Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:39:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084389.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_SRR3084389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084389.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:39:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,261,608
Mapped reads	2,024,090 / 89.5%
Unmapped reads	237,518 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,586 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	63,054 / 2.79%
Duplication rate	2.58%
Clipped reads	936,022 / 41.39%

2.2. ACGT Content

Number/percentage of A's	37,780,780 / 28.01%
Number/percentage of C's	25,591,352 / 18.98%
Number/percentage of T's	41,514,465 / 30.78%
Number/percentage of G's	29,802,381 / 22.1%
Number/percentage of N's	173,490 / 0.13%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.3111

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

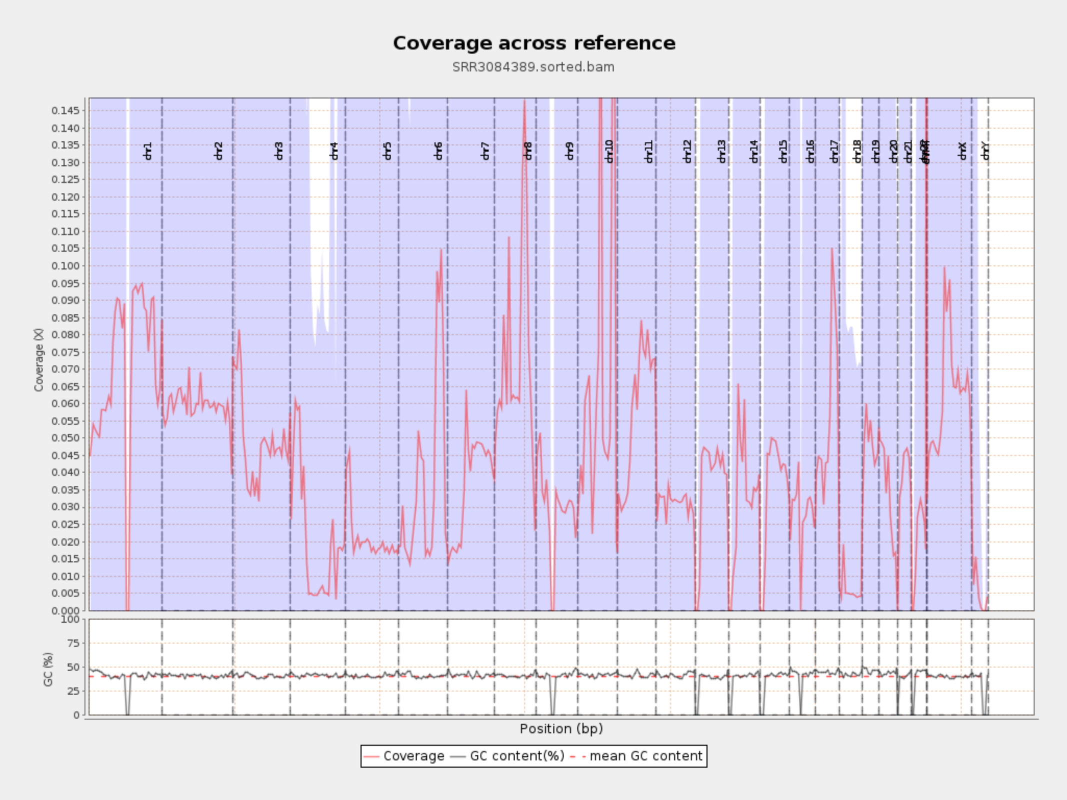
General error rate	1.02%
Mismatches	1,363,082
Insertions	9,863
Mapped reads with at least one insertion	0.48%
Deletions	27,180
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.33%

2.6. Chromosome stats

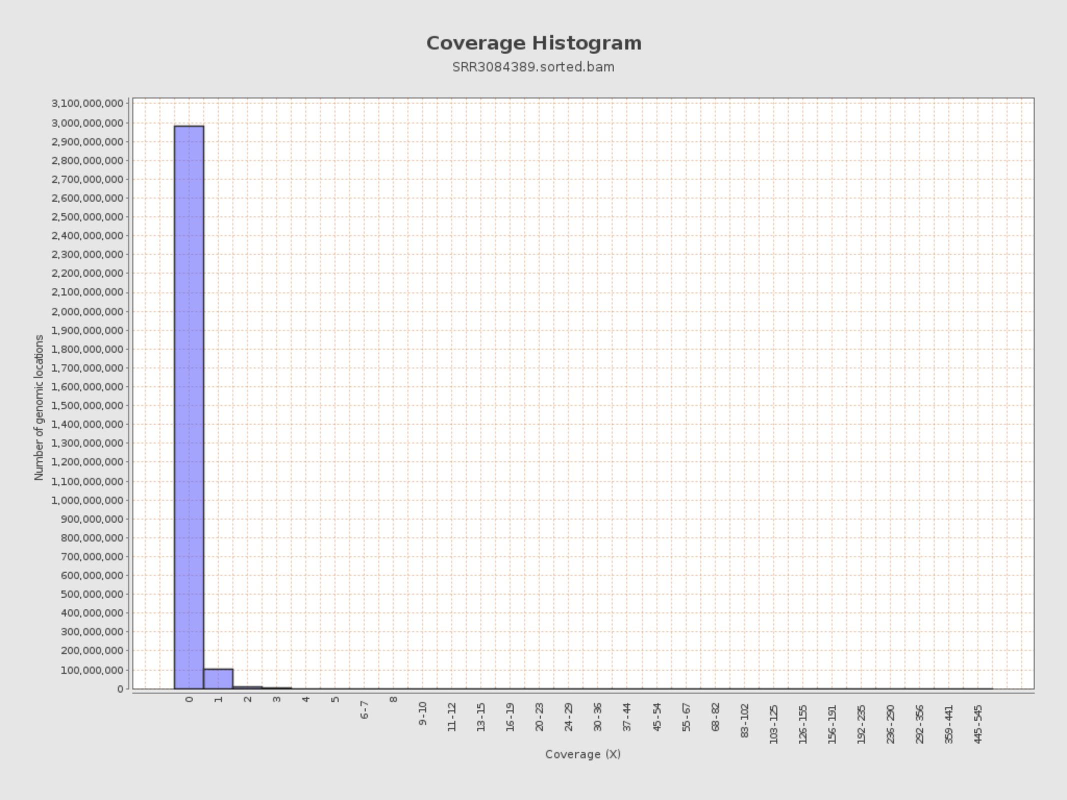
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17270459	0.0693	0.5568
chr2	243199373	14473203	0.0595	0.3459
chr3	198022430	9739285	0.0492	0.2509
chr4	191154276	3902003	0.0204	0.1718
chr5	180915260	3803312	0.021	0.1621
chr6	171115067	6383532	0.0373	0.228
chr7	159138663	5916555	0.0372	0.3631

chr8	146364022	10773662	0.0736	0.3925
chr9	141213431	4145541	0.0294	0.2272
chr10	135534747	9757521	0.072	0.4373
chr11	135006516	7763827	0.0575	0.3294
chr12	133851895	4162425	0.0311	0.1964
chr13	115169878	4155833	0.0361	0.2102
chr14	107349540	3504728	0.0326	0.2049
chr15	102531392	3674078	0.0358	0.2199
chr16	90354753	2537760	0.0281	0.2111
chr17	81195210	4622111	0.0569	0.2885
chr18	78077248	473909	0.0061	0.3315
chr19	59128983	2893501	0.0489	0.3696
chr20	63025520	2123739	0.0337	0.2071
chr21	48129895	1757870	0.0365	0.2233
chr22	51304566	988308	0.0193	0.152
chrMT	16571	11979	0.7229	0.9508
chrX	155270560	9748008	0.0628	0.308
chrY	59373566	326631	0.0055	0.114

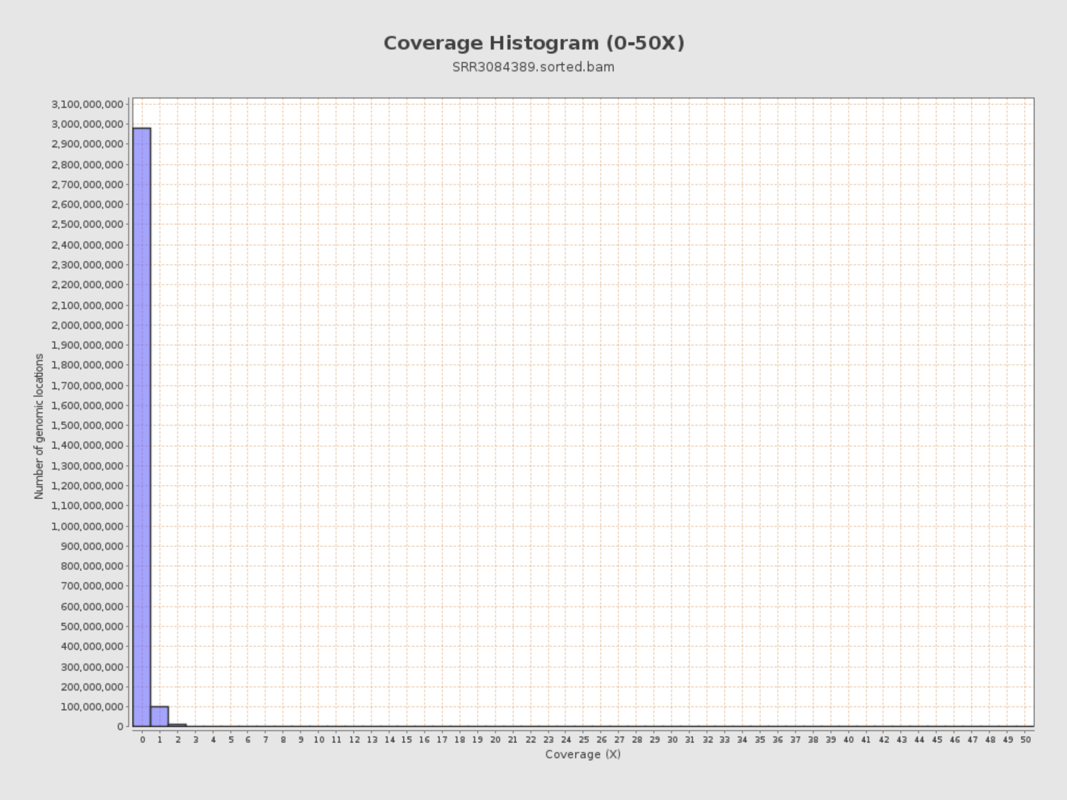
3. Results : Coverage across reference



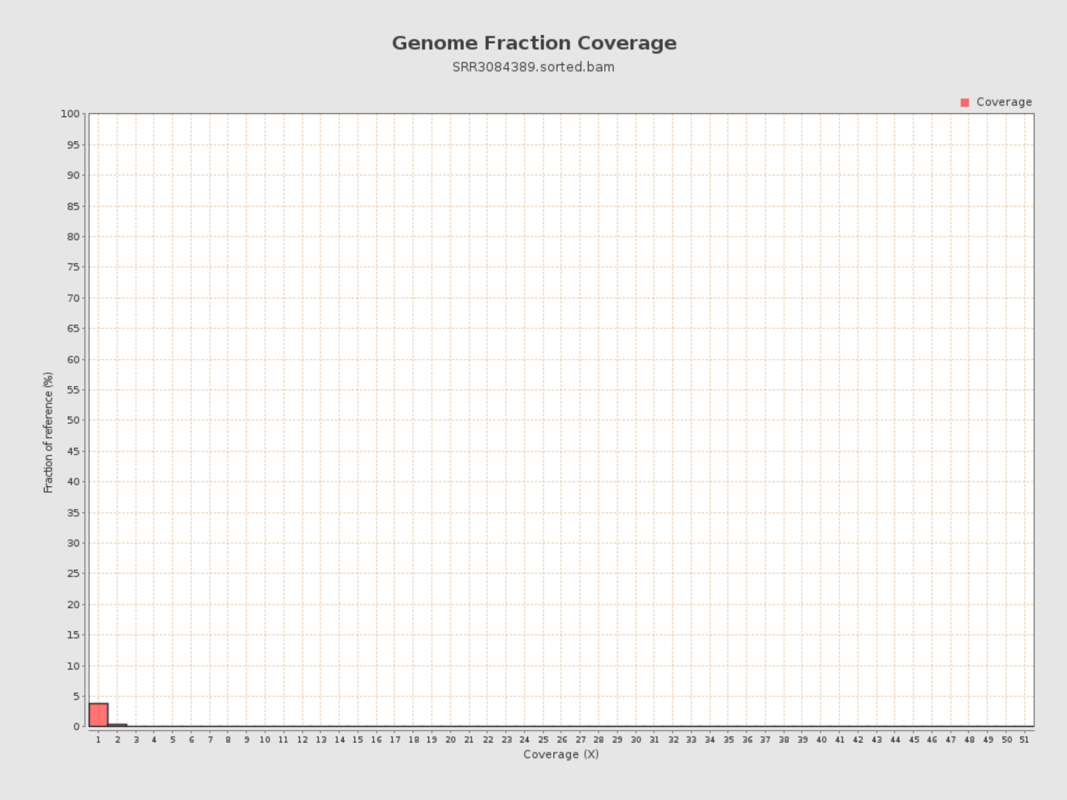
4. Results : Coverage Histogram



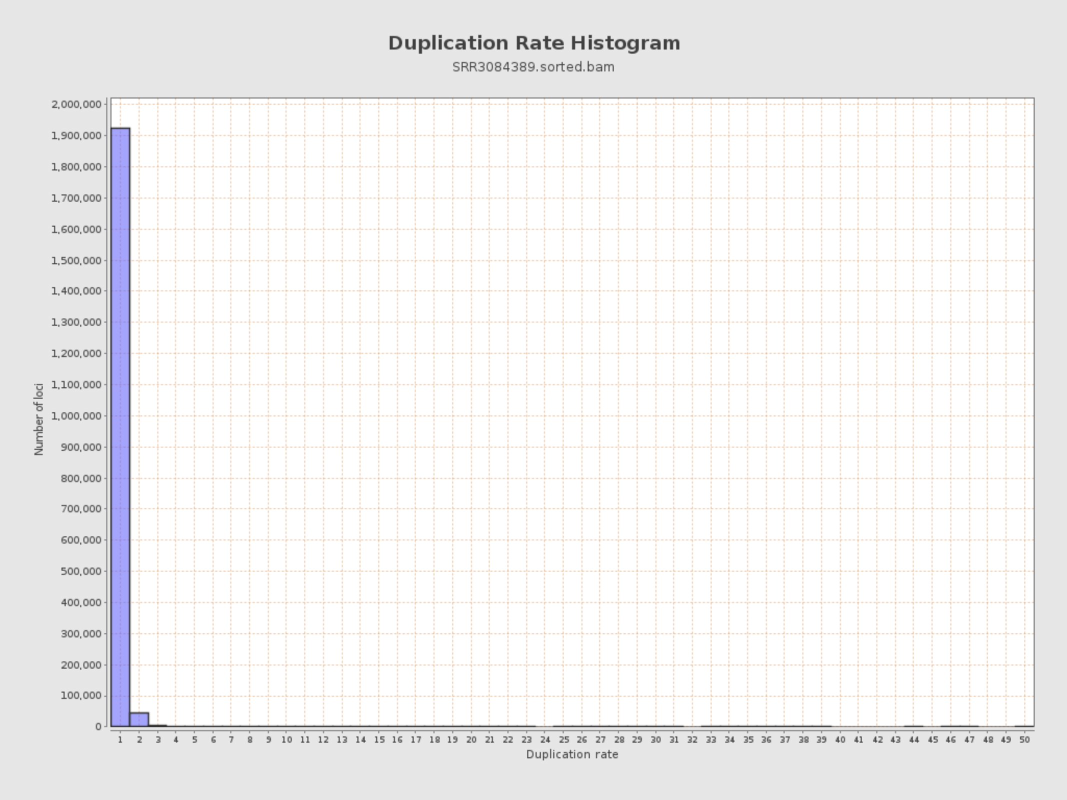
5. Results : Coverage Histogram (0-50X)



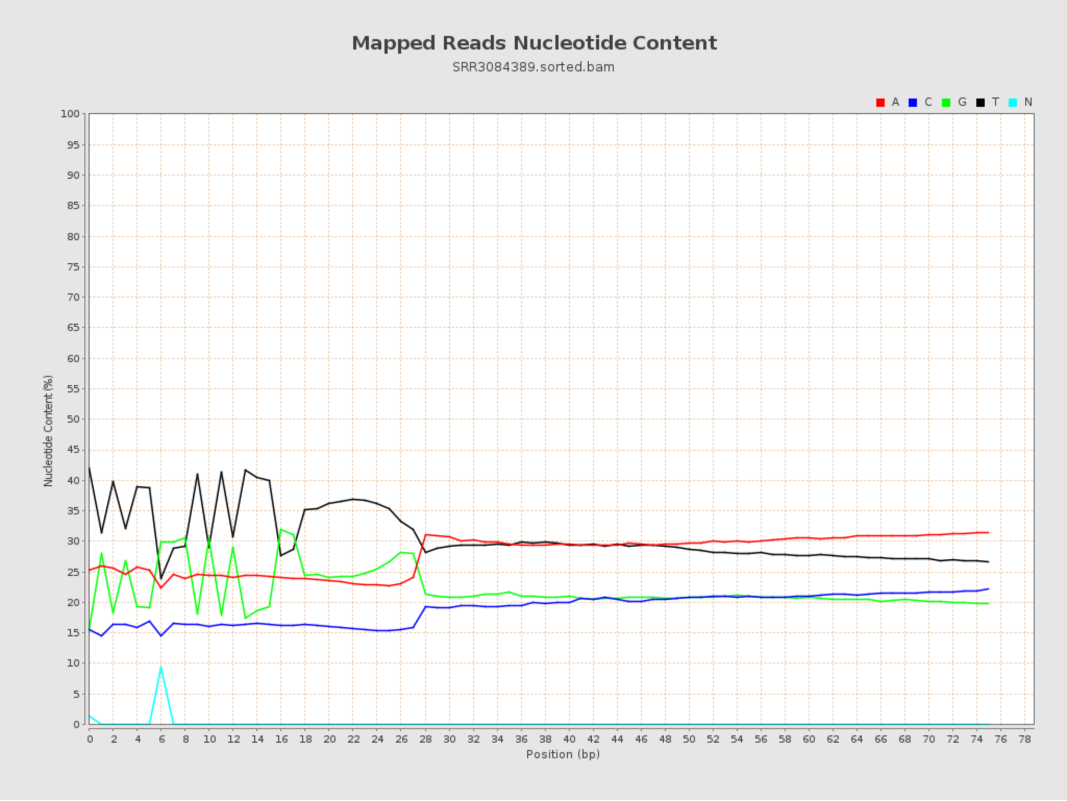
6. Results : Genome Fraction Coverage



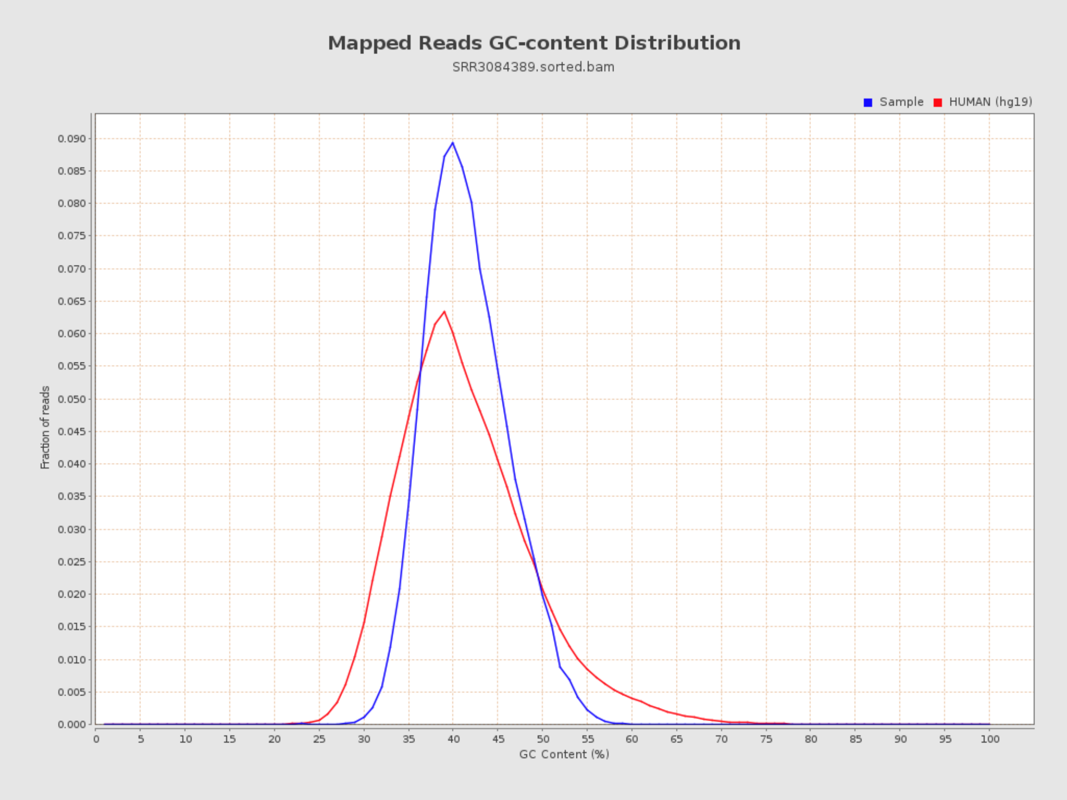
7. Results : Duplication Rate Histogram



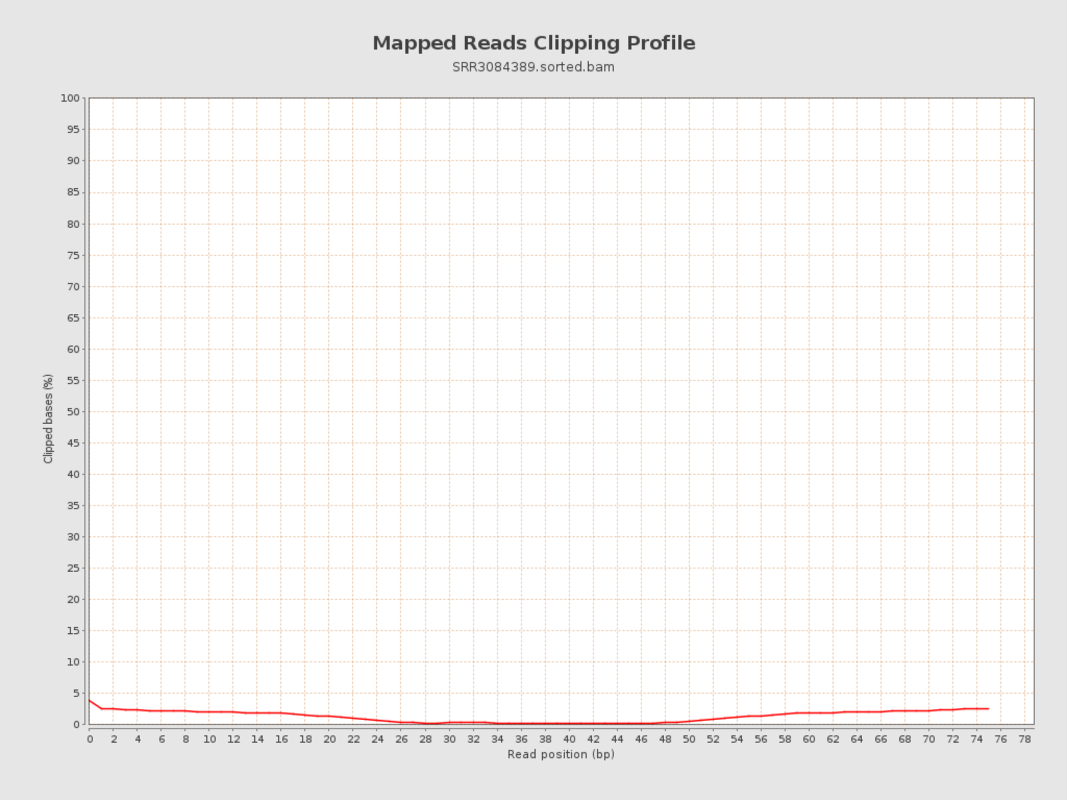
8. Results : Mapped Reads Nucleotide Content



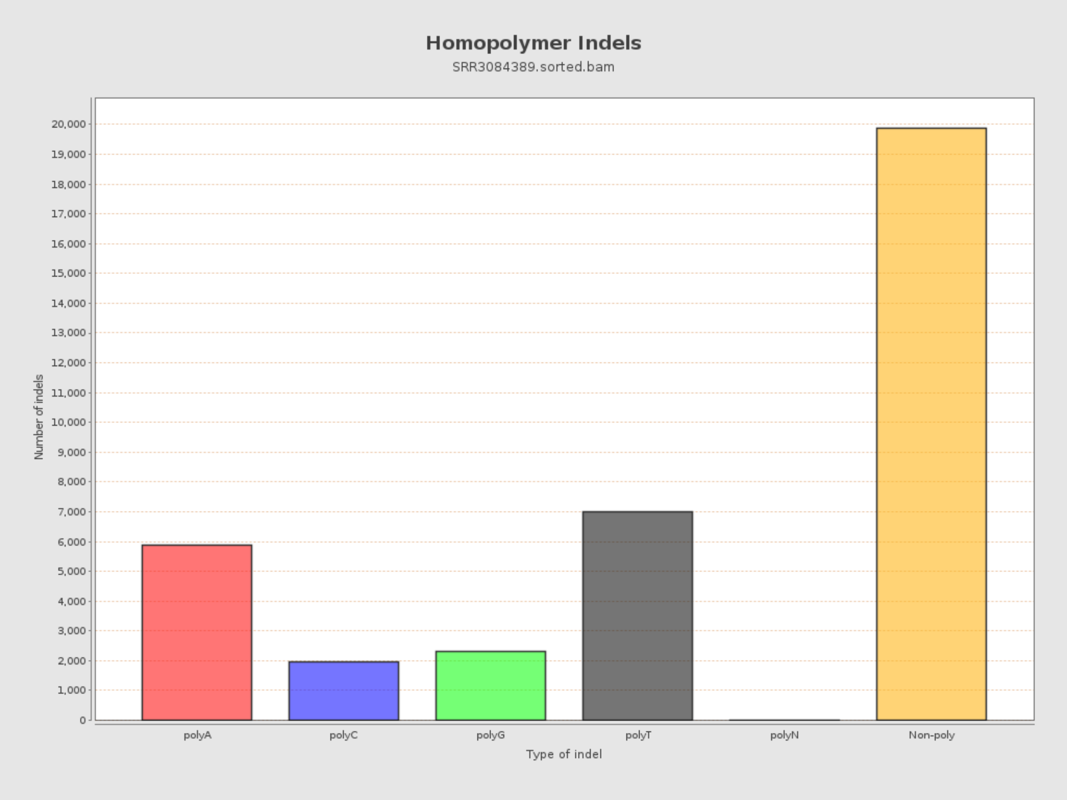
9. Results : Mapped Reads GC-content Distribution



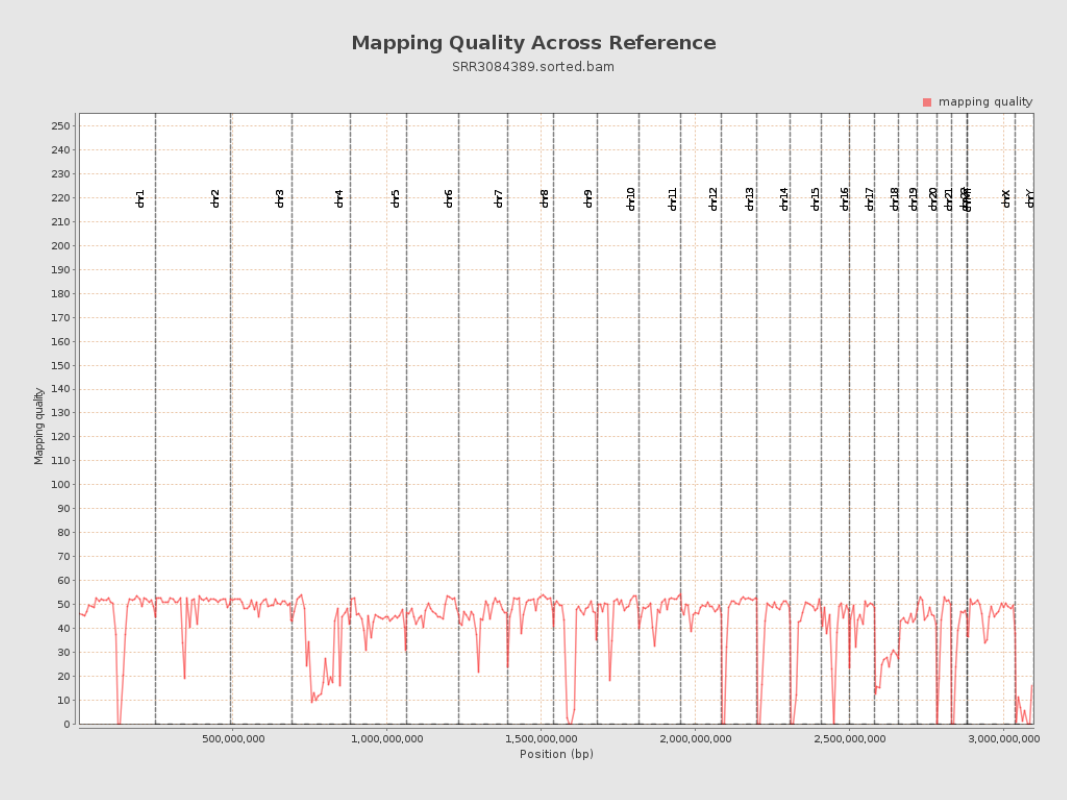
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram