Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:02:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080774.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_SRR3080774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080774.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:02:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,222,195
Mapped reads	2,878,697 / 89.34%
Unmapped reads	343,498 / 10.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,036 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	144,179 / 4.47%
Duplication rate	4.14%
Clipped reads	1,350,352 / 41.91%

2.2. ACGT Content

Number/percentage of A's	55,298,567 / 28.79%
Number/percentage of C's	36,757,652 / 19.14%
Number/percentage of T's	58,756,523 / 30.6%
Number/percentage of G's	41,228,922 / 21.47%
Number/percentage of N's	3,920 / 0%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0621

Standard Deviation	0.4209

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

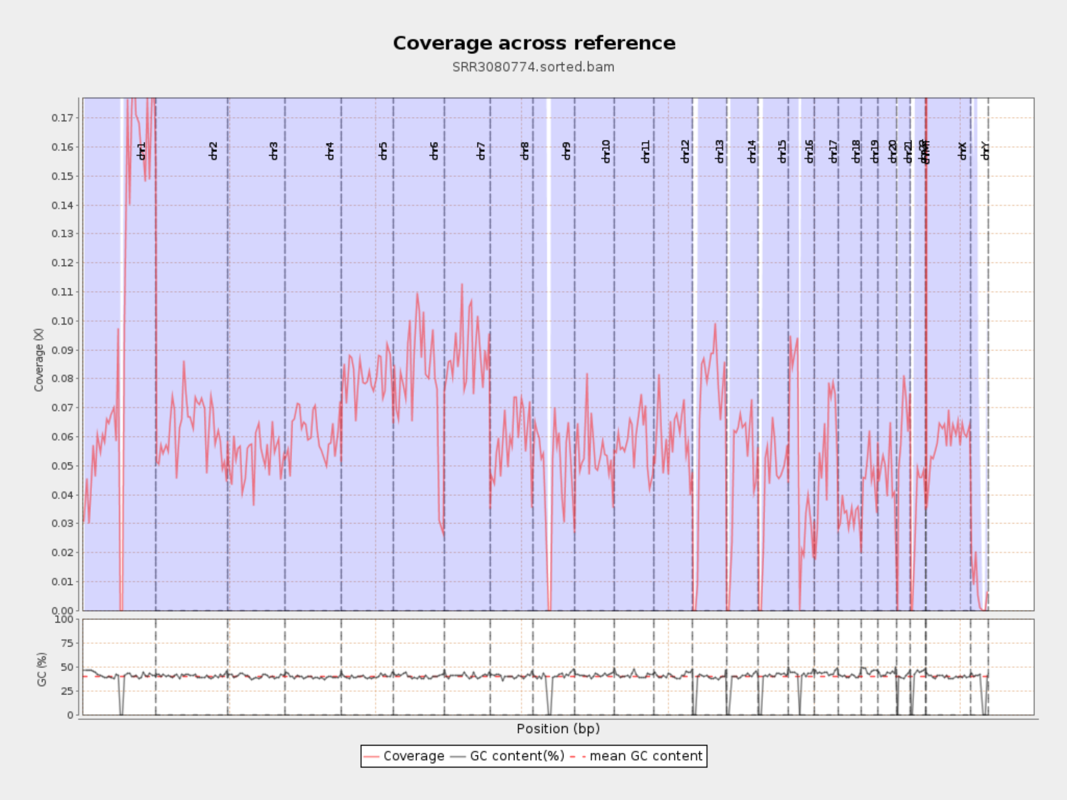
General error rate	0.76%
Mismatches	1,431,910
Insertions	14,576
Mapped reads with at least one insertion	0.5%
Deletions	42,217
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.41%

2.6. Chromosome stats

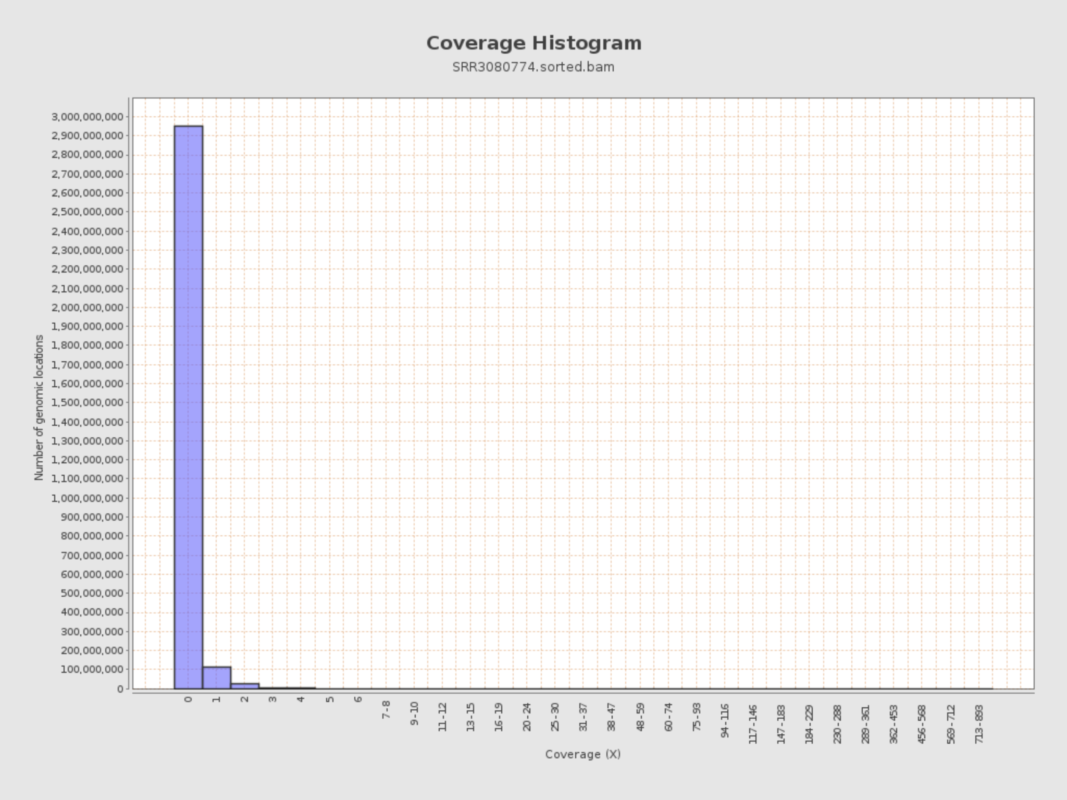
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24861868	0.0997	0.7051
chr2	243199373	15288745	0.0629	0.4683
chr3	198022430	10607816	0.0536	0.2873
chr4	191154276	11654007	0.061	0.3134
chr5	180915260	14536014	0.0803	0.3536
chr6	171115067	13560824	0.0792	0.404
chr7	159138663	14160348	0.089	0.5372

chr8	146364022	8652125	0.0591	0.6172
chr9	141213431	6634170	0.047	0.3311
chr10	135534747	7428316	0.0548	0.3862
chr11	135006516	7929730	0.0587	0.4284
chr12	133851895	8000107	0.0598	0.3051
chr13	115169878	7806128	0.0678	0.3269
chr14	107349540	5324087	0.0496	0.2847
chr15	102531392	4358756	0.0425	0.2602
chr16	90354753	4271583	0.0473	0.2858
chr17	81195210	4509218	0.0555	0.3153
chr18	78077248	2561157	0.0328	0.5312
chr19	59128983	2761128	0.0467	0.4662
chr20	63025520	2955486	0.0469	0.2769
chr21	48129895	2864582	0.0595	0.3146
chr22	51304566	1672024	0.0326	0.2201
chrMT	16571	186800	11.2727	6.854
chrX	155270560	9102027	0.0586	0.3163
chrY	59373566	425122	0.0072	0.1365

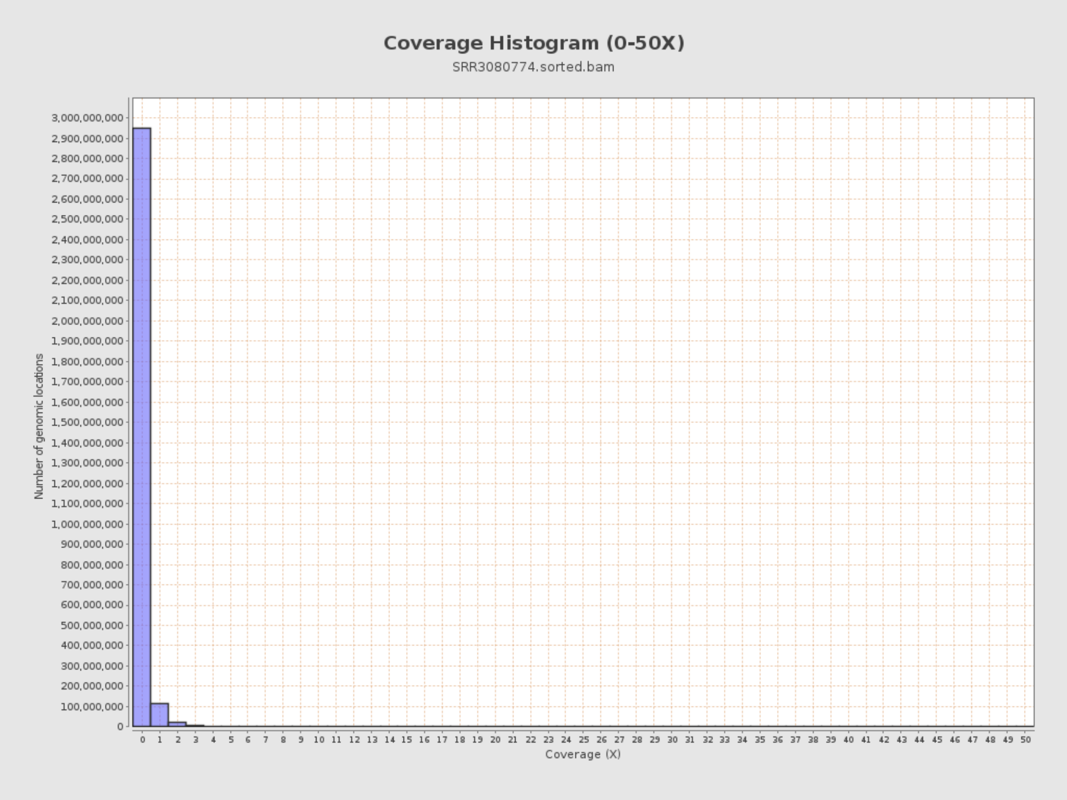
3. Results : Coverage across reference



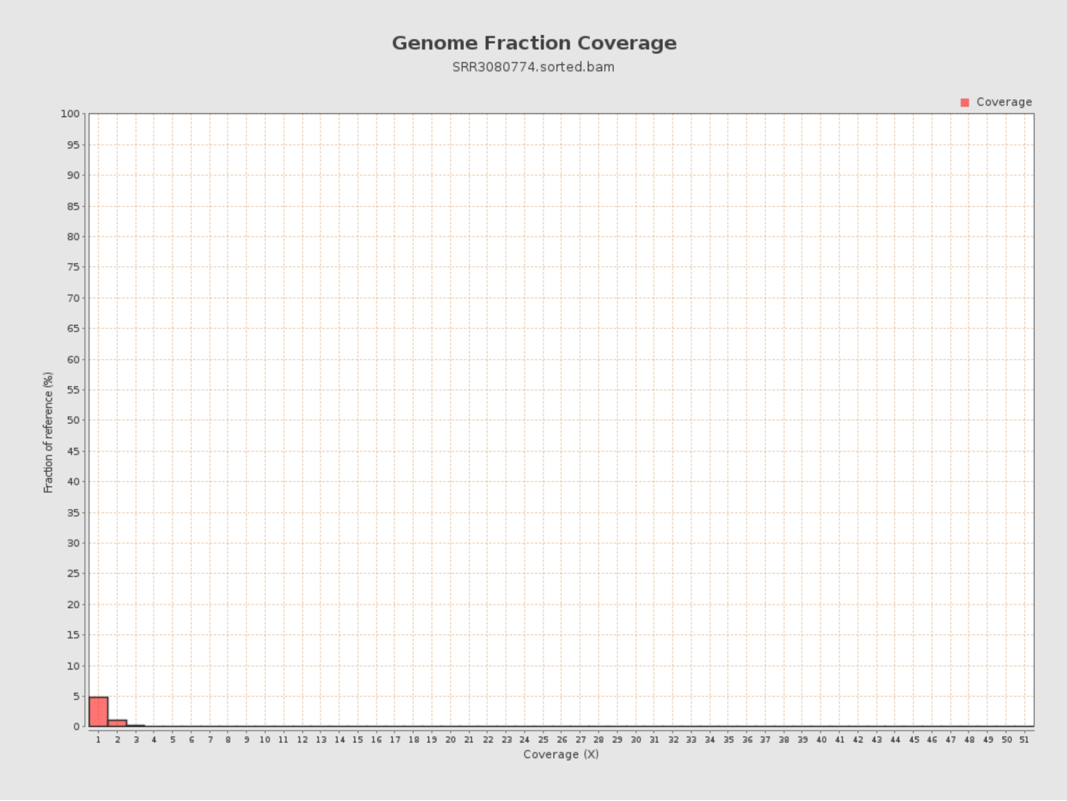
4. Results : Coverage Histogram



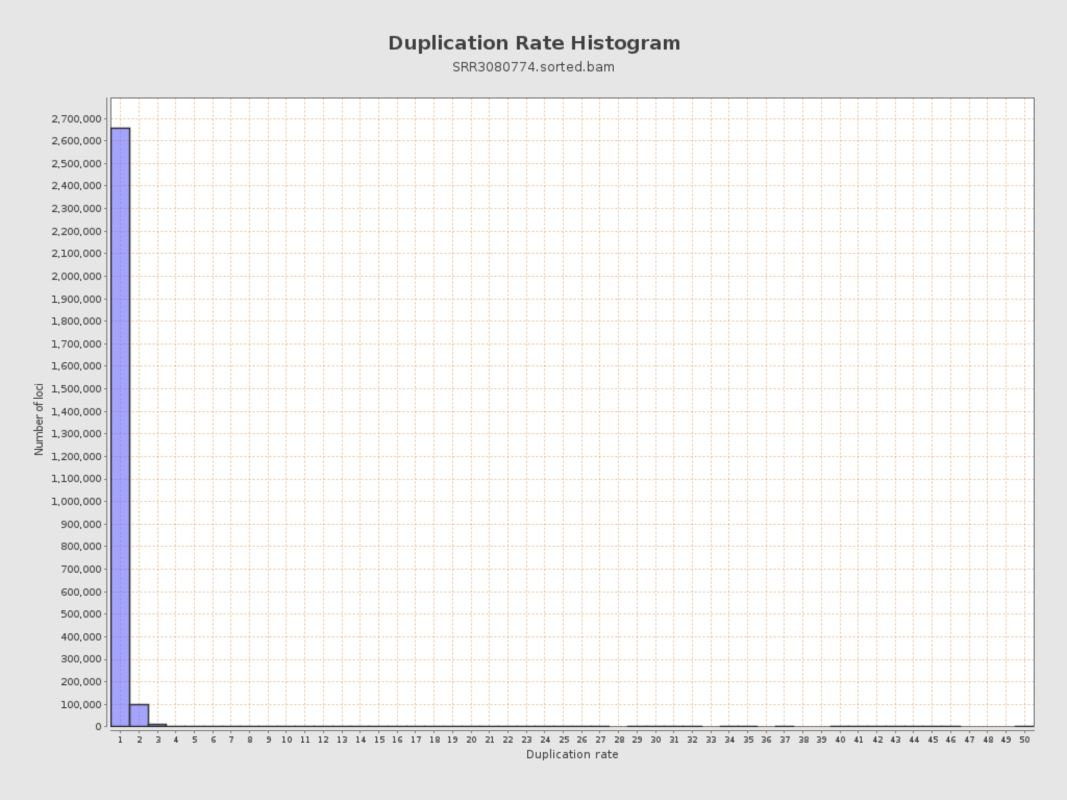
5. Results : Coverage Histogram (0-50X)



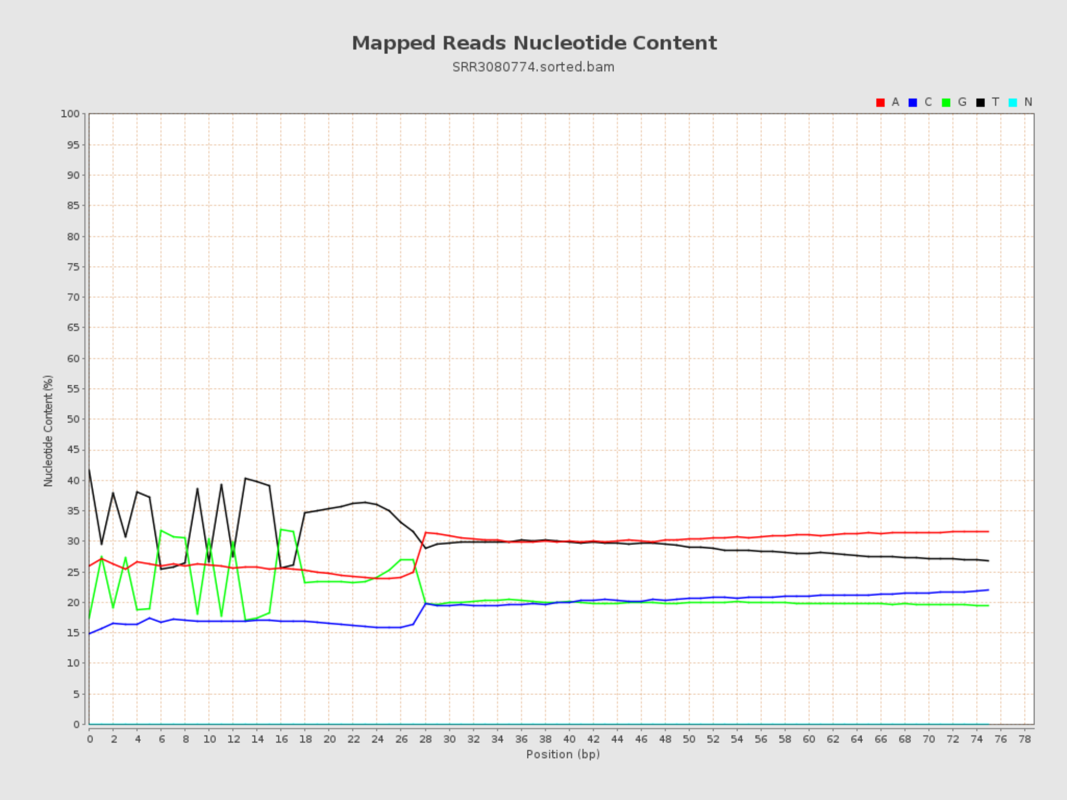
6. Results : Genome Fraction Coverage



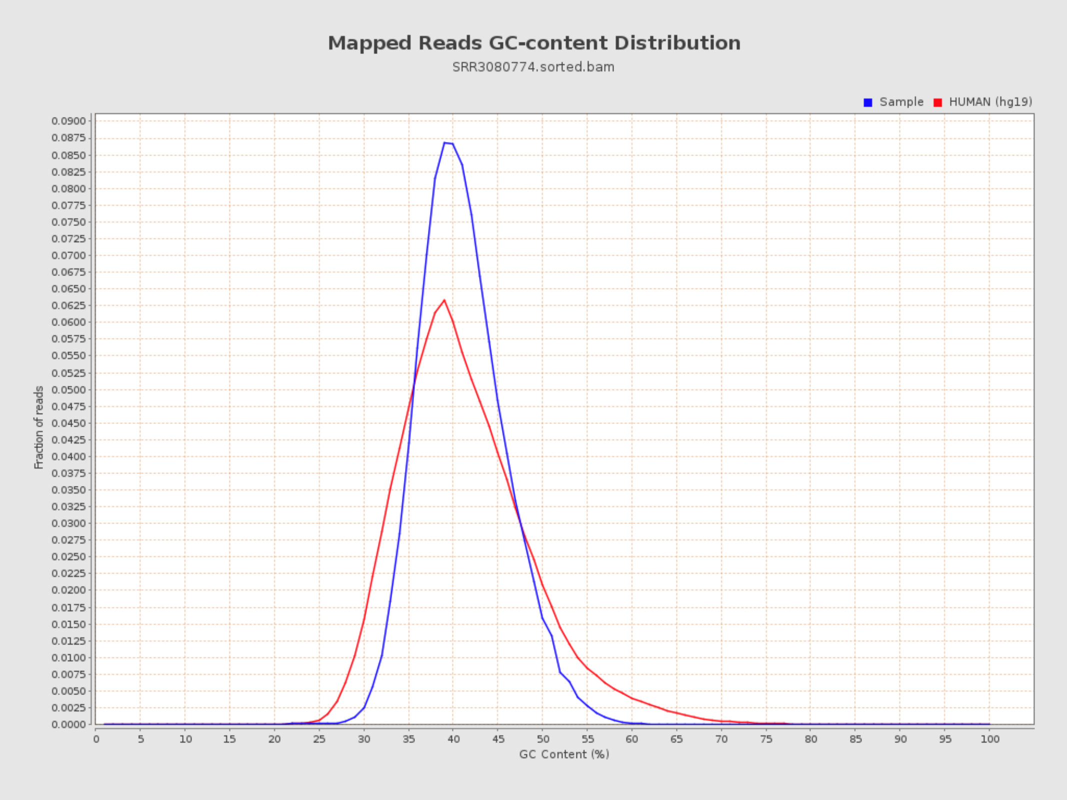
7. Results : Duplication Rate Histogram



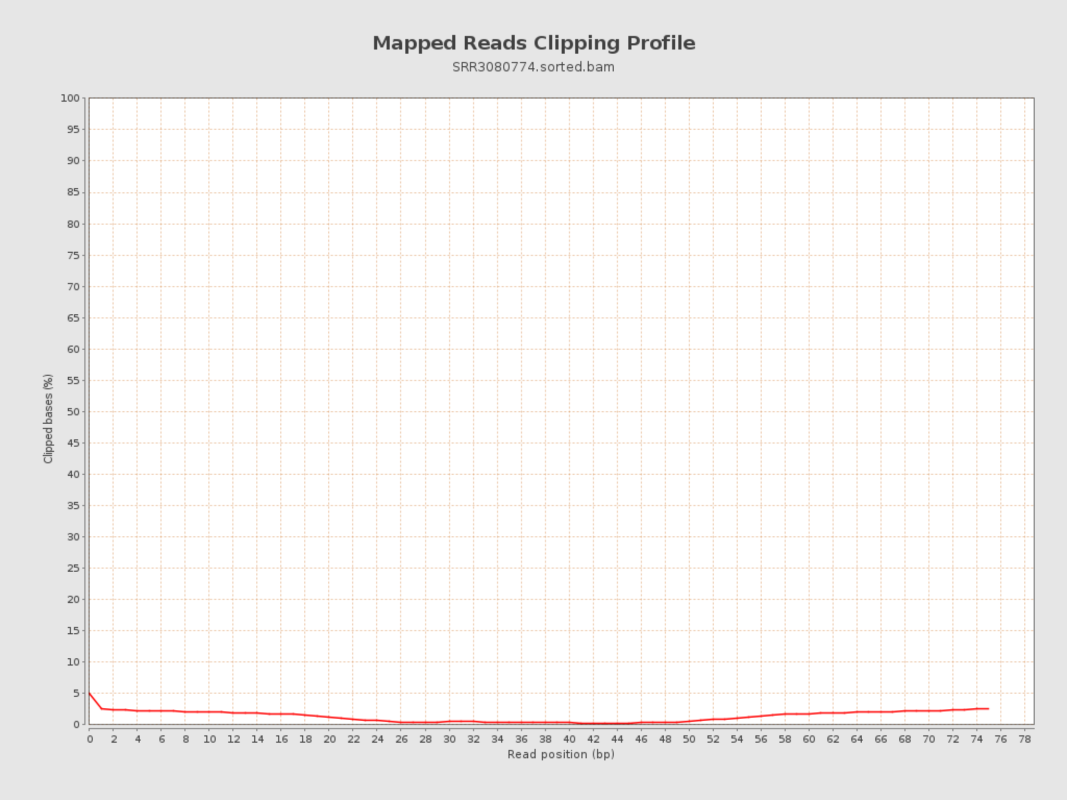
8. Results : Mapped Reads Nucleotide Content



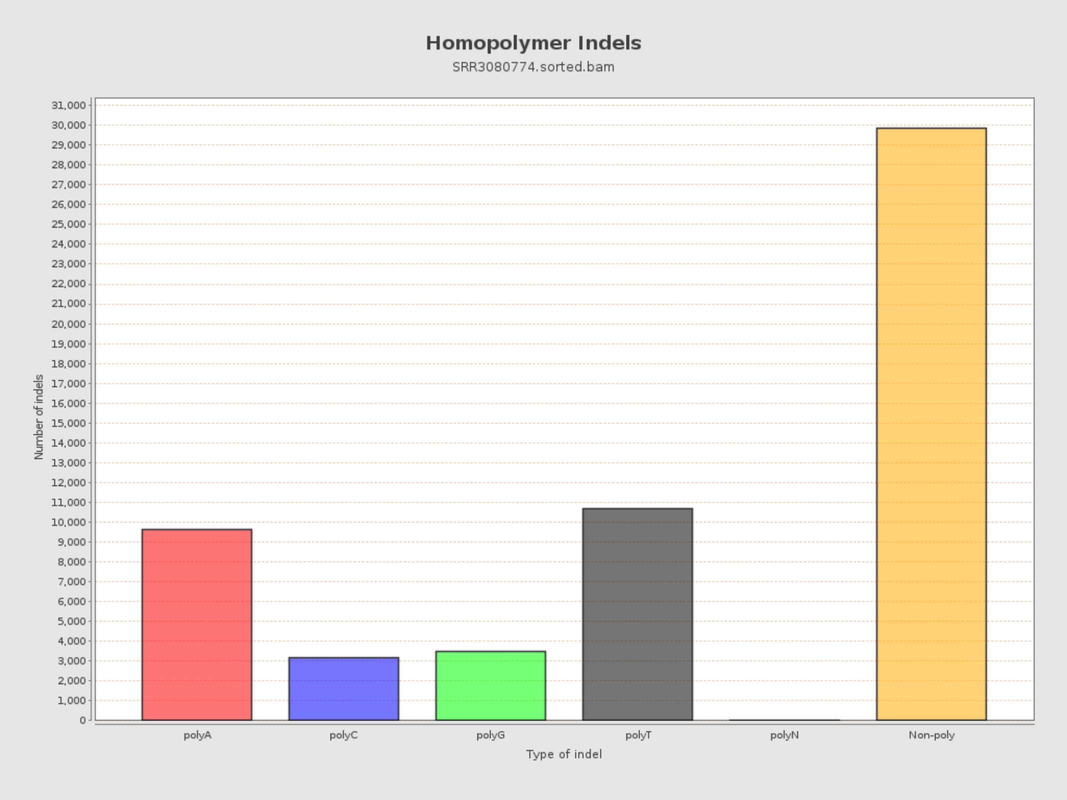
9. Results : Mapped Reads GC-content Distribution



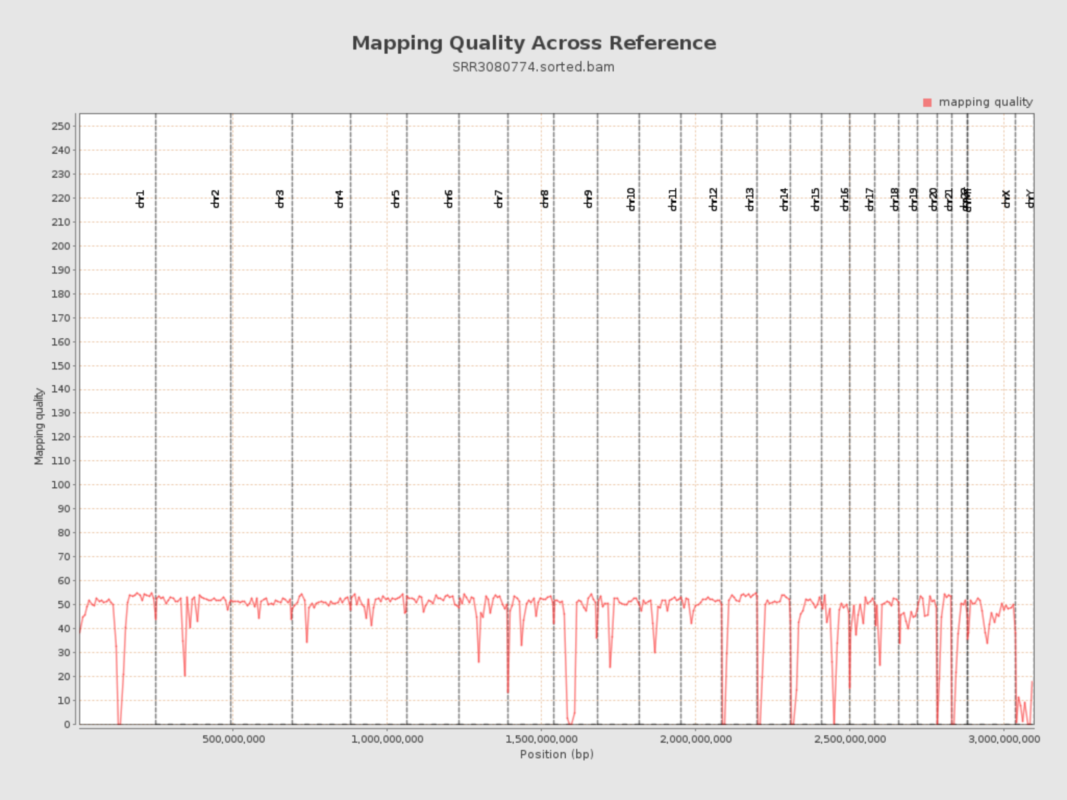
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram