Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:38:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818872.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_SRR1818872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818872.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:38:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,731,851
Mapped reads	1,709,268 / 98.7%
Unmapped reads	22,583 / 1.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,633 / 1.77%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	426,534 / 24.63%
Duplication rate	21.57%
Clipped reads	1,728,871 / 99.83%

2.2. ACGT Content

Number/percentage of A's	44,869,991 / 28.41%
Number/percentage of C's	34,440,682 / 21.81%
Number/percentage of T's	44,548,499 / 28.2%
Number/percentage of G's	34,085,821 / 21.58%
Number/percentage of N's	2,283 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0511

Standard Deviation	0.5733

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

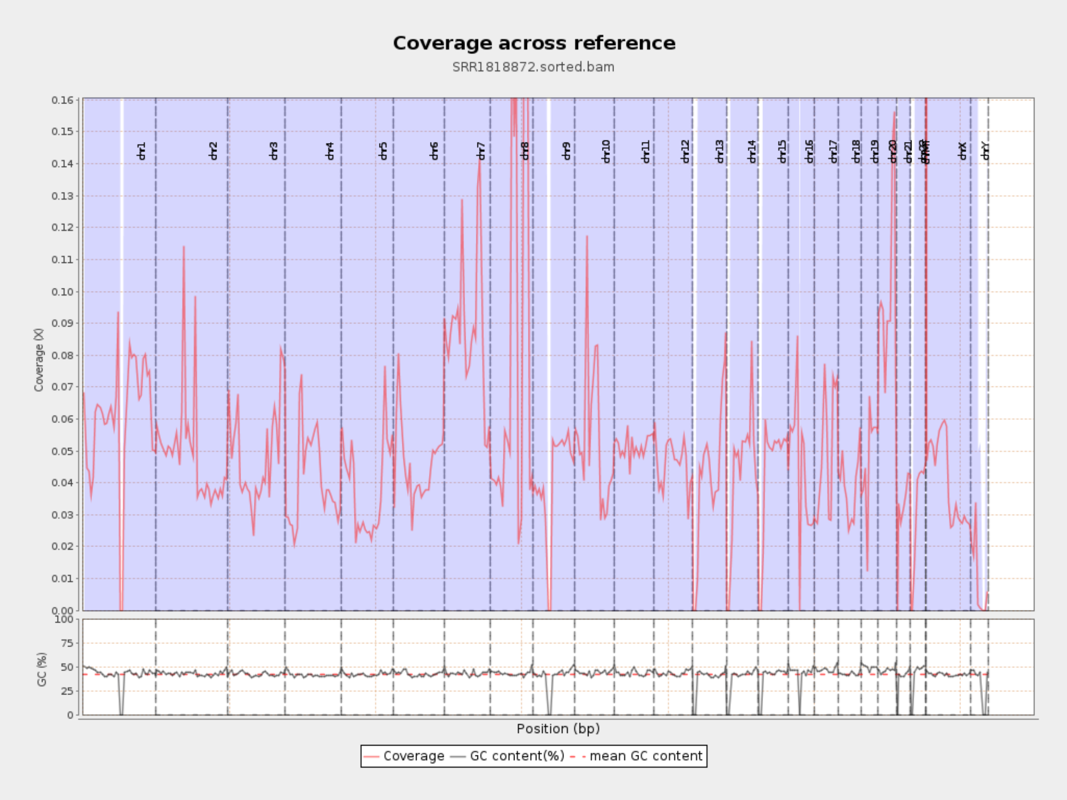
General error rate	0.64%
Mismatches	958,016
Insertions	22,228
Mapped reads with at least one insertion	1.26%
Deletions	52,283
Mapped reads with at least one deletion	2.99%
Homopolymer indels	39.72%

2.6. Chromosome stats

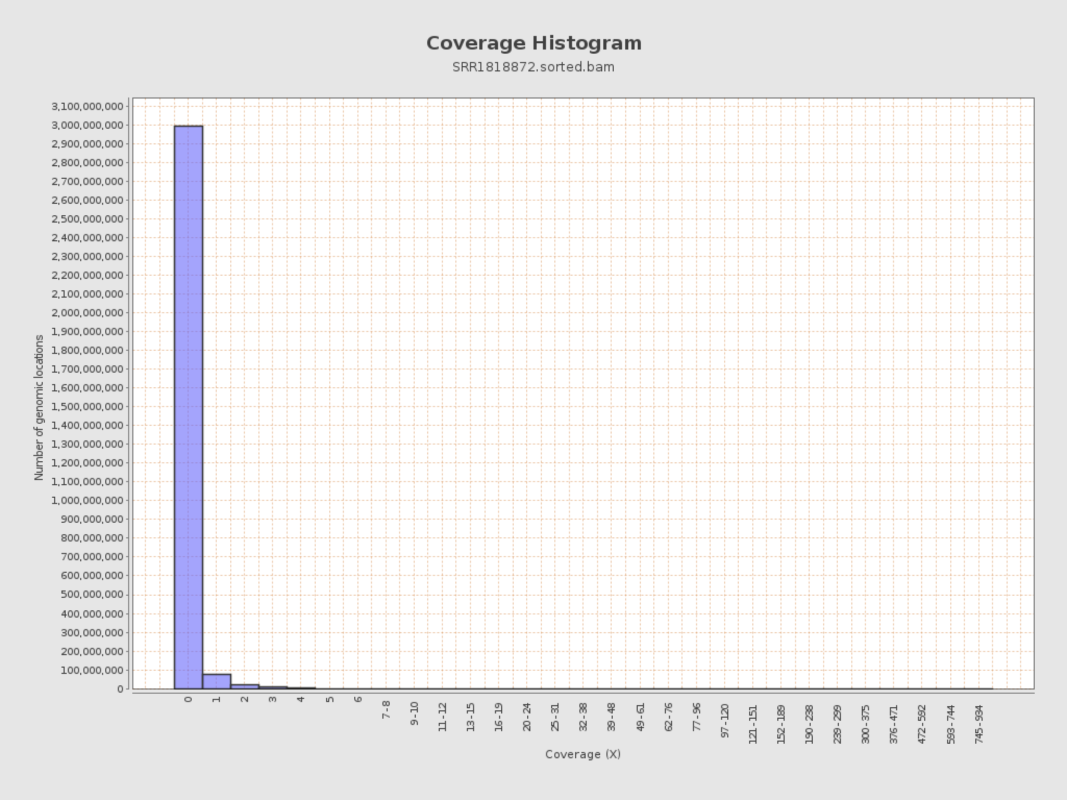
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15037830	0.0603	0.8476
chr2	243199373	12019001	0.0494	0.8891
chr3	198022430	9691217	0.0489	0.3065
chr4	191154276	7910897	0.0414	0.3585
chr5	180915260	7021188	0.0388	0.2951
chr6	171115067	7838966	0.0458	0.328
chr7	159138663	14039167	0.0882	1.0669

chr8	146364022	13838480	0.0945	0.5242
chr9	141213431	5785435	0.041	0.469
chr10	135534747	7277198	0.0537	0.7547
chr11	135006516	6931074	0.0513	0.3819
chr12	133851895	6203576	0.0463	0.3005
chr13	115169878	4839509	0.042	0.2829
chr14	107349540	4703978	0.0438	0.312
chr15	102531392	4416068	0.0431	0.2857
chr16	90354753	3937720	0.0436	0.6562
chr17	81195210	3965551	0.0488	0.3916
chr18	78077248	3026849	0.0388	0.5568
chr19	59128983	2794603	0.0473	0.7191
chr20	63025520	6522748	0.1035	0.4762
chr21	48129895	1553477	0.0323	0.2896
chr22	51304566	1516987	0.0296	0.2737
chrMT	16571	265908	16.0466	10.6035
chrX	155270560	6339176	0.0408	0.3337
chrY	59373566	571469	0.0096	0.6717

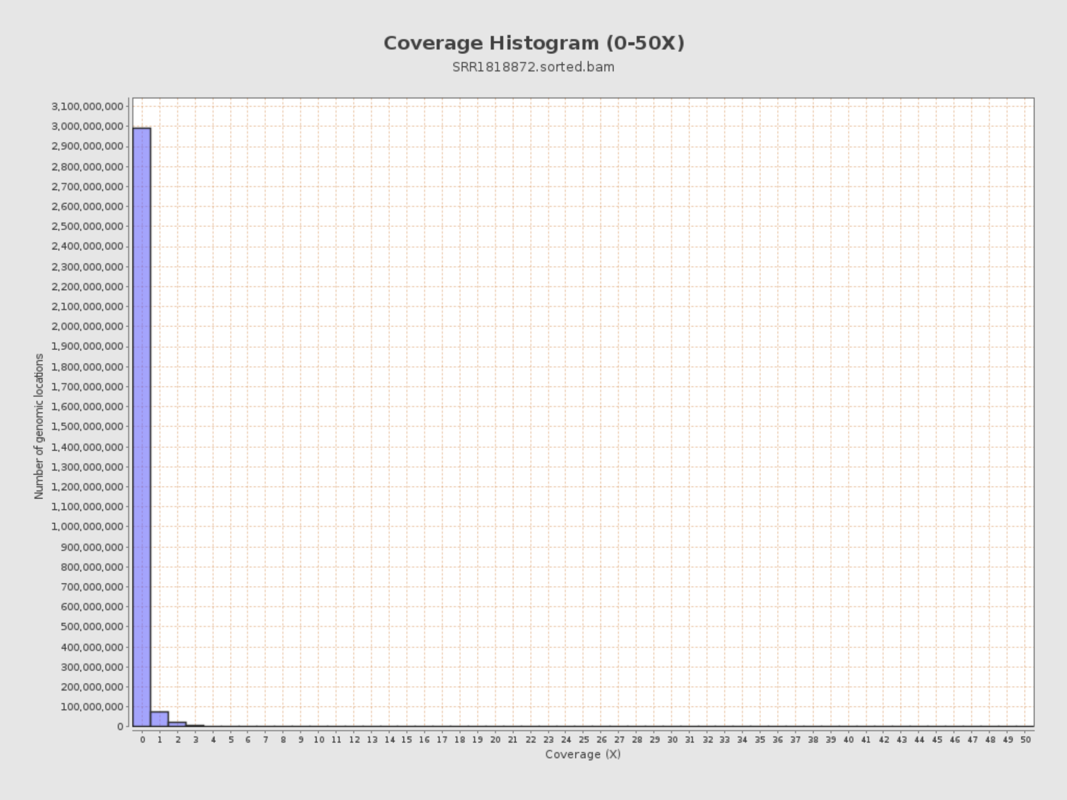
3. Results : Coverage across reference



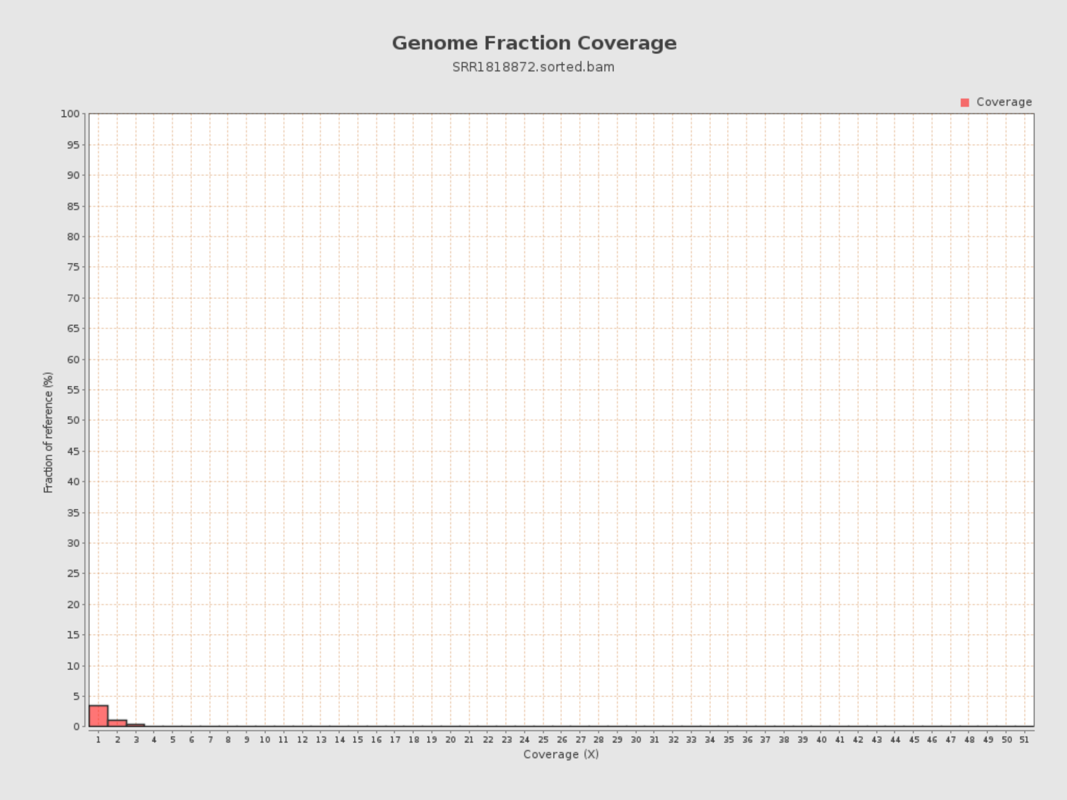
4. Results : Coverage Histogram



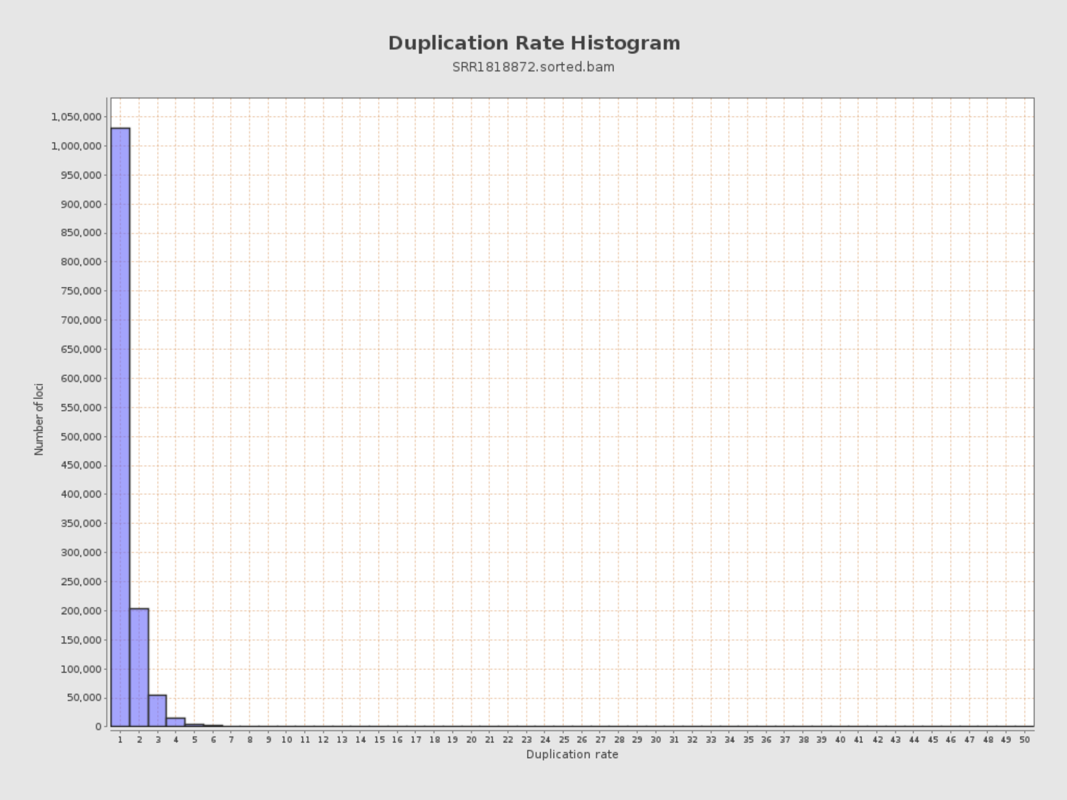
5. Results : Coverage Histogram (0-50X)



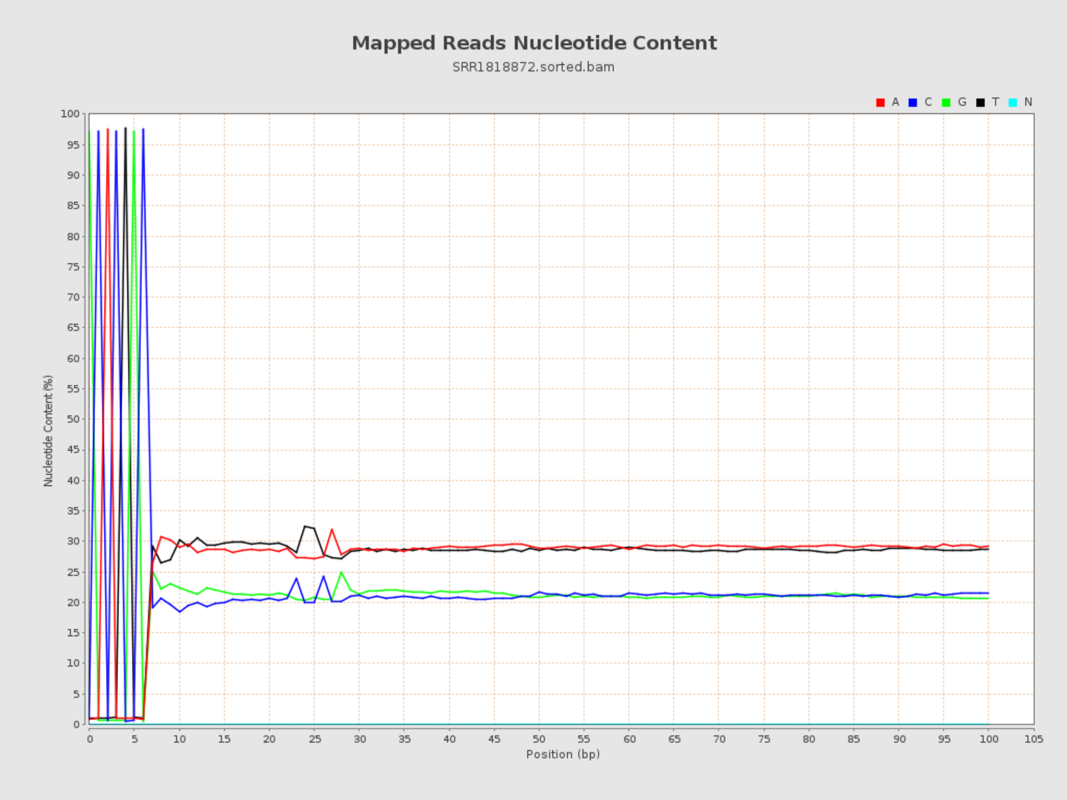
6. Results : Genome Fraction Coverage



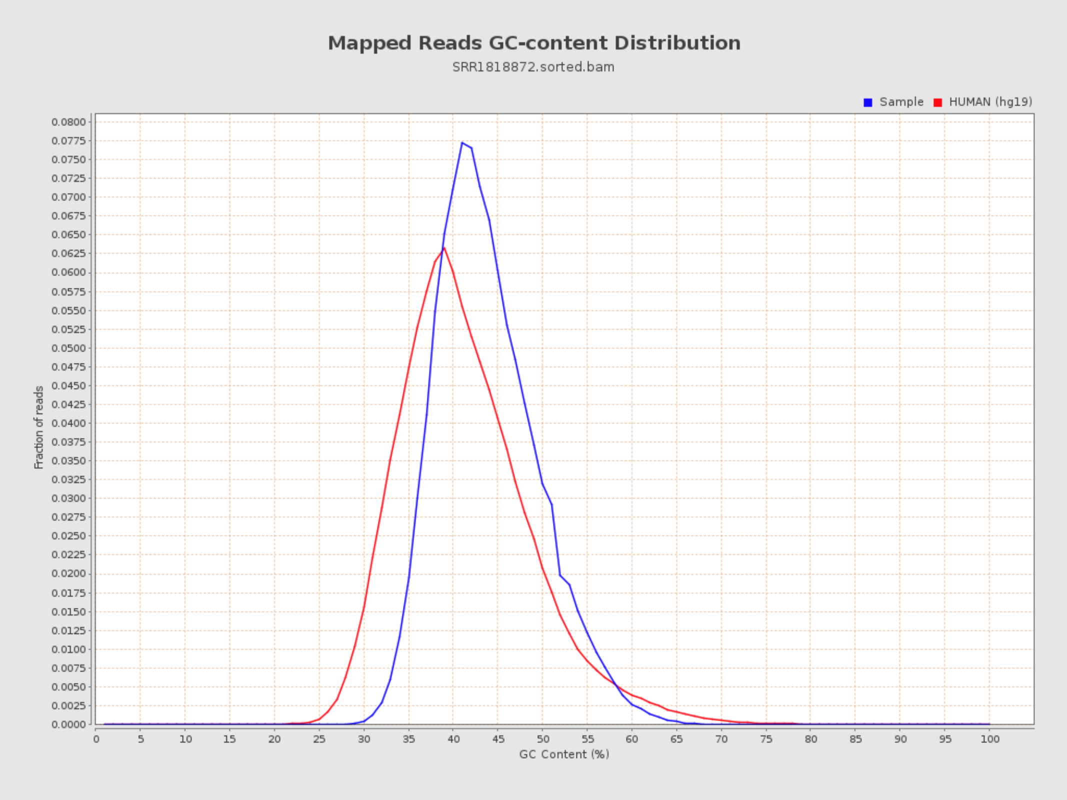
7. Results : Duplication Rate Histogram



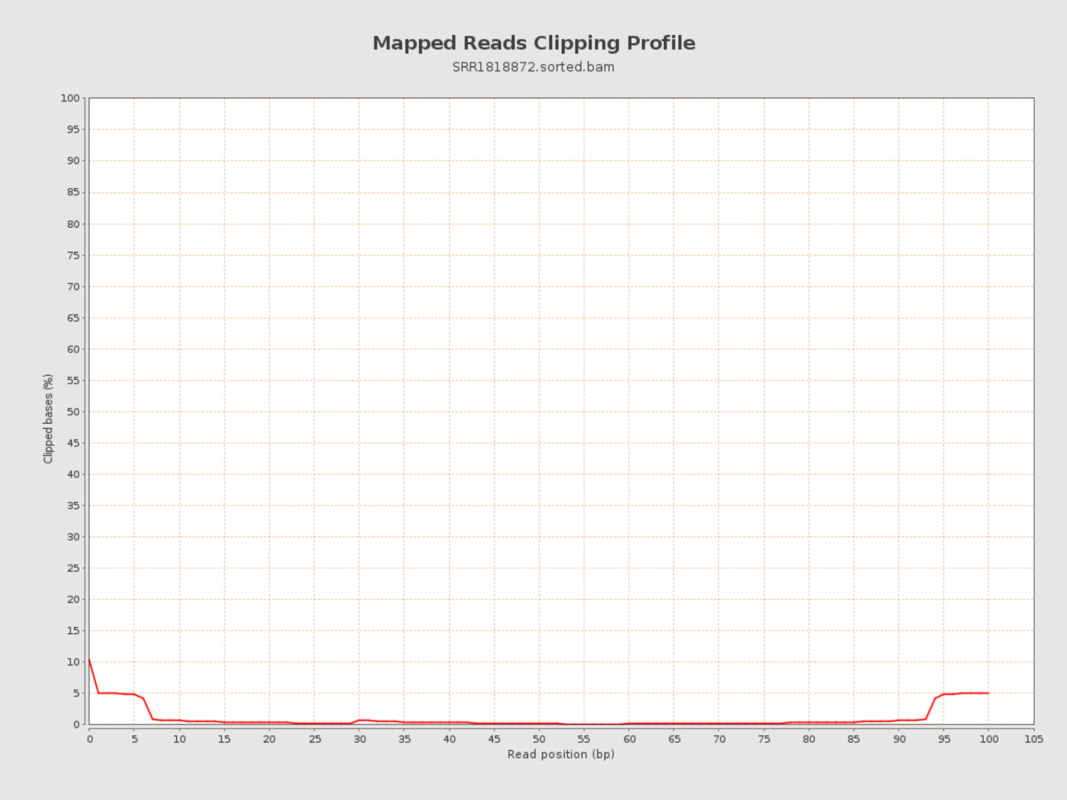
8. Results : Mapped Reads Nucleotide Content



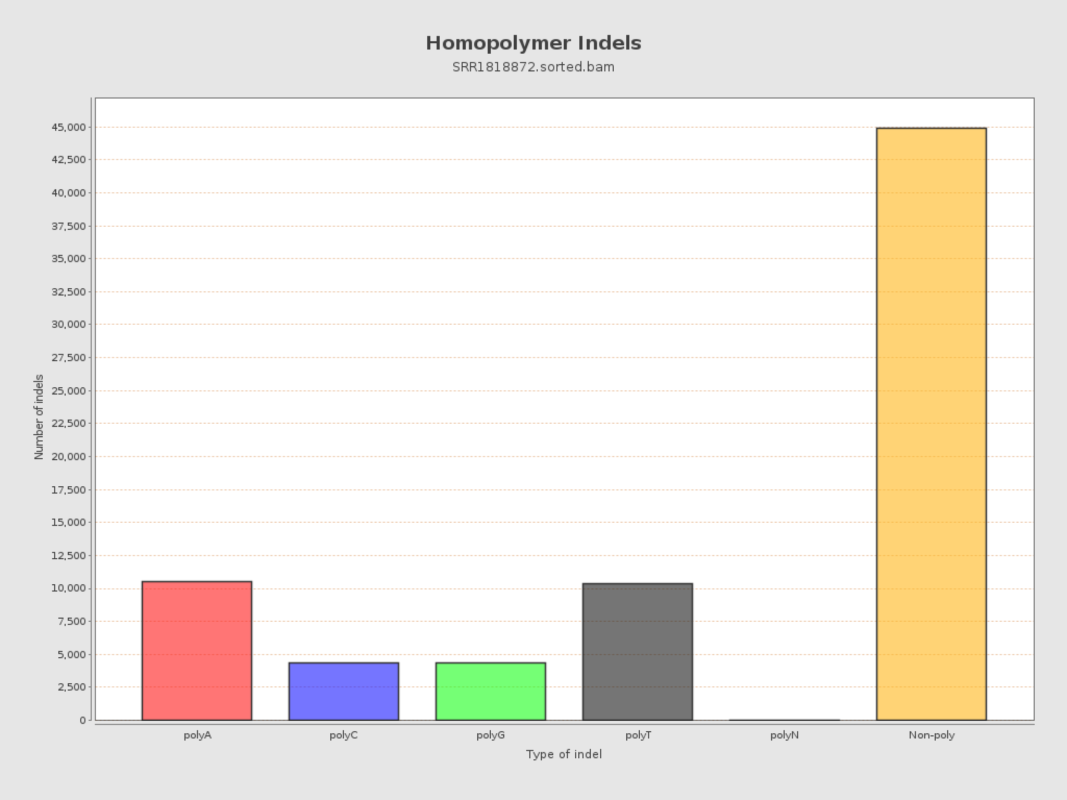
9. Results : Mapped Reads GC-content Distribution



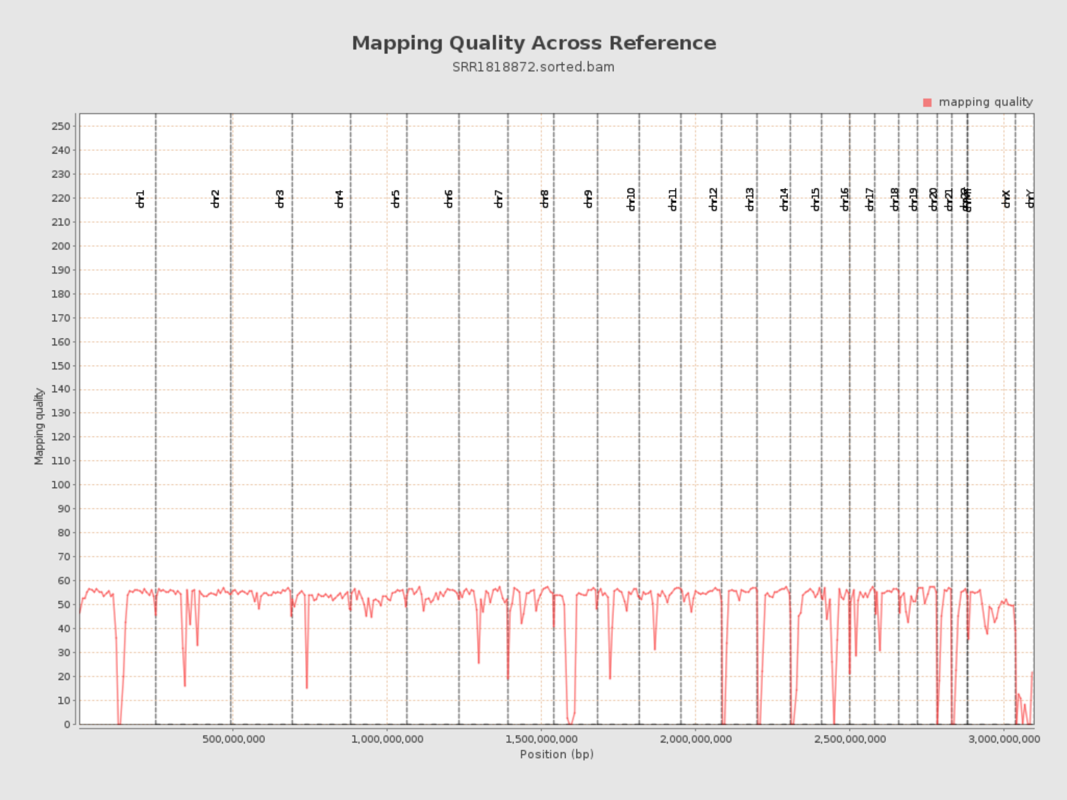
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram