Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:51:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230369.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_SRR6230369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230369.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:51:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,387,083
Mapped reads	1,782,801 / 74.69%
Unmapped reads	604,282 / 25.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,022 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	221,774 / 9.29%
Duplication rate	9.99%
Clipped reads	1,116,956 / 46.79%

2.2. ACGT Content

Number/percentage of A's	30,020,506 / 27.03%
Number/percentage of C's	19,930,339 / 17.95%
Number/percentage of T's	35,709,891 / 32.15%
Number/percentage of G's	25,346,968 / 22.82%
Number/percentage of N's	48,759 / 0.04%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3417

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

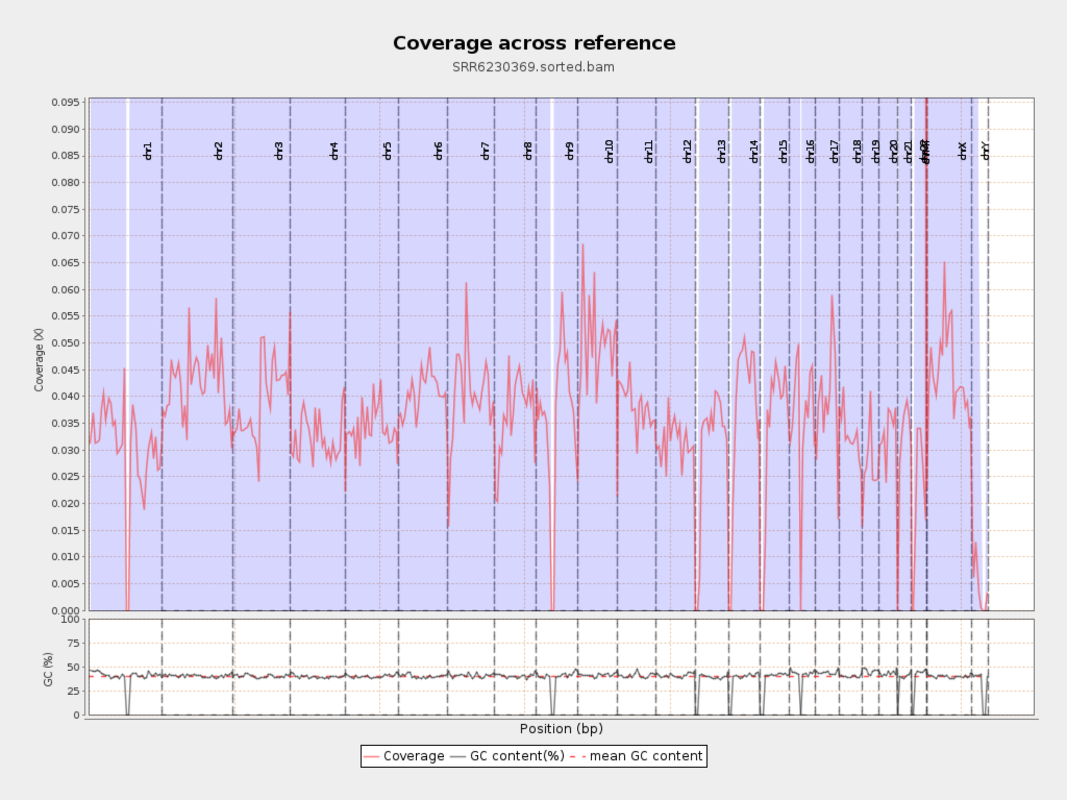
General error rate	1.02%
Mismatches	1,121,316
Insertions	8,924
Mapped reads with at least one insertion	0.5%
Deletions	36,789
Mapped reads with at least one deletion	2.04%
Homopolymer indels	48.05%

2.6. Chromosome stats

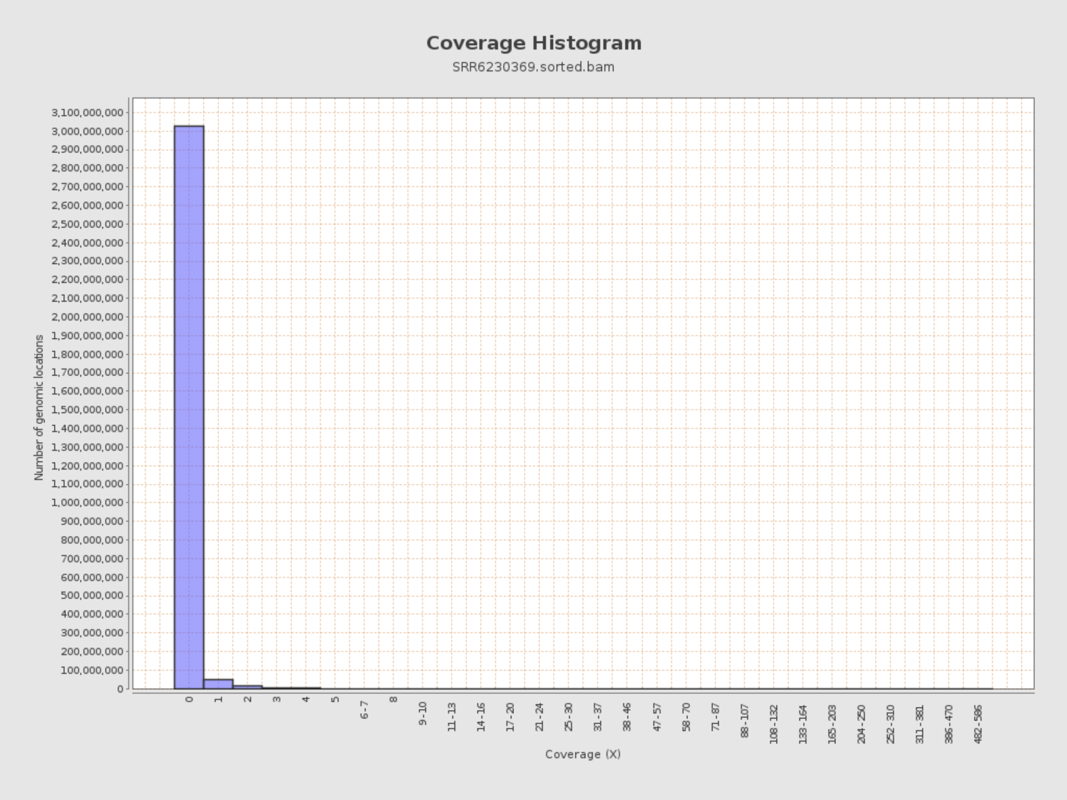
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7476129	0.03	0.4561
chr2	243199373	10364674	0.0426	0.4208
chr3	198022430	7719545	0.039	0.287
chr4	191154276	6179979	0.0323	0.2702
chr5	180915260	6206507	0.0343	0.2691
chr6	171115067	6956467	0.0407	0.3201
chr7	159138663	6514123	0.0409	0.4785

chr8	146364022	5340218	0.0365	0.3662
chr9	141213431	5041571	0.0357	0.3354
chr10	135534747	6814743	0.0503	0.3512
chr11	135006516	5139797	0.0381	0.3502
chr12	133851895	4198708	0.0314	0.264
chr13	115169878	3421811	0.0297	0.2566
chr14	107349540	4001349	0.0373	0.3011
chr15	102531392	3373941	0.0329	0.2991
chr16	90354753	3261723	0.0361	0.2852
chr17	81195210	3152450	0.0388	0.2981
chr18	78077248	2570795	0.0329	0.4596
chr19	59128983	1633904	0.0276	0.3356
chr20	63025520	2077648	0.033	0.2674
chr21	48129895	1483154	0.0308	0.2606
chr22	51304566	1050121	0.0205	0.2011
chrMT	16571	17938	1.0825	1.497
chrX	155270560	6846571	0.0441	0.3235
chrY	59373566	271225	0.0046	0.1048

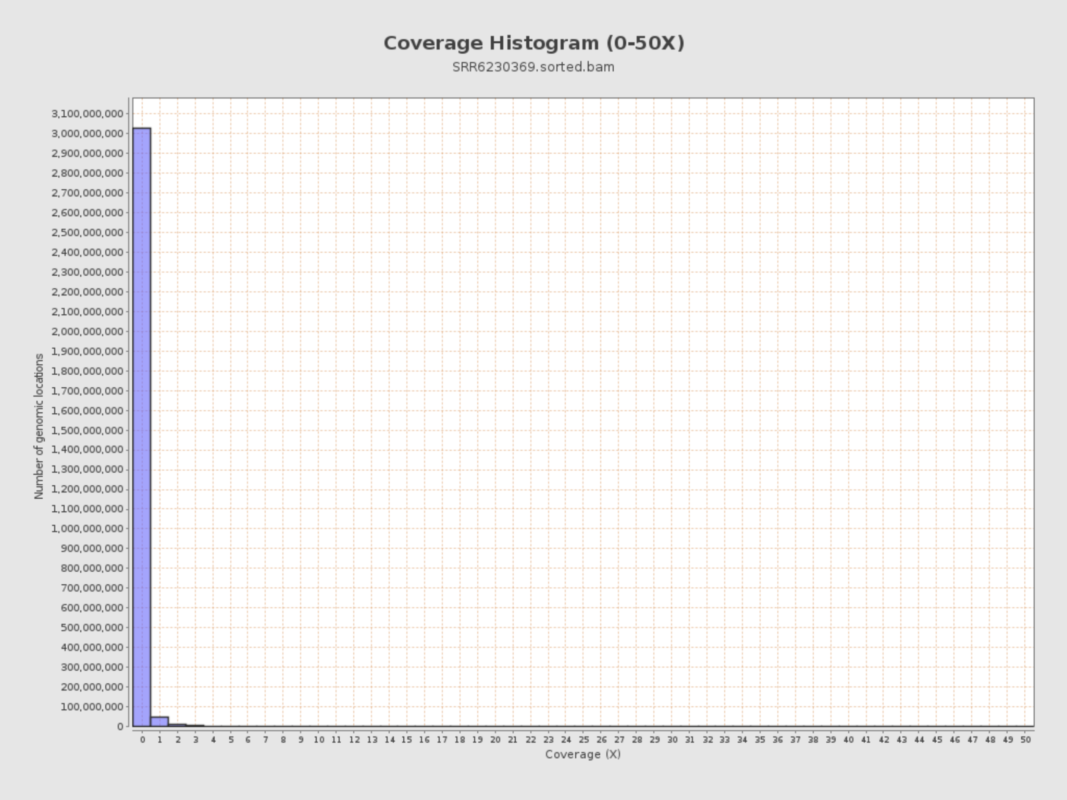
3. Results : Coverage across reference



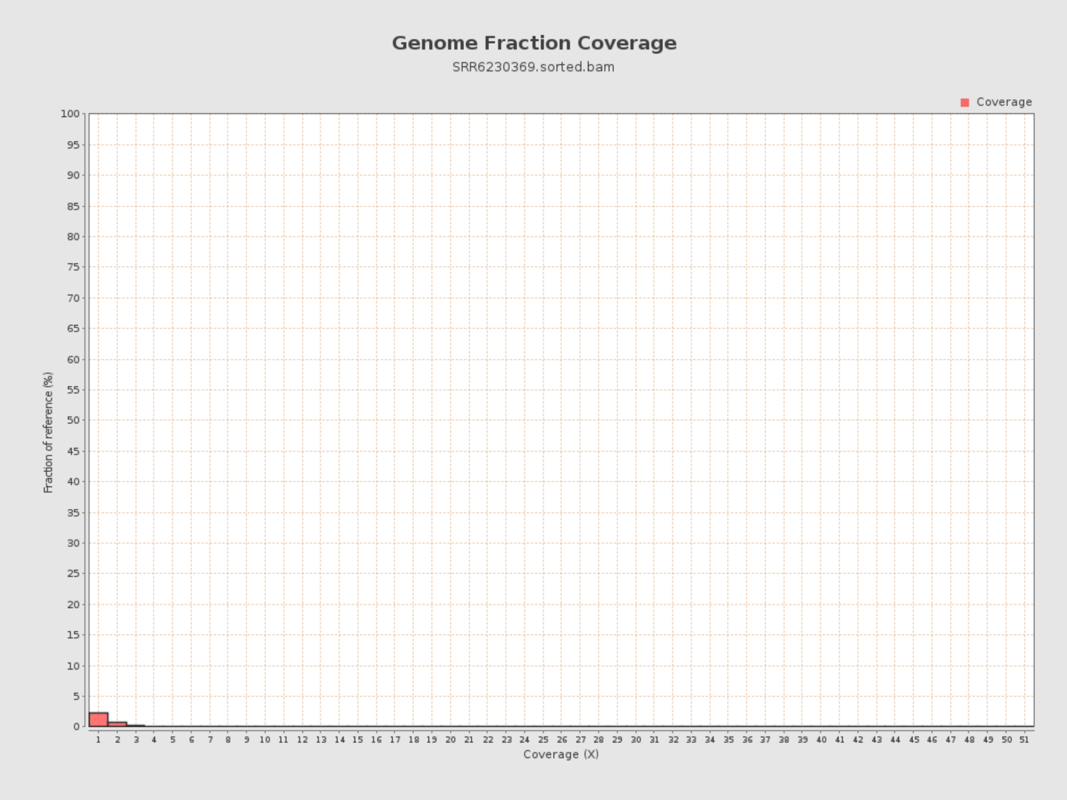
4. Results : Coverage Histogram



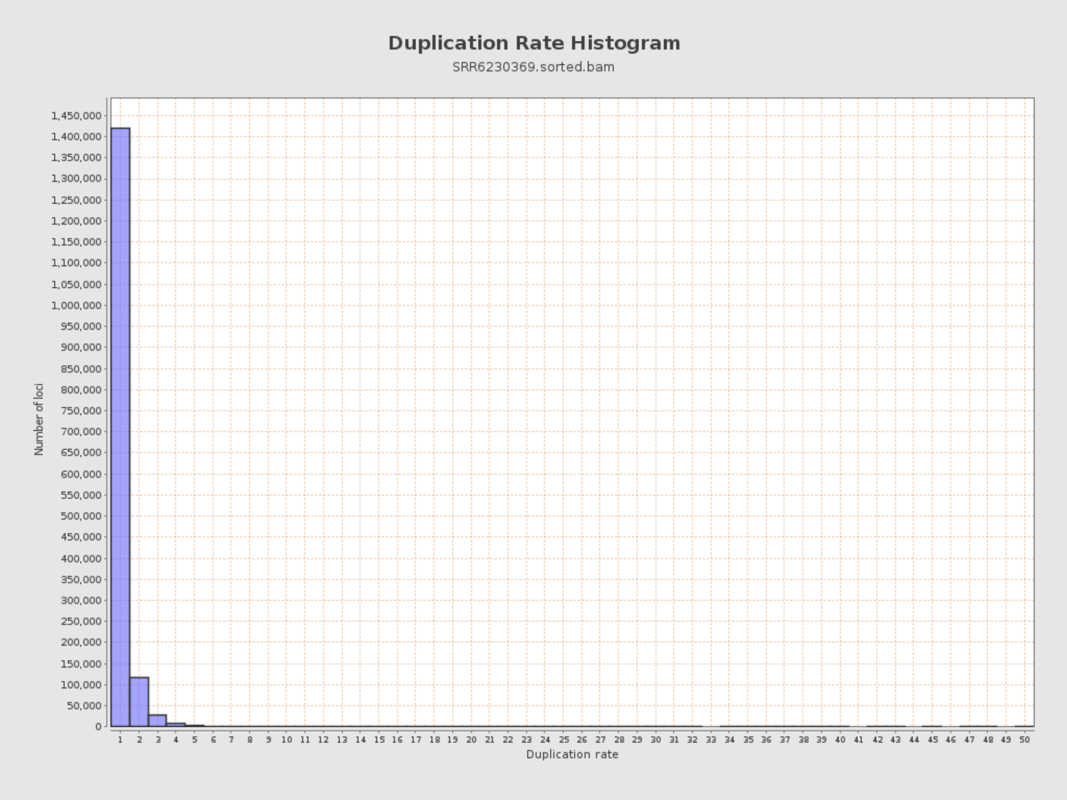
5. Results : Coverage Histogram (0-50X)



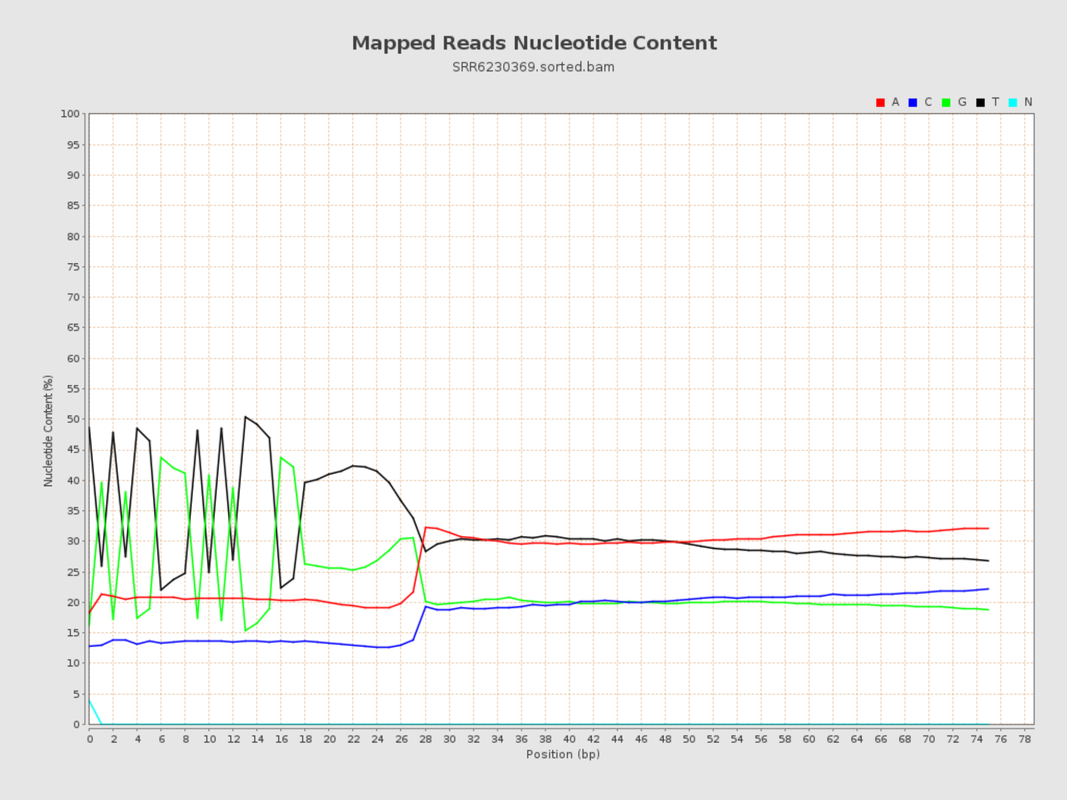
6. Results : Genome Fraction Coverage



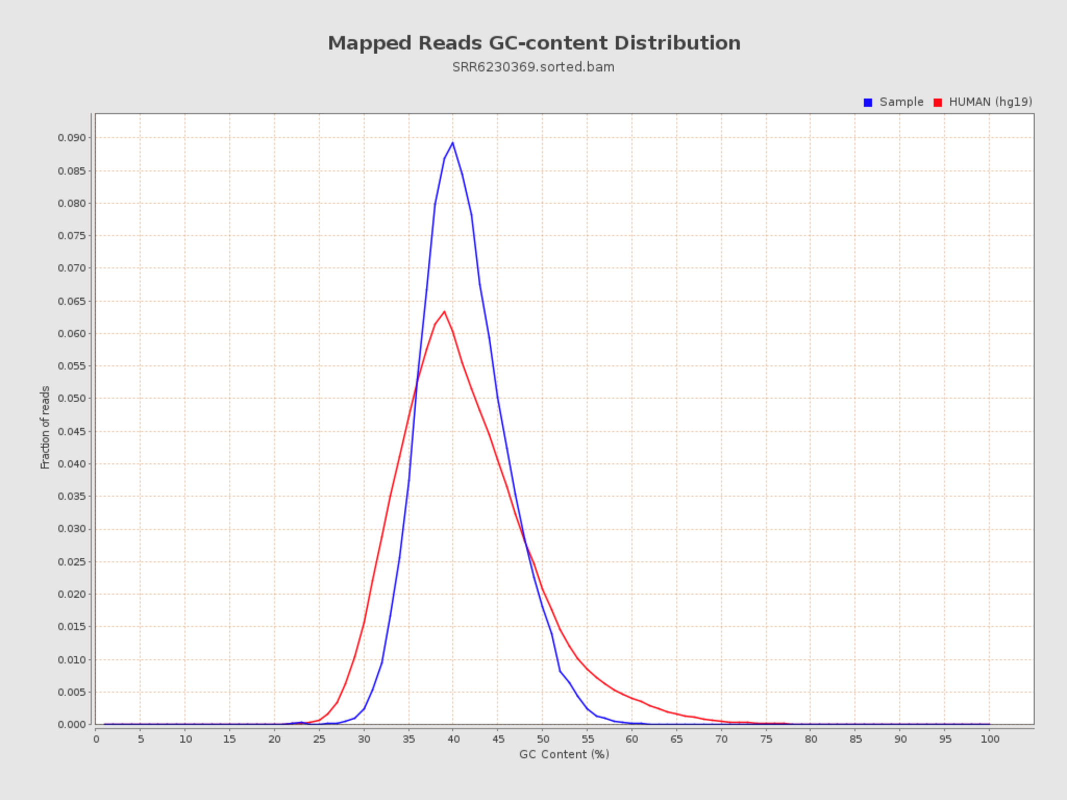
7. Results : Duplication Rate Histogram



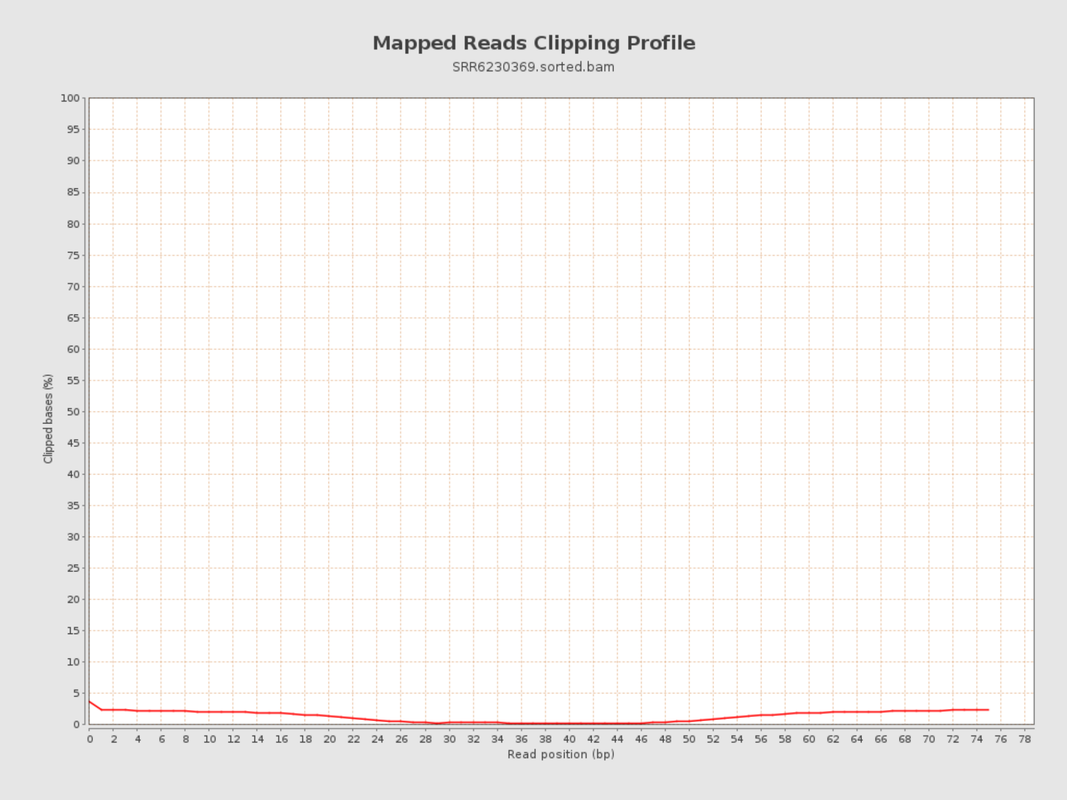
8. Results : Mapped Reads Nucleotide Content



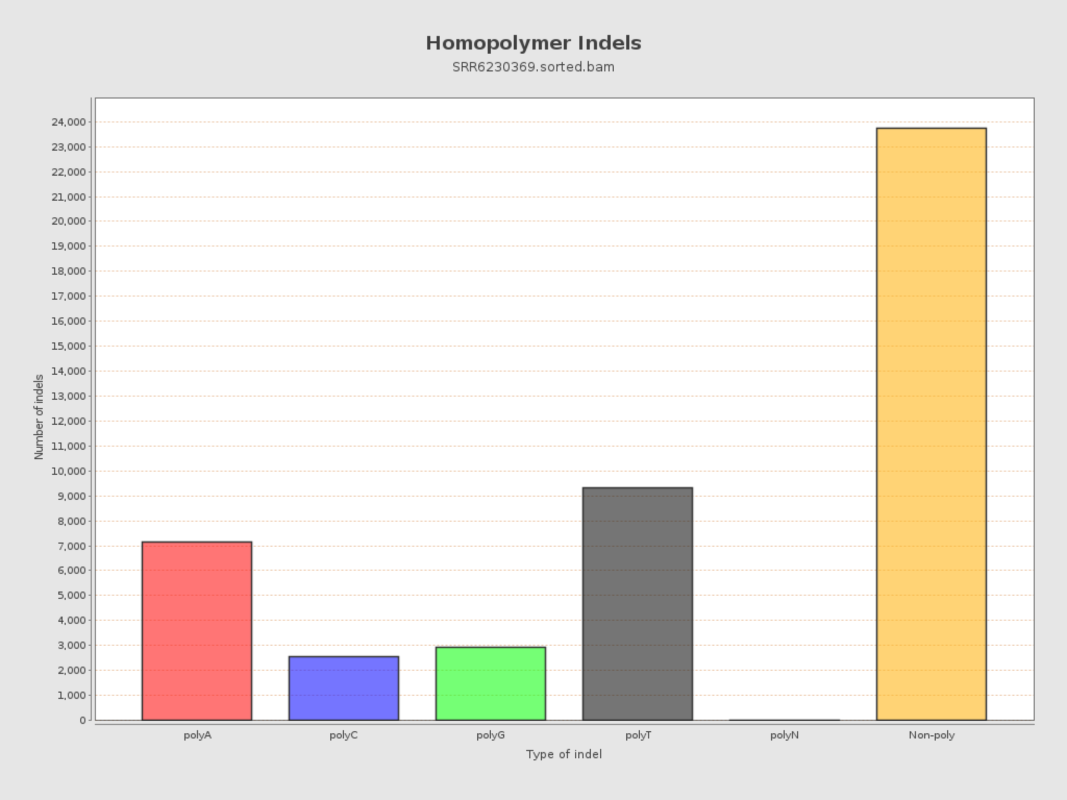
9. Results : Mapped Reads GC-content Distribution



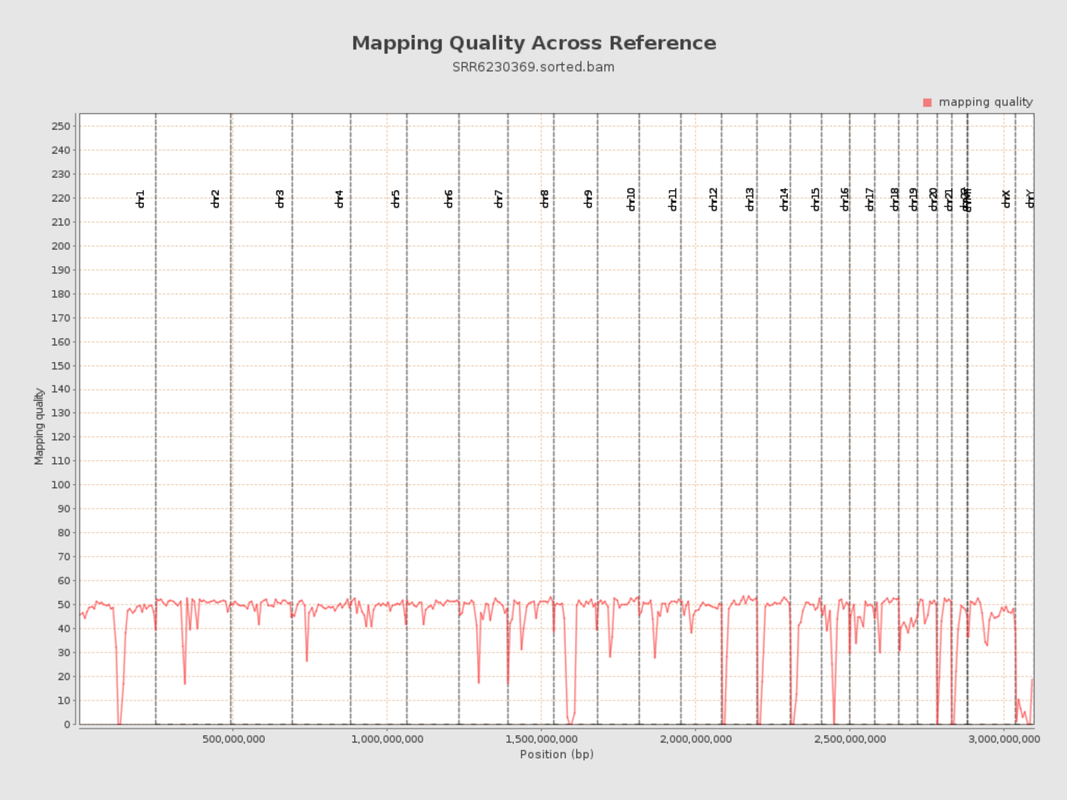
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram