Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:00:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818785.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_SRR1818785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:00:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,014,509
Mapped reads	1,963,172 / 97.45%
Unmapped reads	51,337 / 2.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,995 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	913,698 / 45.36%
Duplication rate	38.95%
Clipped reads	1,969,374 / 97.76%

2.2. ACGT Content

Number/percentage of A's	36,710,266 / 27.52%
Number/percentage of C's	27,954,670 / 20.96%
Number/percentage of T's	38,514,241 / 28.88%
Number/percentage of G's	30,191,967 / 22.64%
Number/percentage of N's	7,830 / 0.01%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.5066

2.4. Mapping Quality

Mean Mapping Quality	47.77

2.5. Mismatches and indels

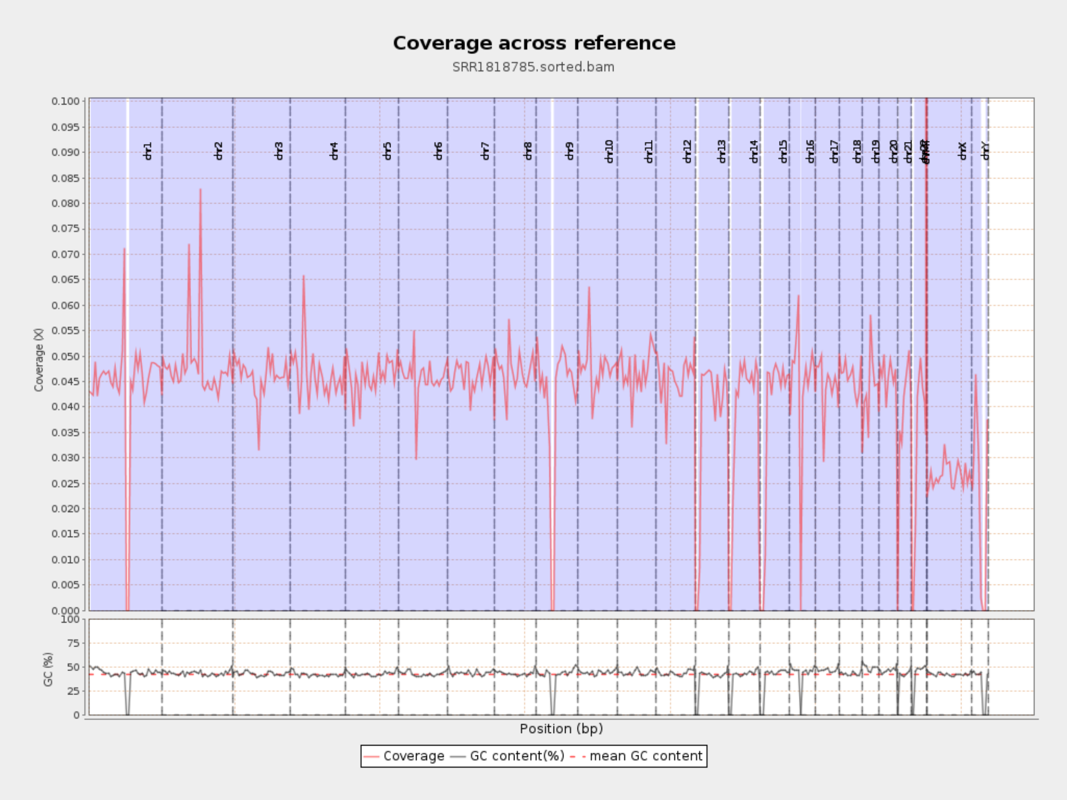
General error rate	0.5%
Mismatches	643,755
Insertions	11,696
Mapped reads with at least one insertion	0.59%
Deletions	32,805
Mapped reads with at least one deletion	1.66%
Homopolymer indels	43.93%

2.6. Chromosome stats

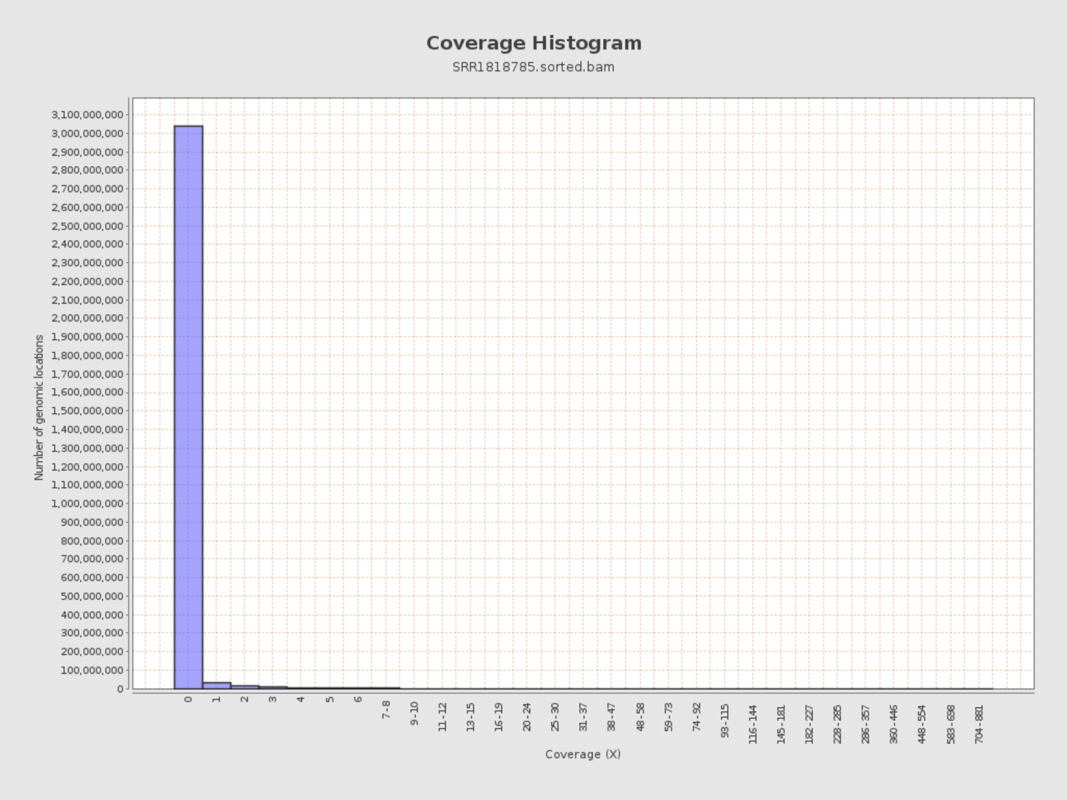
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10969585	0.044	0.7262
chr2	243199373	11779161	0.0484	0.7256
chr3	198022430	9106462	0.046	0.4114
chr4	191154276	8846156	0.0463	0.4427
chr5	180915260	8297038	0.0459	0.4264
chr6	171115067	7834768	0.0458	0.448
chr7	159138663	7361653	0.0463	0.4735

chr8	146364022	6913544	0.0472	0.4734
chr9	141213431	5757191	0.0408	0.461
chr10	135534747	6470300	0.0477	0.5346
chr11	135006516	6373174	0.0472	0.4604
chr12	133851895	6118440	0.0457	0.4238
chr13	115169878	4255039	0.0369	0.3733
chr14	107349540	4095981	0.0382	0.4062
chr15	102531392	3778769	0.0369	0.3732
chr16	90354753	4026570	0.0446	0.5185
chr17	81195210	3574616	0.044	0.4311
chr18	78077248	3587865	0.046	0.5936
chr19	59128983	2593032	0.0439	0.6556
chr20	63025520	2893043	0.0459	0.4372
chr21	48129895	1817423	0.0378	0.3942
chr22	51304566	1554991	0.0303	0.3593
chrMT	16571	61554	3.7146	4.6316
chrX	155270560	4121580	0.0265	0.3309
chrY	59373566	1243523	0.0209	0.617

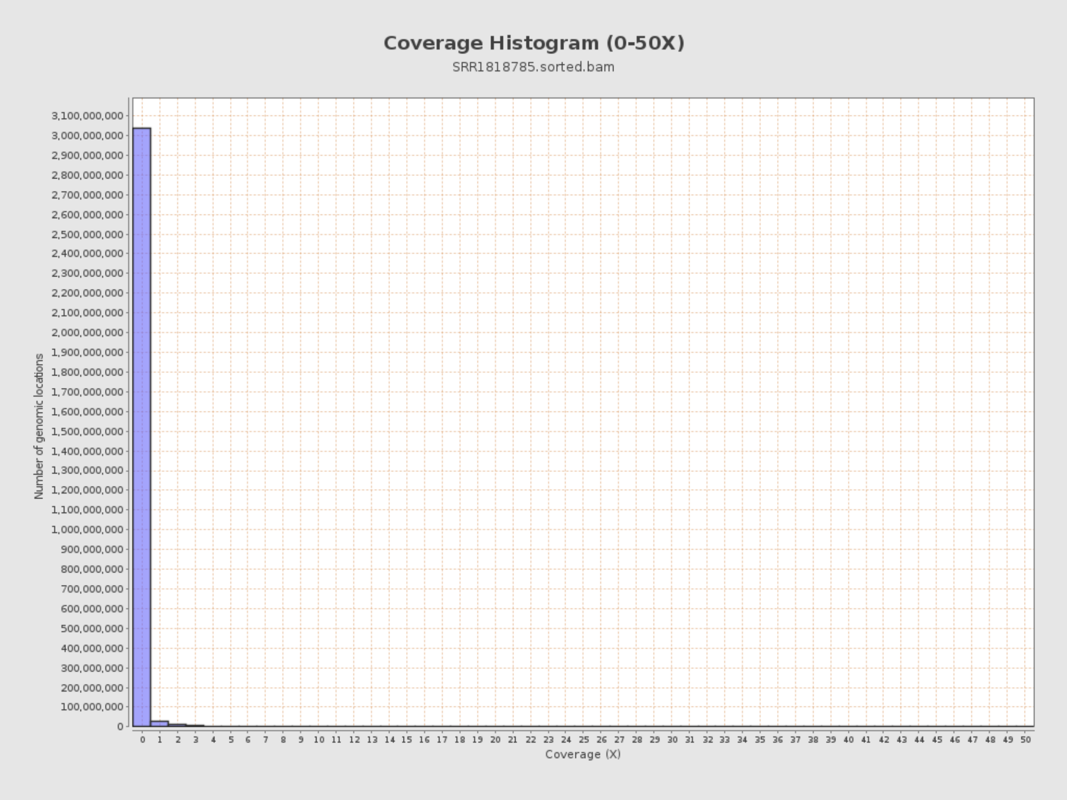
3. Results : Coverage across reference



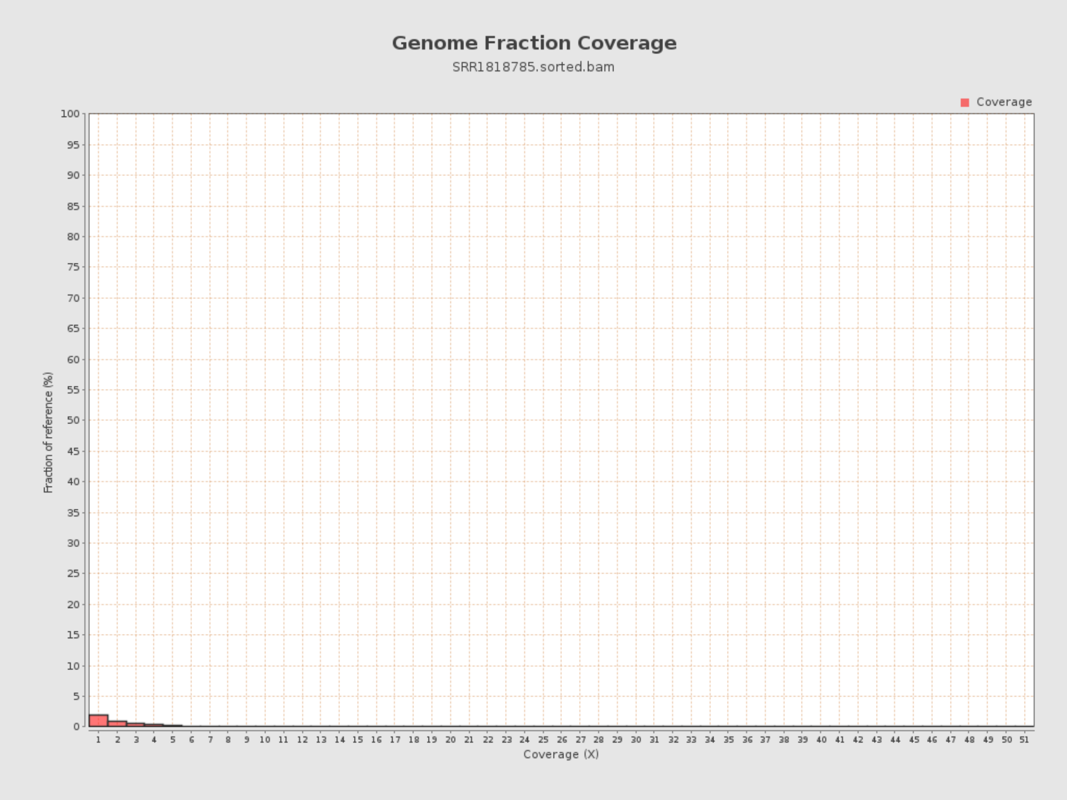
4. Results : Coverage Histogram



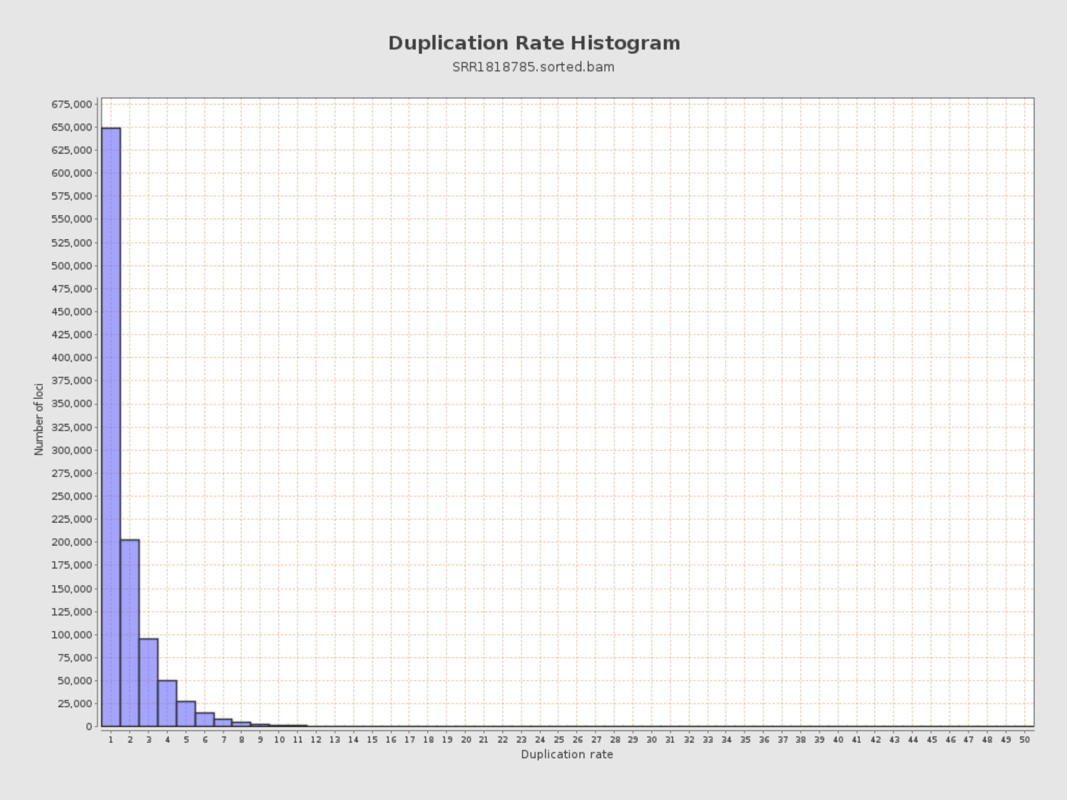
5. Results : Coverage Histogram (0-50X)



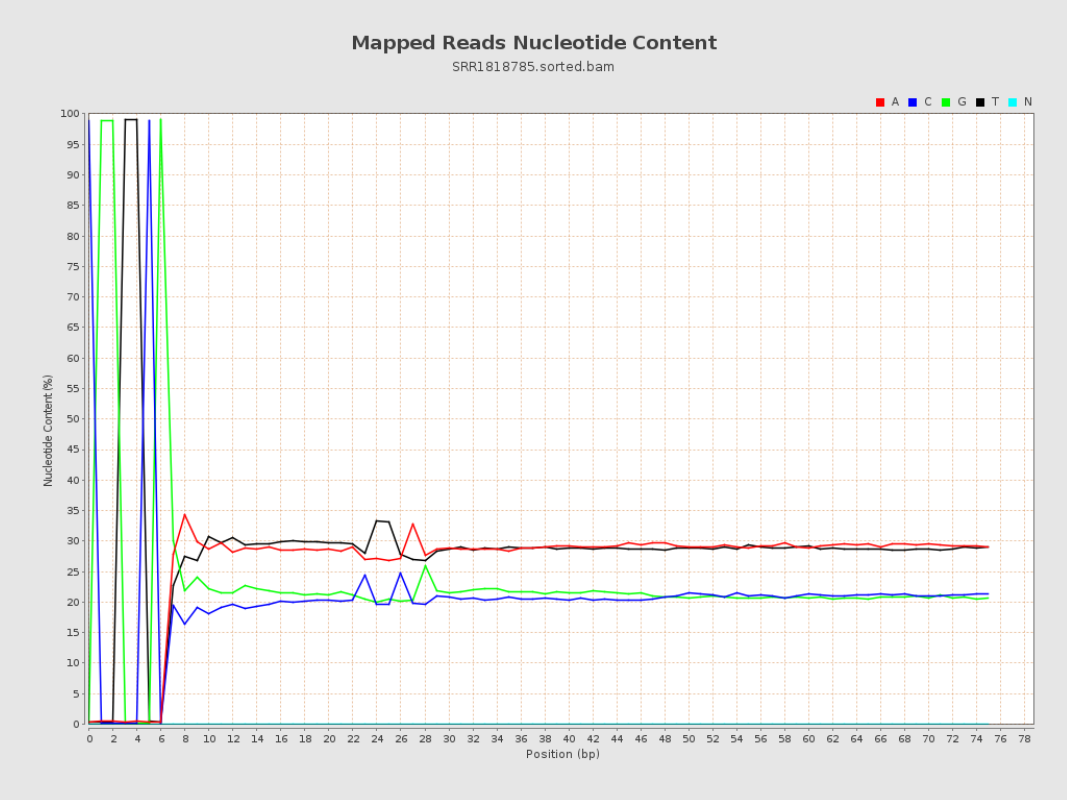
6. Results : Genome Fraction Coverage



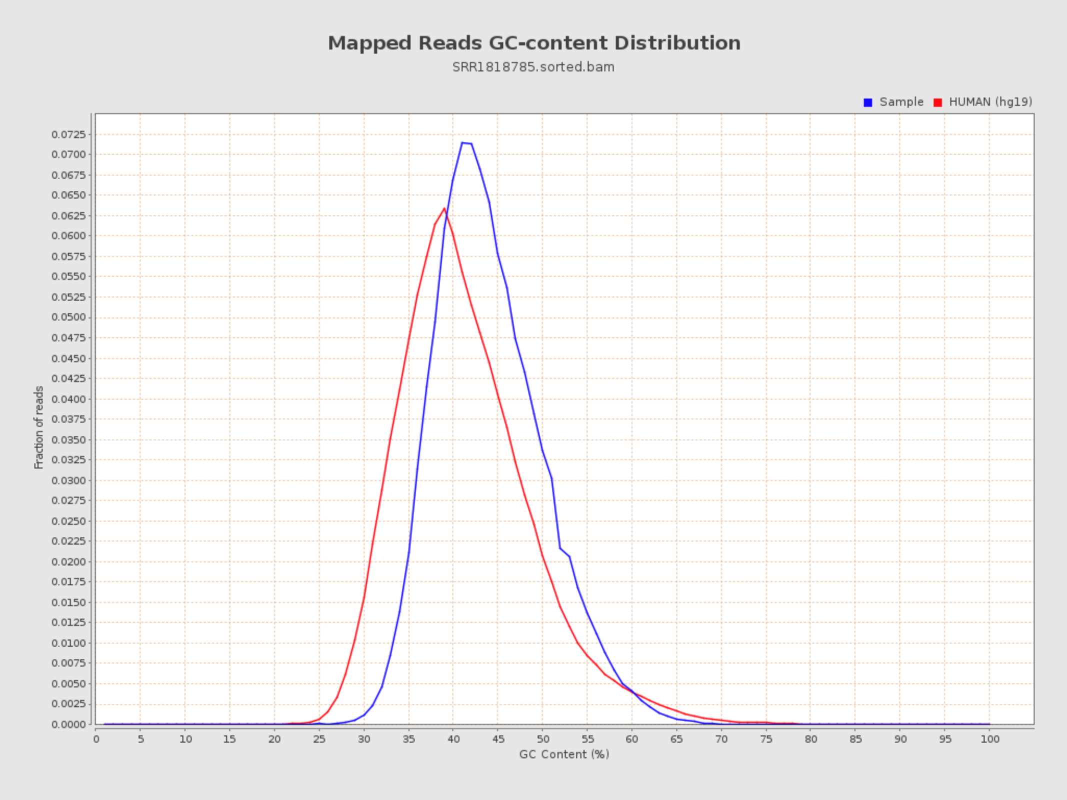
7. Results : Duplication Rate Histogram



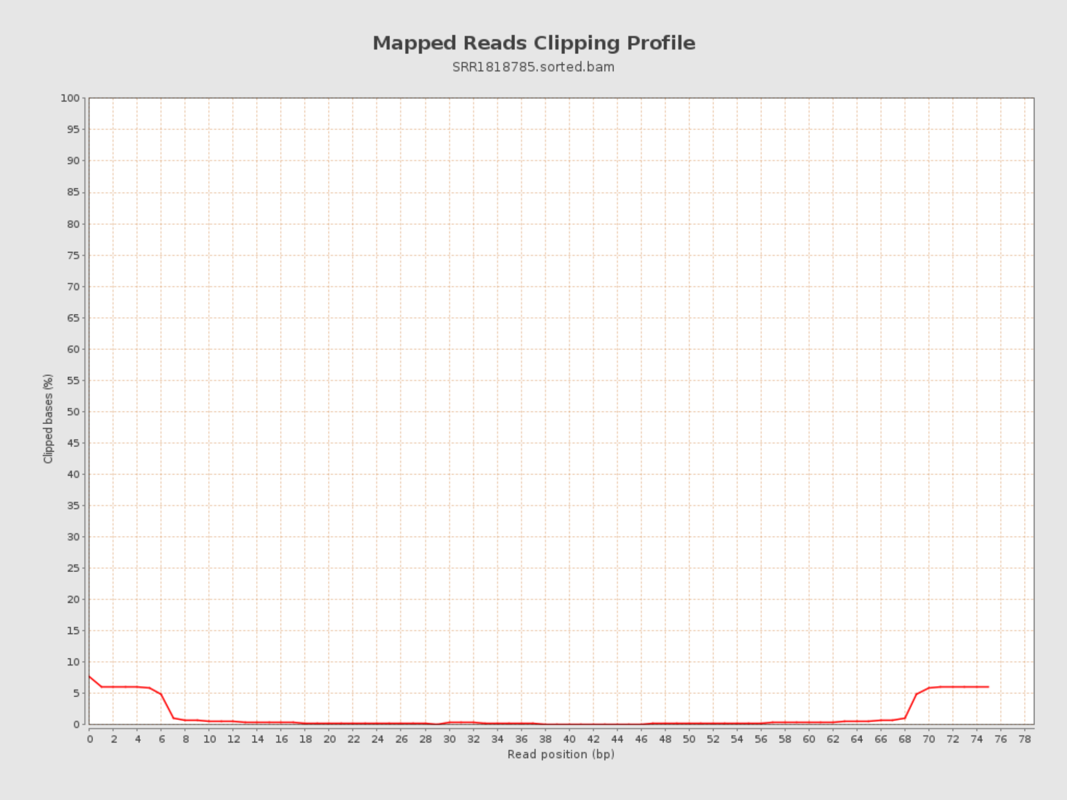
8. Results : Mapped Reads Nucleotide Content



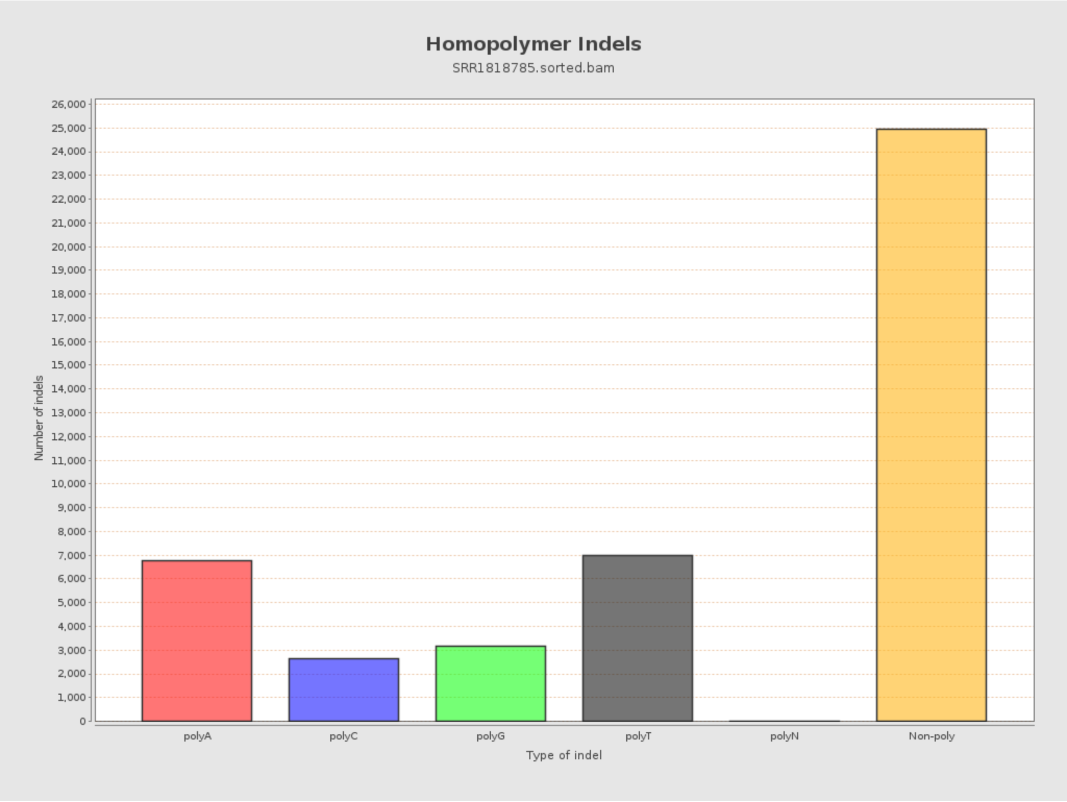
9. Results : Mapped Reads GC-content Distribution



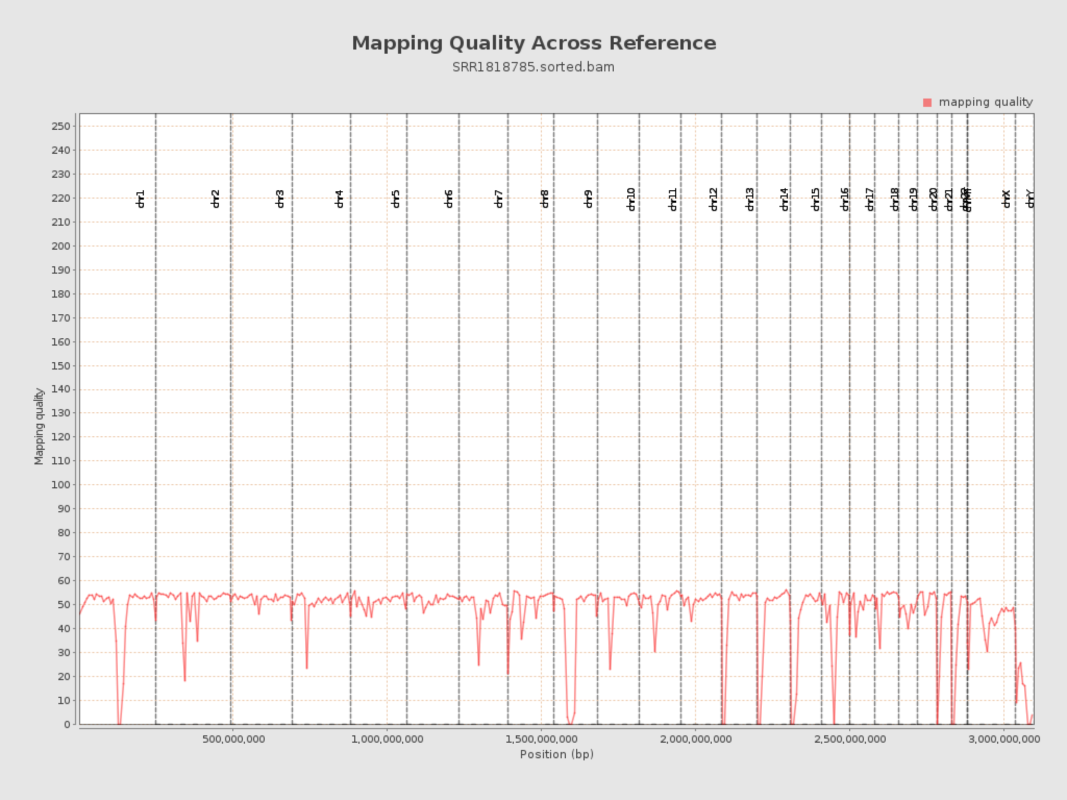
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram