Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:39:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124872.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_SRR3124872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124872_1.fastq.gz SRR3124872_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:39:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,086,044
Mapped reads	4,994,593 / 98.2%
Unmapped reads	91,451 / 1.8%
Mapped paired reads	4,994,593 / 98.2%
Mapped reads, first in pair	2,498,780 / 49.13%
Mapped reads, second in pair	2,495,813 / 49.07%
Mapped reads, both in pair	4,978,760 / 97.89%
Mapped reads, singletons	15,833 / 0.31%
Secondary alignments	0
Supplementary alignments	19,674 / 0.39%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	294,829 / 5.8%
Duplication rate	3.91%
Clipped reads	2,092,100 / 41.13%

2.2. ACGT Content

Number/percentage of A's	128,420,081 / 28.4%
Number/percentage of C's	88,106,677 / 19.48%
Number/percentage of T's	132,944,674 / 29.4%
Number/percentage of G's	102,783,040 / 22.73%
Number/percentage of N's	6,294 / 0%

GC Percentage	42.21%

2.3. Coverage

Mean	0.1462
Standard Deviation	1.2993

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	48,185.29
Standard Deviation	2,099,326.97
P25/Median/P75	144 / 186 / 249

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	3,140,586
Insertions	54,616
Mapped reads with at least one insertion	1.07%
Deletions	134,833
Mapped reads with at least one deletion	2.65%
Homopolymer indels	47.35%

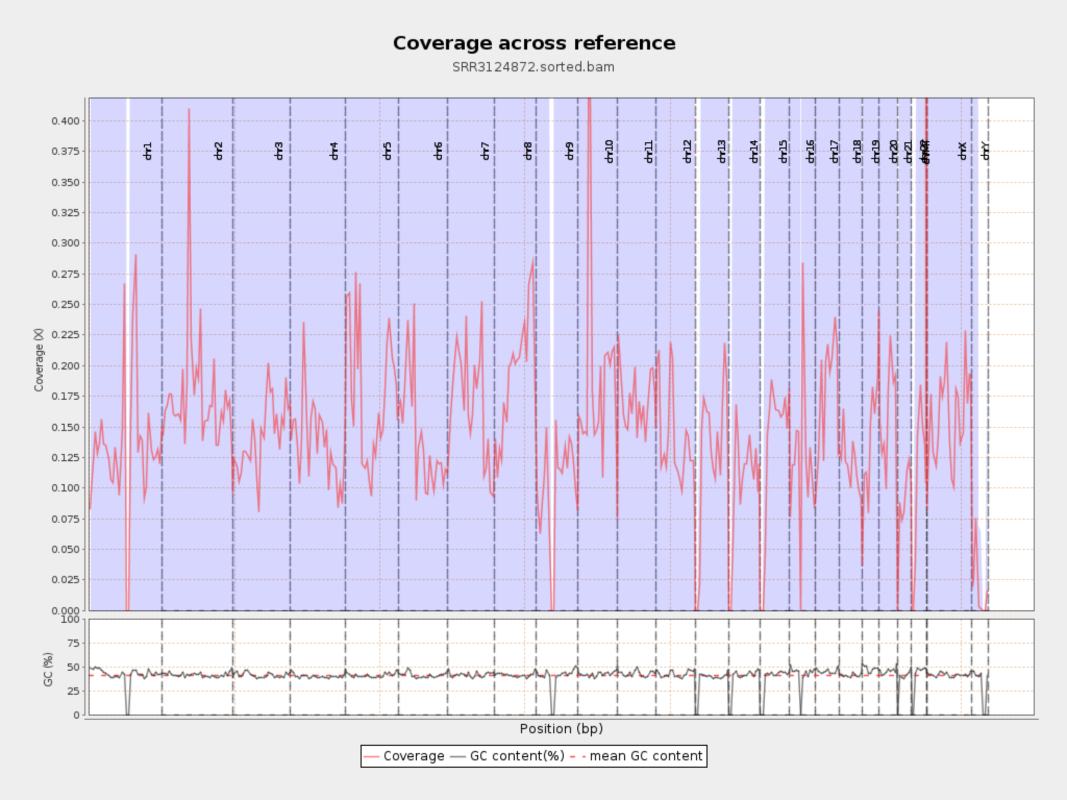
2.7. Chromosome stats

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

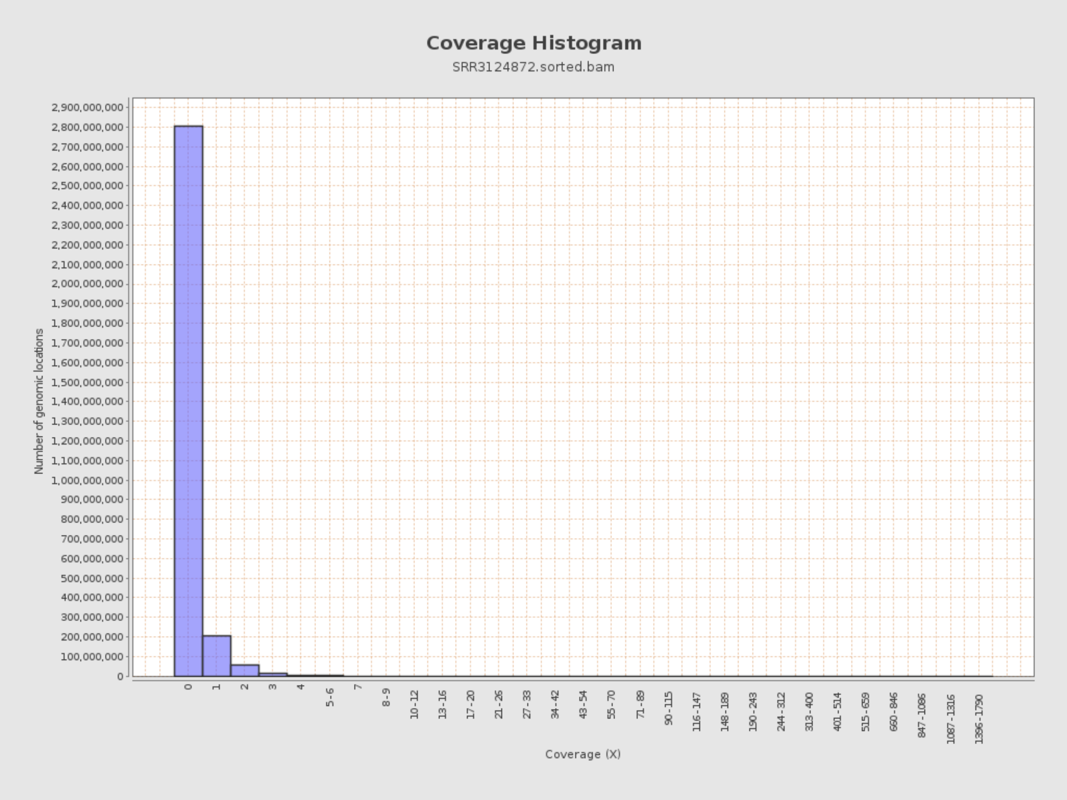
		bases	coverage	deviation
chr1	249250621	32915452	0.1321	1.4324
chr2	243199373	43111615	0.1773	1.6209
chr3	198022430	28301771	0.1429	0.5663
chr4	191154276	26070297	0.1364	0.856
chr5	180915260	31983324	0.1768	0.6399
chr6	171115067	24206634	0.1415	1.0378
chr7	159138663	27229886	0.1711	1.9445
chr8	146364022	28745401	0.1964	0.7592
chr9	141213431	14121905	0.1	1.5125
chr10	135534747	25916997	0.1912	3.1892
chr11	135006516	22857862	0.1693	0.9883
chr12	133851895	19017117	0.1421	0.6176
chr13	115169878	14625792	0.127	0.505
chr14	107349540	10898335	0.1015	0.5493
chr15	102531392	13603359	0.1327	0.5522
chr16	90354753	10925172	0.1209	1.4059
chr17	81195210	14651599	0.1804	1.5653
chr18	78077248	9430185	0.1208	1.7498
chr19	59128983	8301184	0.1404	1.022
chr20	63025520	10038390	0.1593	0.7576
chr21	48129895	4230127	0.0879	0.5484
chr22	51304566	5259514	0.1025	0.526
chrMT	16571	460861	27.8113	15.3488
chrX	155270560	24532062	0.158	0.8605

chrY	59373566	1046457	0.0176	1.1048

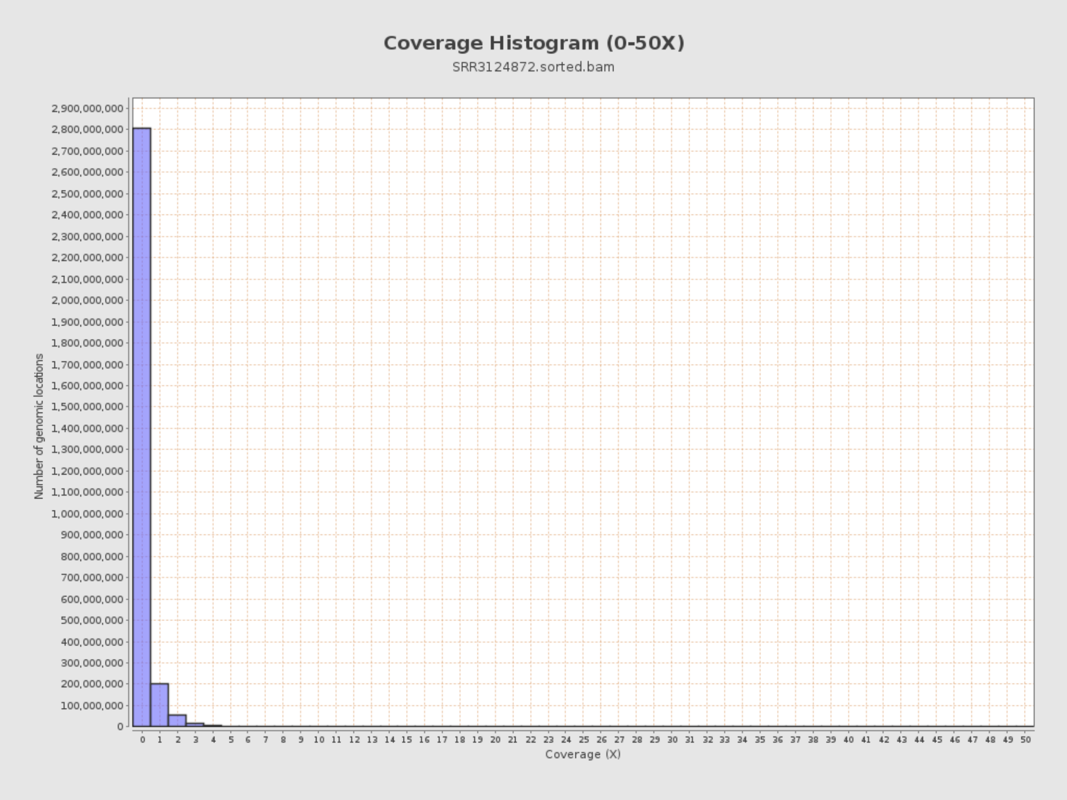
3. Results : Coverage across reference



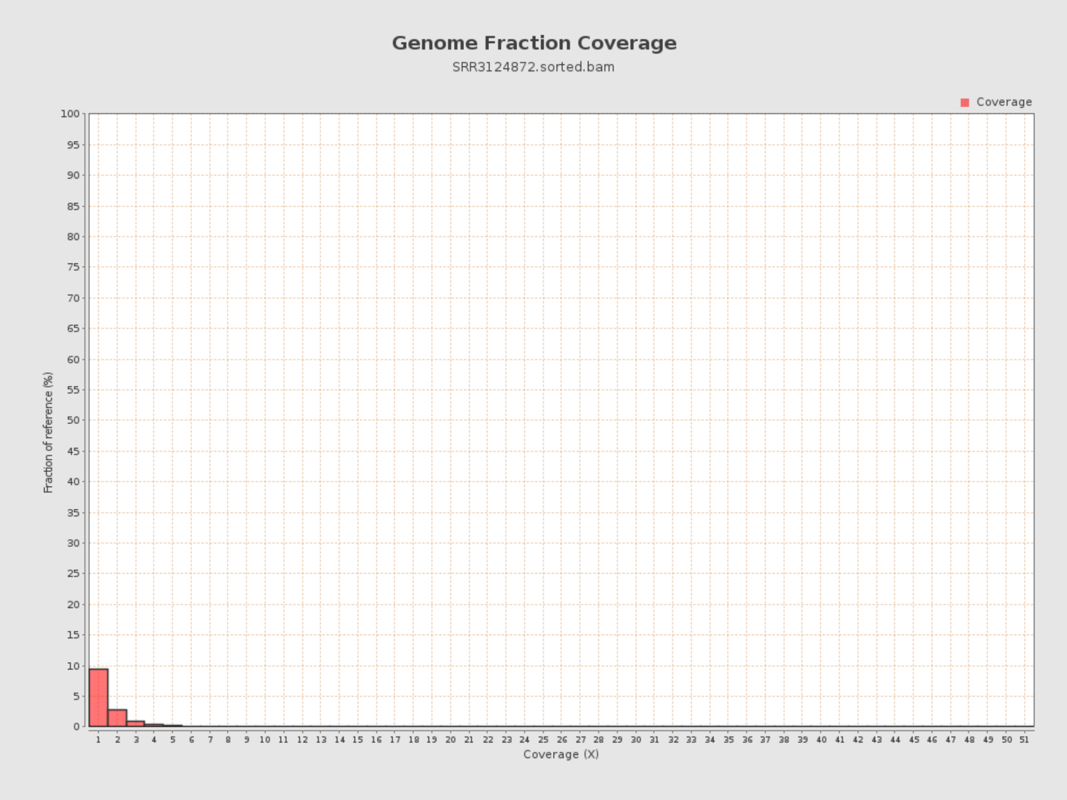
4. Results : Coverage Histogram



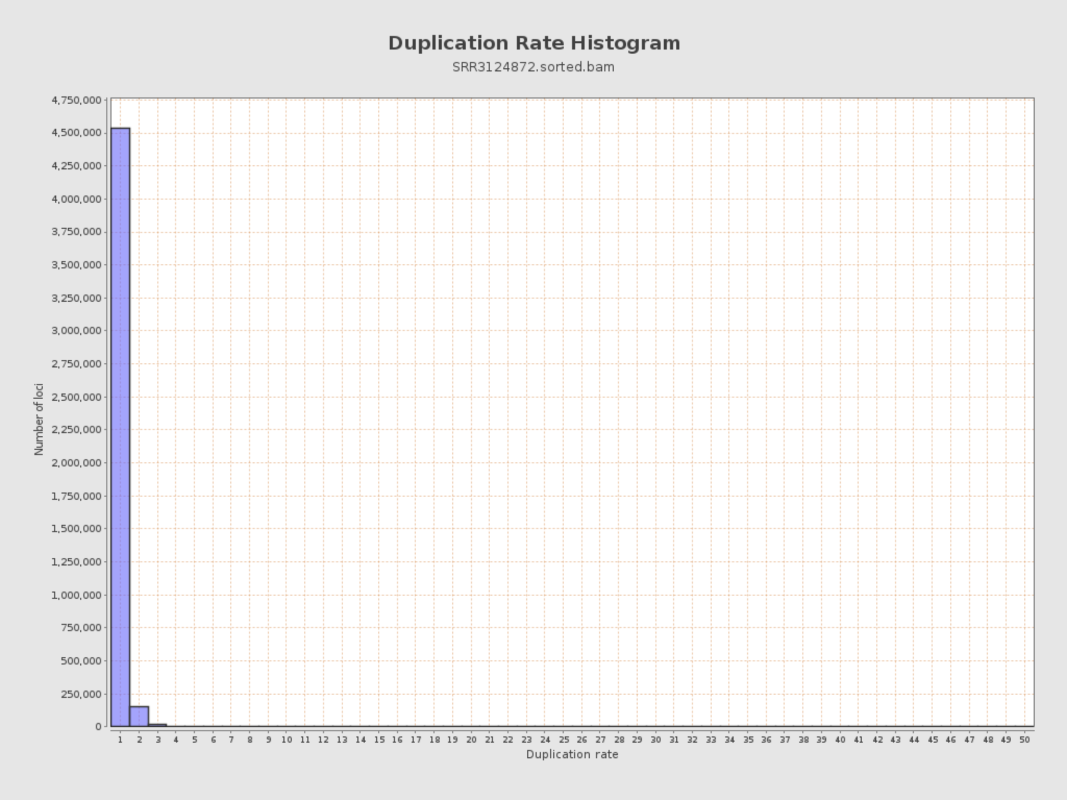
5. Results : Coverage Histogram (0-50X)



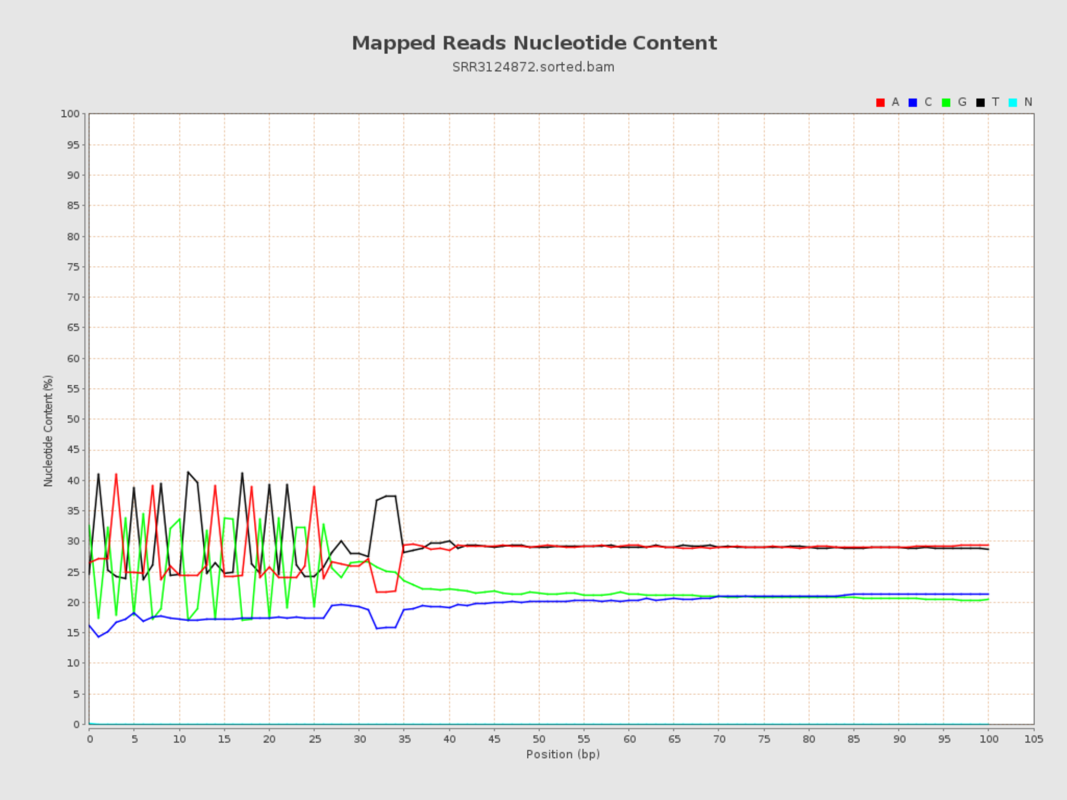
6. Results : Genome Fraction Coverage



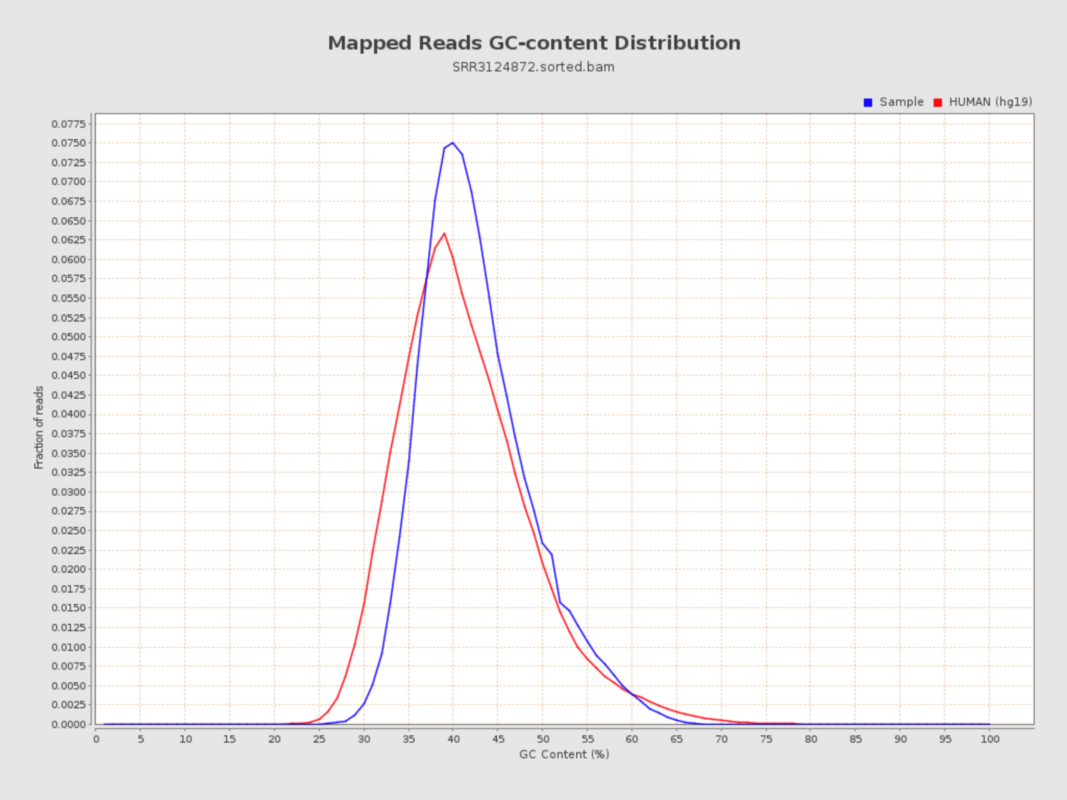
7. Results : Duplication Rate Histogram



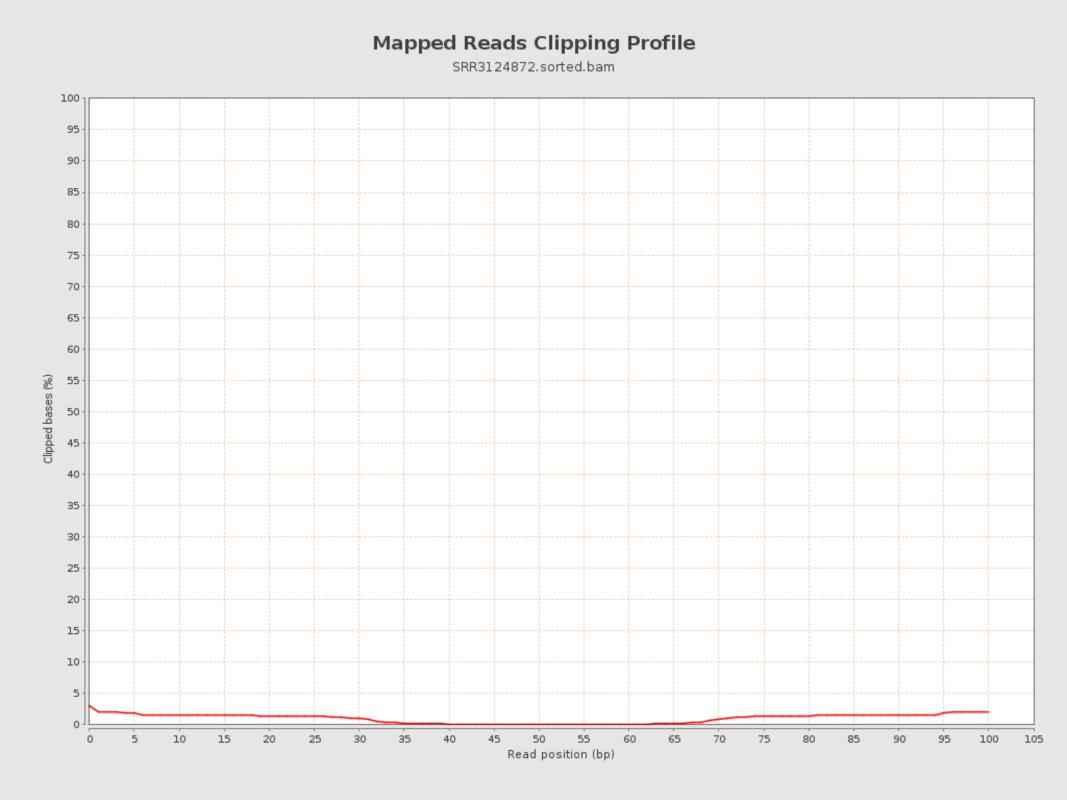
8. Results : Mapped Reads Nucleotide Content



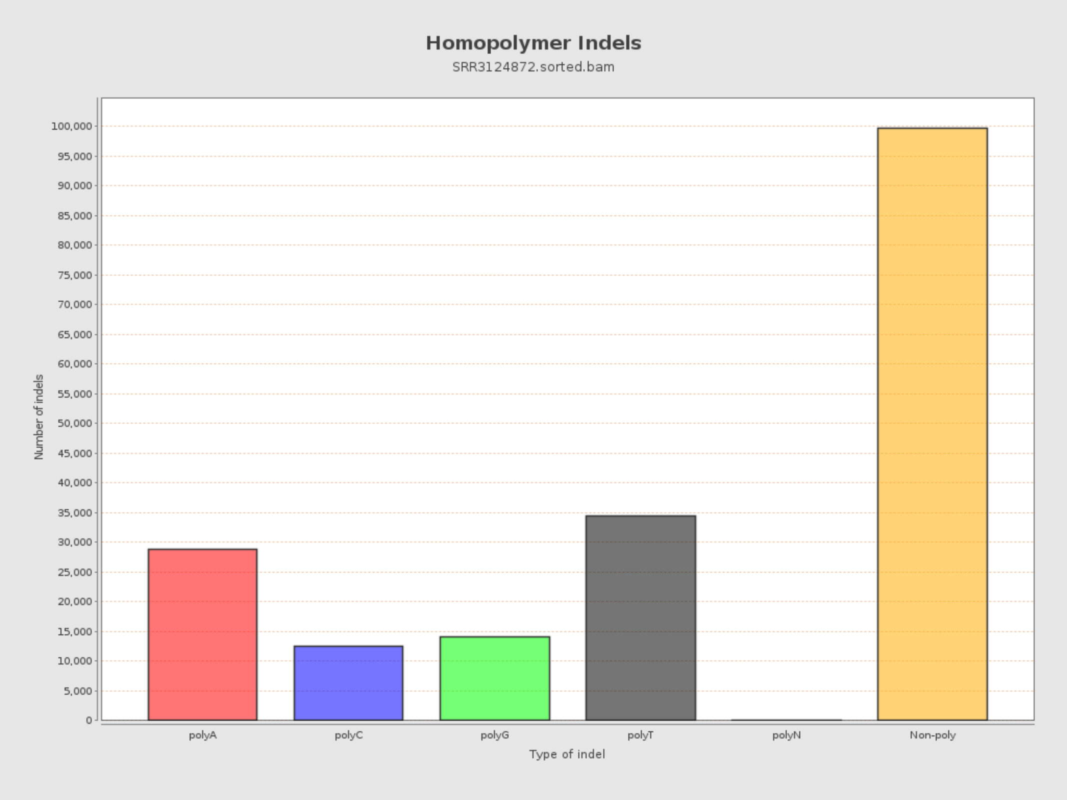
9. Results : Mapped Reads GC-content Distribution



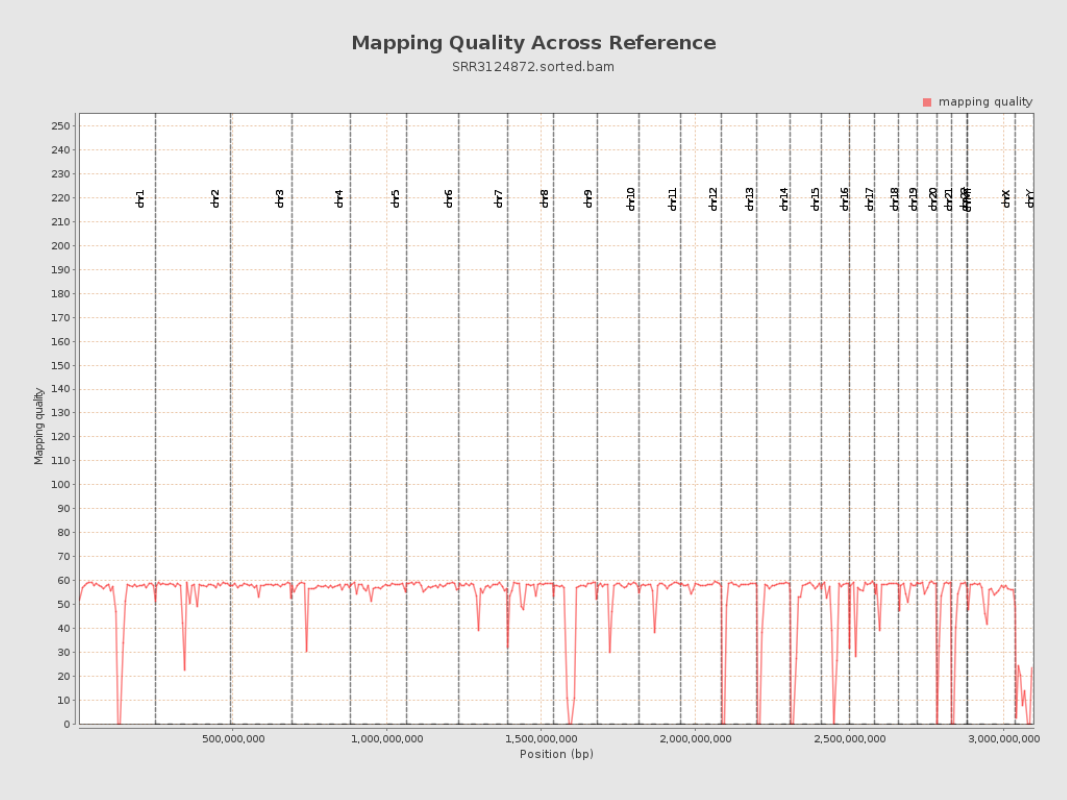
10. Results : Mapped Reads Clipping Profile



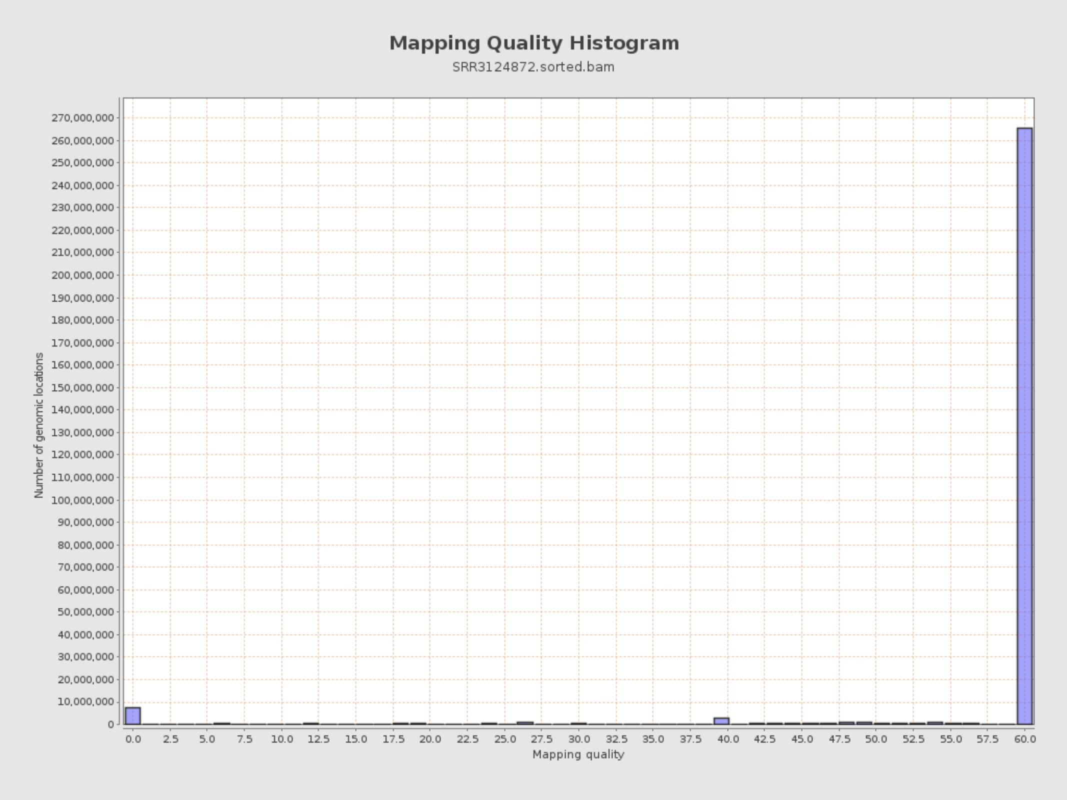
11. Results : Homopolymer Indels



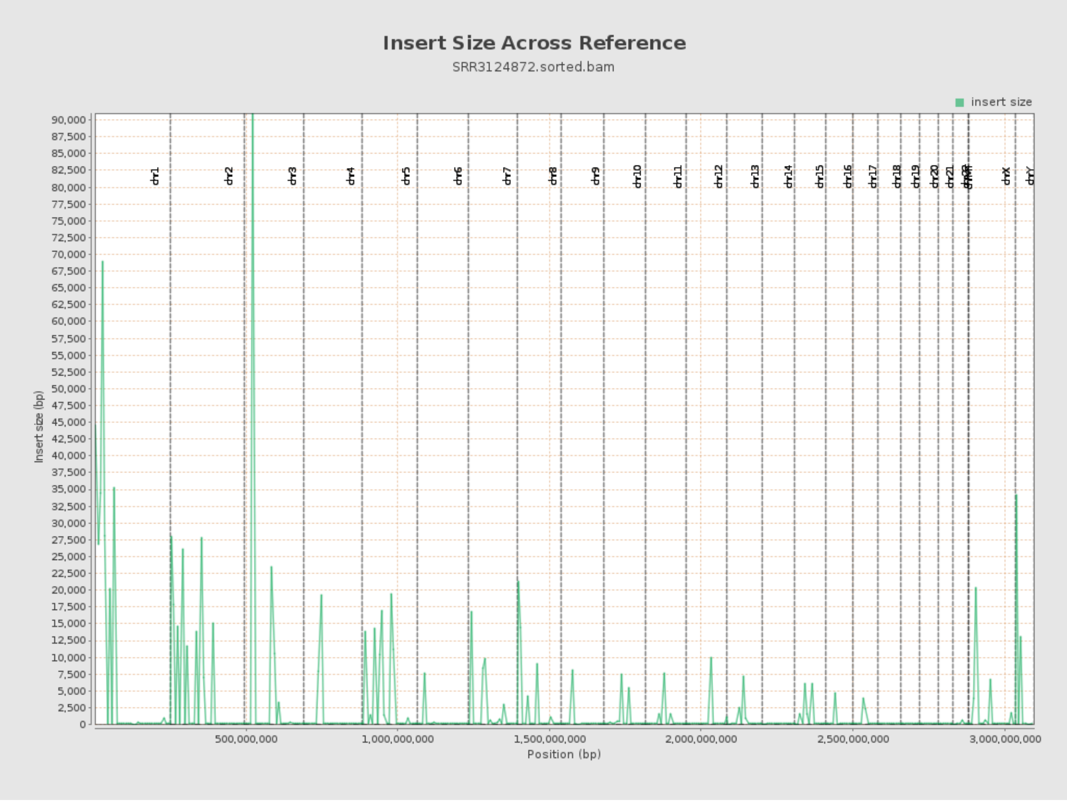
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram