Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:11:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819054.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_SRR1819054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:11:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,703,161
Mapped reads	1,559,186 / 91.55%
Unmapped reads	143,975 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,465 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	45,977 / 2.7%
Duplication rate	2.31%
Clipped reads	1,561,718 / 91.7%

2.2. ACGT Content

Number/percentage of A's	22,634,430 / 25.28%
Number/percentage of C's	18,009,087 / 20.12%
Number/percentage of T's	27,448,613 / 30.66%
Number/percentage of G's	21,424,671 / 23.93%
Number/percentage of N's	1,883 / 0%
GC Percentage	44.05%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2294

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

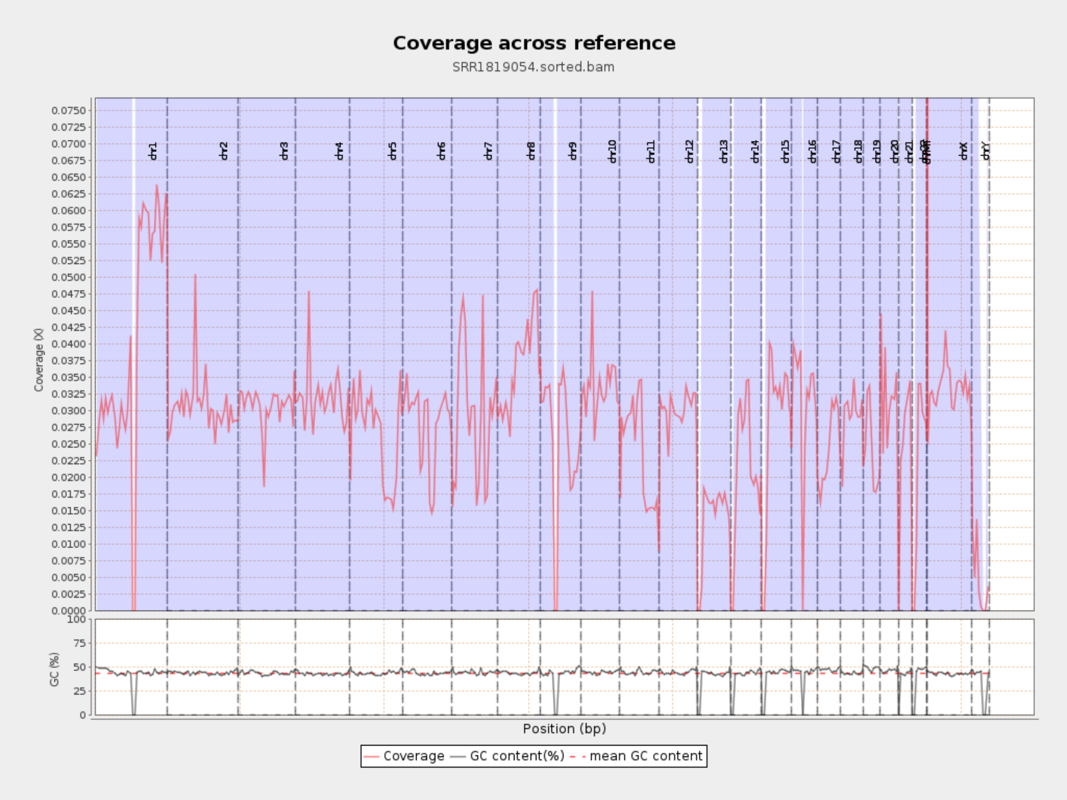
General error rate	0.49%
Mismatches	430,225
Insertions	5,051
Mapped reads with at least one insertion	0.32%
Deletions	13,156
Mapped reads with at least one deletion	0.84%
Homopolymer indels	41.76%

2.6. Chromosome stats

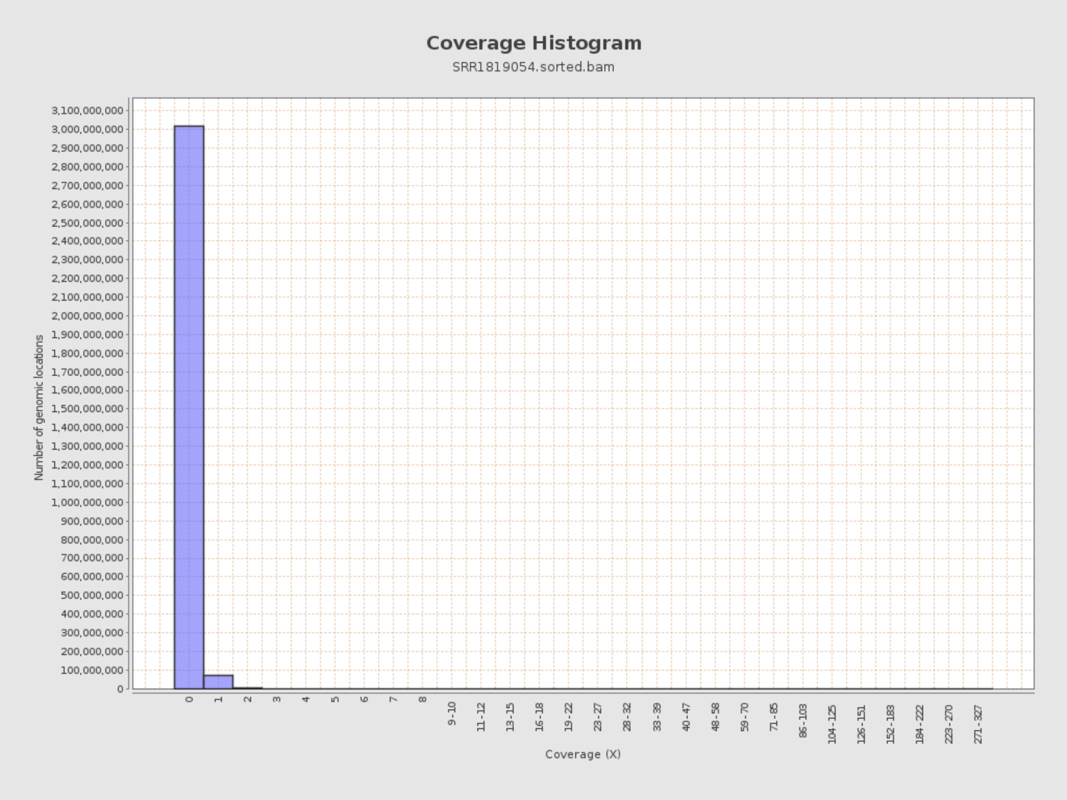
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9975662	0.04	0.3365
chr2	243199373	7463431	0.0307	0.2675
chr3	198022430	6052440	0.0306	0.1917
chr4	191154276	6095692	0.0319	0.2084
chr5	180915260	4830925	0.0267	0.1797
chr6	171115067	4795932	0.028	0.1917
chr7	159138663	4721248	0.0297	0.2209

chr8	146364022	5368140	0.0367	0.2342
chr9	141213431	3567058	0.0253	0.2396
chr10	135534747	4545896	0.0335	0.2532
chr11	135006516	3233069	0.0239	0.2243
chr12	133851895	4054103	0.0303	0.1924
chr13	115169878	1569277	0.0136	0.1261
chr14	107349540	2260445	0.0211	0.1686
chr15	102531392	2814679	0.0275	0.1811
chr16	90354753	2782698	0.0308	0.2052
chr17	81195210	1969437	0.0243	0.1756
chr18	78077248	2256516	0.0289	0.4057
chr19	59128983	1433349	0.0242	0.2541
chr20	63025520	1993046	0.0316	0.2002
chr21	48129895	1207540	0.0251	0.1911
chr22	51304566	1095730	0.0214	0.1603
chrMT	16571	15950	0.9625	1.0522
chrX	155270560	5179436	0.0334	0.2213
chrY	59373566	259474	0.0044	0.1002

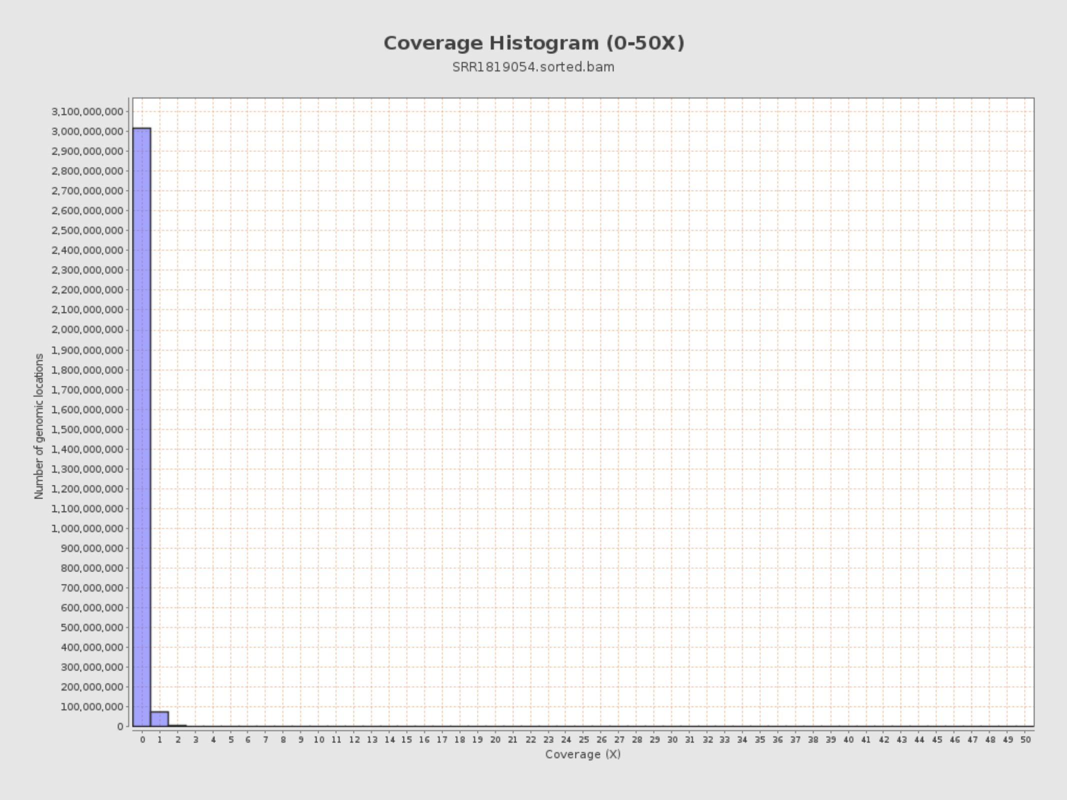
3. Results : Coverage across reference



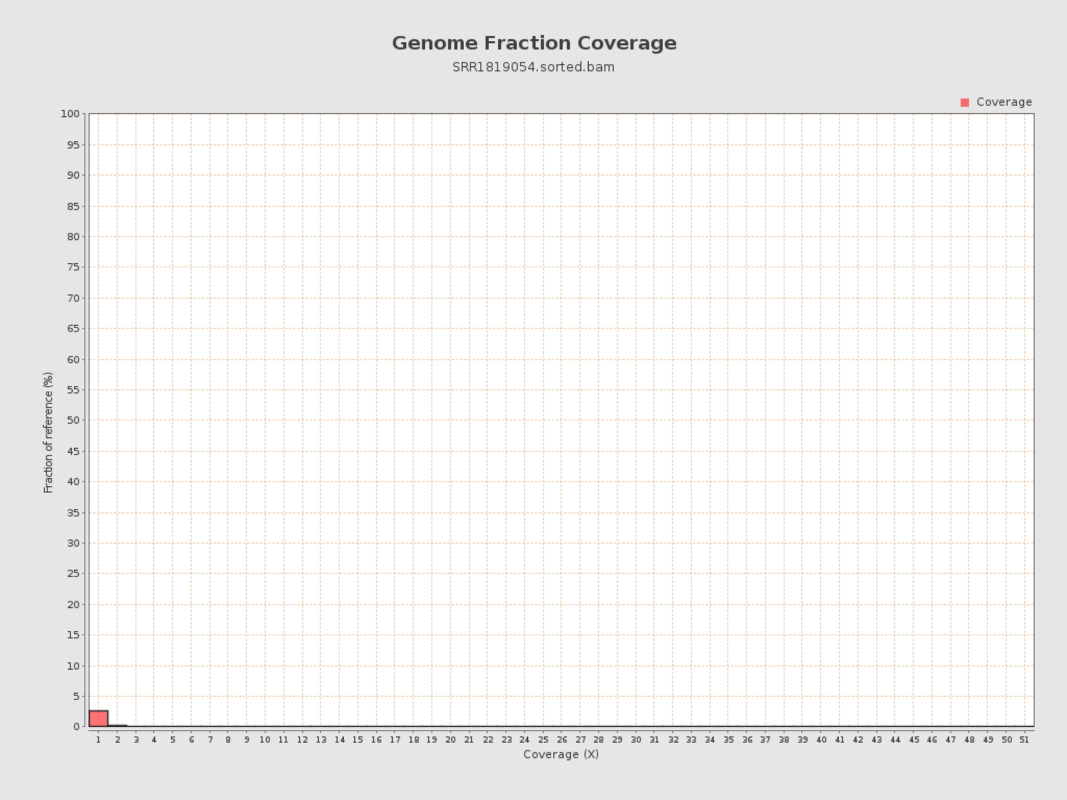
4. Results : Coverage Histogram



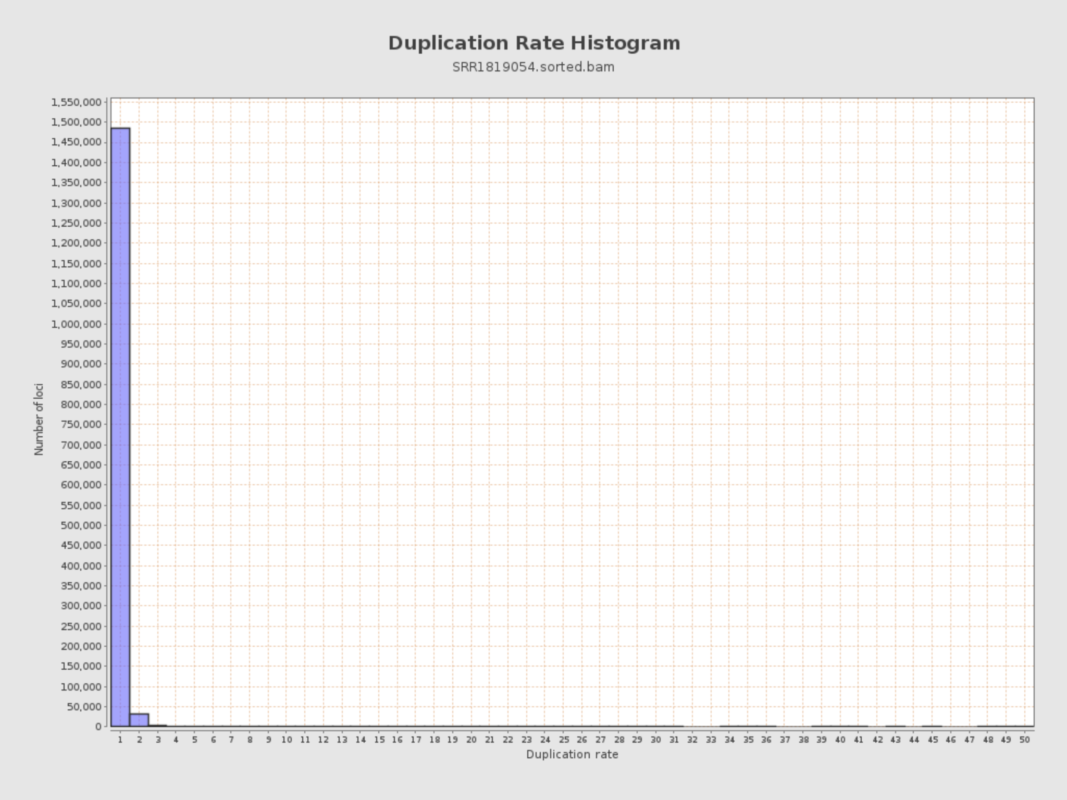
5. Results : Coverage Histogram (0-50X)



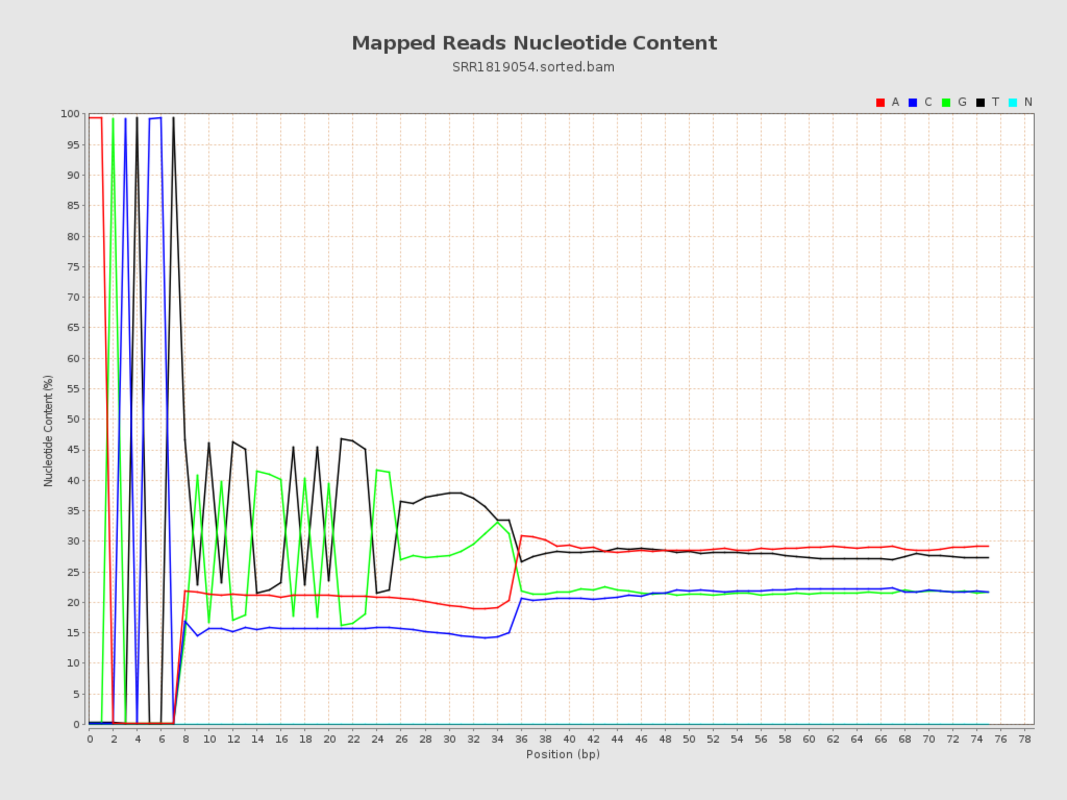
6. Results : Genome Fraction Coverage



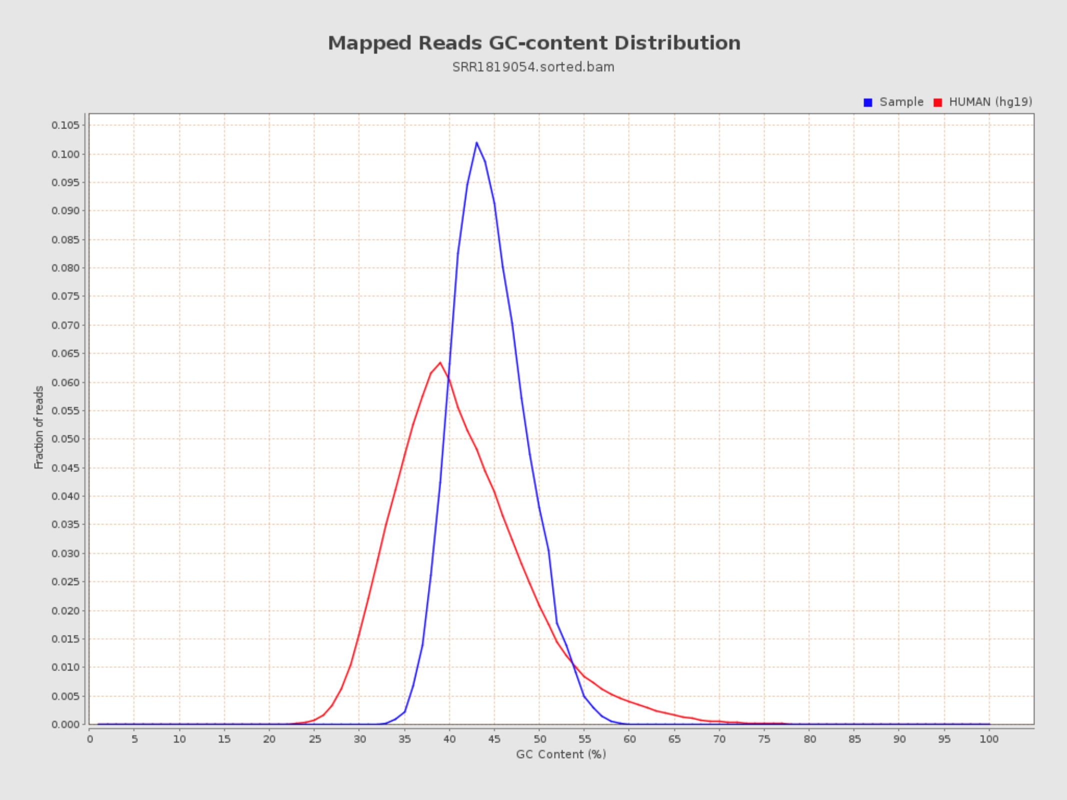
7. Results : Duplication Rate Histogram



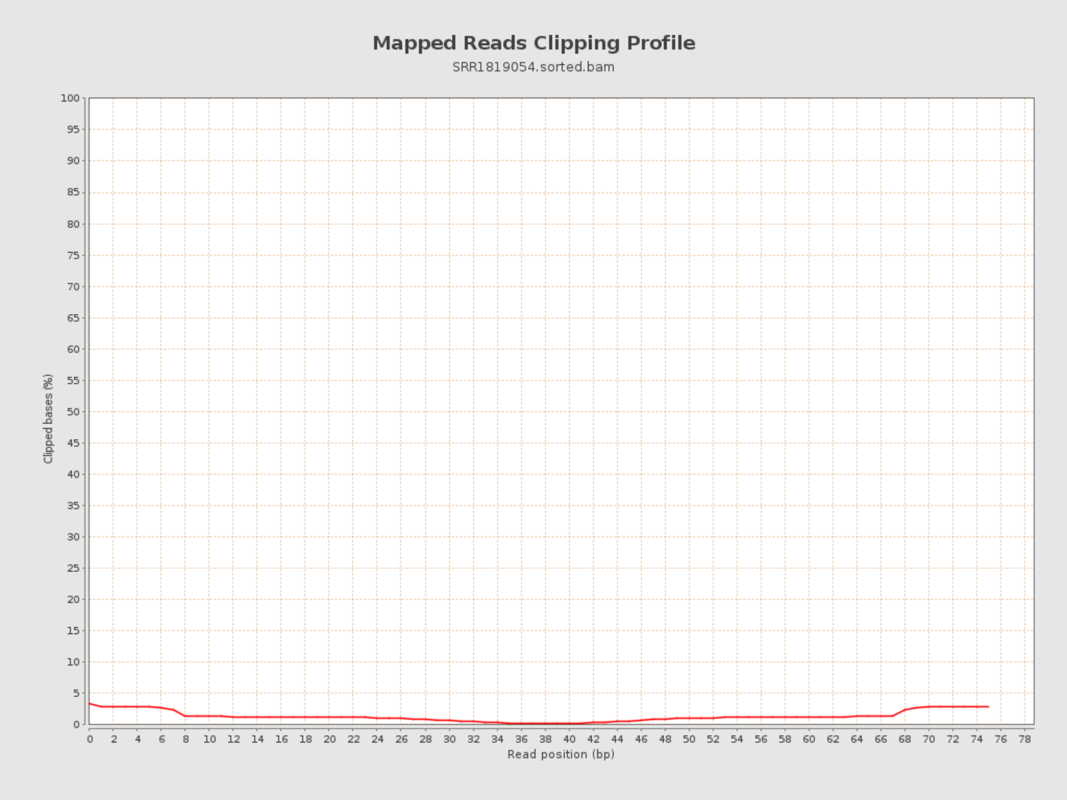
8. Results : Mapped Reads Nucleotide Content



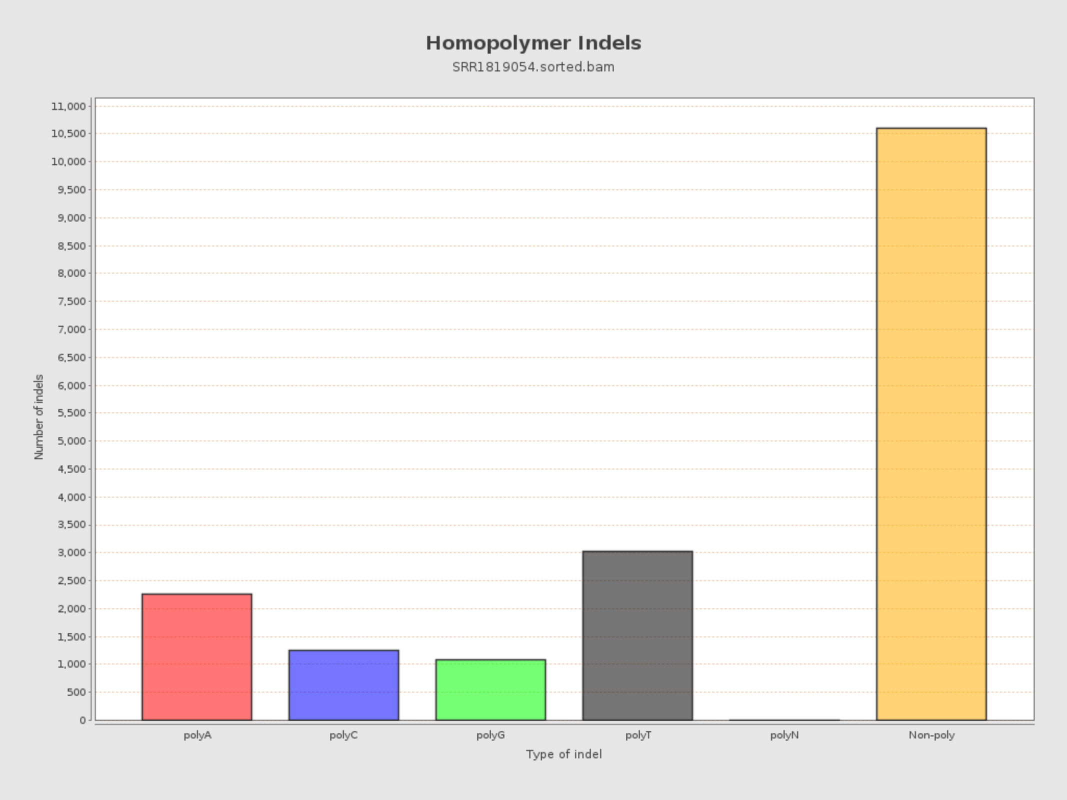
9. Results : Mapped Reads GC-content Distribution



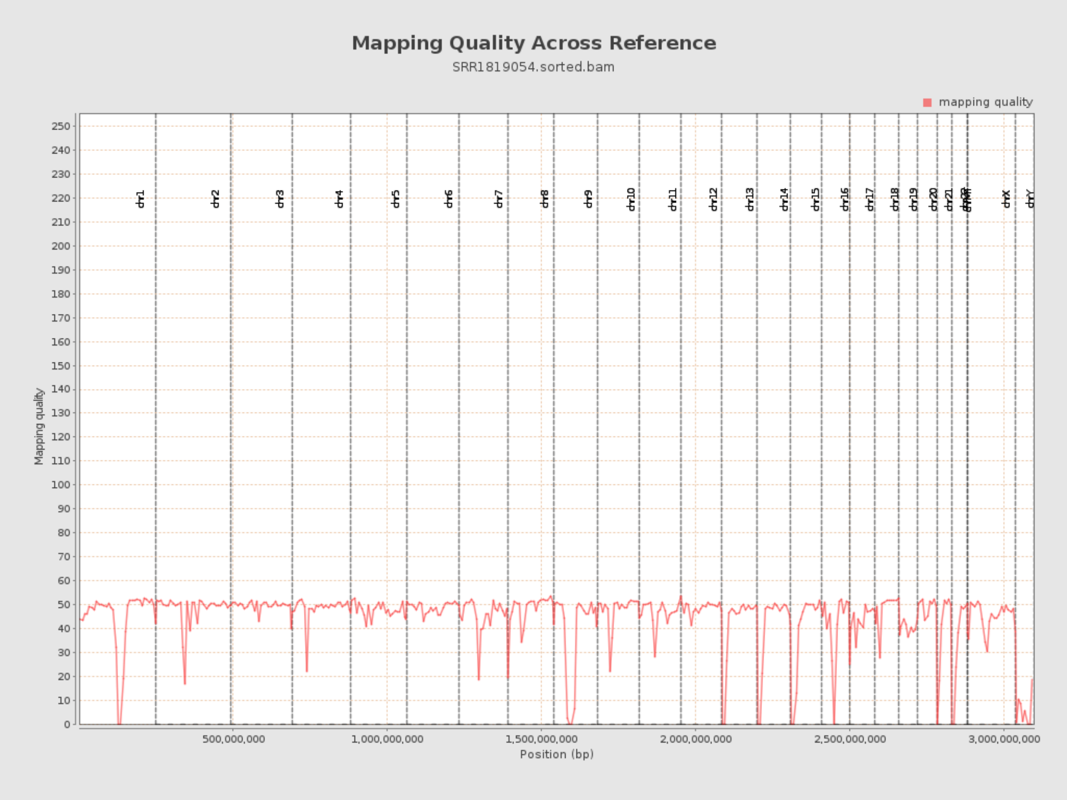
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram