Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:10:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068935.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_SRR6068935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:10:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,177,259
Mapped reads	1,846,347 / 84.8%
Unmapped reads	330,912 / 15.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,955 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	62,888 / 2.89%
Duplication rate	2.4%
Clipped reads	1,023,430 / 47.01%

2.2. ACGT Content

Number/percentage of A's	30,996,850 / 26.11%
Number/percentage of C's	20,494,246 / 17.26%
Number/percentage of T's	39,141,320 / 32.97%
Number/percentage of G's	27,791,112 / 23.41%
Number/percentage of N's	283,084 / 0.24%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3579

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

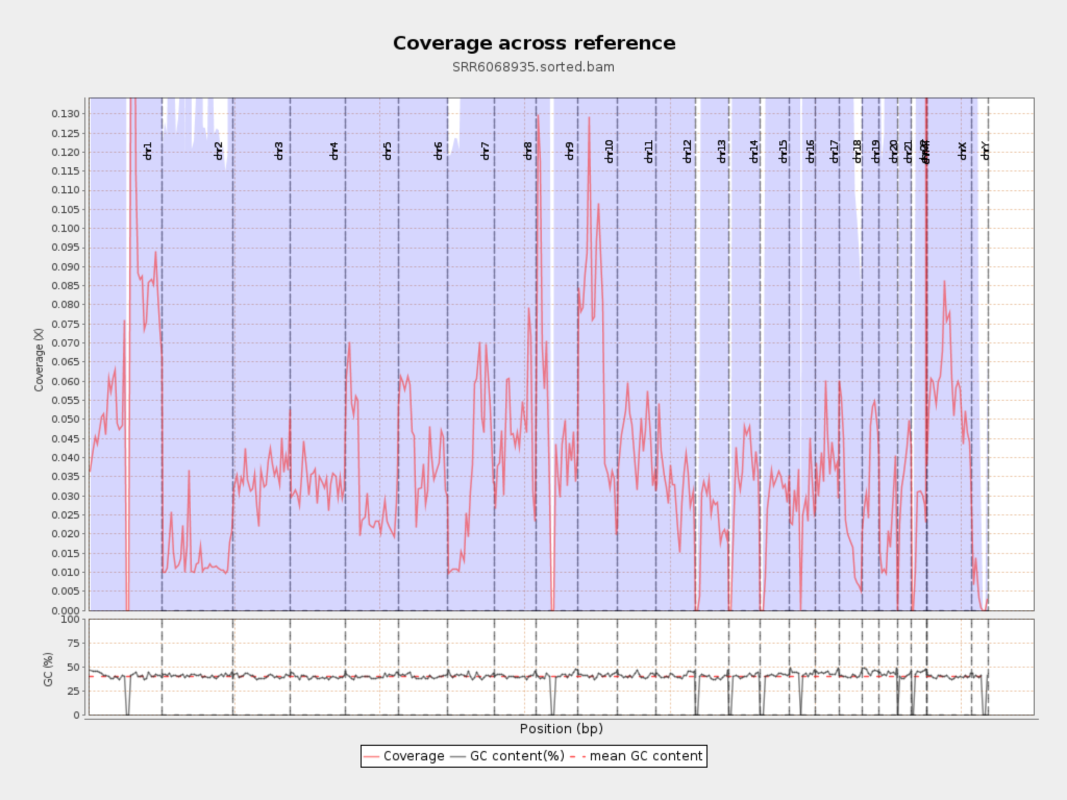
General error rate	0.94%
Mismatches	1,100,058
Insertions	10,695
Mapped reads with at least one insertion	0.57%
Deletions	33,059
Mapped reads with at least one deletion	1.77%
Homopolymer indels	48.5%

2.6. Chromosome stats

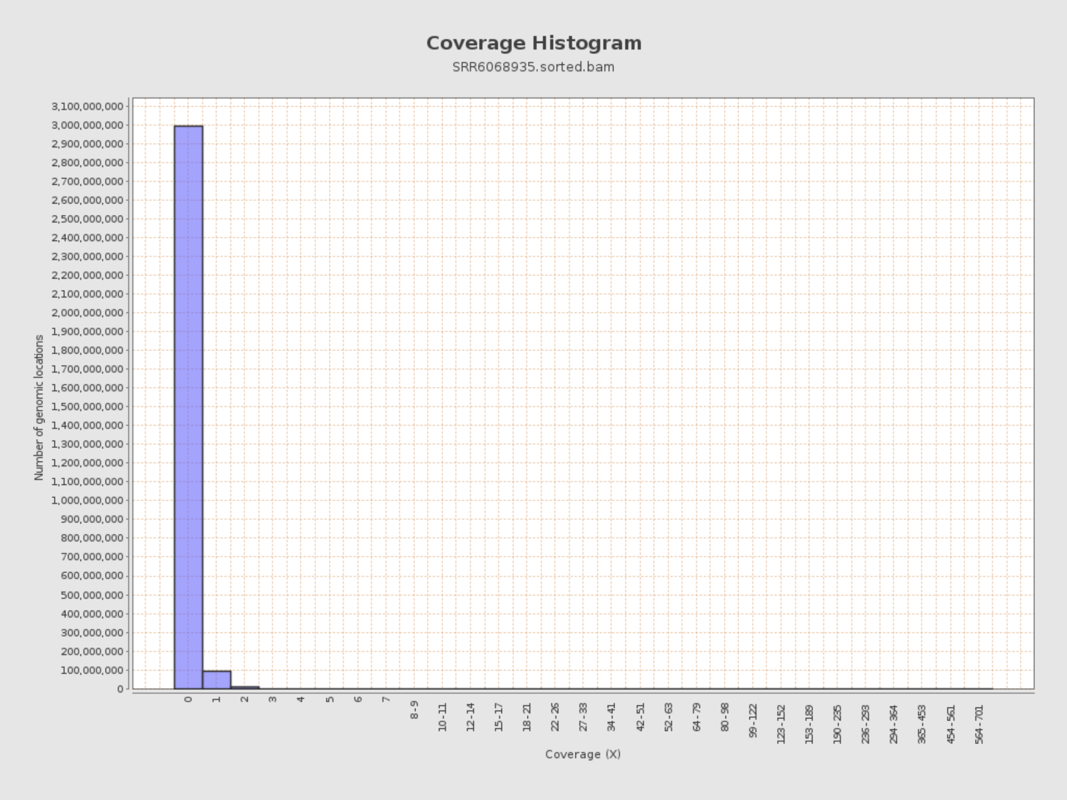
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17537121	0.0704	0.6159
chr2	243199373	3373355	0.0139	0.2452
chr3	198022430	6958040	0.0351	0.2609
chr4	191154276	6305768	0.033	0.2116
chr5	180915260	5886683	0.0325	0.1989
chr6	171115067	7332830	0.0429	0.2641
chr7	159138663	5465890	0.0343	0.2717

chr8	146364022	6828370	0.0467	0.4378
chr9	141213431	6890721	0.0488	0.3547
chr10	135534747	9771088	0.0721	0.7701
chr11	135006516	6018013	0.0446	0.4404
chr12	133851895	4413699	0.033	0.2078
chr13	115169878	2527917	0.0219	0.1604
chr14	107349540	3567524	0.0332	0.2318
chr15	102531392	2698128	0.0263	0.1778
chr16	90354753	2440148	0.027	0.2205
chr17	81195210	3239531	0.0399	0.2579
chr18	78077248	1803015	0.0231	0.5125
chr19	59128983	2351225	0.0398	0.4173
chr20	63025520	1236713	0.0196	0.1675
chr21	48129895	1633395	0.0339	0.2207
chr22	51304566	1053156	0.0205	0.1584
chrMT	16571	64433	3.8883	3.1331
chrX	155270560	9066322	0.0584	0.3237
chrY	59373566	297402	0.005	0.1112

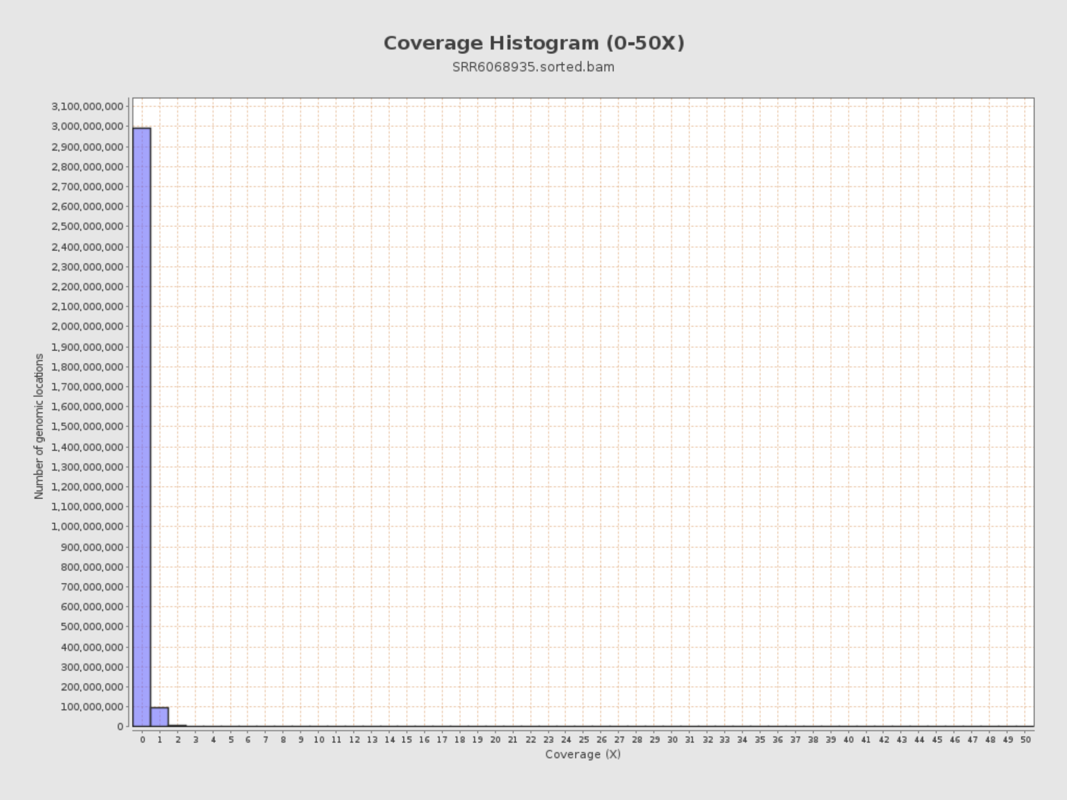
3. Results : Coverage across reference



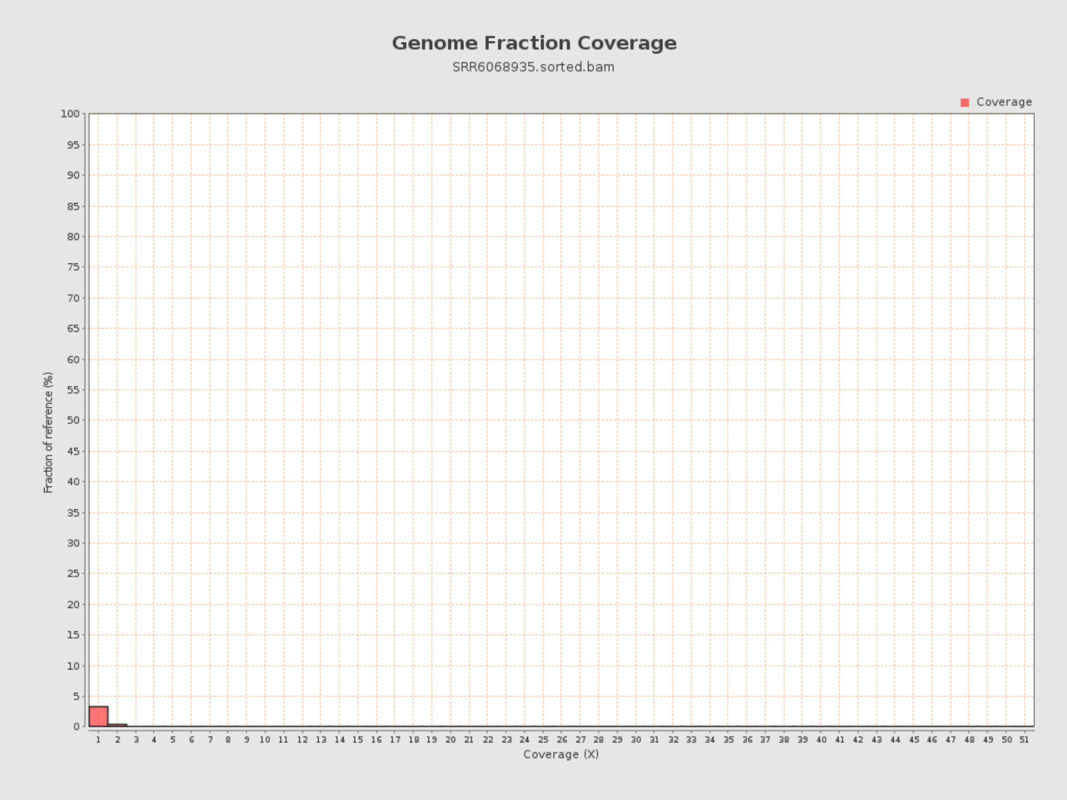
4. Results : Coverage Histogram



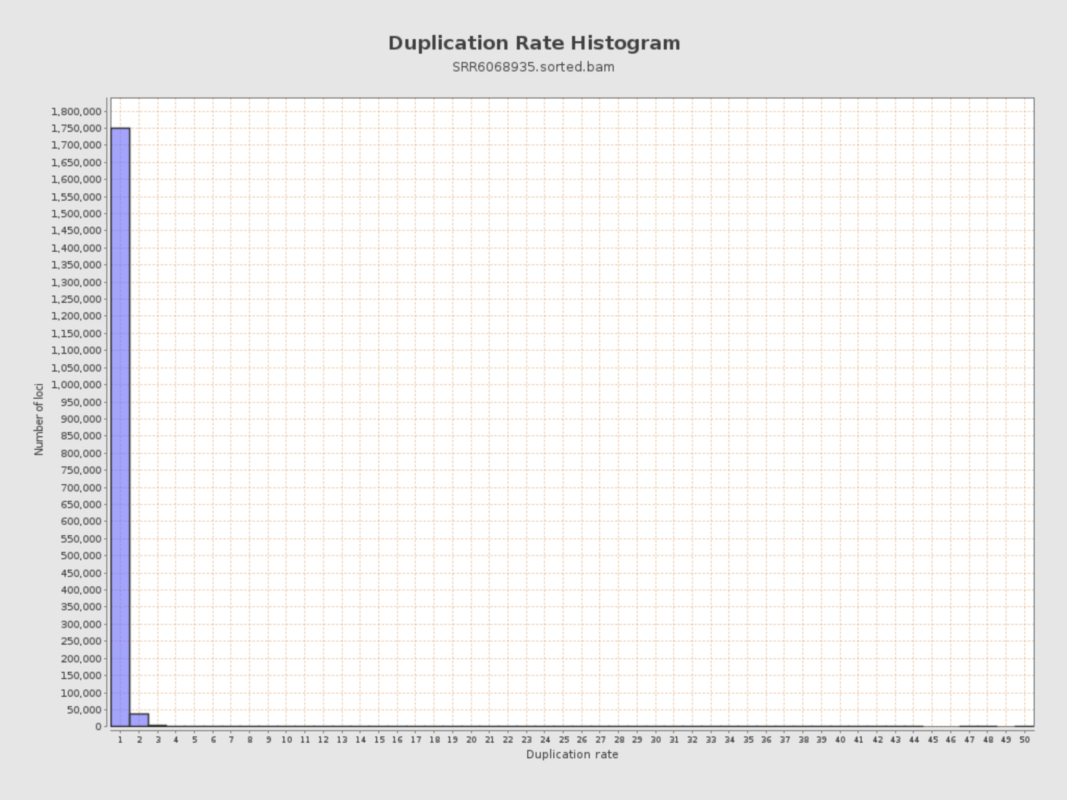
5. Results : Coverage Histogram (0-50X)



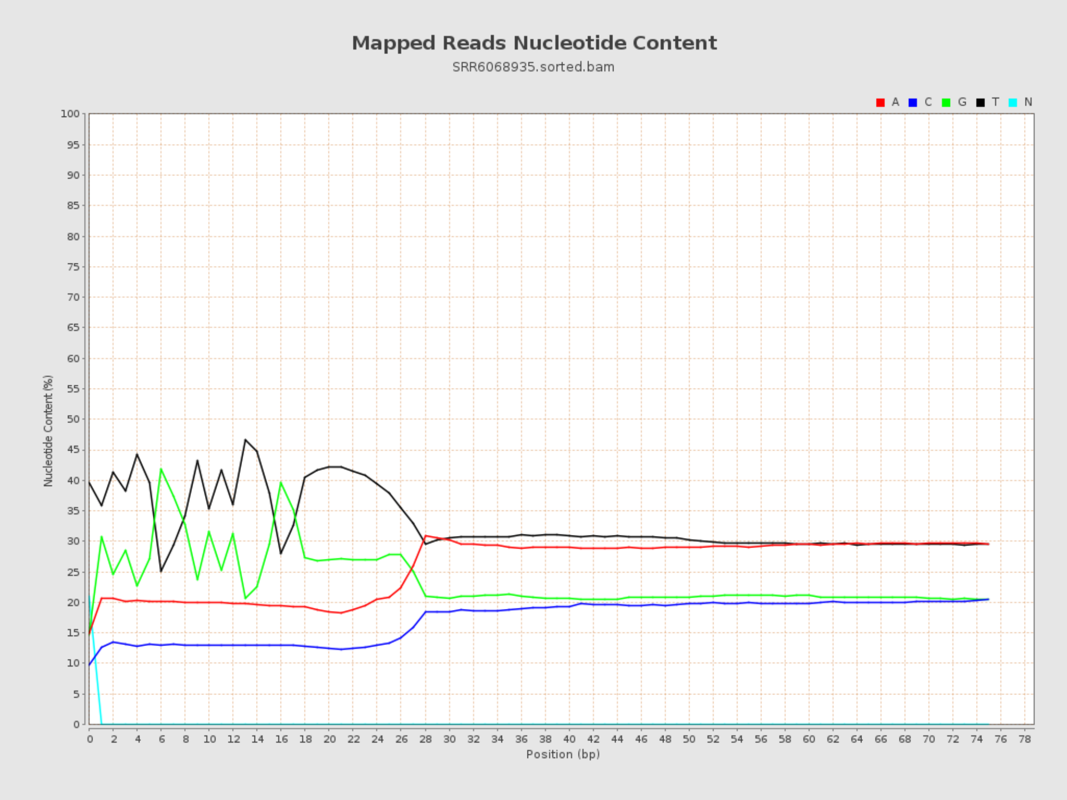
6. Results : Genome Fraction Coverage



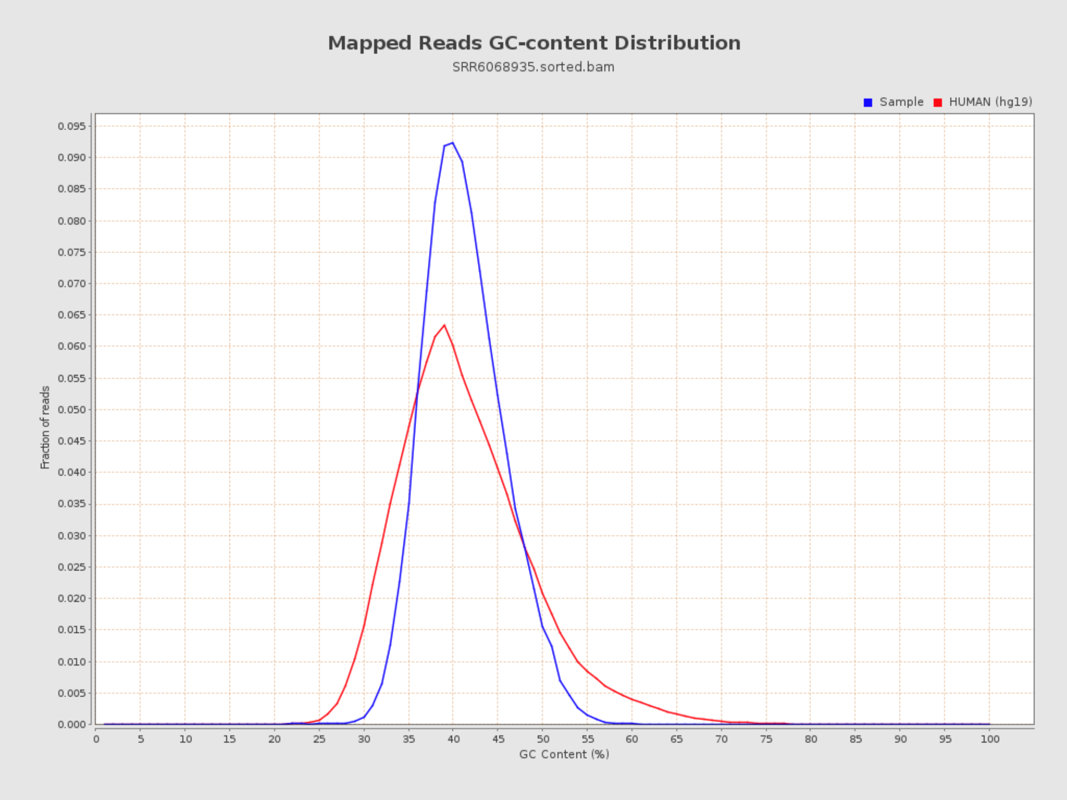
7. Results : Duplication Rate Histogram



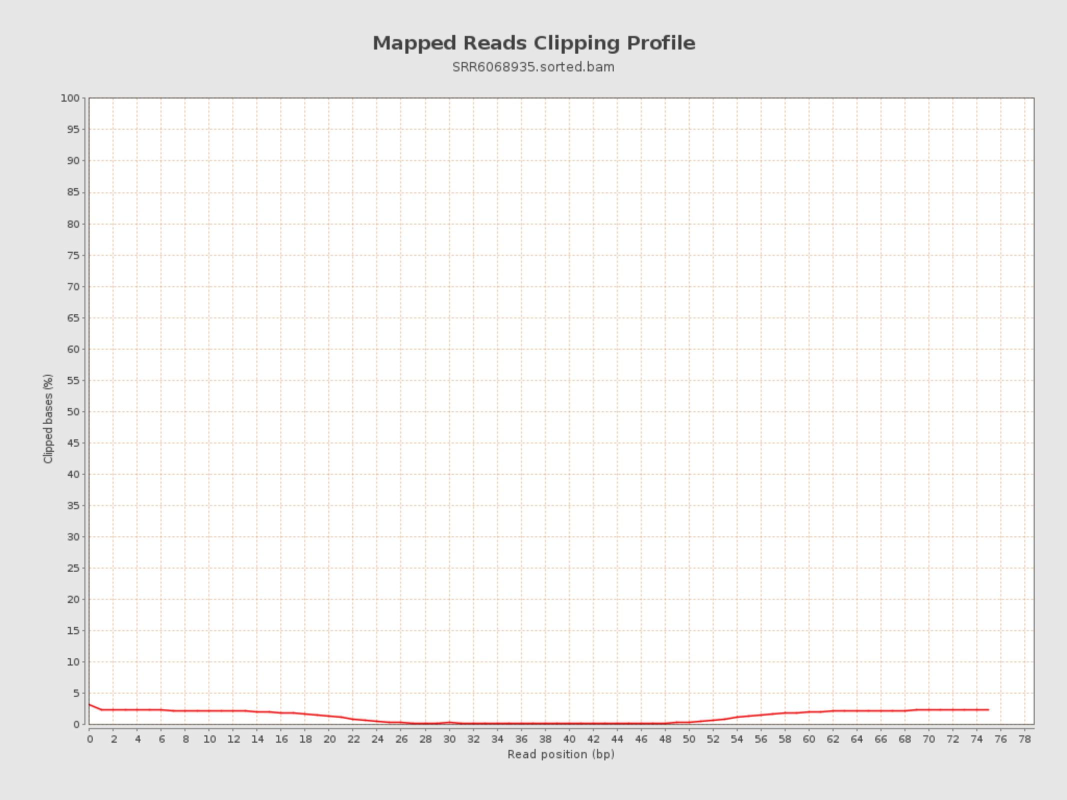
8. Results : Mapped Reads Nucleotide Content



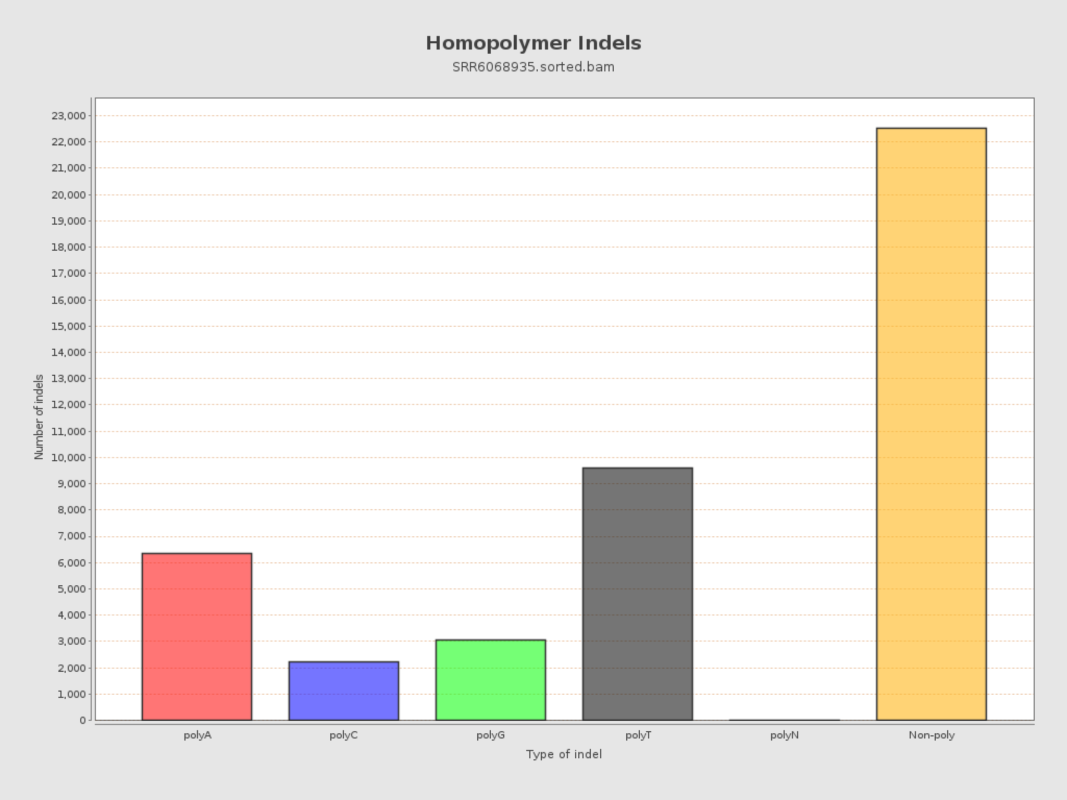
9. Results : Mapped Reads GC-content Distribution



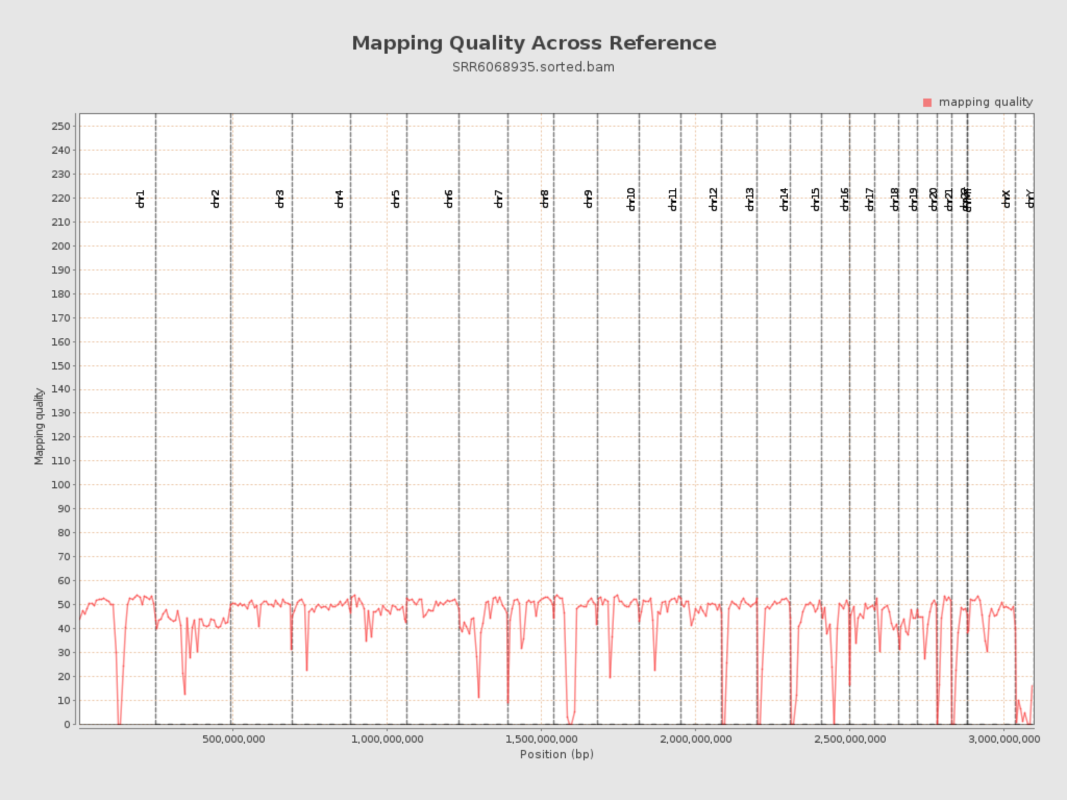
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram