Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:24:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230361.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_SRR6230361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230361.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:24:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230361.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	299,676
Mapped reads	262,981 / 87.76%
Unmapped reads	36,695 / 12.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,182 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	5,592 / 1.87%
Duplication rate	1.89%
Clipped reads	116,808 / 38.98%

2.2. ACGT Content

Number/percentage of A's	5,104,287 / 29.02%
Number/percentage of C's	3,181,563 / 18.09%
Number/percentage of T's	5,634,746 / 32.04%
Number/percentage of G's	3,658,125 / 20.8%
Number/percentage of N's	8,579 / 0.05%
GC Percentage	38.89%

2.3. Coverage

Mean	0.0057

Standard Deviation	0.0869

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

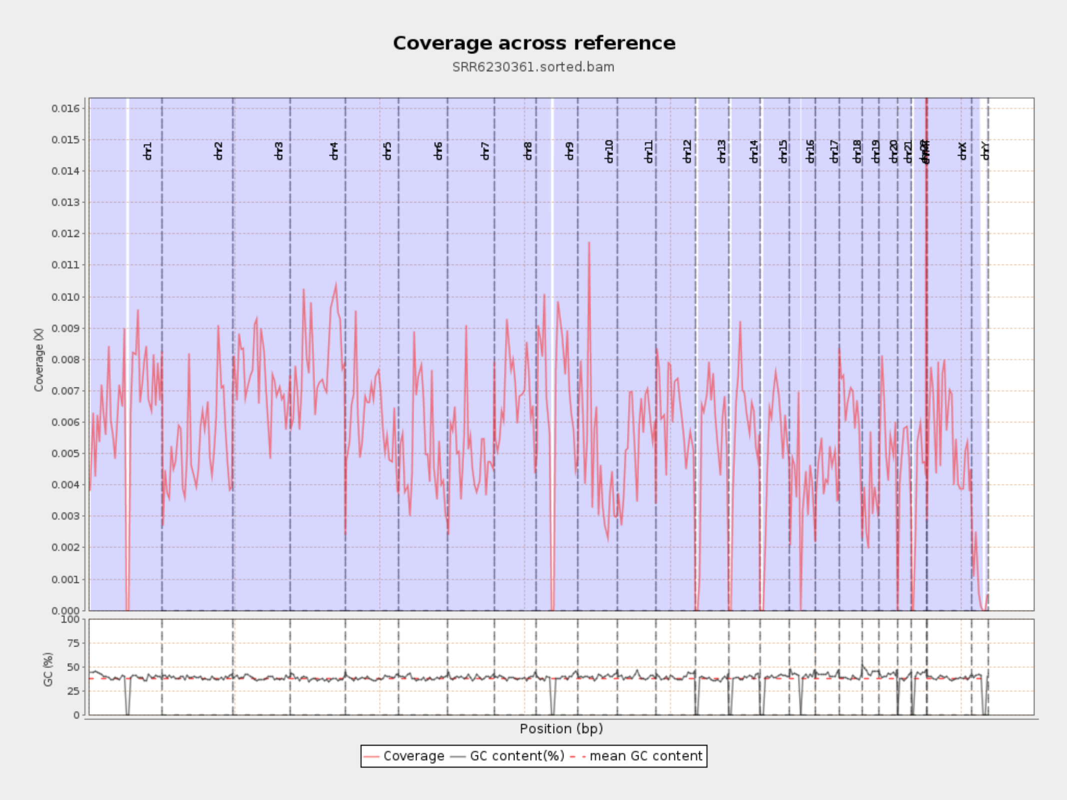
General error rate	0.91%
Mismatches	157,936
Insertions	1,523
Mapped reads with at least one insertion	0.58%
Deletions	5,368
Mapped reads with at least one deletion	2.02%
Homopolymer indels	46.7%

2.6. Chromosome stats

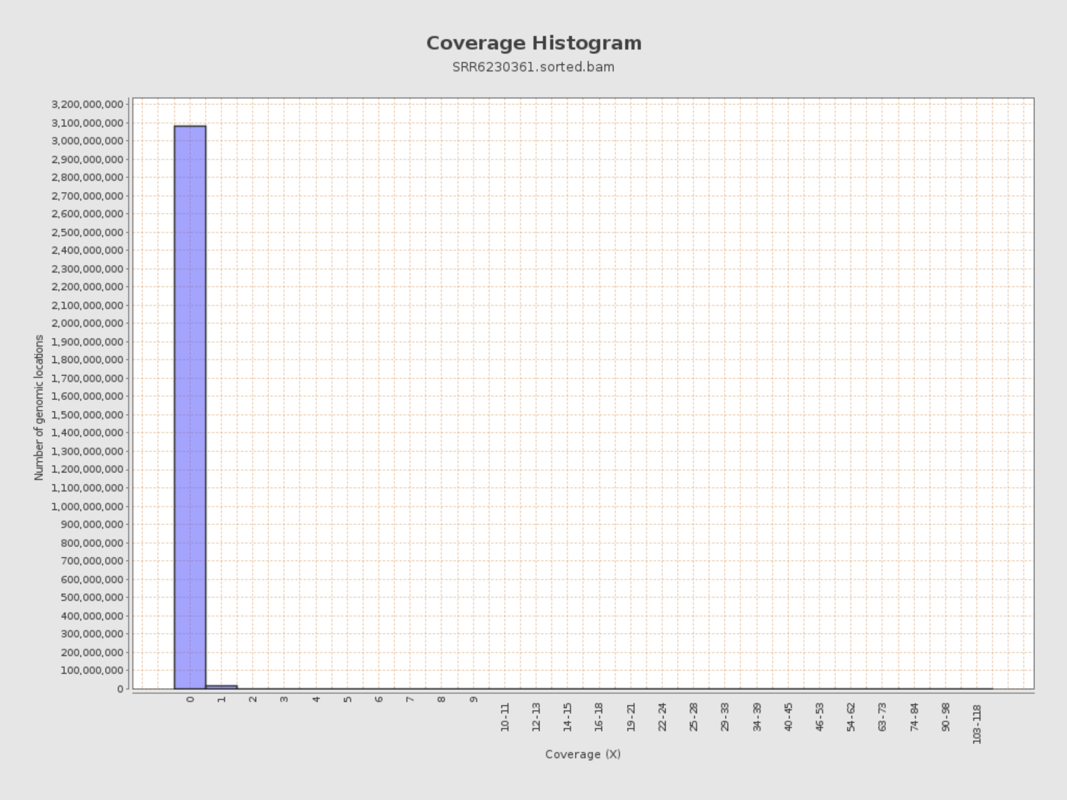
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1588570	0.0064	0.1032
chr2	243199373	1263467	0.0052	0.0842
chr3	198022430	1457049	0.0074	0.0898
chr4	191154276	1518136	0.0079	0.0939
chr5	180915260	1112975	0.0062	0.0817
chr6	171115067	883710	0.0052	0.0782
chr7	159138663	801439	0.005	0.0907

chr8	146364022	996523	0.0068	0.1154
chr9	141213431	969003	0.0069	0.0946
chr10	135534747	665008	0.0049	0.0879
chr11	135006516	724842	0.0054	0.0837
chr12	133851895	839817	0.0063	0.0826
chr13	115169878	602004	0.0052	0.0754
chr14	107349540	594710	0.0055	0.0784
chr15	102531392	502020	0.0049	0.0727
chr16	90354753	338608	0.0037	0.0672
chr17	81195210	357464	0.0044	0.0696
chr18	78077248	512200	0.0066	0.1231
chr19	59128983	201789	0.0034	0.0718
chr20	63025520	353554	0.0056	0.0784
chr21	48129895	212916	0.0044	0.0695
chr22	51304566	186453	0.0036	0.0626
chrMT	16571	1089	0.0657	0.2636
chrX	155270560	867350	0.0056	0.0788
chrY	59373566	45642	0.0008	0.0336

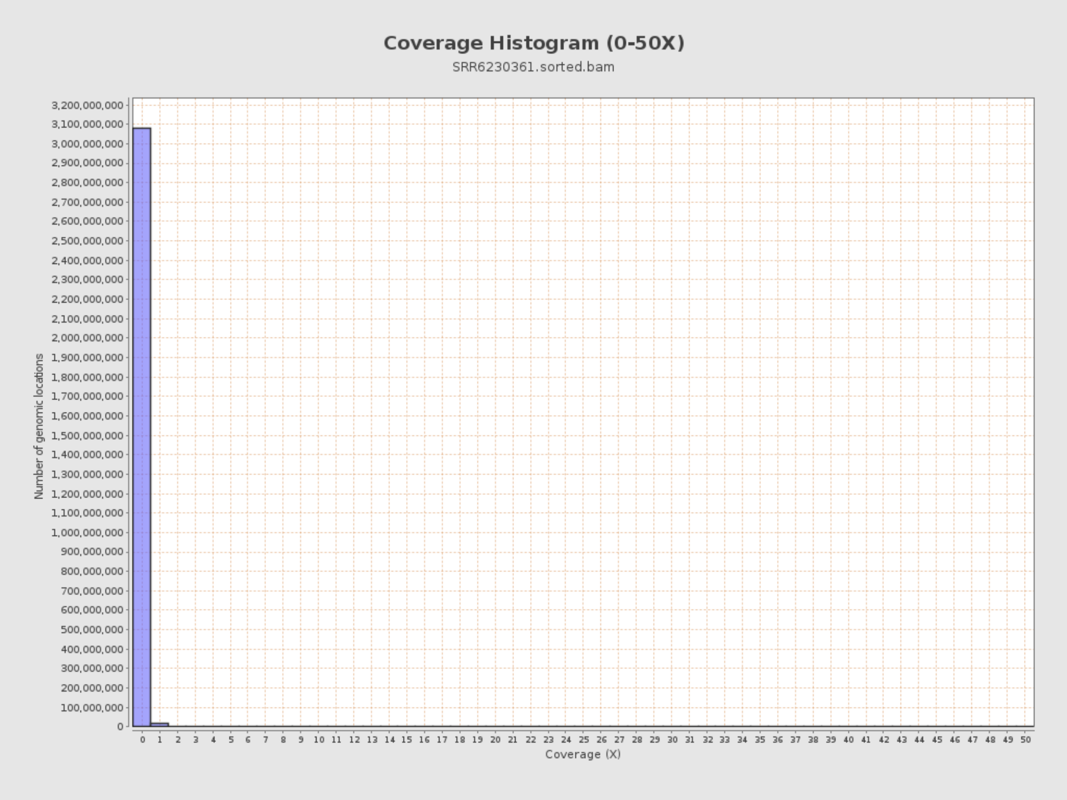
3. Results : Coverage across reference



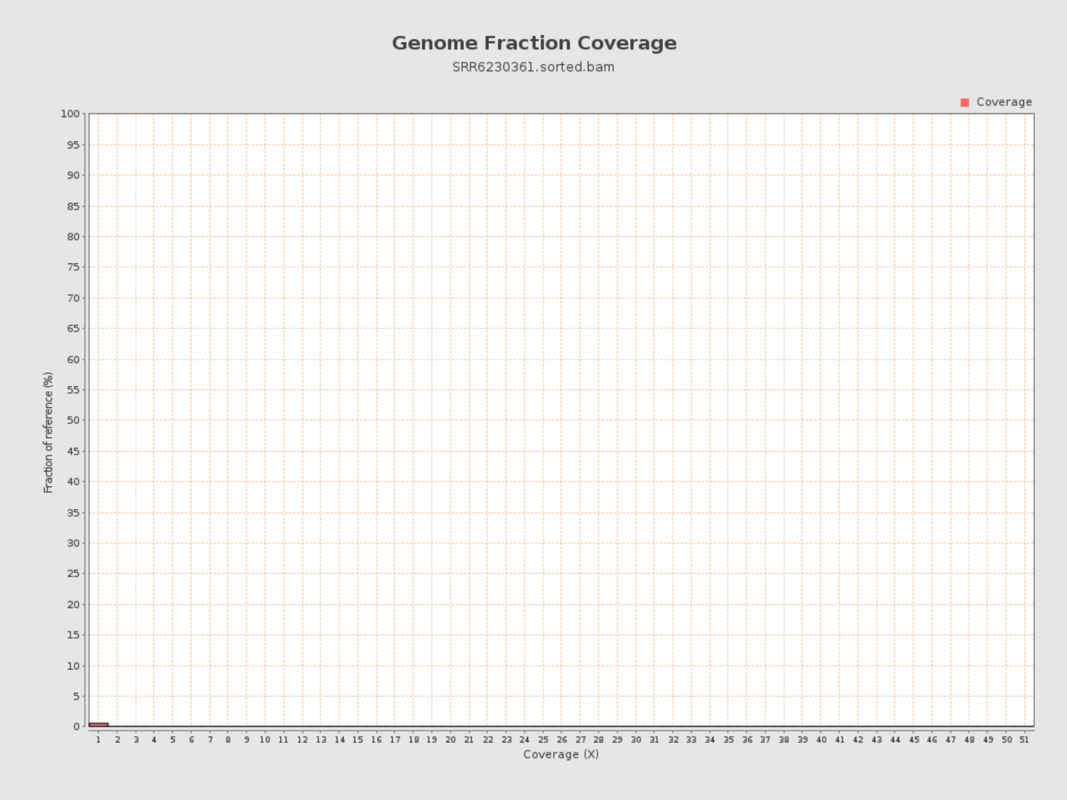
4. Results : Coverage Histogram



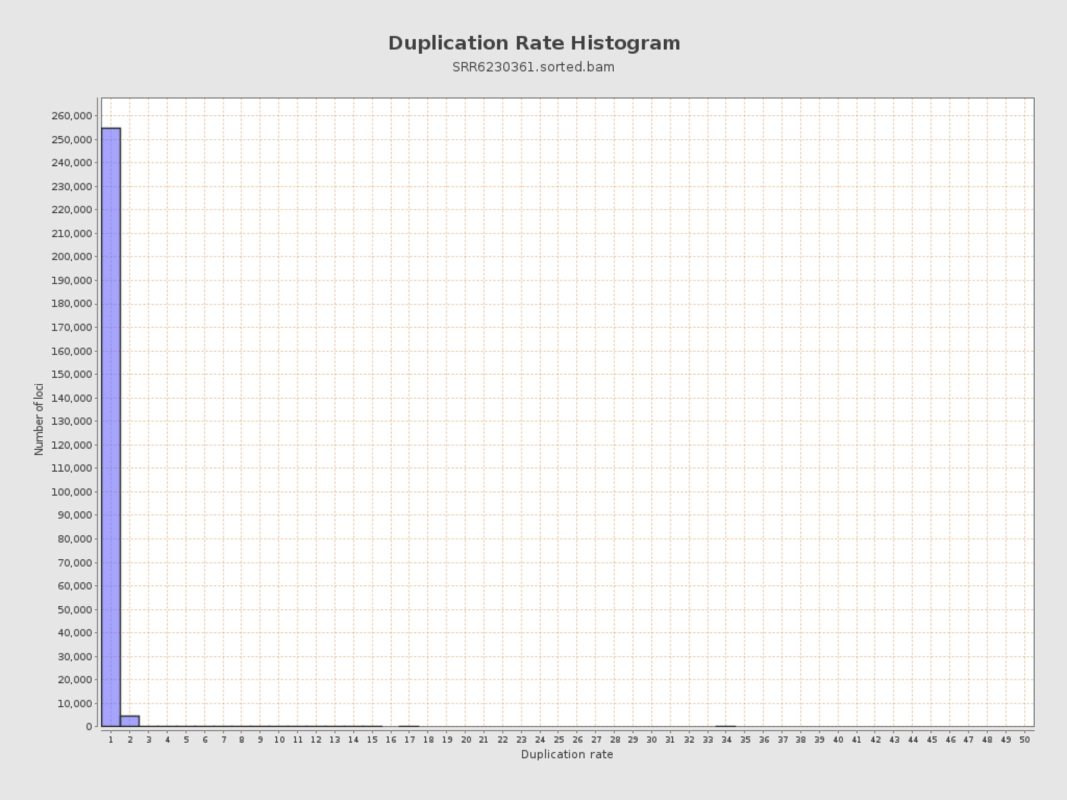
5. Results : Coverage Histogram (0-50X)



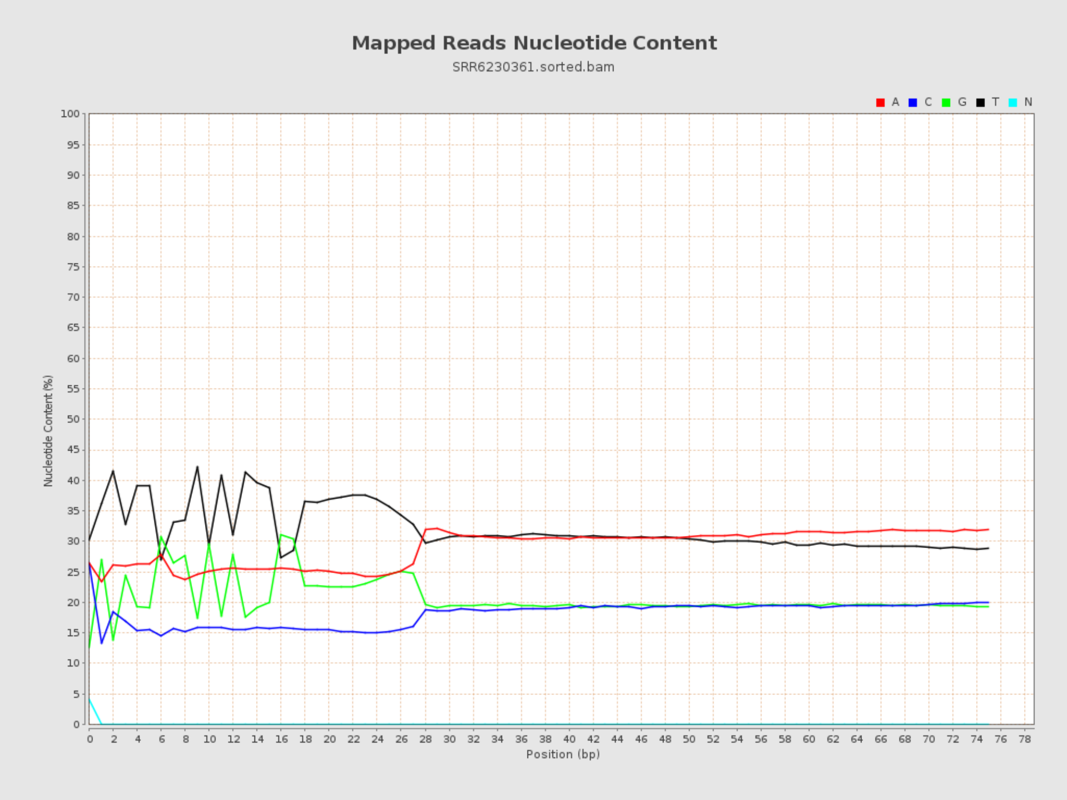
6. Results : Genome Fraction Coverage



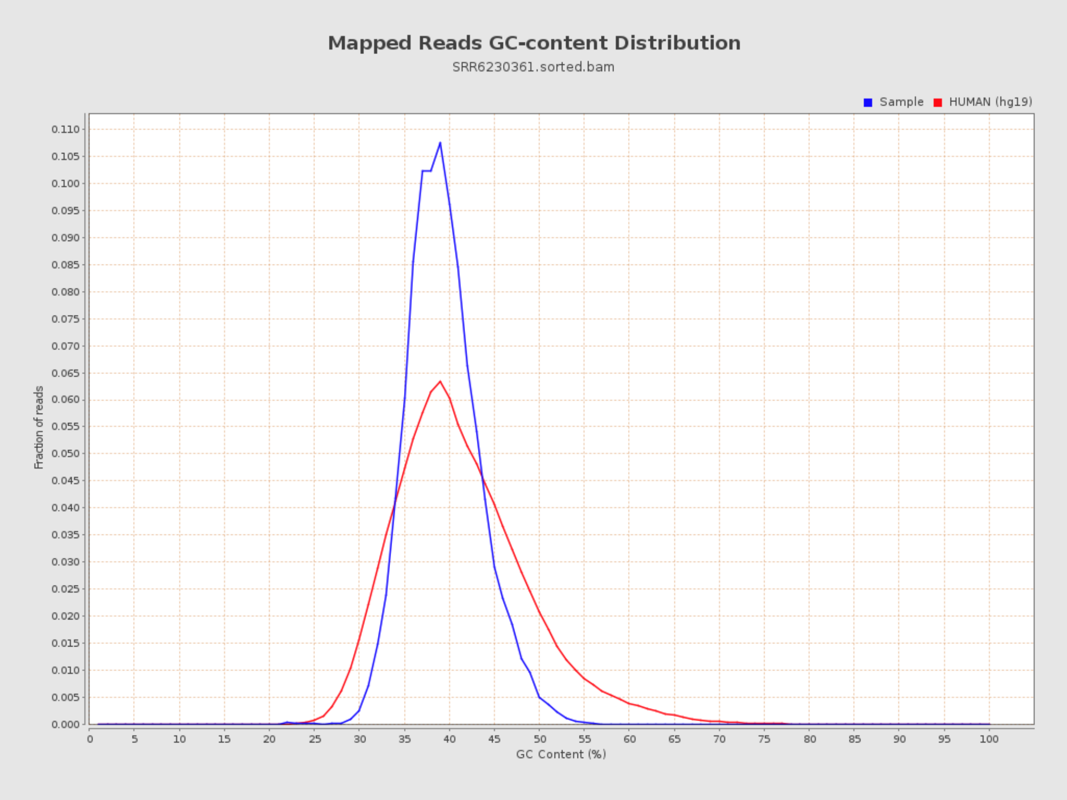
7. Results : Duplication Rate Histogram



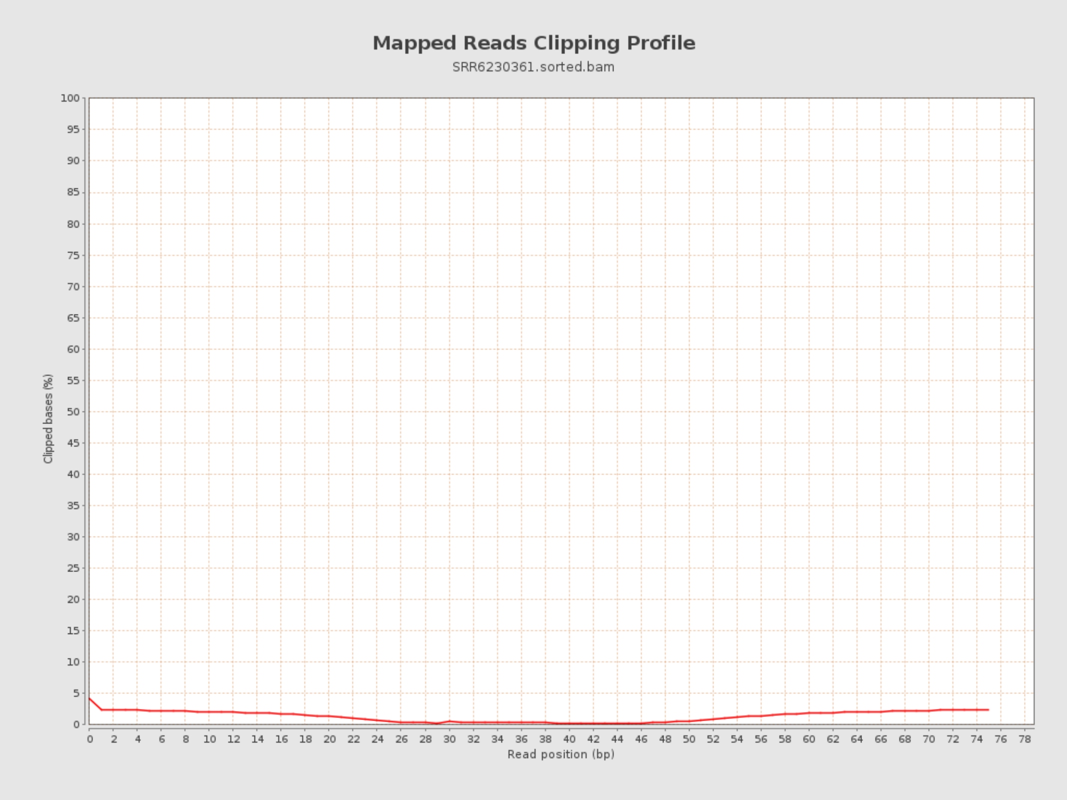
8. Results : Mapped Reads Nucleotide Content



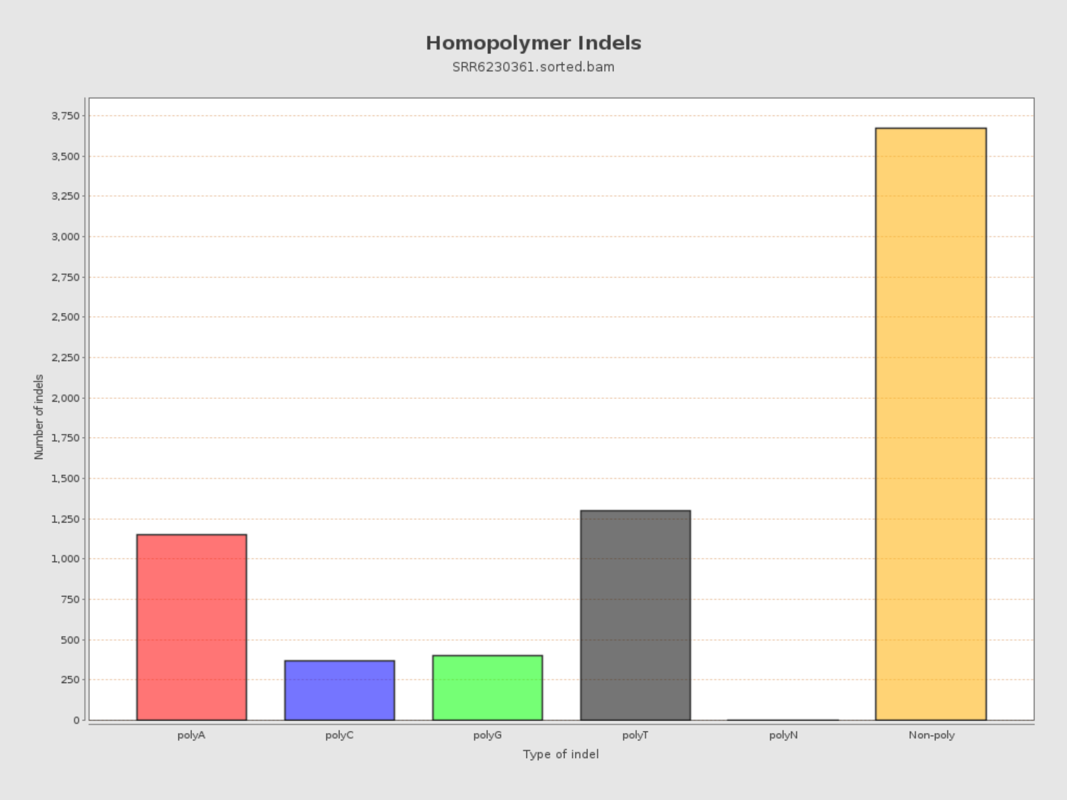
9. Results : Mapped Reads GC-content Distribution



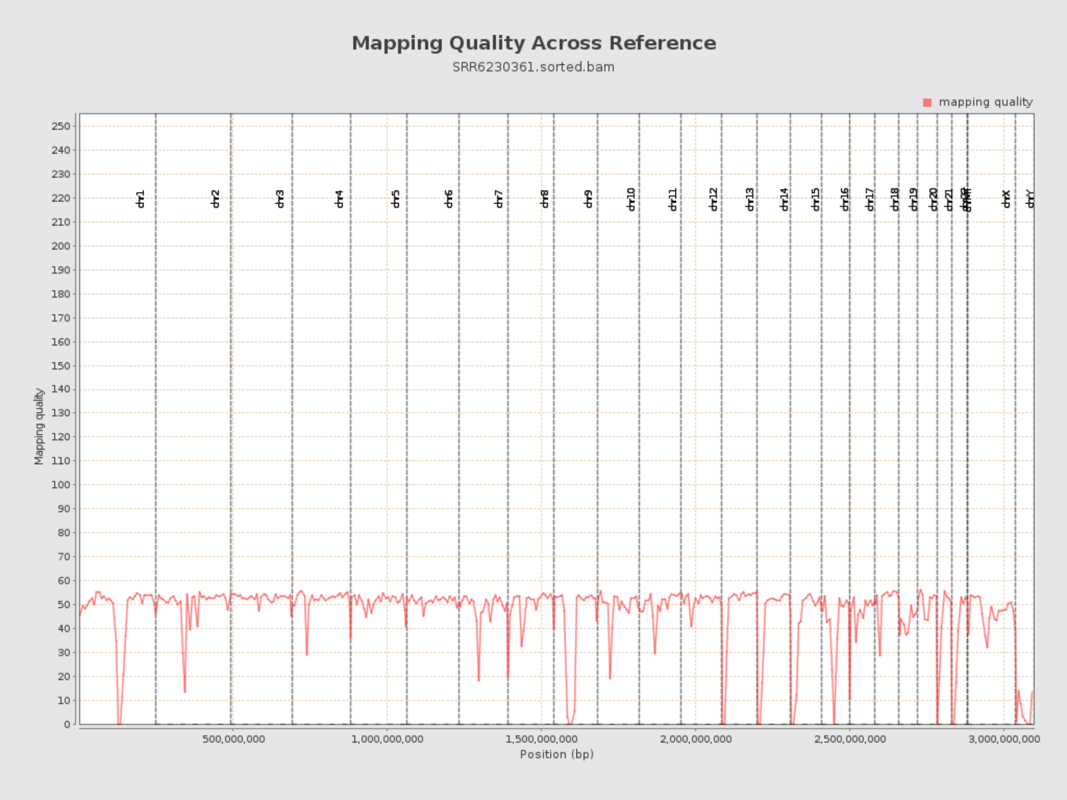
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram