Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:51:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818737.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_SRR1818737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,370,791
Mapped reads	2,309,821 / 97.43%
Unmapped reads	60,970 / 2.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,717 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	1,198,627 / 50.56%
Duplication rate	43.18%
Clipped reads	2,310,433 / 97.45%

2.2. ACGT Content

Number/percentage of A's	45,600,619 / 29.06%
Number/percentage of C's	32,799,720 / 20.9%
Number/percentage of T's	43,183,885 / 27.52%
Number/percentage of G's	35,345,744 / 22.52%
Number/percentage of N's	9,240 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.6489

2.4. Mapping Quality

Mean Mapping Quality	47.62

2.5. Mismatches and indels

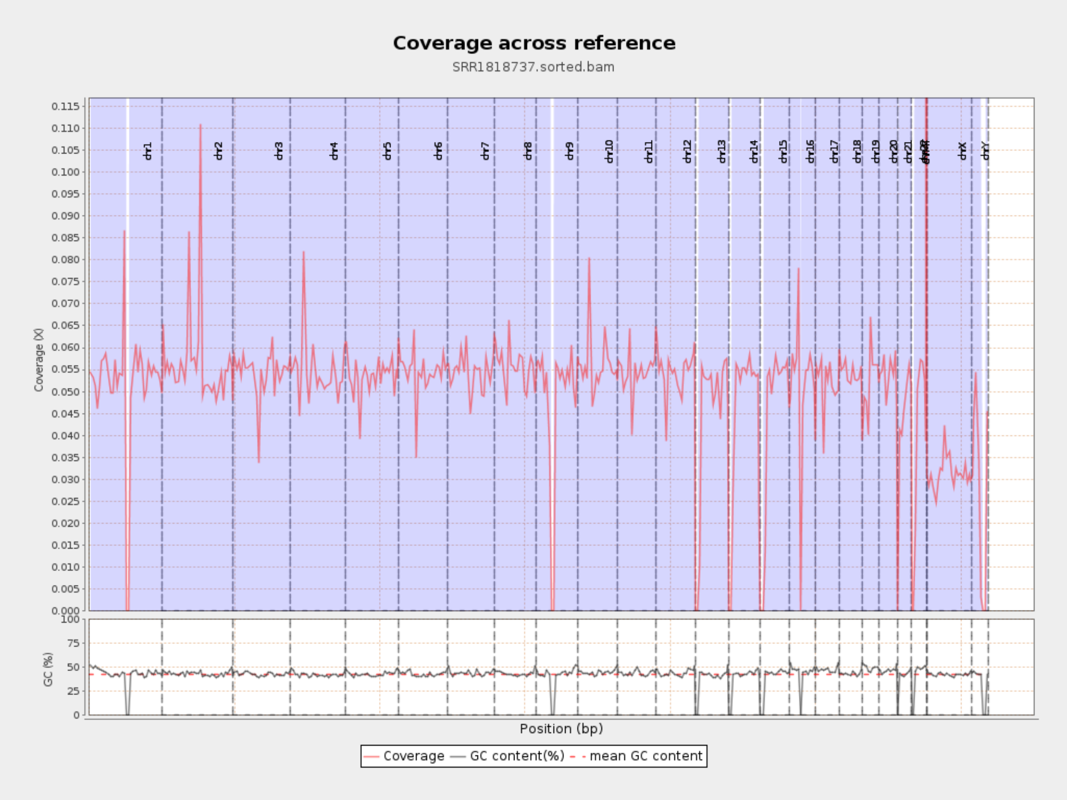
General error rate	0.53%
Mismatches	793,447
Insertions	19,414
Mapped reads with at least one insertion	0.83%
Deletions	40,177
Mapped reads with at least one deletion	1.72%
Homopolymer indels	40.42%

2.6. Chromosome stats

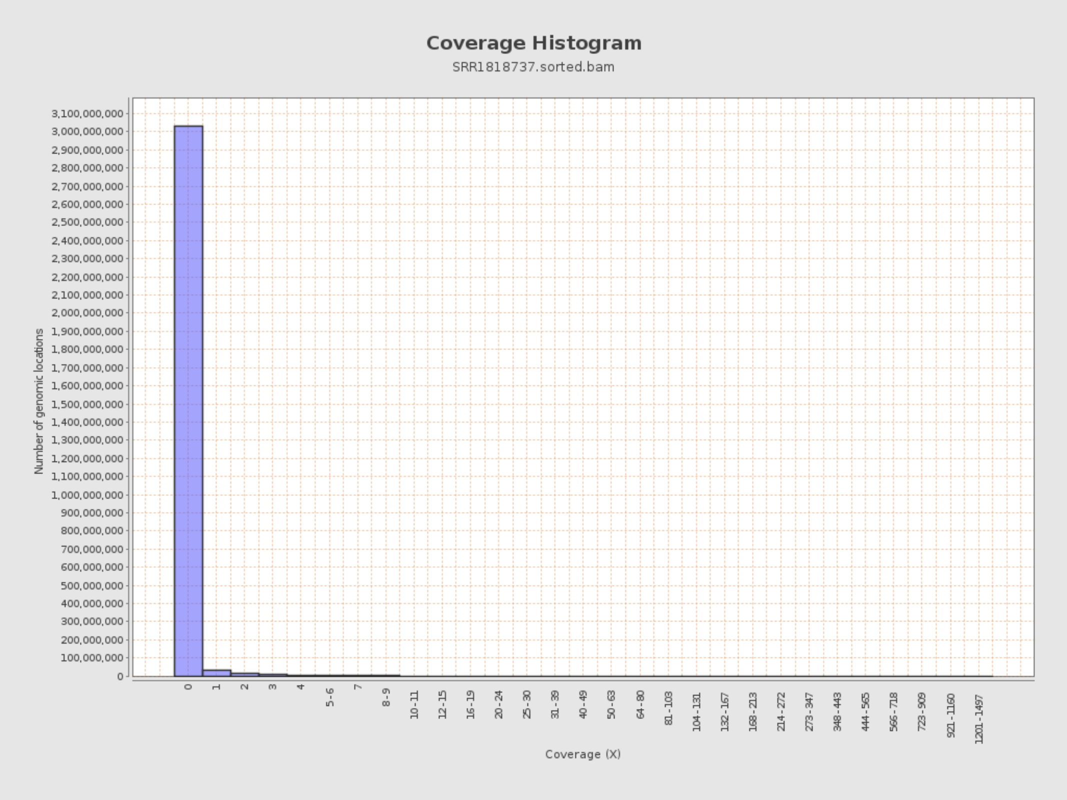
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12807149	0.0514	0.9274
chr2	243199373	13869667	0.057	1.0625
chr3	198022430	10726068	0.0542	0.4716
chr4	191154276	10408516	0.0545	0.56
chr5	180915260	9652335	0.0534	0.4888
chr6	171115067	9336431	0.0546	0.5274
chr7	159138663	8620895	0.0542	0.5722

chr8	146364022	8153582	0.0557	0.5474
chr9	141213431	6675491	0.0473	0.5176
chr10	135534747	7584119	0.056	0.7193
chr11	135006516	7336521	0.0543	0.5243
chr12	133851895	7257488	0.0542	0.5105
chr13	115169878	5067541	0.044	0.4262
chr14	107349540	4892965	0.0456	0.4831
chr15	102531392	4469553	0.0436	0.4259
chr16	90354753	4665765	0.0516	0.7186
chr17	81195210	4199025	0.0517	0.4963
chr18	78077248	4249701	0.0544	0.6729
chr19	59128983	3097707	0.0524	0.8176
chr20	63025520	3413875	0.0542	0.5086
chr21	48129895	2075405	0.0431	0.4583
chr22	51304566	1897842	0.037	0.4421
chrMT	16571	104014	6.2769	7.2046
chrX	155270560	4880701	0.0314	0.405
chrY	59373566	1563074	0.0263	1.1186

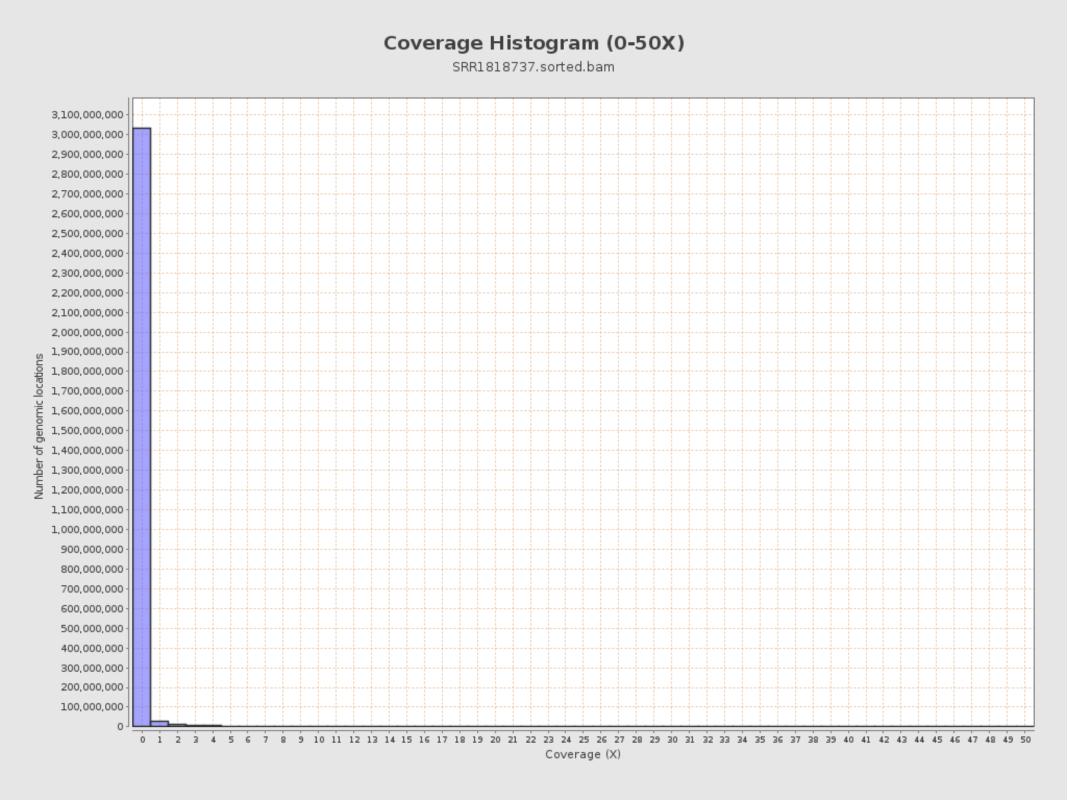
3. Results : Coverage across reference



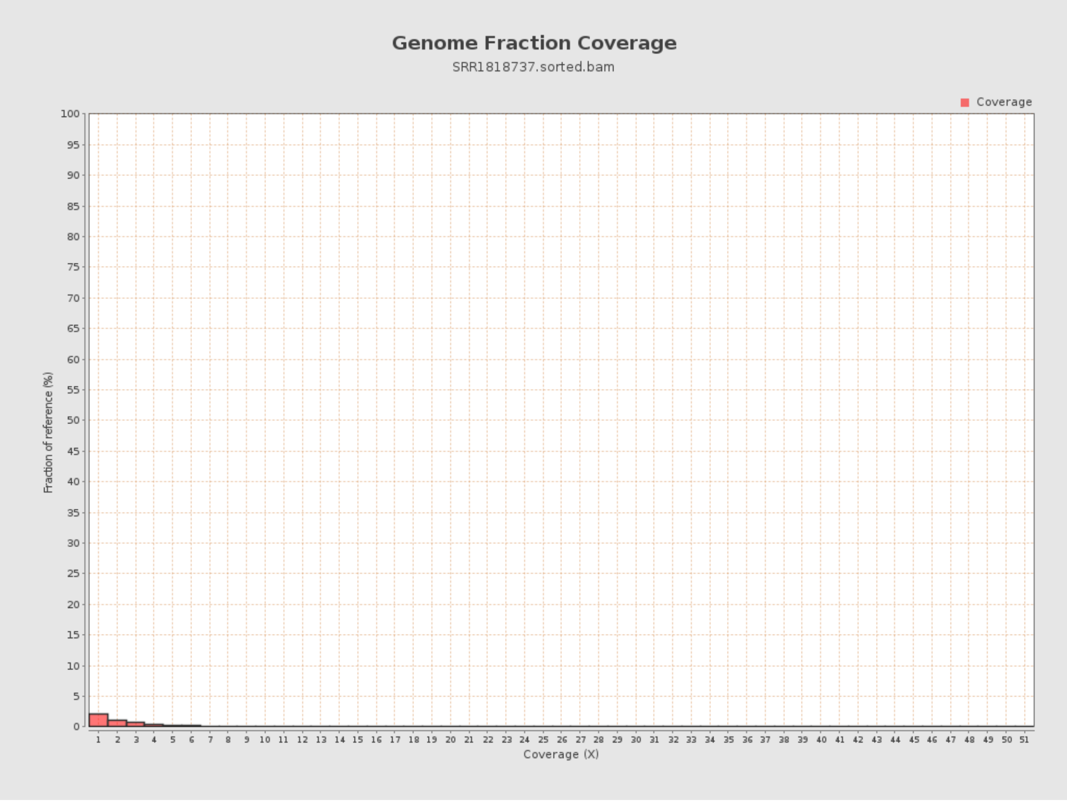
4. Results : Coverage Histogram



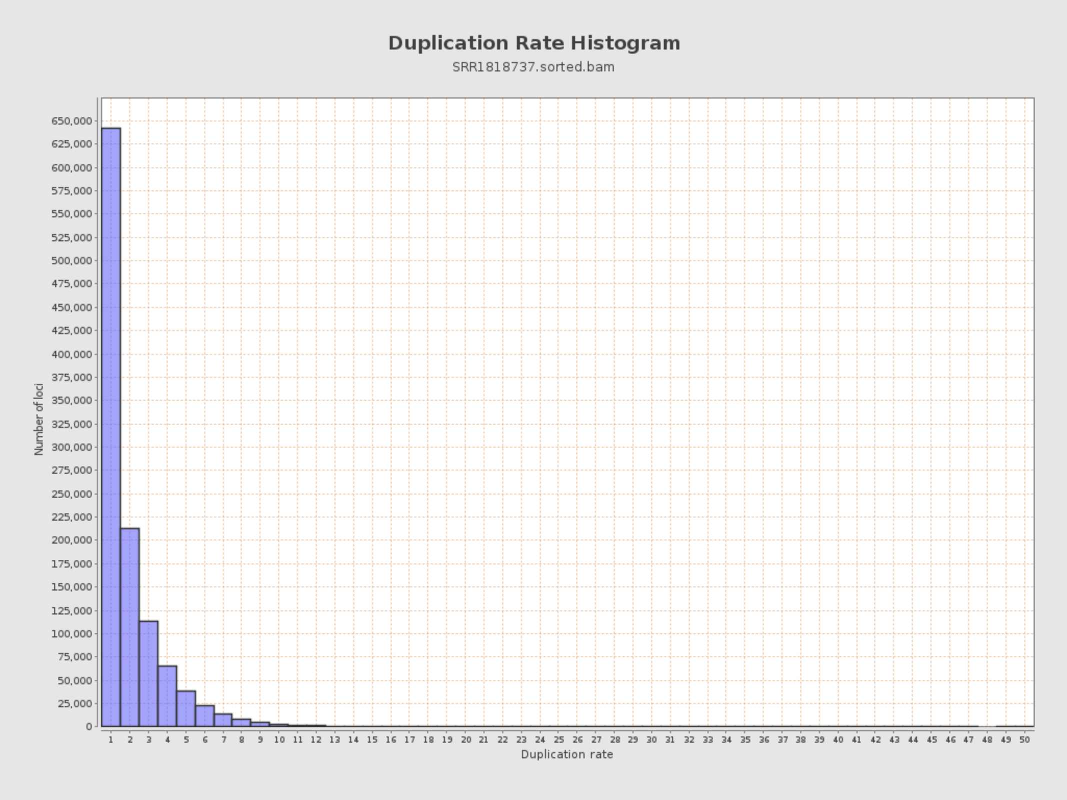
5. Results : Coverage Histogram (0-50X)



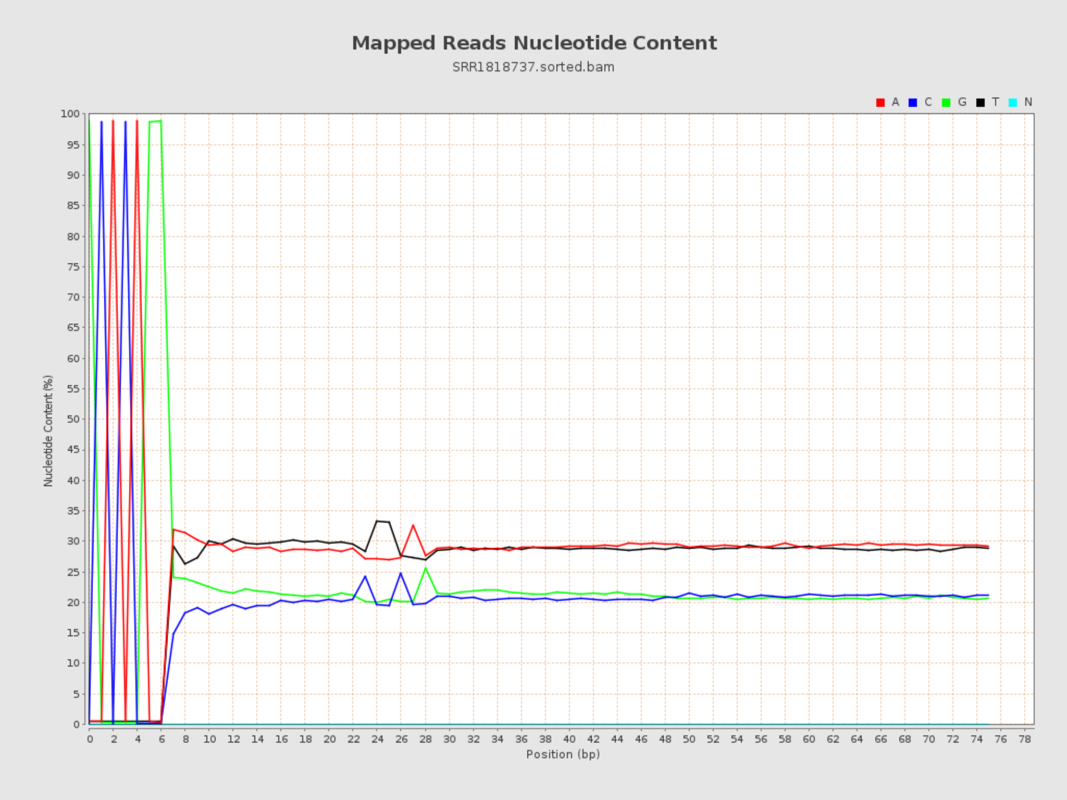
6. Results : Genome Fraction Coverage



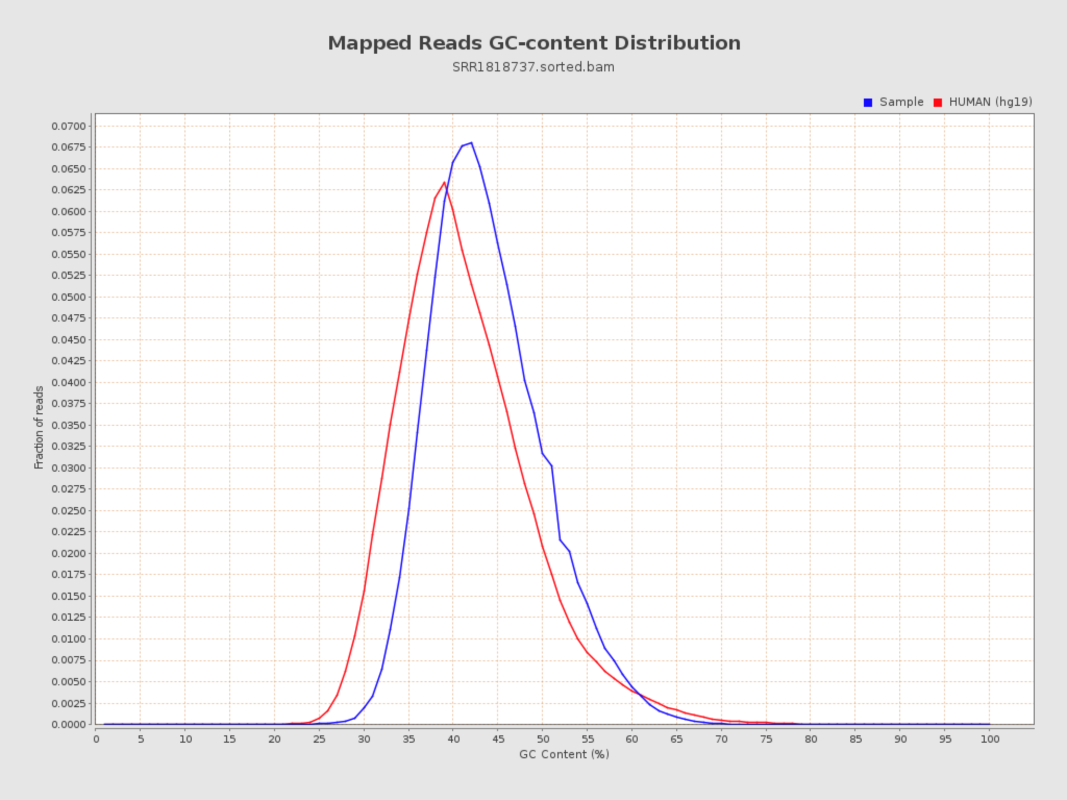
7. Results : Duplication Rate Histogram



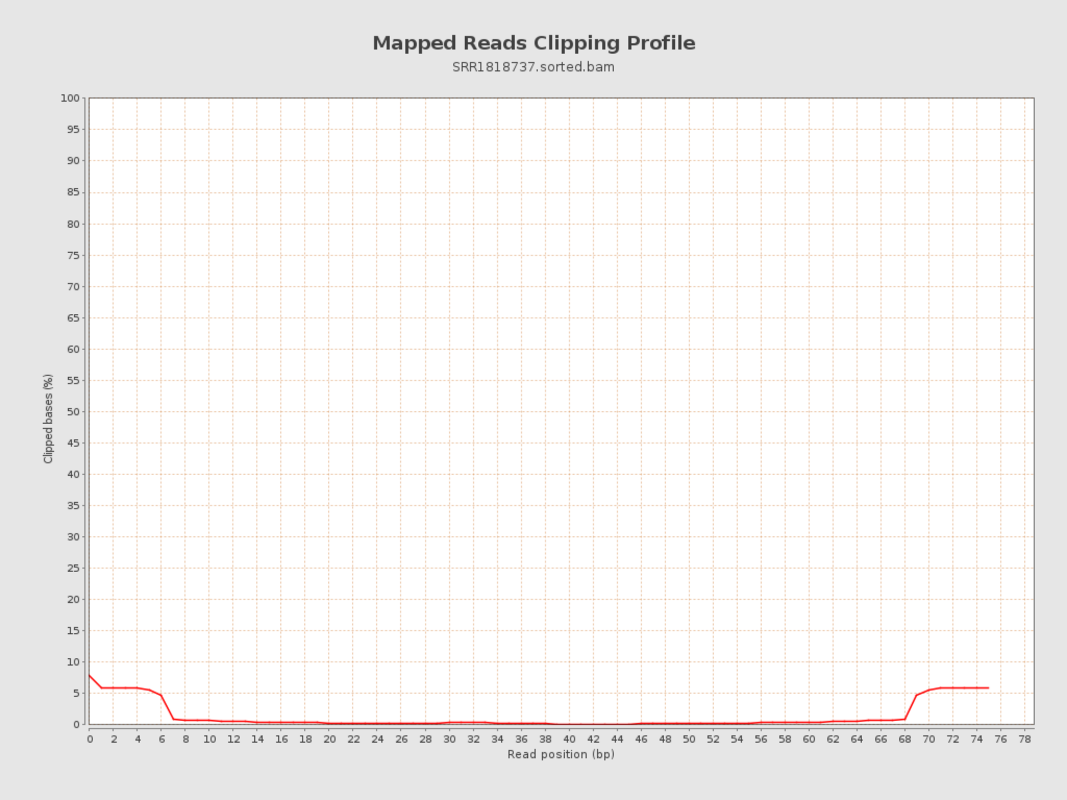
8. Results : Mapped Reads Nucleotide Content



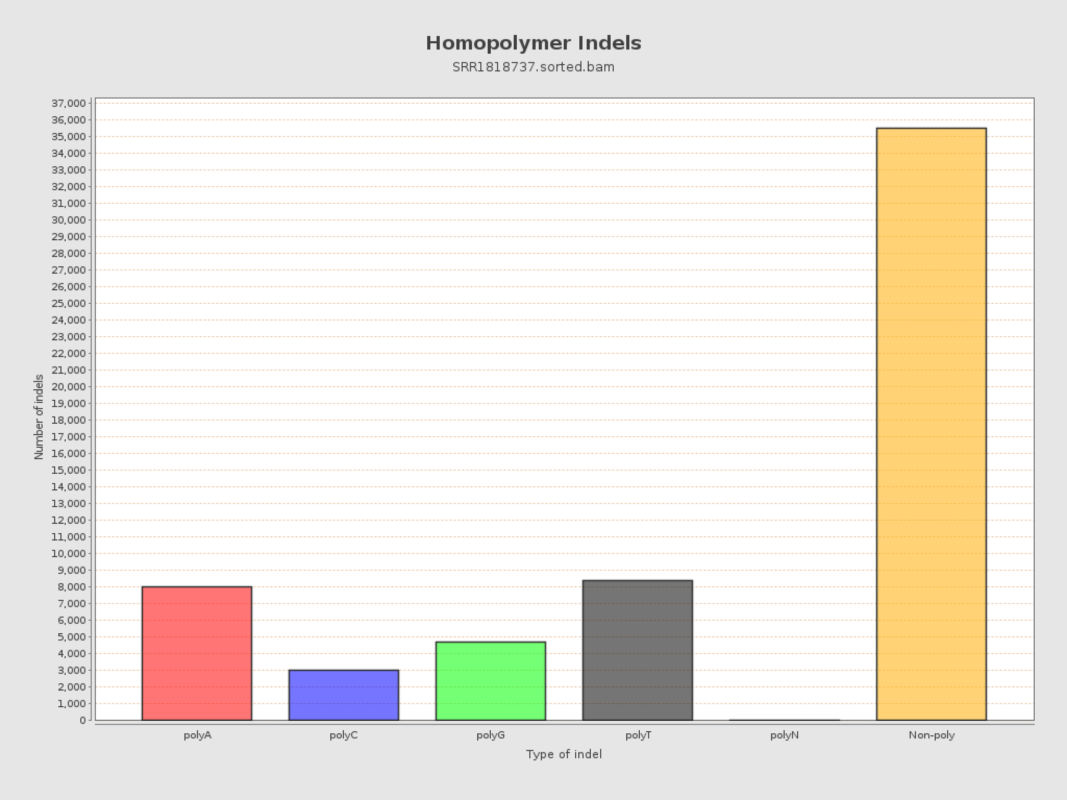
9. Results : Mapped Reads GC-content Distribution



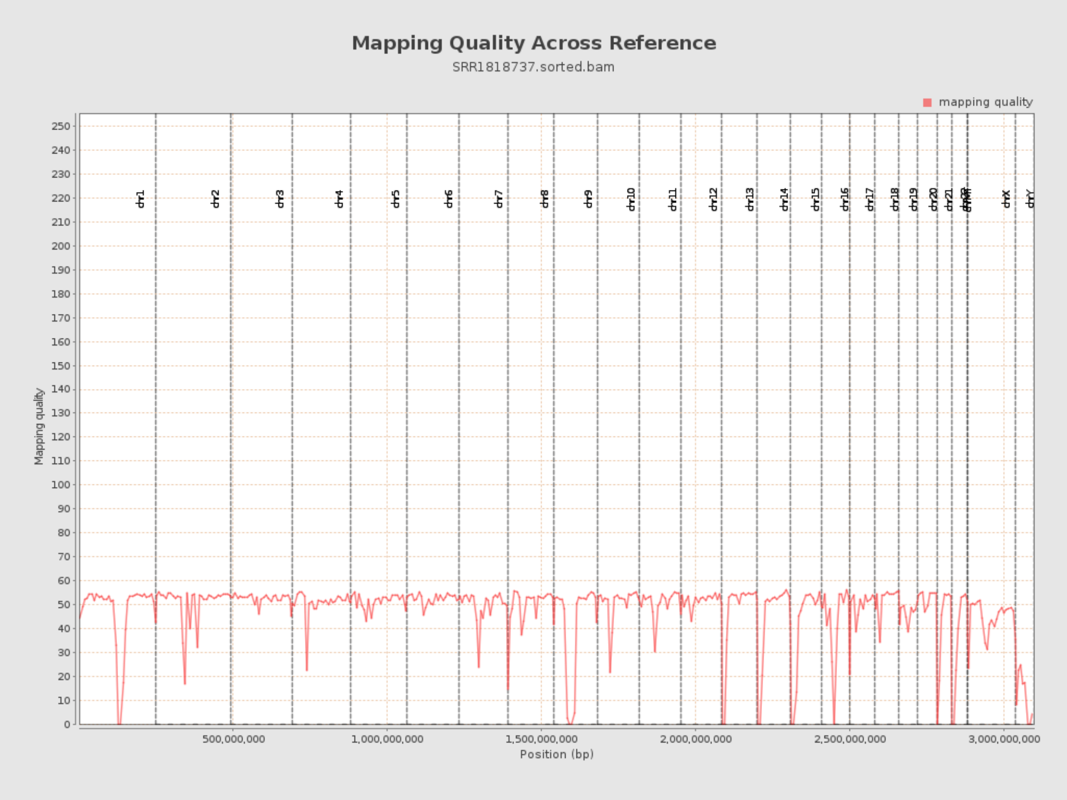
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram