Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:27:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230362.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_SRR6230362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230362.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:27:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,555,510
Mapped reads	3,140,526 / 88.33%
Unmapped reads	414,984 / 11.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,955 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	179,010 / 5.03%
Duplication rate	4.48%
Clipped reads	1,615,899 / 45.45%

2.2. ACGT Content

Number/percentage of A's	55,139,621 / 27.02%
Number/percentage of C's	37,507,583 / 18.38%
Number/percentage of T's	64,441,361 / 31.58%
Number/percentage of G's	46,852,507 / 22.96%
Number/percentage of N's	102,738 / 0.05%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0659

Standard Deviation	0.5145

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

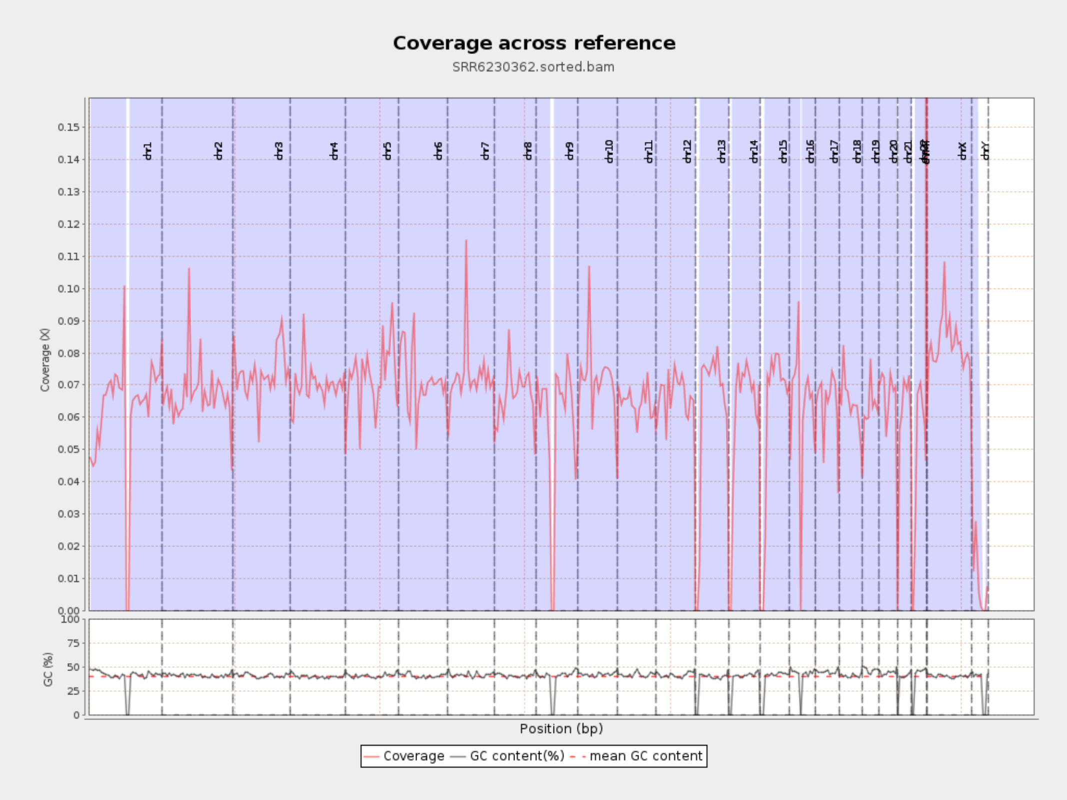
General error rate	0.88%
Mismatches	1,758,324
Insertions	16,037
Mapped reads with at least one insertion	0.51%
Deletions	54,003
Mapped reads with at least one deletion	1.7%
Homopolymer indels	45.86%

2.6. Chromosome stats

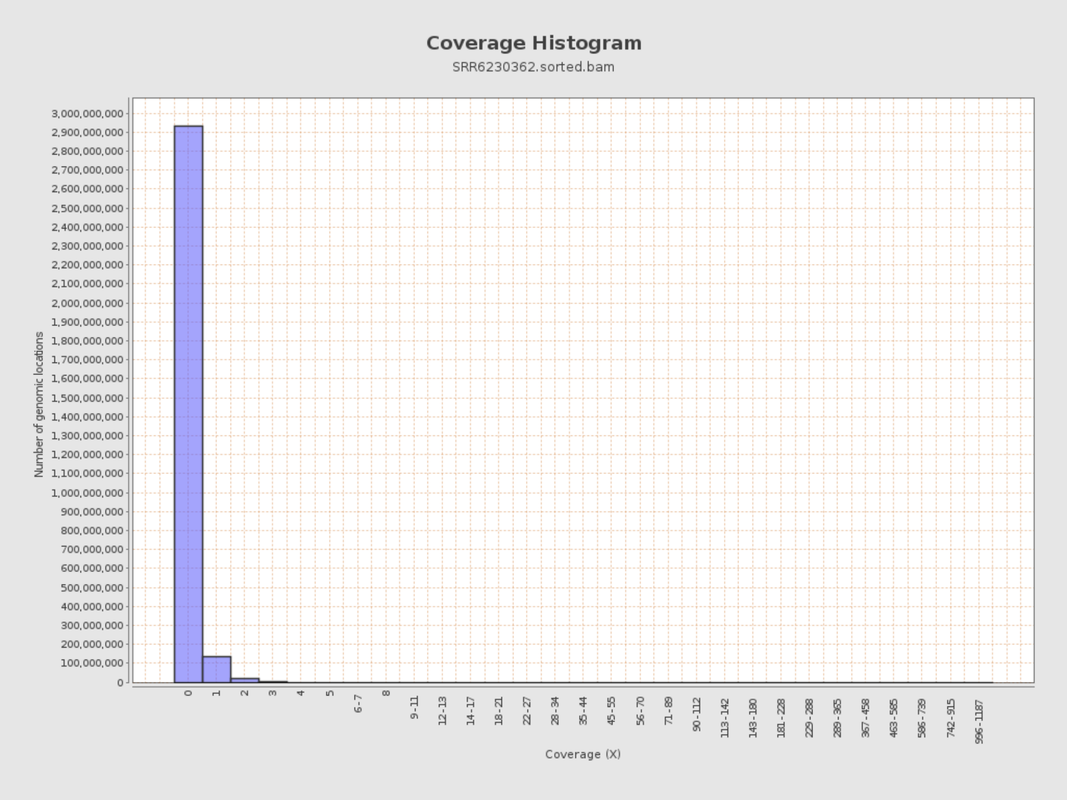
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15472688	0.0621	0.9257
chr2	243199373	16420706	0.0675	0.6684
chr3	198022430	14626681	0.0739	0.3247
chr4	191154276	13389313	0.07	0.342
chr5	180915260	13159020	0.0727	0.3225
chr6	171115067	12233486	0.0715	0.4165
chr7	159138663	11677815	0.0734	0.6791

chr8	146364022	9814315	0.0671	0.5865
chr9	141213431	8205314	0.0581	0.4604
chr10	135534747	9782390	0.0722	0.5048
chr11	135006516	8671295	0.0642	0.4465
chr12	133851895	8891747	0.0664	0.3124
chr13	115169878	6966492	0.0605	0.2958
chr14	107349540	6307910	0.0588	0.3176
chr15	102531392	6084398	0.0593	0.2948
chr16	90354753	5699107	0.0631	0.3541
chr17	81195210	5200983	0.0641	0.3337
chr18	78077248	5079307	0.0651	0.901
chr19	59128983	3732473	0.0631	0.6198
chr20	63025520	4194612	0.0666	0.3242
chr21	48129895	2828536	0.0588	0.3182
chr22	51304566	2301723	0.0449	0.2508
chrMT	16571	26294	1.5867	1.6717
chrX	155270560	12810529	0.0825	0.3927
chrY	59373566	554763	0.0093	0.1845

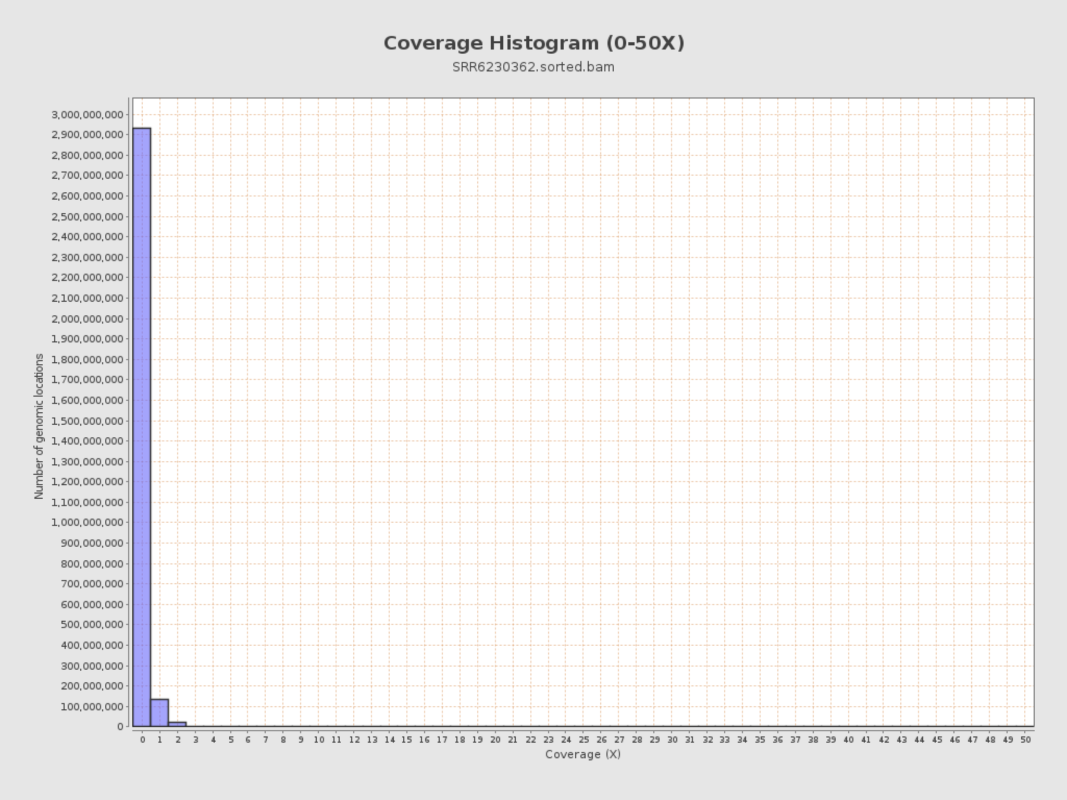
3. Results : Coverage across reference



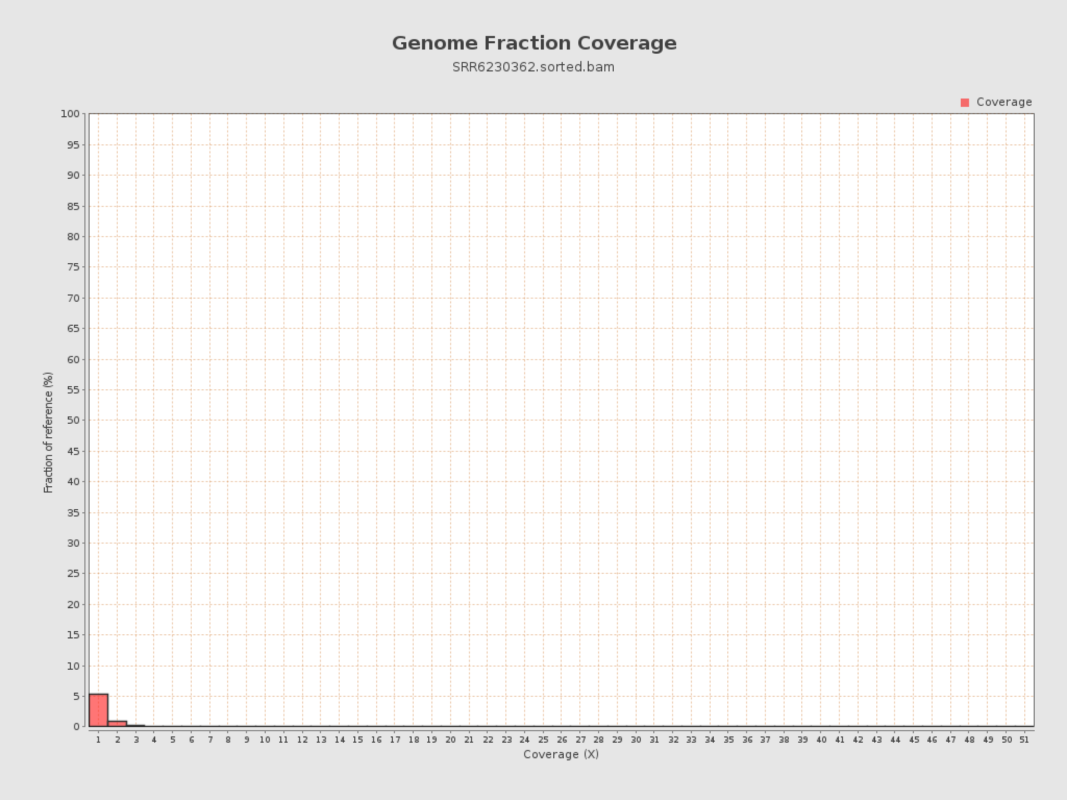
4. Results : Coverage Histogram



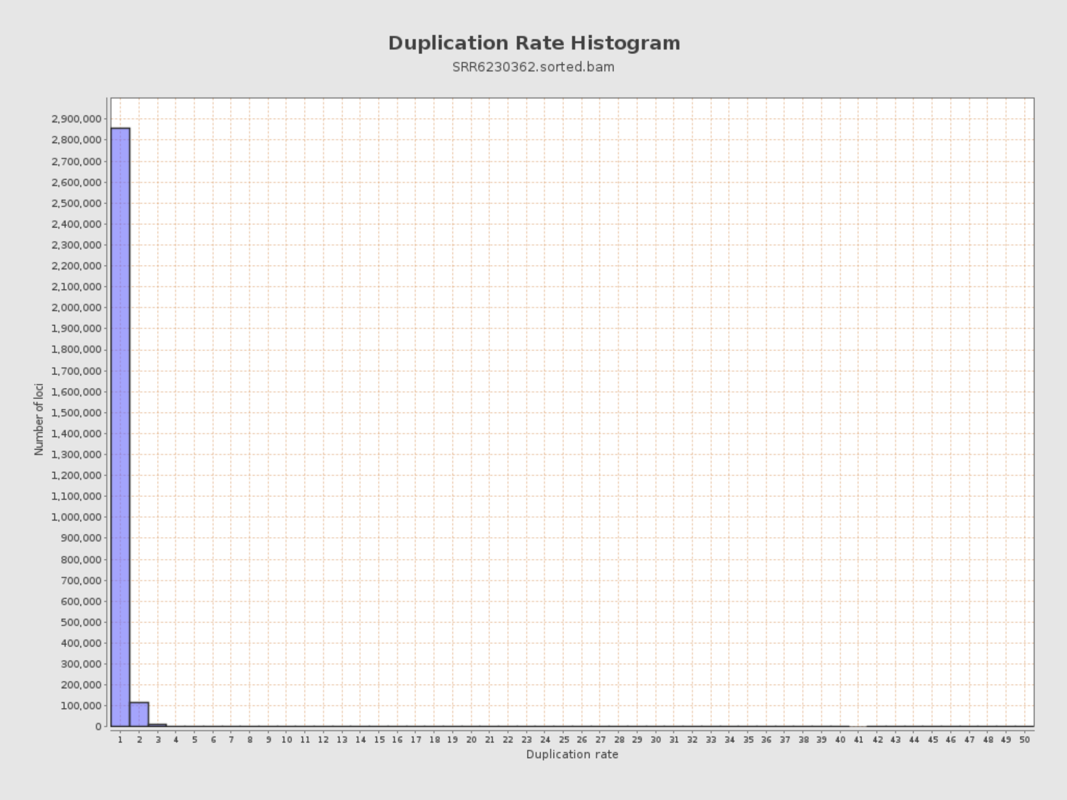
5. Results : Coverage Histogram (0-50X)



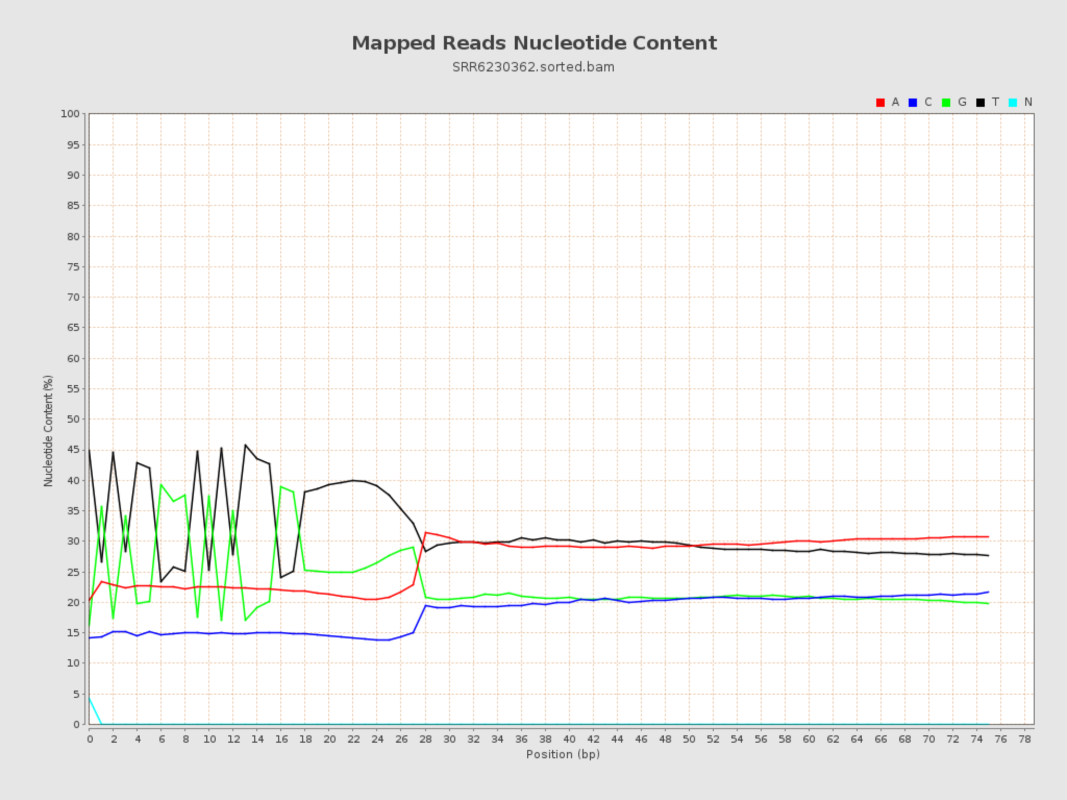
6. Results : Genome Fraction Coverage



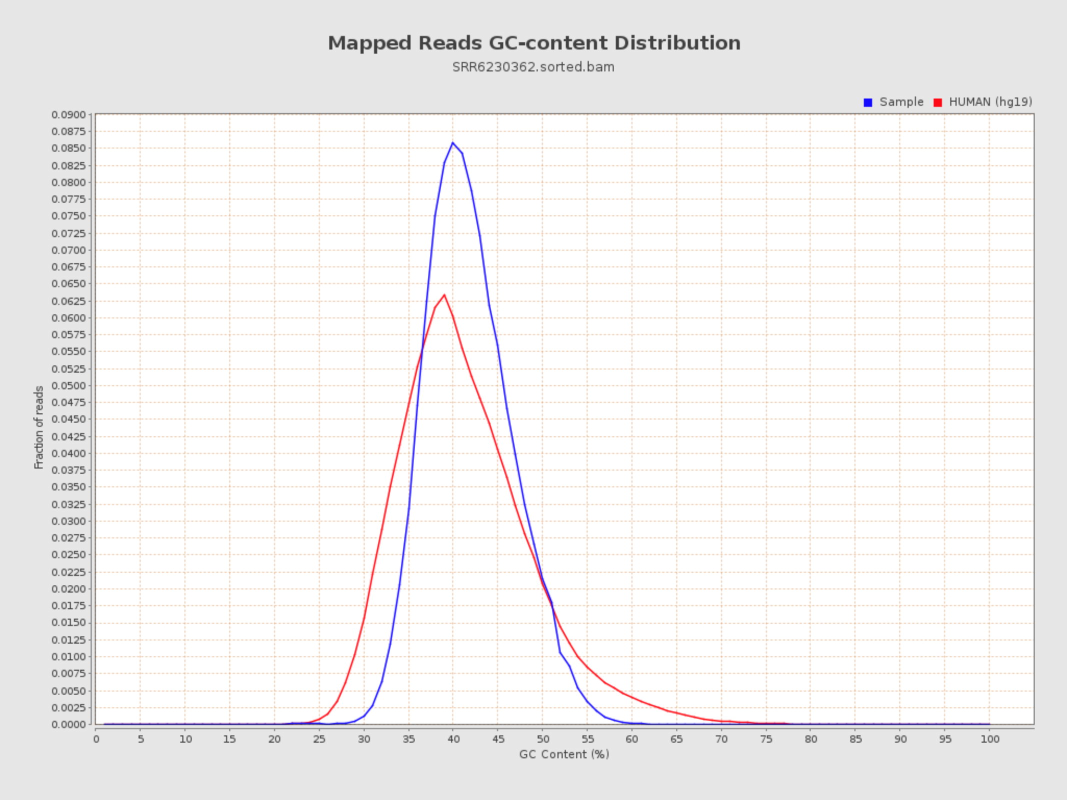
7. Results : Duplication Rate Histogram



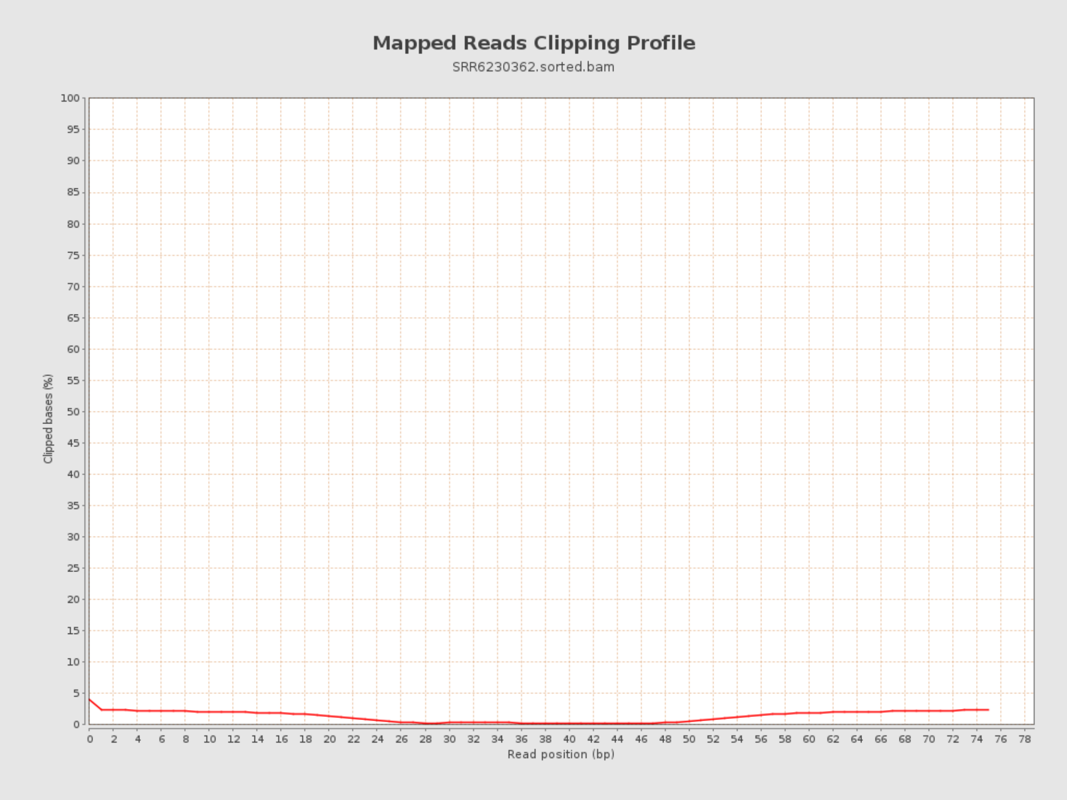
8. Results : Mapped Reads Nucleotide Content



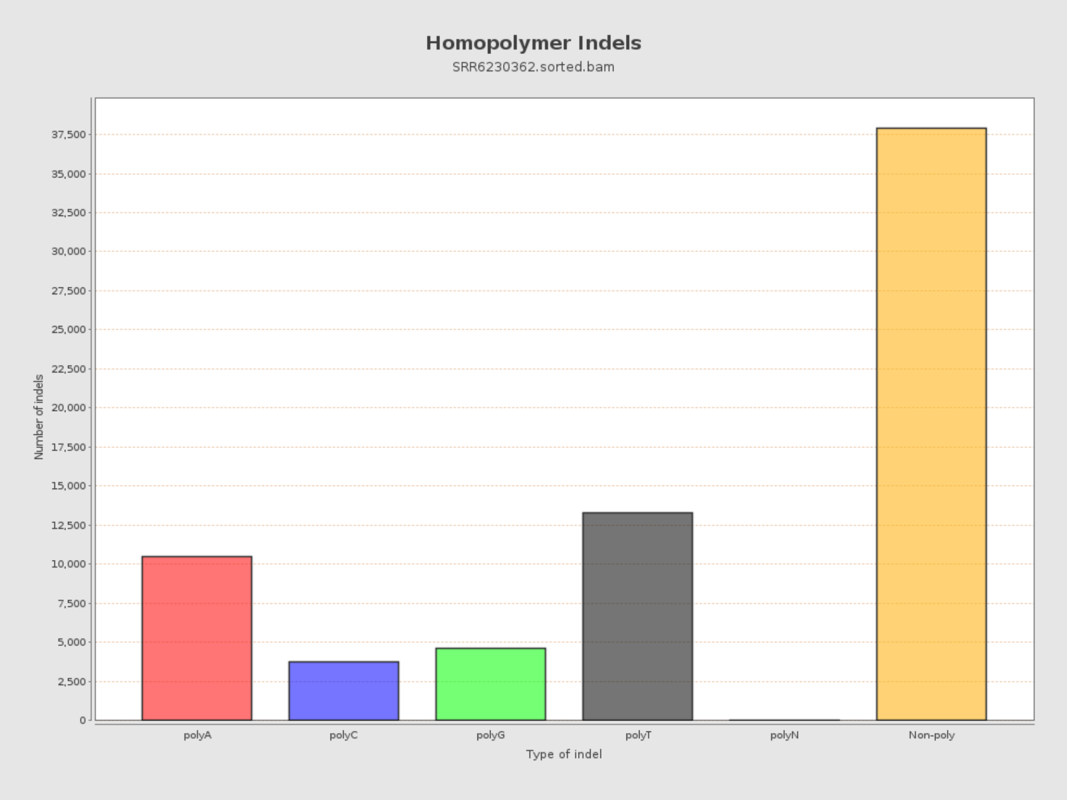
9. Results : Mapped Reads GC-content Distribution



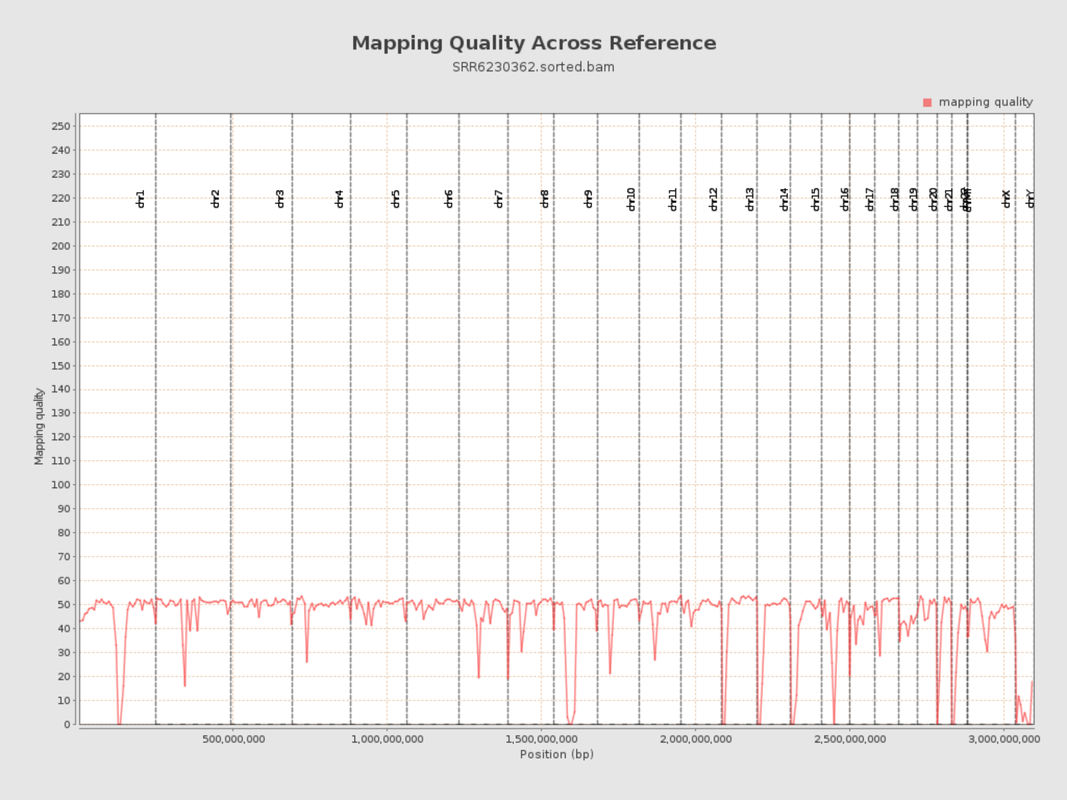
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram