Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:07:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013172.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_SRR6013172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:07:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,081,393
Mapped reads	1,843,595 / 88.58%
Unmapped reads	237,798 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,703 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	75,169 / 3.61%
Duplication rate	3.25%
Clipped reads	891,762 / 42.84%

2.2. ACGT Content

Number/percentage of A's	33,276,383 / 27.43%
Number/percentage of C's	22,996,848 / 18.96%
Number/percentage of T's	37,713,315 / 31.09%
Number/percentage of G's	27,289,341 / 22.5%
Number/percentage of N's	28,887 / 0.02%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0392

Standard Deviation	0.3429

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

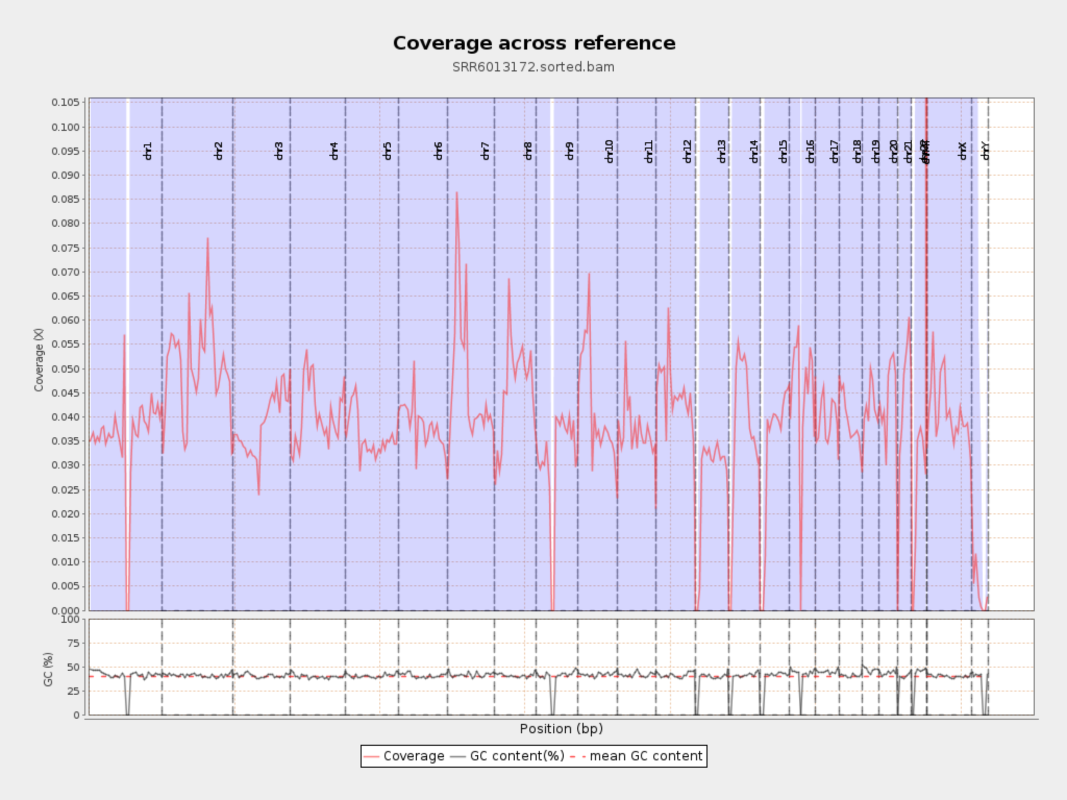
General error rate	0.84%
Mismatches	998,422
Insertions	8,123
Mapped reads with at least one insertion	0.44%
Deletions	34,841
Mapped reads with at least one deletion	1.87%
Homopolymer indels	44.67%

2.6. Chromosome stats

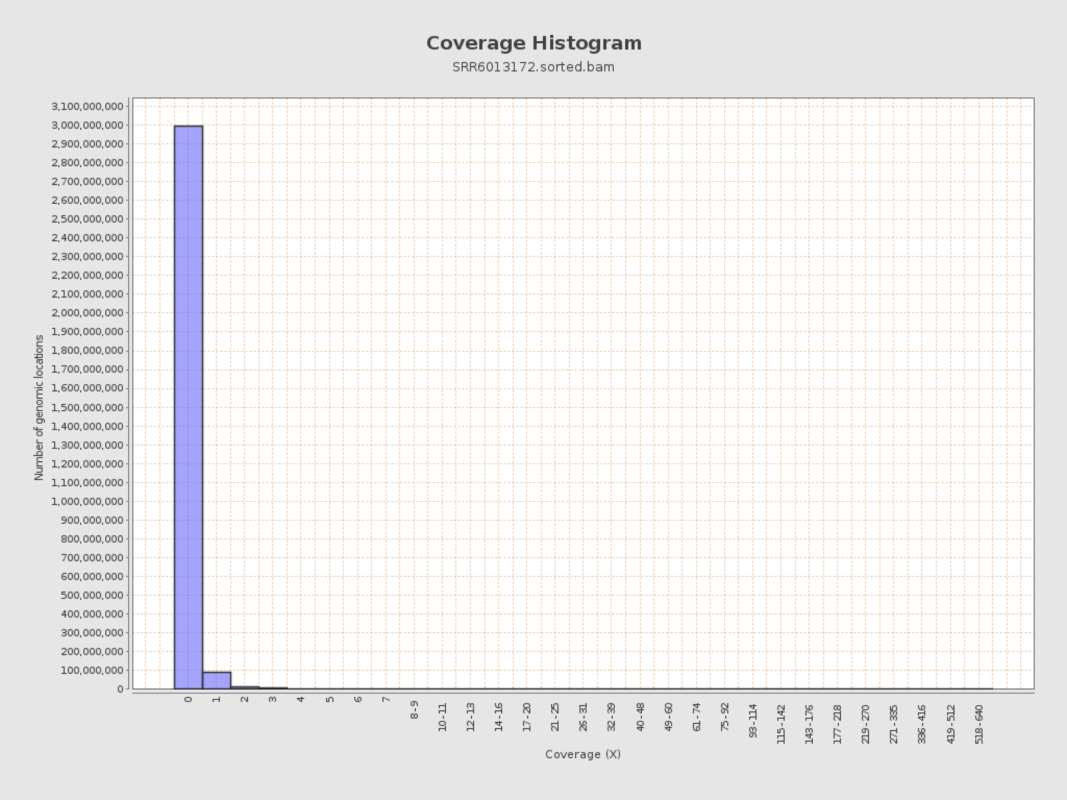
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8942156	0.0359	0.583
chr2	243199373	12340293	0.0507	0.3994
chr3	198022430	7585030	0.0383	0.2262
chr4	191154276	7731703	0.0404	0.2392
chr5	180915260	6505356	0.036	0.2197
chr6	171115067	6541854	0.0382	0.274
chr7	159138663	7580166	0.0476	0.5447

chr8	146364022	6764921	0.0462	0.3503
chr9	141213431	4385798	0.0311	0.2674
chr10	135534747	5727287	0.0423	0.3706
chr11	135006516	5049383	0.0374	0.2621
chr12	133851895	6011459	0.0449	0.2472
chr13	115169878	3058091	0.0266	0.1896
chr14	107349540	3958786	0.0369	0.2373
chr15	102531392	3370151	0.0329	0.2094
chr16	90354753	4018973	0.0445	0.2659
chr17	81195210	3159312	0.0389	0.2472
chr18	78077248	3073582	0.0394	0.4789
chr19	59128983	2488257	0.0421	0.4623
chr20	63025520	2755163	0.0437	0.2471
chr21	48129895	2054960	0.0427	0.2501
chr22	51304566	1237248	0.0241	0.1779
chrMT	16571	372967	22.5072	12.1638
chrX	155270560	6389345	0.0411	0.2526
chrY	59373566	263030	0.0044	0.098

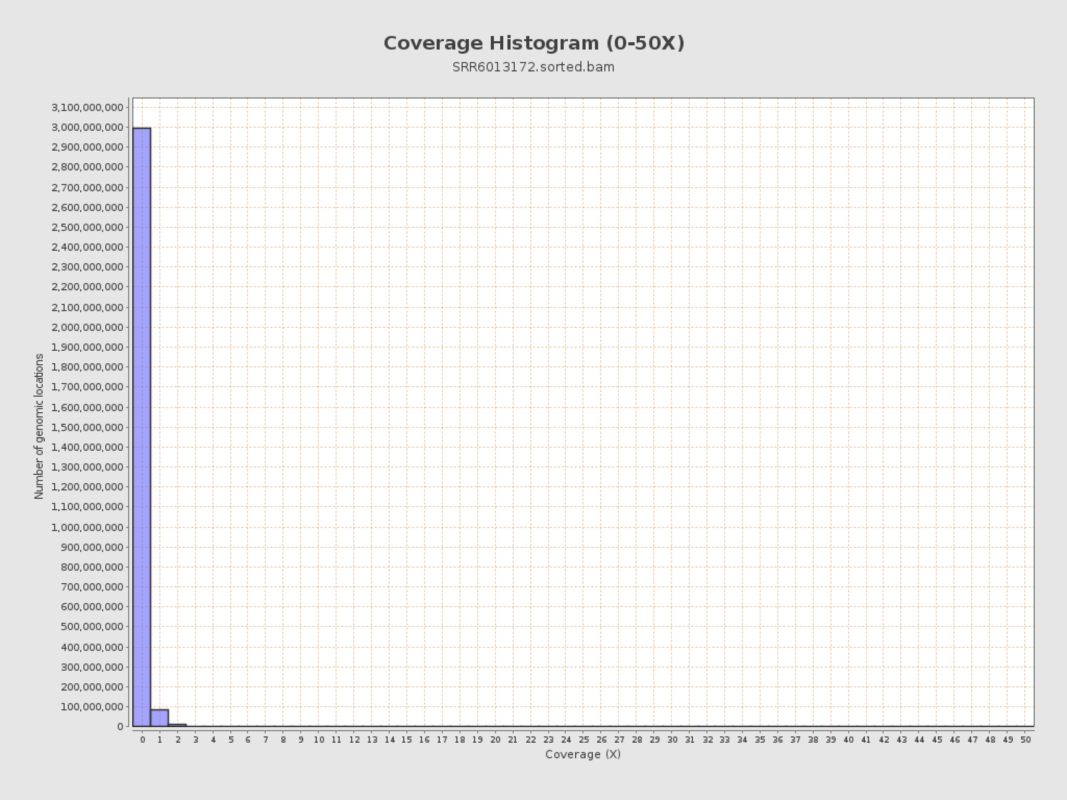
3. Results : Coverage across reference



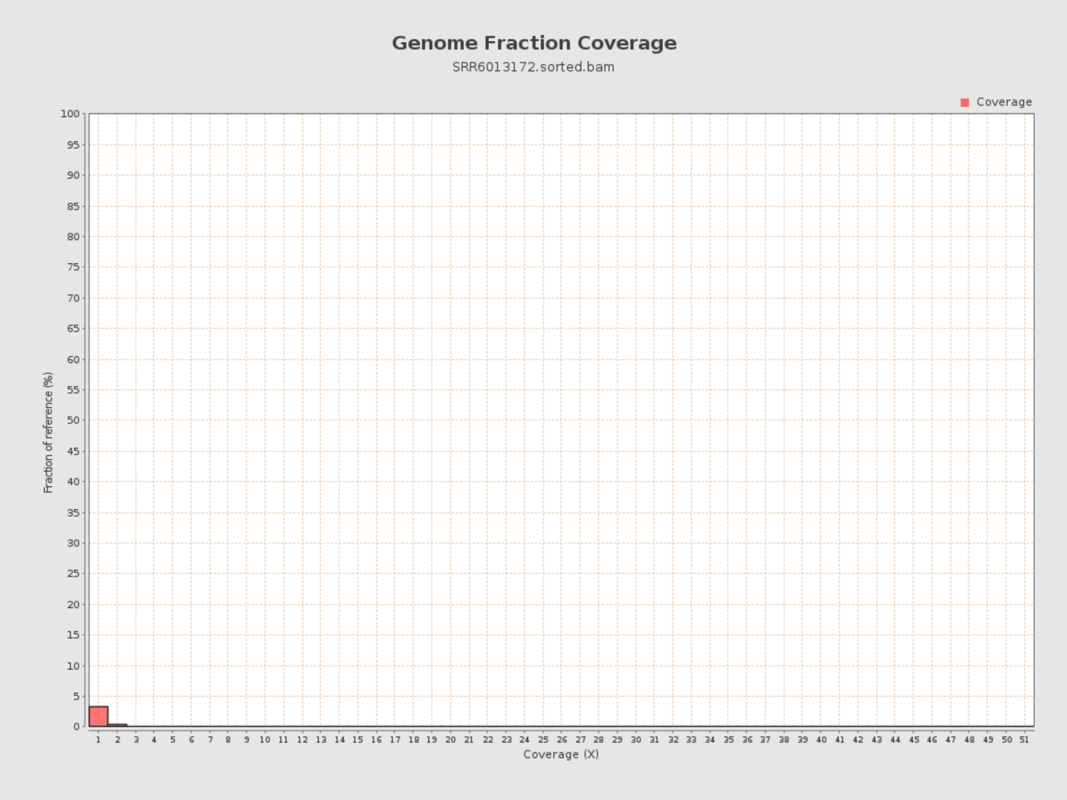
4. Results : Coverage Histogram



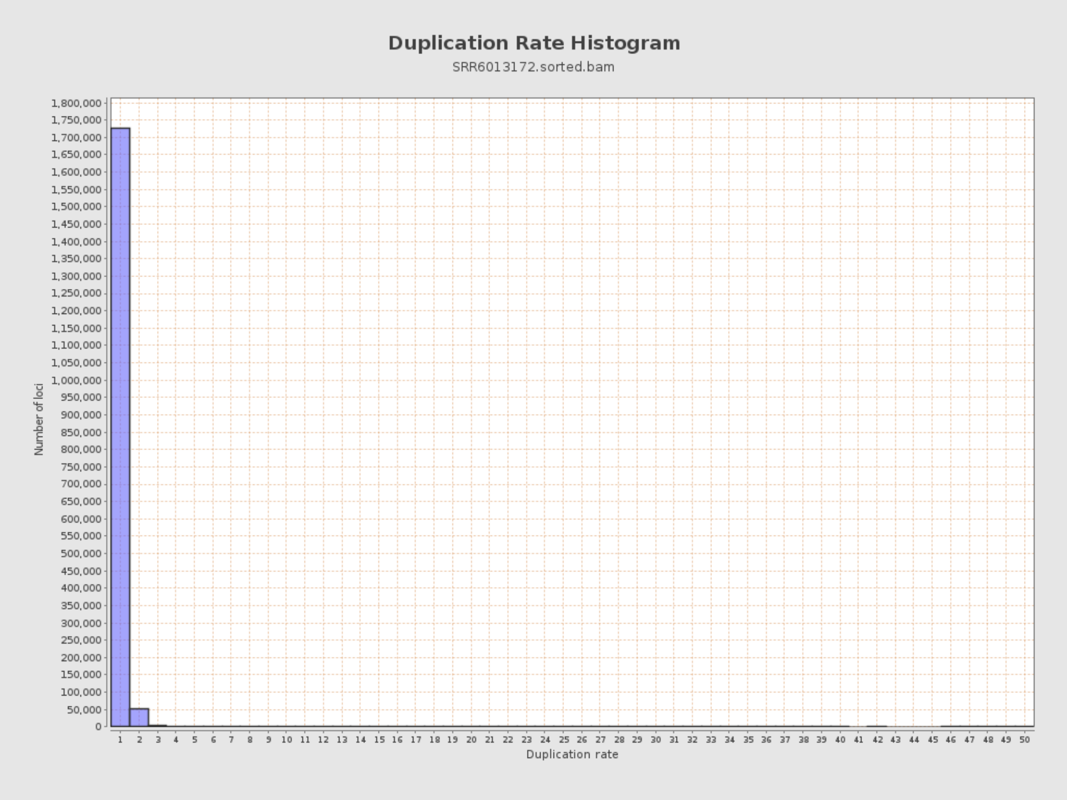
5. Results : Coverage Histogram (0-50X)



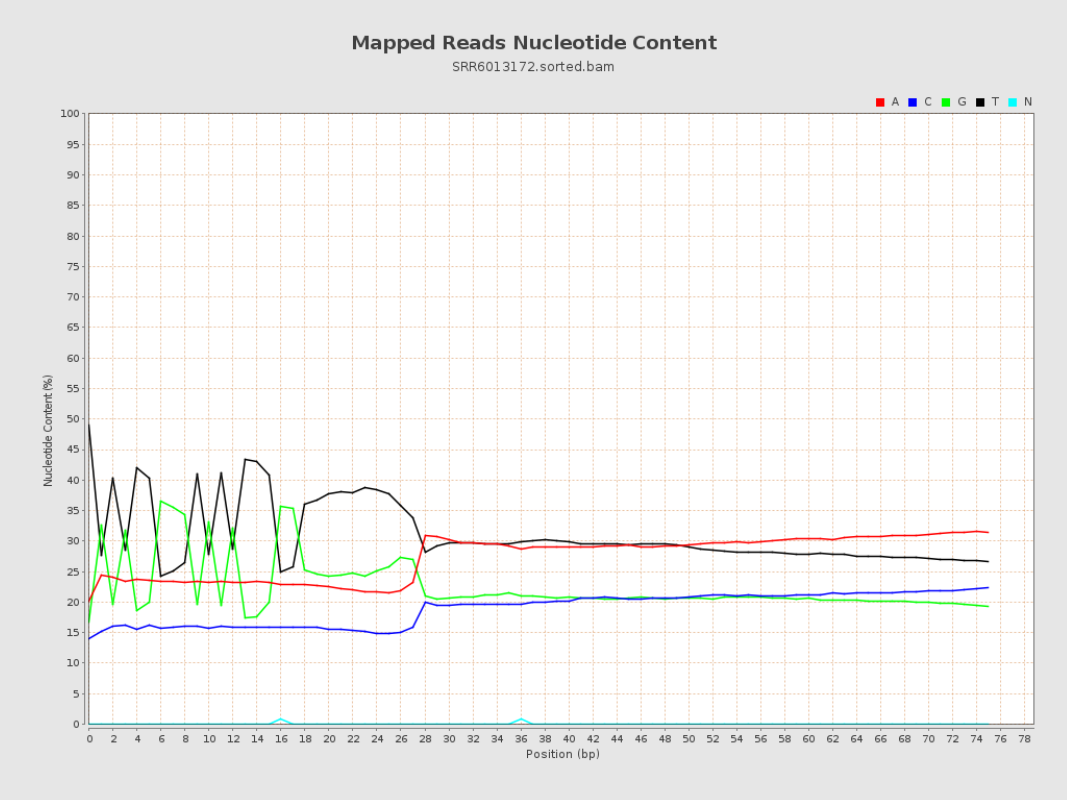
6. Results : Genome Fraction Coverage



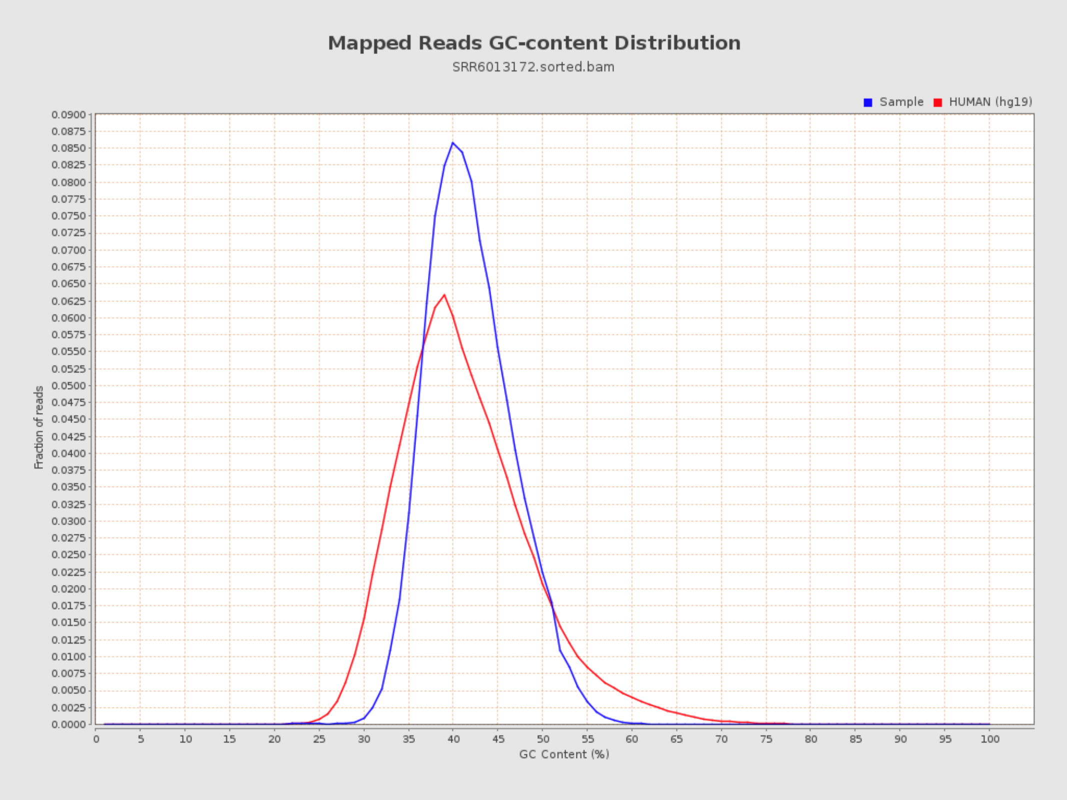
7. Results : Duplication Rate Histogram



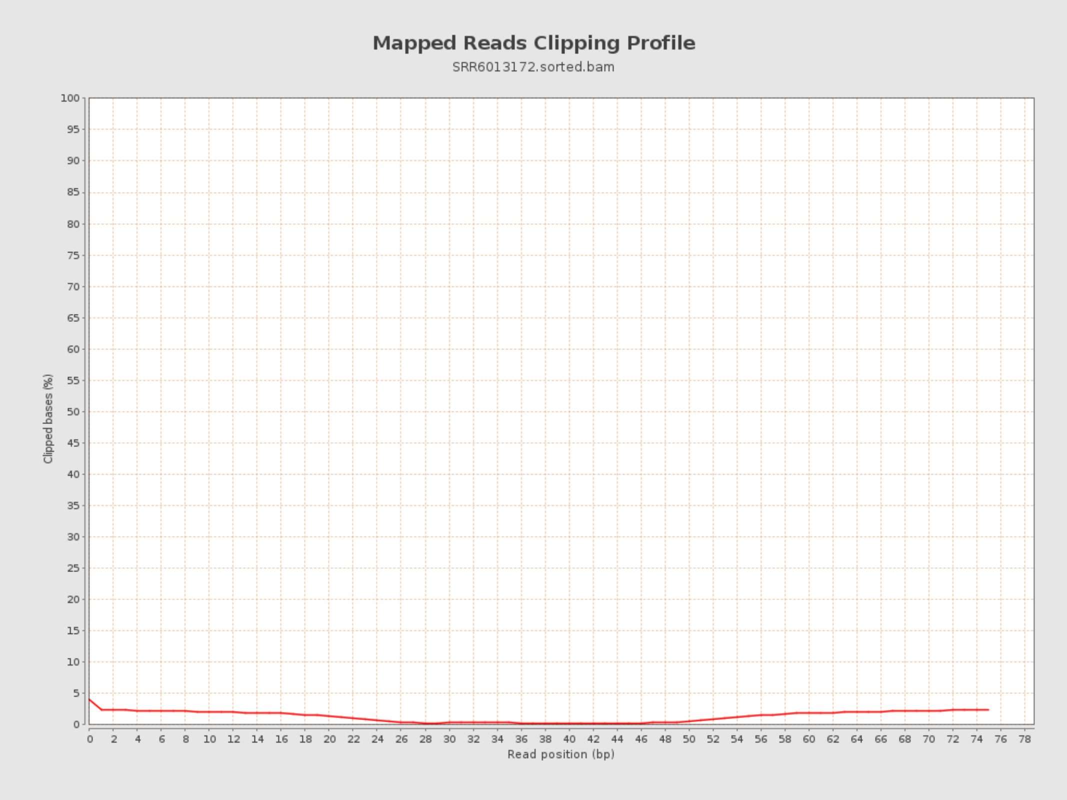
8. Results : Mapped Reads Nucleotide Content



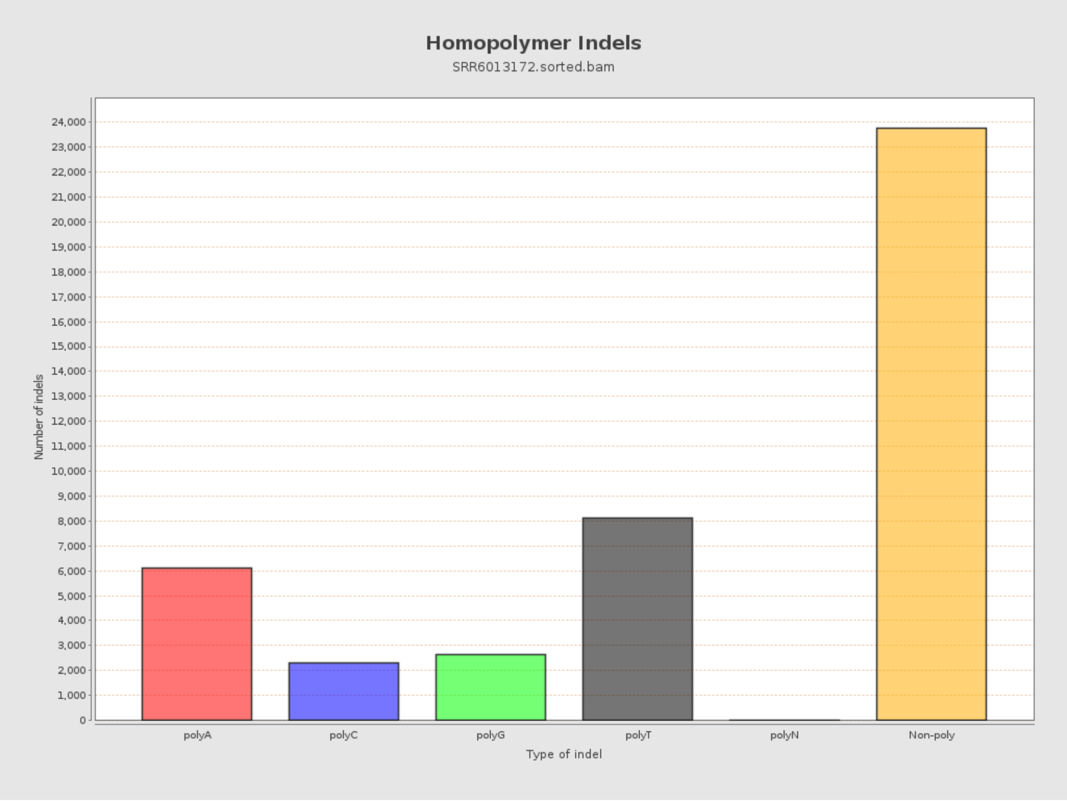
9. Results : Mapped Reads GC-content Distribution



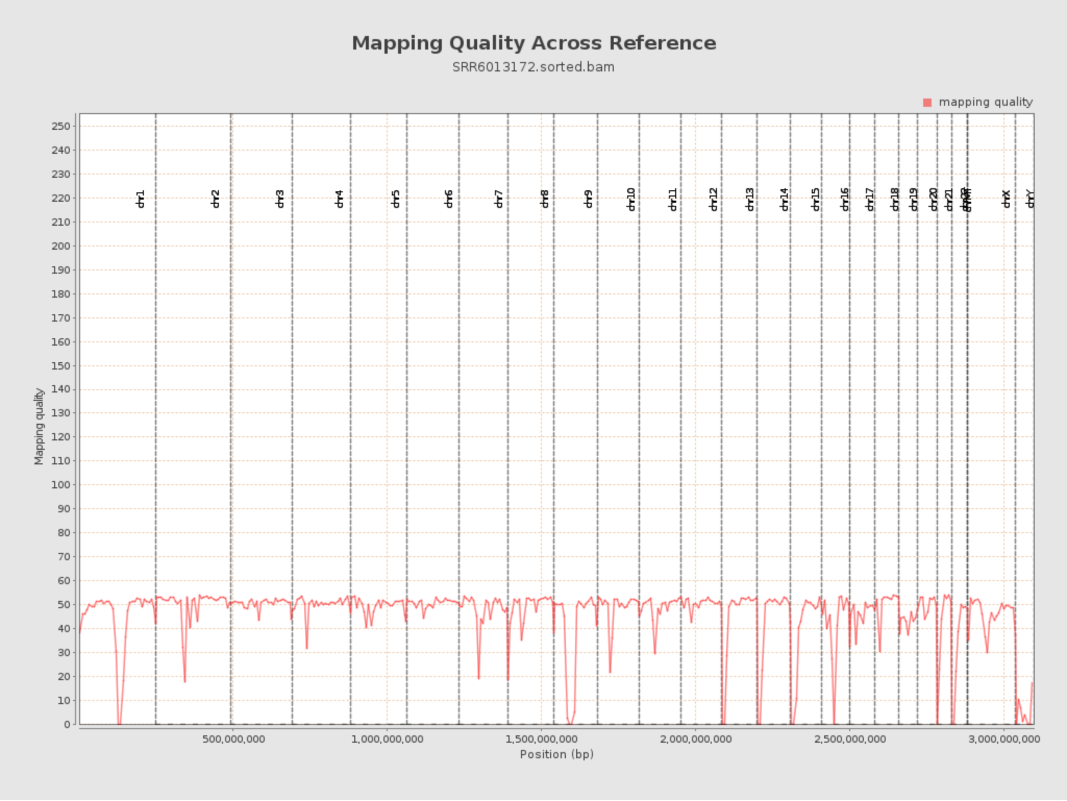
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram