Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:35:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082743.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_SRR3082743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:35:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,912,446
Mapped reads	3,403,369 / 86.99%
Unmapped reads	509,077 / 13.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,835 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	169,235 / 4.33%
Duplication rate	3.99%
Clipped reads	1,343,641 / 34.34%

2.2. ACGT Content

Number/percentage of A's	66,753,557 / 28.78%
Number/percentage of C's	41,870,646 / 18.05%
Number/percentage of T's	75,571,520 / 32.58%
Number/percentage of G's	47,744,556 / 20.58%
Number/percentage of N's	12,985 / 0.01%
GC Percentage	38.64%

2.3. Coverage

Mean	0.075

Standard Deviation	0.537

2.4. Mapping Quality

Mean Mapping Quality	47.4

2.5. Mismatches and indels

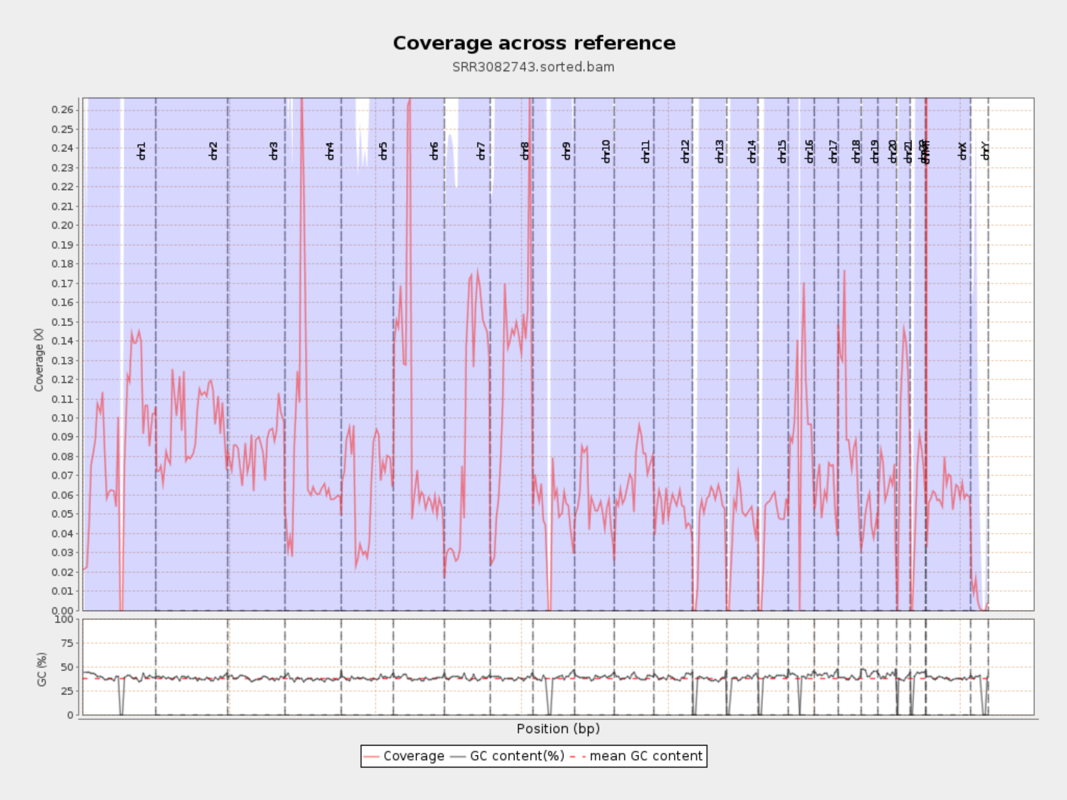
General error rate	0.88%
Mismatches	2,014,987
Insertions	18,373
Mapped reads with at least one insertion	0.54%
Deletions	51,835
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.49%

2.6. Chromosome stats

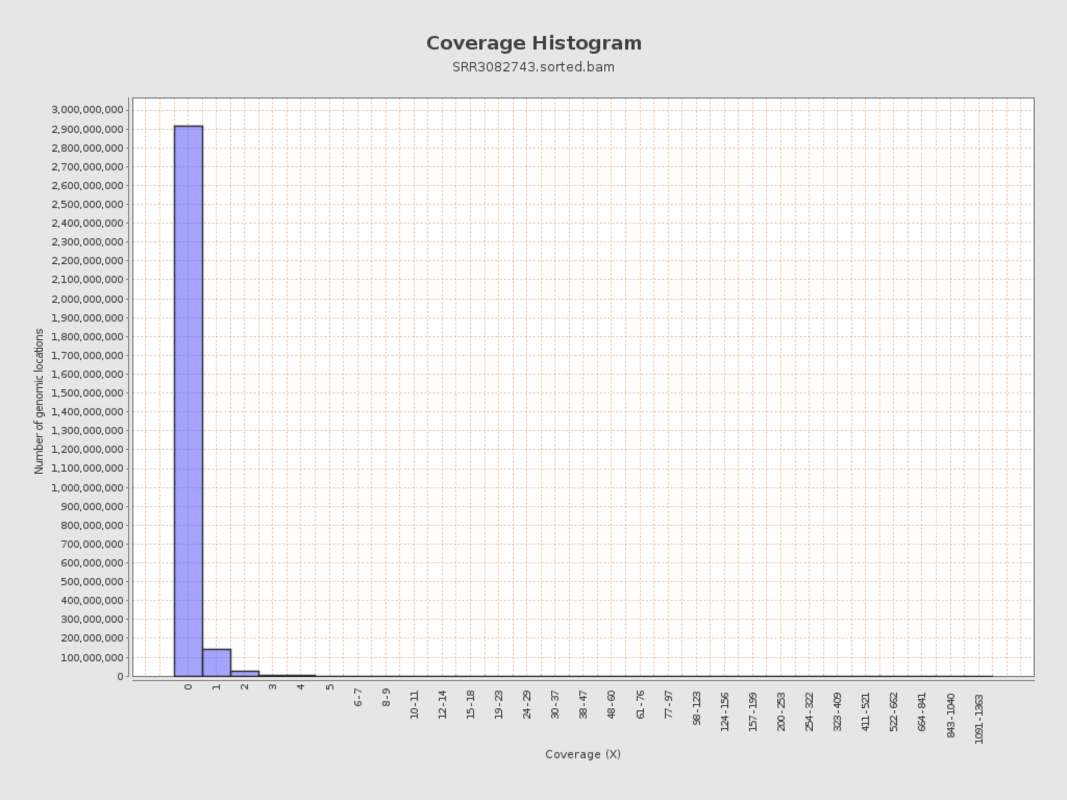
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21521237	0.0863	0.8772
chr2	243199373	23570050	0.0969	0.6669
chr3	198022430	16771736	0.0847	0.353
chr4	191154276	15553816	0.0814	0.358
chr5	180915260	11719499	0.0648	0.3099
chr6	171115067	16755095	0.0979	0.5456
chr7	159138663	15685620	0.0986	0.5156

chr8	146364022	18019575	0.1231	0.9431
chr9	141213431	6985821	0.0495	0.4883
chr10	135534747	7711311	0.0569	0.388
chr11	135006516	9429521	0.0698	0.4425
chr12	133851895	7049501	0.0527	0.2949
chr13	115169878	5517435	0.0479	0.2638
chr14	107349540	4835293	0.045	0.295
chr15	102531392	4528975	0.0442	0.2546
chr16	90354753	8721055	0.0965	0.437
chr17	81195210	5153042	0.0635	0.3601
chr18	78077248	7857206	0.1006	1.0838
chr19	59128983	2783957	0.0471	0.6059
chr20	63025520	4247205	0.0674	0.3348
chr21	48129895	4744225	0.0986	0.394
chr22	51304566	2851438	0.0556	0.2827
chrMT	16571	260355	15.7115	9.0238
chrX	155270560	9409143	0.0606	0.3496
chrY	59373566	359028	0.006	0.1192

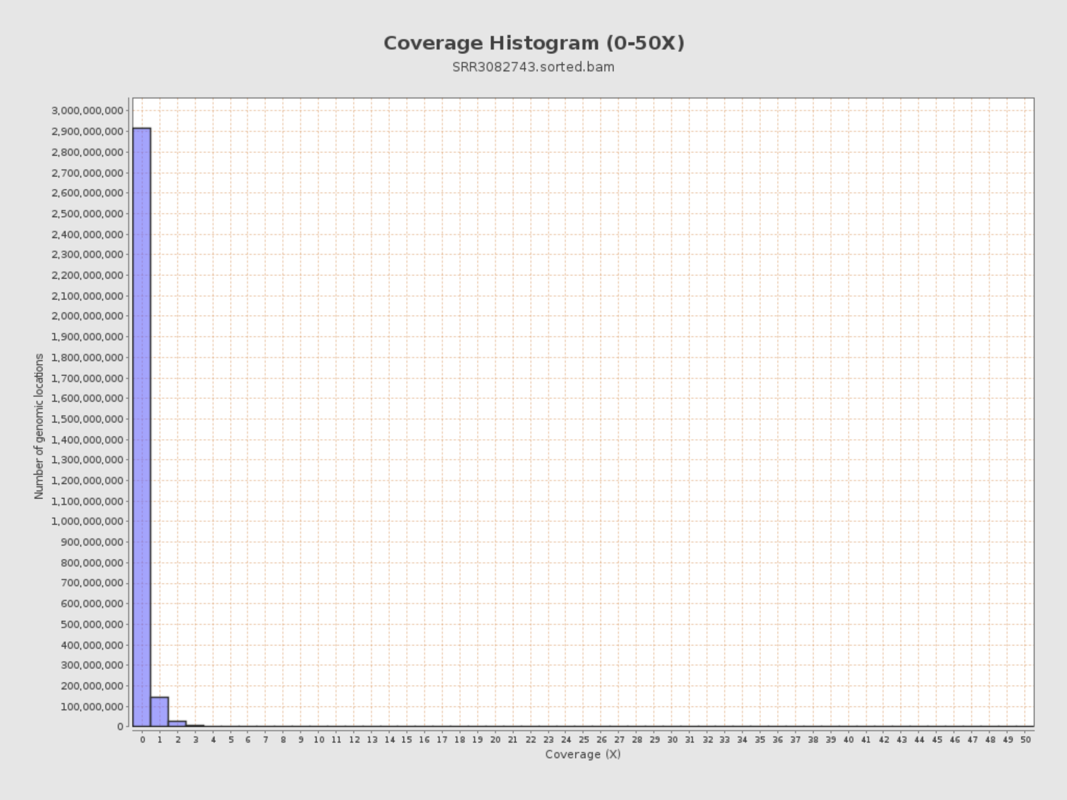
3. Results : Coverage across reference



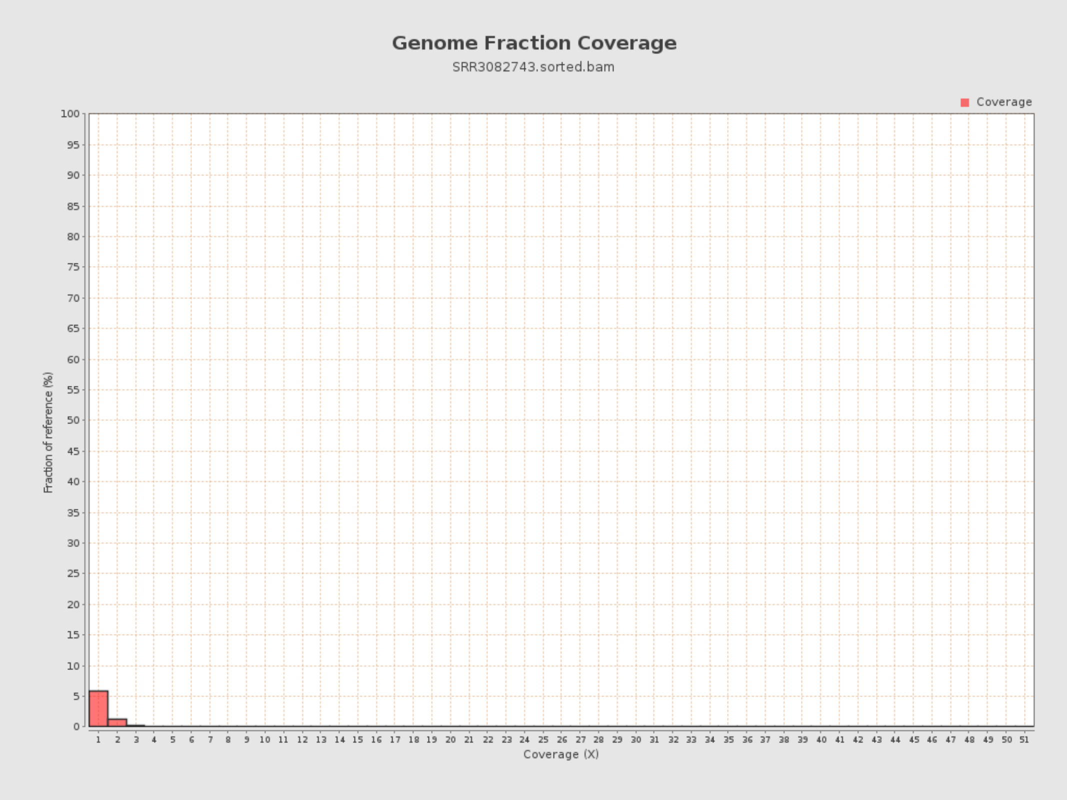
4. Results : Coverage Histogram



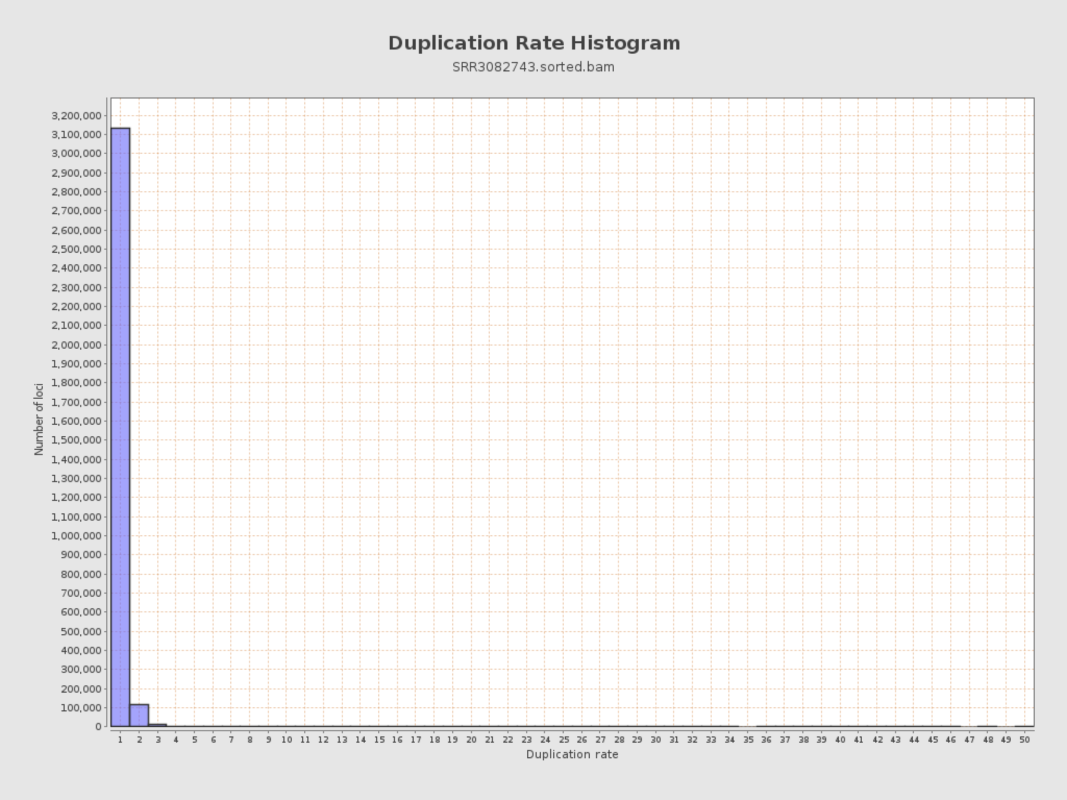
5. Results : Coverage Histogram (0-50X)



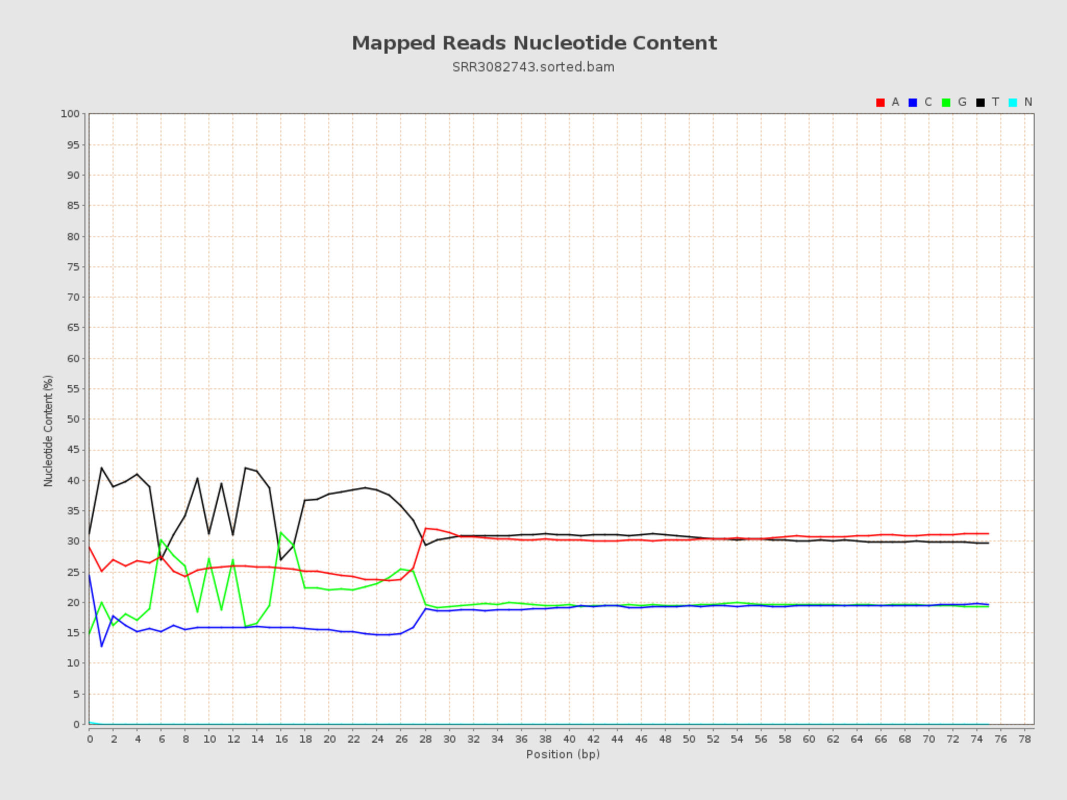
6. Results : Genome Fraction Coverage



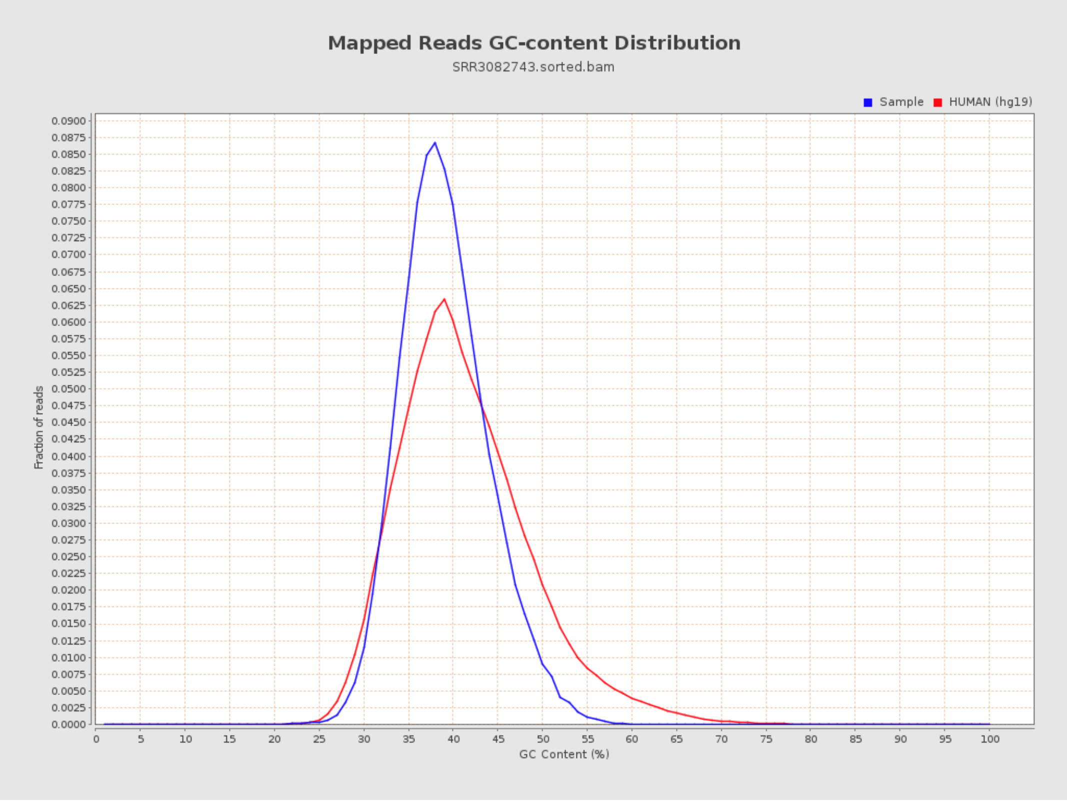
7. Results : Duplication Rate Histogram



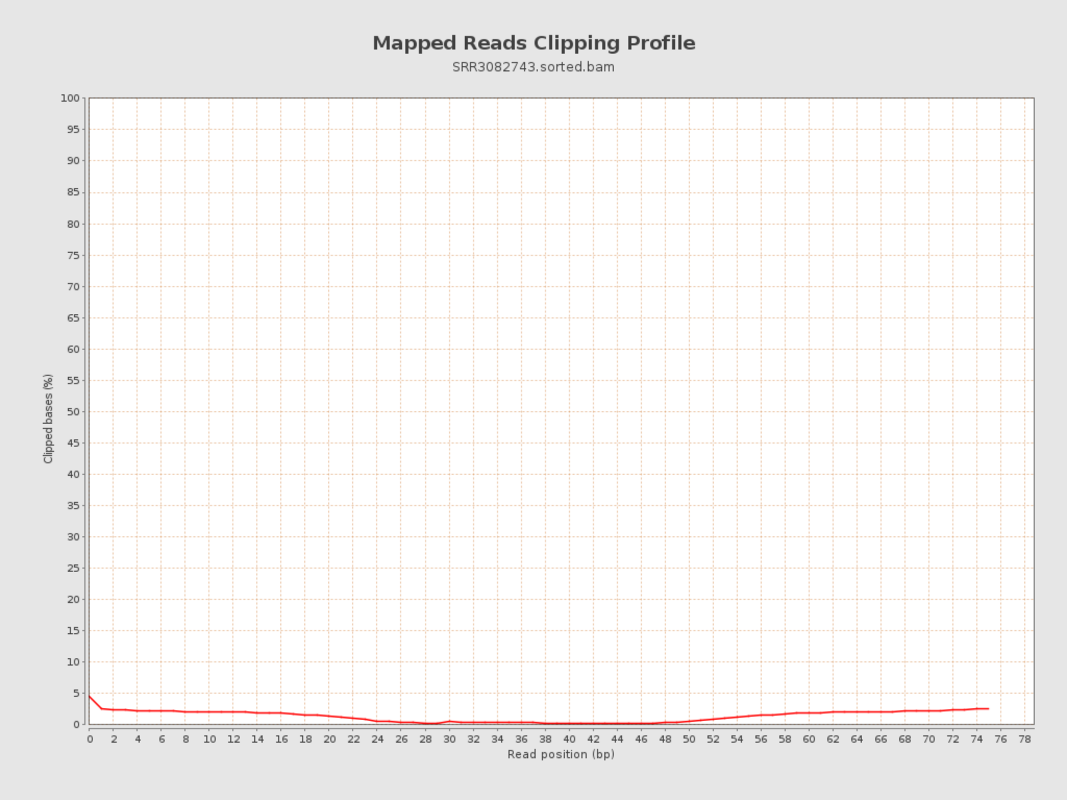
8. Results : Mapped Reads Nucleotide Content



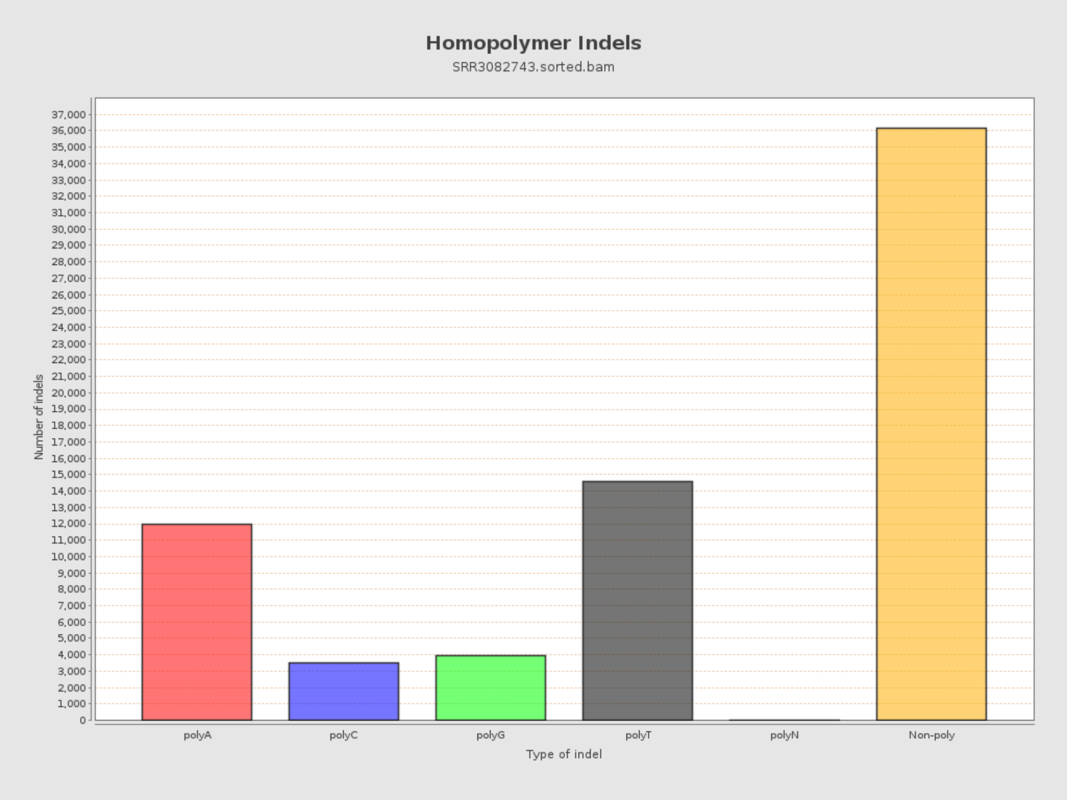
9. Results : Mapped Reads GC-content Distribution



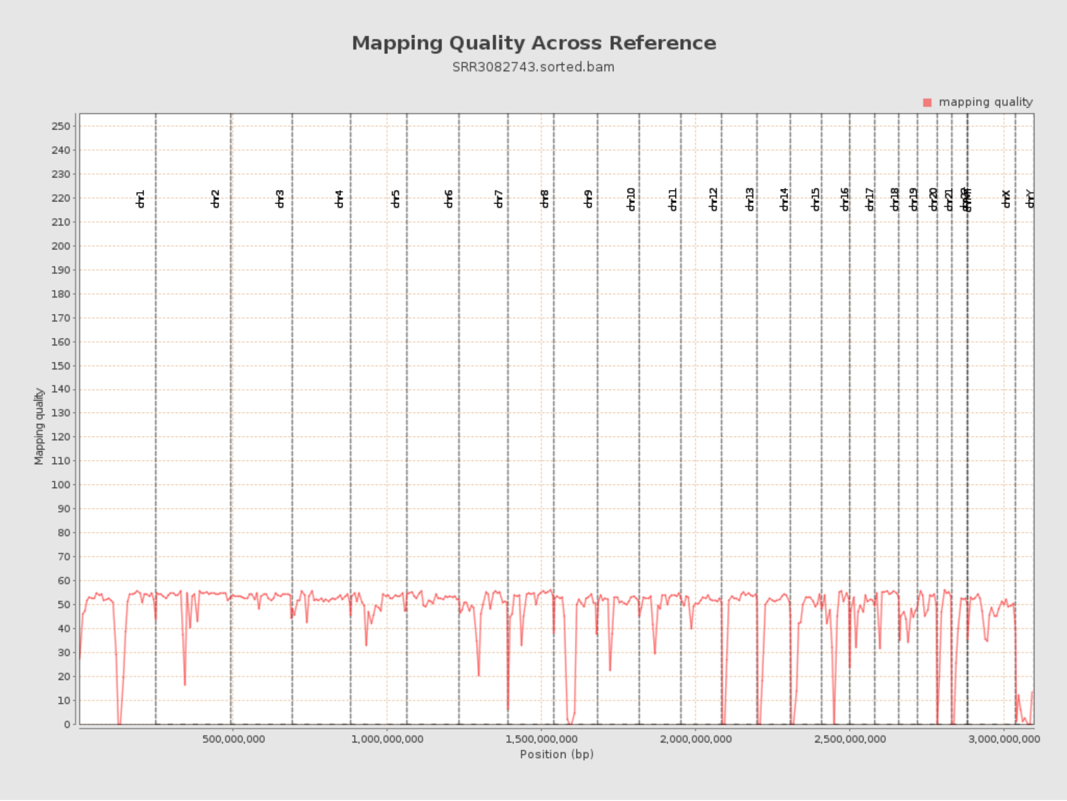
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram