Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:40:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013221.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_SRR6013221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:40:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,771,986
Mapped reads	1,549,852 / 87.46%
Unmapped reads	222,134 / 12.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,788 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	85,860 / 4.85%
Duplication rate	4.58%
Clipped reads	776,735 / 43.83%

2.2. ACGT Content

Number/percentage of A's	27,558,597 / 27.31%
Number/percentage of C's	18,157,265 / 17.99%
Number/percentage of T's	32,639,930 / 32.34%
Number/percentage of G's	22,559,935 / 22.35%
Number/percentage of N's	1,432 / 0%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.2952

2.4. Mapping Quality

Mean Mapping Quality	44.01

2.5. Mismatches and indels

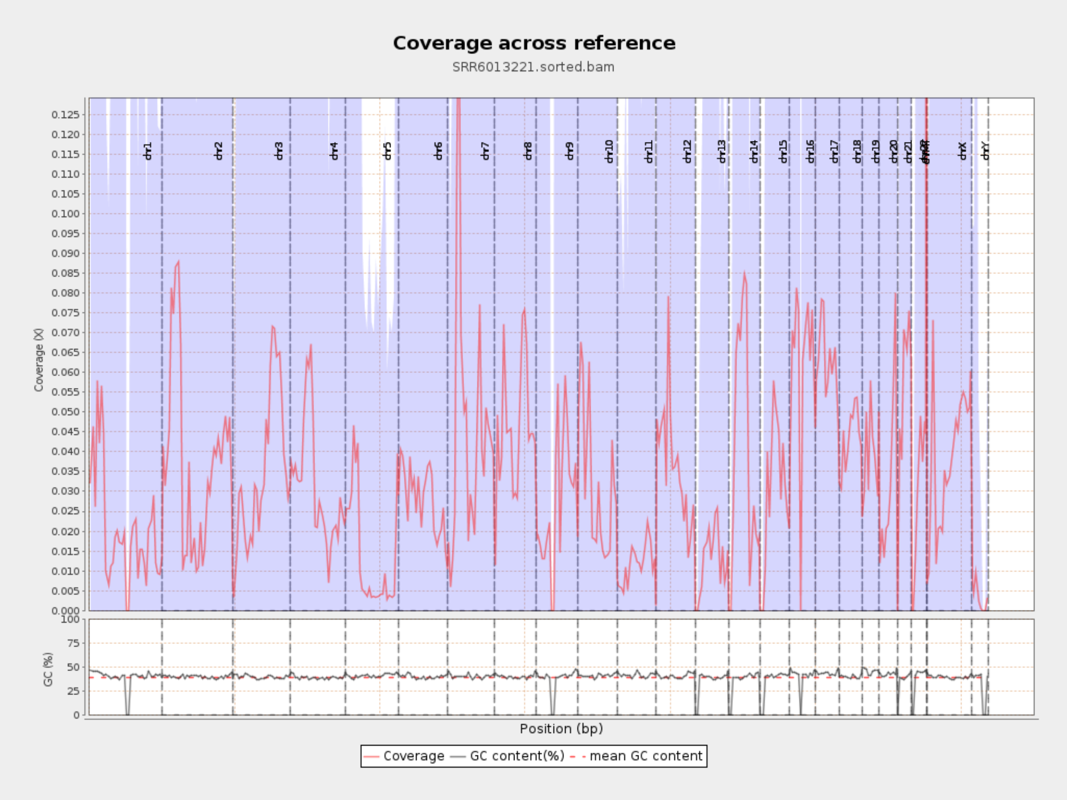
General error rate	0.78%
Mismatches	770,748
Insertions	7,409
Mapped reads with at least one insertion	0.48%
Deletions	31,418
Mapped reads with at least one deletion	2%
Homopolymer indels	45.15%

2.6. Chromosome stats

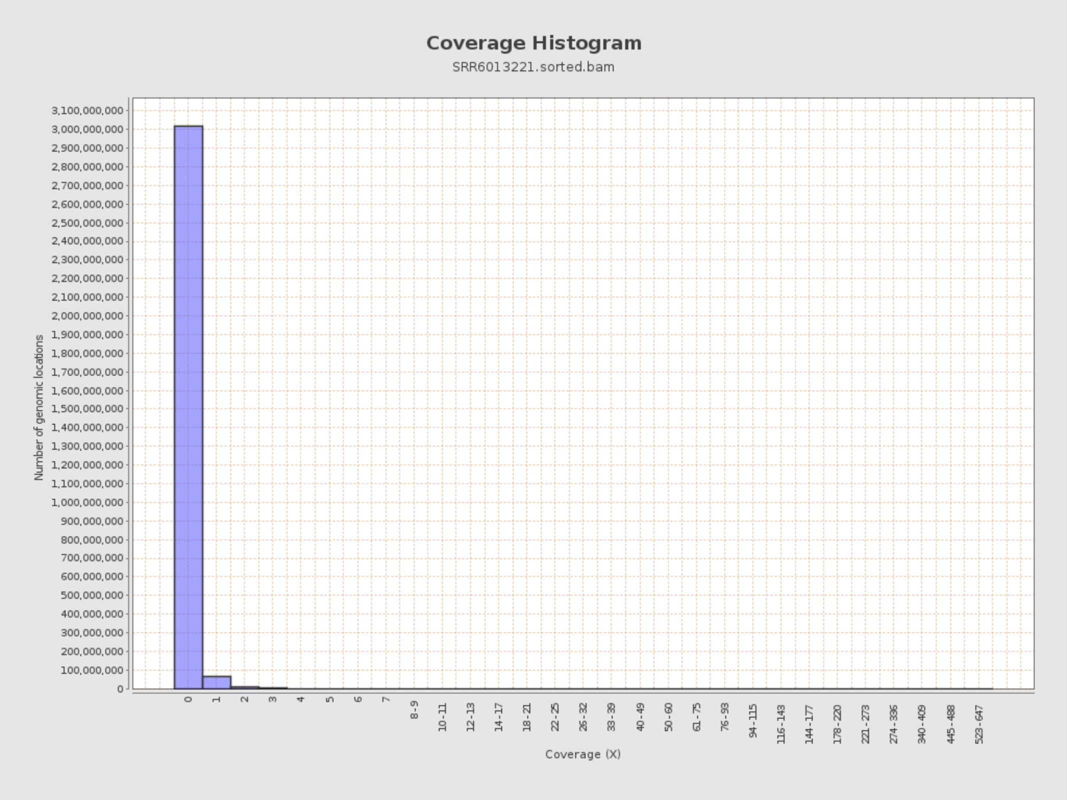
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5126400	0.0206	0.28
chr2	243199373	9153750	0.0376	0.4092
chr3	198022430	6967908	0.0352	0.2281
chr4	191154276	6003618	0.0314	0.2241
chr5	180915260	2477521	0.0137	0.1457
chr6	171115067	4886882	0.0286	0.2427
chr7	159138663	7444315	0.0468	0.4602

chr8	146364022	6673718	0.0456	0.4308
chr9	141213431	3830188	0.0271	0.2771
chr10	135534747	4374030	0.0323	0.3341
chr11	135006516	1585231	0.0117	0.1696
chr12	133851895	4892751	0.0366	0.2347
chr13	115169878	1457112	0.0127	0.1372
chr14	107349540	4343408	0.0405	0.2513
chr15	102531392	3125015	0.0305	0.2104
chr16	90354753	5656039	0.0626	0.3167
chr17	81195210	5081529	0.0626	0.3609
chr18	78077248	3412742	0.0437	0.452
chr19	59128983	2342766	0.0396	0.3734
chr20	63025520	2073843	0.0329	0.2248
chr21	48129895	2597565	0.054	0.2951
chr22	51304566	1458667	0.0284	0.2017
chrMT	16571	13296	0.8024	1.2188
chrX	155270560	5802267	0.0374	0.2498
chrY	59373566	190158	0.0032	0.0937

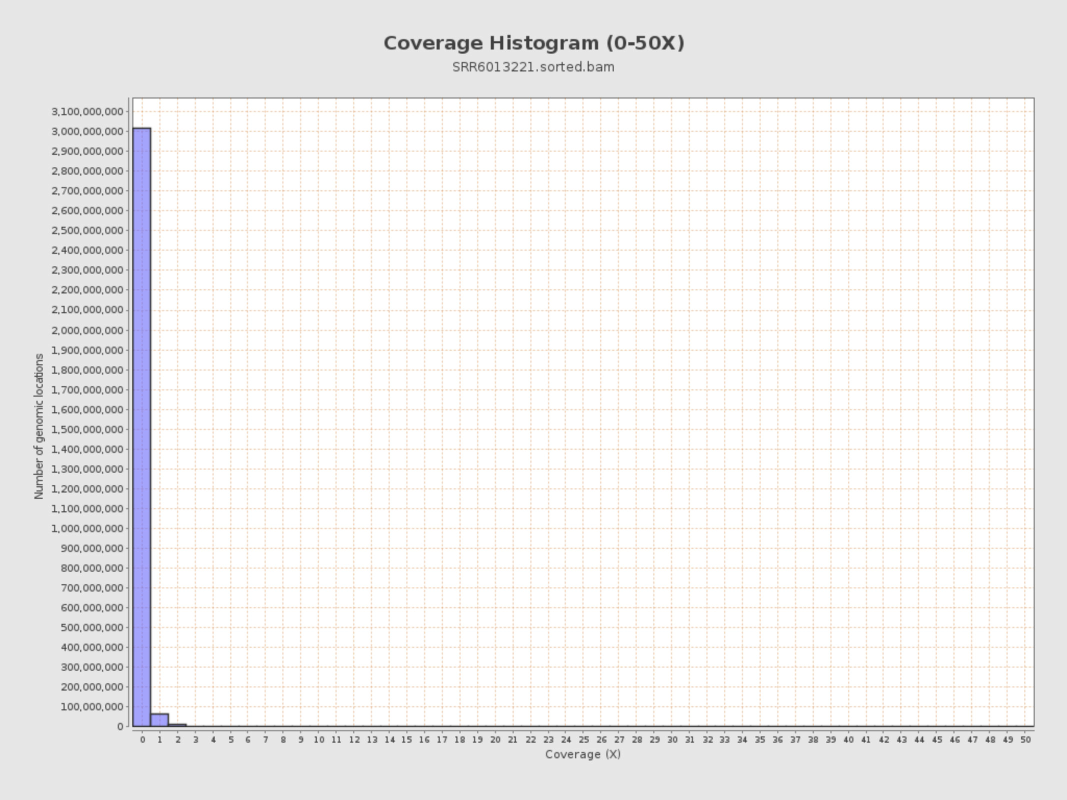
3. Results : Coverage across reference



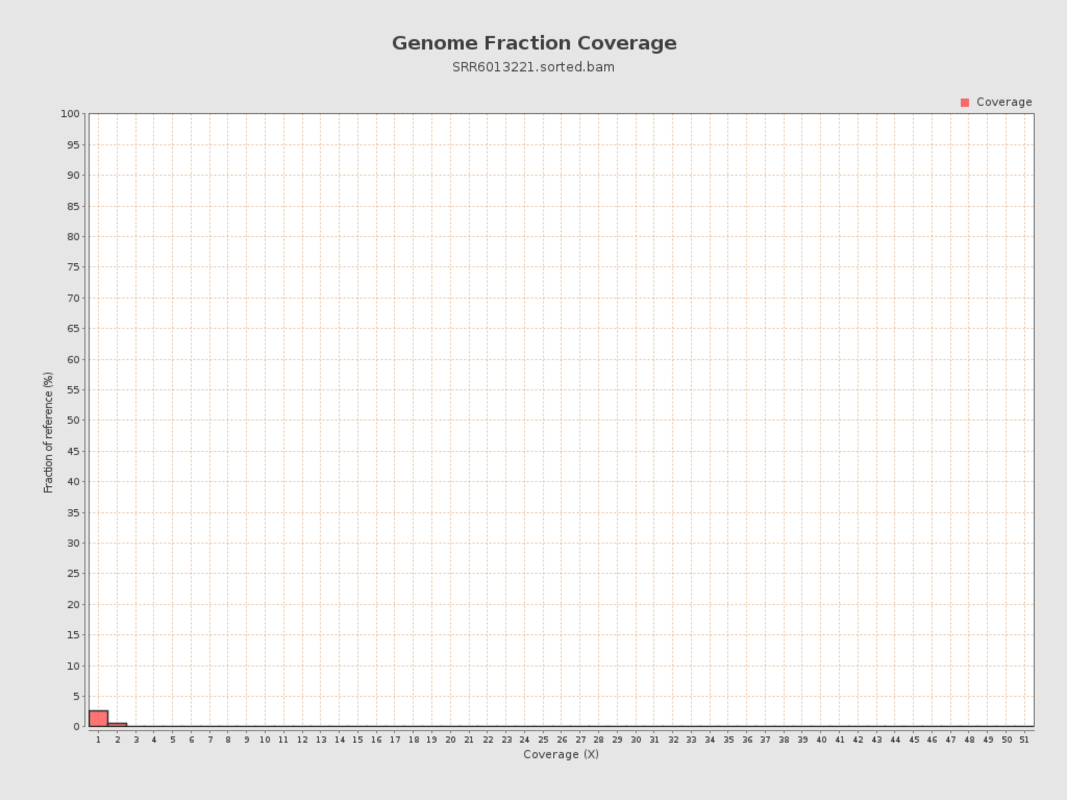
4. Results : Coverage Histogram



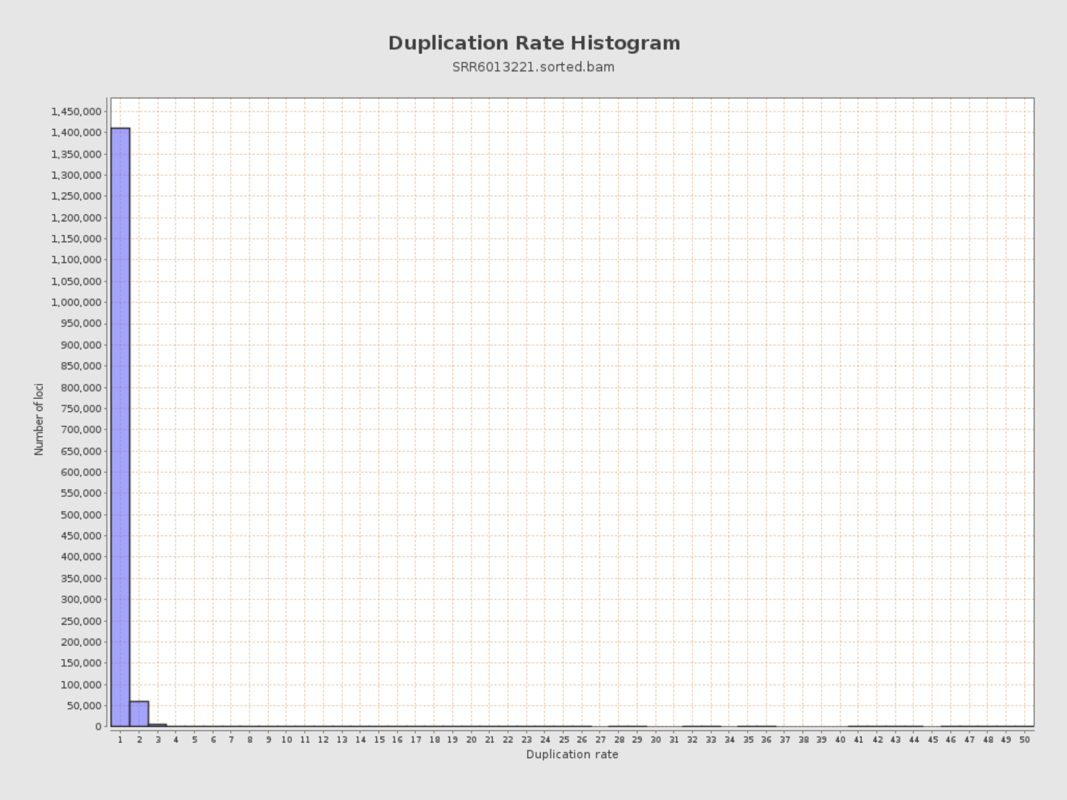
5. Results : Coverage Histogram (0-50X)



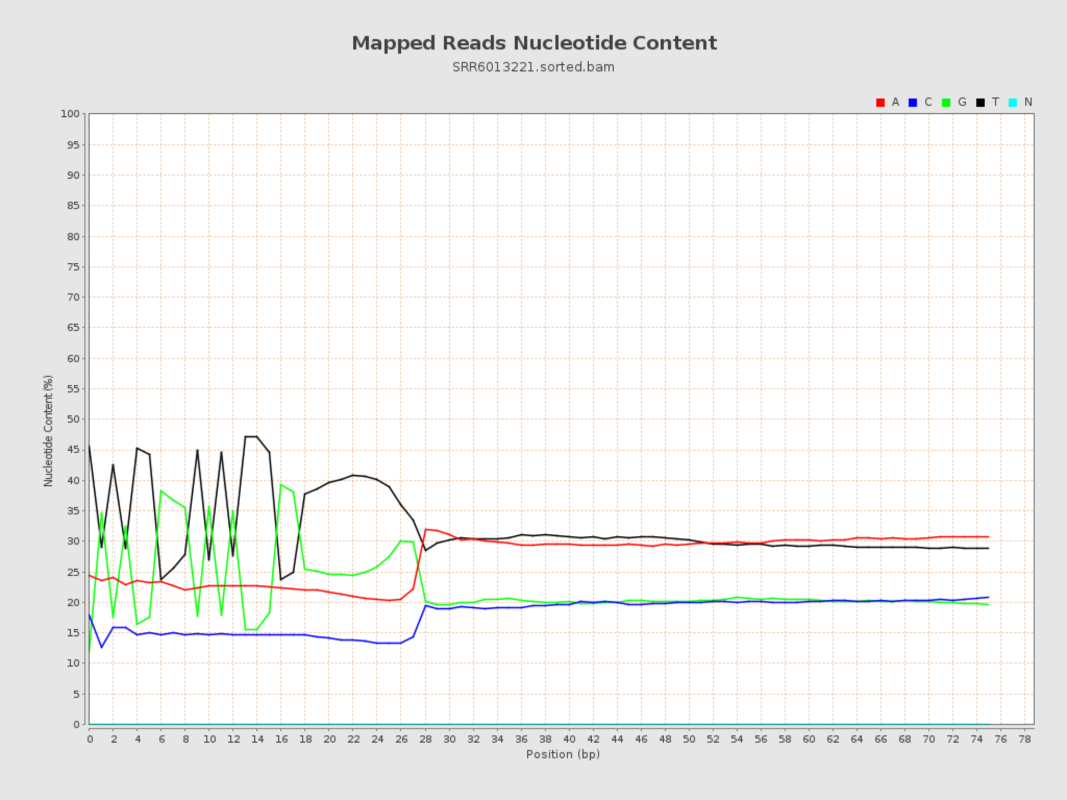
6. Results : Genome Fraction Coverage



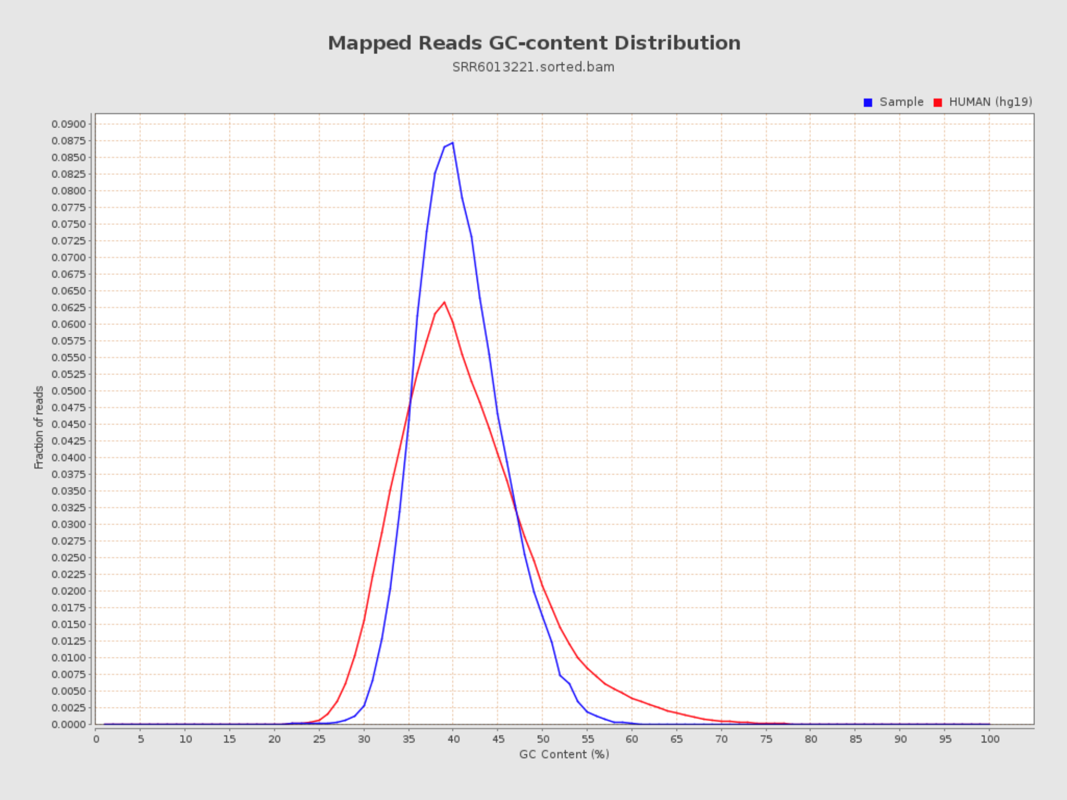
7. Results : Duplication Rate Histogram



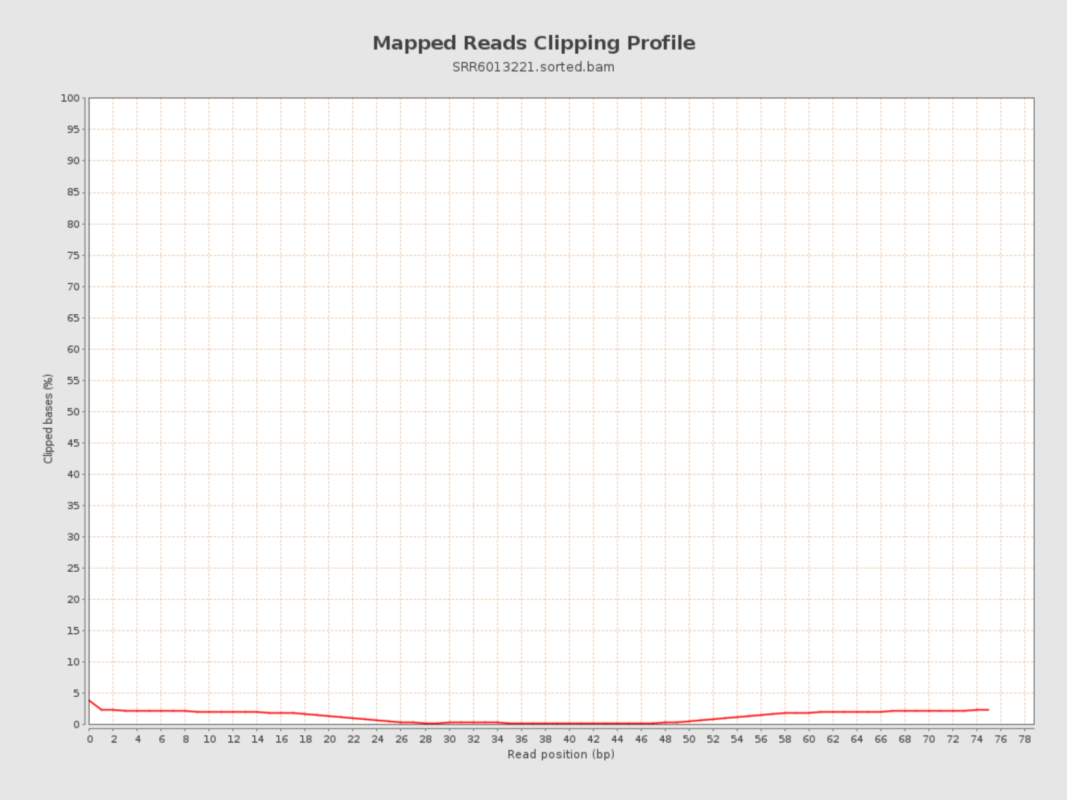
8. Results : Mapped Reads Nucleotide Content



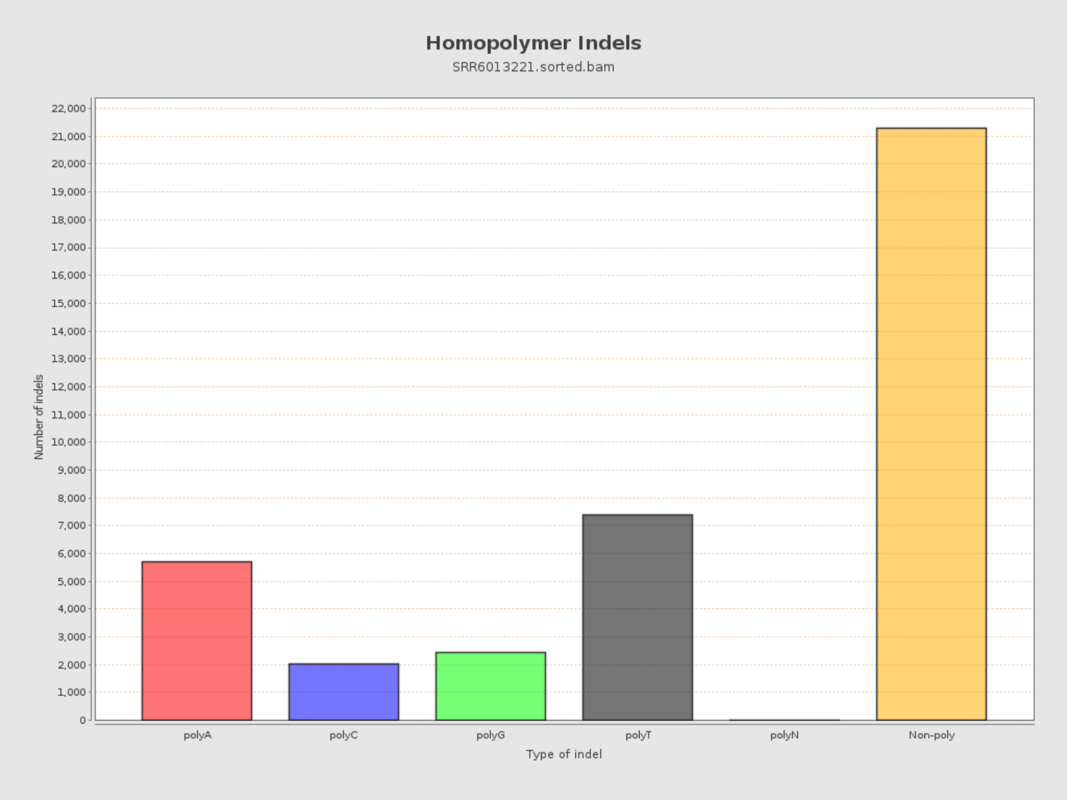
9. Results : Mapped Reads GC-content Distribution



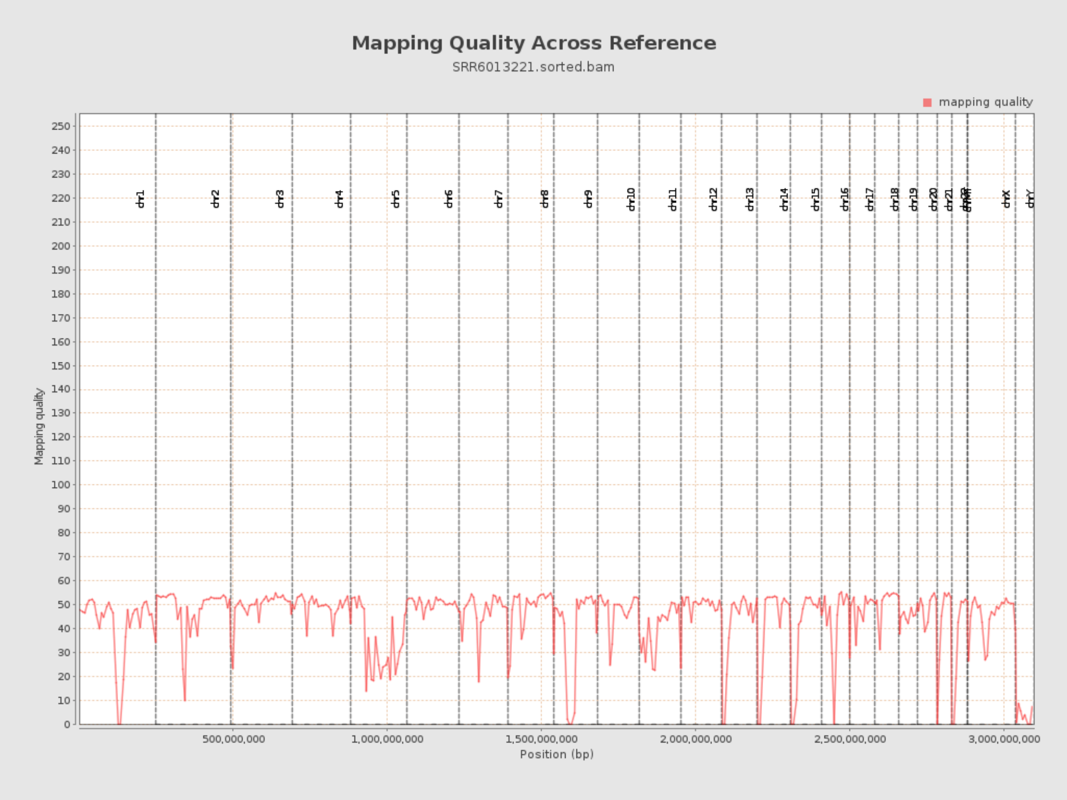
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram