Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:28:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818922.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_SRR1818922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:28:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,676,464
Mapped reads	1,643,543 / 98.04%
Unmapped reads	32,921 / 1.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,534 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	458,030 / 27.32%
Duplication rate	23.65%
Clipped reads	1,657,132 / 98.85%

2.2. ACGT Content

Number/percentage of A's	43,774,987 / 28.82%
Number/percentage of C's	31,753,252 / 20.9%
Number/percentage of T's	44,096,198 / 29.03%
Number/percentage of G's	32,280,775 / 21.25%
Number/percentage of N's	2,335 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.6196

2.4. Mapping Quality

Mean Mapping Quality	49.24

2.5. Mismatches and indels

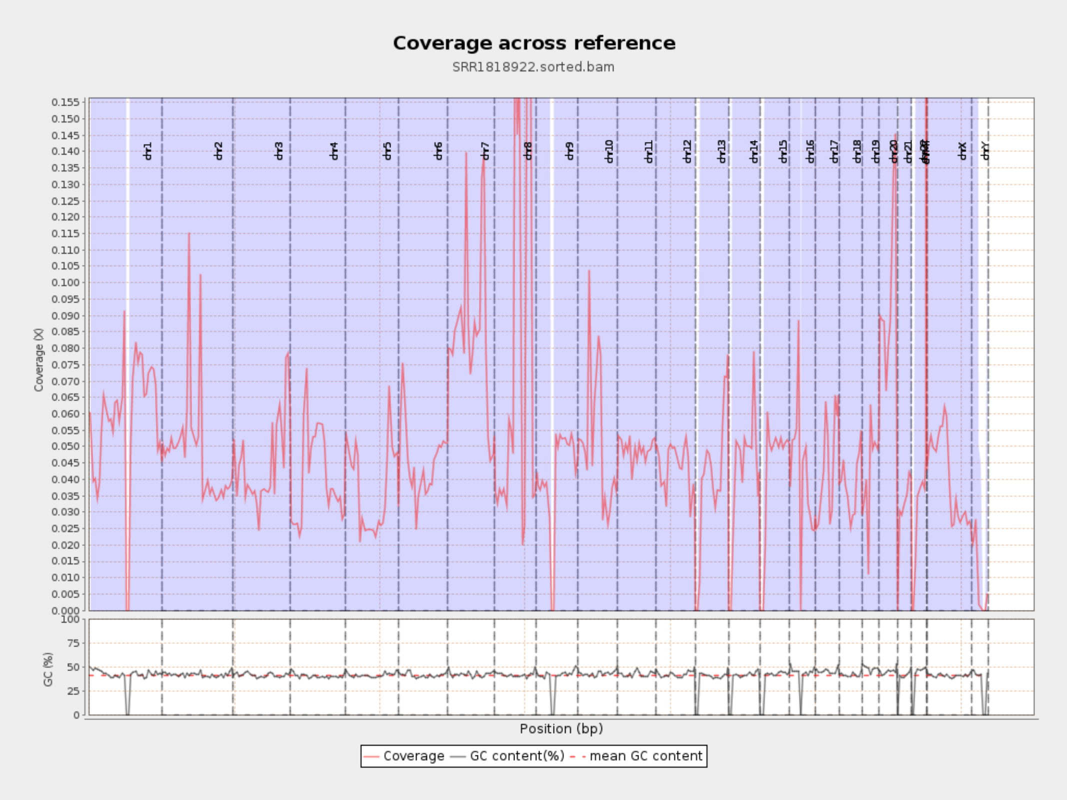
General error rate	0.65%
Mismatches	926,963
Insertions	23,890
Mapped reads with at least one insertion	1.41%
Deletions	51,605
Mapped reads with at least one deletion	3.06%
Homopolymer indels	40.43%

2.6. Chromosome stats

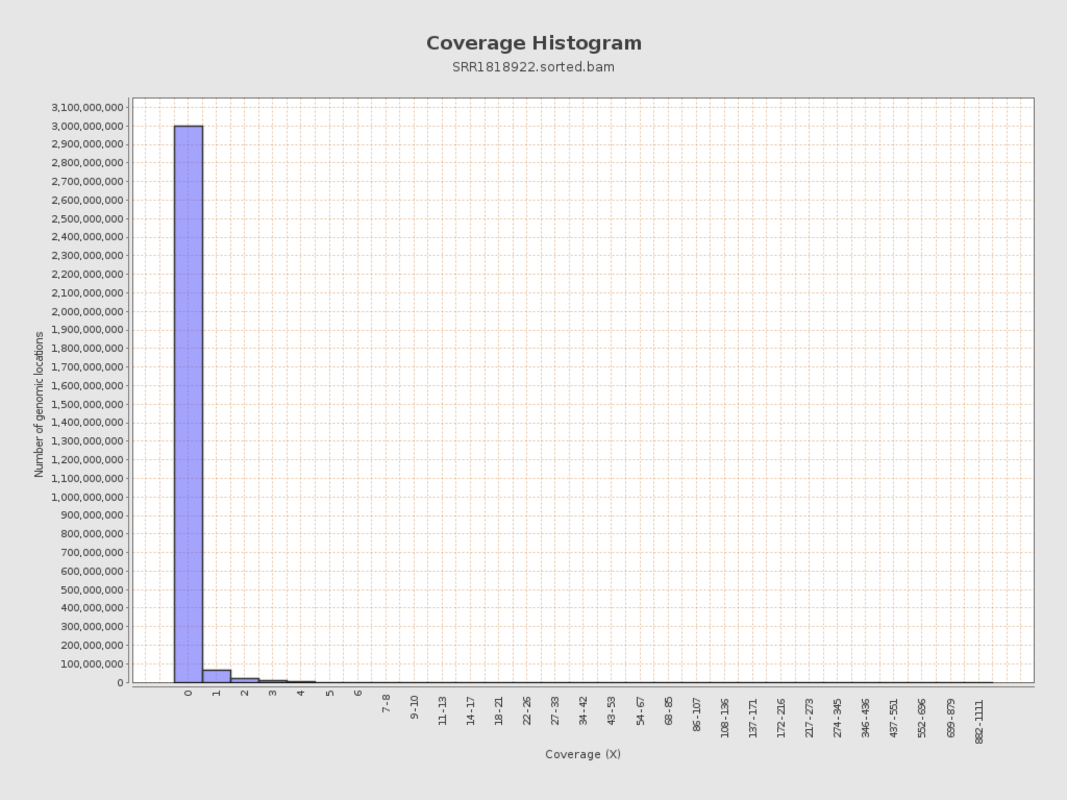
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14516448	0.0582	0.8436
chr2	243199373	11851738	0.0487	1.0703
chr3	198022430	8891266	0.0449	0.3031
chr4	191154276	7764444	0.0406	0.3719
chr5	180915260	6736263	0.0372	0.3003
chr6	171115067	7739690	0.0452	0.3323
chr7	159138663	13694114	0.0861	1.2428

chr8	146364022	13170386	0.09	0.5229
chr9	141213431	5736675	0.0406	0.4758
chr10	135534747	7016119	0.0518	0.7271
chr11	135006516	6627511	0.0491	0.3688
chr12	133851895	5915432	0.0442	0.3091
chr13	115169878	4578641	0.0398	0.2822
chr14	107349540	4531848	0.0422	0.3301
chr15	102531392	4324507	0.0422	0.2996
chr16	90354753	3713685	0.0411	0.7514
chr17	81195210	3589606	0.0442	0.3798
chr18	78077248	2998339	0.0384	0.5192
chr19	59128983	2495451	0.0422	0.6595
chr20	63025520	6085137	0.0966	0.4872
chr21	48129895	1506886	0.0313	0.2917
chr22	51304566	1351537	0.0263	0.259
chrMT	16571	279838	16.8872	10.4435
chrX	155270560	6347527	0.0409	0.3421
chrY	59373566	544247	0.0092	0.8643

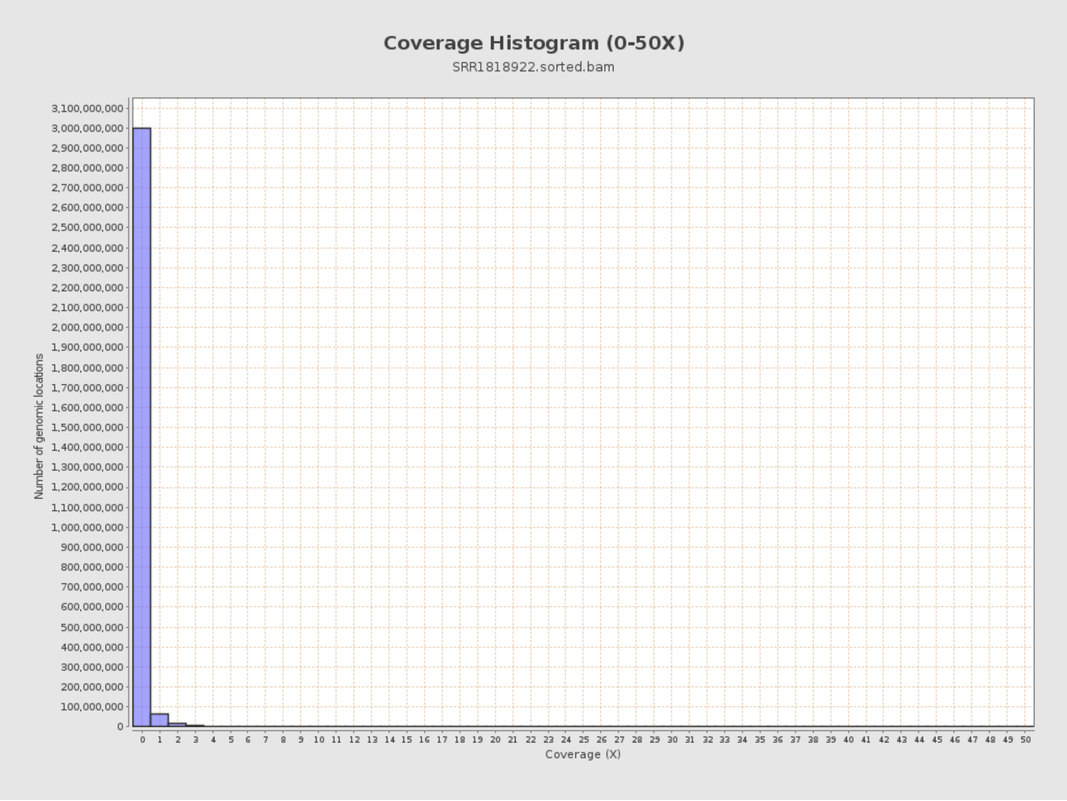
3. Results : Coverage across reference



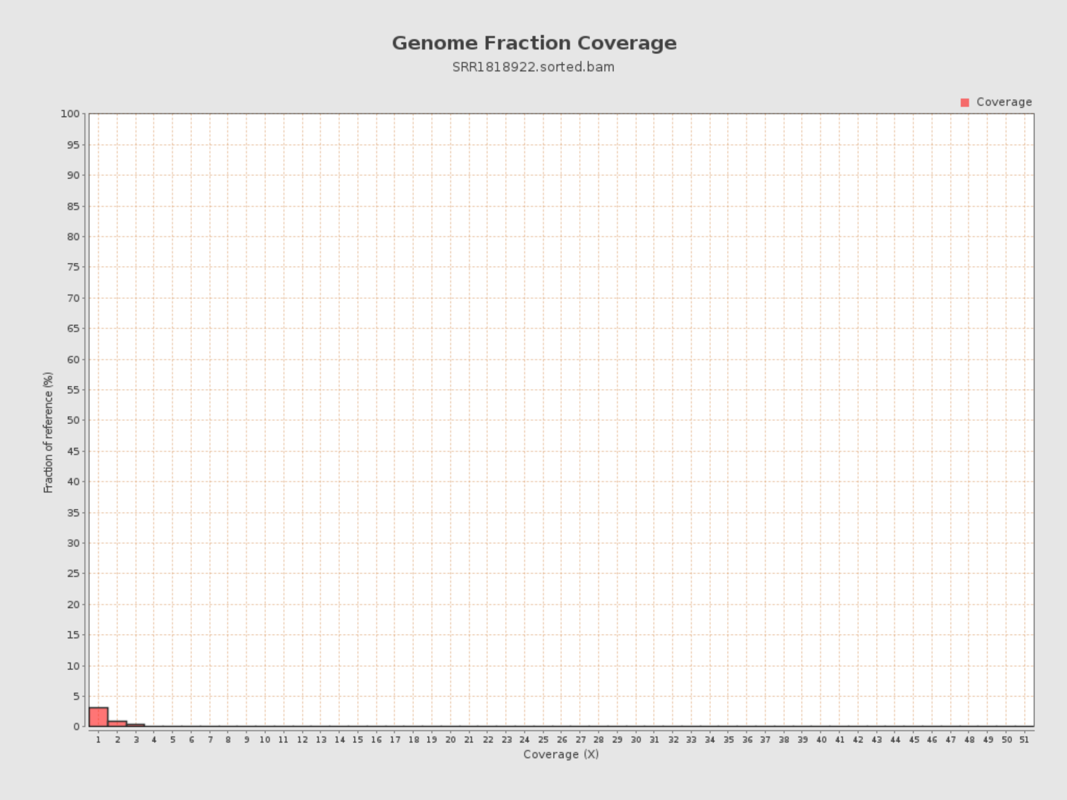
4. Results : Coverage Histogram



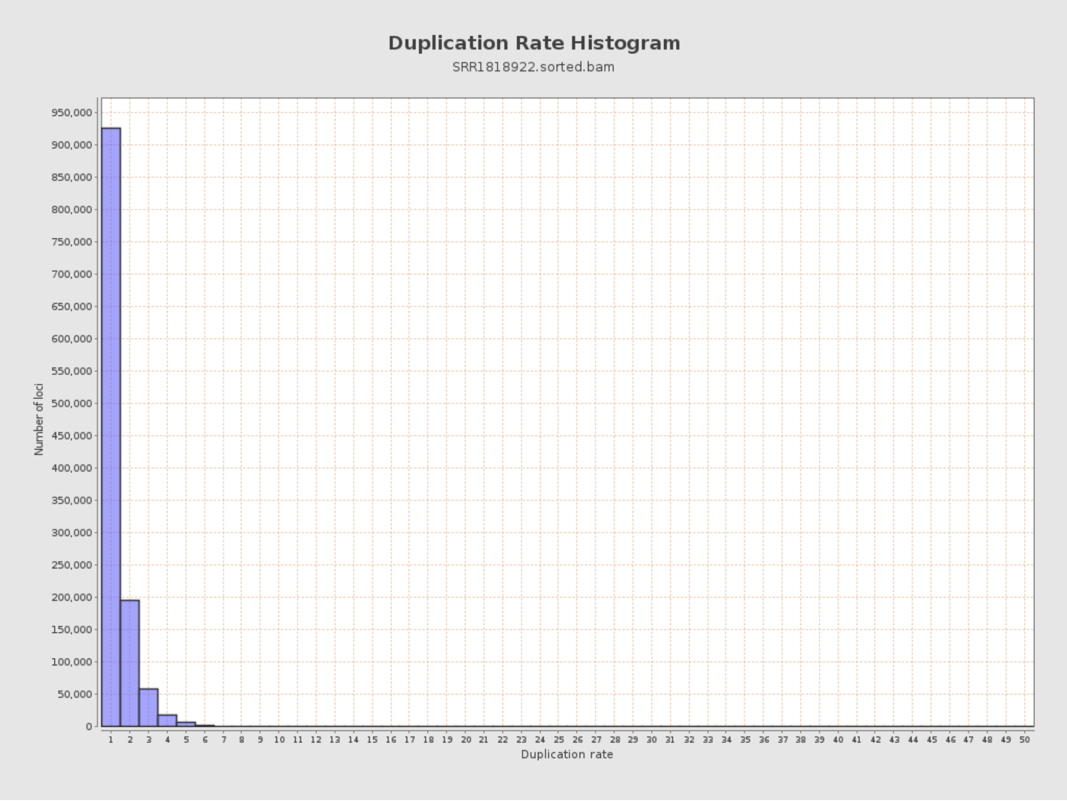
5. Results : Coverage Histogram (0-50X)



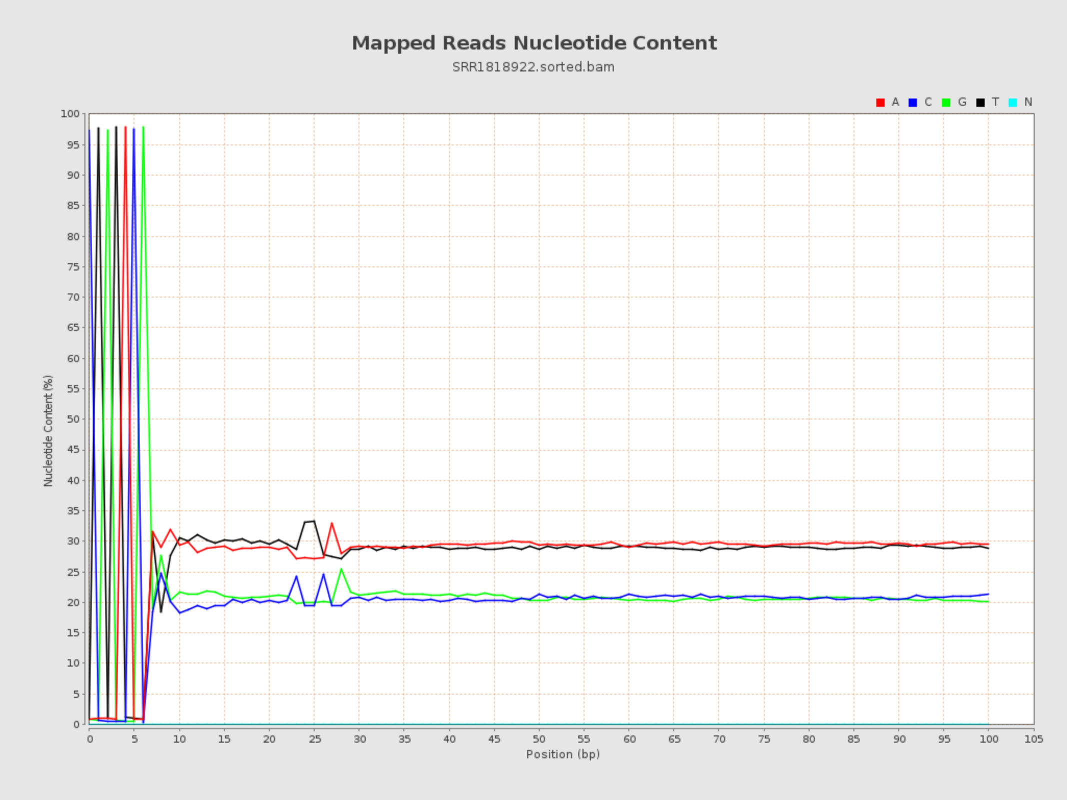
6. Results : Genome Fraction Coverage



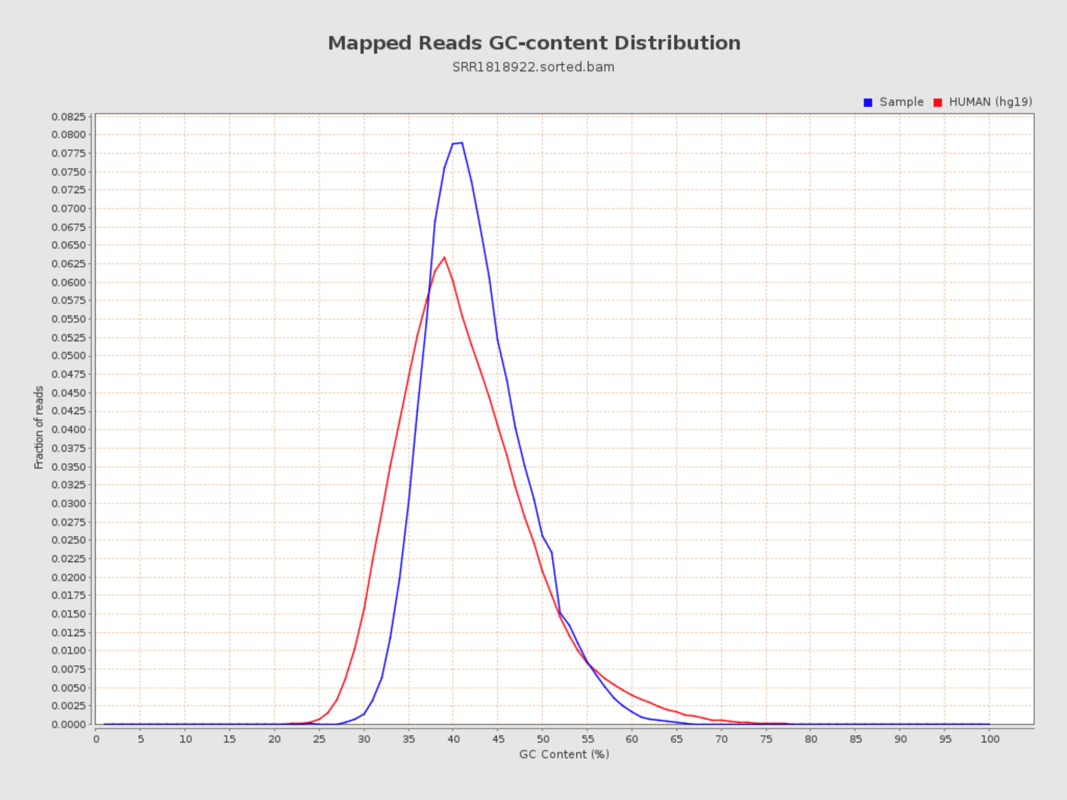
7. Results : Duplication Rate Histogram



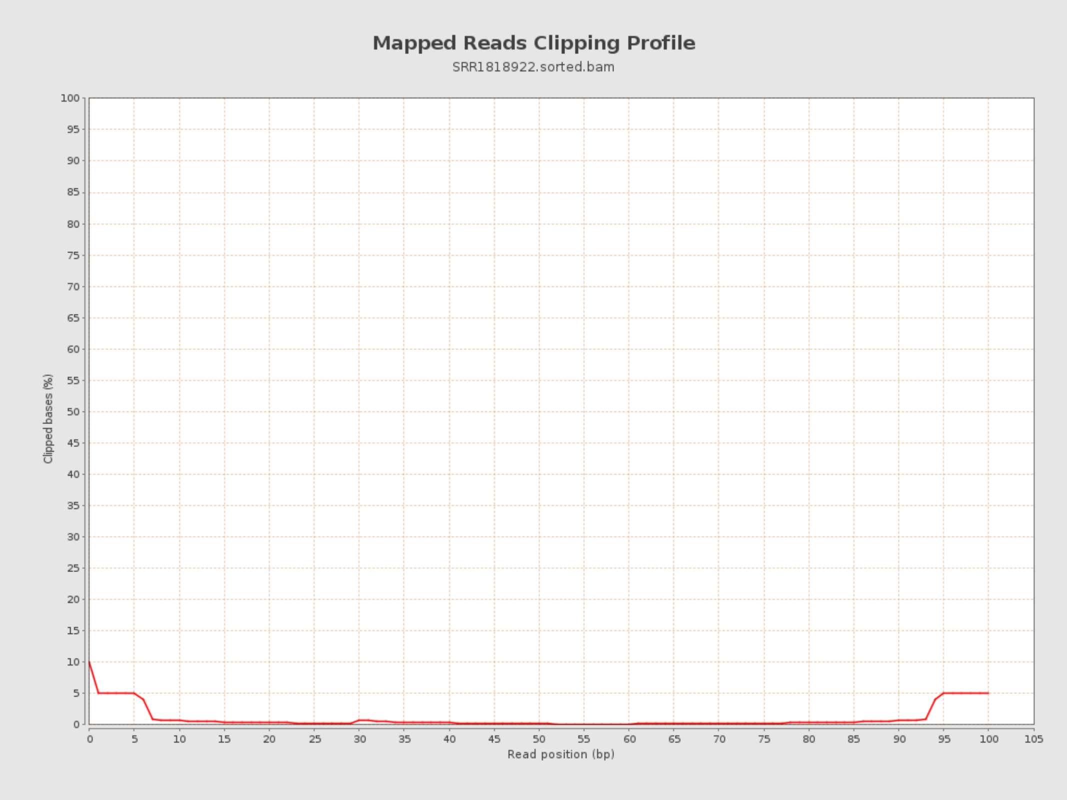
8. Results : Mapped Reads Nucleotide Content



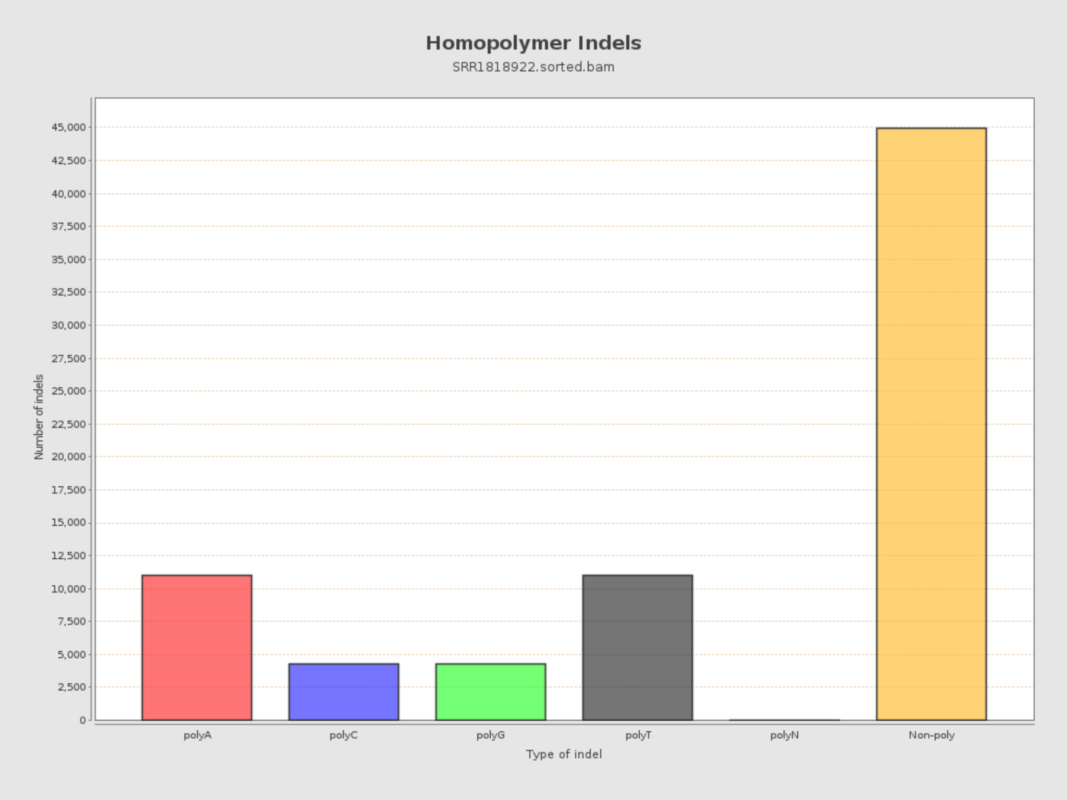
9. Results : Mapped Reads GC-content Distribution



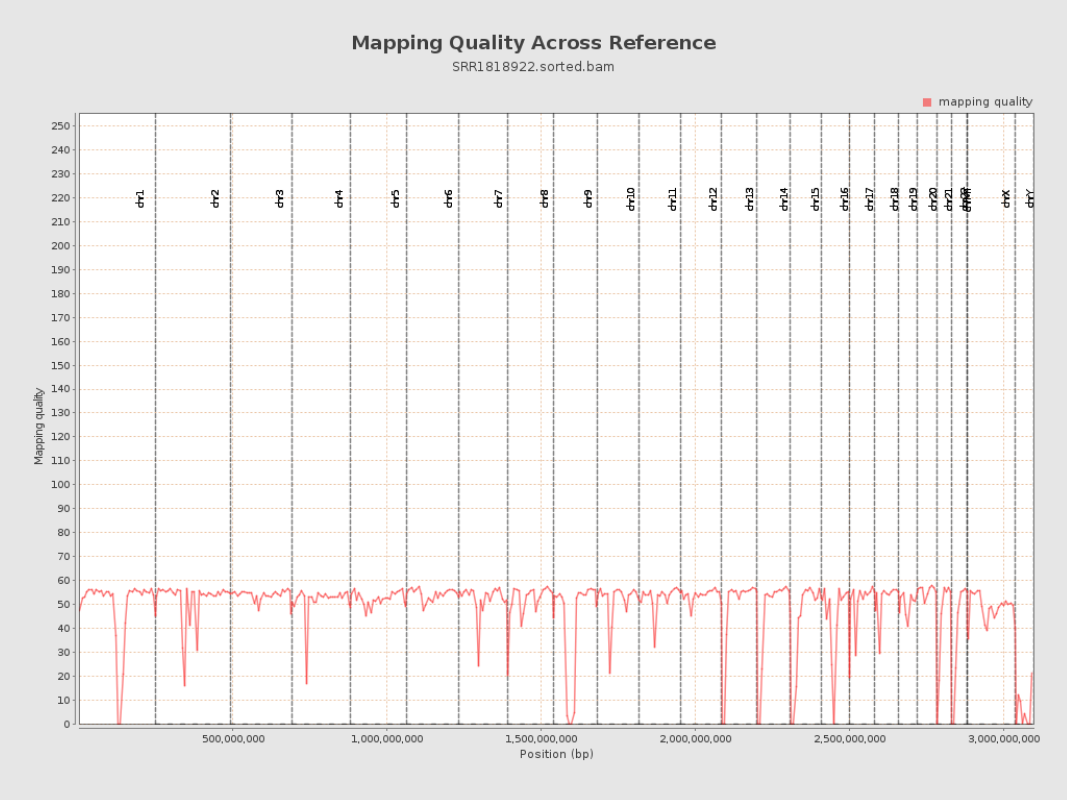
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram