Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:41:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080963.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_SRR3080963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:41:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,069,328
Mapped reads	5,354,176 / 88.22%
Unmapped reads	715,152 / 11.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,503 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	457,968 / 7.55%
Duplication rate	6.85%
Clipped reads	2,315,512 / 38.15%

2.2. ACGT Content

Number/percentage of A's	100,250,809 / 27.92%
Number/percentage of C's	63,127,910 / 17.58%
Number/percentage of T's	117,044,292 / 32.59%
Number/percentage of G's	77,978,172 / 21.71%
Number/percentage of N's	706,515 / 0.2%
GC Percentage	39.29%

2.3. Coverage

Mean	0.116

Standard Deviation	0.73

2.4. Mapping Quality

Mean Mapping Quality	47.23

2.5. Mismatches and indels

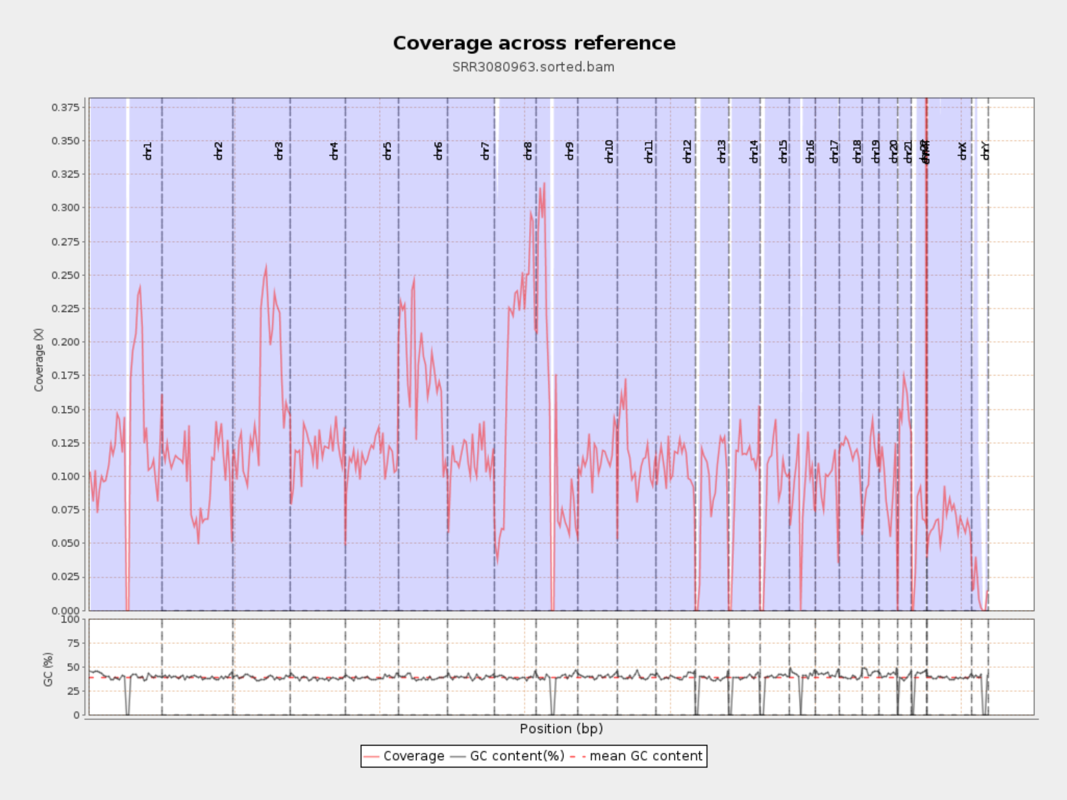
General error rate	0.99%
Mismatches	3,507,830
Insertions	27,749
Mapped reads with at least one insertion	0.51%
Deletions	78,123
Mapped reads with at least one deletion	1.44%
Homopolymer indels	49.64%

2.6. Chromosome stats

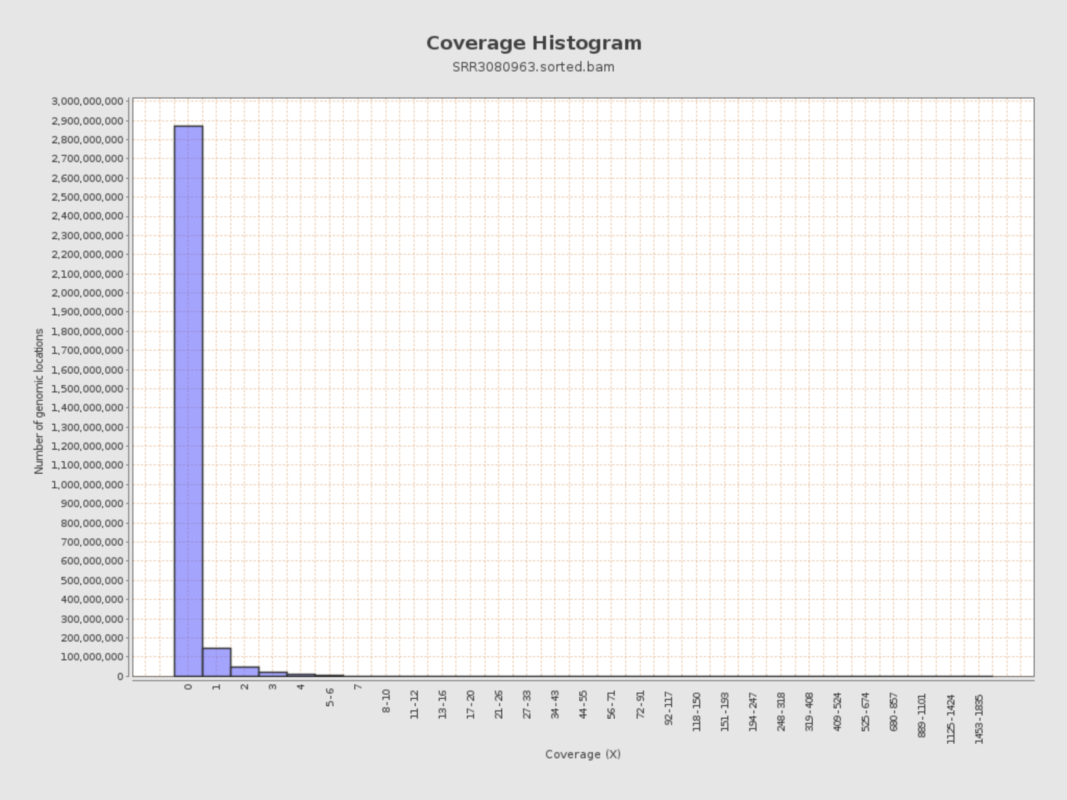
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30542744	0.1225	0.8812
chr2	243199373	24753452	0.1018	0.7133
chr3	198022430	31938475	0.1613	0.5986
chr4	191154276	22852329	0.1195	0.5332
chr5	180915260	20596741	0.1138	0.4983
chr6	171115067	30734908	0.1796	0.8788
chr7	159138663	18085581	0.1136	0.6603

chr8	146364022	27484686	0.1878	1.2958
chr9	141213431	18773530	0.1329	0.9606
chr10	135534747	15530618	0.1146	0.6129
chr11	135006516	15635042	0.1158	0.6198
chr12	133851895	14577182	0.1089	0.5172
chr13	115169878	10211053	0.0887	0.4378
chr14	107349540	10563217	0.0984	0.594
chr15	102531392	9183191	0.0896	0.4407
chr16	90354753	8153914	0.0902	0.5487
chr17	81195210	7517271	0.0926	0.4529
chr18	78077248	9243149	0.1184	1.6118
chr19	59128983	6338924	0.1072	0.6991
chr20	63025520	5822959	0.0924	0.4742
chr21	48129895	6618059	0.1375	0.6888
chr22	51304566	2767016	0.0539	0.3378
chrMT	16571	405452	24.4676	14.3754
chrX	155270560	10205709	0.0657	0.4212
chrY	59373566	700746	0.0118	0.2361

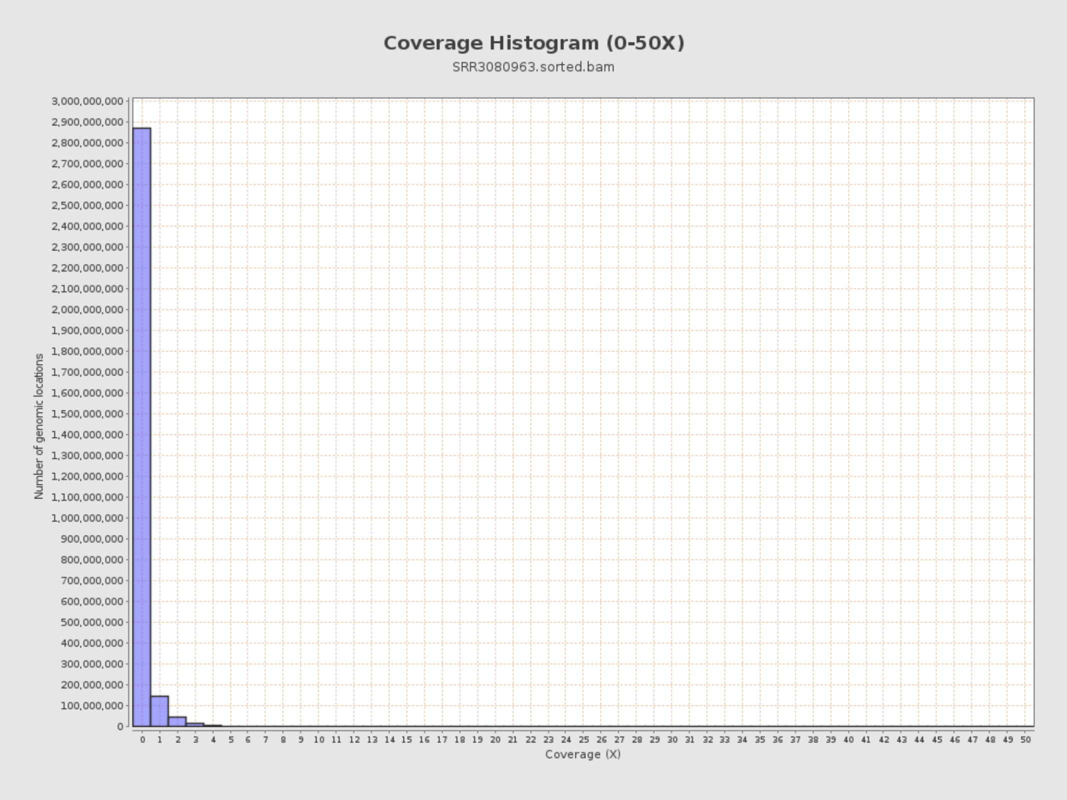
3. Results : Coverage across reference



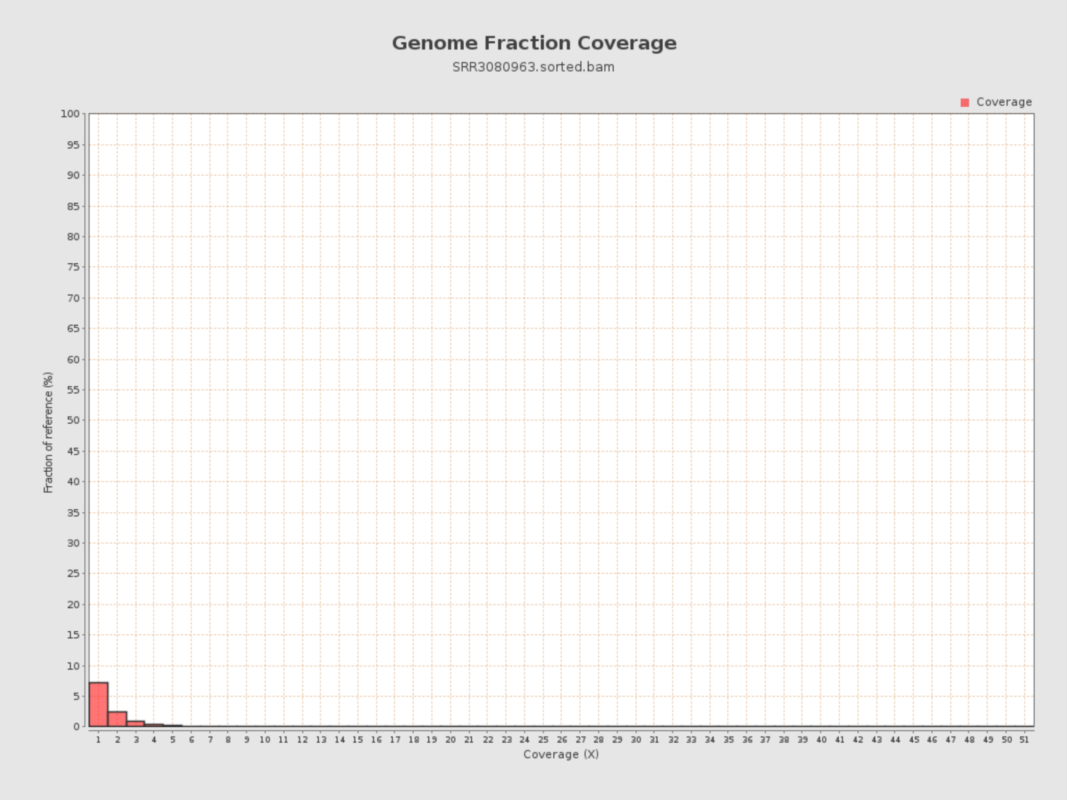
4. Results : Coverage Histogram



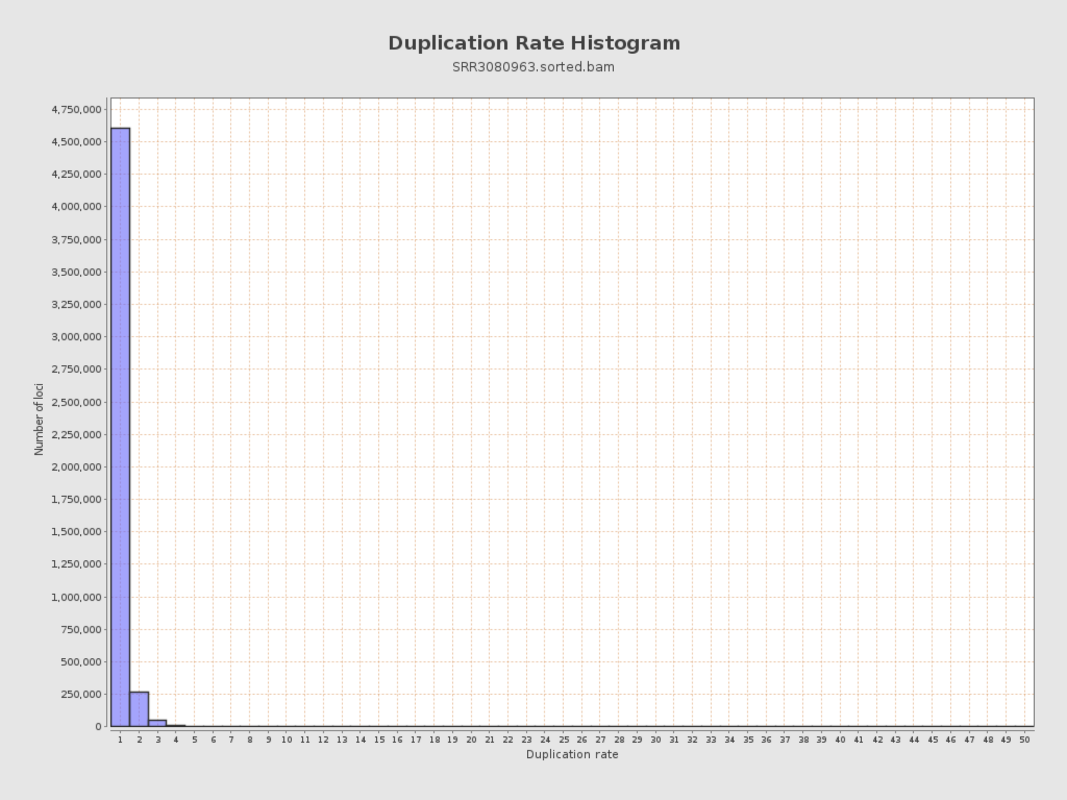
5. Results : Coverage Histogram (0-50X)



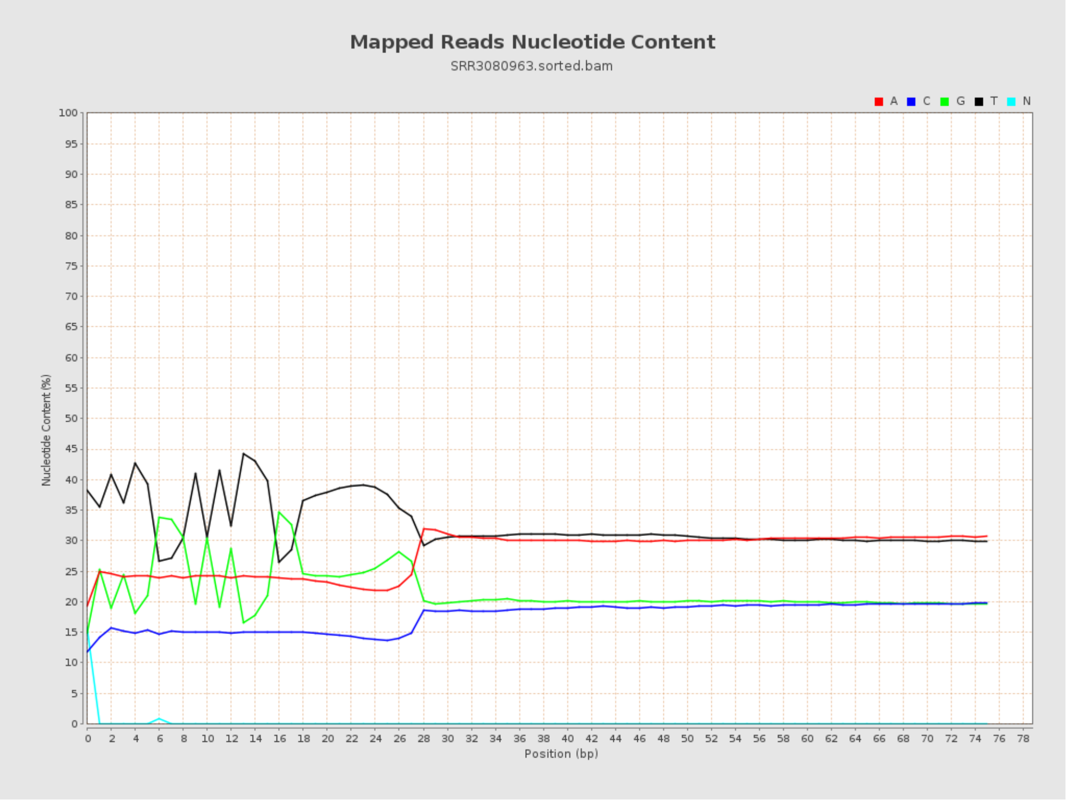
6. Results : Genome Fraction Coverage



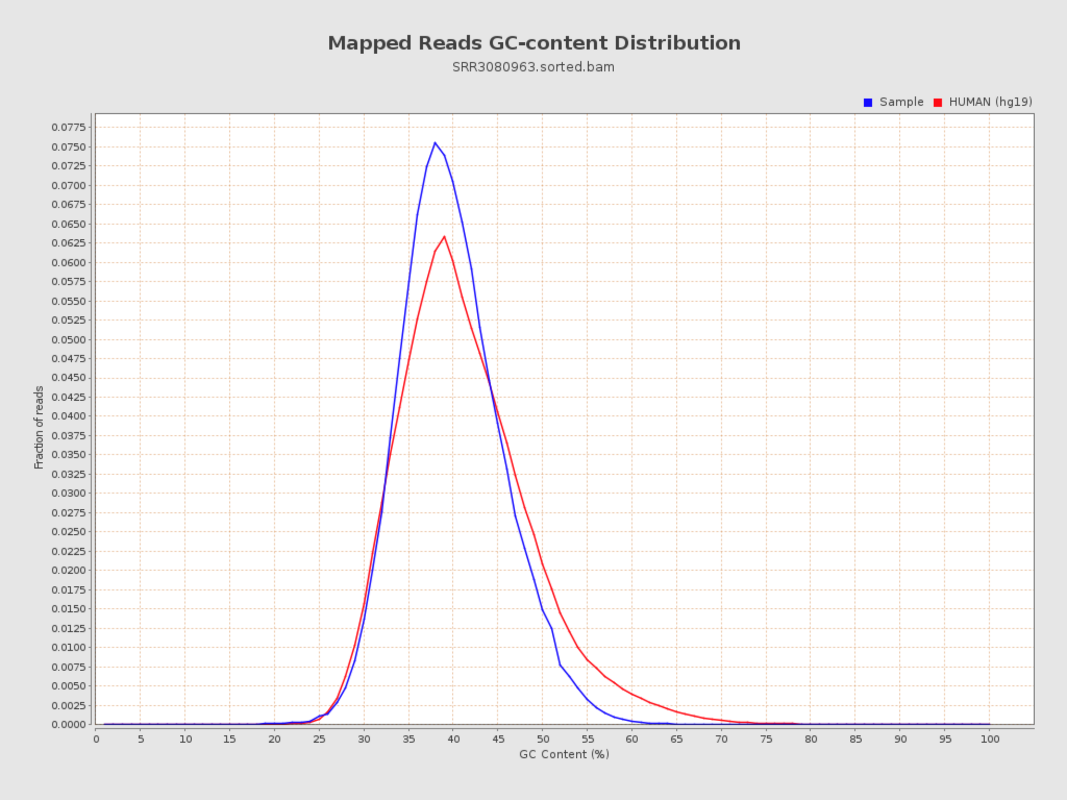
7. Results : Duplication Rate Histogram



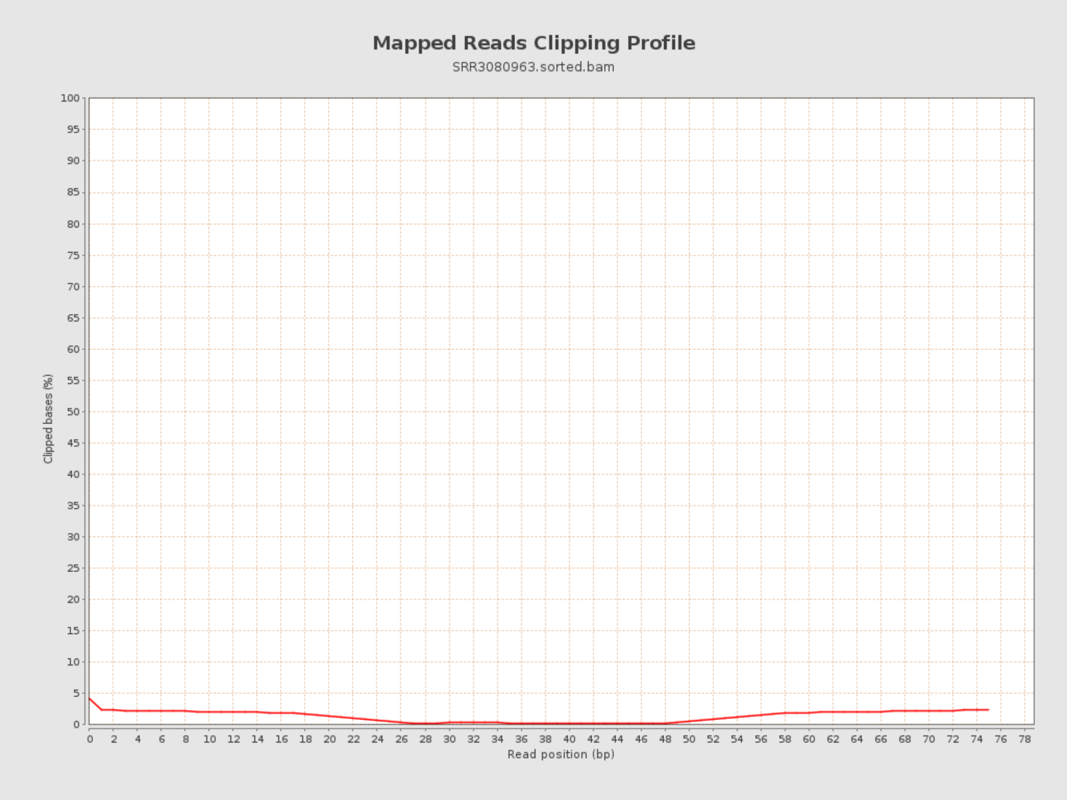
8. Results : Mapped Reads Nucleotide Content



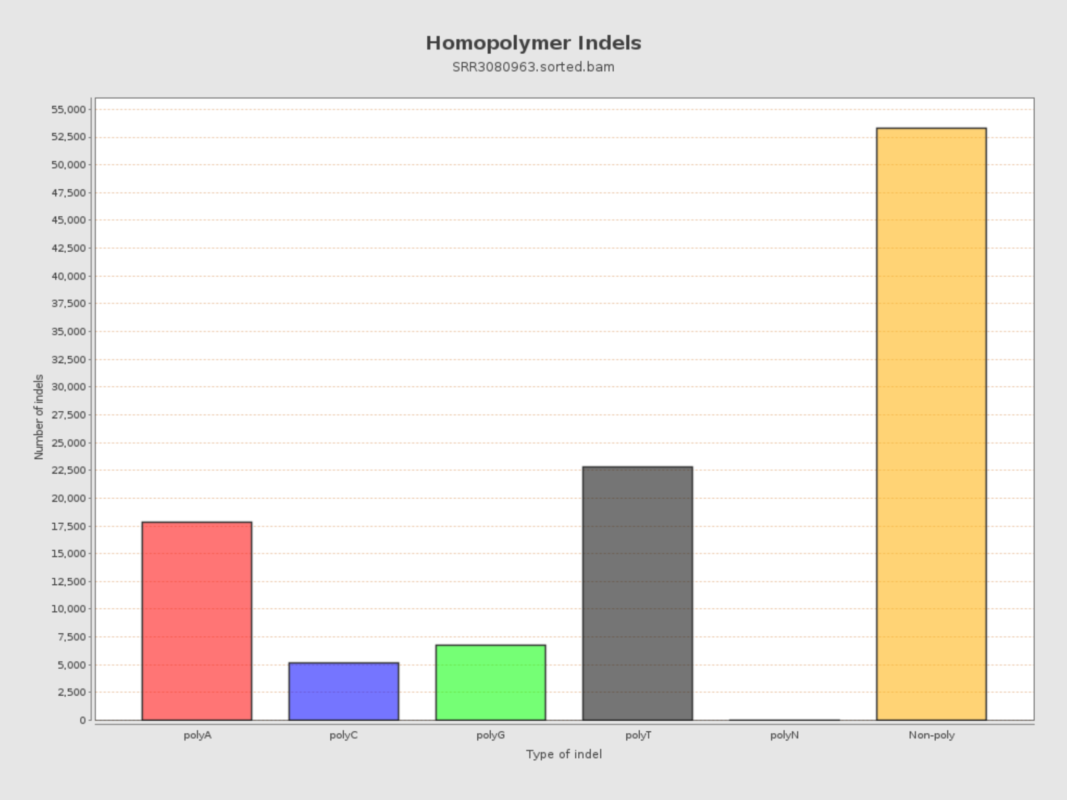
9. Results : Mapped Reads GC-content Distribution



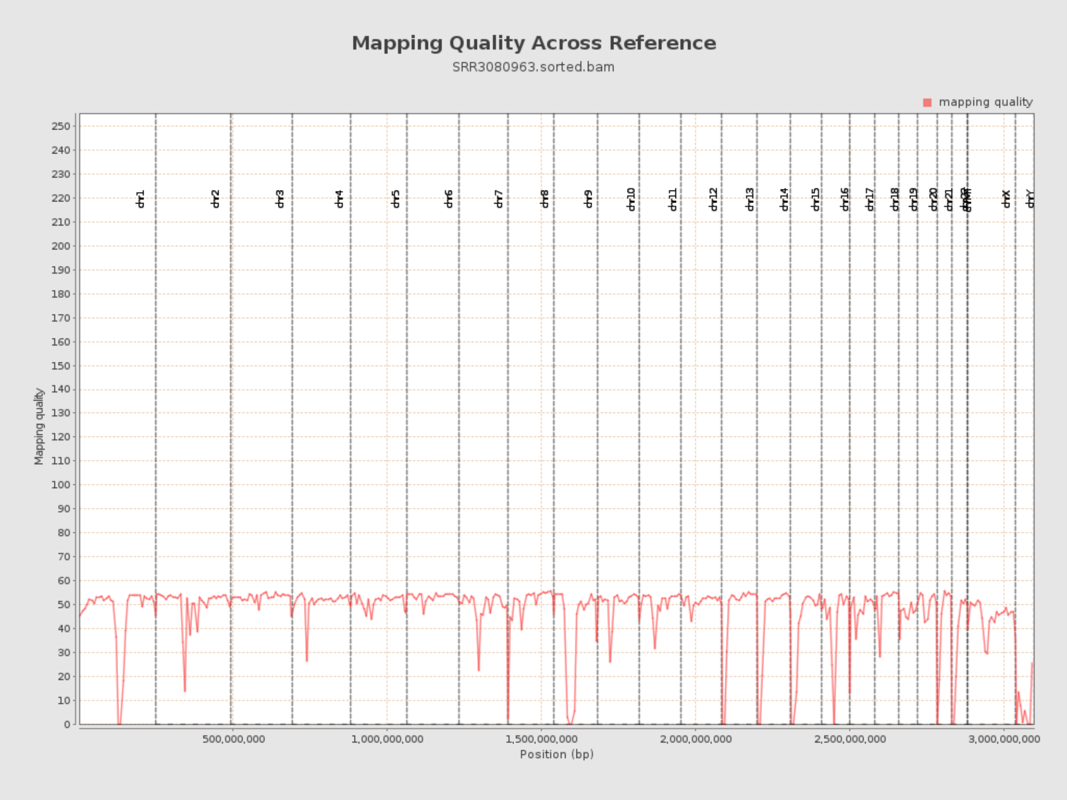
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram