Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:07:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082926.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_SRR3082926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:07:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,876,825
Mapped reads	1,690,990 / 90.1%
Unmapped reads	185,835 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,830 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	79,351 / 4.23%
Duplication rate	4.09%
Clipped reads	749,316 / 39.92%

2.2. ACGT Content

Number/percentage of A's	30,756,630 / 27.23%
Number/percentage of C's	21,389,979 / 18.93%
Number/percentage of T's	35,253,881 / 31.21%
Number/percentage of G's	25,561,756 / 22.63%
Number/percentage of N's	5,010 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.2661

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

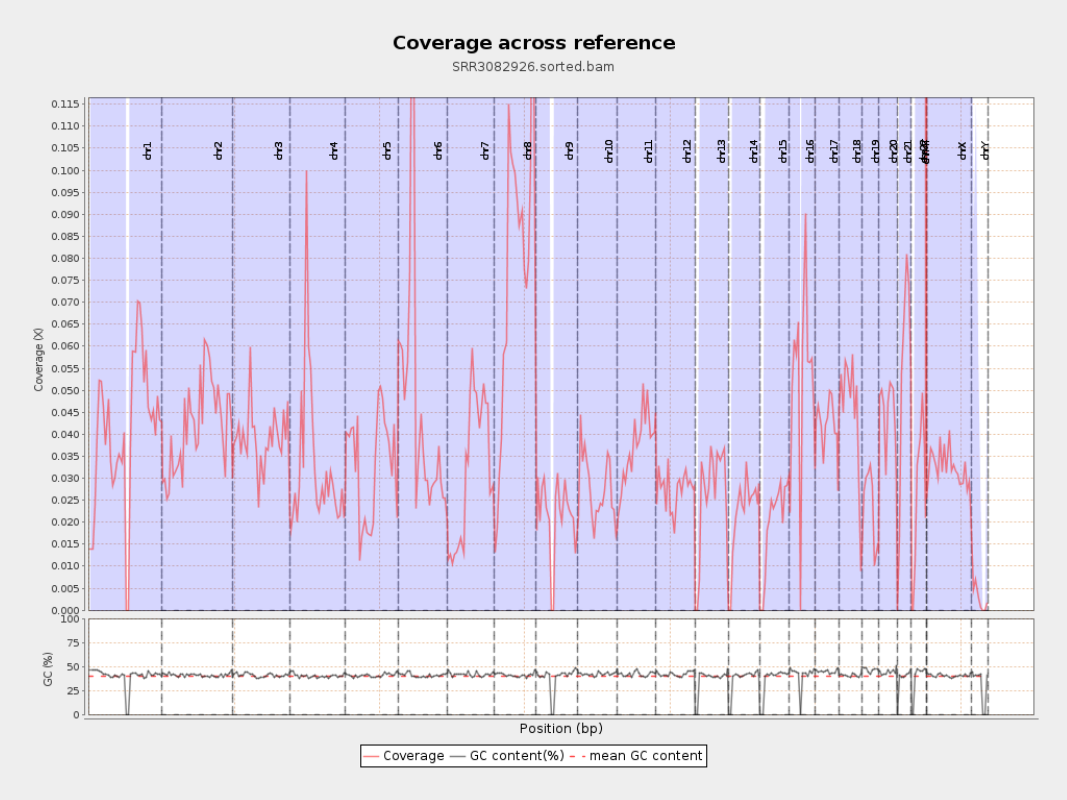
General error rate	0.72%
Mismatches	798,516
Insertions	8,641
Mapped reads with at least one insertion	0.51%
Deletions	25,687
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.49%

2.6. Chromosome stats

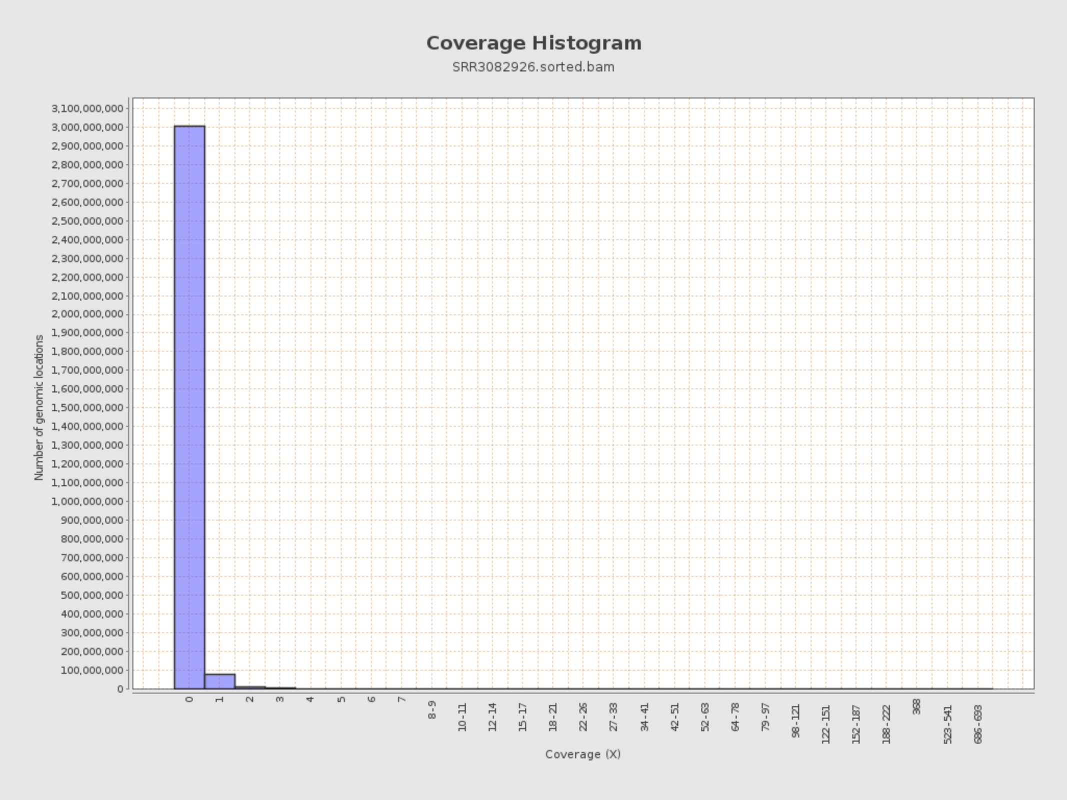
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10125268	0.0406	0.3017
chr2	243199373	10184007	0.0419	0.3919
chr3	198022430	7709548	0.0389	0.2327
chr4	191154276	6280323	0.0329	0.2183
chr5	180915260	5978777	0.033	0.2145
chr6	171115067	8059197	0.0471	0.3021
chr7	159138663	5155317	0.0324	0.2448

chr8	146364022	11503645	0.0786	0.3757
chr9	141213431	3022933	0.0214	0.2115
chr10	135534747	3753833	0.0277	0.2082
chr11	135006516	4961265	0.0367	0.2516
chr12	133851895	3670905	0.0274	0.1955
chr13	115169878	2984403	0.0259	0.1906
chr14	107349540	2314879	0.0216	0.1831
chr15	102531392	2022408	0.0197	0.1728
chr16	90354753	4775455	0.0529	0.2784
chr17	81195210	3429552	0.0422	0.2519
chr18	78077248	3617688	0.0463	0.4162
chr19	59128983	1422046	0.024	0.2296
chr20	63025520	2818371	0.0447	0.2577
chr21	48129895	2505223	0.0521	0.2741
chr22	51304566	1358645	0.0265	0.1932
chrMT	16571	147686	8.9123	5.5589
chrX	155270560	5016858	0.0323	0.2183
chrY	59373566	190884	0.0032	0.0672

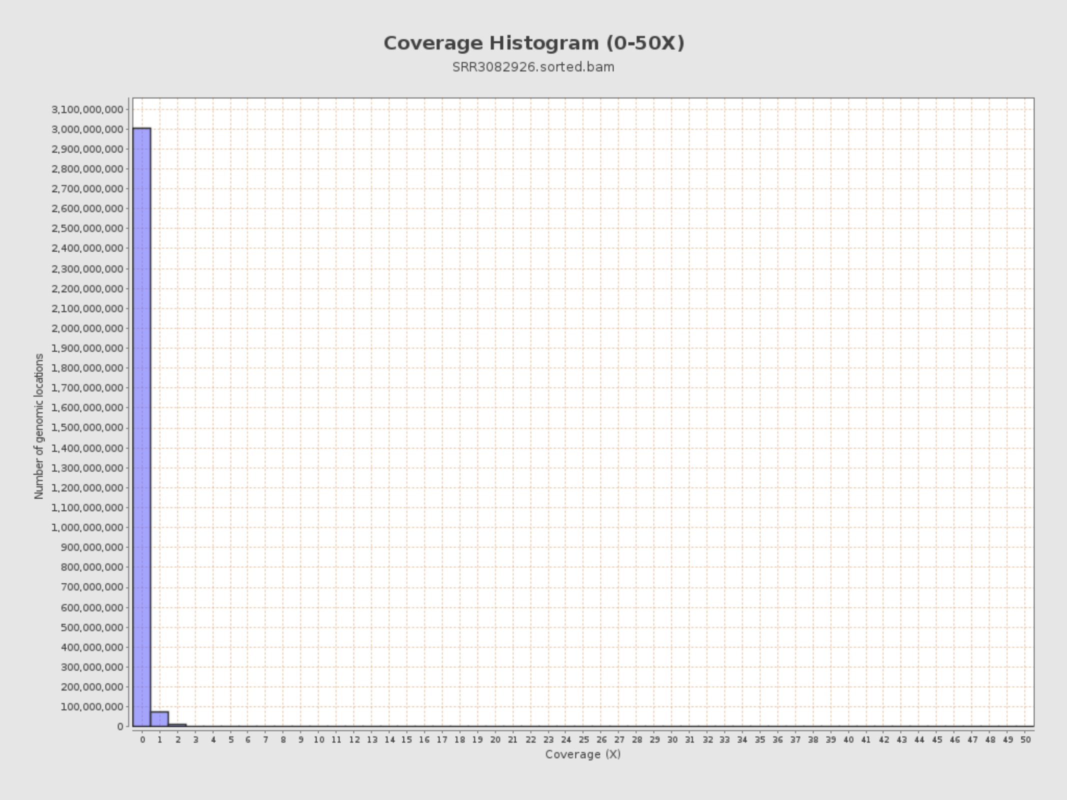
3. Results : Coverage across reference



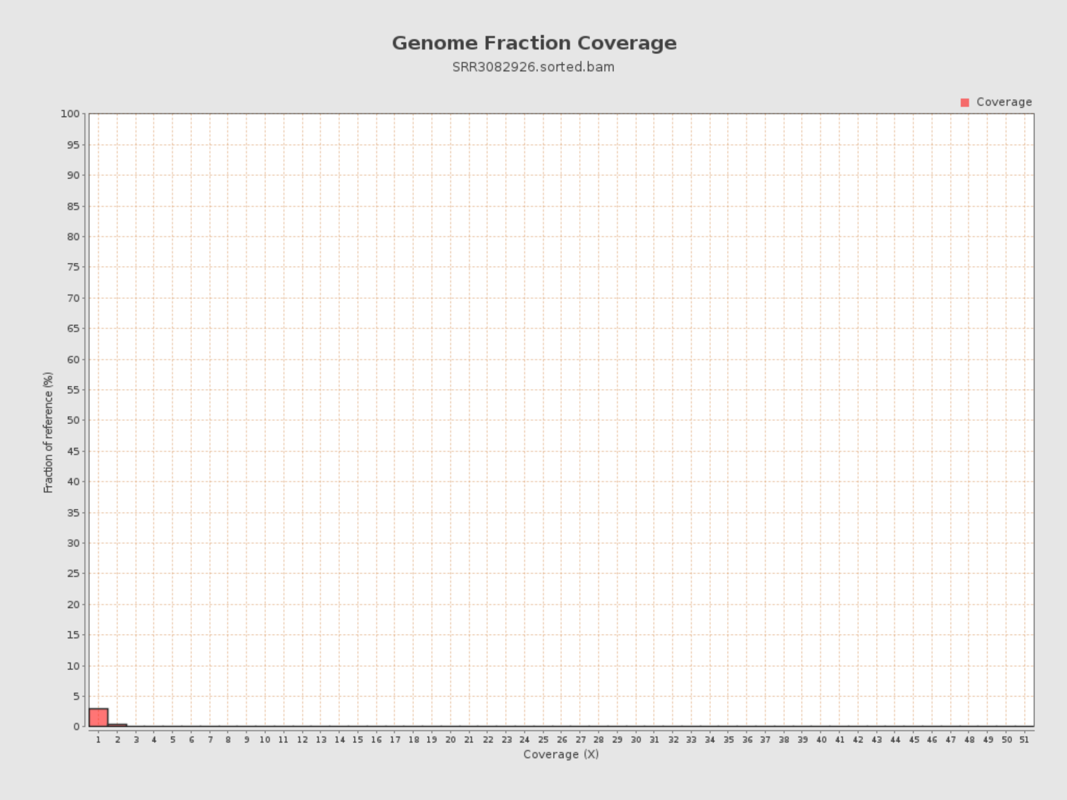
4. Results : Coverage Histogram



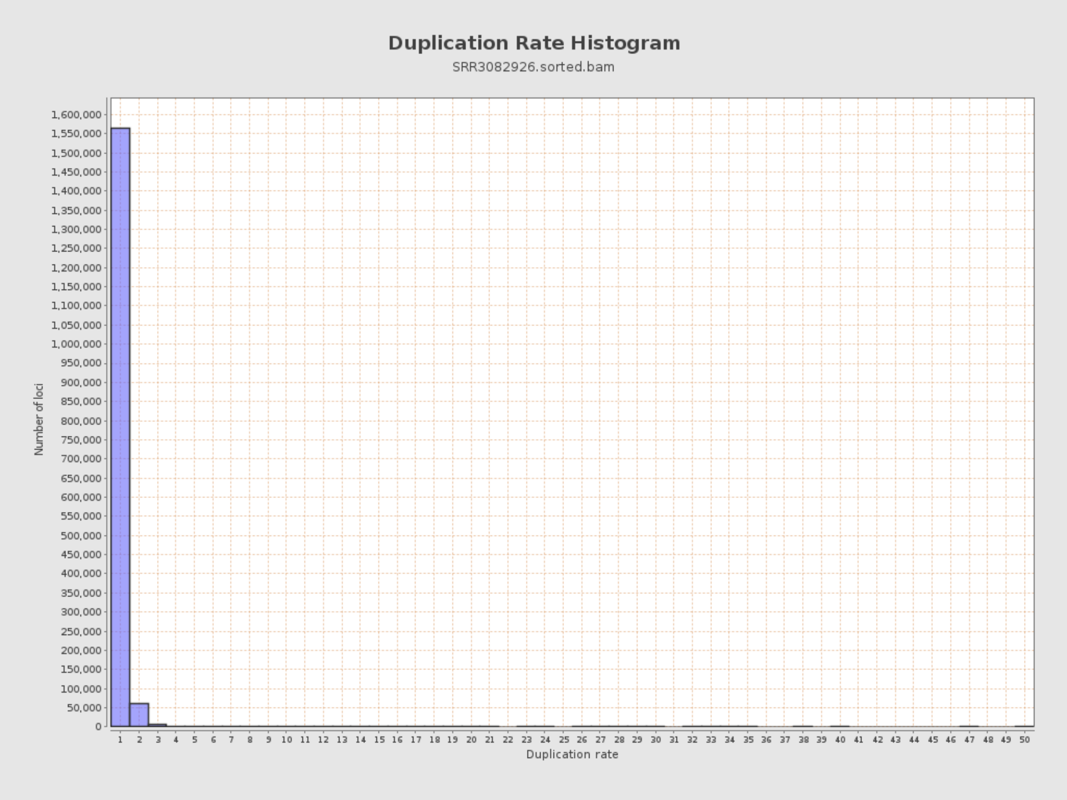
5. Results : Coverage Histogram (0-50X)



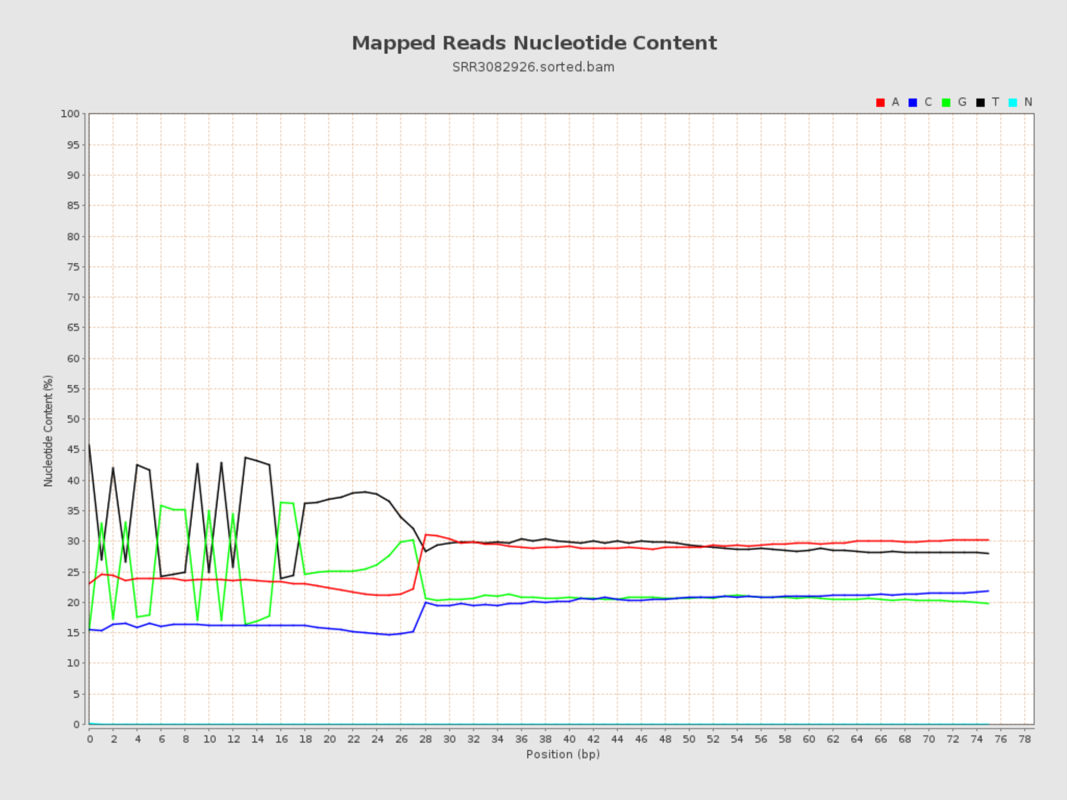
6. Results : Genome Fraction Coverage



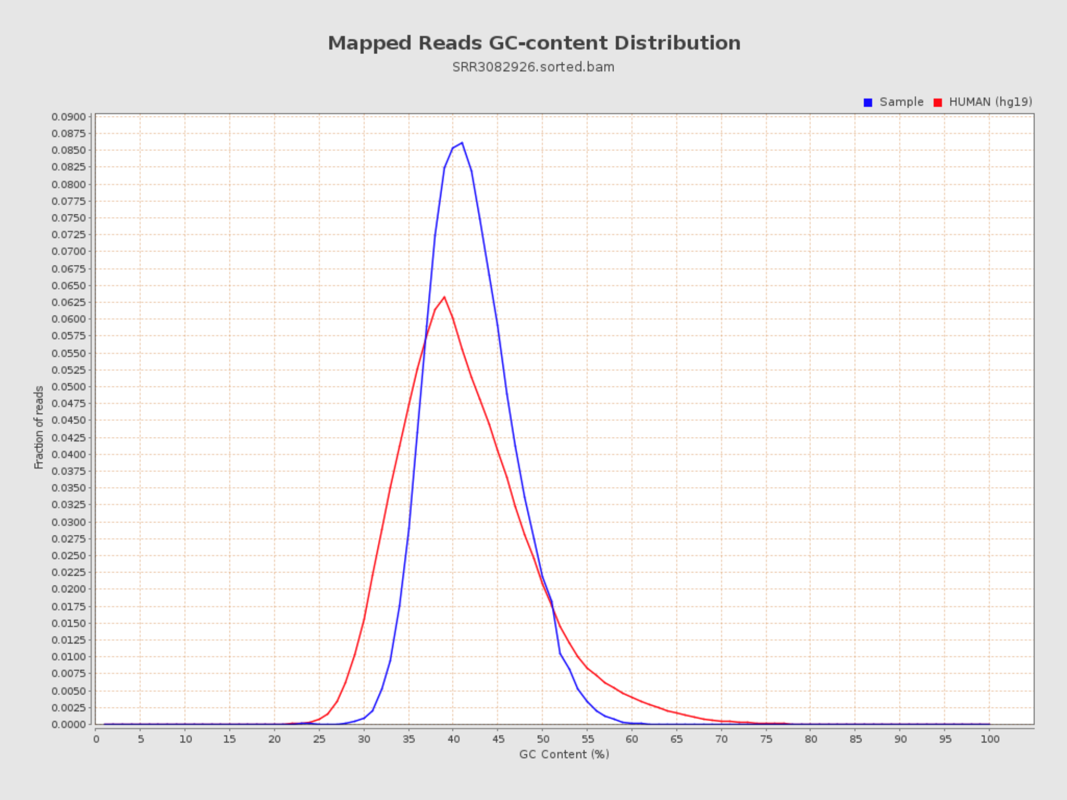
7. Results : Duplication Rate Histogram



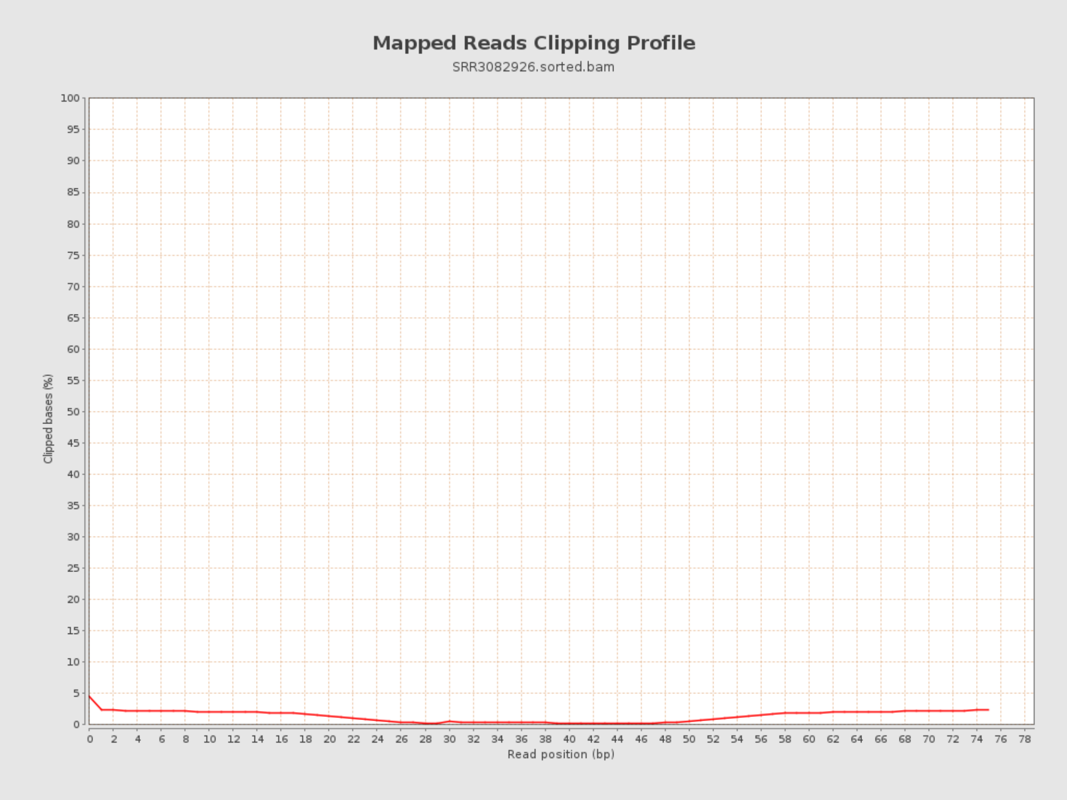
8. Results : Mapped Reads Nucleotide Content



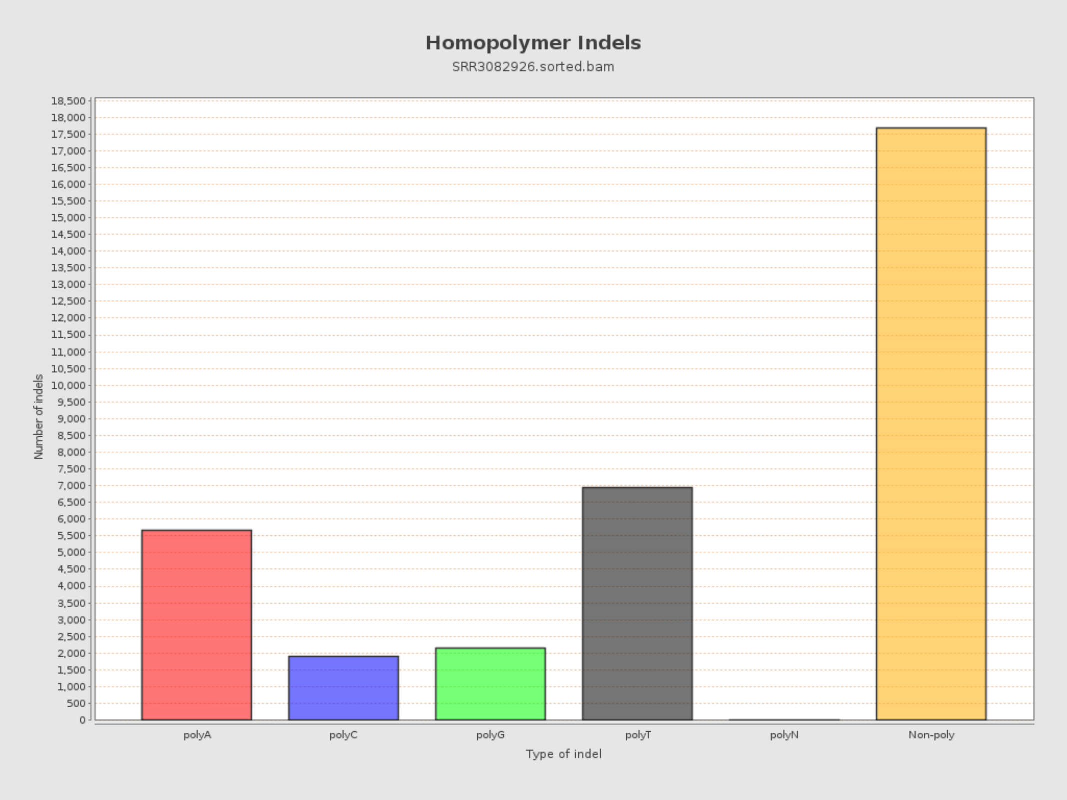
9. Results : Mapped Reads GC-content Distribution



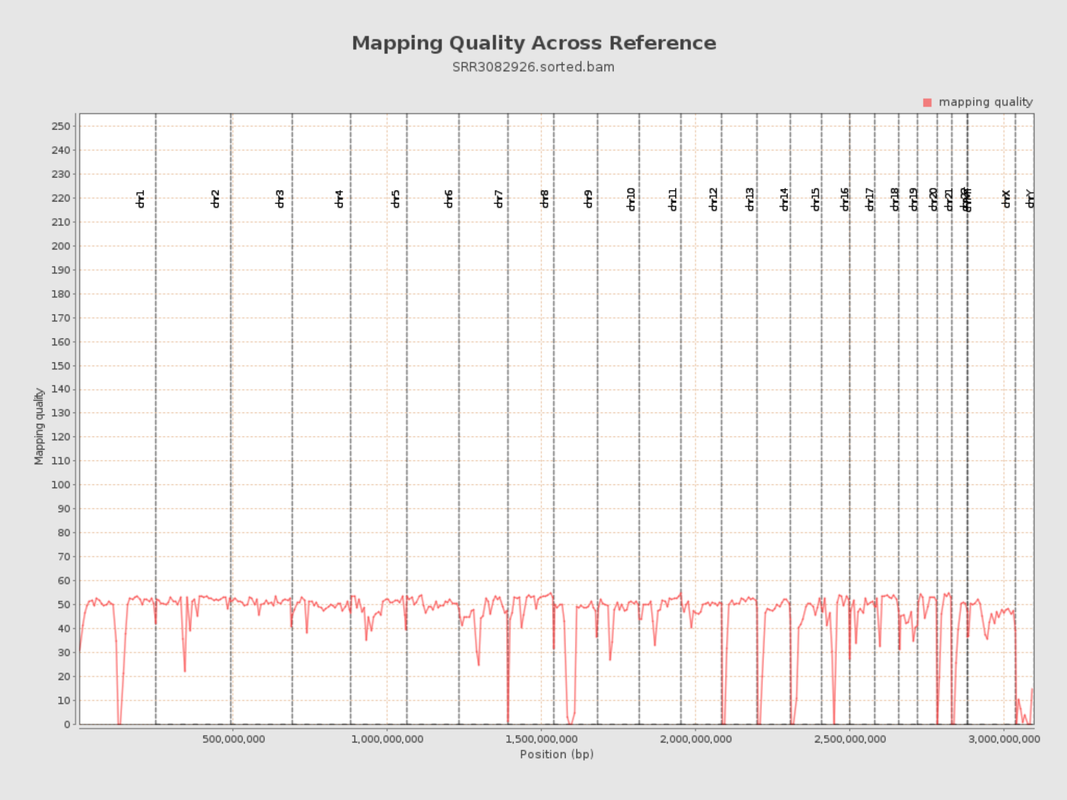
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram