Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:30:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004082.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_SRR6004082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:30:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,225,438
Mapped reads	2,023,019 / 90.9%
Unmapped reads	202,419 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,371 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	56,590 / 2.54%
Duplication rate	1.72%
Clipped reads	1,055,509 / 47.43%

2.2. ACGT Content

Number/percentage of A's	37,453,127 / 28.5%
Number/percentage of C's	24,950,920 / 18.98%
Number/percentage of T's	39,580,039 / 30.11%
Number/percentage of G's	29,437,209 / 22.4%
Number/percentage of N's	16,231 / 0.01%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.4102

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Mismatches and indels

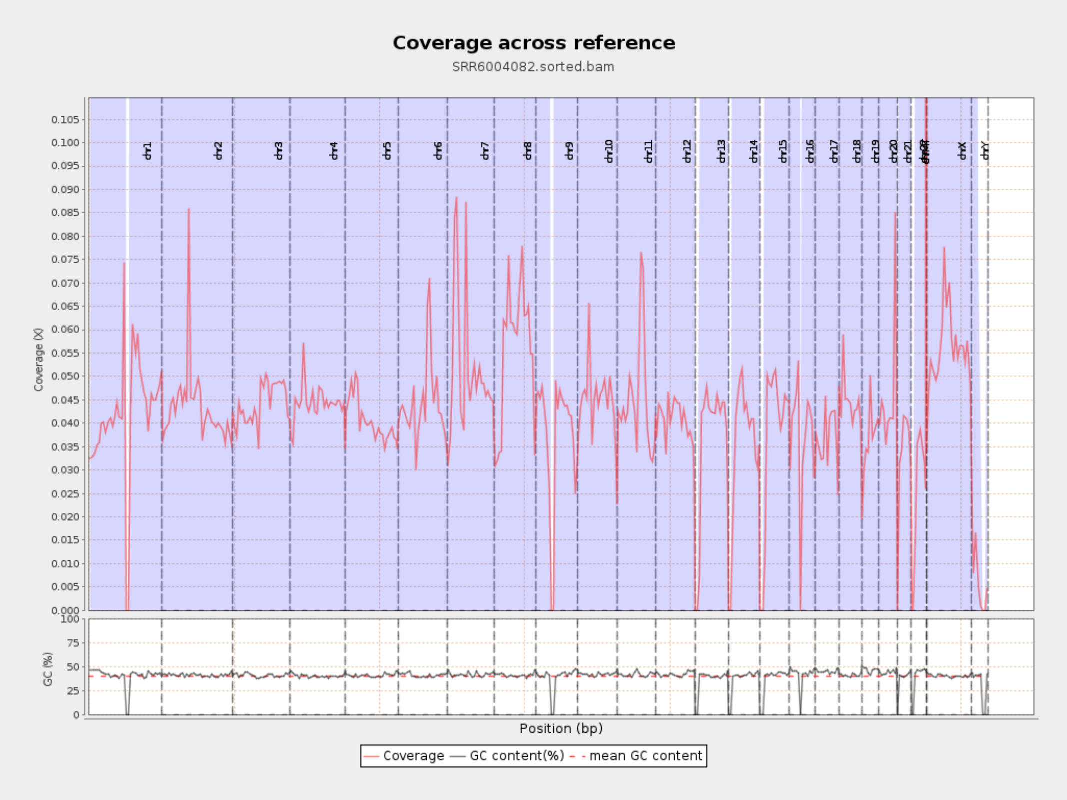
General error rate	0.79%
Mismatches	1,020,384
Insertions	9,844
Mapped reads with at least one insertion	0.48%
Deletions	34,533
Mapped reads with at least one deletion	1.69%
Homopolymer indels	44.28%

2.6. Chromosome stats

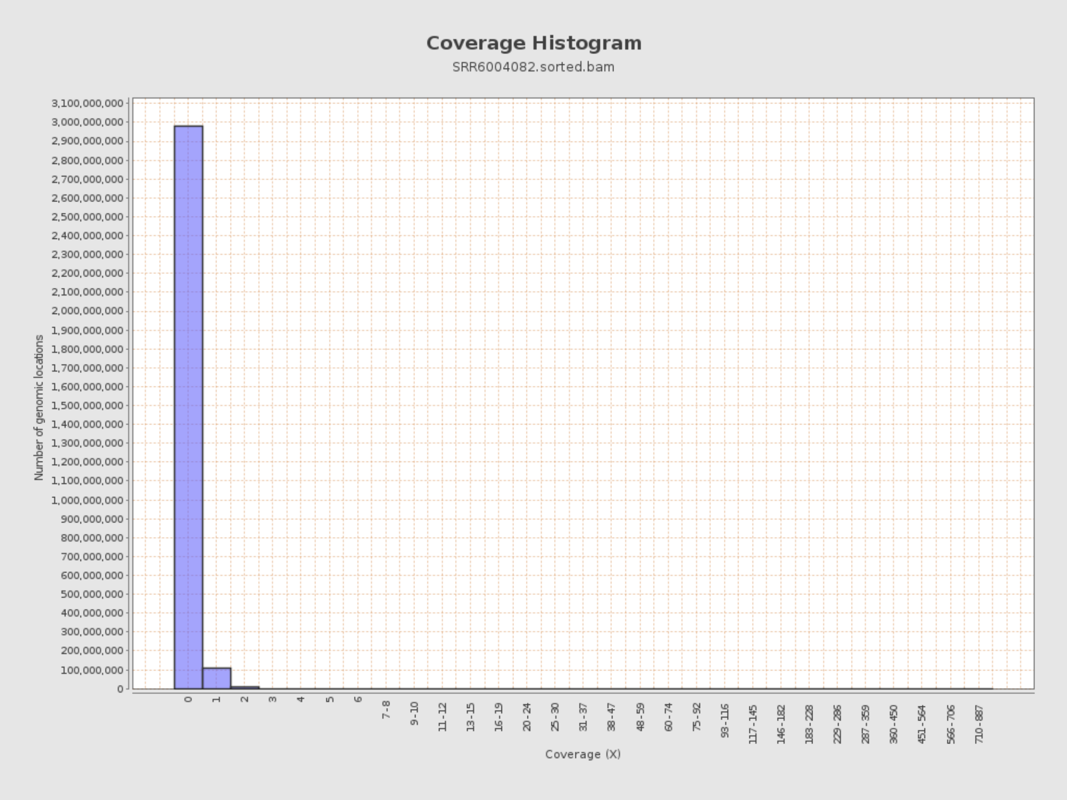
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10390872	0.0417	0.7333
chr2	243199373	10558115	0.0434	0.4757
chr3	198022430	8766503	0.0443	0.2276
chr4	191154276	8470653	0.0443	0.2514
chr5	180915260	7338193	0.0406	0.2213
chr6	171115067	7606214	0.0445	0.2624
chr7	159138663	8397686	0.0528	0.6639

chr8	146364022	8111855	0.0554	0.4584
chr9	141213431	5223524	0.037	0.3775
chr10	135534747	6178231	0.0456	0.3356
chr11	135006516	6095952	0.0452	0.4252
chr12	133851895	5436525	0.0406	0.2237
chr13	115169878	4125213	0.0358	0.205
chr14	107349540	3737630	0.0348	0.2307
chr15	102531392	3801714	0.0371	0.228
chr16	90354753	3336403	0.0369	0.2458
chr17	81195210	2988918	0.0368	0.2499
chr18	78077248	3498204	0.0448	0.7201
chr19	59128983	2183978	0.0369	0.5157
chr20	63025520	2939997	0.0466	0.2453
chr21	48129895	1596832	0.0332	0.2249
chr22	51304566	1252844	0.0244	0.1664
chrMT	16571	426980	25.7667	17.5789
chrX	155270560	8677234	0.0559	0.2999
chrY	59373566	356615	0.006	0.118

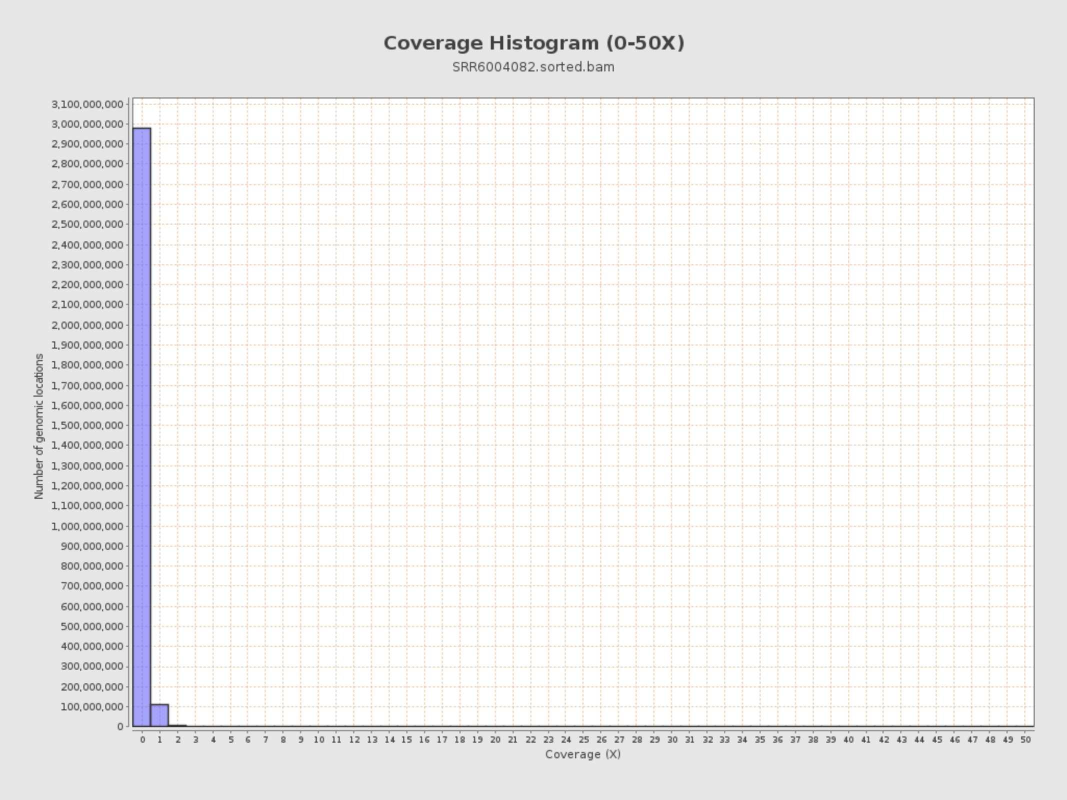
3. Results : Coverage across reference



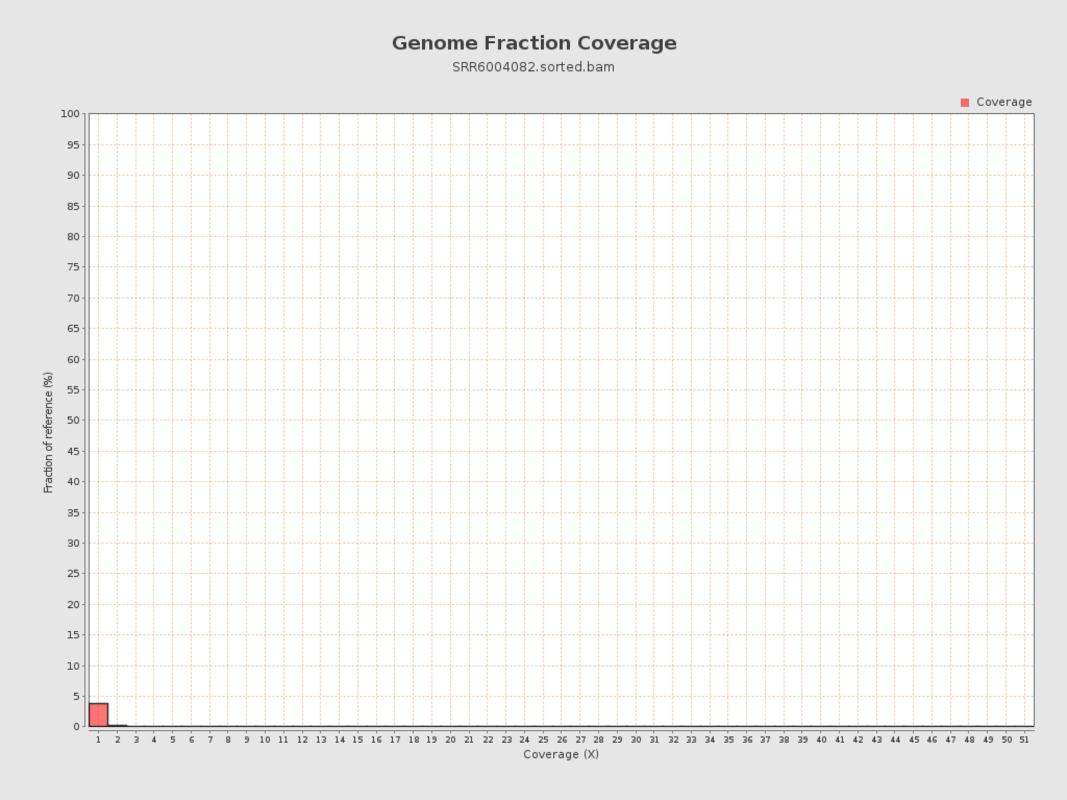
4. Results : Coverage Histogram



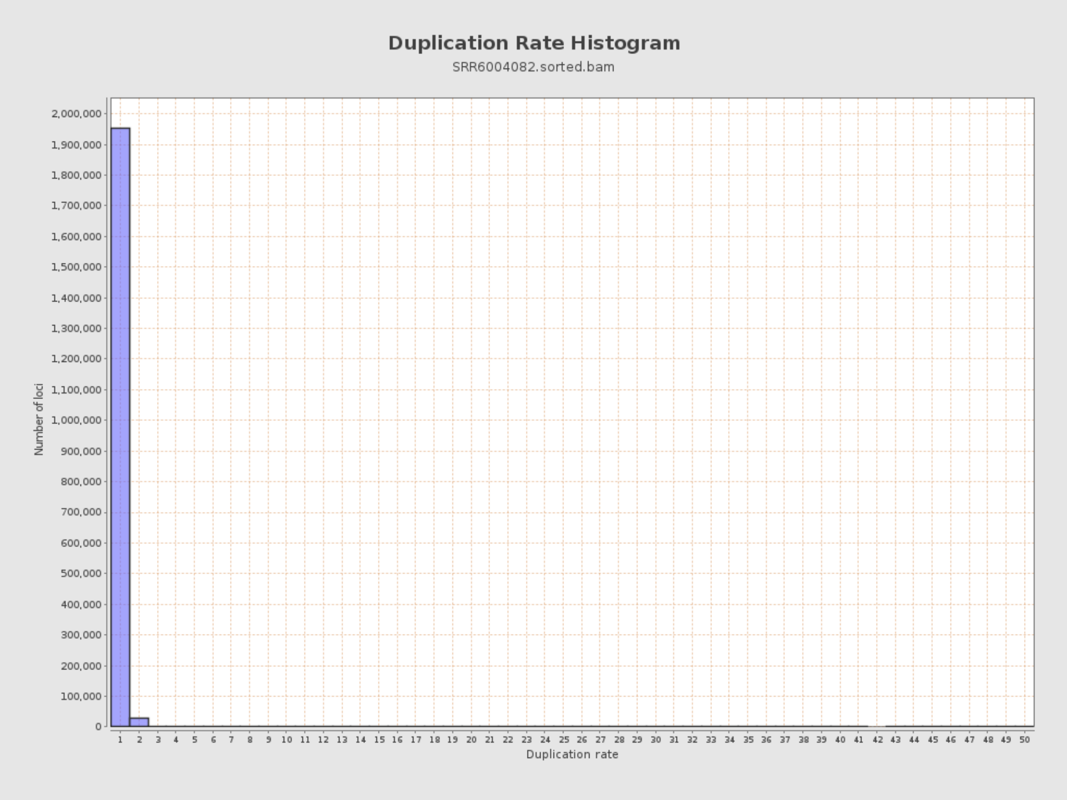
5. Results : Coverage Histogram (0-50X)



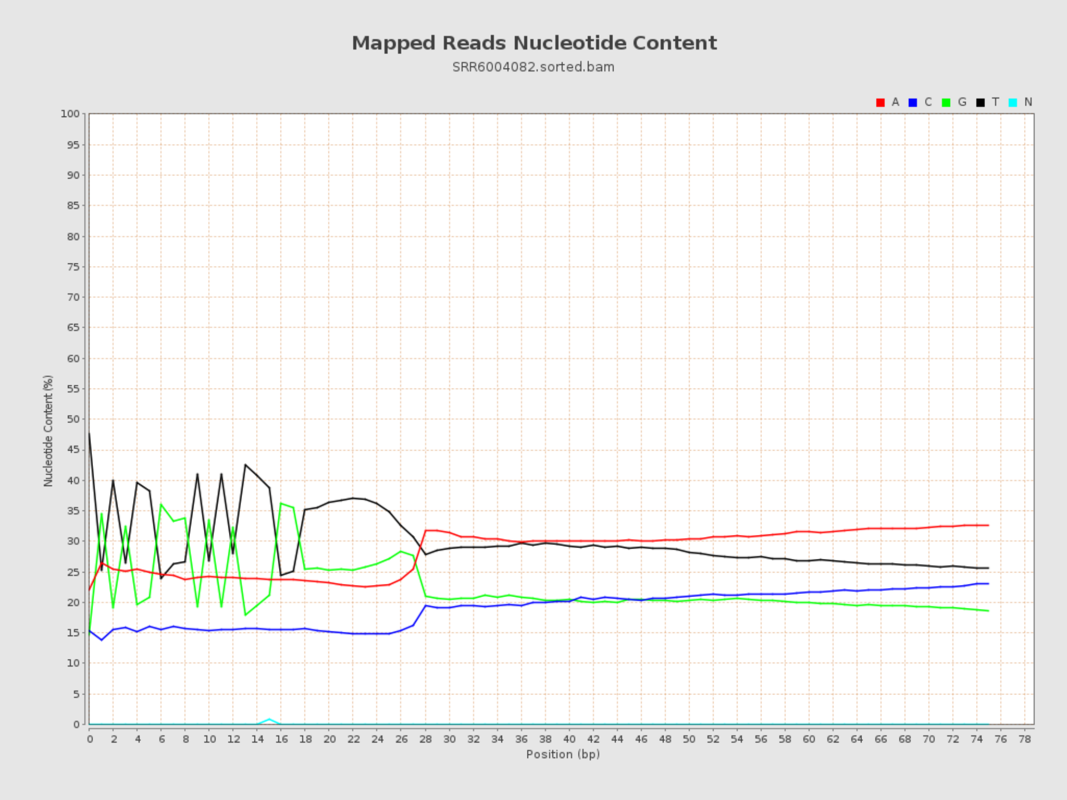
6. Results : Genome Fraction Coverage



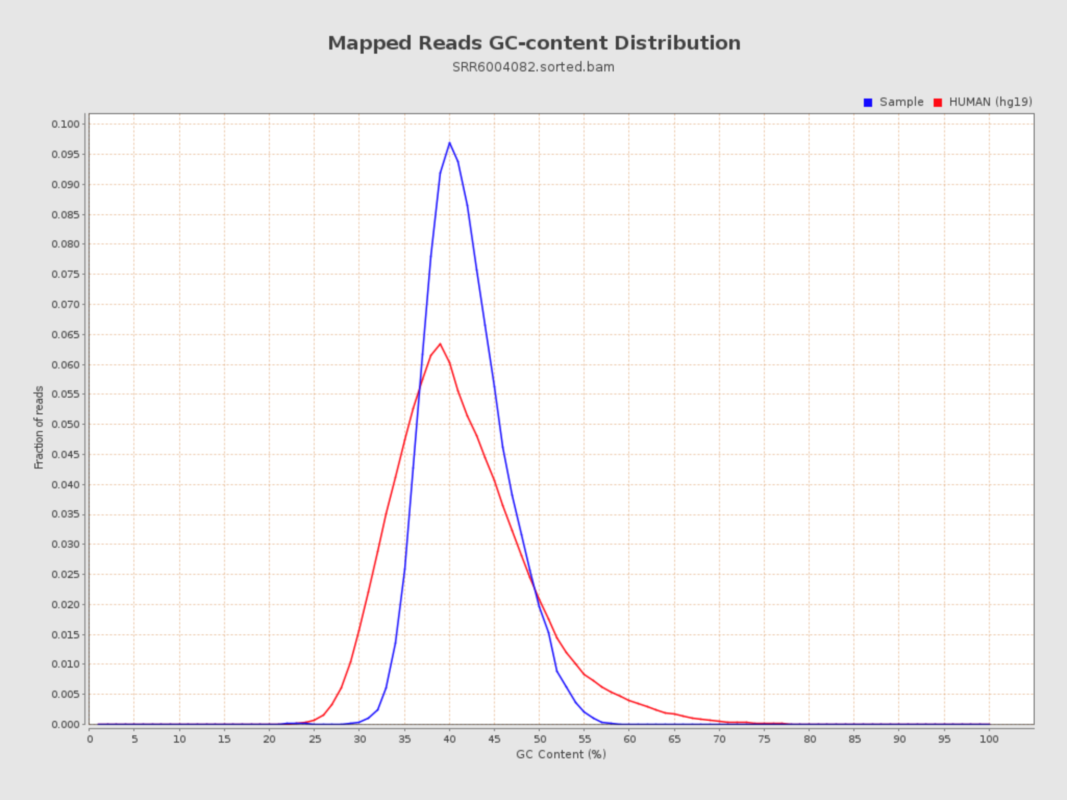
7. Results : Duplication Rate Histogram



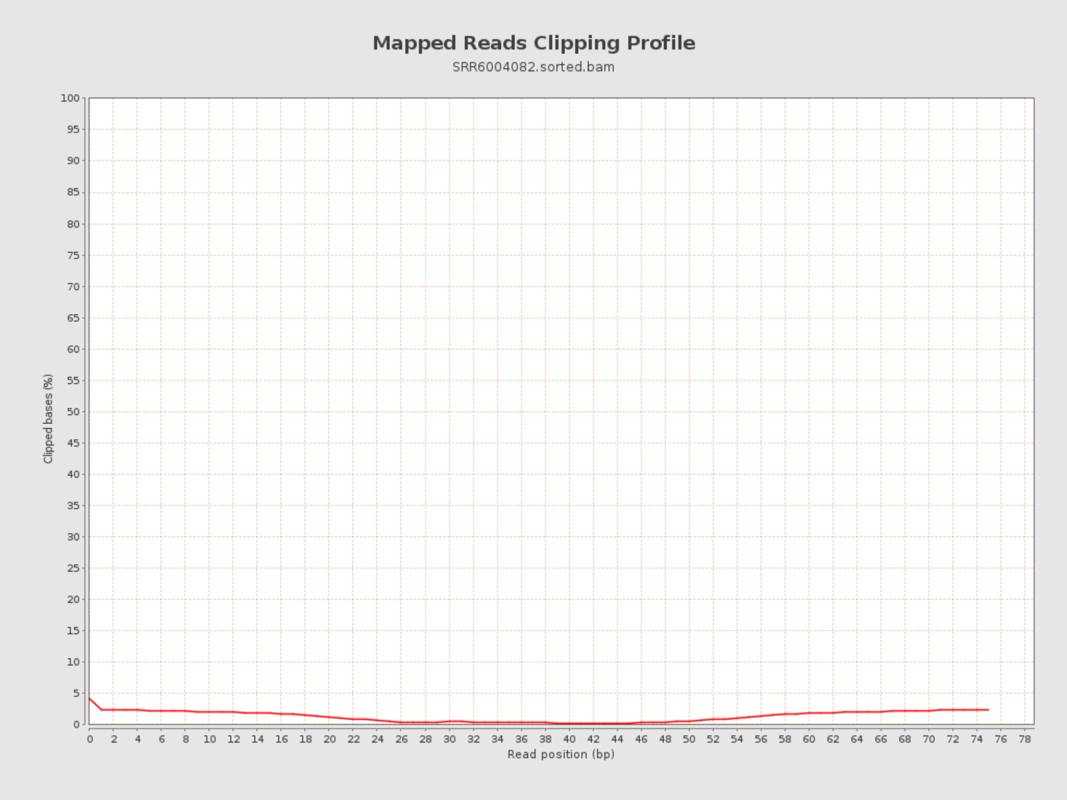
8. Results : Mapped Reads Nucleotide Content



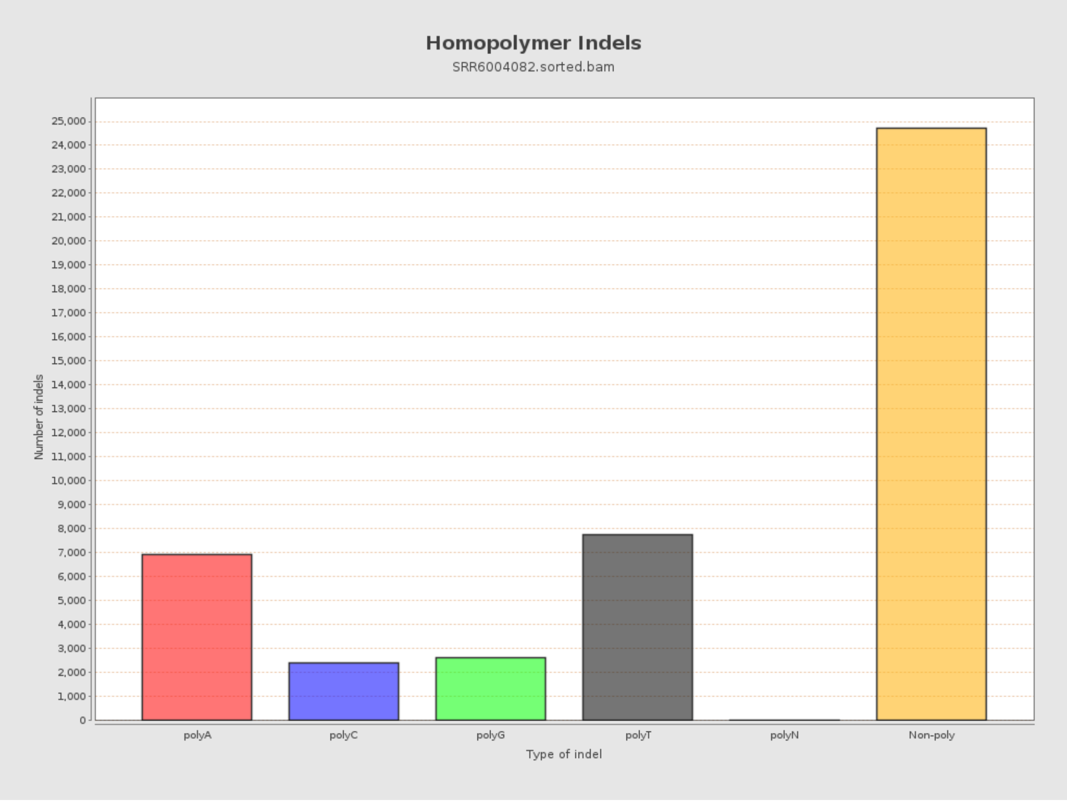
9. Results : Mapped Reads GC-content Distribution



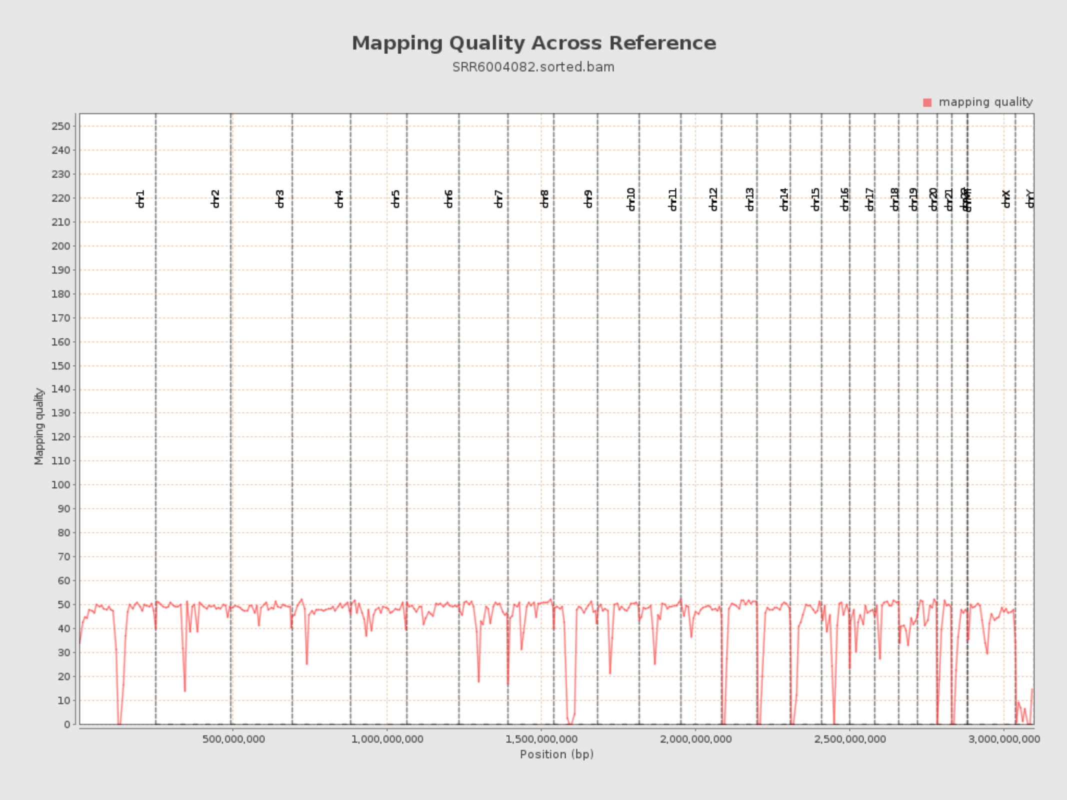
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram