Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:08:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082953.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_SRR3082953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:08:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,583,464
Mapped reads	1,458,122 / 92.08%
Unmapped reads	125,342 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,723 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	65,442 / 4.13%
Duplication rate	3.69%
Clipped reads	599,235 / 37.84%

2.2. ACGT Content

Number/percentage of A's	27,605,767 / 28.06%
Number/percentage of C's	17,842,326 / 18.14%
Number/percentage of T's	31,747,100 / 32.27%
Number/percentage of G's	21,170,478 / 21.52%
Number/percentage of N's	4,561 / 0%
GC Percentage	39.66%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.2797

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

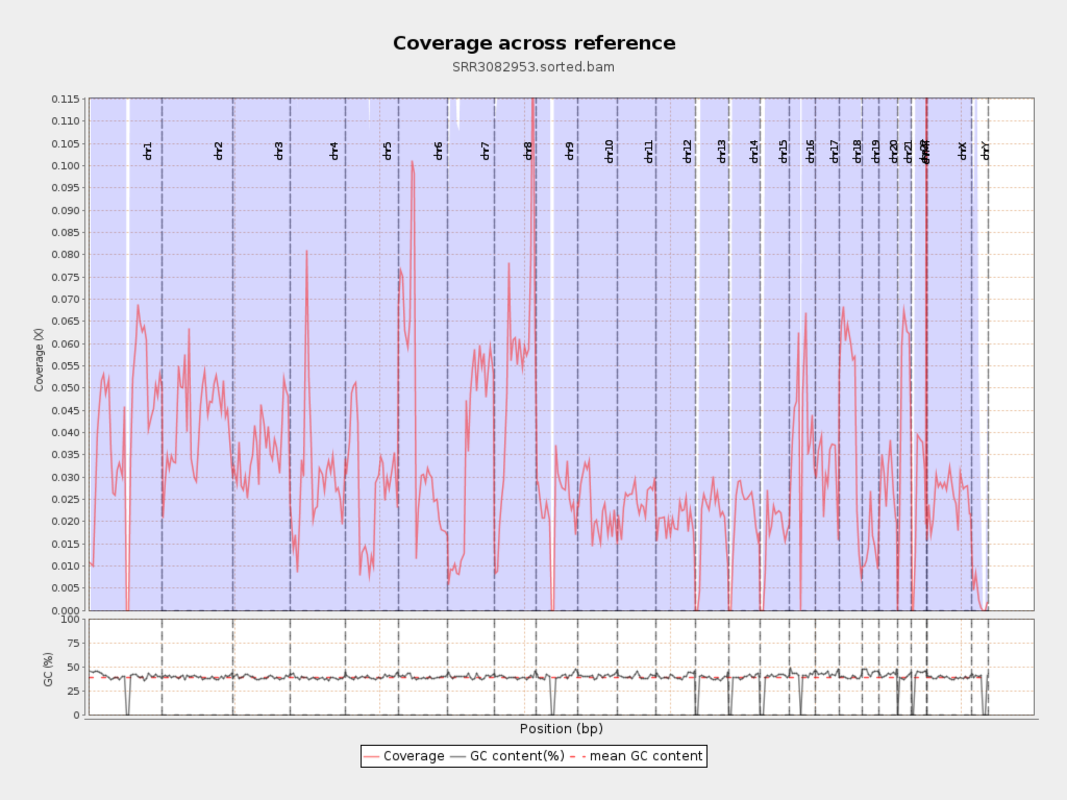
General error rate	0.74%
Mismatches	713,130
Insertions	8,242
Mapped reads with at least one insertion	0.56%
Deletions	23,005
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.62%

2.6. Chromosome stats

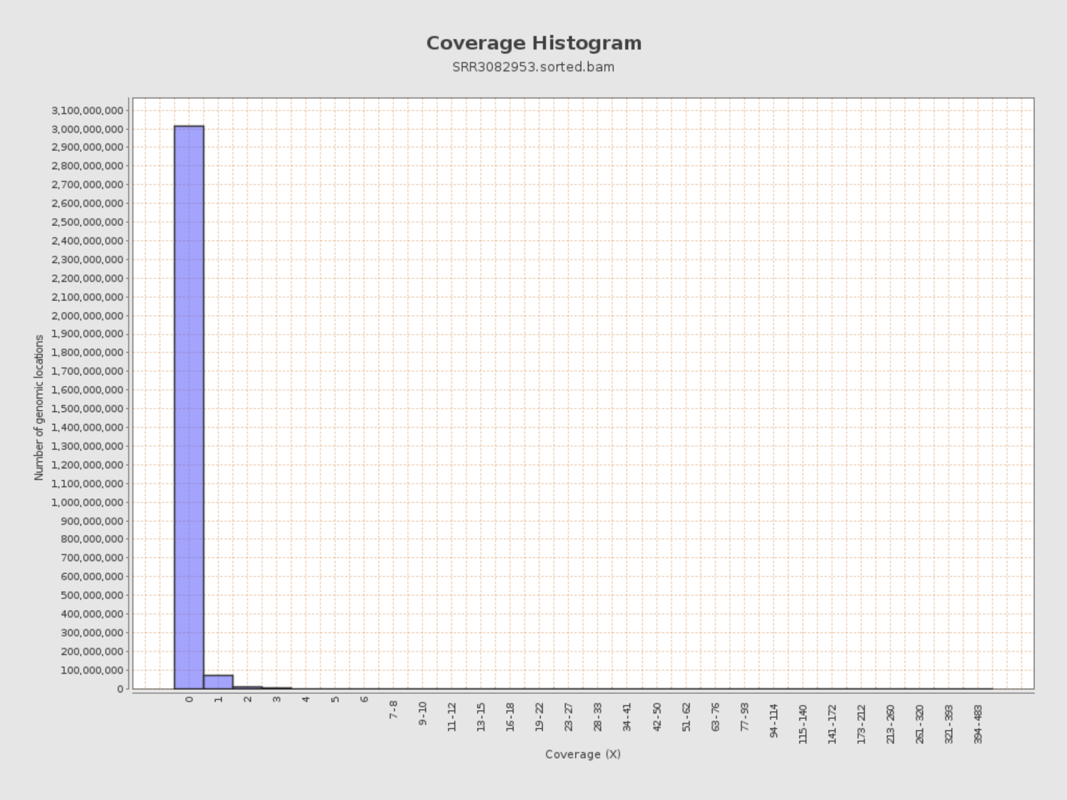
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10272249	0.0412	0.4
chr2	243199373	10422780	0.0429	0.4028
chr3	198022430	7222808	0.0365	0.2174
chr4	191154276	5607685	0.0293	0.1993
chr5	180915260	5058323	0.028	0.1905
chr6	171115067	7237202	0.0423	0.271
chr7	159138663	5824872	0.0366	0.3098

chr8	146364022	7801256	0.0533	0.4111
chr9	141213431	3254727	0.023	0.2776
chr10	135534747	3105309	0.0229	0.2029
chr11	135006516	3309519	0.0245	0.2071
chr12	133851895	2673321	0.02	0.1677
chr13	115169878	2229053	0.0194	0.1587
chr14	107349540	2208699	0.0206	0.1798
chr15	102531392	1712448	0.0167	0.1531
chr16	90354753	3684998	0.0408	0.2451
chr17	81195210	2522915	0.0311	0.2069
chr18	78077248	3831089	0.0491	0.5607
chr19	59128983	865052	0.0146	0.274
chr20	63025520	1816053	0.0288	0.197
chr21	48129895	2299051	0.0478	0.2583
chr22	51304566	1278010	0.0249	0.1786
chrMT	16571	4341	0.262	0.5702
chrX	155270560	3984764	0.0257	0.1967
chrY	59373566	181162	0.0031	0.0735

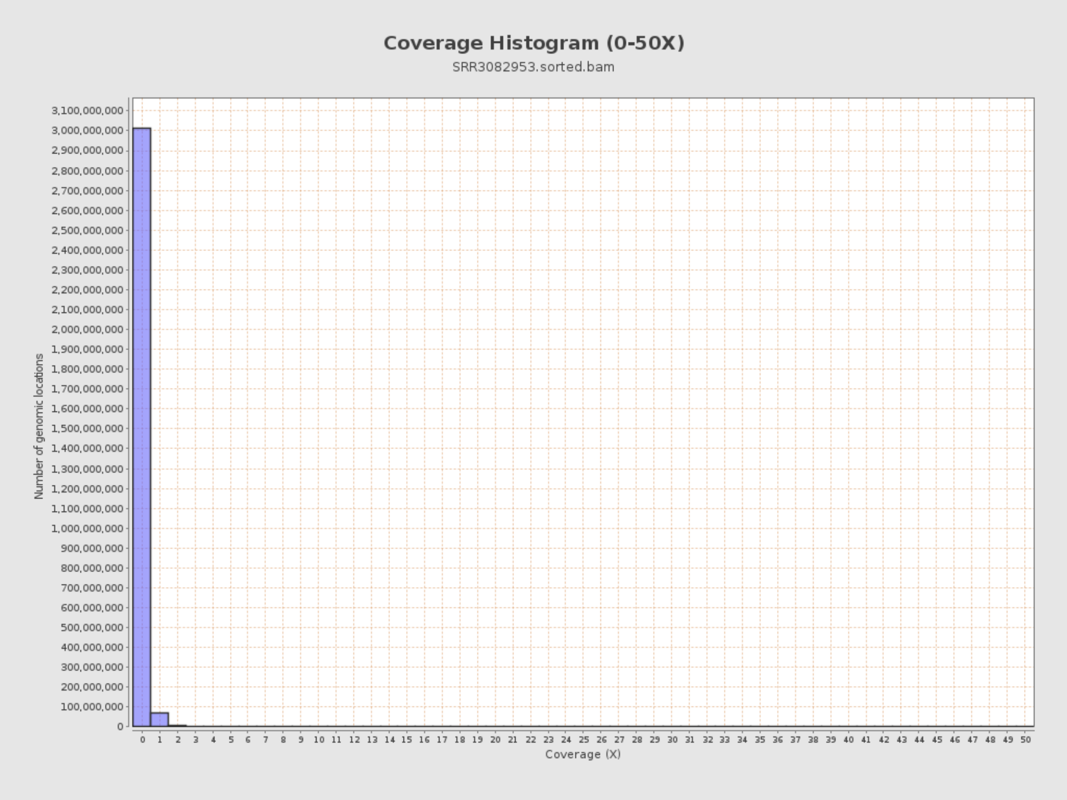
3. Results : Coverage across reference



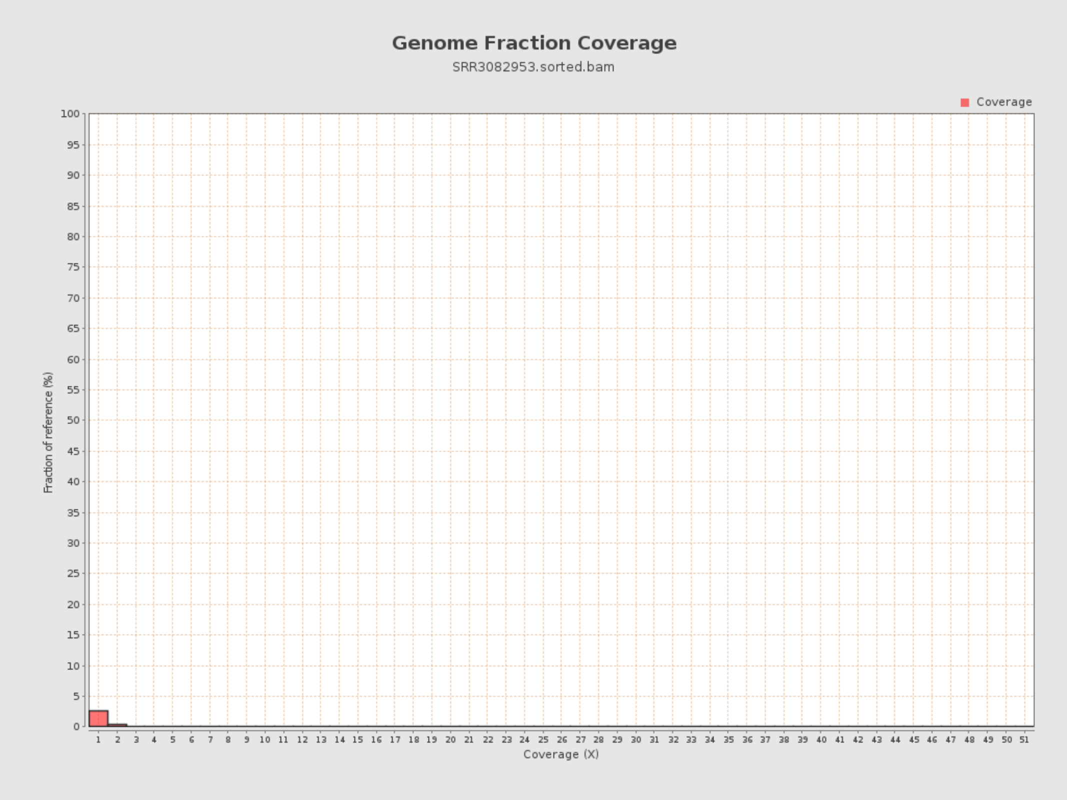
4. Results : Coverage Histogram



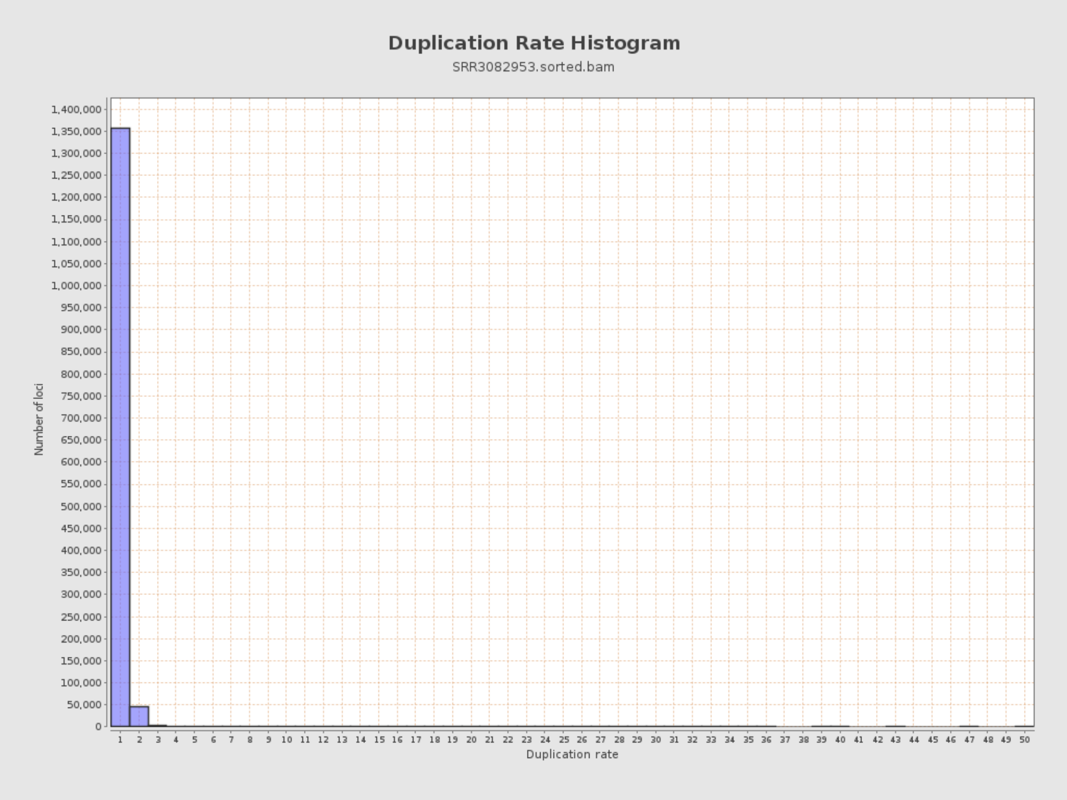
5. Results : Coverage Histogram (0-50X)



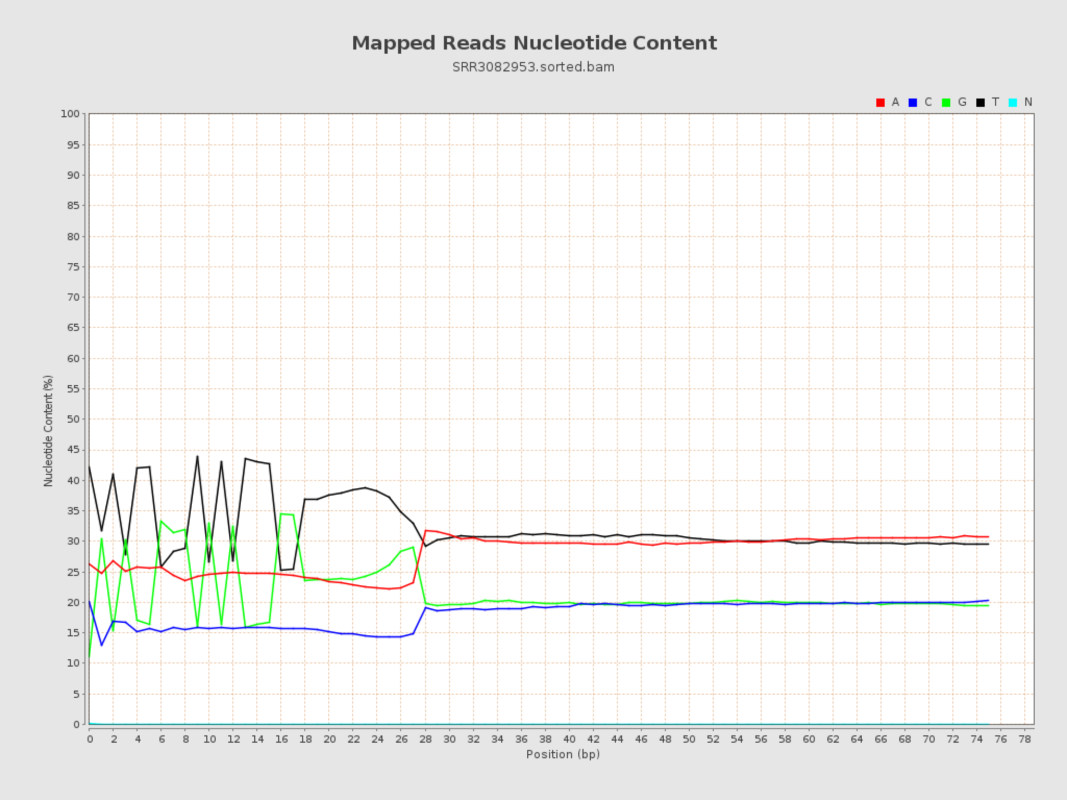
6. Results : Genome Fraction Coverage



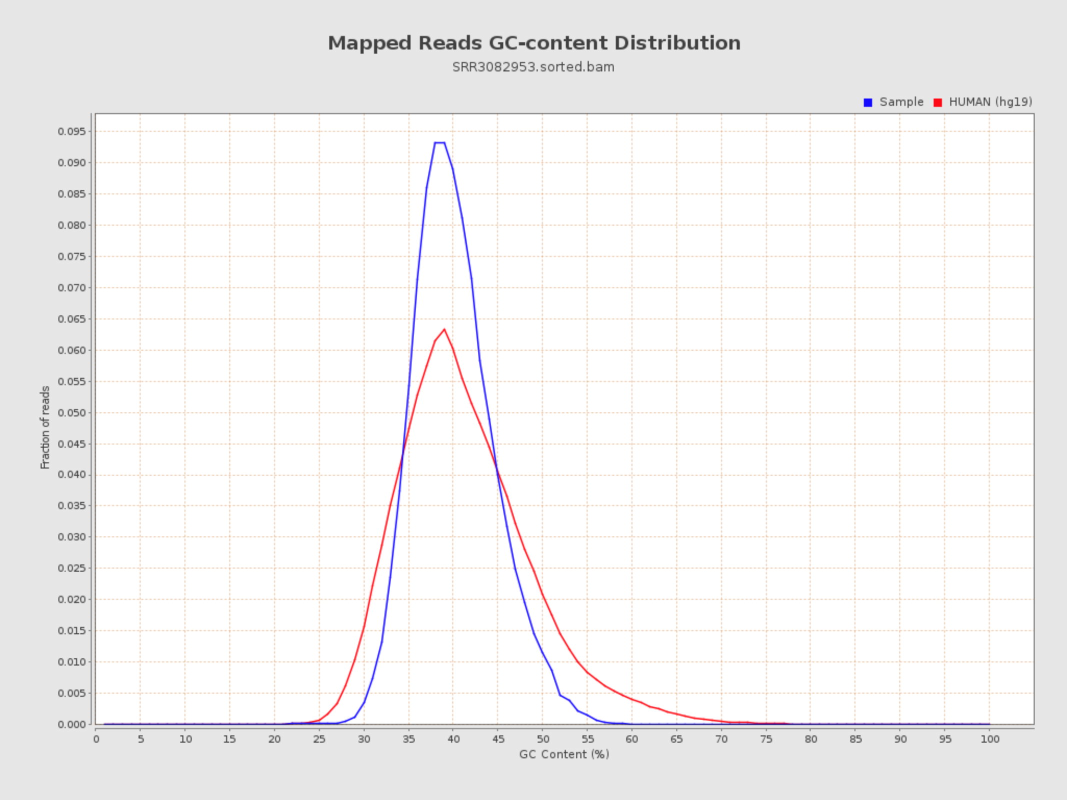
7. Results : Duplication Rate Histogram



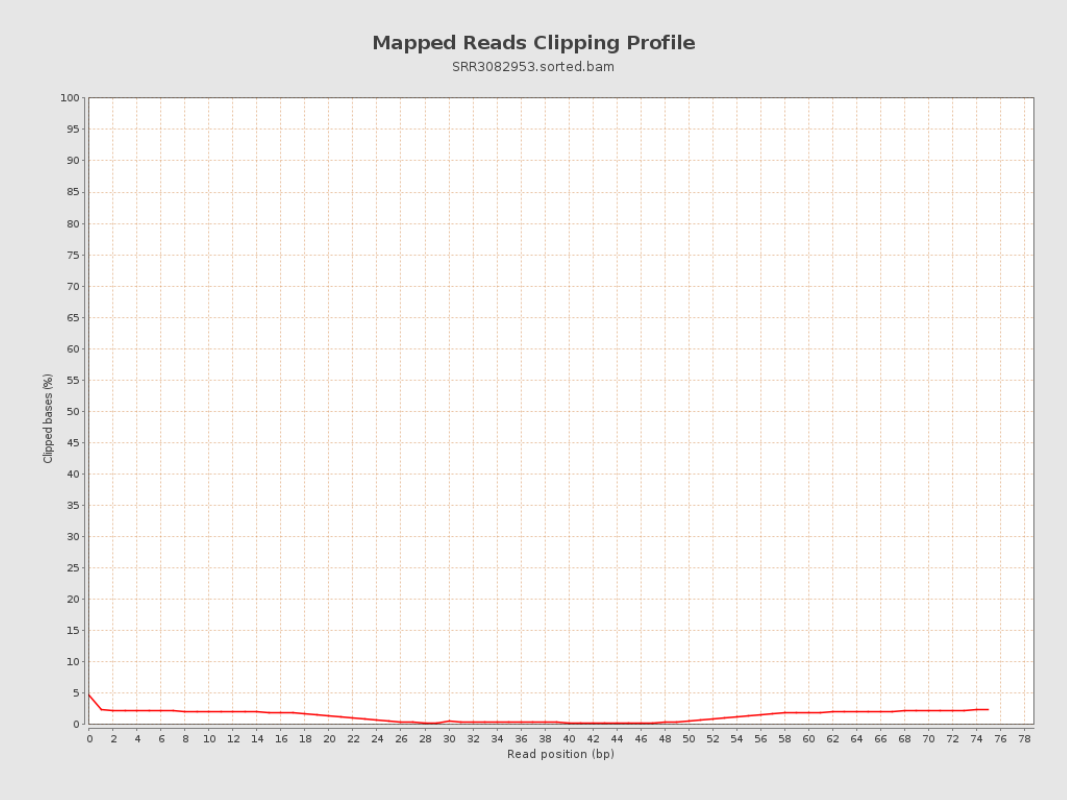
8. Results : Mapped Reads Nucleotide Content



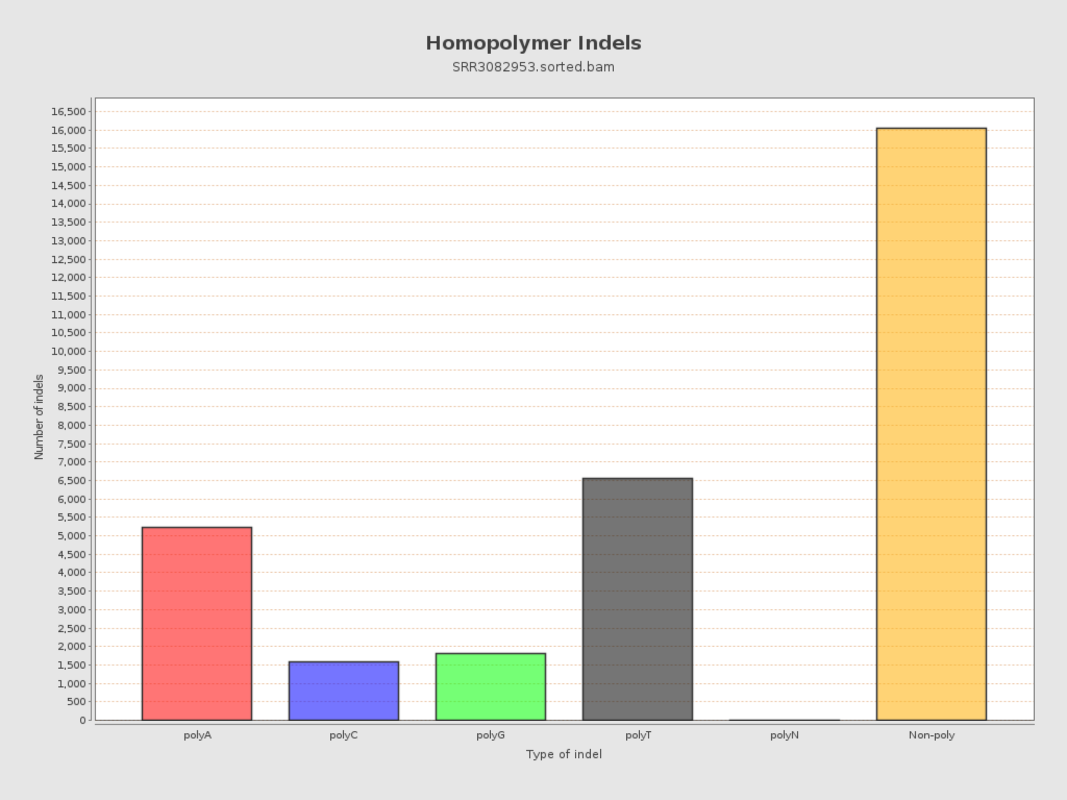
9. Results : Mapped Reads GC-content Distribution



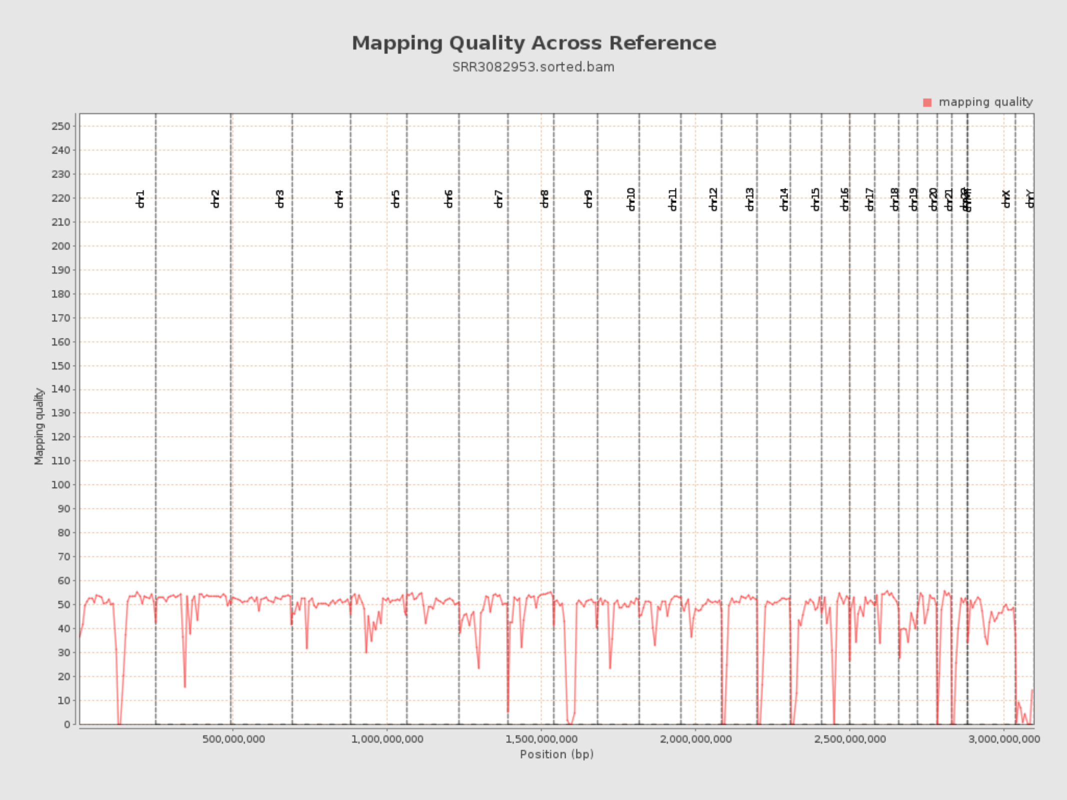
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram