Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:03:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818761.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_SRR1818761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:03:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,119,275
Mapped reads	1,065,554 / 95.2%
Unmapped reads	53,721 / 4.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,497 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	382,828 / 34.2%
Duplication rate	31.87%
Clipped reads	1,062,937 / 94.97%

2.2. ACGT Content

Number/percentage of A's	21,066,263 / 29.14%
Number/percentage of C's	15,273,429 / 21.13%
Number/percentage of T's	20,991,820 / 29.04%
Number/percentage of G's	14,954,803 / 20.69%
Number/percentage of N's	4,346 / 0.01%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.3095

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

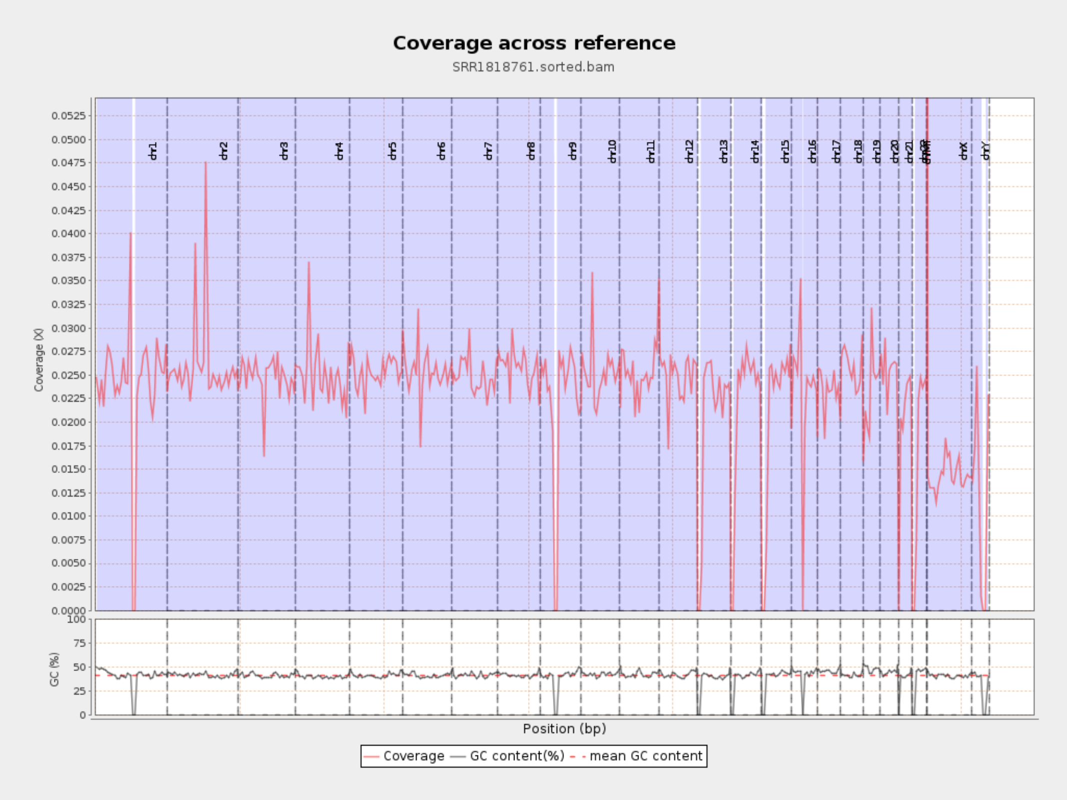
General error rate	0.55%
Mismatches	377,627
Insertions	9,451
Mapped reads with at least one insertion	0.88%
Deletions	18,619
Mapped reads with at least one deletion	1.73%
Homopolymer indels	39.17%

2.6. Chromosome stats

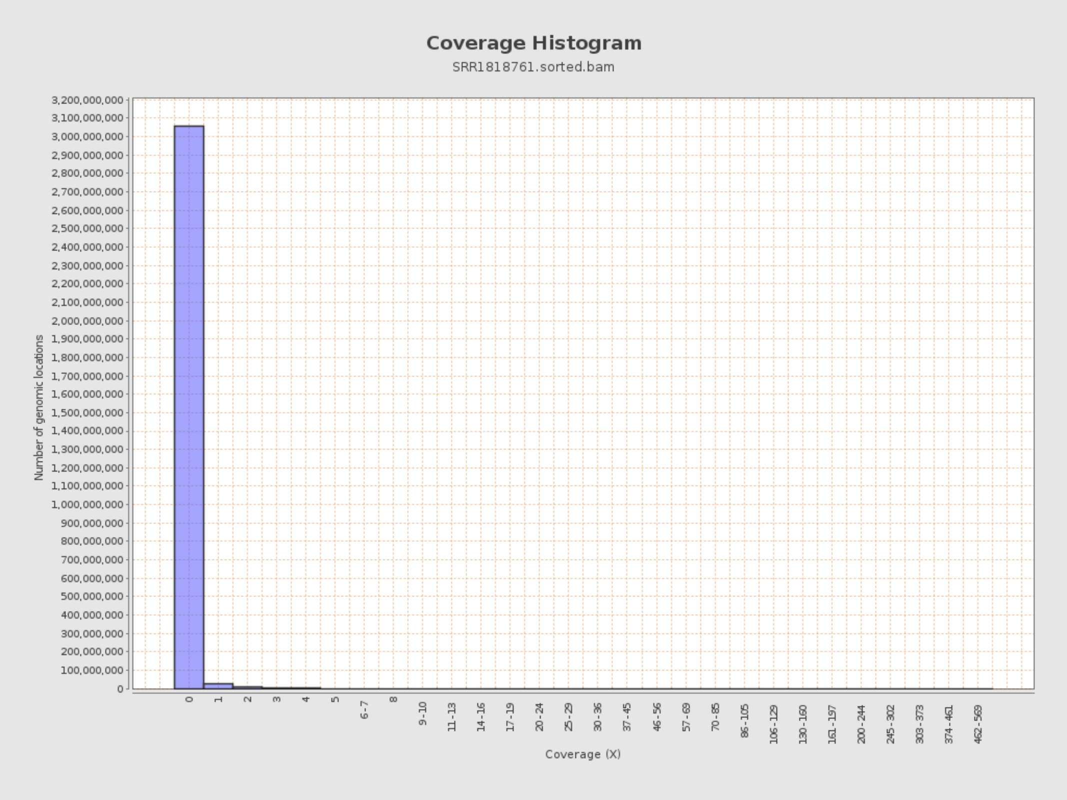
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5943667	0.0238	0.4348
chr2	243199373	6335329	0.026	0.4578
chr3	198022430	4899607	0.0247	0.2474
chr4	191154276	4786079	0.025	0.2778
chr5	180915260	4582838	0.0253	0.2577
chr6	171115067	4342838	0.0254	0.2702
chr7	159138663	3967432	0.0249	0.282

chr8	146364022	3783648	0.0259	0.2886
chr9	141213431	3122420	0.0221	0.2684
chr10	135534747	3436082	0.0254	0.313
chr11	135006516	3380549	0.025	0.2711
chr12	133851895	3322401	0.0248	0.261
chr13	115169878	2310711	0.0201	0.2228
chr14	107349540	2279489	0.0212	0.2514
chr15	102531392	2081994	0.0203	0.229
chr16	90354753	2069430	0.0229	0.3352
chr17	81195210	1901688	0.0234	0.2511
chr18	78077248	2016229	0.0258	0.346
chr19	59128983	1387469	0.0235	0.3802
chr20	63025520	1593080	0.0253	0.2703
chr21	48129895	967286	0.0201	0.2398
chr22	51304566	842423	0.0164	0.2228
chrMT	16571	33868	2.0438	2.5312
chrX	155270560	2228286	0.0144	0.2032
chrY	59373566	706019	0.0119	0.4516

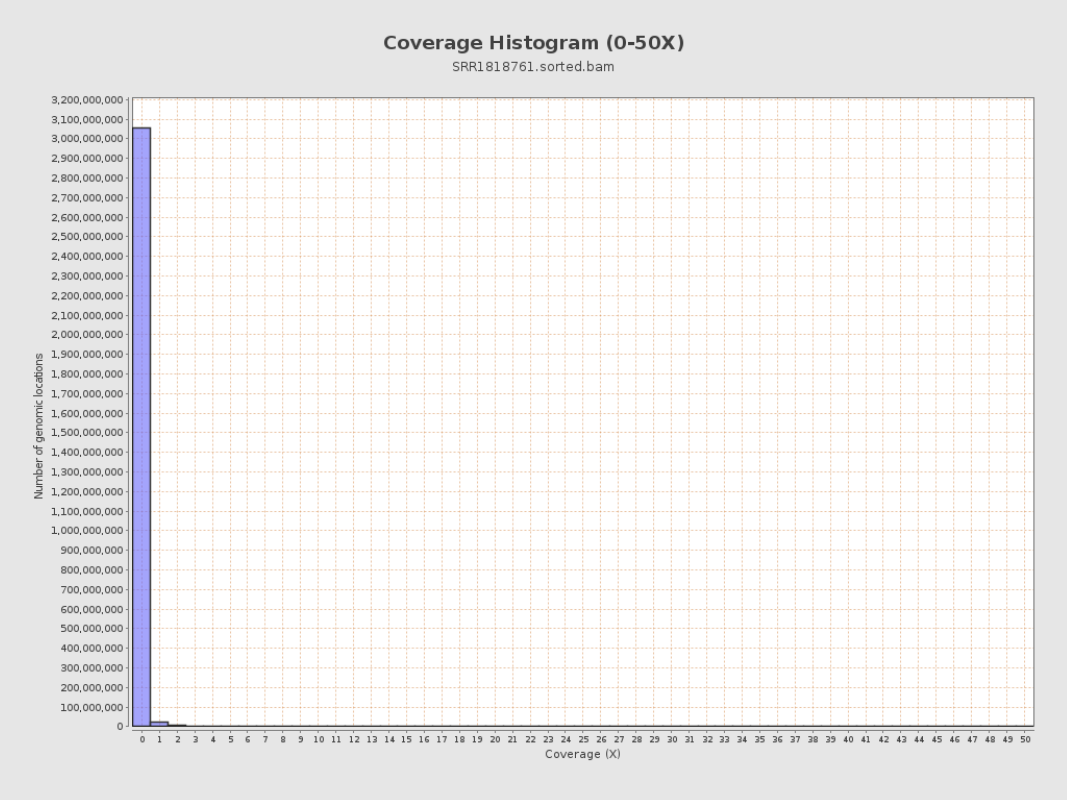
3. Results : Coverage across reference



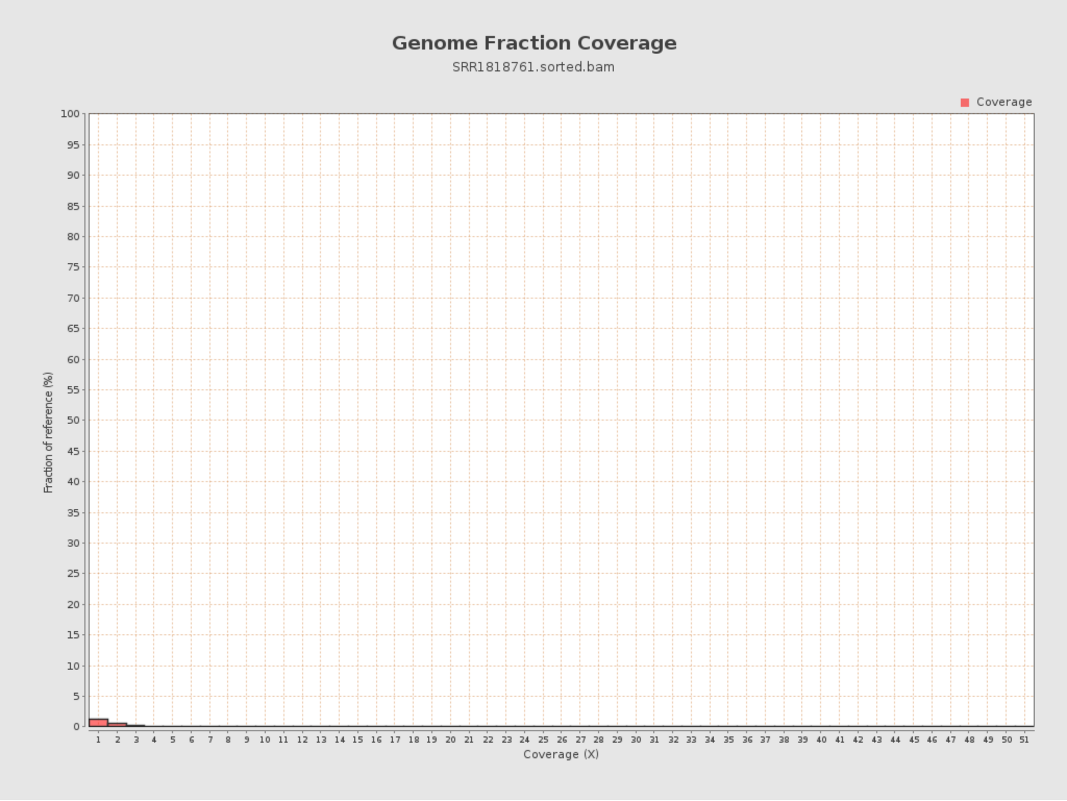
4. Results : Coverage Histogram



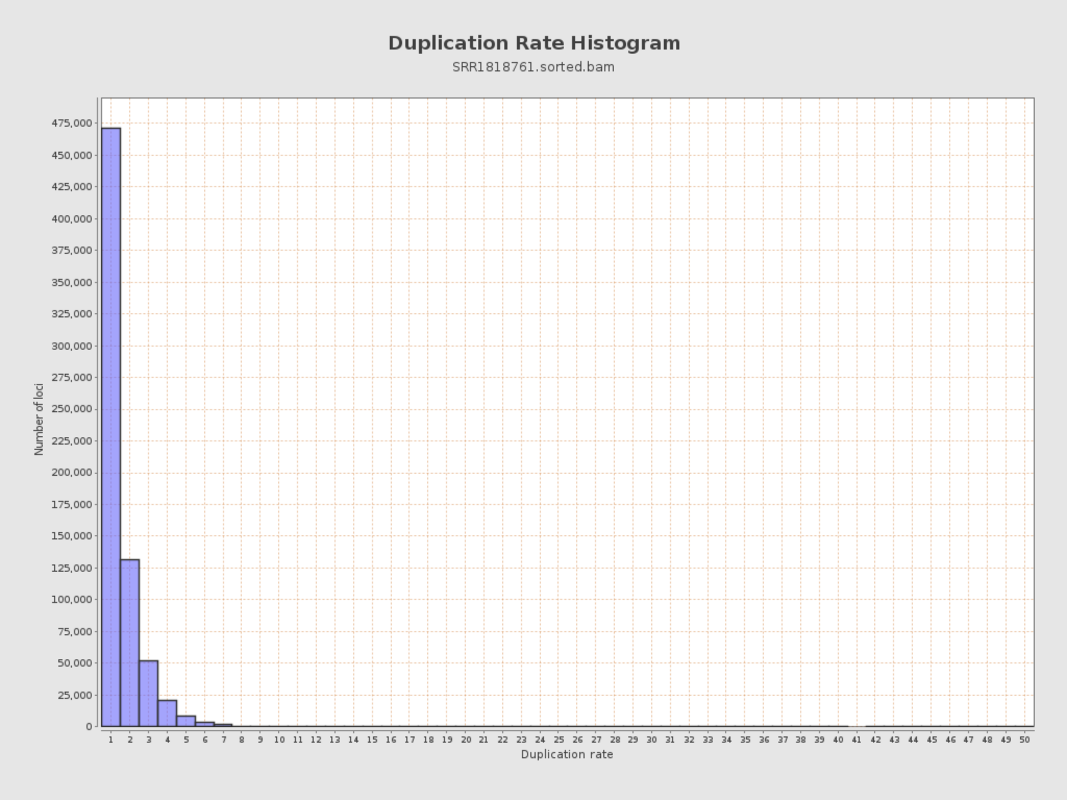
5. Results : Coverage Histogram (0-50X)



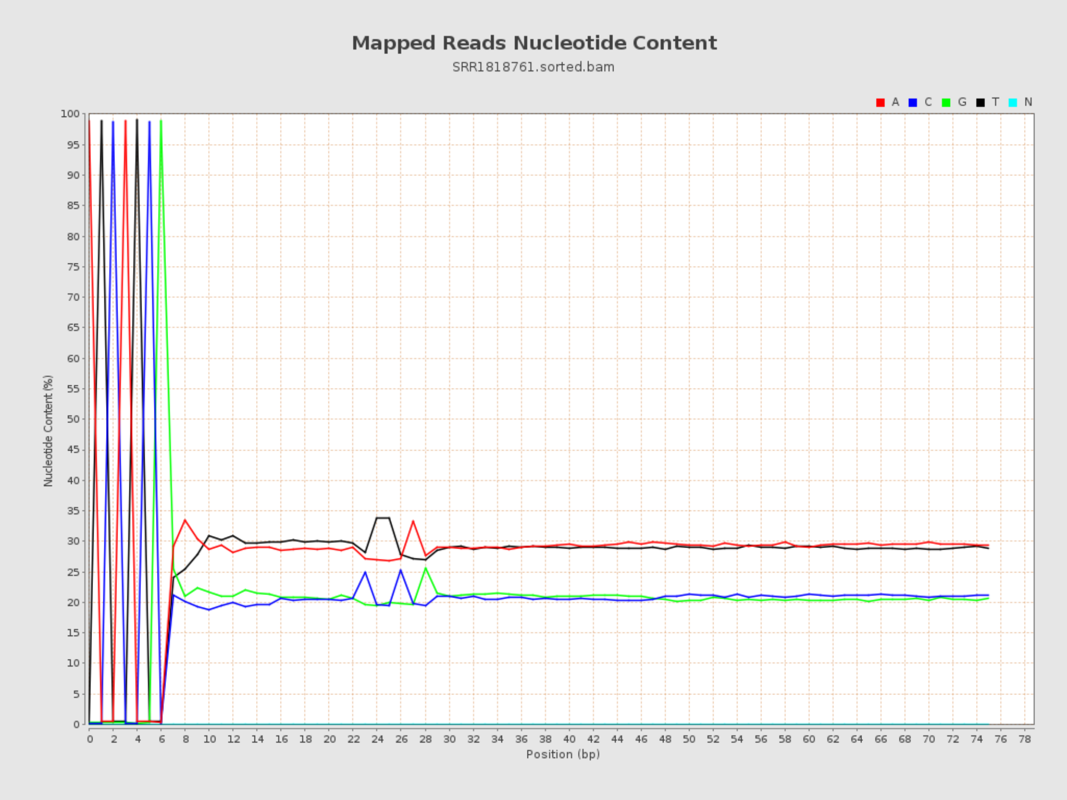
6. Results : Genome Fraction Coverage



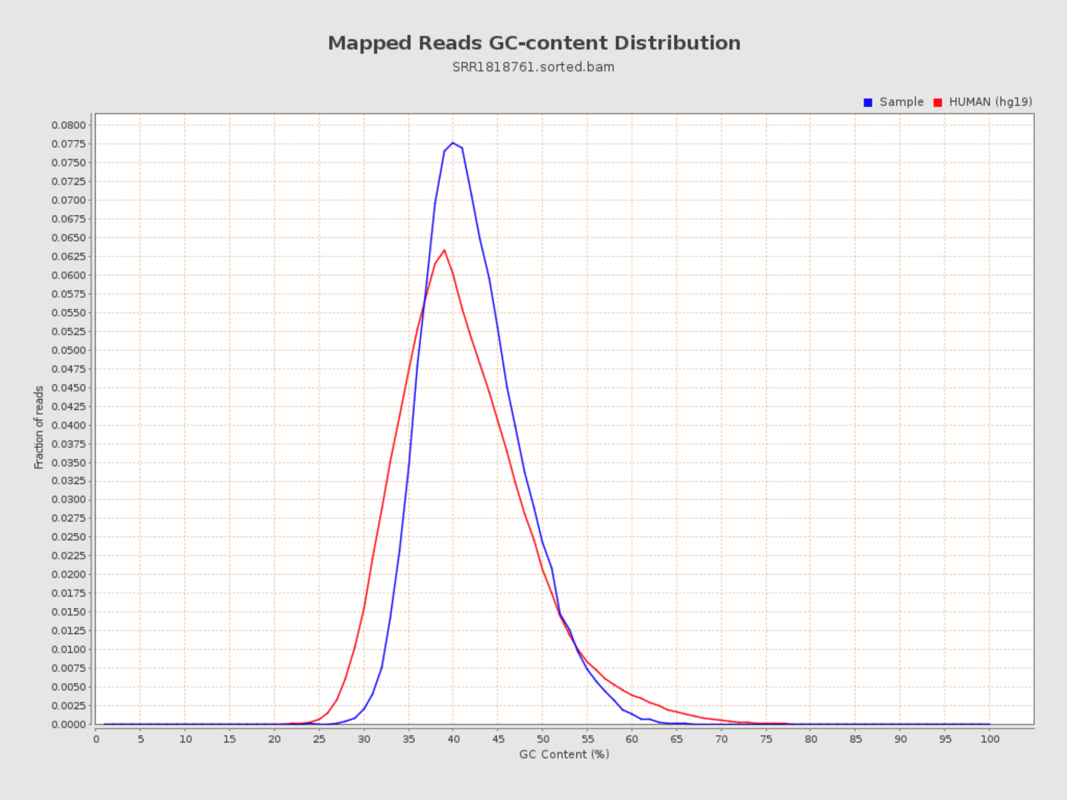
7. Results : Duplication Rate Histogram



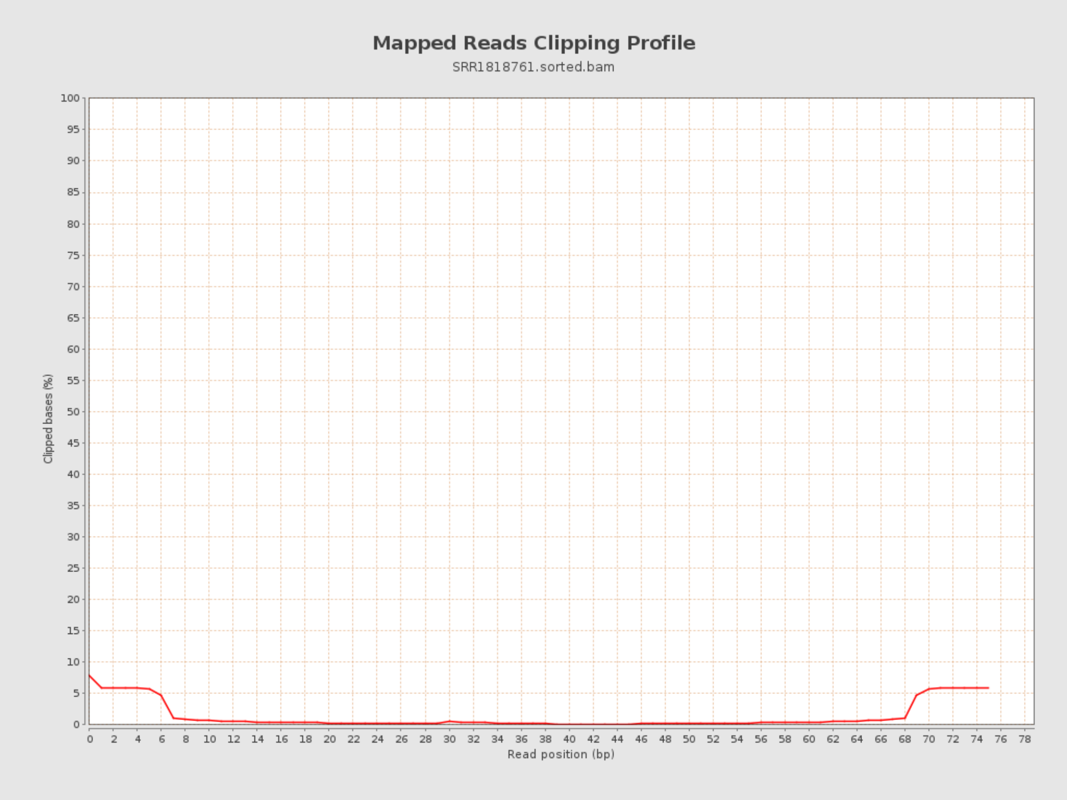
8. Results : Mapped Reads Nucleotide Content



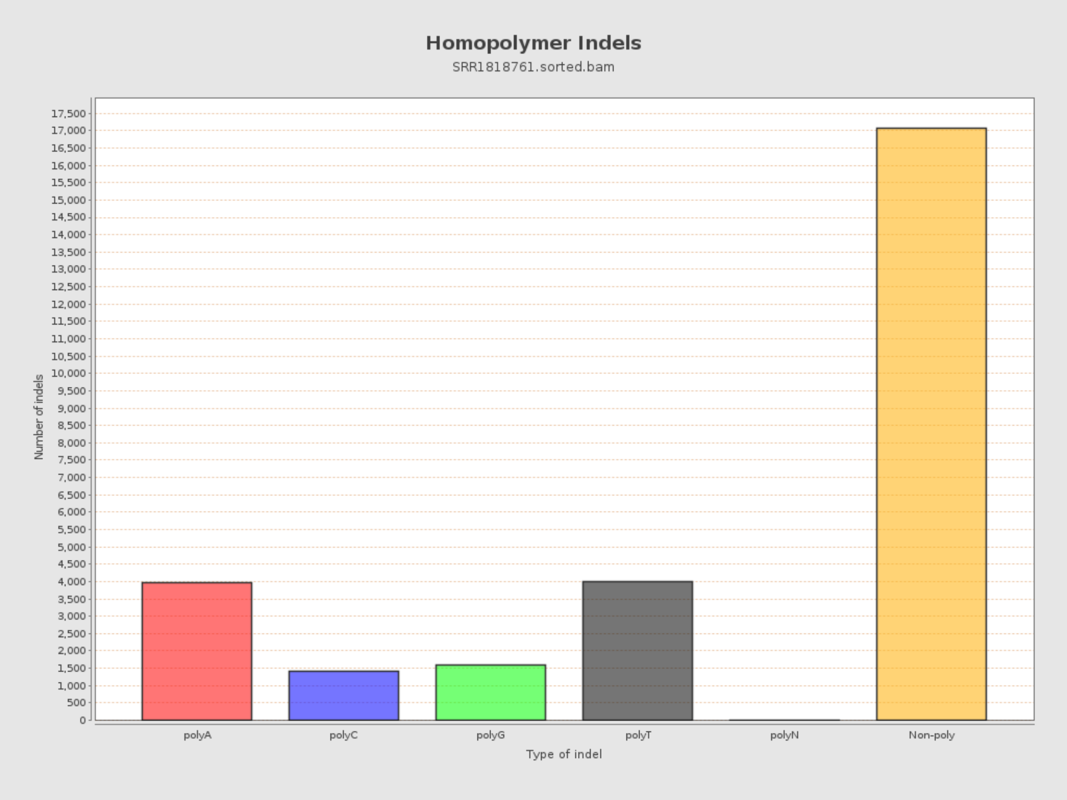
9. Results : Mapped Reads GC-content Distribution



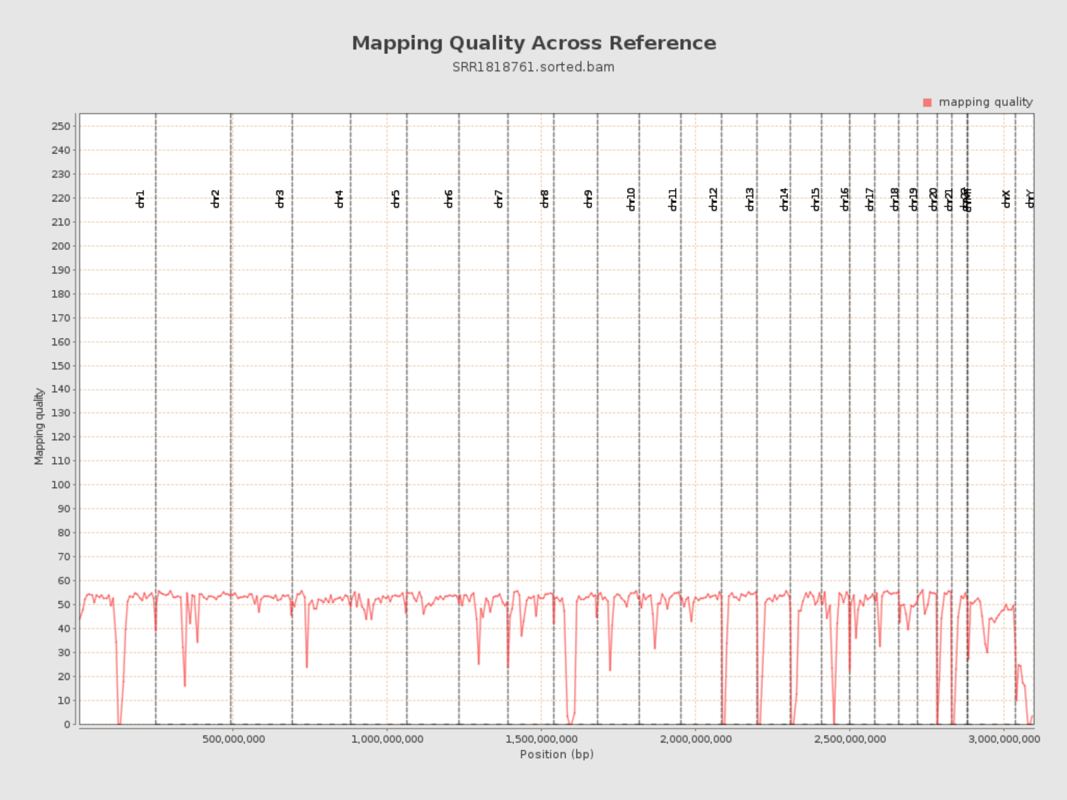
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram