Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:08:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818794.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_SRR1818794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:08:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,152,292
Mapped reads	3,075,726 / 97.57%
Unmapped reads	76,566 / 2.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,424 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,539,699 / 48.84%
Duplication rate	42.28%
Clipped reads	3,055,555 / 96.93%

2.2. ACGT Content

Number/percentage of A's	60,476,618 / 28.92%
Number/percentage of C's	42,378,948 / 20.27%
Number/percentage of T's	59,368,374 / 28.39%
Number/percentage of G's	46,867,143 / 22.41%
Number/percentage of N's	12,847 / 0.01%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0676

Standard Deviation	0.8057

2.4. Mapping Quality

Mean Mapping Quality	47.48

2.5. Mismatches and indels

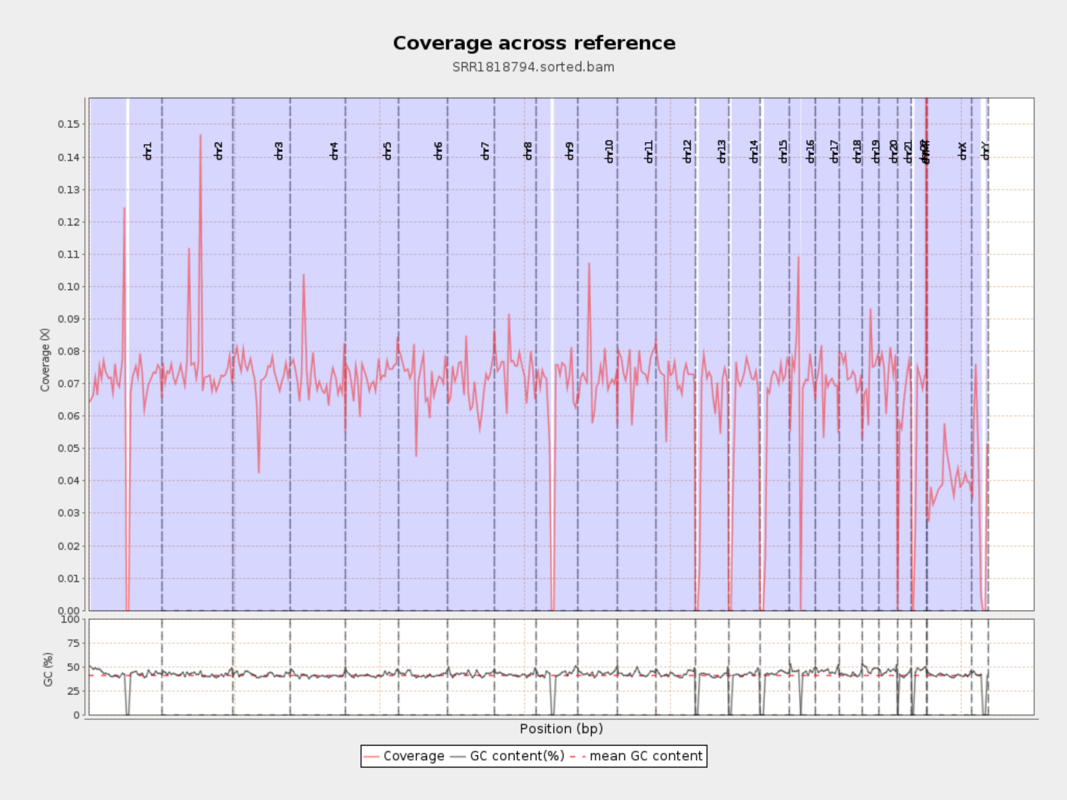
General error rate	0.54%
Mismatches	1,072,220
Insertions	28,281
Mapped reads with at least one insertion	0.91%
Deletions	54,663
Mapped reads with at least one deletion	1.76%
Homopolymer indels	39.38%

2.6. Chromosome stats

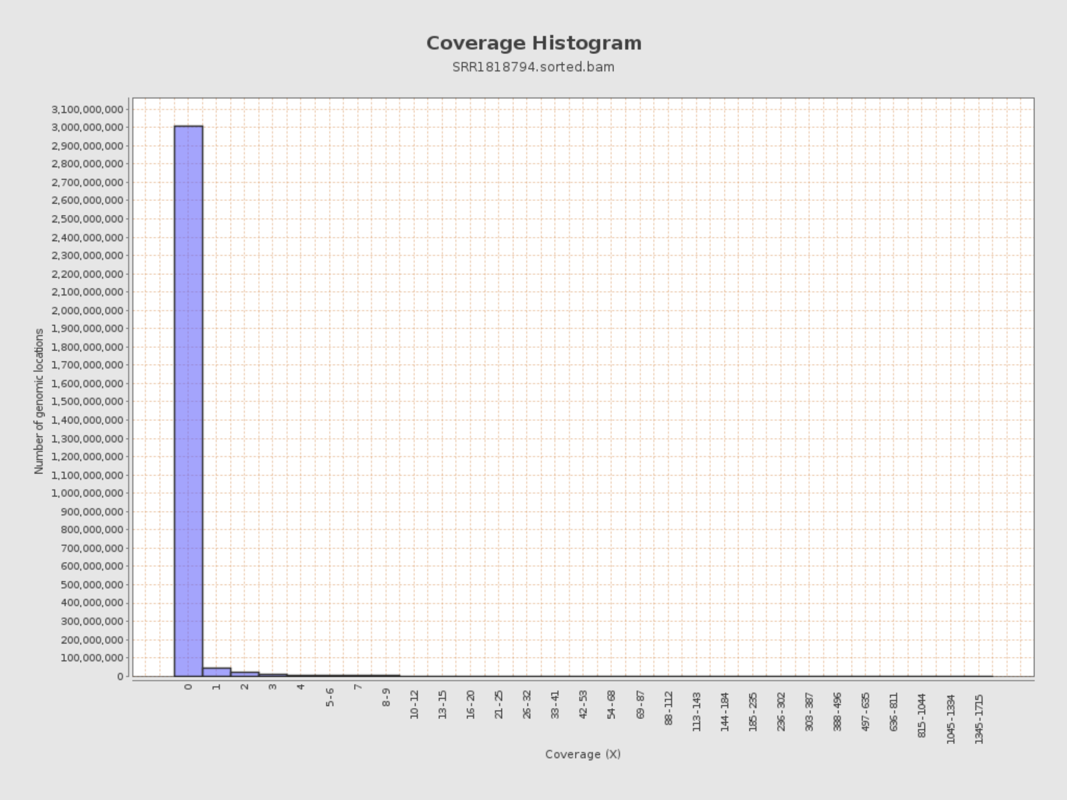
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17153173	0.0688	1.2817
chr2	243199373	18576131	0.0764	1.314
chr3	198022430	14406950	0.0728	0.5333
chr4	191154276	13858080	0.0725	0.6379
chr5	180915260	13071911	0.0723	0.5495
chr6	171115067	12245454	0.0716	0.6229
chr7	159138663	11094251	0.0697	0.6934

chr8	146364022	10975324	0.075	0.6523
chr9	141213431	8939293	0.0633	0.6505
chr10	135534747	9786622	0.0722	0.8301
chr11	135006516	10043334	0.0744	0.6348
chr12	133851895	9632987	0.072	0.5732
chr13	115169878	6721362	0.0584	0.4786
chr14	107349540	6535582	0.0609	0.5913
chr15	102531392	5927810	0.0578	0.4794
chr16	90354753	6321260	0.07	0.9145
chr17	81195210	5641938	0.0695	0.5758
chr18	78077248	5752678	0.0737	0.8982
chr19	59128983	4300938	0.0727	1.0997
chr20	63025520	4650942	0.0738	0.5843
chr21	48129895	2879521	0.0598	0.5272
chr22	51304566	2565450	0.05	0.506
chrMT	16571	15639	0.9438	2.0174
chrX	155270560	6124712	0.0394	0.5114
chrY	59373566	1971172	0.0332	1.428

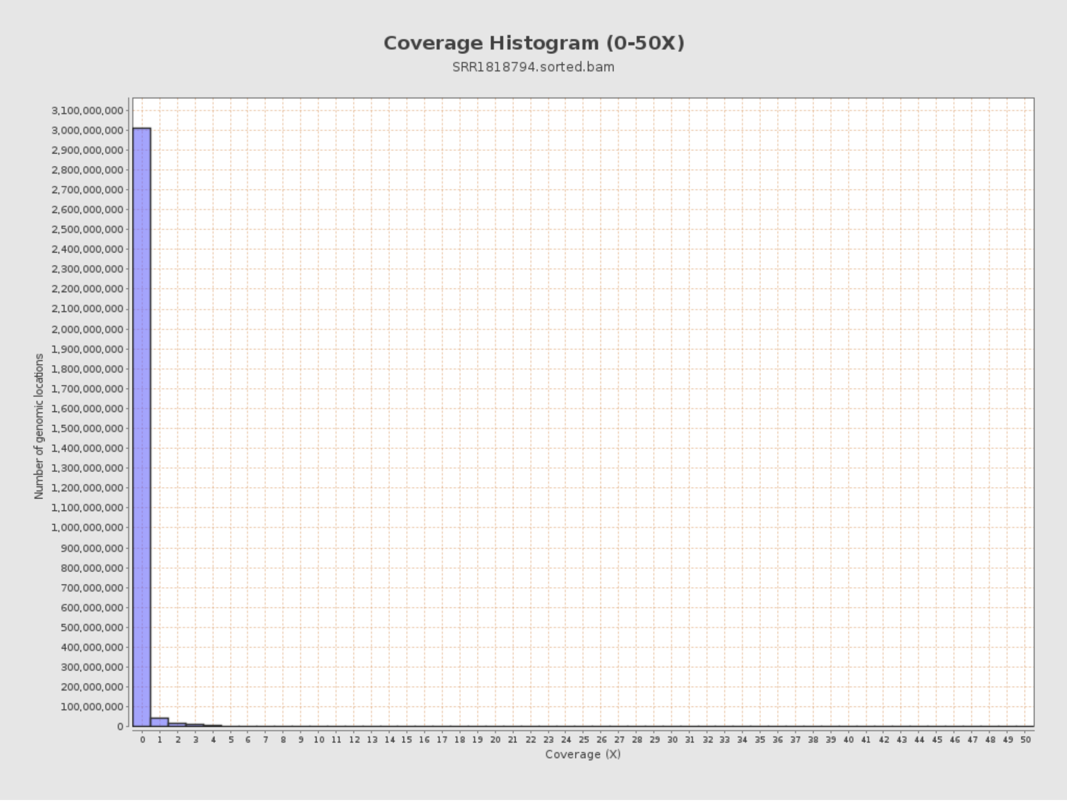
3. Results : Coverage across reference



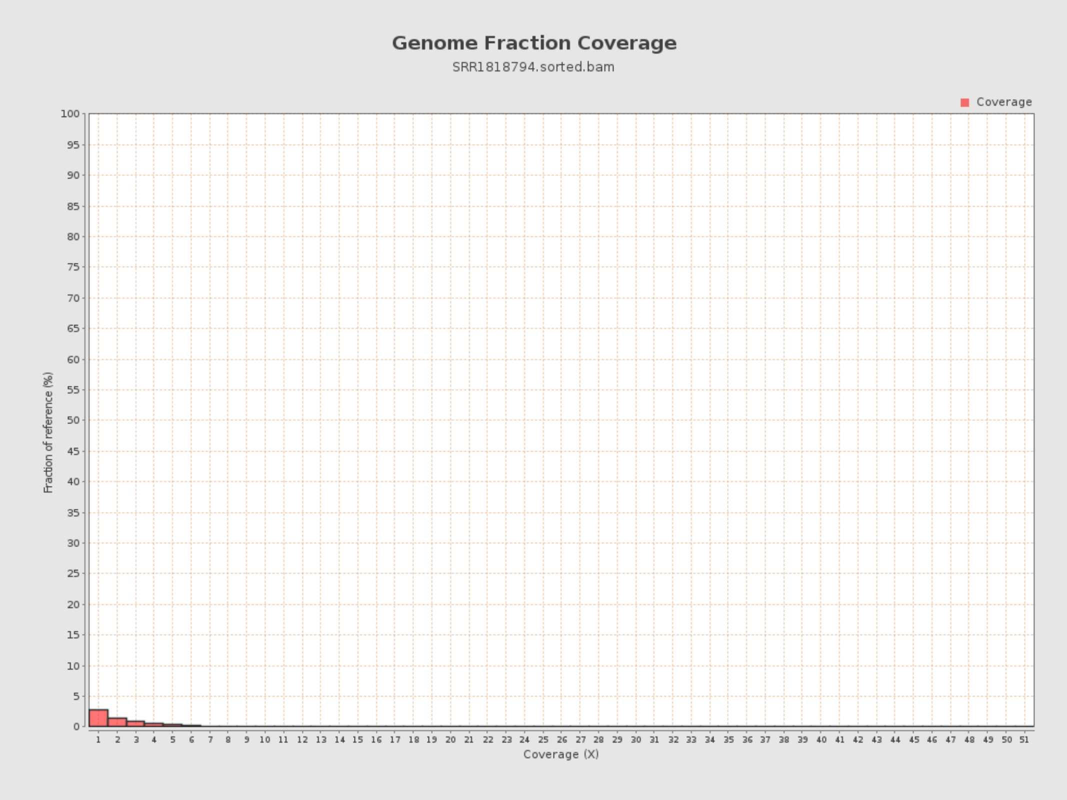
4. Results : Coverage Histogram



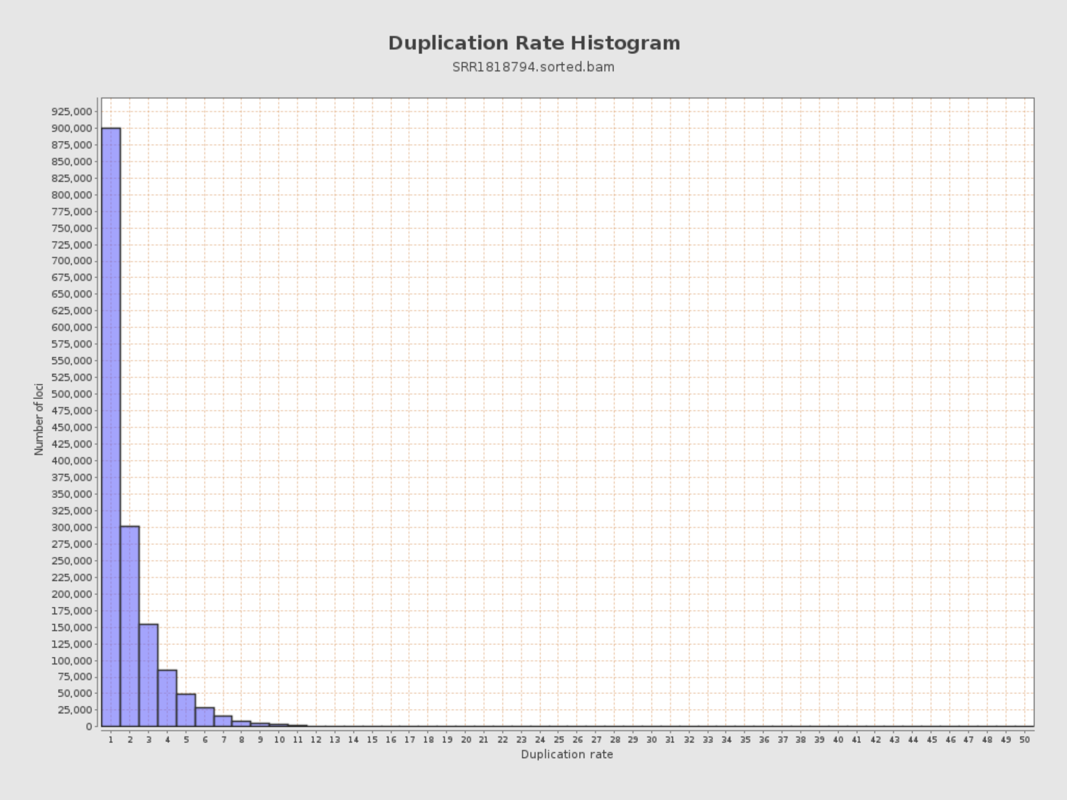
5. Results : Coverage Histogram (0-50X)



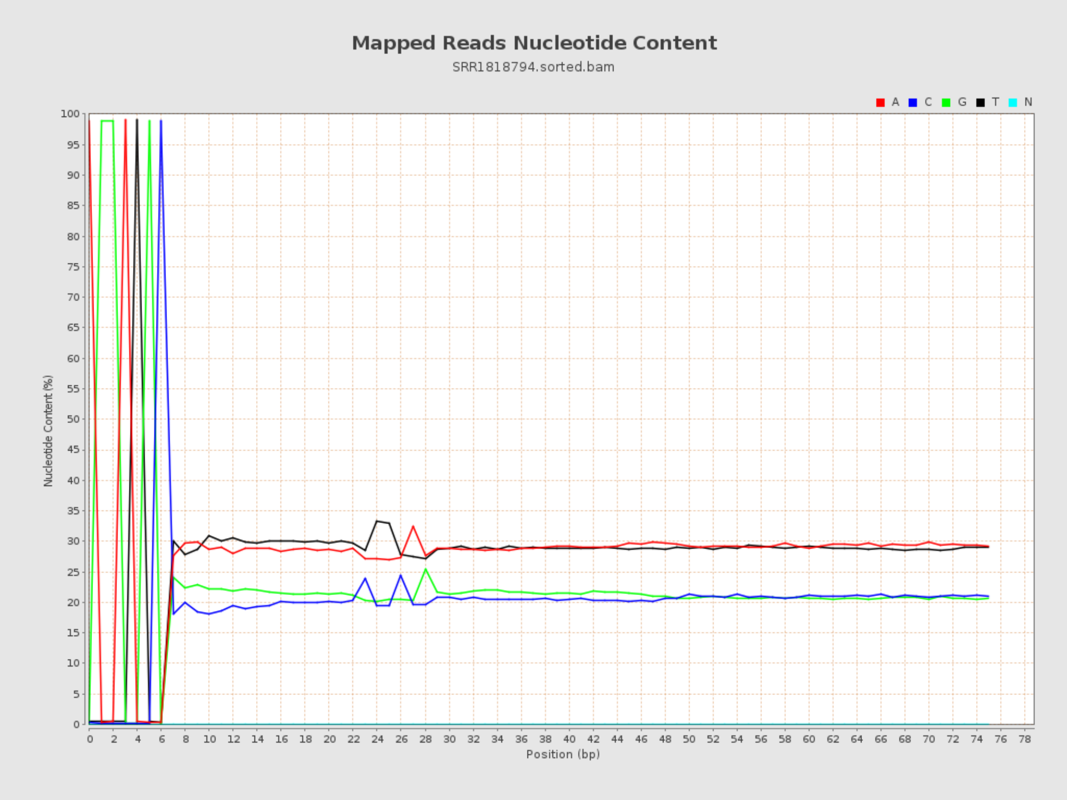
6. Results : Genome Fraction Coverage



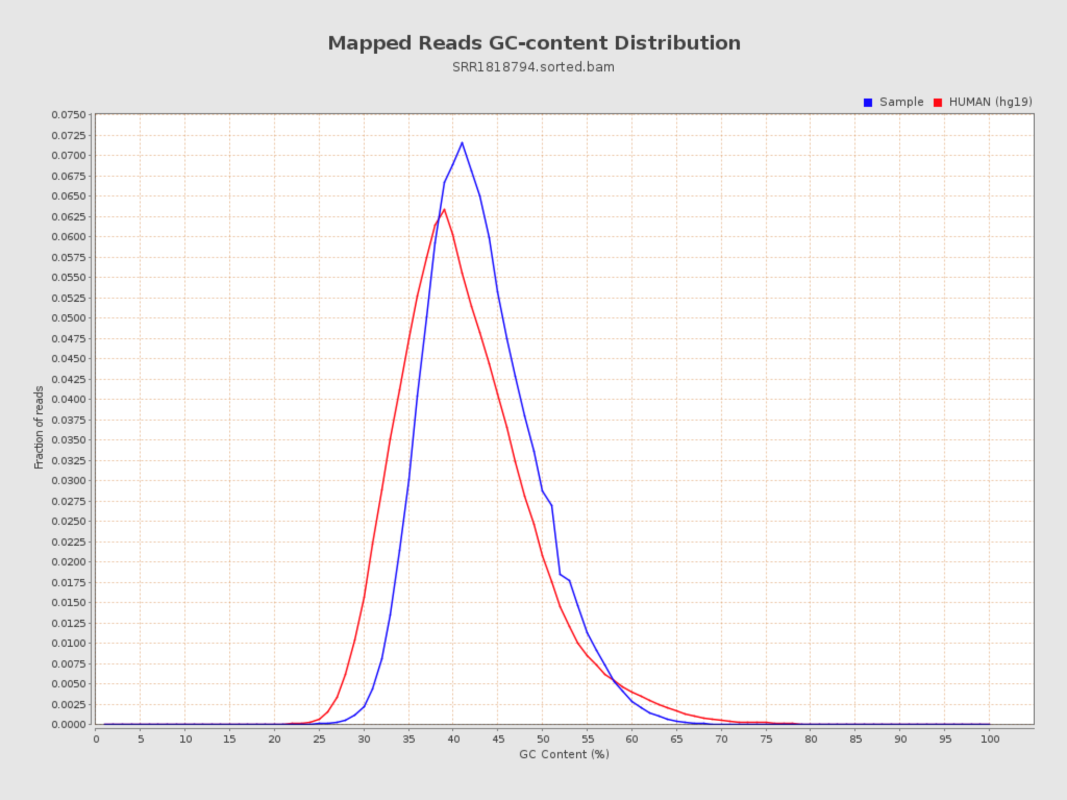
7. Results : Duplication Rate Histogram



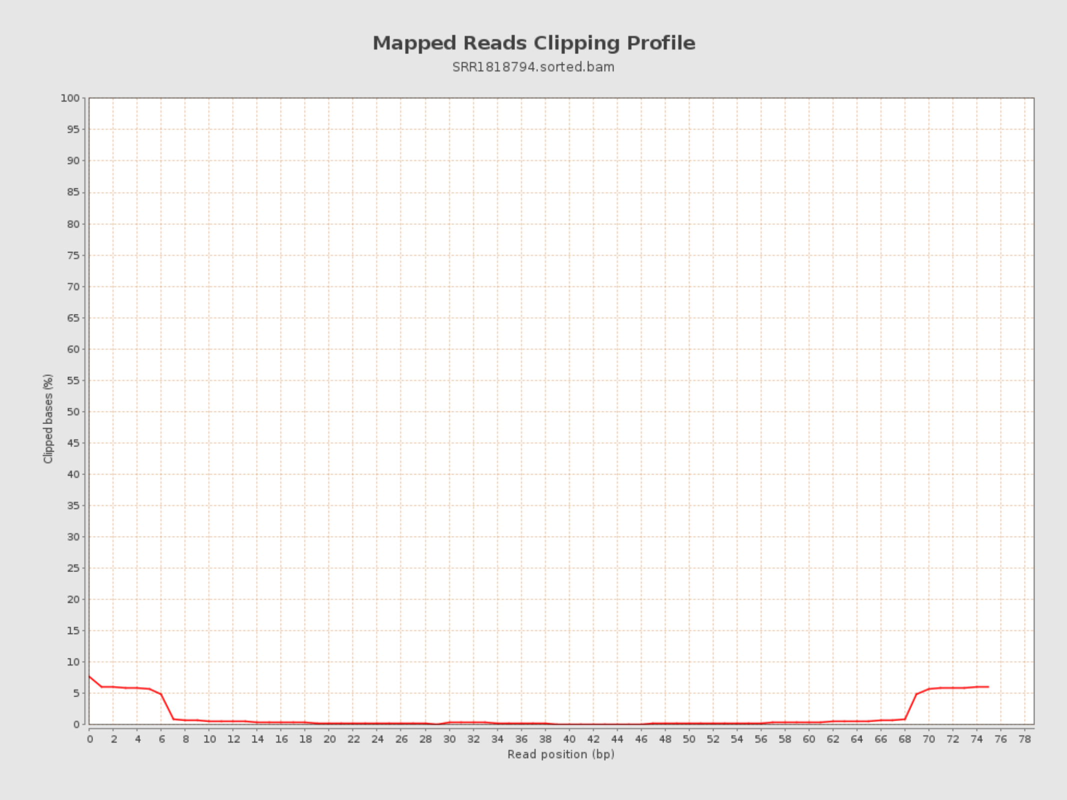
8. Results : Mapped Reads Nucleotide Content



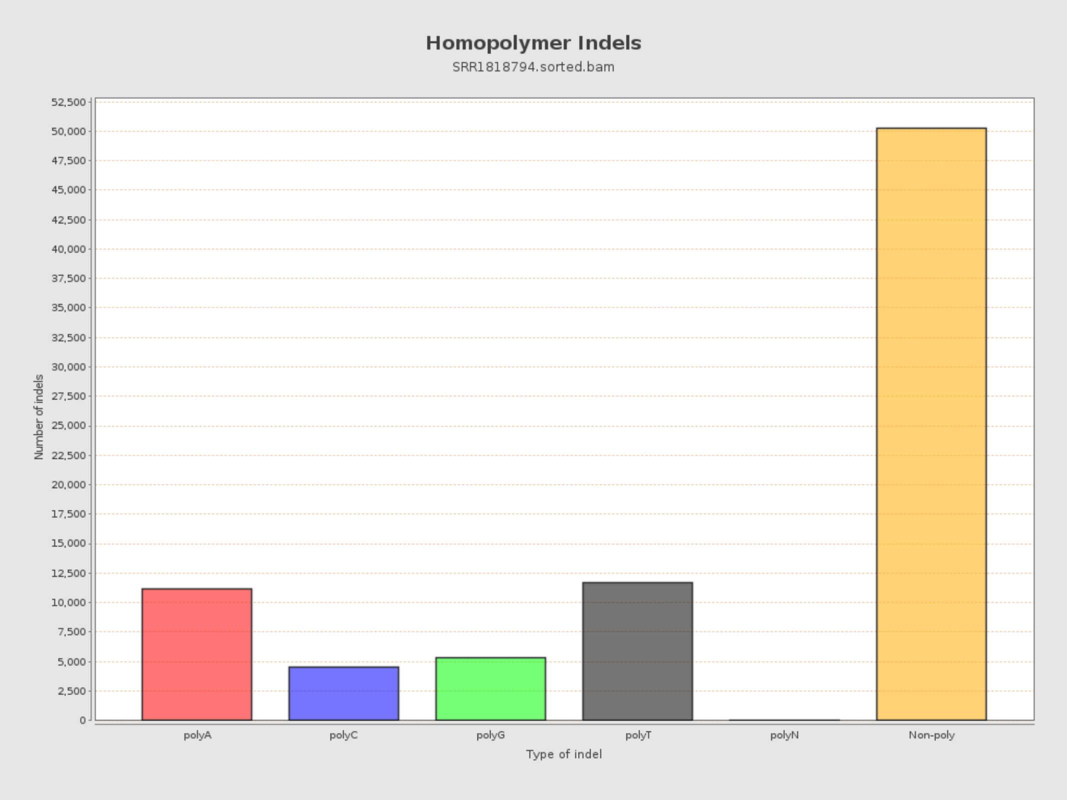
9. Results : Mapped Reads GC-content Distribution



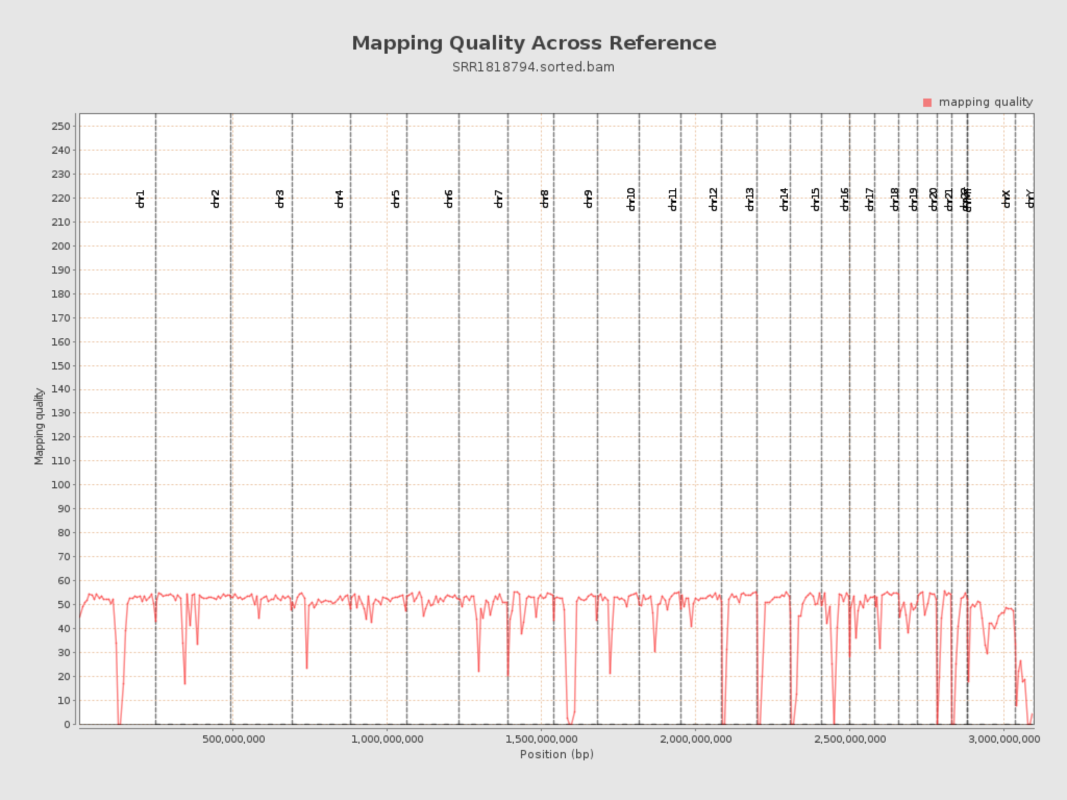
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram