Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 11:28:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960911.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_SRR960911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960911_1.fastq.gz SRR960911_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 11:28:52 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	130,591,606
Mapped reads	124,119,392 / 95.04%
Unmapped reads	6,472,214 / 4.96%
Mapped paired reads	124,119,392 / 95.04%
Mapped reads, first in pair	62,286,071 / 47.7%
Mapped reads, second in pair	61,833,321 / 47.35%
Mapped reads, both in pair	121,521,958 / 93.05%
Mapped reads, singletons	2,597,434 / 1.99%
Secondary alignments	0
Supplementary alignments	2,027,303 / 1.55%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	13,729,006 / 10.51%
Duplication rate	5.63%
Clipped reads	63,278,590 / 48.46%

2.2. ACGT Content

Number/percentage of A's	3,145,842,593 / 29.04%
Number/percentage of C's	2,224,224,651 / 20.53%
Number/percentage of T's	3,207,137,336 / 29.61%
Number/percentage of G's	2,253,206,918 / 20.8%
Number/percentage of N's	1,430,737 / 0.01%

GC Percentage	41.34%

2.3. Coverage

Mean	3.5
Standard Deviation	48.0037

2.4. Mapping Quality

Mean Mapping Quality	52.38

2.5. Insert size

Mean	156,552.66
Standard Deviation	4,092,208.81
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.6%
Mismatches	169,613,332
Insertions	1,668,734
Mapped reads with at least one insertion	1.32%
Deletions	1,399,578
Mapped reads with at least one deletion	1.1%
Homopolymer indels	37.06%

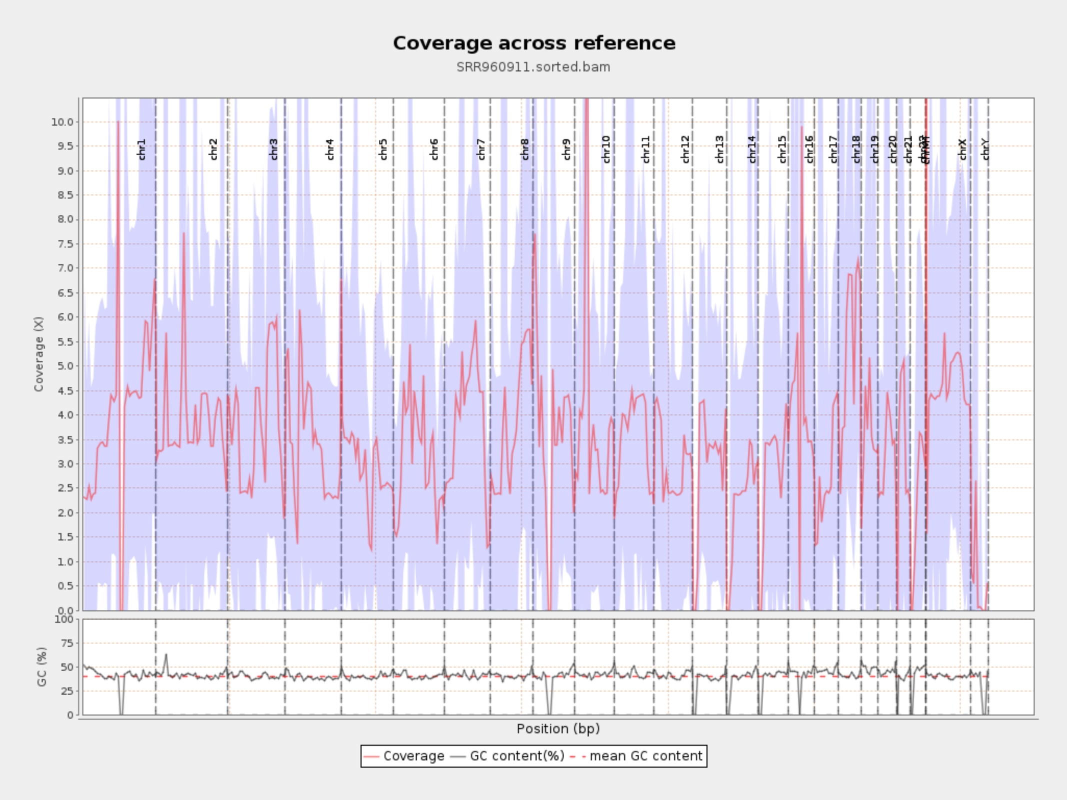
2.7. Chromosome stats

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

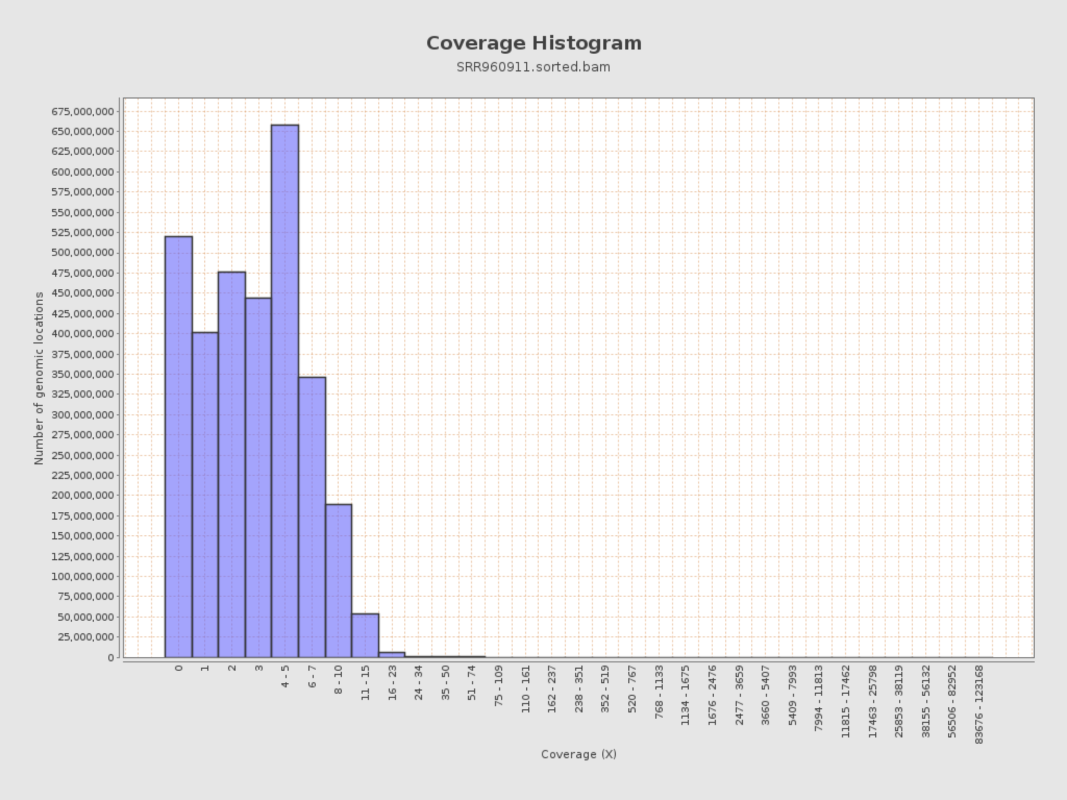
		bases	coverage	deviation
chr1	249250621	1000980674	4.016	121.0161
chr2	243199373	940235239	3.8661	69.2897
chr3	198022430	748040420	3.7776	7.9982
chr4	191154276	656202141	3.4328	21.5624
chr5	180915260	528858085	2.9232	4.7716
chr6	171115067	540782336	3.1603	14.8661
chr7	159138663	613520286	3.8553	31.2709
chr8	146364022	562925854	3.8461	39.39
chr9	141213431	516868790	3.6602	36.8138
chr10	135534747	524773148	3.8719	80.7344
chr11	135006516	490110763	3.6303	23.2712
chr12	133851895	405591702	3.0302	4.3992
chr13	115169878	338462032	2.9388	3.0185
chr14	107349540	238771107	2.2242	19.3558
chr15	102531392	282239353	2.7527	3.5231
chr16	90354753	381792783	4.2255	40.524
chr17	81195210	215770935	2.6574	11.8639
chr18	78077248	419108930	5.3679	45.341
chr19	59128983	216758396	3.6659	54.9884
chr20	63025520	203008915	3.2211	9.8958
chr21	48129895	153235990	3.1838	14.2721
chr22	51304566	113616347	2.2145	3.3685
chrMT	16571	2279132	137.5374	30.2726
chrX	155270560	706828559	4.5522	15.8178

chrY	59373566	34055661	0.5736	25.9371

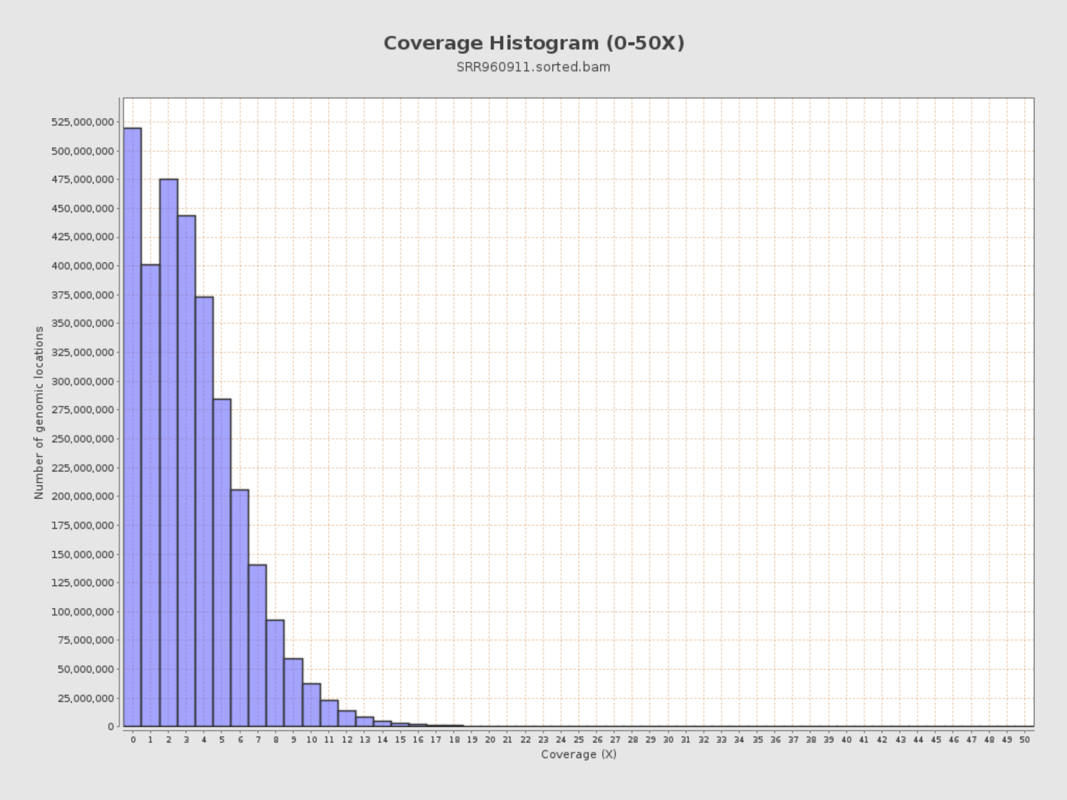
3. Results : Coverage across reference



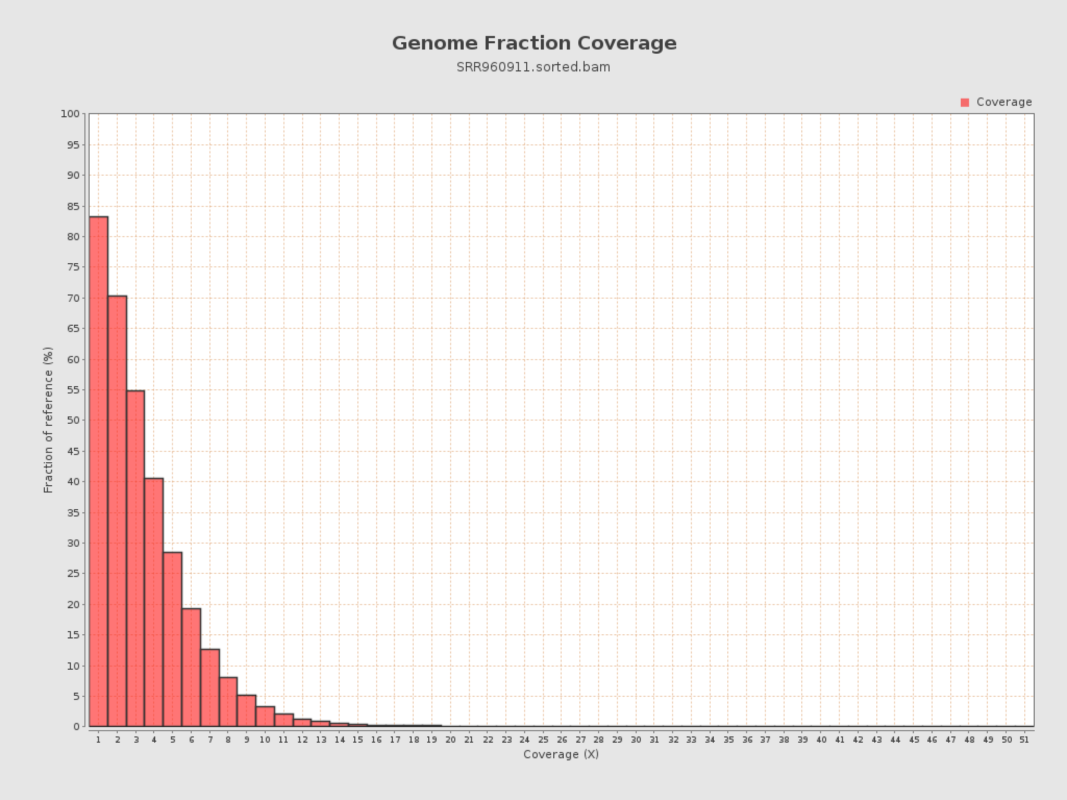
4. Results : Coverage Histogram



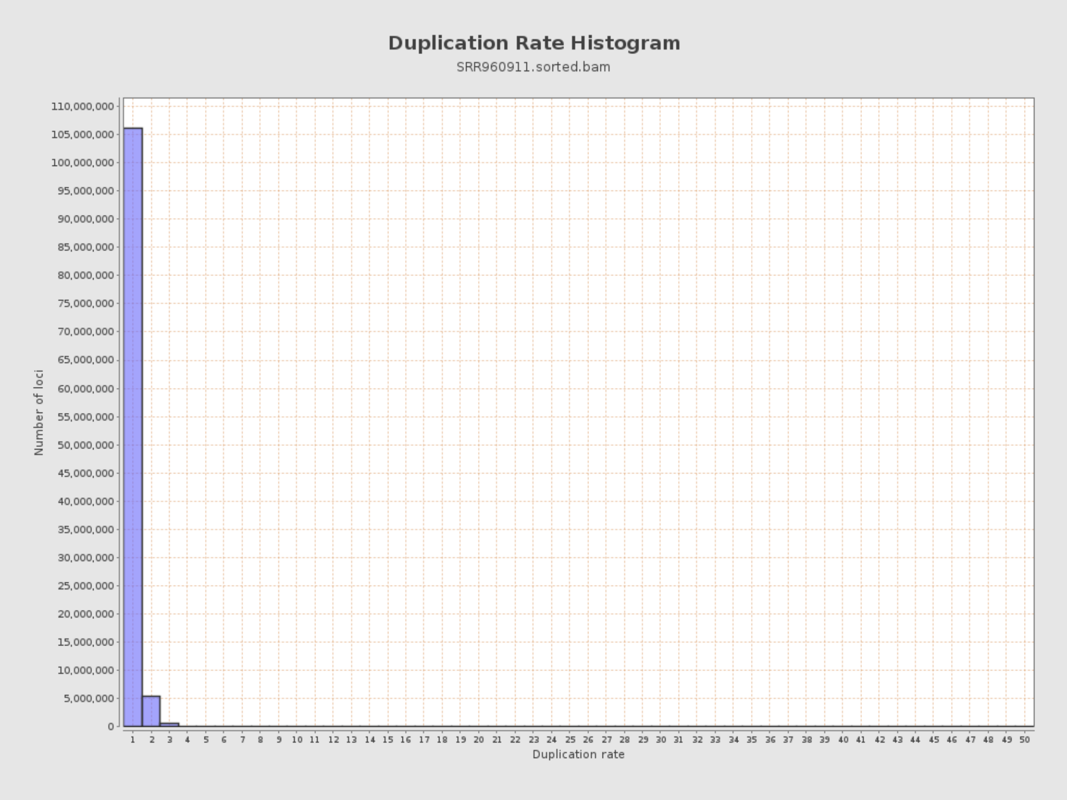
5. Results : Coverage Histogram (0-50X)



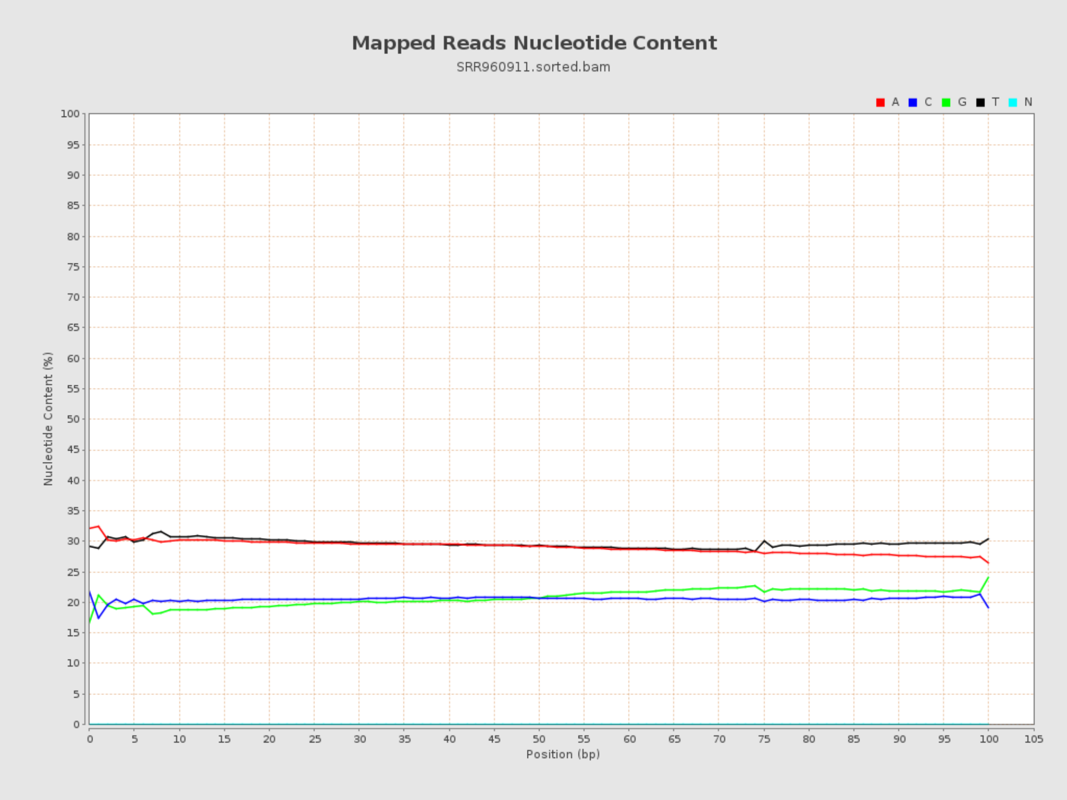
6. Results : Genome Fraction Coverage



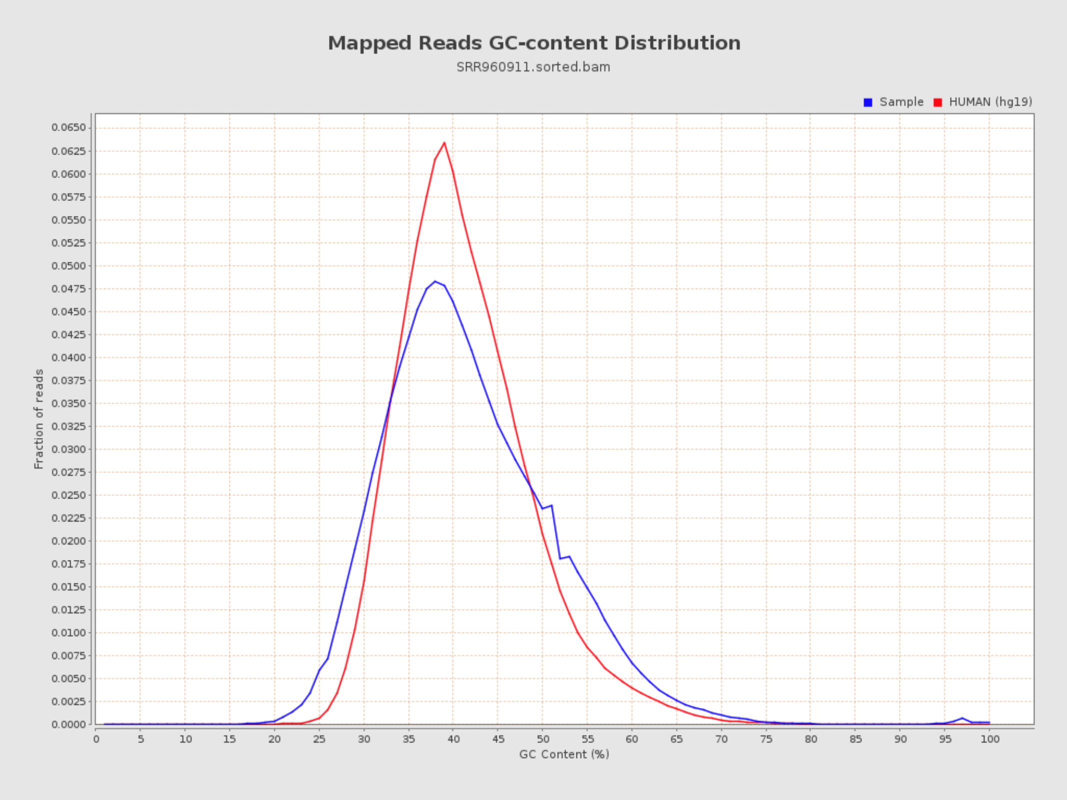
7. Results : Duplication Rate Histogram



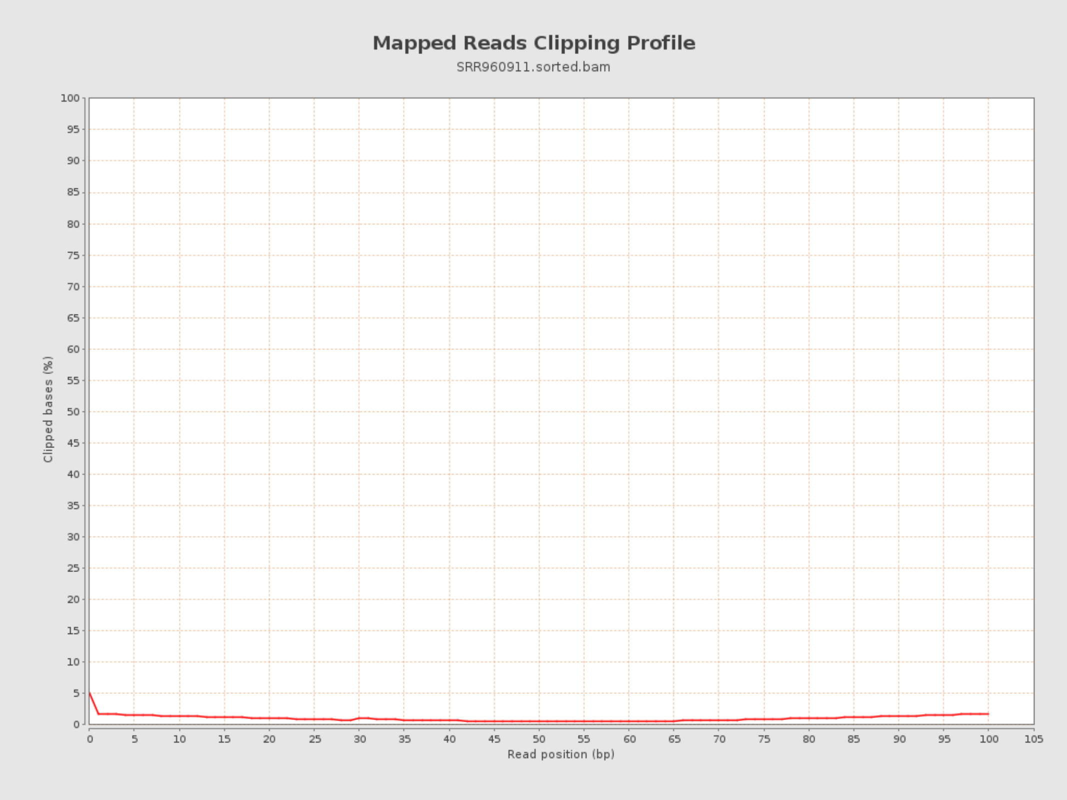
8. Results : Mapped Reads Nucleotide Content



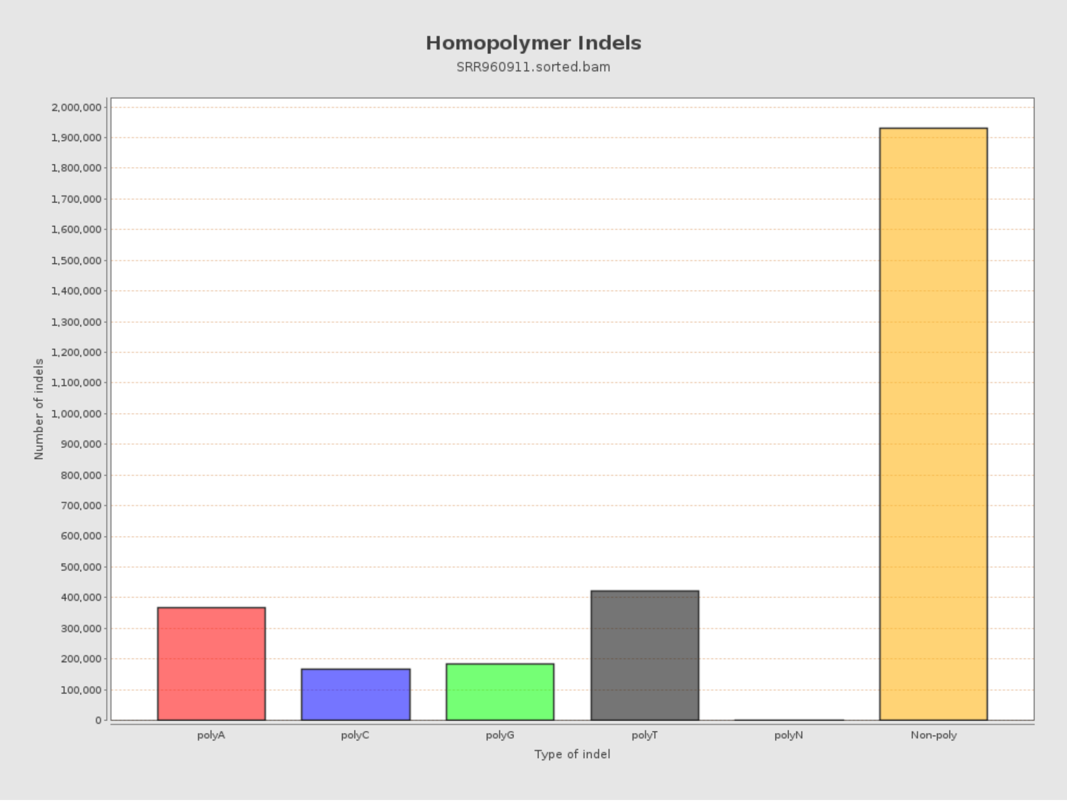
9. Results : Mapped Reads GC-content Distribution



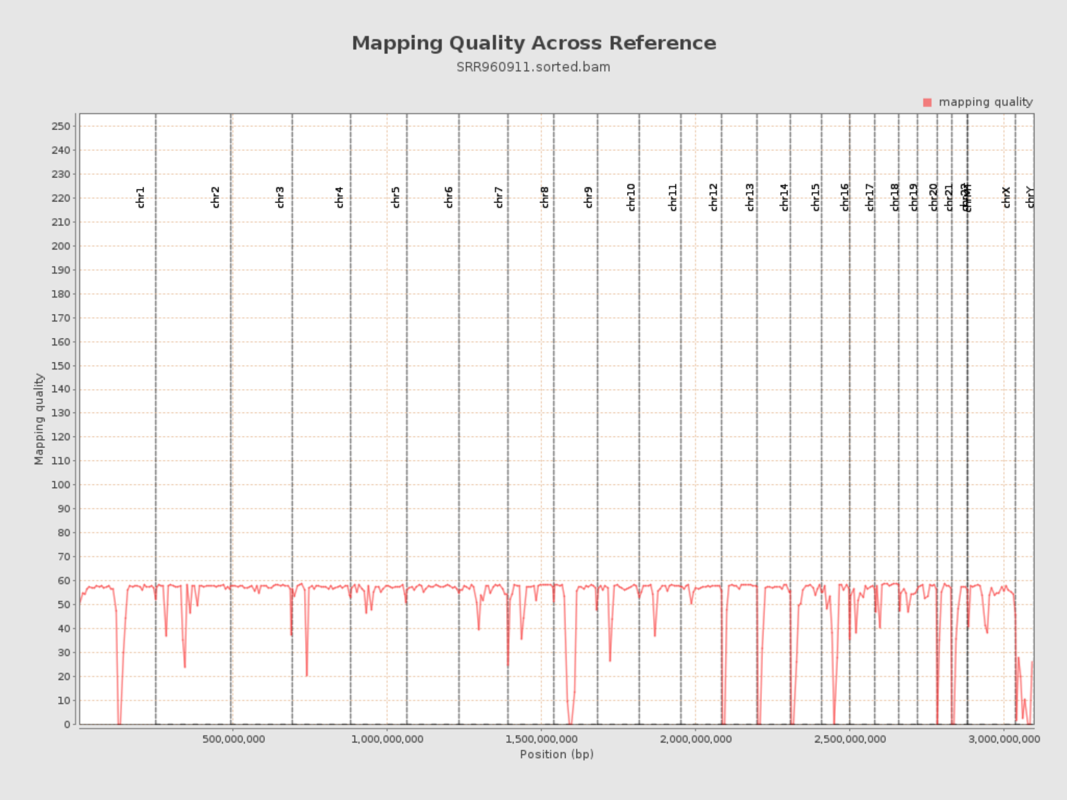
10. Results : Mapped Reads Clipping Profile



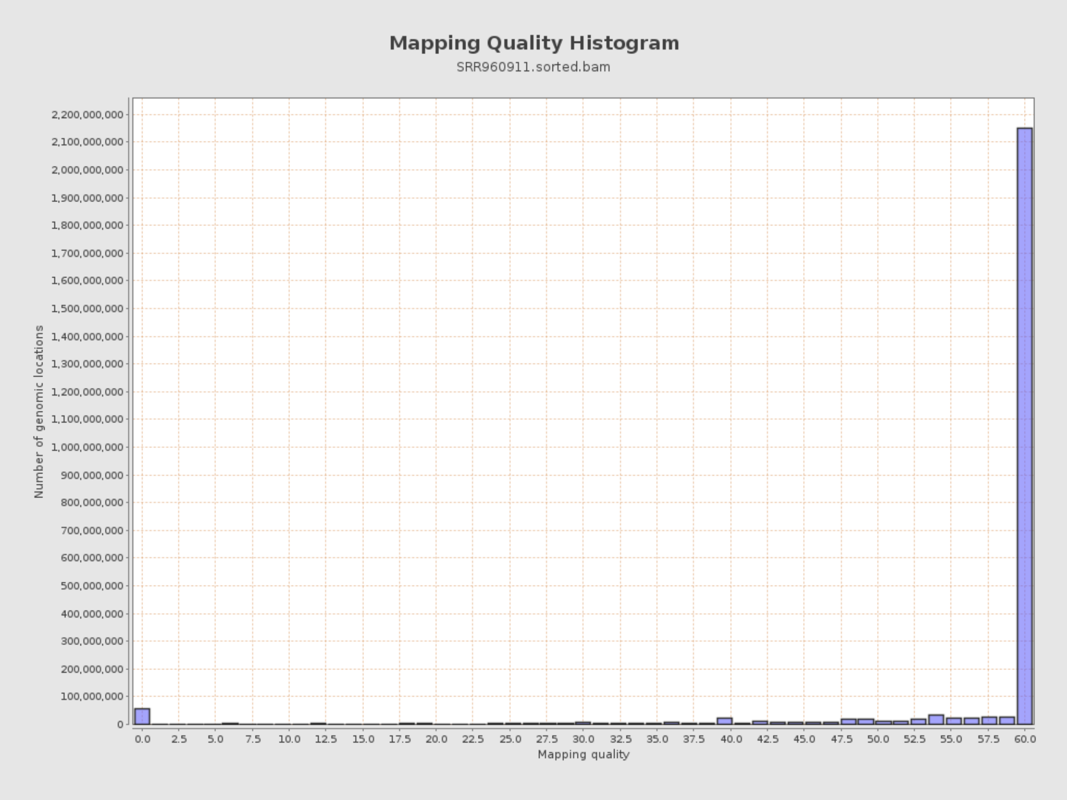
11. Results : Homopolymer Indels



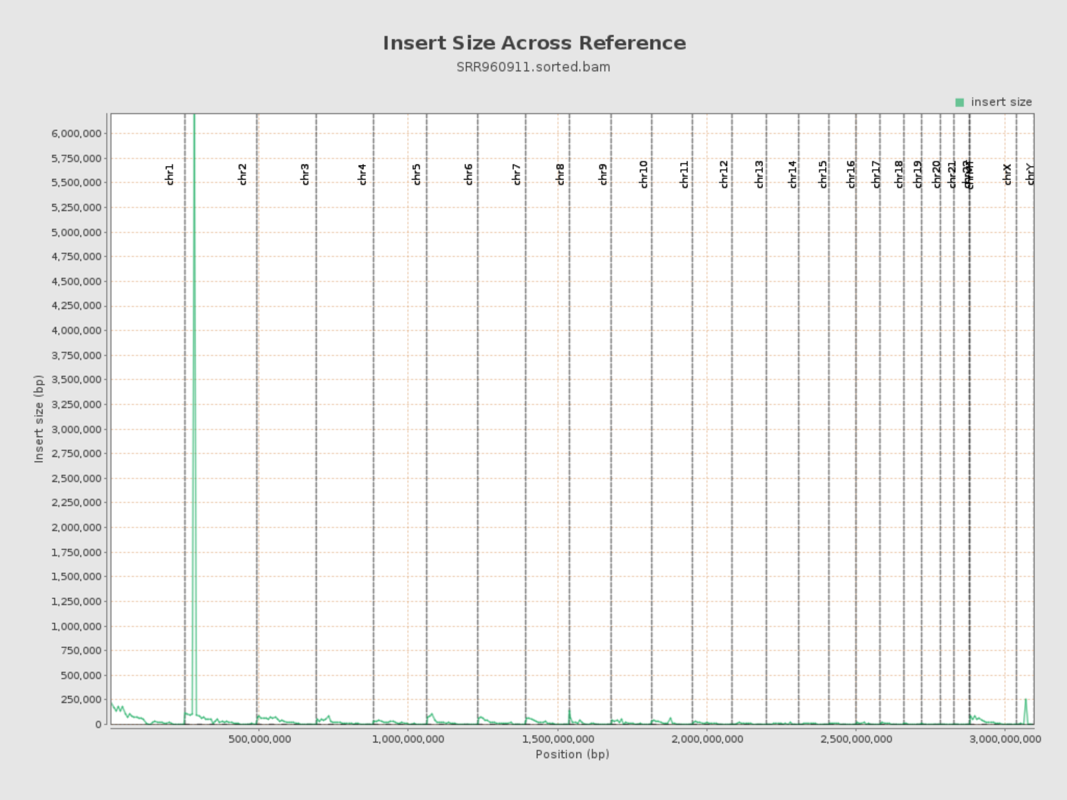
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram