Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:35:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083675.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_SRR3083675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:35:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,878,565
Mapped reads	1,339,641 / 71.31%
Unmapped reads	538,924 / 28.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,204 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	38,396 / 2.04%
Duplication rate	2.31%
Clipped reads	795,914 / 42.37%

2.2. ACGT Content

Number/percentage of A's	23,993,181 / 28.74%
Number/percentage of C's	15,434,435 / 18.49%
Number/percentage of T's	24,959,452 / 29.9%
Number/percentage of G's	19,073,485 / 22.85%
Number/percentage of N's	11,404 / 0.01%
GC Percentage	41.34%

2.3. Coverage

Mean	0.027

Standard Deviation	0.253

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

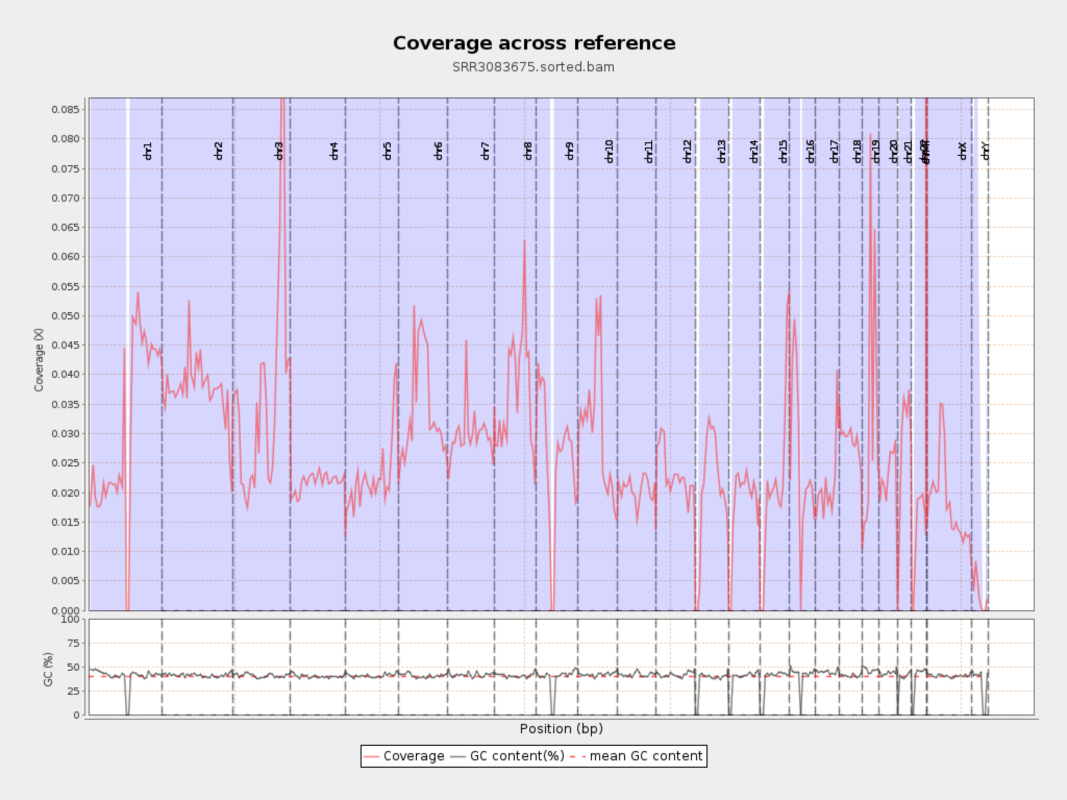
General error rate	0.89%
Mismatches	734,590
Insertions	5,968
Mapped reads with at least one insertion	0.44%
Deletions	16,777
Mapped reads with at least one deletion	1.24%
Homopolymer indels	46.11%

2.6. Chromosome stats

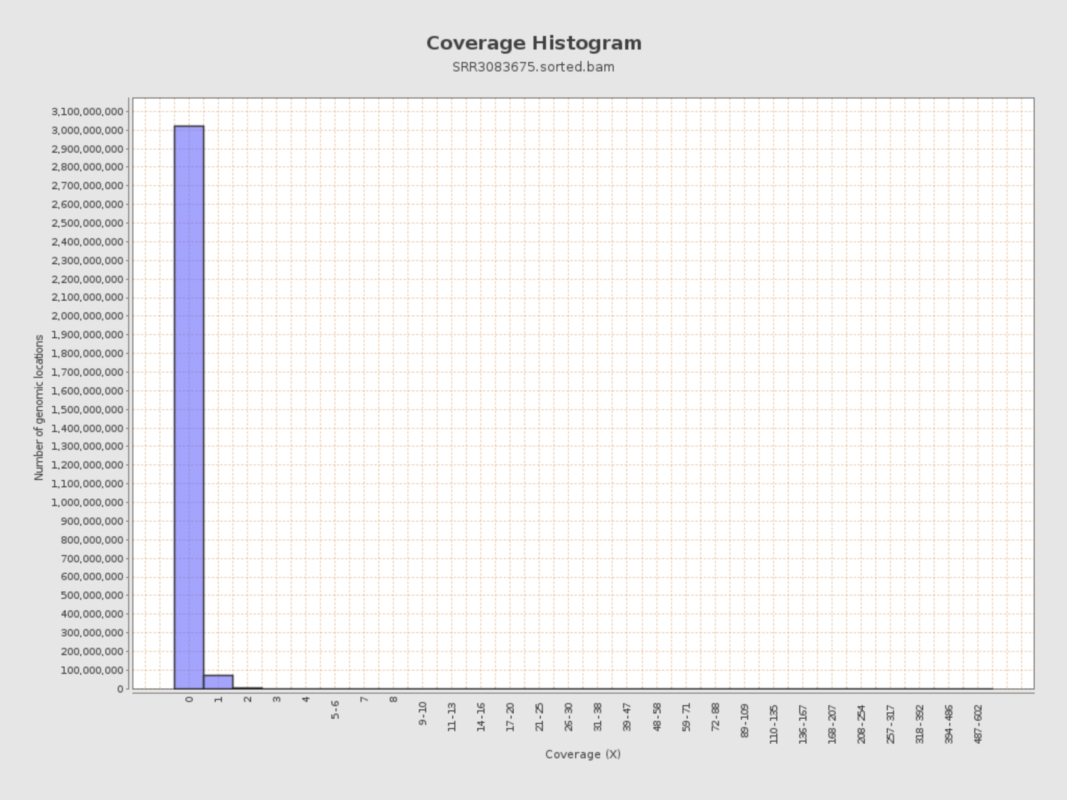
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7687484	0.0308	0.5226
chr2	243199373	9143477	0.0376	0.2594
chr3	198022430	7213296	0.0364	0.2036
chr4	191154276	4167465	0.0218	0.158
chr5	180915260	4157786	0.023	0.1614
chr6	171115067	5846527	0.0342	0.2341
chr7	159138663	4768349	0.03	0.3153

chr8	146364022	5445020	0.0372	0.2942
chr9	141213431	3684754	0.0261	0.2
chr10	135534747	4261125	0.0314	0.2335
chr11	135006516	2769351	0.0205	0.1873
chr12	133851895	3092831	0.0231	0.1612
chr13	115169878	2355896	0.0205	0.1509
chr14	107349540	1910061	0.0178	0.1432
chr15	102531392	2162912	0.0211	0.1541
chr16	90354753	2307785	0.0255	0.1745
chr17	81195210	1770031	0.0218	0.1635
chr18	78077248	2269078	0.0291	0.3342
chr19	59128983	1968120	0.0333	0.3619
chr20	63025520	1454133	0.0231	0.163
chr21	48129895	1319507	0.0274	0.1773
chr22	51304566	678656	0.0132	0.1208
chrMT	16571	37034	2.2349	1.9863
chrX	155270560	2867750	0.0185	0.1544
chrY	59373566	160236	0.0027	0.0637

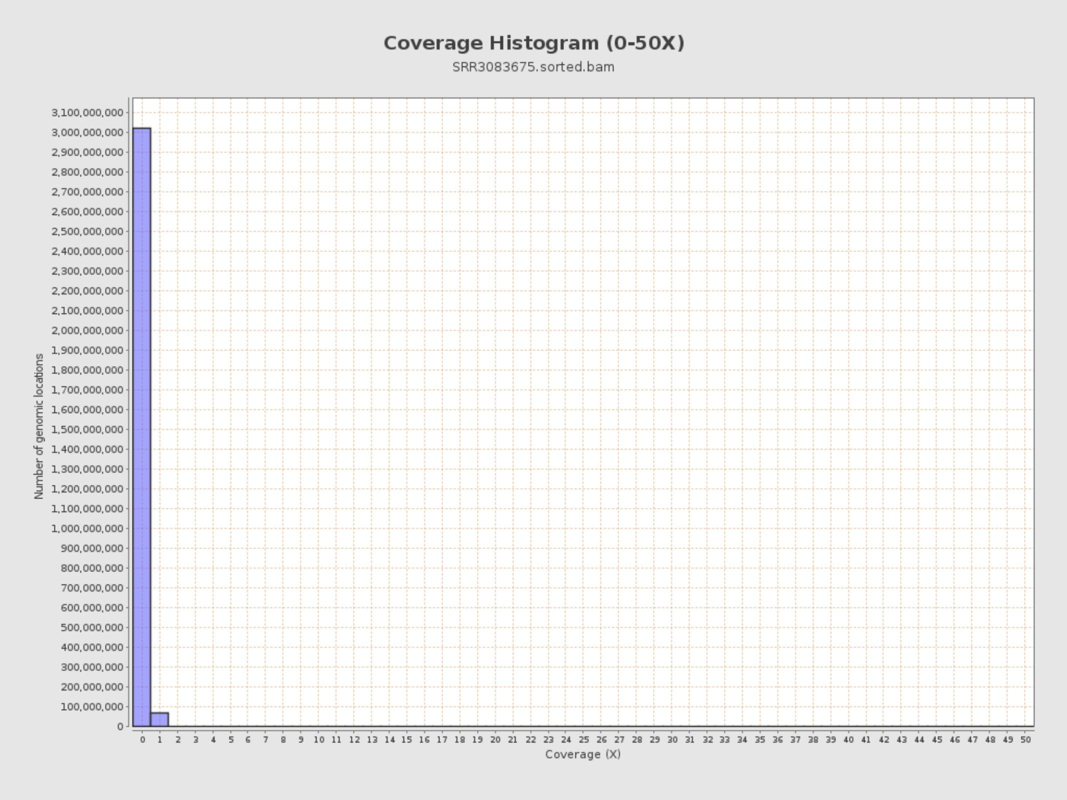
3. Results : Coverage across reference



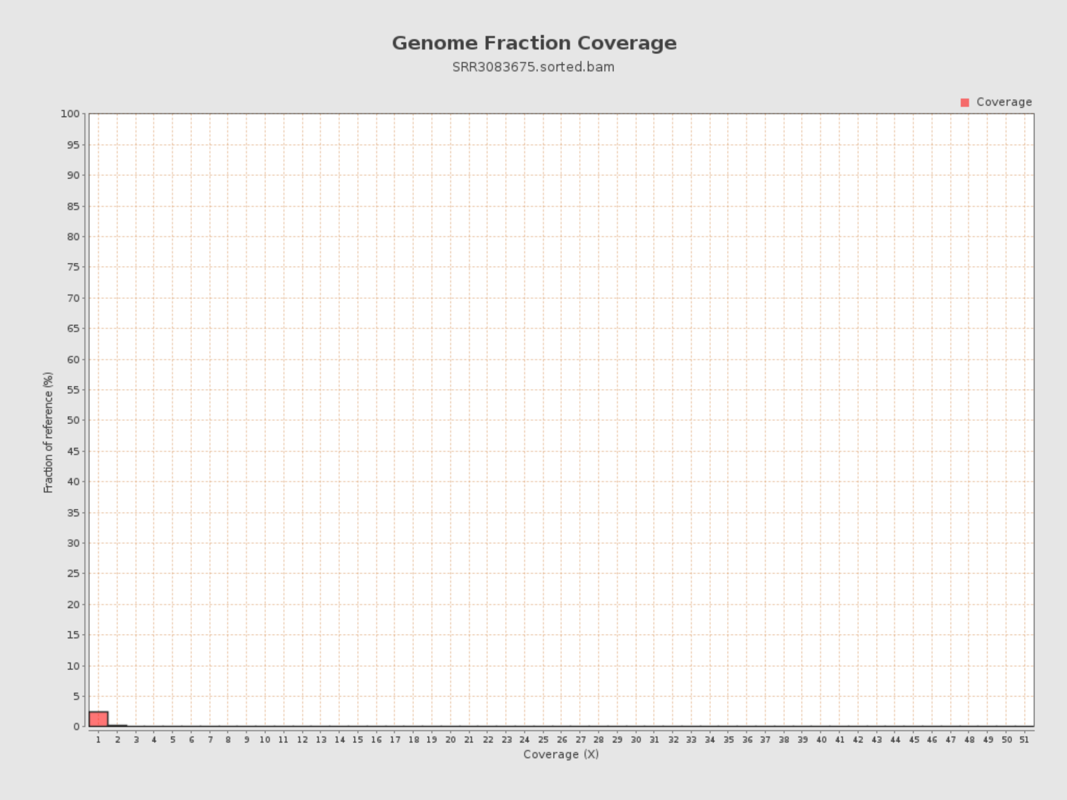
4. Results : Coverage Histogram



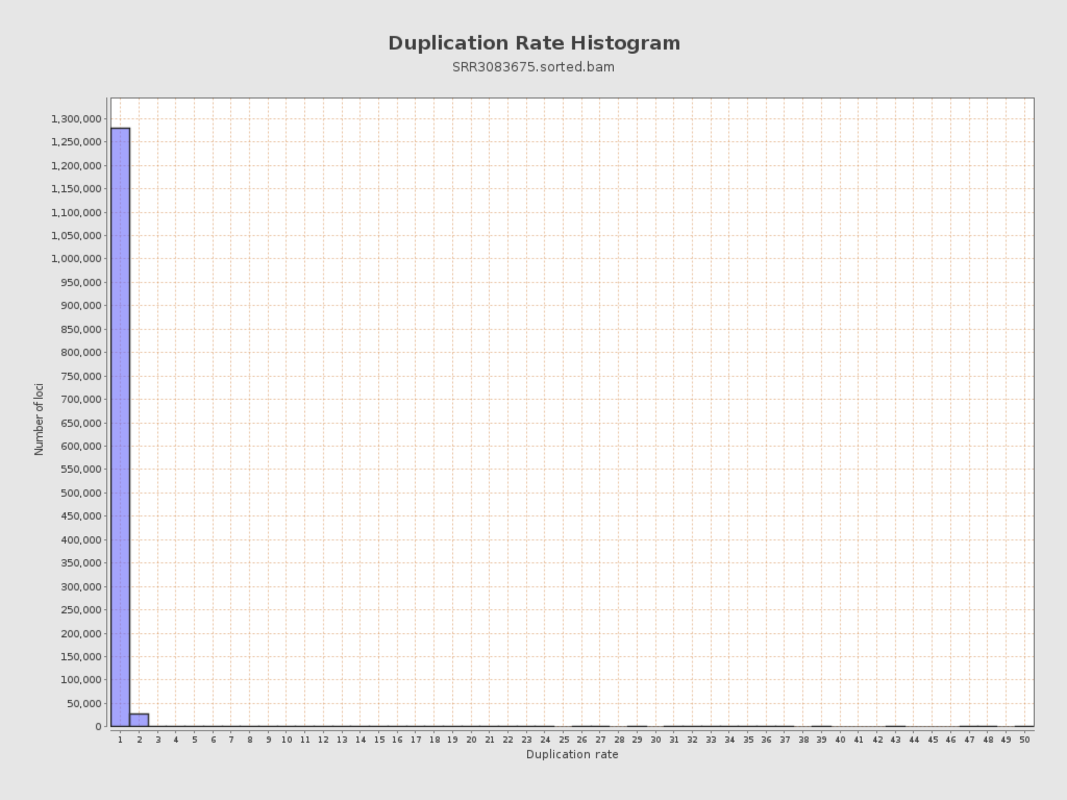
5. Results : Coverage Histogram (0-50X)



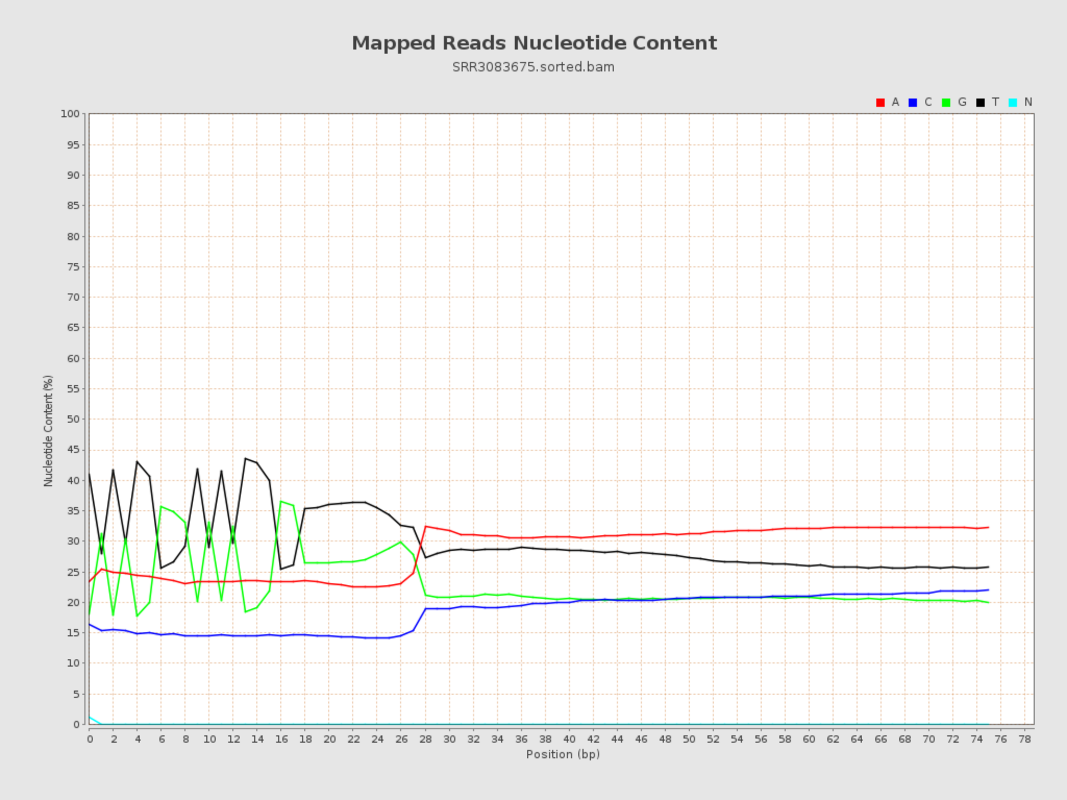
6. Results : Genome Fraction Coverage



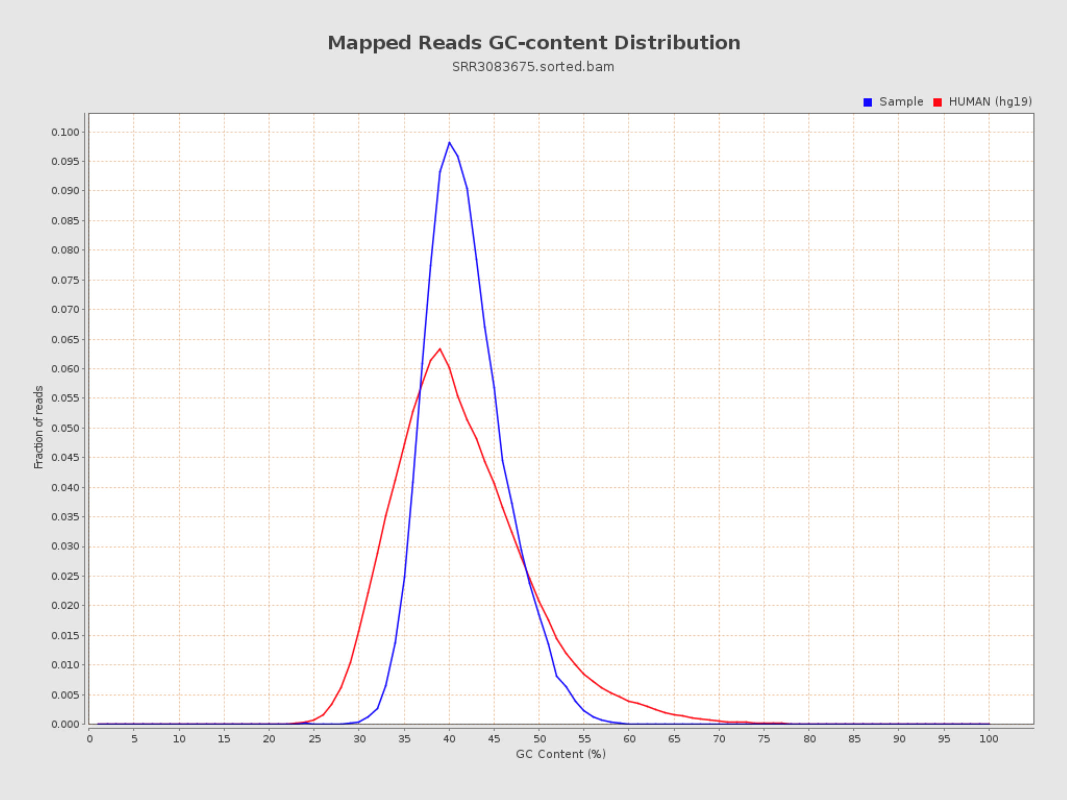
7. Results : Duplication Rate Histogram



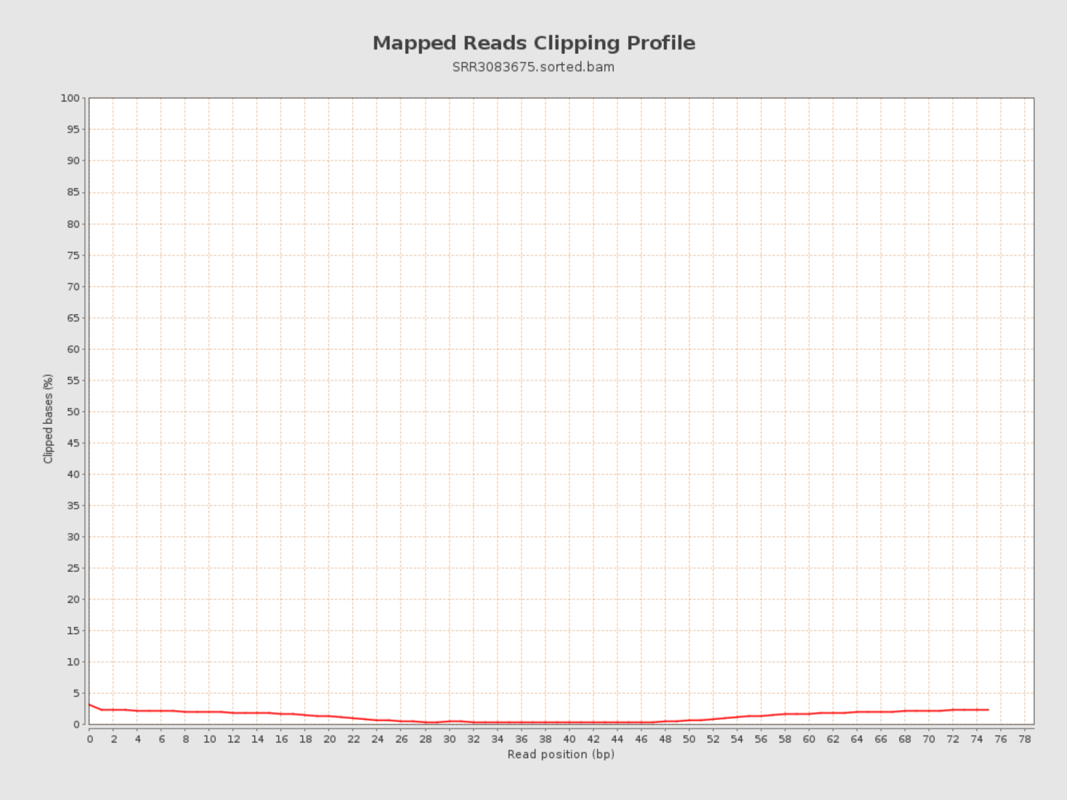
8. Results : Mapped Reads Nucleotide Content



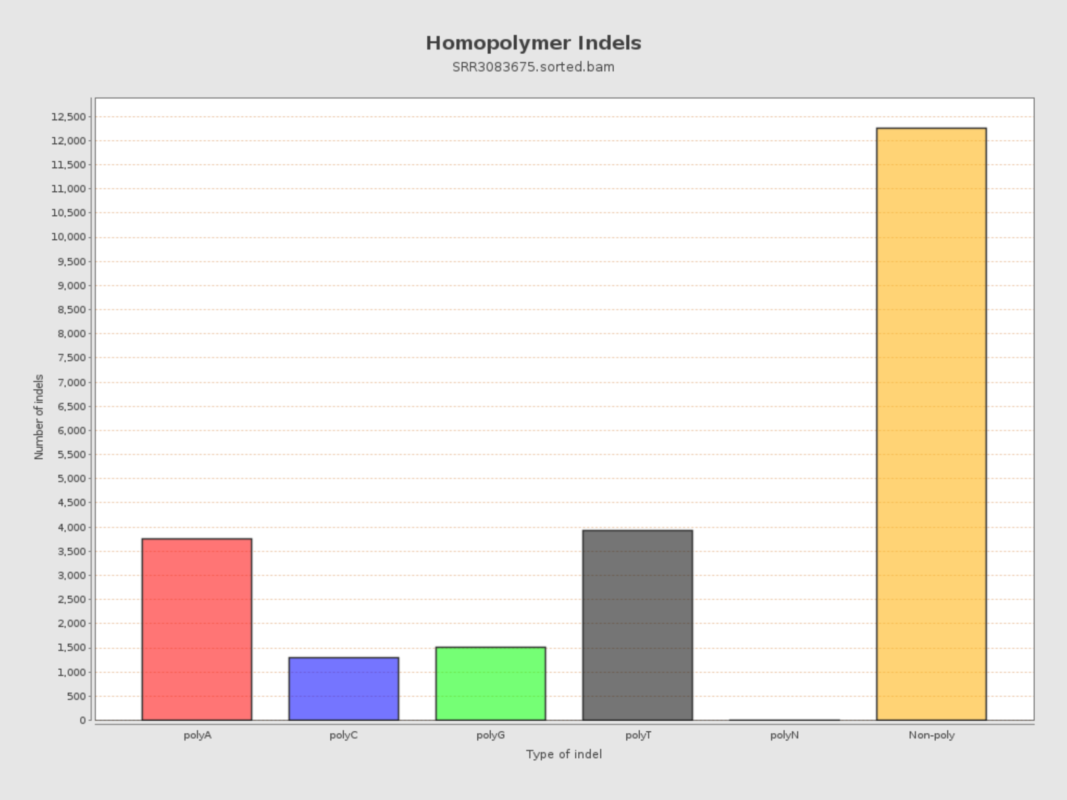
9. Results : Mapped Reads GC-content Distribution



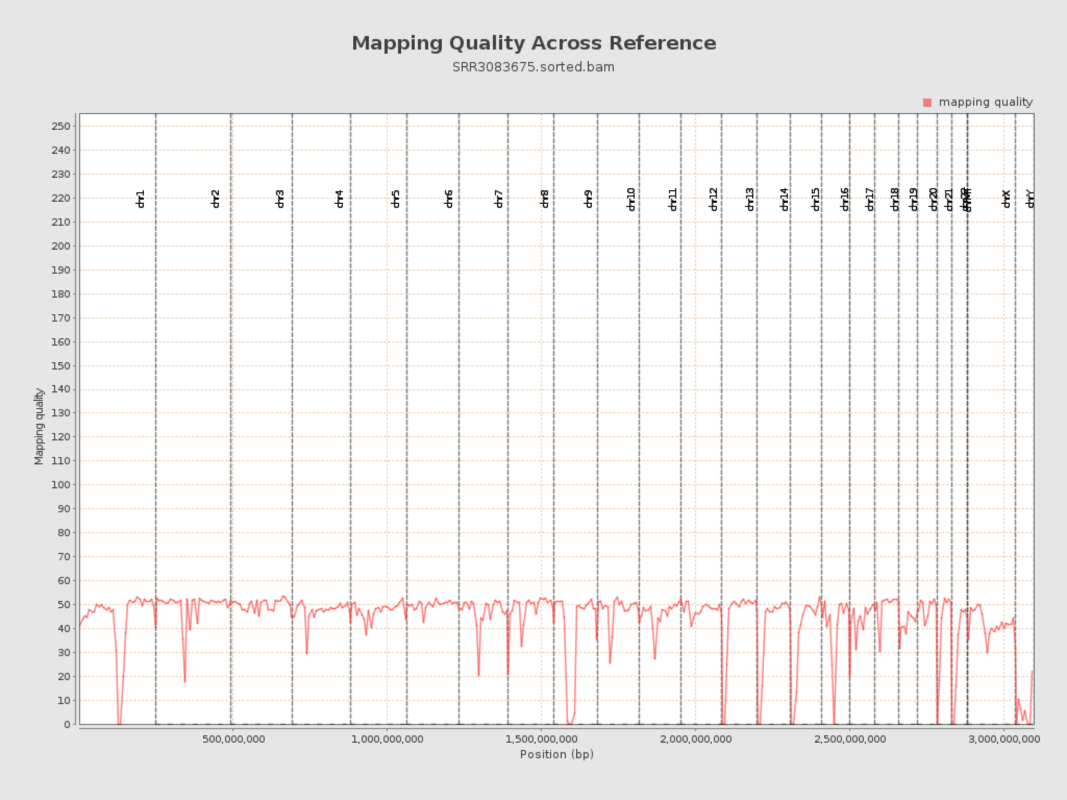
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram