Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:13:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084362.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_SRR3084362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084362.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:13:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,539,362
Mapped reads	2,291,361 / 90.23%
Unmapped reads	248,001 / 9.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,771 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	84,000 / 3.31%
Duplication rate	3.09%
Clipped reads	963,485 / 37.94%

2.2. ACGT Content

Number/percentage of A's	42,582,045 / 27.57%
Number/percentage of C's	29,992,775 / 19.42%
Number/percentage of T's	47,291,145 / 30.62%
Number/percentage of G's	34,402,054 / 22.27%
Number/percentage of N's	196,567 / 0.13%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.3366

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

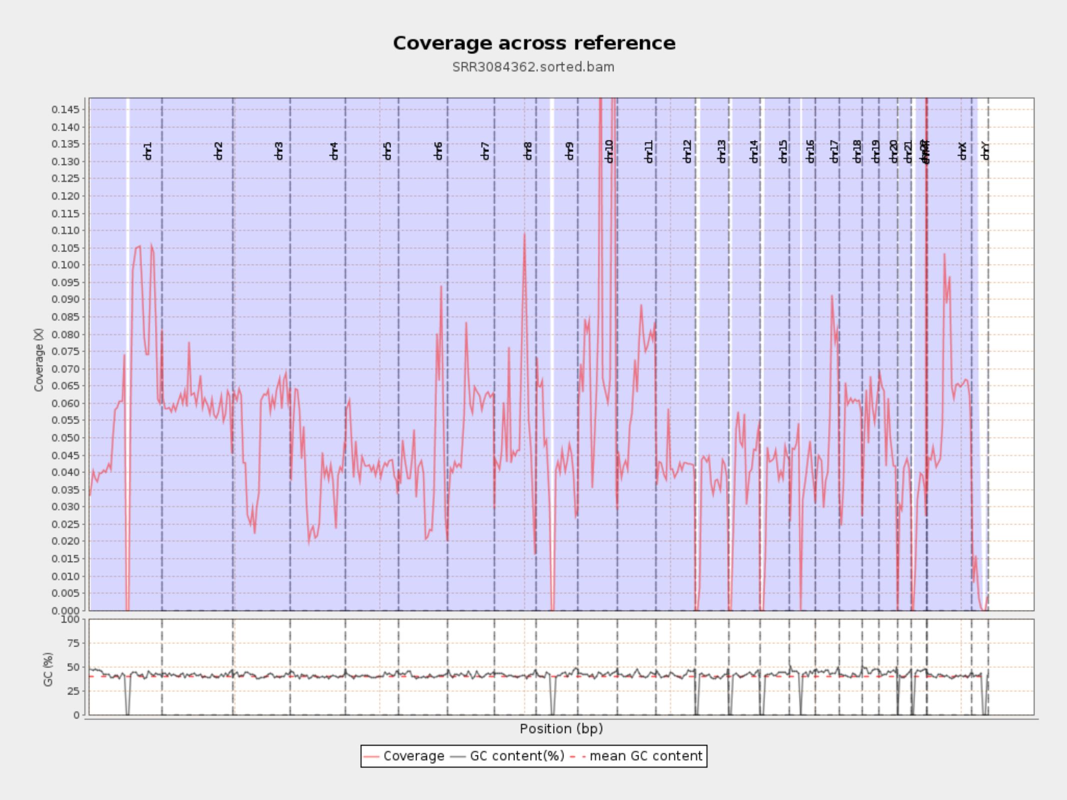
General error rate	1.02%
Mismatches	1,549,030
Insertions	10,754
Mapped reads with at least one insertion	0.46%
Deletions	30,443
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.29%

2.6. Chromosome stats

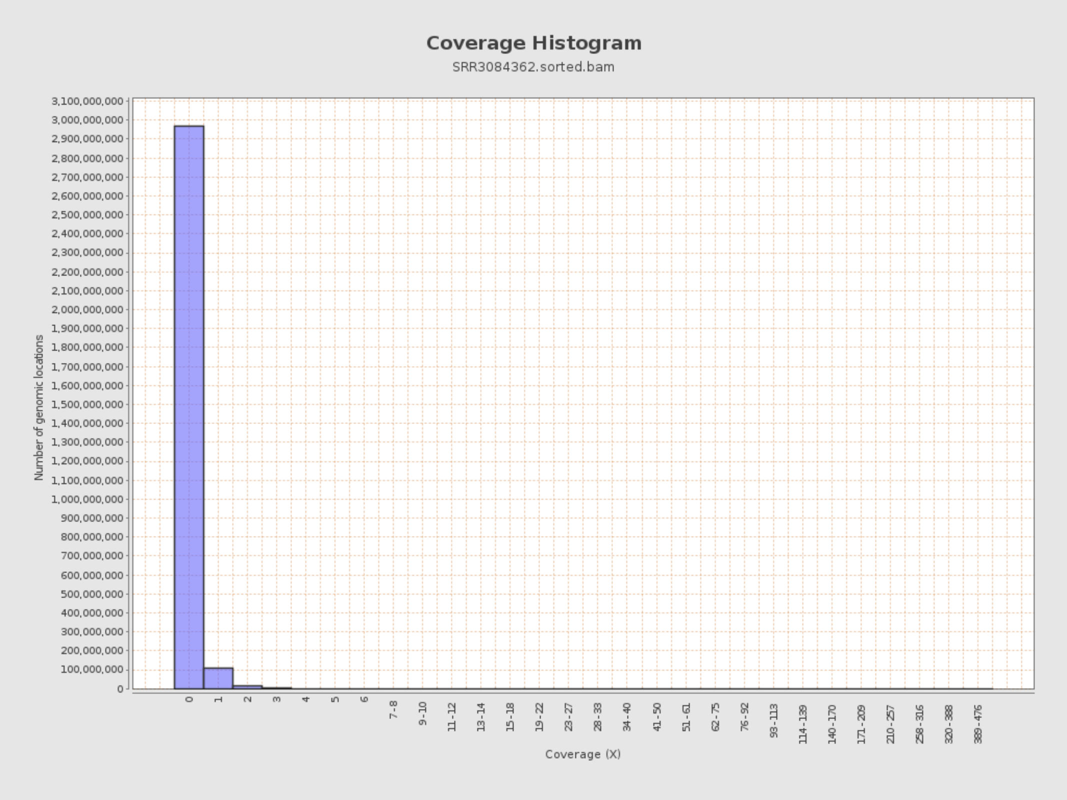
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15349108	0.0616	0.5109
chr2	243199373	14673152	0.0603	0.3718
chr3	198022430	10482871	0.0529	0.2667
chr4	191154276	7465694	0.0391	0.2398
chr5	180915260	7825003	0.0433	0.2386
chr6	171115067	7320664	0.0428	0.265
chr7	159138663	8915252	0.056	0.5392

chr8	146364022	7812252	0.0534	0.3203
chr9	141213431	5814907	0.0412	0.2805
chr10	135534747	11405512	0.0842	0.4797
chr11	135006516	8614516	0.0638	0.3438
chr12	133851895	5618314	0.042	0.2368
chr13	115169878	3828738	0.0332	0.2082
chr14	107349540	4233945	0.0394	0.2356
chr15	102531392	3592488	0.035	0.2175
chr16	90354753	3514731	0.0389	0.2467
chr17	81195210	4444500	0.0547	0.2868
chr18	78077248	4196883	0.0538	0.4484
chr19	59128983	3365366	0.0569	0.3901
chr20	63025520	3291842	0.0522	0.2672
chr21	48129895	1587835	0.033	0.2209
chr22	51304566	1280425	0.025	0.1802
chrMT	16571	10626	0.6412	0.9166
chrX	155270560	9537397	0.0614	0.3115
chrY	59373566	336972	0.0057	0.1187

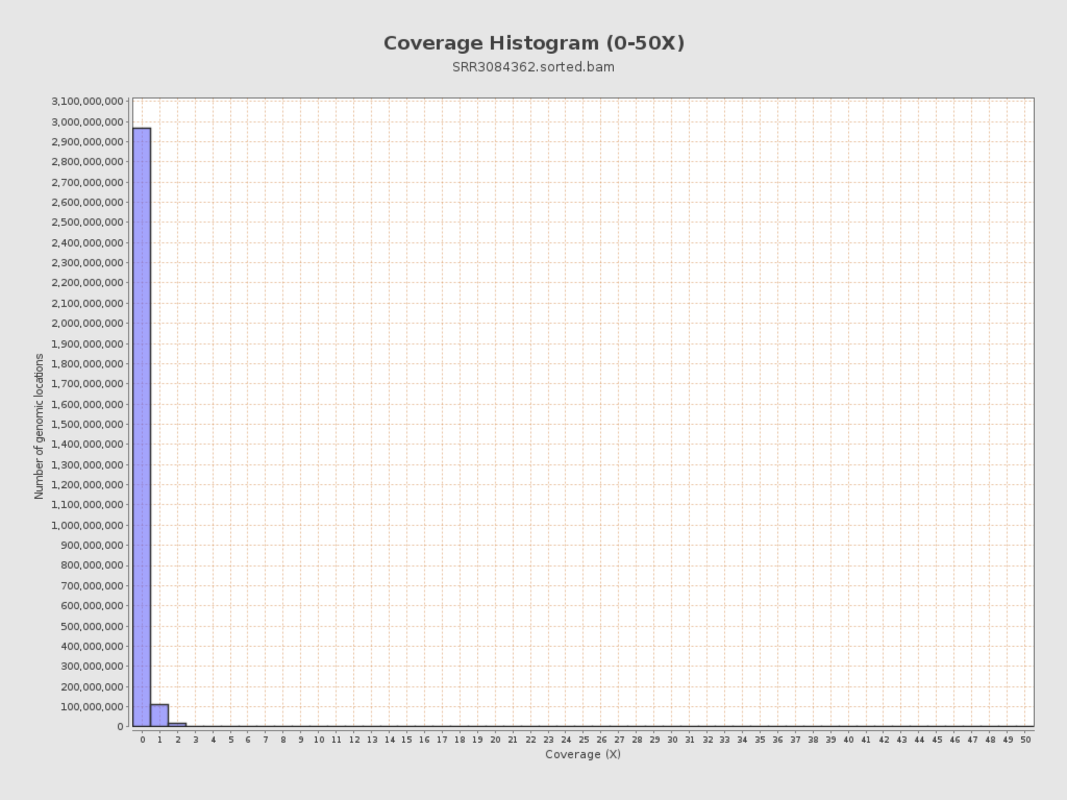
3. Results : Coverage across reference



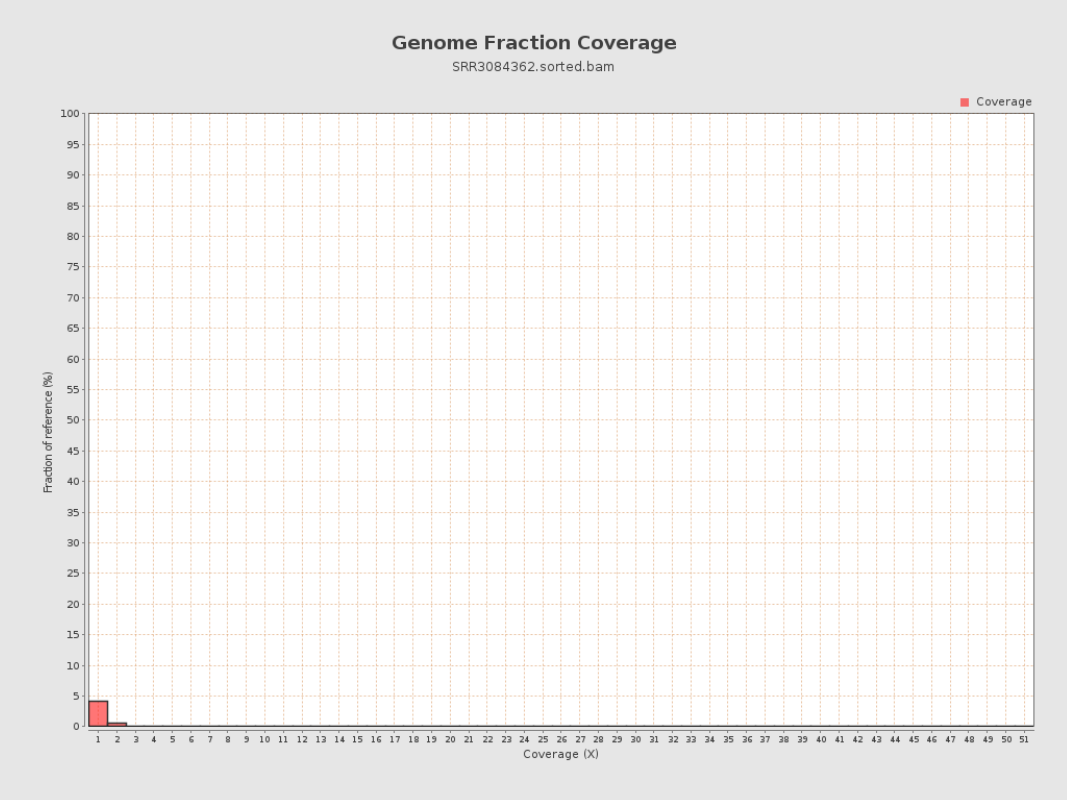
4. Results : Coverage Histogram



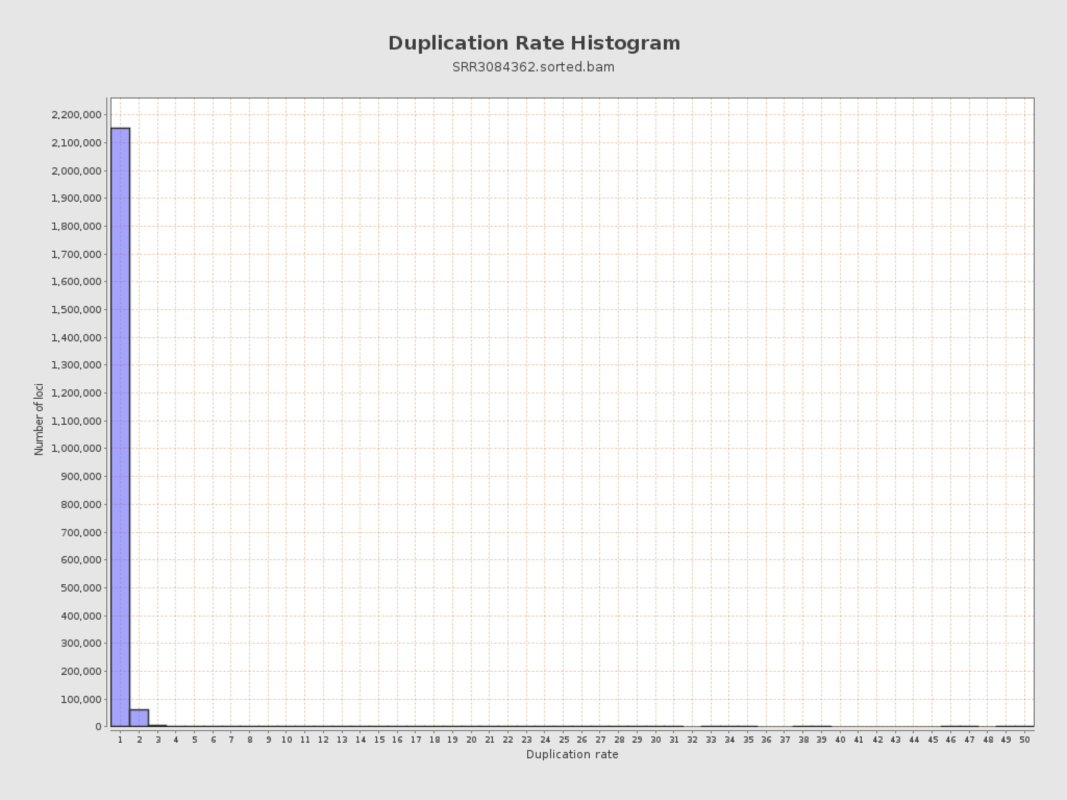
5. Results : Coverage Histogram (0-50X)



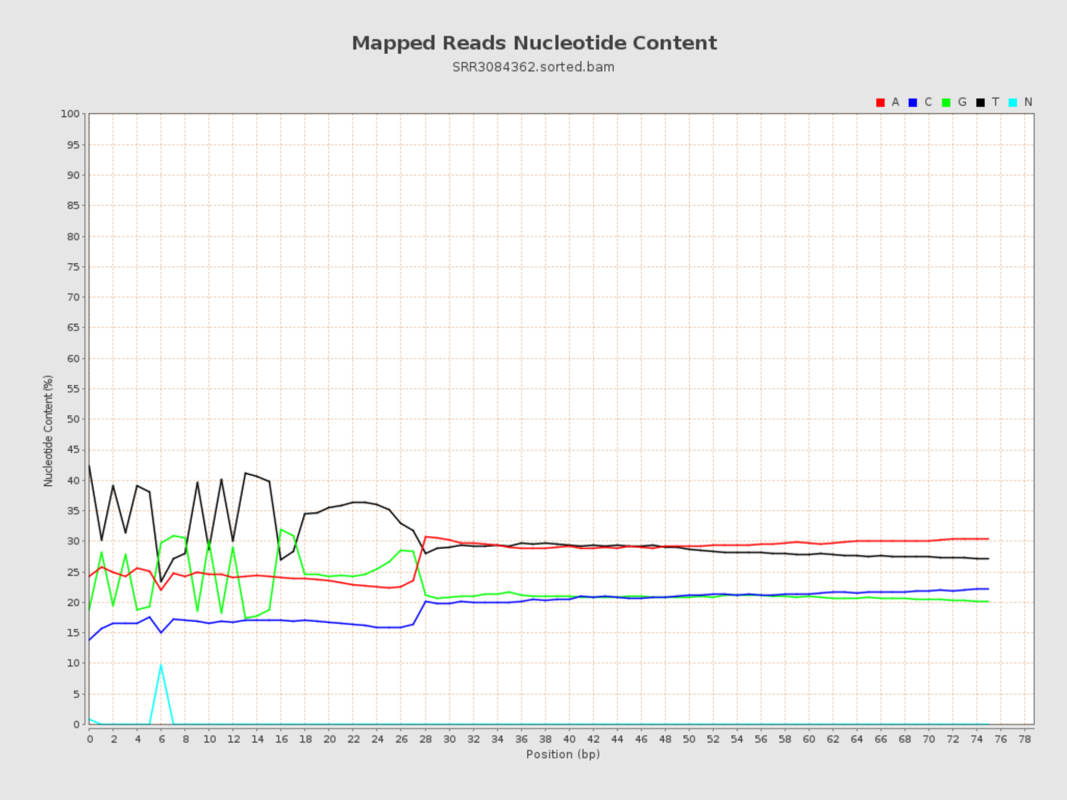
6. Results : Genome Fraction Coverage



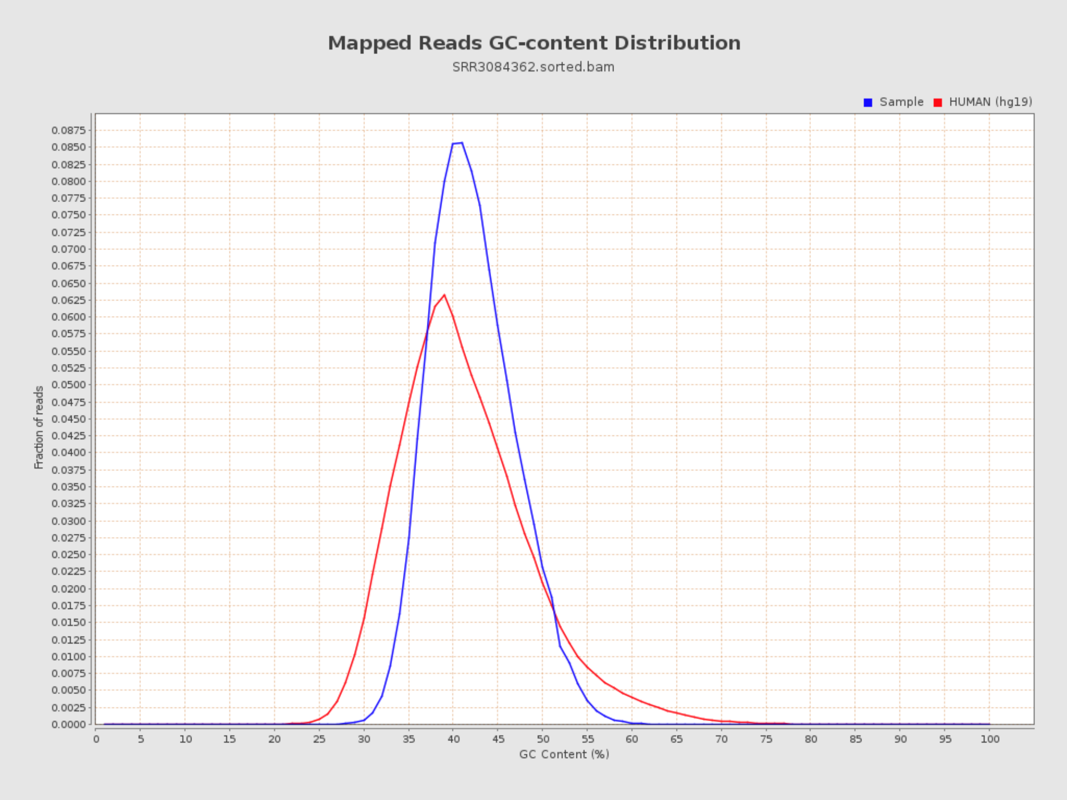
7. Results : Duplication Rate Histogram



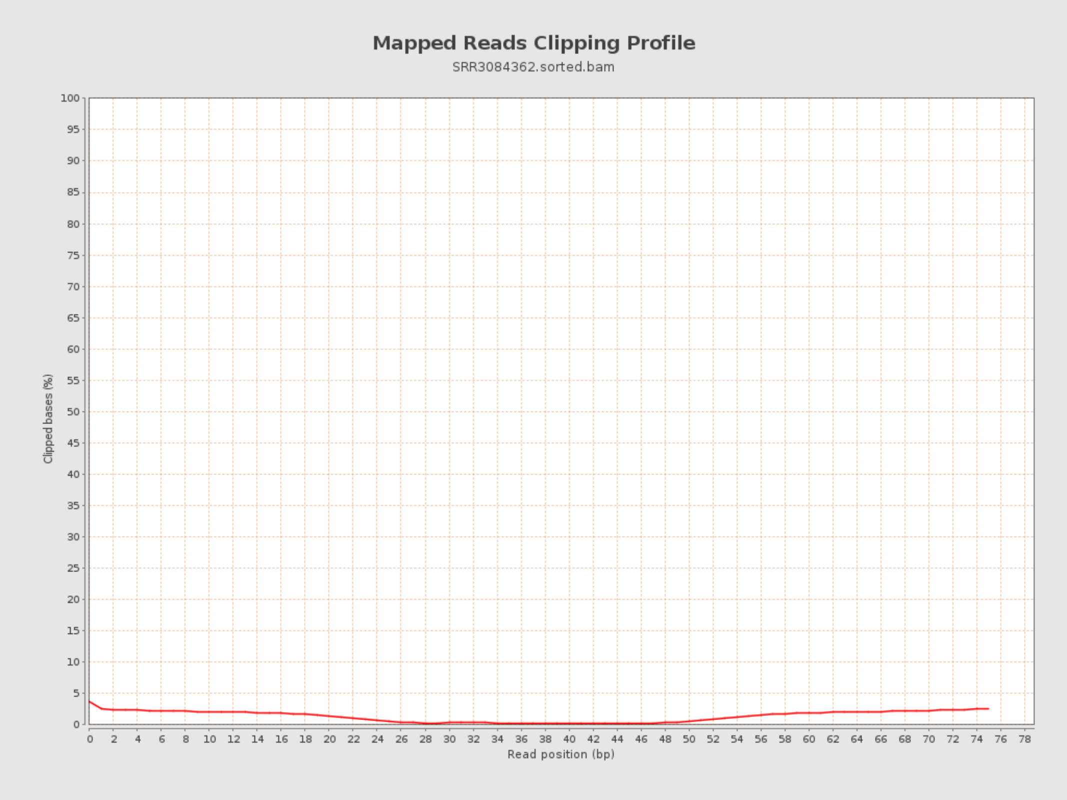
8. Results : Mapped Reads Nucleotide Content



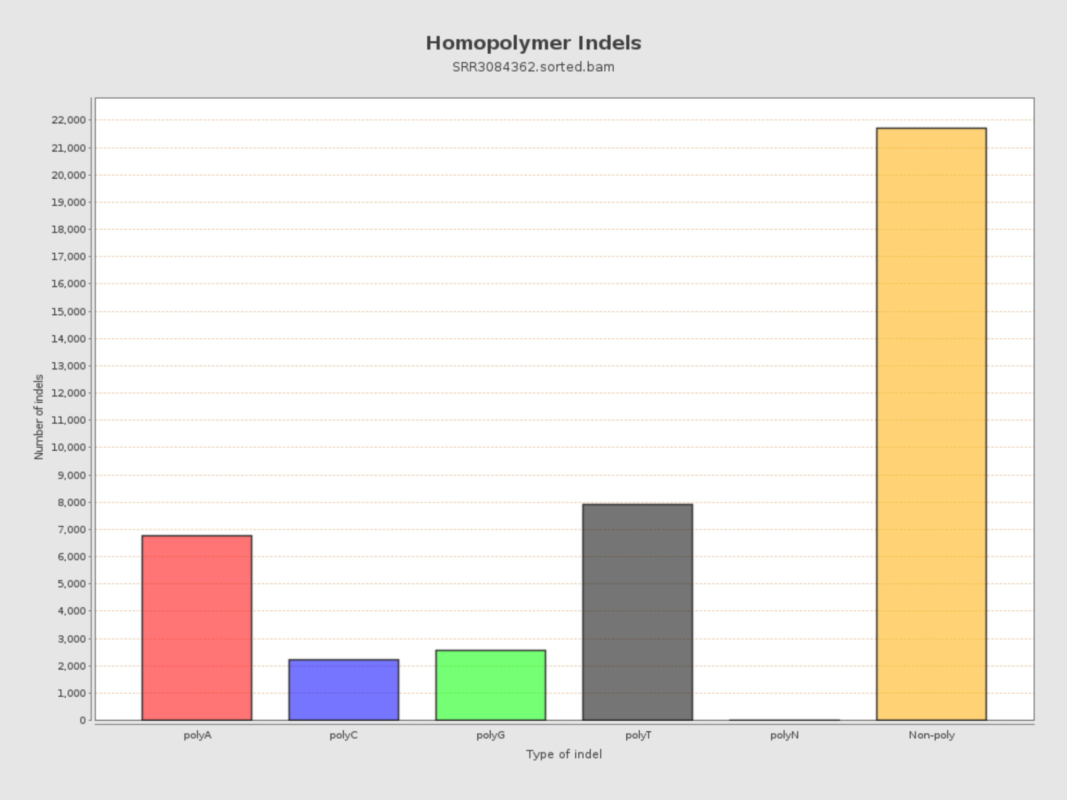
9. Results : Mapped Reads GC-content Distribution



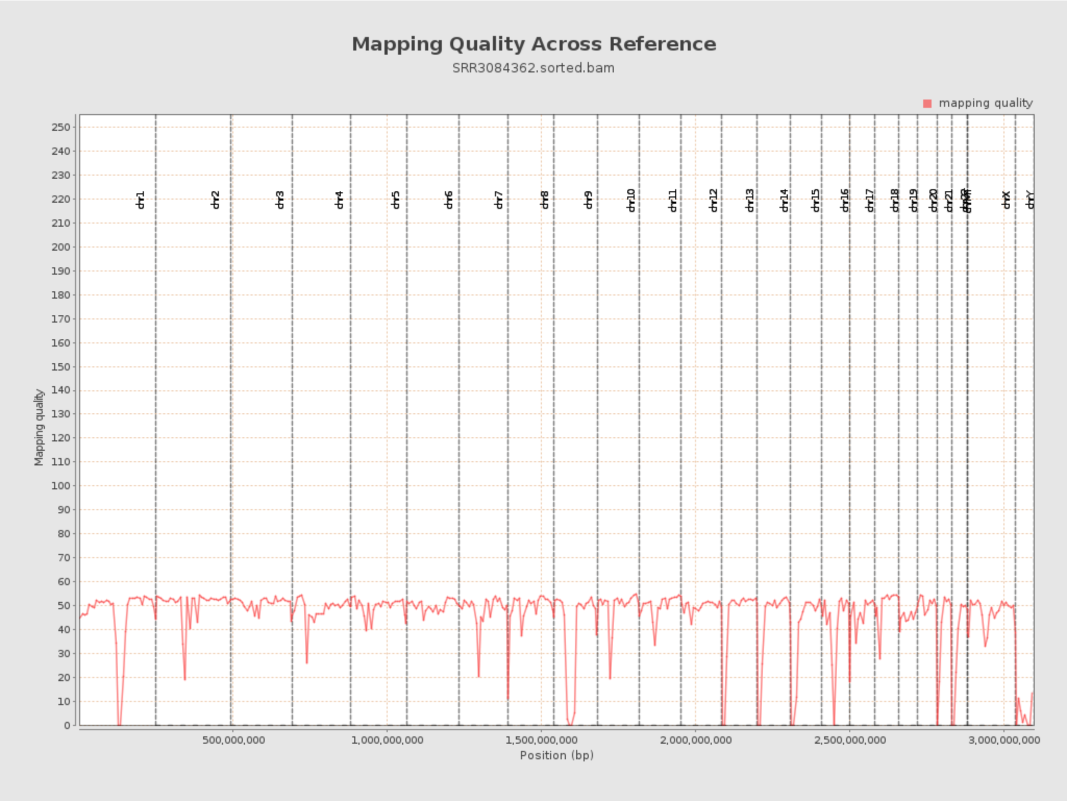
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram