Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:16:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082458.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_SRR3082458 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082458.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:16:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082458.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,322
Mapped reads	1,777,020 / 92.01%
Unmapped reads	154,302 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,795 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	51,783 / 2.68%
Duplication rate	2.14%
Clipped reads	587,893 / 30.44%

2.2. ACGT Content

Number/percentage of A's	36,973,829 / 29.72%
Number/percentage of C's	23,304,805 / 18.73%
Number/percentage of T's	38,093,778 / 30.62%
Number/percentage of G's	26,023,113 / 20.92%
Number/percentage of N's	2,677 / 0%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3683

2.4. Mapping Quality

Mean Mapping Quality	47.54

2.5. Mismatches and indels

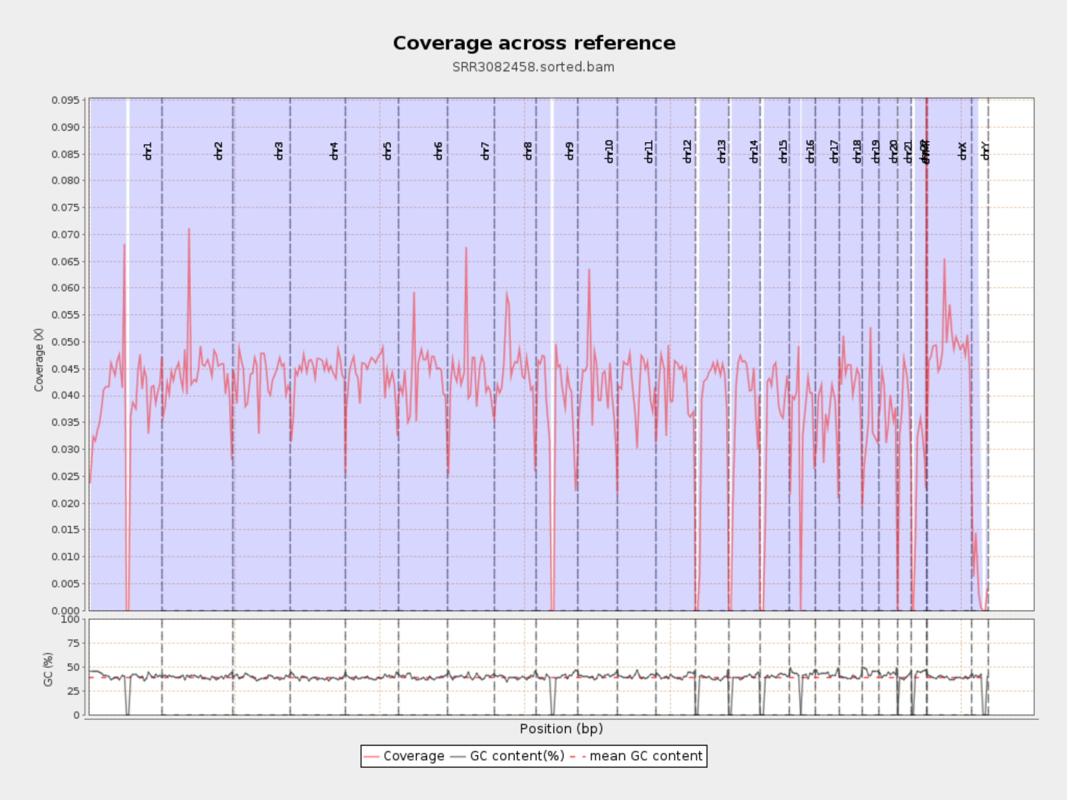
General error rate	0.85%
Mismatches	1,039,851
Insertions	10,307
Mapped reads with at least one insertion	0.58%
Deletions	27,626
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.76%

2.6. Chromosome stats

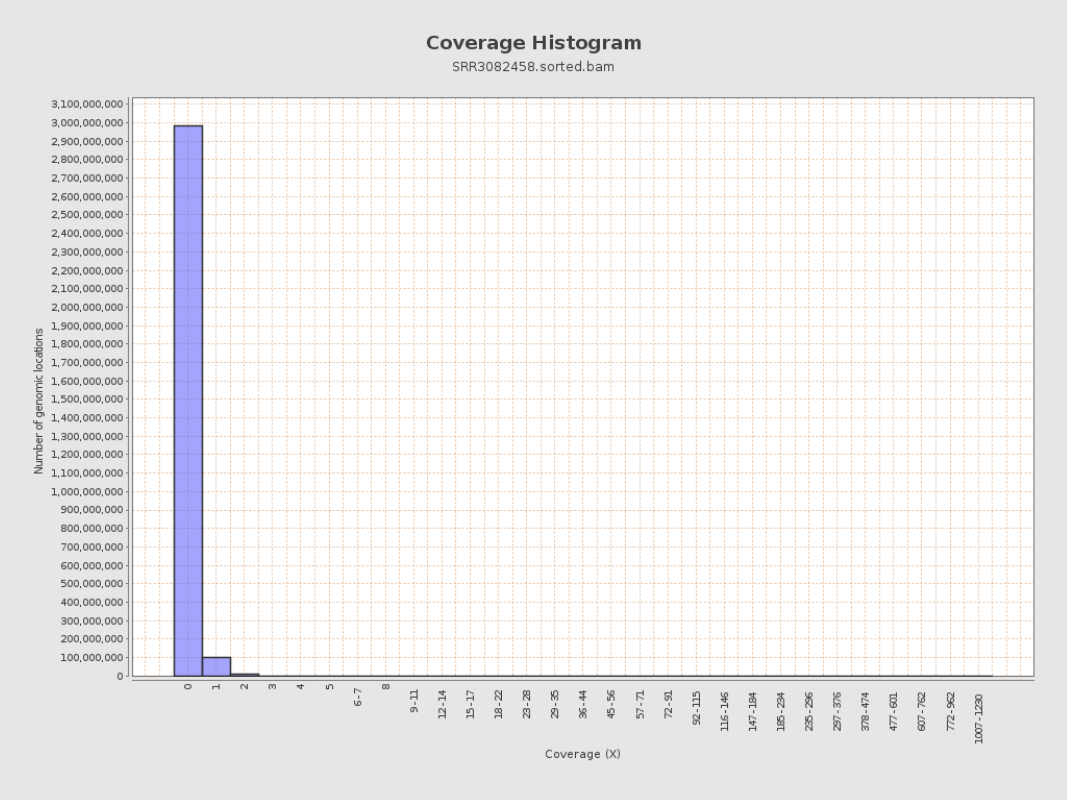
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9589393	0.0385	0.63
chr2	243199373	10798590	0.0444	0.3628
chr3	198022430	8614739	0.0435	0.2265
chr4	191154276	8524892	0.0446	0.2347
chr5	180915260	7968454	0.044	0.2281
chr6	171115067	7489804	0.0438	0.2681
chr7	159138663	6954536	0.0437	0.4507

chr8	146364022	6491407	0.0444	0.7686
chr9	141213431	5165783	0.0366	0.3149
chr10	135534747	5757039	0.0425	0.3241
chr11	135006516	5673716	0.042	0.2838
chr12	133851895	5543417	0.0414	0.2248
chr13	115169878	4145427	0.036	0.2037
chr14	107349540	3816180	0.0355	0.2183
chr15	102531392	3436554	0.0335	0.1984
chr16	90354753	3146113	0.0348	0.2299
chr17	81195210	2858310	0.0352	0.2316
chr18	78077248	3428638	0.0439	0.6036
chr19	59128983	2007036	0.0339	0.4625
chr20	63025520	2324375	0.0369	0.2131
chr21	48129895	1676614	0.0348	0.2154
chr22	51304566	1138097	0.0222	0.1594
chrMT	16571	2934	0.1771	0.4507
chrX	155270560	7598939	0.0489	0.2601
chrY	59373566	292857	0.0049	0.1111

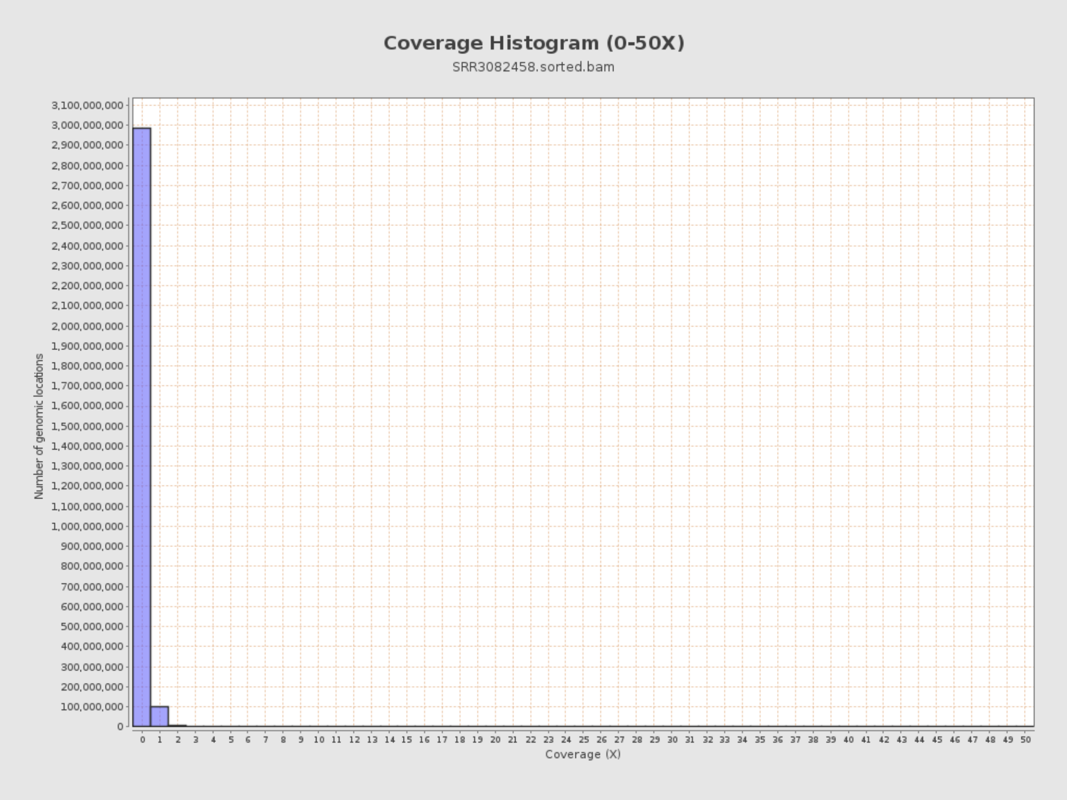
3. Results : Coverage across reference



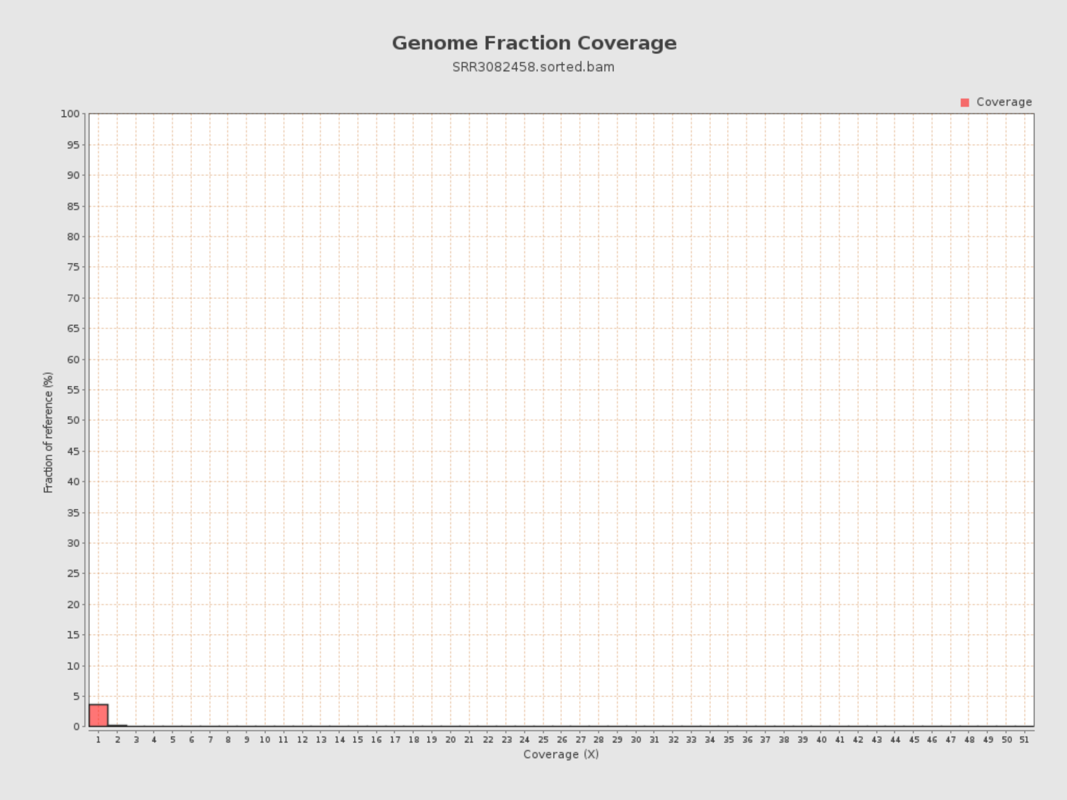
4. Results : Coverage Histogram



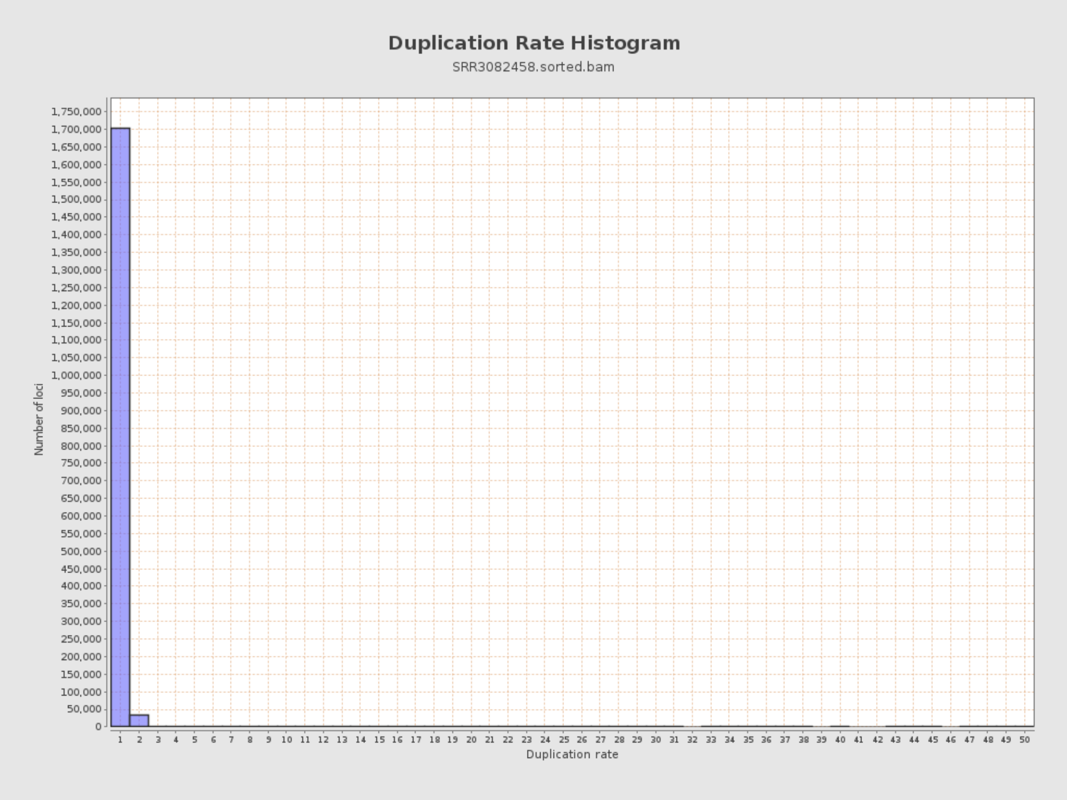
5. Results : Coverage Histogram (0-50X)



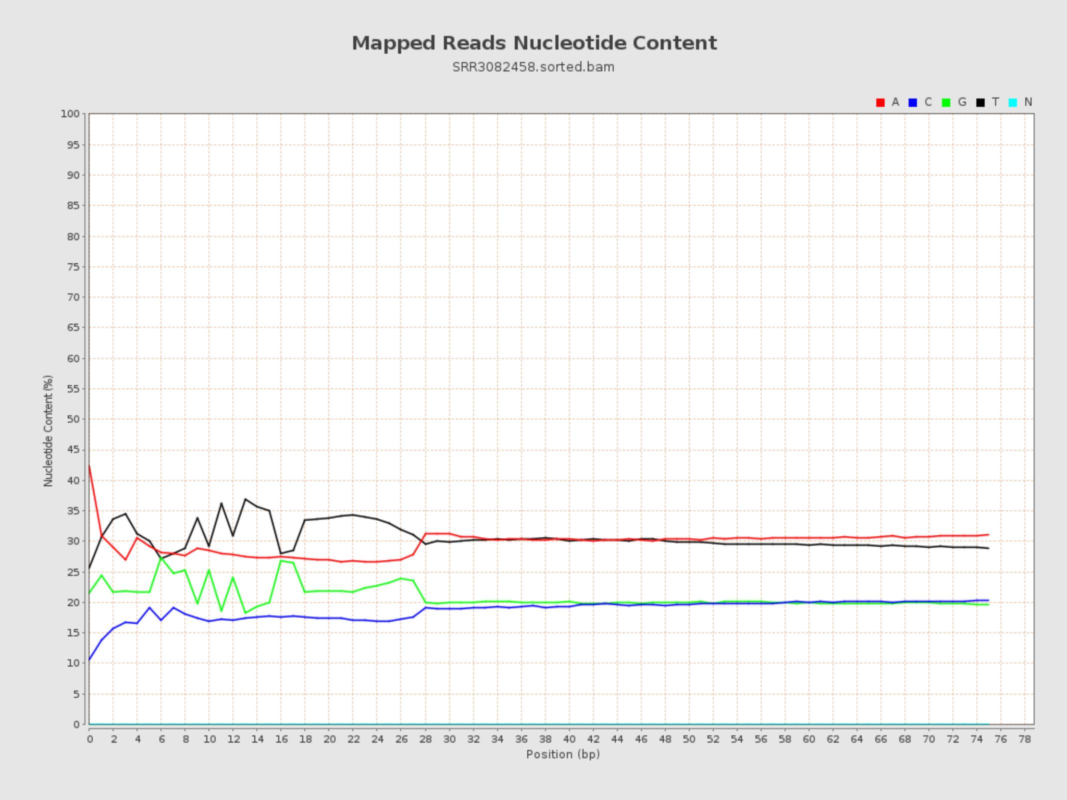
6. Results : Genome Fraction Coverage



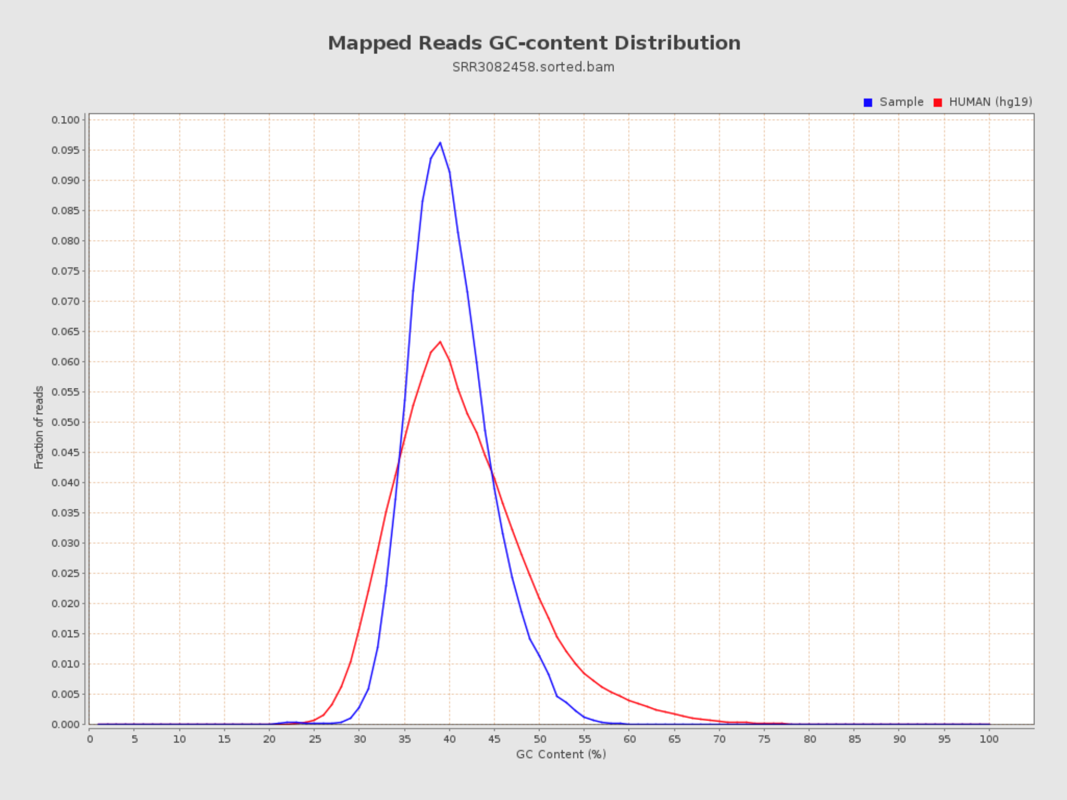
7. Results : Duplication Rate Histogram



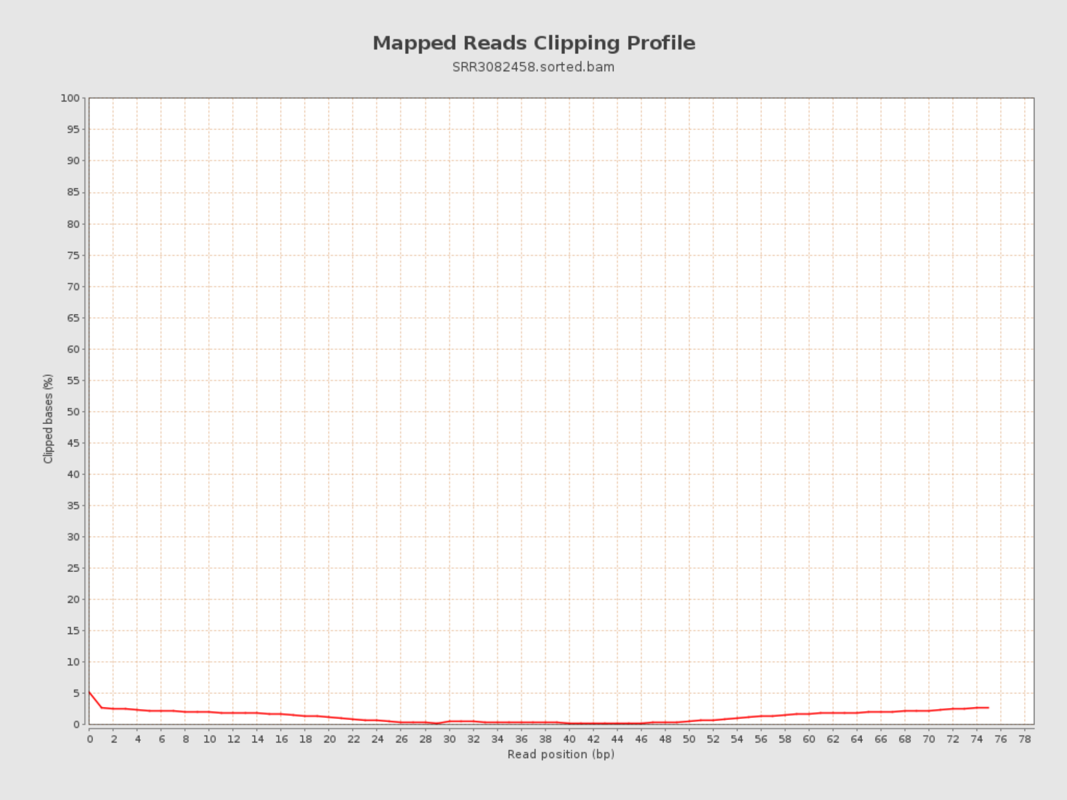
8. Results : Mapped Reads Nucleotide Content



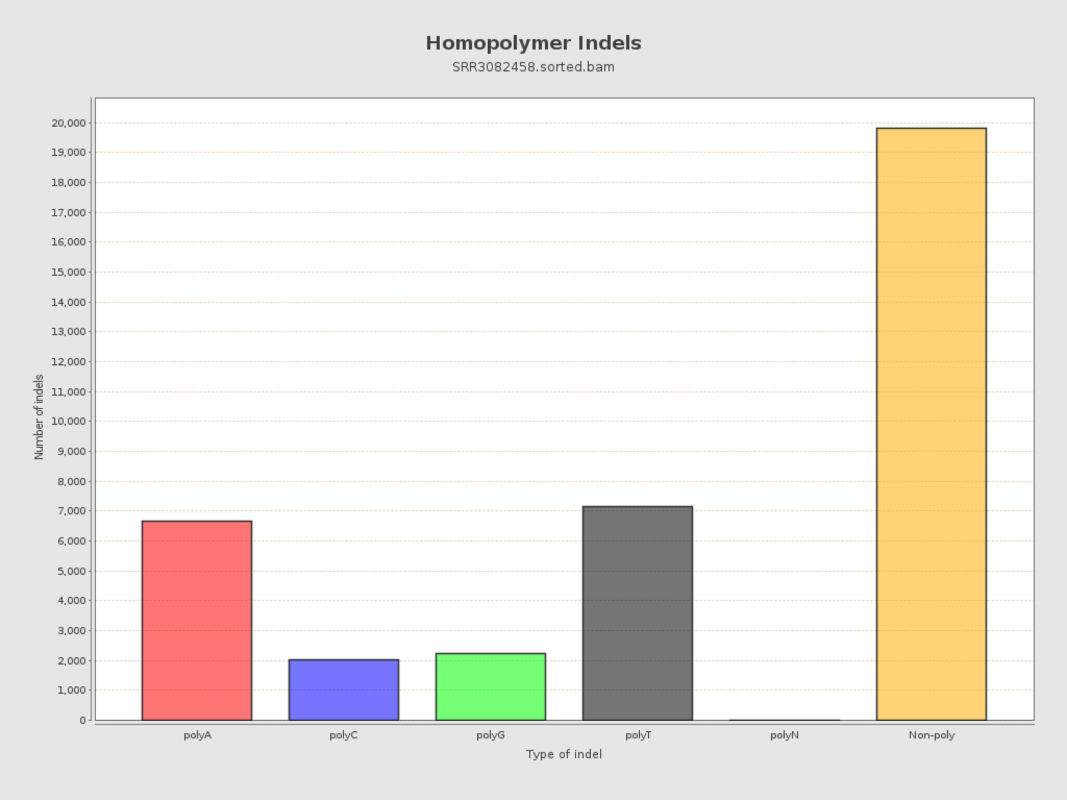
9. Results : Mapped Reads GC-content Distribution



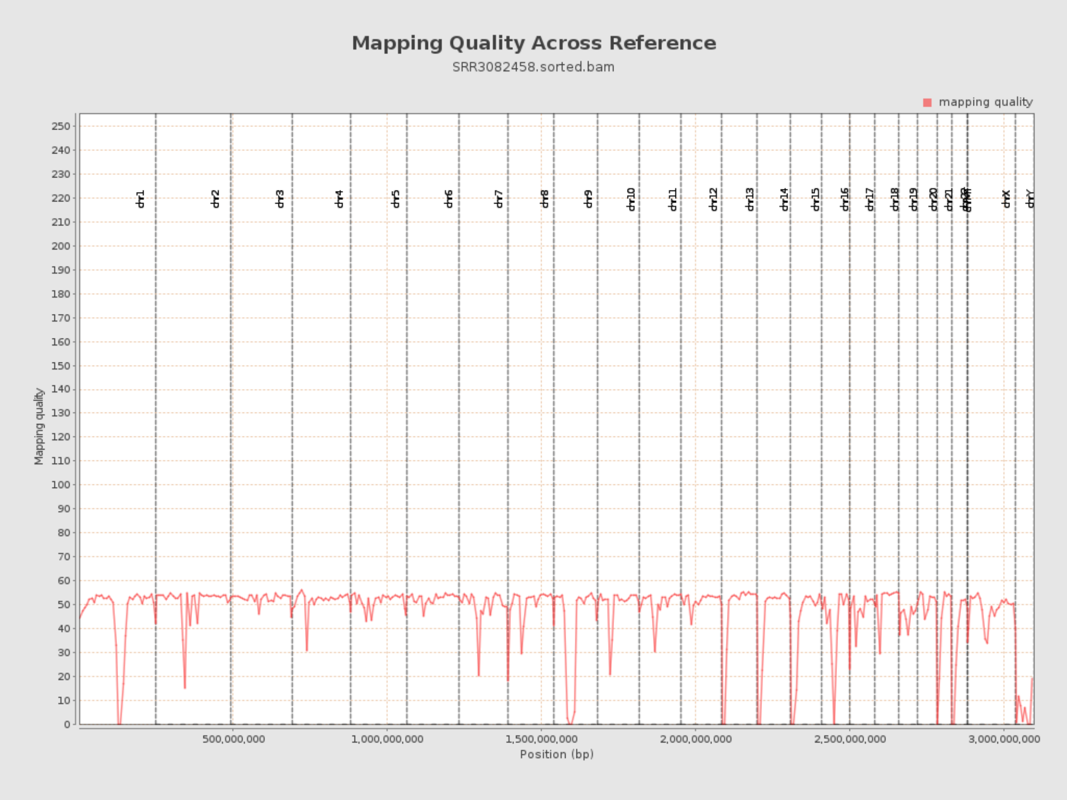
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram