Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:46:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818953.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_SRR1818953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818953.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:46:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,622,875
Mapped reads	2,566,299 / 97.84%
Unmapped reads	56,576 / 2.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,491 / 1.09%
Read min/max/mean length	30 / 101 / 101.42
Duplicated reads (estimated)	1,239,371 / 47.25%
Duplication rate	39.35%
Clipped reads	2,586,105 / 98.6%

2.2. ACGT Content

Number/percentage of A's	68,234,299 / 28.7%
Number/percentage of C's	51,212,156 / 21.54%
Number/percentage of T's	66,494,186 / 27.97%
Number/percentage of G's	51,774,050 / 21.78%
Number/percentage of N's	10,194 / 0%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0768

Standard Deviation	0.921

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

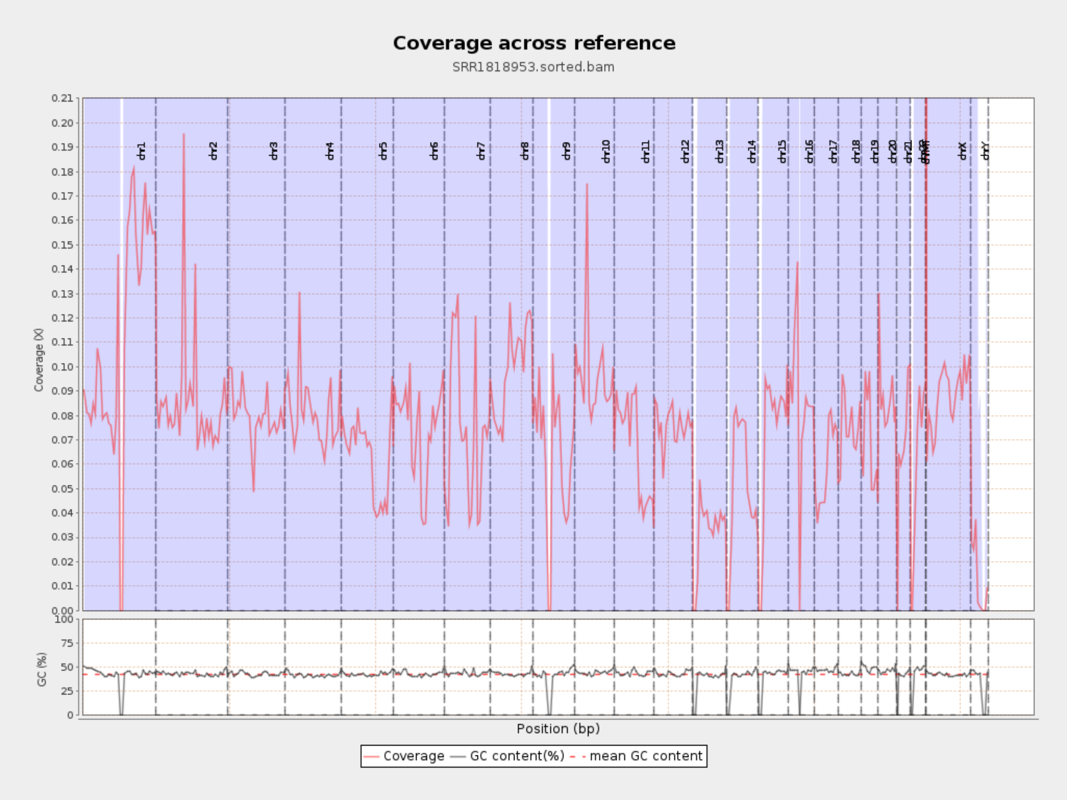
General error rate	0.68%
Mismatches	1,547,052
Insertions	28,008
Mapped reads with at least one insertion	1.06%
Deletions	71,928
Mapped reads with at least one deletion	2.74%
Homopolymer indels	42.69%

2.6. Chromosome stats

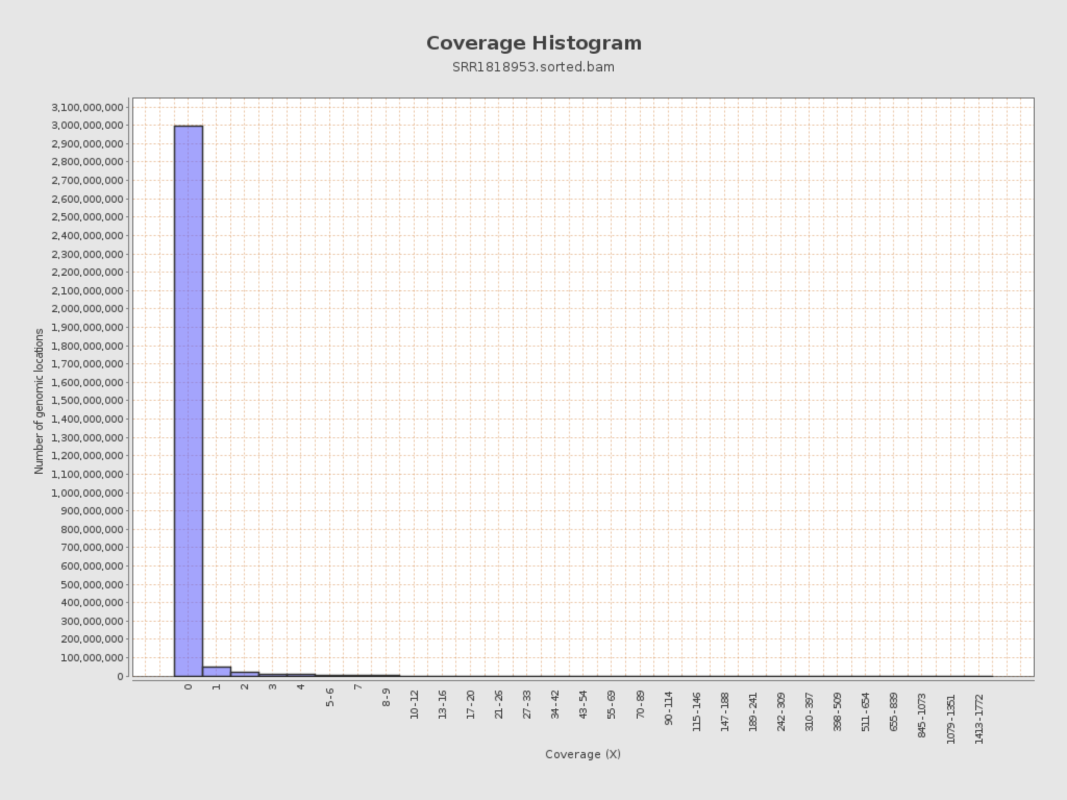
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27840296	0.1117	1.6712
chr2	243199373	20754780	0.0853	1.3411
chr3	198022430	15854642	0.0801	0.5663
chr4	191154276	15653630	0.0819	0.6432
chr5	180915260	11568965	0.0639	0.5226
chr6	171115067	12878772	0.0753	0.6212
chr7	159138663	11632565	0.0731	0.7409

chr8	146364022	14577061	0.0996	0.7383
chr9	141213431	8873805	0.0628	0.966
chr10	135534747	13144914	0.097	1.1047
chr11	135006516	9039712	0.067	0.6462
chr12	133851895	10211057	0.0763	0.5646
chr13	115169878	3725699	0.0323	0.357
chr14	107349540	5576931	0.052	0.4998
chr15	102531392	7156459	0.0698	0.5393
chr16	90354753	7562612	0.0837	0.9805
chr17	81195210	4809289	0.0592	0.5604
chr18	78077248	5832666	0.0747	1.267
chr19	59128983	4107199	0.0695	1.4025
chr20	63025520	5522589	0.0876	0.6261
chr21	48129895	3306958	0.0687	0.5942
chr22	51304566	2971306	0.0579	0.5583
chrMT	16571	876837	52.9139	34.5221
chrX	155270560	13641573	0.0879	0.7425
chrY	59373566	738104	0.0124	0.769

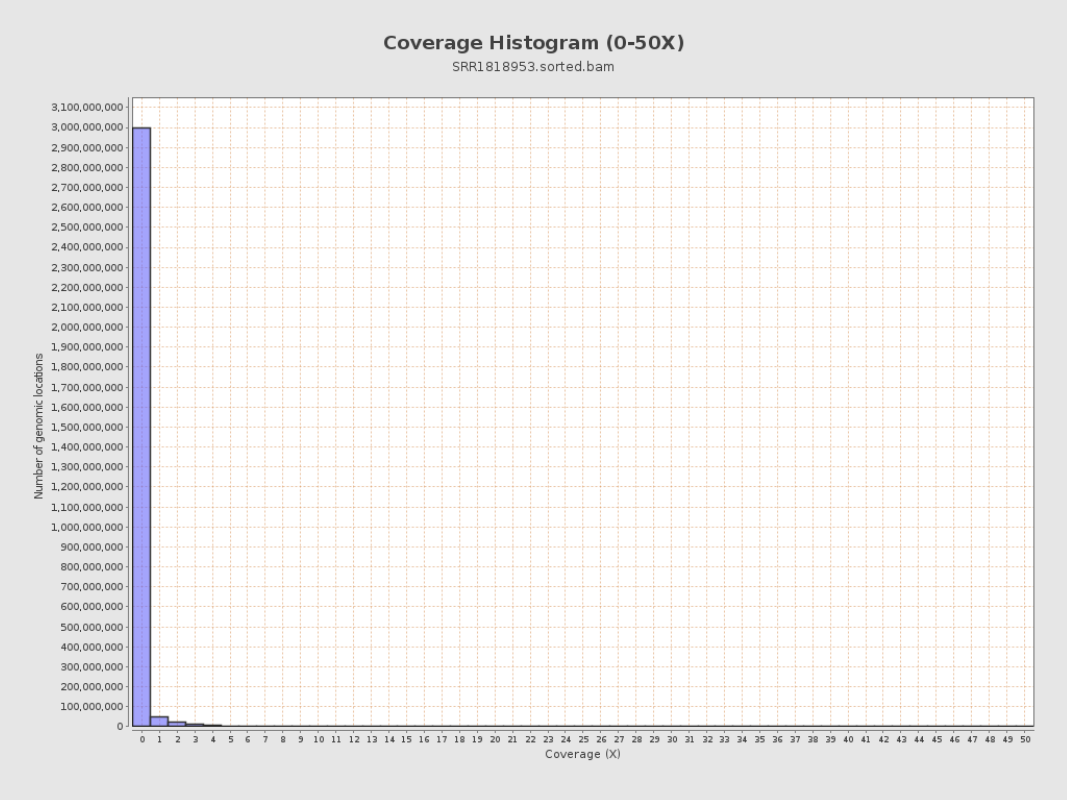
3. Results : Coverage across reference



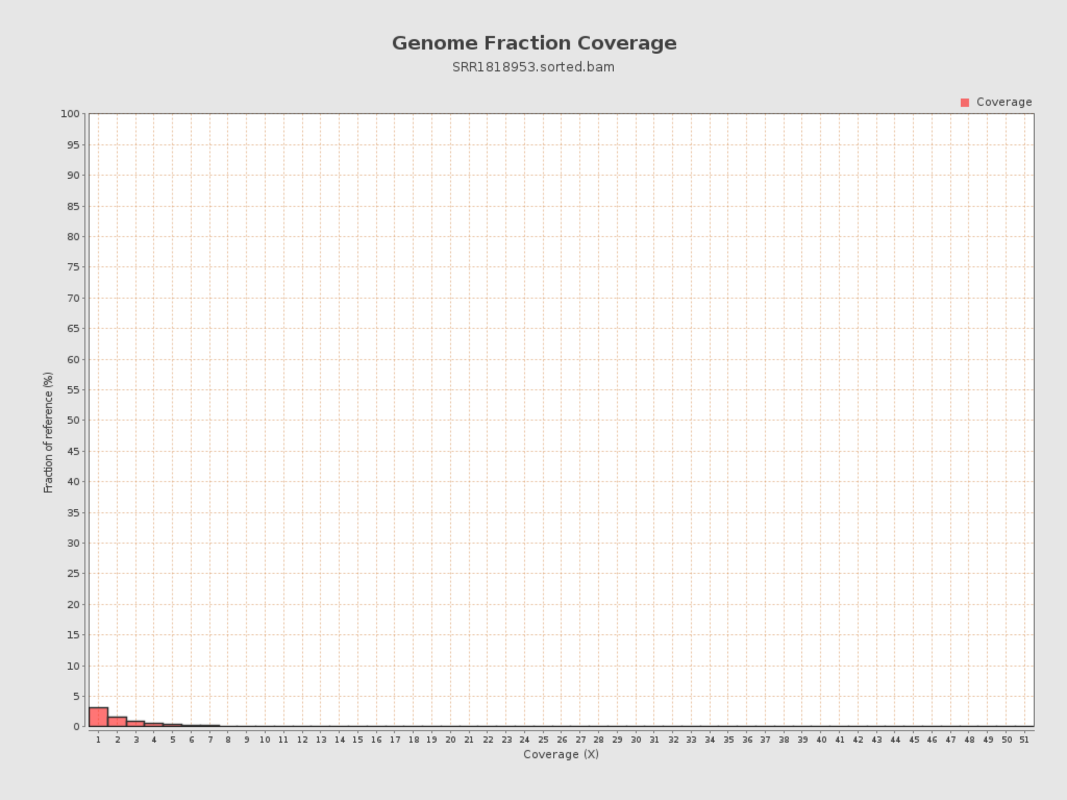
4. Results : Coverage Histogram



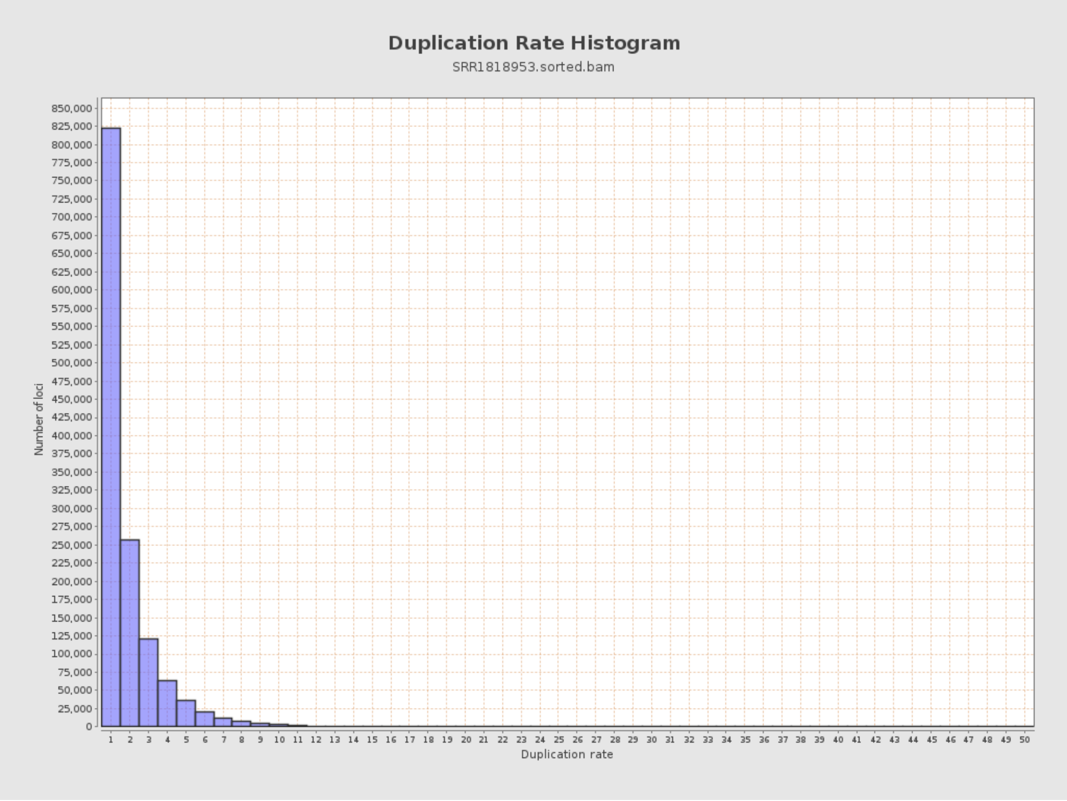
5. Results : Coverage Histogram (0-50X)



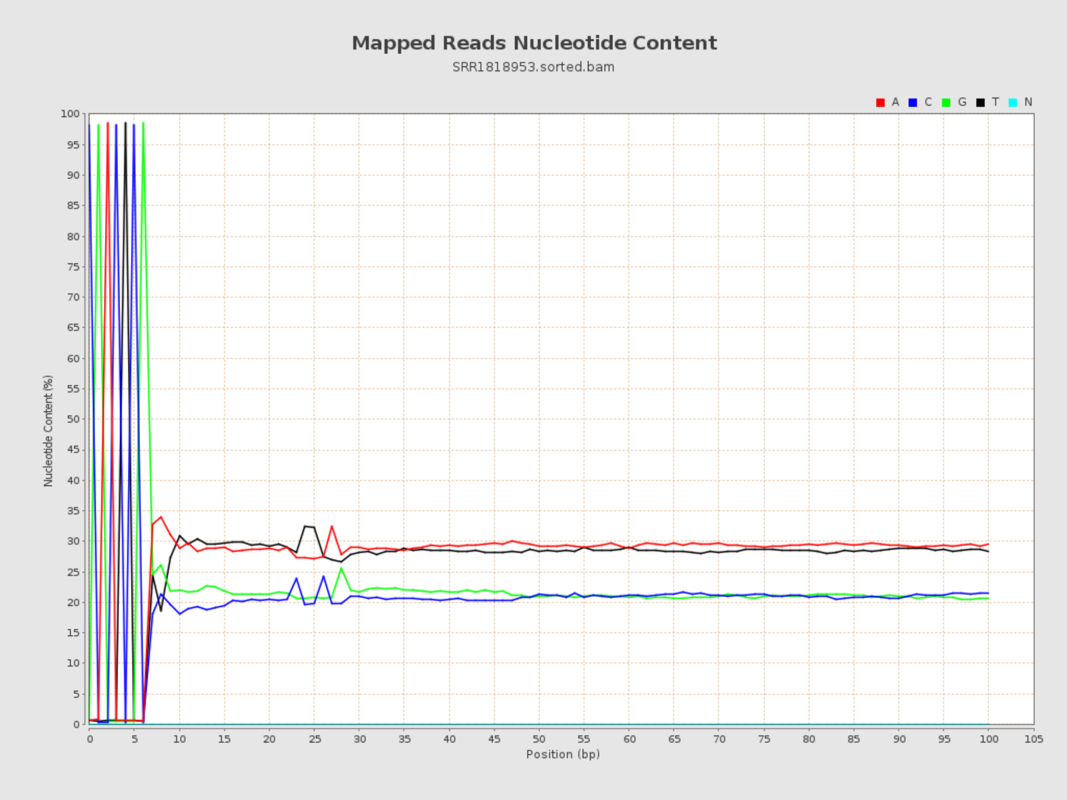
6. Results : Genome Fraction Coverage



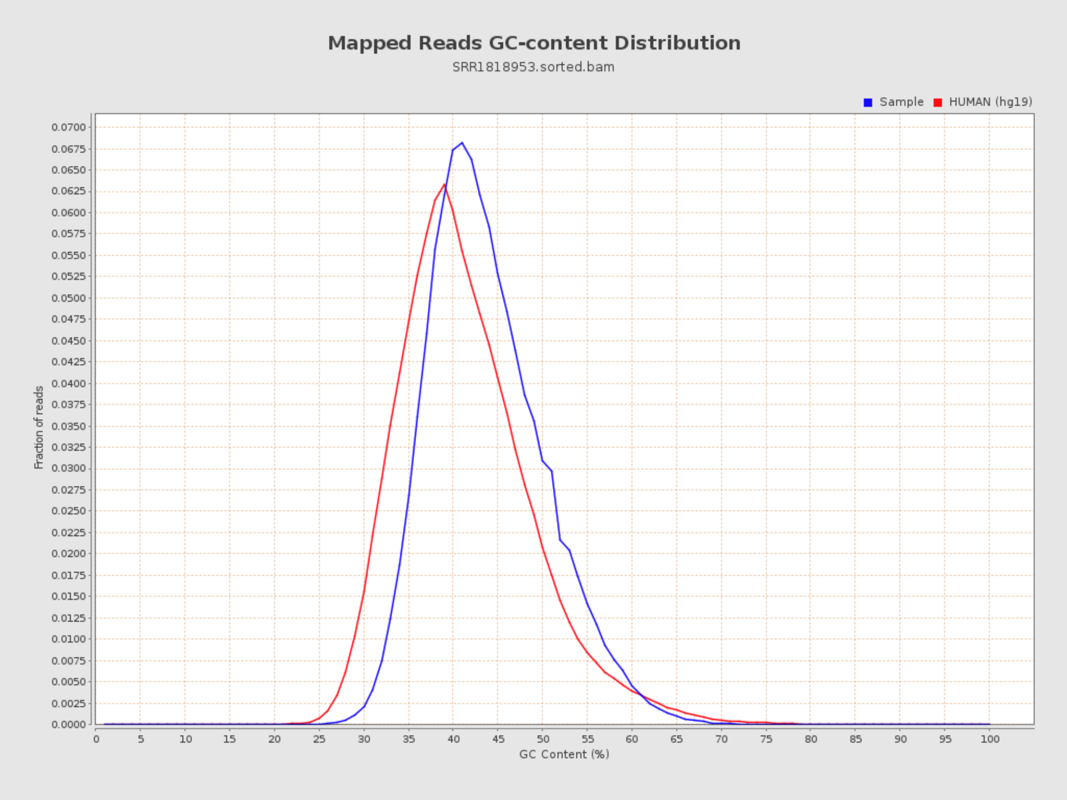
7. Results : Duplication Rate Histogram



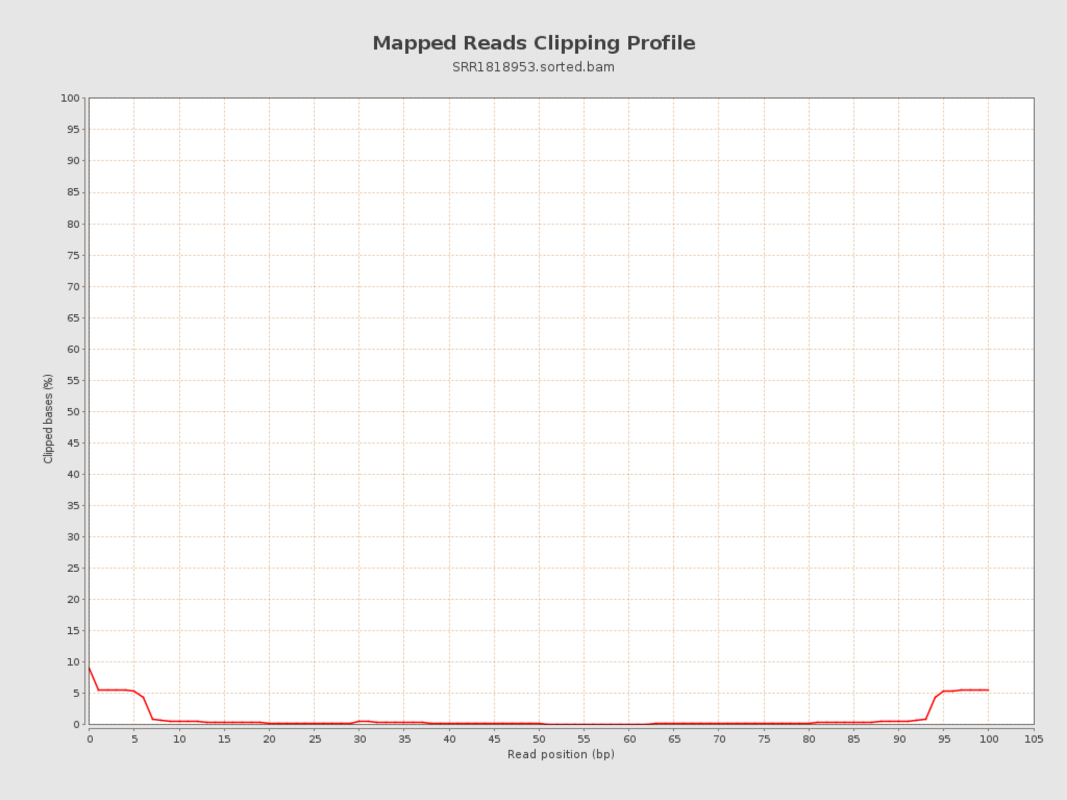
8. Results : Mapped Reads Nucleotide Content



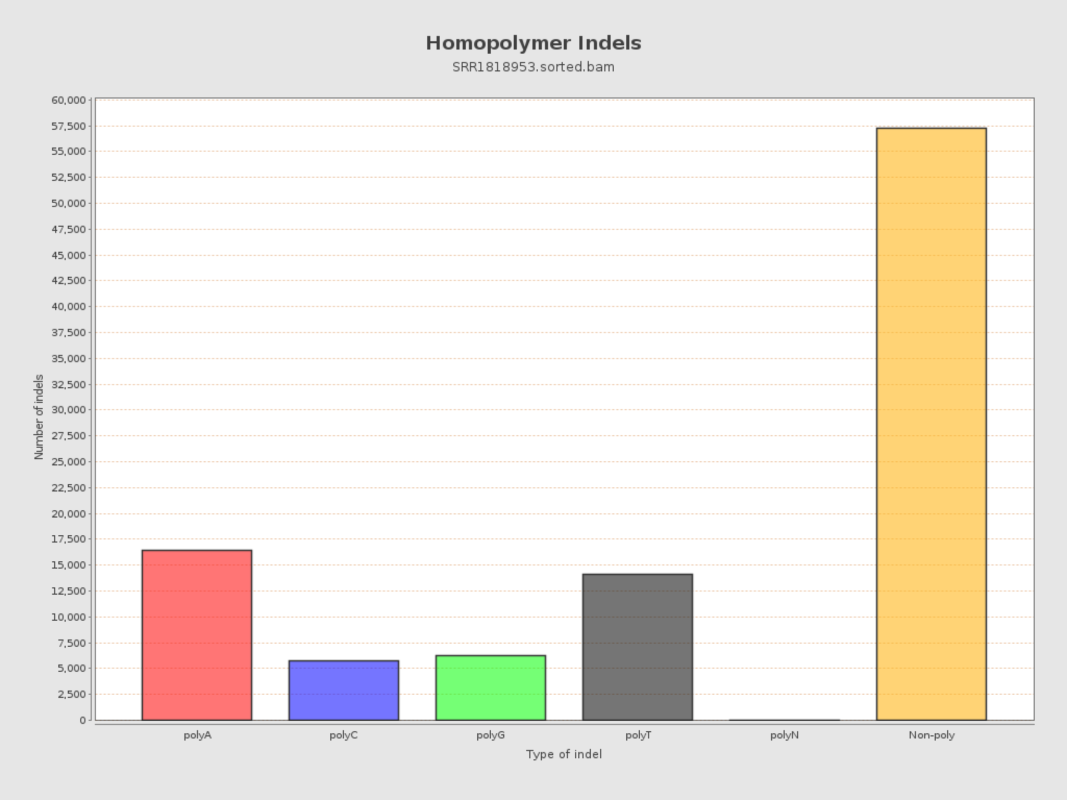
9. Results : Mapped Reads GC-content Distribution



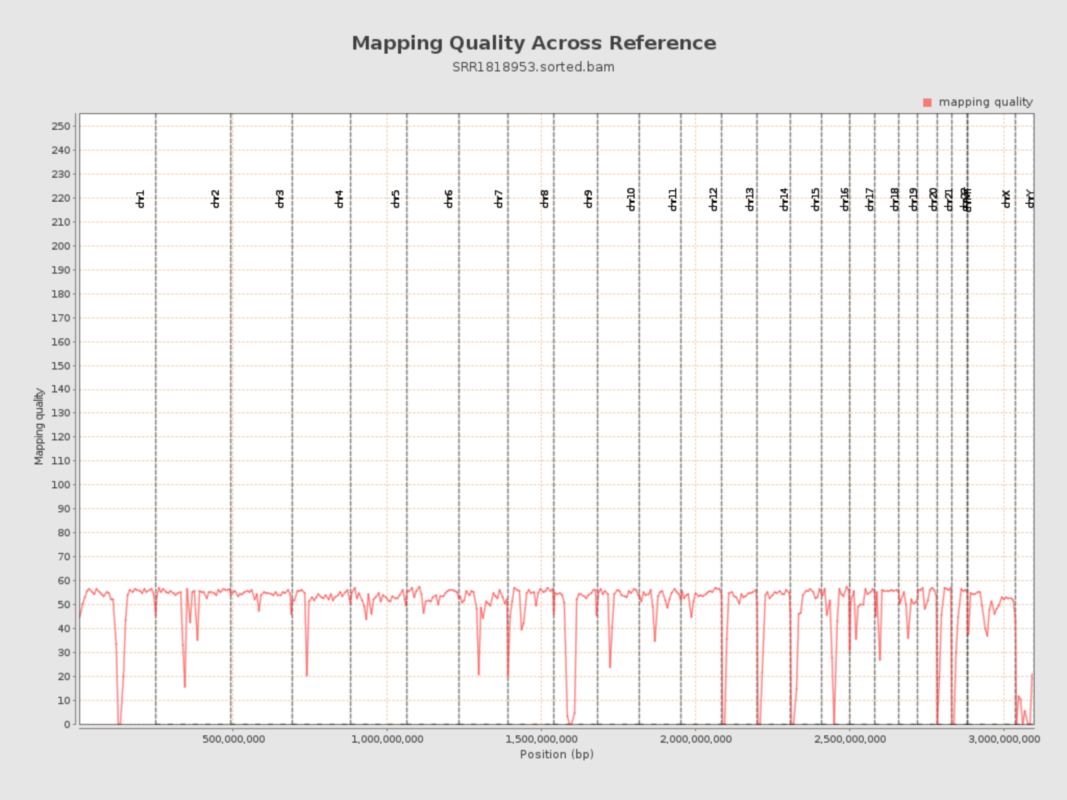
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram