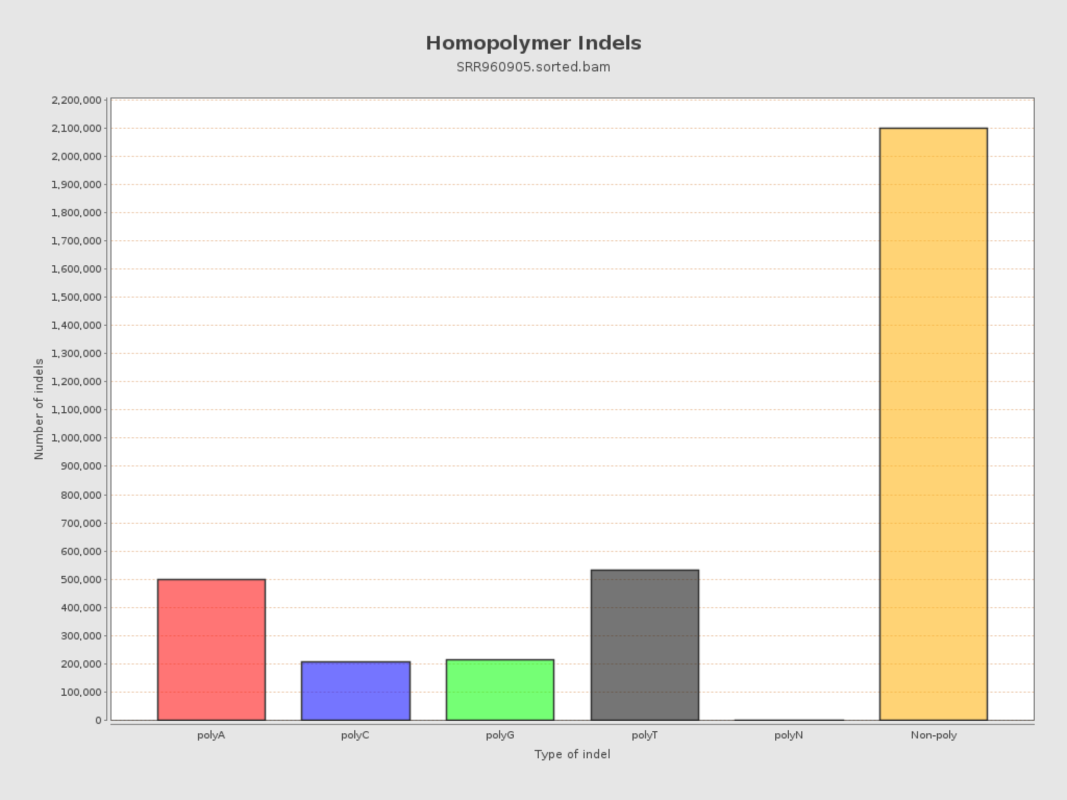
9. Results : Mapped Reads GC-content Distribution



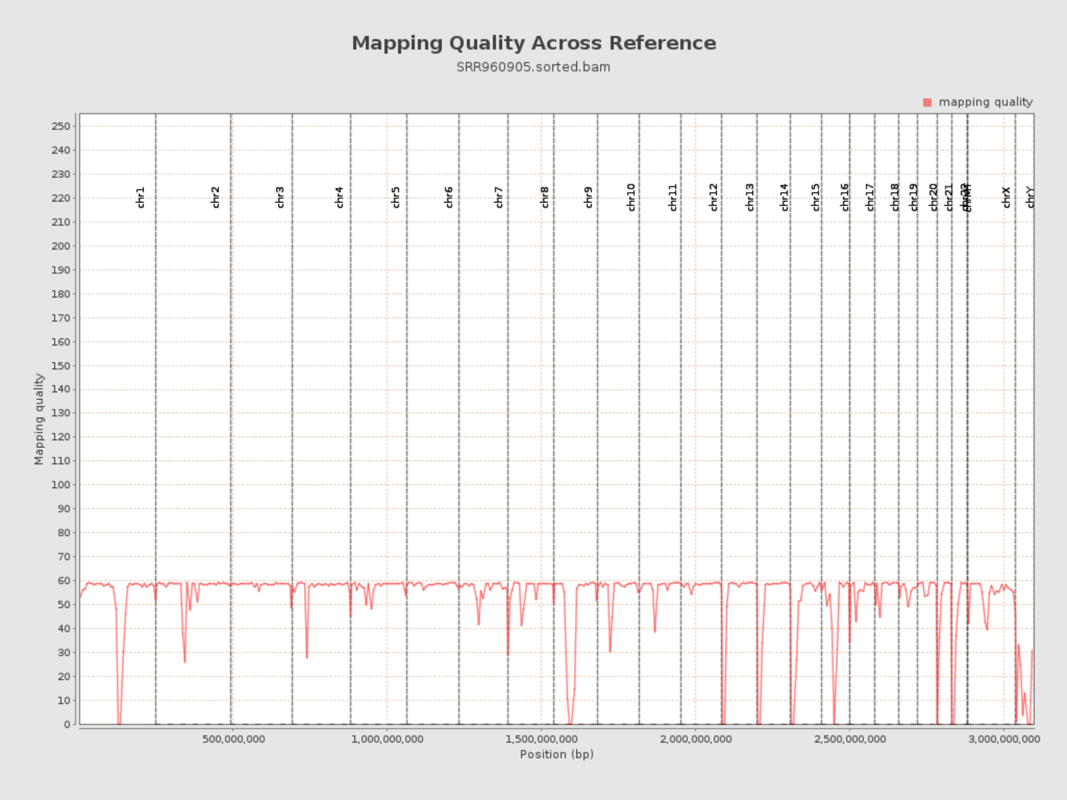
10. Results : Mapped Reads Clipping Profile



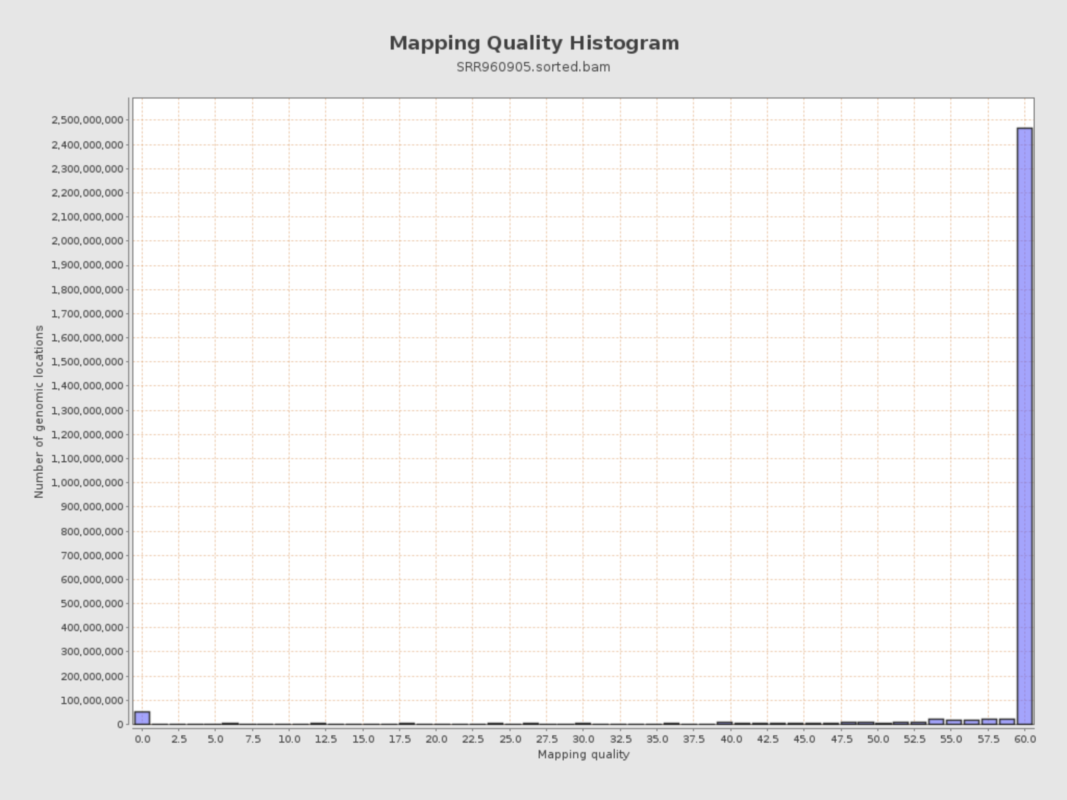
11. Results : Homopolymer Indels



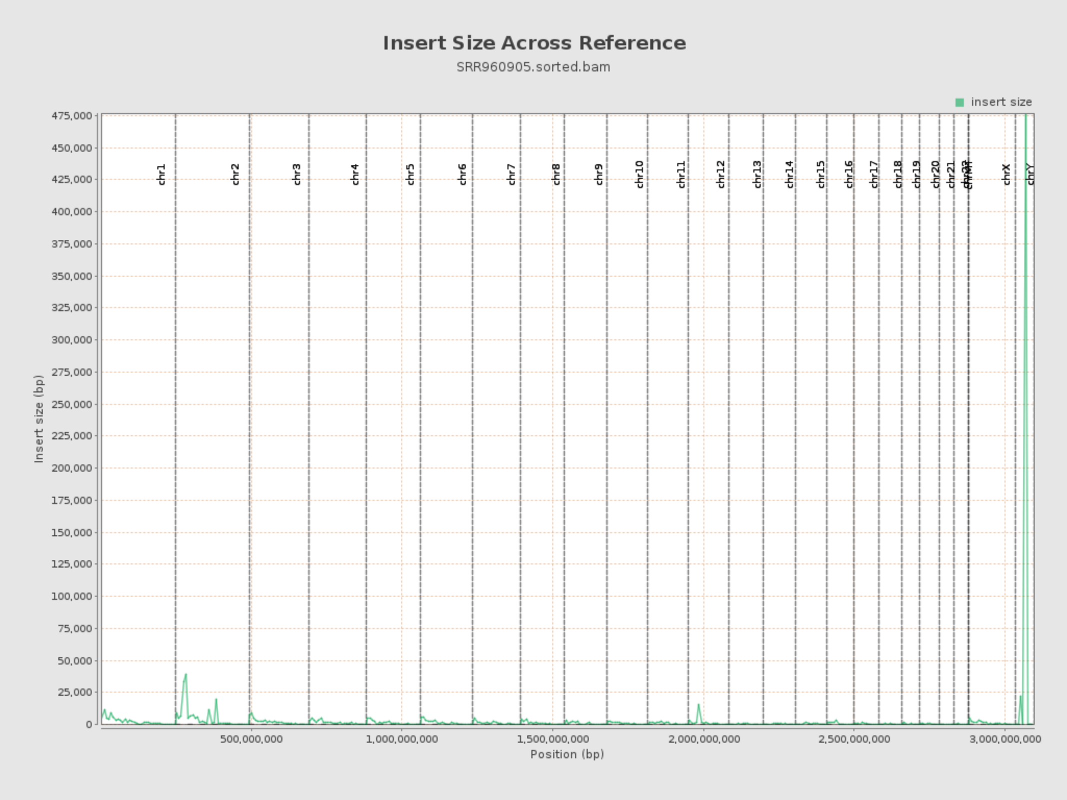
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram