Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 04:37:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472674.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_SRR3472674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472674_1.fastq.gz SRR3472674_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 04:37:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,627,986
Mapped reads	20,442,567 / 99.1%
Unmapped reads	185,419 / 0.9%
Mapped paired reads	20,442,567 / 99.1%
Mapped reads, first in pair	10,250,819 / 49.69%
Mapped reads, second in pair	10,191,748 / 49.41%
Mapped reads, both in pair	20,324,042 / 98.53%
Mapped reads, singletons	118,525 / 0.57%
Secondary alignments	0
Supplementary alignments	111,625 / 0.54%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	14,894,543 / 72.21%
Duplication rate	49.79%
Clipped reads	1,445,686 / 7.01%

2.2. ACGT Content

Number/percentage of A's	525,274,099 / 26.11%
Number/percentage of C's	484,134,719 / 24.06%
Number/percentage of T's	526,406,859 / 26.16%
Number/percentage of G's	475,822,114 / 23.65%
Number/percentage of N's	364,194 / 0.02%

GC Percentage	47.71%

2.3. Coverage

Mean	0.65
Standard Deviation	31.6379

2.4. Mapping Quality

Mean Mapping Quality	54.77

2.5. Insert size

Mean	20,928.54
Standard Deviation	1,442,879.85
P25/Median/P75	162 / 221 / 291

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	12,619,938
Insertions	125,064
Mapped reads with at least one insertion	0.61%
Deletions	100,184
Mapped reads with at least one deletion	0.48%
Homopolymer indels	47.1%

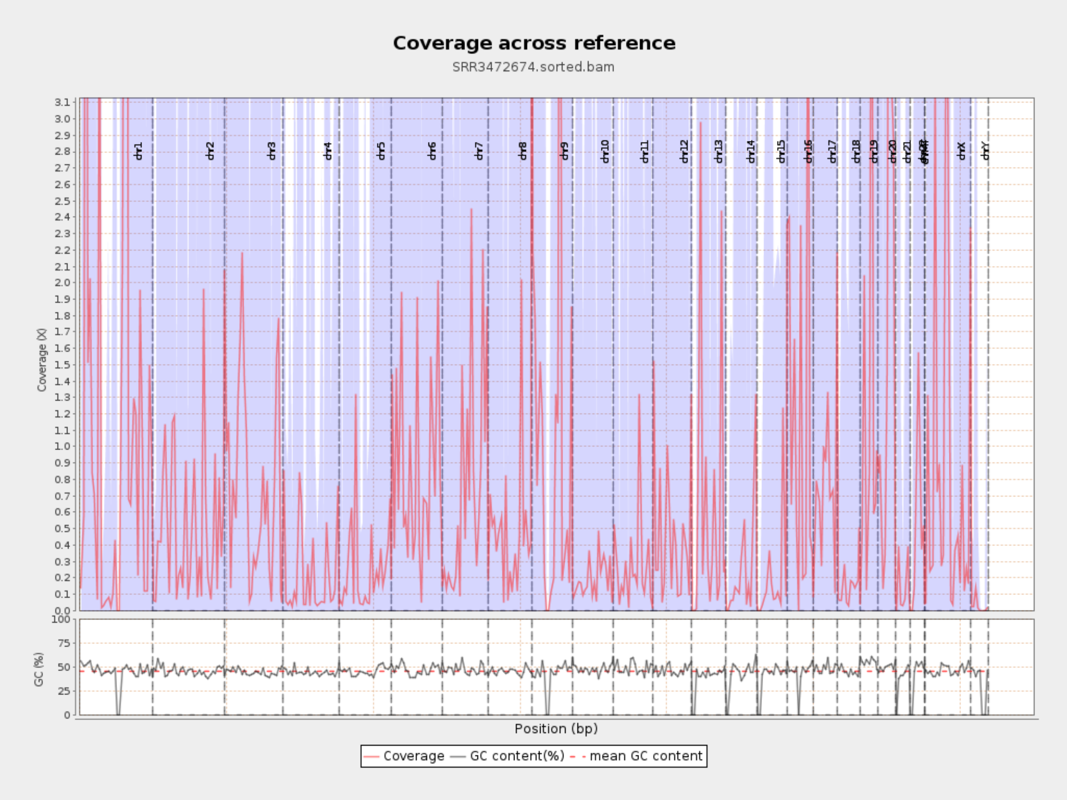
2.7. Chromosome stats

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

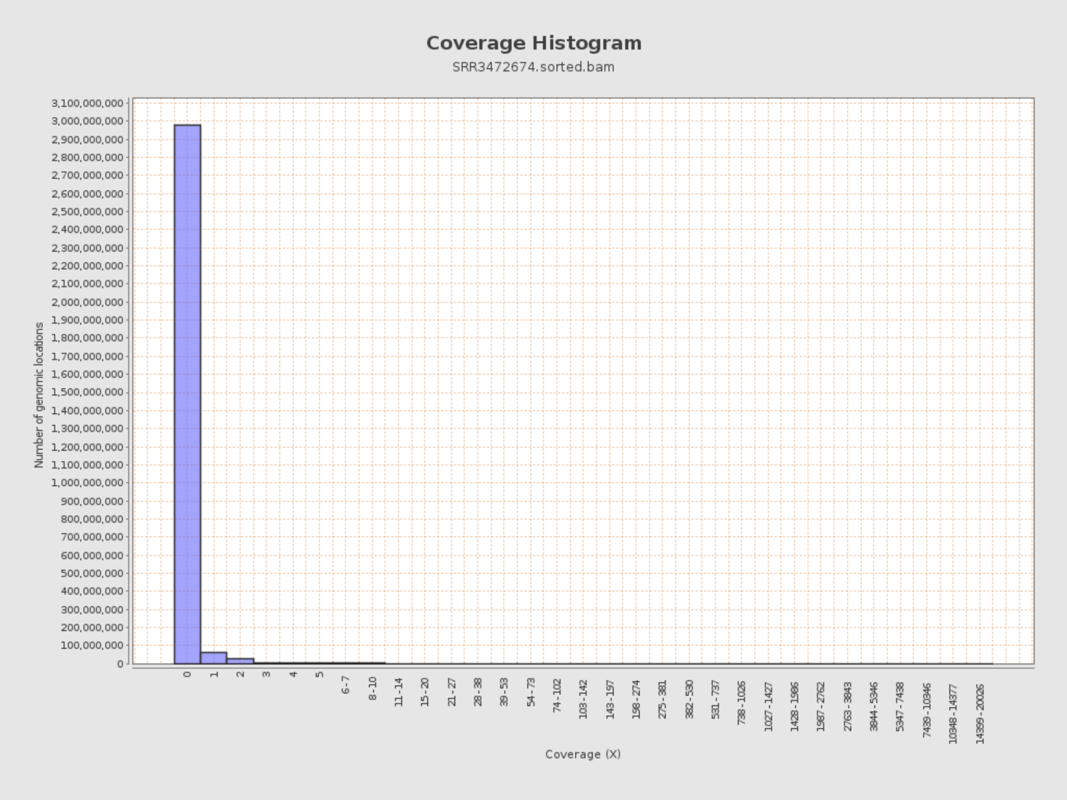
		bases	coverage	deviation
chr1	249250621	327715348	1.3148	55.4883
chr2	243199373	121434683	0.4993	20.255
chr3	198022430	157931580	0.7975	26.2144
chr4	191154276	40920009	0.2141	12.5359
chr5	180915260	47420812	0.2621	9.9411
chr6	171115067	148077297	0.8654	31.3225
chr7	159138663	120769933	0.7589	26.9871
chr8	146364022	70718571	0.4832	15.7952
chr9	141213431	162096669	1.1479	50.9893
chr10	135534747	26277427	0.1939	7.2973
chr11	135006516	37407973	0.2771	11.3229
chr12	133851895	60429643	0.4515	16.2423
chr13	115169878	75358156	0.6543	29.4976
chr14	107349540	26502135	0.2469	16.8685
chr15	102531392	20513303	0.2001	11.8905
chr16	90354753	115277882	1.2758	54.282
chr17	81195210	61832792	0.7615	24.0848
chr18	78077248	11712055	0.15	7.6605
chr19	59128983	79652631	1.3471	62.437
chr20	63025520	129764062	2.0589	79.0479
chr21	48129895	7534949	0.1566	9.2416
chr22	51304566	26713989	0.5207	16.9419
chrMT	16571	4449	0.2685	0.6097
chrX	155270560	134512063	0.8663	35.2575

chrY	59373566	1661868	0.028	2.0775

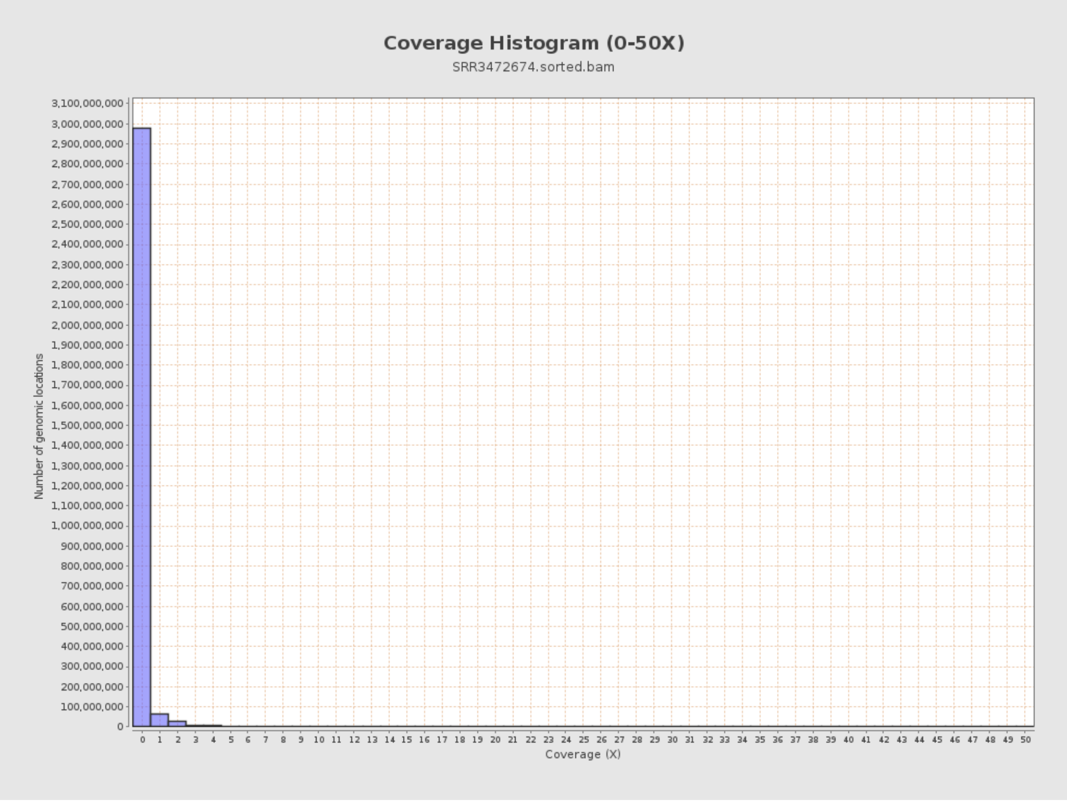
3. Results : Coverage across reference



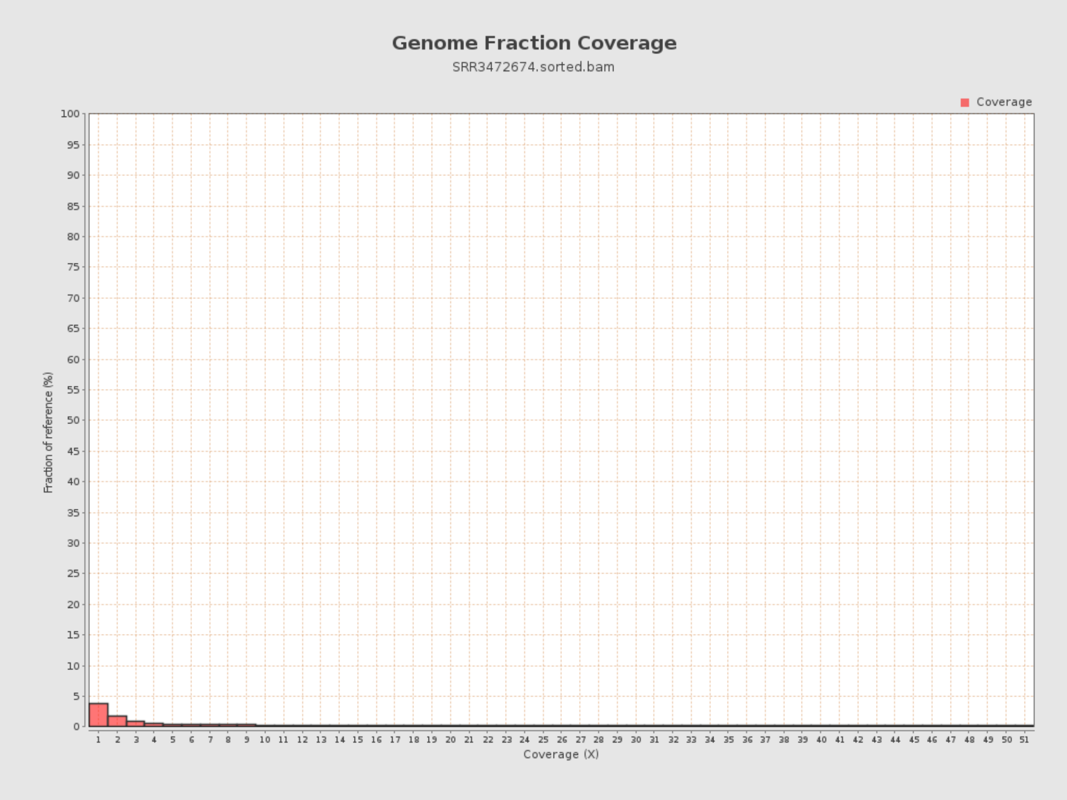
4. Results : Coverage Histogram



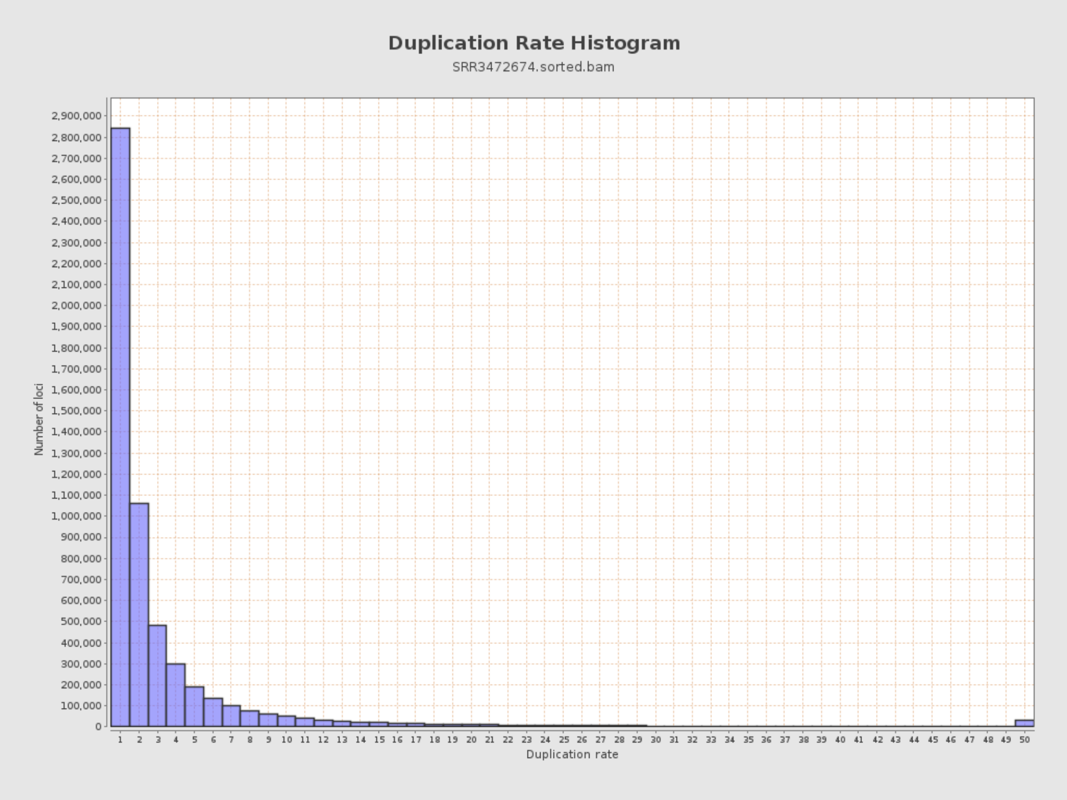
5. Results : Coverage Histogram (0-50X)



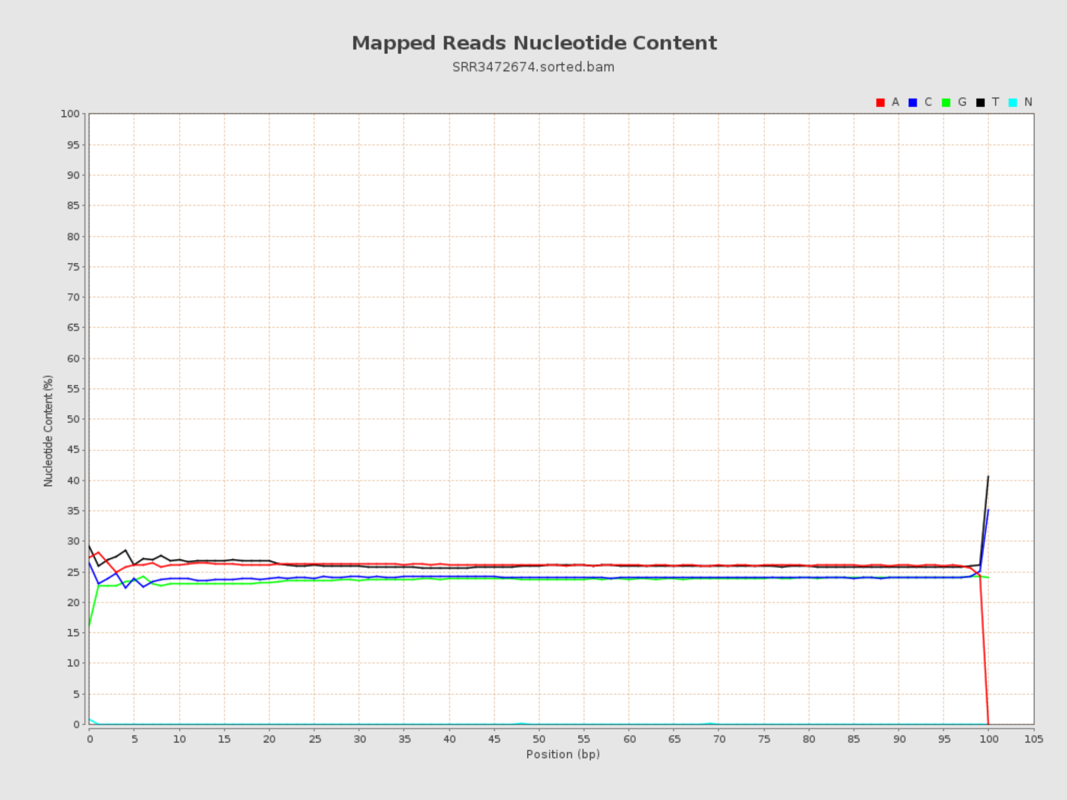
6. Results : Genome Fraction Coverage



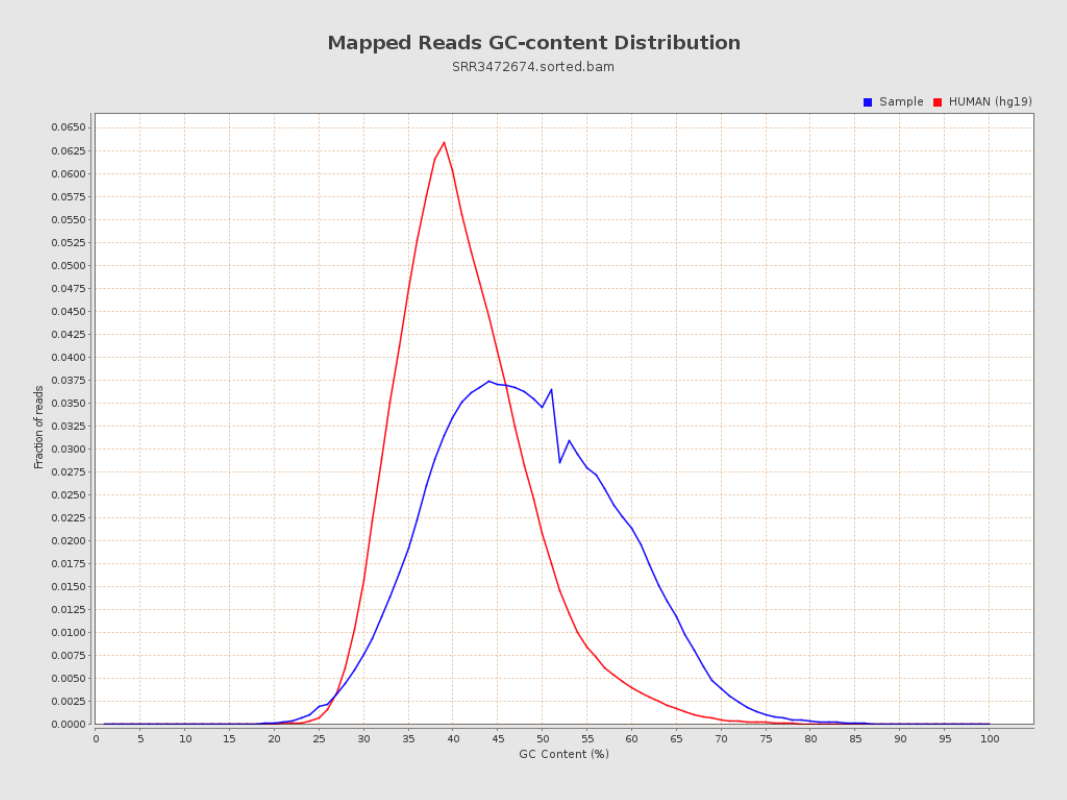
7. Results : Duplication Rate Histogram



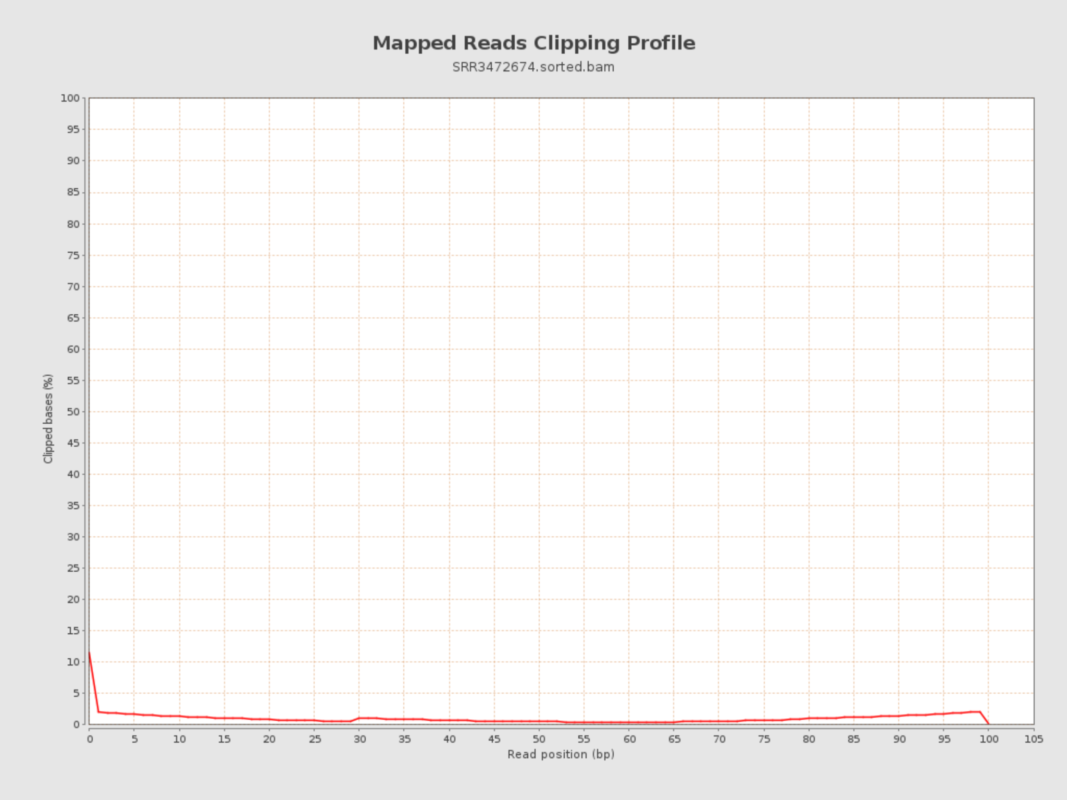
8. Results : Mapped Reads Nucleotide Content



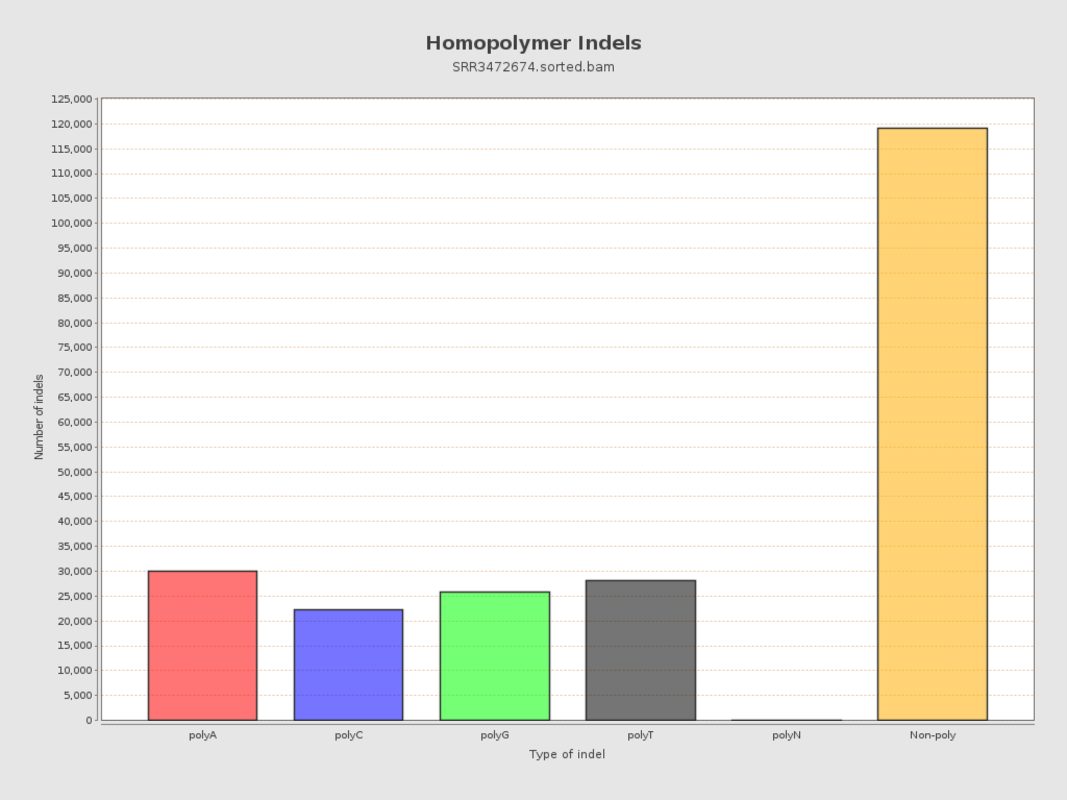
9. Results : Mapped Reads GC-content Distribution



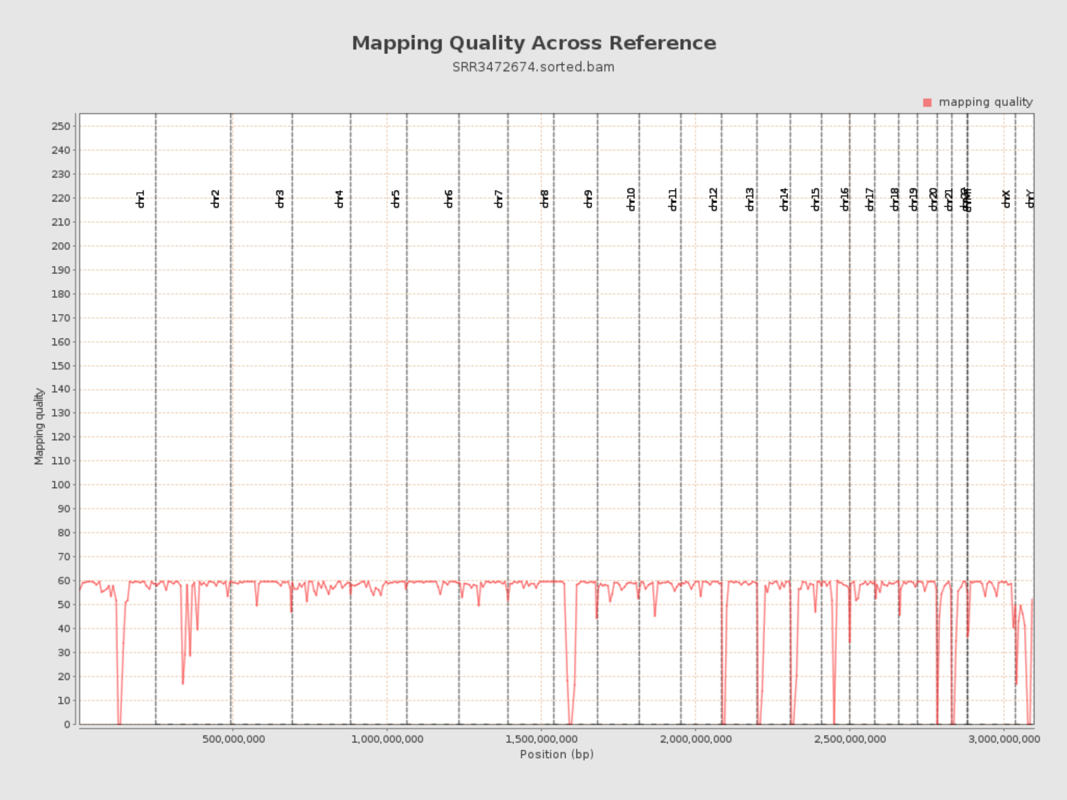
10. Results : Mapped Reads Clipping Profile



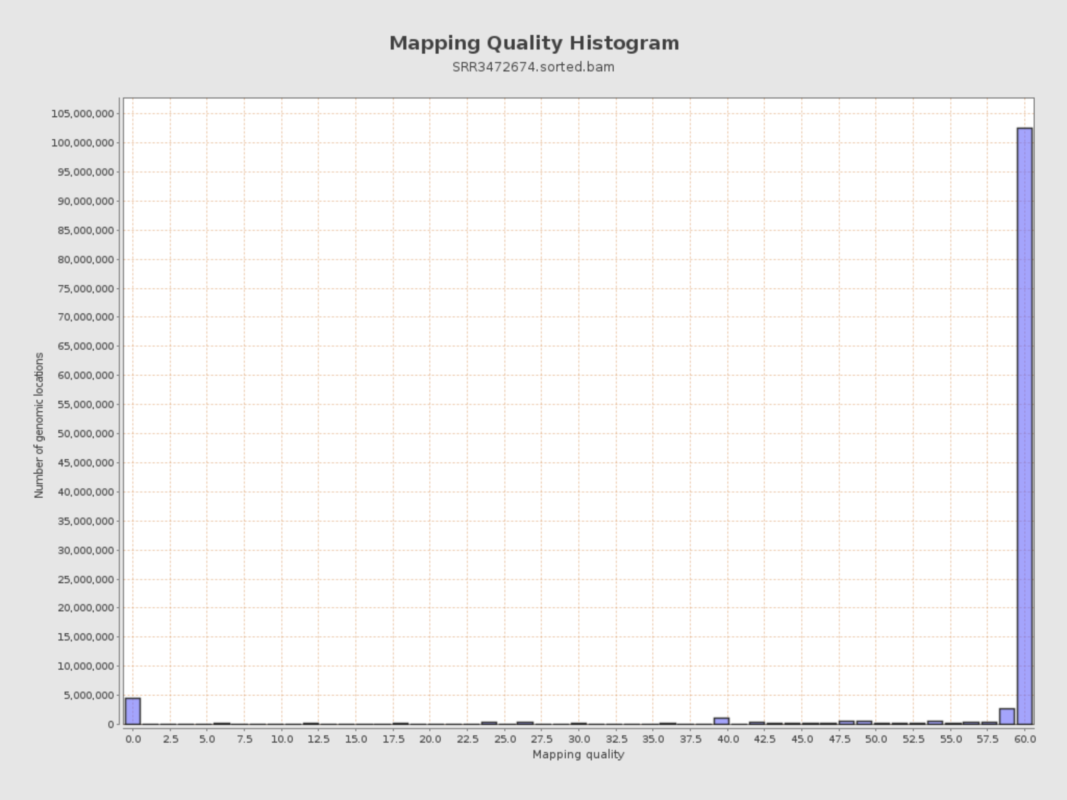
11. Results : Homopolymer Indels



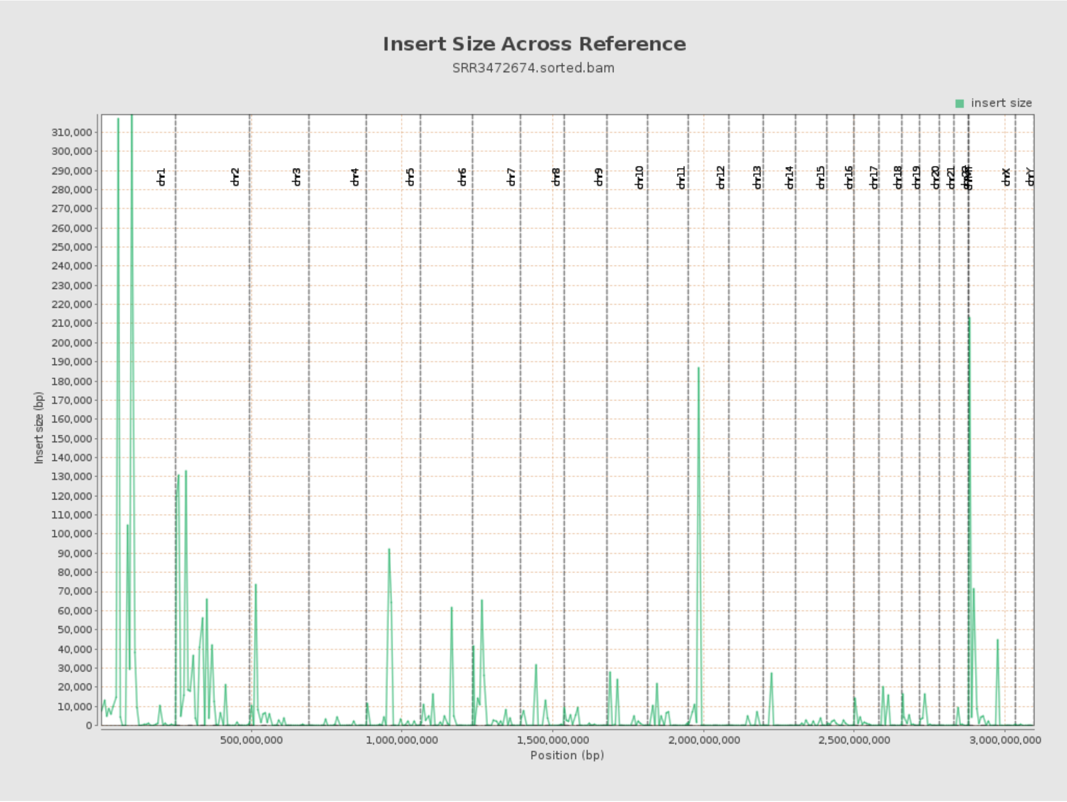
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram