Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 19:29:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960922.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_SRR960922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960922_1.fastq.gz SRR960922_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 19:29:32 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	225,220,794
Mapped reads	219,961,387 / 97.66%
Unmapped reads	5,259,407 / 2.34%
Mapped paired reads	219,961,387 / 97.66%
Mapped reads, first in pair	110,578,419 / 49.1%
Mapped reads, second in pair	109,382,968 / 48.57%
Mapped reads, both in pair	217,738,228 / 96.68%
Mapped reads, singletons	2,223,159 / 0.99%
Secondary alignments	0
Supplementary alignments	445,200 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	36,624,113 / 16.26%
Duplication rate	11.89%
Clipped reads	43,338,665 / 19.24%

2.2. ACGT Content

Number/percentage of A's	6,545,335,085 / 30.63%
Number/percentage of C's	4,149,460,348 / 19.42%
Number/percentage of T's	6,546,975,883 / 30.64%
Number/percentage of G's	4,123,452,924 / 19.3%
Number/percentage of N's	1,595,979 / 0.01%

GC Percentage	38.72%

2.3. Coverage

Mean	6.9041
Standard Deviation	101.7521

2.4. Mapping Quality

Mean Mapping Quality	53.54

2.5. Insert size

Mean	18,755.34
Standard Deviation	1,268,897.72
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	323,317,007
Insertions	2,623,198
Mapped reads with at least one insertion	1.16%
Deletions	2,876,454
Mapped reads with at least one deletion	1.27%
Homopolymer indels	39.89%

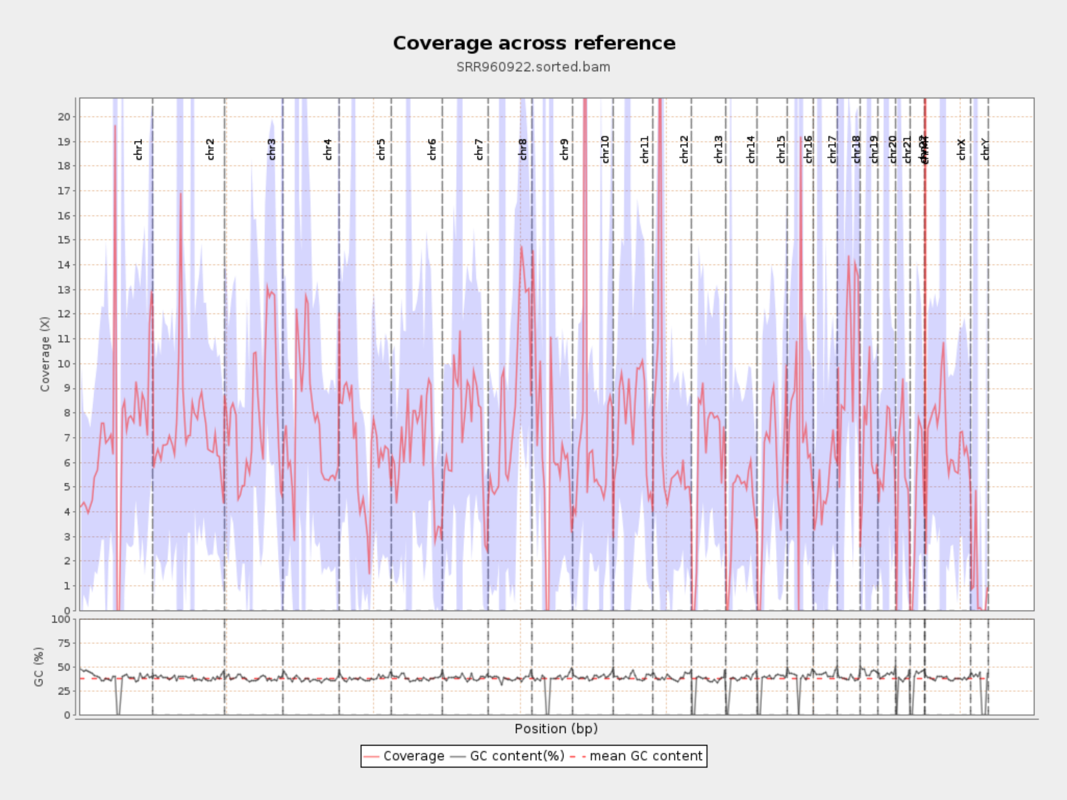
2.7. Chromosome stats

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

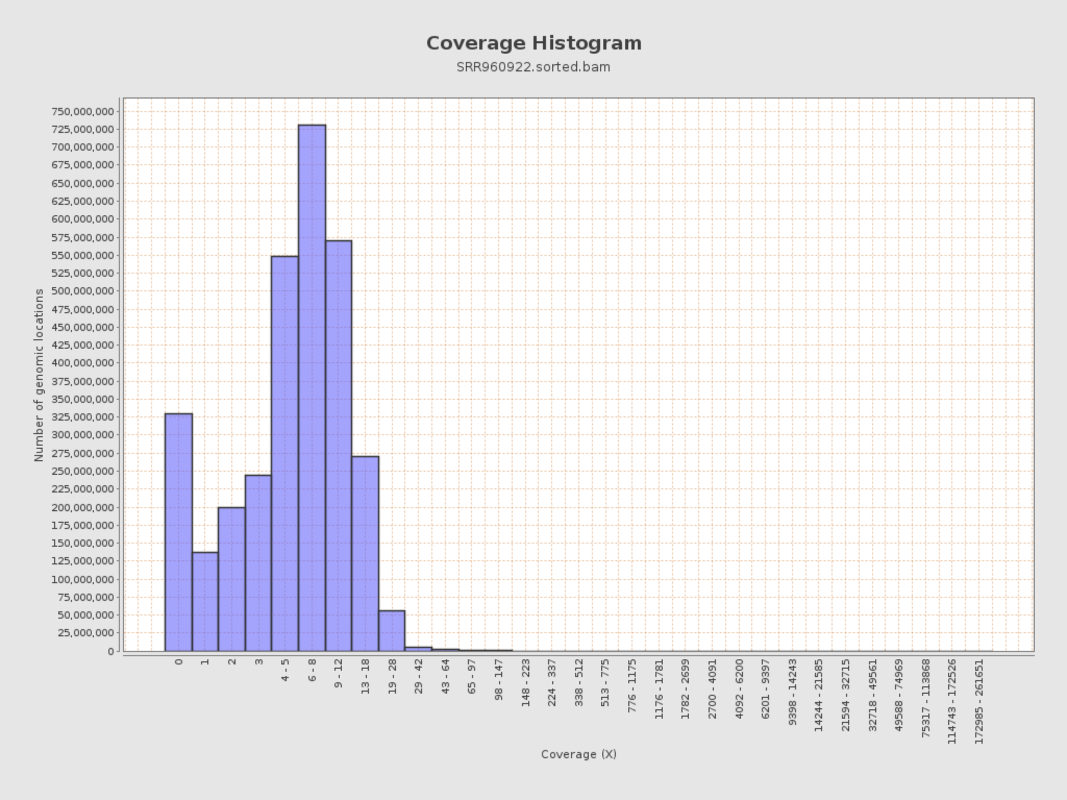
		bases	coverage	deviation
chr1	249250621	1774178570	7.1181	269.7841
chr2	243199373	1801458458	7.4073	53.8439
chr3	198022430	1592032523	8.0397	9.3109
chr4	191154276	1414419849	7.3994	54.01
chr5	180915260	1163923786	6.4335	9.1944
chr6	171115067	1125669256	6.5784	26.7396
chr7	159138663	1177617590	7.3999	67.2065
chr8	146364022	1254456768	8.5708	132.3059
chr9	141213431	912054120	6.4587	95.2601
chr10	135534747	1015775918	7.4946	194.4509
chr11	135006516	1040982226	7.7106	42.1221
chr12	133851895	967037932	7.2247	11.449
chr13	115169878	739778126	6.4234	4.8236
chr14	107349540	455182581	4.2402	7.2847
chr15	102531392	574302337	5.6012	5.1102
chr16	90354753	698532011	7.731	83.9734
chr17	81195210	404522663	4.9821	25.5102
chr18	78077248	822008549	10.5281	98.2219
chr19	59128983	391443004	6.6202	113.597
chr20	63025520	399016615	6.331	18.0992
chr21	48129895	285484460	5.9315	21.6994
chr22	51304566	217687562	4.243	5.5938
chrMT	16571	4771731	287.9567	60.5187
chrX	155270560	1082693757	6.9729	28.6107

chrY	59373566	57959080	0.9762	50.5405

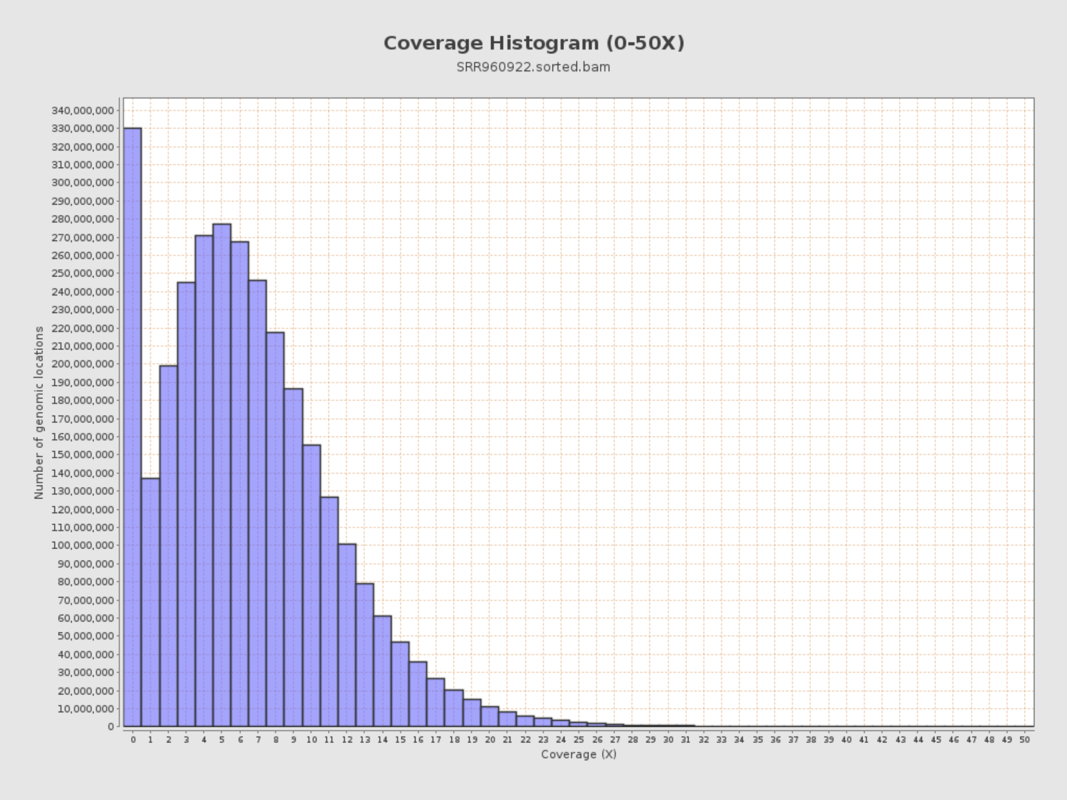
3. Results : Coverage across reference



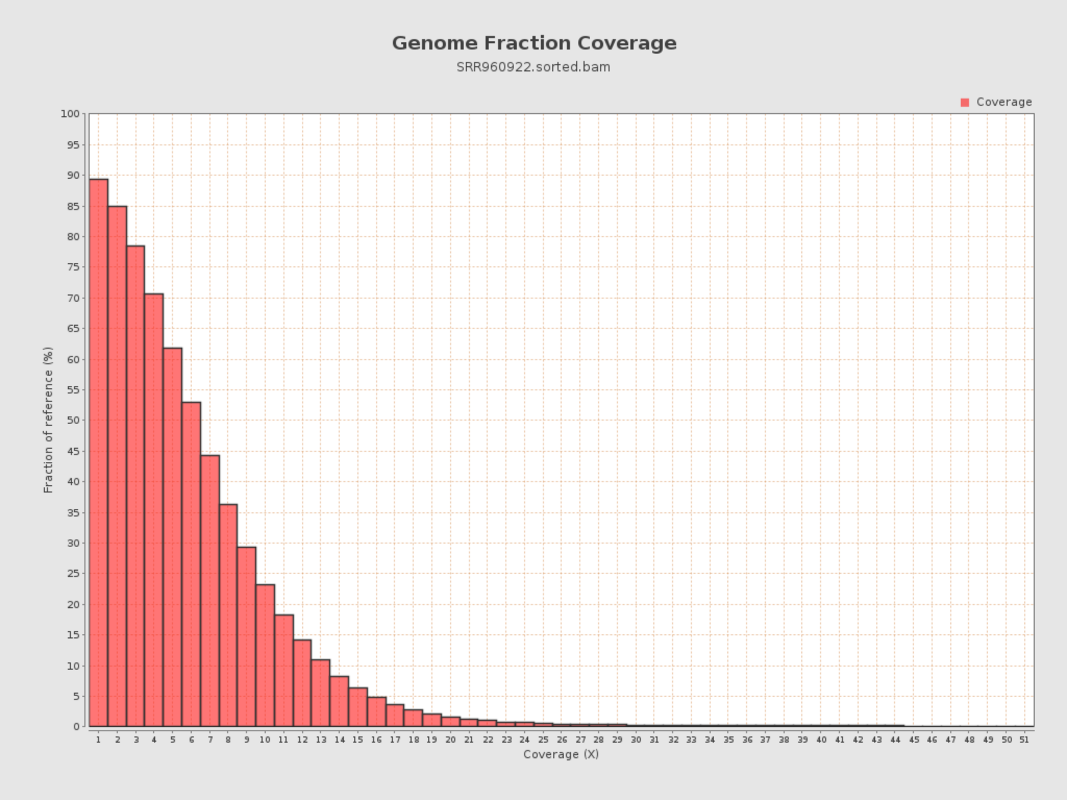
4. Results : Coverage Histogram



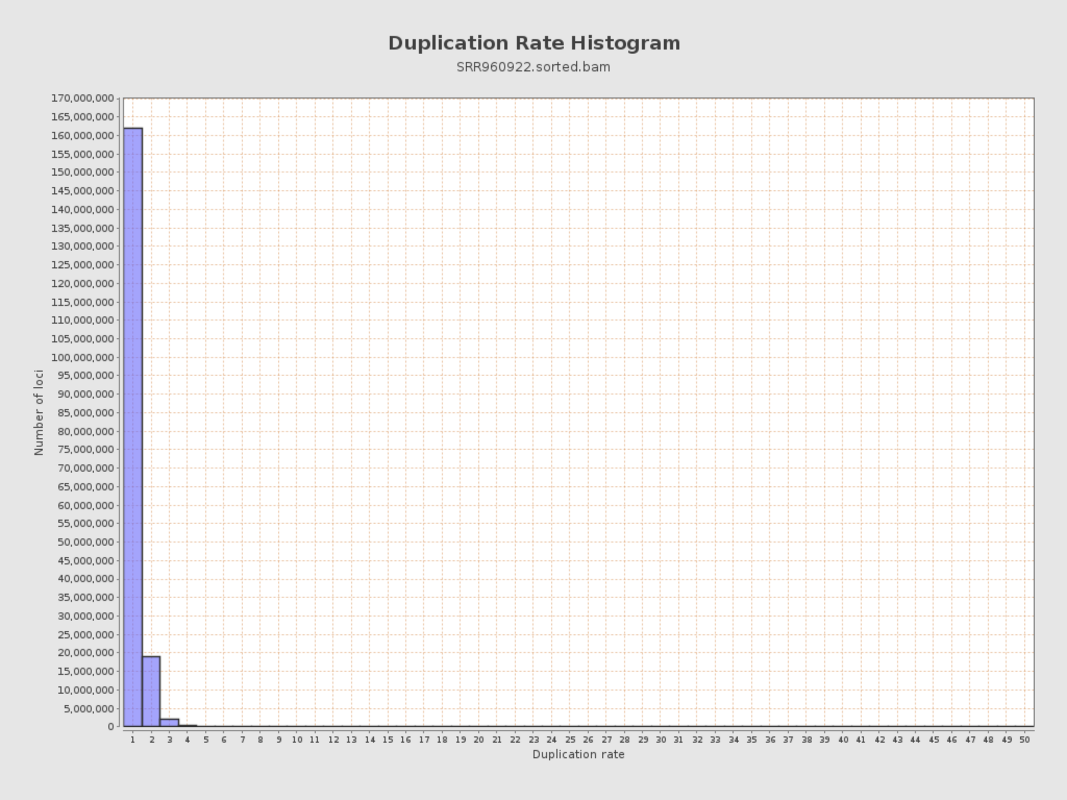
5. Results : Coverage Histogram (0-50X)



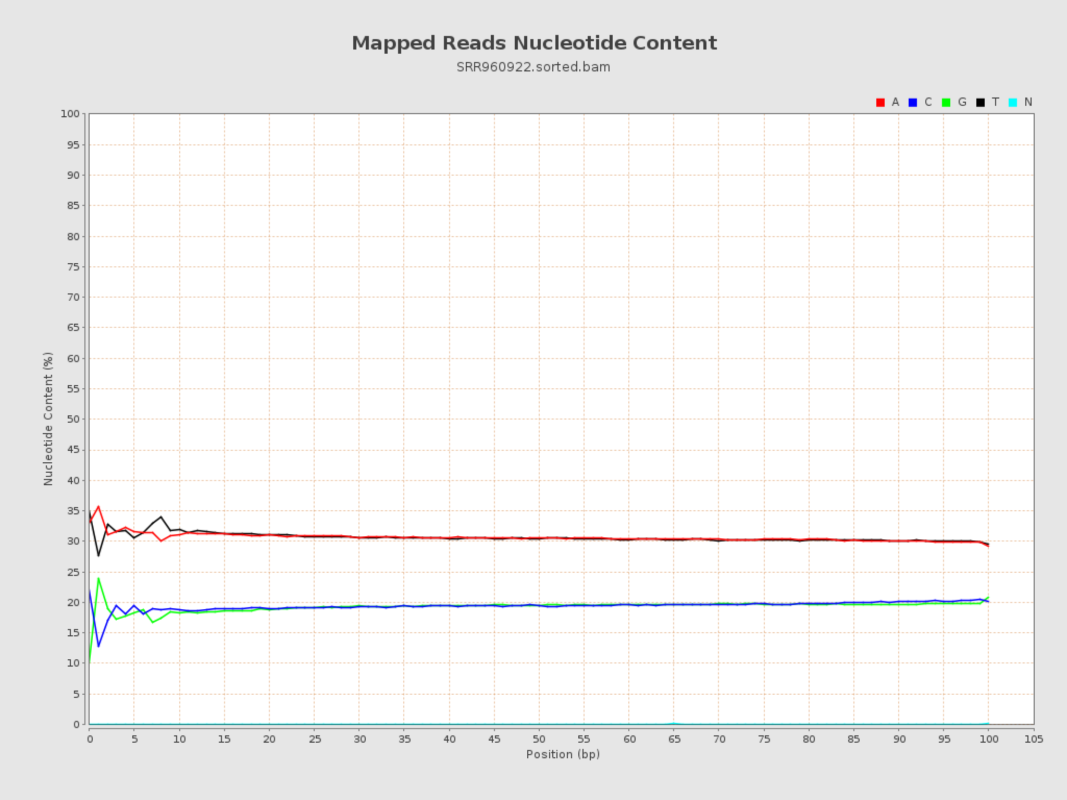
6. Results : Genome Fraction Coverage



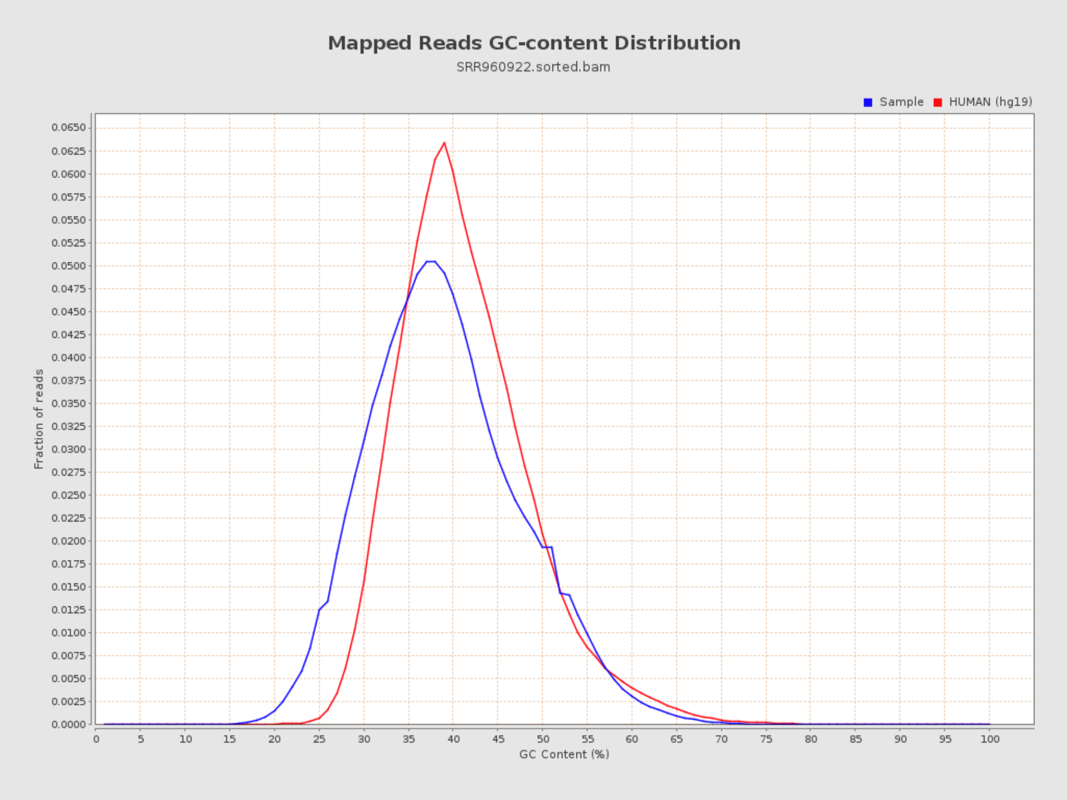
7. Results : Duplication Rate Histogram



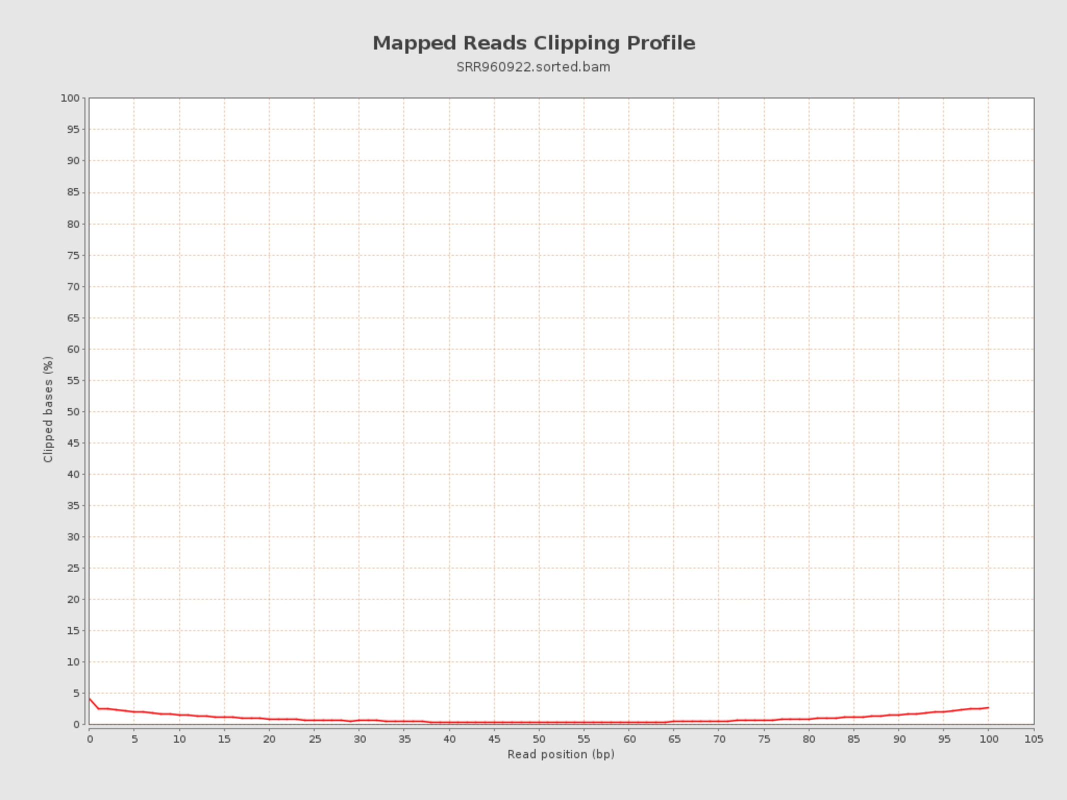
8. Results : Mapped Reads Nucleotide Content



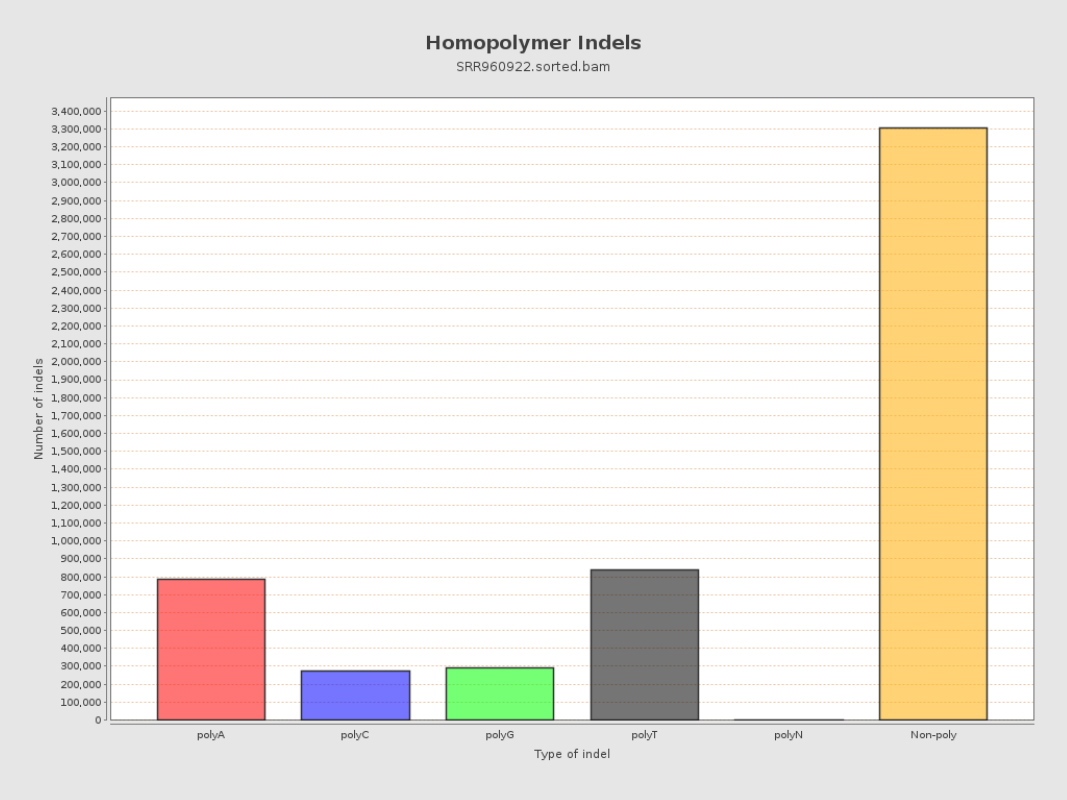
9. Results : Mapped Reads GC-content Distribution



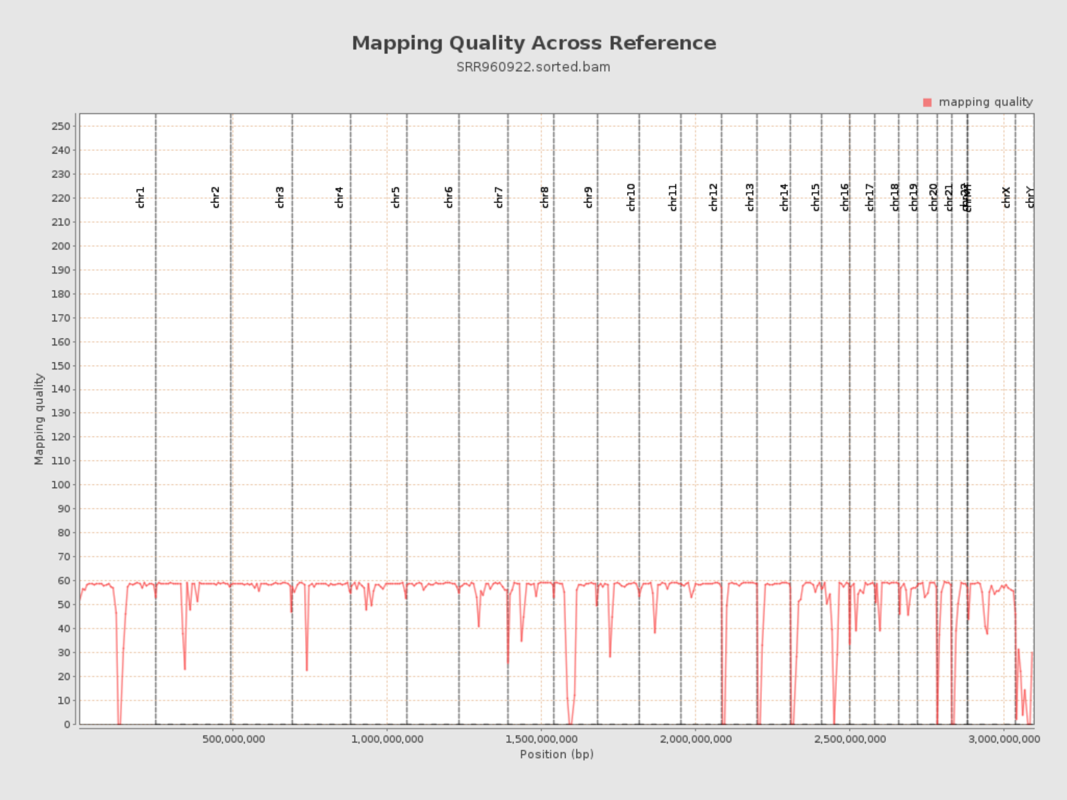
10. Results : Mapped Reads Clipping Profile



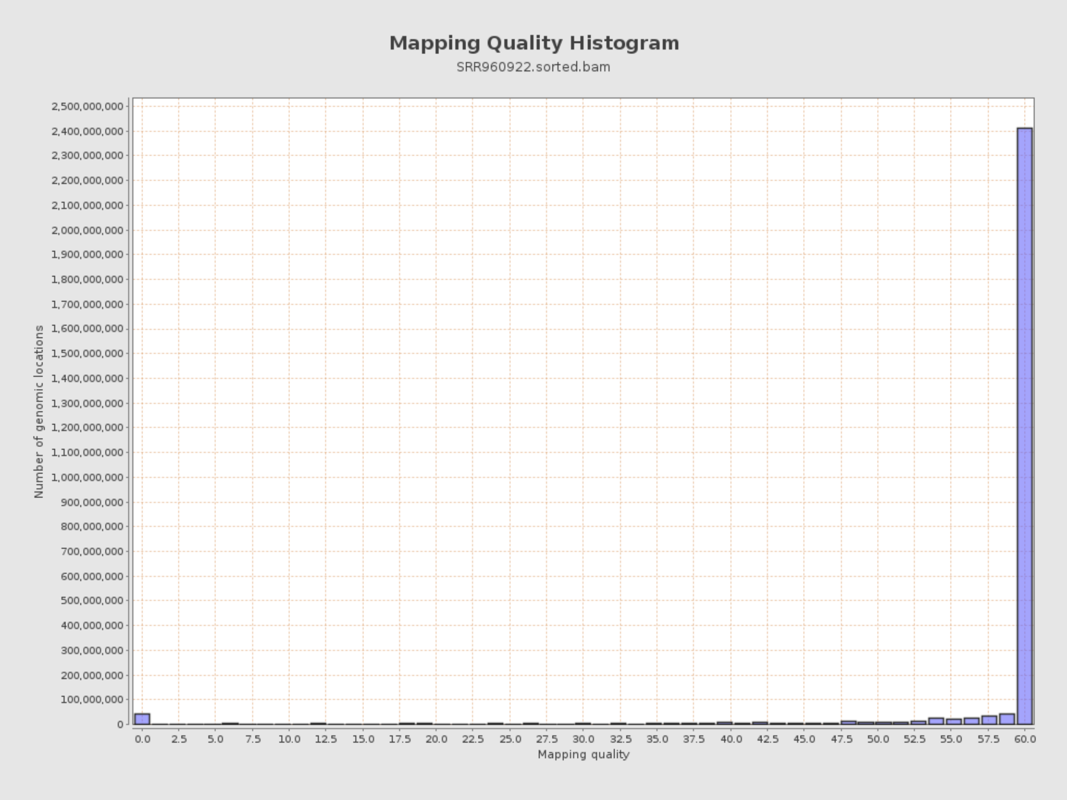
11. Results : Homopolymer Indels



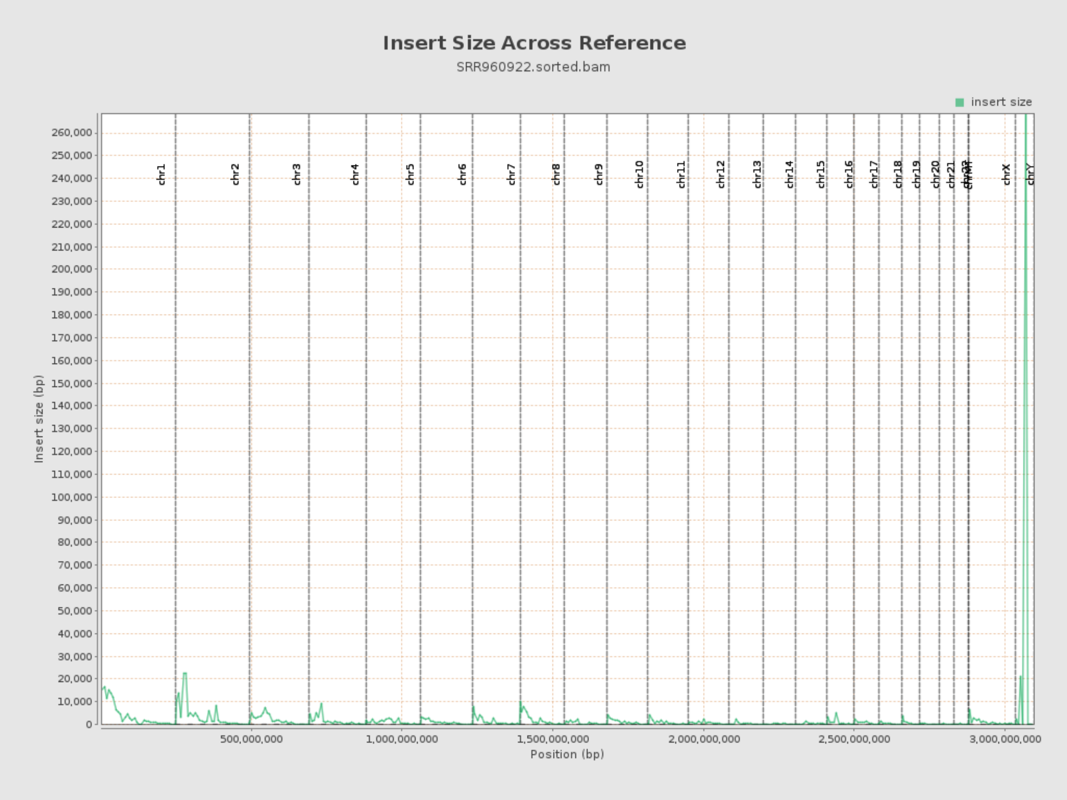
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram