Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:19:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082904.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_SRR3082904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082904.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:19:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,065
Mapped reads	1,547,957 / 88.86%
Unmapped reads	194,108 / 11.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,614 / 1.13%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	89,685 / 5.15%
Duplication rate	4.99%
Clipped reads	731,405 / 41.98%

2.2. ACGT Content

Number/percentage of A's	27,860,481 / 27.25%
Number/percentage of C's	18,829,320 / 18.42%
Number/percentage of T's	32,706,014 / 31.99%
Number/percentage of G's	22,841,441 / 22.34%
Number/percentage of N's	4,927 / 0%
GC Percentage	40.76%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2773

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

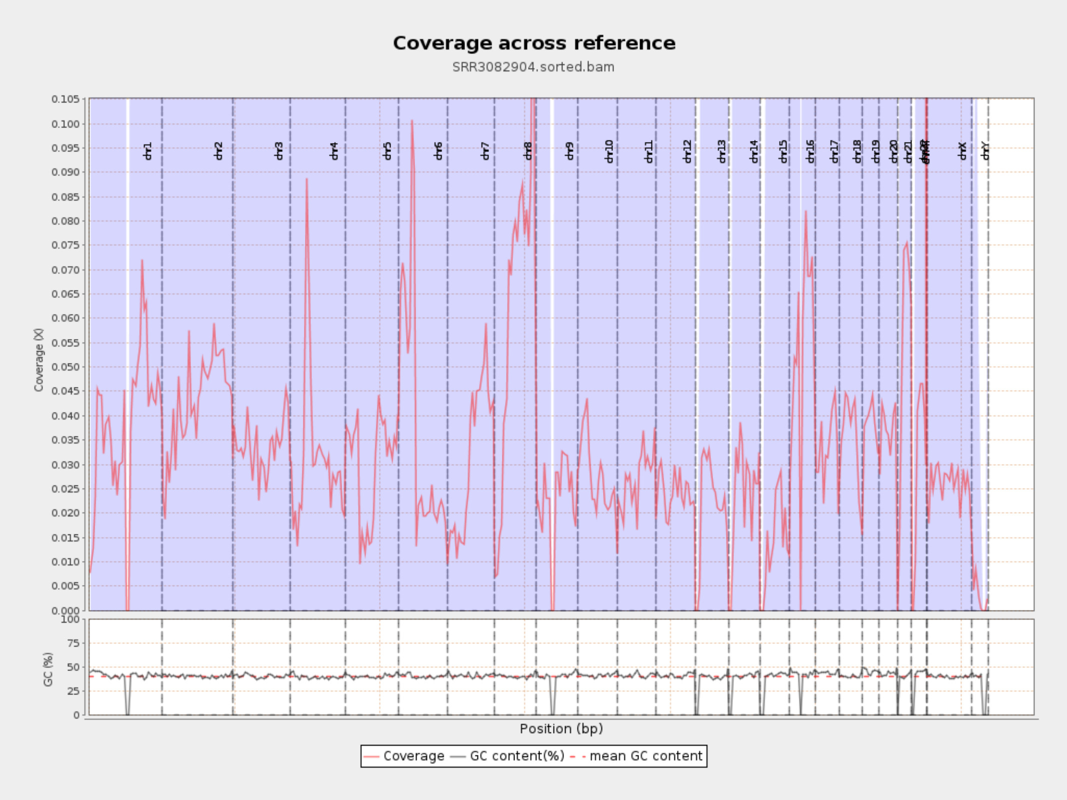
General error rate	0.73%
Mismatches	726,497
Insertions	8,456
Mapped reads with at least one insertion	0.54%
Deletions	23,398
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.91%

2.6. Chromosome stats

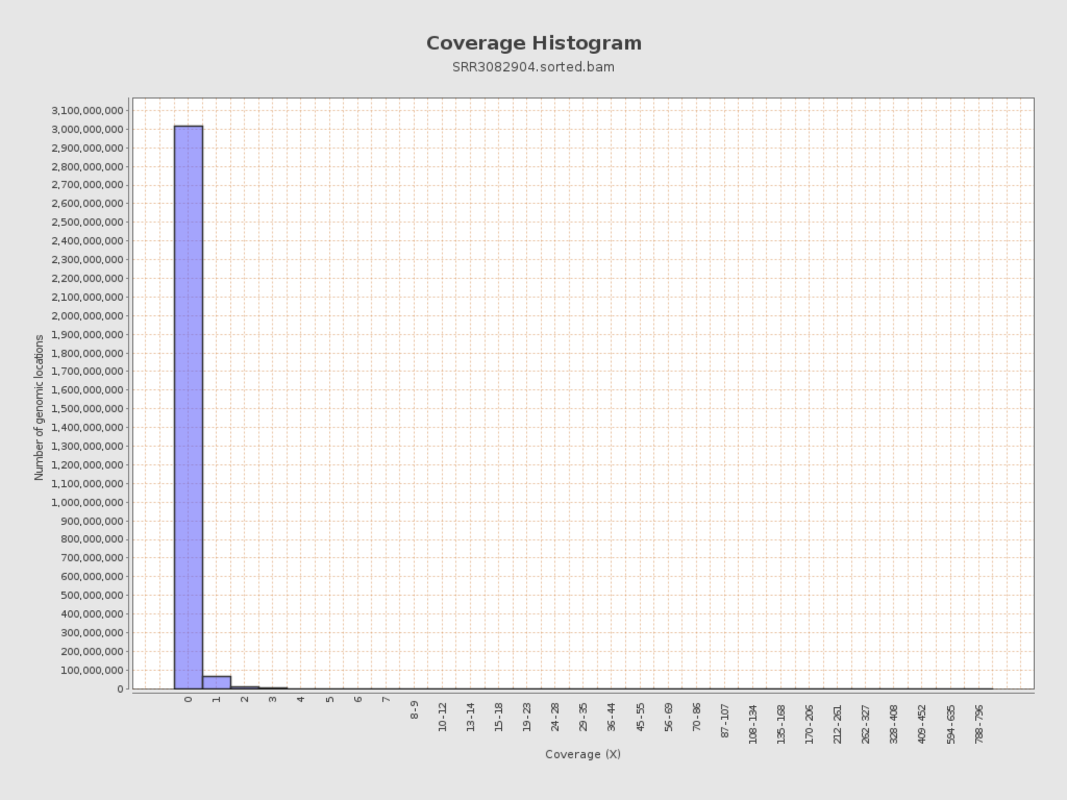
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9431926	0.0378	0.4446
chr2	243199373	10432956	0.0429	0.428
chr3	198022430	6688165	0.0338	0.2226
chr4	191154276	5993490	0.0314	0.2165
chr5	180915260	5403226	0.0299	0.209
chr6	171115067	6374153	0.0373	0.267
chr7	159138663	5067226	0.0318	0.2278

chr8	146364022	9425633	0.0644	0.358
chr9	141213431	3147917	0.0223	0.2187
chr10	135534747	3799977	0.028	0.2212
chr11	135006516	3641264	0.027	0.2133
chr12	133851895	3235668	0.0242	0.1903
chr13	115169878	2455643	0.0213	0.1769
chr14	107349540	2492432	0.0232	0.194
chr15	102531392	1435113	0.014	0.1467
chr16	90354753	4856911	0.0538	0.2865
chr17	81195210	2686490	0.0331	0.2271
chr18	78077248	2815456	0.0361	0.3378
chr19	59128983	2238329	0.0379	0.3246
chr20	63025520	2330874	0.037	0.2369
chr21	48129895	2513112	0.0522	0.2823
chr22	51304566	1482645	0.0289	0.2069
chrMT	16571	74497	4.4956	3.8465
chrX	155270560	4059267	0.0261	0.2049
chrY	59373566	198045	0.0033	0.0732

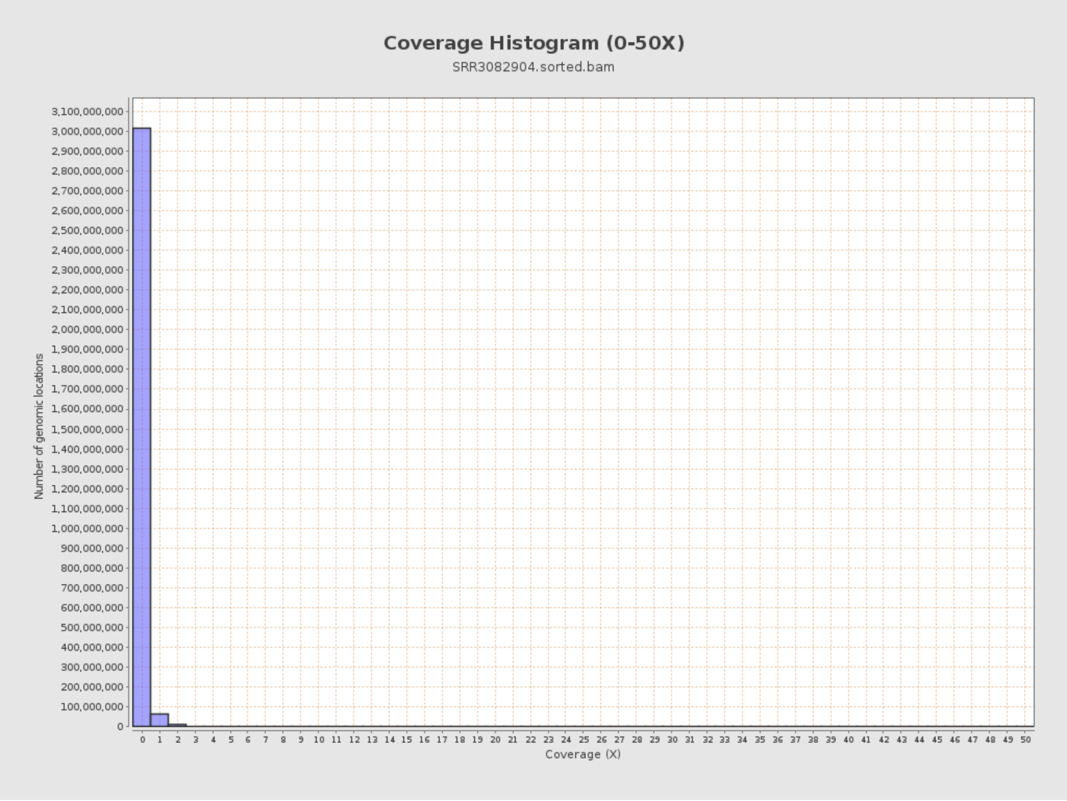
3. Results : Coverage across reference



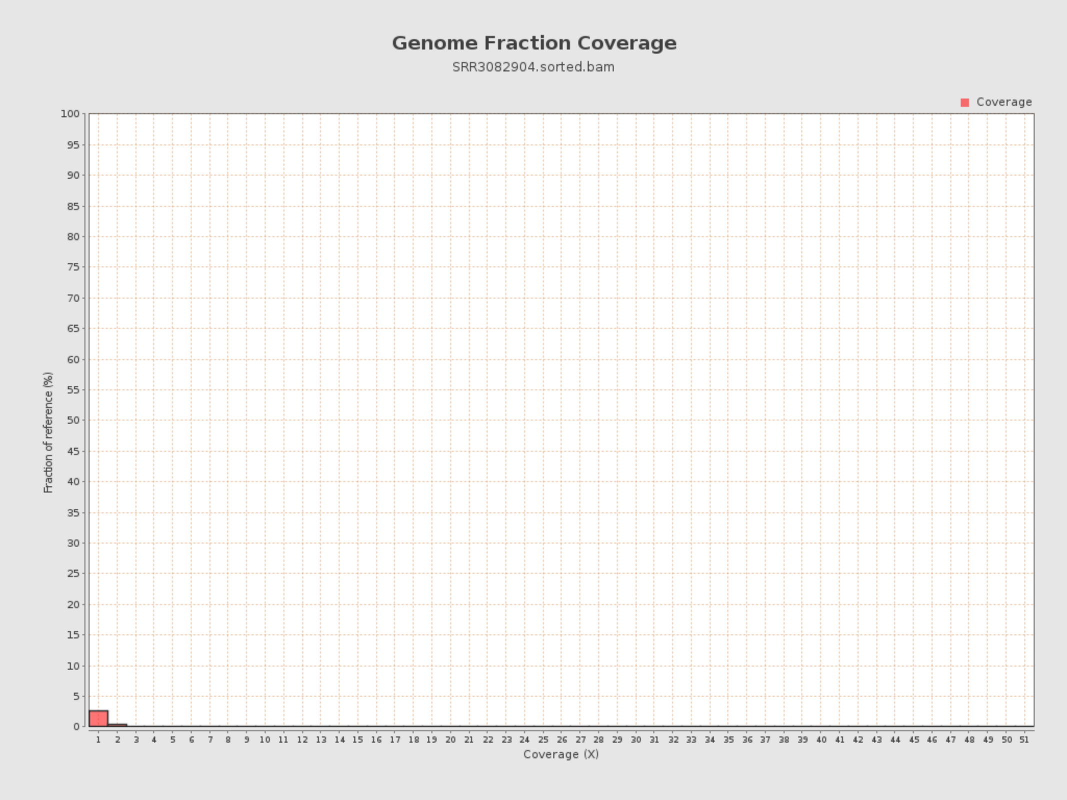
4. Results : Coverage Histogram



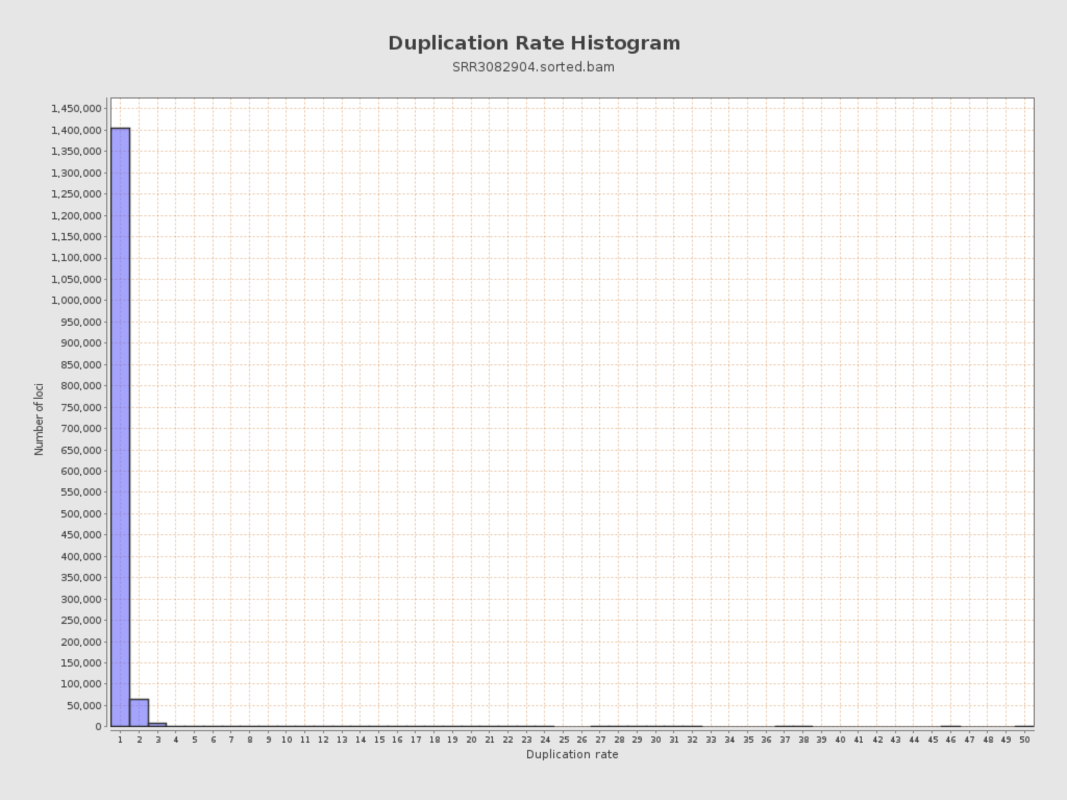
5. Results : Coverage Histogram (0-50X)



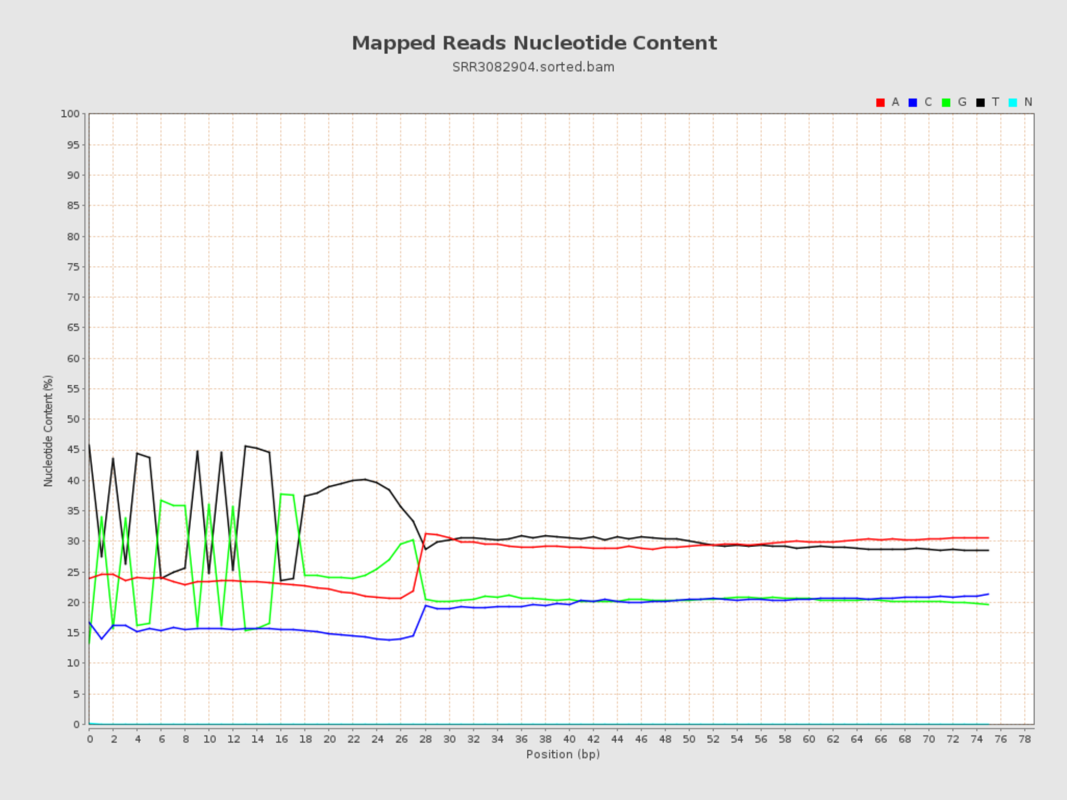
6. Results : Genome Fraction Coverage



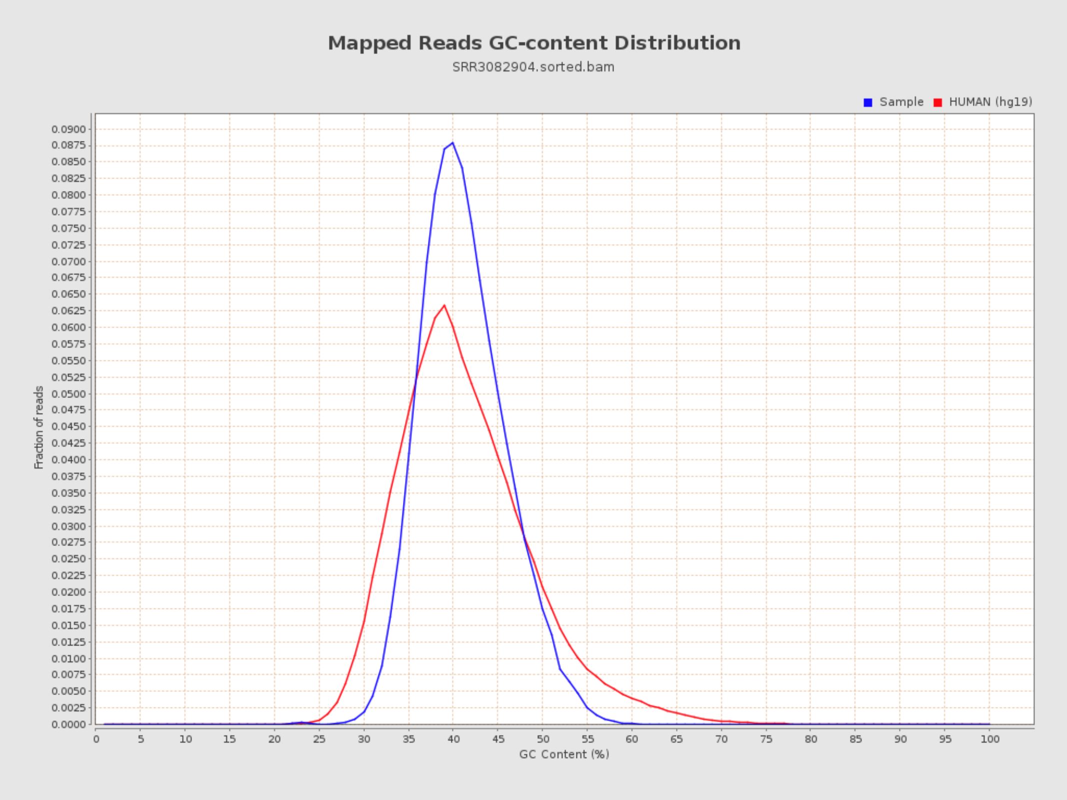
7. Results : Duplication Rate Histogram



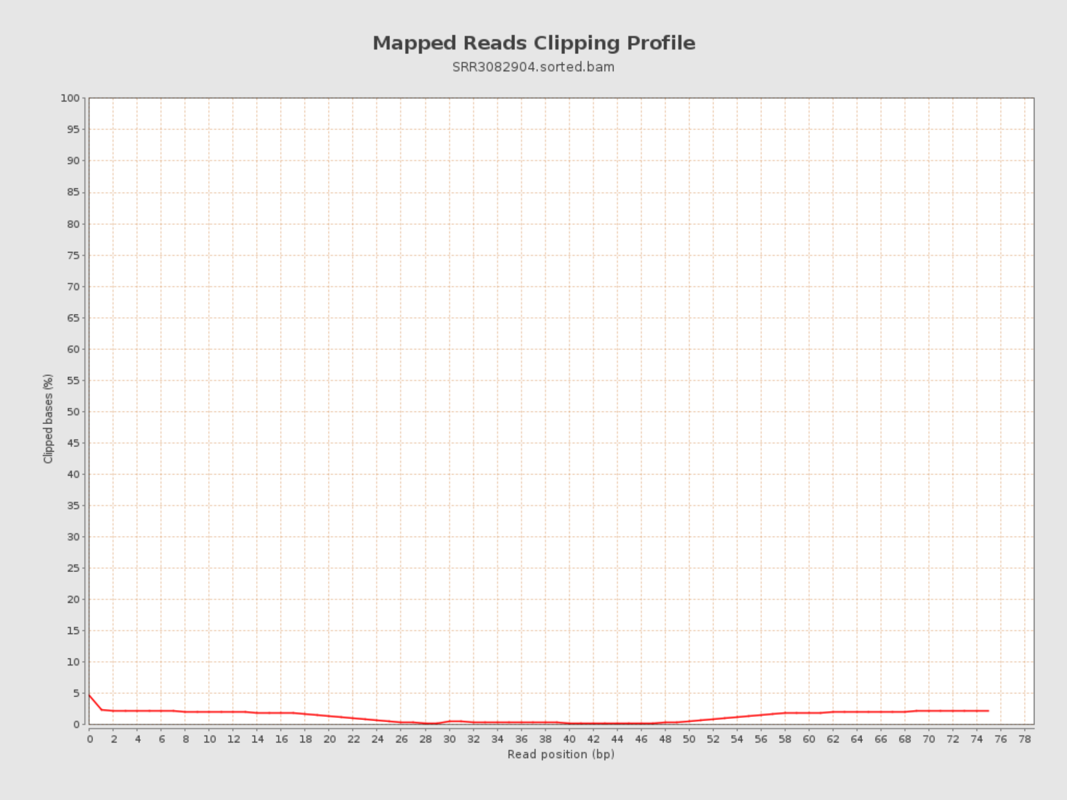
8. Results : Mapped Reads Nucleotide Content



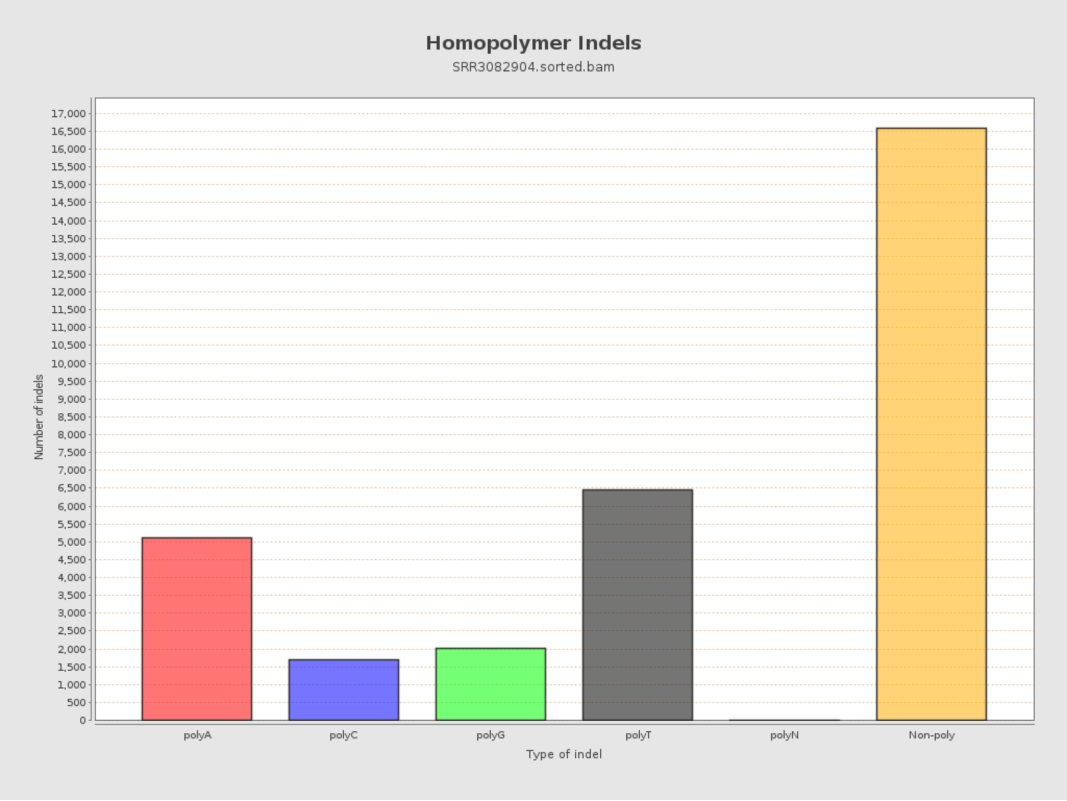
9. Results : Mapped Reads GC-content Distribution



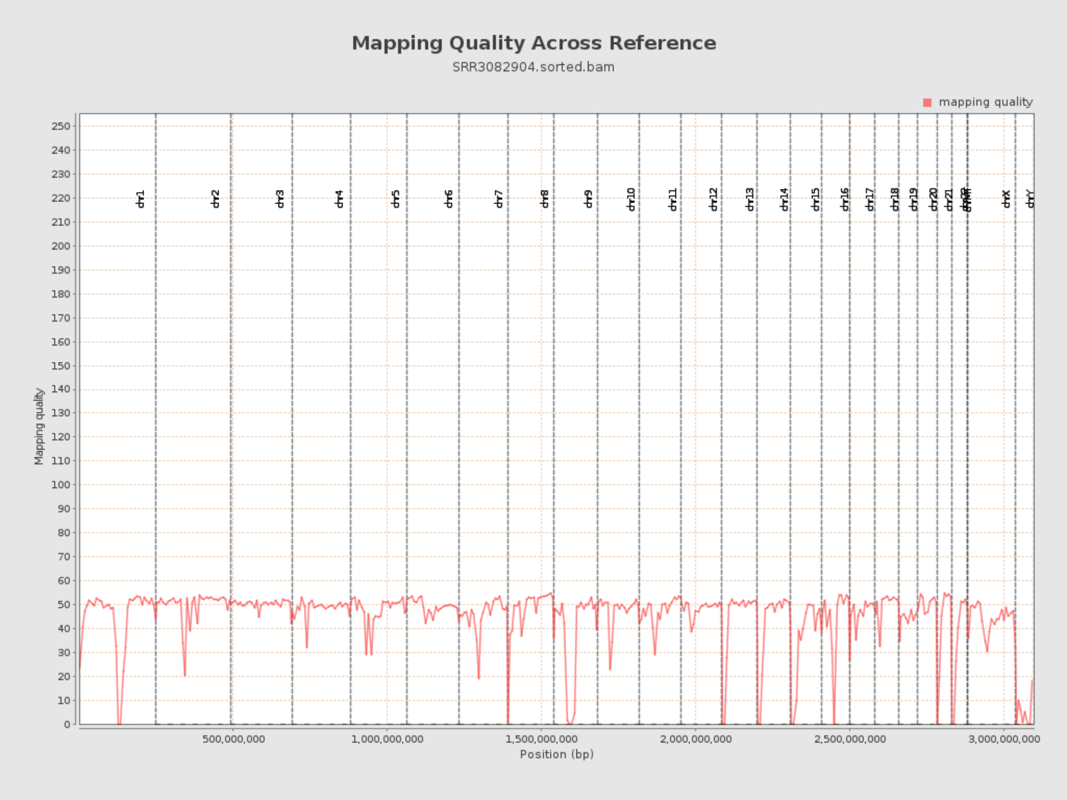
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram