Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:50:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818755.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_SRR1818755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,832,032
Mapped reads	1,784,476 / 97.4%
Unmapped reads	47,556 / 2.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,575 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	875,491 / 47.79%
Duplication rate	42.1%
Clipped reads	1,788,780 / 97.64%

2.2. ACGT Content

Number/percentage of A's	33,082,824 / 27.3%
Number/percentage of C's	27,596,427 / 22.78%
Number/percentage of T's	35,282,263 / 29.12%
Number/percentage of G's	25,191,242 / 20.79%
Number/percentage of N's	7,653 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0392

Standard Deviation	0.4696

2.4. Mapping Quality

Mean Mapping Quality	47.79

2.5. Mismatches and indels

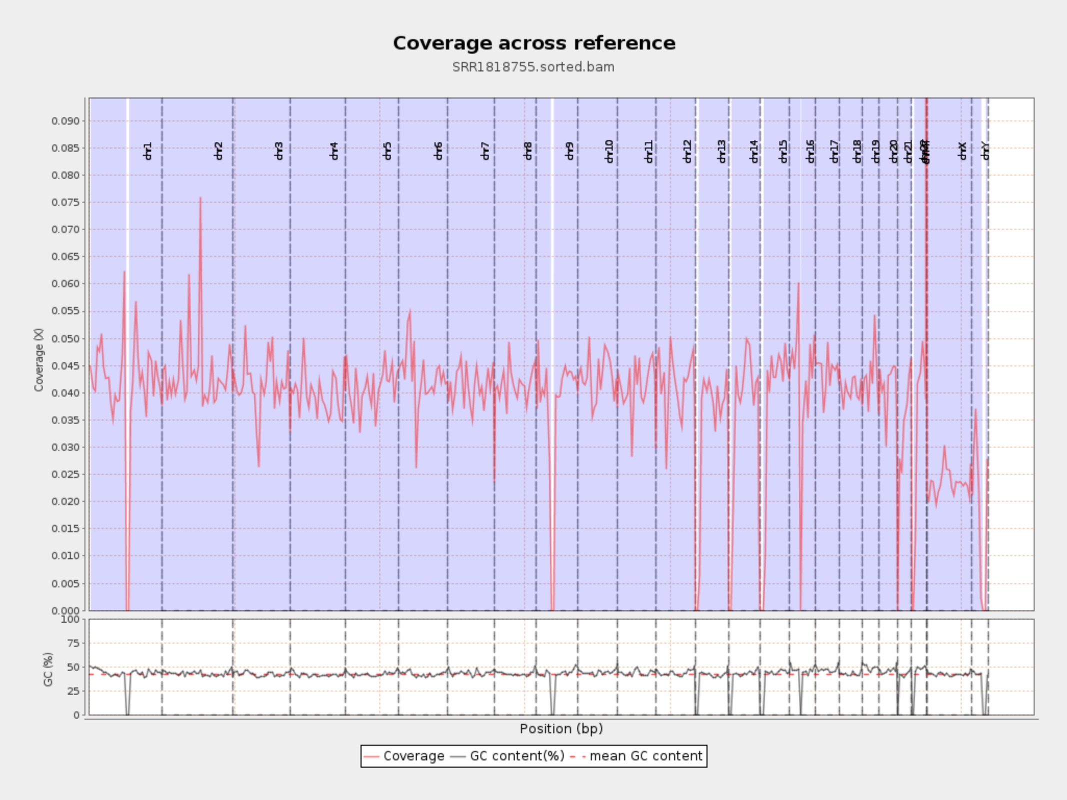
General error rate	0.52%
Mismatches	606,002
Insertions	14,397
Mapped reads with at least one insertion	0.8%
Deletions	30,941
Mapped reads with at least one deletion	1.71%
Homopolymer indels	41.35%

2.6. Chromosome stats

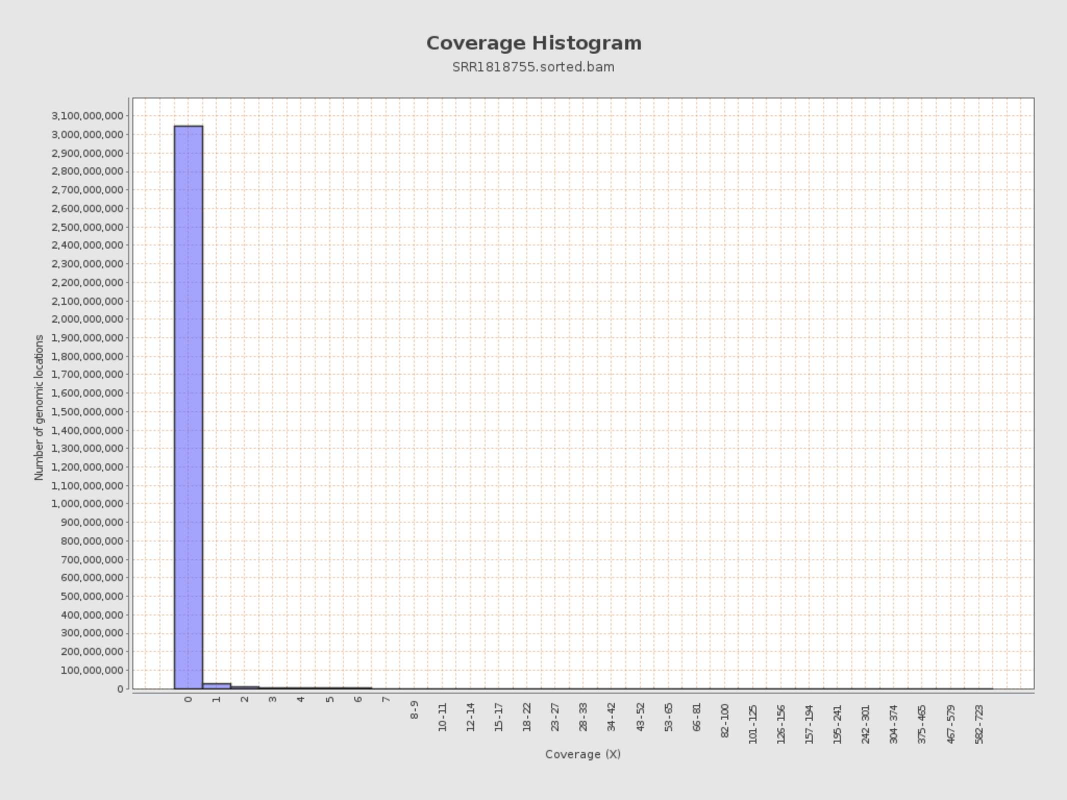
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10189453	0.0409	0.6621
chr2	243199373	10705012	0.044	0.6297
chr3	198022430	8227368	0.0415	0.3926
chr4	191154276	7564220	0.0396	0.408
chr5	180915260	7393203	0.0409	0.4012
chr6	171115067	7357851	0.043	0.4218
chr7	159138663	6558103	0.0412	0.4322

chr8	146364022	6098640	0.0417	0.4368
chr9	141213431	5203794	0.0369	0.4152
chr10	135534747	5817525	0.0429	0.4829
chr11	135006516	5581550	0.0413	0.4261
chr12	133851895	5589113	0.0418	0.406
chr13	115169878	3790024	0.0329	0.3472
chr14	107349540	3797474	0.0354	0.3885
chr15	102531392	3644545	0.0355	0.3661
chr16	90354753	3770689	0.0417	0.5034
chr17	81195210	3552043	0.0437	0.4232
chr18	78077248	3175931	0.0407	0.5395
chr19	59128983	2538609	0.0429	0.5713
chr20	63025520	2601069	0.0413	0.4113
chr21	48129895	1536904	0.0319	0.3578
chr22	51304566	1569169	0.0306	0.3593
chrMT	16571	297761	17.9688	16.1497
chrX	155270560	3629506	0.0234	0.3084
chrY	59373566	1019940	0.0172	0.6307

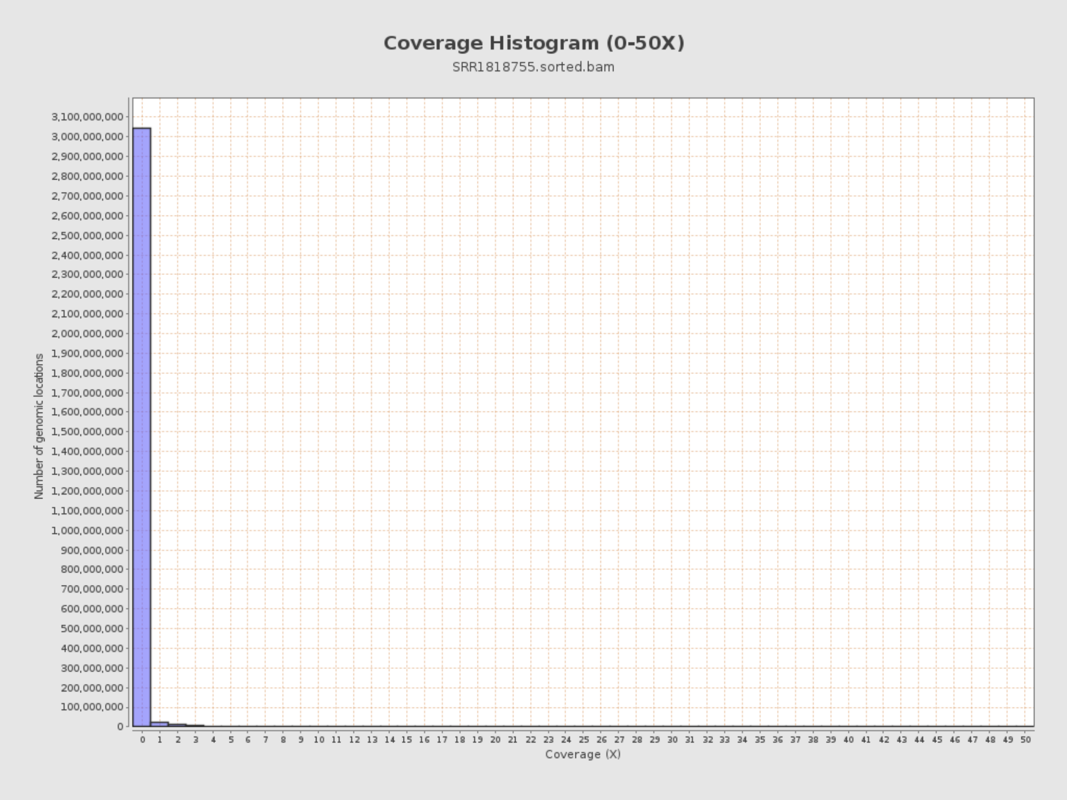
3. Results : Coverage across reference



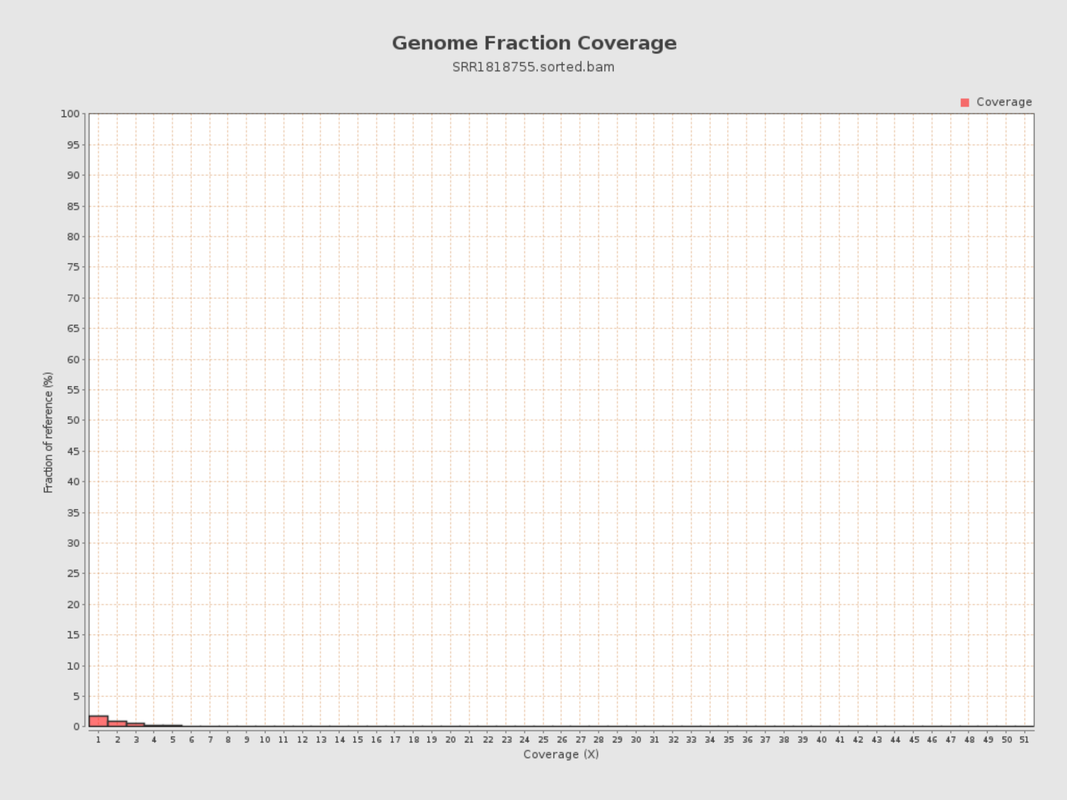
4. Results : Coverage Histogram



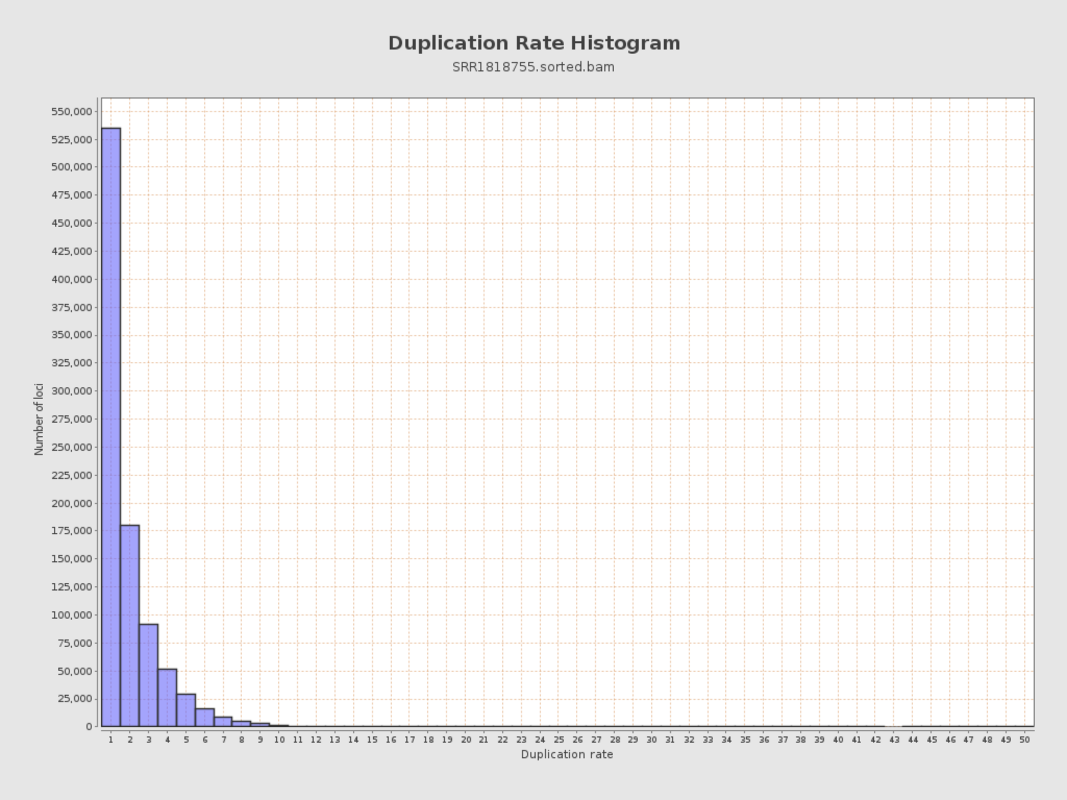
5. Results : Coverage Histogram (0-50X)



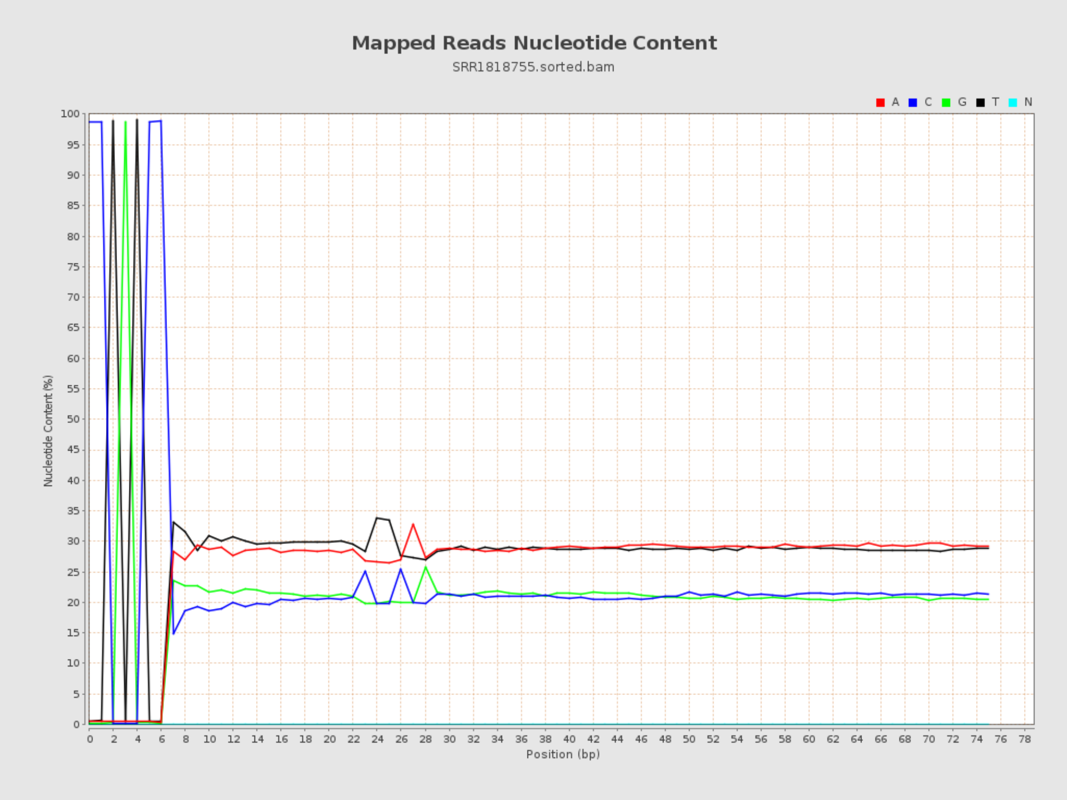
6. Results : Genome Fraction Coverage



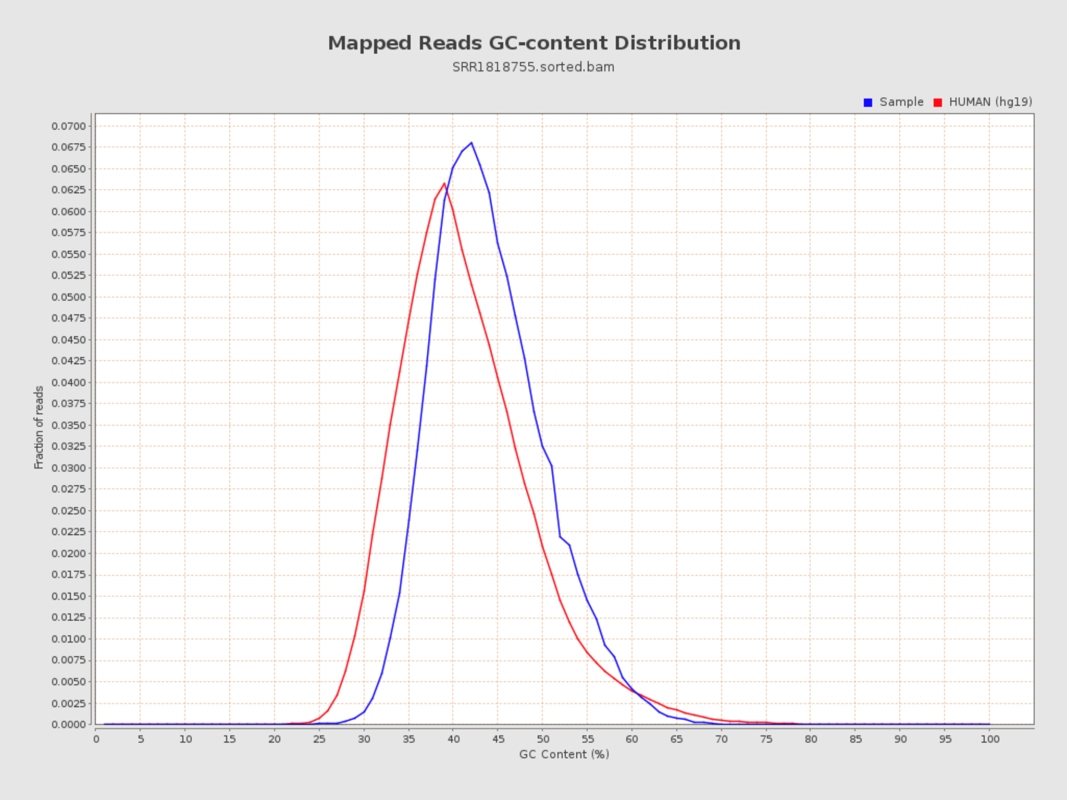
7. Results : Duplication Rate Histogram



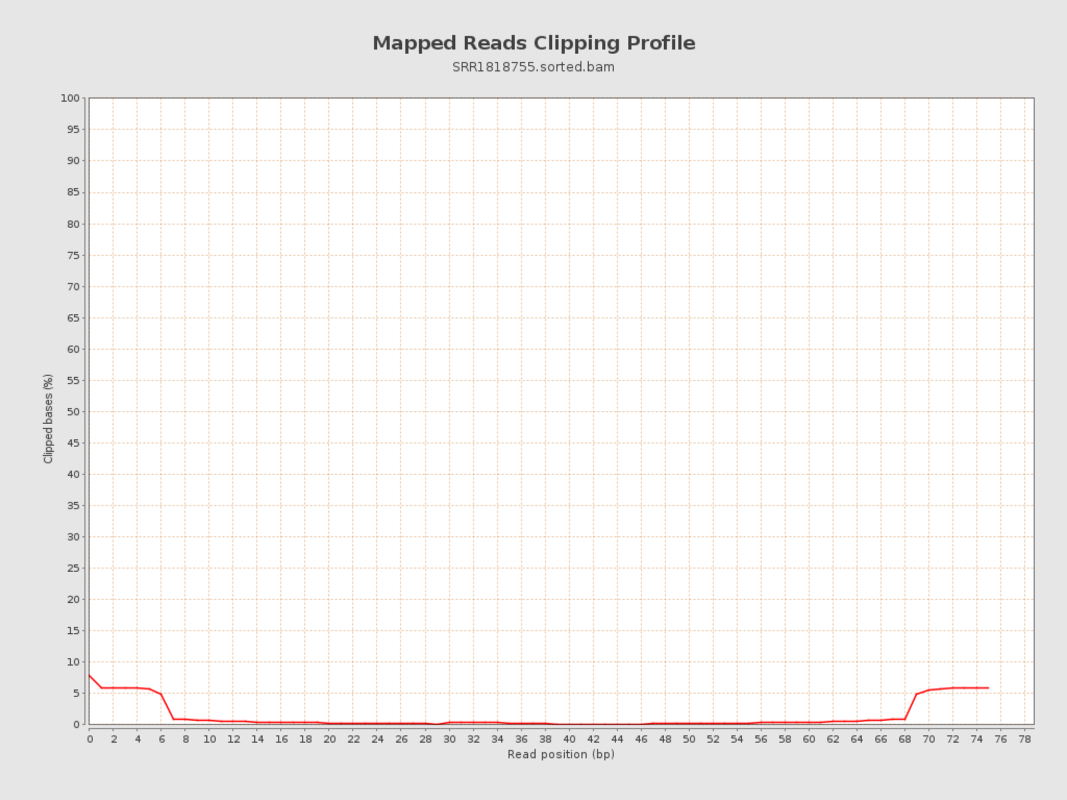
8. Results : Mapped Reads Nucleotide Content



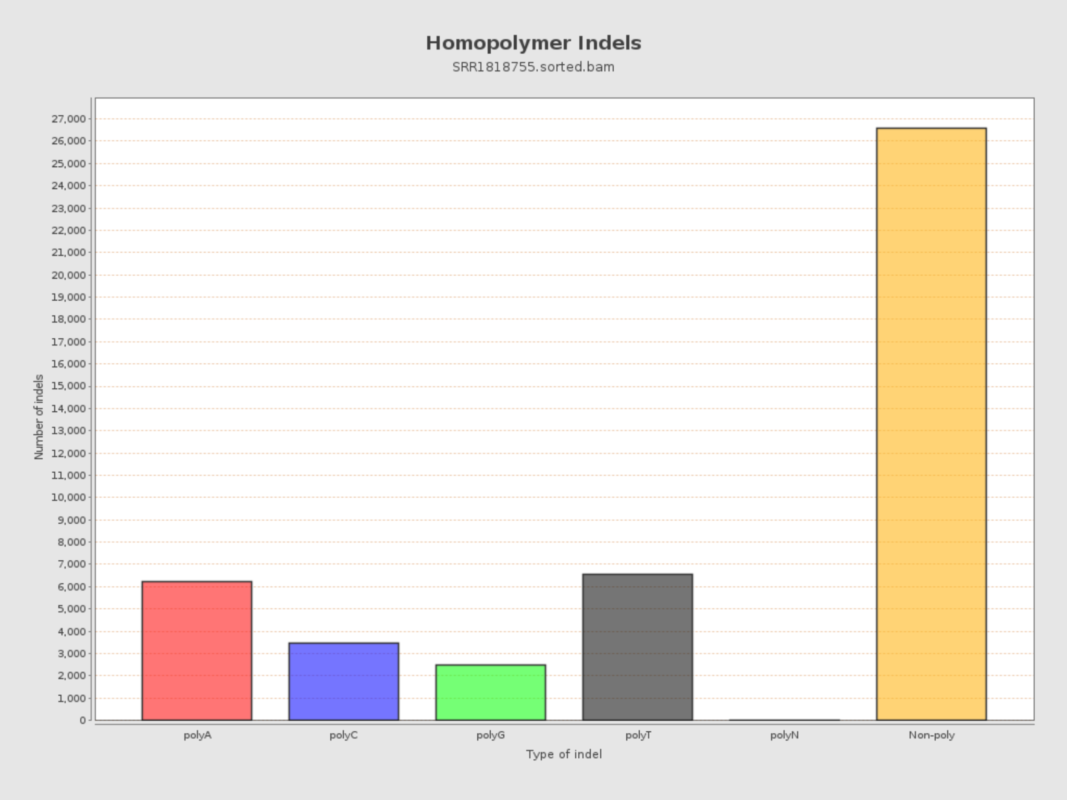
9. Results : Mapped Reads GC-content Distribution



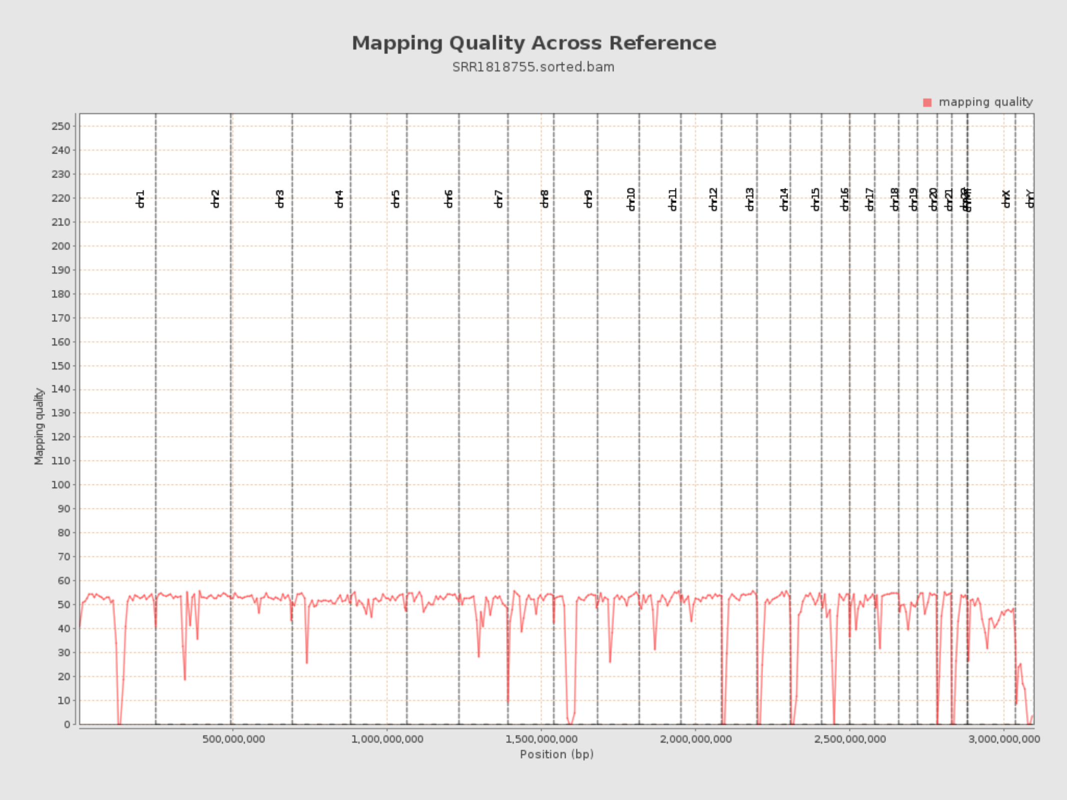
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram