Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 16:35:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975262.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_SRR975262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975262_1.fastq.gz SRR975262_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 16:35:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,977,258
Mapped reads	5,782,989 / 96.75%
Unmapped reads	194,269 / 3.25%
Mapped paired reads	5,782,989 / 96.75%
Mapped reads, first in pair	2,911,288 / 48.71%
Mapped reads, second in pair	2,871,701 / 48.04%
Mapped reads, both in pair	5,720,486 / 95.7%
Mapped reads, singletons	62,503 / 1.05%
Secondary alignments	0
Supplementary alignments	88,246 / 1.48%
Read min/max/mean length	30 / 151 / 151.72
Duplicated reads (estimated)	739,738 / 12.38%
Duplication rate	9.65%
Clipped reads	2,667,947 / 44.63%

2.2. ACGT Content

Number/percentage of A's	226,816,923 / 28.61%
Number/percentage of C's	161,061,678 / 20.32%
Number/percentage of T's	229,447,508 / 28.94%
Number/percentage of G's	175,335,684 / 22.12%
Number/percentage of N's	68,995 / 0.01%

GC Percentage	42.44%

2.3. Coverage

Mean	0.2563
Standard Deviation	2.3633

2.4. Mapping Quality

Mean Mapping Quality	53.6

2.5. Insert size

Mean	70,717.3
Standard Deviation	2,486,963.35
P25/Median/P75	158 / 200 / 260

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	9,385,467
Insertions	153,909
Mapped reads with at least one insertion	2.48%
Deletions	329,580
Mapped reads with at least one deletion	5.44%
Homopolymer indels	46.4%

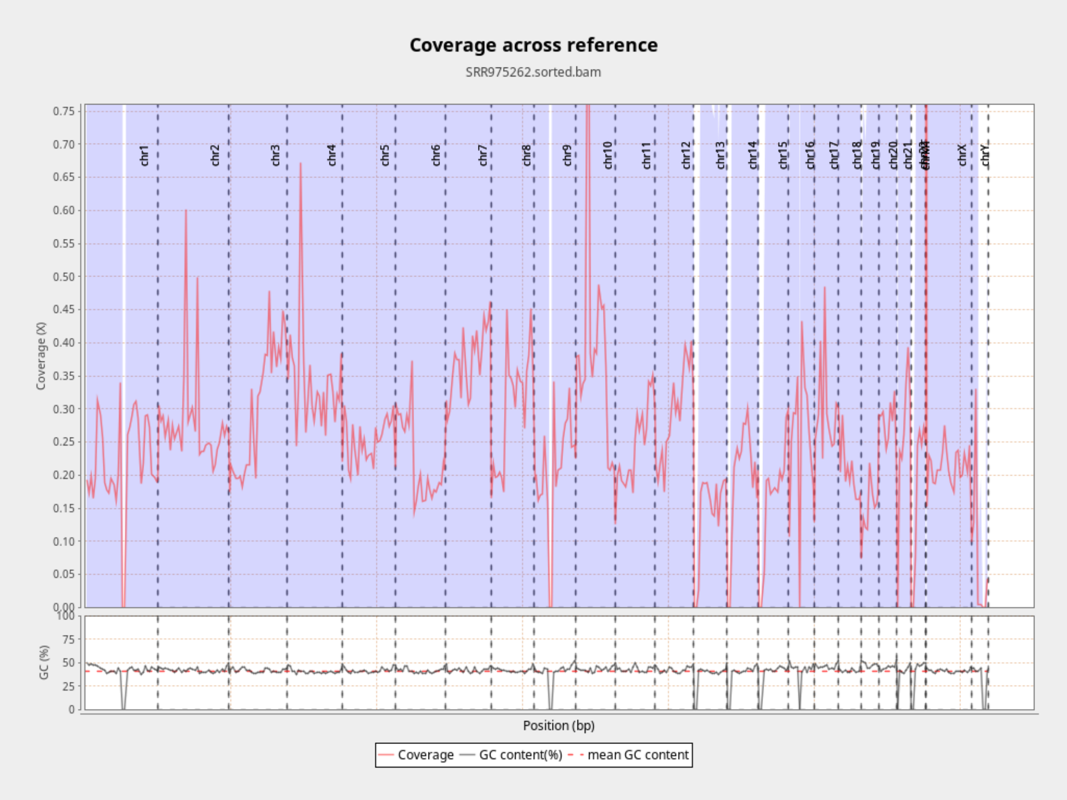
2.7. Chromosome stats

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

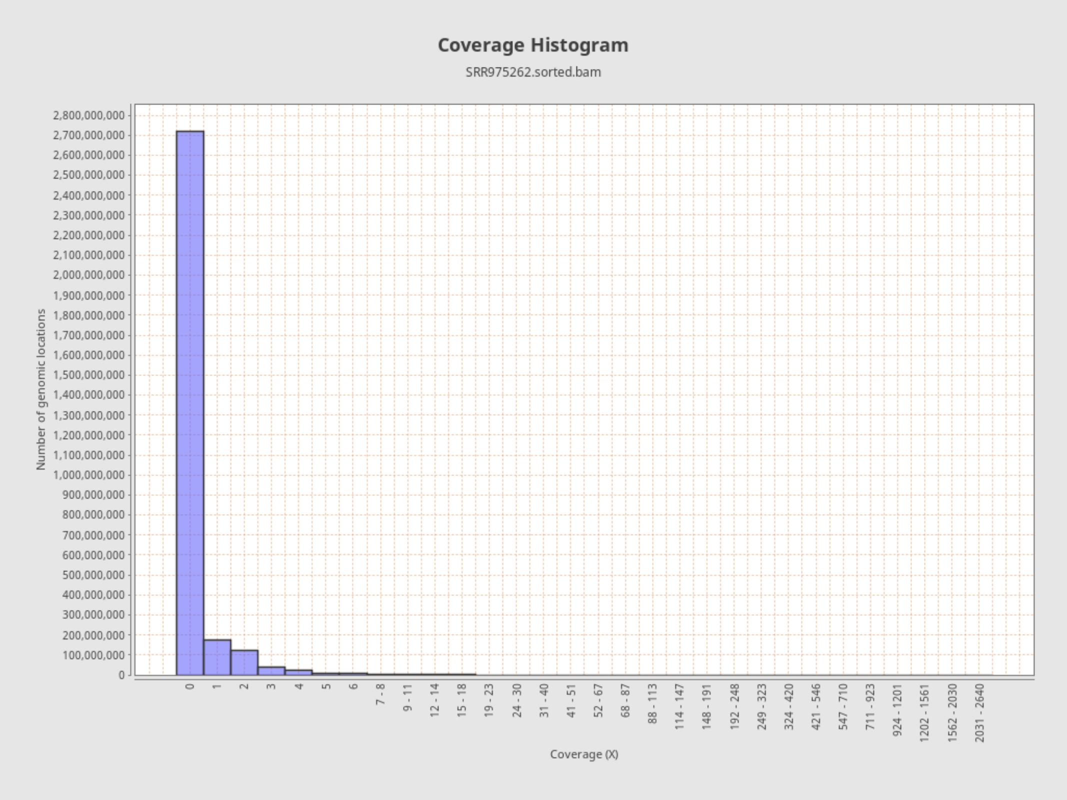
		bases	coverage	deviation
chr1	249250621	54319402	0.2179	2.2623
chr2	243199373	68193938	0.2804	3.1995
chr3	198022430	60163730	0.3038	0.931
chr4	191154276	64850210	0.3393	2.6771
chr5	180915260	45790189	0.2531	0.8432
chr6	171115067	37571148	0.2196	1.6083
chr7	159138663	59259617	0.3724	3.1132
chr8	146364022	44835155	0.3063	1.294
chr9	141213431	29009710	0.2054	3.4198
chr10	135534747	52848850	0.3899	5.5201
chr11	135006516	33140135	0.2455	1.524
chr12	133851895	39248687	0.2932	0.9167
chr13	115169878	16309860	0.1416	0.6125
chr14	107349540	20934118	0.195	0.7894
chr15	102531392	16651576	0.1624	0.6593
chr16	90354753	23328714	0.2582	2.3988
chr17	81195210	24544035	0.3023	2.2931
chr18	78077248	15892796	0.2036	3.2151
chr19	59128983	8862161	0.1499	1.2211
chr20	63025520	17765233	0.2819	1.2205
chr21	48129895	12804787	0.266	1.7178
chr22	51304566	9045345	0.1763	0.7316
chrMT	16571	477508	28.8159	16.1445
chrX	155270560	33081368	0.2131	0.9074

chrY	59373566	4455273	0.075	4.096

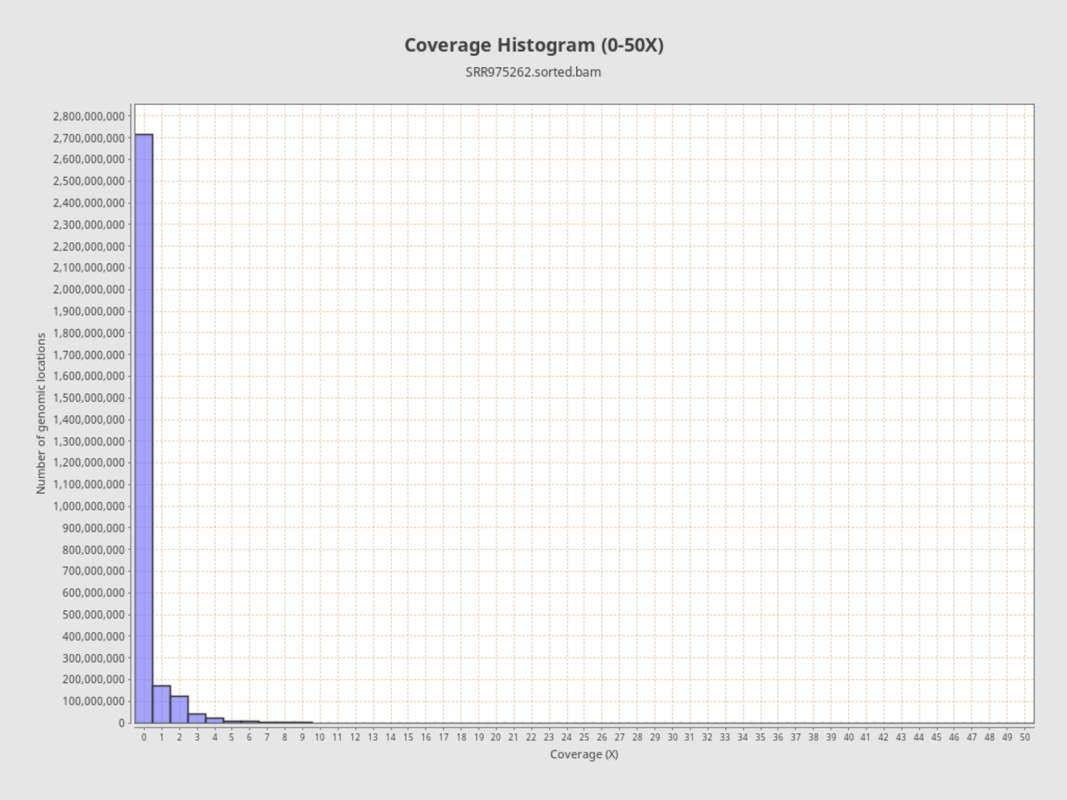
3. Results : Coverage across reference



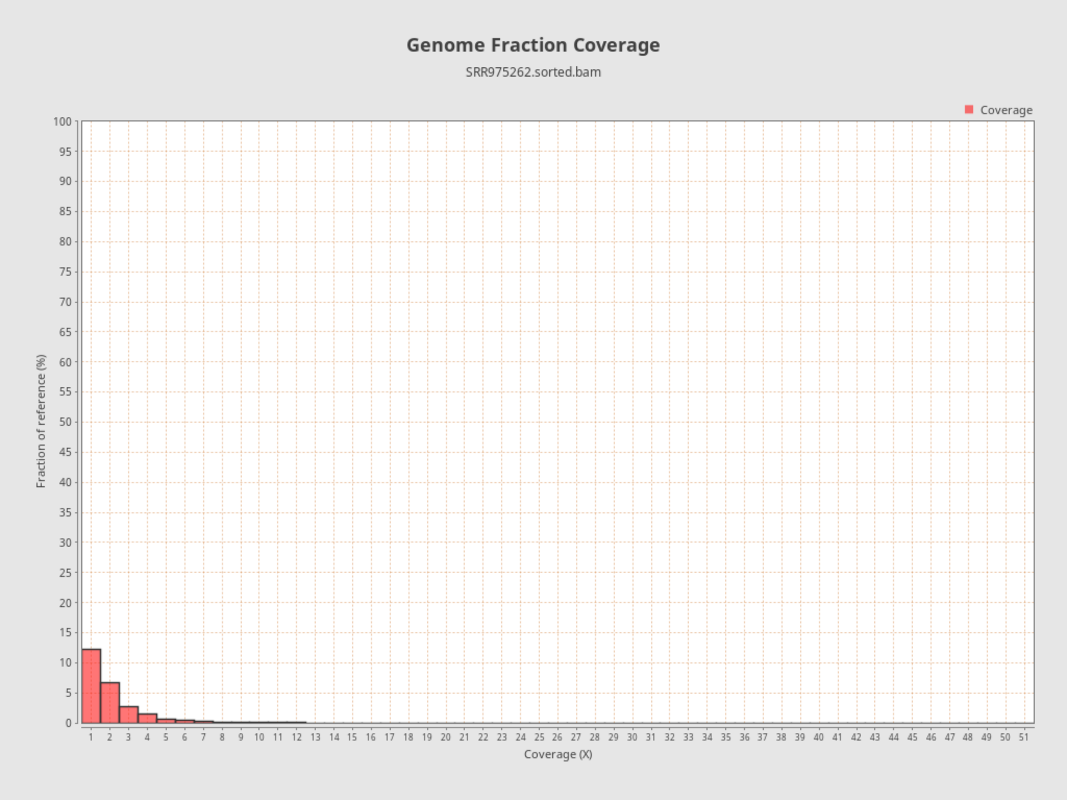
4. Results : Coverage Histogram



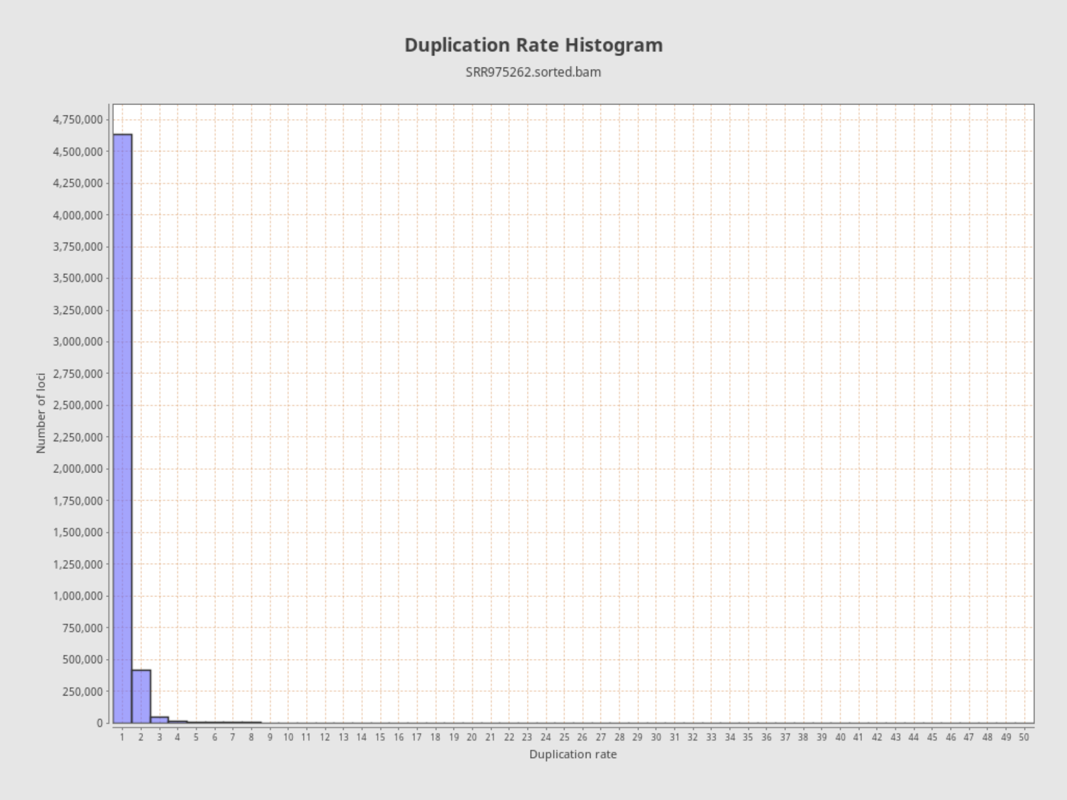
5. Results : Coverage Histogram (0-50X)



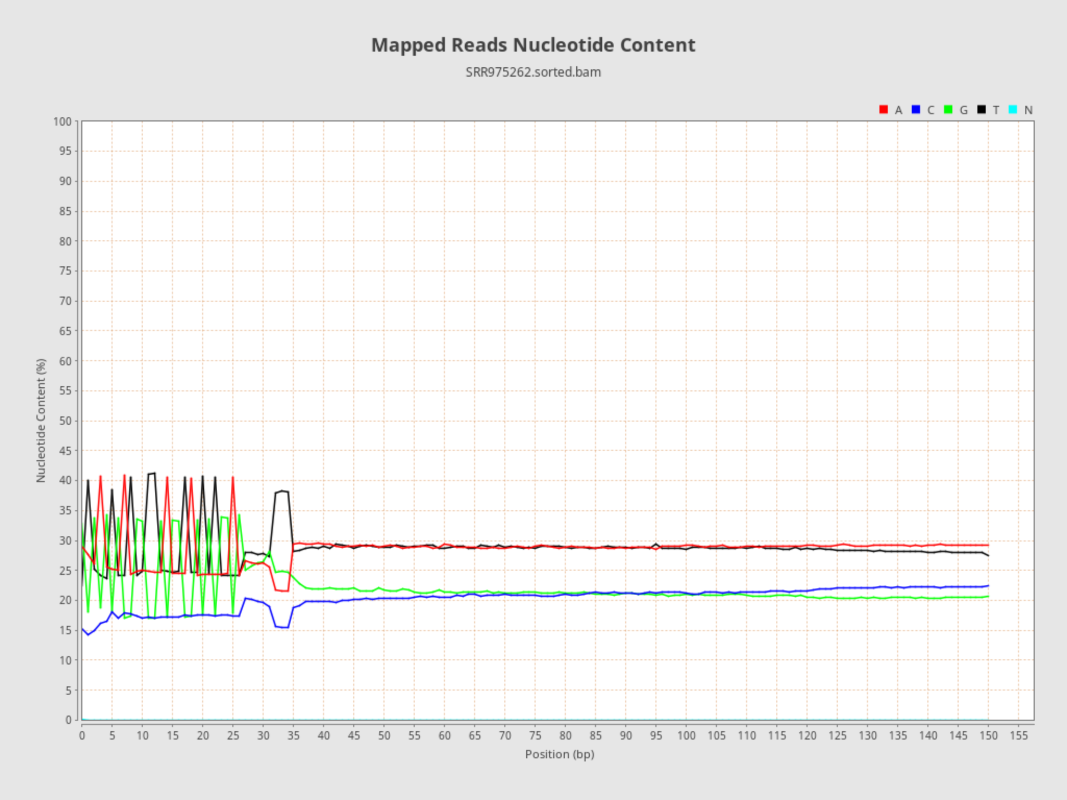
6. Results : Genome Fraction Coverage



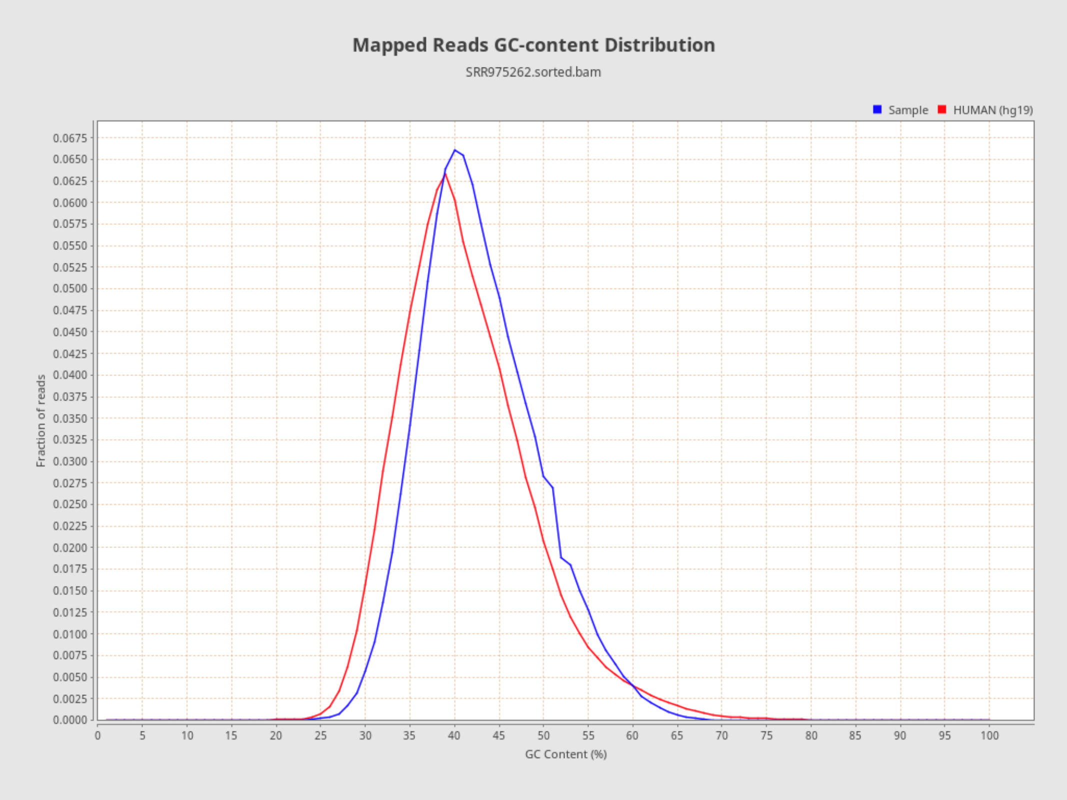
7. Results : Duplication Rate Histogram



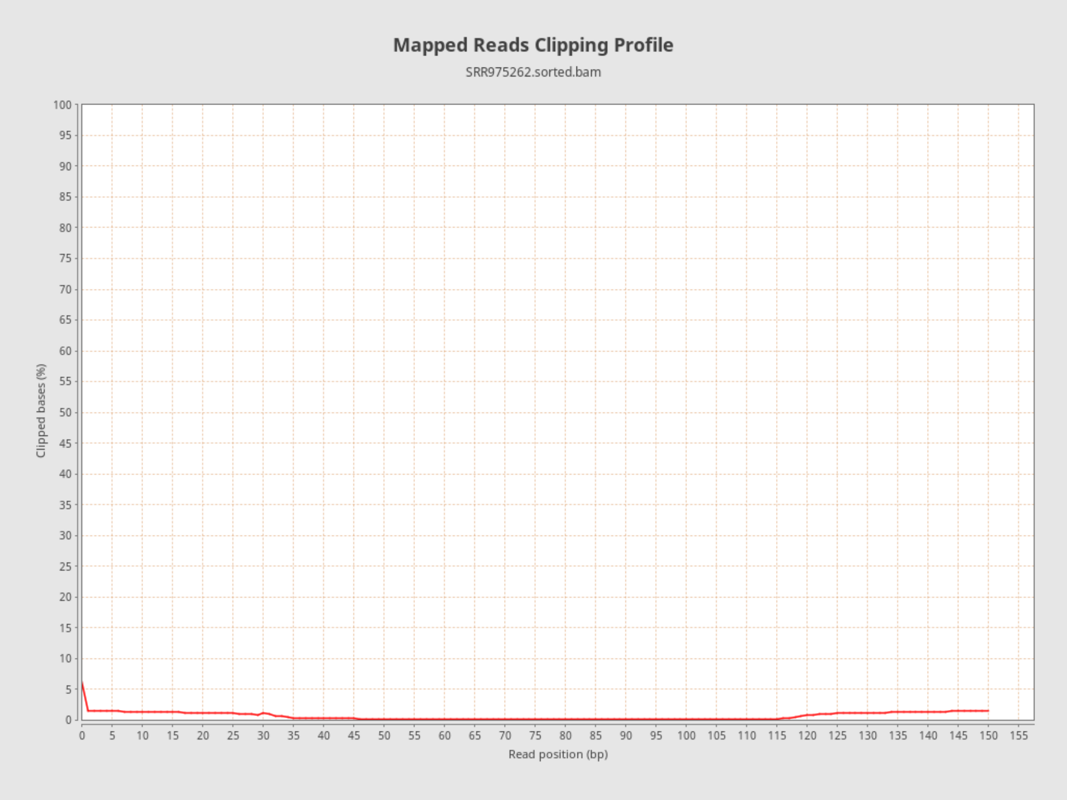
8. Results : Mapped Reads Nucleotide Content



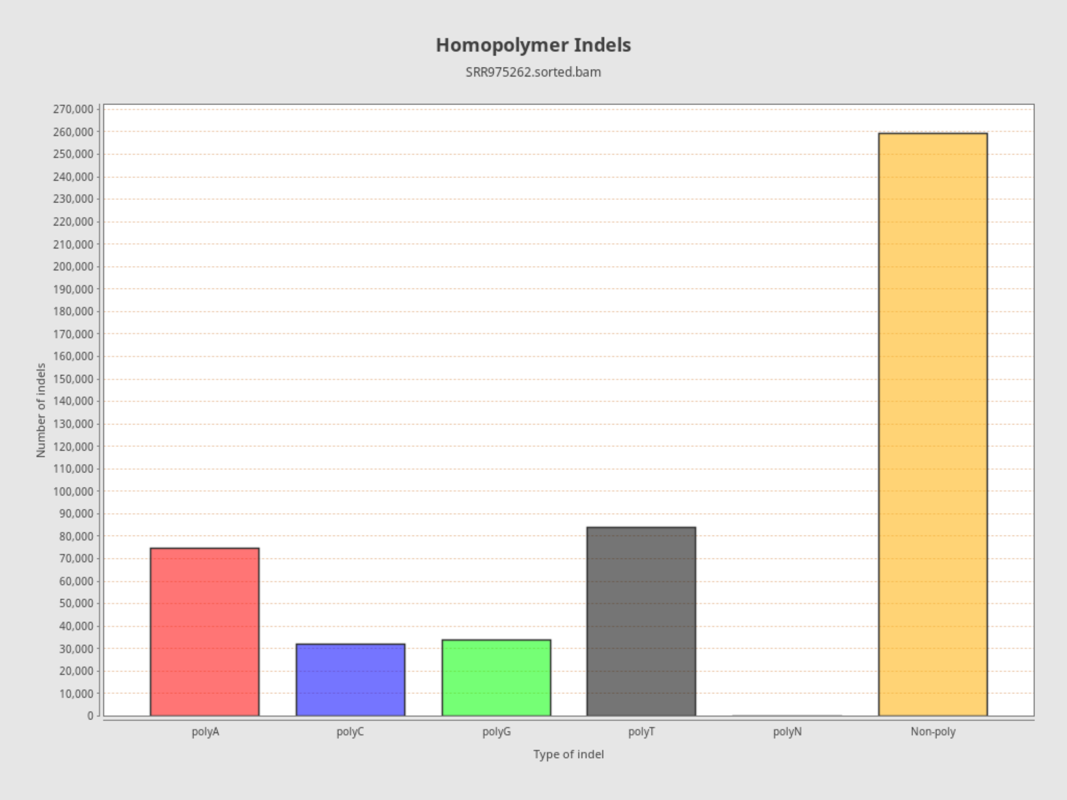
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

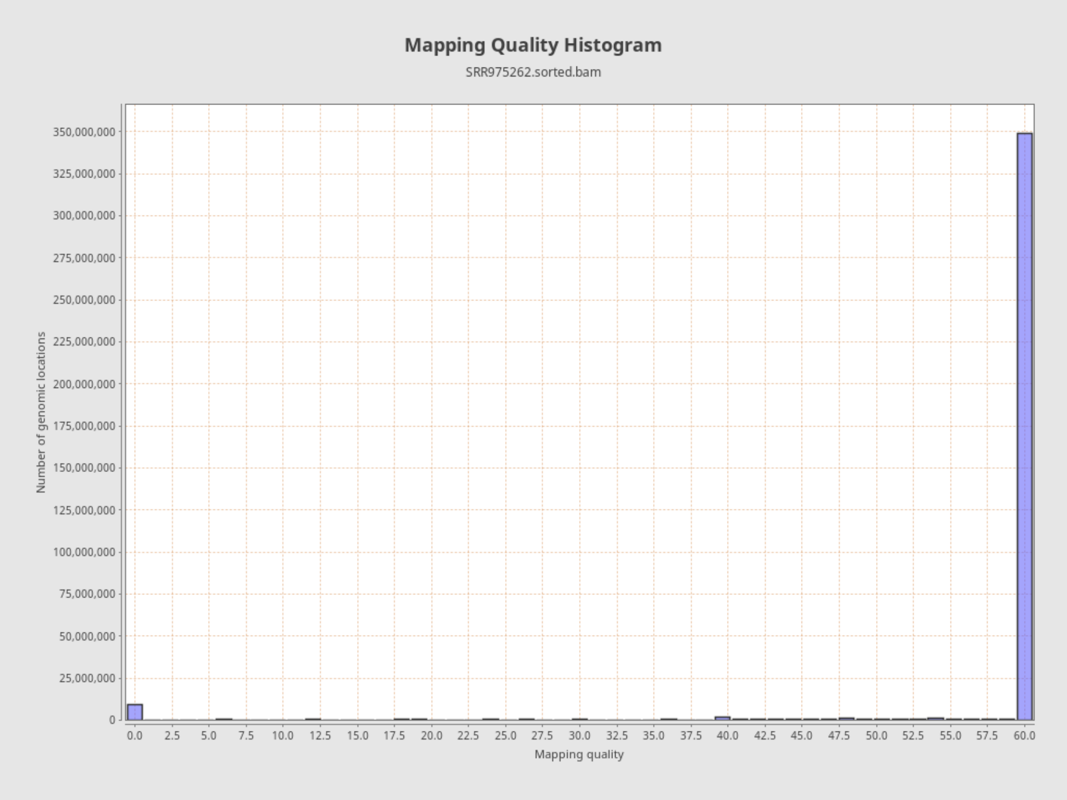


11. Results : Homopolymer Indels

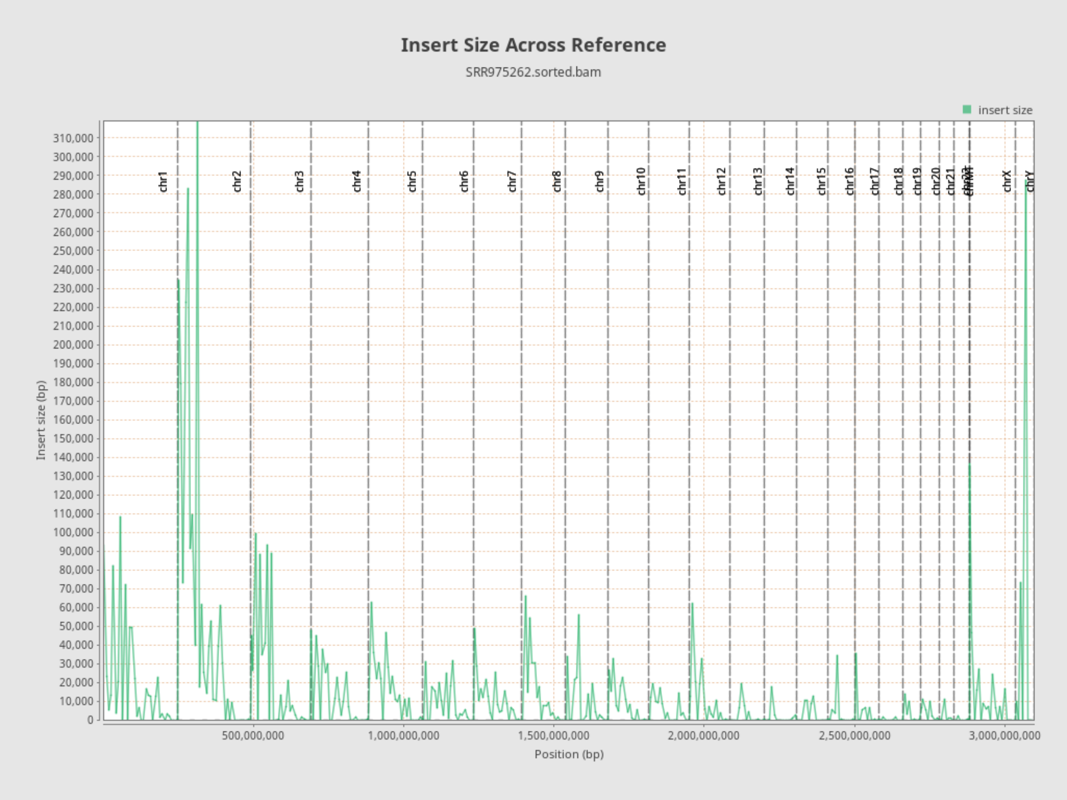


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram