Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:44:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013369.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_SRR6013369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013369.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:44:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,187,732
Mapped reads	1,977,619 / 90.4%
Unmapped reads	210,113 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,652 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	90,415 / 4.13%
Duplication rate	3.31%
Clipped reads	794,188 / 36.3%

2.2. ACGT Content

Number/percentage of A's	38,104,777 / 28.47%
Number/percentage of C's	24,540,725 / 18.33%
Number/percentage of T's	42,566,550 / 31.8%
Number/percentage of G's	28,619,075 / 21.38%
Number/percentage of N's	29,249 / 0.02%
GC Percentage	39.71%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.4637

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

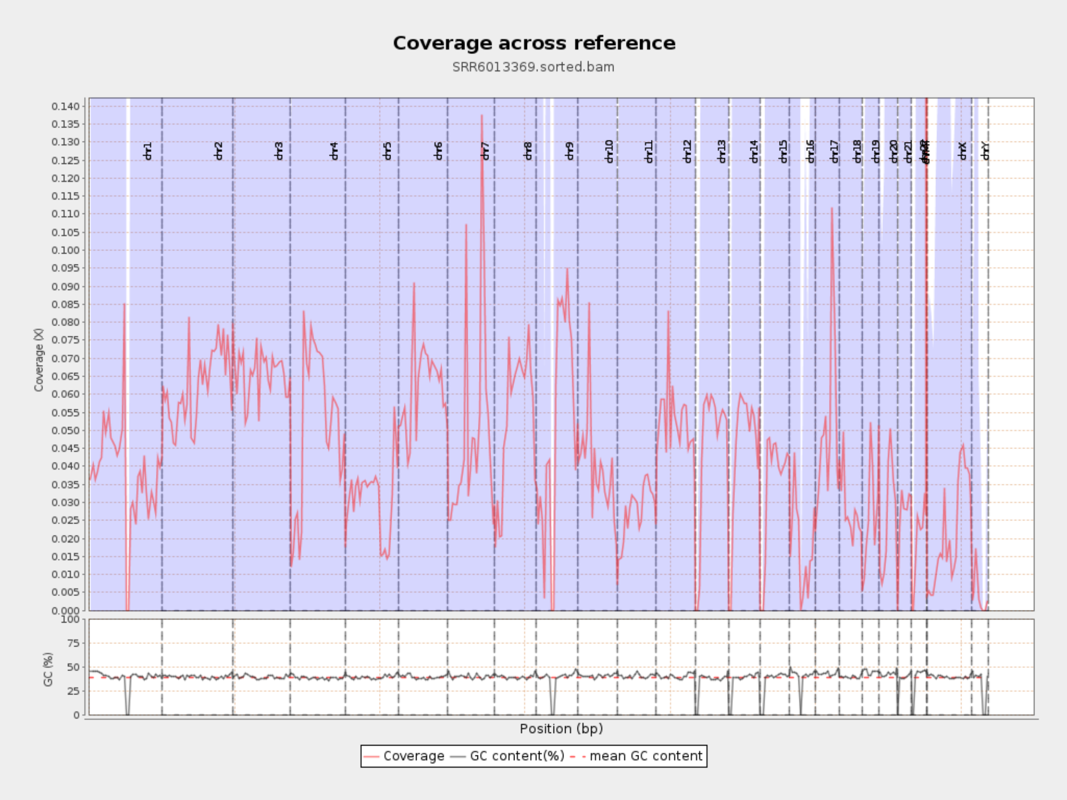
General error rate	0.8%
Mismatches	1,056,487
Insertions	10,263
Mapped reads with at least one insertion	0.51%
Deletions	31,847
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.69%

2.6. Chromosome stats

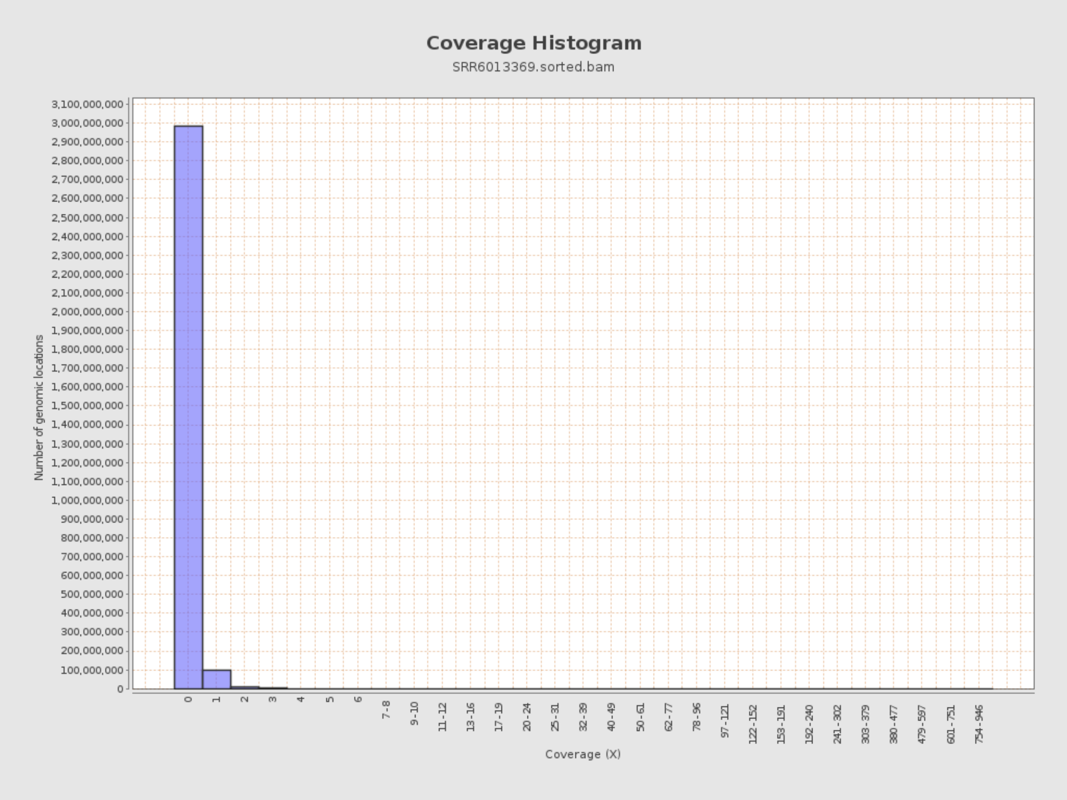
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9536287	0.0383	0.8288
chr2	243199373	15212752	0.0626	0.4857
chr3	198022430	13055963	0.0659	0.2893
chr4	191154276	9842938	0.0515	0.3054
chr5	180915260	5660570	0.0313	0.2025
chr6	171115067	10667064	0.0623	0.3864
chr7	159138663	7947677	0.0499	0.9616

chr8	146364022	7945077	0.0543	0.5164
chr9	141213431	7156207	0.0507	0.4029
chr10	135534747	5421288	0.04	0.501
chr11	135006516	3705740	0.0274	0.2589
chr12	133851895	7107602	0.0531	0.2716
chr13	115169878	5179528	0.045	0.2387
chr14	107349540	4795686	0.0447	0.262
chr15	102531392	3561156	0.0347	0.2139
chr16	90354753	1620509	0.0179	0.2088
chr17	81195210	4114716	0.0507	0.2895
chr18	78077248	2208861	0.0283	0.7416
chr19	59128983	1622914	0.0274	0.5506
chr20	63025520	1603074	0.0254	0.2008
chr21	48129895	1279655	0.0266	0.2381
chr22	51304566	956933	0.0187	0.1507
chrMT	16571	171408	10.3439	5.9854
chrX	155270560	3309248	0.0213	0.1972
chrY	59373566	233648	0.0039	0.1818

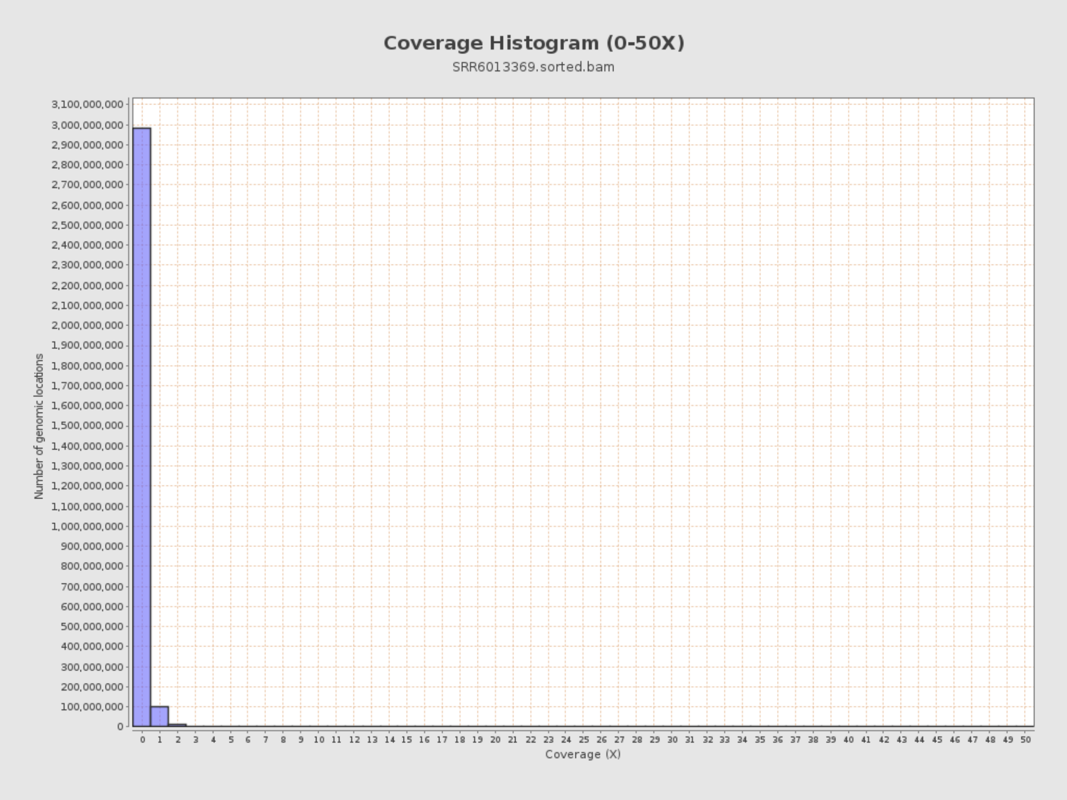
3. Results : Coverage across reference



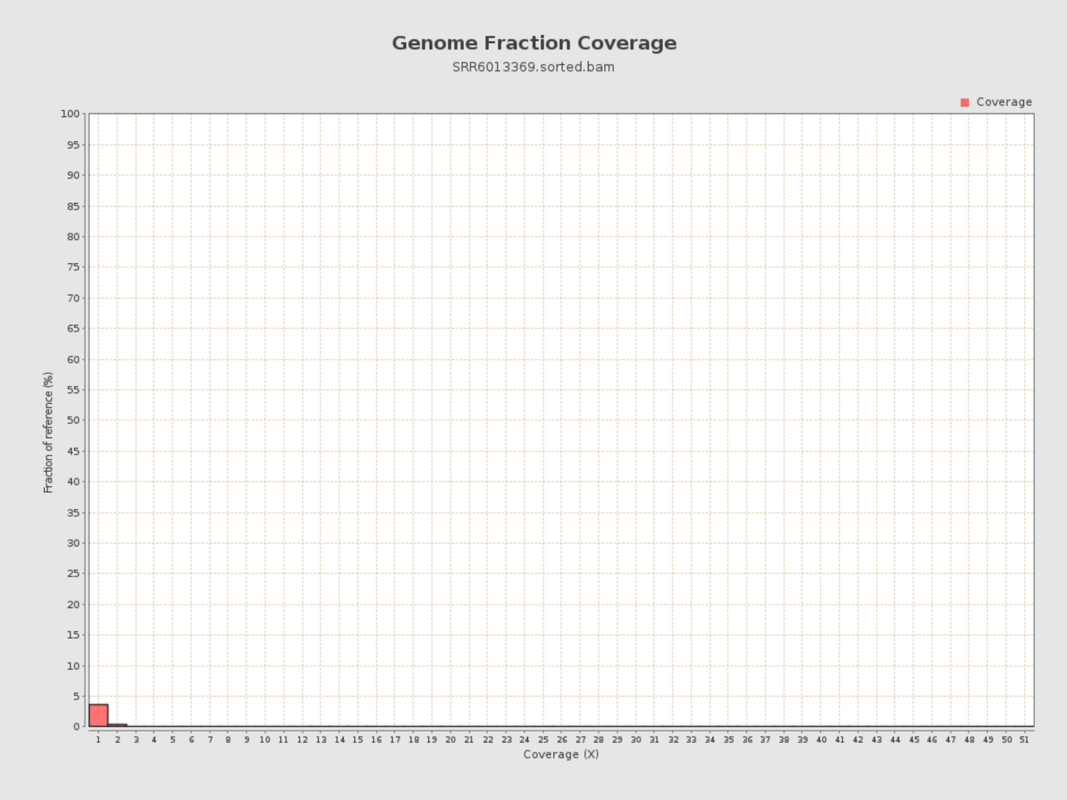
4. Results : Coverage Histogram



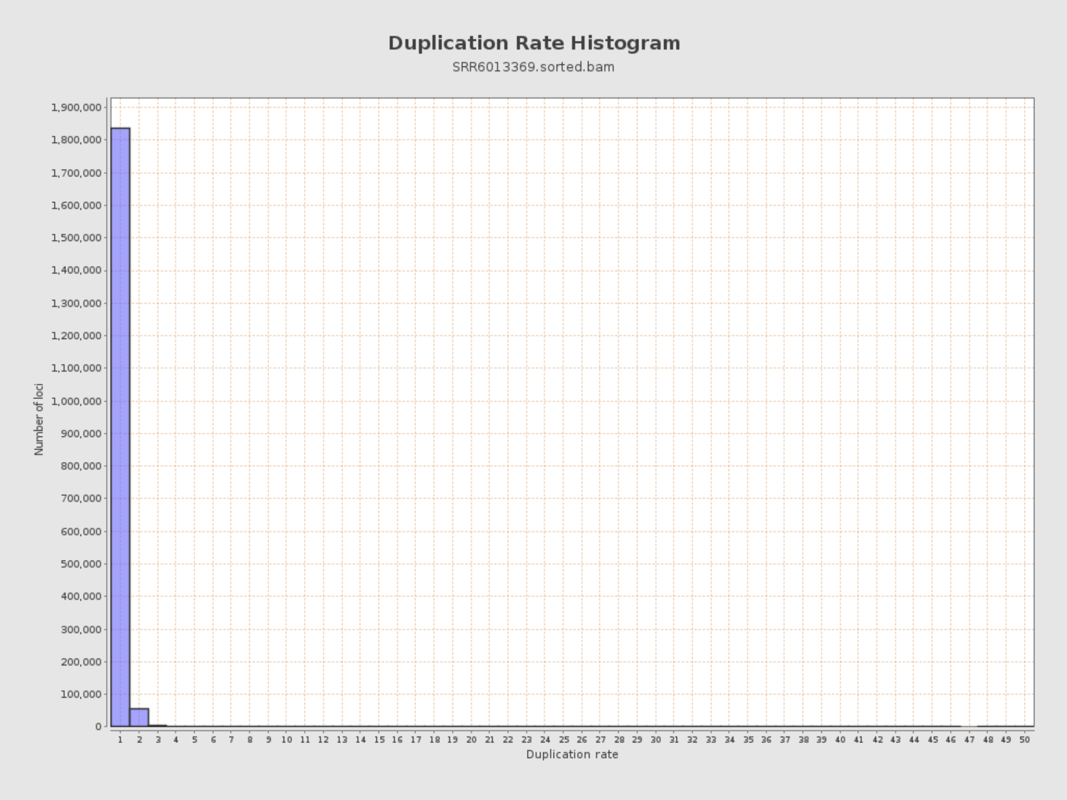
5. Results : Coverage Histogram (0-50X)



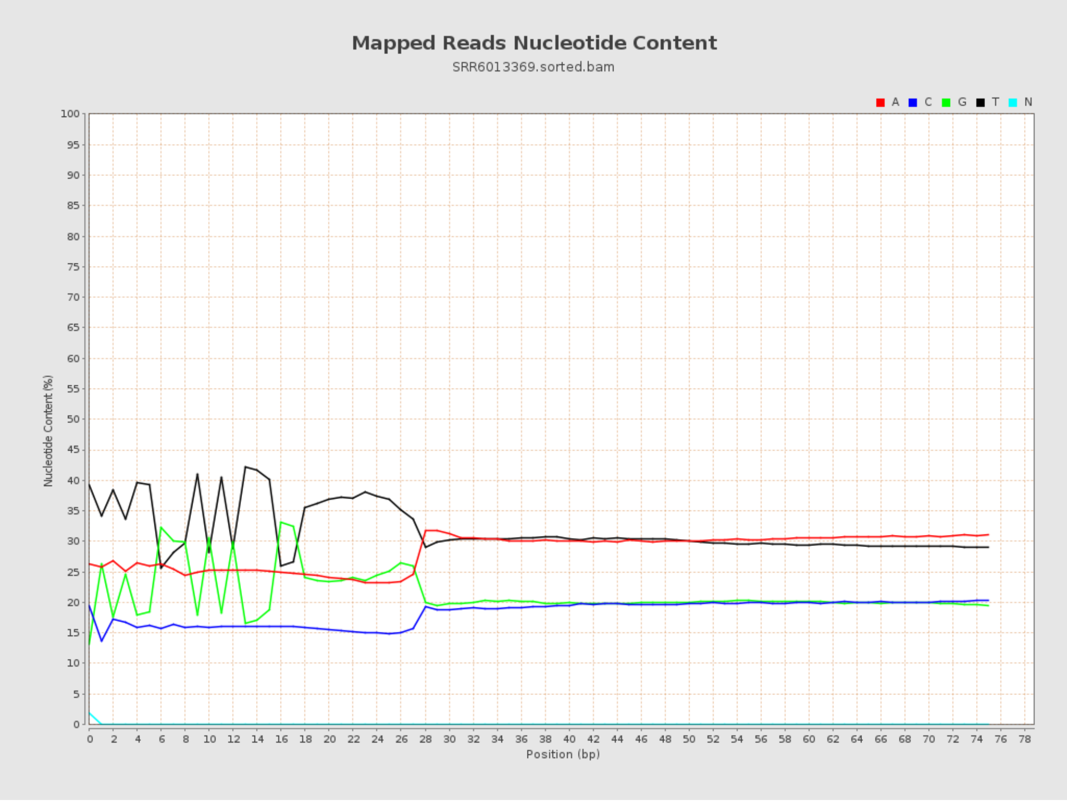
6. Results : Genome Fraction Coverage



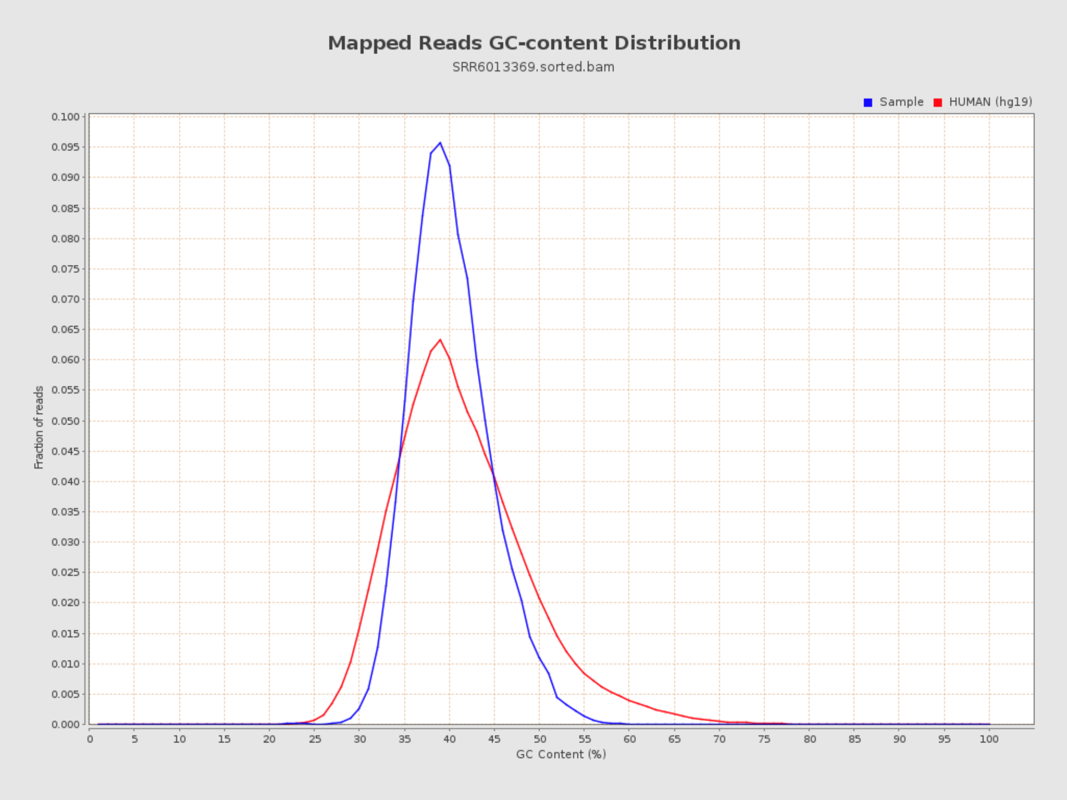
7. Results : Duplication Rate Histogram



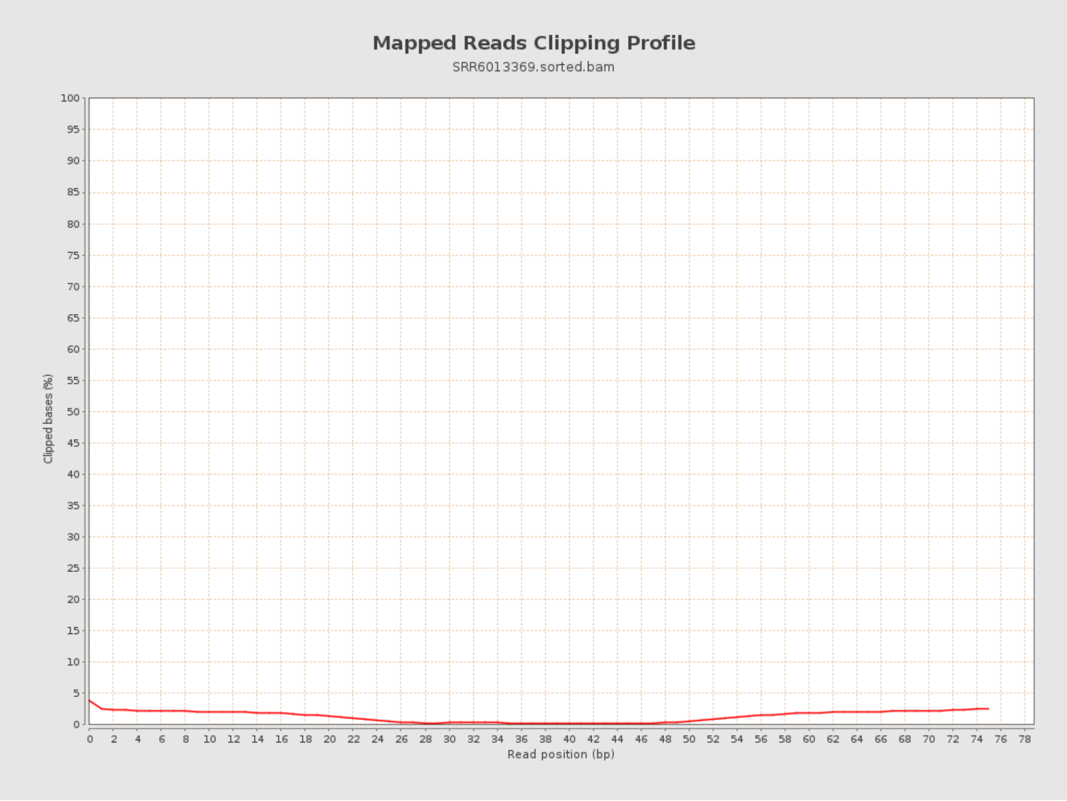
8. Results : Mapped Reads Nucleotide Content



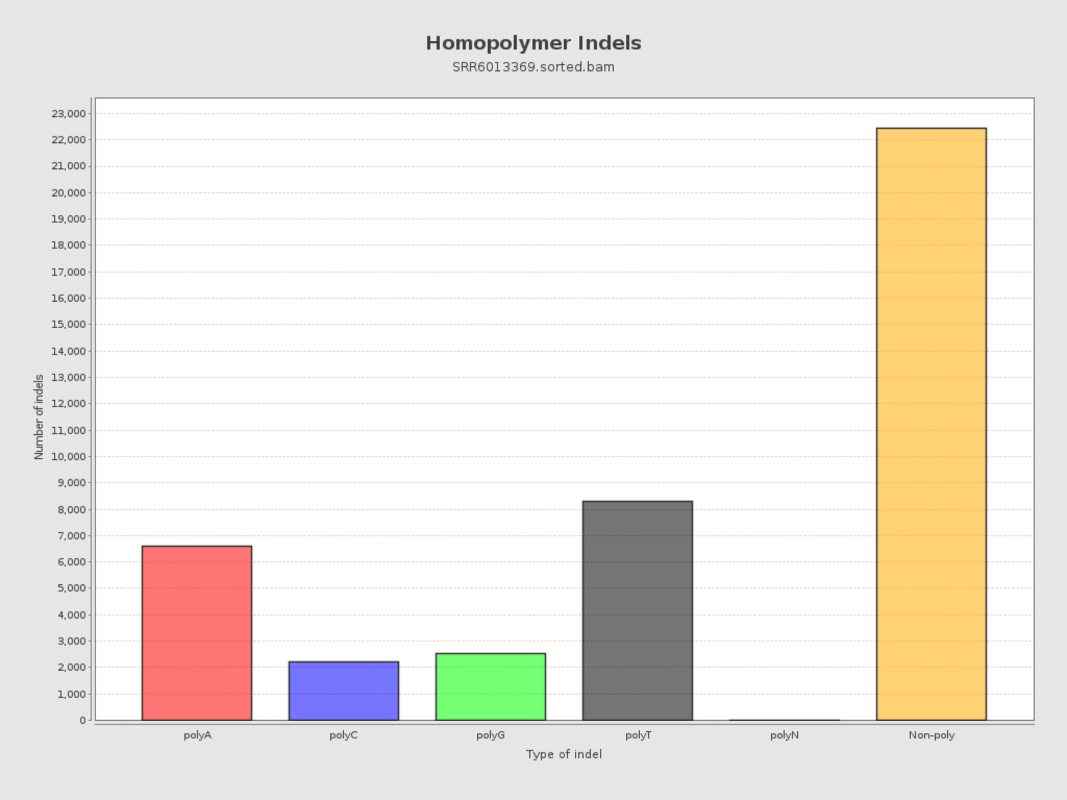
9. Results : Mapped Reads GC-content Distribution



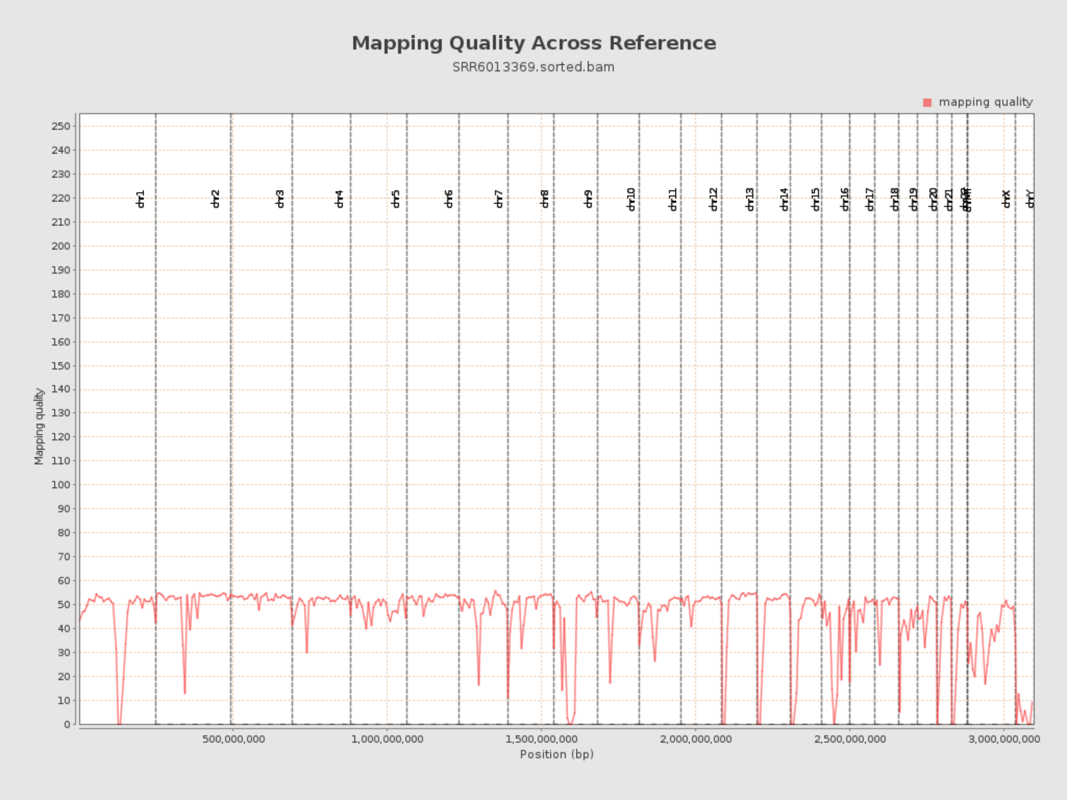
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram