Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:22:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082691.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_SRR3082691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:22:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,631,486
Mapped reads	3,374,909 / 92.93%
Unmapped reads	256,577 / 7.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,000 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	139,300 / 3.84%
Duplication rate	3.19%
Clipped reads	1,611,336 / 44.37%

2.2. ACGT Content

Number/percentage of A's	61,388,312 / 27.5%
Number/percentage of C's	38,158,520 / 17.09%
Number/percentage of T's	74,594,712 / 33.41%
Number/percentage of G's	49,054,174 / 21.97%
Number/percentage of N's	59,319 / 0.03%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0721

Standard Deviation	0.4975

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

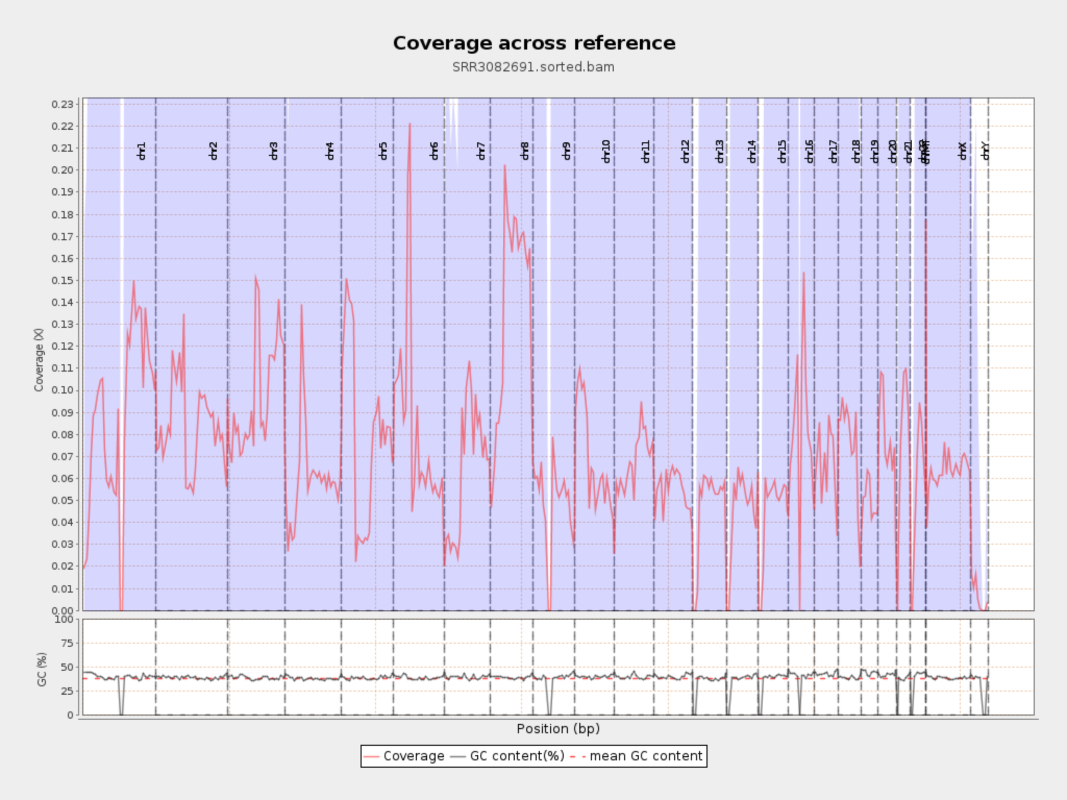
General error rate	0.9%
Mismatches	1,984,903
Insertions	19,806
Mapped reads with at least one insertion	0.58%
Deletions	52,176
Mapped reads with at least one deletion	1.53%
Homopolymer indels	49.38%

2.6. Chromosome stats

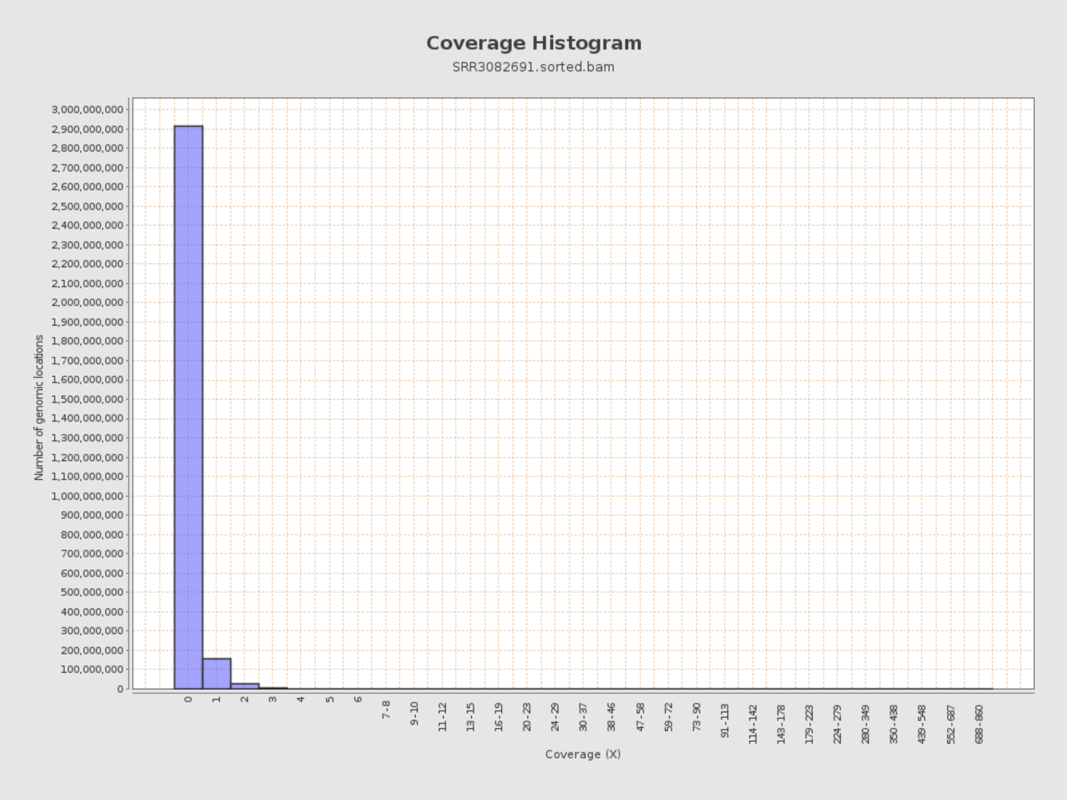
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21788296	0.0874	0.7058
chr2	243199373	20551244	0.0845	0.6786
chr3	198022430	19213771	0.097	0.3677
chr4	191154276	11658804	0.061	0.2963
chr5	180915260	14413404	0.0797	0.3368
chr6	171115067	14317083	0.0837	0.5682
chr7	159138663	10284145	0.0646	0.572

chr8	146364022	20271881	0.1385	0.6385
chr9	141213431	6853298	0.0485	0.577
chr10	135534747	9394855	0.0693	0.4115
chr11	135006516	9111593	0.0675	0.4338
chr12	133851895	7351794	0.0549	0.2823
chr13	115169878	5350155	0.0465	0.2467
chr14	107349540	4837963	0.0451	0.2948
chr15	102531392	4513007	0.044	0.2424
chr16	90354753	7350268	0.0813	0.3711
chr17	81195210	5515593	0.0679	0.408
chr18	78077248	6022097	0.0771	1.0658
chr19	59128983	2970862	0.0502	0.529
chr20	63025520	4990868	0.0792	0.3462
chr21	48129895	3594219	0.0747	0.3364
chr22	51304566	2821589	0.055	0.2751
chrMT	16571	2941	0.1775	0.4586
chrX	155270560	9792866	0.0631	0.3589
chrY	59373566	365828	0.0062	0.1149

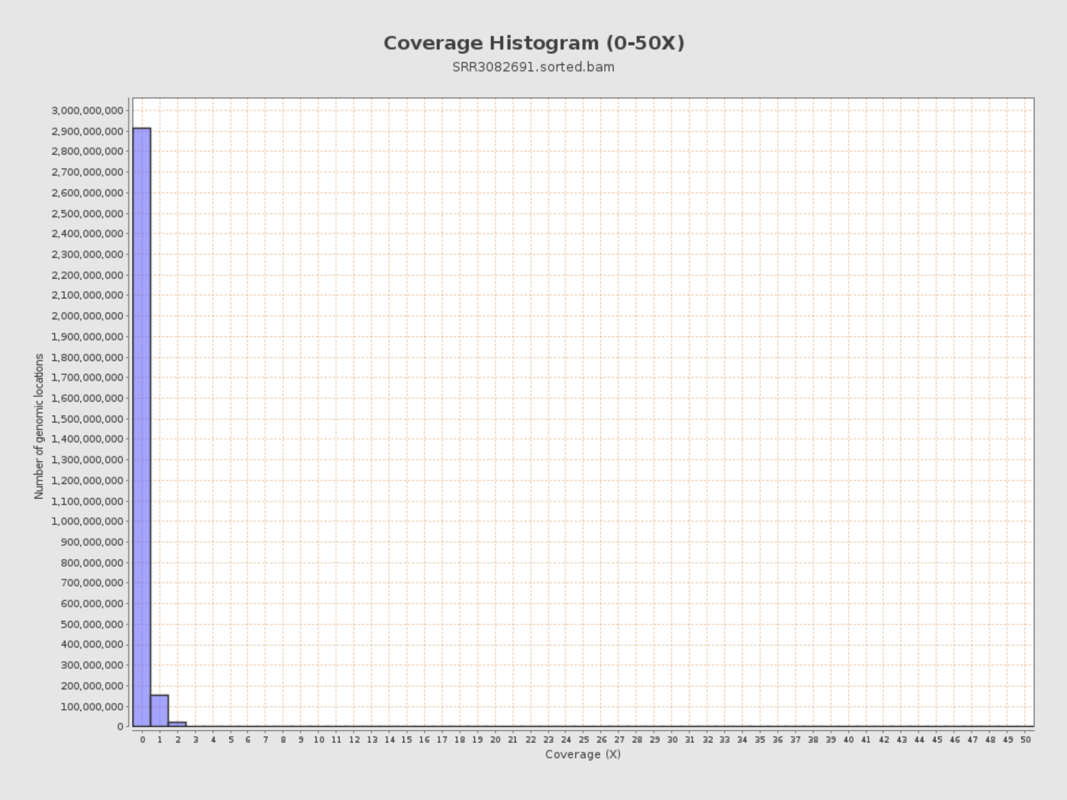
3. Results : Coverage across reference



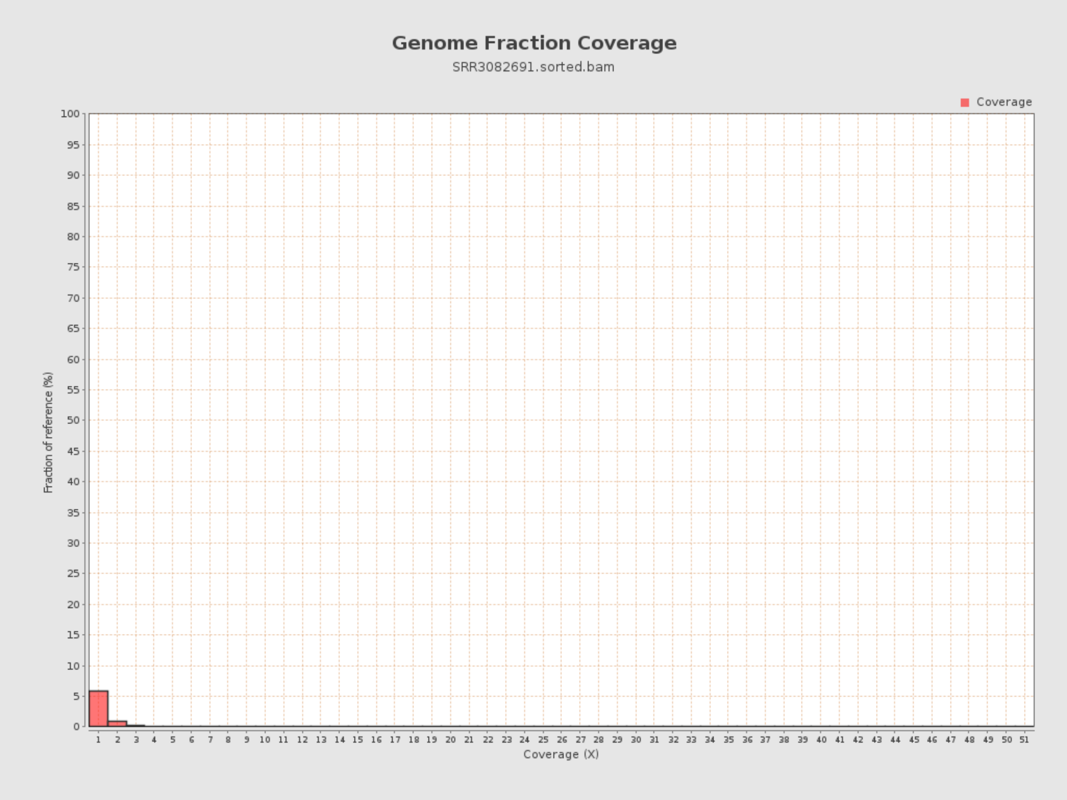
4. Results : Coverage Histogram



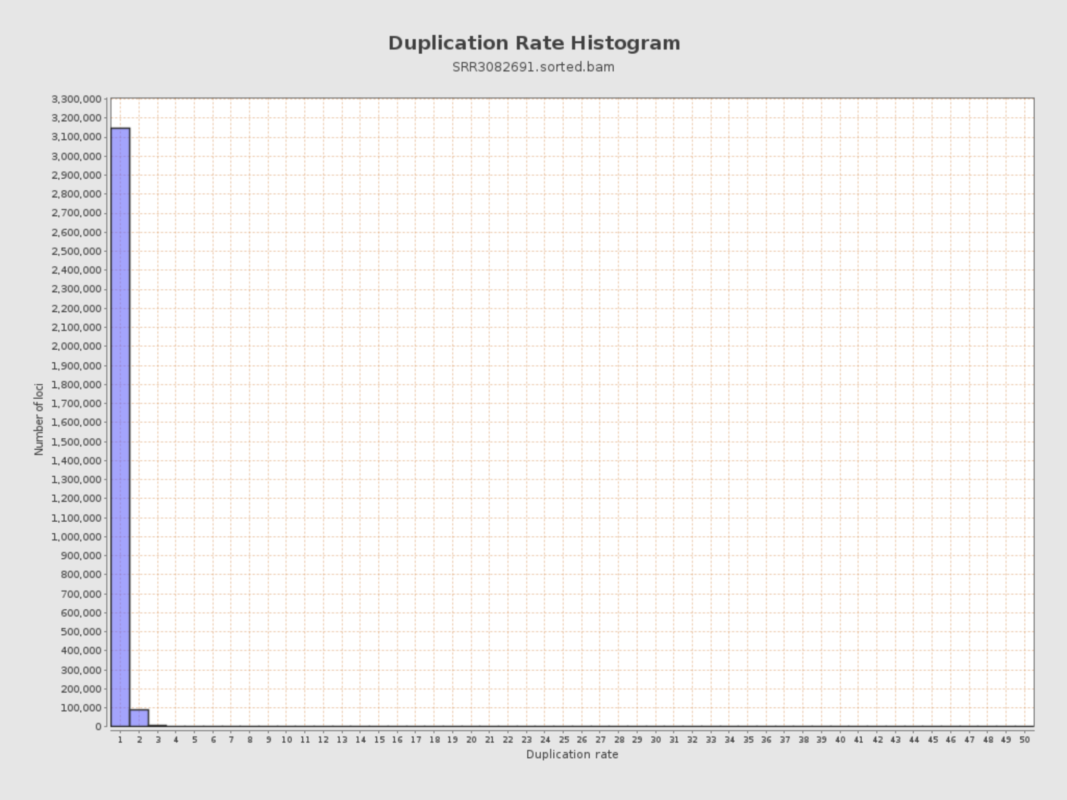
5. Results : Coverage Histogram (0-50X)



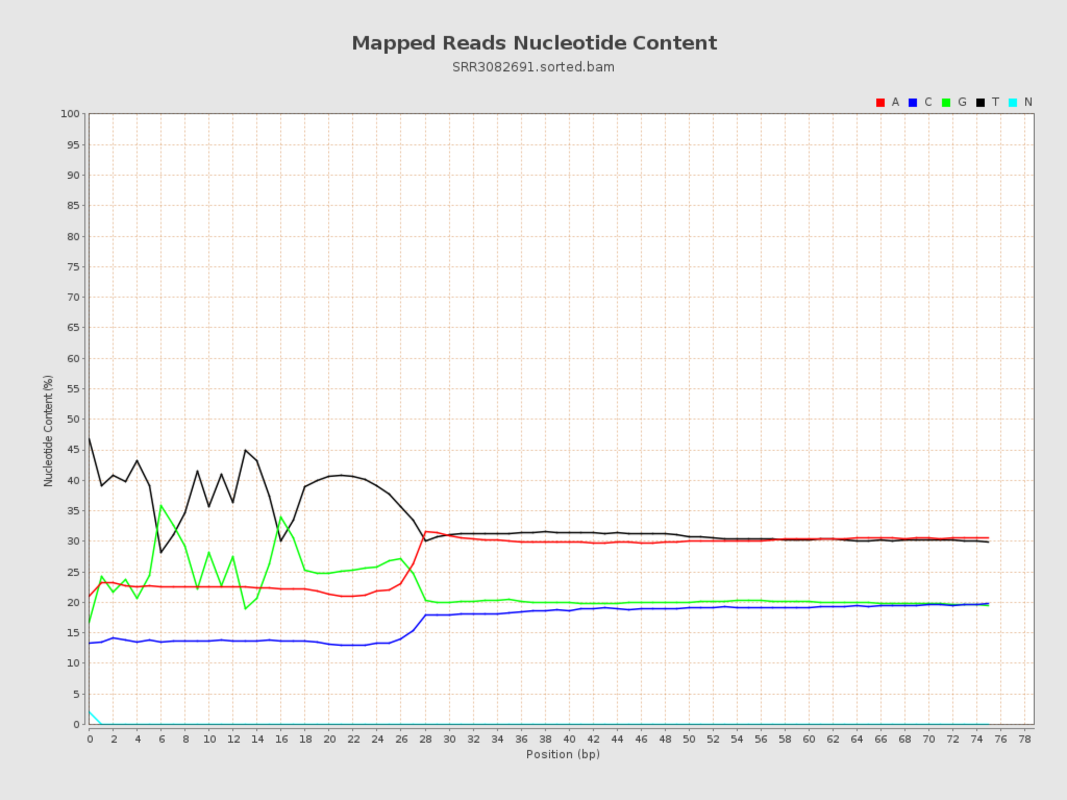
6. Results : Genome Fraction Coverage



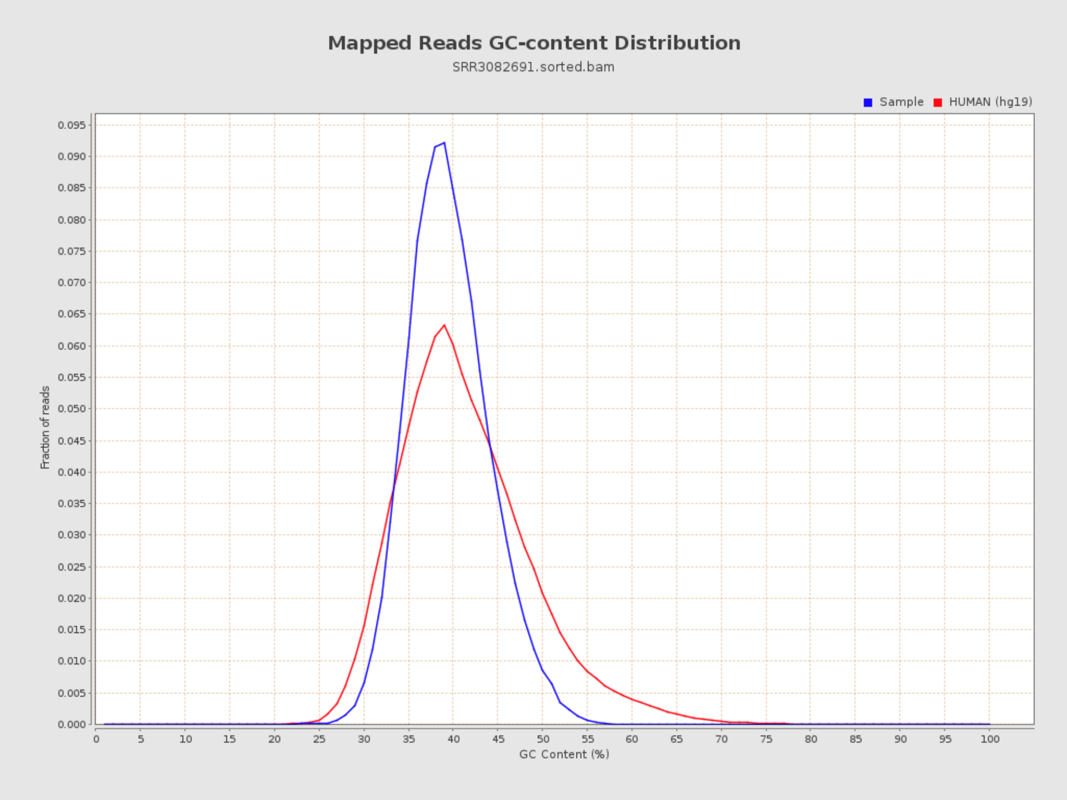
7. Results : Duplication Rate Histogram



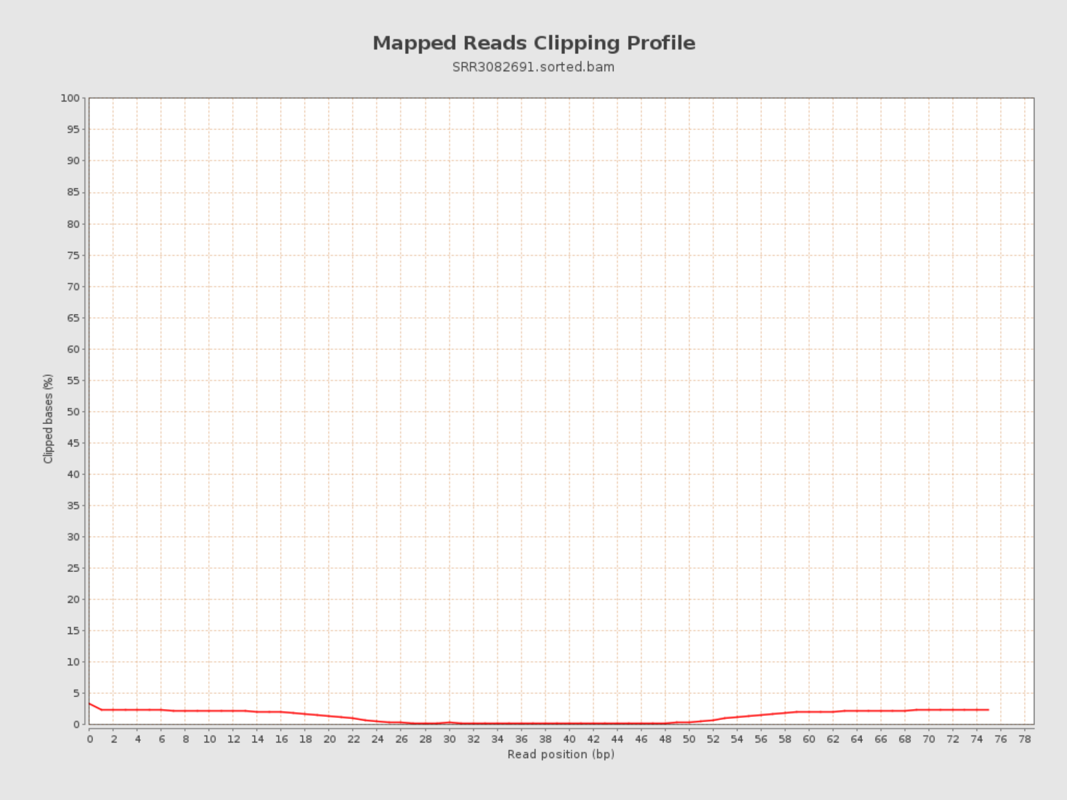
8. Results : Mapped Reads Nucleotide Content



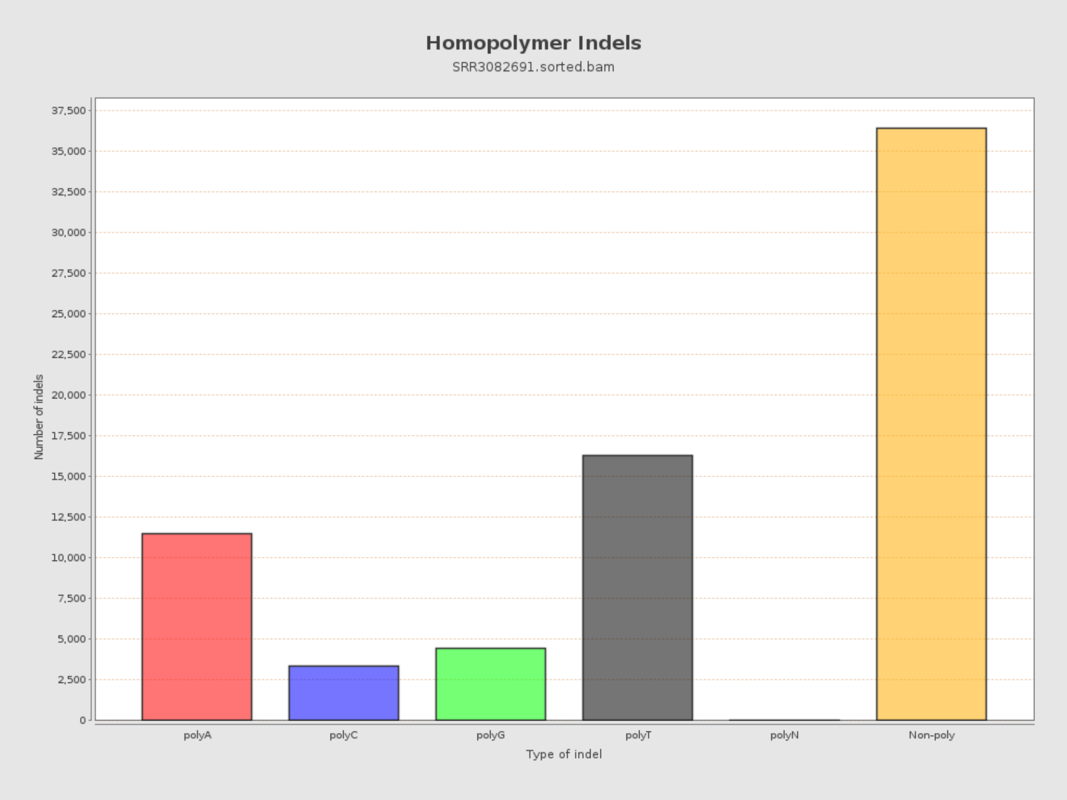
9. Results : Mapped Reads GC-content Distribution



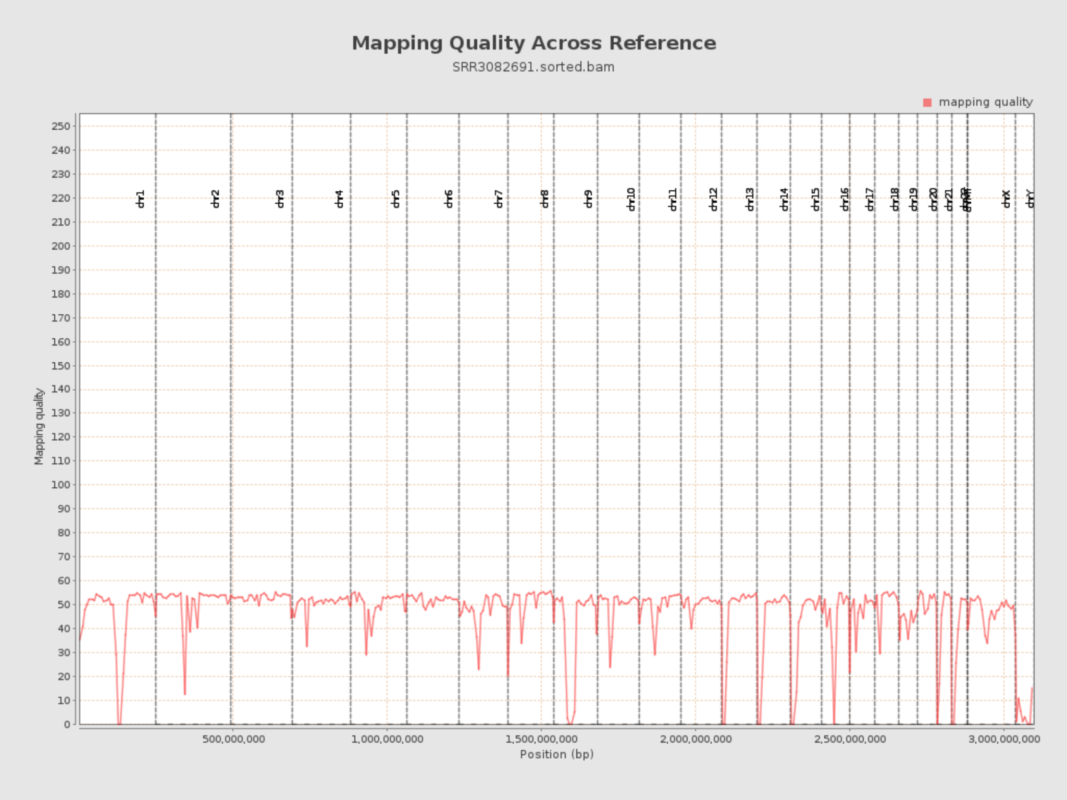
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram