Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:13:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818743.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_SRR1818743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:13:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,353,975
Mapped reads	1,319,047 / 97.42%
Unmapped reads	34,928 / 2.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,872 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	558,419 / 41.24%
Duplication rate	36.67%
Clipped reads	1,325,315 / 97.88%

2.2. ACGT Content

Number/percentage of A's	25,403,246 / 28.36%
Number/percentage of C's	19,531,742 / 21.81%
Number/percentage of T's	25,167,183 / 28.1%
Number/percentage of G's	19,466,349 / 21.73%
Number/percentage of N's	5,316 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.371

2.4. Mapping Quality

Mean Mapping Quality	47.74

2.5. Mismatches and indels

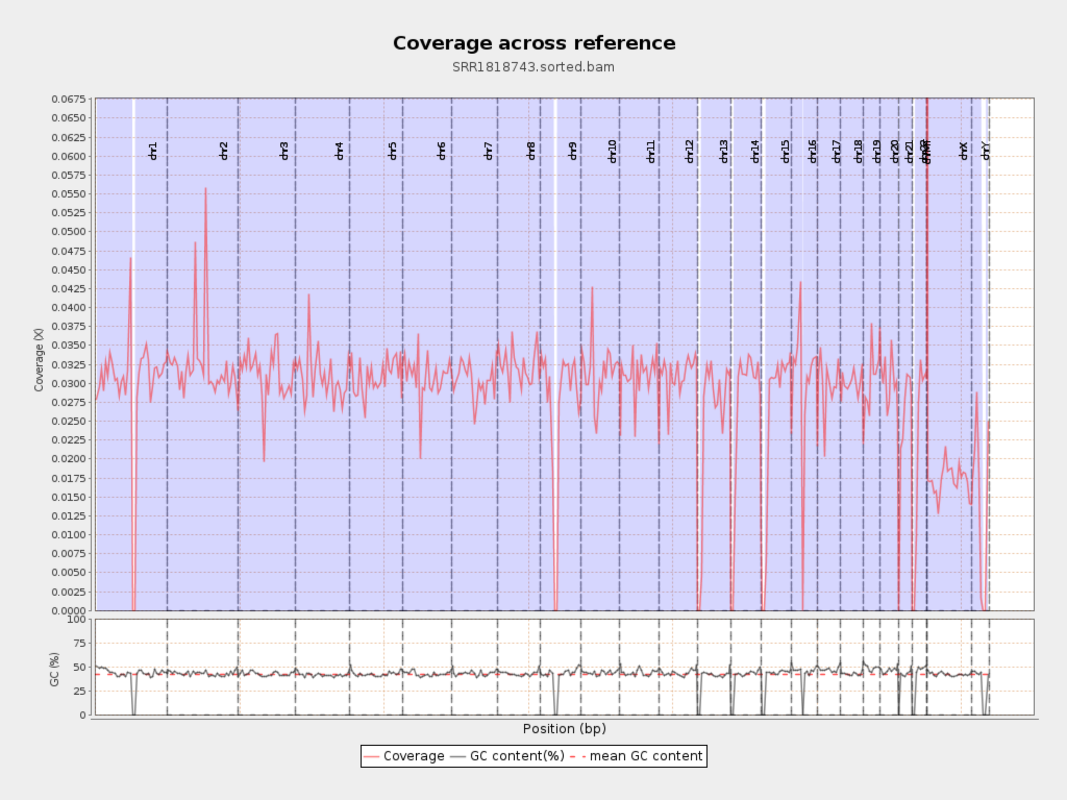
General error rate	0.51%
Mismatches	440,983
Insertions	7,945
Mapped reads with at least one insertion	0.59%
Deletions	22,724
Mapped reads with at least one deletion	1.71%
Homopolymer indels	43.74%

2.6. Chromosome stats

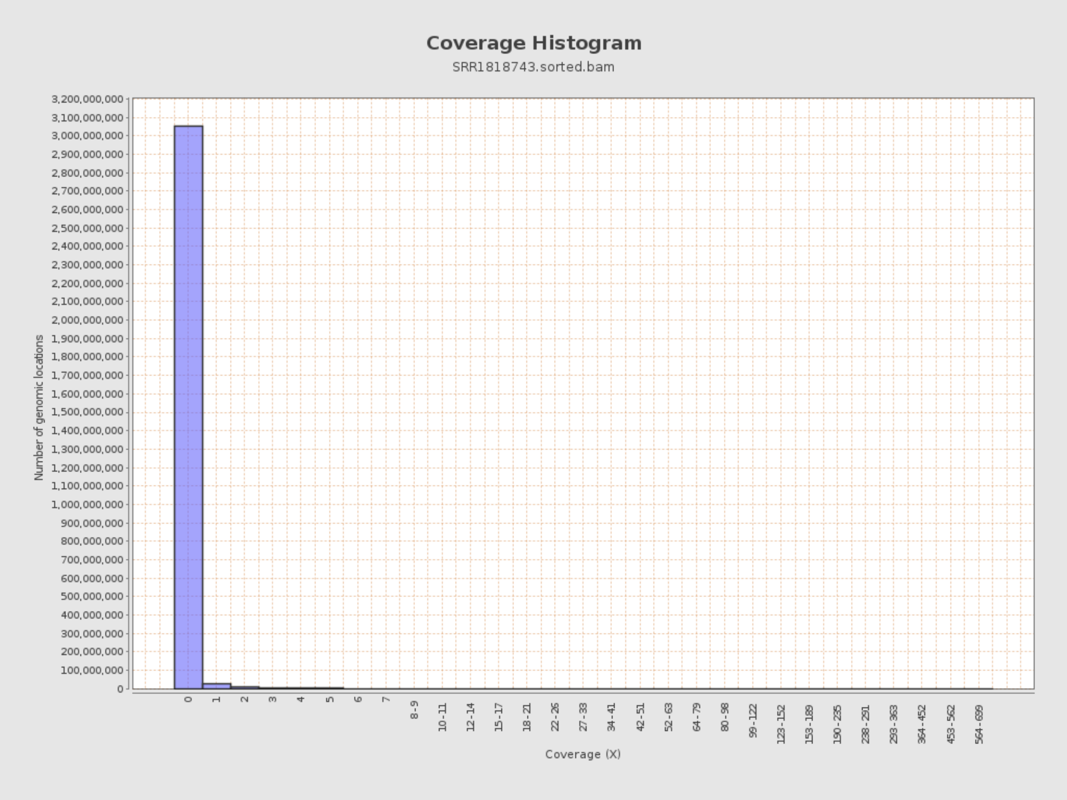
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7401818	0.0297	0.5205
chr2	243199373	7904464	0.0325	0.5432
chr3	198022430	6180992	0.0312	0.3098
chr4	191154276	5897288	0.0309	0.3369
chr5	180915260	5600807	0.031	0.3164
chr6	171115067	5273266	0.0308	0.3244
chr7	159138663	4832875	0.0304	0.3487

chr8	146364022	4712076	0.0322	0.3457
chr9	141213431	3781398	0.0268	0.3124
chr10	135534747	4293435	0.0317	0.3801
chr11	135006516	4208510	0.0312	0.3358
chr12	133851895	4184700	0.0313	0.323
chr13	115169878	2825891	0.0245	0.2706
chr14	107349540	2812202	0.0262	0.2972
chr15	102531392	2584560	0.0252	0.2763
chr16	90354753	2679311	0.0297	0.3919
chr17	81195210	2428643	0.0299	0.3159
chr18	78077248	2351324	0.0301	0.3905
chr19	59128983	1803846	0.0305	0.4479
chr20	63025520	1903450	0.0302	0.317
chr21	48129895	1176683	0.0244	0.2926
chr22	51304566	1084291	0.0211	0.278
chrMT	16571	180853	10.9138	9.9764
chrX	155270560	2684744	0.0173	0.2397
chrY	59373566	823262	0.0139	0.4493

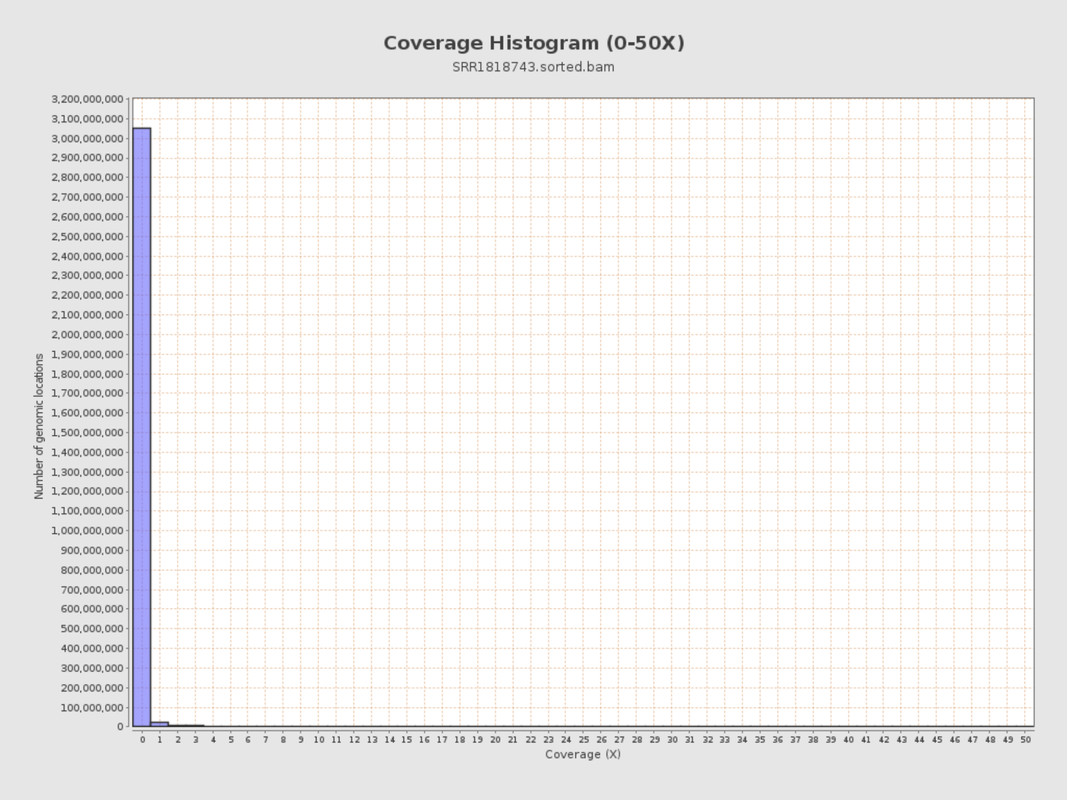
3. Results : Coverage across reference



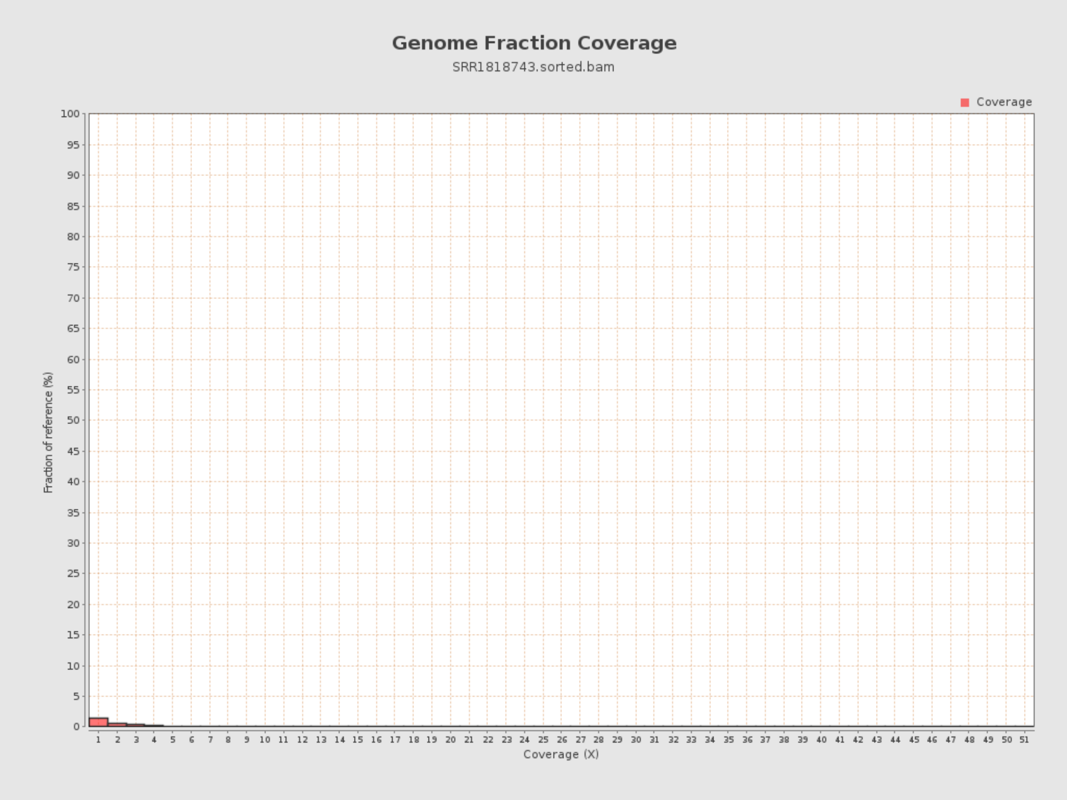
4. Results : Coverage Histogram



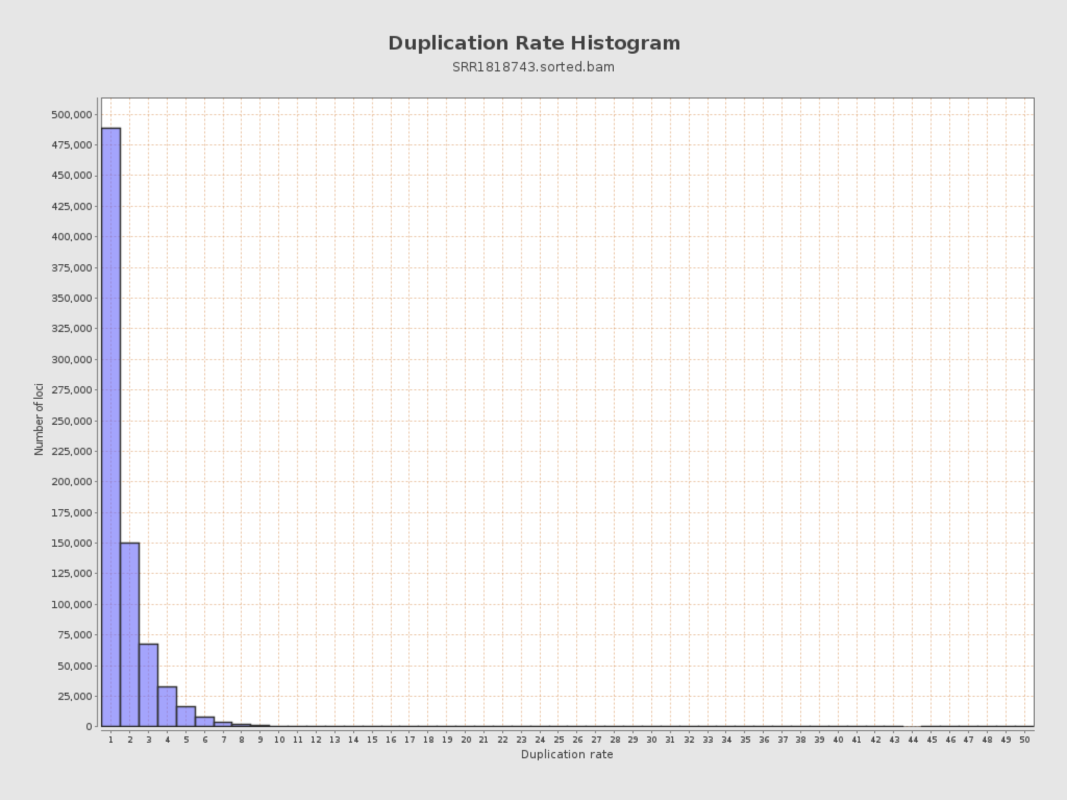
5. Results : Coverage Histogram (0-50X)



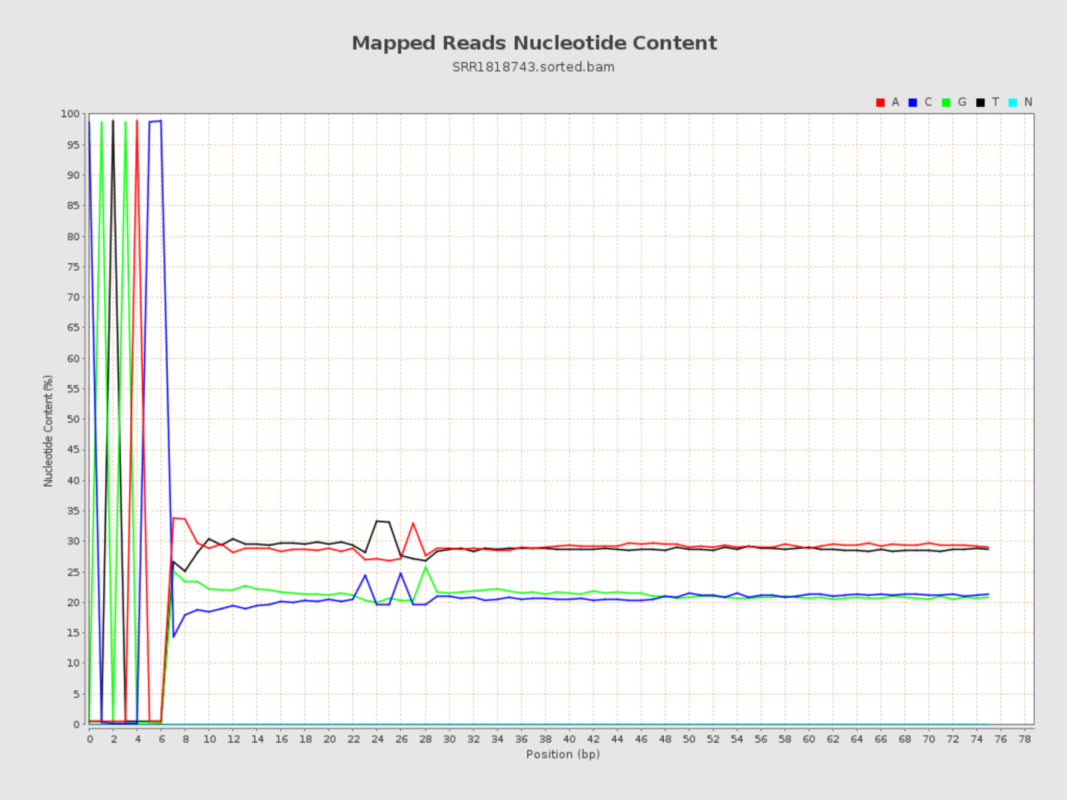
6. Results : Genome Fraction Coverage



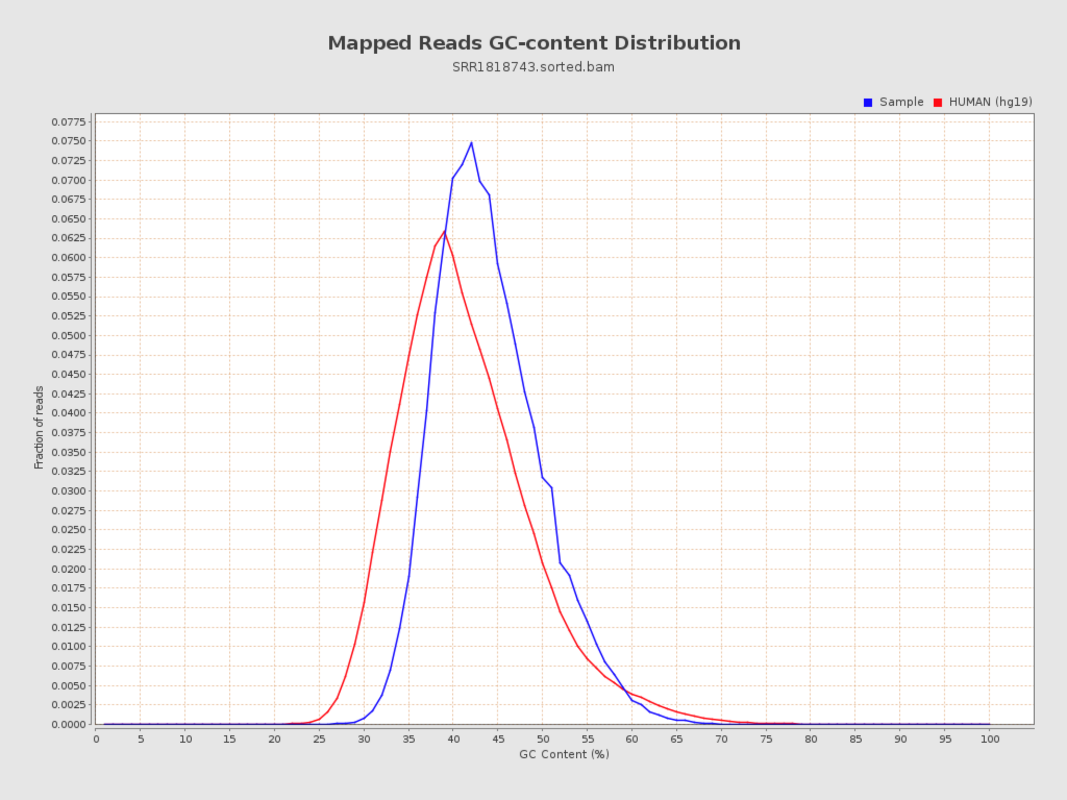
7. Results : Duplication Rate Histogram



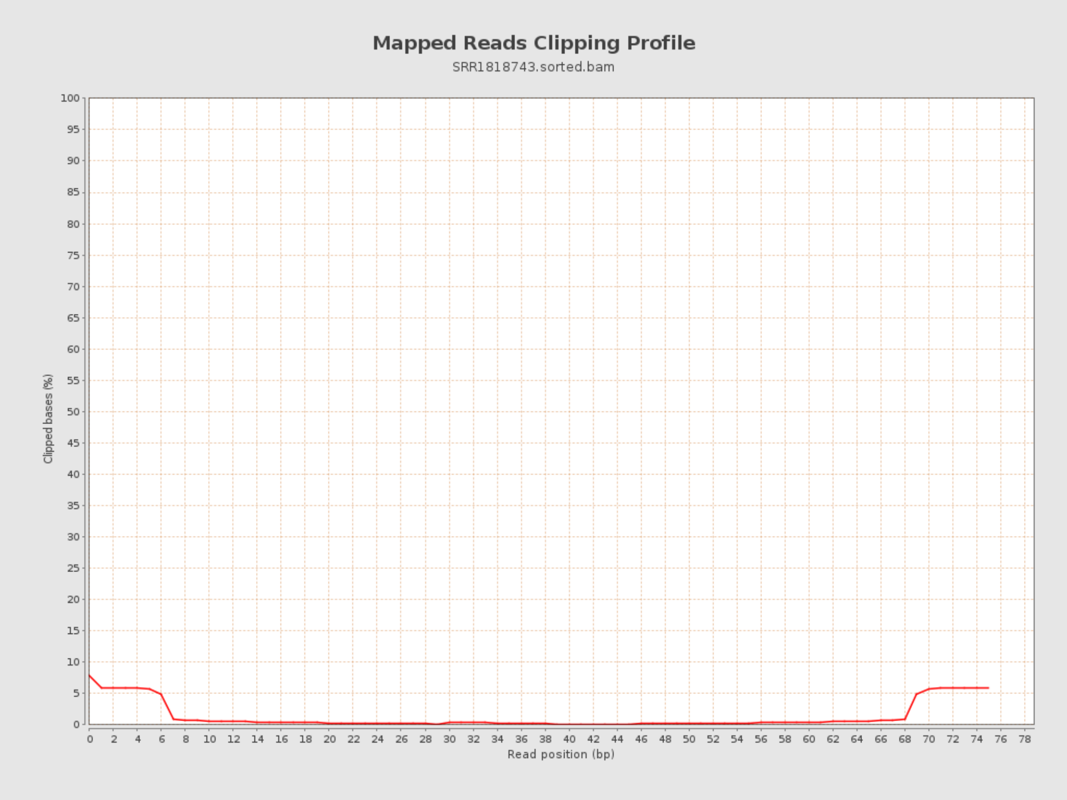
8. Results : Mapped Reads Nucleotide Content



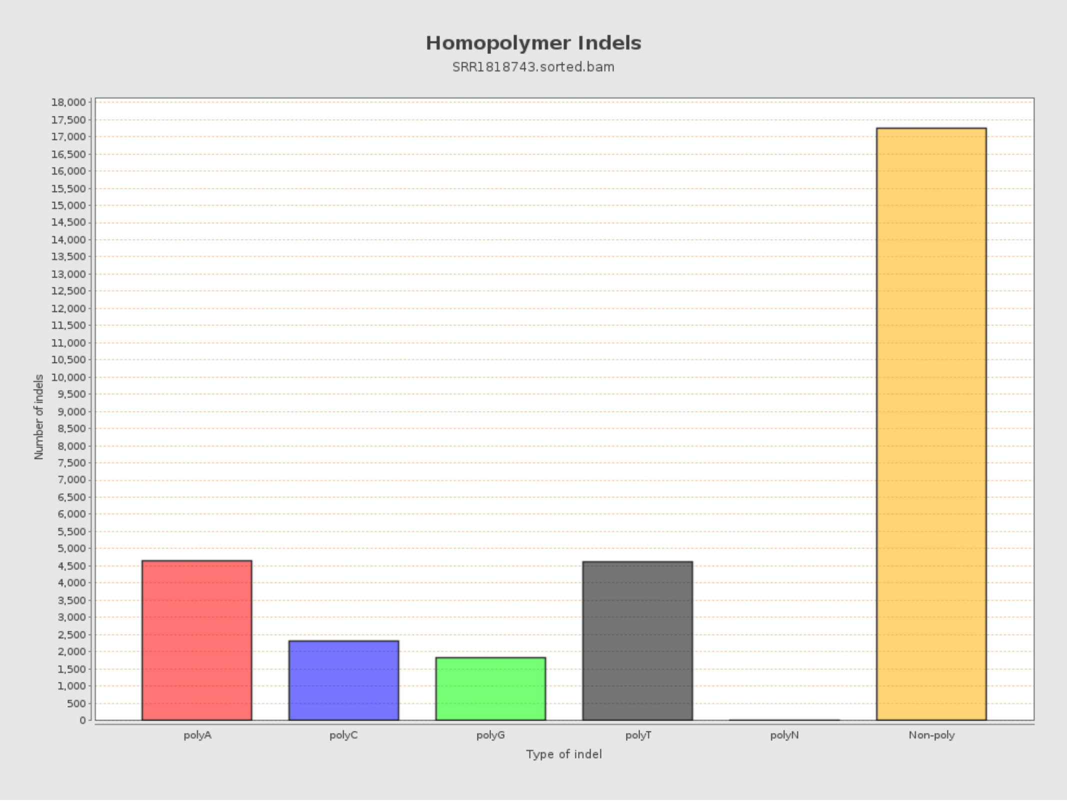
9. Results : Mapped Reads GC-content Distribution



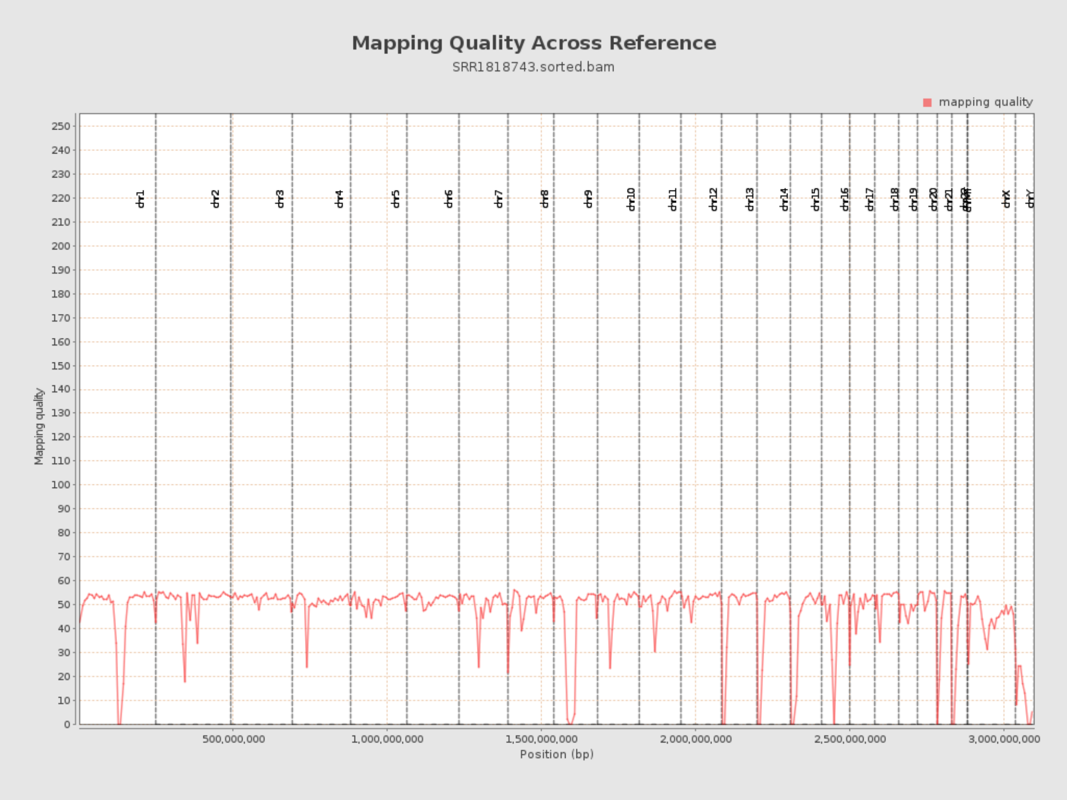
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram