Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:43:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013222.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_SRR6013222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:43:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,998,340
Mapped reads	1,688,439 / 84.49%
Unmapped reads	309,901 / 15.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,128 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	97,108 / 4.86%
Duplication rate	4.45%
Clipped reads	895,739 / 44.82%

2.2. ACGT Content

Number/percentage of A's	29,645,144 / 27.19%
Number/percentage of C's	19,423,870 / 17.81%
Number/percentage of T's	35,383,439 / 32.45%
Number/percentage of G's	24,579,009 / 22.54%
Number/percentage of N's	1,322 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0352

Standard Deviation	0.4307

2.4. Mapping Quality

Mean Mapping Quality	43.32

2.5. Mismatches and indels

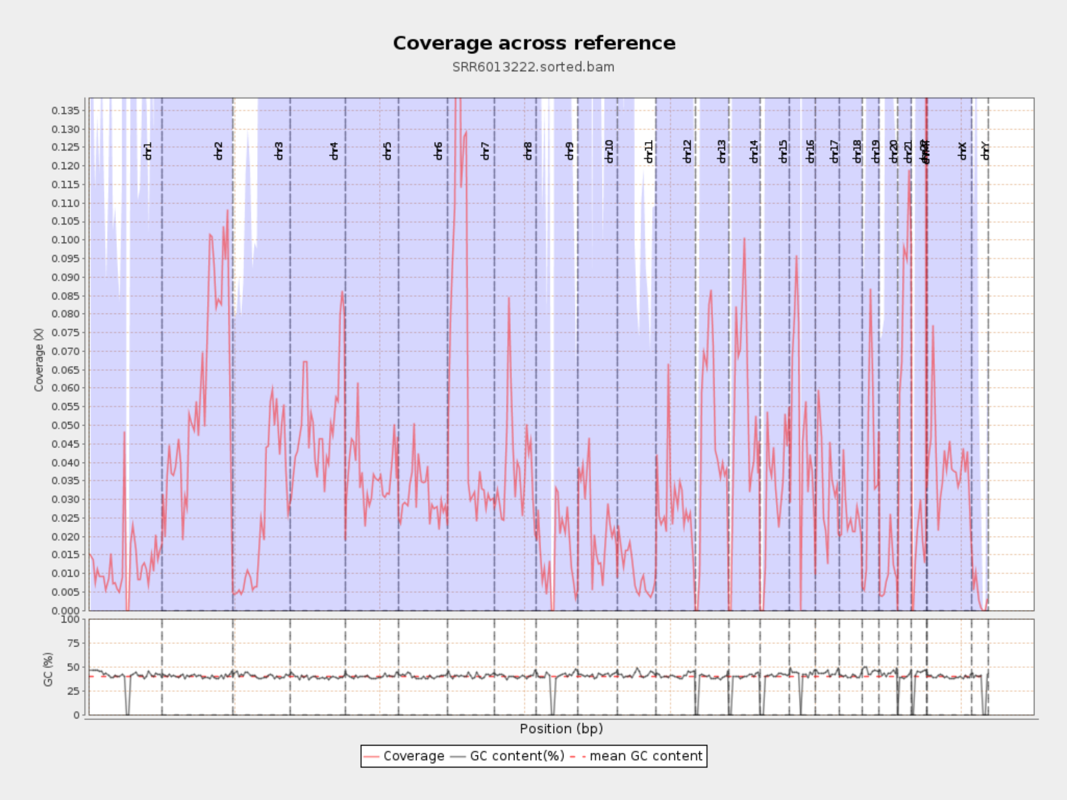
General error rate	0.8%
Mismatches	854,187
Insertions	7,631
Mapped reads with at least one insertion	0.45%
Deletions	30,813
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.93%

2.6. Chromosome stats

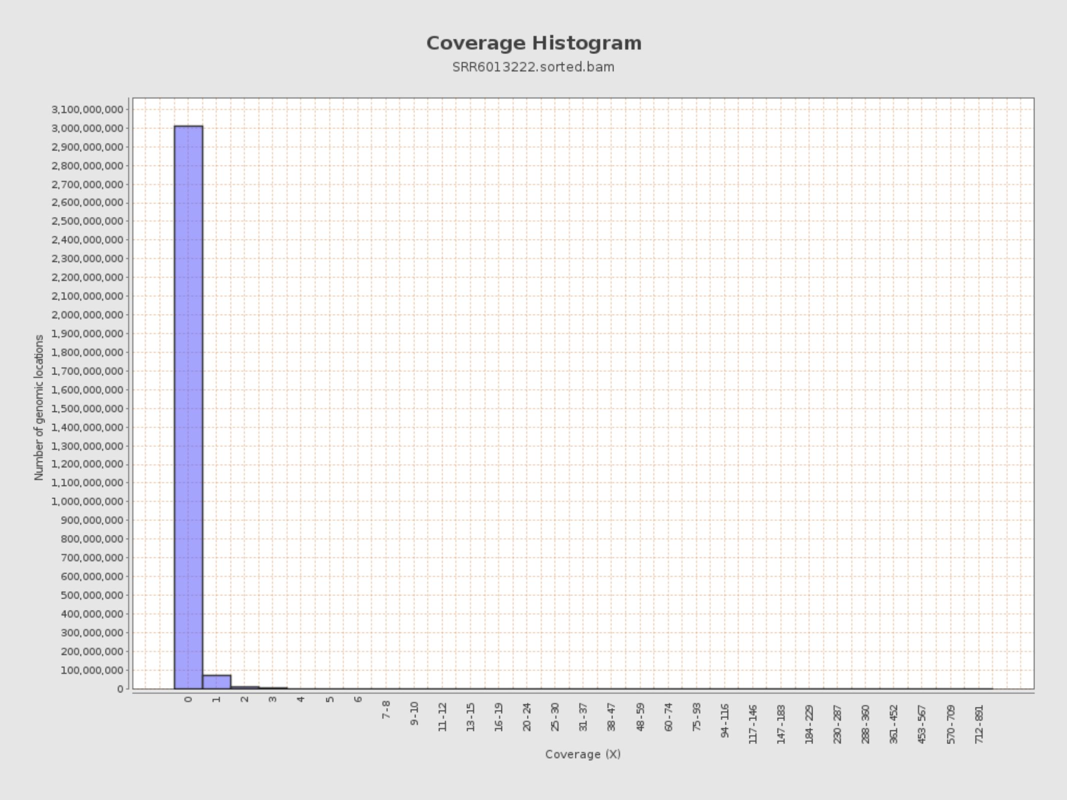
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2977243	0.0119	0.7234
chr2	243199373	14286536	0.0587	0.4577
chr3	198022430	5132045	0.0259	0.1906
chr4	191154276	9725956	0.0509	0.2698
chr5	180915260	6654252	0.0368	0.2293
chr6	171115067	5309029	0.031	0.2858
chr7	159138663	11198308	0.0704	1.0928

chr8	146364022	5682006	0.0388	0.5236
chr9	141213431	2208803	0.0156	0.2363
chr10	135534747	3235177	0.0239	0.2624
chr11	135006516	1391892	0.0103	0.1775
chr12	133851895	3891140	0.0291	0.2066
chr13	115169878	5302408	0.046	0.2558
chr14	107349540	5582434	0.052	0.2909
chr15	102531392	3259383	0.0318	0.2117
chr16	90354753	4483580	0.0496	0.2799
chr17	81195210	2745337	0.0338	0.2405
chr18	78077248	1997288	0.0256	0.578
chr19	59128983	2342867	0.0396	0.4462
chr20	63025520	624762	0.0099	0.1415
chr21	48129895	3876206	0.0805	0.3544
chr22	51304566	790312	0.0154	0.1454
chrMT	16571	60347	3.6417	2.9766
chrX	155270560	6092319	0.0392	0.2514
chrY	59373566	235529	0.004	0.0837

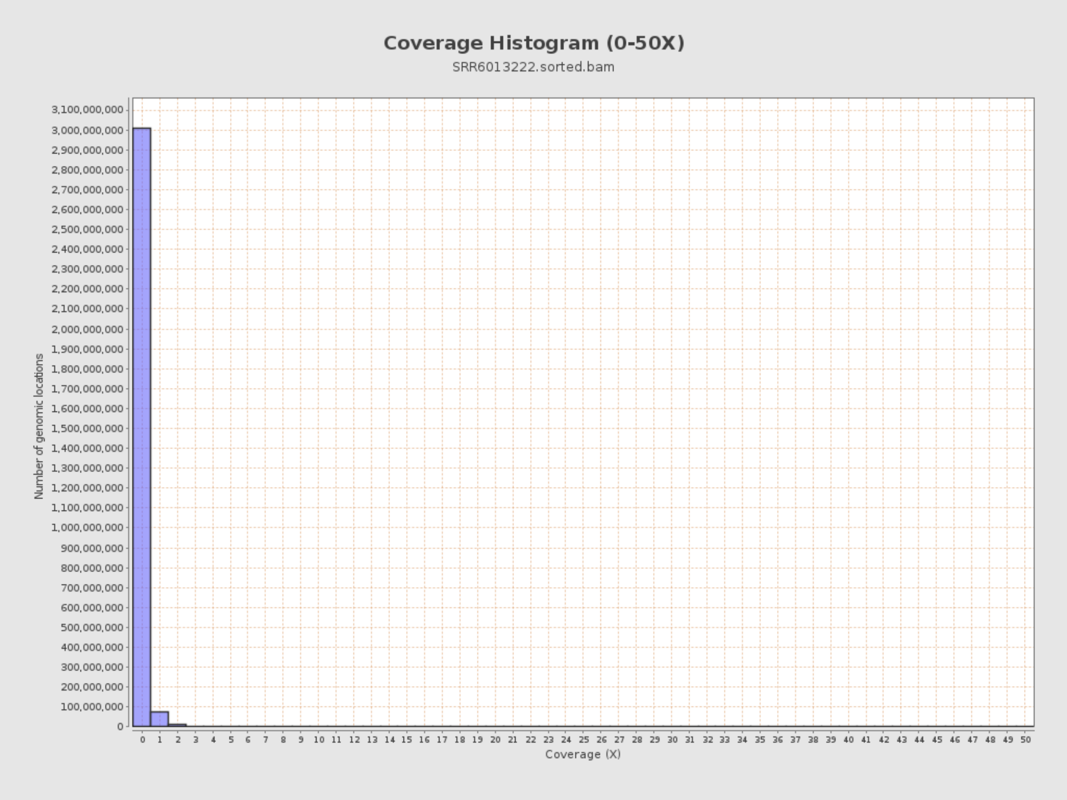
3. Results : Coverage across reference



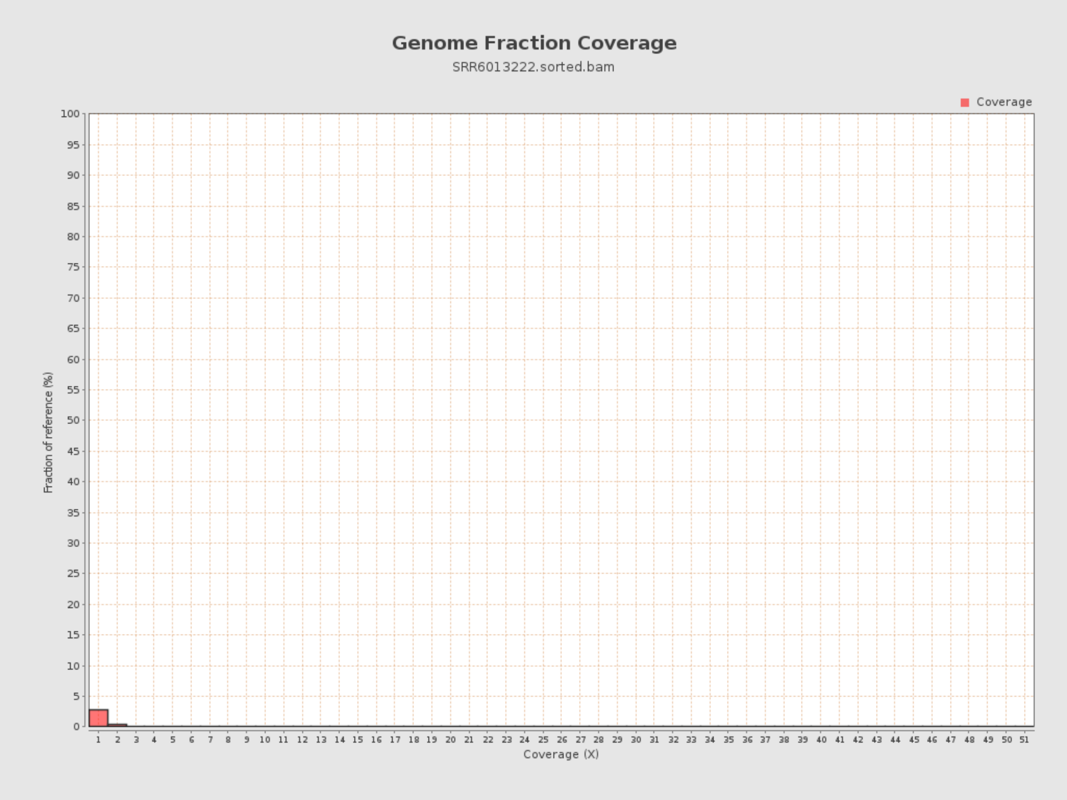
4. Results : Coverage Histogram



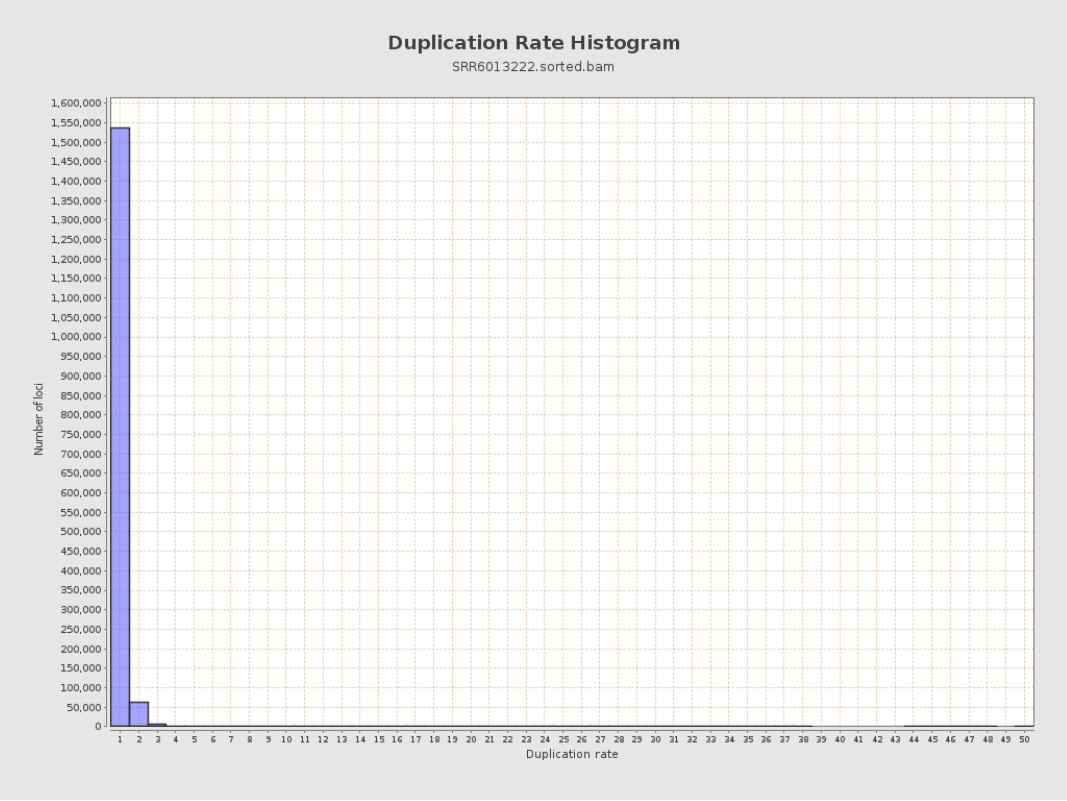
5. Results : Coverage Histogram (0-50X)



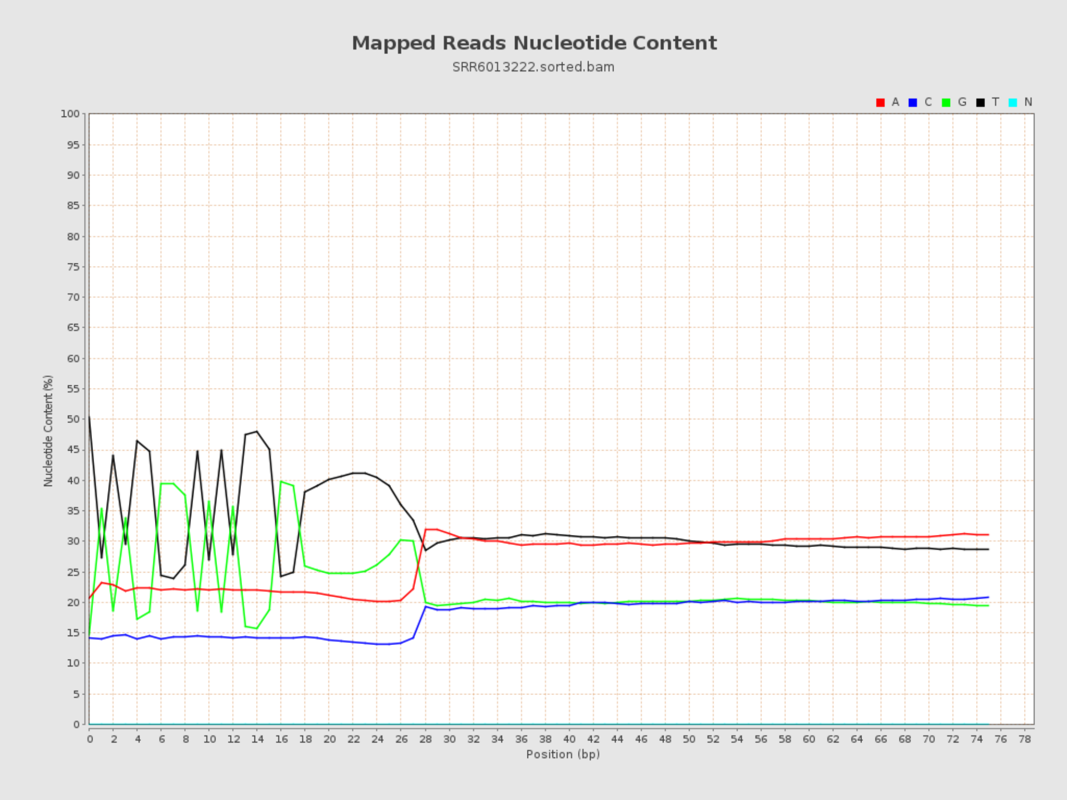
6. Results : Genome Fraction Coverage



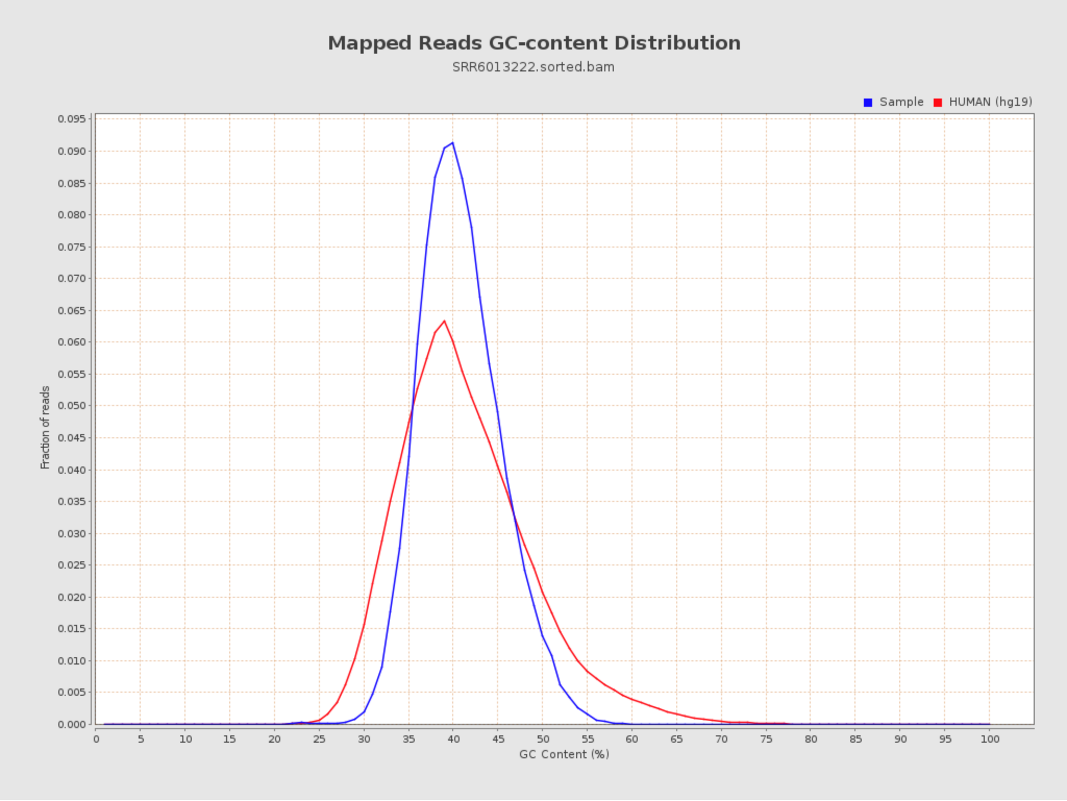
7. Results : Duplication Rate Histogram



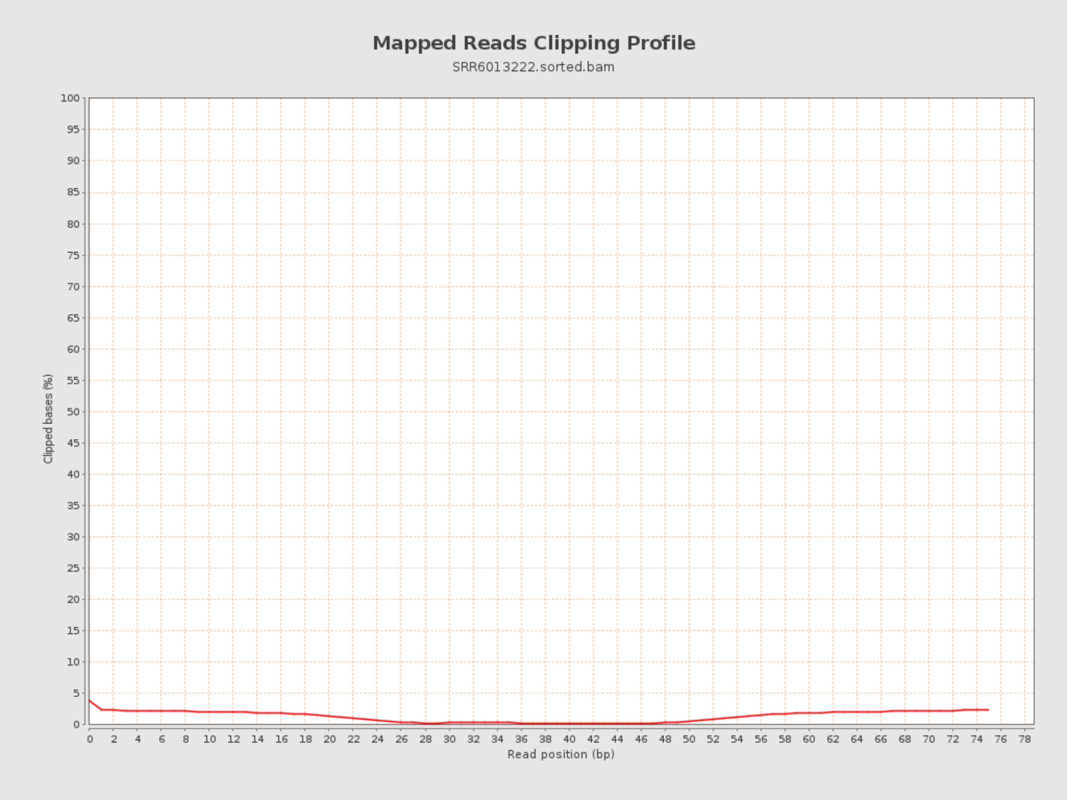
8. Results : Mapped Reads Nucleotide Content



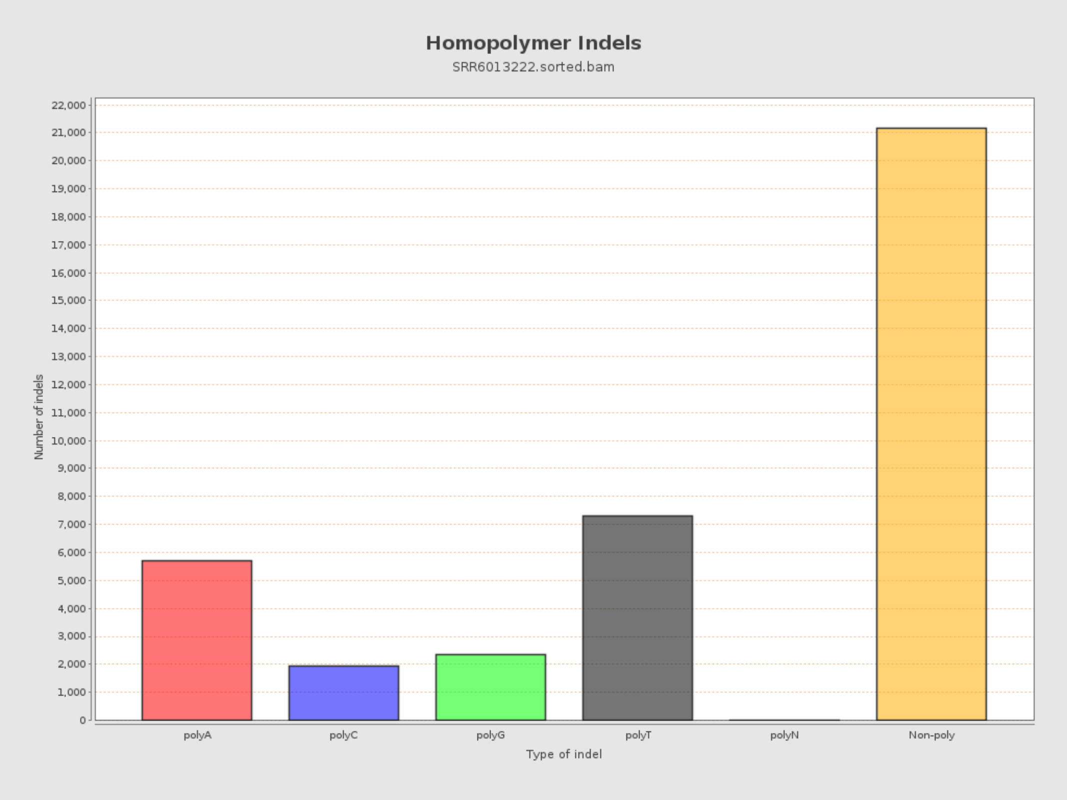
9. Results : Mapped Reads GC-content Distribution



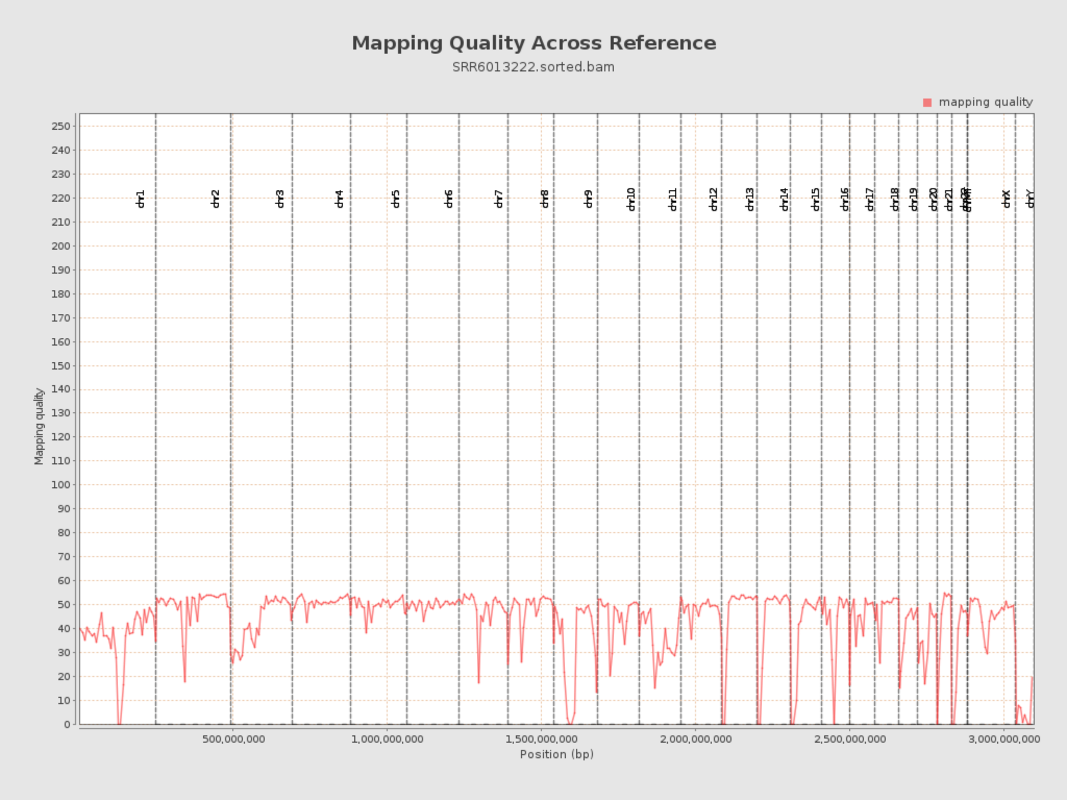
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram