Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:05:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818752.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_SRR1818752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:05:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,647,534
Mapped reads	1,359,507 / 82.52%
Unmapped reads	288,027 / 17.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,922 / 0.6%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	451,267 / 27.39%
Duplication rate	29.26%
Clipped reads	1,358,726 / 82.47%

2.2. ACGT Content

Number/percentage of A's	26,835,676 / 29.07%
Number/percentage of C's	19,347,878 / 20.96%
Number/percentage of T's	26,932,222 / 29.18%
Number/percentage of G's	19,183,744 / 20.78%
Number/percentage of N's	5,913 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.4068

2.4. Mapping Quality

Mean Mapping Quality	47.23

2.5. Mismatches and indels

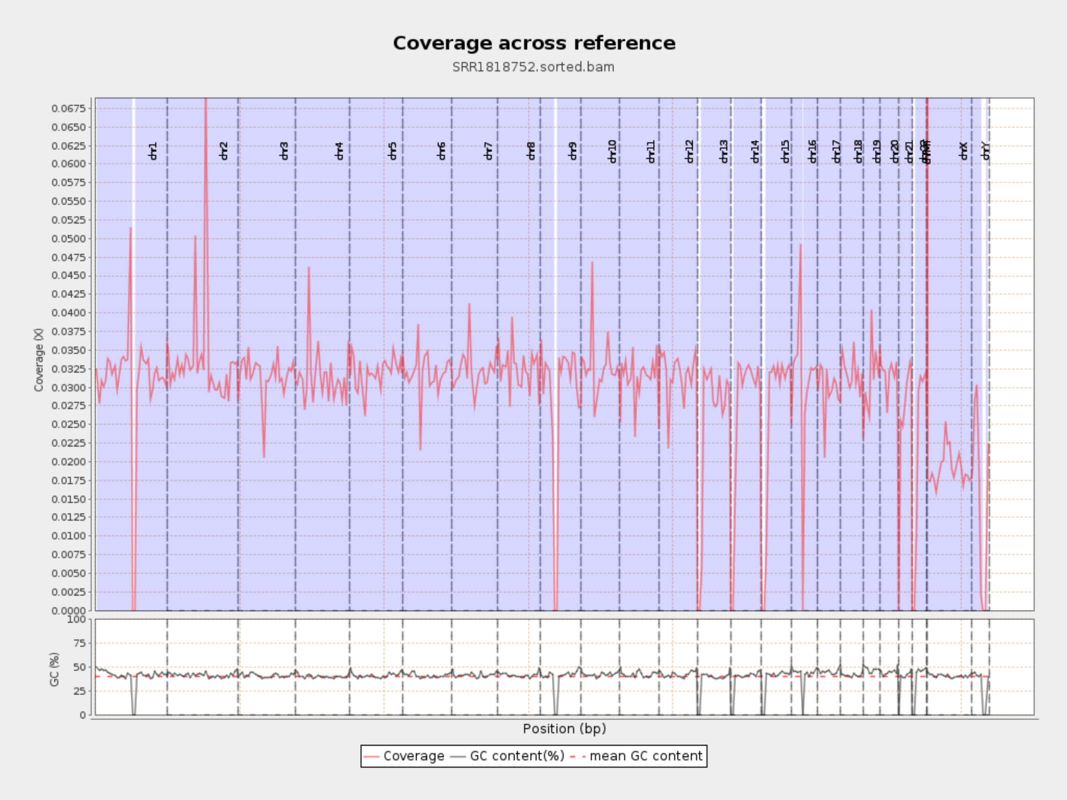
General error rate	0.55%
Mismatches	487,602
Insertions	11,158
Mapped reads with at least one insertion	0.81%
Deletions	25,344
Mapped reads with at least one deletion	1.85%
Homopolymer indels	39.87%

2.6. Chromosome stats

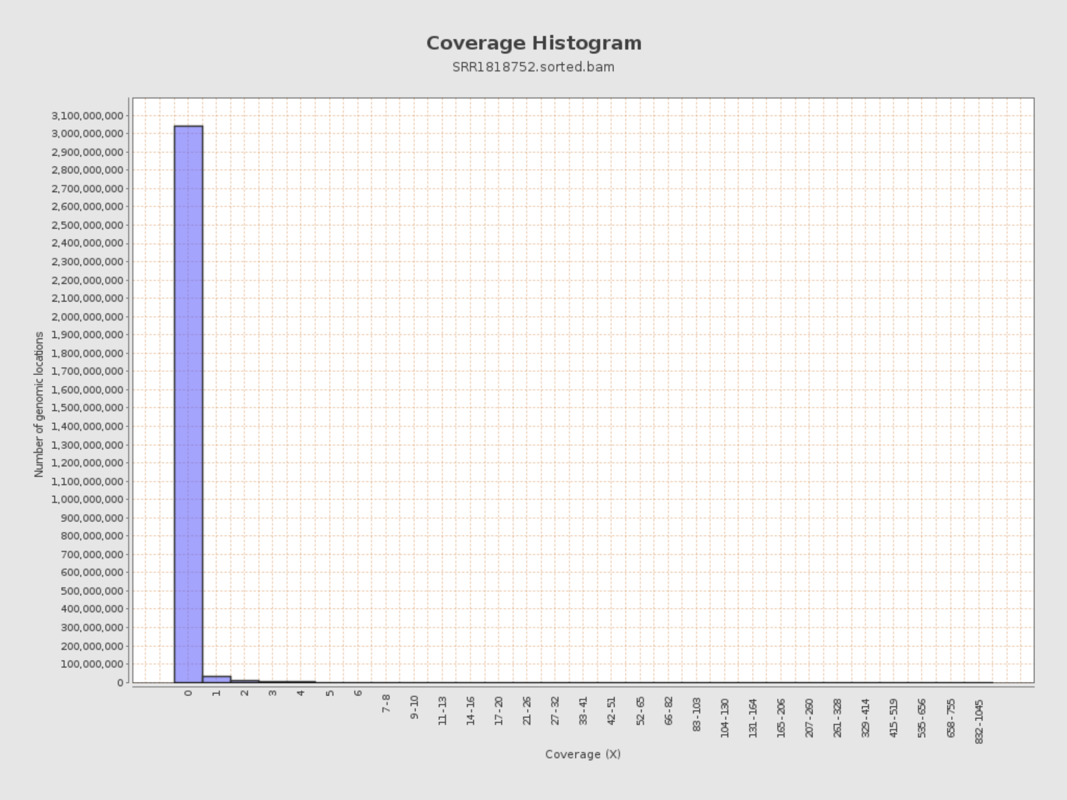
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7614314	0.0305	0.5621
chr2	243199373	8203556	0.0337	0.7316
chr3	198022430	6256159	0.0316	0.2712
chr4	191154276	6001396	0.0314	0.3251
chr5	180915260	5807100	0.0321	0.2903
chr6	171115067	5456666	0.0319	0.3181
chr7	159138663	5135721	0.0323	0.3641

chr8	146364022	4772311	0.0326	0.3128
chr9	141213431	4024046	0.0285	0.316
chr10	135534747	4447806	0.0328	0.4531
chr11	135006516	4259231	0.0315	0.3026
chr12	133851895	4253428	0.0318	0.299
chr13	115169878	2863455	0.0249	0.2416
chr14	107349540	2827915	0.0263	0.2882
chr15	102531392	2644881	0.0258	0.2447
chr16	90354753	2731660	0.0302	0.5126
chr17	81195210	2404900	0.0296	0.2788
chr18	78077248	2500045	0.032	0.3978
chr19	59128983	1847042	0.0312	0.4552
chr20	63025520	1980941	0.0314	0.2939
chr21	48129895	1262216	0.0262	0.2677
chr22	51304566	1084618	0.0211	0.2616
chrMT	16571	98987	5.9735	6.0293
chrX	155270560	2975017	0.0192	0.2568
chrY	59373566	893682	0.0151	0.7579

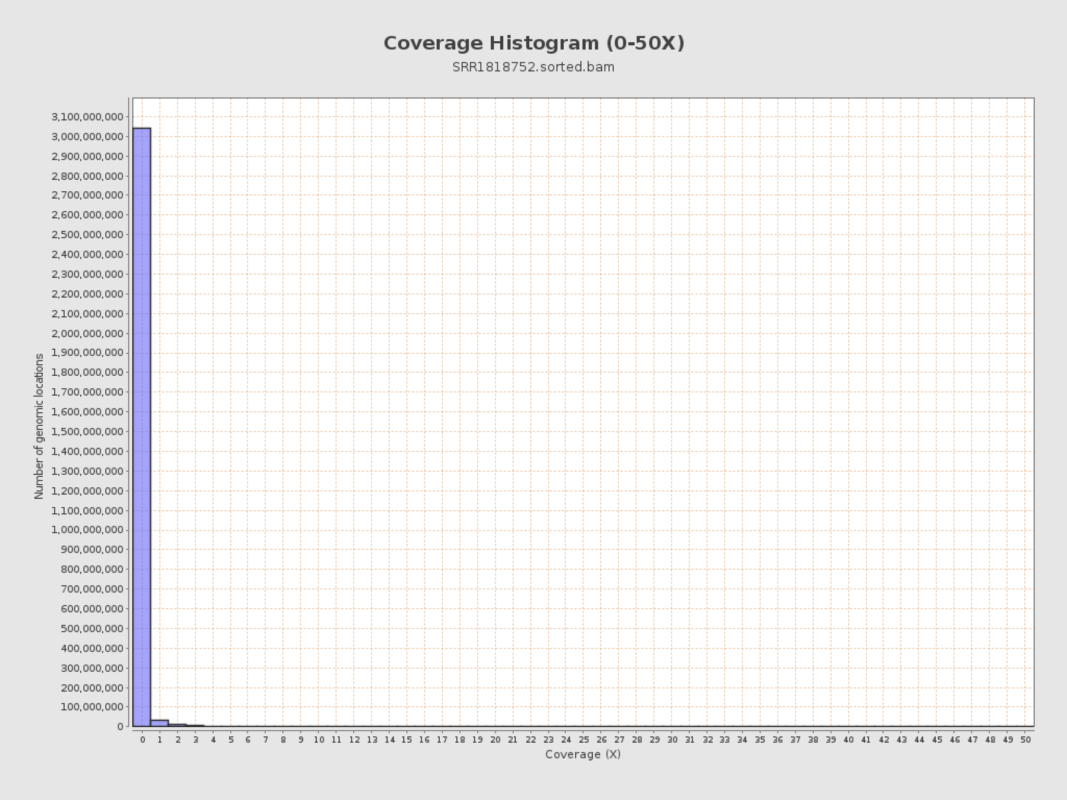
3. Results : Coverage across reference



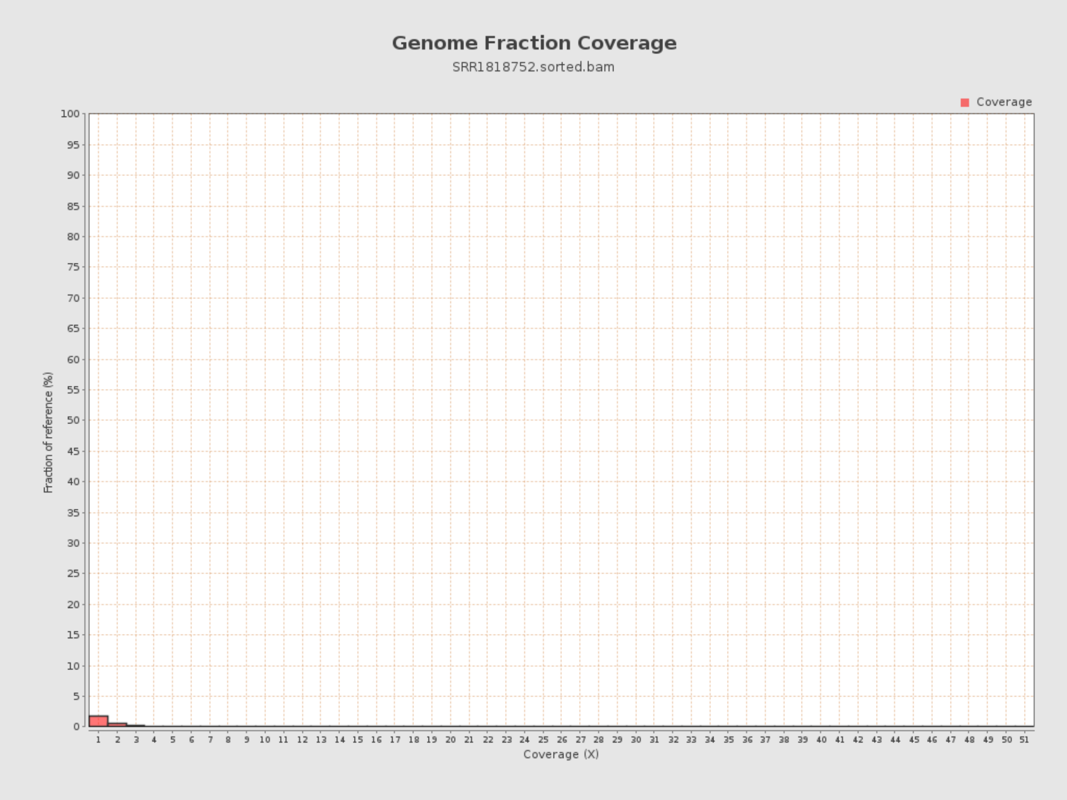
4. Results : Coverage Histogram



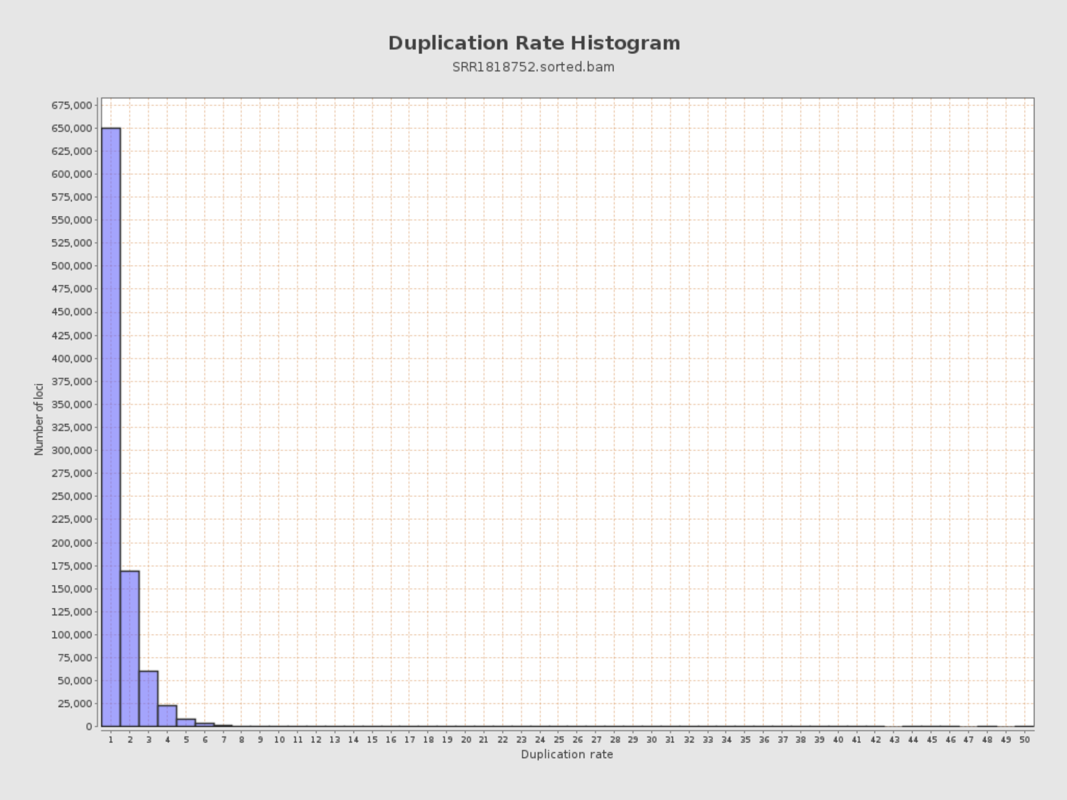
5. Results : Coverage Histogram (0-50X)



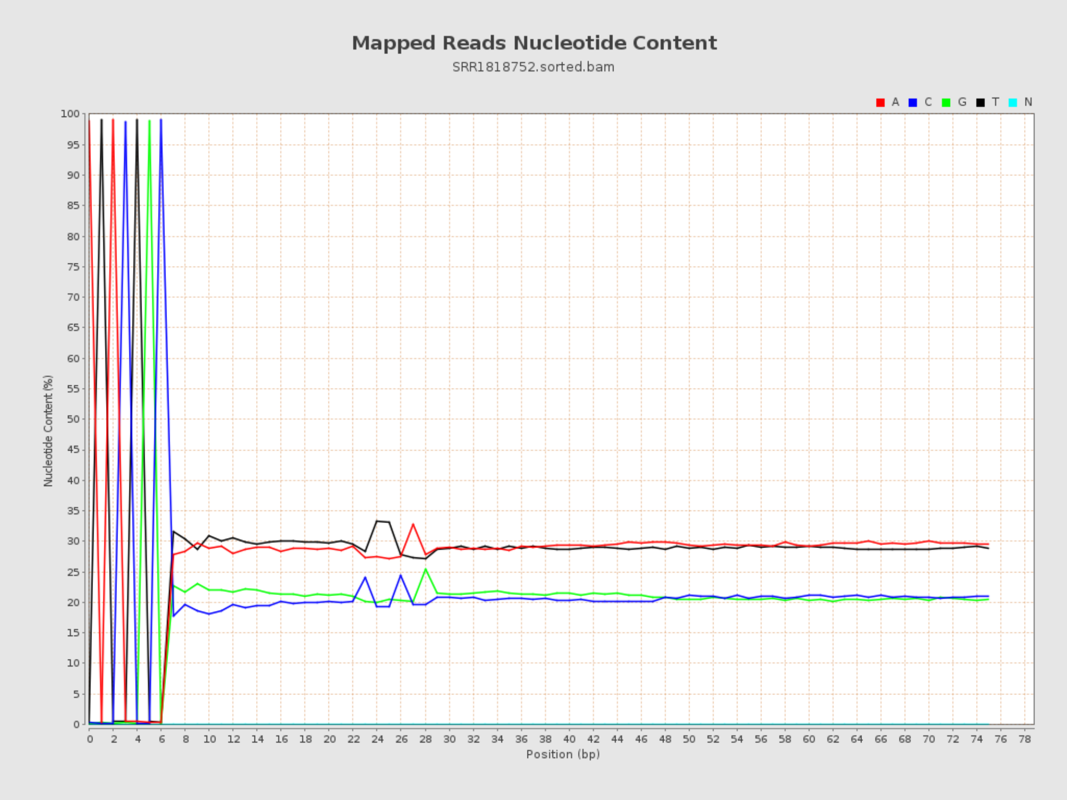
6. Results : Genome Fraction Coverage



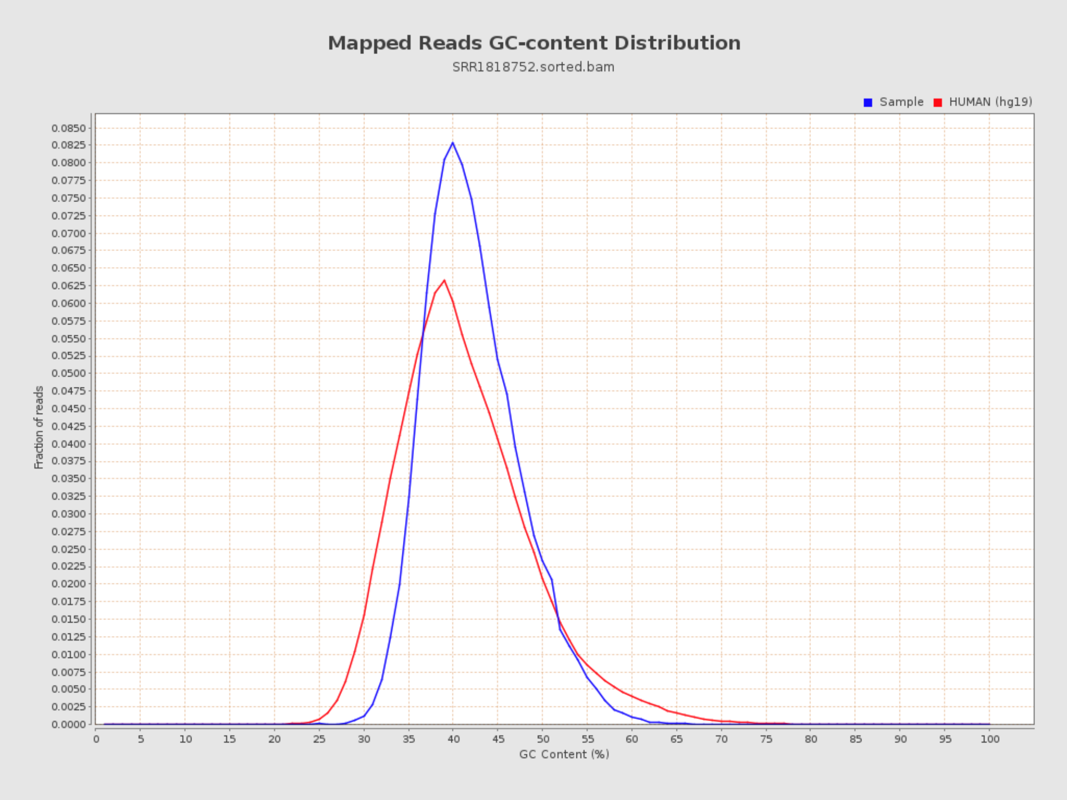
7. Results : Duplication Rate Histogram



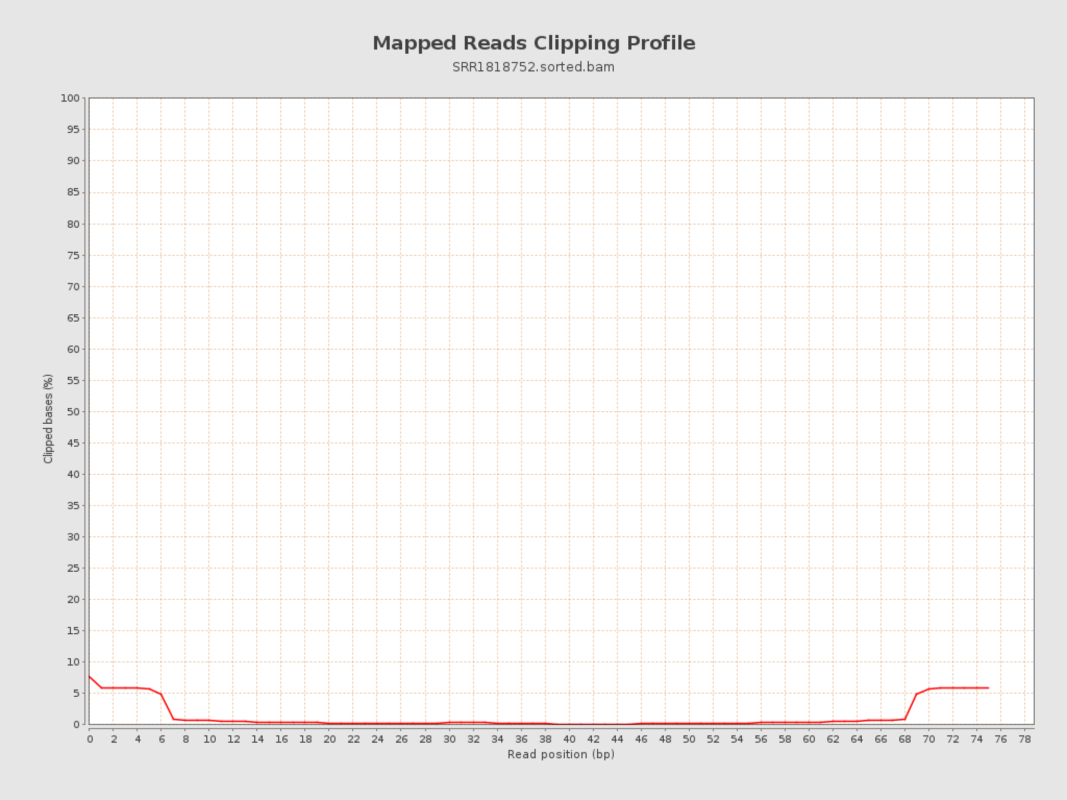
8. Results : Mapped Reads Nucleotide Content



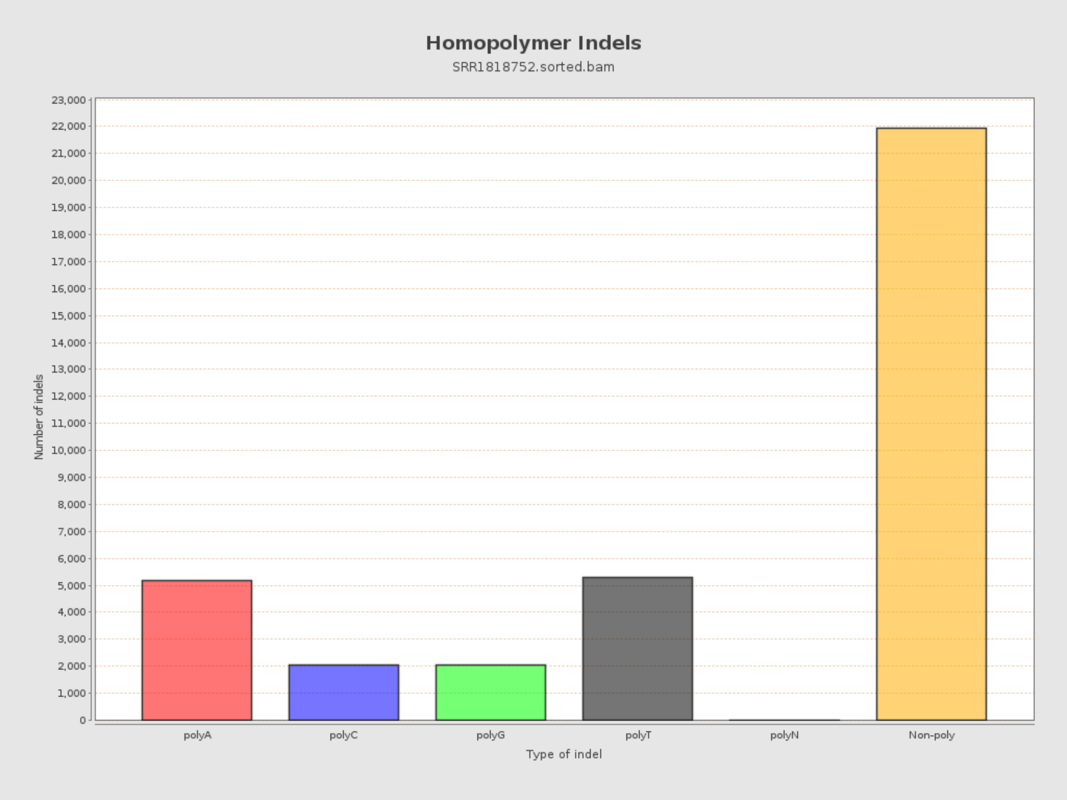
9. Results : Mapped Reads GC-content Distribution



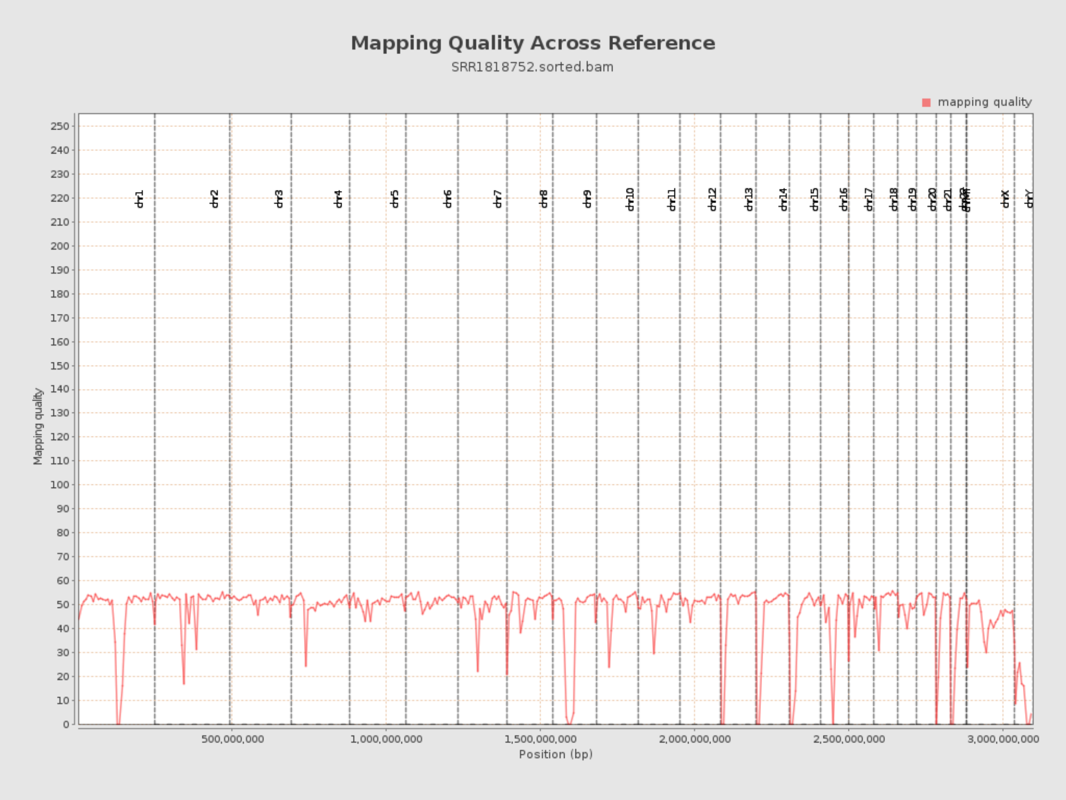
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram