Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:11:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082902.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_SRR3082902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:11:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,776,748
Mapped reads	1,562,010 / 87.91%
Unmapped reads	214,738 / 12.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,150 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	86,242 / 4.85%
Duplication rate	4.79%
Clipped reads	742,036 / 41.76%

2.2. ACGT Content

Number/percentage of A's	27,975,811 / 27.13%
Number/percentage of C's	19,160,076 / 18.58%
Number/percentage of T's	32,632,979 / 31.65%
Number/percentage of G's	23,348,178 / 22.64%
Number/percentage of N's	4,529 / 0%
GC Percentage	41.22%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.2628

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

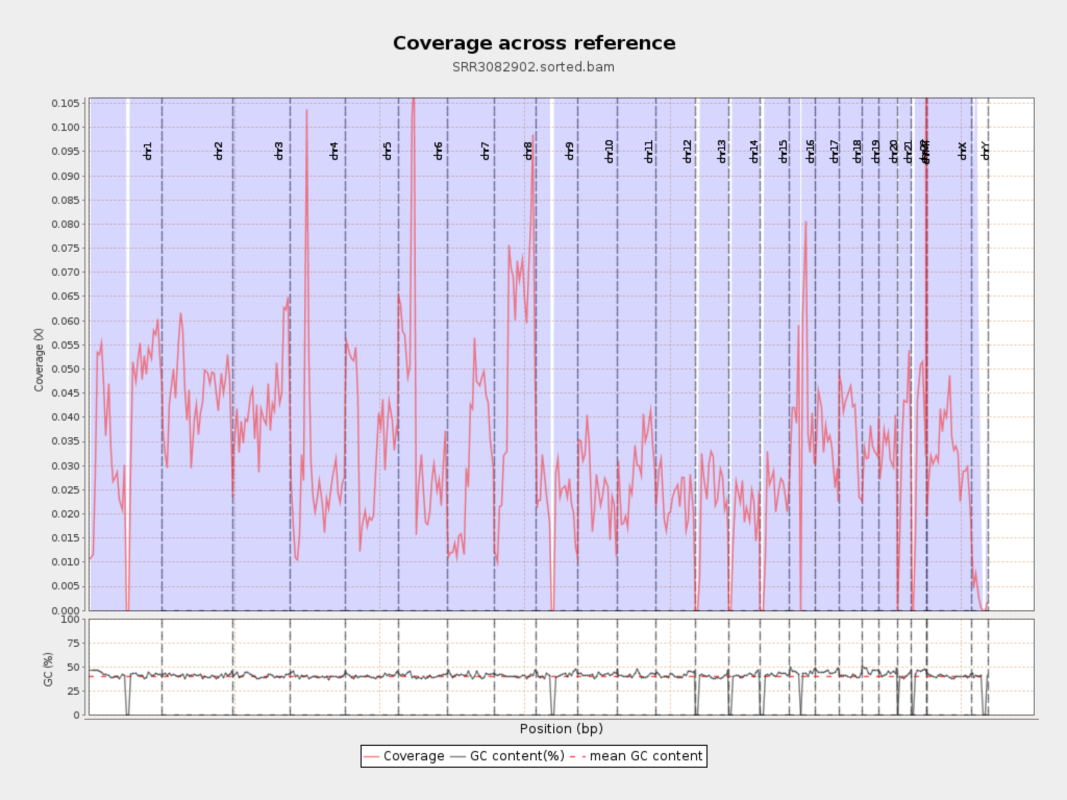
General error rate	0.73%
Mismatches	742,043
Insertions	8,247
Mapped reads with at least one insertion	0.52%
Deletions	23,132
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.41%

2.6. Chromosome stats

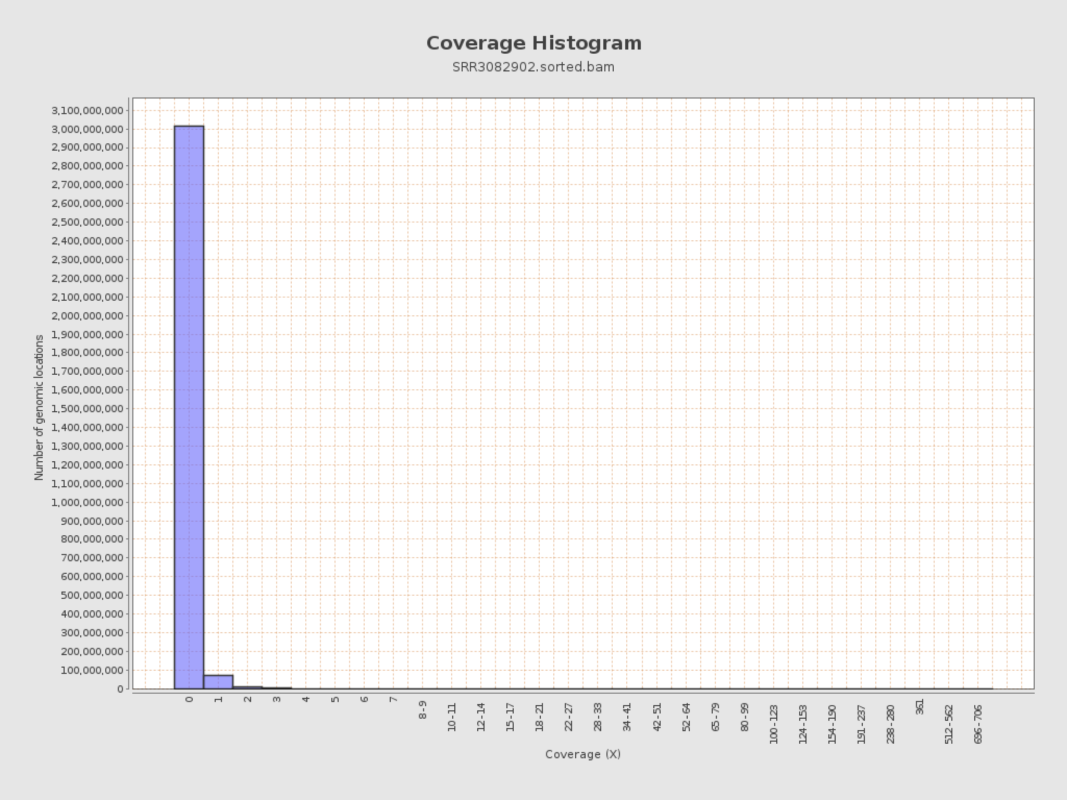
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9778712	0.0392	0.3368
chr2	243199373	10893852	0.0448	0.4025
chr3	198022430	8454071	0.0427	0.2487
chr4	191154276	5263871	0.0275	0.2021
chr5	180915260	6365573	0.0352	0.2263
chr6	171115067	6924388	0.0405	0.2935
chr7	159138663	4939919	0.031	0.2388

chr8	146364022	8023765	0.0548	0.3225
chr9	141213431	3040340	0.0215	0.2203
chr10	135534747	3565610	0.0263	0.211
chr11	135006516	3887205	0.0288	0.2262
chr12	133851895	3075614	0.023	0.1852
chr13	115169878	2586236	0.0225	0.1798
chr14	107349540	1984623	0.0185	0.1756
chr15	102531392	2162755	0.0211	0.177
chr16	90354753	3758108	0.0416	0.2518
chr17	81195210	2810408	0.0346	0.2397
chr18	78077248	3108309	0.0398	0.3908
chr19	59128983	1961907	0.0332	0.2673
chr20	63025520	2120824	0.0337	0.2248
chr21	48129895	1612429	0.0335	0.2207
chr22	51304566	1609177	0.0314	0.2155
chrMT	16571	9531	0.5752	0.8701
chrX	155270560	5040846	0.0325	0.2288
chrY	59373566	180681	0.003	0.0686

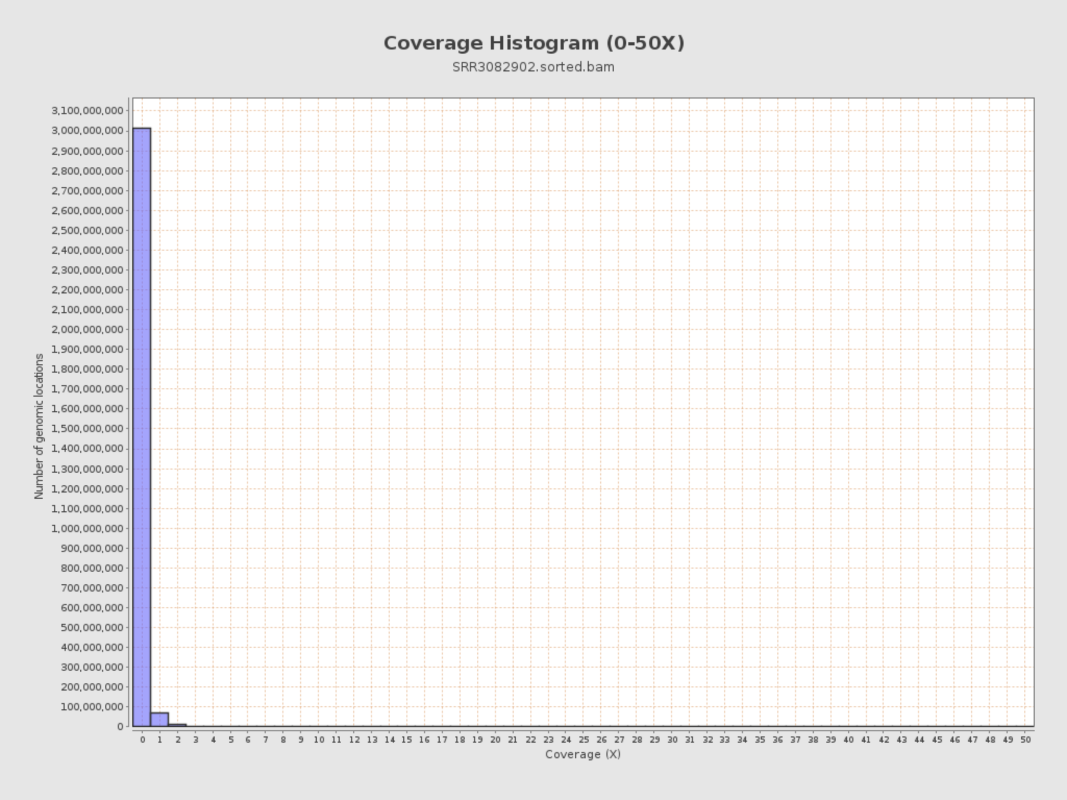
3. Results : Coverage across reference



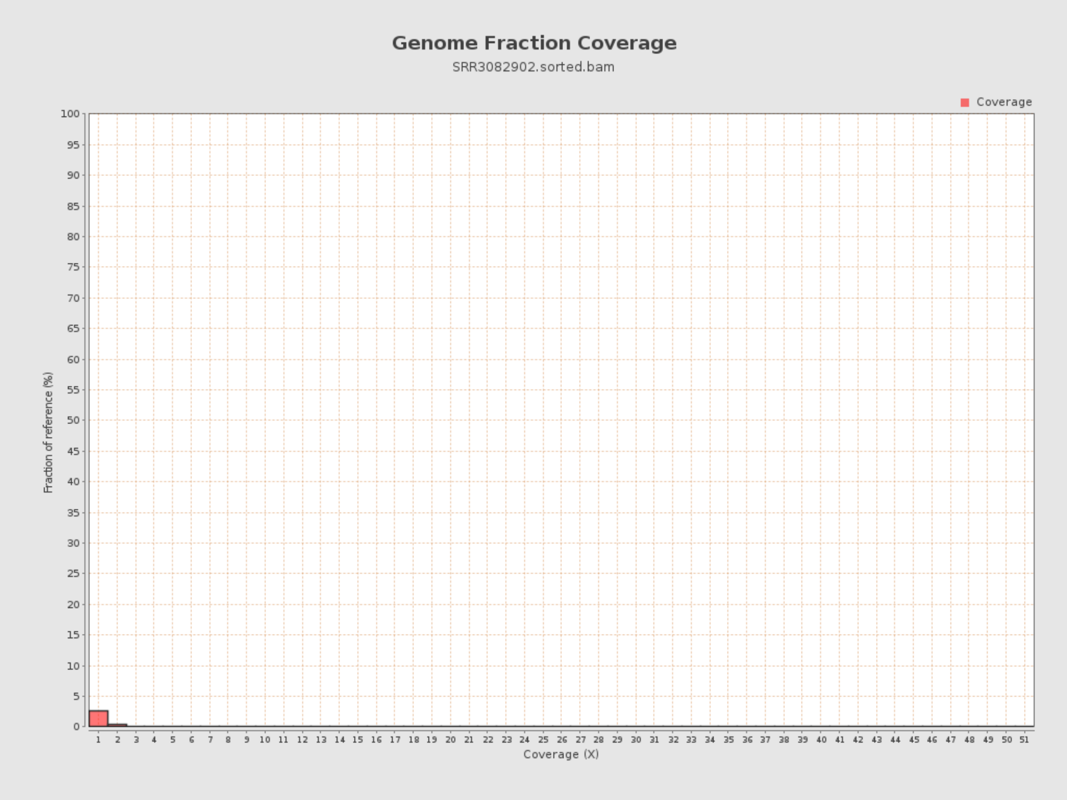
4. Results : Coverage Histogram



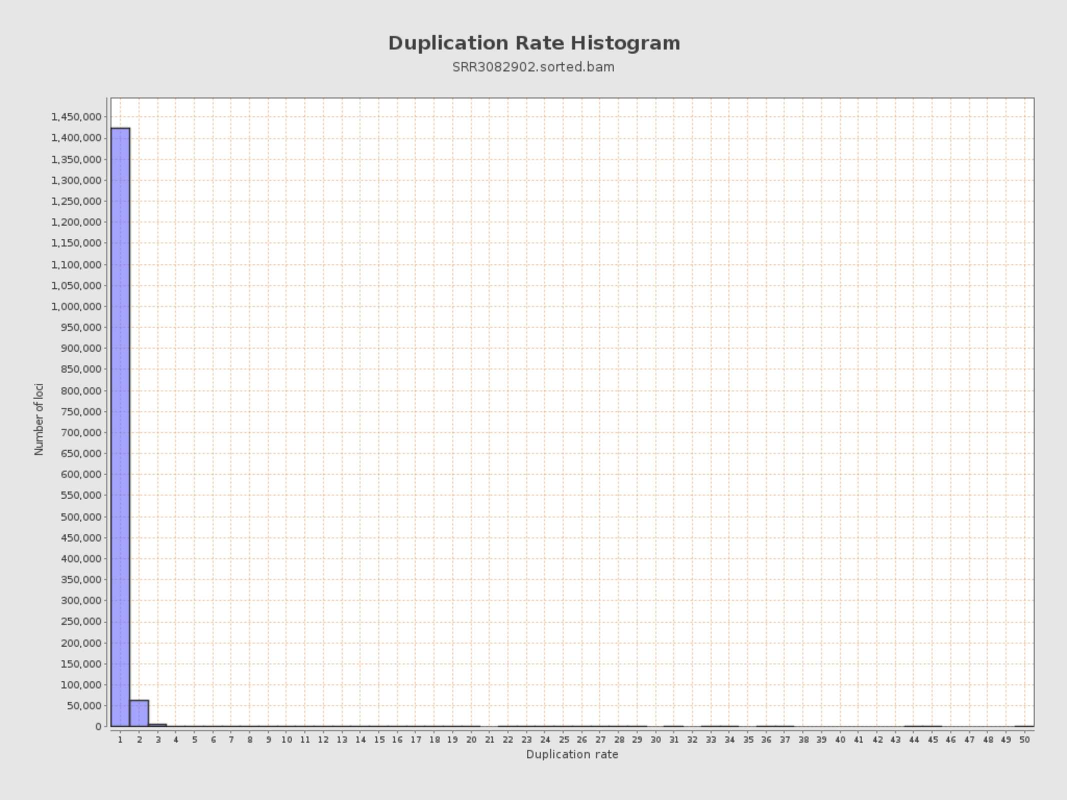
5. Results : Coverage Histogram (0-50X)



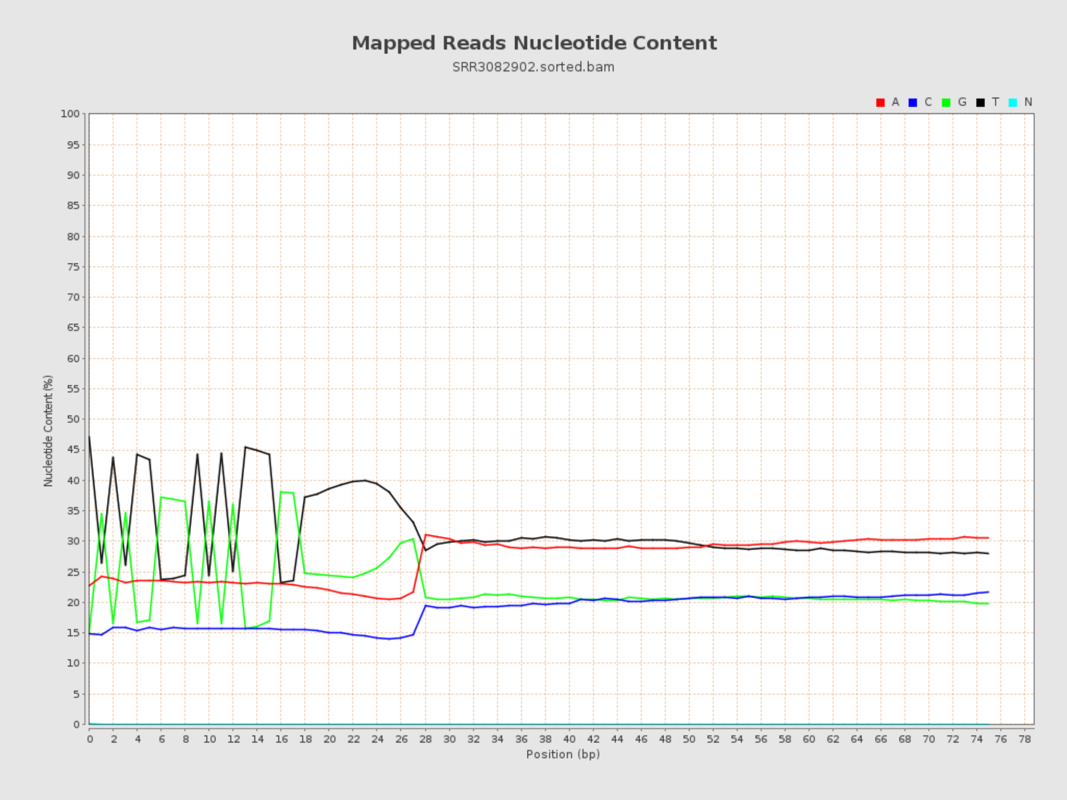
6. Results : Genome Fraction Coverage



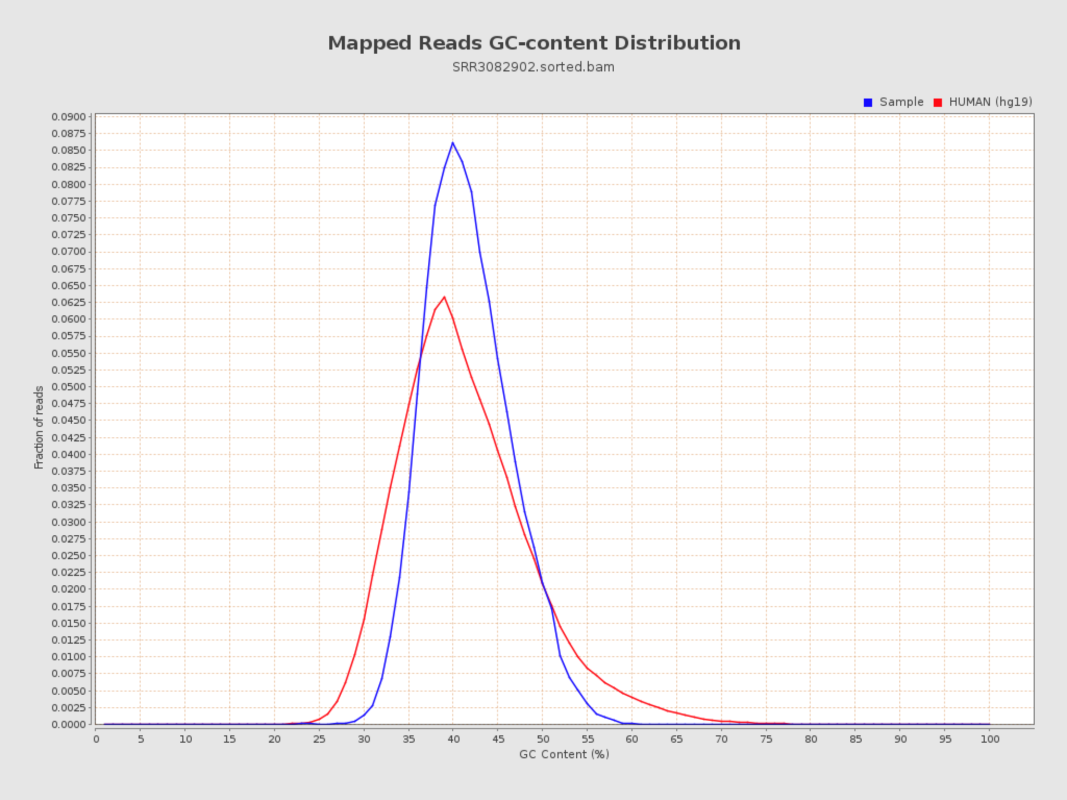
7. Results : Duplication Rate Histogram



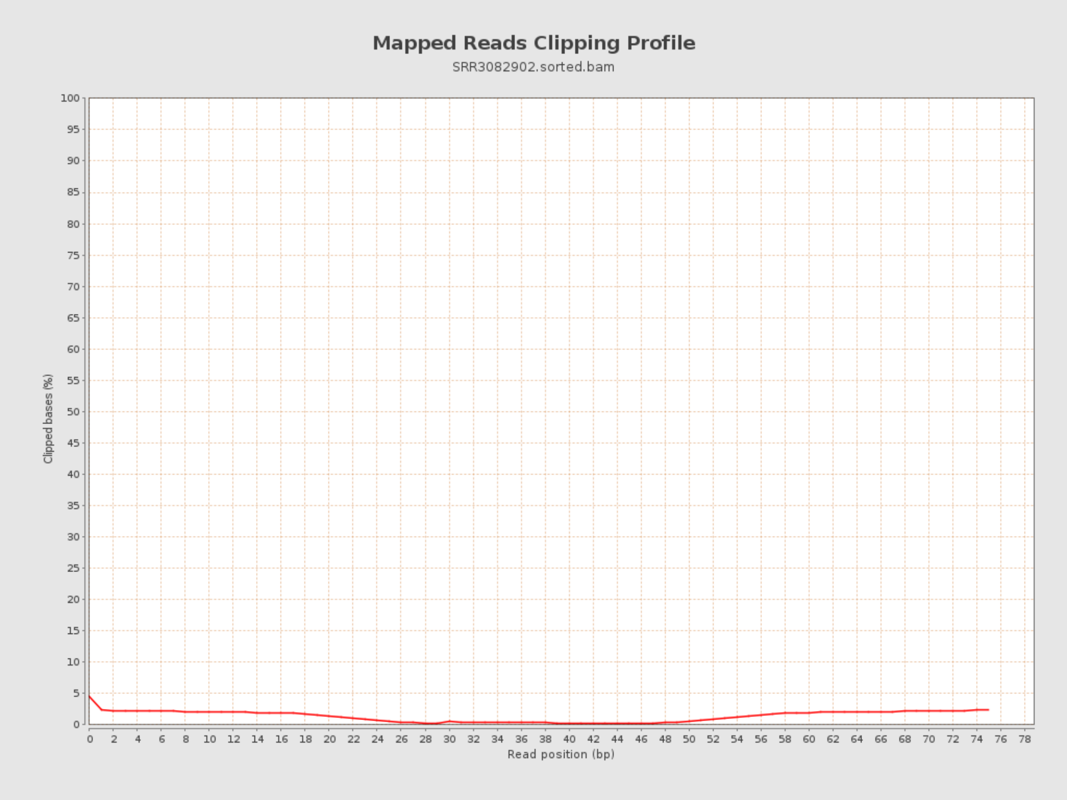
8. Results : Mapped Reads Nucleotide Content



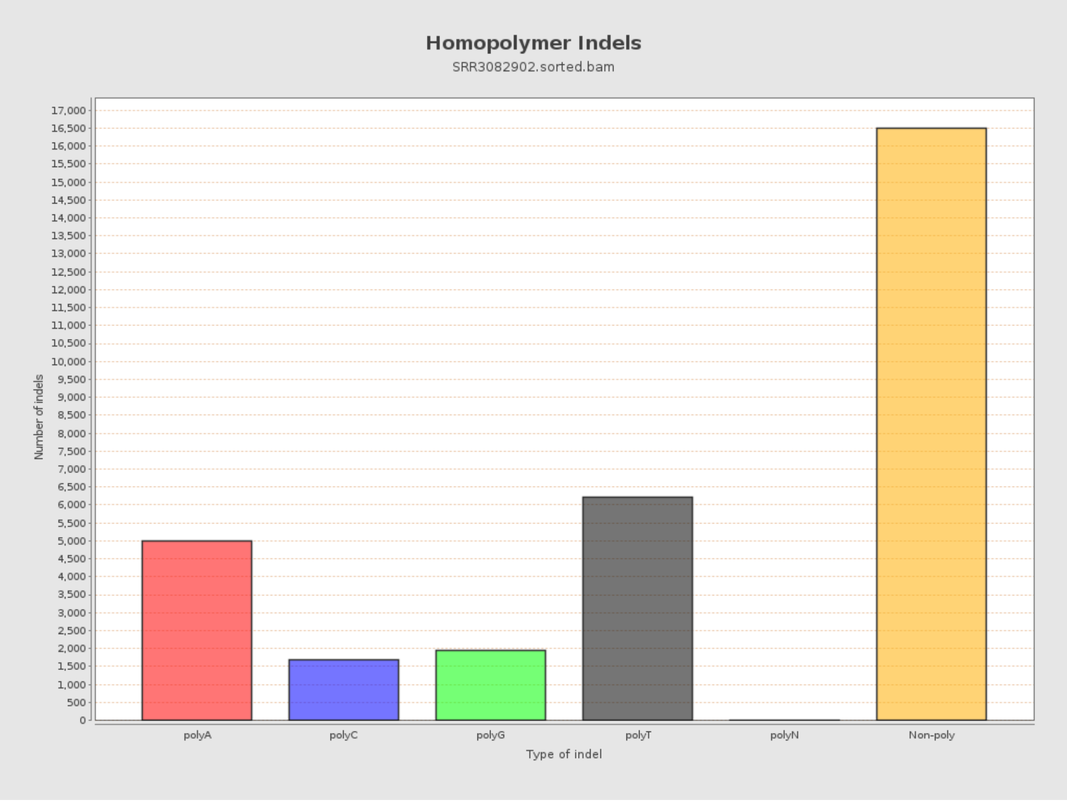
9. Results : Mapped Reads GC-content Distribution



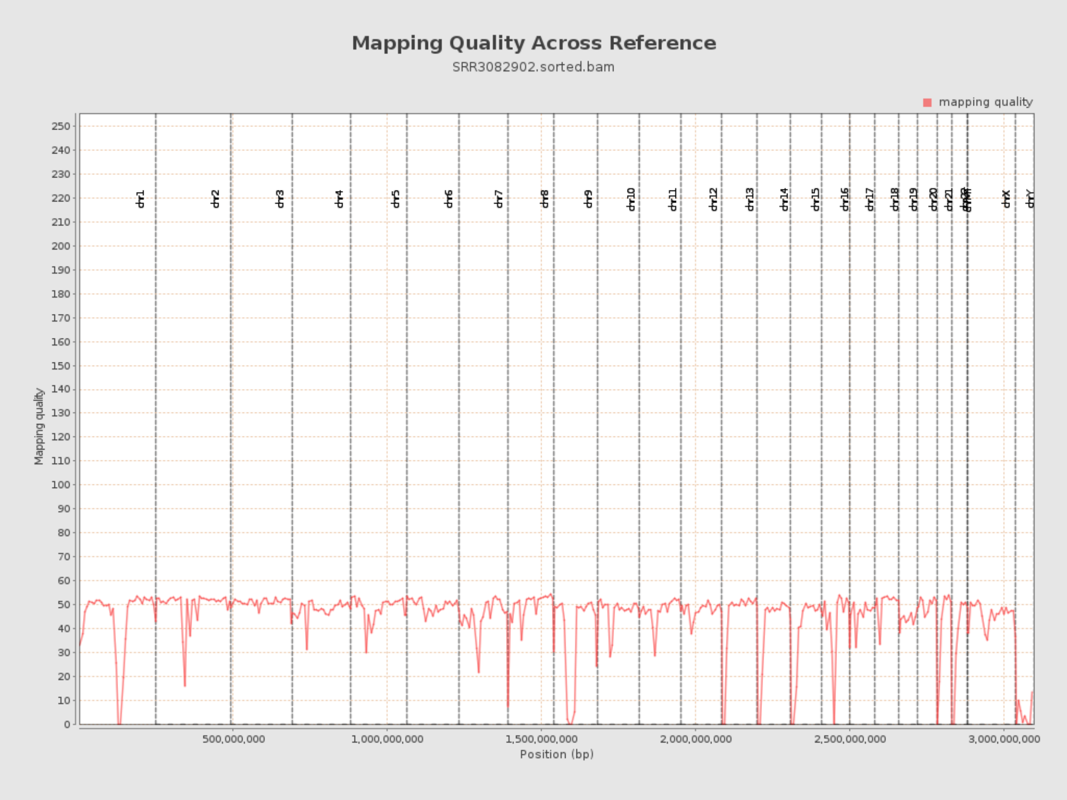
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram