Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:26:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548969.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_SRR1548969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:26:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,161,850
Mapped reads	4,907,079 / 43.96%
Unmapped reads	6,254,771 / 56.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	159,267 / 1.43%
Duplication rate	2.49%
Clipped reads	484,558 / 4.34%

2.2. ACGT Content

Number/percentage of A's	59,838,883 / 30.89%
Number/percentage of C's	36,763,712 / 18.98%
Number/percentage of T's	60,009,981 / 30.98%
Number/percentage of G's	37,066,481 / 19.14%
Number/percentage of N's	9,841 / 0.01%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0626
Standard Deviation	0.4251

2.4. Mapping Quality

Mean Mapping Quality	43.41

2.5. Mismatches and indels

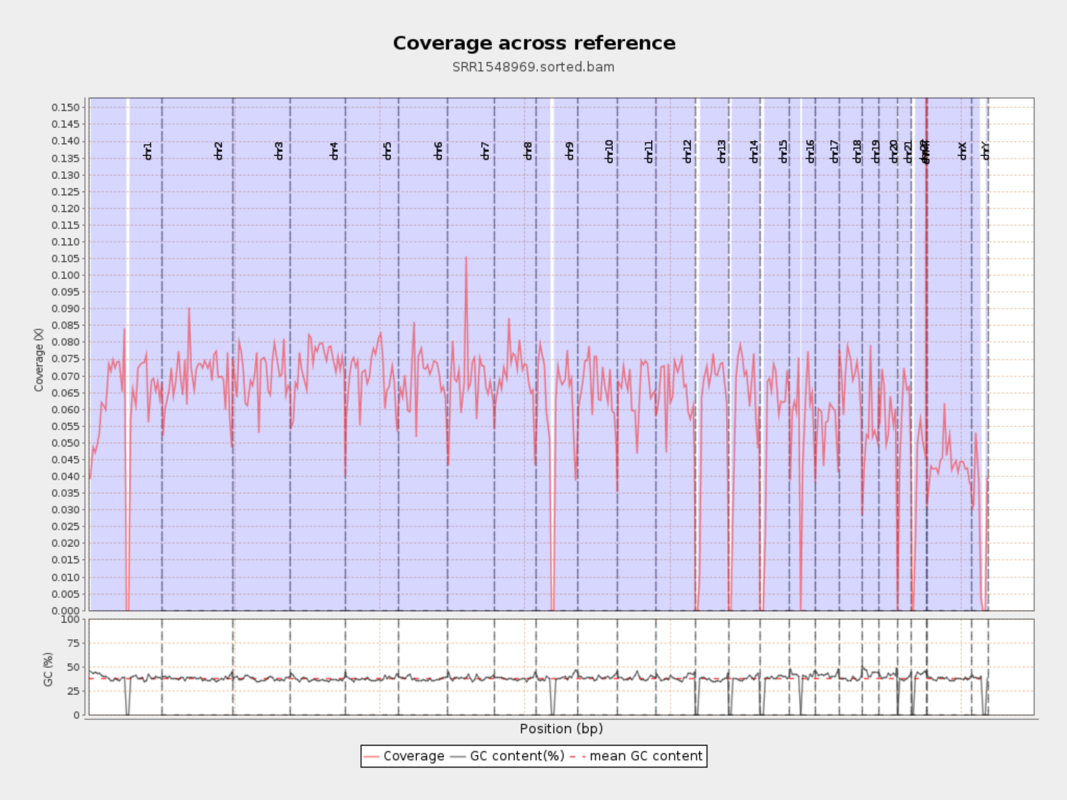
General error rate	0.32%
Mismatches	612,008
Insertions	8,446
Mapped reads with at least one insertion	0.17%
Deletions	20,838
Mapped reads with at least one deletion	0.42%
Homopolymer indels	45.41%

2.6. Chromosome stats

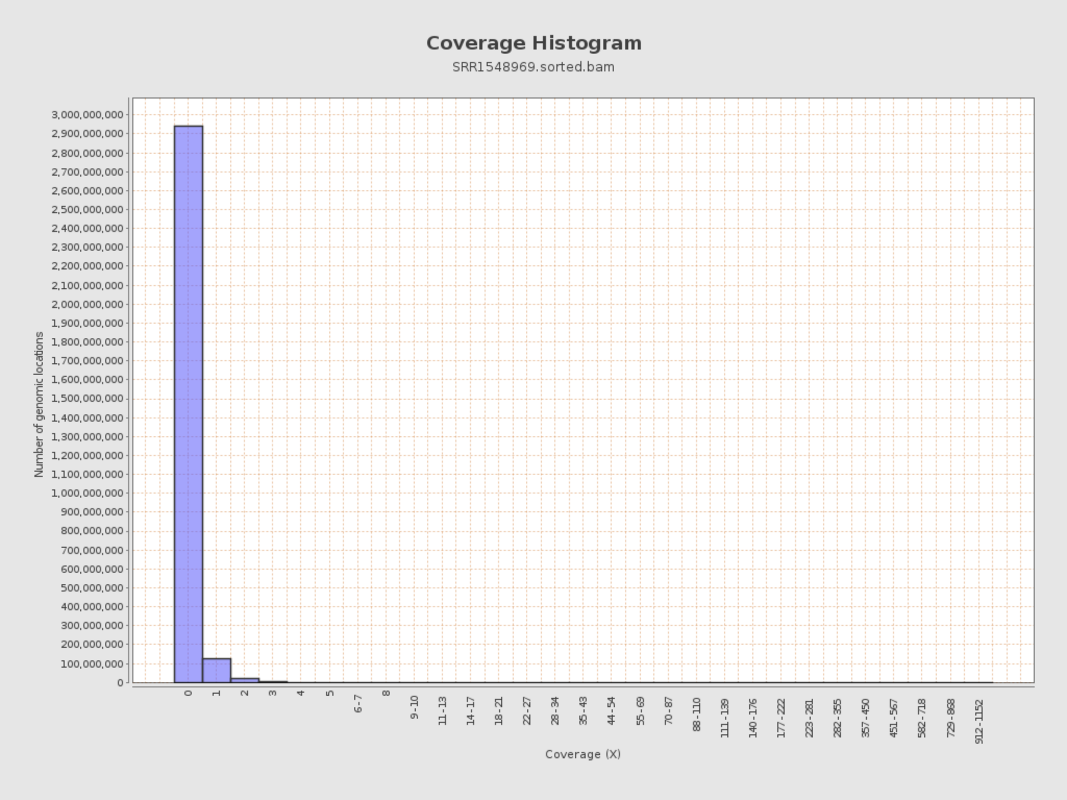
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15253398	0.0612	0.6753
chr2	243199373	16868421	0.0694	0.4098
chr3	198022430	13955314	0.0705	0.3225
chr4	191154276	14038588	0.0734	0.3347
chr5	180915260	12677704	0.0701	0.3241
chr6	171115067	11798199	0.0689	0.3699
chr7	159138663	11123982	0.0699	0.6152
chr8	146364022	10280140	0.0702	0.6582

chr9	141213431	8319246	0.0589	0.3657
chr10	135534747	9086852	0.067	0.3635
chr11	135006516	8886861	0.0658	0.3965
chr12	133851895	8768086	0.0655	0.319
chr13	115169878	6635015	0.0576	0.2895
chr14	107349540	6120058	0.057	0.3348
chr15	102531392	5505977	0.0537	0.28
chr16	90354753	4983338	0.0552	0.2947
chr17	81195210	4435300	0.0546	0.2972
chr18	78077248	5489688	0.0703	0.5941
chr19	59128983	3176732	0.0537	0.6229
chr20	63025520	3675593	0.0583	0.2979
chr21	48129895	2586249	0.0537	0.3053
chr22	51304566	1828269	0.0356	0.2575
chrMT	16571	10225	0.617	0.9096
chrX	155270560	6767241	0.0436	0.2846
chrY	59373566	1444543	0.0243	0.2486

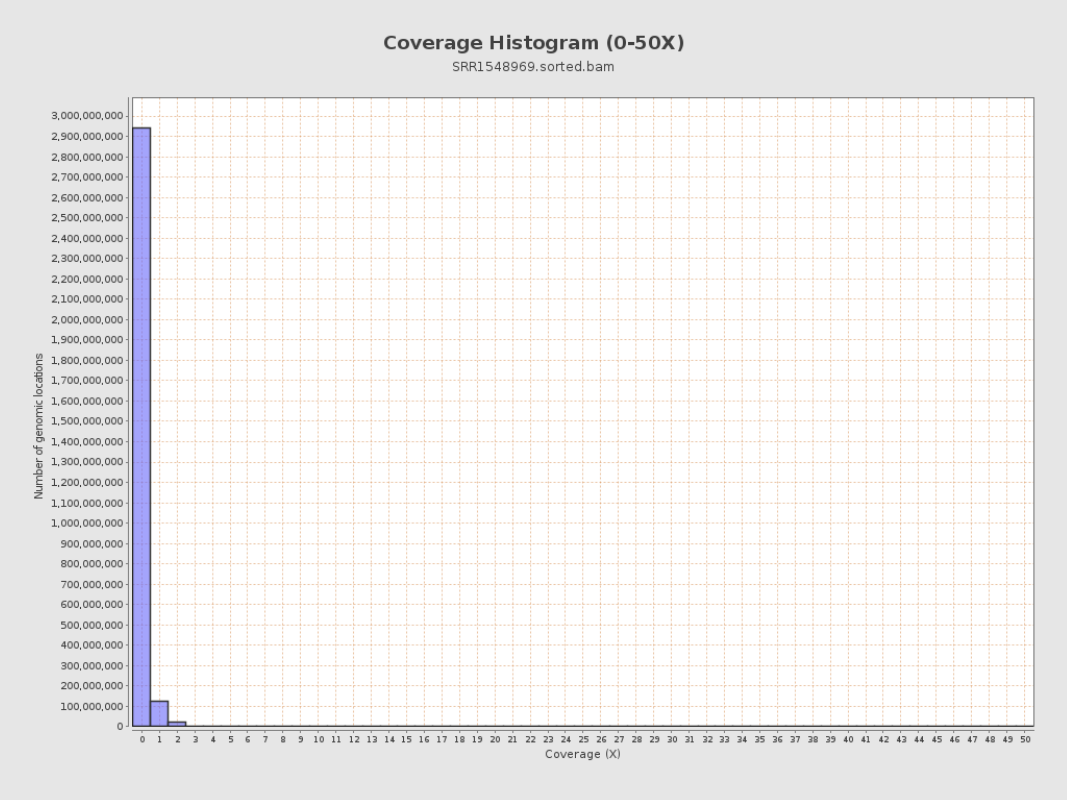
3. Results : Coverage across reference



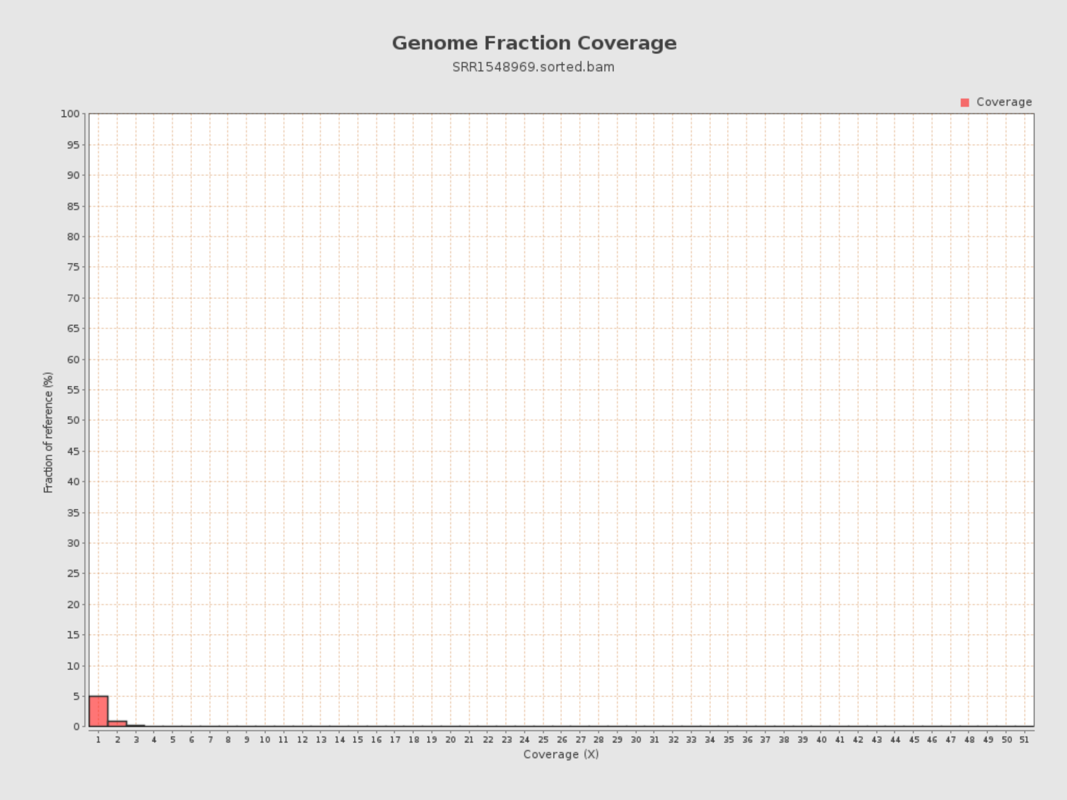
4. Results : Coverage Histogram



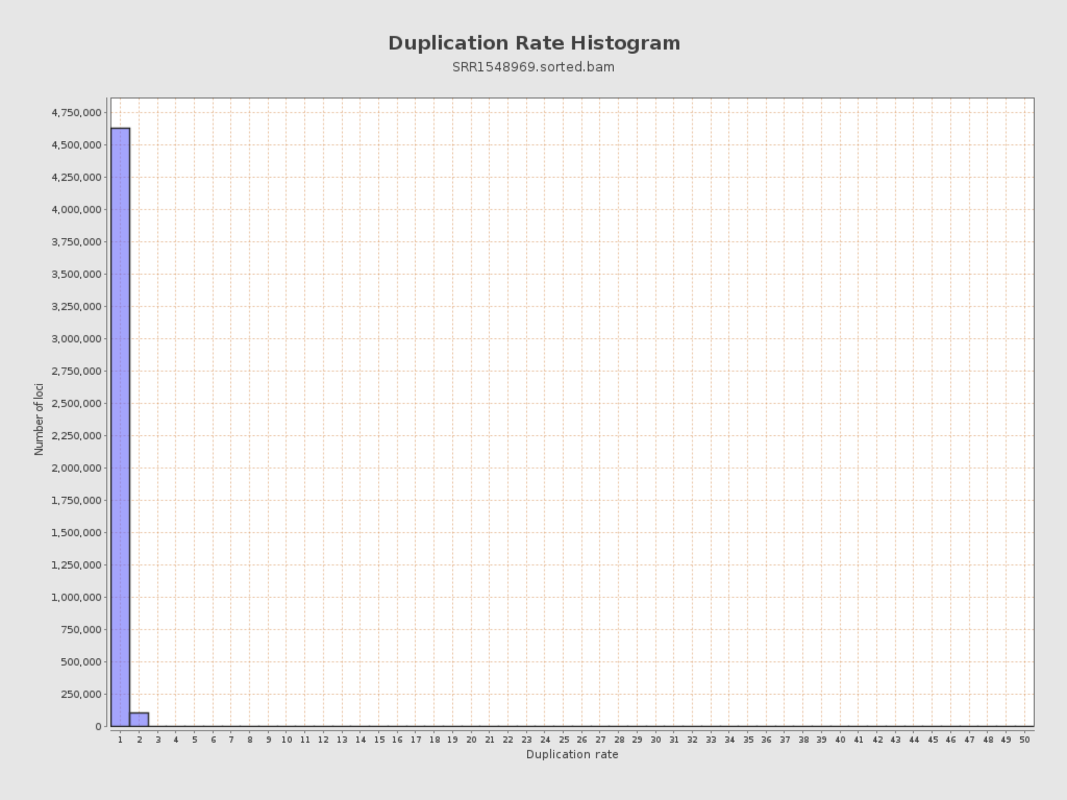
5. Results : Coverage Histogram (0-50X)



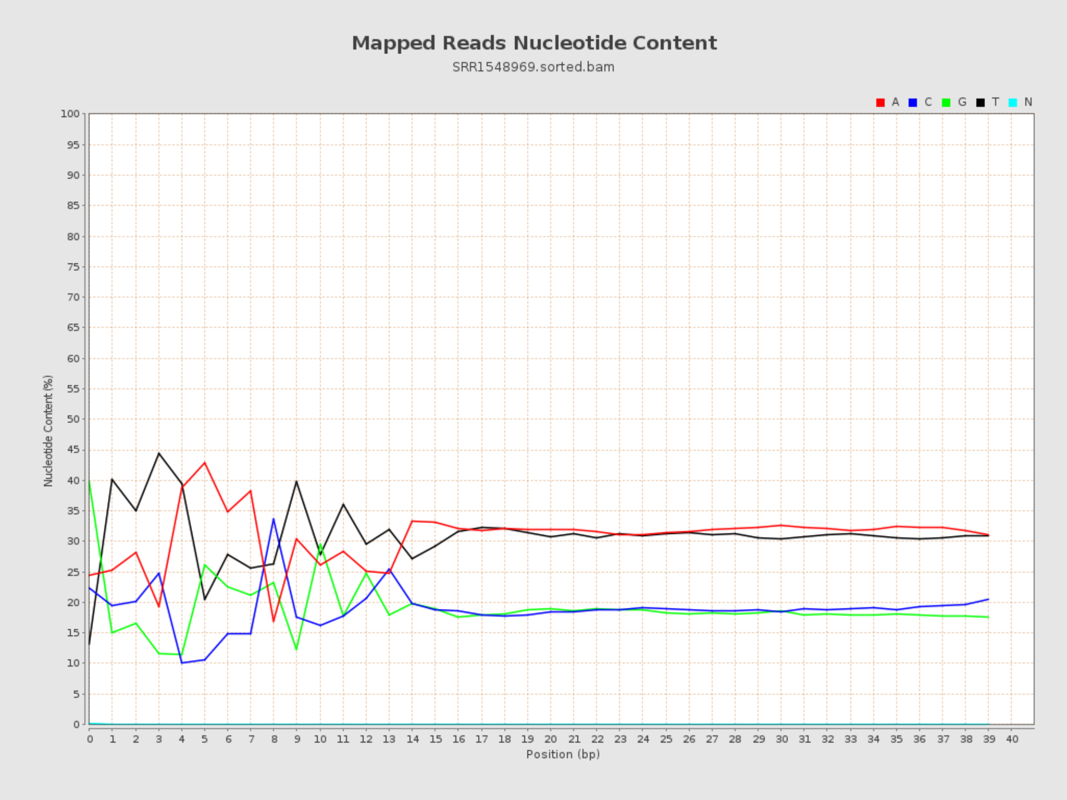
6. Results : Genome Fraction Coverage



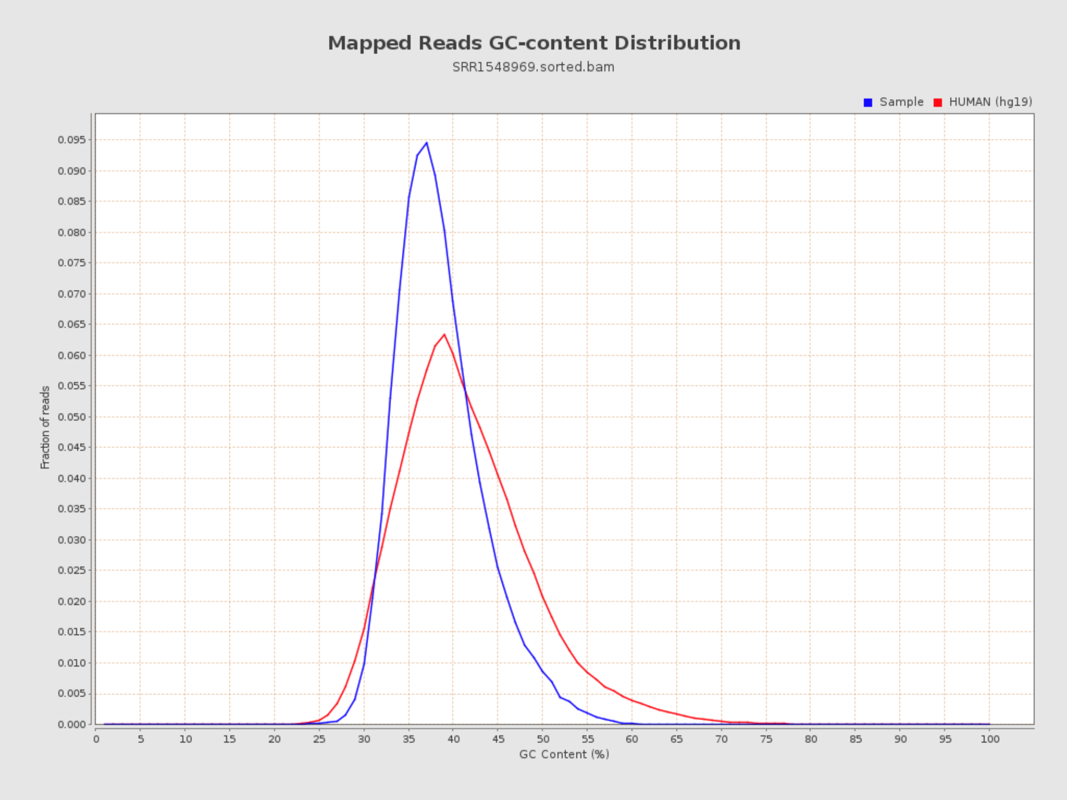
7. Results : Duplication Rate Histogram



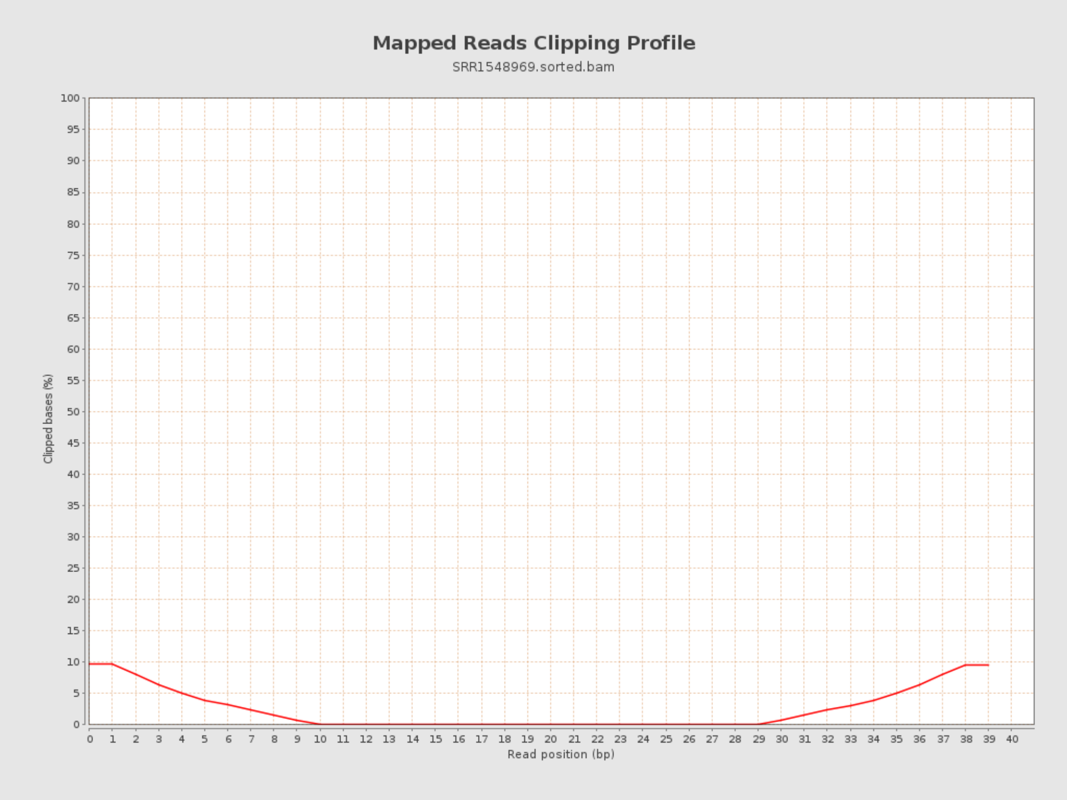
8. Results : Mapped Reads Nucleotide Content



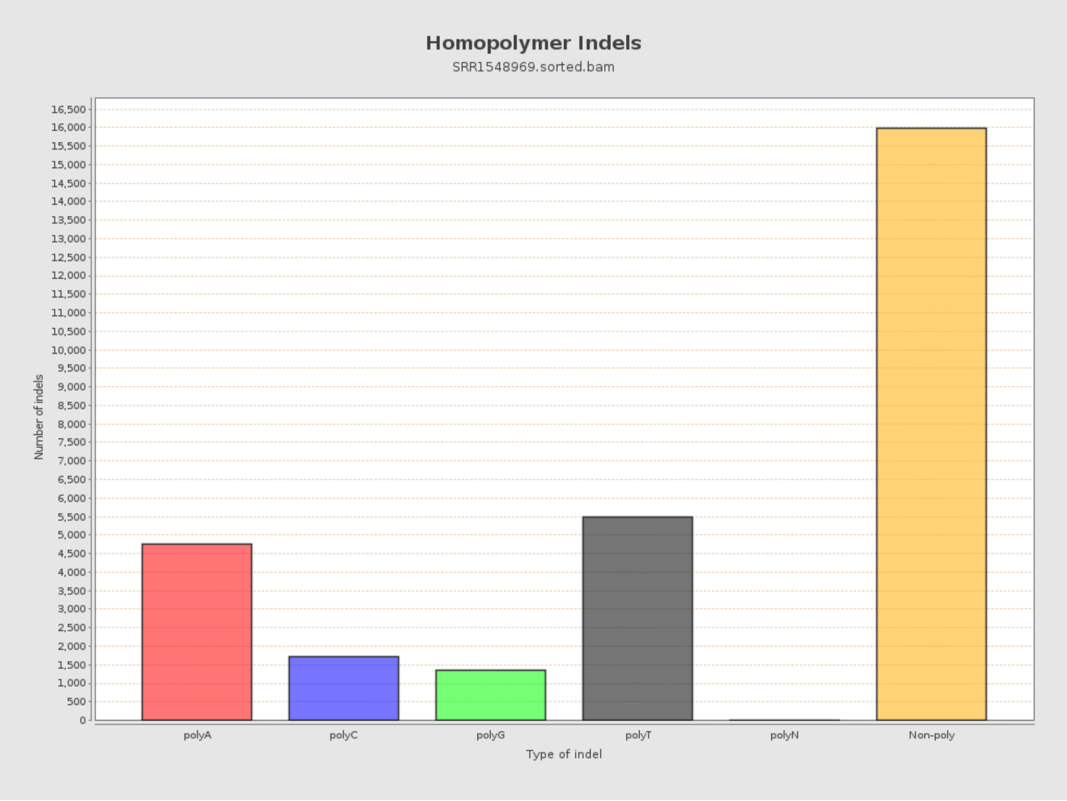
9. Results : Mapped Reads GC-content Distribution



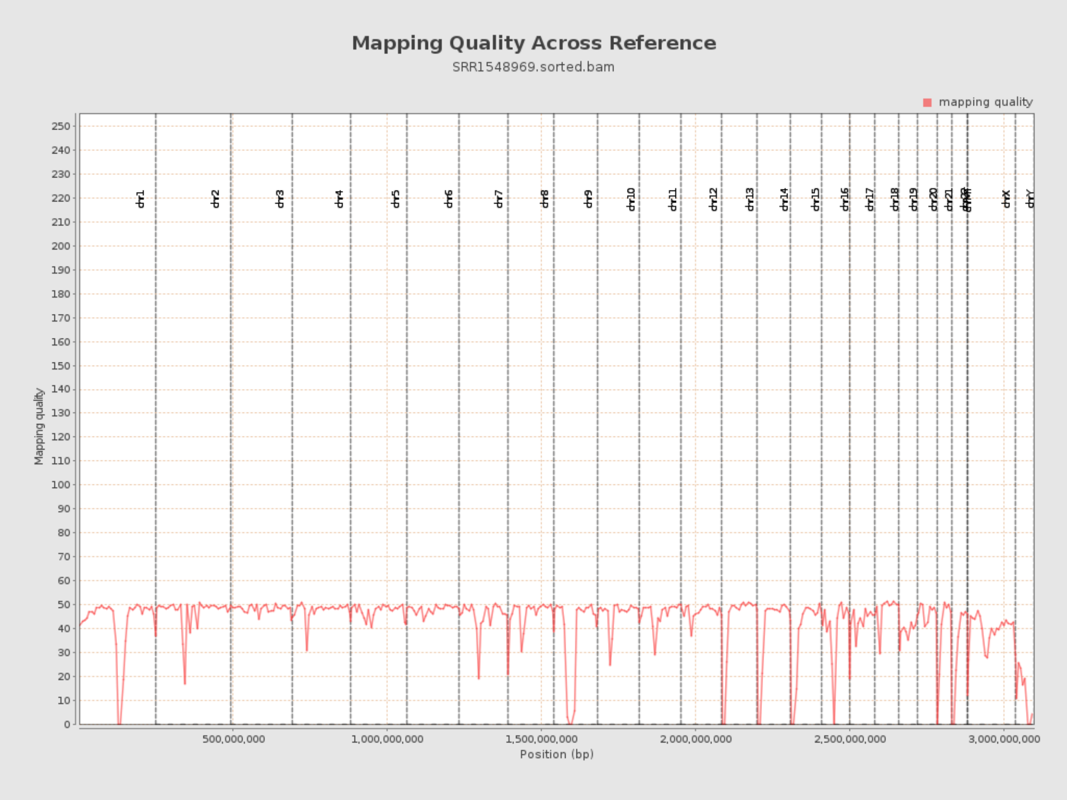
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram