Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:55:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818773.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_SRR1818773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:55:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,048,732
Mapped reads	1,926,402 / 94.03%
Unmapped reads	122,330 / 5.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,040 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	934,605 / 45.62%
Duplication rate	41.31%
Clipped reads	1,921,740 / 93.8%

2.2. ACGT Content

Number/percentage of A's	37,903,248 / 28.97%
Number/percentage of C's	27,725,662 / 21.19%
Number/percentage of T's	38,181,264 / 29.19%
Number/percentage of G's	27,004,656 / 20.64%
Number/percentage of N's	8,361 / 0.01%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.5353

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

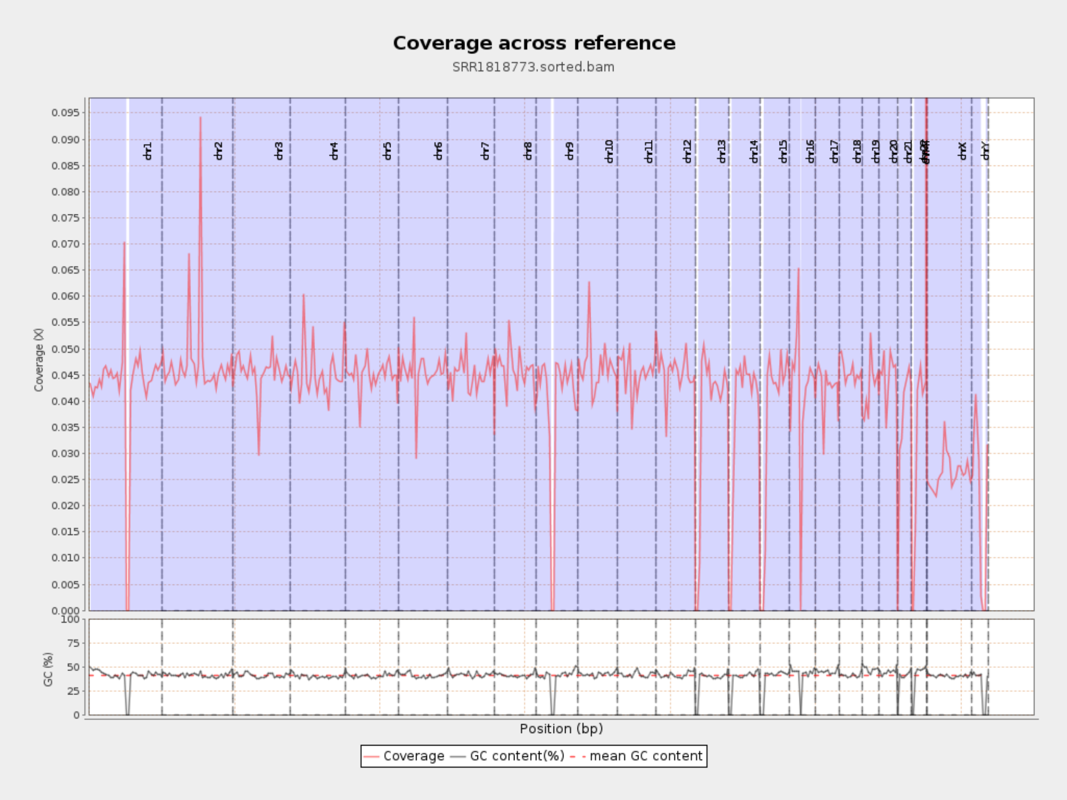
General error rate	0.55%
Mismatches	683,961
Insertions	15,466
Mapped reads with at least one insertion	0.79%
Deletions	34,060
Mapped reads with at least one deletion	1.75%
Homopolymer indels	41.16%

2.6. Chromosome stats

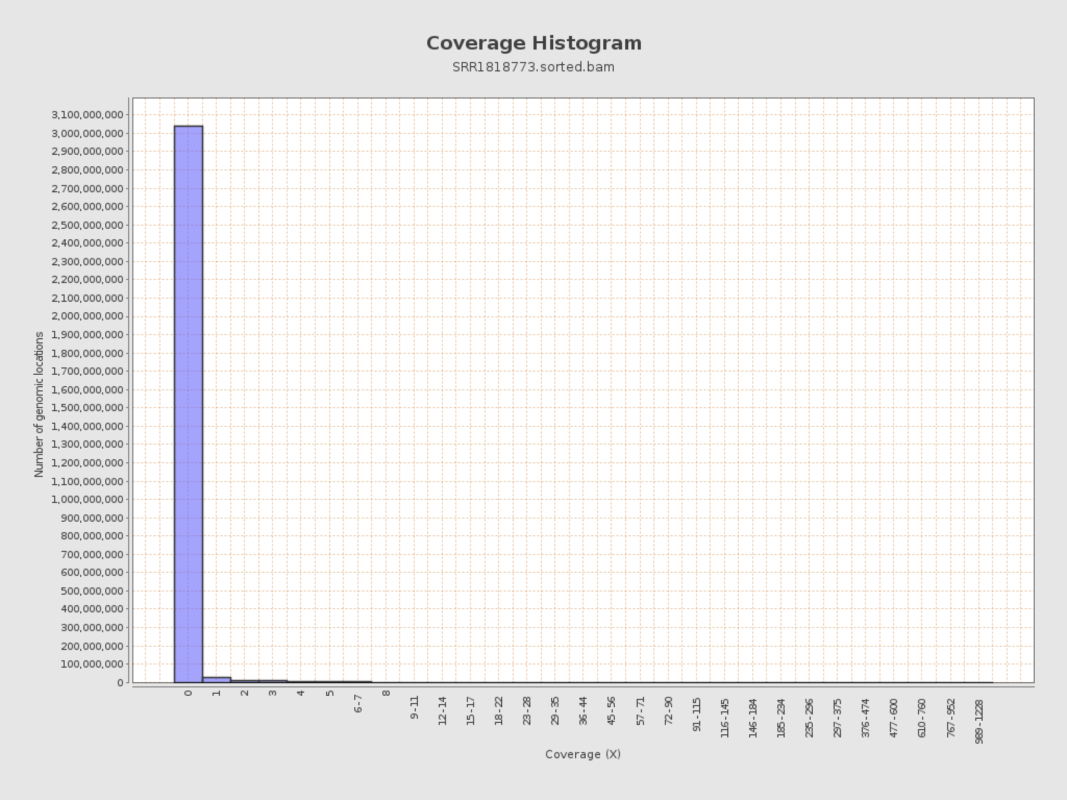
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10656695	0.0428	0.6975
chr2	243199373	11629125	0.0478	0.911
chr3	198022430	8988013	0.0454	0.4101
chr4	191154276	8660695	0.0453	0.4693
chr5	180915260	8166996	0.0451	0.4232
chr6	171115067	7811006	0.0456	0.4521
chr7	159138663	7195757	0.0452	0.4692

chr8	146364022	6783236	0.0463	0.4672
chr9	141213431	5548228	0.0393	0.4412
chr10	135534747	6314957	0.0466	0.5718
chr11	135006516	6115339	0.0453	0.4531
chr12	133851895	6098160	0.0456	0.4448
chr13	115169878	4279996	0.0372	0.3697
chr14	107349540	3994851	0.0372	0.4192
chr15	102531392	3737665	0.0365	0.3694
chr16	90354753	3814839	0.0422	0.5777
chr17	81195210	3451990	0.0425	0.4171
chr18	78077248	3567714	0.0457	0.577
chr19	59128983	2516537	0.0426	0.615
chr20	63025520	2828832	0.0449	0.4356
chr21	48129895	1732271	0.036	0.3829
chr22	51304566	1544882	0.0301	0.3724
chrMT	16571	166437	10.0439	10.656
chrX	155270560	4079321	0.0263	0.3353
chrY	59373566	1194706	0.0201	0.8194

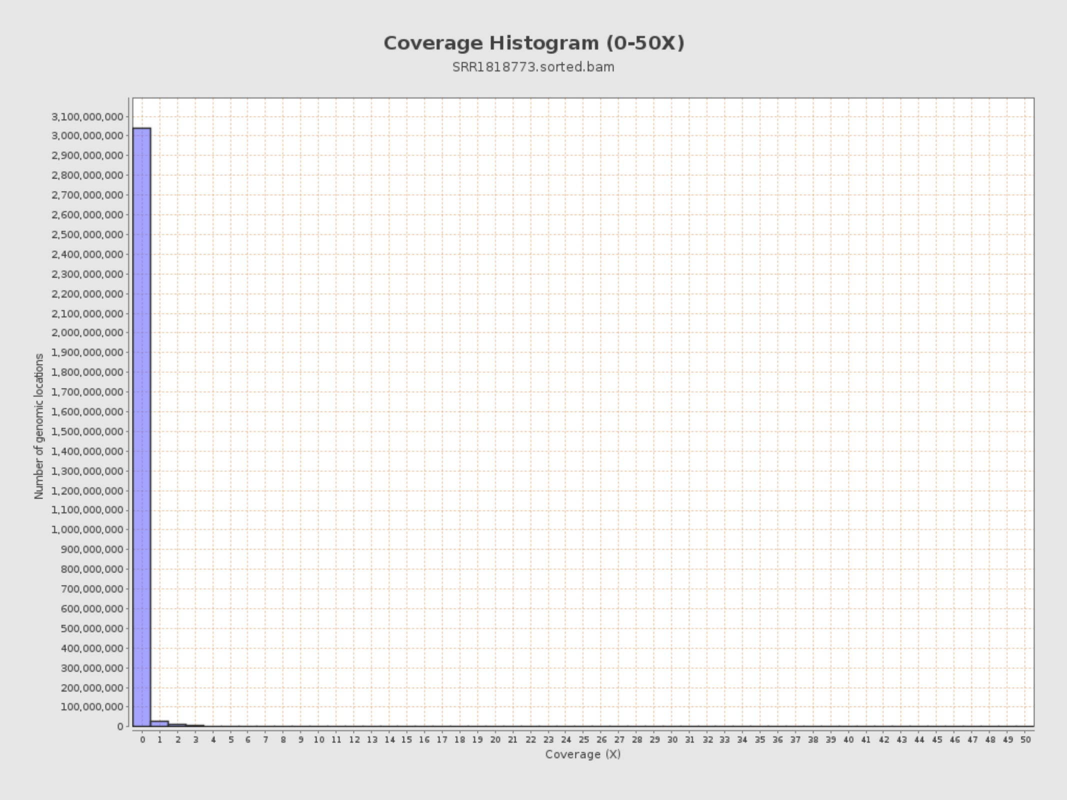
3. Results : Coverage across reference



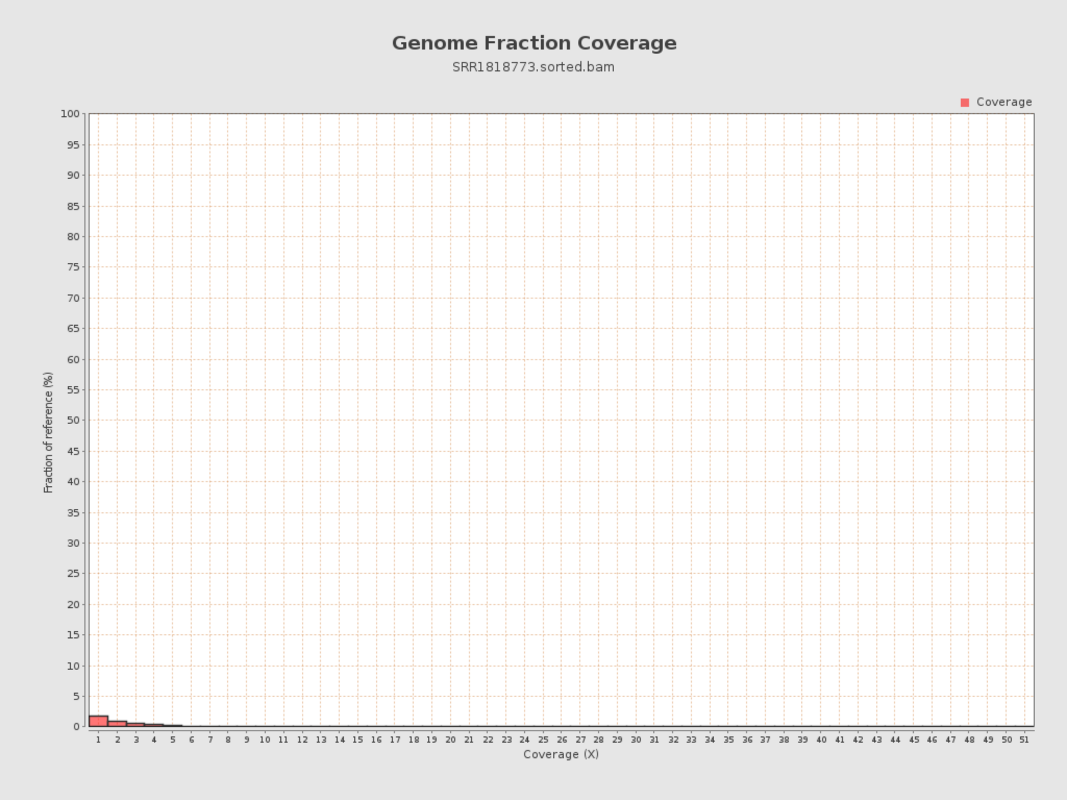
4. Results : Coverage Histogram



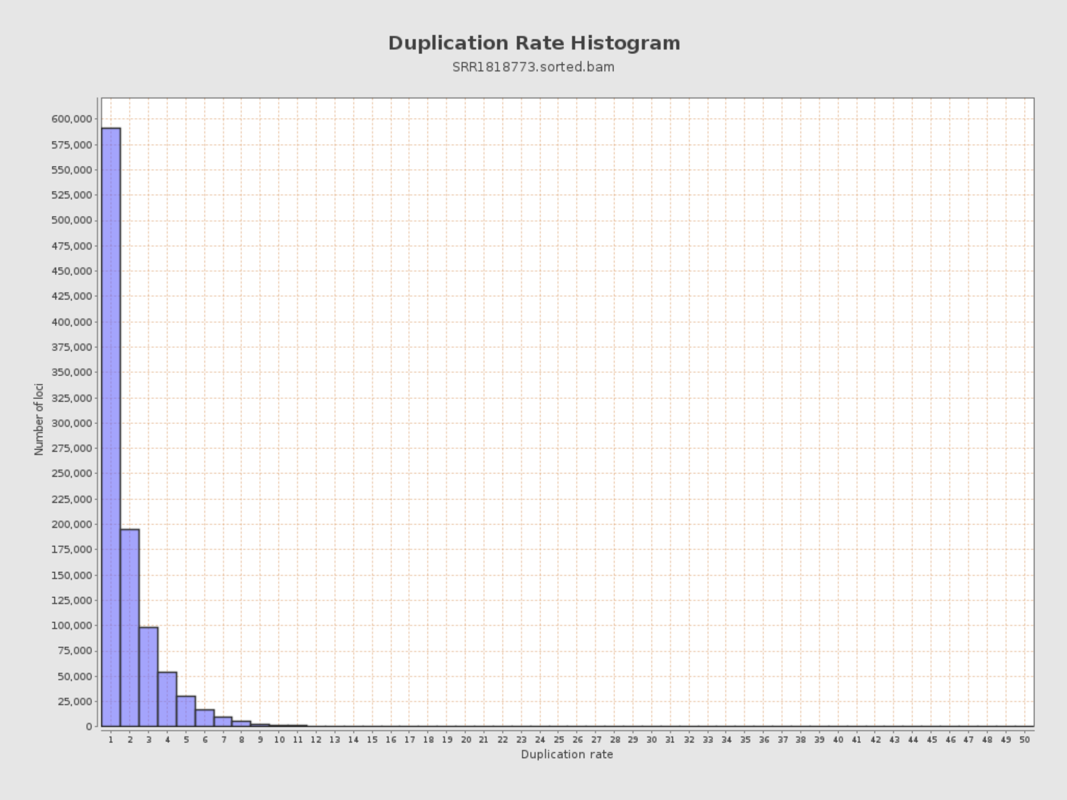
5. Results : Coverage Histogram (0-50X)



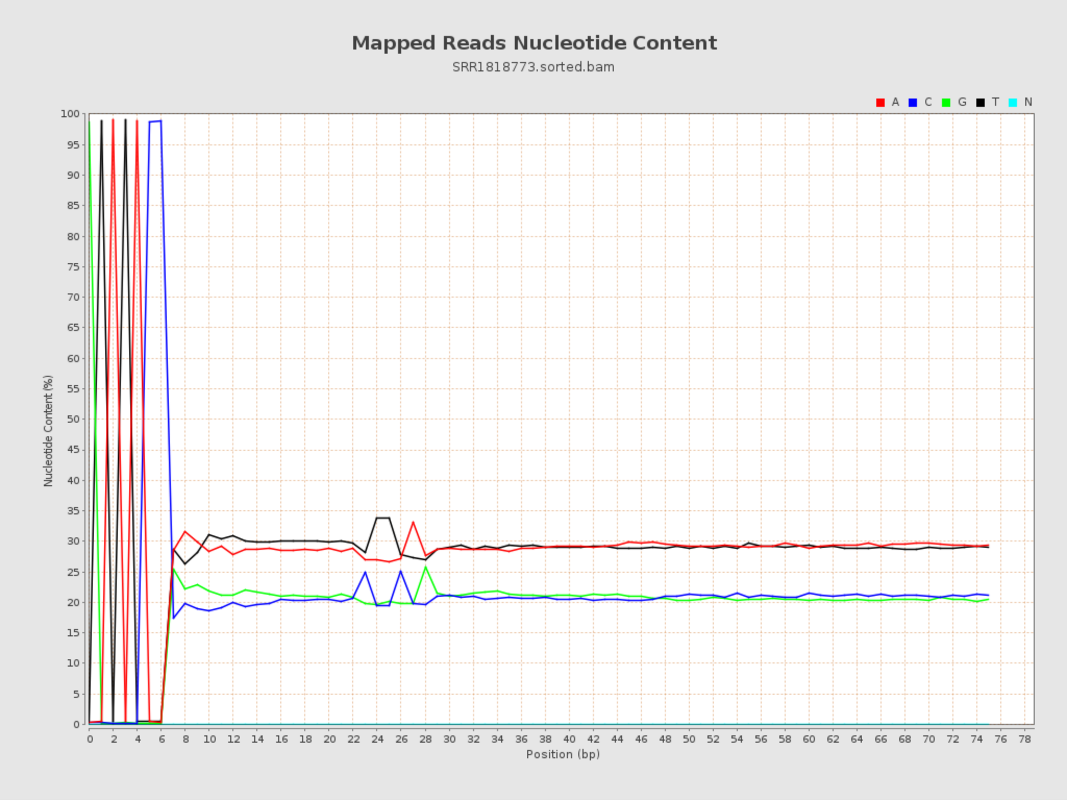
6. Results : Genome Fraction Coverage



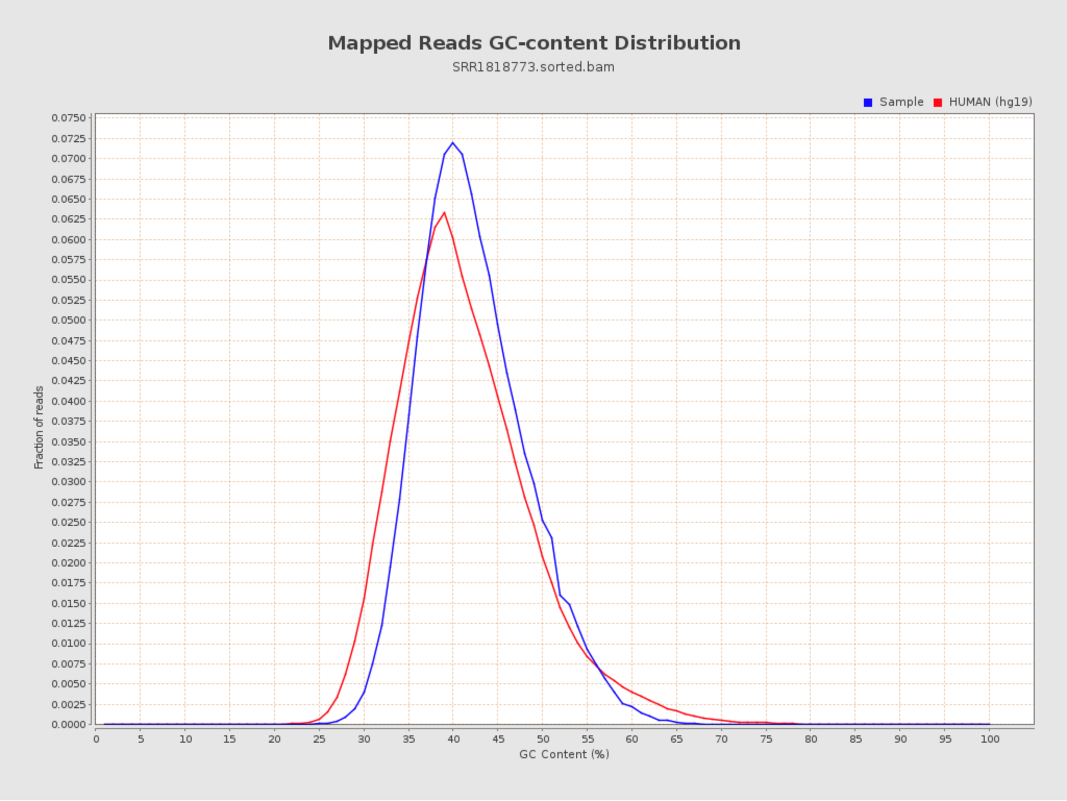
7. Results : Duplication Rate Histogram



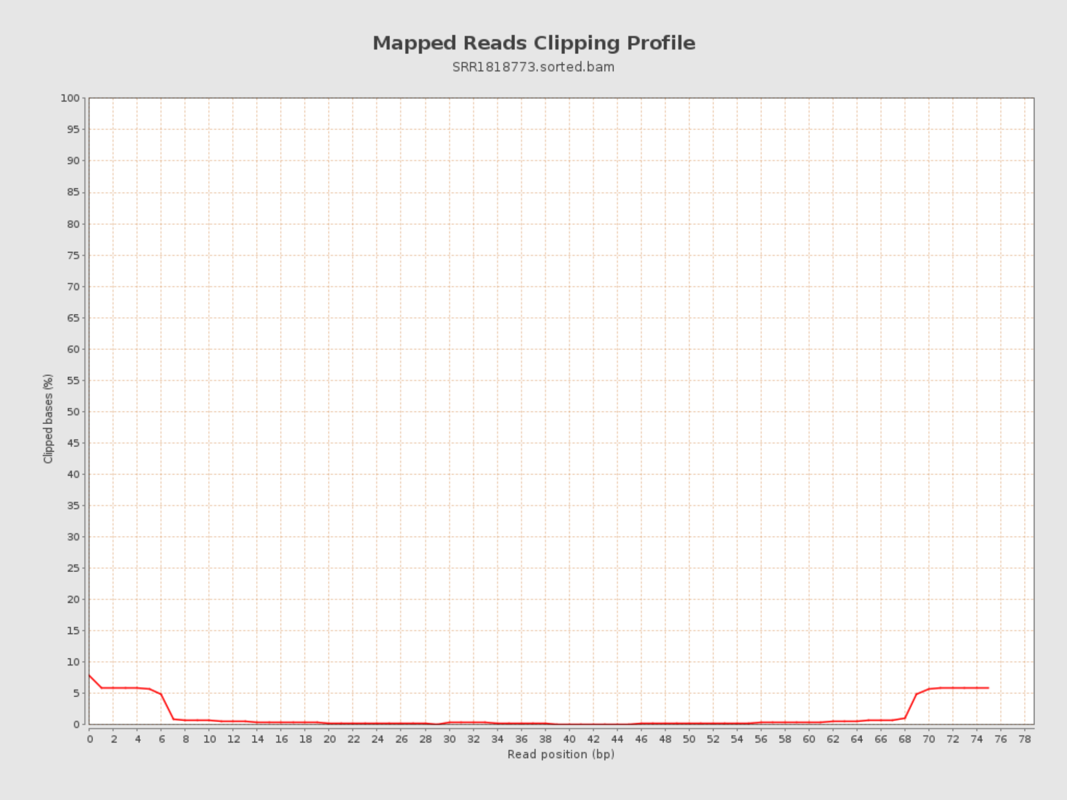
8. Results : Mapped Reads Nucleotide Content



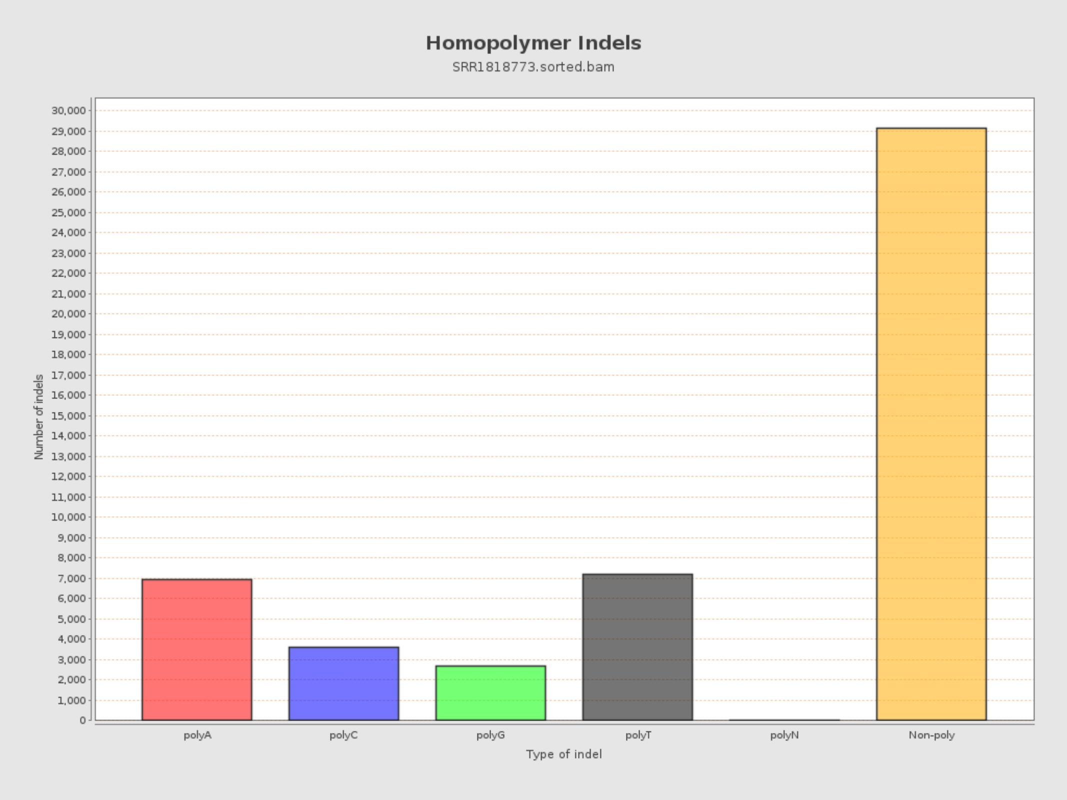
9. Results : Mapped Reads GC-content Distribution



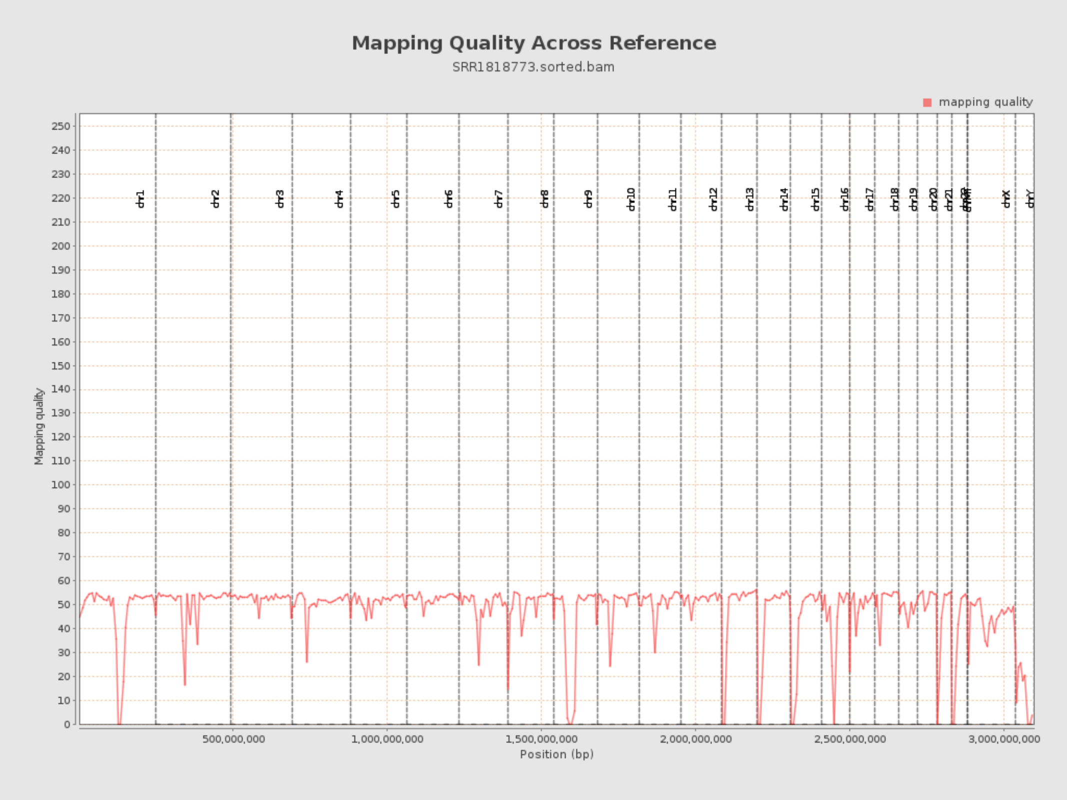
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram