Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 04:06:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960907.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_SRR960907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960907_1.fastq.gz SRR960907_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 04:06:04 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	84,324,010
Mapped reads	79,296,825 / 94.04%
Unmapped reads	5,027,185 / 5.96%
Mapped paired reads	79,296,825 / 94.04%
Mapped reads, first in pair	39,731,274 / 47.12%
Mapped reads, second in pair	39,565,551 / 46.92%
Mapped reads, both in pair	77,889,248 / 92.37%
Mapped reads, singletons	1,407,577 / 1.67%
Secondary alignments	0
Supplementary alignments	1,376,968 / 1.63%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	7,547,142 / 8.95%
Duplication rate	4.39%
Clipped reads	38,050,792 / 45.12%

2.2. ACGT Content

Number/percentage of A's	2,027,250,245 / 28.92%
Number/percentage of C's	1,447,498,254 / 20.65%
Number/percentage of T's	2,062,187,550 / 29.41%
Number/percentage of G's	1,472,986,895 / 21.01%
Number/percentage of N's	778,960 / 0.01%

GC Percentage	41.66%

2.3. Coverage

Mean	2.2653
Standard Deviation	31.9401

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	159,131.77
Standard Deviation	4,147,371.29
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	105,736,839
Insertions	1,119,064
Mapped reads with at least one insertion	1.38%
Deletions	920,587
Mapped reads with at least one deletion	1.13%
Homopolymer indels	37.29%

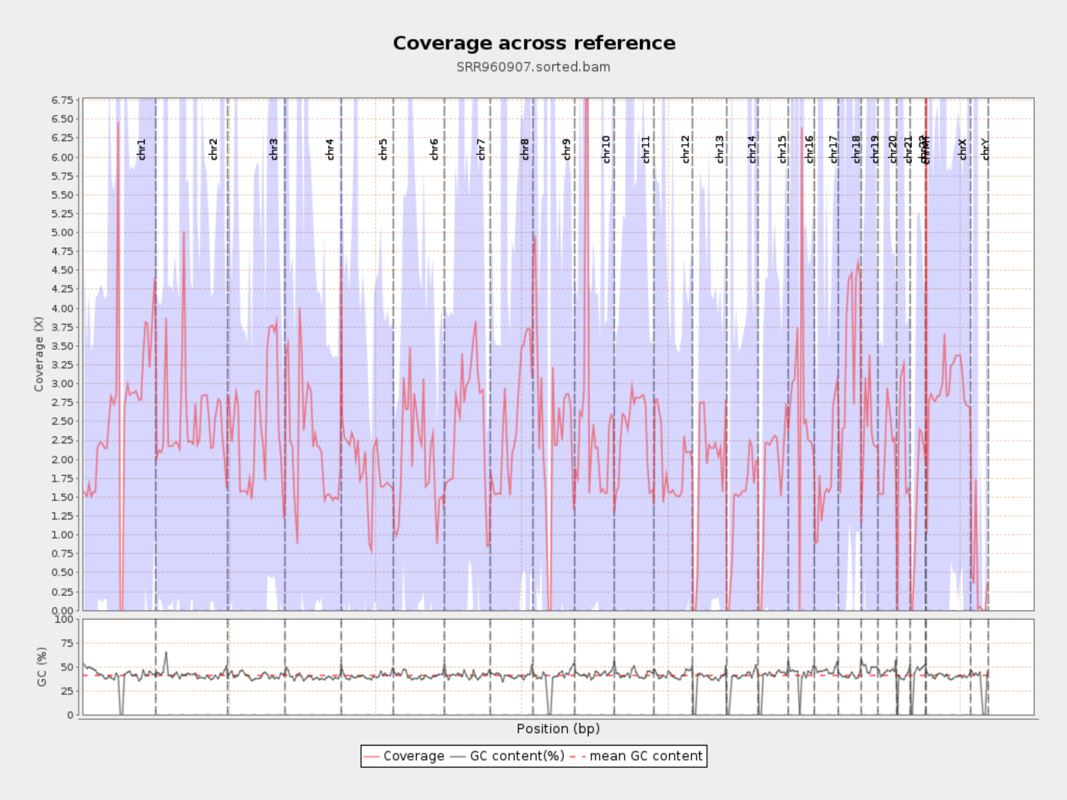
2.7. Chromosome stats

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

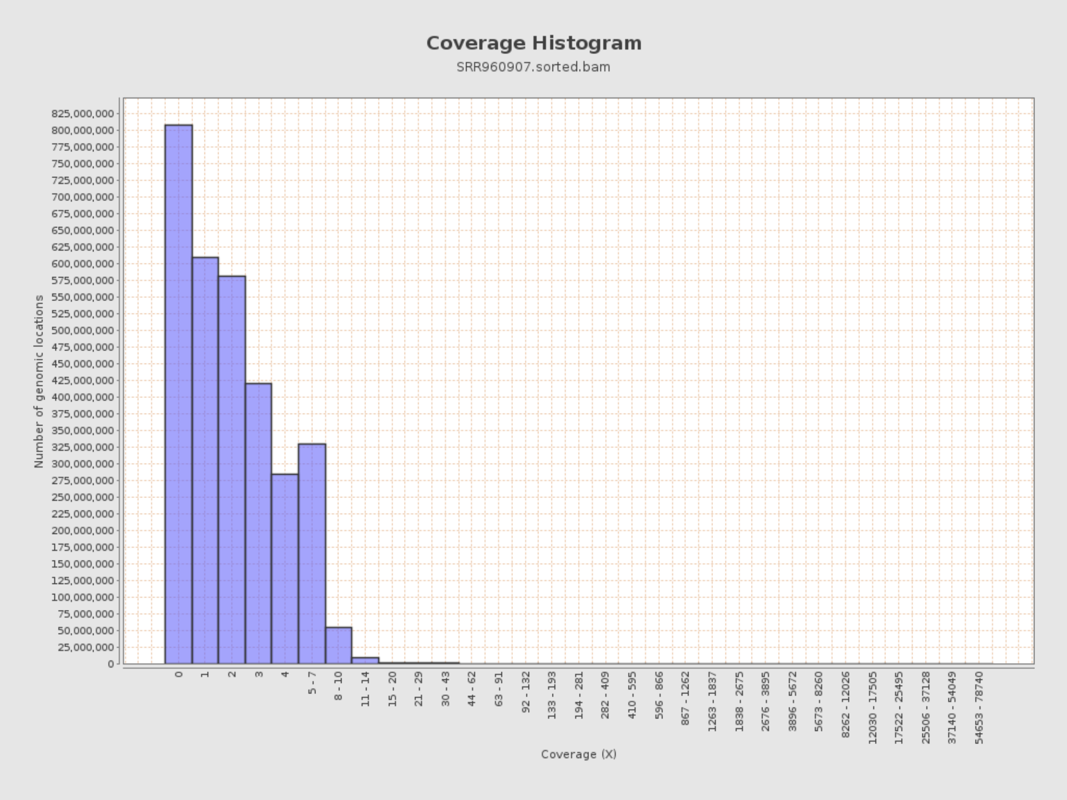
		bases	coverage	deviation
chr1	249250621	648164099	2.6005	78.193
chr2	243199373	608492335	2.502	50.9646
chr3	198022430	481433866	2.4312	5.3178
chr4	191154276	422400492	2.2097	14.4861
chr5	180915260	340715758	1.8833	3.2853
chr6	171115067	348307416	2.0355	9.4964
chr7	159138663	396597171	2.4921	20.0536
chr8	146364022	363606477	2.4843	24.9918
chr9	141213431	334988110	2.3722	24.3203
chr10	135534747	341222373	2.5176	53.5513
chr11	135006516	317805182	2.354	15.6956
chr12	133851895	262384357	1.9603	3.1041
chr13	115169878	217930117	1.8922	2.1921
chr14	107349540	154629826	1.4404	13.5789
chr15	102531392	183617398	1.7908	2.476
chr16	90354753	248788614	2.7535	26.2663
chr17	81195210	141987738	1.7487	7.8163
chr18	78077248	270463727	3.4641	29.4132
chr19	59128983	143852873	2.4329	36.4019
chr20	63025520	132771291	2.1066	6.685
chr21	48129895	98785365	2.0525	9.5451
chr22	51304566	75371819	1.4691	2.3533
chrMT	16571	1500099	90.5256	19.796
chrX	155270560	454749357	2.9288	10.3685

chrY	59373566	22099623	0.3722	17.4312

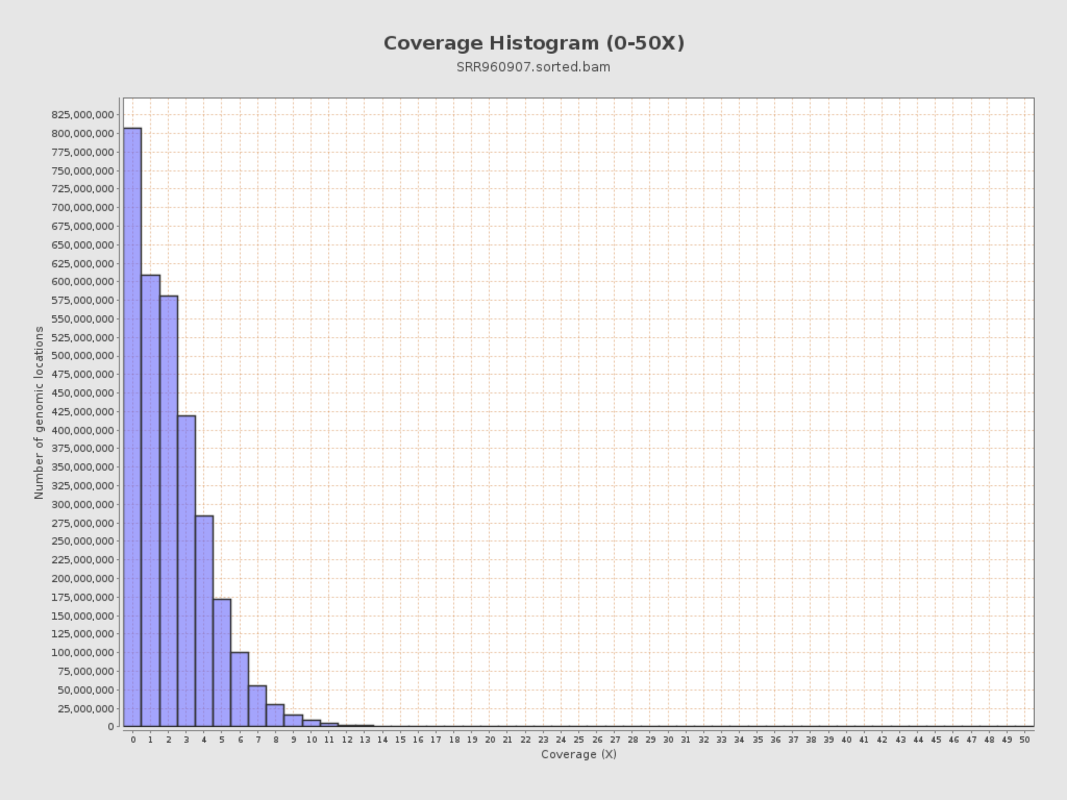
3. Results : Coverage across reference



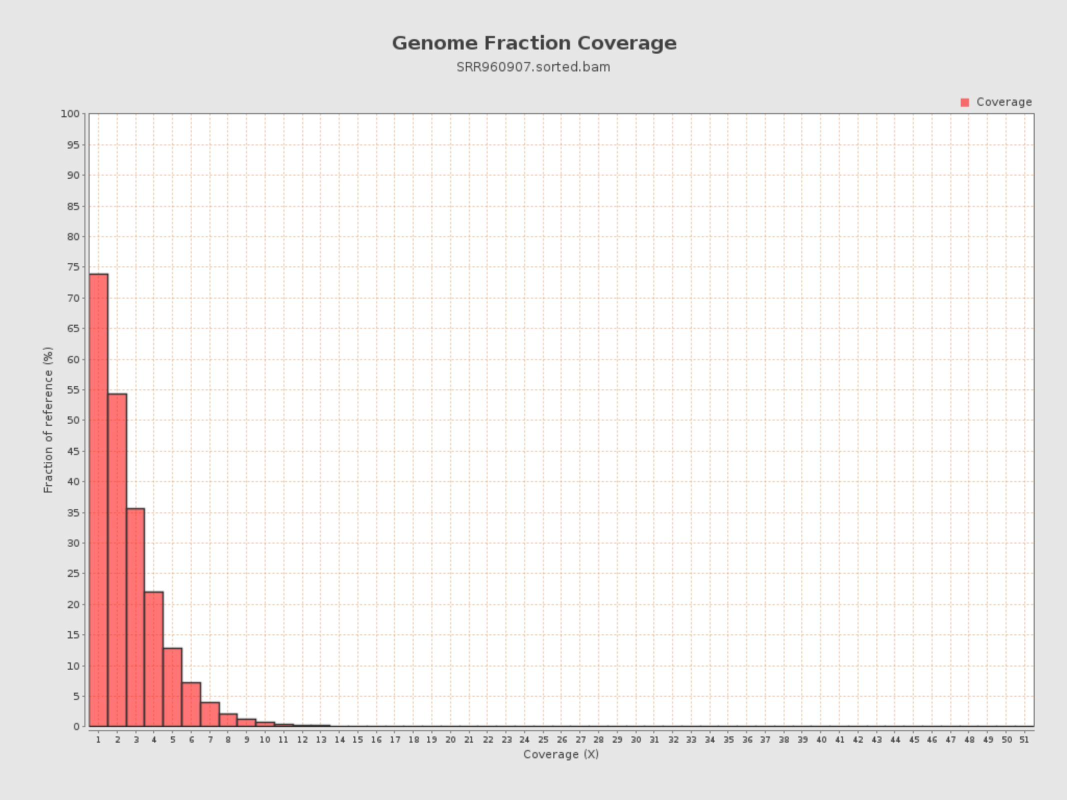
4. Results : Coverage Histogram



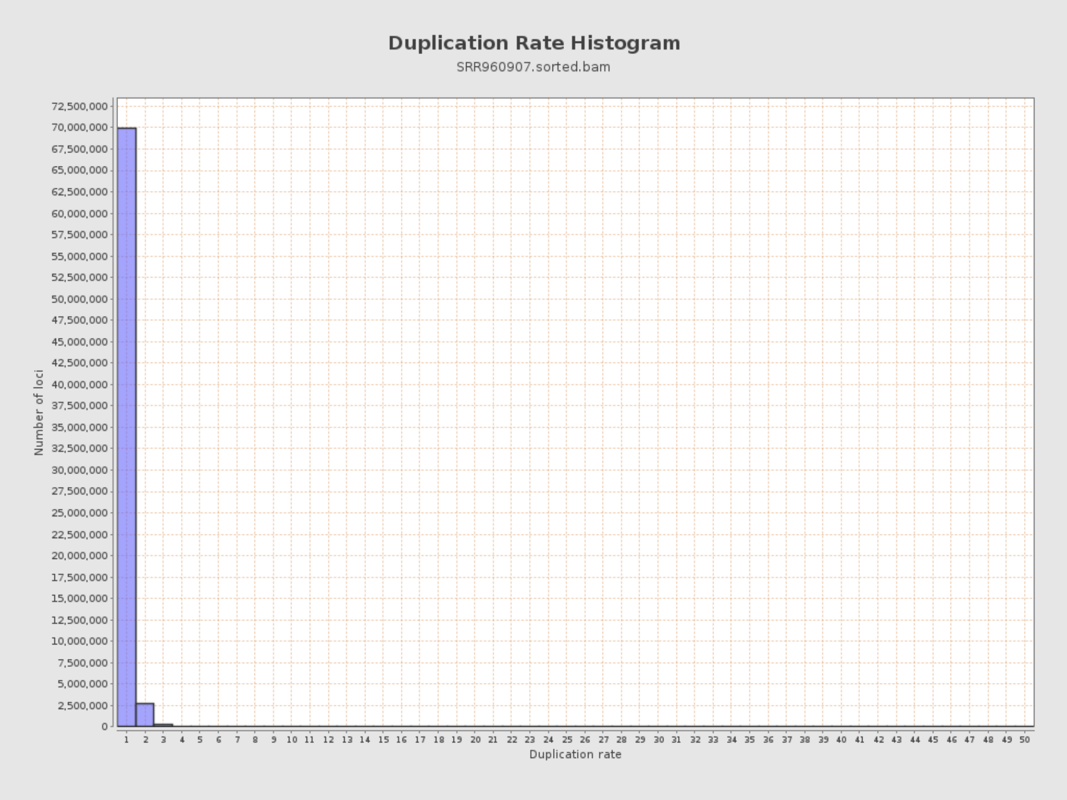
5. Results : Coverage Histogram (0-50X)



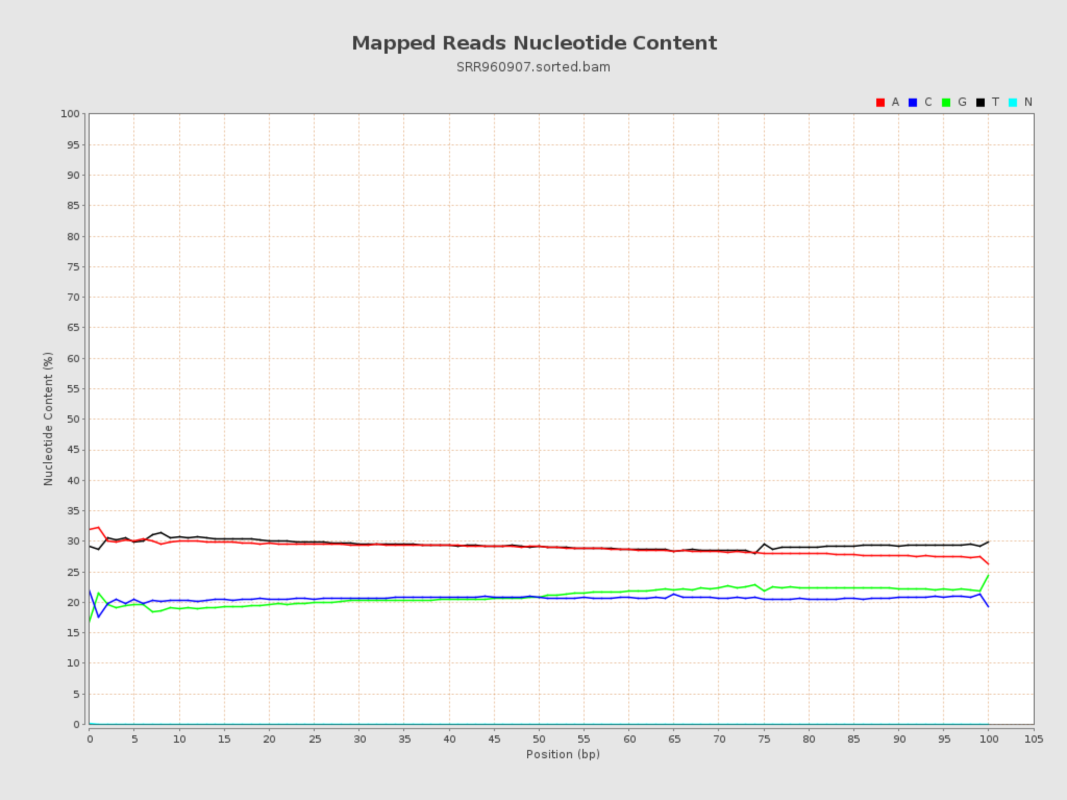
6. Results : Genome Fraction Coverage



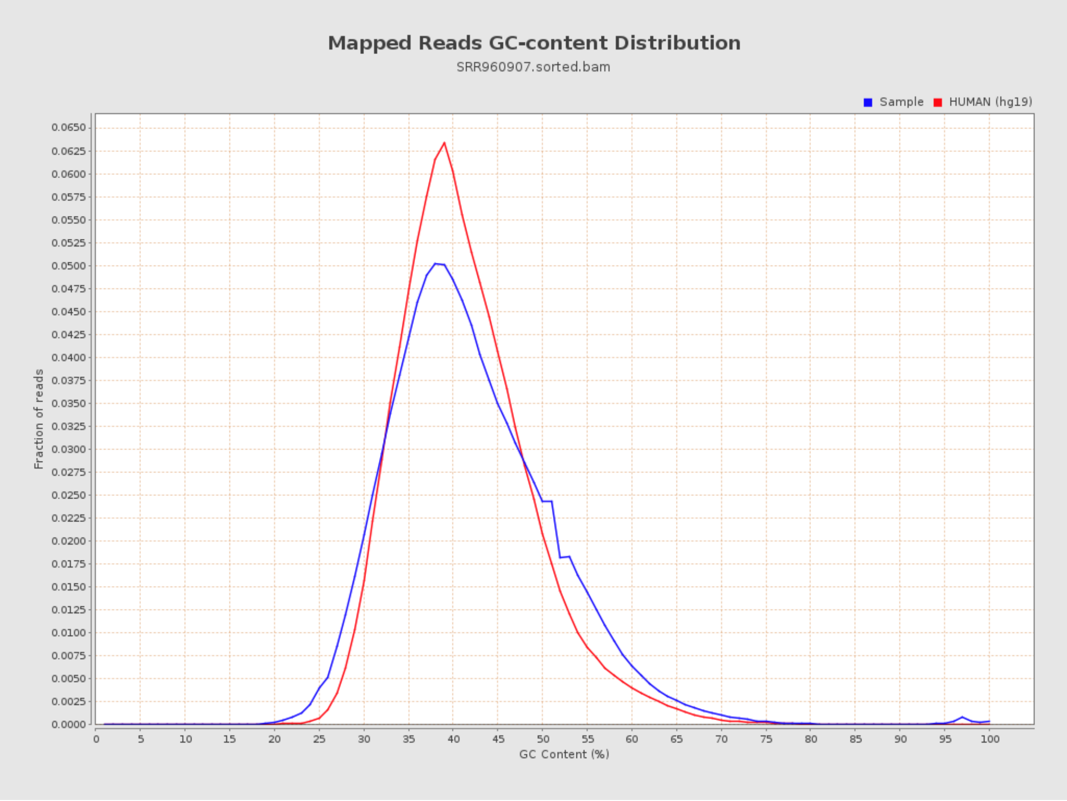
7. Results : Duplication Rate Histogram



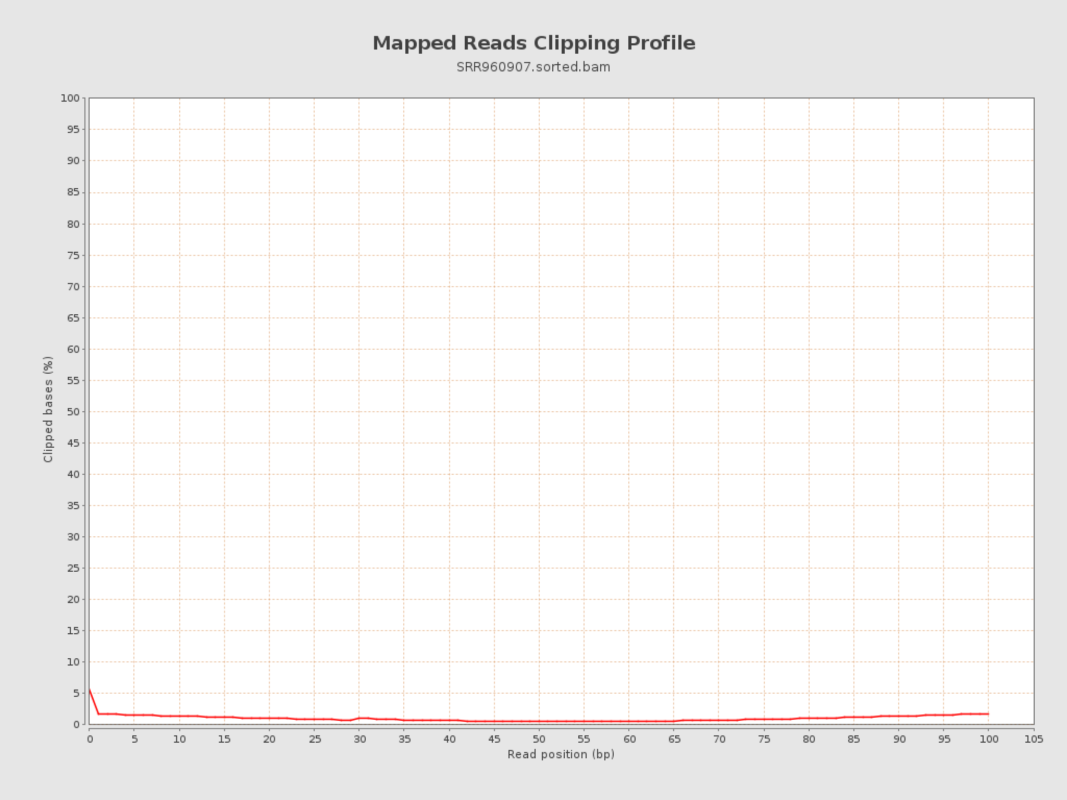
8. Results : Mapped Reads Nucleotide Content



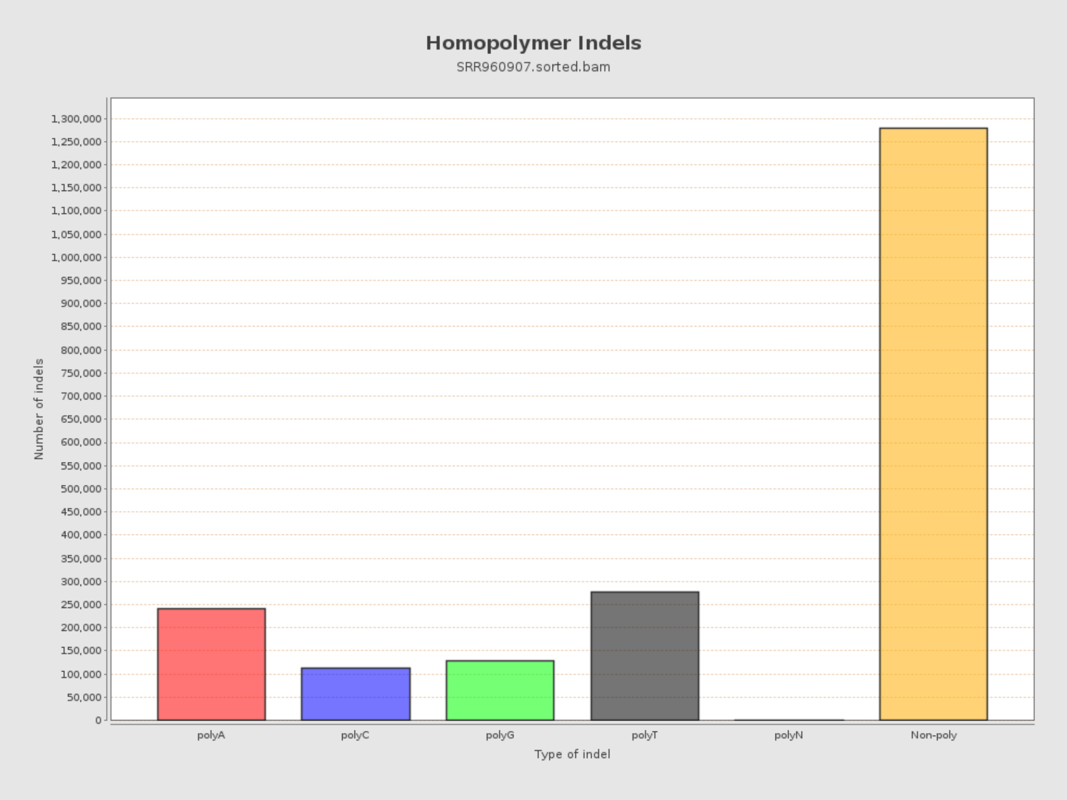
9. Results : Mapped Reads GC-content Distribution



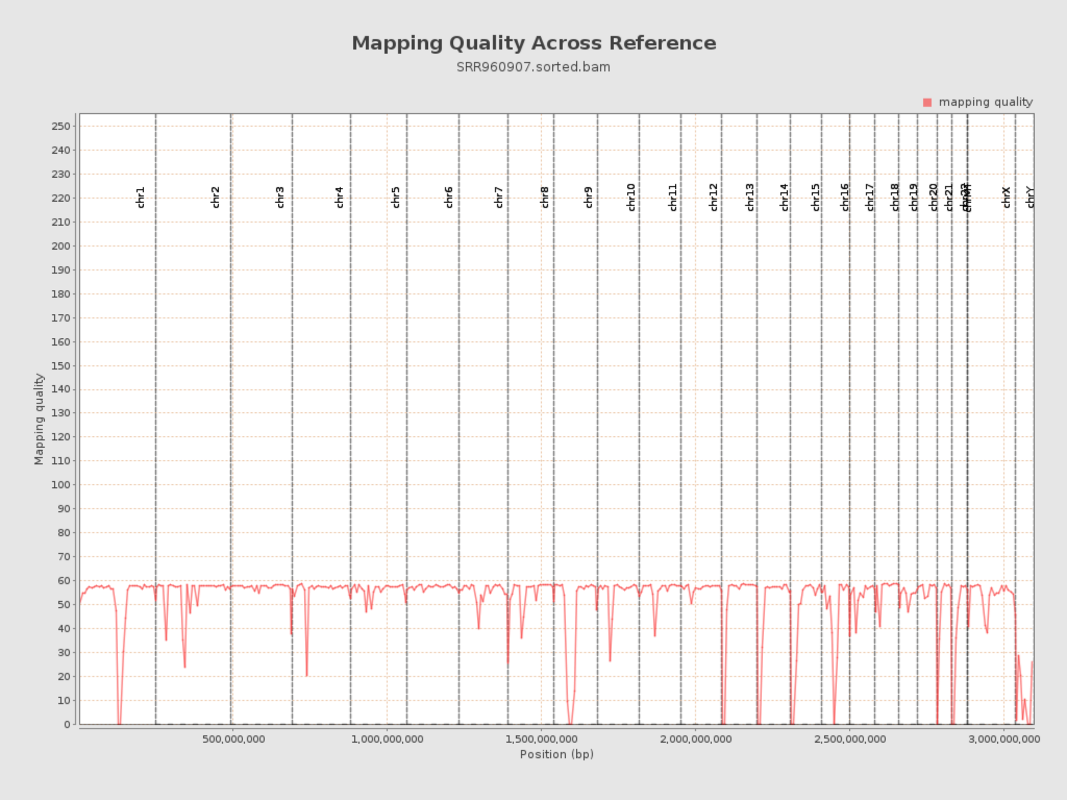
10. Results : Mapped Reads Clipping Profile



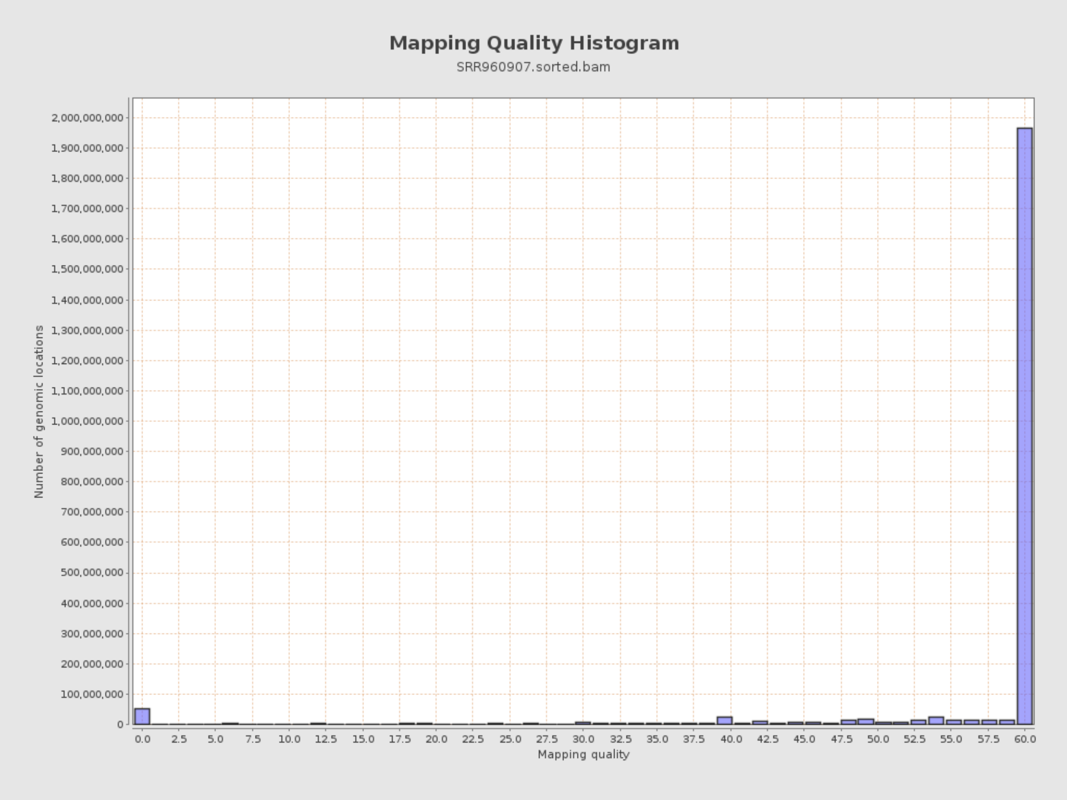
11. Results : Homopolymer Indels



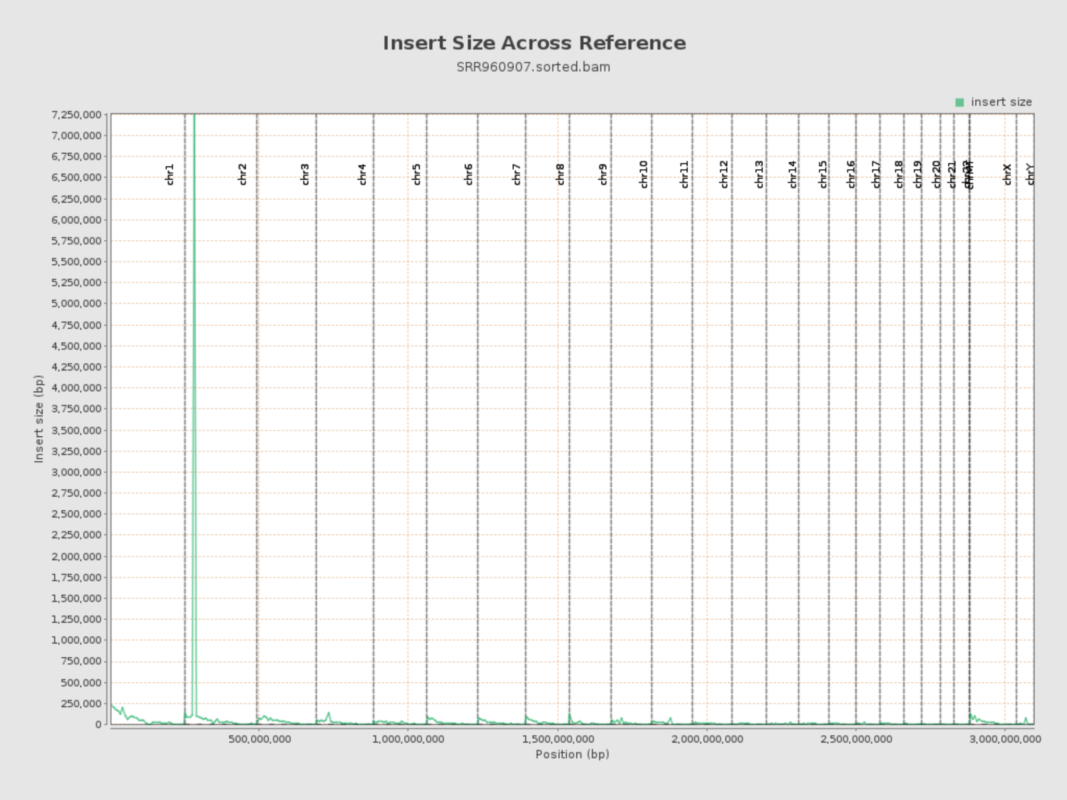
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram