Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818817.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_SRR1818817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:04:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	196,254
Mapped reads	183,108 / 93.3%
Unmapped reads	13,146 / 6.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,683 / 0.86%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	16,490 / 8.4%
Duplication rate	8.1%
Clipped reads	182,376 / 92.93%

2.2. ACGT Content

Number/percentage of A's	3,545,081 / 28.59%
Number/percentage of C's	2,440,787 / 19.69%
Number/percentage of T's	3,589,491 / 28.95%
Number/percentage of G's	2,822,436 / 22.76%
Number/percentage of N's	705 / 0.01%
GC Percentage	42.45%

2.3. Coverage

Mean	0.004

Standard Deviation	0.0808

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

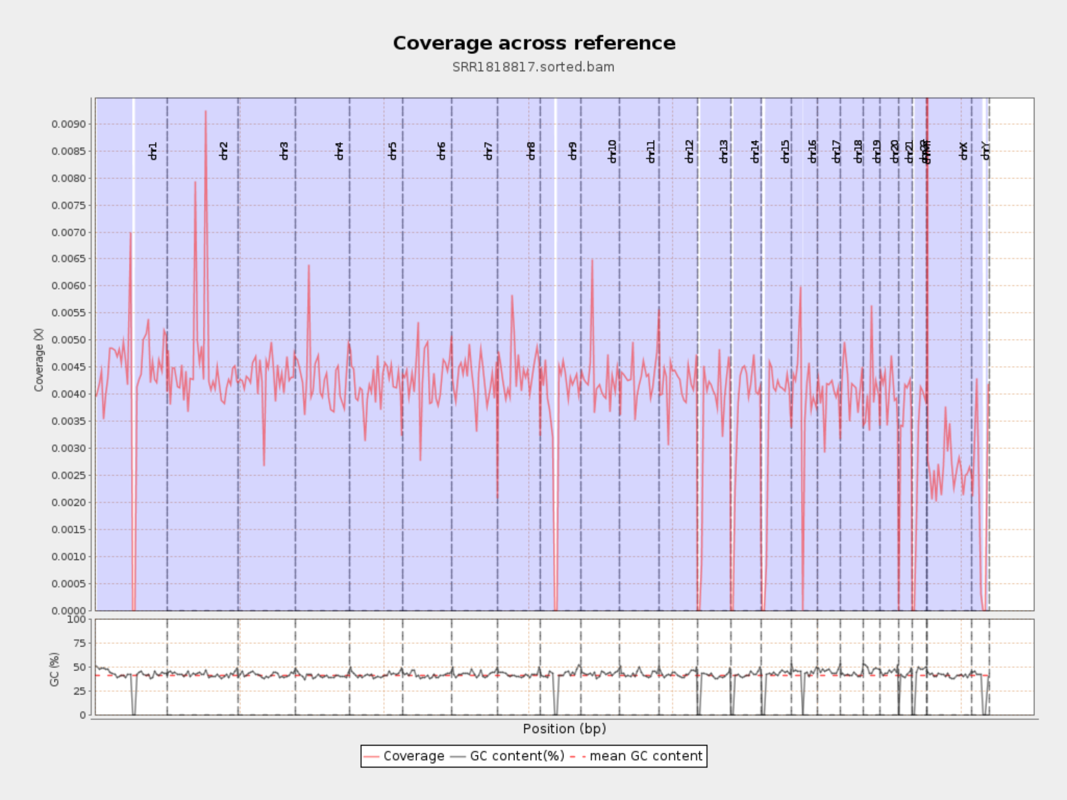
General error rate	0.55%
Mismatches	64,685
Insertions	1,412
Mapped reads with at least one insertion	0.76%
Deletions	3,078
Mapped reads with at least one deletion	1.66%
Homopolymer indels	42.25%

2.6. Chromosome stats

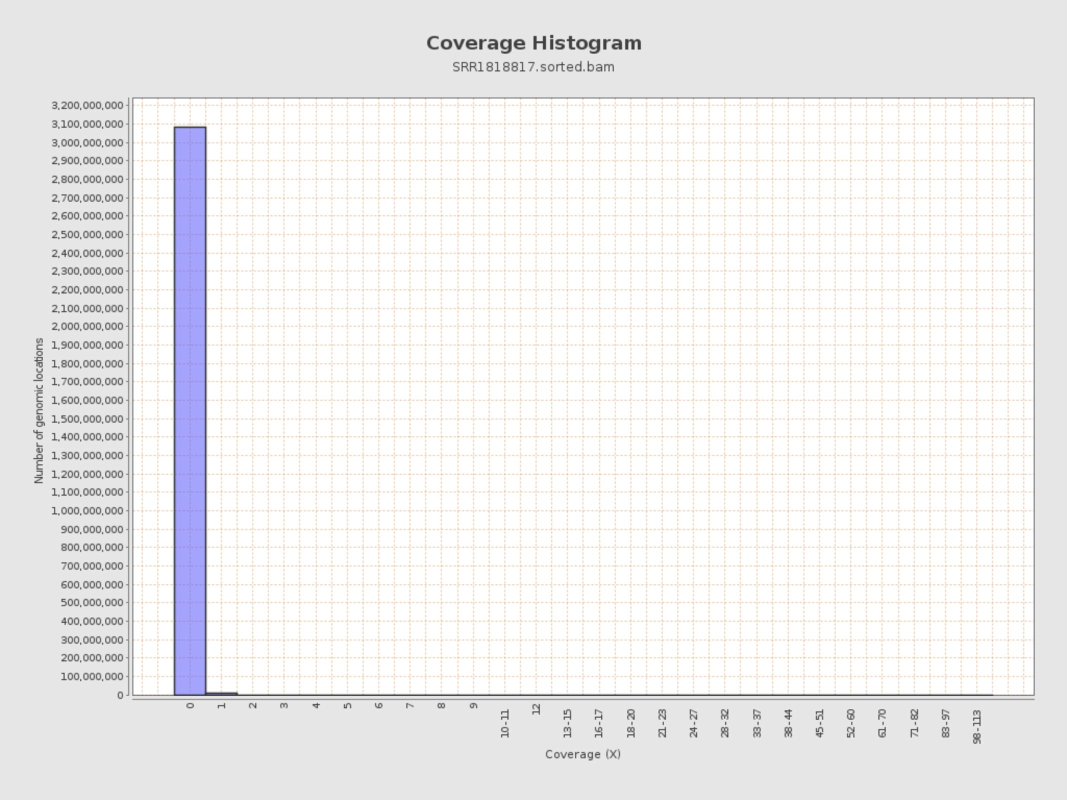
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1080707	0.0043	0.0985
chr2	243199373	1107956	0.0046	0.1155
chr3	198022430	851652	0.0043	0.0728
chr4	191154276	820520	0.0043	0.0753
chr5	180915260	753772	0.0042	0.0723
chr6	171115067	736213	0.0043	0.0748
chr7	159138663	681766	0.0043	0.0776

chr8	146364022	654156	0.0045	0.0773
chr9	141213431	526651	0.0037	0.0723
chr10	135534747	583760	0.0043	0.0861
chr11	135006516	580209	0.0043	0.0756
chr12	133851895	560434	0.0042	0.0735
chr13	115169878	401239	0.0035	0.0652
chr14	107349540	379475	0.0035	0.0707
chr15	102531392	344435	0.0034	0.0639
chr16	90354753	350255	0.0039	0.0813
chr17	81195210	320709	0.0039	0.0706
chr18	78077248	326124	0.0042	0.0866
chr19	59128983	237570	0.004	0.0936
chr20	63025520	257292	0.0041	0.0727
chr21	48129895	168243	0.0035	0.0666
chr22	51304566	141221	0.0028	0.0597
chrMT	16571	8590	0.5184	0.8351
chrX	155270560	407759	0.0026	0.059
chrY	59373566	122563	0.0021	0.1017

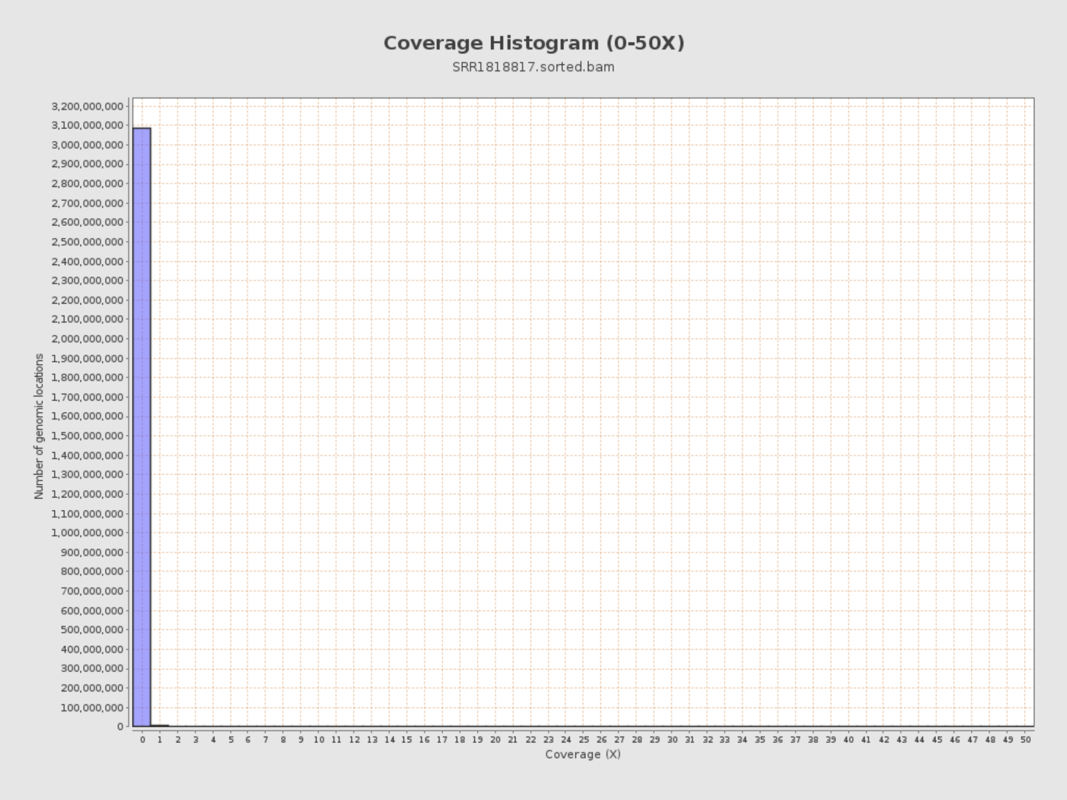
3. Results : Coverage across reference



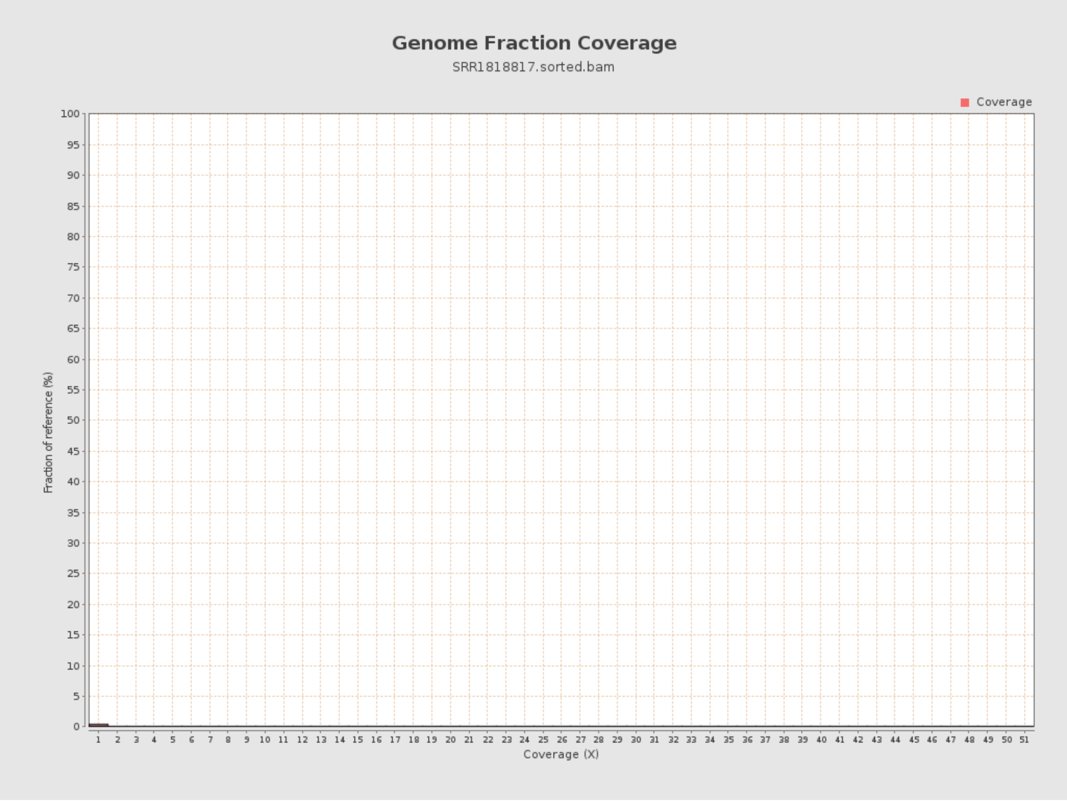
4. Results : Coverage Histogram



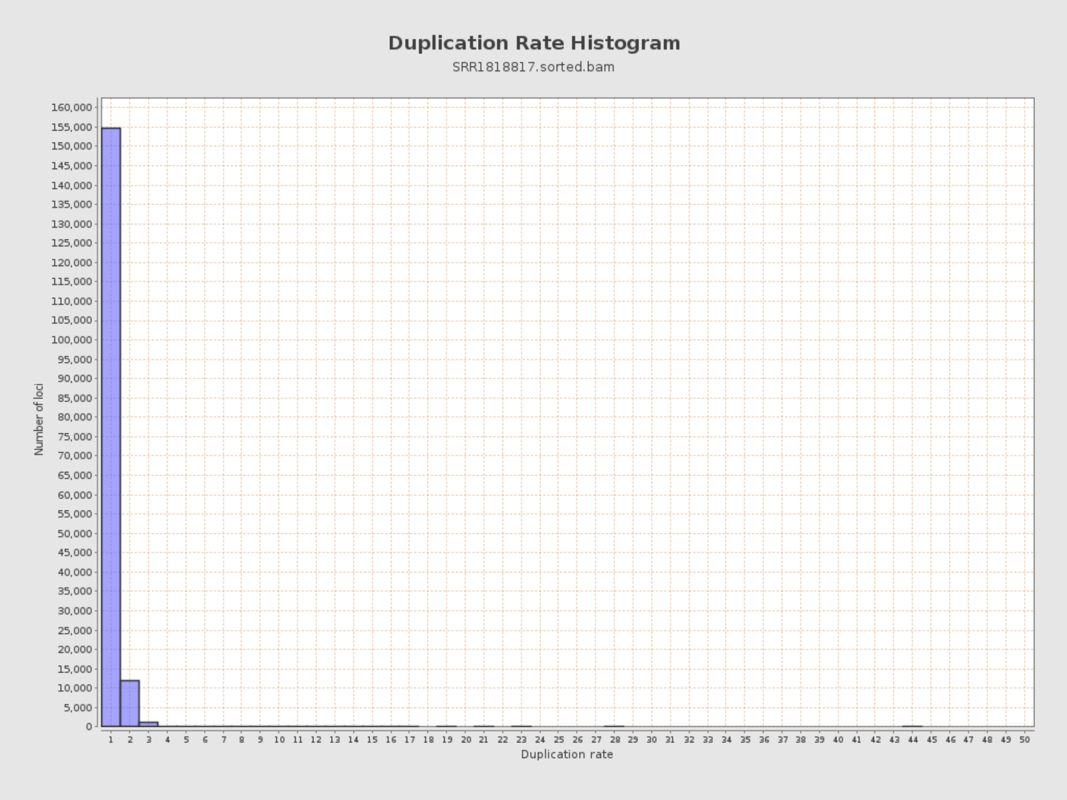
5. Results : Coverage Histogram (0-50X)



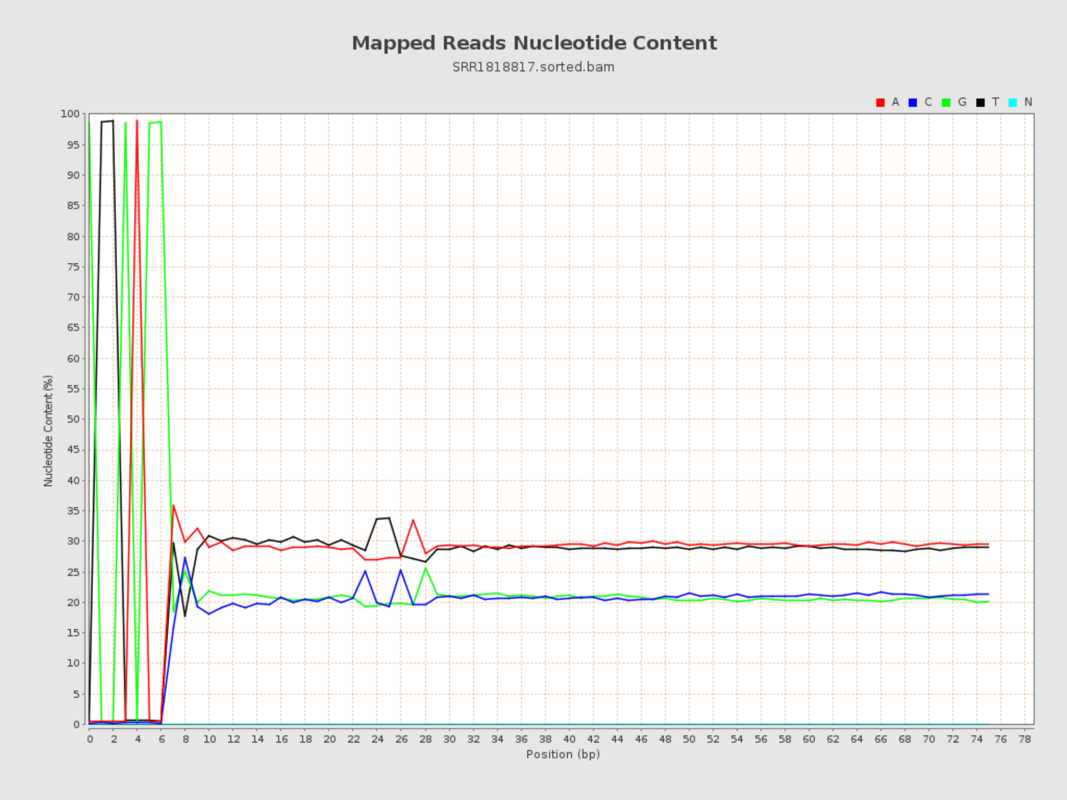
6. Results : Genome Fraction Coverage



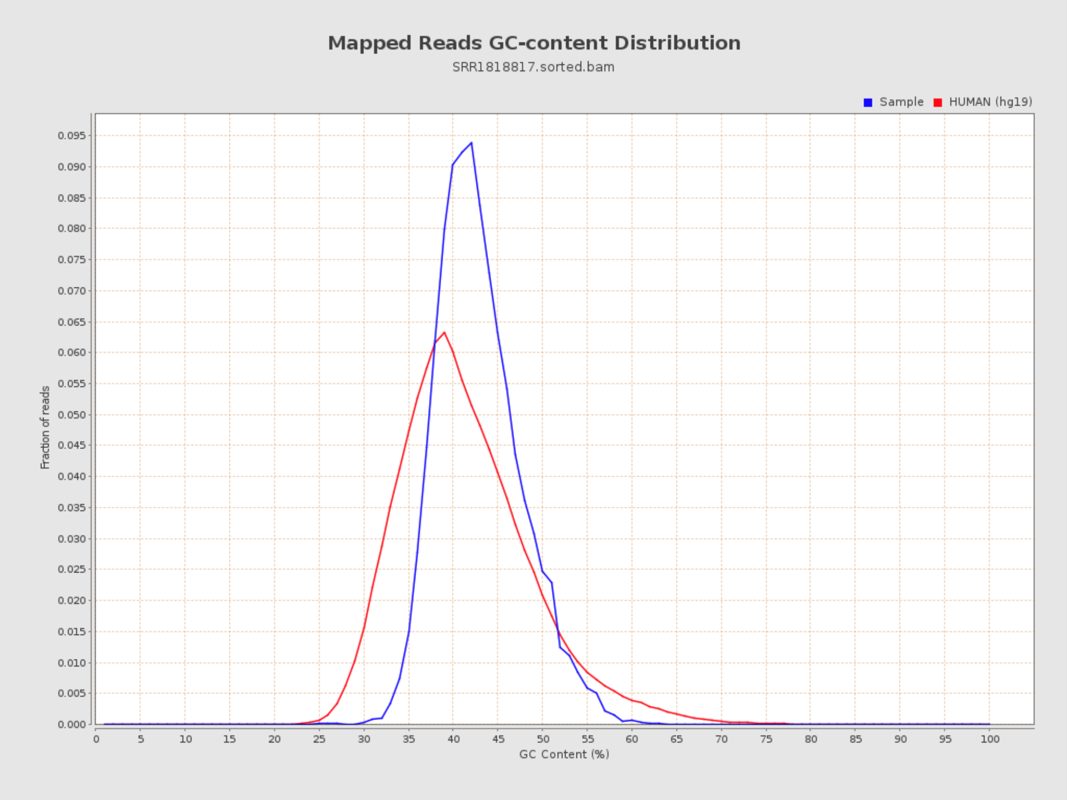
7. Results : Duplication Rate Histogram



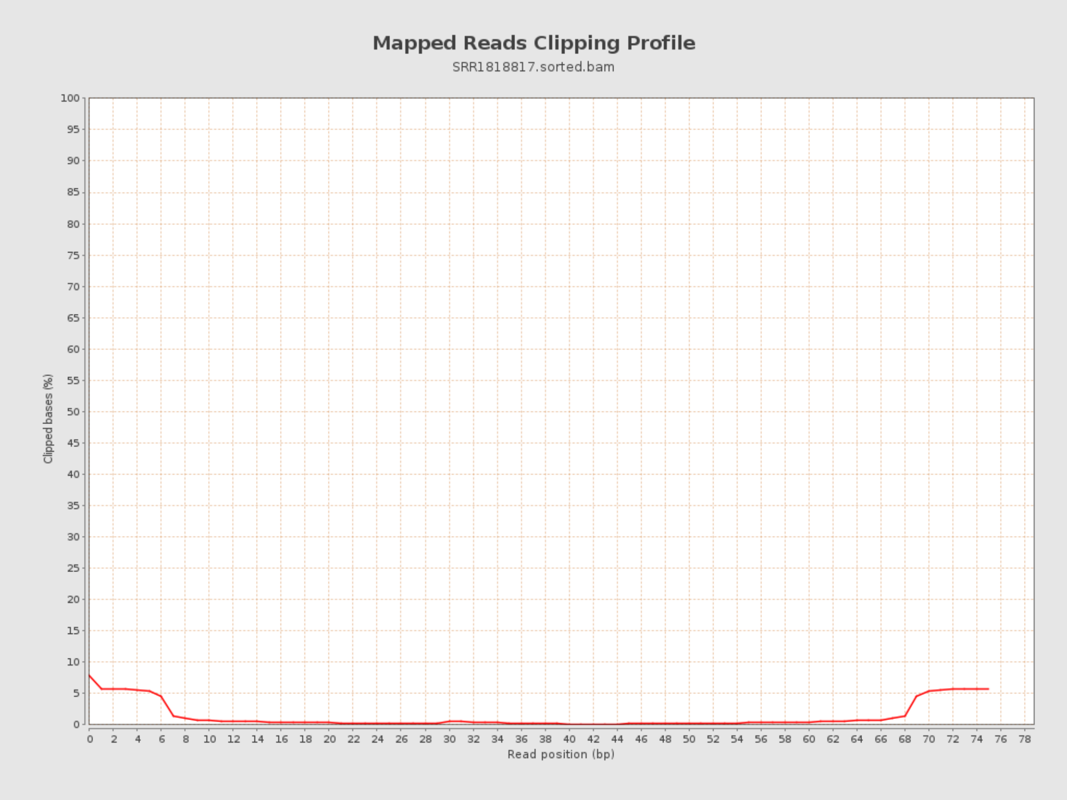
8. Results : Mapped Reads Nucleotide Content



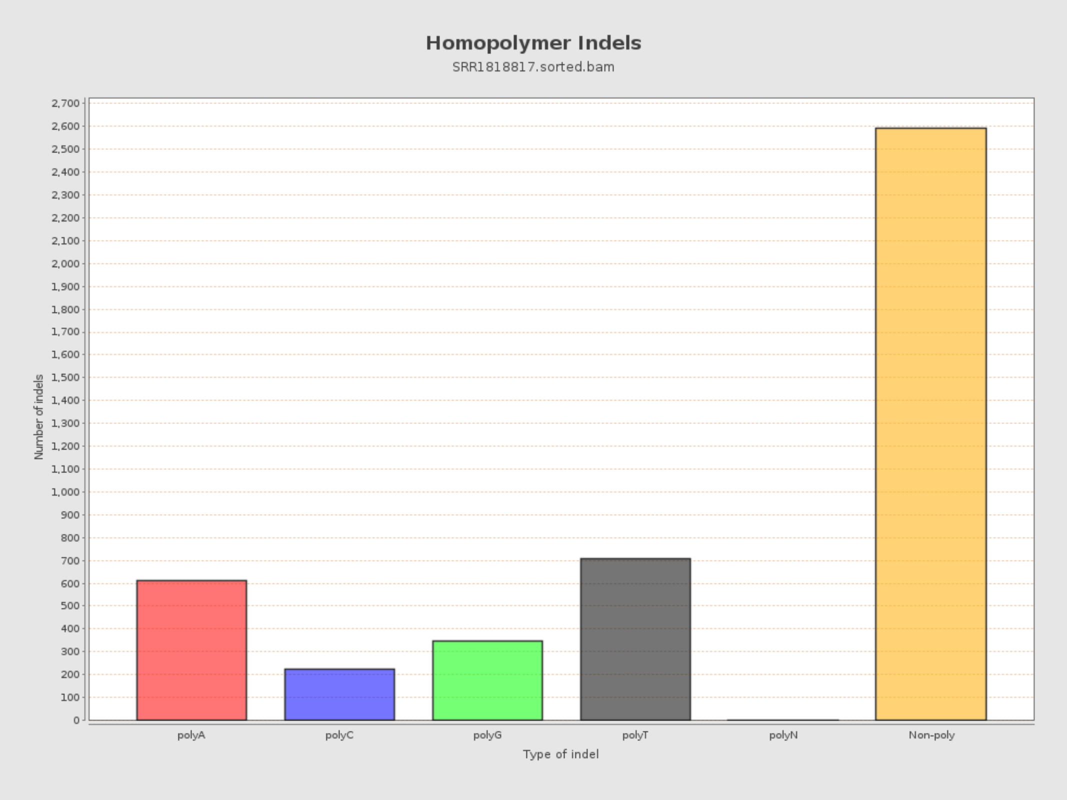
9. Results : Mapped Reads GC-content Distribution



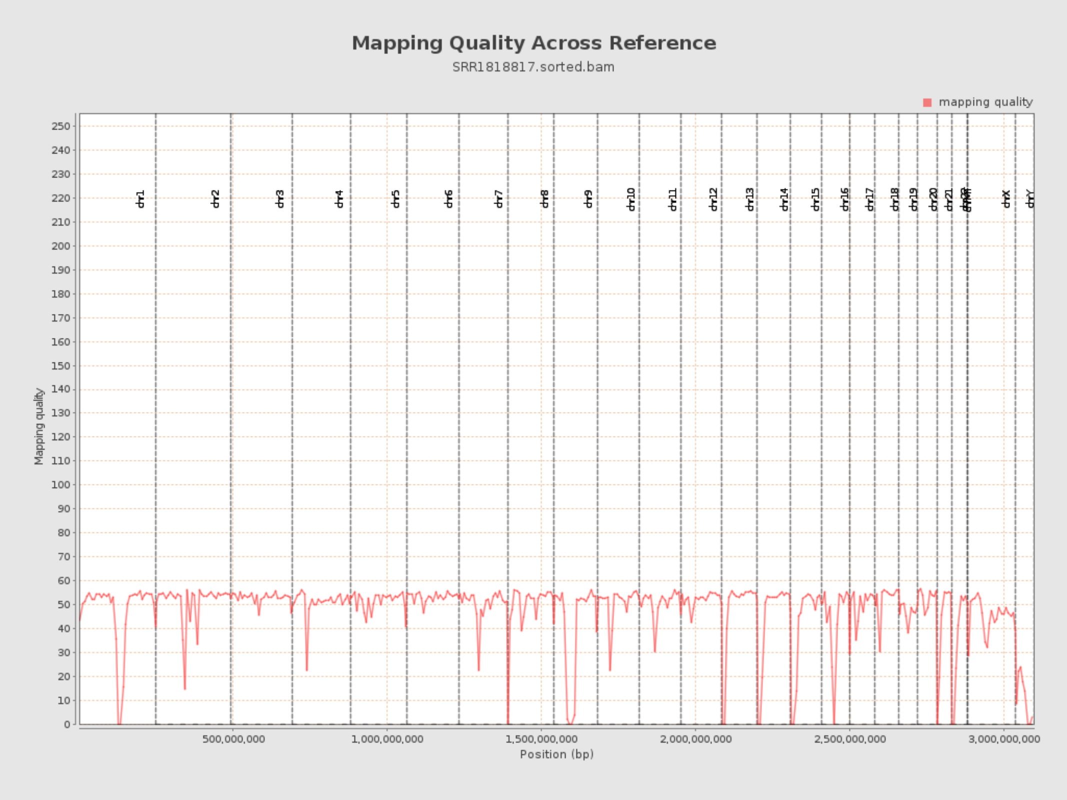
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram