Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:22:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818735.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_SRR1818735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:22:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,342,416
Mapped reads	3,258,516 / 97.49%
Unmapped reads	83,900 / 2.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,073 / 0.69%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,747,637 / 52.29%
Duplication rate	43.23%
Clipped reads	3,238,632 / 96.89%

2.2. ACGT Content

Number/percentage of A's	64,634,949 / 29.16%
Number/percentage of C's	46,513,523 / 20.98%
Number/percentage of T's	63,983,261 / 28.87%
Number/percentage of G's	46,506,930 / 20.98%
Number/percentage of N's	14,693 / 0.01%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0716

Standard Deviation	0.8512

2.4. Mapping Quality

Mean Mapping Quality	47.63

2.5. Mismatches and indels

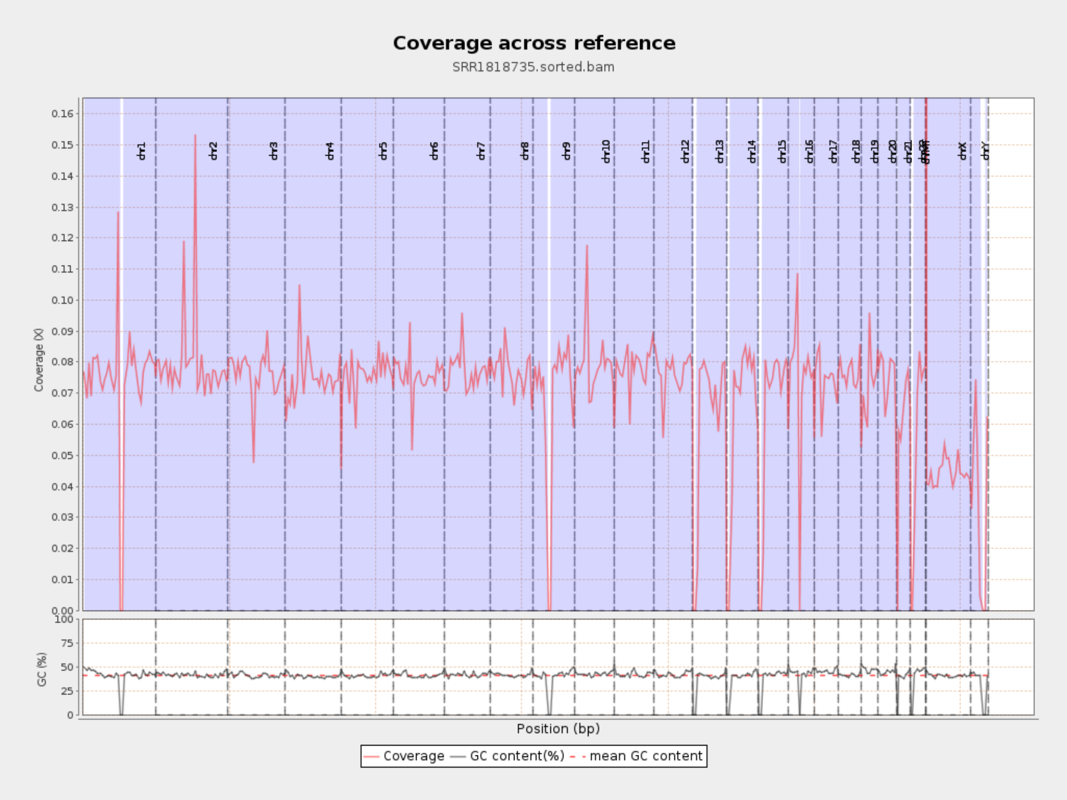
General error rate	0.55%
Mismatches	1,167,998
Insertions	27,120
Mapped reads with at least one insertion	0.82%
Deletions	57,113
Mapped reads with at least one deletion	1.74%
Homopolymer indels	41.93%

2.6. Chromosome stats

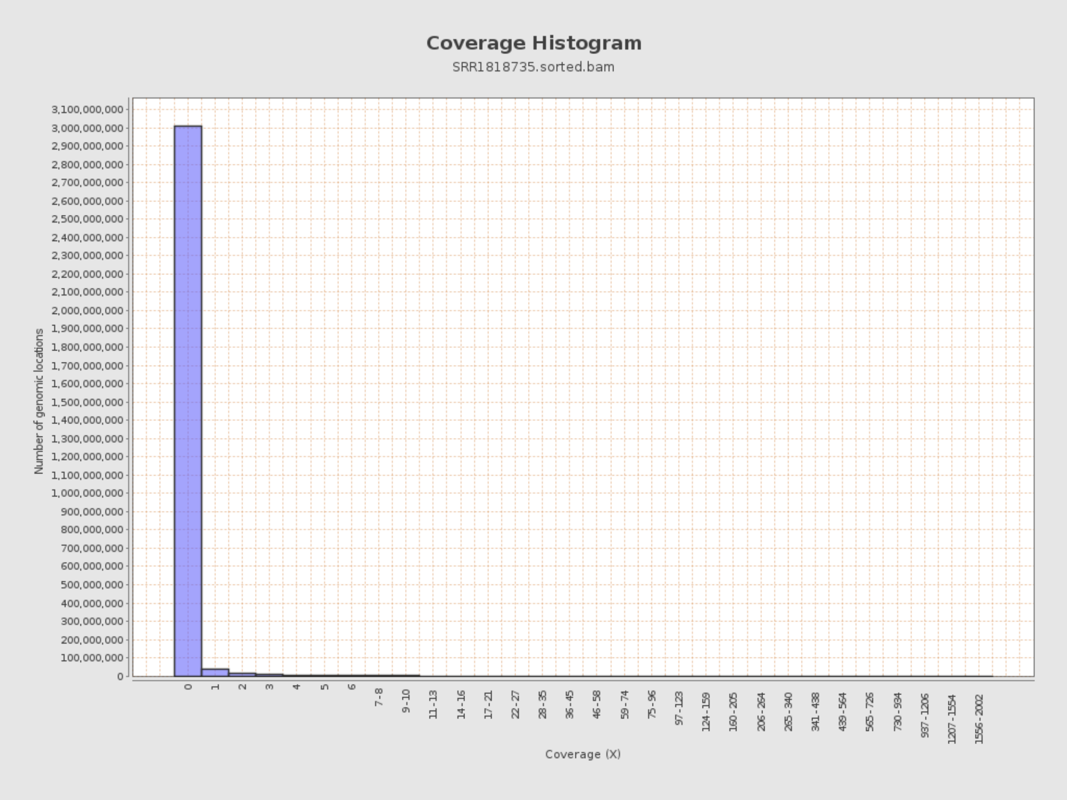
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18433925	0.074	1.3206
chr2	243199373	19519720	0.0803	1.4058
chr3	198022430	15118408	0.0763	0.5902
chr4	191154276	14413704	0.0754	0.6783
chr5	180915260	13782924	0.0762	0.6099
chr6	171115067	12953559	0.0757	0.6624
chr7	159138663	12311563	0.0774	0.7804

chr8	146364022	11201322	0.0765	0.6967
chr9	141213431	9549122	0.0676	0.6913
chr10	135534747	10781624	0.0795	0.874
chr11	135006516	10579969	0.0784	0.6858
chr12	133851895	10305869	0.077	0.6376
chr13	115169878	7041164	0.0611	0.531
chr14	107349540	6880867	0.0641	0.6281
chr15	102531392	6337015	0.0618	0.5317
chr16	90354753	6600977	0.0731	0.9045
chr17	81195210	6067881	0.0747	0.6372
chr18	78077248	5971176	0.0765	0.877
chr19	59128983	4297181	0.0727	1.0441
chr20	63025520	4794291	0.0761	0.6413
chr21	48129895	2886787	0.06	0.5516
chr22	51304566	2722748	0.0531	0.5551
chrMT	16571	263486	15.9004	14.217
chrX	155270560	6899200	0.0444	0.5145
chrY	59373566	2032601	0.0342	1.4852

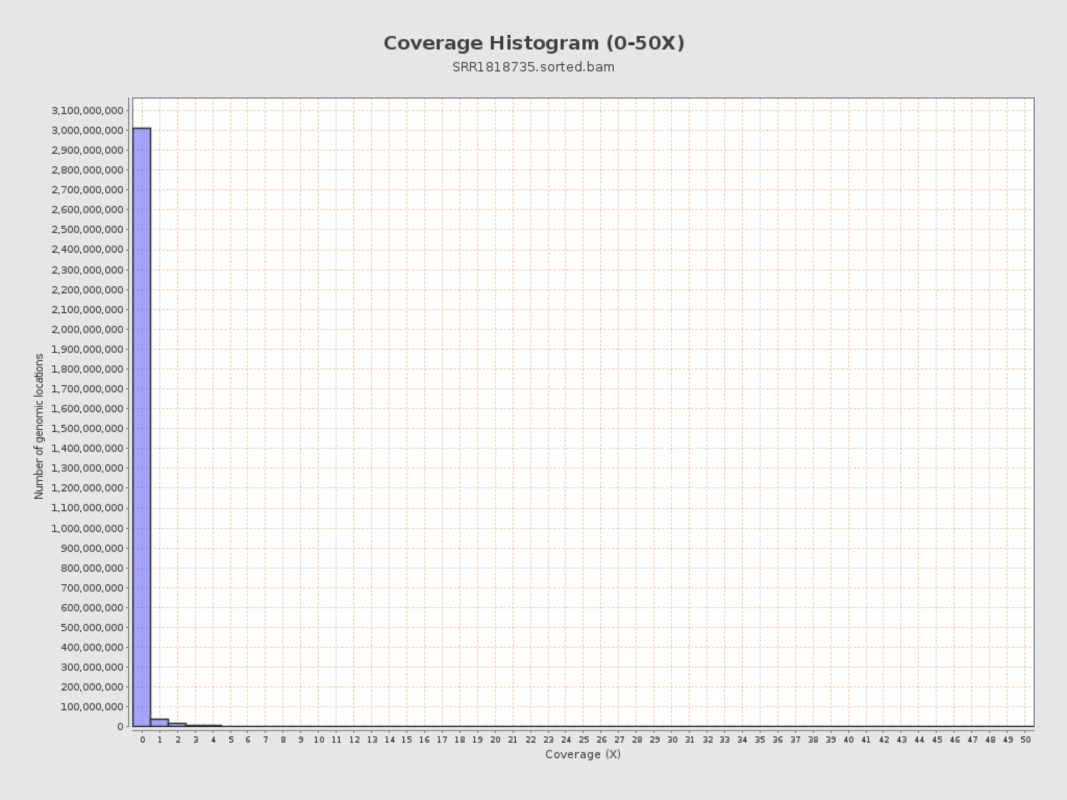
3. Results : Coverage across reference



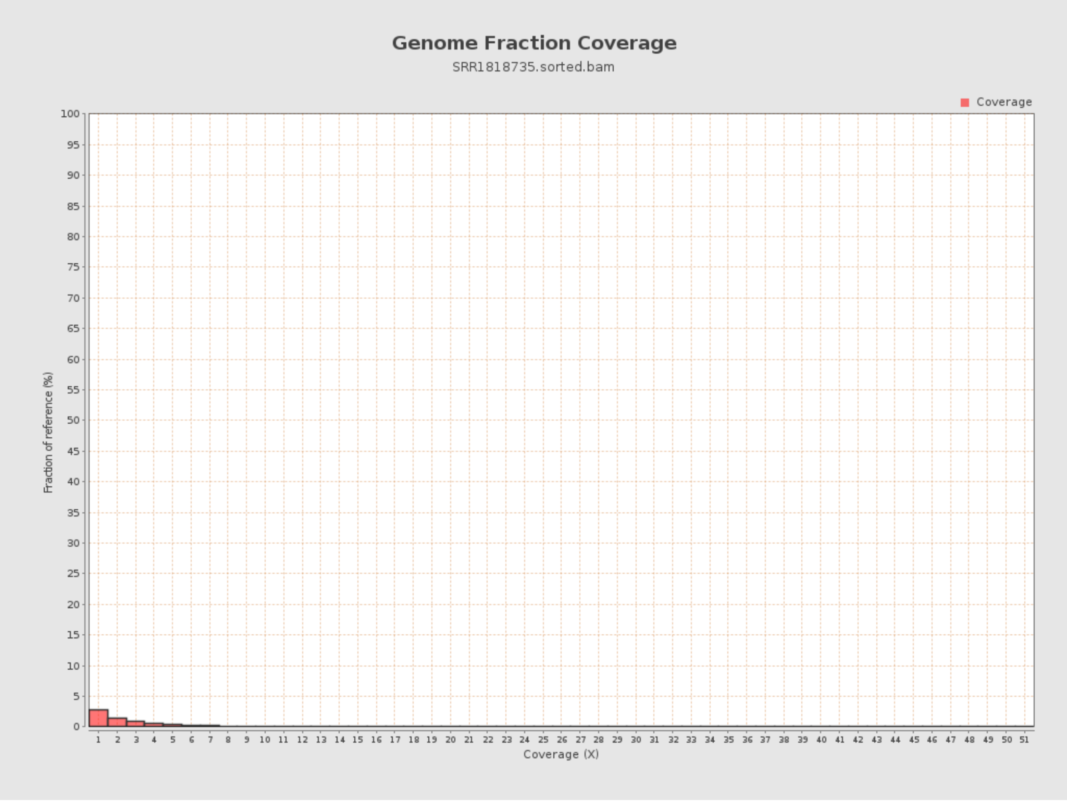
4. Results : Coverage Histogram



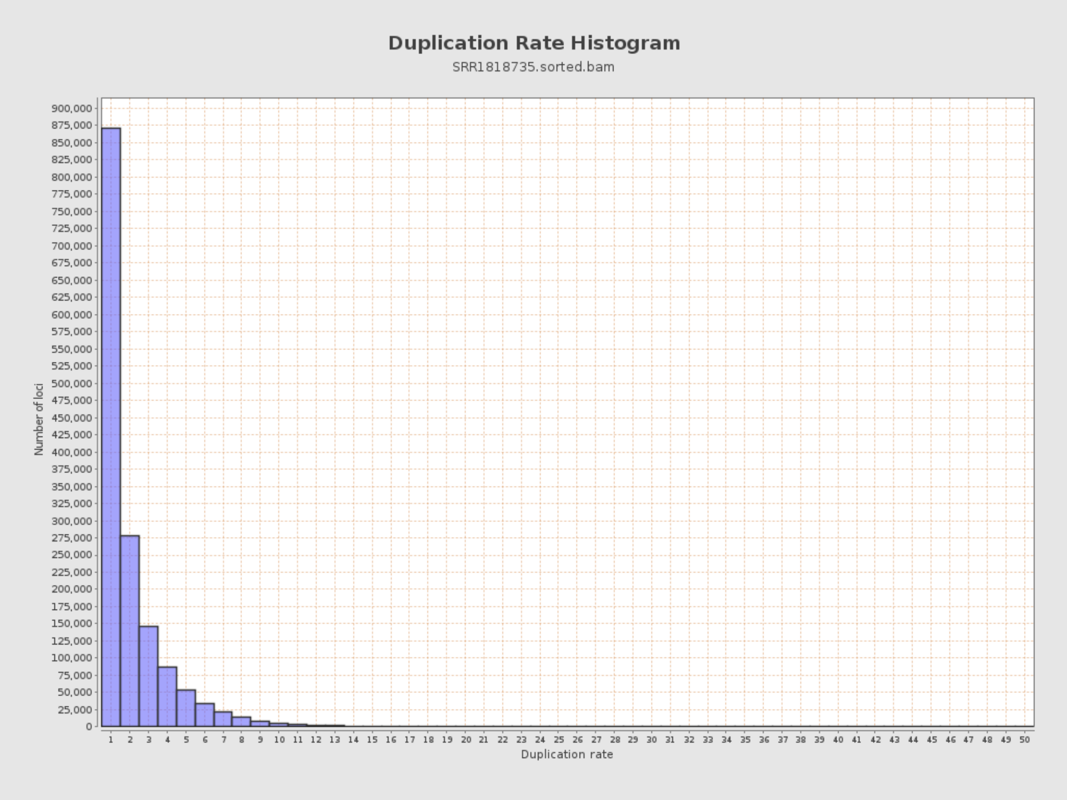
5. Results : Coverage Histogram (0-50X)



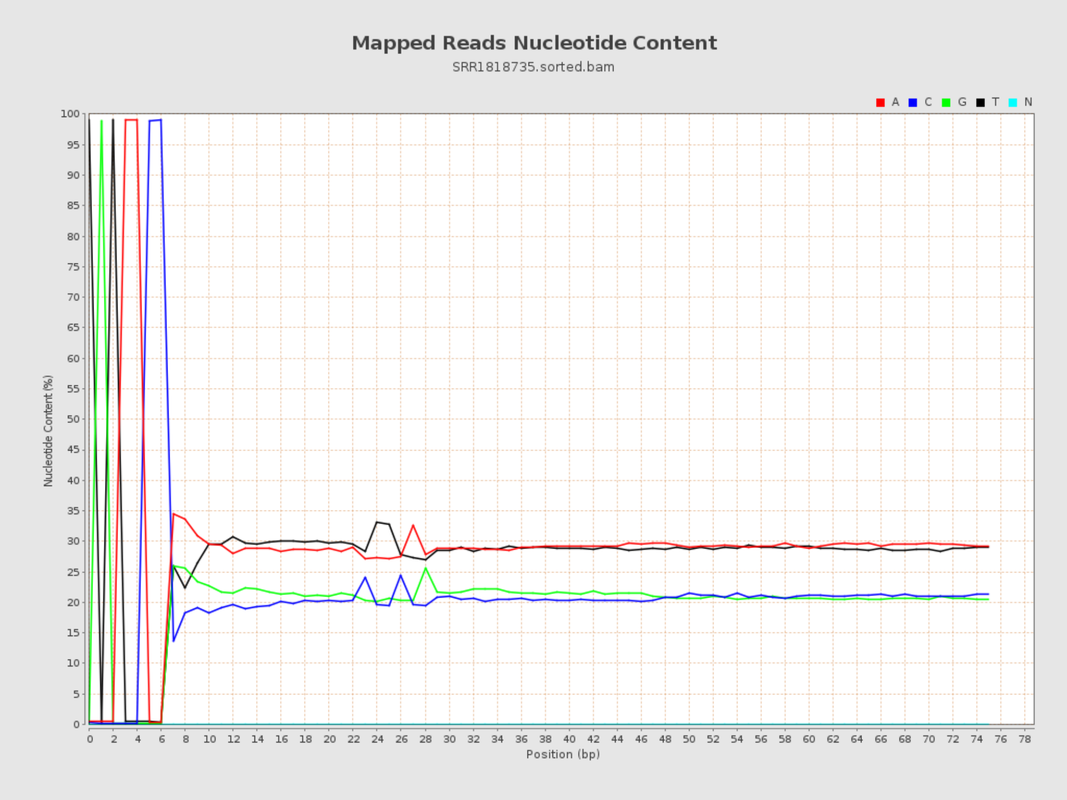
6. Results : Genome Fraction Coverage



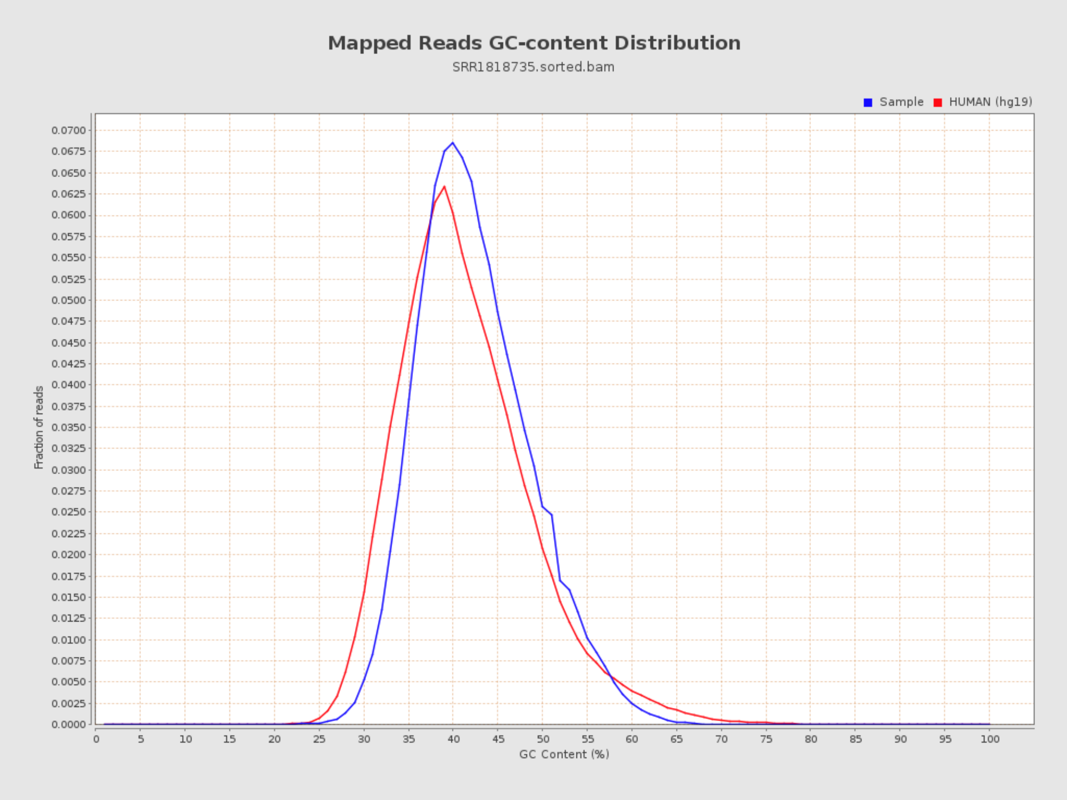
7. Results : Duplication Rate Histogram



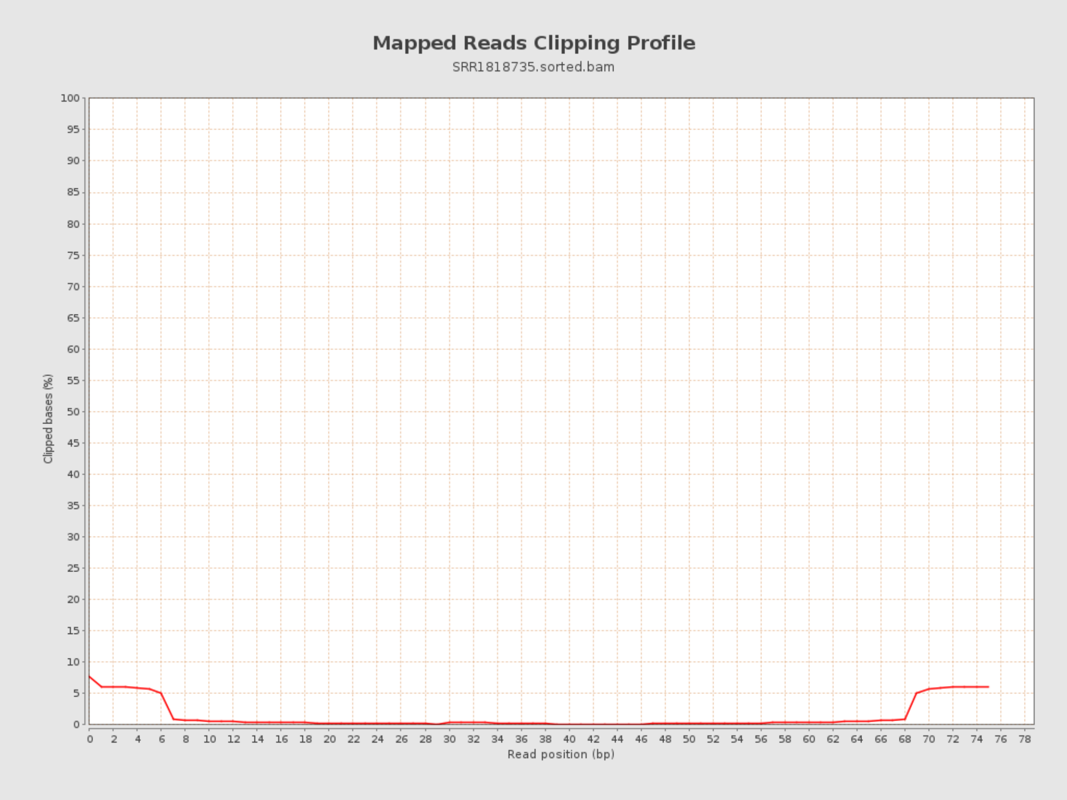
8. Results : Mapped Reads Nucleotide Content



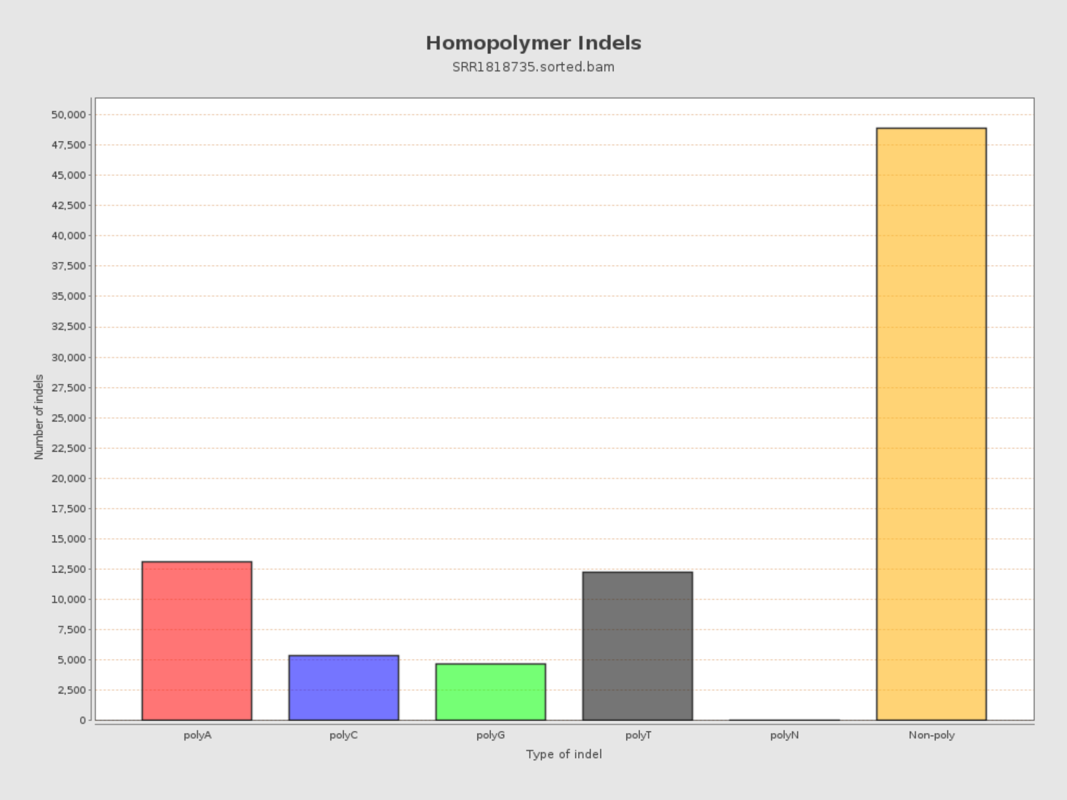
9. Results : Mapped Reads GC-content Distribution



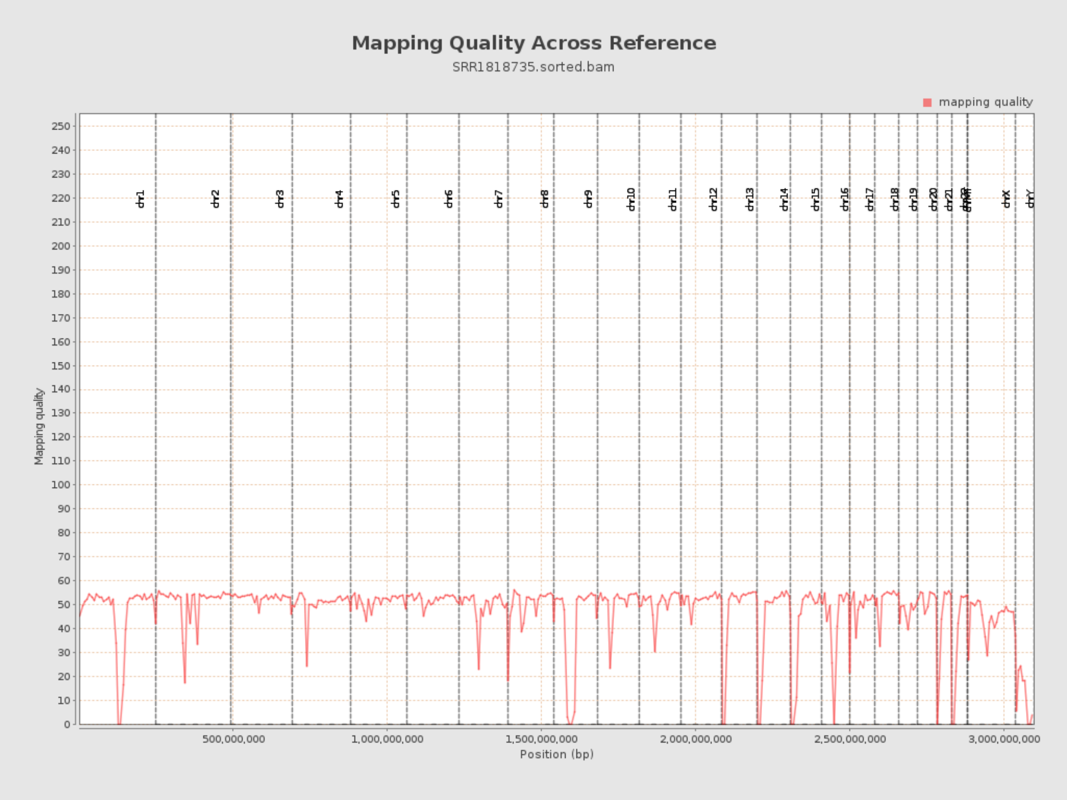
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram