Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:53:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081884.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_SRR3081884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081884.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:52:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,188,660
Mapped reads	2,927,864 / 91.82%
Unmapped reads	260,796 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,331 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	122,342 / 3.84%
Duplication rate	3.13%
Clipped reads	1,255,810 / 39.38%

2.2. ACGT Content

Number/percentage of A's	53,878,370 / 27.4%
Number/percentage of C's	38,551,752 / 19.6%
Number/percentage of T's	59,408,034 / 30.21%
Number/percentage of G's	44,803,063 / 22.78%
Number/percentage of N's	2,136 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0635

Standard Deviation	0.4919

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

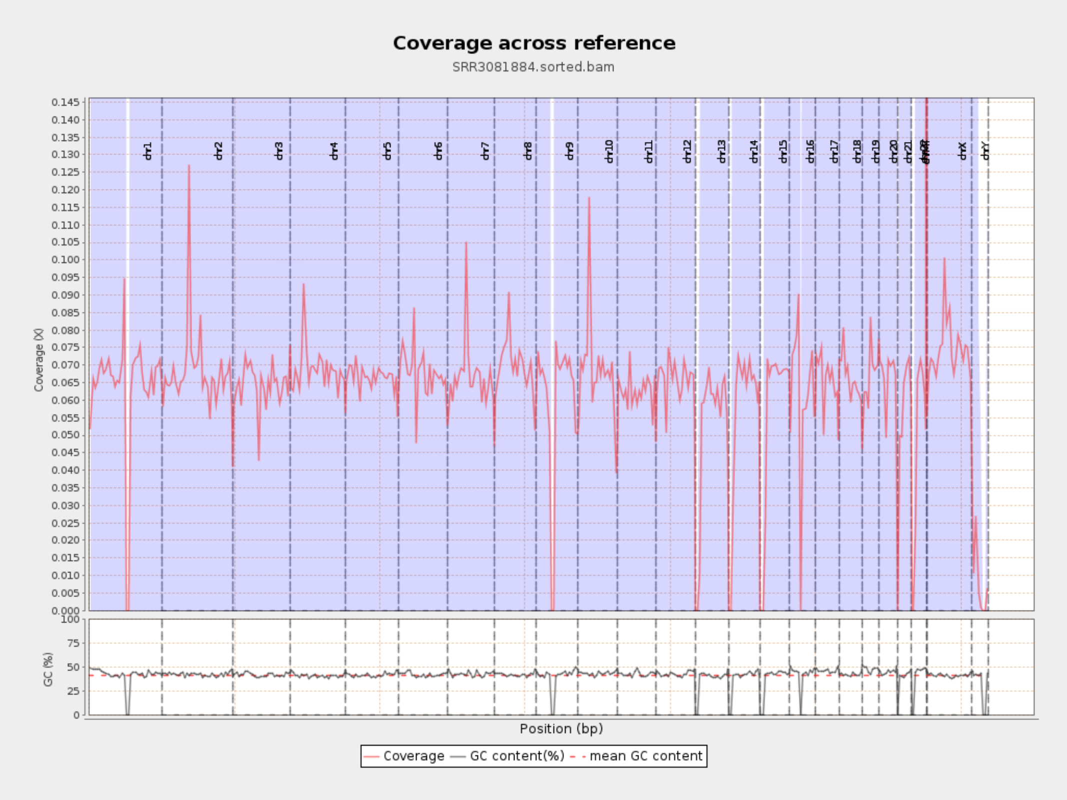
General error rate	0.83%
Mismatches	1,605,755
Insertions	14,087
Mapped reads with at least one insertion	0.48%
Deletions	39,433
Mapped reads with at least one deletion	1.33%
Homopolymer indels	45.91%

2.6. Chromosome stats

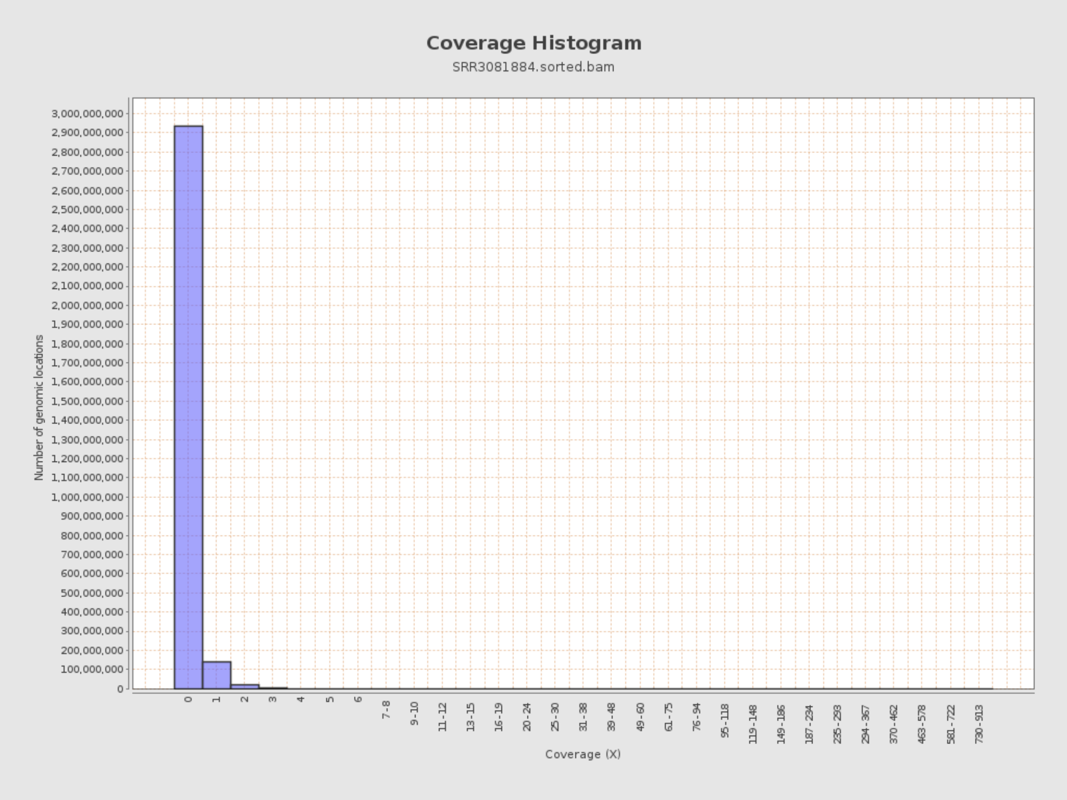
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15868722	0.0637	0.846
chr2	243199373	16668534	0.0685	0.6238
chr3	198022430	12645033	0.0639	0.296
chr4	191154276	13137769	0.0687	0.3436
chr5	180915260	12049441	0.0666	0.3005
chr6	171115067	11561418	0.0676	0.3754
chr7	159138663	10661922	0.067	0.685

chr8	146364022	10172925	0.0695	0.5579
chr9	141213431	8443919	0.0598	0.4722
chr10	135534747	9328980	0.0688	0.5533
chr11	135006516	8402622	0.0622	0.415
chr12	133851895	8853805	0.0661	0.3039
chr13	115169878	5902629	0.0513	0.2614
chr14	107349540	5996199	0.0559	0.3059
chr15	102531392	5722020	0.0558	0.2791
chr16	90354753	5613235	0.0621	0.3543
chr17	81195210	5311950	0.0654	0.3346
chr18	78077248	5215128	0.0668	0.8492
chr19	59128983	3965747	0.0671	0.6483
chr20	63025520	4130325	0.0655	0.3119
chr21	48129895	2670661	0.0555	0.3167
chr22	51304566	2341036	0.0456	0.2478
chrMT	16571	12390	0.7477	0.9957
chrX	155270560	11523149	0.0742	0.3779
chrY	59373566	514233	0.0087	0.2197

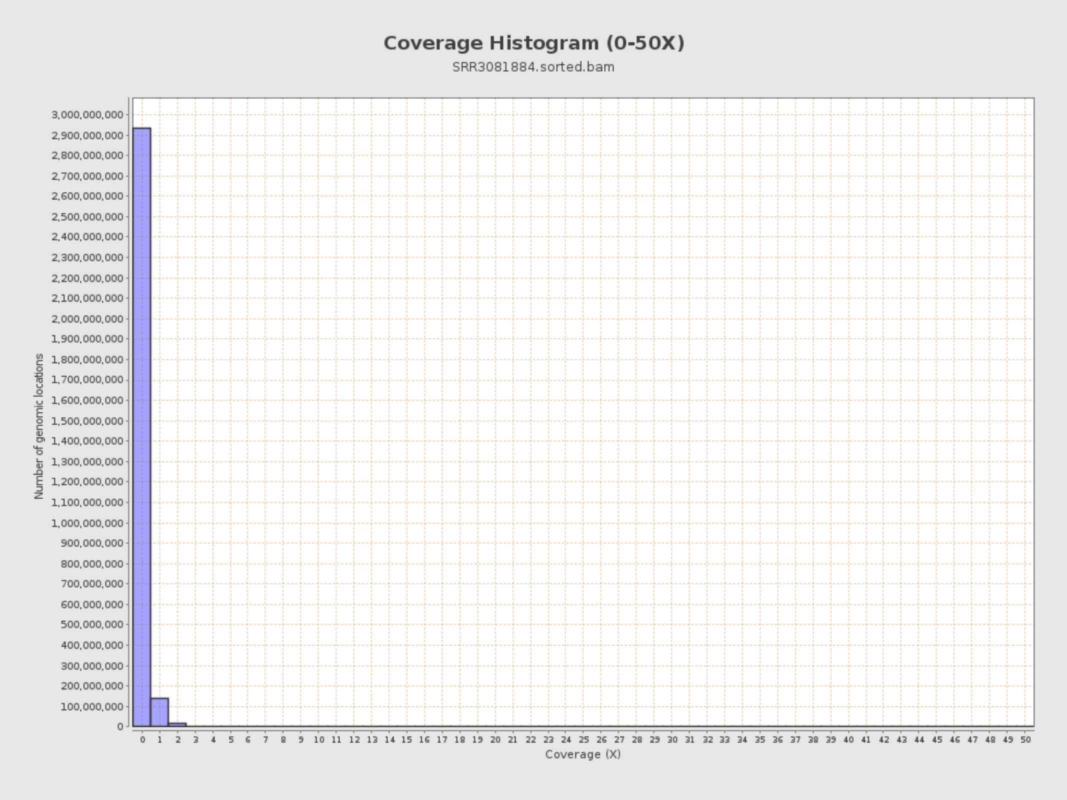
3. Results : Coverage across reference



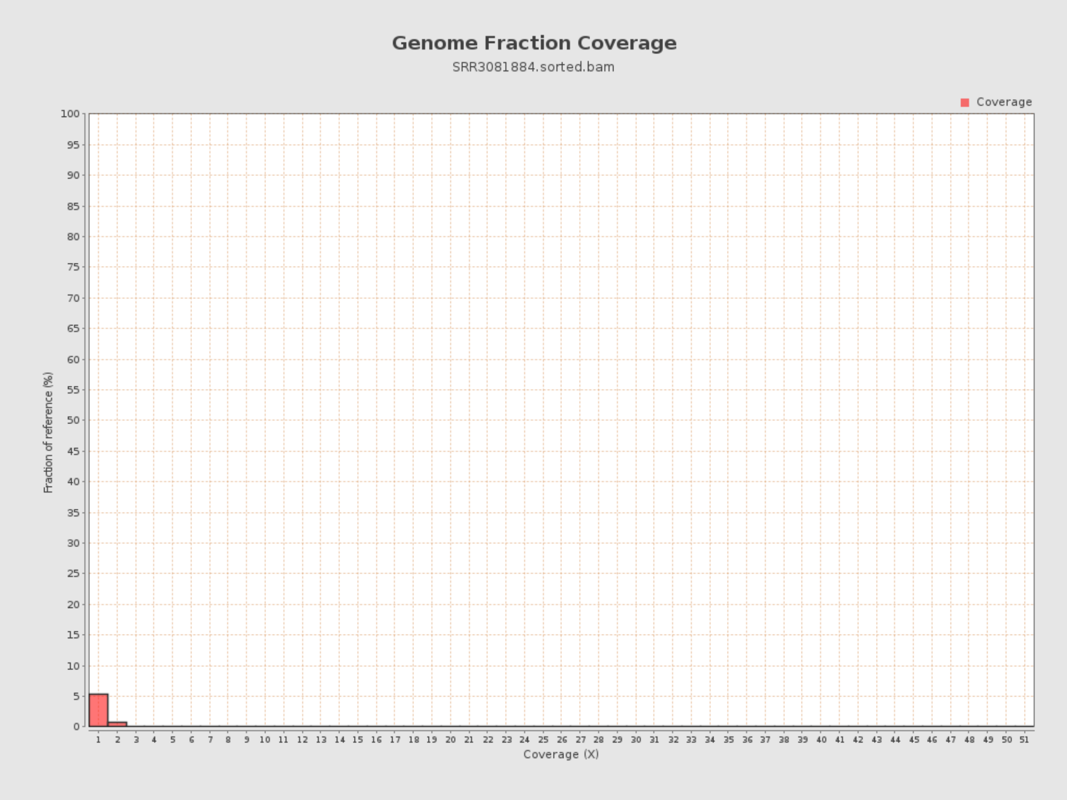
4. Results : Coverage Histogram



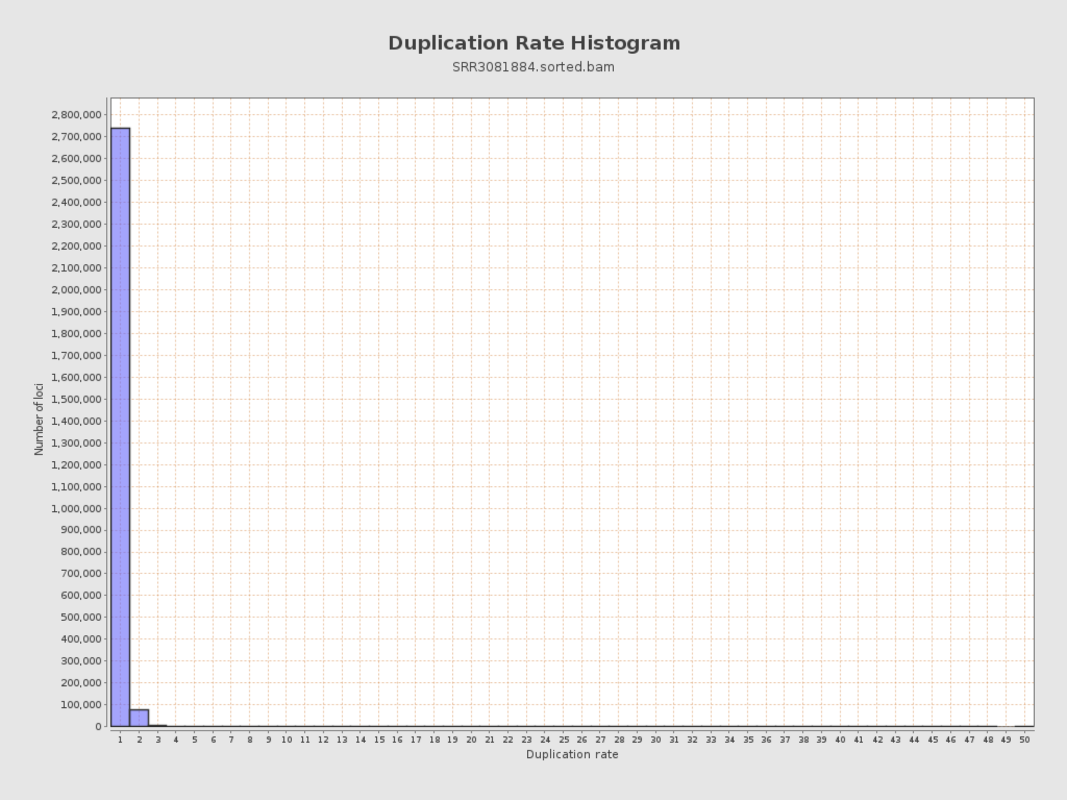
5. Results : Coverage Histogram (0-50X)



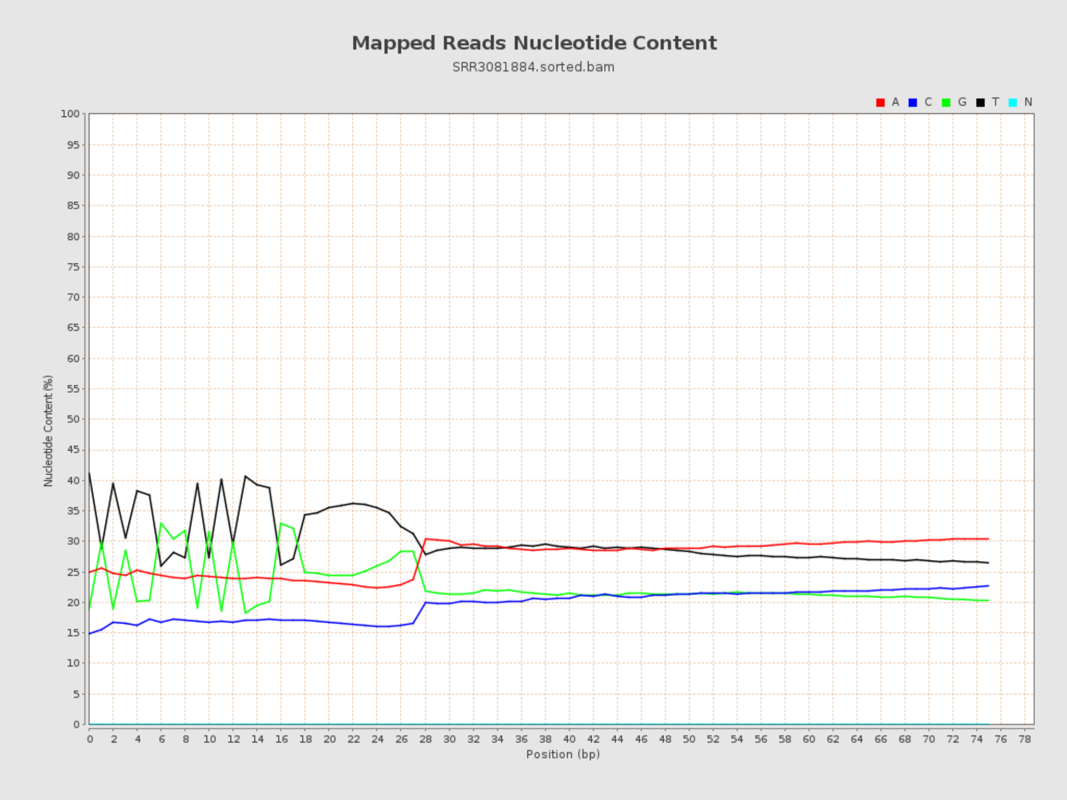
6. Results : Genome Fraction Coverage



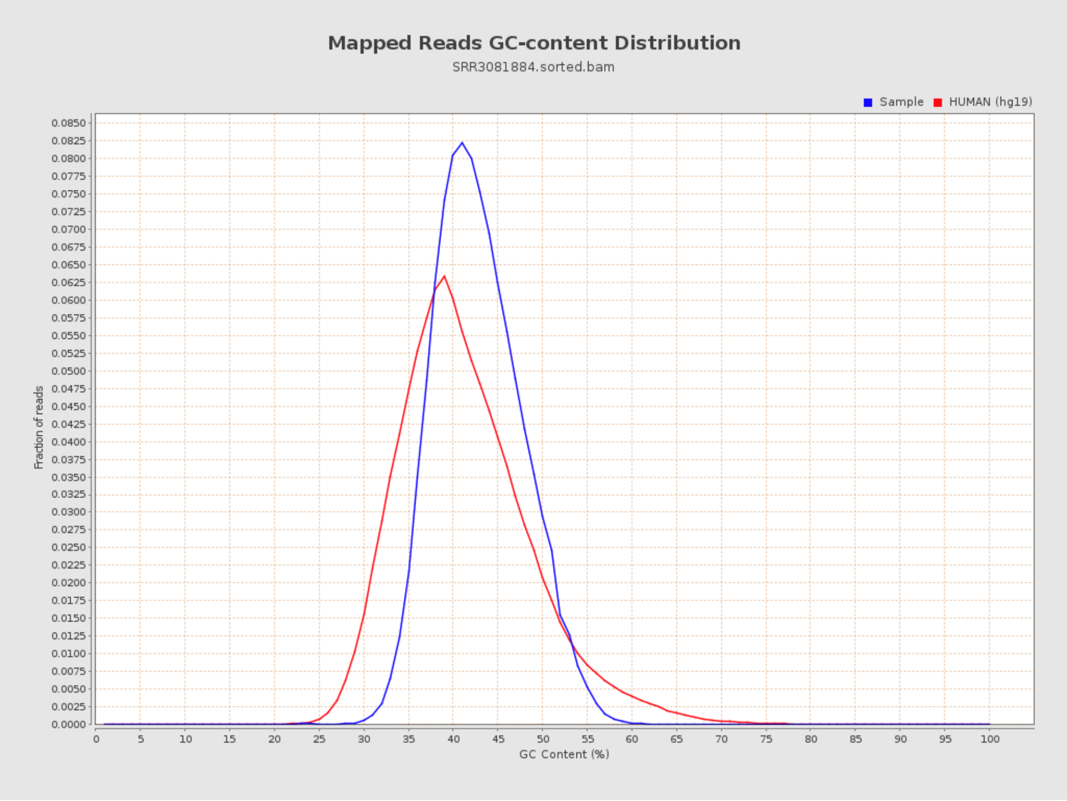
7. Results : Duplication Rate Histogram



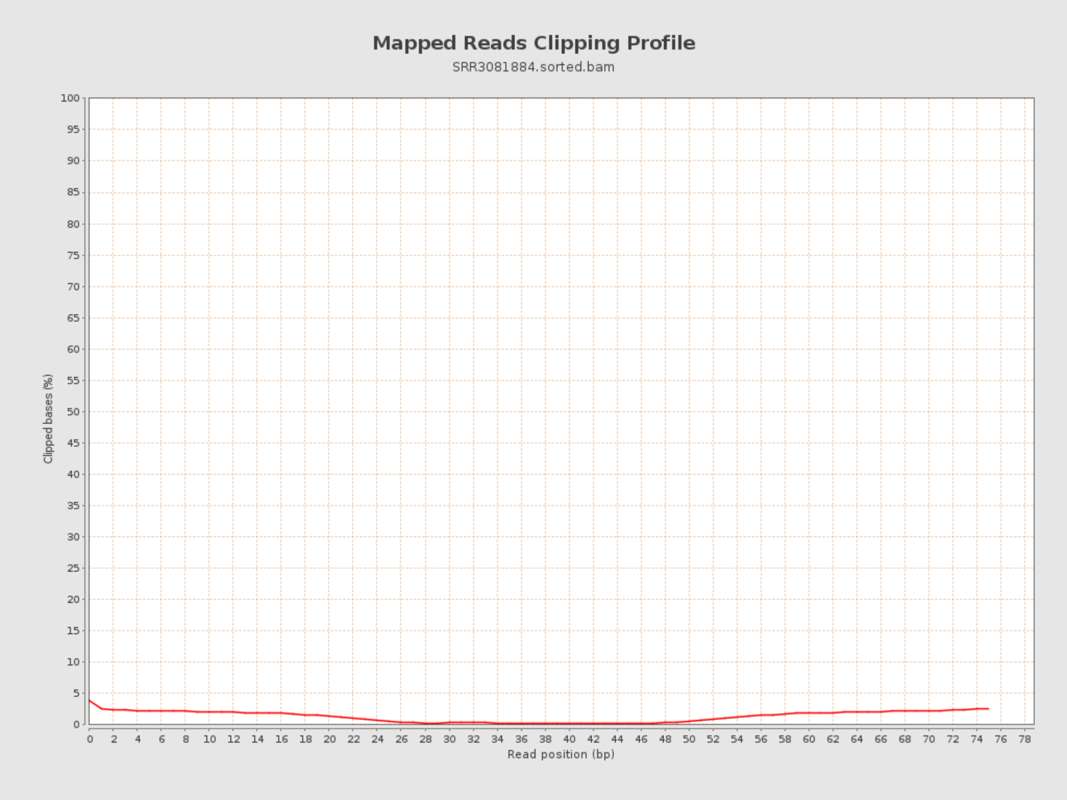
8. Results : Mapped Reads Nucleotide Content



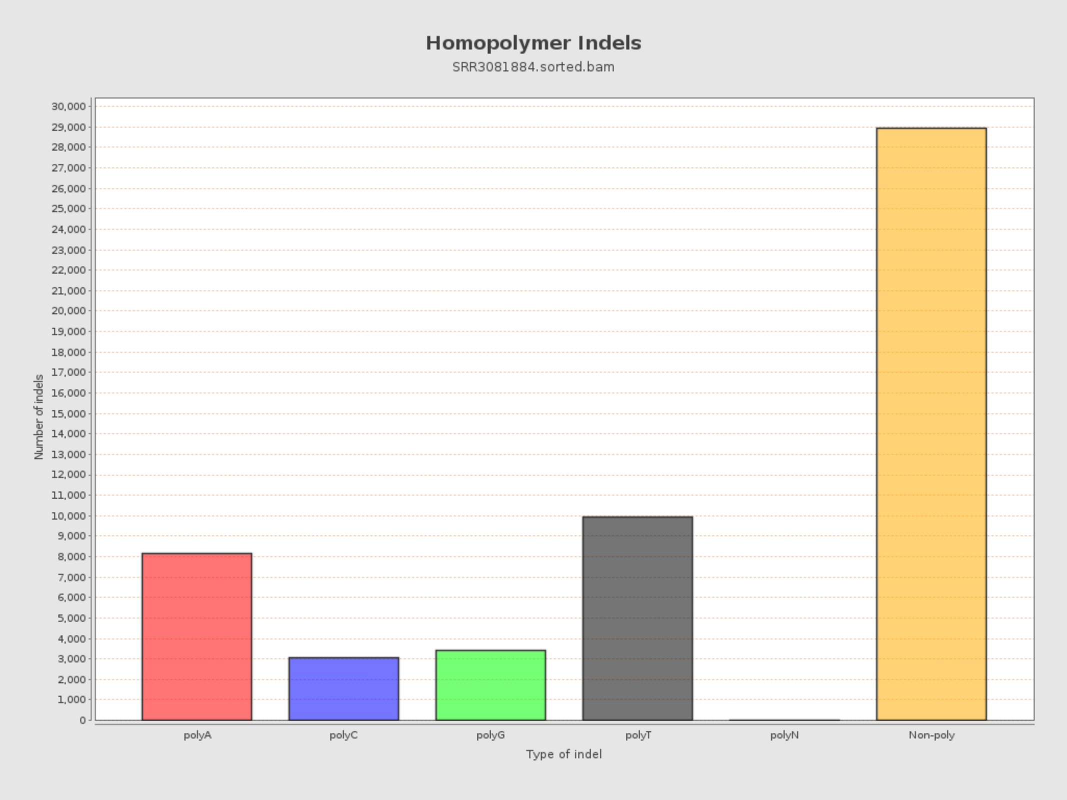
9. Results : Mapped Reads GC-content Distribution



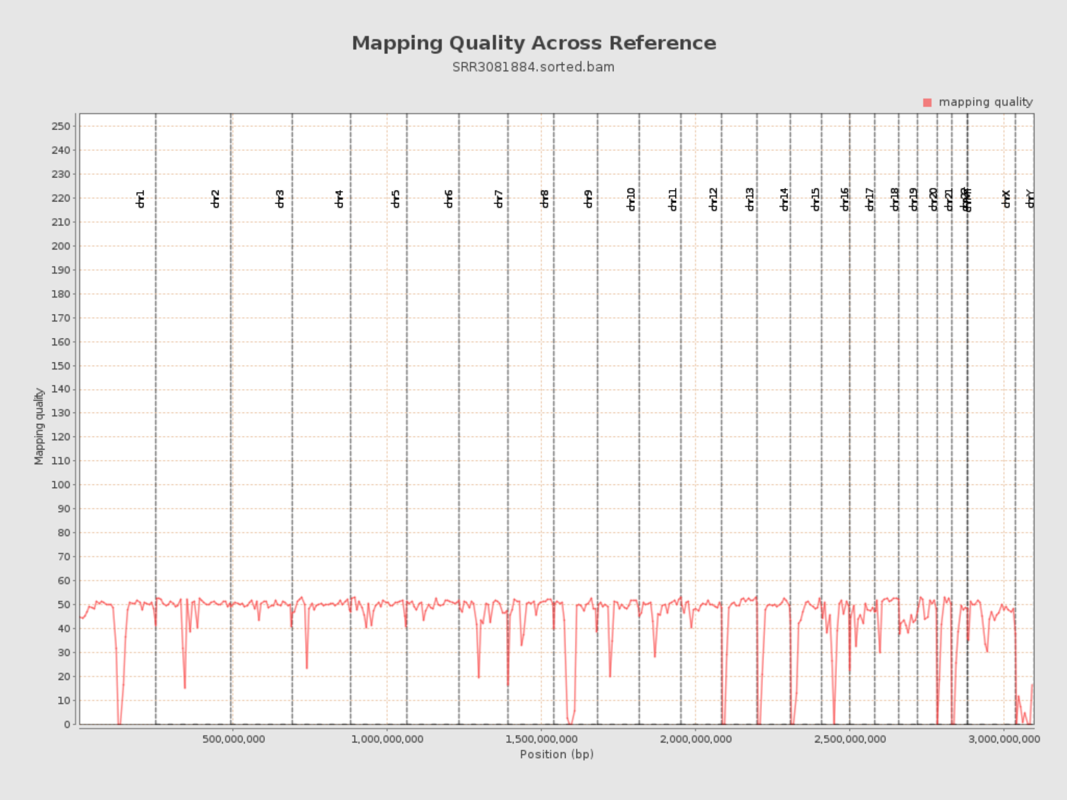
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram