Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:55:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818967.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_SRR1818967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:55:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,958,320
Mapped reads	1,933,411 / 98.73%
Unmapped reads	24,909 / 1.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,813 / 1.62%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	923,925 / 47.18%
Duplication rate	40.88%
Clipped reads	1,956,259 / 99.89%

2.2. ACGT Content

Number/percentage of A's	51,108,905 / 28.58%
Number/percentage of C's	38,217,990 / 21.37%
Number/percentage of T's	51,250,553 / 28.66%
Number/percentage of G's	38,241,270 / 21.38%
Number/percentage of N's	9,151 / 0.01%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.6395

2.4. Mapping Quality

Mean Mapping Quality	49.06

2.5. Mismatches and indels

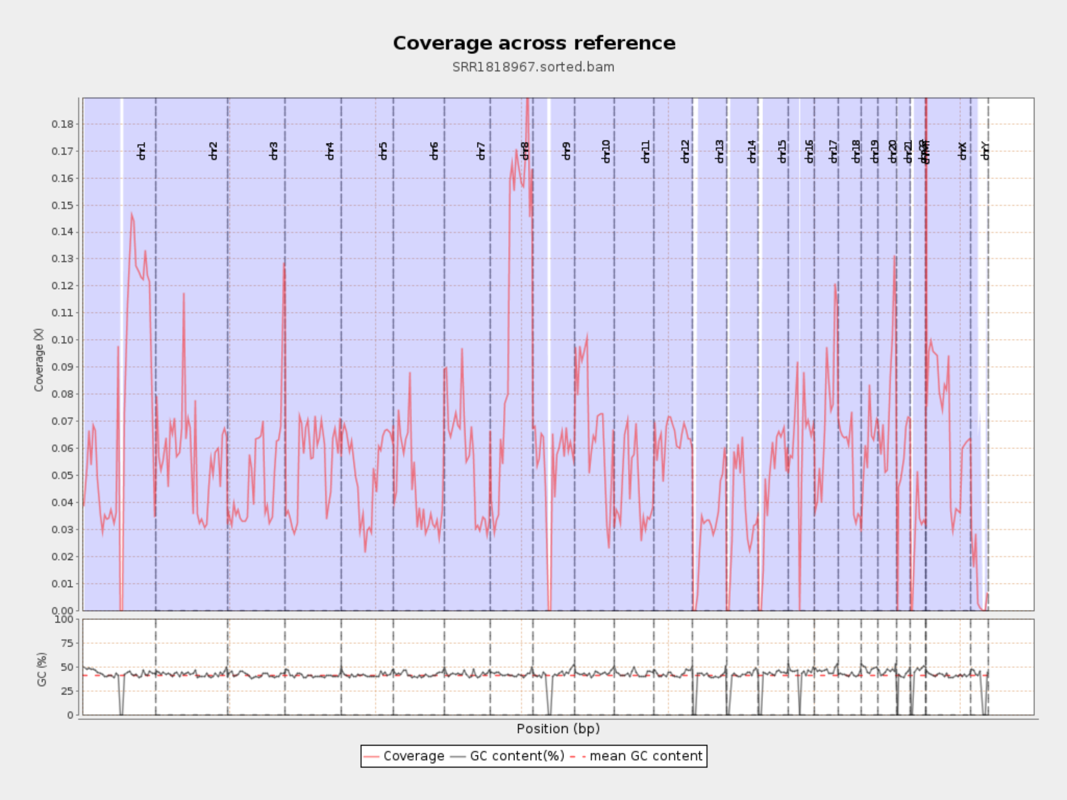
General error rate	0.64%
Mismatches	1,082,483
Insertions	27,903
Mapped reads with at least one insertion	1.41%
Deletions	56,928
Mapped reads with at least one deletion	2.88%
Homopolymer indels	41.34%

2.6. Chromosome stats

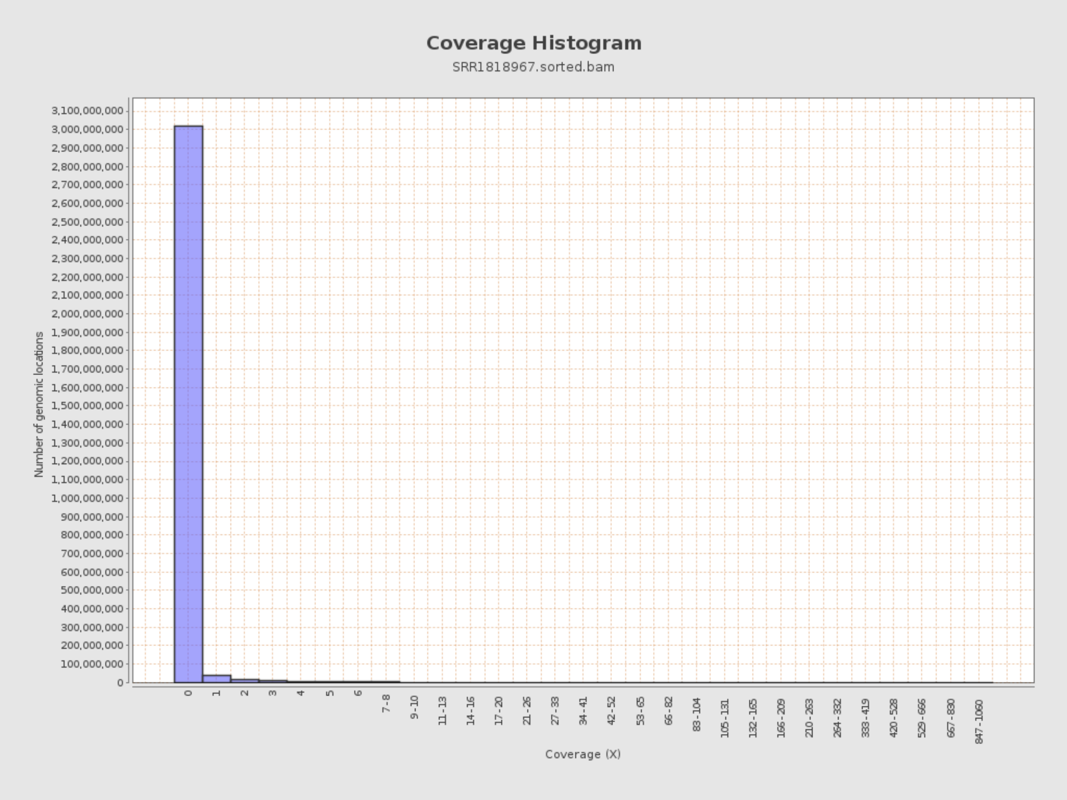
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18320985	0.0735	1.0474
chr2	243199373	14033645	0.0577	0.8465
chr3	198022430	9911052	0.0501	0.4199
chr4	191154276	10372043	0.0543	0.4751
chr5	180915260	9409491	0.052	0.4344
chr6	171115067	7729301	0.0452	0.4725
chr7	159138663	9120188	0.0573	0.784

chr8	146364022	17051512	0.1165	0.7187
chr9	141213431	7445532	0.0527	0.5828
chr10	135534747	9267668	0.0684	0.7144
chr11	135006516	5949350	0.0441	0.4367
chr12	133851895	8618232	0.0644	0.4907
chr13	115169878	3575125	0.031	0.3368
chr14	107349540	3813530	0.0355	0.3705
chr15	102531392	4634382	0.0452	0.4133
chr16	90354753	5574320	0.0617	0.6988
chr17	81195210	5803211	0.0715	0.5628
chr18	78077248	4268231	0.0547	0.6469
chr19	59128983	3667667	0.062	1.1016
chr20	63025520	4983331	0.0791	0.5702
chr21	48129895	2592453	0.0539	0.4831
chr22	51304566	1391608	0.0271	0.3378
chrMT	16571	19865	1.1988	2.1846
chrX	155270560	10806824	0.0696	0.535
chrY	59373566	571144	0.0096	0.5265

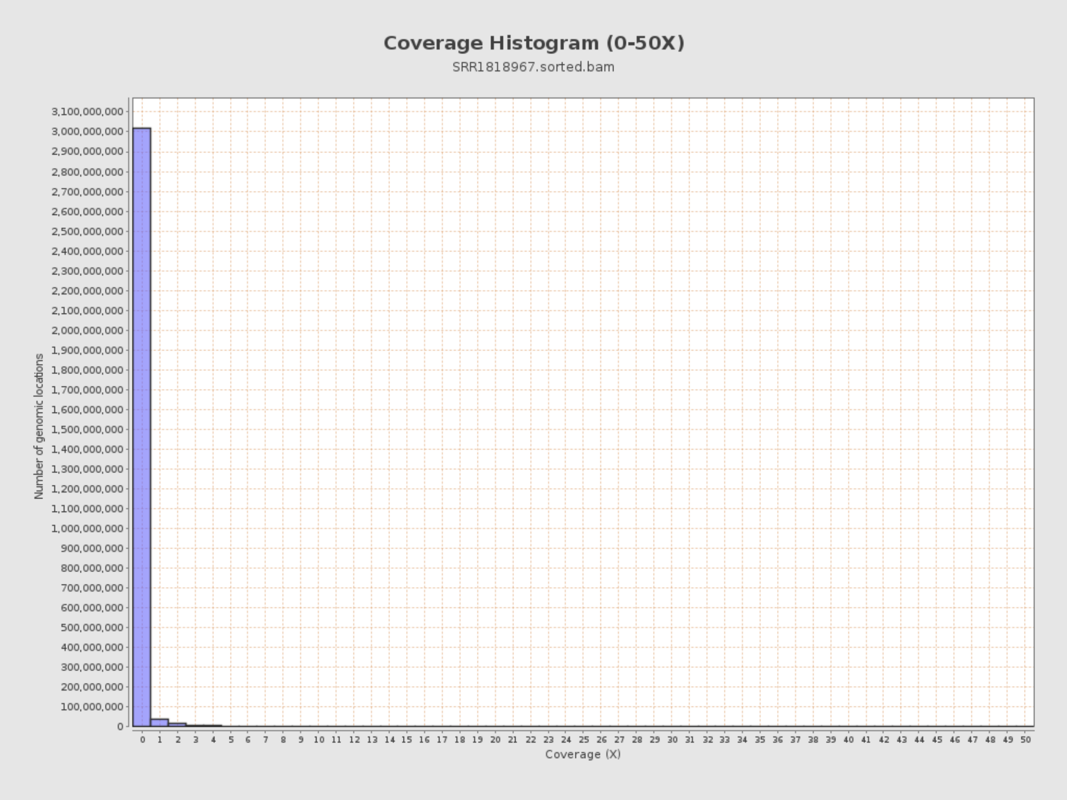
3. Results : Coverage across reference



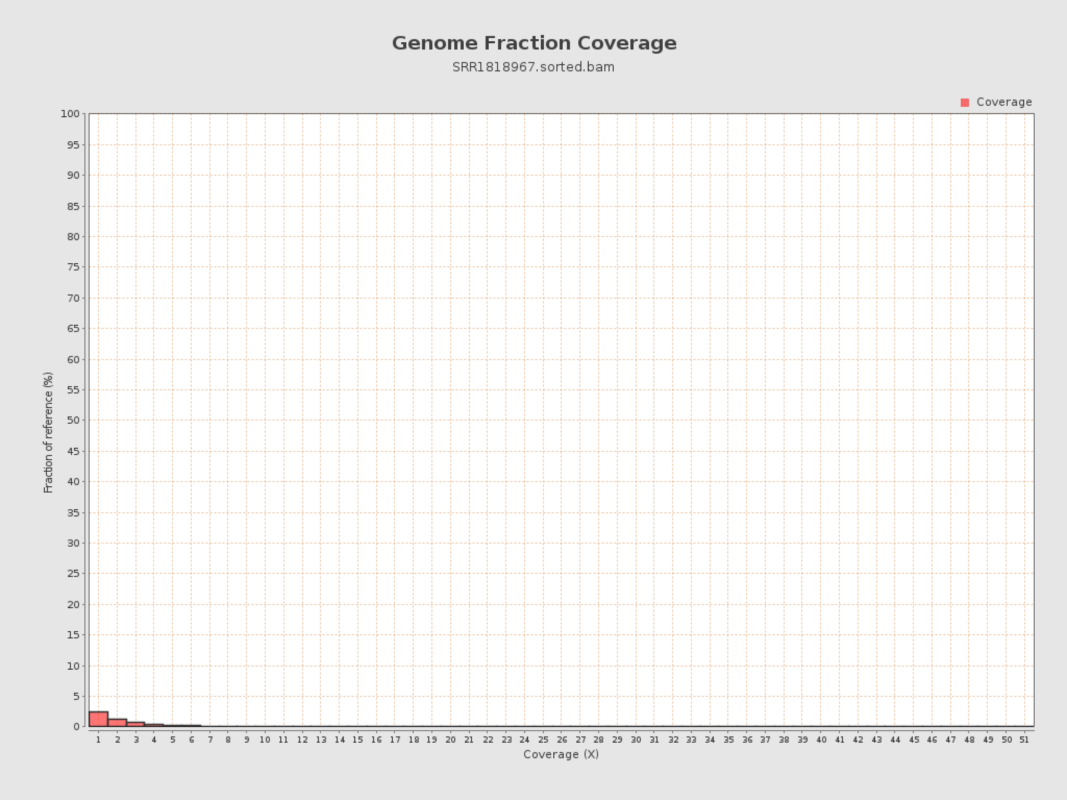
4. Results : Coverage Histogram



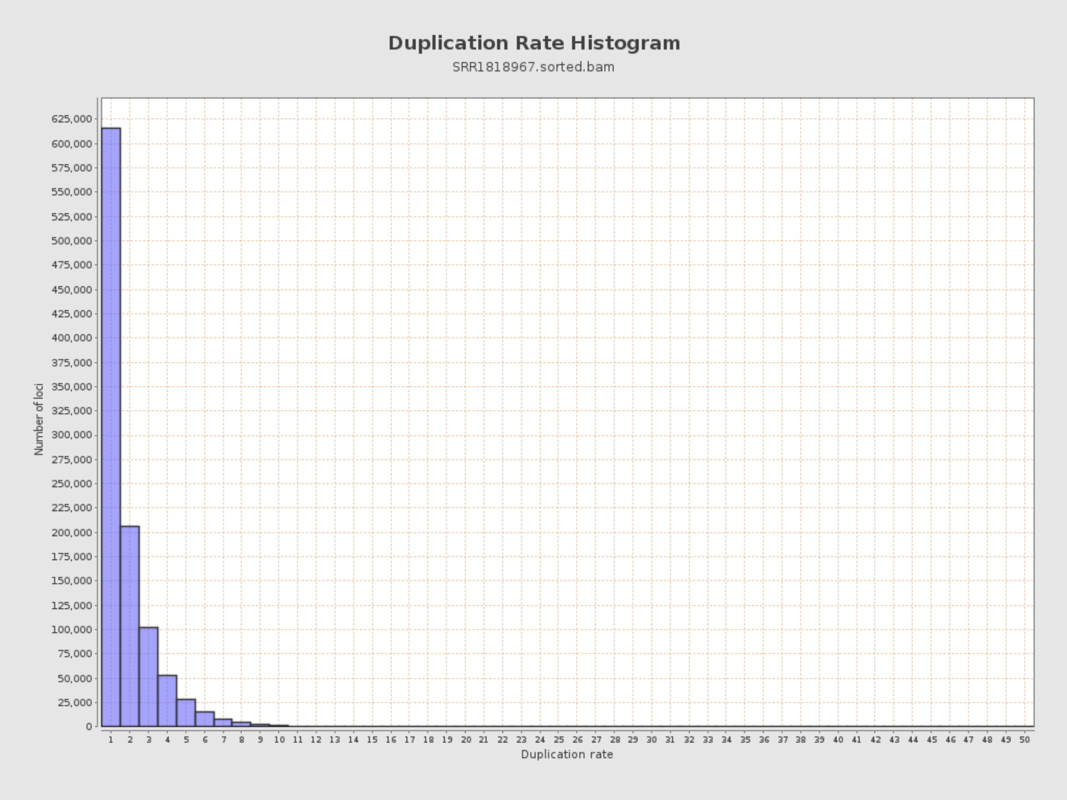
5. Results : Coverage Histogram (0-50X)



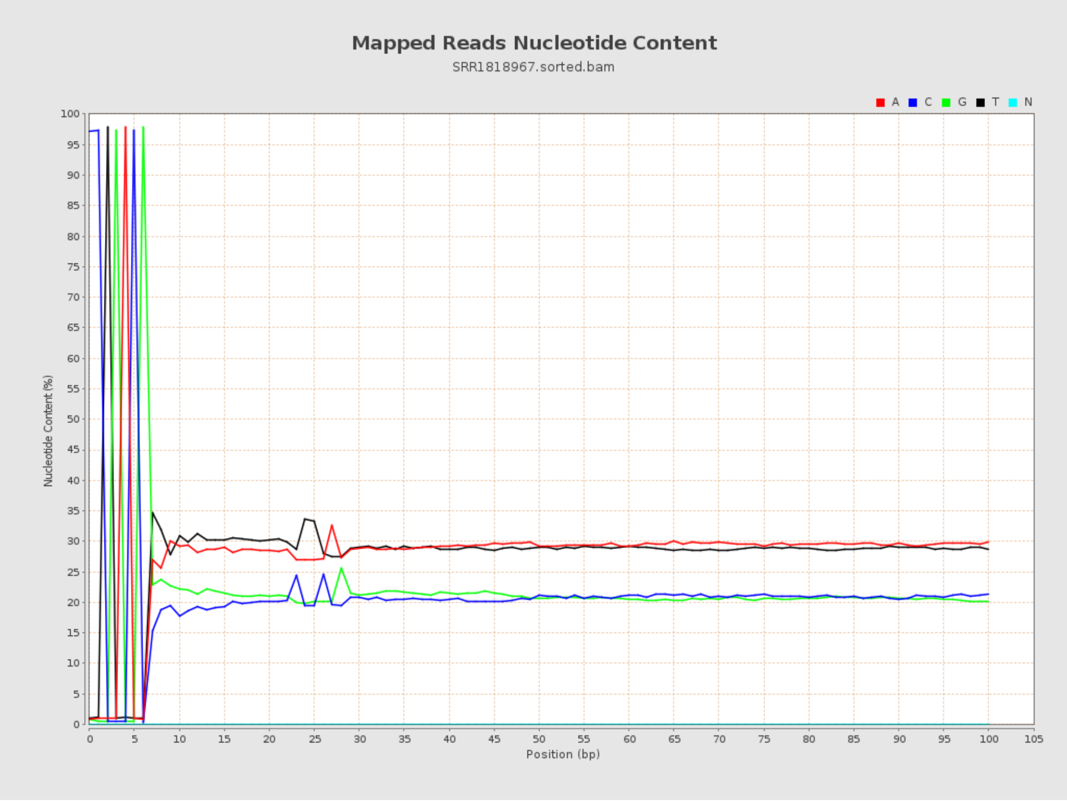
6. Results : Genome Fraction Coverage



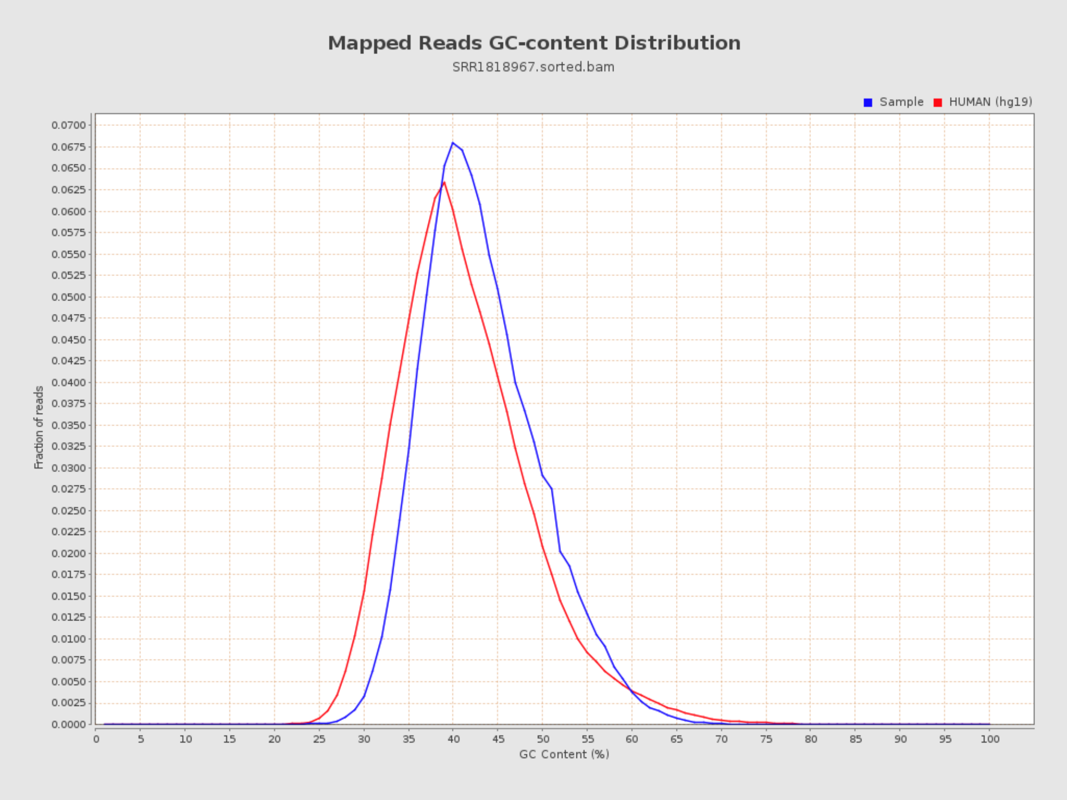
7. Results : Duplication Rate Histogram



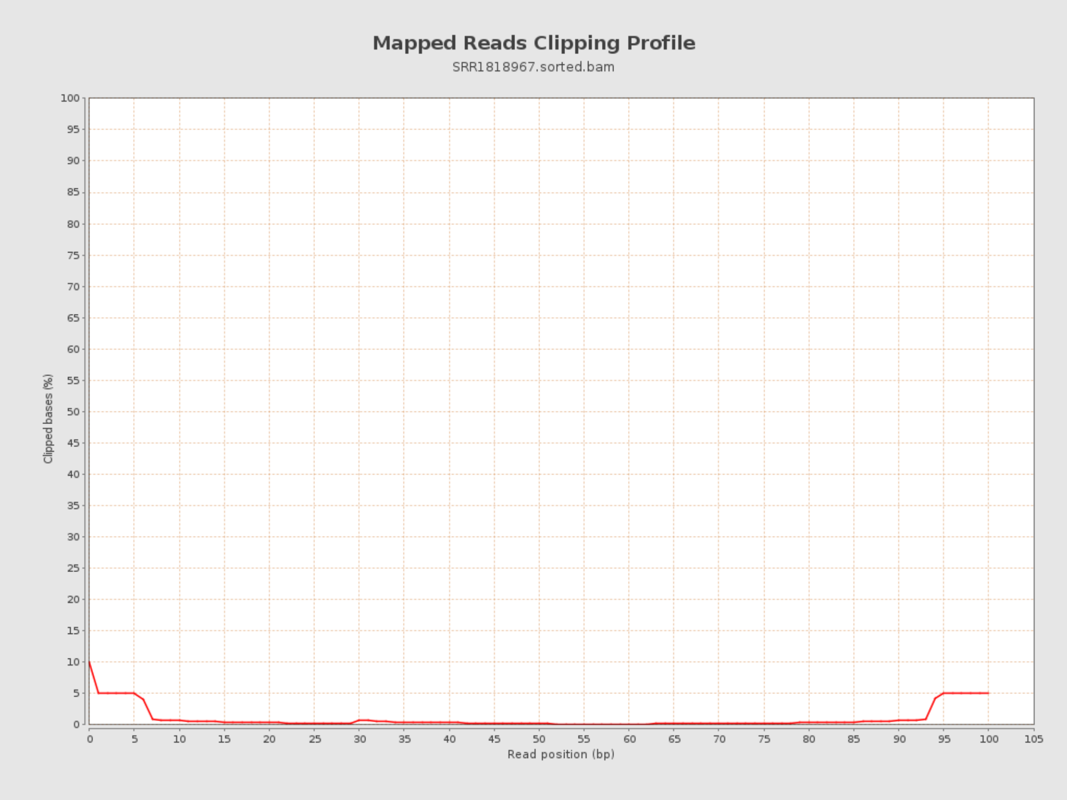
8. Results : Mapped Reads Nucleotide Content



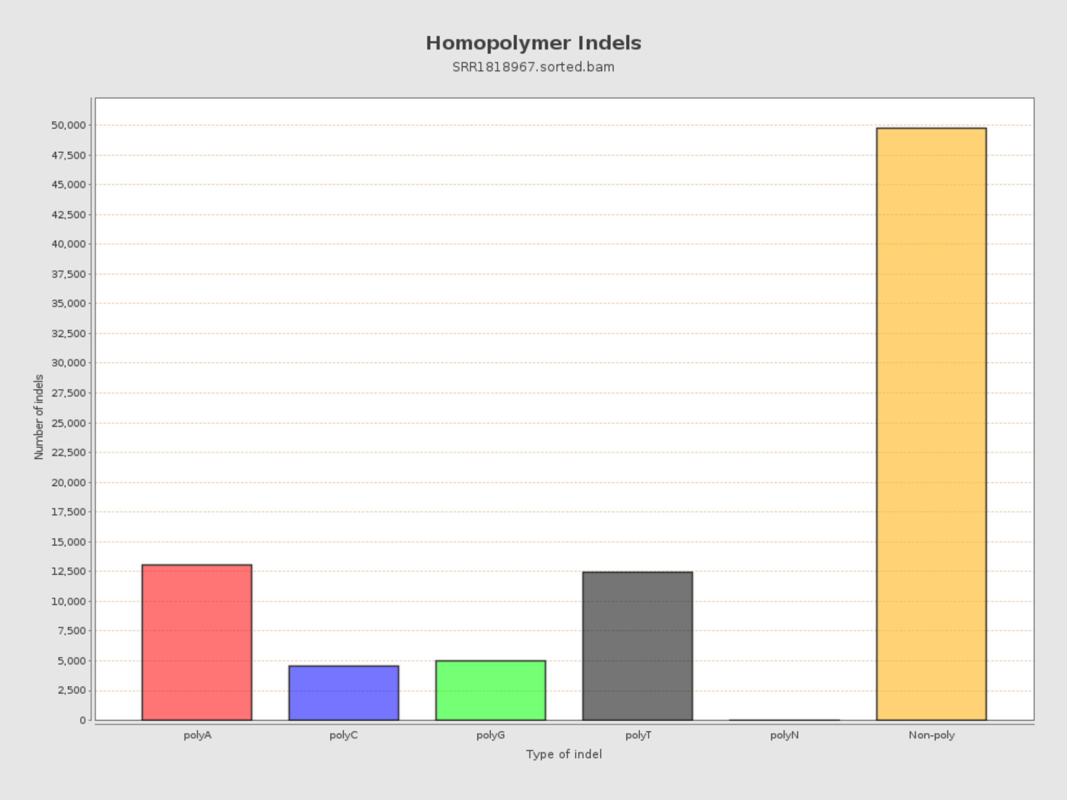
9. Results : Mapped Reads GC-content Distribution



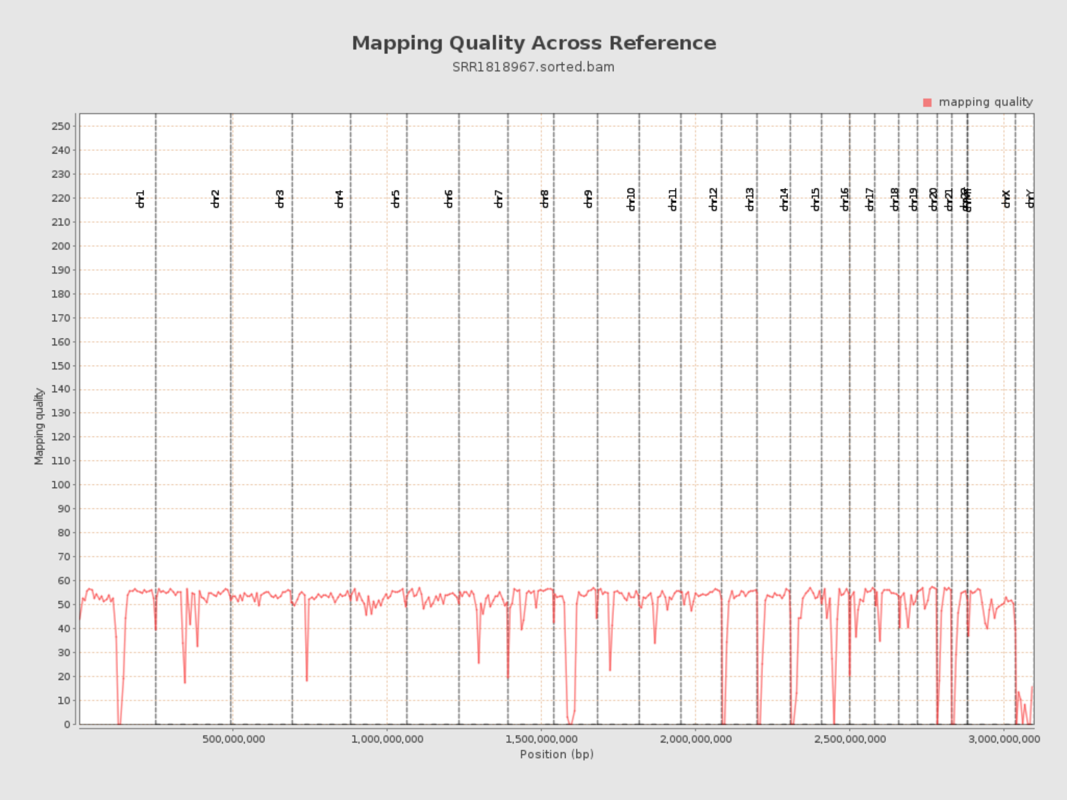
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram