Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:23:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818744.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_SRR1818744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:23:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,447,429
Mapped reads	1,228,160 / 84.85%
Unmapped reads	219,269 / 15.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,446 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	428,008 / 29.57%
Duplication rate	30.93%
Clipped reads	1,225,000 / 84.63%

2.2. ACGT Content

Number/percentage of A's	23,246,088 / 27.86%
Number/percentage of C's	17,027,845 / 20.41%
Number/percentage of T's	24,970,666 / 29.93%
Number/percentage of G's	18,176,867 / 21.79%
Number/percentage of N's	4,951 / 0.01%
GC Percentage	42.2%

2.3. Coverage

Mean	0.027

Standard Deviation	0.3297

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

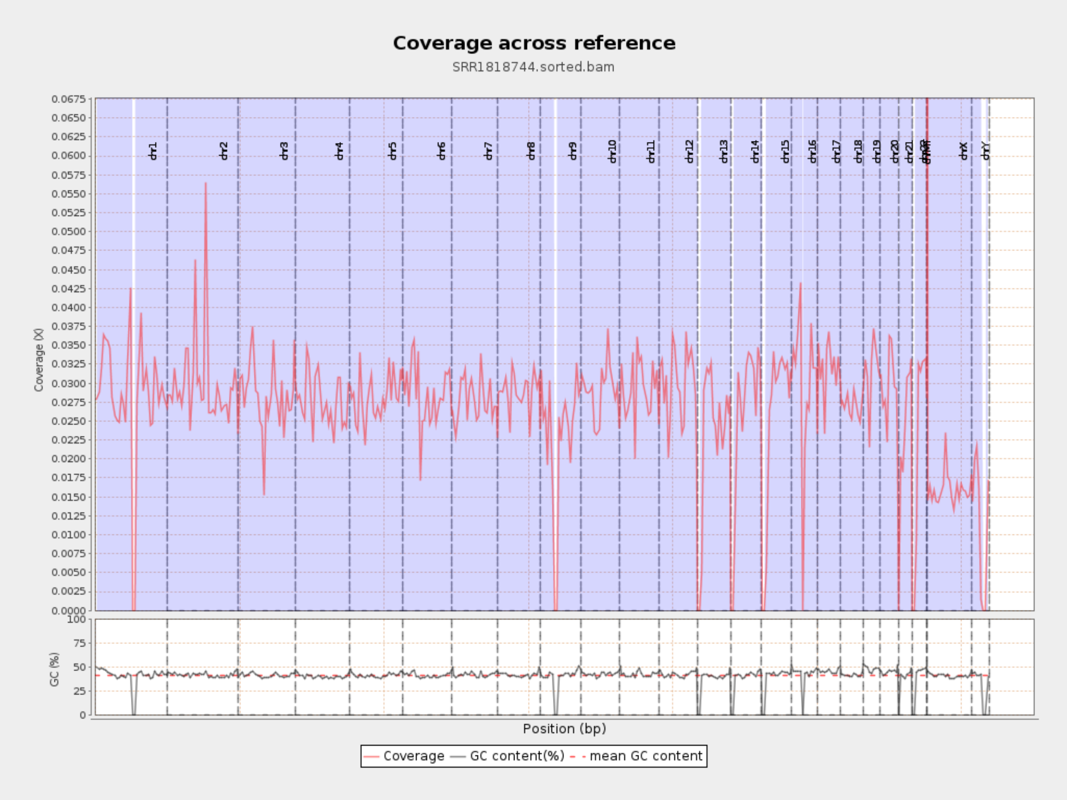
General error rate	0.52%
Mismatches	414,962
Insertions	10,007
Mapped reads with at least one insertion	0.8%
Deletions	21,596
Mapped reads with at least one deletion	1.74%
Homopolymer indels	41.56%

2.6. Chromosome stats

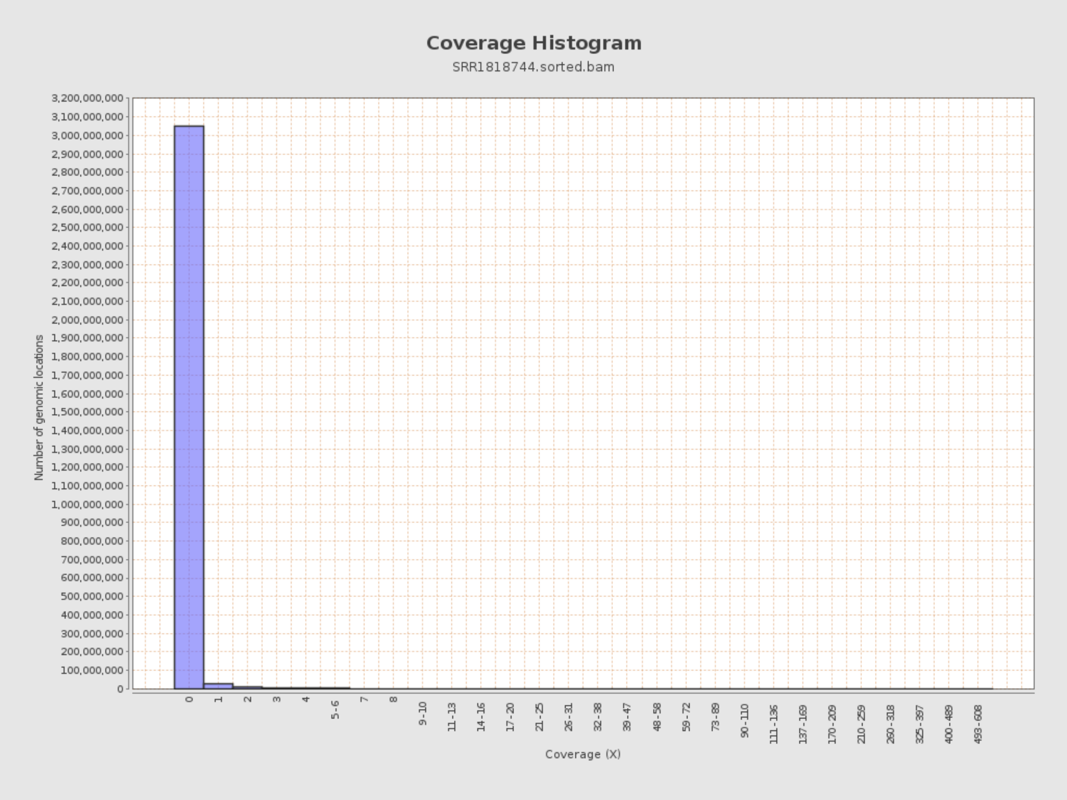
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7063009	0.0283	0.4175
chr2	243199373	7312308	0.0301	0.512
chr3	198022430	5591591	0.0282	0.2693
chr4	191154276	5285643	0.0277	0.2839
chr5	180915260	5081156	0.0281	0.2749
chr6	171115067	4879617	0.0285	0.2851
chr7	159138663	4428766	0.0278	0.2935

chr8	146364022	4235995	0.0289	0.293
chr9	141213431	3206366	0.0227	0.2863
chr10	135534747	3944895	0.0291	0.3443
chr11	135006516	3974186	0.0294	0.289
chr12	133851895	4006554	0.0299	0.2905
chr13	115169878	2592400	0.0225	0.2366
chr14	107349540	2724466	0.0254	0.2749
chr15	102531392	2525966	0.0246	0.2501
chr16	90354753	2663756	0.0295	0.3705
chr17	81195210	2603988	0.0321	0.2914
chr18	78077248	2102396	0.0269	0.3446
chr19	59128983	1867095	0.0316	0.3831
chr20	63025520	1843346	0.0292	0.2895
chr21	48129895	1127276	0.0234	0.2625
chr22	51304566	1135284	0.0221	0.2476
chrMT	16571	110525	6.6698	5.9819
chrX	155270560	2486838	0.016	0.212
chrY	59373566	667898	0.0112	0.5364

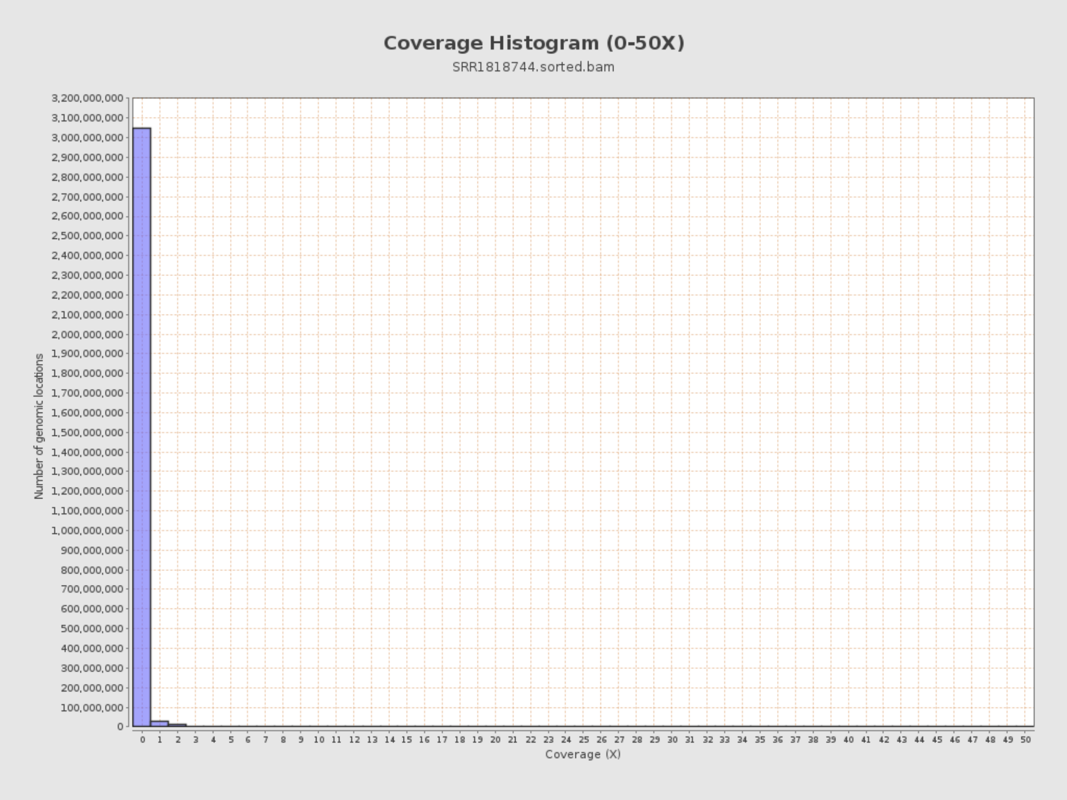
3. Results : Coverage across reference



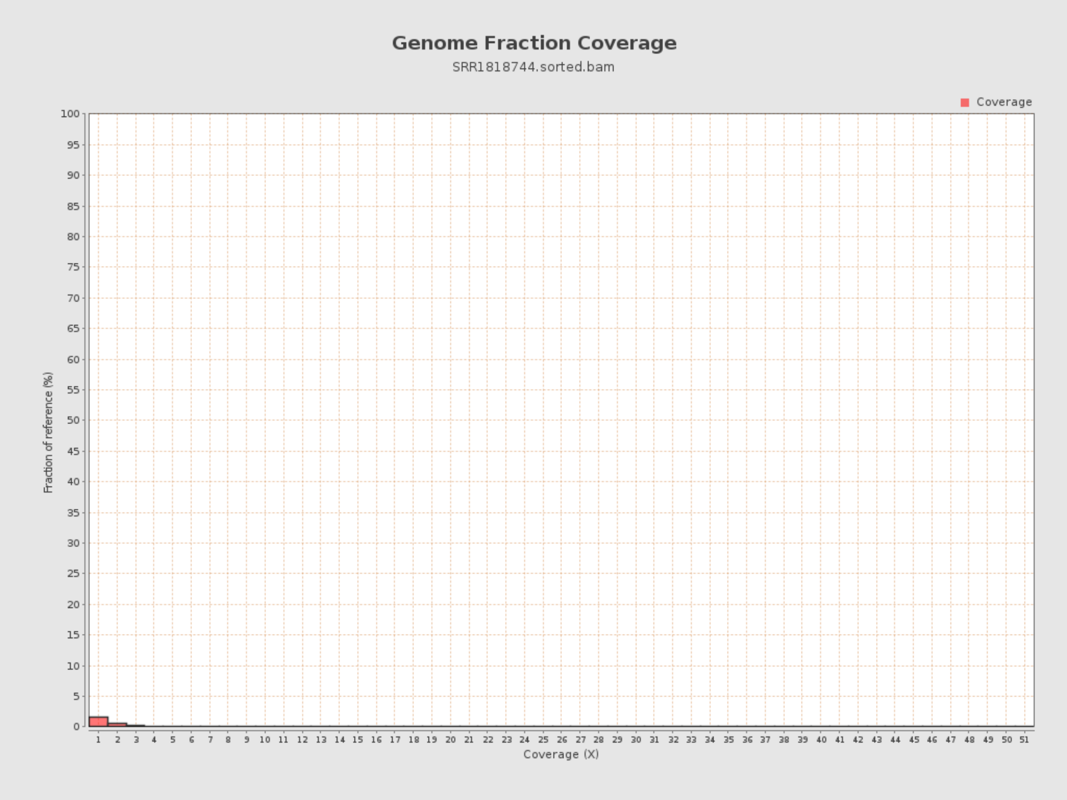
4. Results : Coverage Histogram



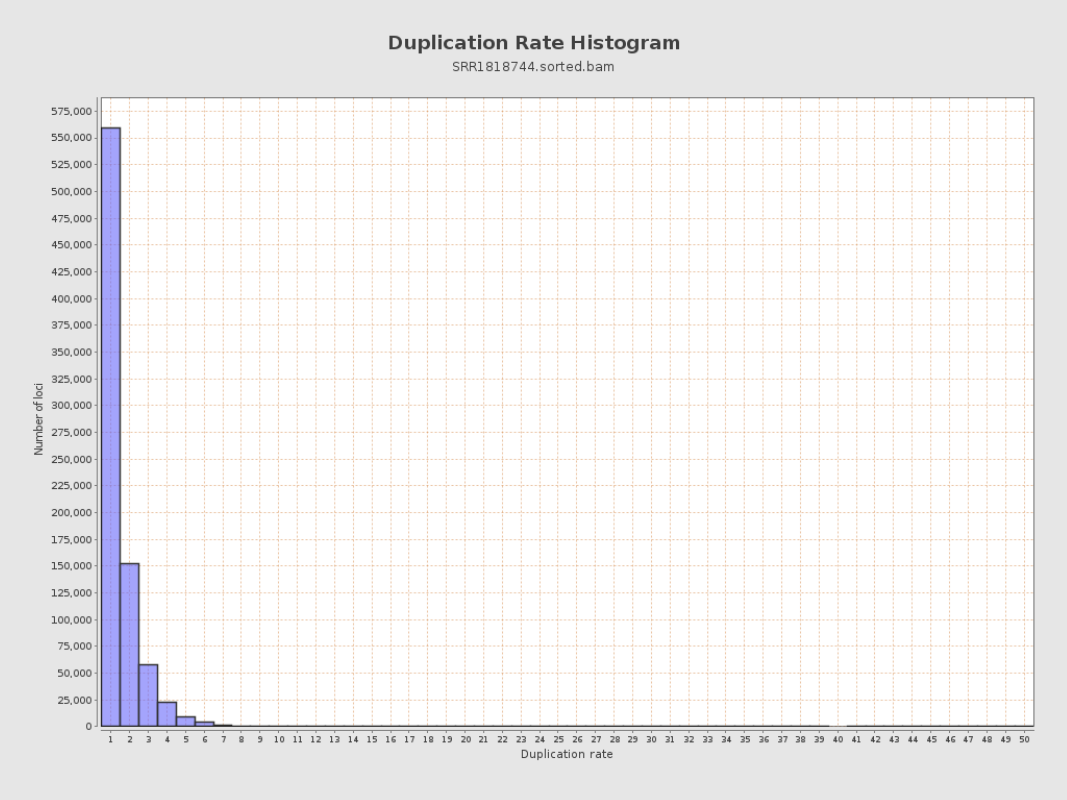
5. Results : Coverage Histogram (0-50X)



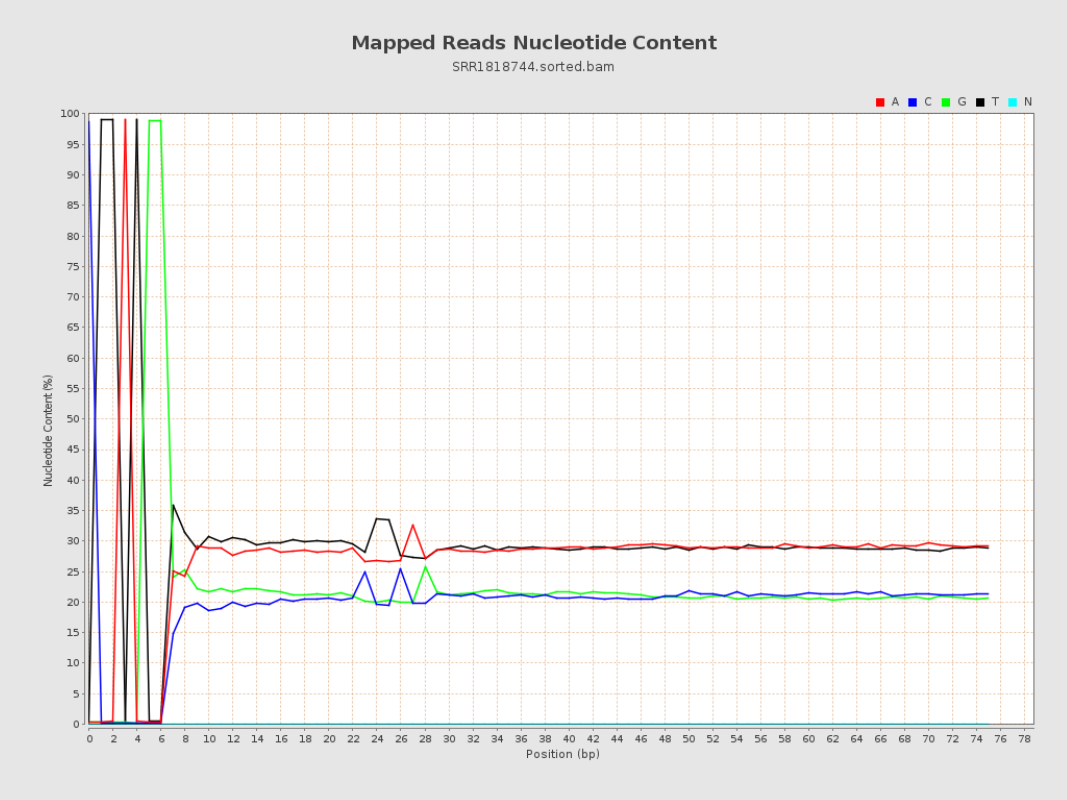
6. Results : Genome Fraction Coverage



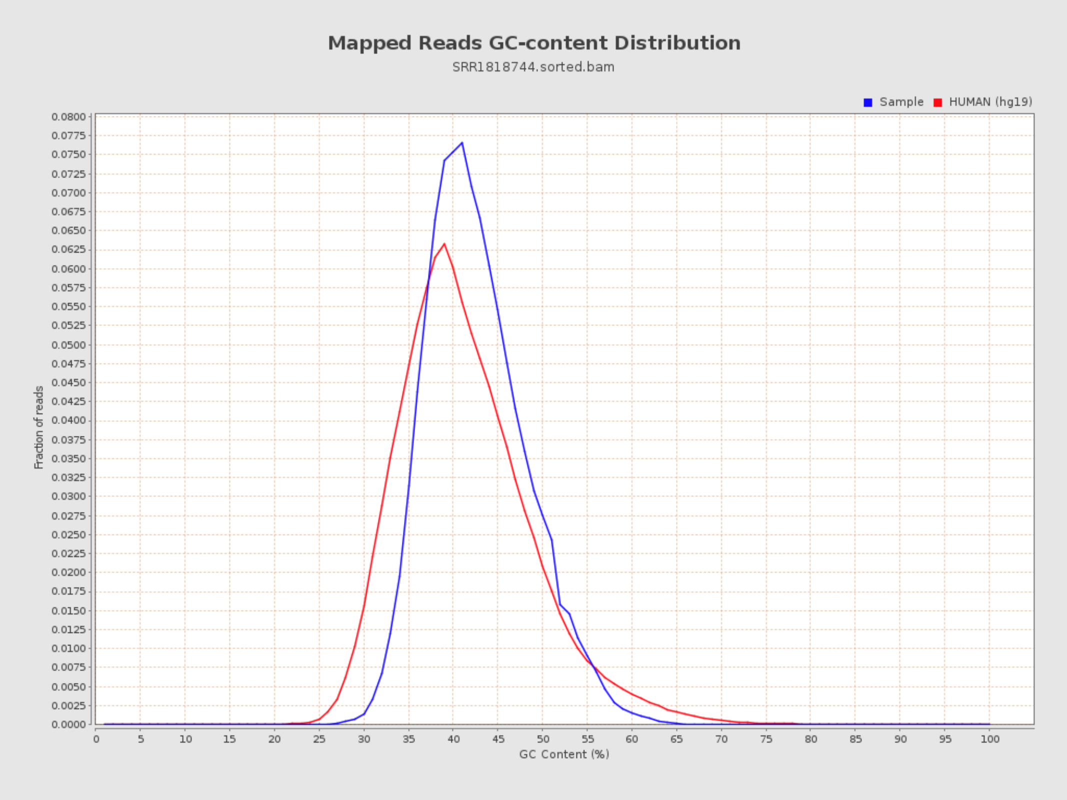
7. Results : Duplication Rate Histogram



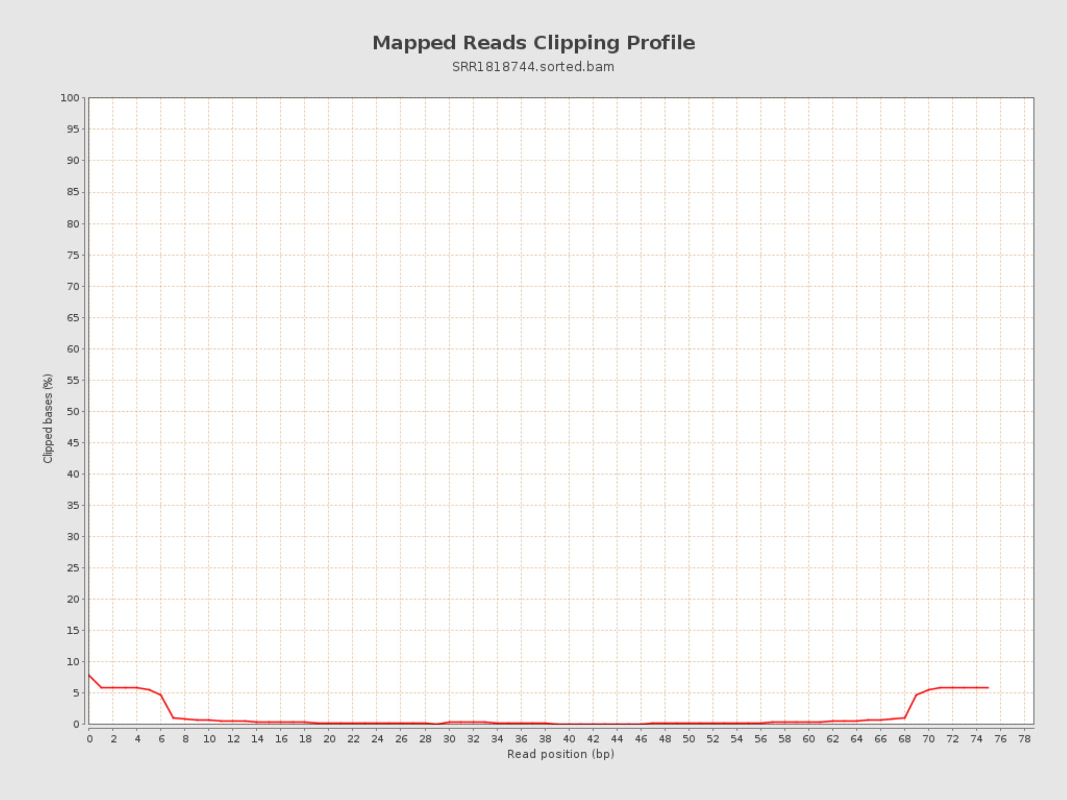
8. Results : Mapped Reads Nucleotide Content



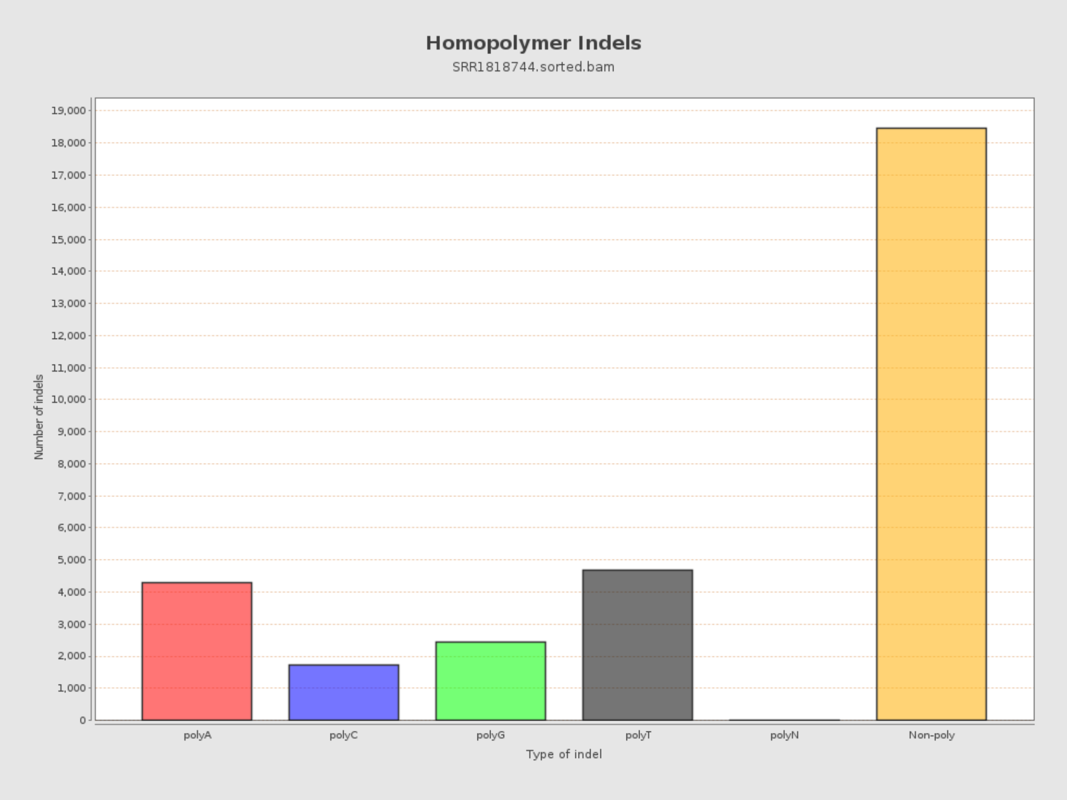
9. Results : Mapped Reads GC-content Distribution



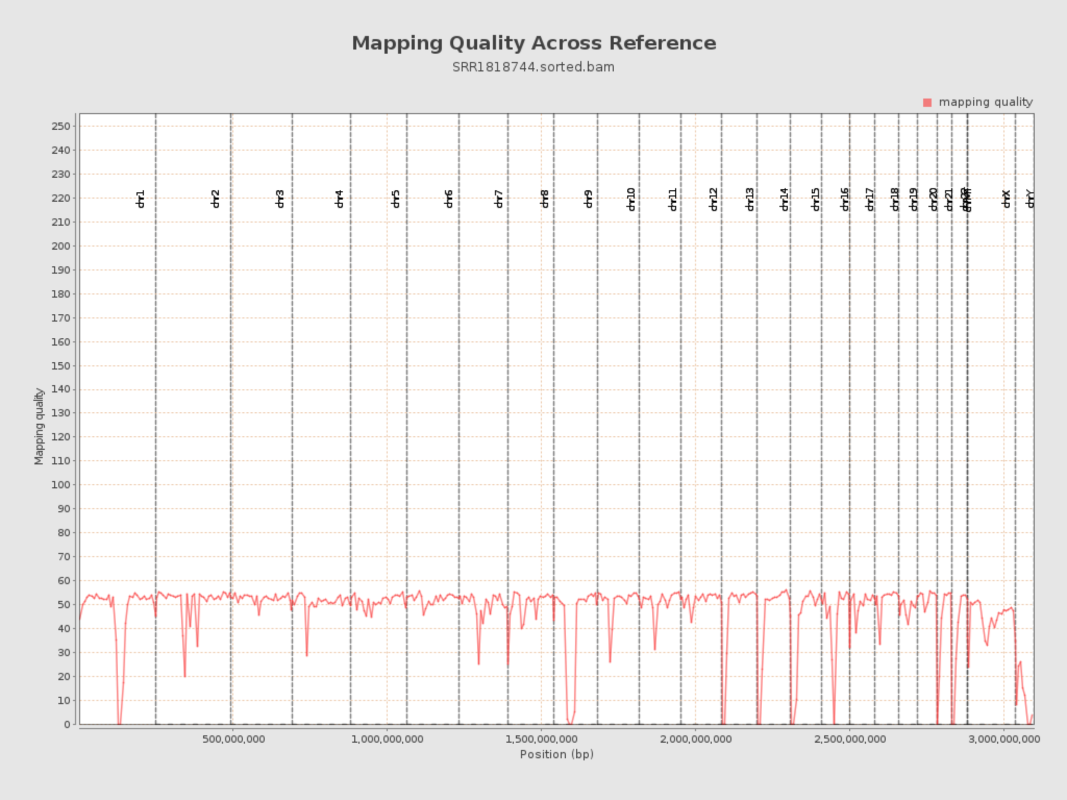
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram