Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:37:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230365.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_SRR6230365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230365.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:37:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,182,883
Mapped reads	2,039,500 / 93.43%
Unmapped reads	143,383 / 6.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,427 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	66,327 / 3.04%
Duplication rate	2.11%
Clipped reads	530,724 / 24.31%

2.2. ACGT Content

Number/percentage of A's	43,789,037 / 29.95%
Number/percentage of C's	29,271,939 / 20.02%
Number/percentage of T's	42,912,173 / 29.35%
Number/percentage of G's	30,173,715 / 20.63%
Number/percentage of N's	80,871 / 0.06%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.5756

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

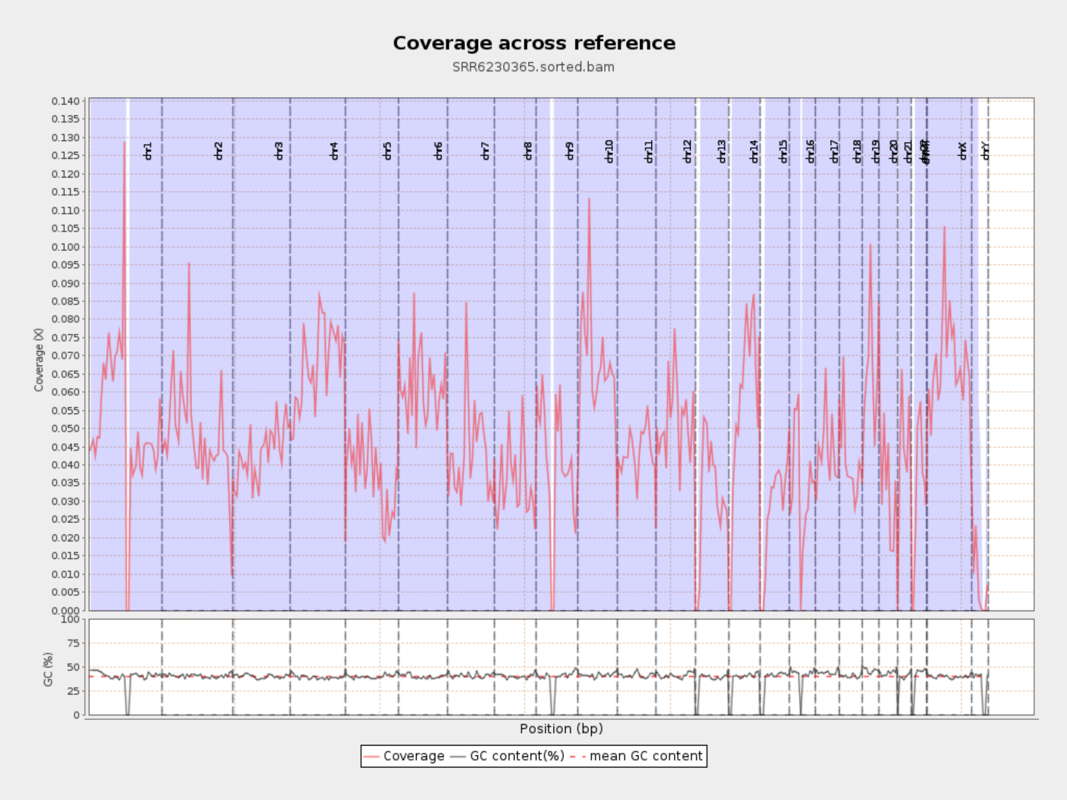
General error rate	0.95%
Mismatches	1,359,170
Insertions	13,153
Mapped reads with at least one insertion	0.64%
Deletions	45,813
Mapped reads with at least one deletion	2.22%
Homopolymer indels	45.22%

2.6. Chromosome stats

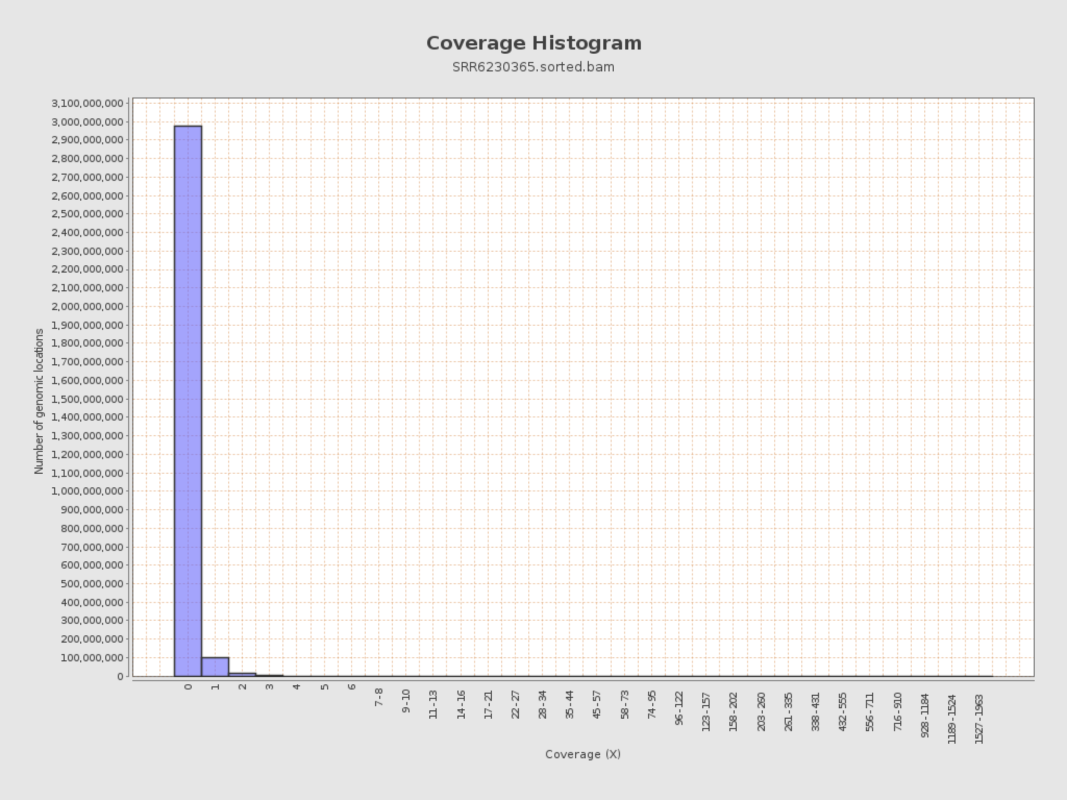
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12895518	0.0517	1.5258
chr2	243199373	11780971	0.0484	0.4591
chr3	198022430	8537886	0.0431	0.2572
chr4	191154276	12920723	0.0676	0.3342
chr5	180915260	6750105	0.0373	0.2292
chr6	171115067	10485016	0.0613	0.3591
chr7	159138663	6986722	0.0439	0.5421

chr8	146364022	5171312	0.0353	0.3538
chr9	141213431	5600586	0.0397	0.4182
chr10	135534747	9272383	0.0684	0.5932
chr11	135006516	5853716	0.0434	0.3818
chr12	133851895	7010306	0.0524	0.2762
chr13	115169878	3527299	0.0306	0.2023
chr14	107349540	6017535	0.0561	0.2985
chr15	102531392	2815841	0.0275	0.1906
chr16	90354753	3117813	0.0345	0.2876
chr17	81195210	3536500	0.0436	0.2654
chr18	78077248	3214857	0.0412	0.878
chr19	59128983	3911131	0.0661	0.7806
chr20	63025520	2181021	0.0346	0.2329
chr21	48129895	2083155	0.0433	0.2737
chr22	51304566	1615368	0.0315	0.2062
chrMT	16571	642	0.0387	0.2123
chrX	155270560	10554099	0.068	0.3684
chrY	59373566	466178	0.0079	0.2012

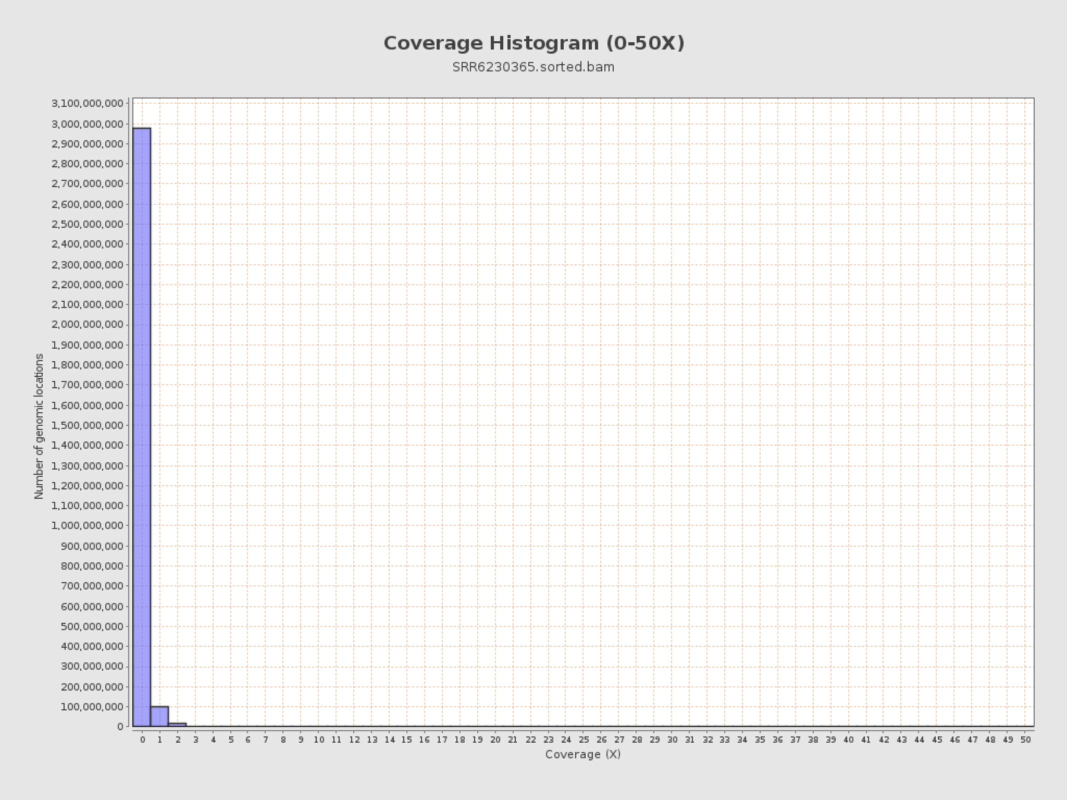
3. Results : Coverage across reference



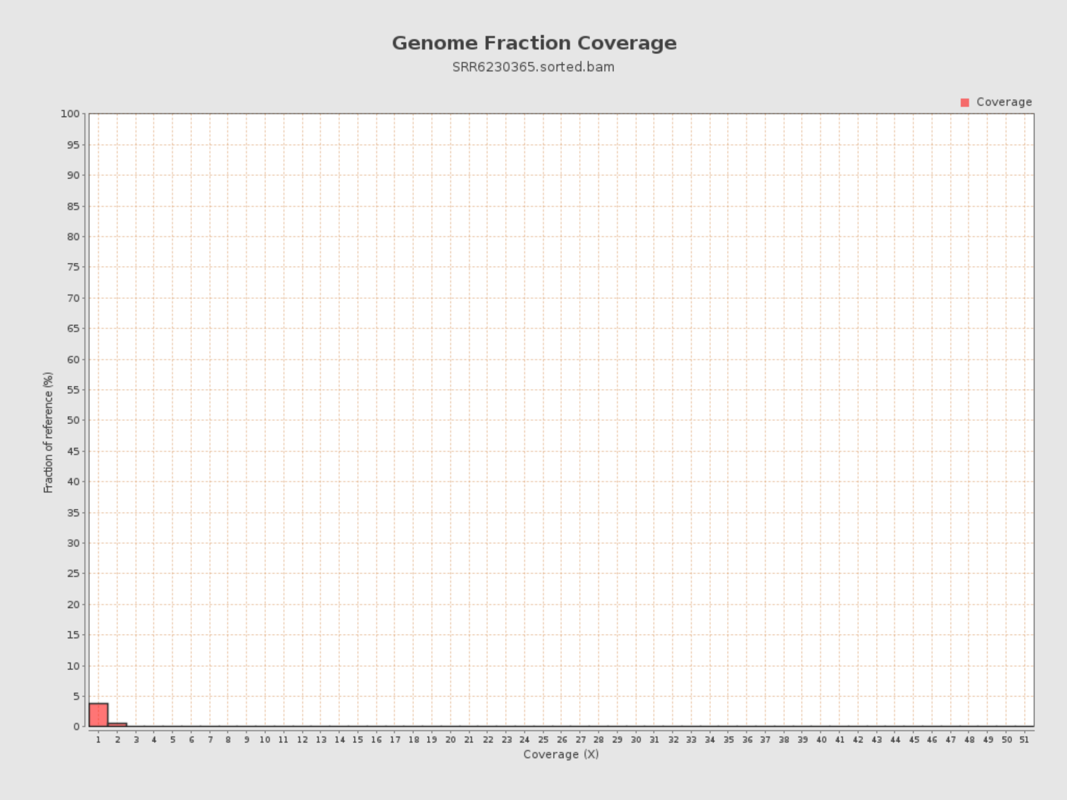
4. Results : Coverage Histogram



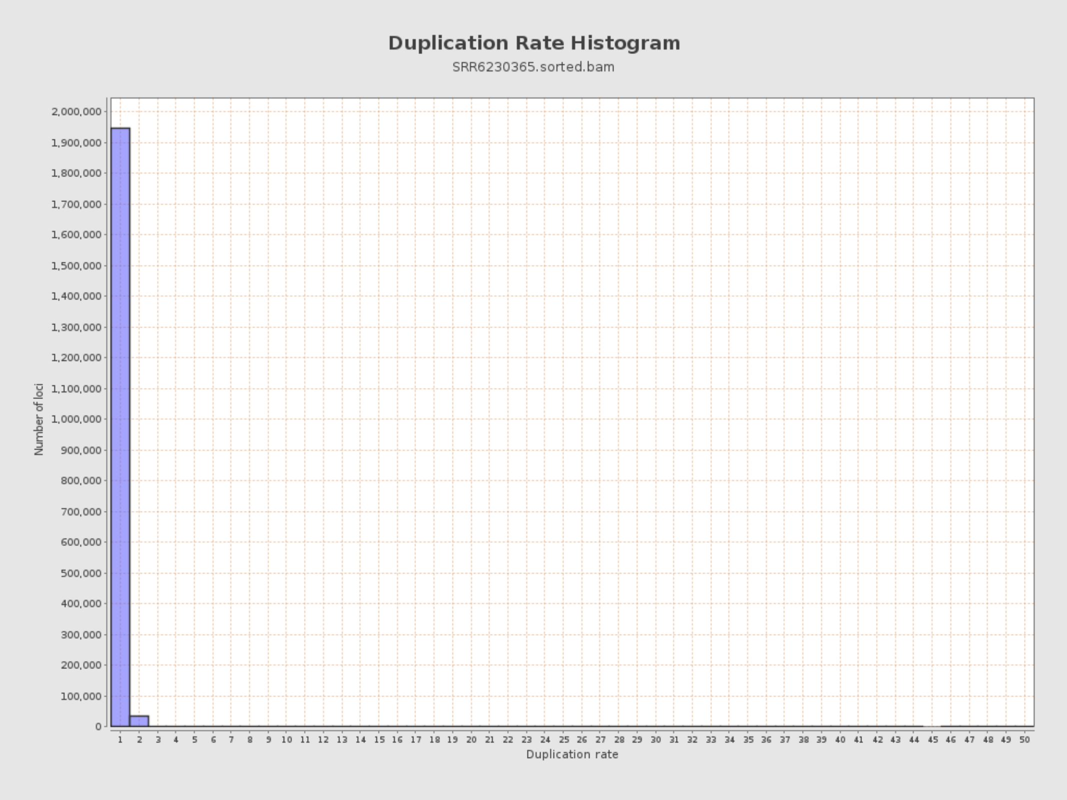
5. Results : Coverage Histogram (0-50X)



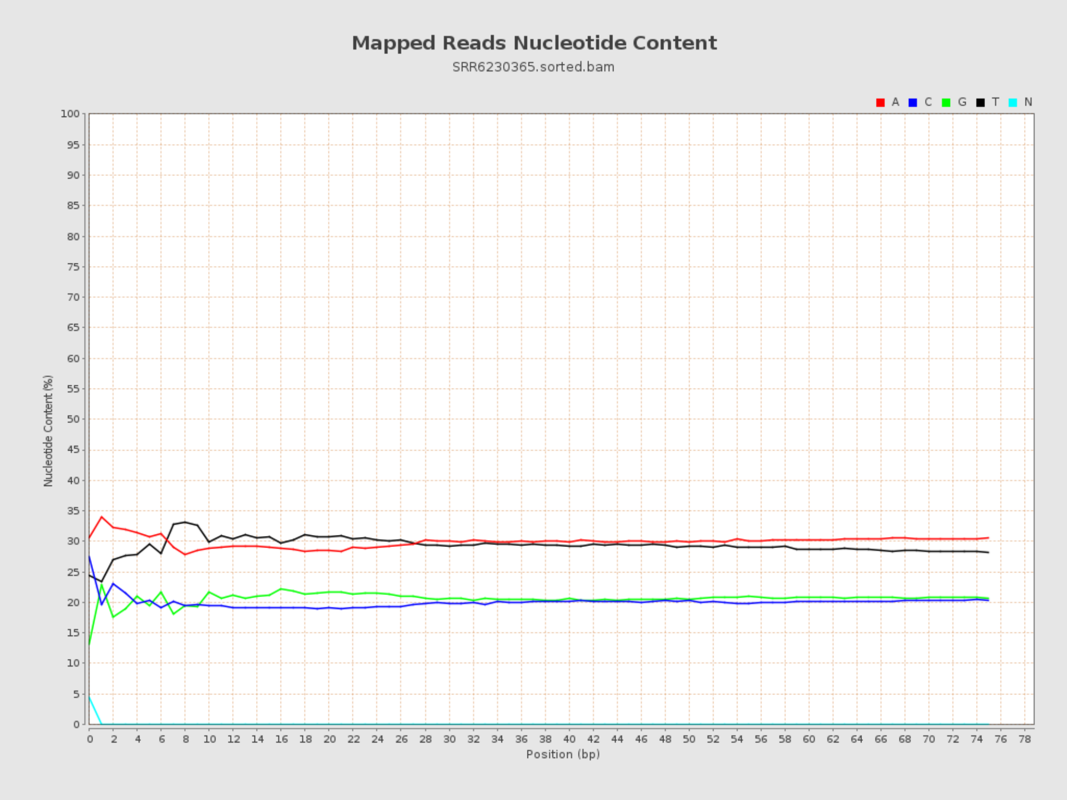
6. Results : Genome Fraction Coverage



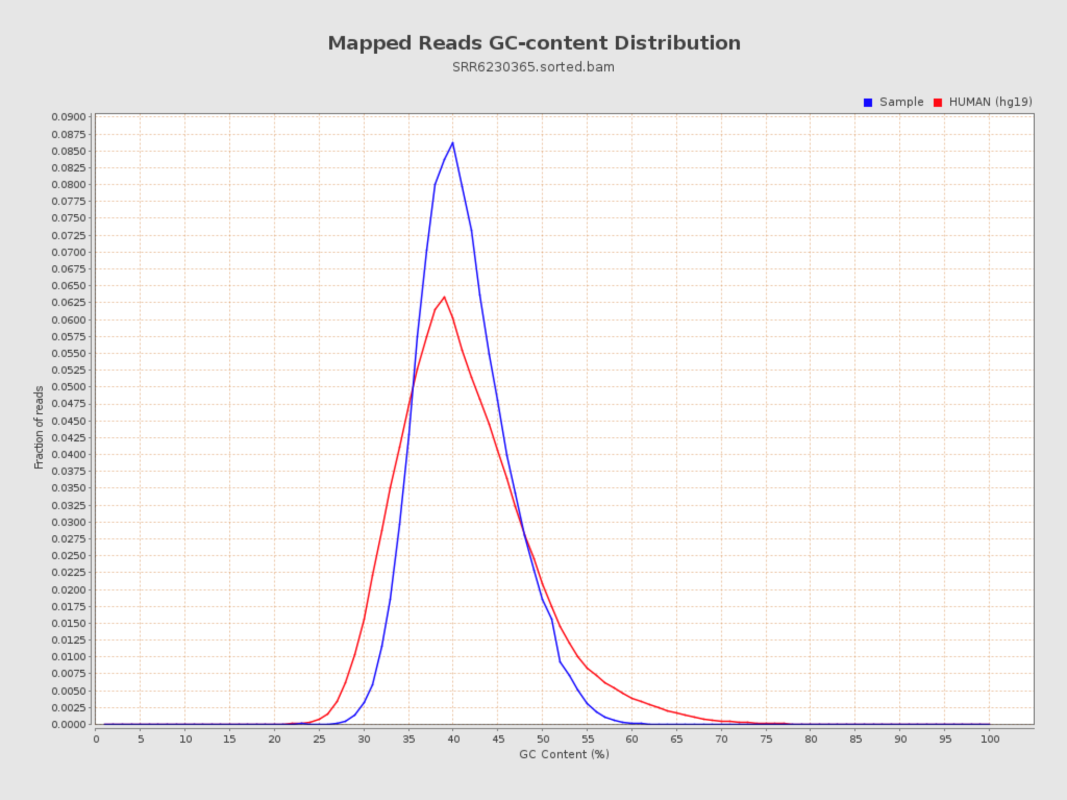
7. Results : Duplication Rate Histogram



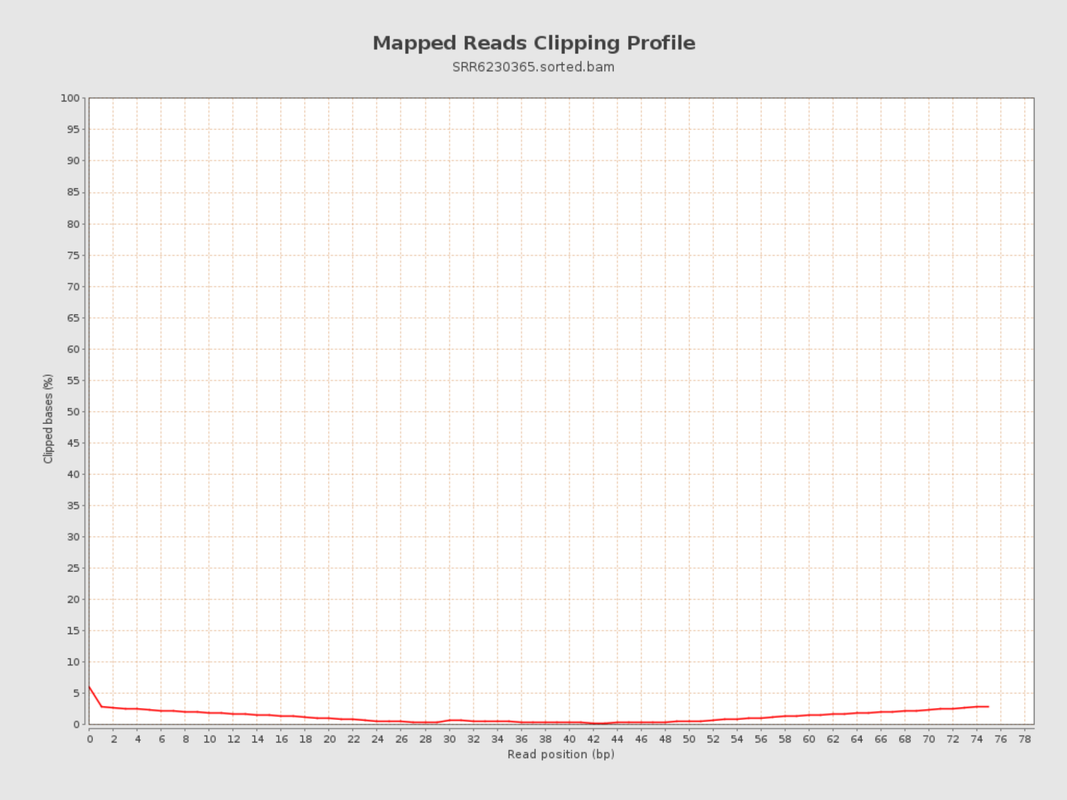
8. Results : Mapped Reads Nucleotide Content



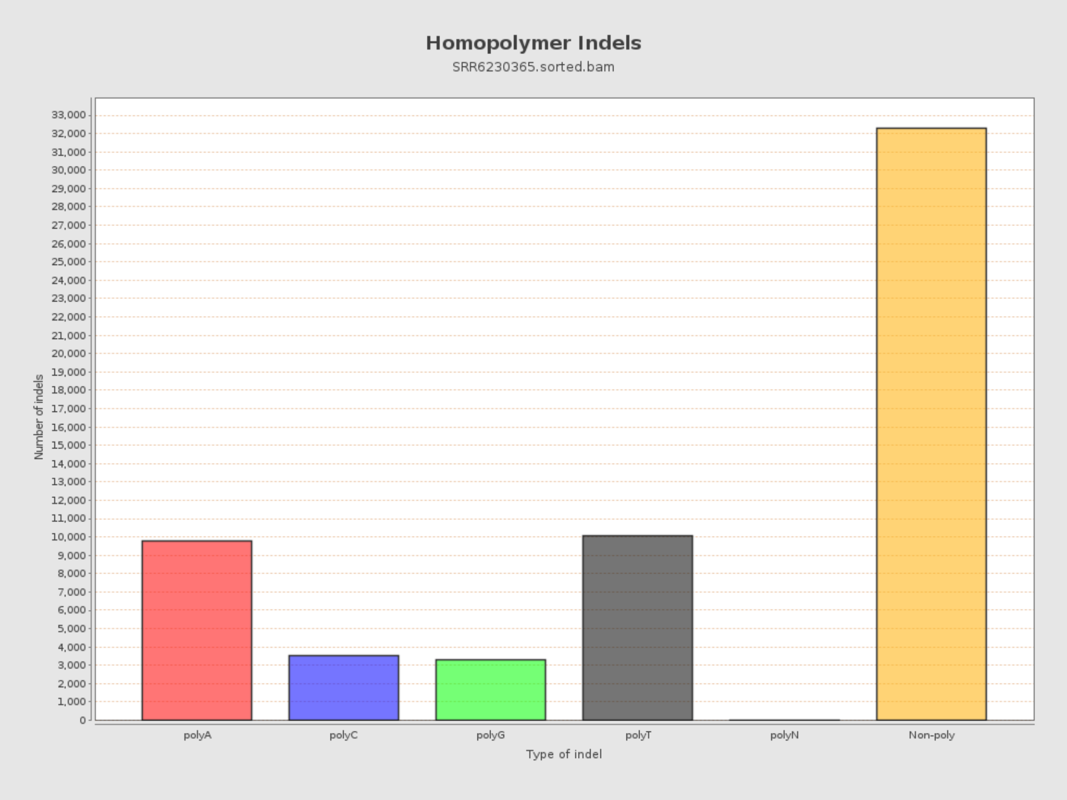
9. Results : Mapped Reads GC-content Distribution



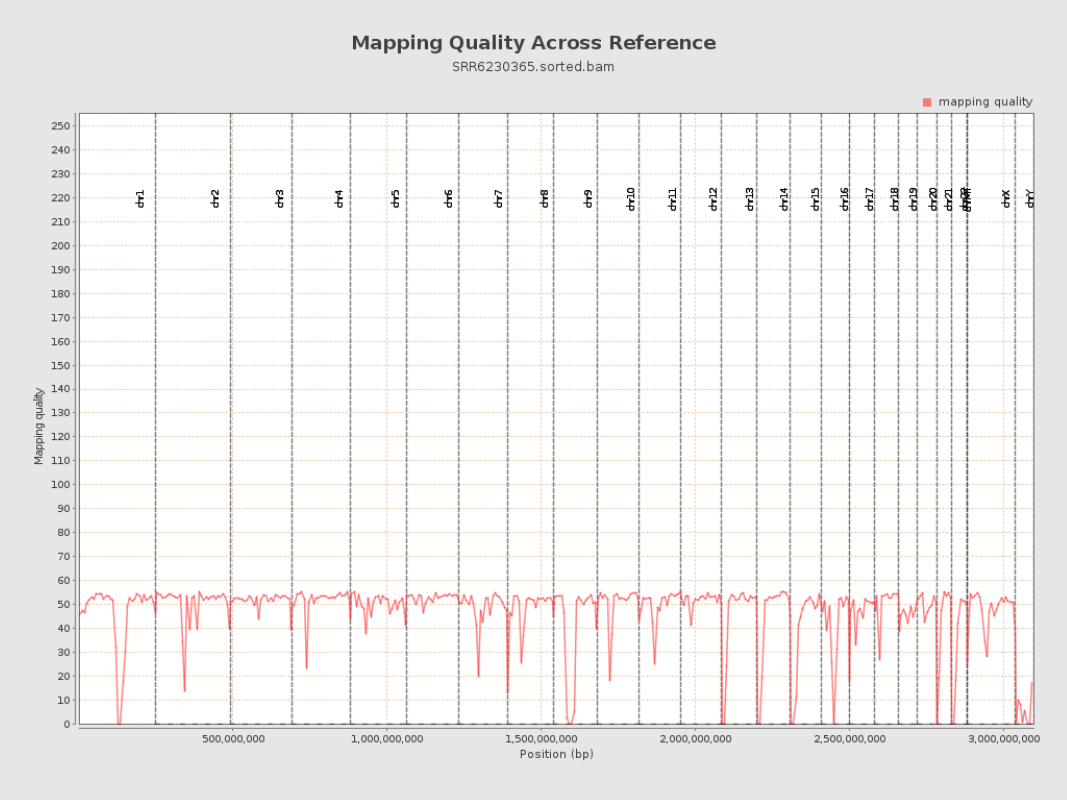
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram