Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/07 01:16:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960917.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_SRR960917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960917_1.fastq.gz SRR960917_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 07 01:16:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	229,224,264
Mapped reads	224,561,281 / 97.97%
Unmapped reads	4,662,983 / 2.03%
Mapped paired reads	224,561,281 / 97.97%
Mapped reads, first in pair	112,747,381 / 49.19%
Mapped reads, second in pair	111,813,900 / 48.78%
Mapped reads, both in pair	222,649,058 / 97.13%
Mapped reads, singletons	1,912,223 / 0.83%
Secondary alignments	0
Supplementary alignments	470,210 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	38,322,175 / 16.72%
Duplication rate	12.29%
Clipped reads	38,407,881 / 16.76%

2.2. ACGT Content

Number/percentage of A's	6,721,112,165 / 30.63%
Number/percentage of C's	4,260,876,133 / 19.42%
Number/percentage of T's	6,715,789,935 / 30.6%
Number/percentage of G's	4,243,376,615 / 19.34%
Number/percentage of N's	2,891,007 / 0.01%

GC Percentage	38.75%

2.3. Coverage

Mean	7.0906
Standard Deviation	105.3469

2.4. Mapping Quality

Mean Mapping Quality	53.58

2.5. Insert size

Mean	18,877.73
Standard Deviation	1,275,135.01
P25/Median/P75	155 / 183 / 213

2.6. Mismatches and indels

General error rate	1.43%
Mismatches	307,934,009
Insertions	2,628,299
Mapped reads with at least one insertion	1.14%
Deletions	2,918,703
Mapped reads with at least one deletion	1.26%
Homopolymer indels	40.48%

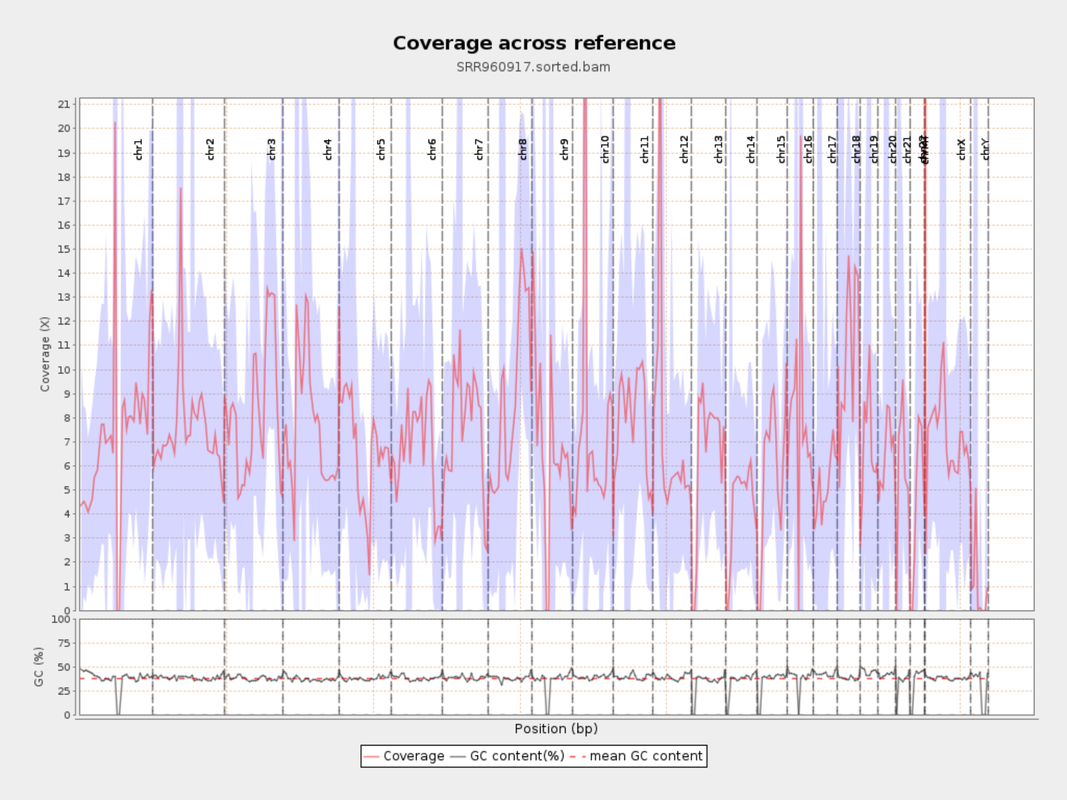
2.7. Chromosome stats

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

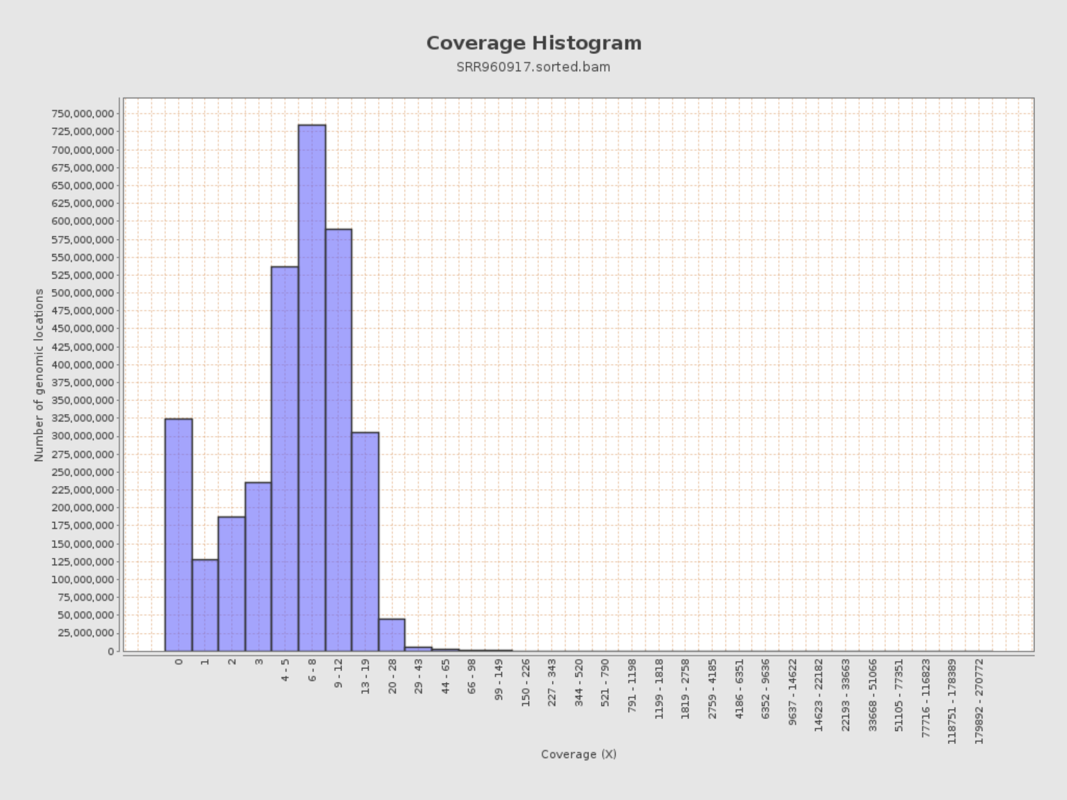
		bases	coverage	deviation
chr1	249250621	1824210475	7.3188	279.3509
chr2	243199373	1848059175	7.5989	56.178
chr3	198022430	1632769263	8.2454	9.6687
chr4	191154276	1449627191	7.5835	57.3871
chr5	180915260	1193500588	6.597	9.4607
chr6	171115067	1154032122	6.7442	27.6872
chr7	159138663	1207073849	7.585	69.1735
chr8	146364022	1287710993	8.798	134.7279
chr9	141213431	936418064	6.6312	99.6617
chr10	135534747	1045827938	7.7163	201.6946
chr11	135006516	1069553640	7.9222	43.9732
chr12	133851895	992096542	7.4119	11.8915
chr13	115169878	757528327	6.5775	4.9007
chr14	107349540	467187418	4.352	7.391
chr15	102531392	590677577	5.7609	5.2025
chr16	90354753	720798711	7.9774	86.2073
chr17	81195210	418394653	5.1529	26.3295
chr18	78077248	843216485	10.7998	102.4126
chr19	59128983	405307462	6.8546	116.8221
chr20	63025520	412276309	6.5414	19.1163
chr21	48129895	292119462	6.0694	23.1207
chr22	51304566	225812593	4.4014	5.7544
chrMT	16571	5006547	302.127	62.1848
chrX	155270560	1110965471	7.155	29.612

chrY	59373566	60225629	1.0144	53.2659

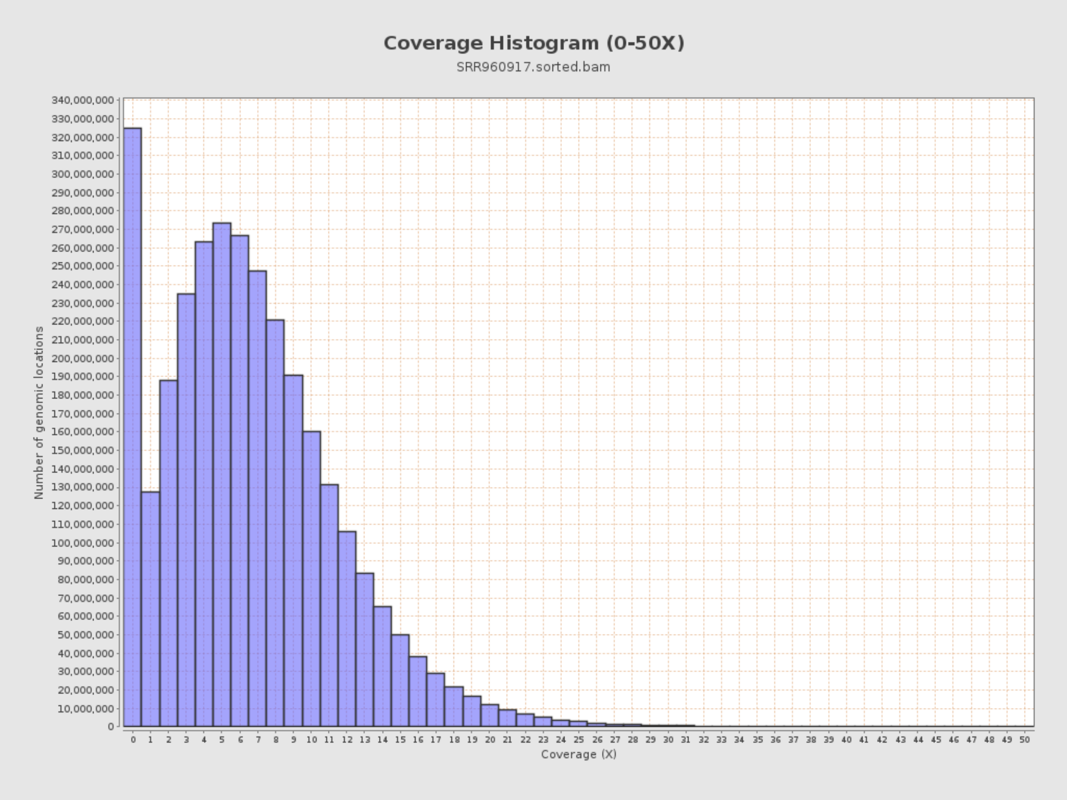
3. Results : Coverage across reference



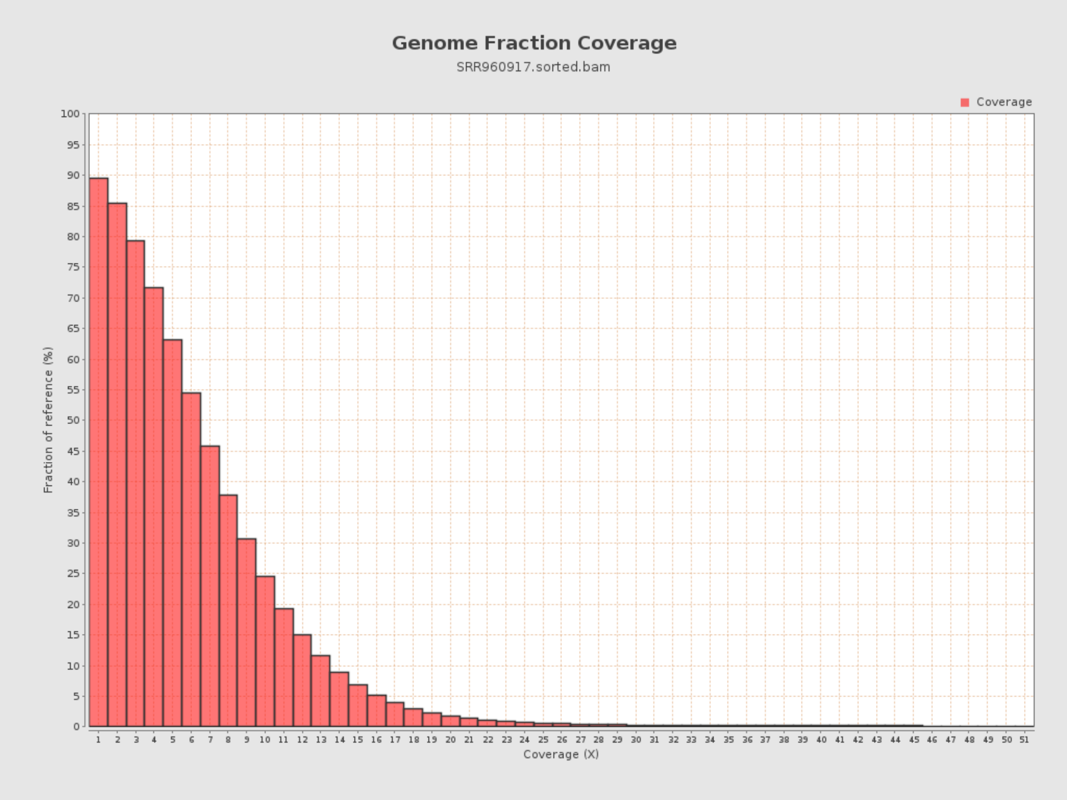
4. Results : Coverage Histogram



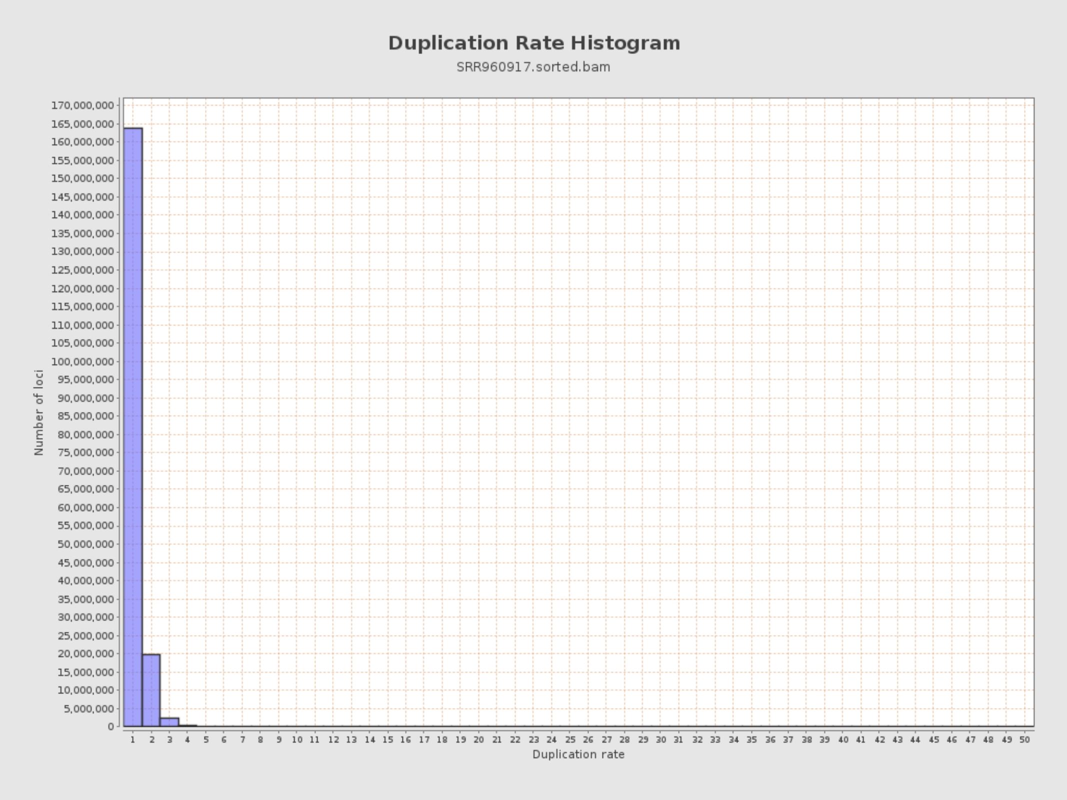
5. Results : Coverage Histogram (0-50X)



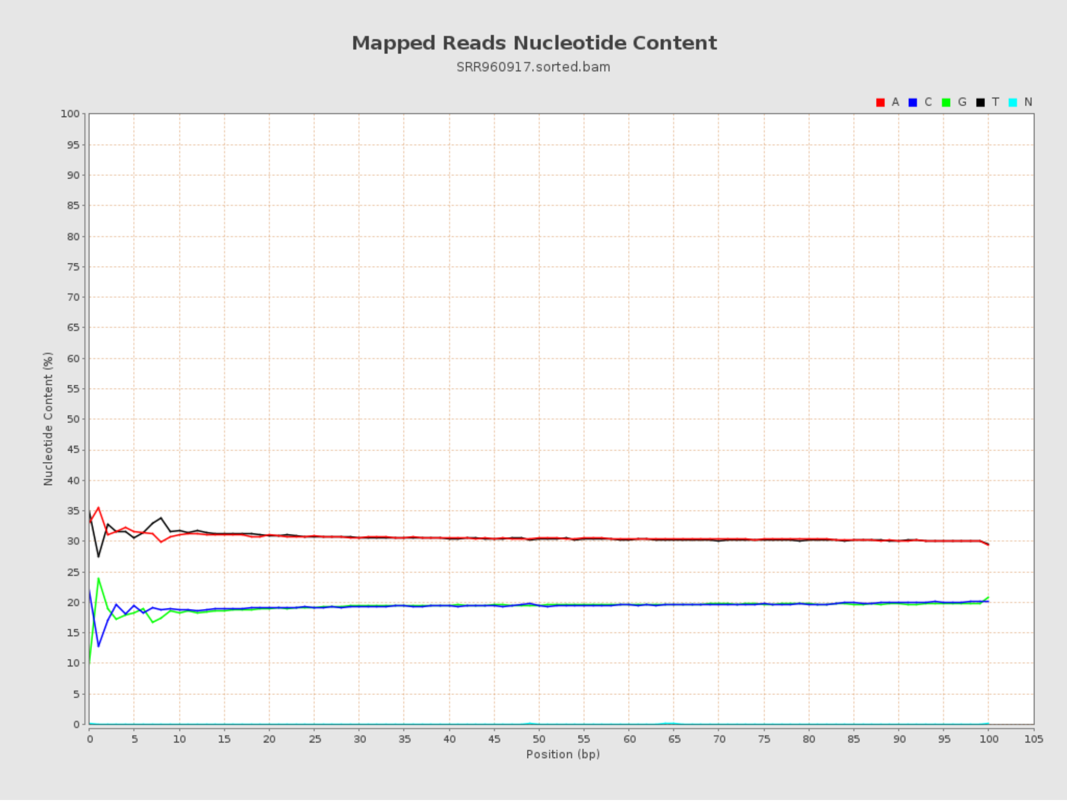
6. Results : Genome Fraction Coverage



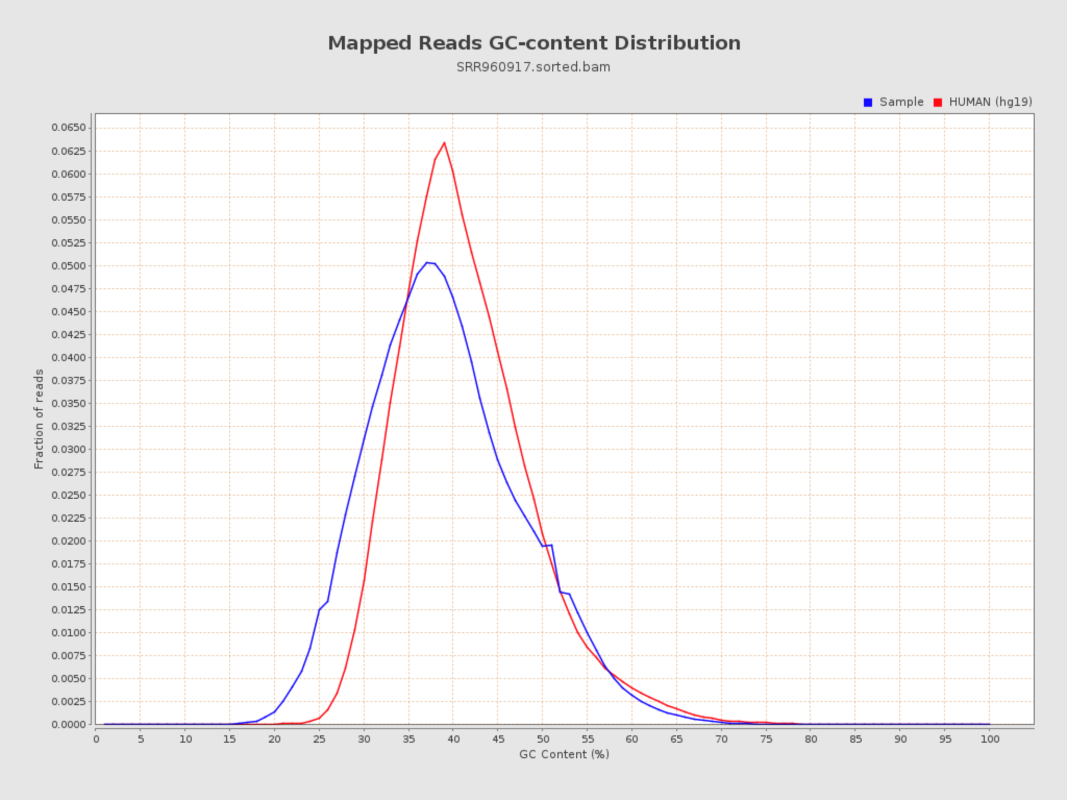
7. Results : Duplication Rate Histogram



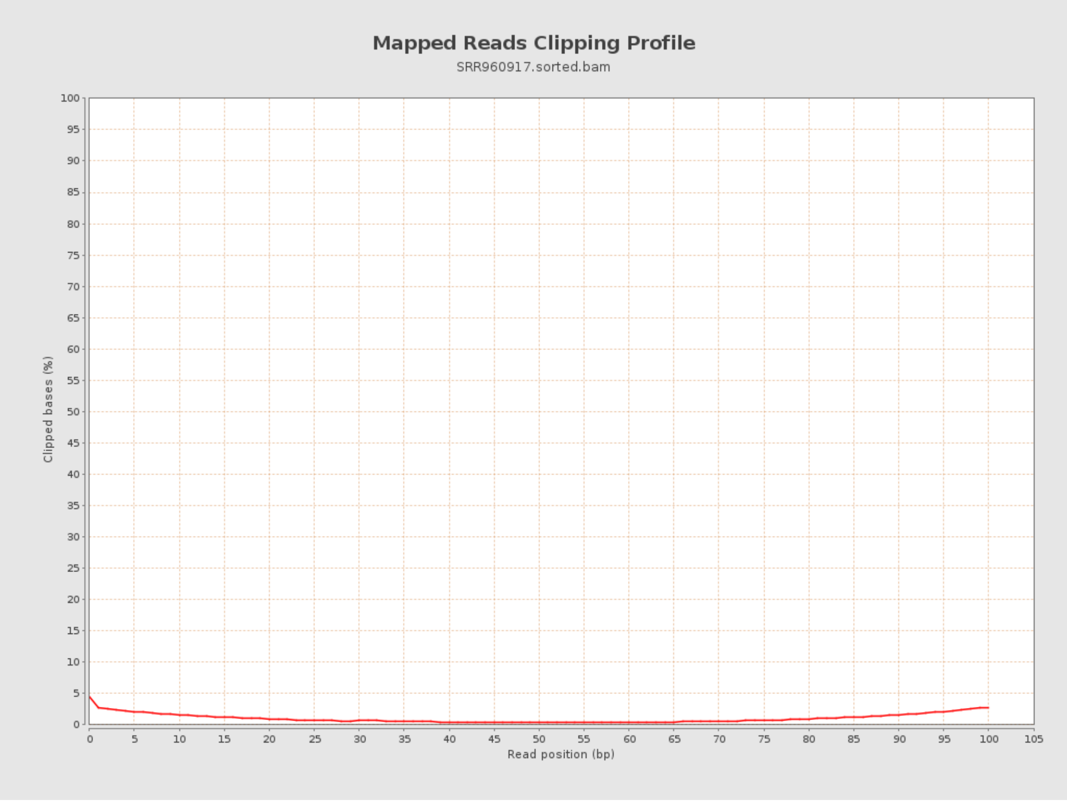
8. Results : Mapped Reads Nucleotide Content



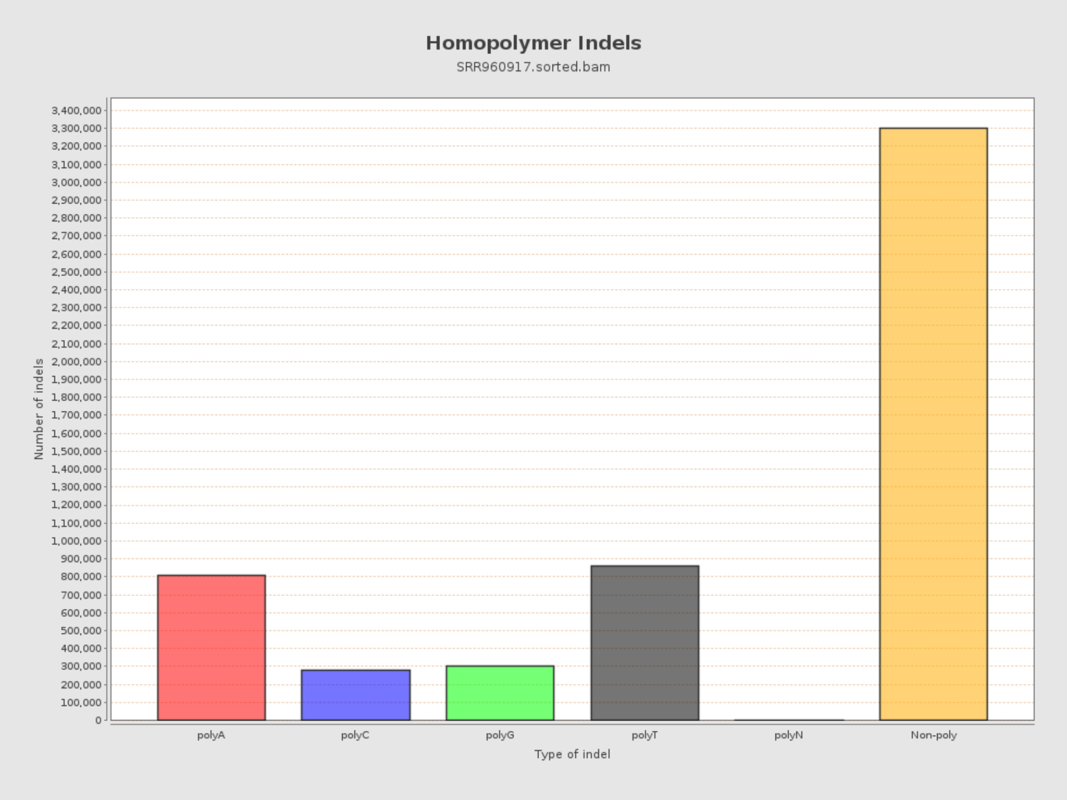
9. Results : Mapped Reads GC-content Distribution



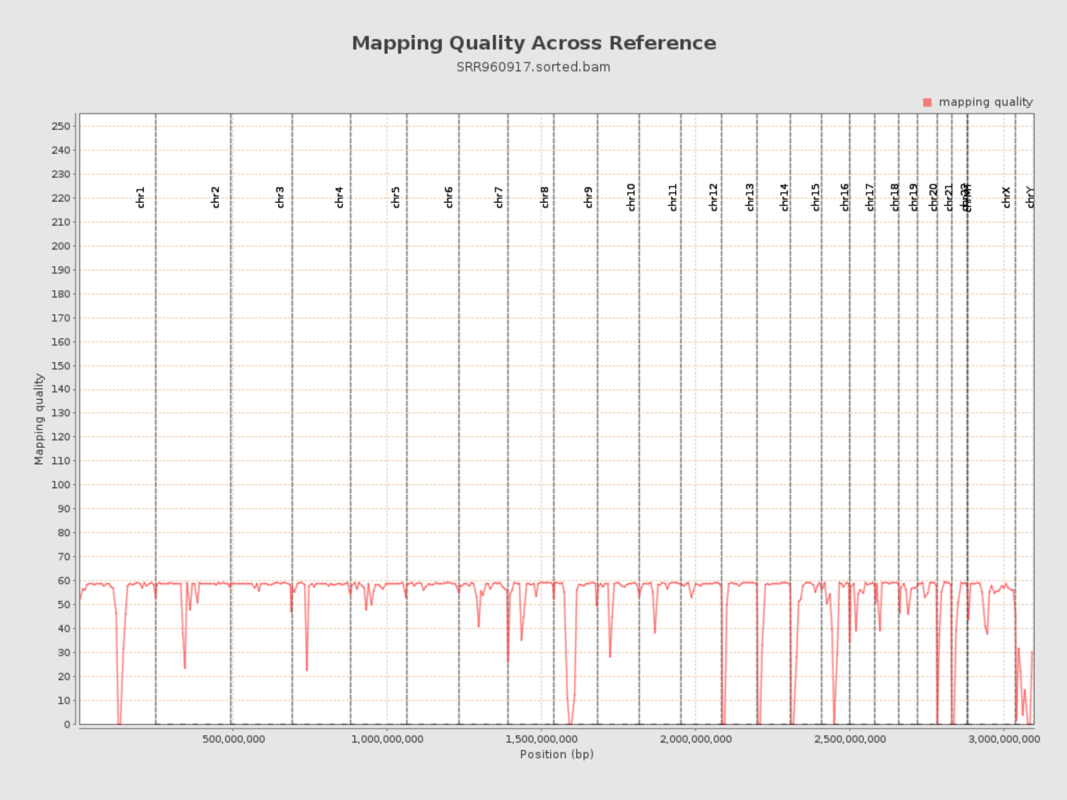
10. Results : Mapped Reads Clipping Profile



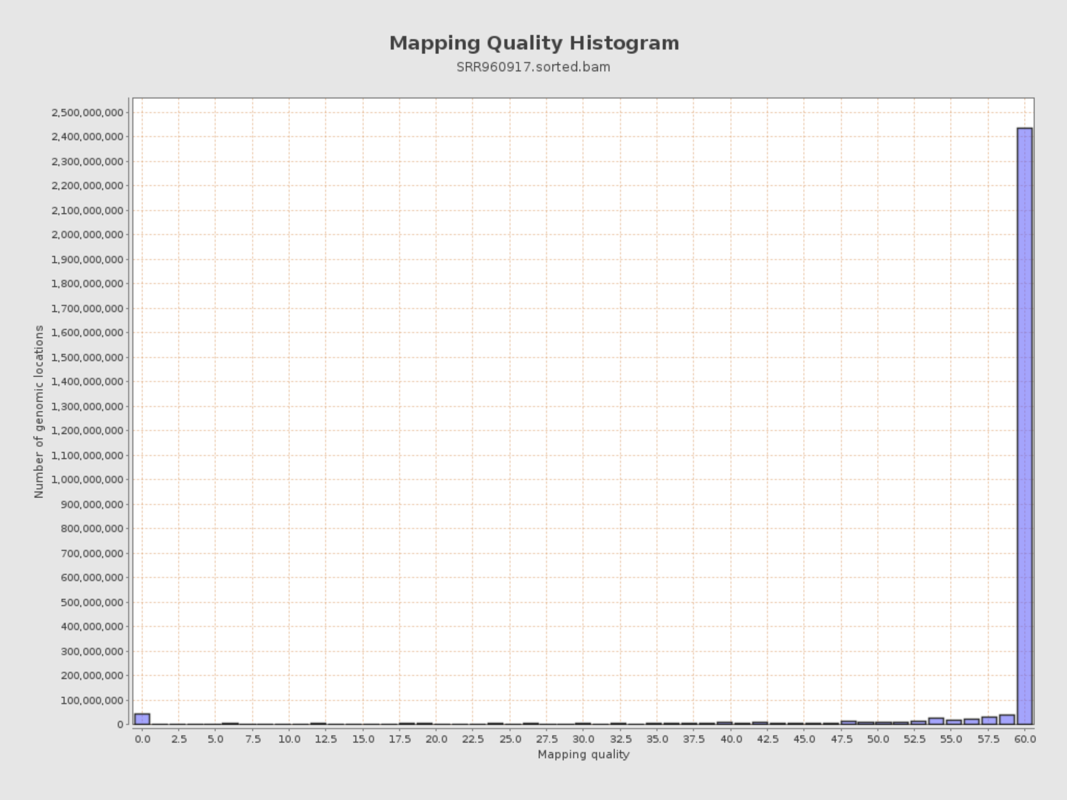
11. Results : Homopolymer Indels



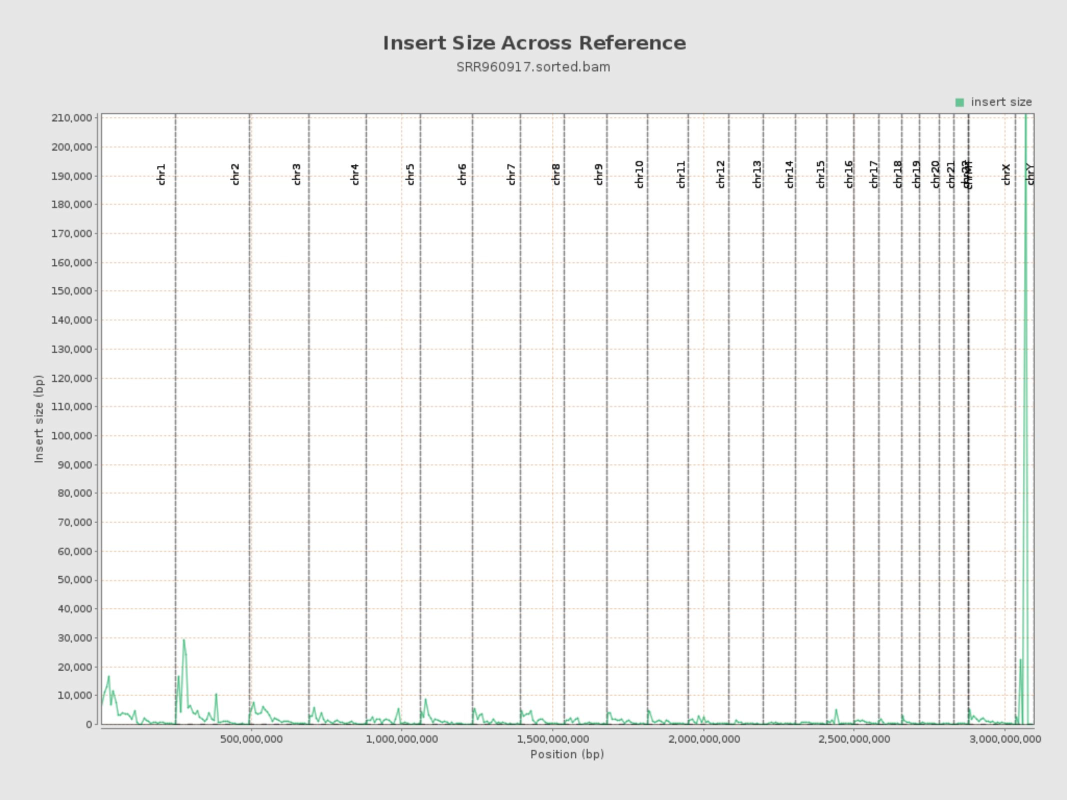
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram