Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:07:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063572.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_SRR6063572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:07:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,701,558
Mapped reads	2,107,719 / 78.02%
Unmapped reads	593,839 / 21.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,912 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	265,555 / 9.83%
Duplication rate	9.94%
Clipped reads	970,926 / 35.94%

2.2. ACGT Content

Number/percentage of A's	38,499,867 / 27.64%
Number/percentage of C's	25,333,745 / 18.19%
Number/percentage of T's	44,775,412 / 32.15%
Number/percentage of G's	30,668,190 / 22.02%
Number/percentage of N's	3,752 / 0%
GC Percentage	40.21%

2.3. Coverage

Mean	0.045

Standard Deviation	0.469

2.4. Mapping Quality

Mean Mapping Quality	47.1

2.5. Mismatches and indels

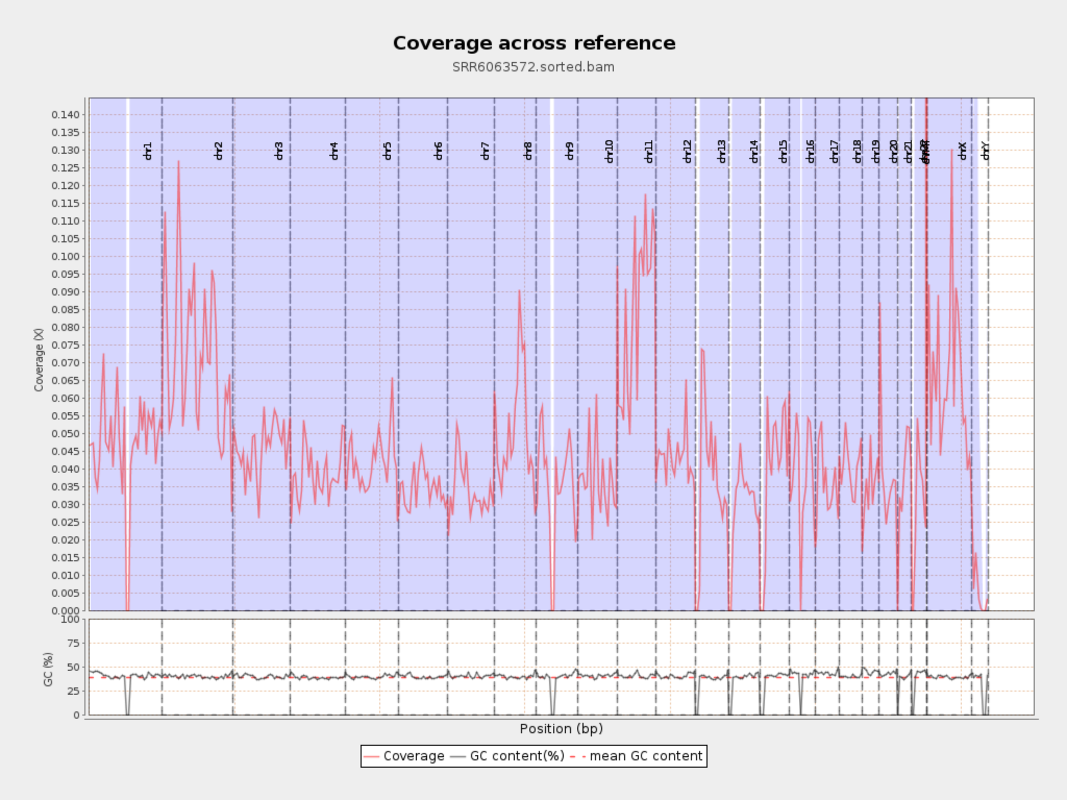
General error rate	0.78%
Mismatches	1,063,289
Insertions	9,873
Mapped reads with at least one insertion	0.46%
Deletions	38,805
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.89%

2.6. Chromosome stats

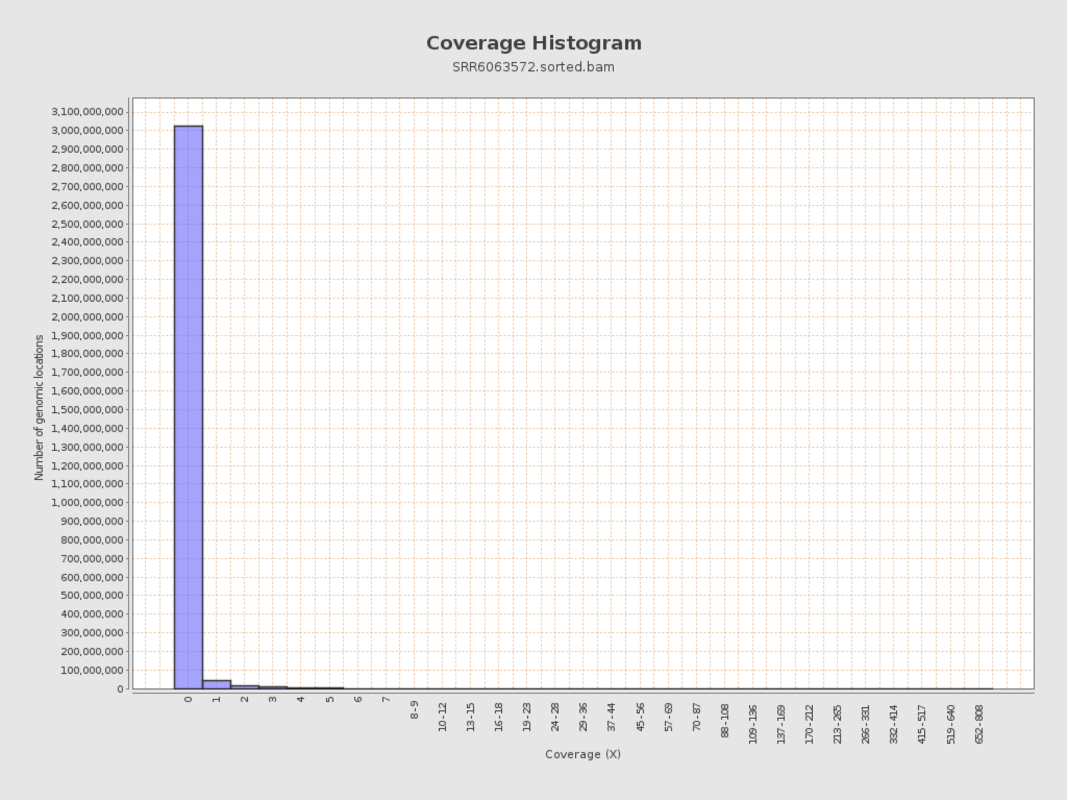
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11663782	0.0468	0.6471
chr2	243199373	17602339	0.0724	0.5199
chr3	198022430	9058455	0.0457	0.3648
chr4	191154276	7352848	0.0385	0.3386
chr5	180915260	7585988	0.0419	0.3464
chr6	171115067	5923875	0.0346	0.3405
chr7	159138663	5412908	0.034	0.3819

chr8	146364022	7411235	0.0506	0.5098
chr9	141213431	5034805	0.0357	0.3728
chr10	135534747	5021415	0.037	0.3895
chr11	135006516	11478257	0.085	0.7515
chr12	133851895	5820255	0.0435	0.356
chr13	115169878	4146798	0.036	0.3227
chr14	107349540	3139955	0.0292	0.3023
chr15	102531392	4021524	0.0392	0.3307
chr16	90354753	3418805	0.0378	0.3437
chr17	81195210	2853959	0.0351	0.3687
chr18	78077248	3161480	0.0405	0.5988
chr19	59128983	2079315	0.0352	0.4496
chr20	63025520	2373713	0.0377	0.3374
chr21	48129895	1764462	0.0367	0.3388
chr22	51304566	1415007	0.0276	0.2729
chrMT	16571	981750	59.2451	36.8954
chrX	155270560	10290715	0.0663	0.4602
chrY	59373566	334926	0.0056	0.1263

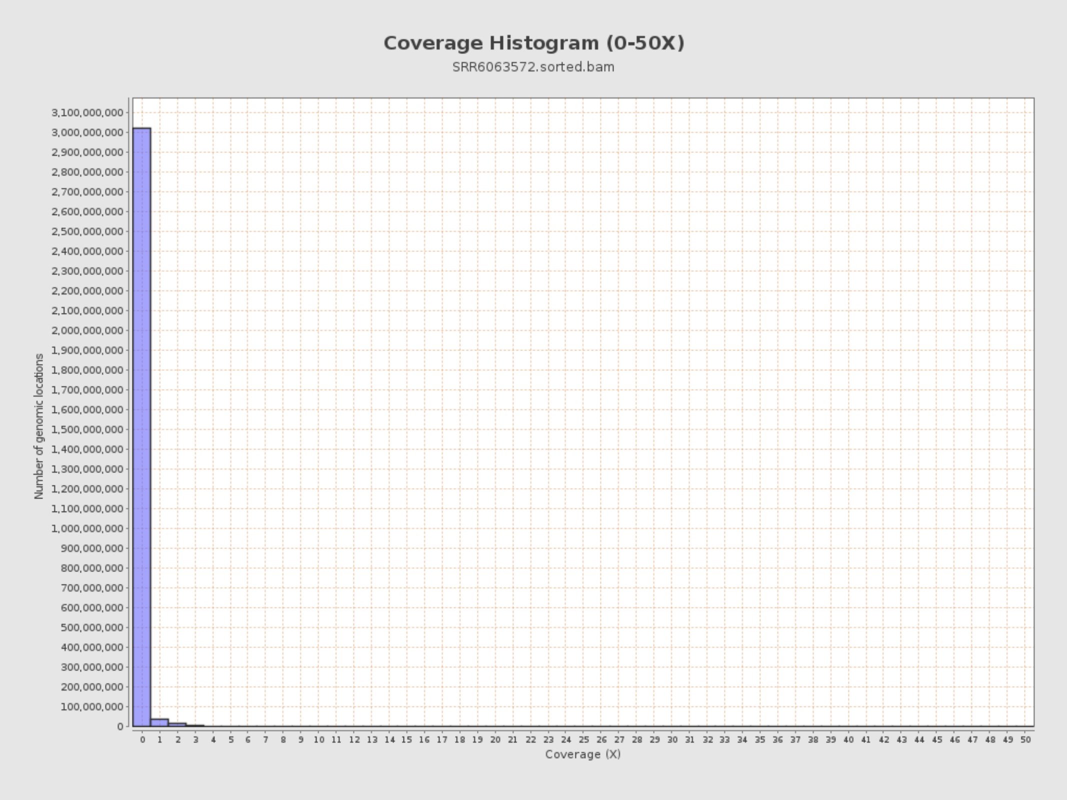
3. Results : Coverage across reference



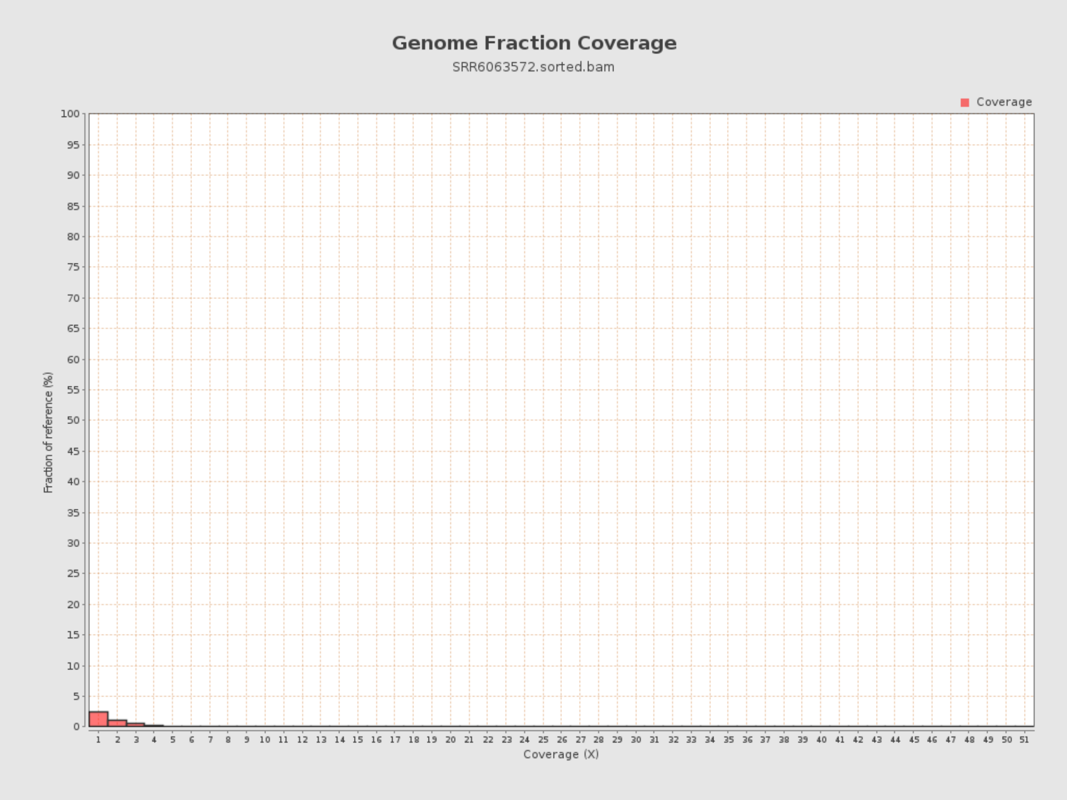
4. Results : Coverage Histogram



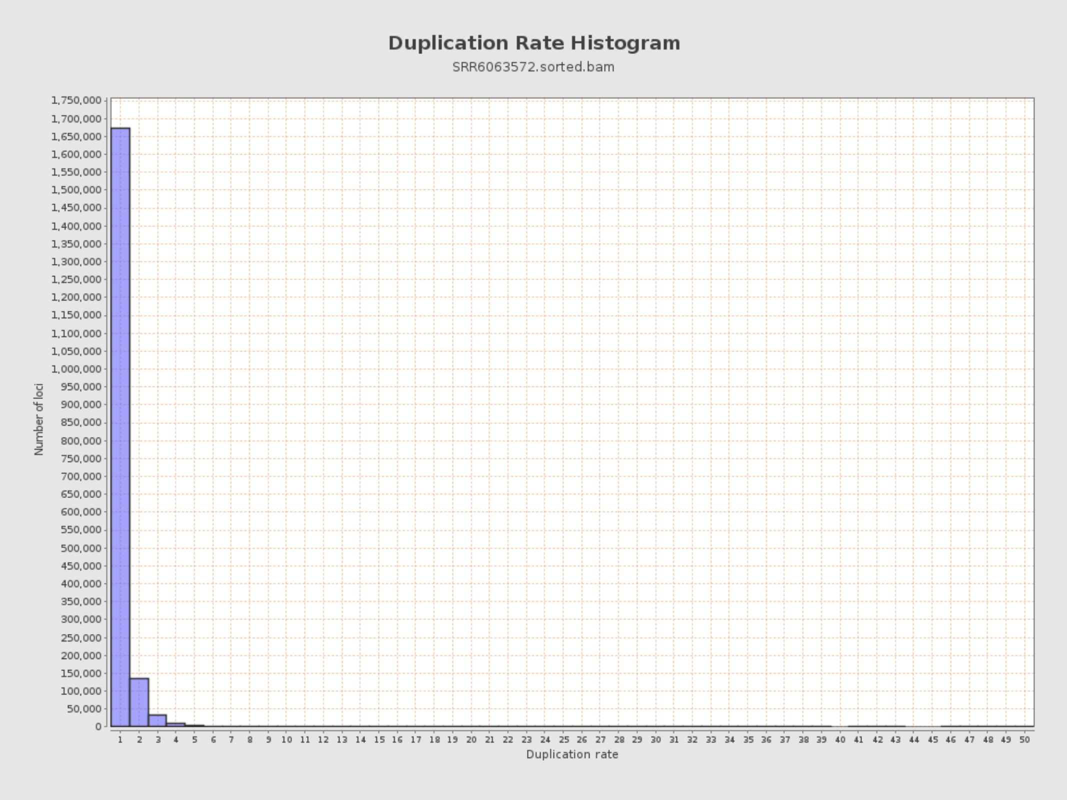
5. Results : Coverage Histogram (0-50X)



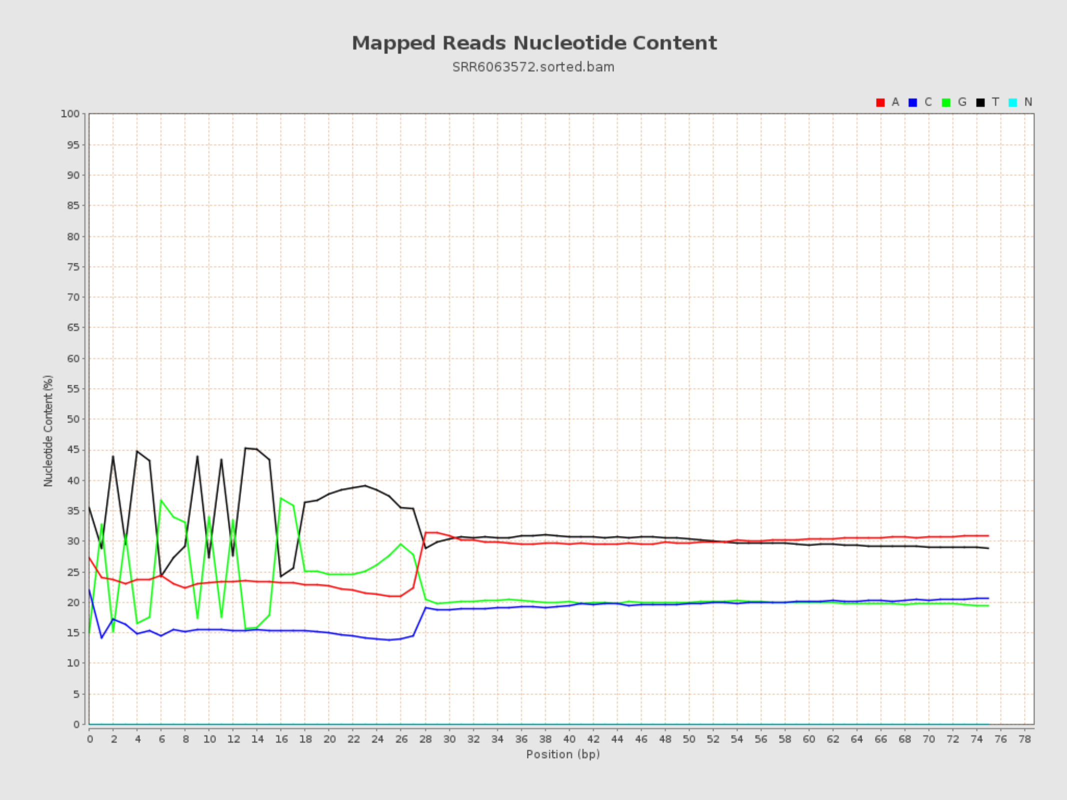
6. Results : Genome Fraction Coverage



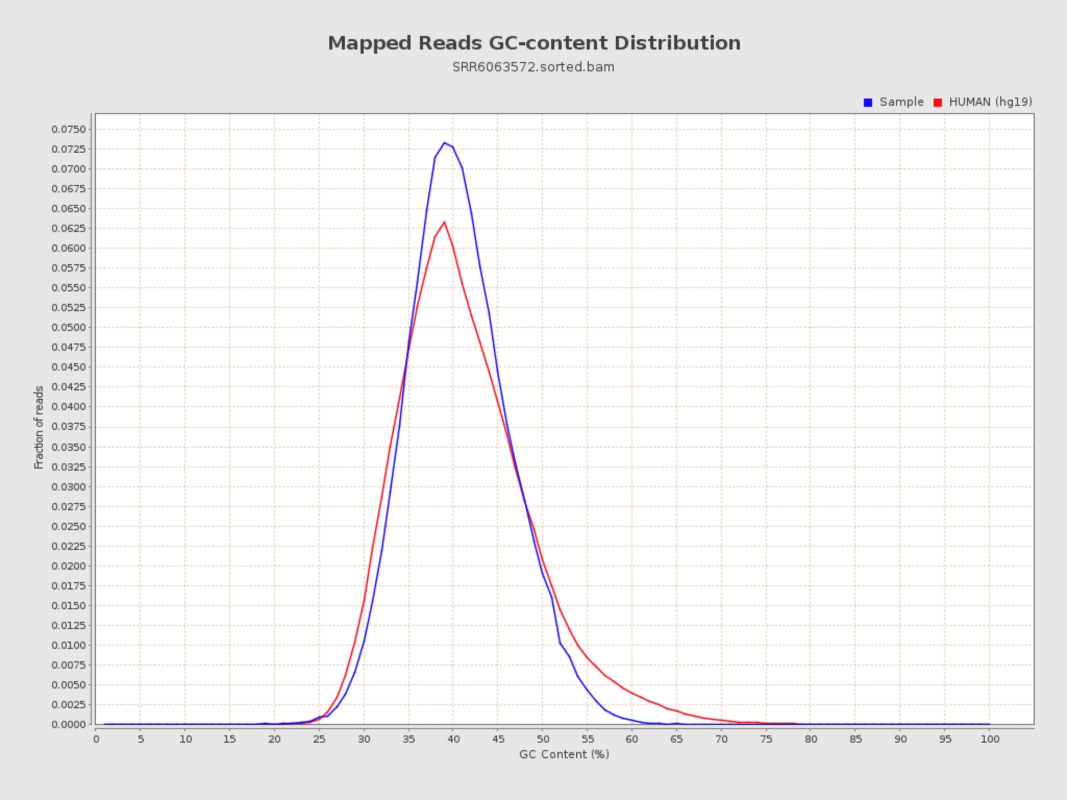
7. Results : Duplication Rate Histogram



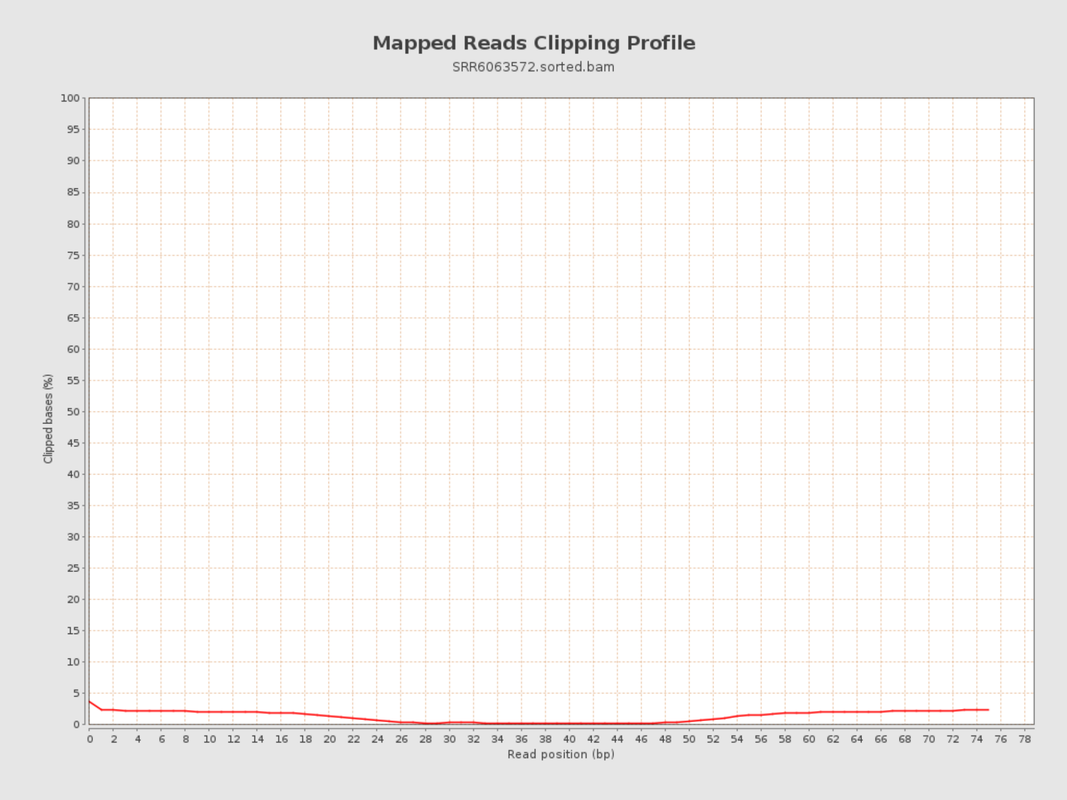
8. Results : Mapped Reads Nucleotide Content



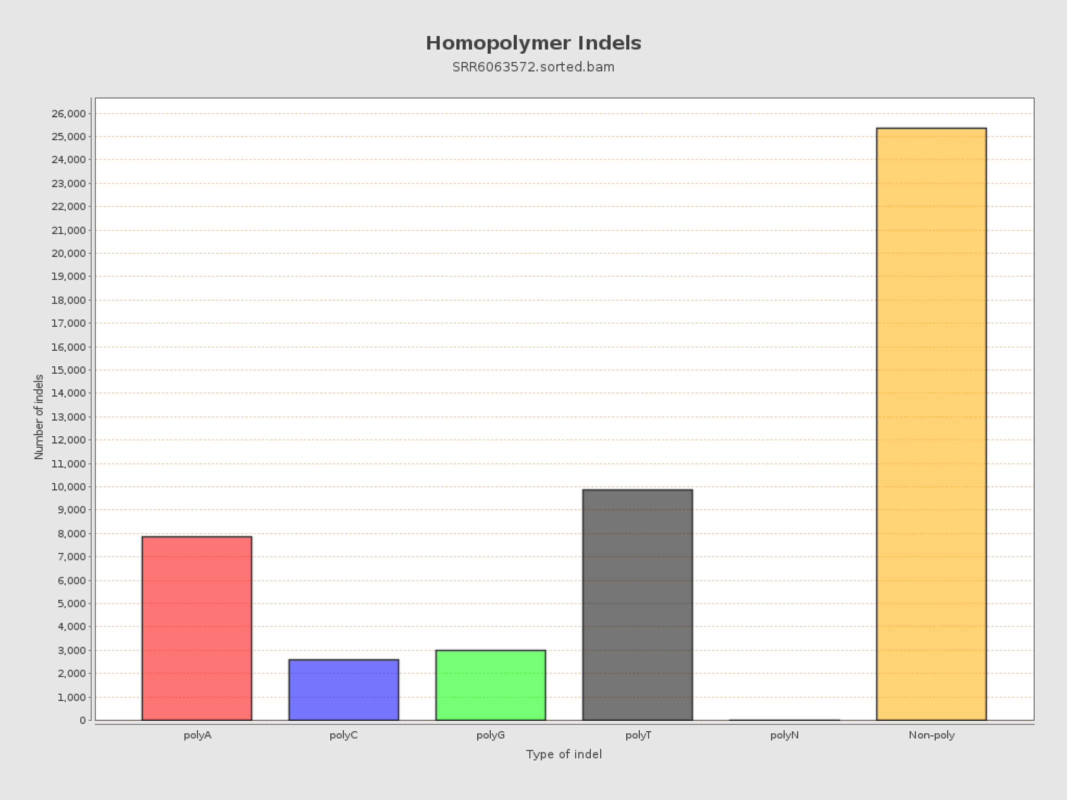
9. Results : Mapped Reads GC-content Distribution



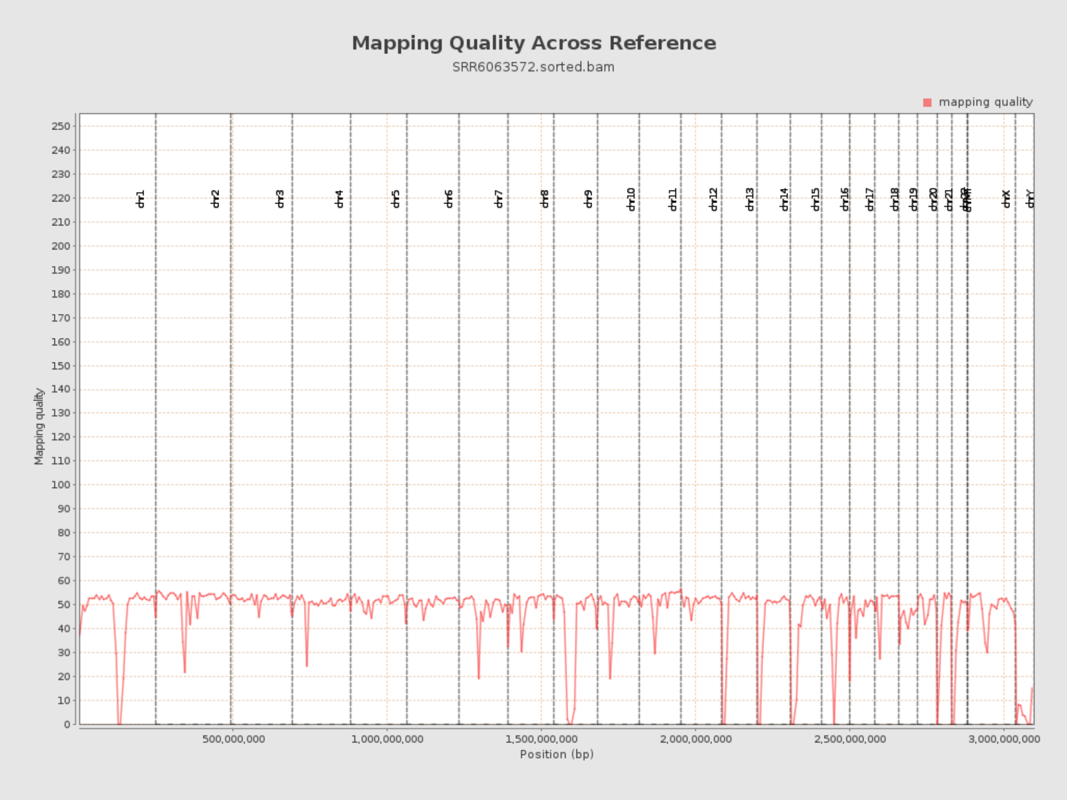
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram