Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:08:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008777.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_SRR6008777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:08:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,733,547
Mapped reads	2,534,302 / 92.71%
Unmapped reads	199,245 / 7.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,227 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	91,399 / 3.34%
Duplication rate	2.45%
Clipped reads	1,069,406 / 39.12%

2.2. ACGT Content

Number/percentage of A's	46,154,286 / 27.14%
Number/percentage of C's	32,636,120 / 19.19%
Number/percentage of T's	52,219,641 / 30.71%
Number/percentage of G's	38,817,914 / 22.83%
Number/percentage of N's	238,852 / 0.14%
GC Percentage	42.02%

2.3. Coverage

Mean	0.055

Standard Deviation	0.522

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

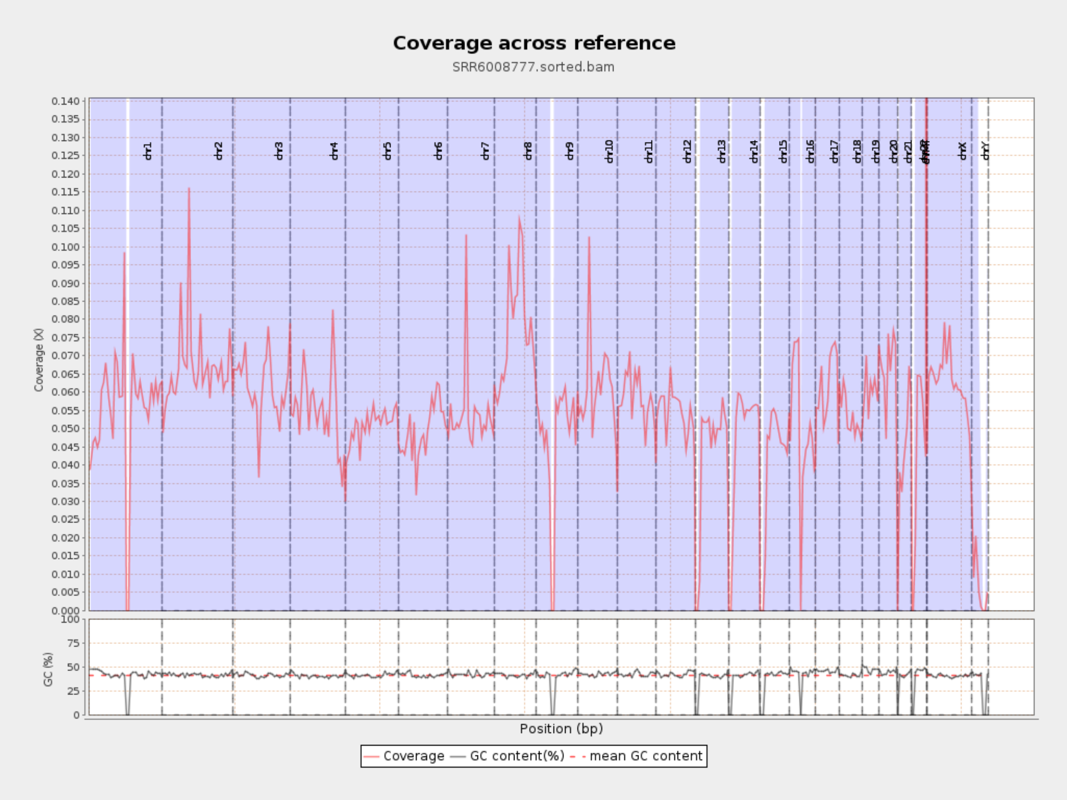
General error rate	0.84%
Mismatches	1,398,985
Insertions	12,415
Mapped reads with at least one insertion	0.49%
Deletions	44,422
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.47%

2.6. Chromosome stats

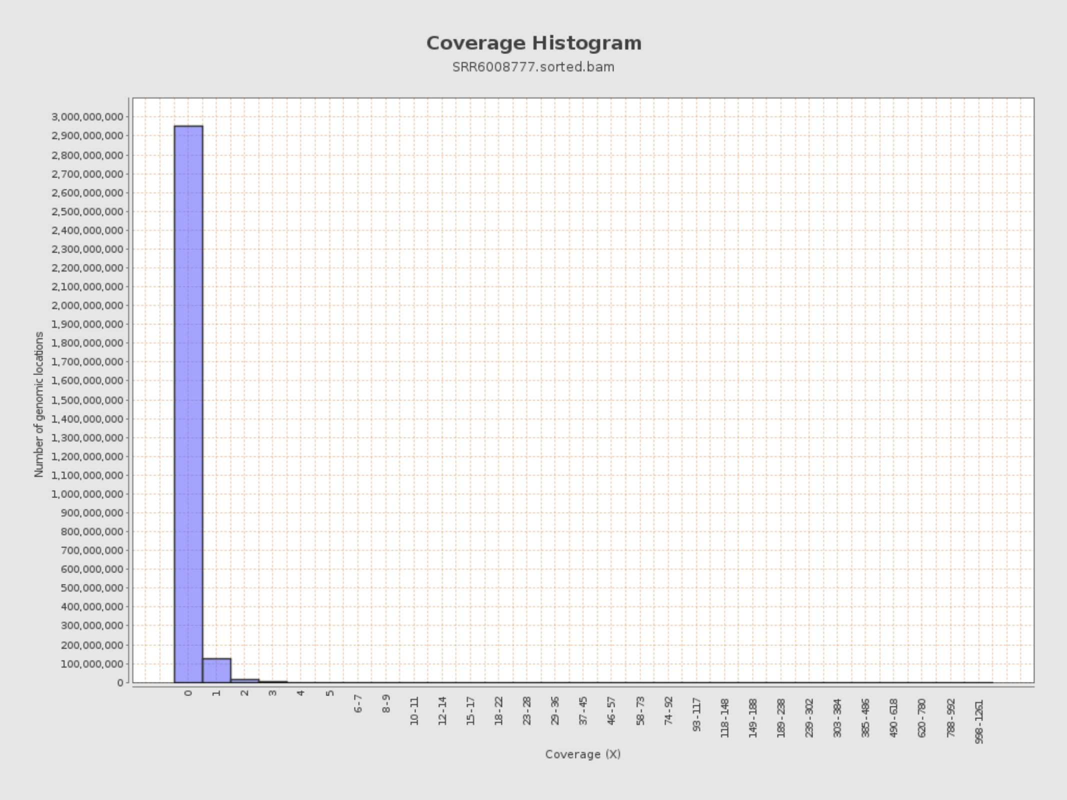
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13734104	0.0551	1.0621
chr2	243199373	16330029	0.0671	0.6942
chr3	198022430	12179623	0.0615	0.2912
chr4	191154276	10481874	0.0548	0.2835
chr5	180915260	9228474	0.051	0.2574
chr6	171115067	8451265	0.0494	0.3088
chr7	159138663	8604290	0.0541	0.7889

chr8	146364022	11349821	0.0775	0.6764
chr9	141213431	6587631	0.0467	0.3782
chr10	135534747	8317947	0.0614	0.533
chr11	135006516	7856046	0.0582	0.3933
chr12	133851895	7310095	0.0546	0.2714
chr13	115169878	4882266	0.0424	0.2356
chr14	107349540	4997664	0.0466	0.2744
chr15	102531392	4051802	0.0395	0.2285
chr16	90354753	4534443	0.0502	0.3175
chr17	81195210	5018405	0.0618	0.3216
chr18	78077248	4186532	0.0536	0.6408
chr19	59128983	3586864	0.0607	0.724
chr20	63025520	4175089	0.0662	0.3041
chr21	48129895	2066931	0.0429	0.2584
chr22	51304566	2041953	0.0398	0.2278
chrMT	16571	42327	2.5543	2.1721
chrX	155270560	9704295	0.0625	0.3135
chrY	59373566	425312	0.0072	0.1565

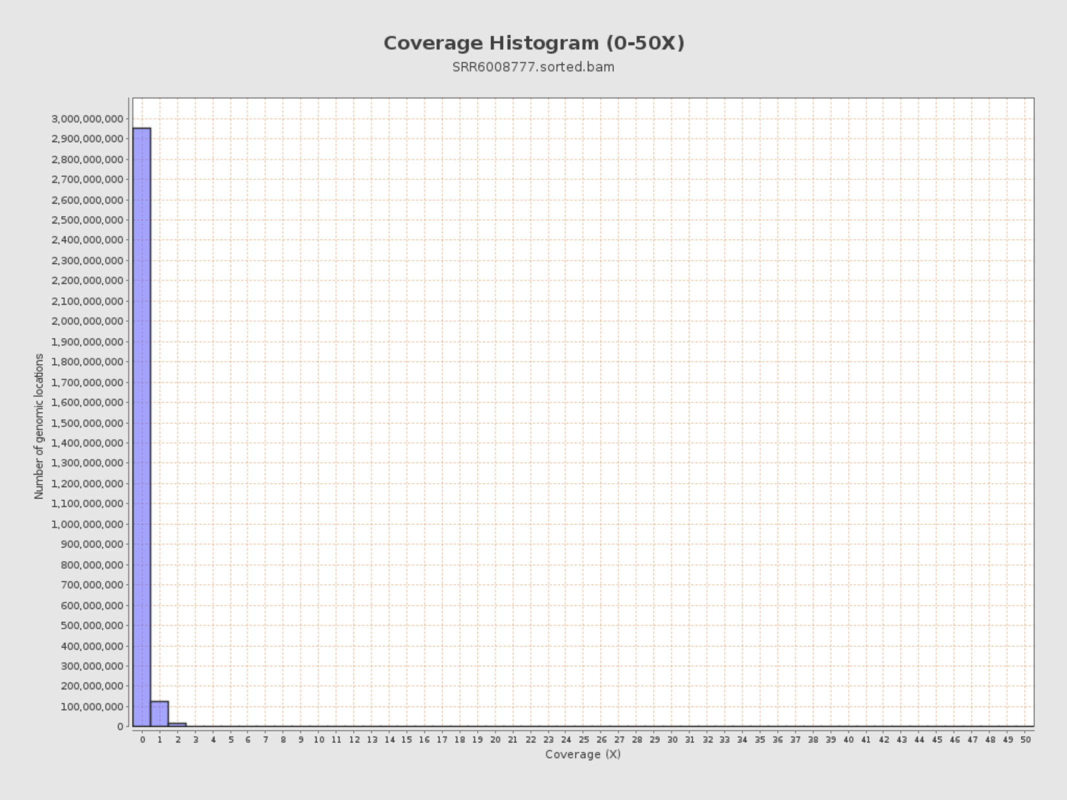
3. Results : Coverage across reference



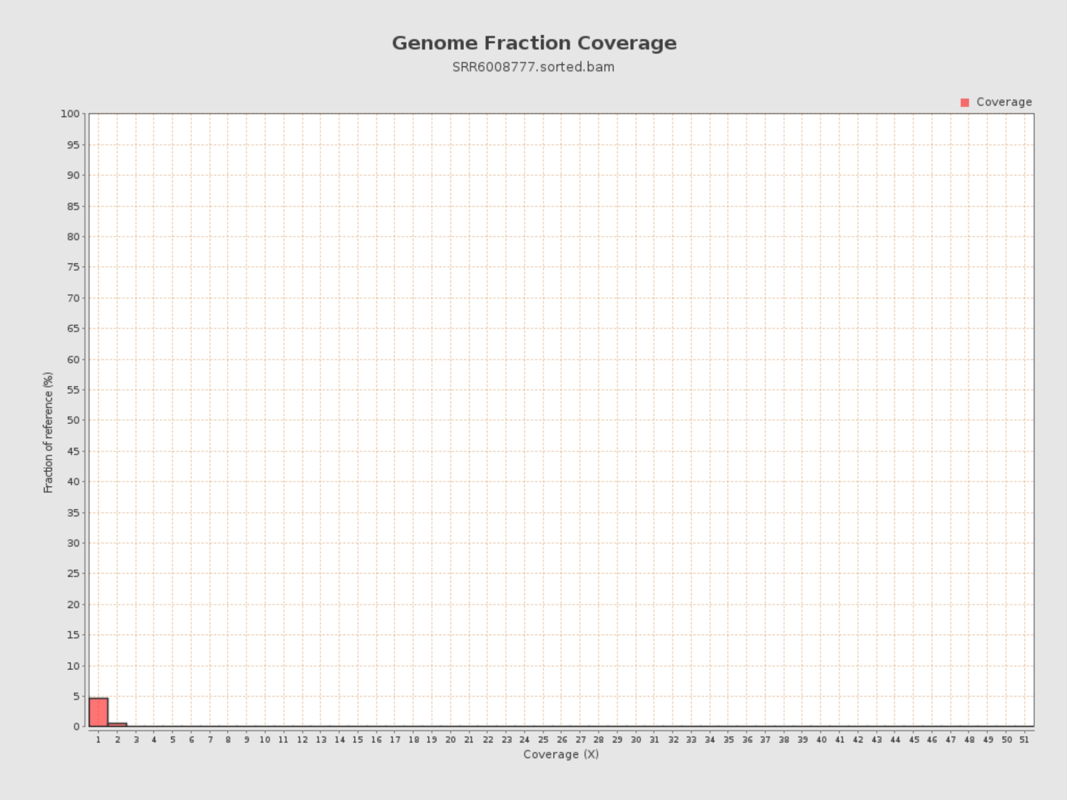
4. Results : Coverage Histogram



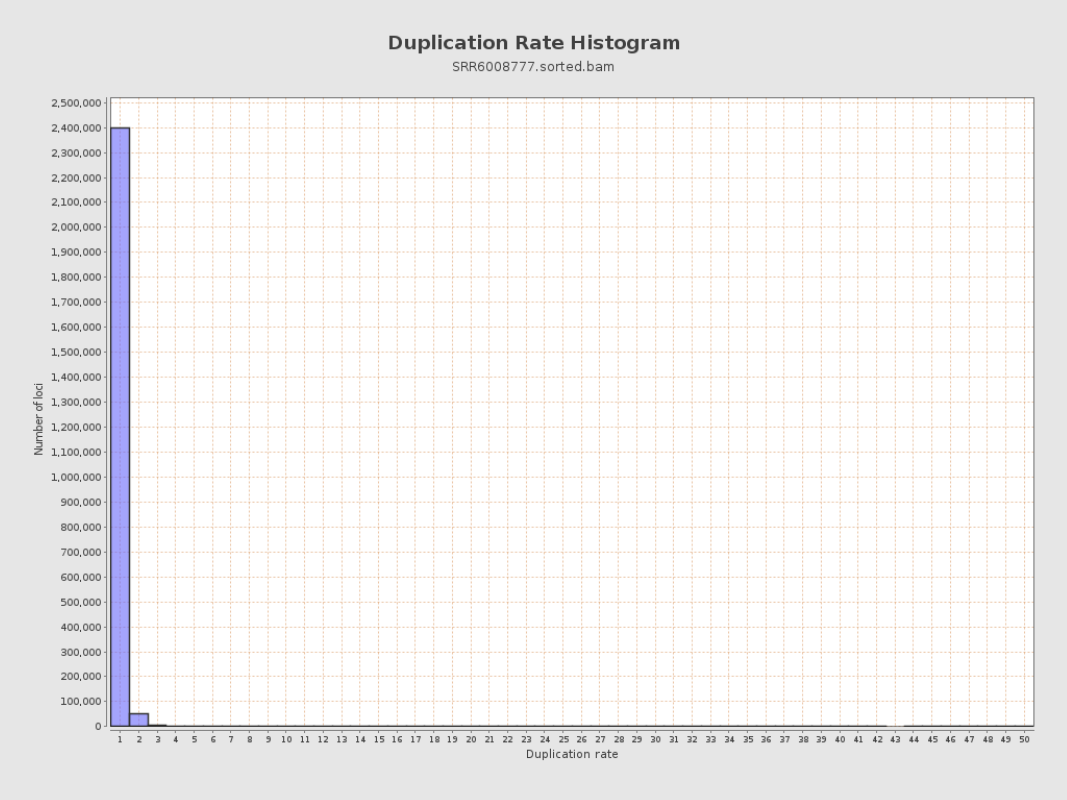
5. Results : Coverage Histogram (0-50X)



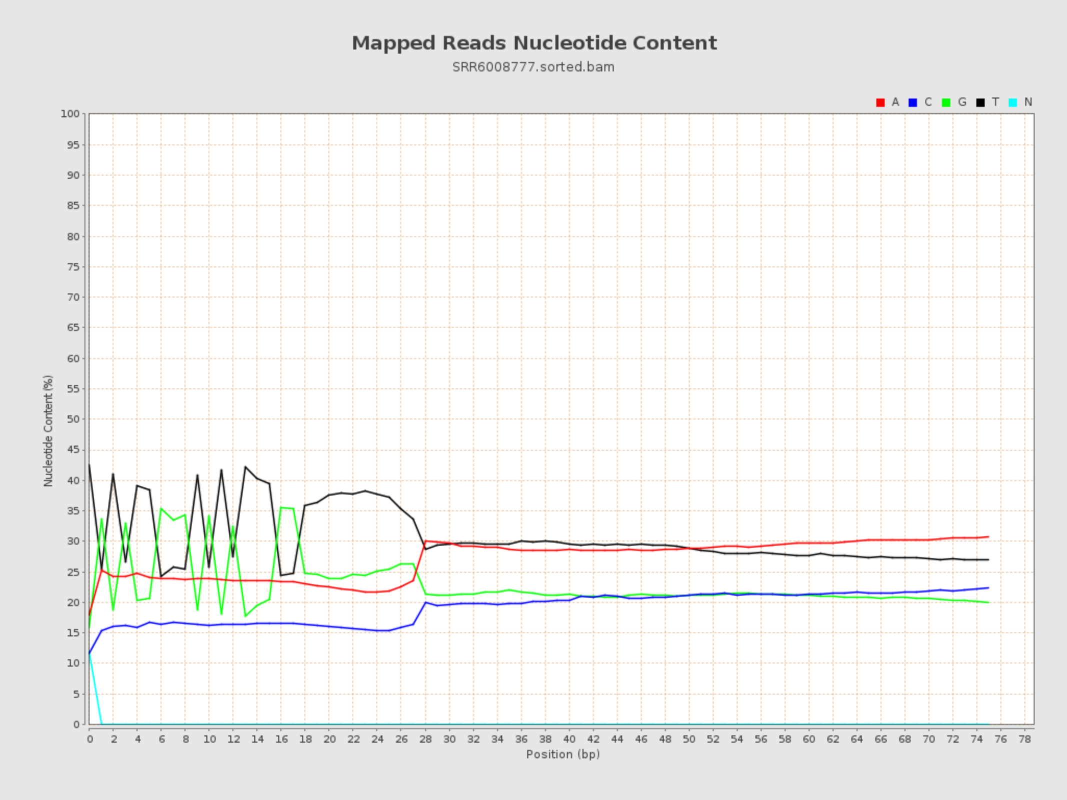
6. Results : Genome Fraction Coverage



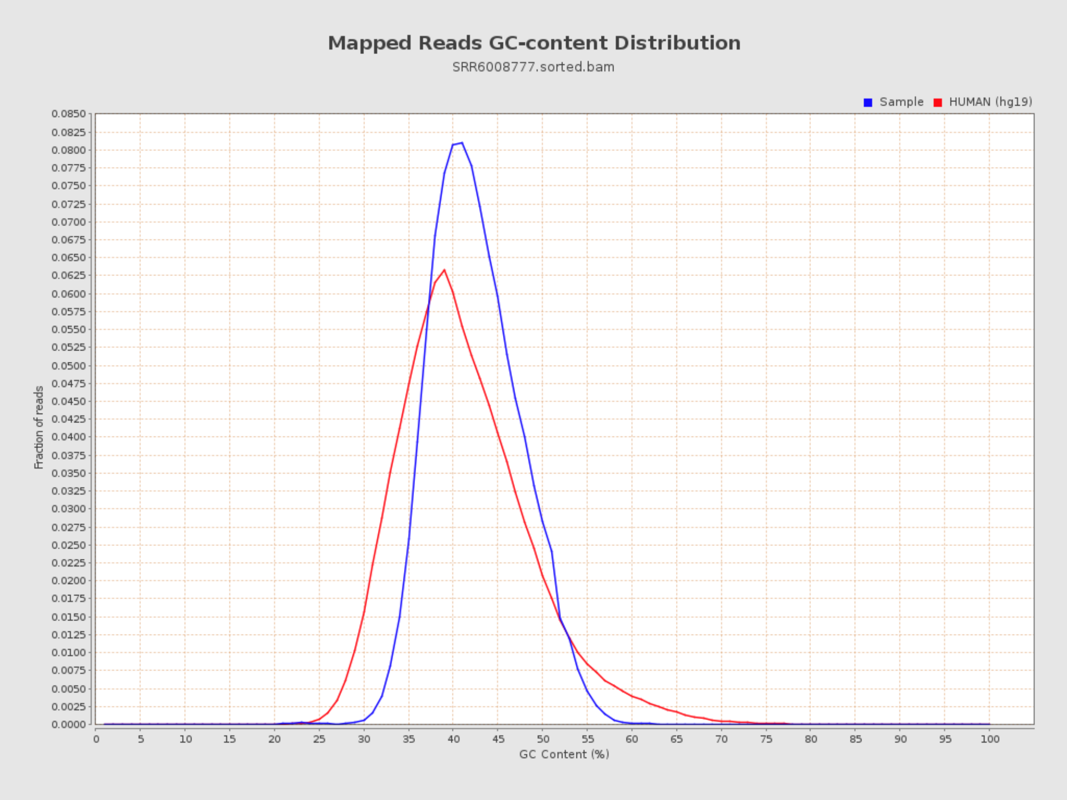
7. Results : Duplication Rate Histogram



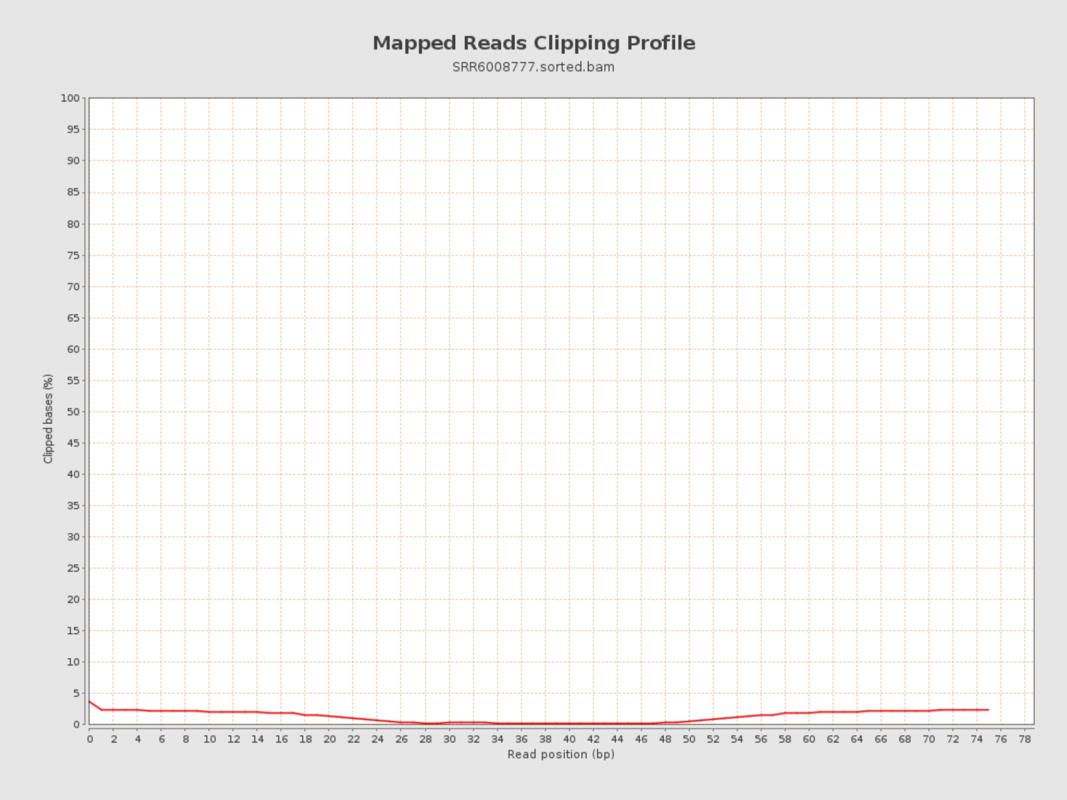
8. Results : Mapped Reads Nucleotide Content



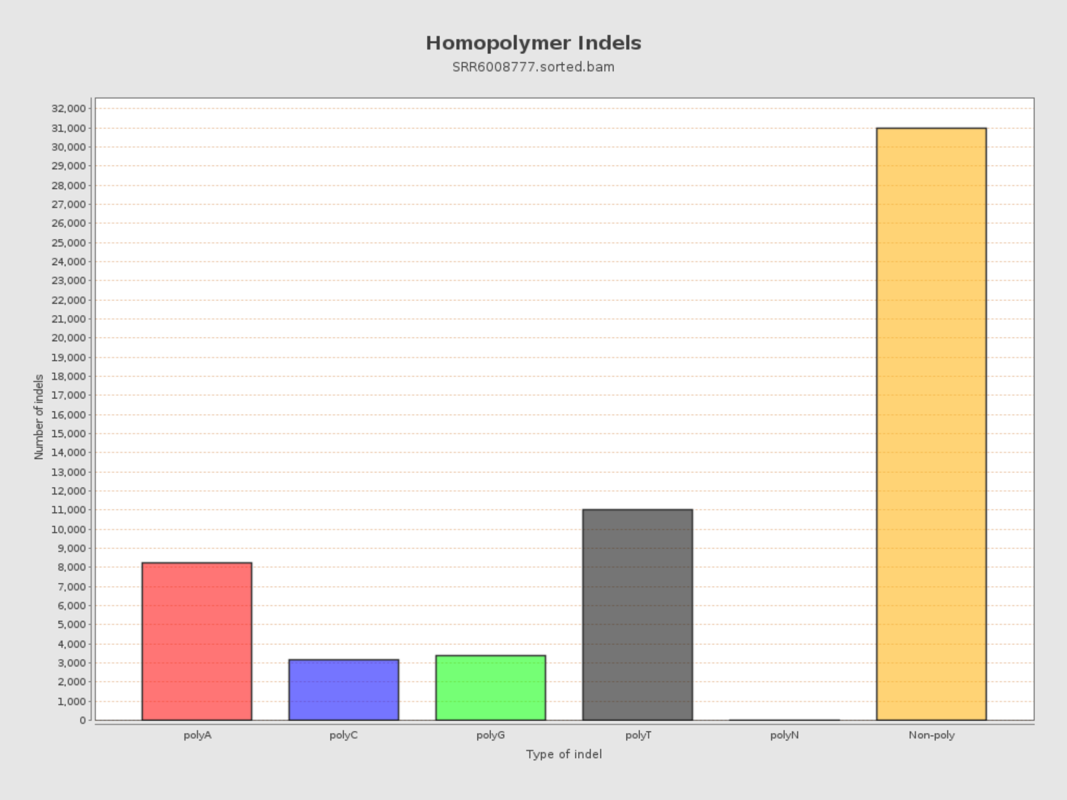
9. Results : Mapped Reads GC-content Distribution



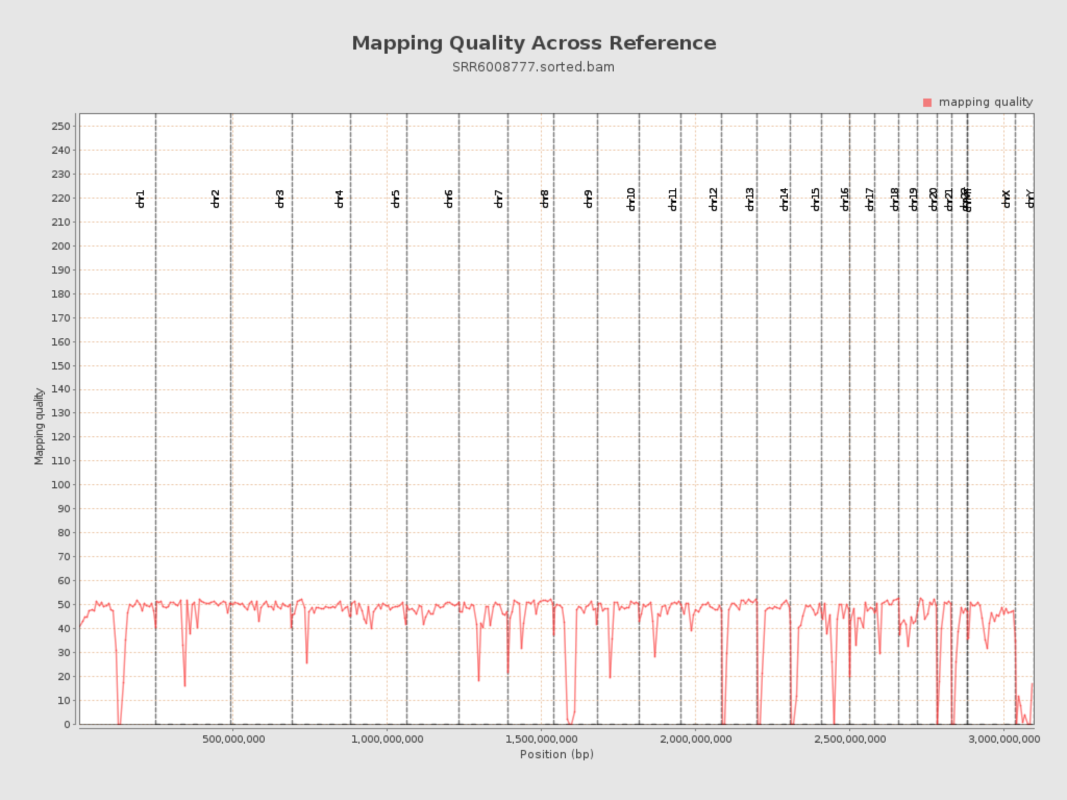
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram