Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:06:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230372.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_SRR6230372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230372.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:06:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,905,754
Mapped reads	3,321,172 / 85.03%
Unmapped reads	584,582 / 14.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,061 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	383,116 / 9.81%
Duplication rate	9.1%
Clipped reads	1,061,359 / 27.17%

2.2. ACGT Content

Number/percentage of A's	68,703,792 / 29.43%
Number/percentage of C's	46,752,243 / 20.03%
Number/percentage of T's	69,001,321 / 29.56%
Number/percentage of G's	48,878,905 / 20.94%
Number/percentage of N's	127,332 / 0.05%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0755

Standard Deviation	1.1713

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

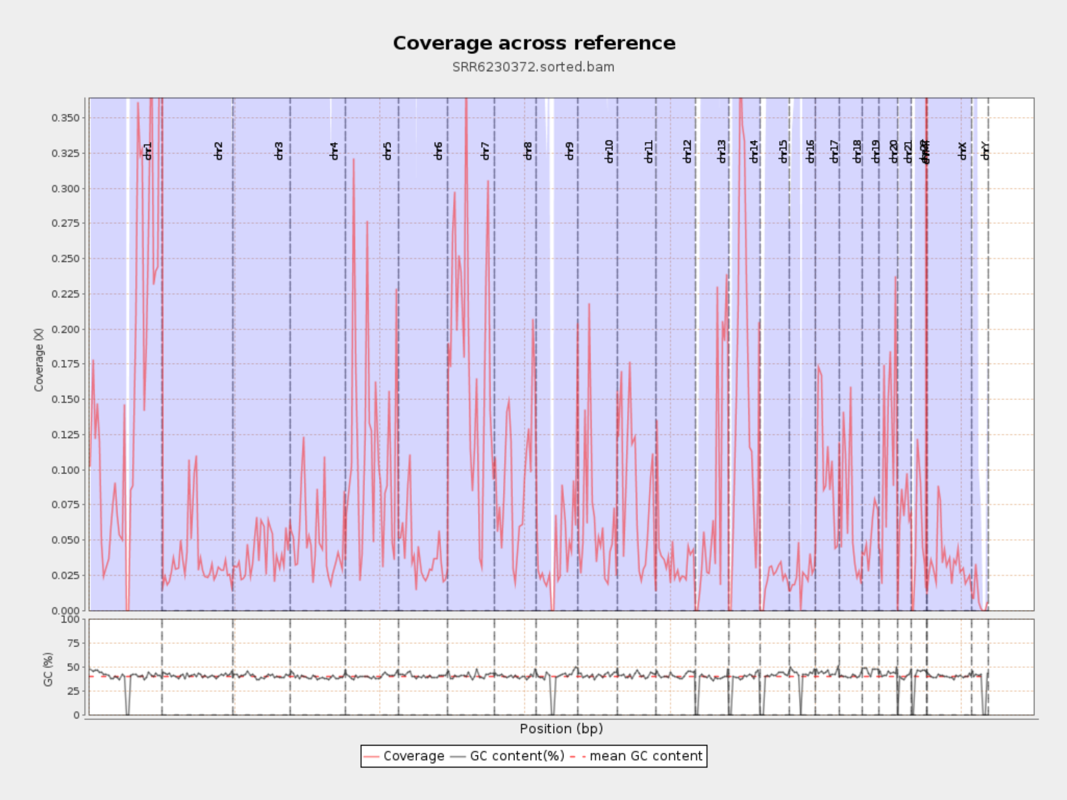
General error rate	0.88%
Mismatches	2,015,842
Insertions	19,510
Mapped reads with at least one insertion	0.58%
Deletions	63,704
Mapped reads with at least one deletion	1.9%
Homopolymer indels	46.83%

2.6. Chromosome stats

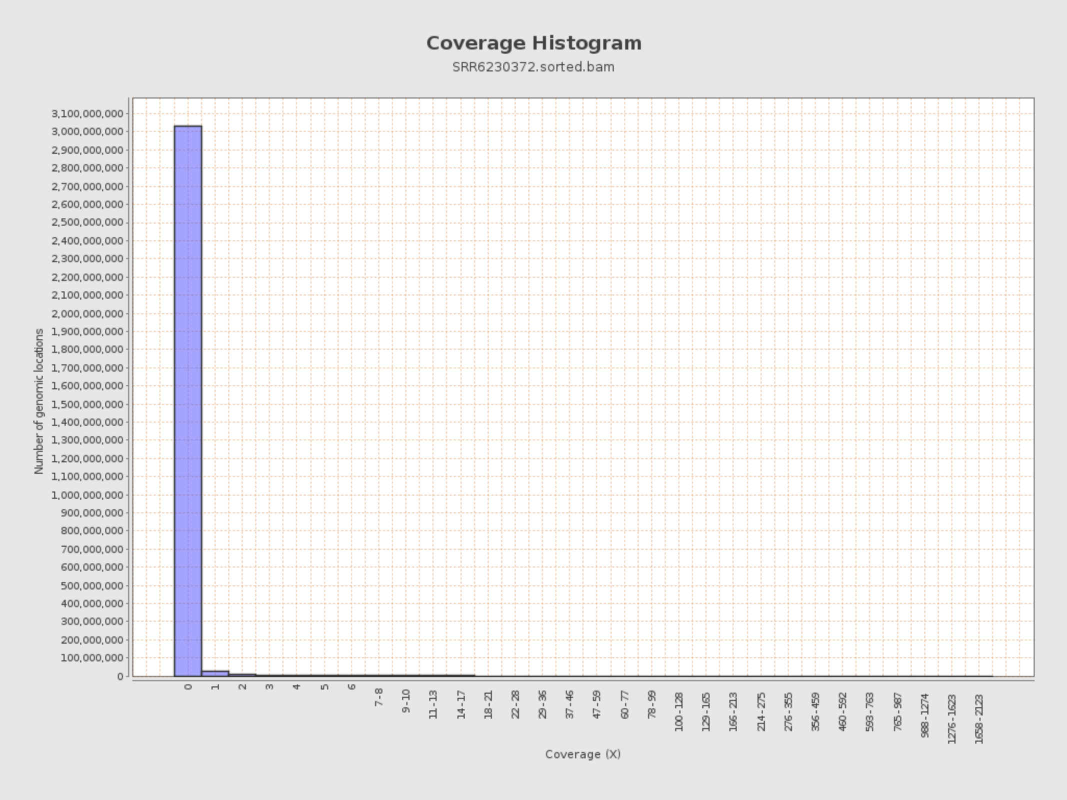
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38970212	0.1563	1.5142
chr2	243199373	8939159	0.0368	0.8246
chr3	198022430	8026797	0.0405	0.6311
chr4	191154276	9673688	0.0506	0.6421
chr5	180915260	20914754	0.1156	1.0061
chr6	171115067	6915289	0.0404	0.601
chr7	159138663	29253478	0.1838	3.3876

chr8	146364022	13706936	0.0936	0.9986
chr9	141213431	5510003	0.039	0.7245
chr10	135534747	8454965	0.0624	1.1759
chr11	135006516	11398346	0.0844	0.9754
chr12	133851895	5117044	0.0382	0.5667
chr13	115169878	9500839	0.0825	0.8452
chr14	107349540	16668986	0.1553	1.1783
chr15	102531392	2270092	0.0221	0.4259
chr16	90354753	2229450	0.0247	0.4707
chr17	81195210	7865376	0.0969	0.9014
chr18	78077248	5507314	0.0705	1.366
chr19	59128983	3135220	0.053	0.9003
chr20	63025520	7804760	0.1238	1.0359
chr21	48129895	3264826	0.0678	0.7459
chr22	51304566	2542447	0.0496	0.6155
chrMT	16571	35151	2.1212	3.7344
chrX	155270560	5397433	0.0348	0.5503
chrY	59373566	468710	0.0079	0.2693

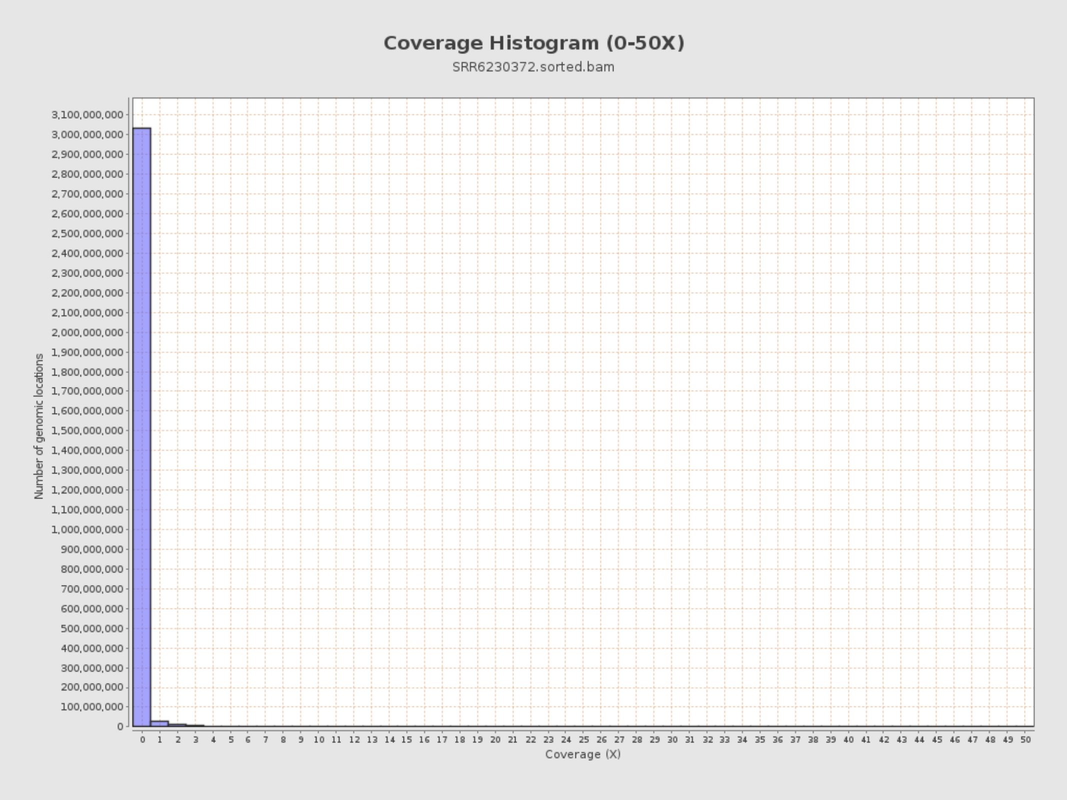
3. Results : Coverage across reference



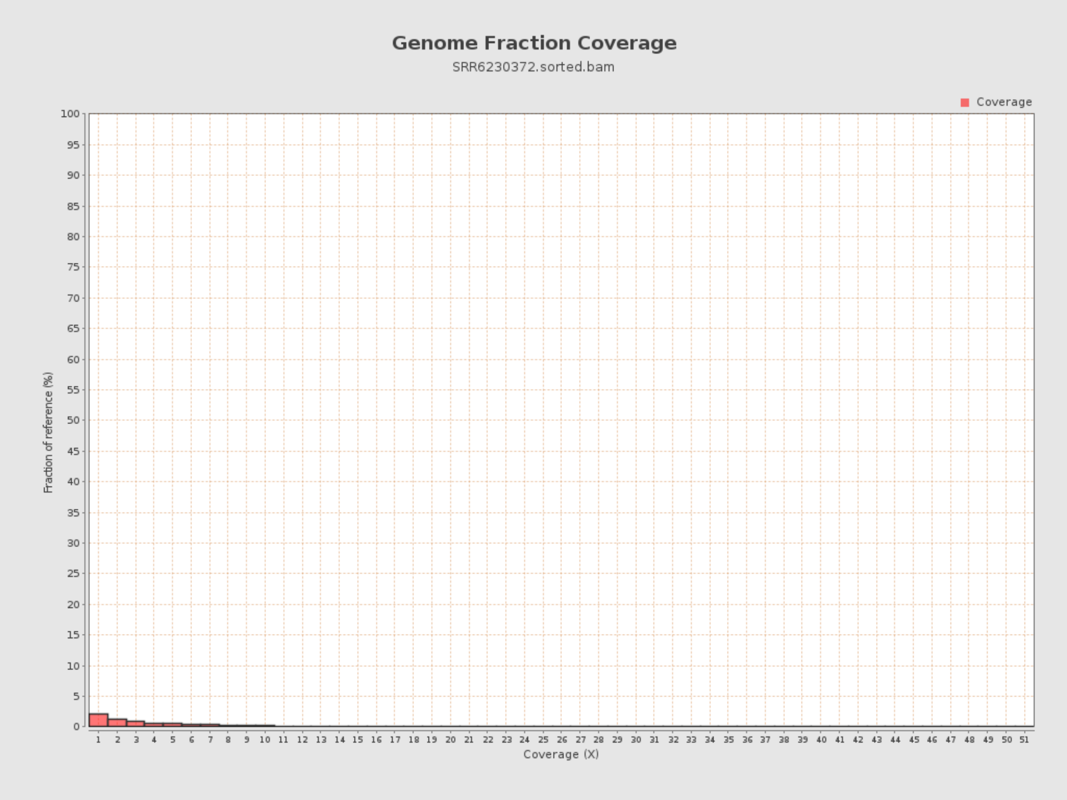
4. Results : Coverage Histogram



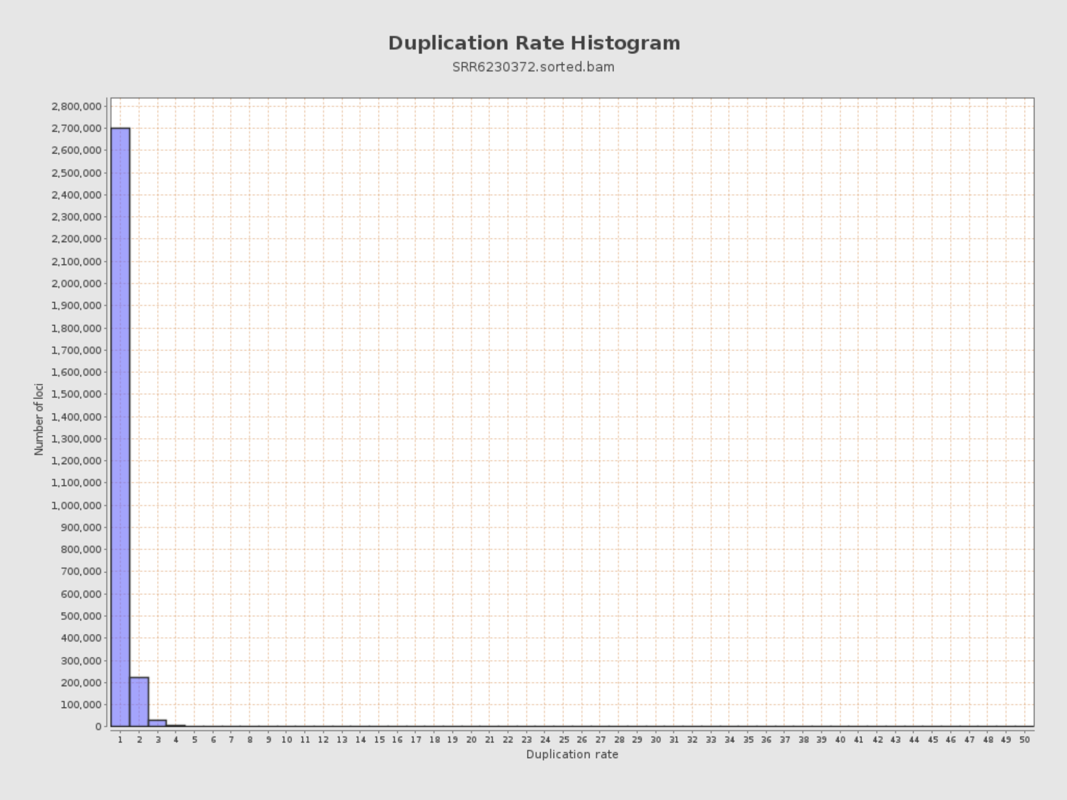
5. Results : Coverage Histogram (0-50X)



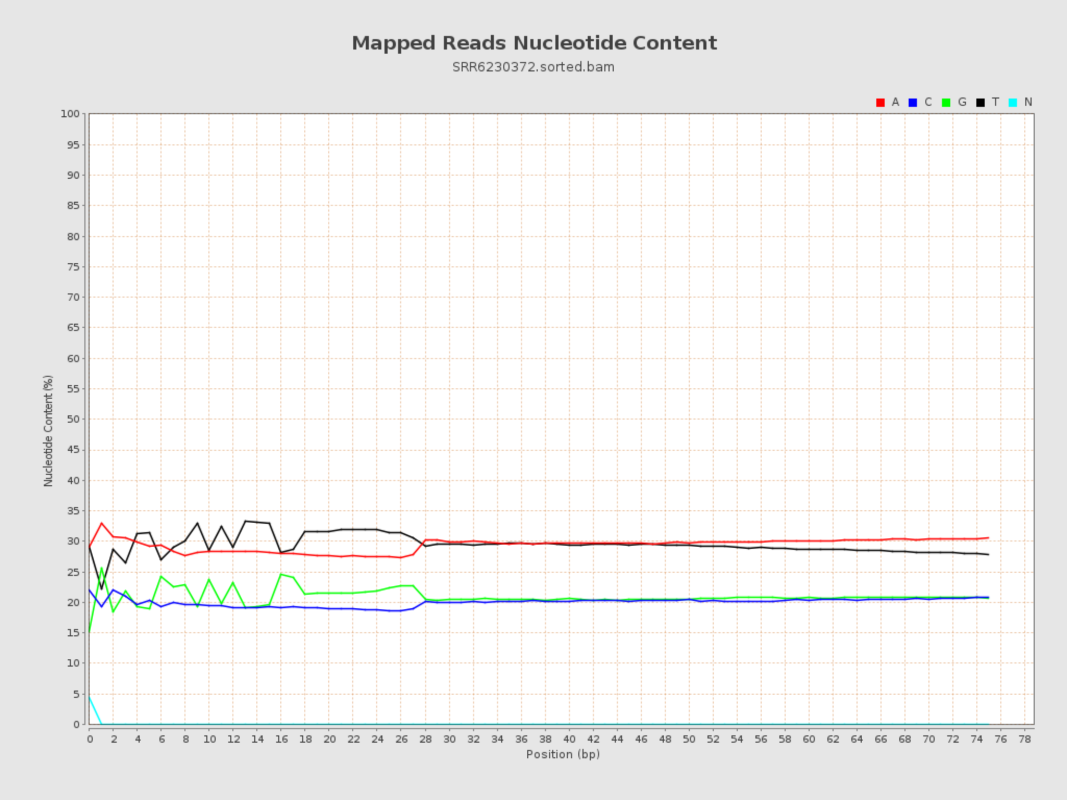
6. Results : Genome Fraction Coverage



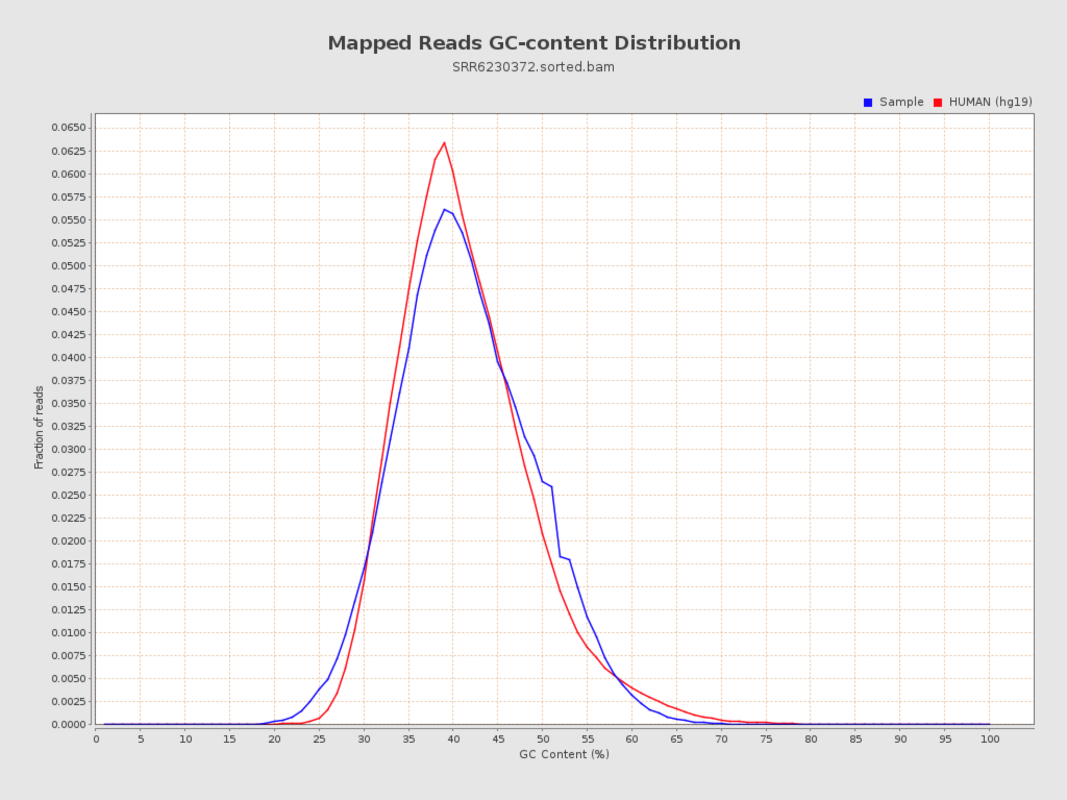
7. Results : Duplication Rate Histogram



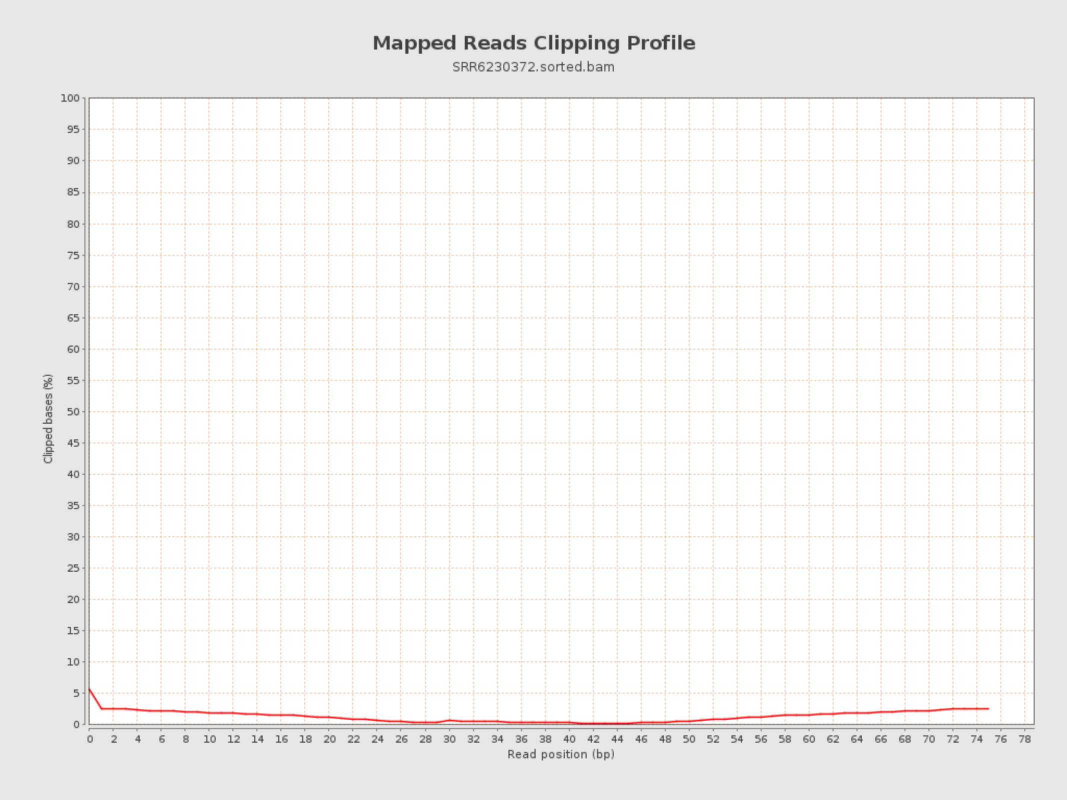
8. Results : Mapped Reads Nucleotide Content



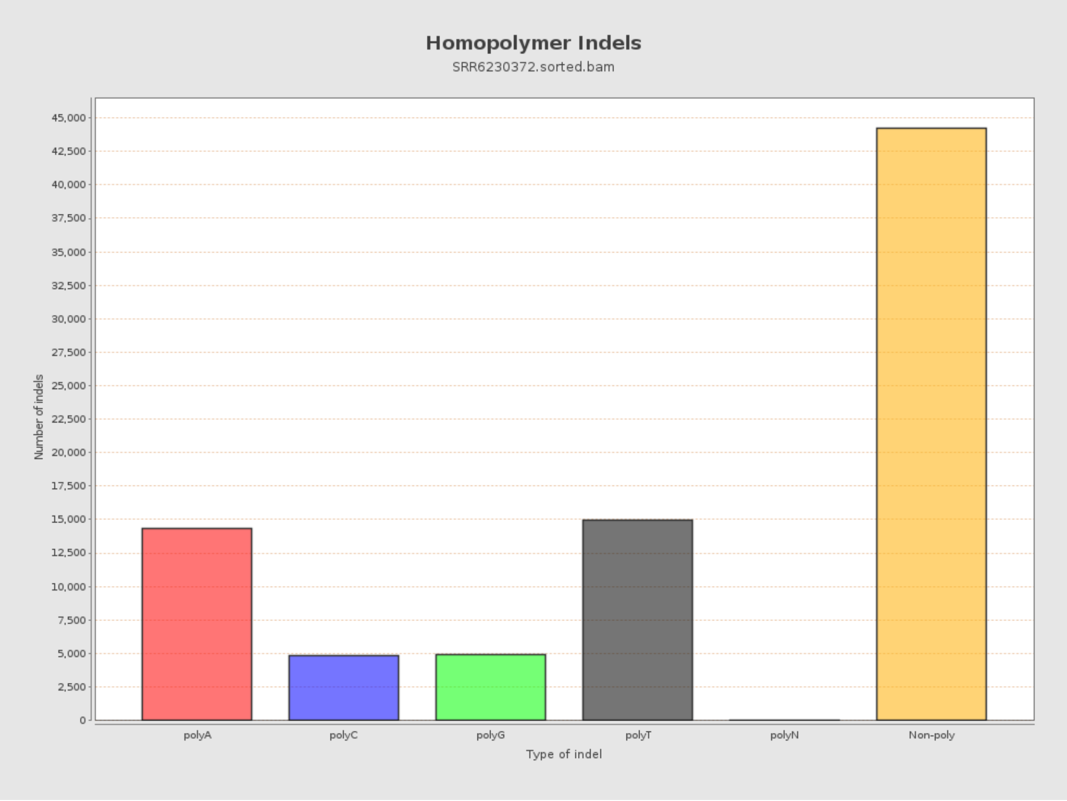
9. Results : Mapped Reads GC-content Distribution



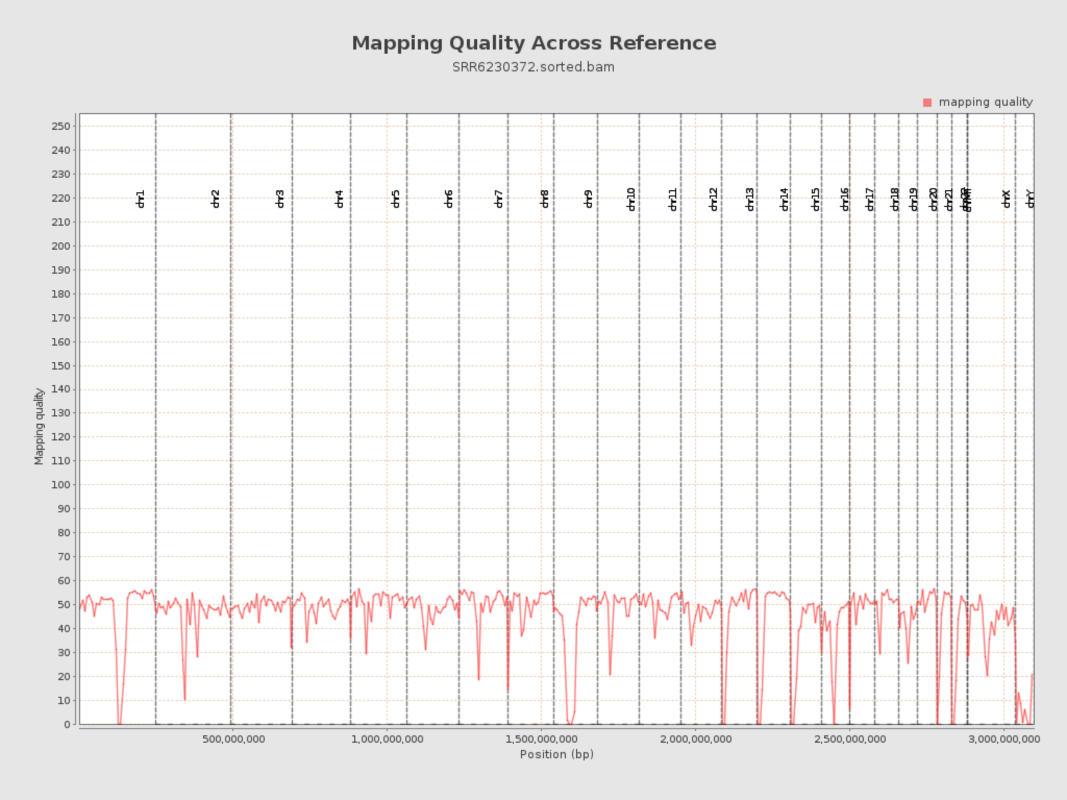
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram