Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:51:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818805.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_SRR1818805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:51:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,263
Mapped reads	73,795 / 94.29%
Unmapped reads	4,468 / 5.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	496 / 0.63%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	2,596 / 3.32%
Duplication rate	3.1%
Clipped reads	74,045 / 94.61%

2.2. ACGT Content

Number/percentage of A's	1,414,077 / 28.31%
Number/percentage of C's	1,098,760 / 22%
Number/percentage of T's	1,394,675 / 27.92%
Number/percentage of G's	1,086,751 / 21.76%
Number/percentage of N's	361 / 0.01%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0016

Standard Deviation	0.0446

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

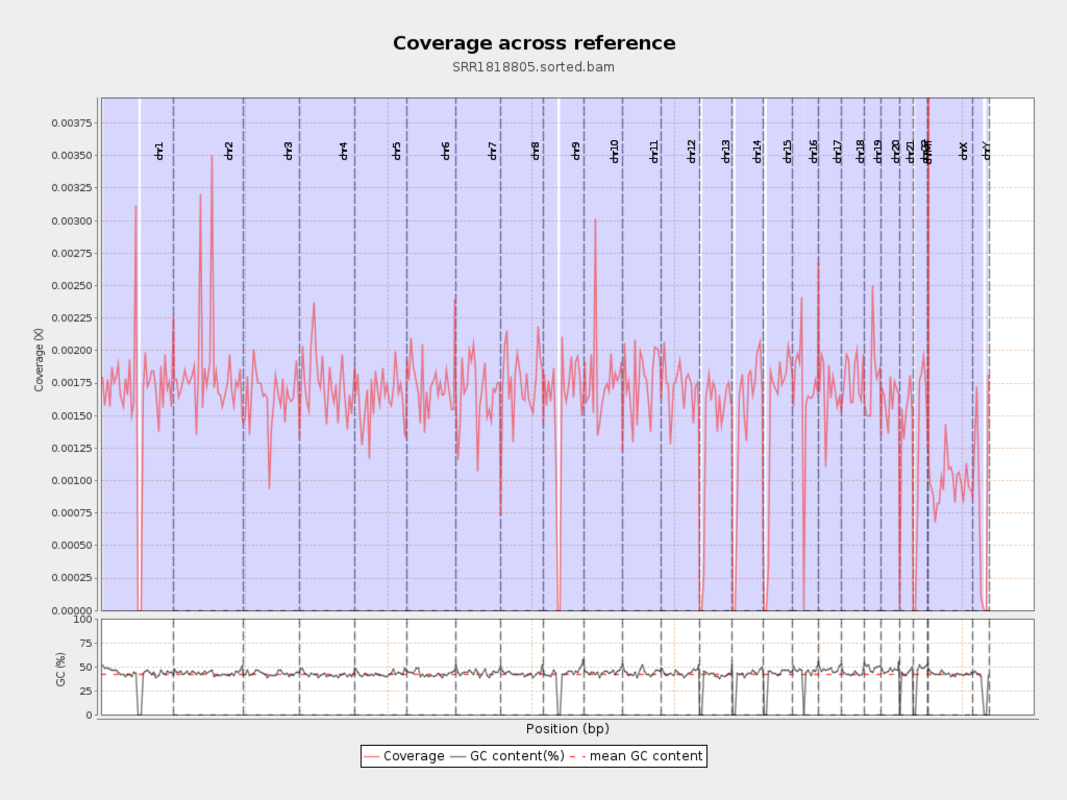
General error rate	0.54%
Mismatches	25,946
Insertions	424
Mapped reads with at least one insertion	0.56%
Deletions	1,252
Mapped reads with at least one deletion	1.69%
Homopolymer indels	44.39%

2.6. Chromosome stats

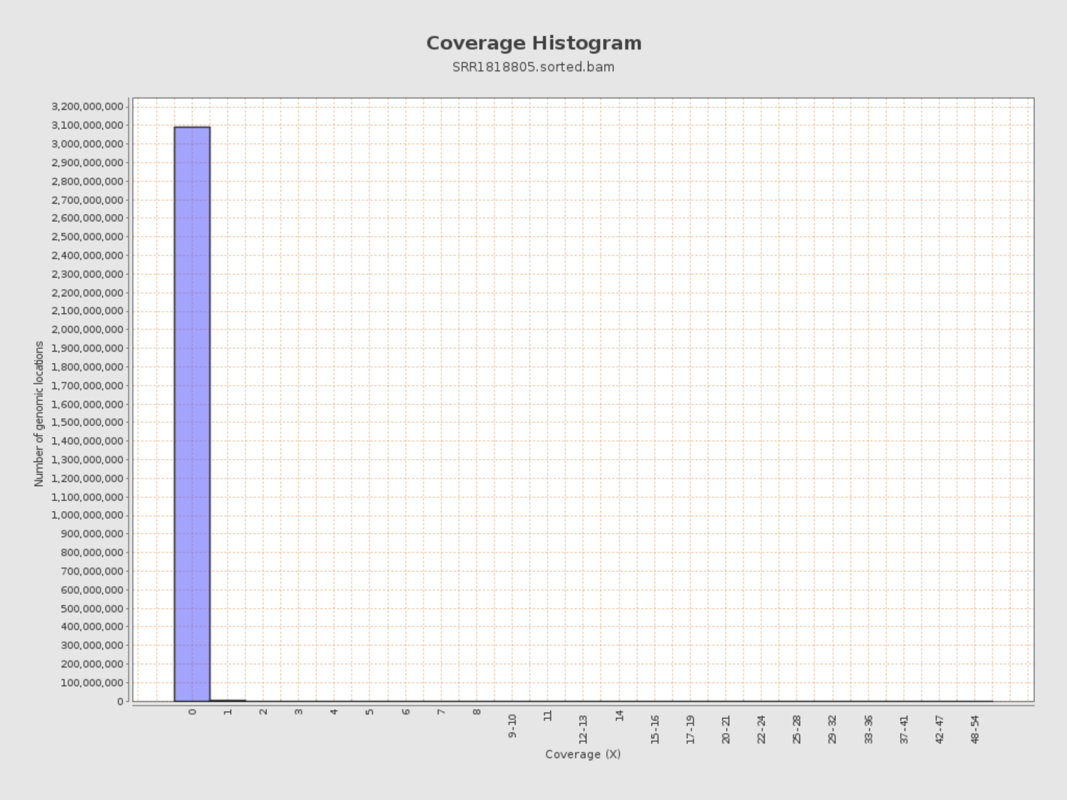
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	415843	0.0017	0.0517
chr2	243199373	446302	0.0018	0.0551
chr3	198022430	323571	0.0016	0.0421
chr4	191154276	332728	0.0017	0.044
chr5	180915260	295399	0.0016	0.0423
chr6	171115067	296265	0.0017	0.0434
chr7	159138663	265381	0.0017	0.0441

chr8	146364022	260413	0.0018	0.0447
chr9	141213431	217332	0.0015	0.0423
chr10	135534747	241842	0.0018	0.0472
chr11	135006516	237976	0.0018	0.0449
chr12	133851895	231308	0.0017	0.0431
chr13	115169878	156916	0.0014	0.0382
chr14	107349540	153920	0.0014	0.0399
chr15	102531392	148858	0.0015	0.0395
chr16	90354753	149432	0.0017	0.0469
chr17	81195210	136519	0.0017	0.043
chr18	78077248	139060	0.0018	0.047
chr19	59128983	104887	0.0018	0.0491
chr20	63025520	102647	0.0016	0.0422
chr21	48129895	68065	0.0014	0.0395
chr22	51304566	64556	0.0013	0.0374
chrMT	16571	4358	0.263	0.565
chrX	155270560	152616	0.001	0.0329
chrY	59373566	50478	0.0009	0.0439

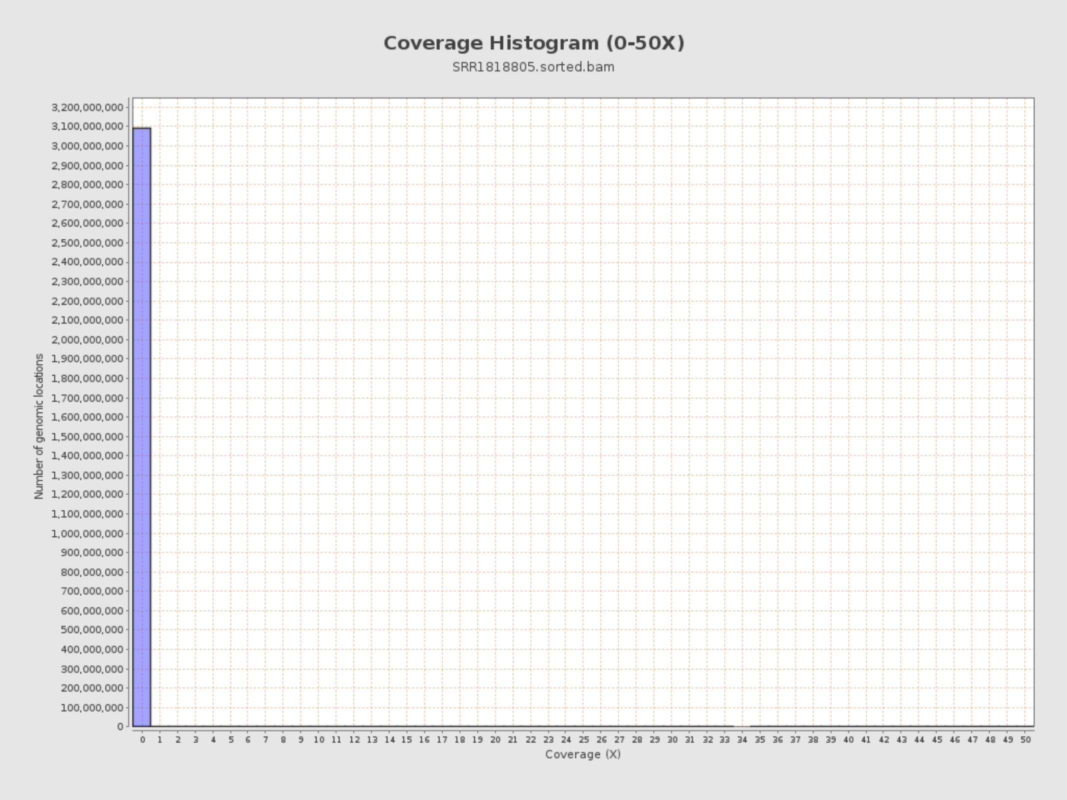
3. Results : Coverage across reference



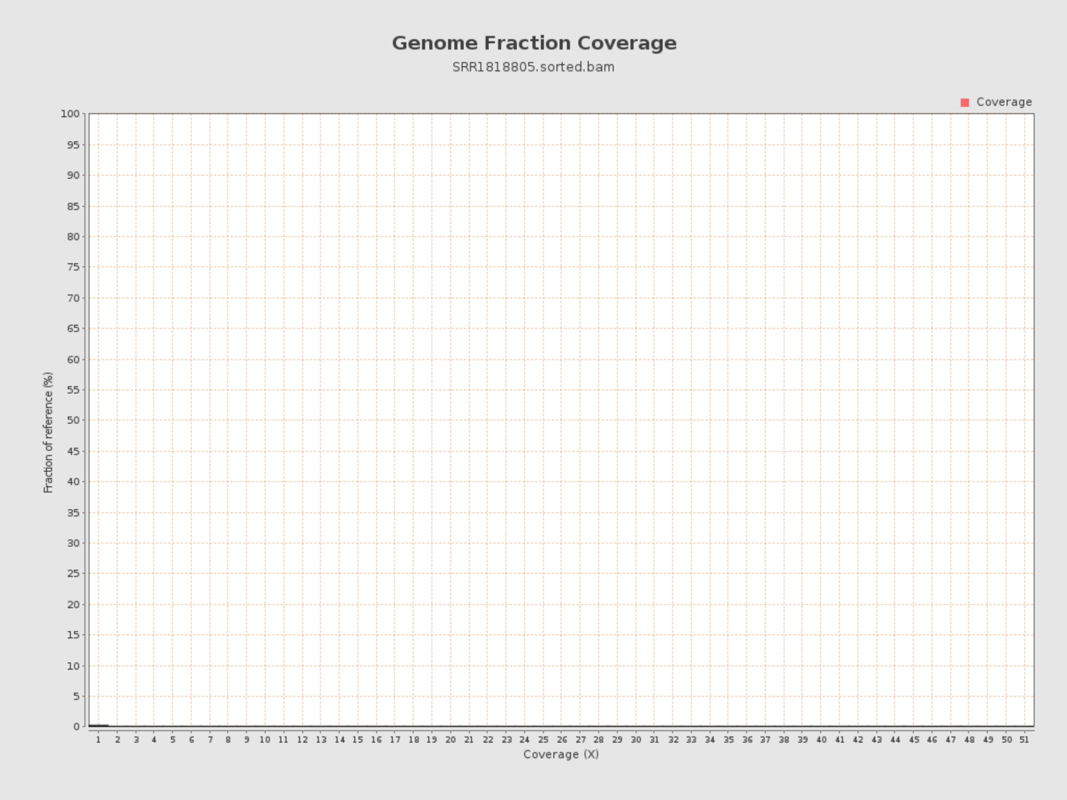
4. Results : Coverage Histogram



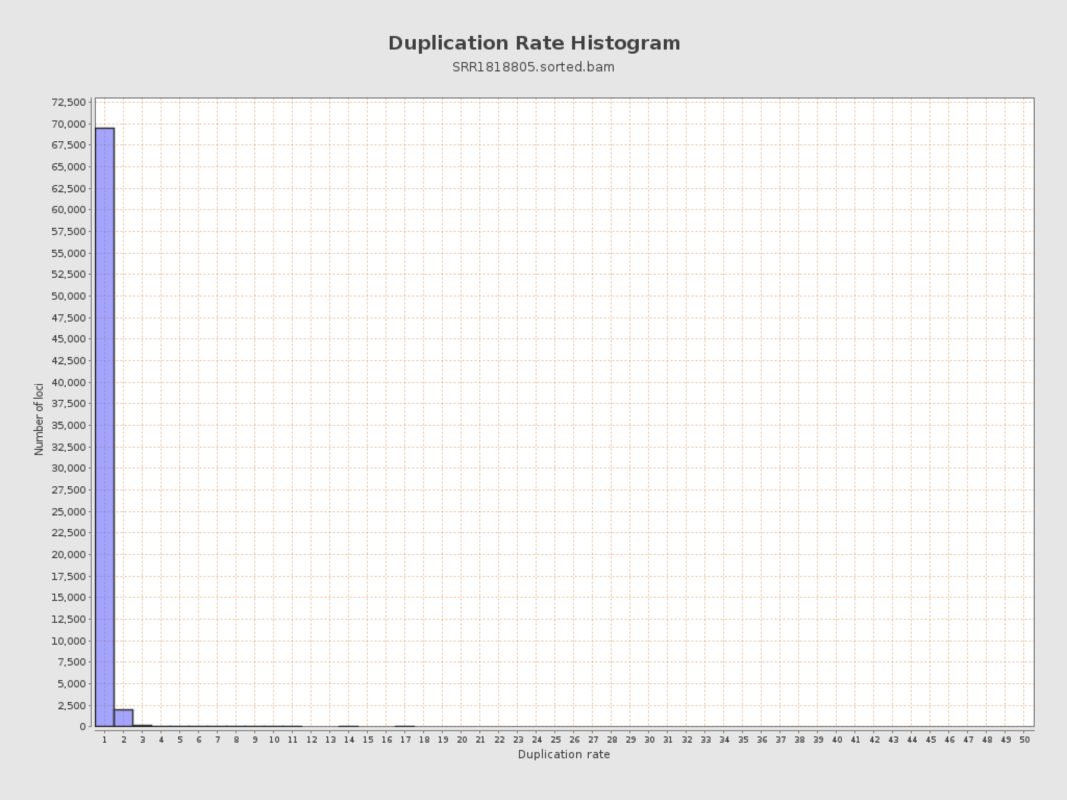
5. Results : Coverage Histogram (0-50X)



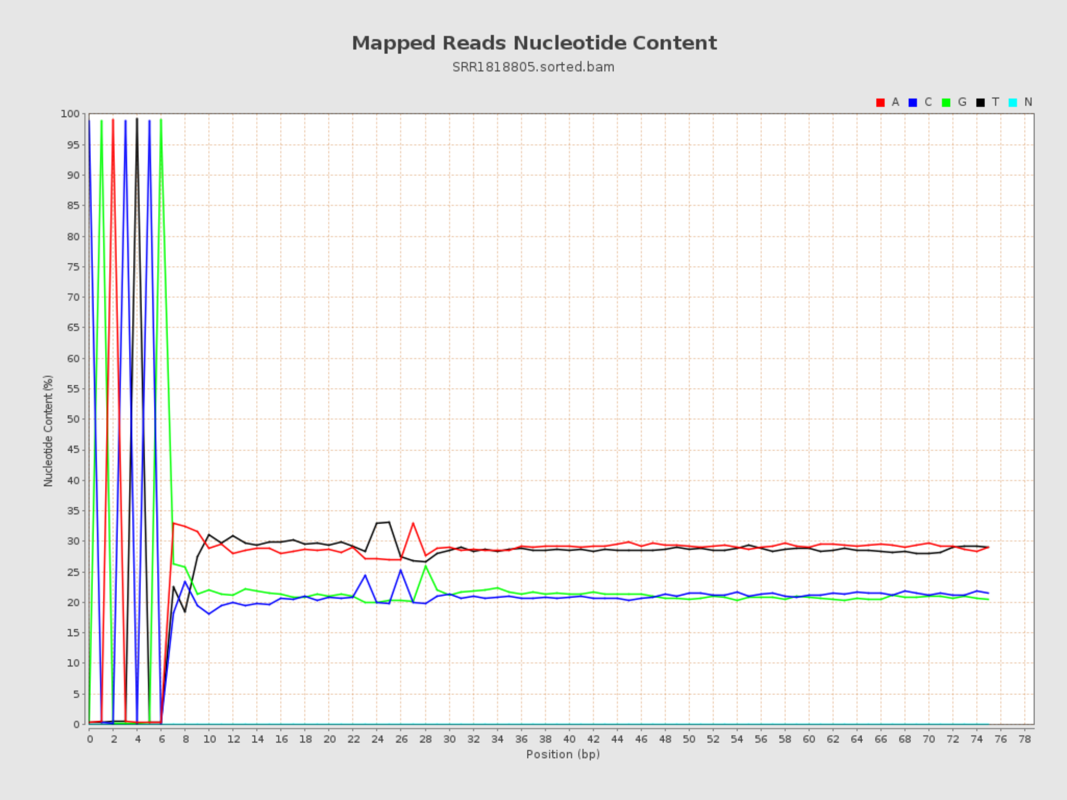
6. Results : Genome Fraction Coverage



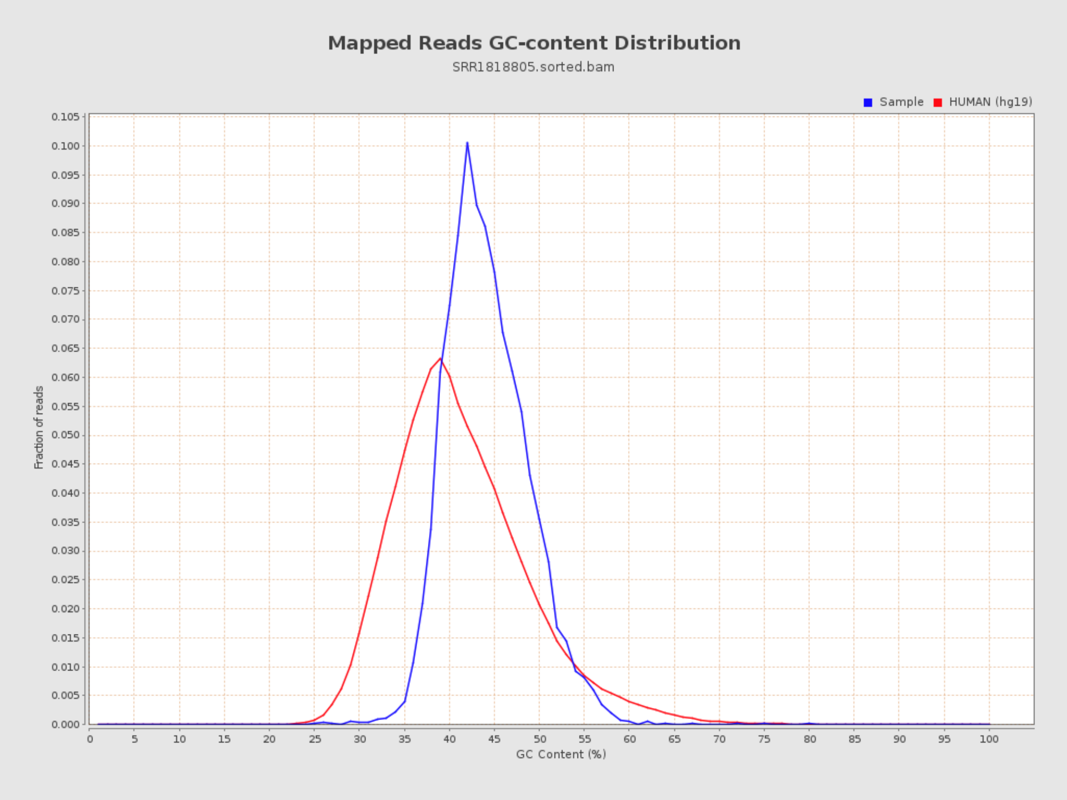
7. Results : Duplication Rate Histogram



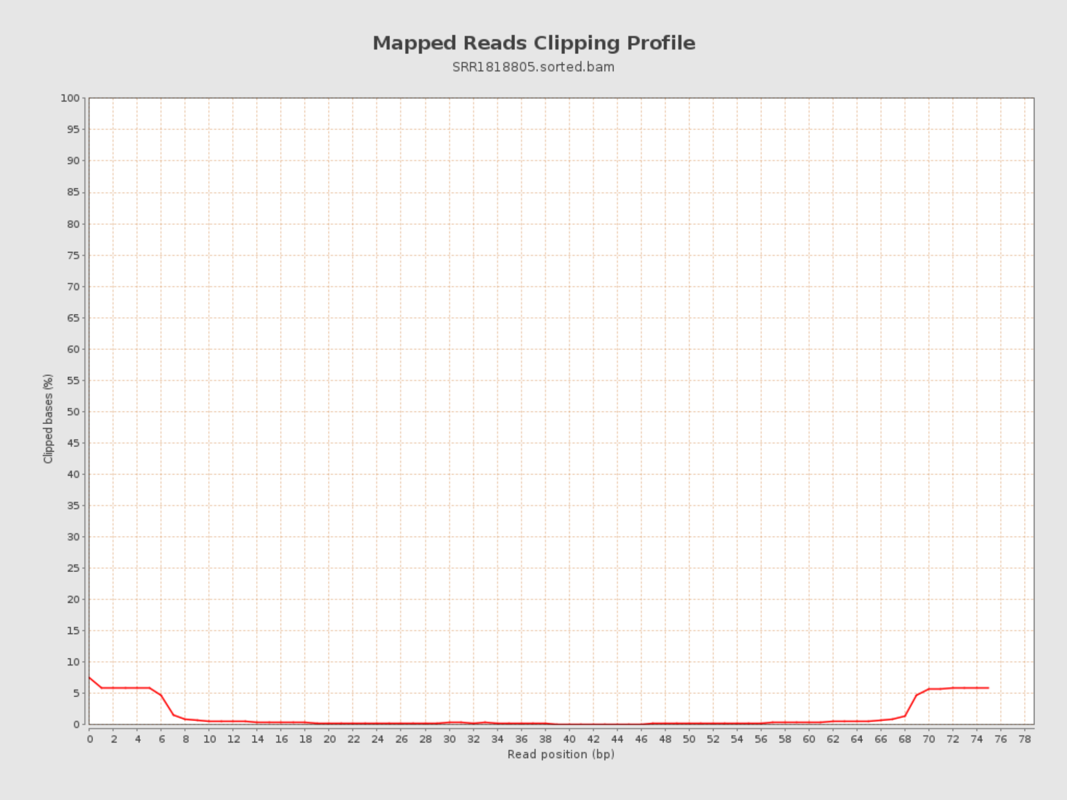
8. Results : Mapped Reads Nucleotide Content



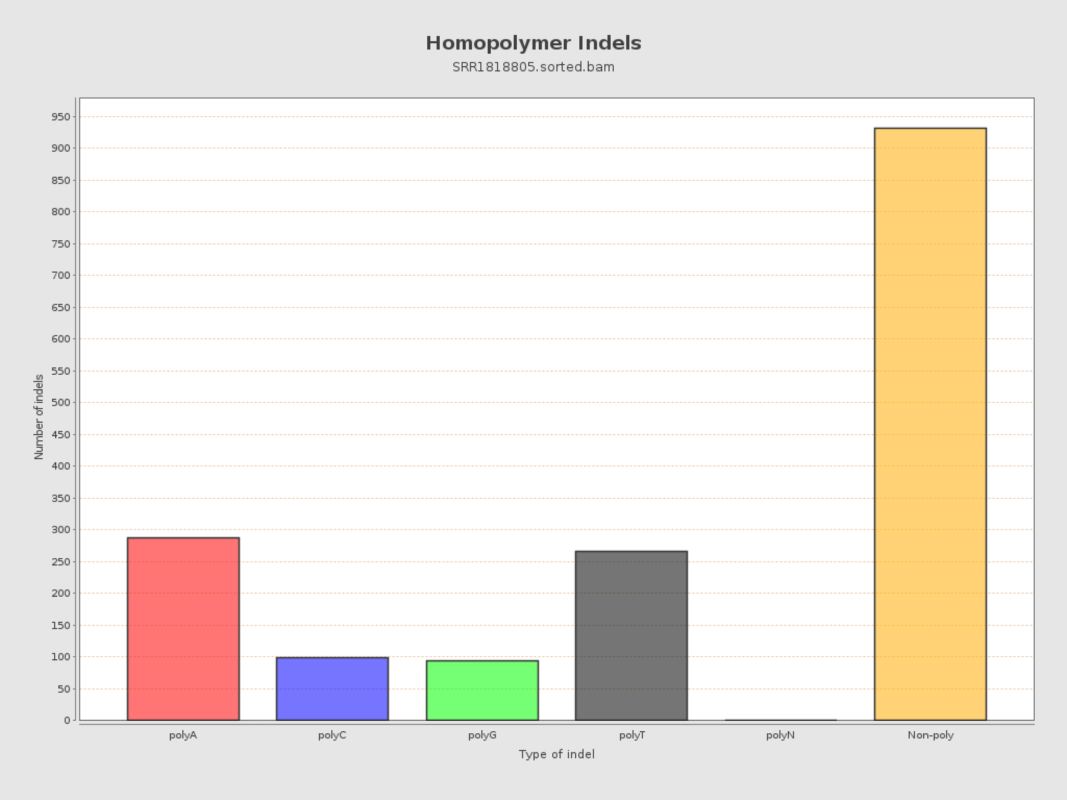
9. Results : Mapped Reads GC-content Distribution



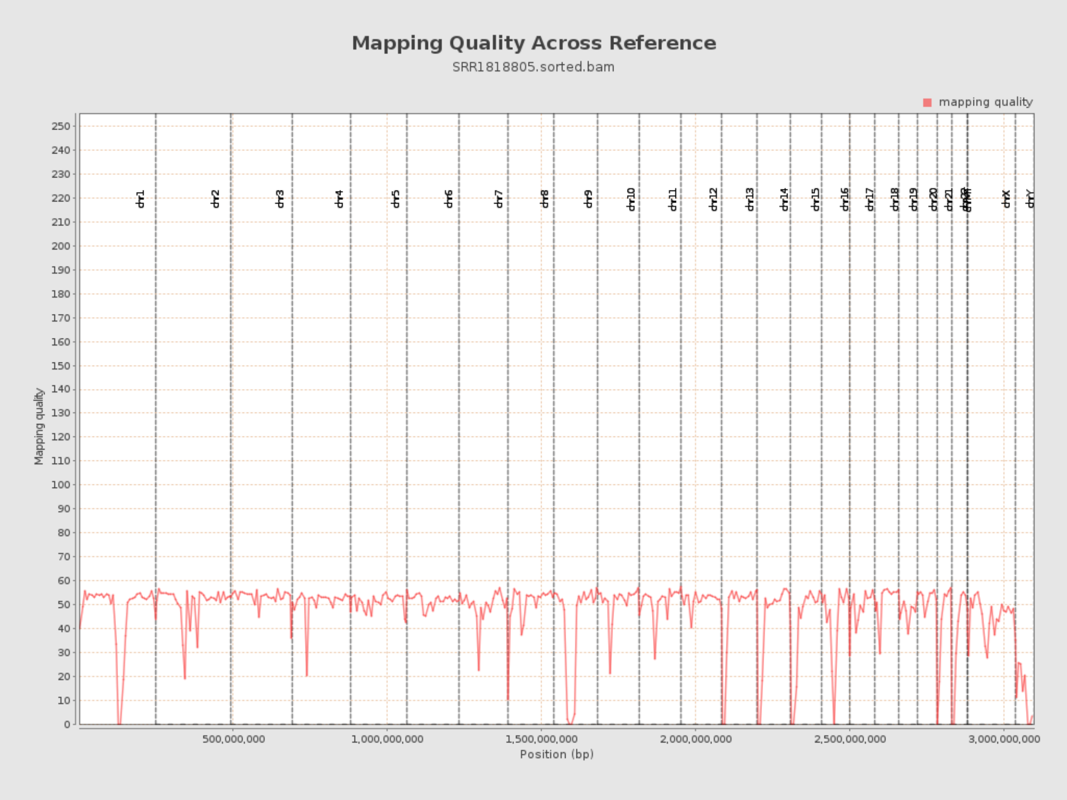
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram