Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:47:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818835.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_SRR1818835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:47:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	975,147
Mapped reads	963,606 / 98.82%
Unmapped reads	11,541 / 1.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,600 / 1.6%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	174,109 / 17.85%
Duplication rate	15.34%
Clipped reads	976,072 / 100.09%

2.2. ACGT Content

Number/percentage of A's	25,174,873 / 28.22%
Number/percentage of C's	18,446,953 / 20.68%
Number/percentage of T's	25,624,180 / 28.72%
Number/percentage of G's	19,969,317 / 22.38%
Number/percentage of N's	1,331 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.338

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

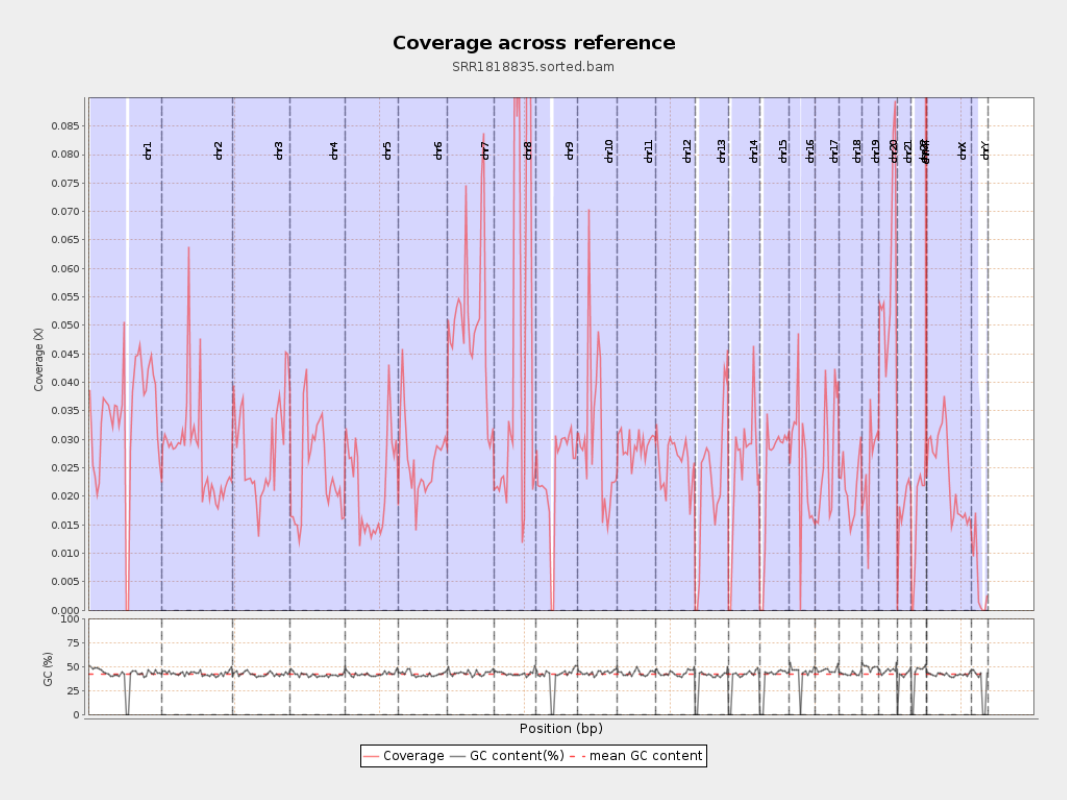
General error rate	0.61%
Mismatches	517,482
Insertions	10,690
Mapped reads with at least one insertion	1.07%
Deletions	27,718
Mapped reads with at least one deletion	2.82%
Homopolymer indels	42.09%

2.6. Chromosome stats

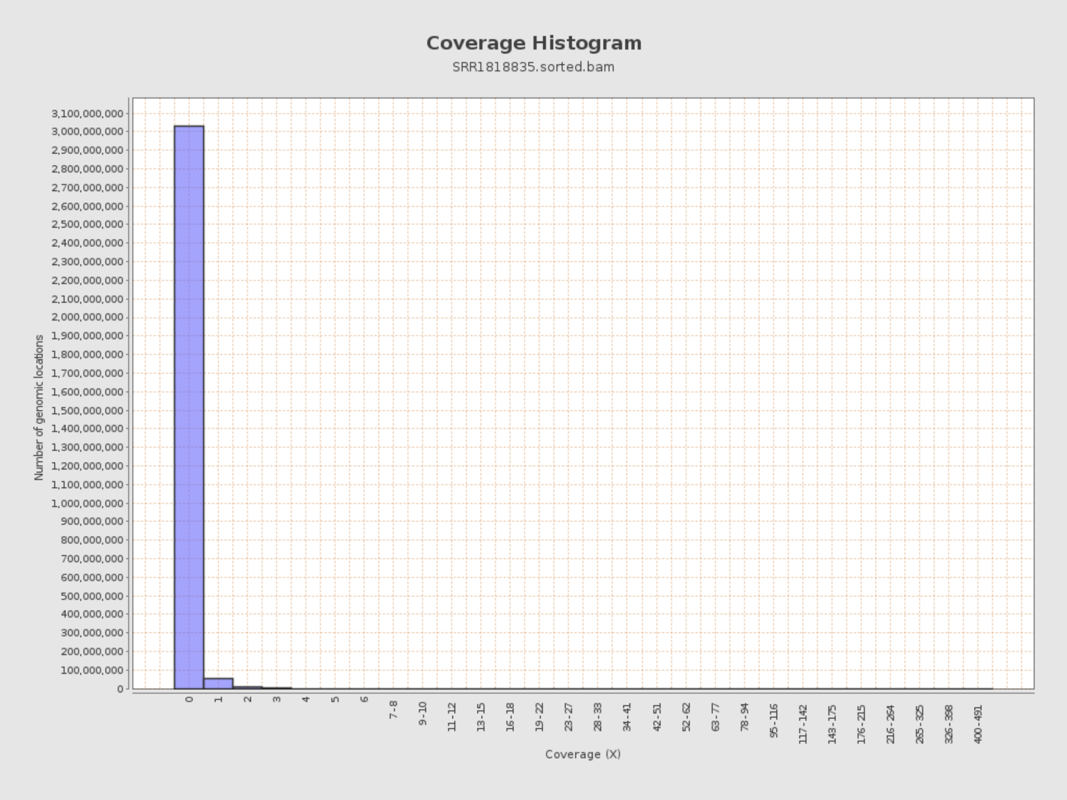
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8363928	0.0336	0.4568
chr2	243199373	6749833	0.0278	0.4553
chr3	198022430	5630157	0.0284	0.2124
chr4	191154276	4555024	0.0238	0.2302
chr5	180915260	3929352	0.0217	0.193
chr6	171115067	4490664	0.0262	0.2169
chr7	159138663	8056608	0.0506	0.6581

chr8	146364022	7773831	0.0531	0.345
chr9	141213431	3296245	0.0233	0.2951
chr10	135534747	4089764	0.0302	0.4668
chr11	135006516	3911463	0.029	0.2386
chr12	133851895	3512088	0.0262	0.2086
chr13	115169878	2617440	0.0227	0.1894
chr14	107349540	2673921	0.0249	0.209
chr15	102531392	2483817	0.0242	0.1944
chr16	90354753	2249679	0.0249	0.3507
chr17	81195210	2218663	0.0273	0.2462
chr18	78077248	1686341	0.0216	0.3311
chr19	59128983	1476211	0.025	0.4053
chr20	63025520	3683817	0.0584	0.3217
chr21	48129895	849423	0.0176	0.1849
chr22	51304566	816215	0.0159	0.1818
chrMT	16571	178824	10.7914	7.5238
chrX	155270560	3679528	0.0237	0.2197
chrY	59373566	296907	0.005	0.3699

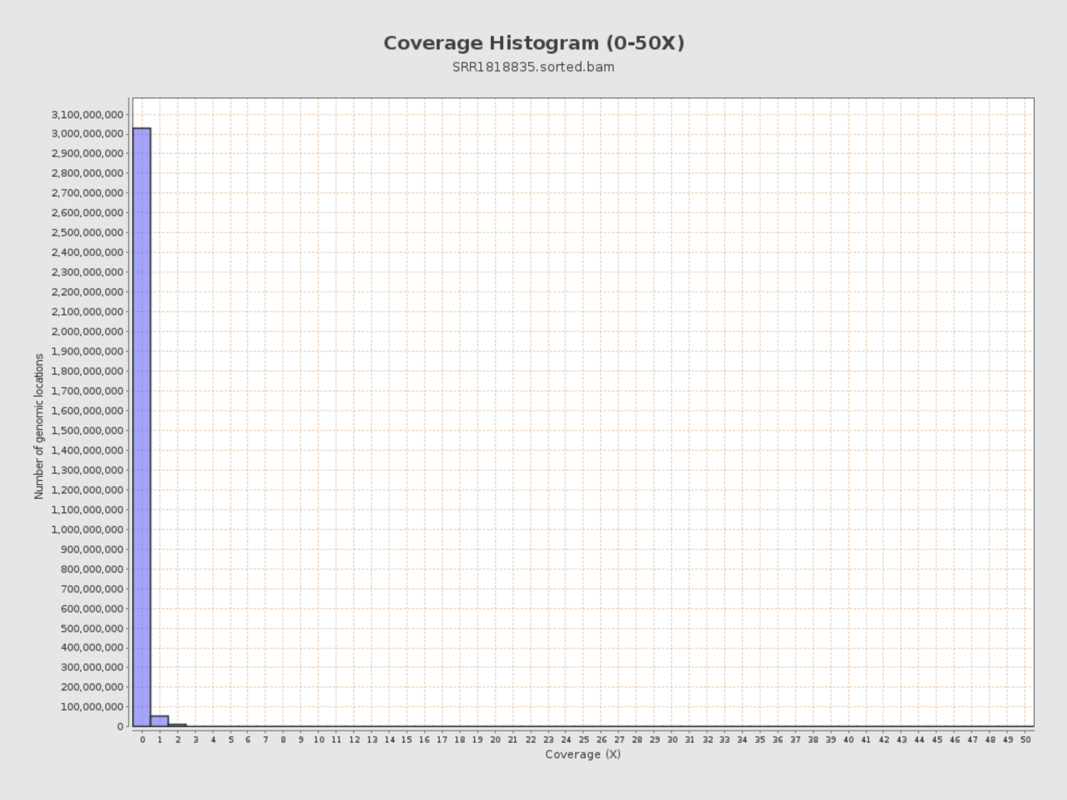
3. Results : Coverage across reference



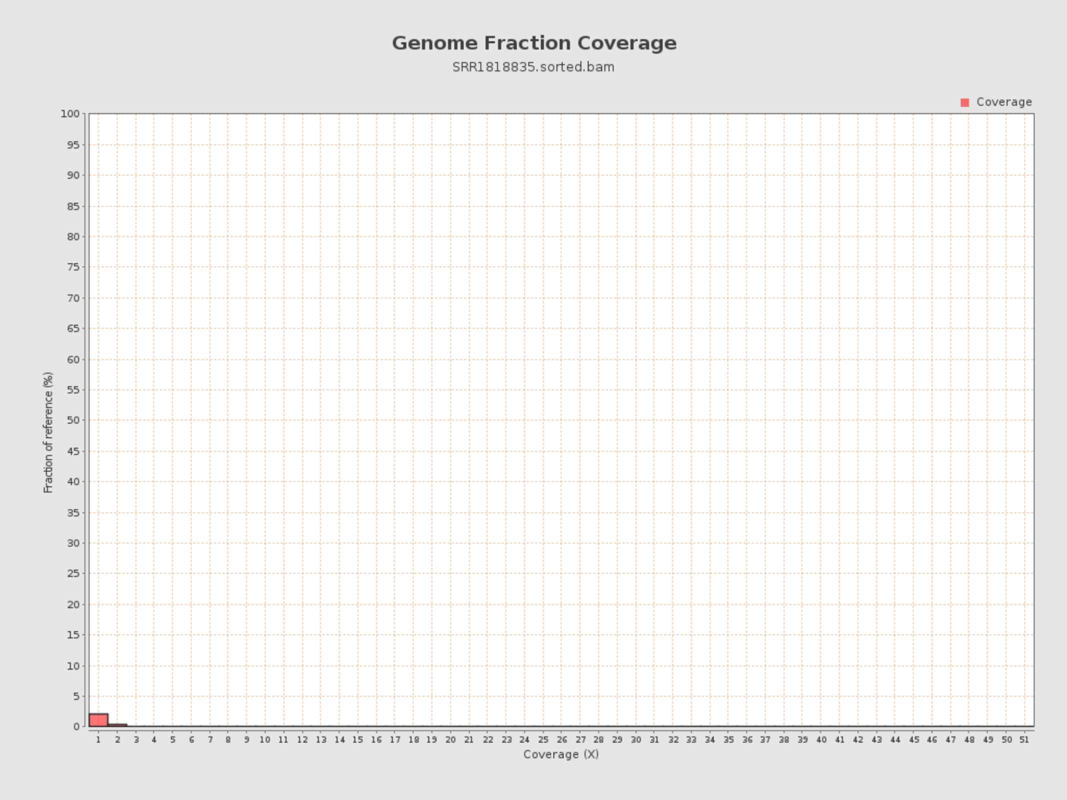
4. Results : Coverage Histogram



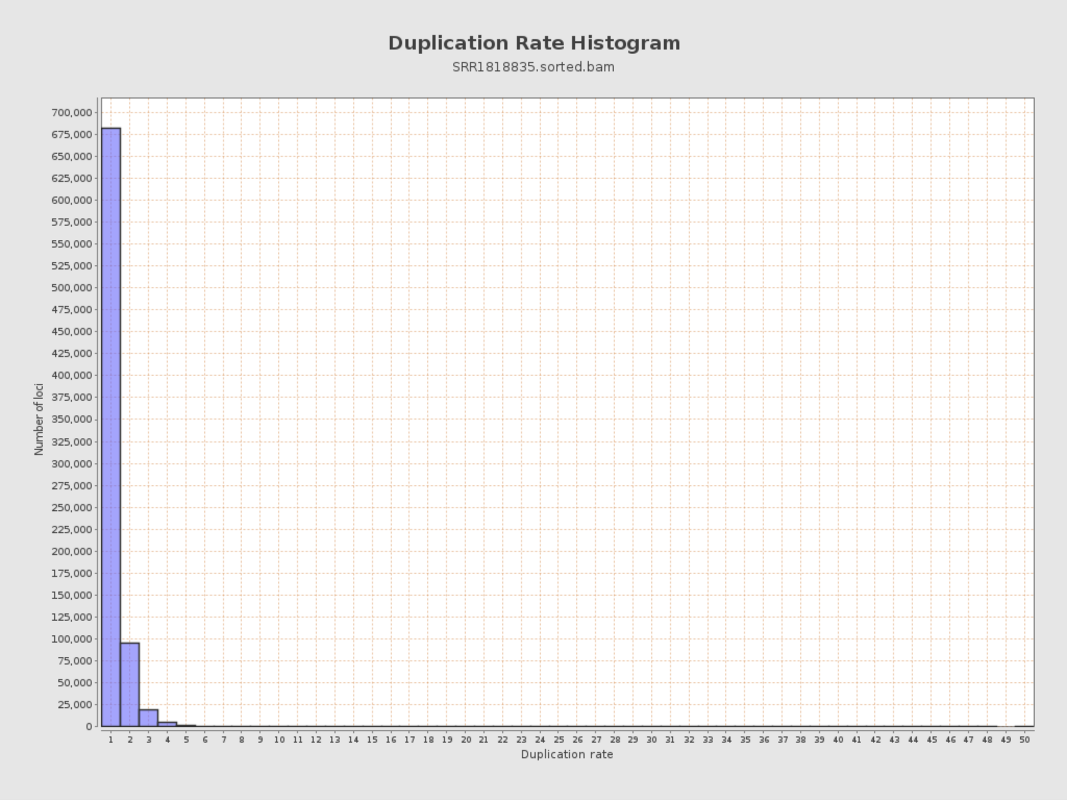
5. Results : Coverage Histogram (0-50X)



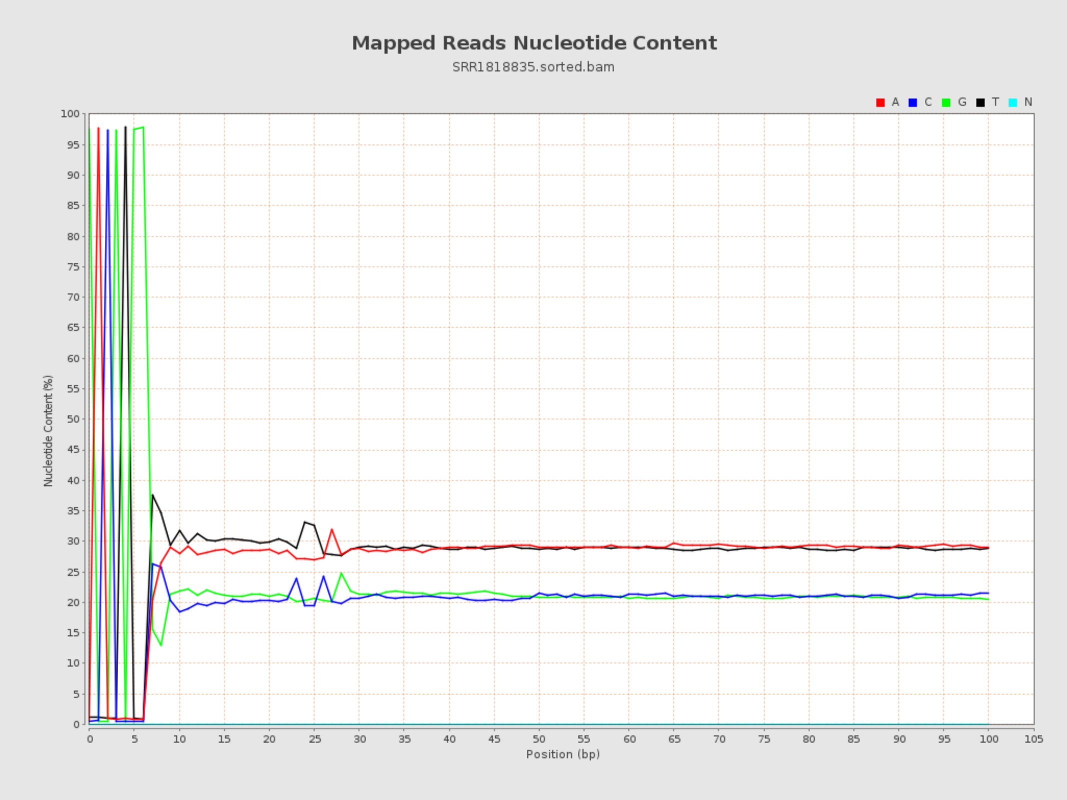
6. Results : Genome Fraction Coverage



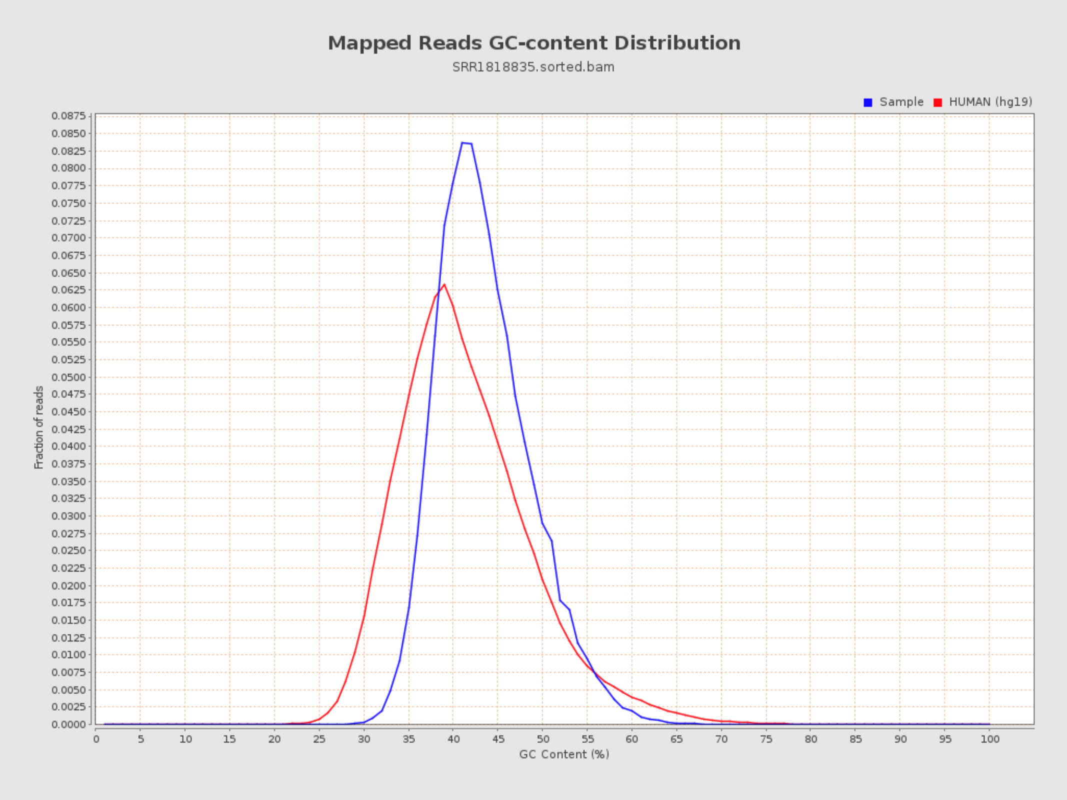
7. Results : Duplication Rate Histogram



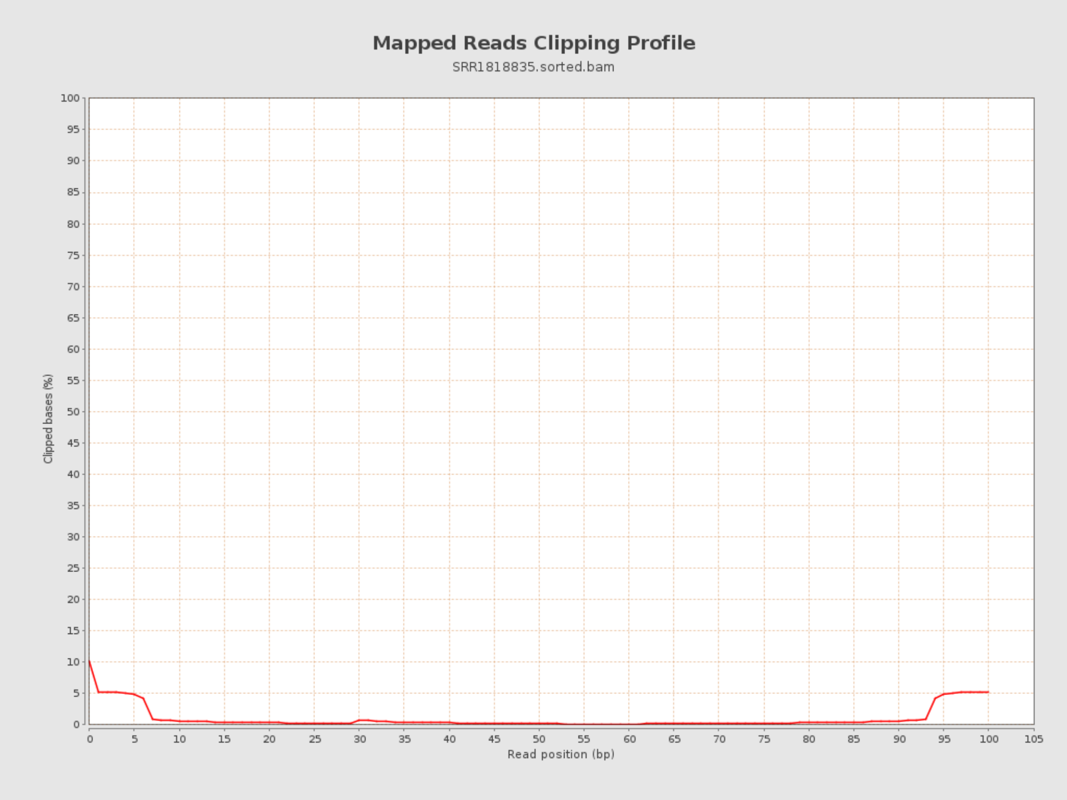
8. Results : Mapped Reads Nucleotide Content



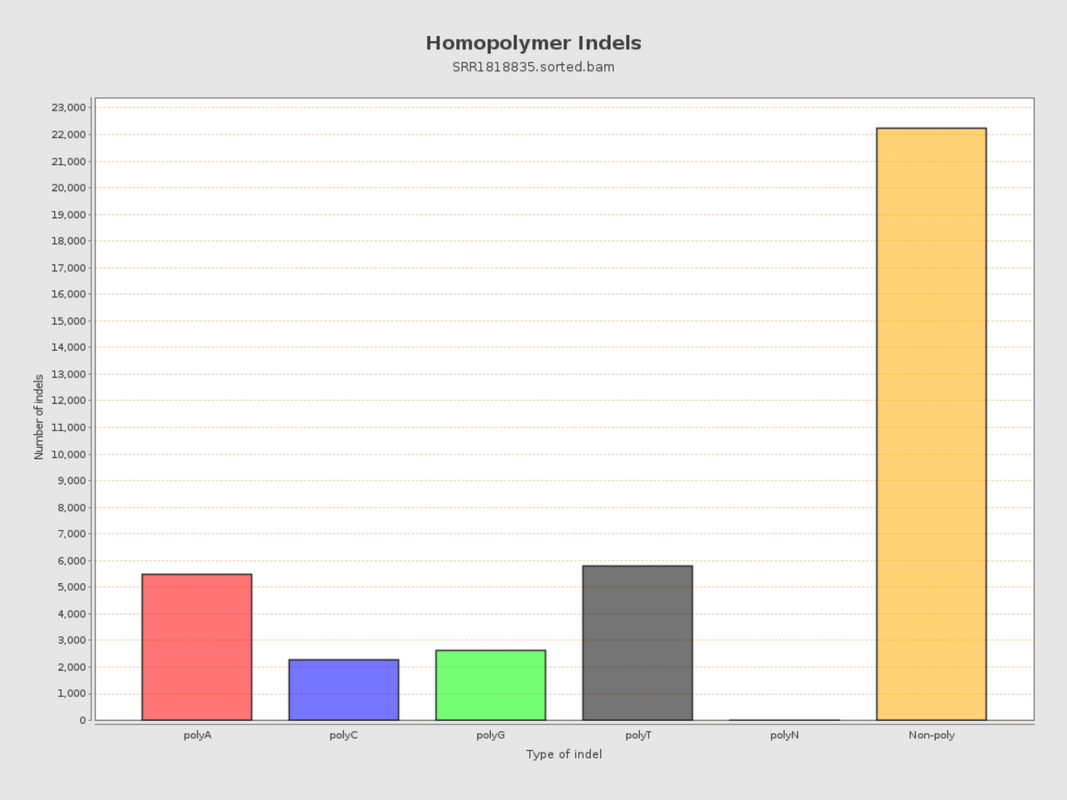
9. Results : Mapped Reads GC-content Distribution



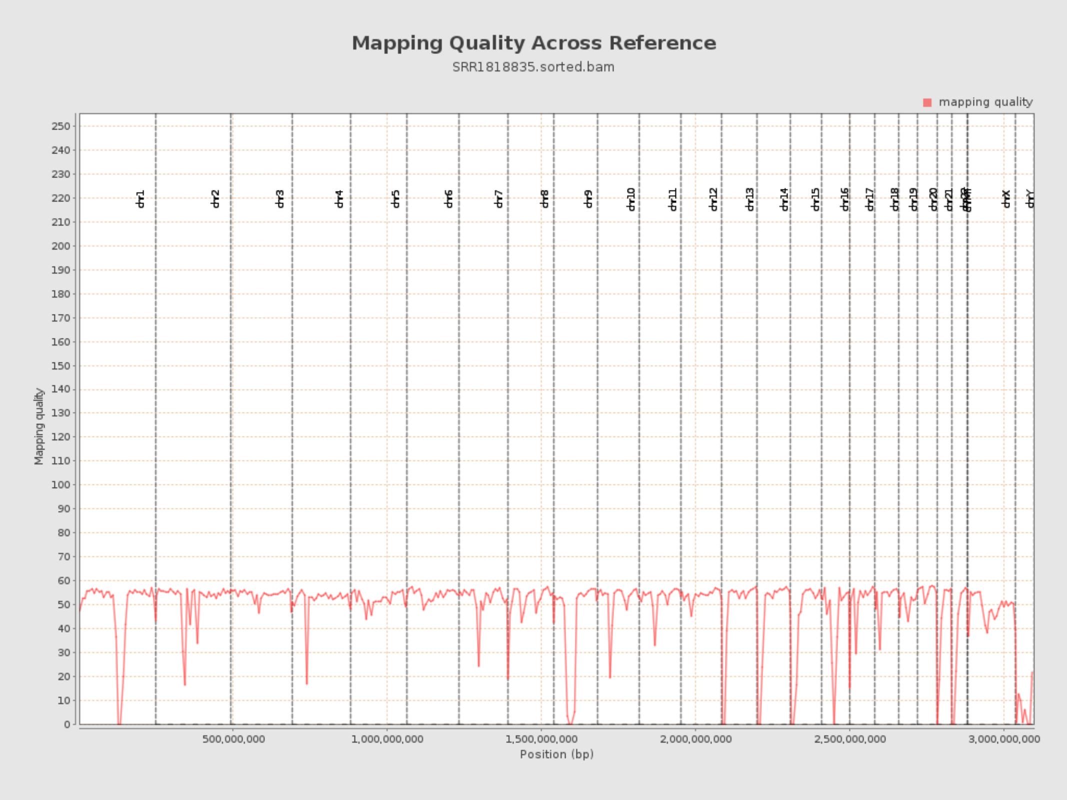
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram