Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013161.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_SRR6013161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:35:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,608,378
Mapped reads	2,426,672 / 67.25%
Unmapped reads	1,181,706 / 32.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,159 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	258,535 / 7.16%
Duplication rate	8.32%
Clipped reads	1,326,183 / 36.75%

2.2. ACGT Content

Number/percentage of A's	41,892,340 / 26.97%
Number/percentage of C's	28,344,078 / 18.25%
Number/percentage of T's	49,375,930 / 31.79%
Number/percentage of G's	35,457,633 / 22.83%
Number/percentage of N's	242,989 / 0.16%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.4875

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

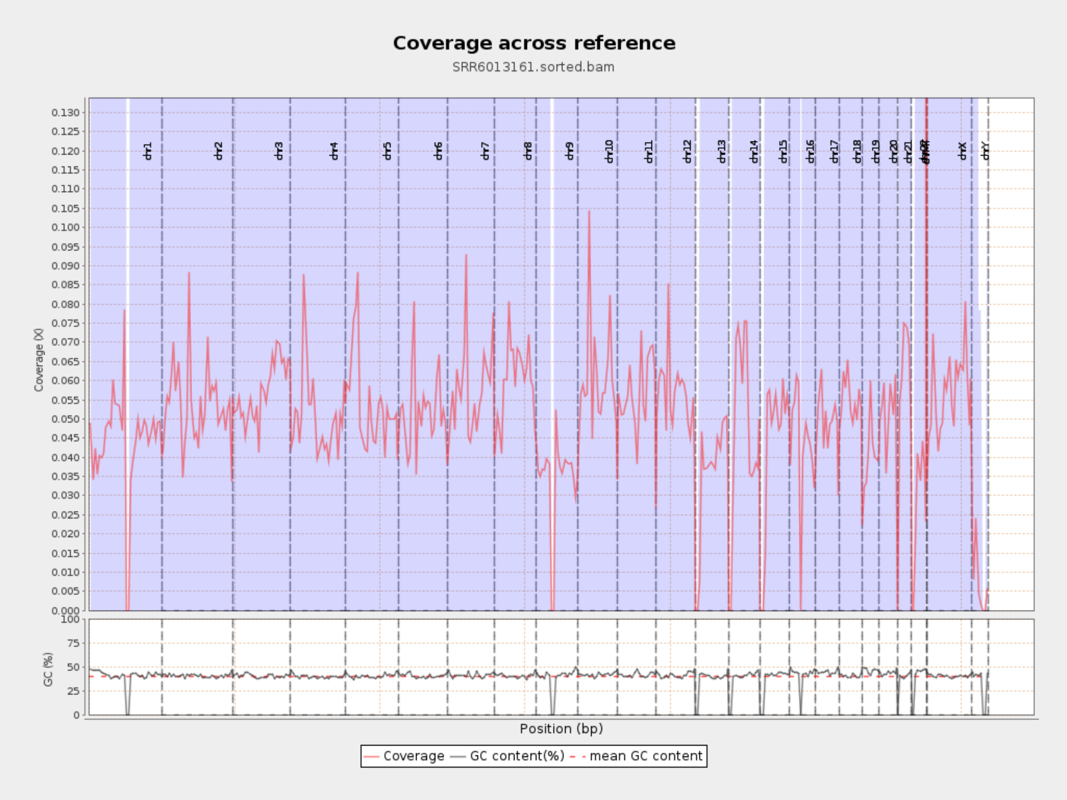
General error rate	0.94%
Mismatches	1,436,012
Insertions	10,291
Mapped reads with at least one insertion	0.42%
Deletions	53,295
Mapped reads with at least one deletion	2.17%
Homopolymer indels	43.39%

2.6. Chromosome stats

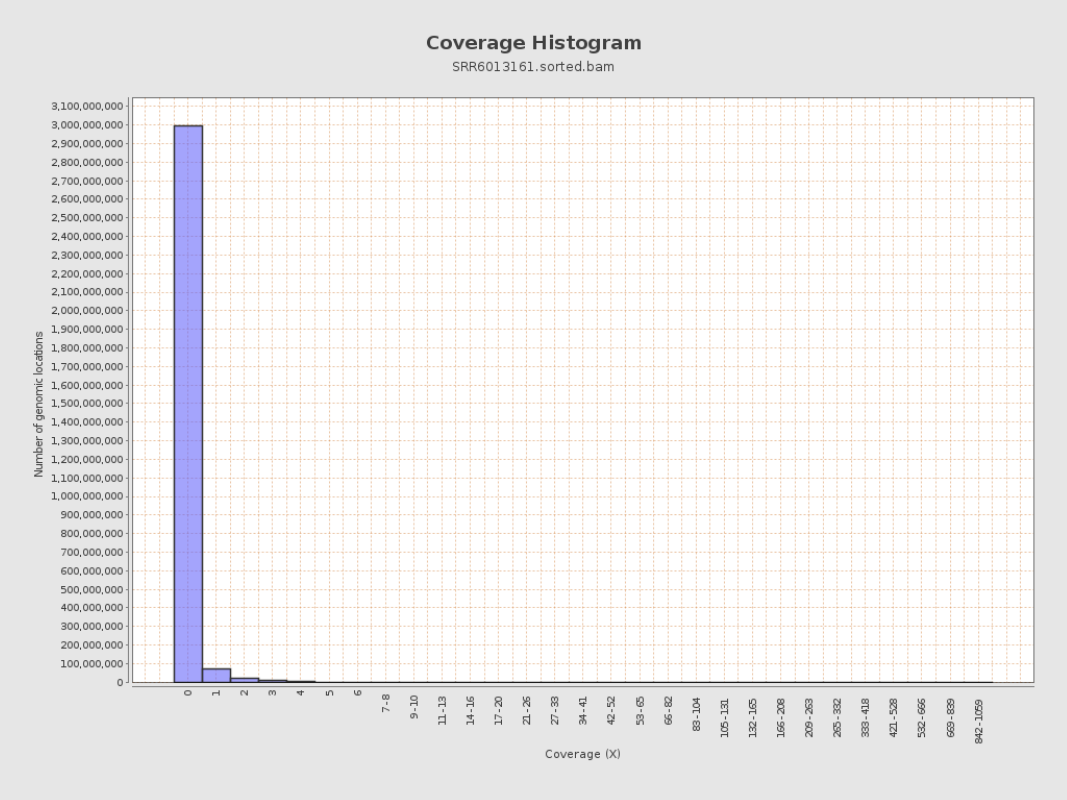
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11021663	0.0442	0.8708
chr2	243199373	13082614	0.0538	0.5754
chr3	198022430	11297999	0.0571	0.3454
chr4	191154276	9622751	0.0503	0.3479
chr5	180915260	9850676	0.0544	0.3346
chr6	171115067	8927574	0.0522	0.4132
chr7	159138663	9239918	0.0581	0.6188

chr8	146364022	8784612	0.06	0.4658
chr9	141213431	4790707	0.0339	0.3675
chr10	135534747	8222496	0.0607	0.5566
chr11	135006516	7643006	0.0566	0.4192
chr12	133851895	7604179	0.0568	0.3412
chr13	115169878	4085758	0.0355	0.2714
chr14	107349540	4983676	0.0464	0.3192
chr15	102531392	4400486	0.0429	0.2962
chr16	90354753	3893922	0.0431	0.317
chr17	81195210	3973117	0.0489	0.3555
chr18	78077248	4297770	0.055	0.6646
chr19	59128983	2396712	0.0405	0.5841
chr20	63025520	3233204	0.0513	0.3318
chr21	48129895	2805124	0.0583	0.3628
chr22	51304566	1386761	0.027	0.2334
chrMT	16571	700121	42.2498	19.831
chrX	155270560	8730303	0.0562	0.3585
chrY	59373566	430314	0.0072	0.1859

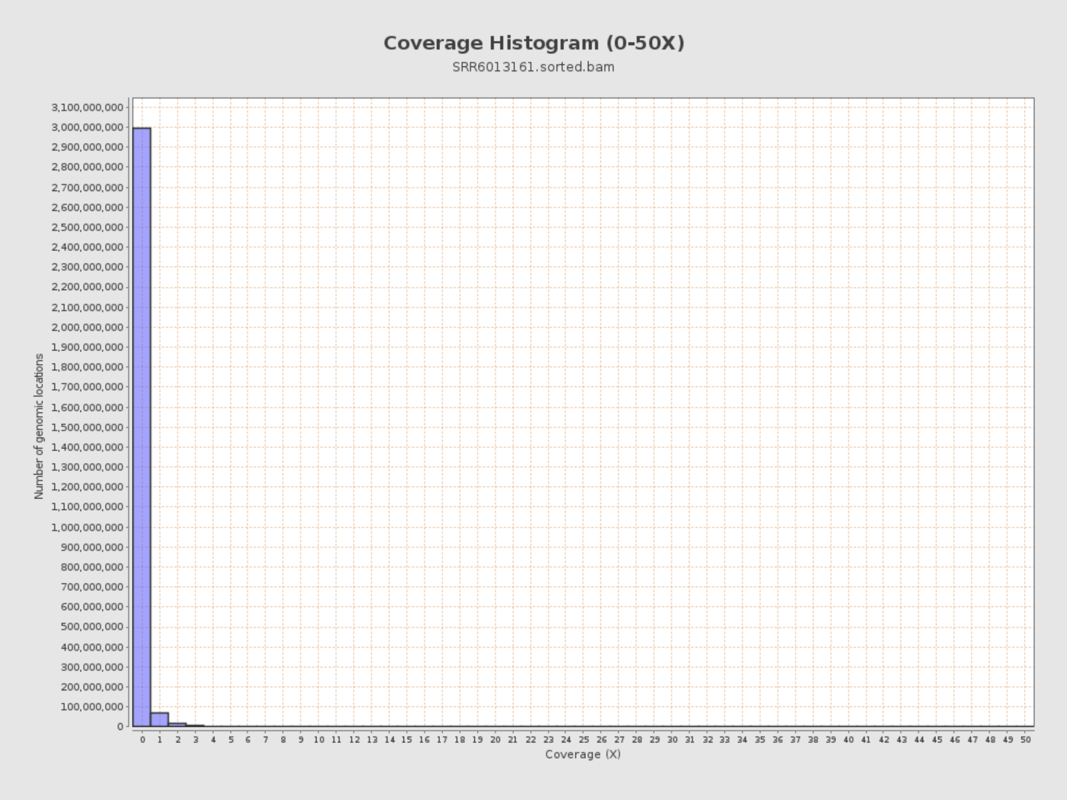
3. Results : Coverage across reference



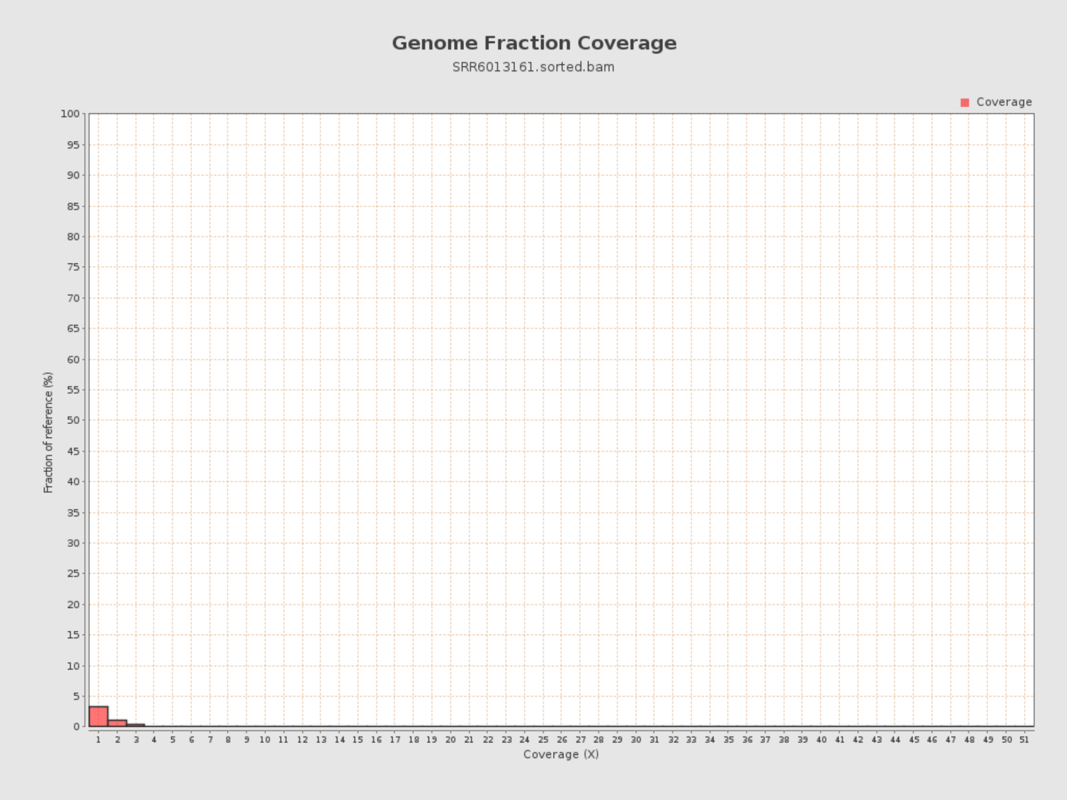
4. Results : Coverage Histogram



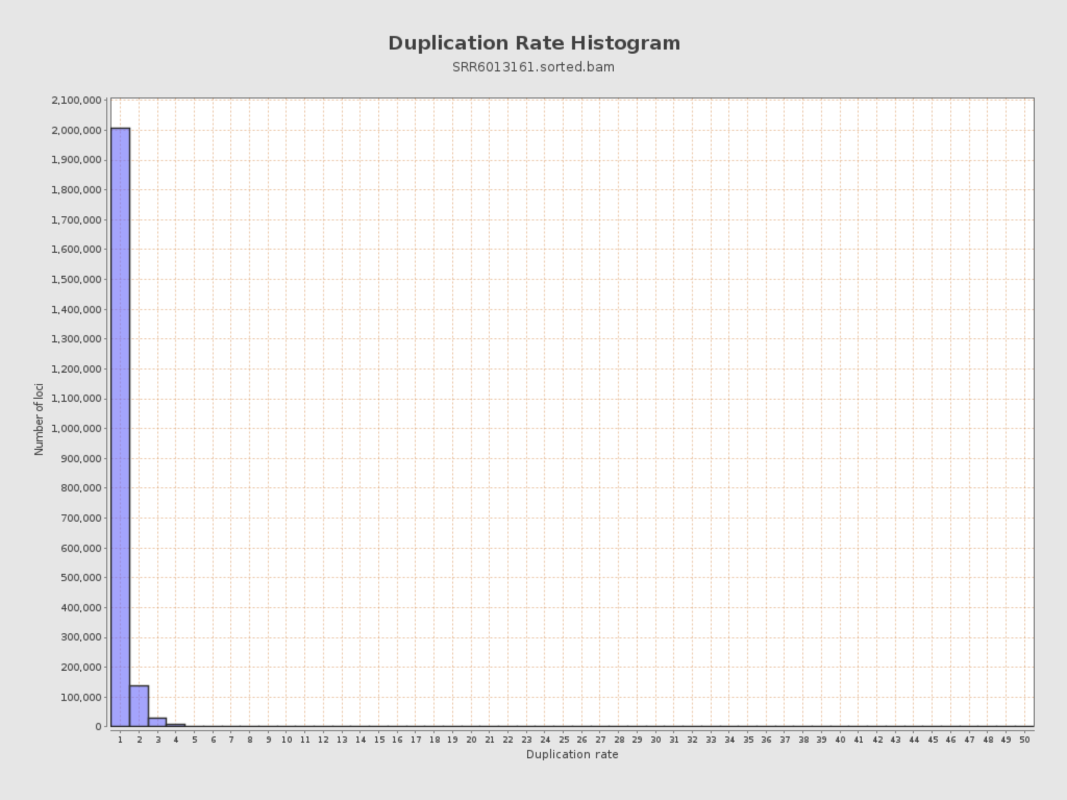
5. Results : Coverage Histogram (0-50X)



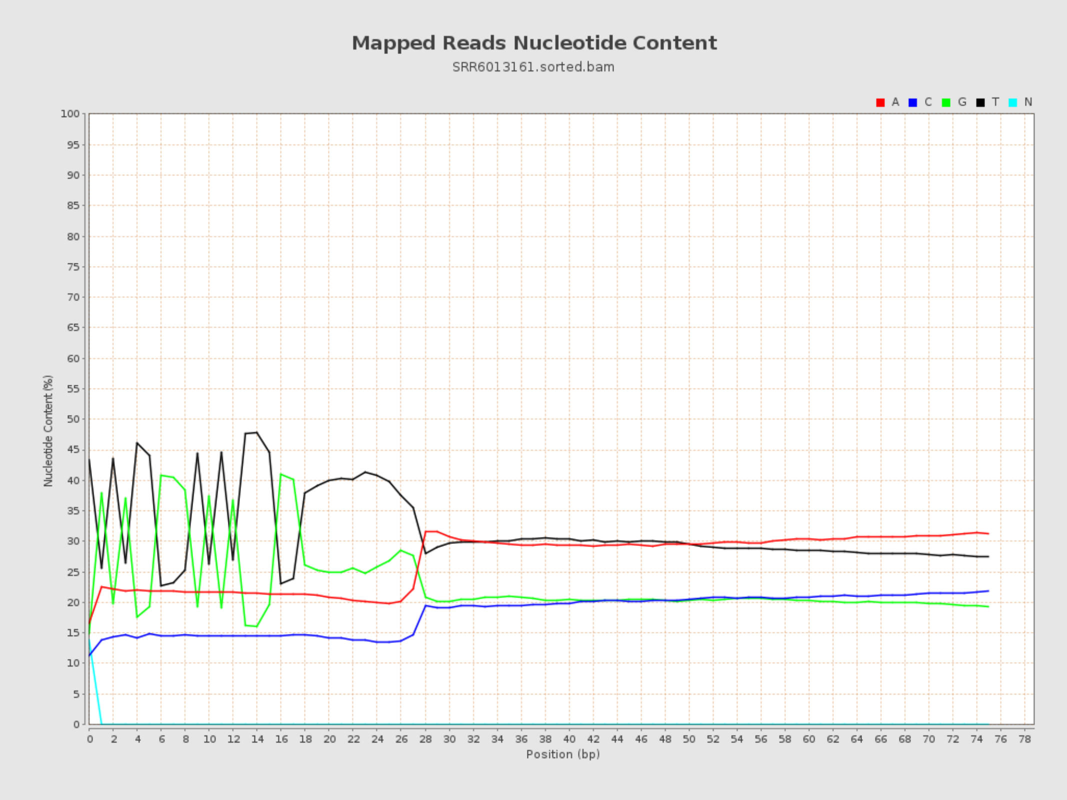
6. Results : Genome Fraction Coverage



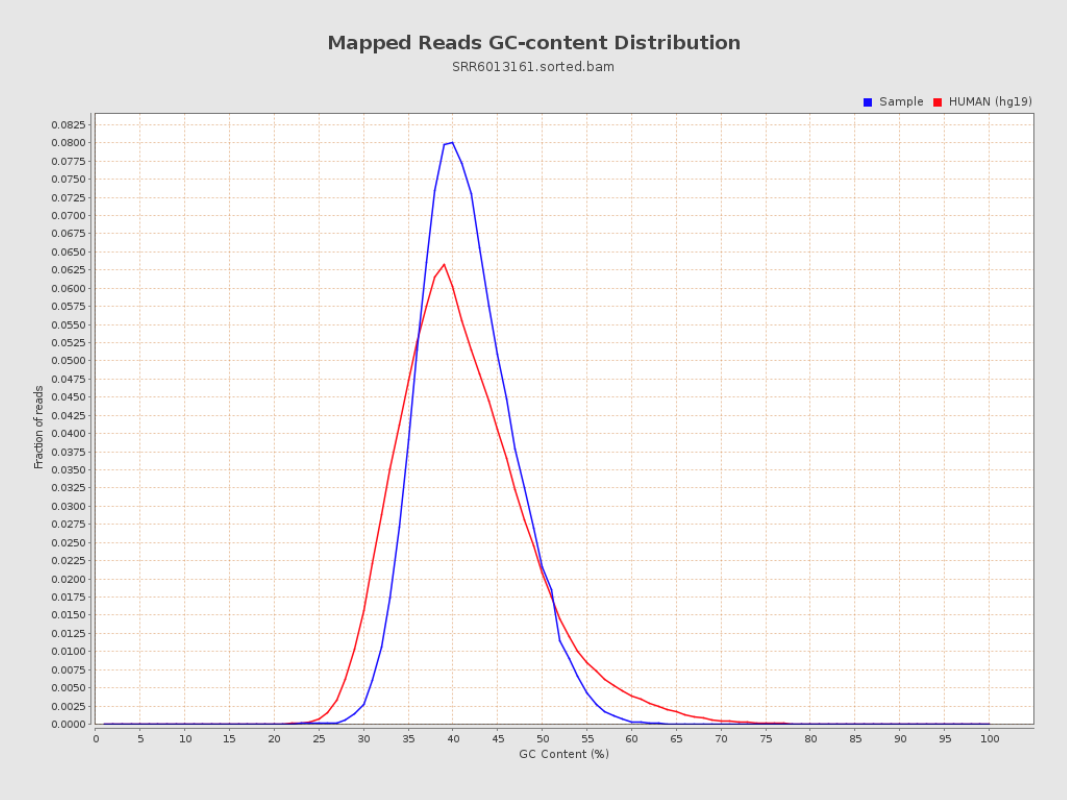
7. Results : Duplication Rate Histogram



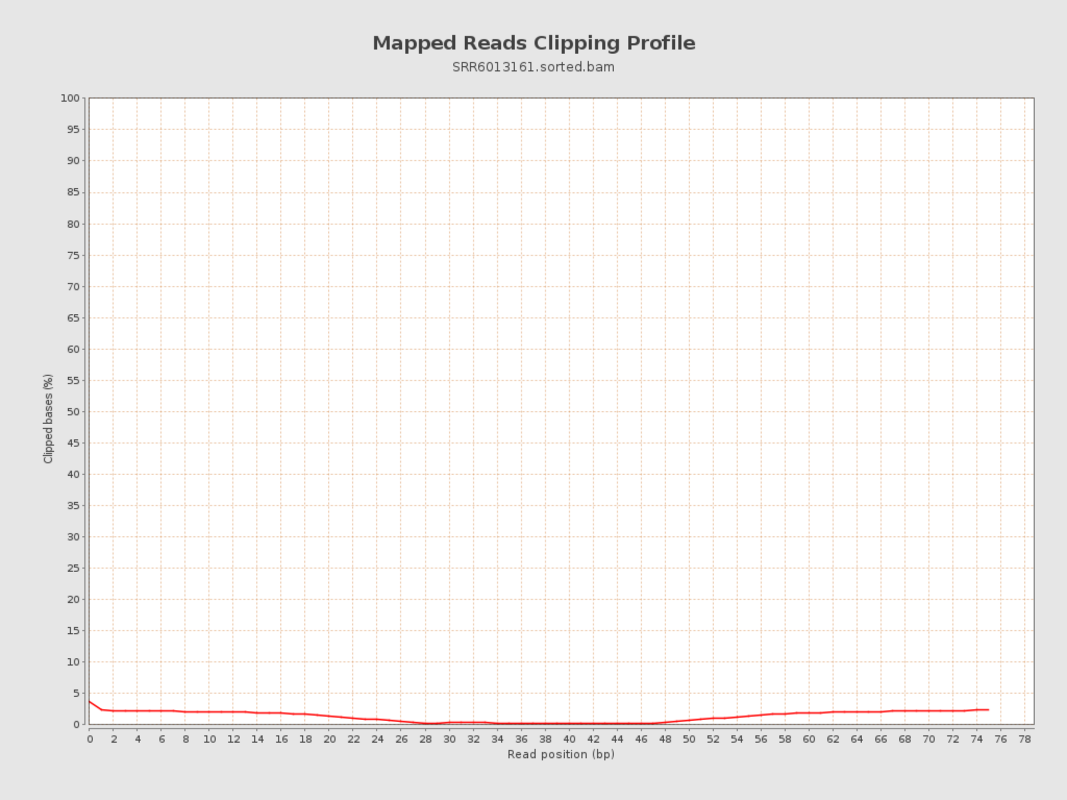
8. Results : Mapped Reads Nucleotide Content



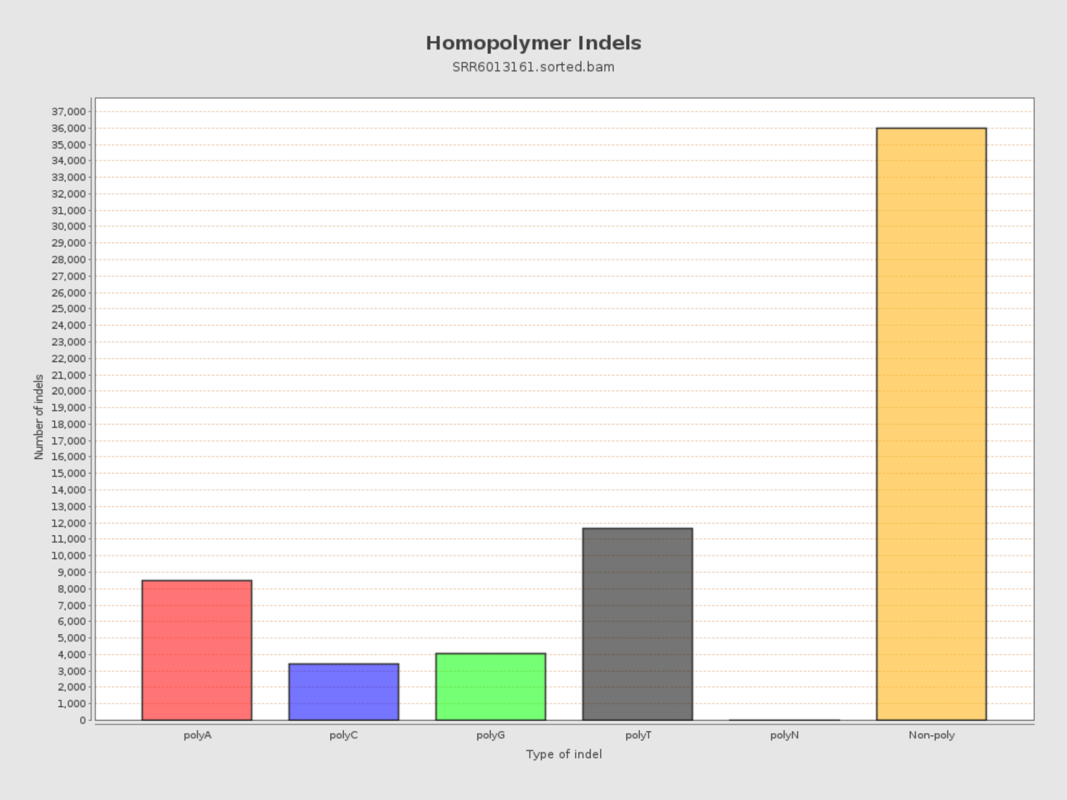
9. Results : Mapped Reads GC-content Distribution



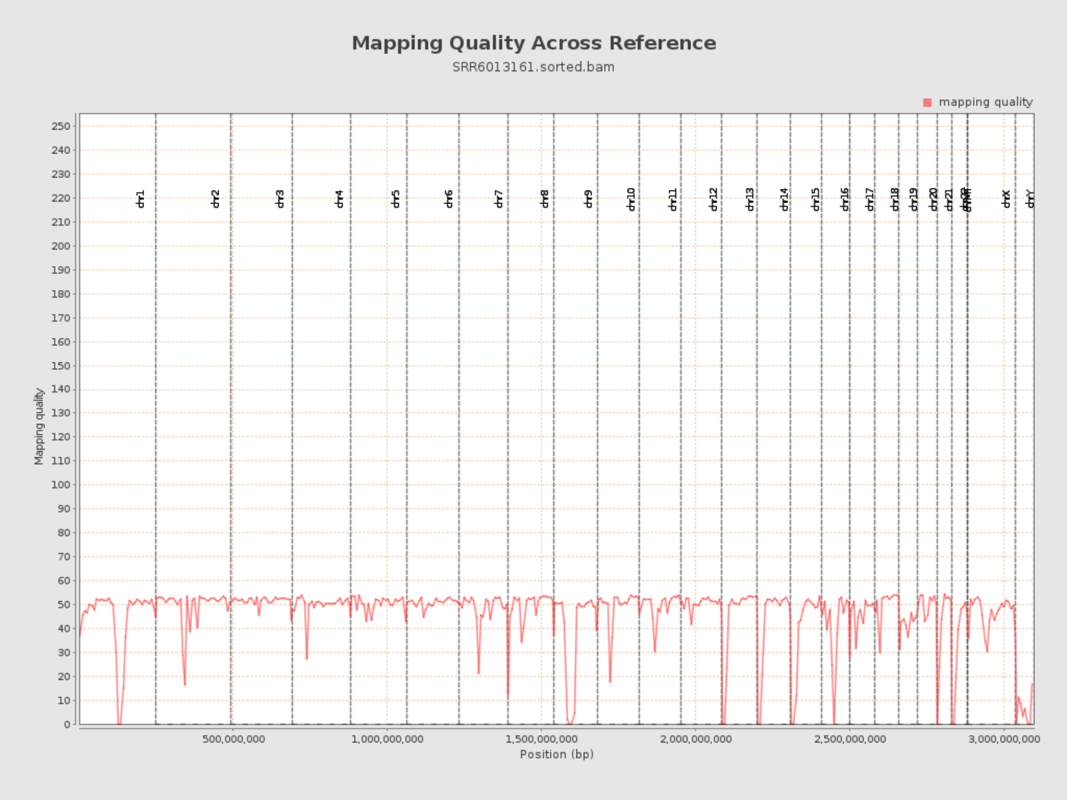
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram