Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:40:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081174.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_SRR3081174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:40:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,868,452
Mapped reads	2,592,274 / 90.37%
Unmapped reads	276,178 / 9.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,823 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	124,204 / 4.33%
Duplication rate	3.88%
Clipped reads	1,098,020 / 38.28%

2.2. ACGT Content

Number/percentage of A's	49,799,143 / 28.4%
Number/percentage of C's	32,350,306 / 18.45%
Number/percentage of T's	55,306,886 / 31.54%
Number/percentage of G's	37,831,615 / 21.58%
Number/percentage of N's	52,465 / 0.03%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.4343

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

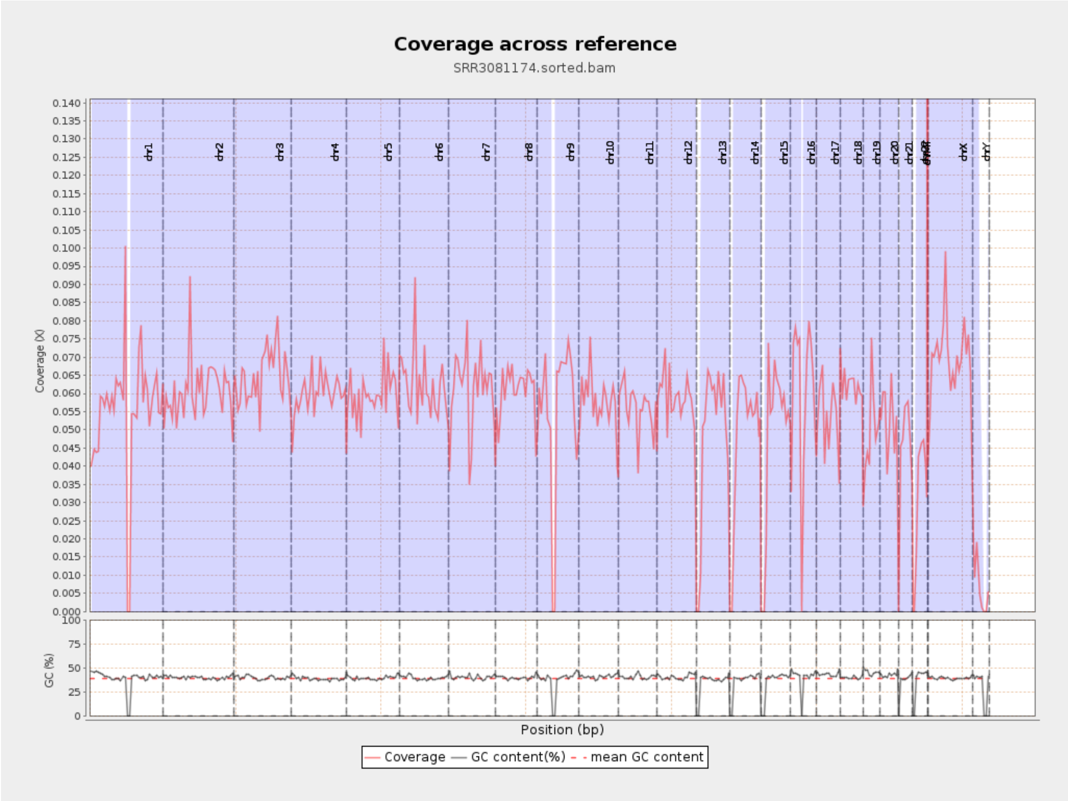
General error rate	0.84%
Mismatches	1,441,481
Insertions	13,503
Mapped reads with at least one insertion	0.52%
Deletions	41,192
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.62%

2.6. Chromosome stats

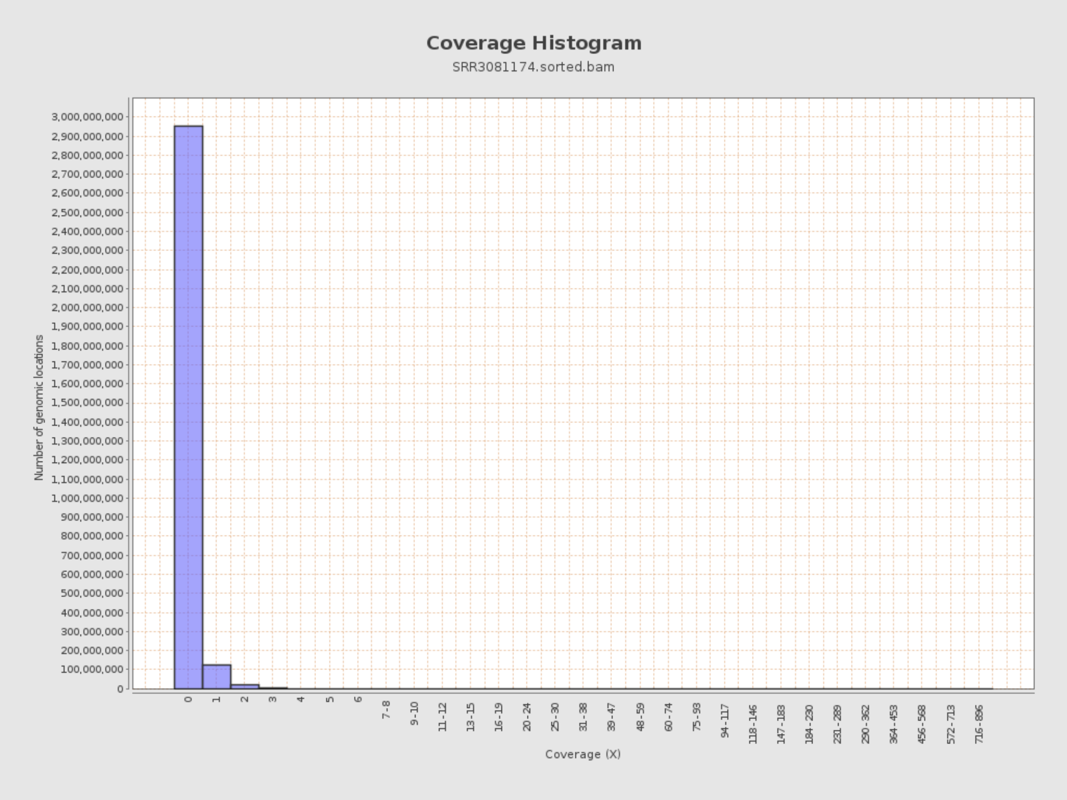
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13793968	0.0553	0.8011
chr2	243199373	14815145	0.0609	0.5076
chr3	198022430	12857740	0.0649	0.2947
chr4	191154276	11458468	0.0599	0.2961
chr5	180915260	10759240	0.0595	0.2845
chr6	171115067	10713353	0.0626	0.3702
chr7	159138663	9779618	0.0615	0.5917

chr8	146364022	8888793	0.0607	0.5594
chr9	141213431	7796161	0.0552	0.3718
chr10	135534747	7866268	0.058	0.3741
chr11	135006516	7508658	0.0556	0.3706
chr12	133851895	7844885	0.0586	0.2858
chr13	115169878	5509428	0.0478	0.2549
chr14	107349540	5158621	0.0481	0.2698
chr15	102531392	4965789	0.0484	0.2595
chr16	90354753	5442033	0.0602	0.2993
chr17	81195210	4287146	0.0528	0.3205
chr18	78077248	4846594	0.0621	0.6321
chr19	59128983	2959405	0.05	0.5827
chr20	63025520	3265290	0.0518	0.2726
chr21	48129895	2144873	0.0446	0.2594
chr22	51304566	1552285	0.0303	0.2005
chrMT	16571	10317	0.6226	0.9012
chrX	155270560	10782793	0.0694	0.3465
chrY	59373566	399336	0.0067	0.1315

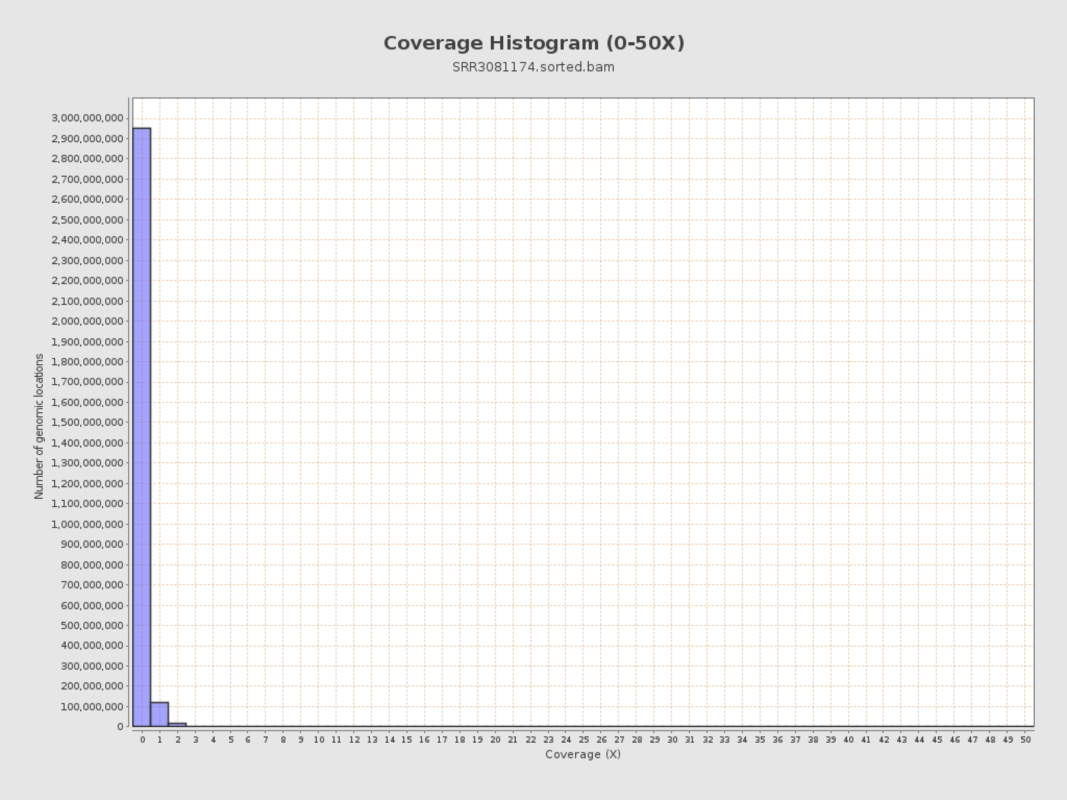
3. Results : Coverage across reference



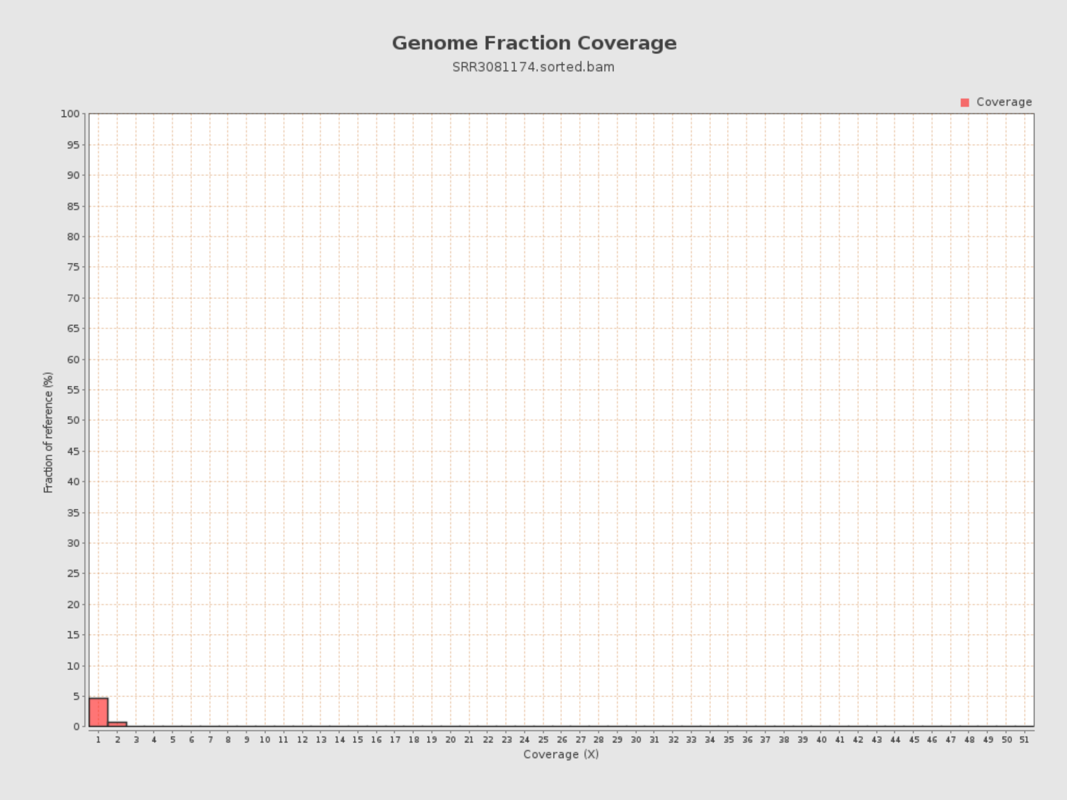
4. Results : Coverage Histogram



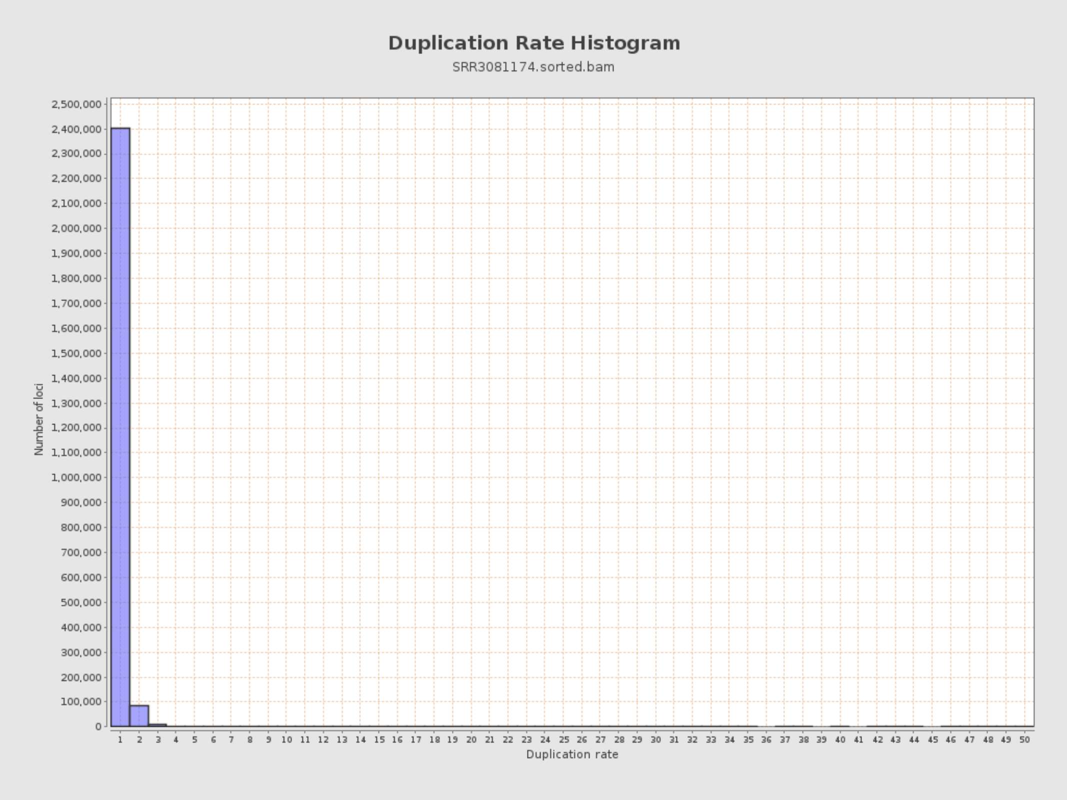
5. Results : Coverage Histogram (0-50X)



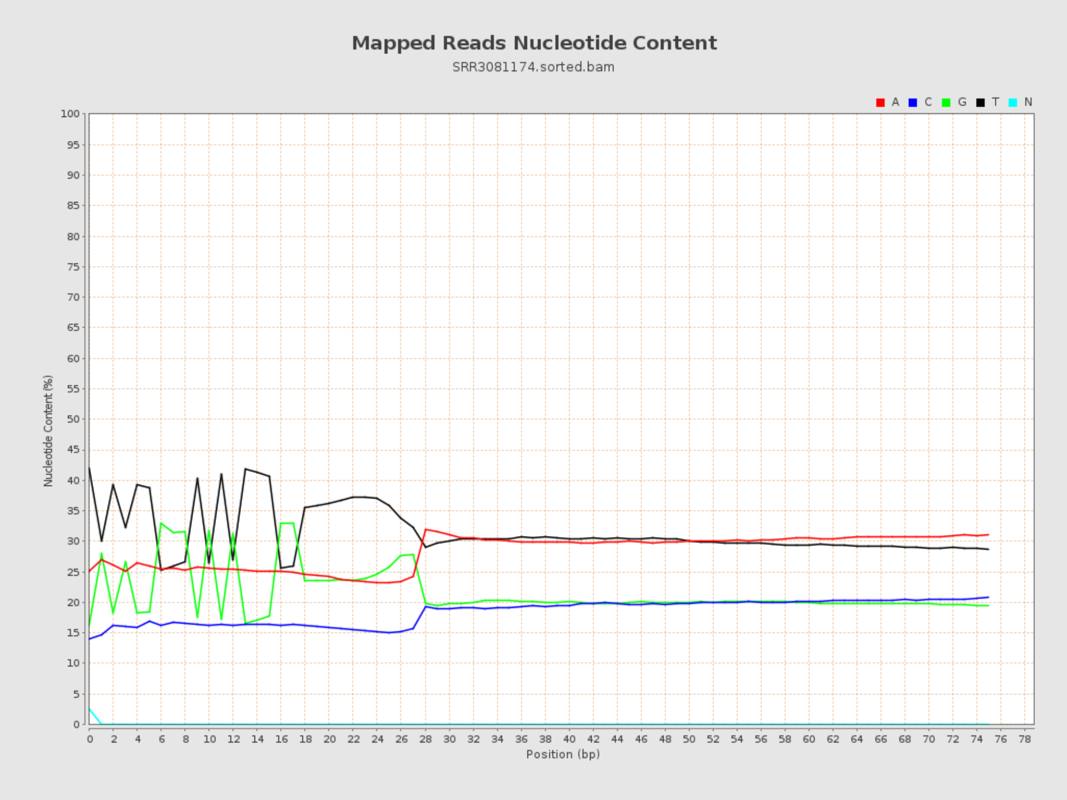
6. Results : Genome Fraction Coverage



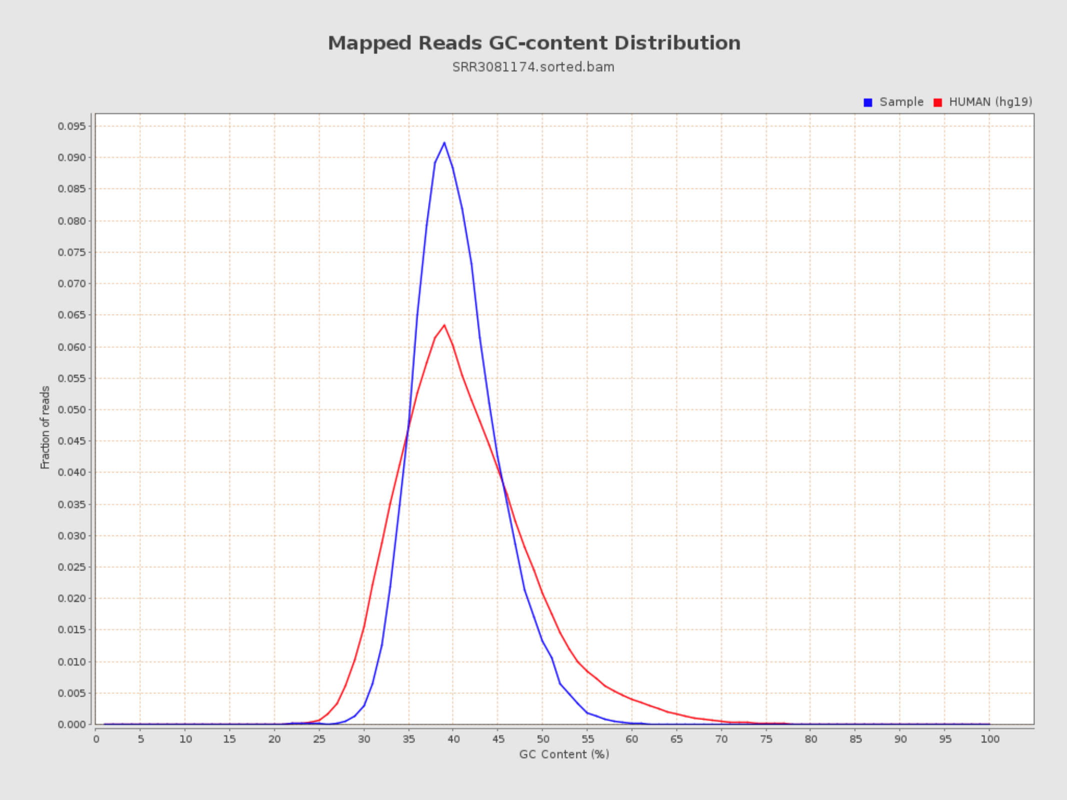
7. Results : Duplication Rate Histogram



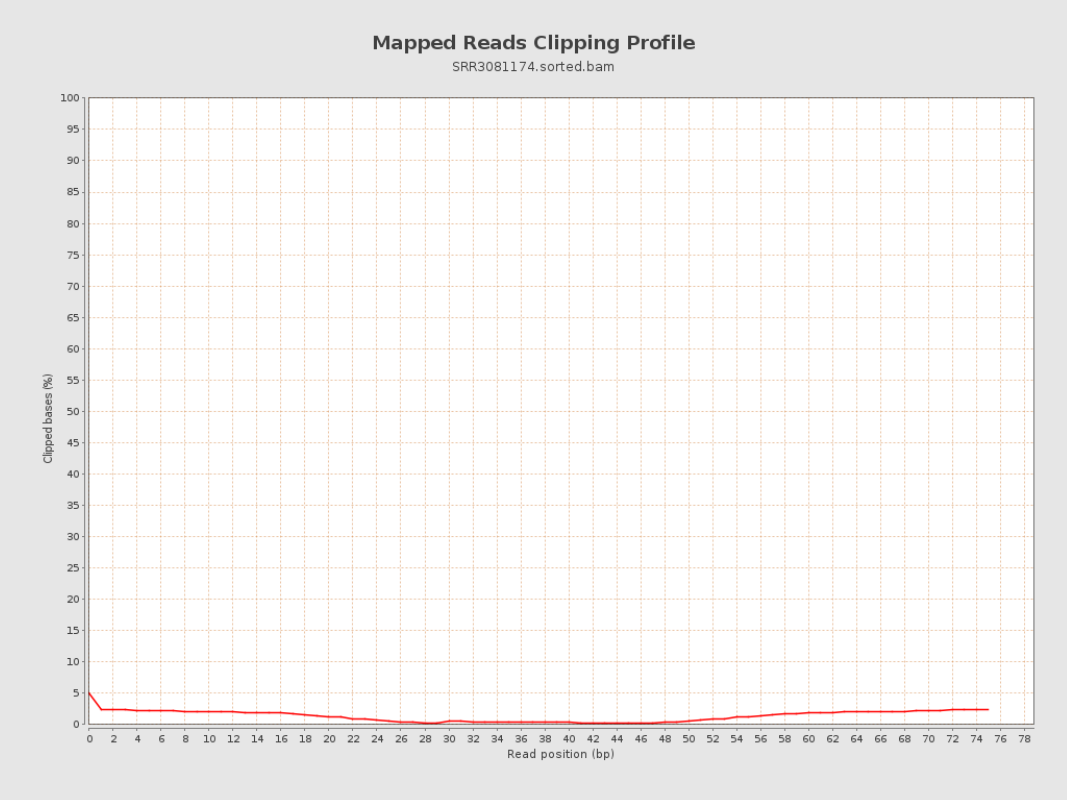
8. Results : Mapped Reads Nucleotide Content



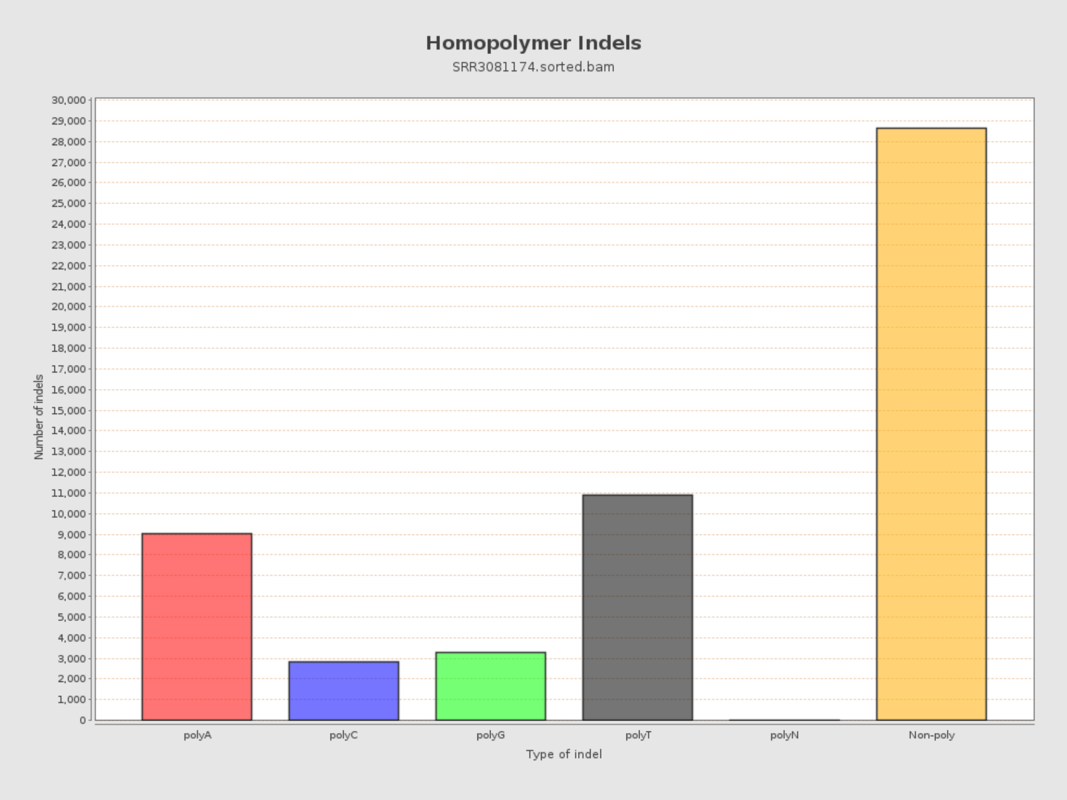
9. Results : Mapped Reads GC-content Distribution



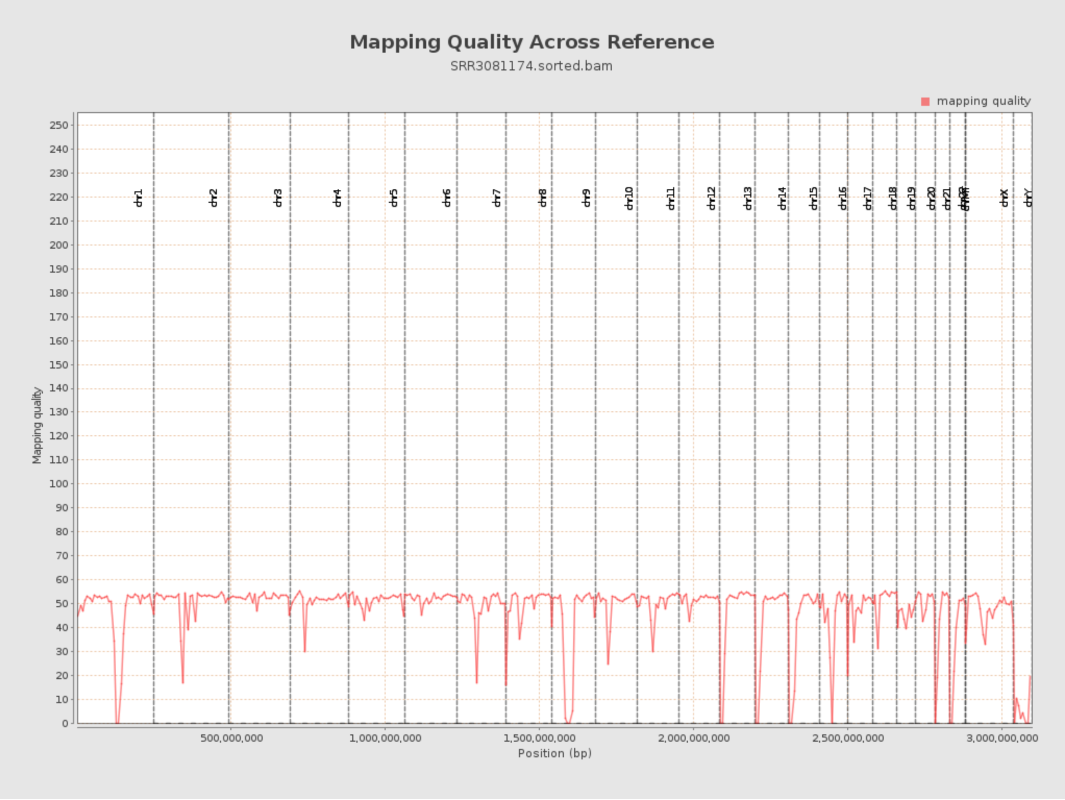
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram