Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:04:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230389.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_SRR6230389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230389.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:04:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,330,595
Mapped reads	1,314,375 / 56.4%
Unmapped reads	1,016,220 / 43.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,198 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	110,287 / 4.73%
Duplication rate	6.85%
Clipped reads	745,977 / 32.01%

2.2. ACGT Content

Number/percentage of A's	22,083,156 / 26.39%
Number/percentage of C's	14,382,843 / 17.19%
Number/percentage of T's	28,139,563 / 33.63%
Number/percentage of G's	18,929,786 / 22.62%
Number/percentage of N's	135,480 / 0.16%
GC Percentage	39.81%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2741

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

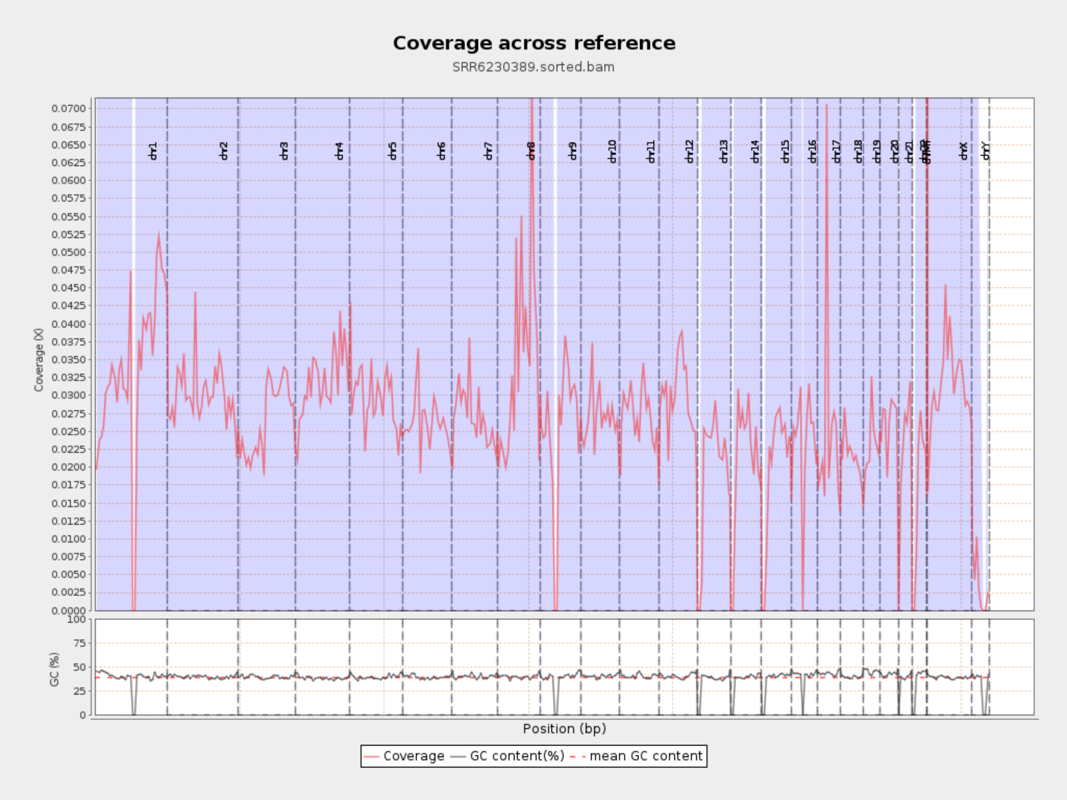
General error rate	1.19%
Mismatches	984,280
Insertions	7,243
Mapped reads with at least one insertion	0.55%
Deletions	27,725
Mapped reads with at least one deletion	2.08%
Homopolymer indels	49.29%

2.6. Chromosome stats

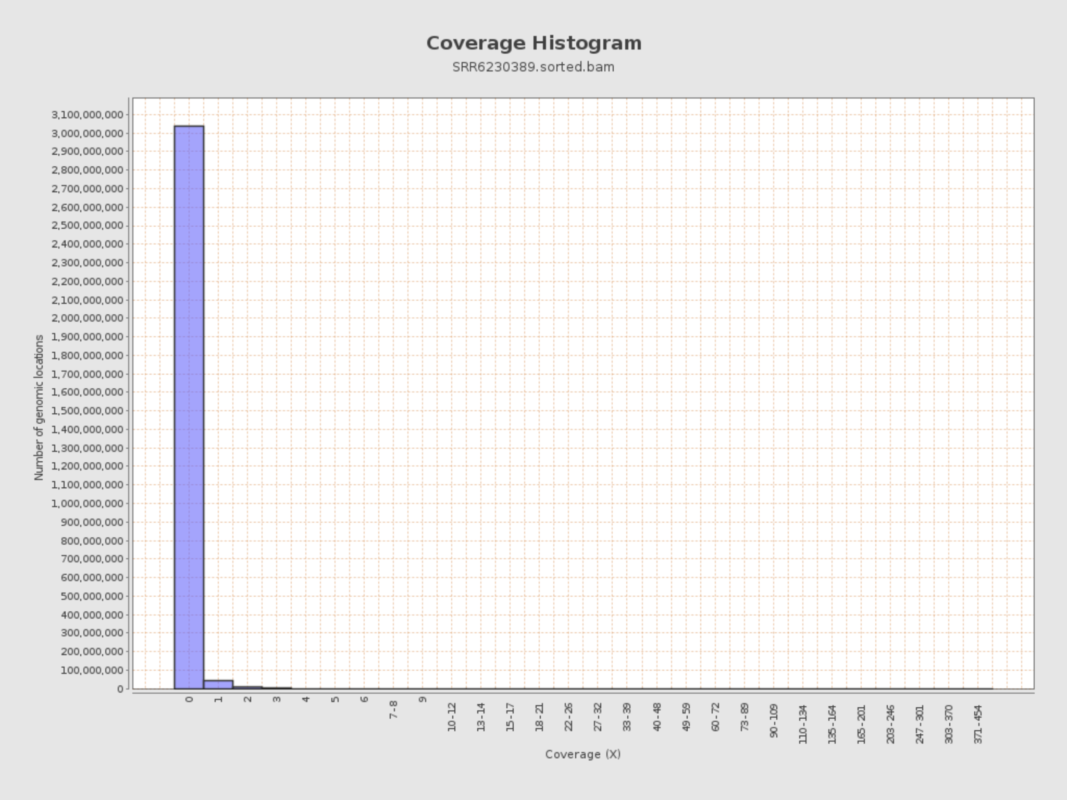
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8338711	0.0335	0.4314
chr2	243199373	7354152	0.0302	0.2892
chr3	198022430	5281485	0.0267	0.2181
chr4	191154276	6077435	0.0318	0.2466
chr5	180915260	5322448	0.0294	0.2323
chr6	171115067	4504574	0.0263	0.2477
chr7	159138663	4305396	0.0271	0.3093

chr8	146364022	5097372	0.0348	0.3537
chr9	141213431	3550430	0.0251	0.2632
chr10	135534747	3640322	0.0269	0.2567
chr11	135006516	3706563	0.0275	0.2659
chr12	133851895	4034354	0.0301	0.2359
chr13	115169878	2246664	0.0195	0.1876
chr14	107349540	2225157	0.0207	0.2014
chr15	102531392	2039100	0.0199	0.1898
chr16	90354753	2084318	0.0231	0.2105
chr17	81195210	2054898	0.0253	0.2269
chr18	78077248	1698902	0.0218	0.3878
chr19	59128983	1362812	0.023	0.2999
chr20	63025520	1638534	0.026	0.2201
chr21	48129895	1079825	0.0224	0.2118
chr22	51304566	842500	0.0164	0.1665
chrMT	16571	97070	5.8578	4.7731
chrX	155270560	4927592	0.0317	0.2509
chrY	59373566	204432	0.0034	0.0857

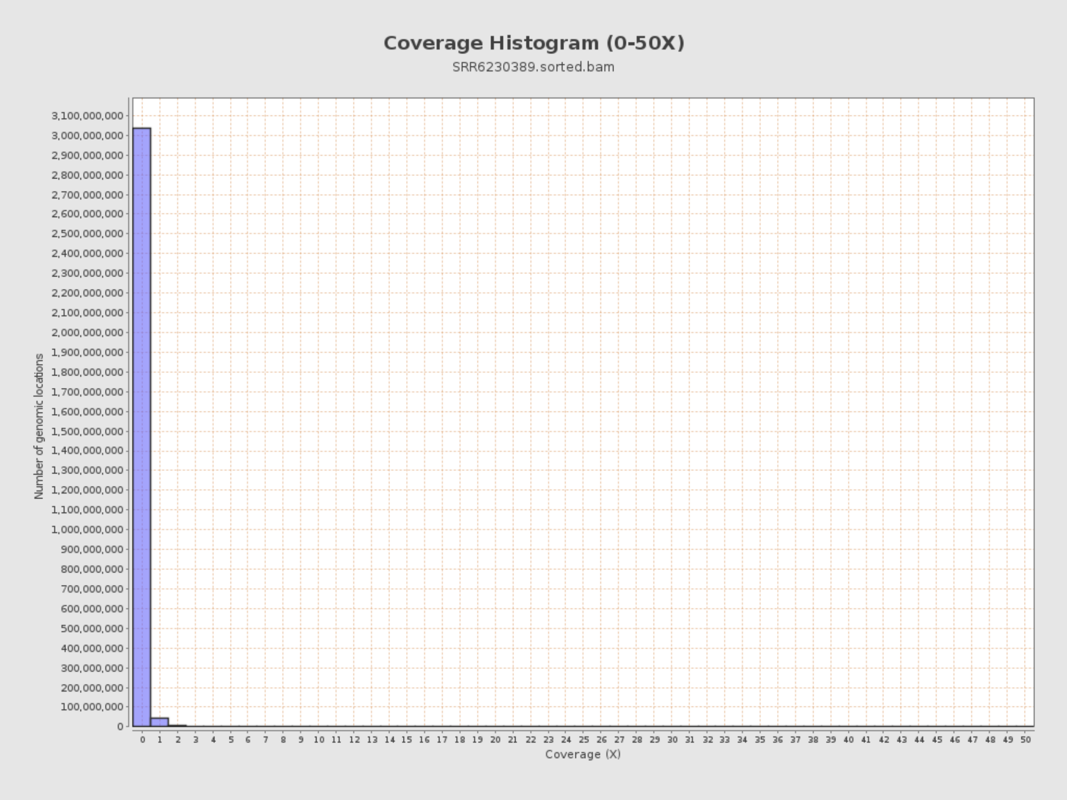
3. Results : Coverage across reference



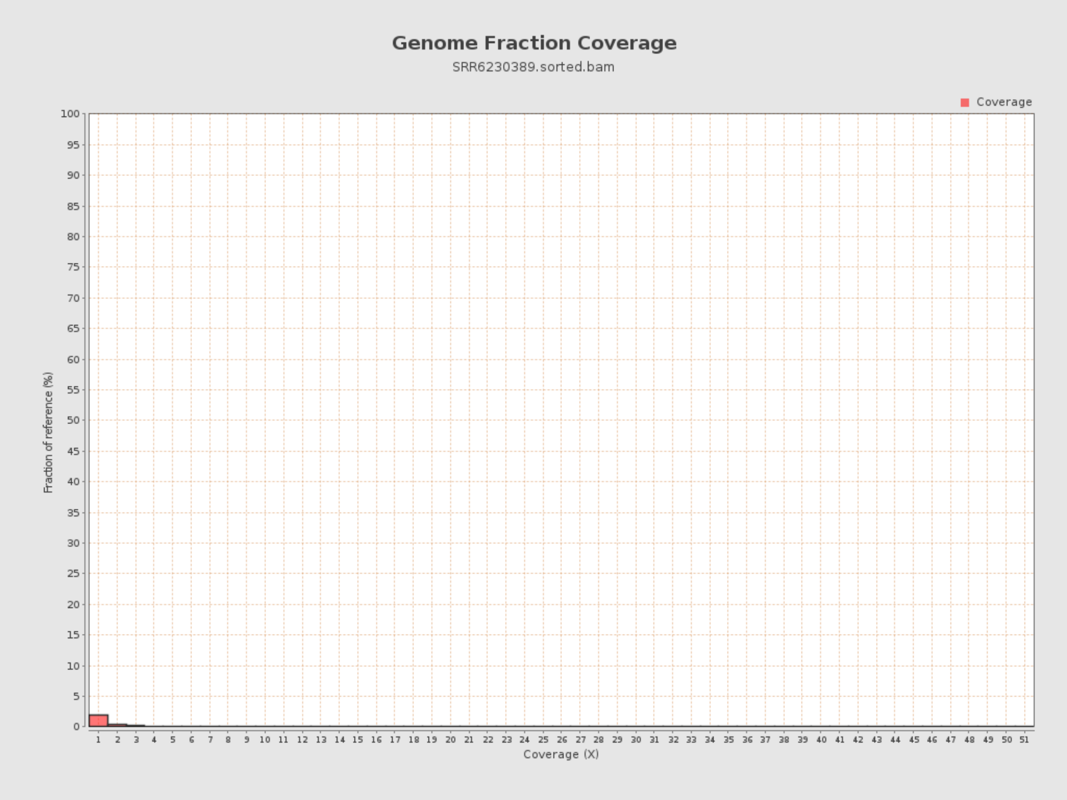
4. Results : Coverage Histogram



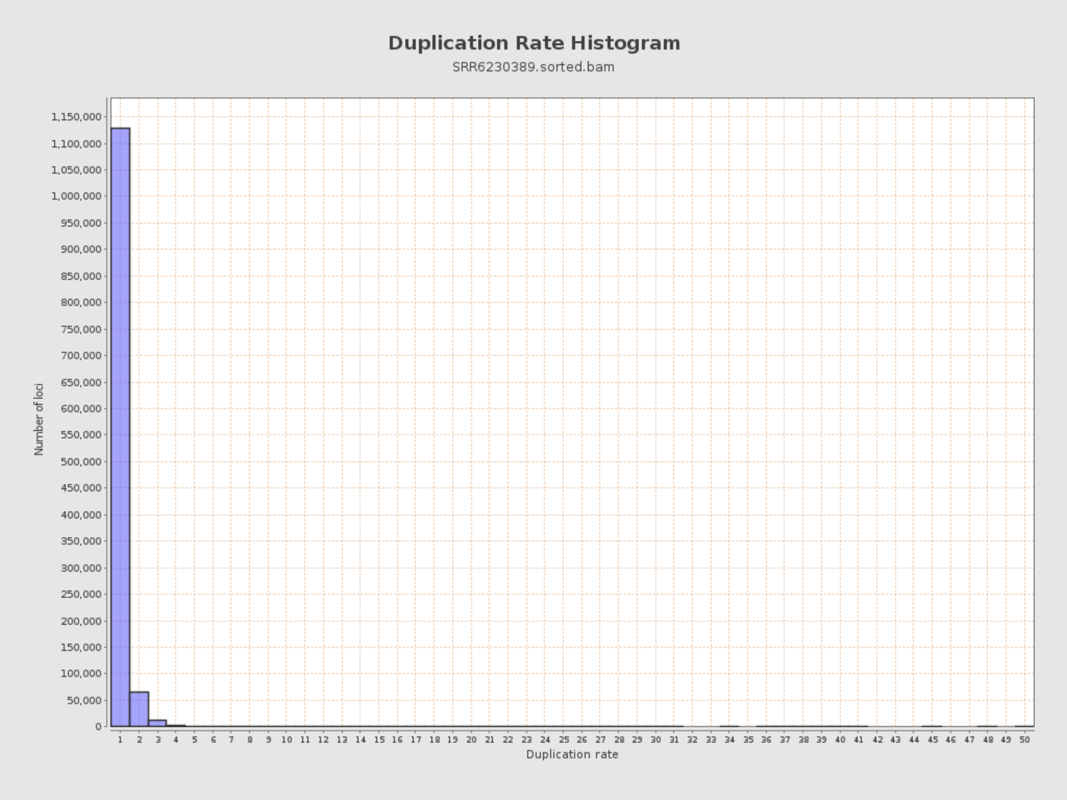
5. Results : Coverage Histogram (0-50X)



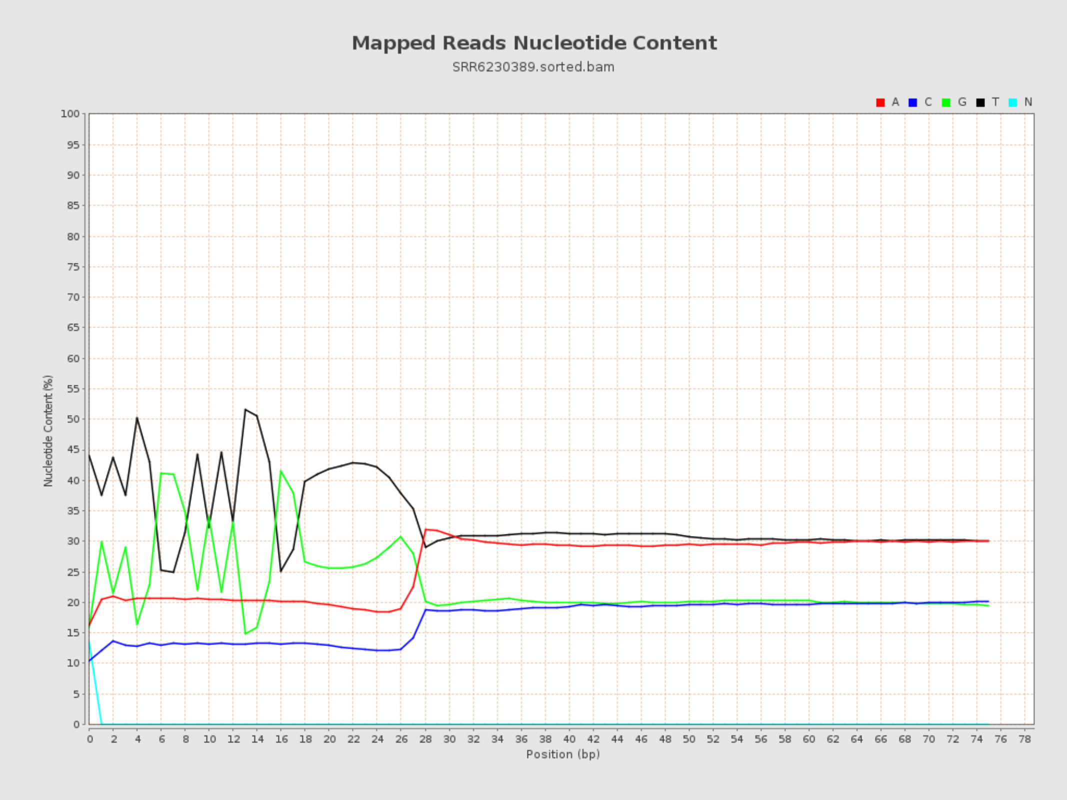
6. Results : Genome Fraction Coverage



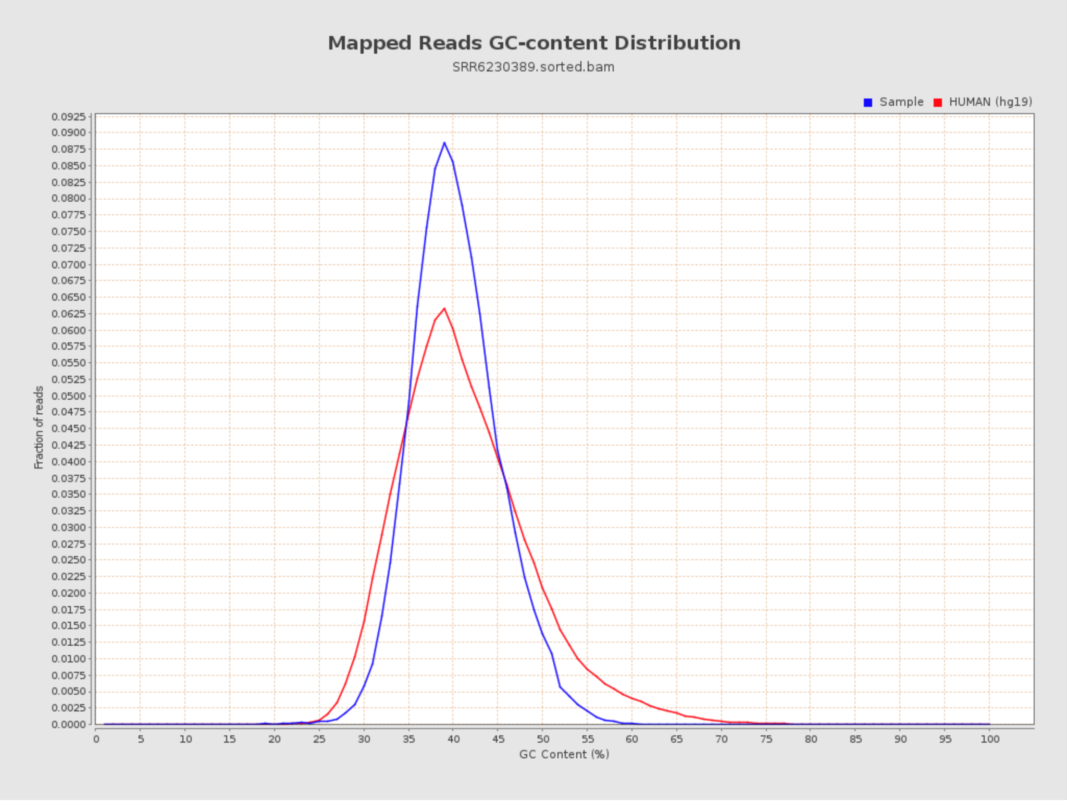
7. Results : Duplication Rate Histogram



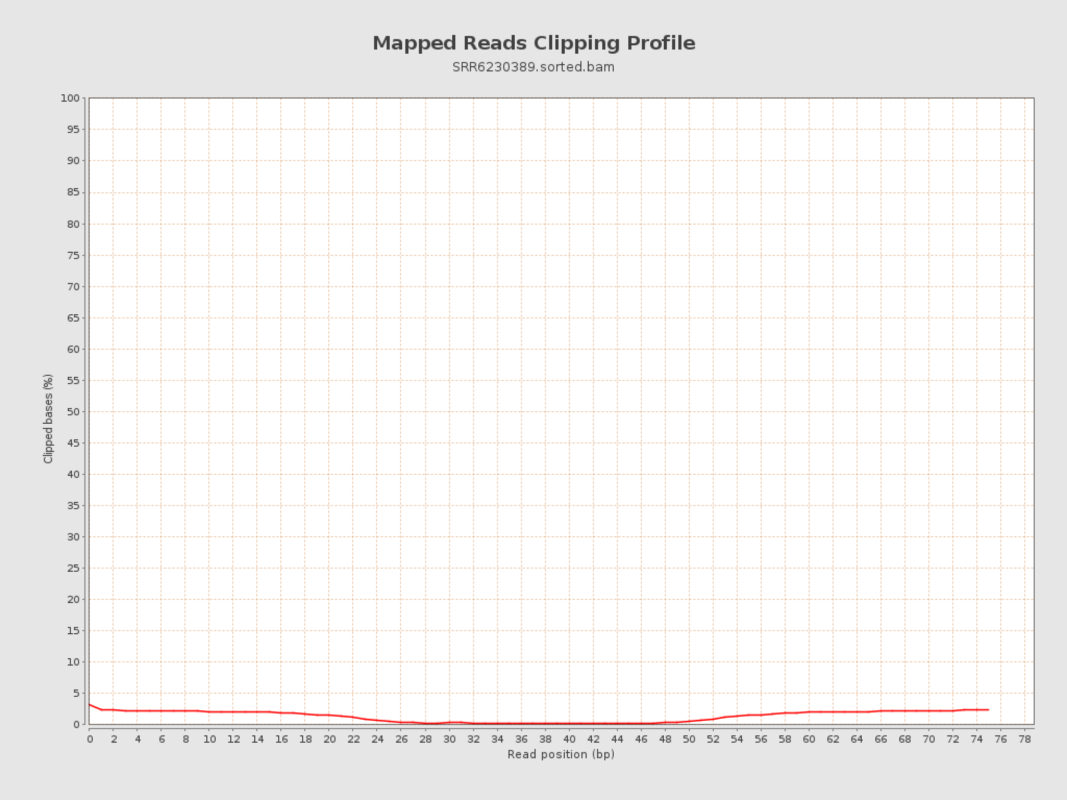
8. Results : Mapped Reads Nucleotide Content



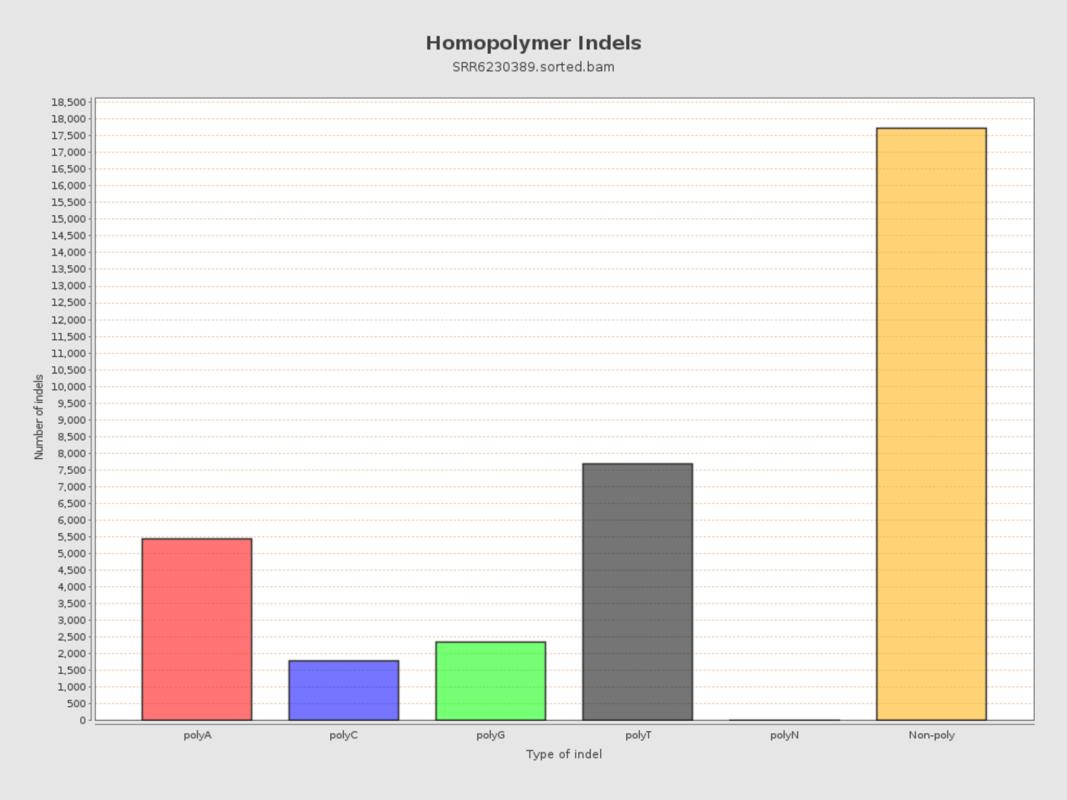
9. Results : Mapped Reads GC-content Distribution



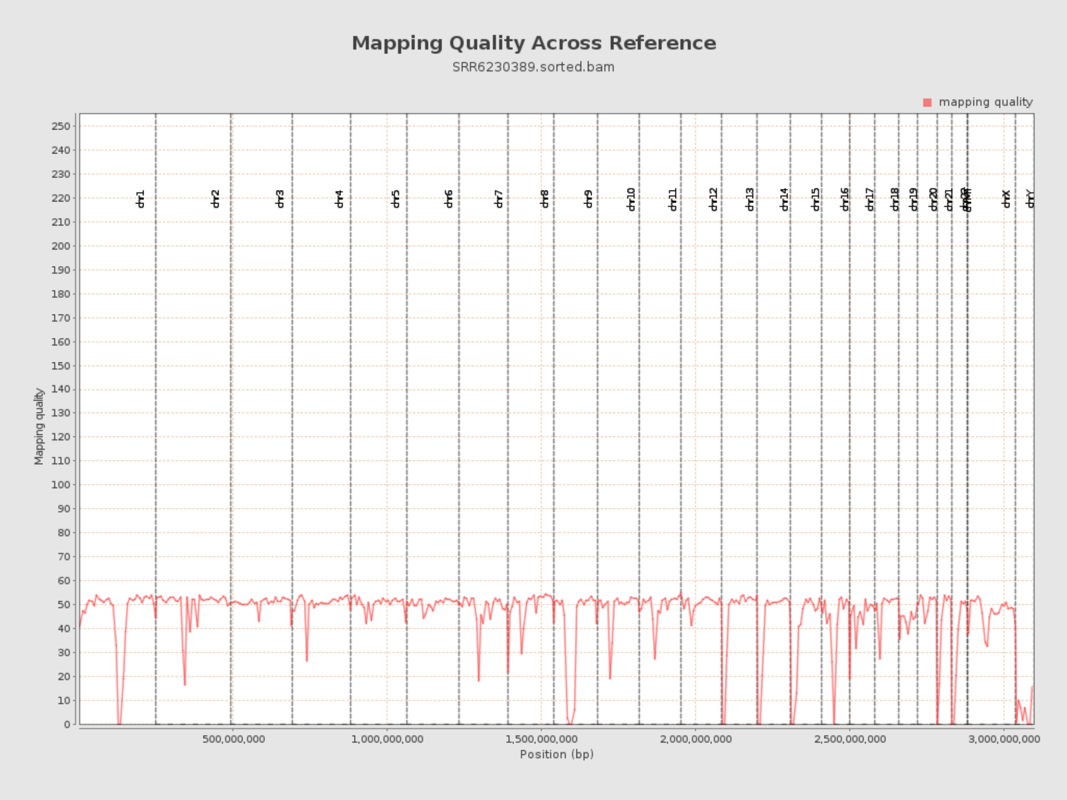
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram