Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:03:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082665.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_SRR3082665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:03:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,322,851
Mapped reads	2,970,033 / 89.38%
Unmapped reads	352,818 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,652 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	121,282 / 3.65%
Duplication rate	2.98%
Clipped reads	1,377,501 / 41.46%

2.2. ACGT Content

Number/percentage of A's	54,186,802 / 27.44%
Number/percentage of C's	34,433,837 / 17.44%
Number/percentage of T's	65,028,273 / 32.93%
Number/percentage of G's	43,753,023 / 22.16%
Number/percentage of N's	53,581 / 0.03%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0638

Standard Deviation	0.5064

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

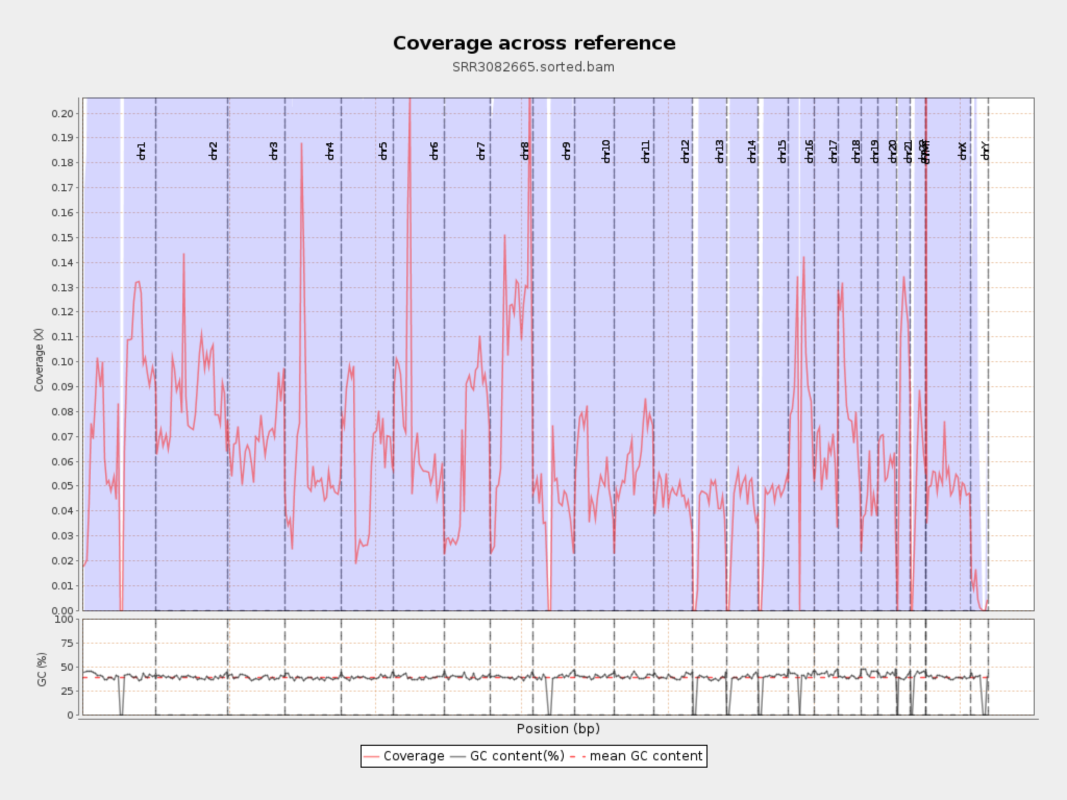
General error rate	0.96%
Mismatches	1,870,168
Insertions	18,221
Mapped reads with at least one insertion	0.61%
Deletions	47,309
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.74%

2.6. Chromosome stats

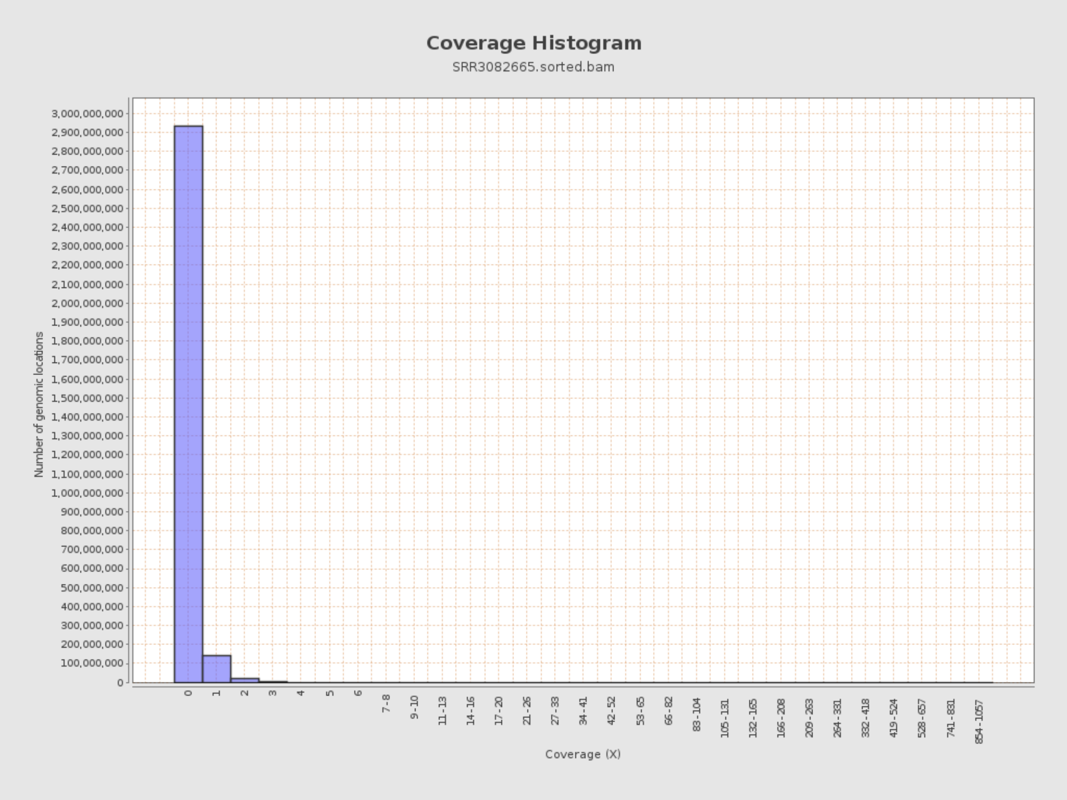
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19355659	0.0777	0.6813
chr2	243199373	21031729	0.0865	0.7667
chr3	198022430	13765758	0.0695	0.3063
chr4	191154276	11586087	0.0606	0.2994
chr5	180915260	10949679	0.0605	0.2873
chr6	171115067	12993541	0.0759	0.5674
chr7	159138663	10410759	0.0654	0.5466

chr8	146364022	15492414	0.1058	0.6053
chr9	141213431	5761309	0.0408	0.552
chr10	135534747	7518548	0.0555	0.4029
chr11	135006516	8249735	0.0611	0.4637
chr12	133851895	6198736	0.0463	0.2638
chr13	115169878	4386126	0.0381	0.2218
chr14	107349540	4383764	0.0408	0.3221
chr15	102531392	4047917	0.0395	0.2281
chr16	90354753	7826316	0.0866	0.3907
chr17	81195210	4952269	0.061	0.3742
chr18	78077248	6855161	0.0878	1.2414
chr19	59128983	2567217	0.0434	0.574
chr20	63025520	3817200	0.0606	0.3298
chr21	48129895	4481914	0.0931	0.3733
chr22	51304566	2571337	0.0501	0.2595
chrMT	16571	6205	0.3744	0.6724
chrX	155270560	7988340	0.0514	0.3459
chrY	59373566	334199	0.0056	0.1244

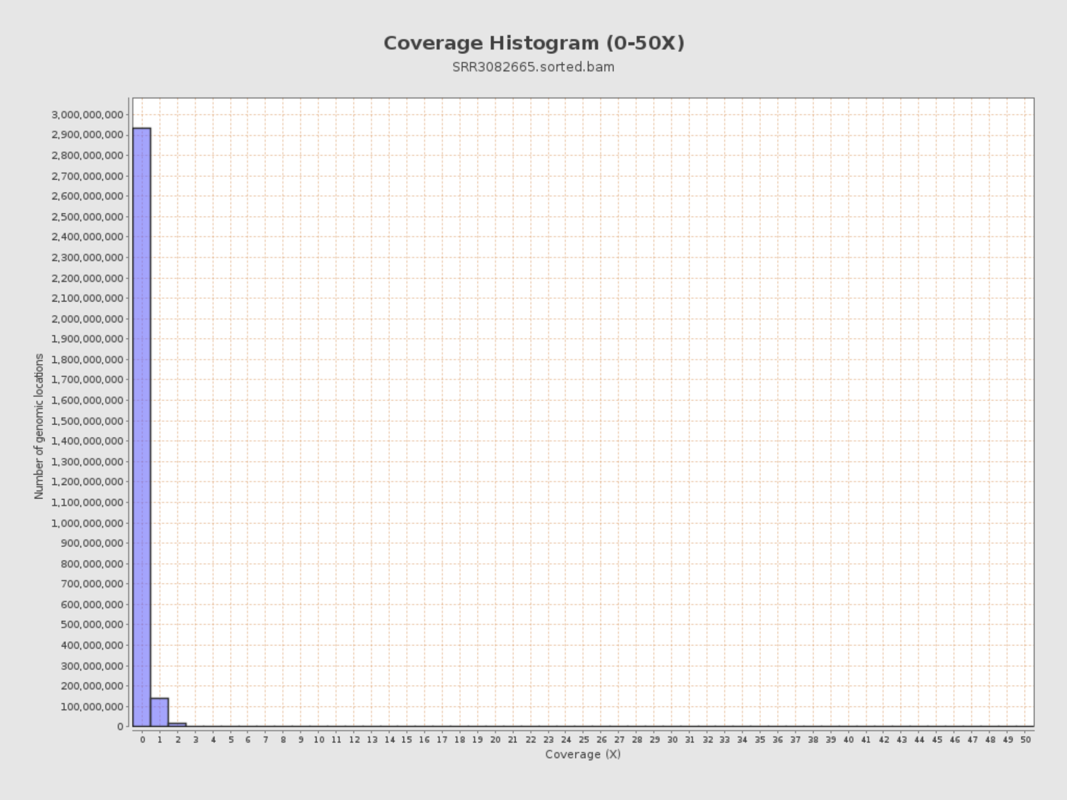
3. Results : Coverage across reference



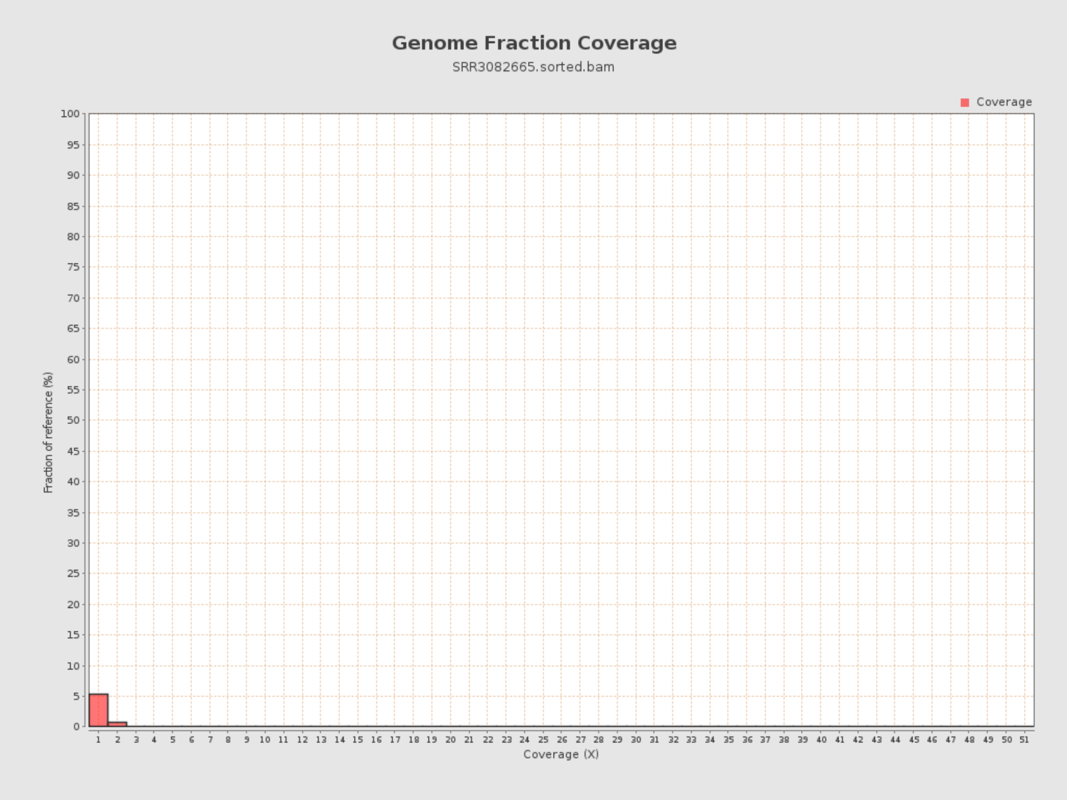
4. Results : Coverage Histogram



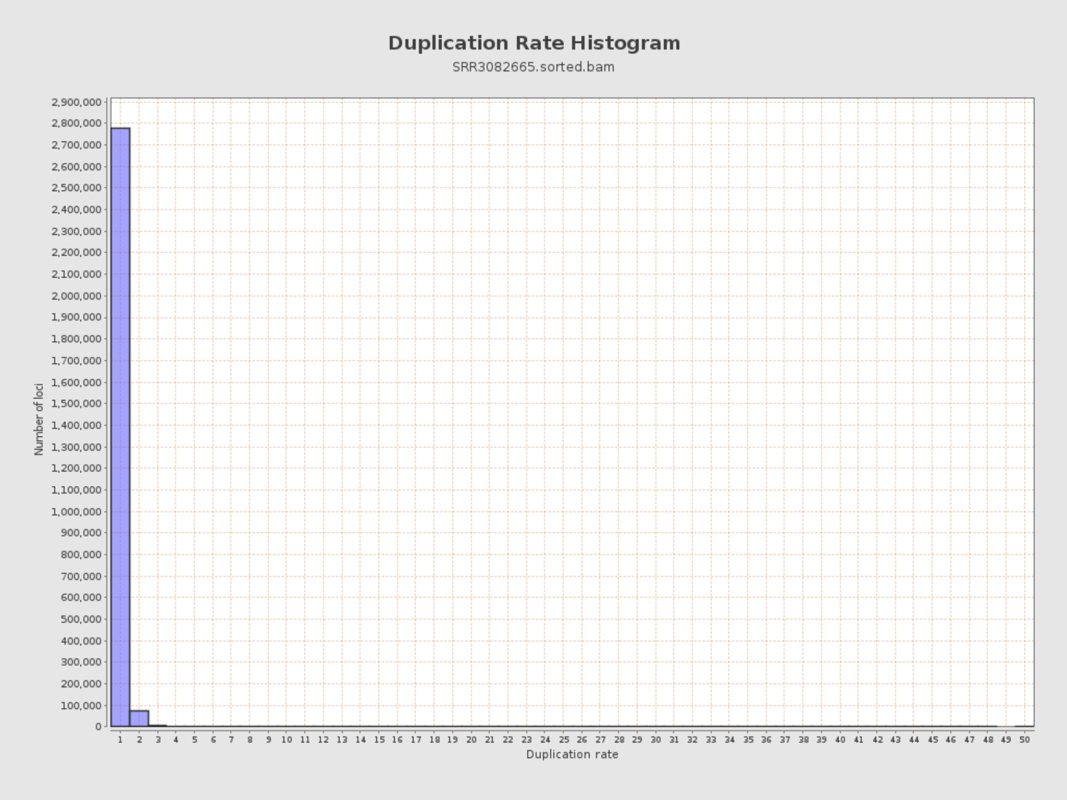
5. Results : Coverage Histogram (0-50X)



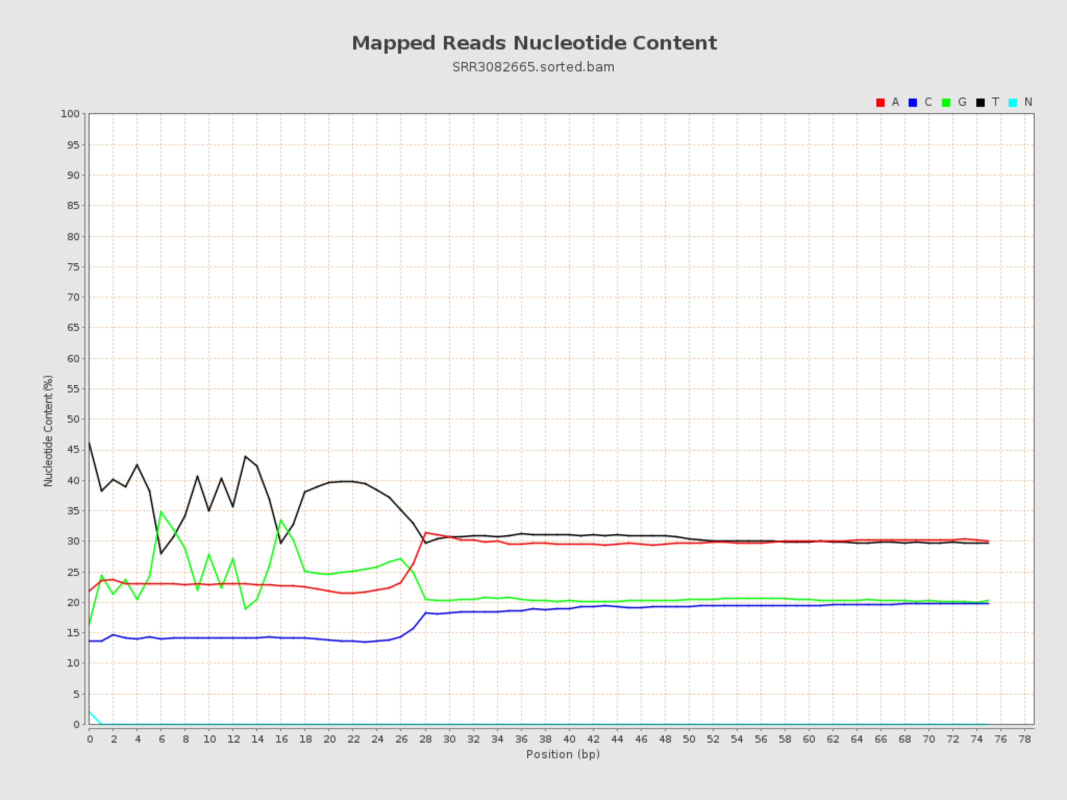
6. Results : Genome Fraction Coverage



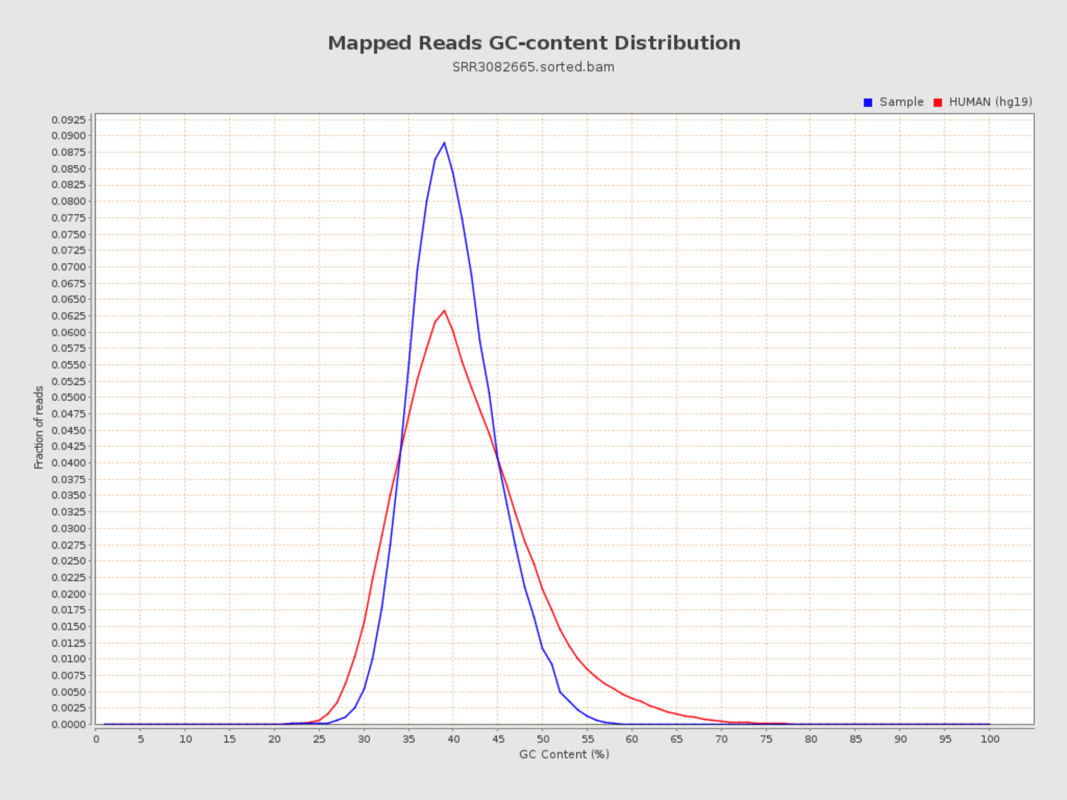
7. Results : Duplication Rate Histogram



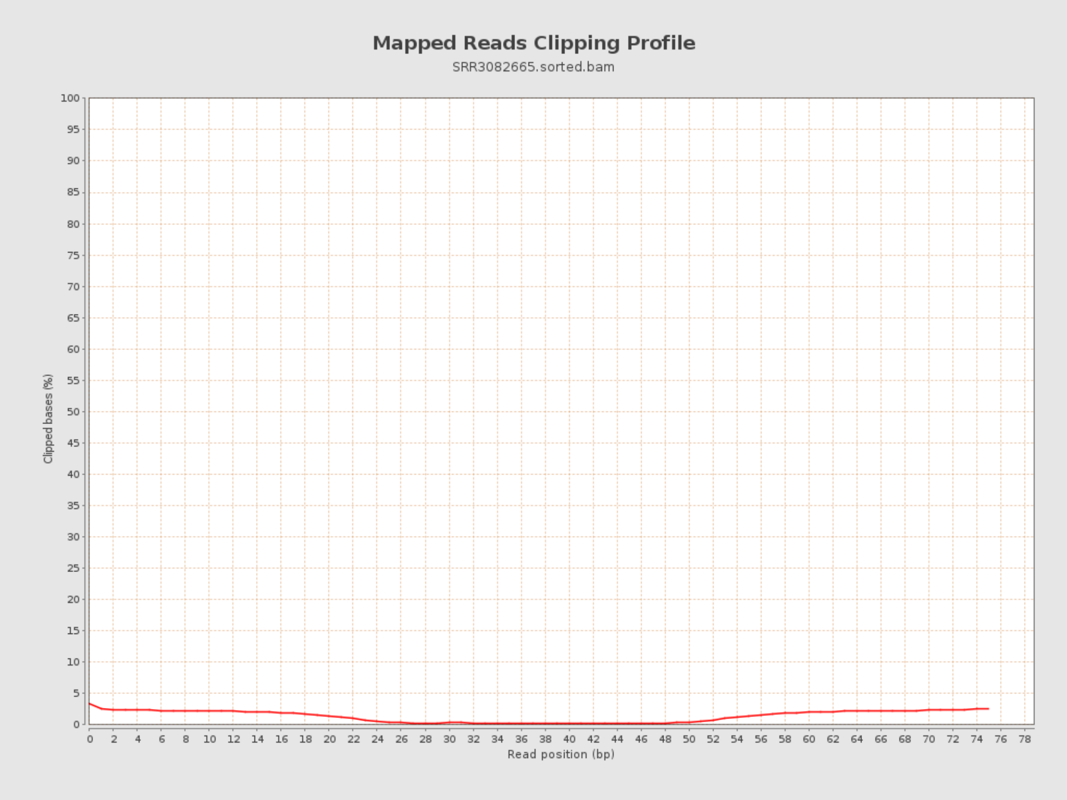
8. Results : Mapped Reads Nucleotide Content



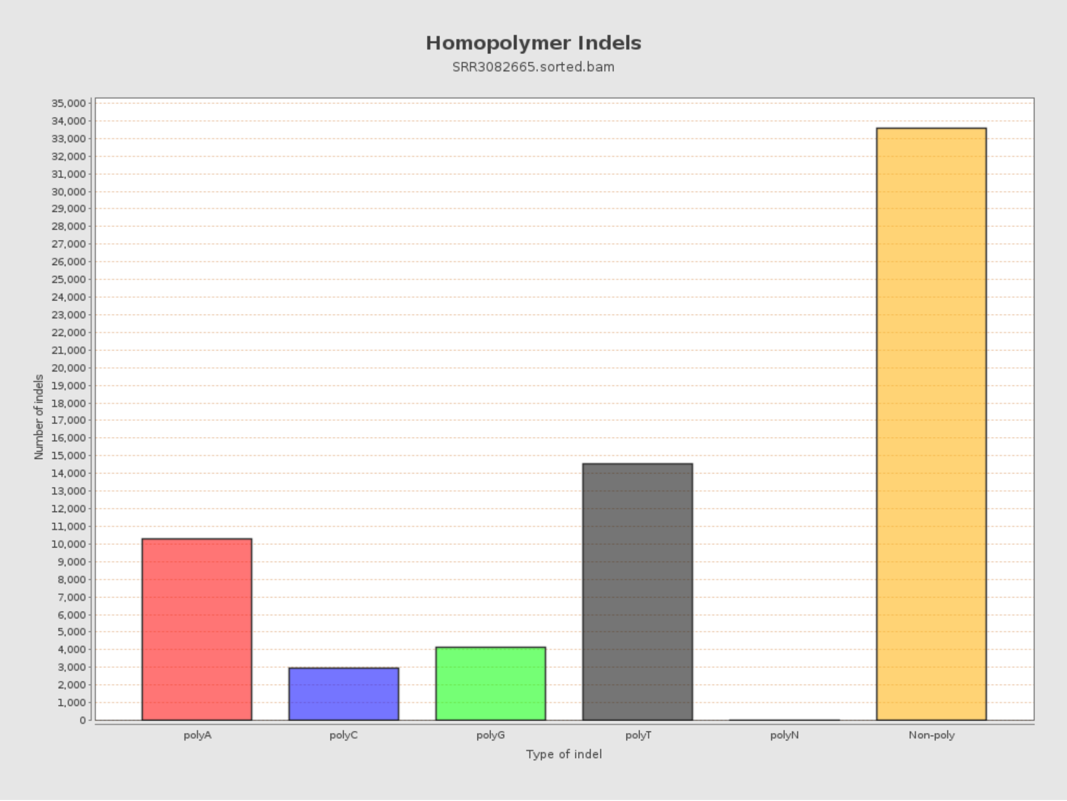
9. Results : Mapped Reads GC-content Distribution



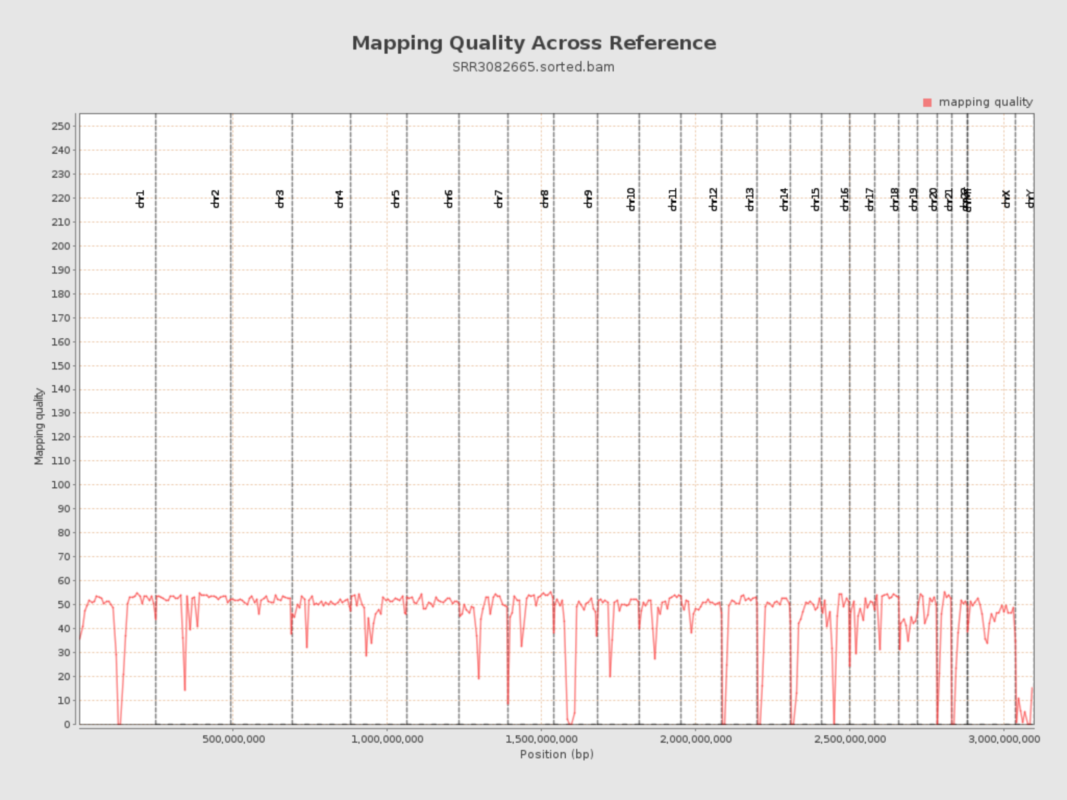
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram