Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:39:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818926.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_SRR1818926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:39:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,313,357
Mapped reads	1,297,589 / 98.8%
Unmapped reads	15,768 / 1.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,713 / 1.42%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	485,062 / 36.93%
Duplication rate	31.18%
Clipped reads	1,312,273 / 99.92%

2.2. ACGT Content

Number/percentage of A's	34,268,284 / 28.5%
Number/percentage of C's	24,681,026 / 20.53%
Number/percentage of T's	34,654,403 / 28.82%
Number/percentage of G's	26,619,468 / 22.14%
Number/percentage of N's	5,268 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0389

Standard Deviation	0.4475

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

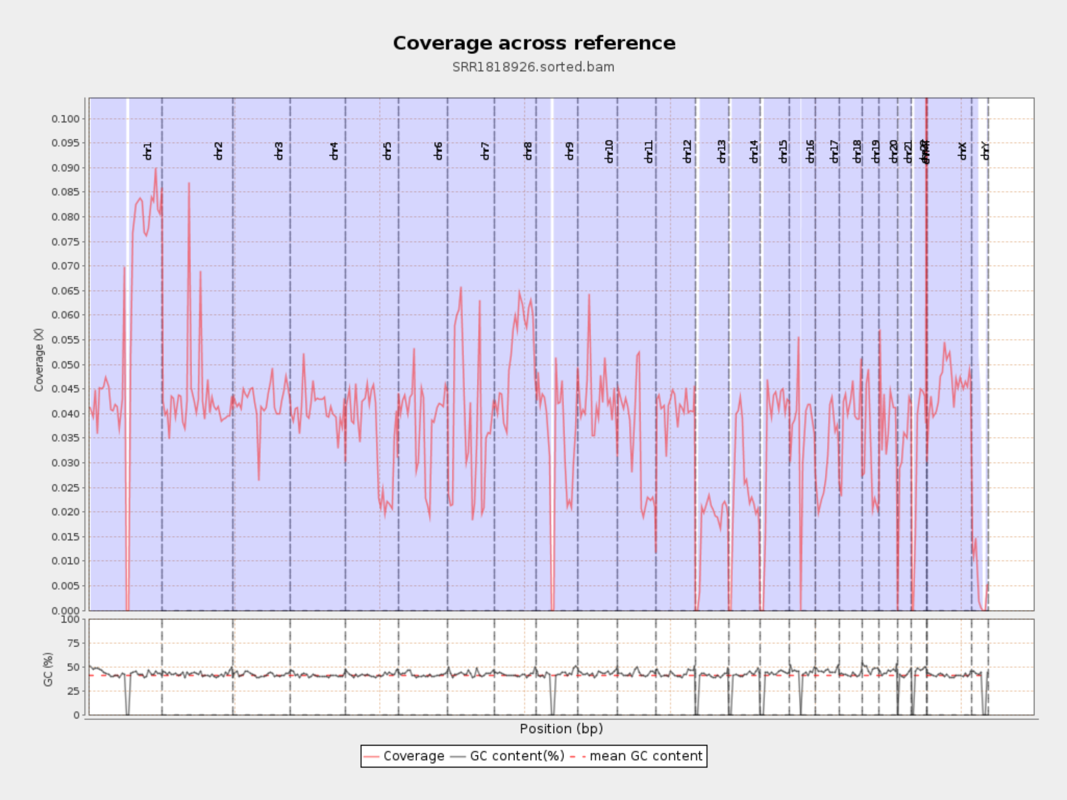
General error rate	0.63%
Mismatches	722,791
Insertions	13,649
Mapped reads with at least one insertion	1.03%
Deletions	36,149
Mapped reads with at least one deletion	2.73%
Homopolymer indels	43.43%

2.6. Chromosome stats

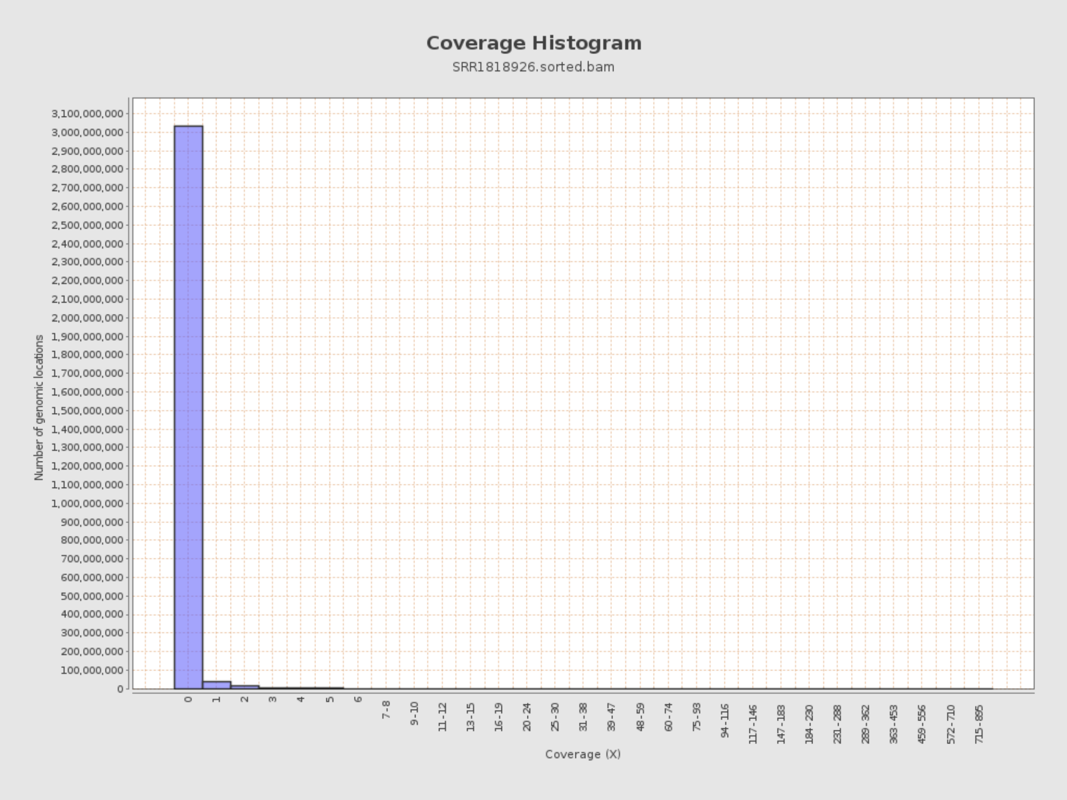
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14193949	0.0569	0.753
chr2	243199373	10564720	0.0434	0.6148
chr3	198022430	8418332	0.0425	0.348
chr4	191154276	7837861	0.041	0.3515
chr5	180915260	6421531	0.0355	0.3225
chr6	171115067	6628213	0.0387	0.3508
chr7	159138663	6000446	0.0377	0.373

chr8	146364022	7667900	0.0524	0.4208
chr9	141213431	4675484	0.0331	0.4981
chr10	135534747	5858663	0.0432	0.489
chr11	135006516	4553777	0.0337	0.3376
chr12	133851895	5533012	0.0413	0.352
chr13	115169878	1988594	0.0173	0.2157
chr14	107349540	2657651	0.0248	0.2874
chr15	102531392	3564066	0.0348	0.3131
chr16	90354753	3268671	0.0362	0.4475
chr17	81195210	2526283	0.0311	0.3166
chr18	78077248	3104531	0.0398	0.6028
chr19	59128983	1843961	0.0312	0.6063
chr20	63025520	2515458	0.0399	0.3521
chr21	48129895	1550252	0.0322	0.3237
chr22	51304566	1535034	0.0299	0.3144
chrMT	16571	5533	0.3339	1.296
chrX	155270560	7052168	0.0454	0.4123
chrY	59373566	325612	0.0055	0.3342

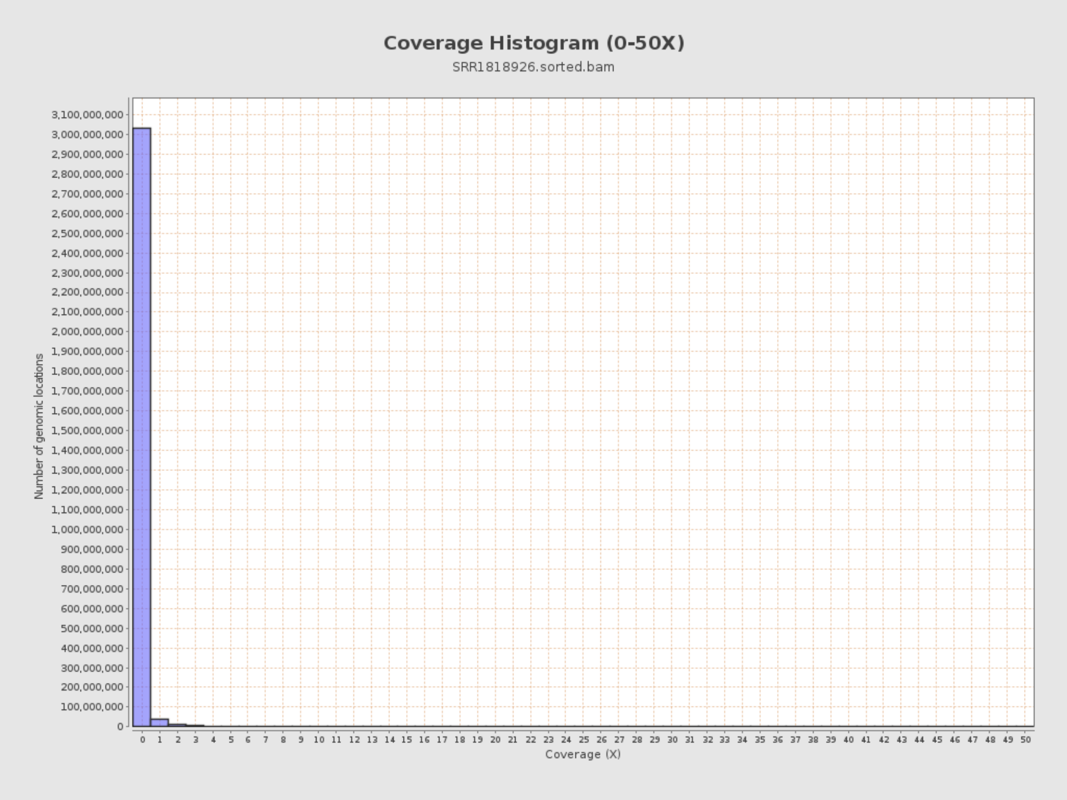
3. Results : Coverage across reference



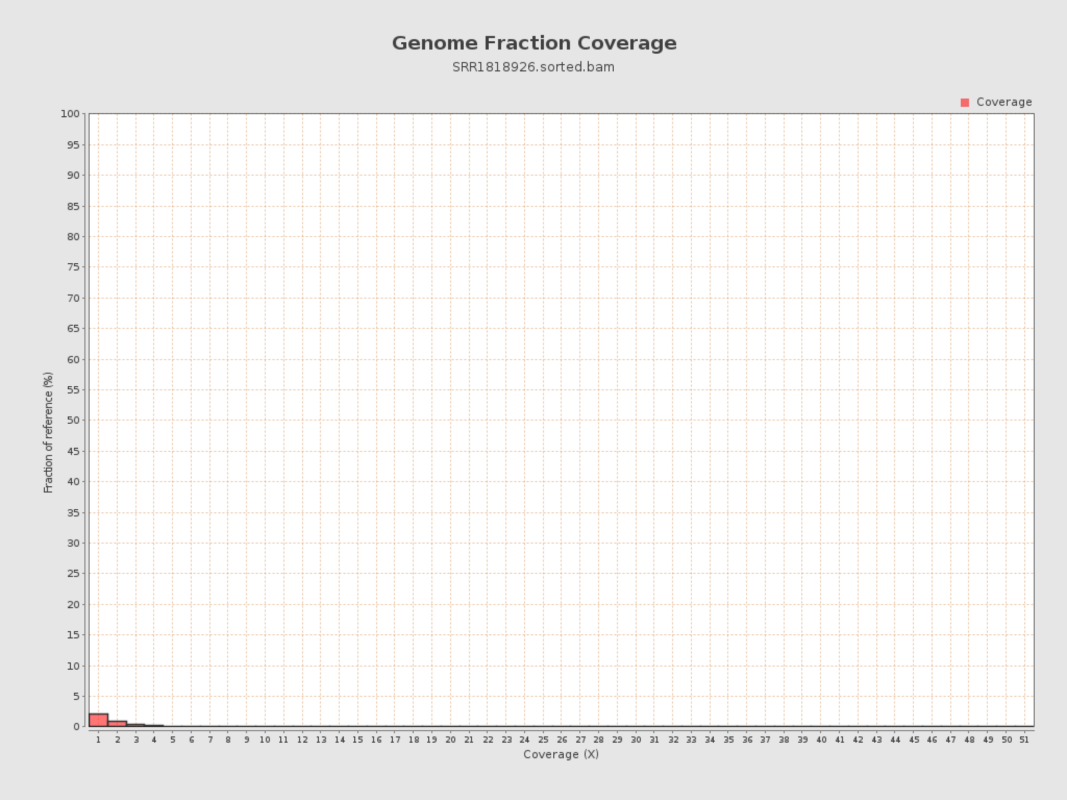
4. Results : Coverage Histogram



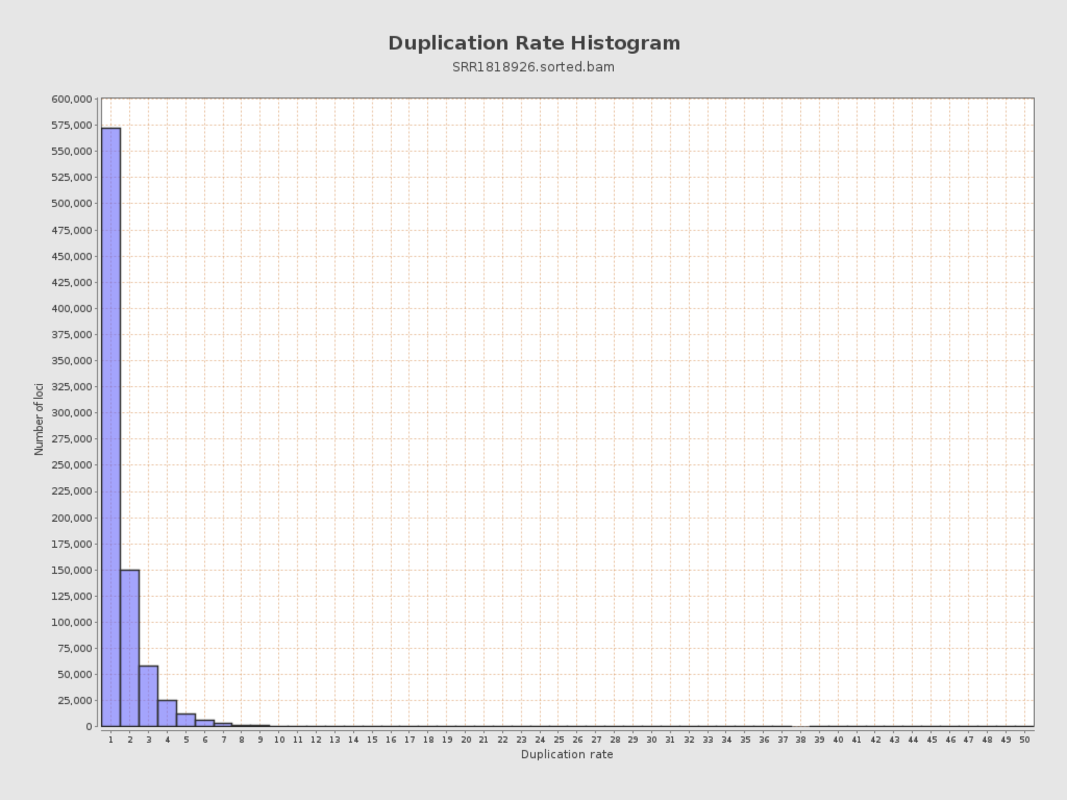
5. Results : Coverage Histogram (0-50X)



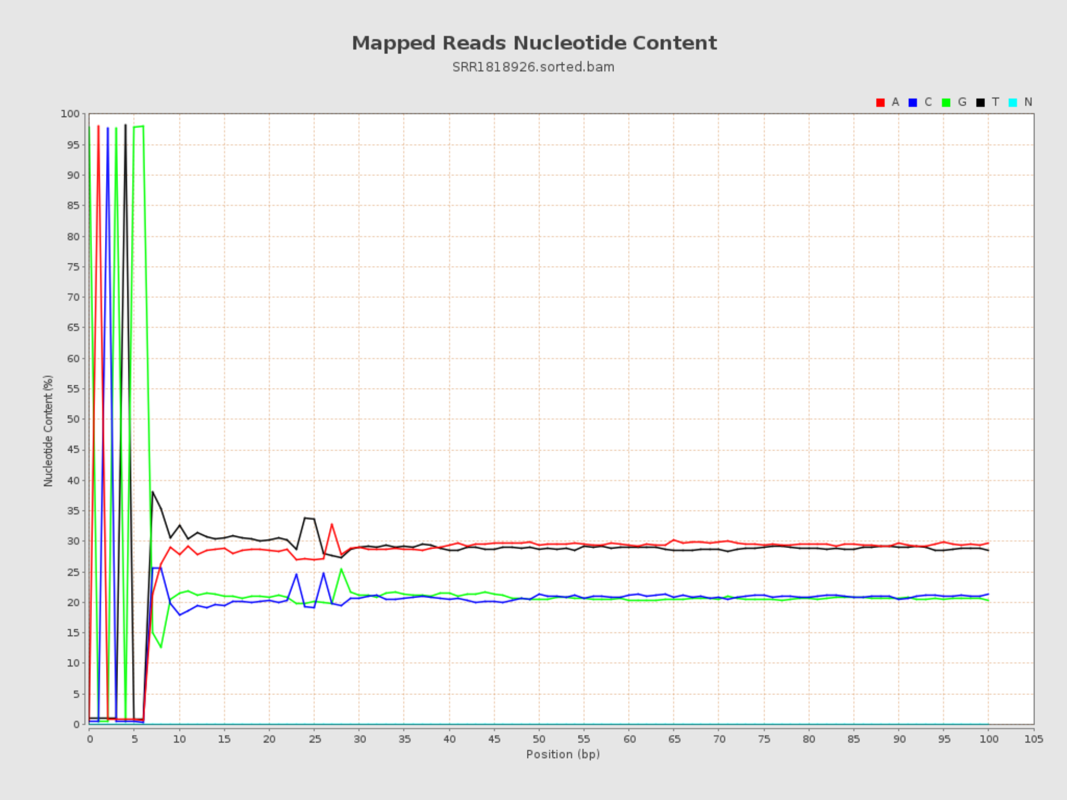
6. Results : Genome Fraction Coverage



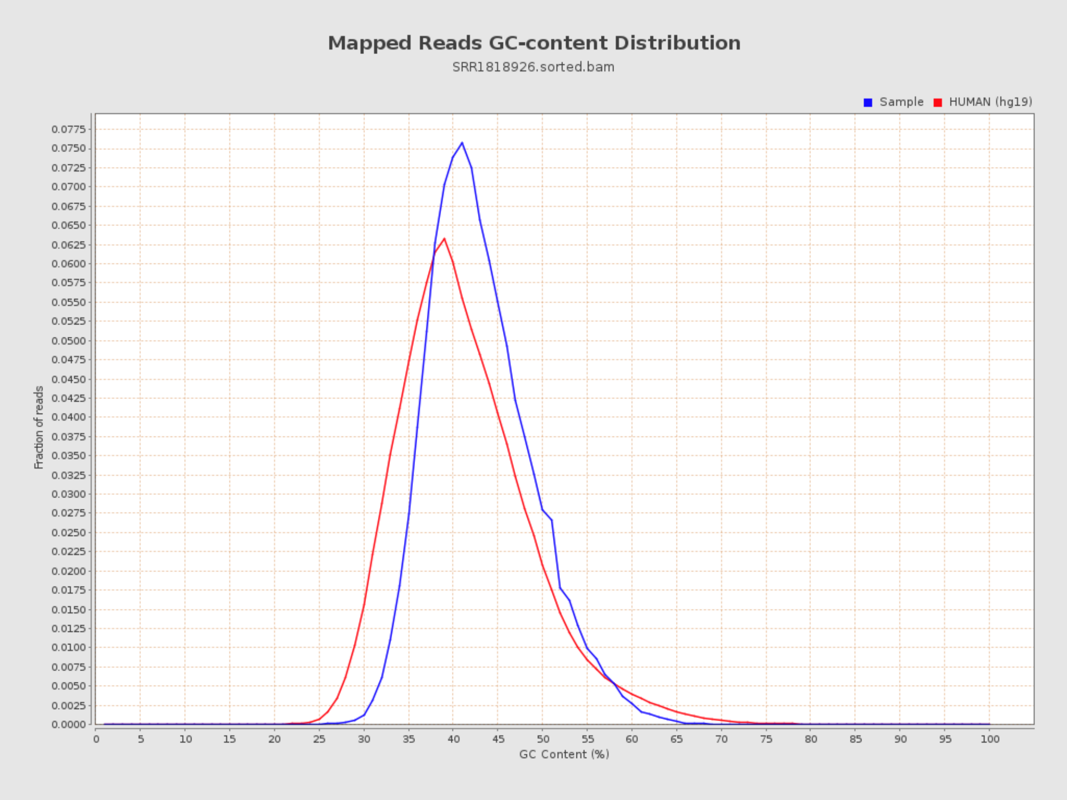
7. Results : Duplication Rate Histogram



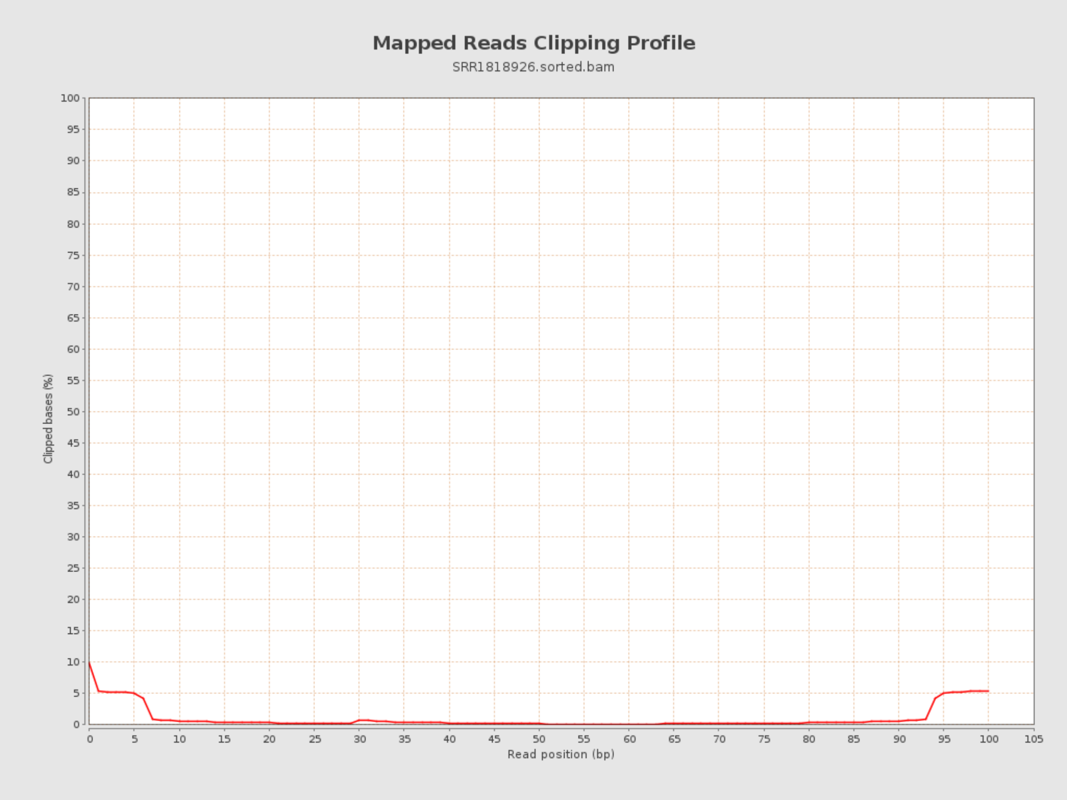
8. Results : Mapped Reads Nucleotide Content



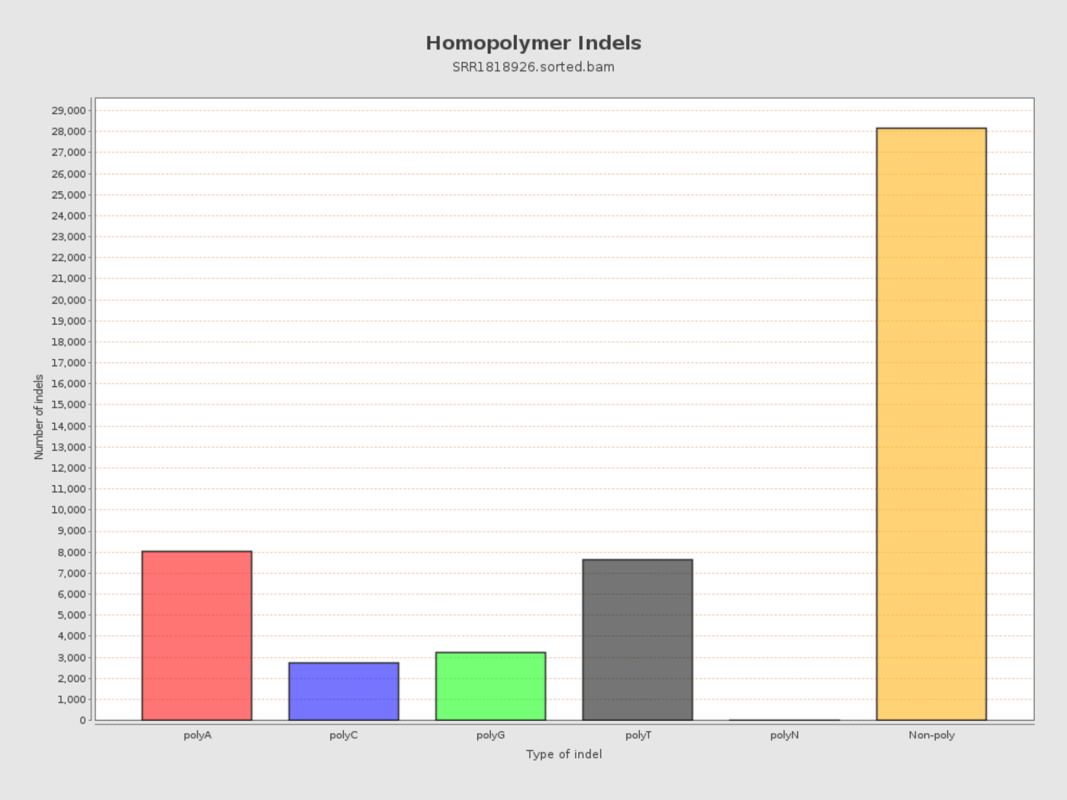
9. Results : Mapped Reads GC-content Distribution



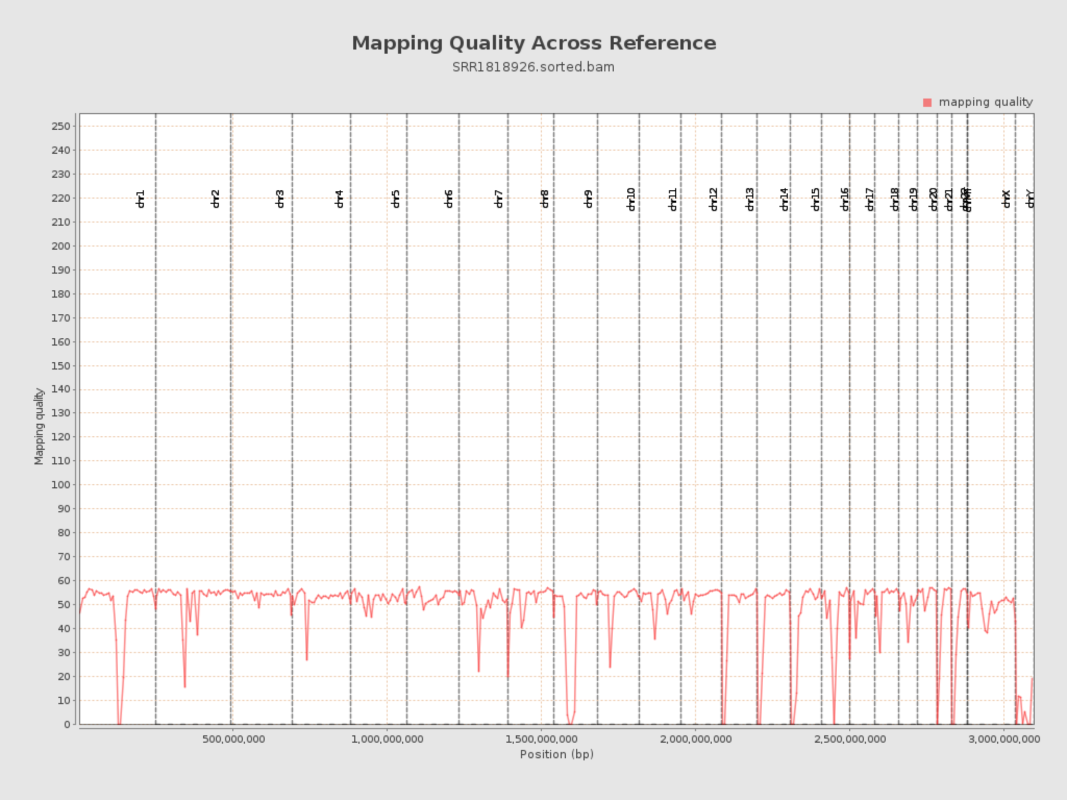
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram