Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:16:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080707.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_SRR3080707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:16:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,092,222
Mapped reads	1,898,411 / 90.74%
Unmapped reads	193,811 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,902 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	101,031 / 4.83%
Duplication rate	4.49%
Clipped reads	771,106 / 36.86%

2.2. ACGT Content

Number/percentage of A's	35,727,098 / 27.89%
Number/percentage of C's	23,577,115 / 18.4%
Number/percentage of T's	40,905,622 / 31.93%
Number/percentage of G's	27,897,681 / 21.78%
Number/percentage of N's	1,887 / 0%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.3651

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

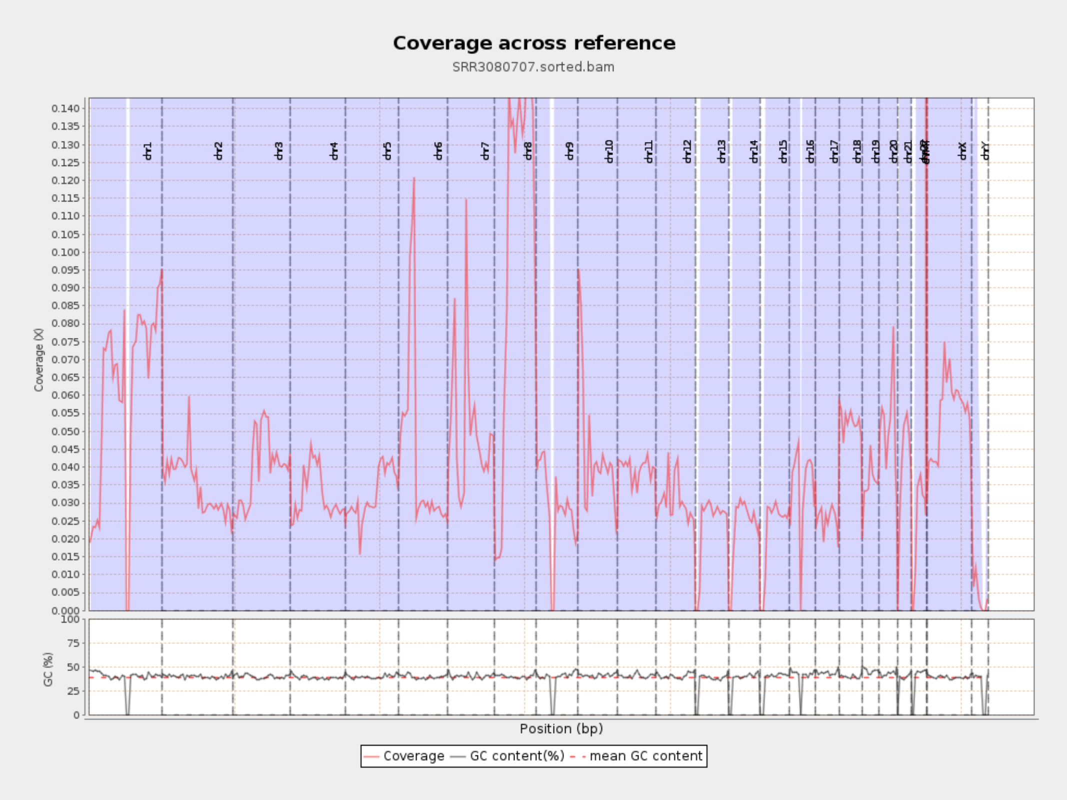
General error rate	0.82%
Mismatches	1,031,365
Insertions	9,163
Mapped reads with at least one insertion	0.48%
Deletions	26,323
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.2%

2.6. Chromosome stats

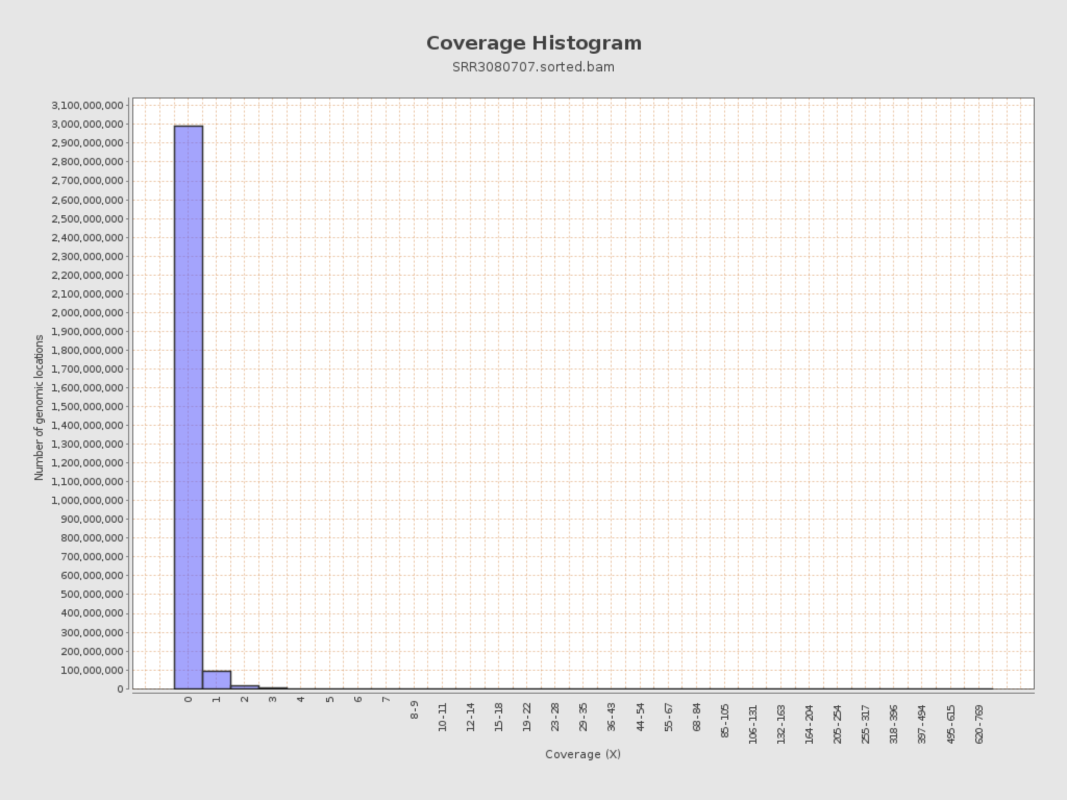
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15255234	0.0612	0.529
chr2	243199373	8484017	0.0349	0.3595
chr3	198022430	7859572	0.0397	0.2286
chr4	191154276	6163420	0.0322	0.2145
chr5	180915260	5880377	0.0325	0.2064
chr6	171115067	7548246	0.0441	0.3264
chr7	159138663	8189748	0.0515	0.9039

chr8	146364022	15217367	0.104	0.4961
chr9	141213431	4033393	0.0286	0.2657
chr10	135534747	6105659	0.045	0.3147
chr11	135006516	5296277	0.0392	0.2634
chr12	133851895	4073073	0.0304	0.2022
chr13	115169878	2702270	0.0235	0.1765
chr14	107349540	2461440	0.0229	0.1804
chr15	102531392	2280824	0.0222	0.1696
chr16	90354753	3164108	0.035	0.2297
chr17	81195210	2047428	0.0252	0.1924
chr18	78077248	4118128	0.0527	0.4201
chr19	59128983	2126520	0.036	0.3405
chr20	63025520	3255384	0.0517	0.2675
chr21	48129895	1913105	0.0397	0.243
chr22	51304566	1189476	0.0232	0.1733
chrMT	16571	20252	1.2221	1.3192
chrX	155270560	8491600	0.0547	0.2891
chrY	59373566	278925	0.0047	0.1003

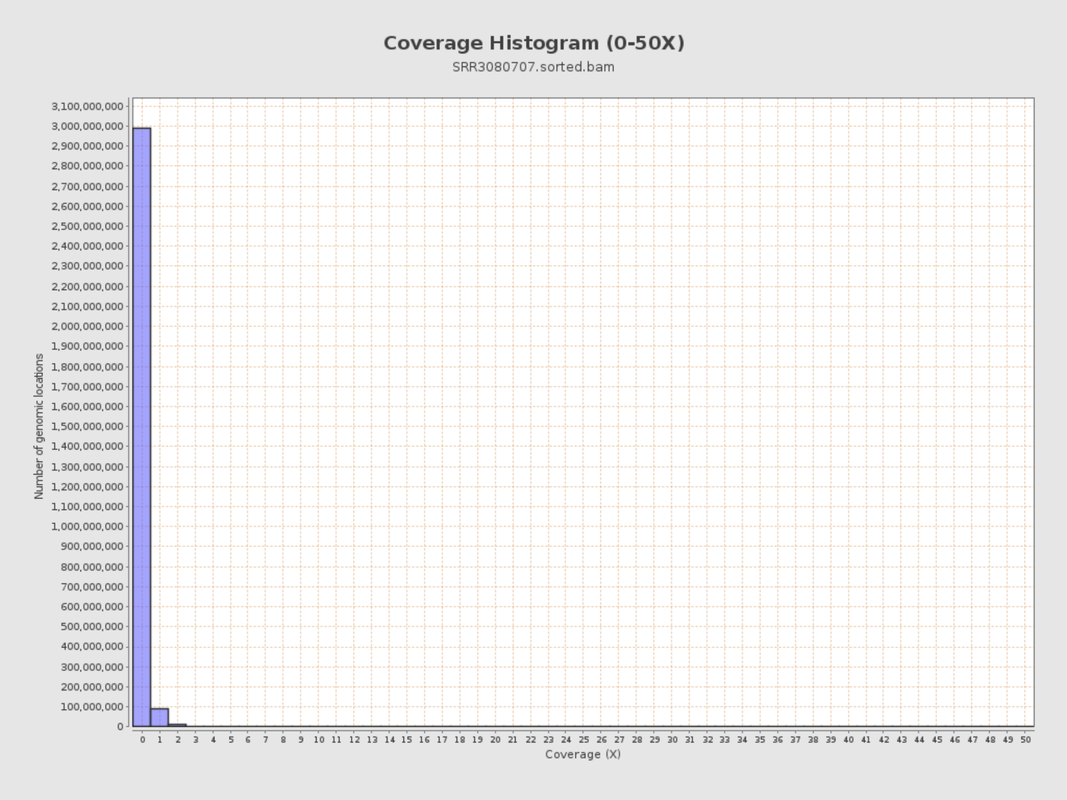
3. Results : Coverage across reference



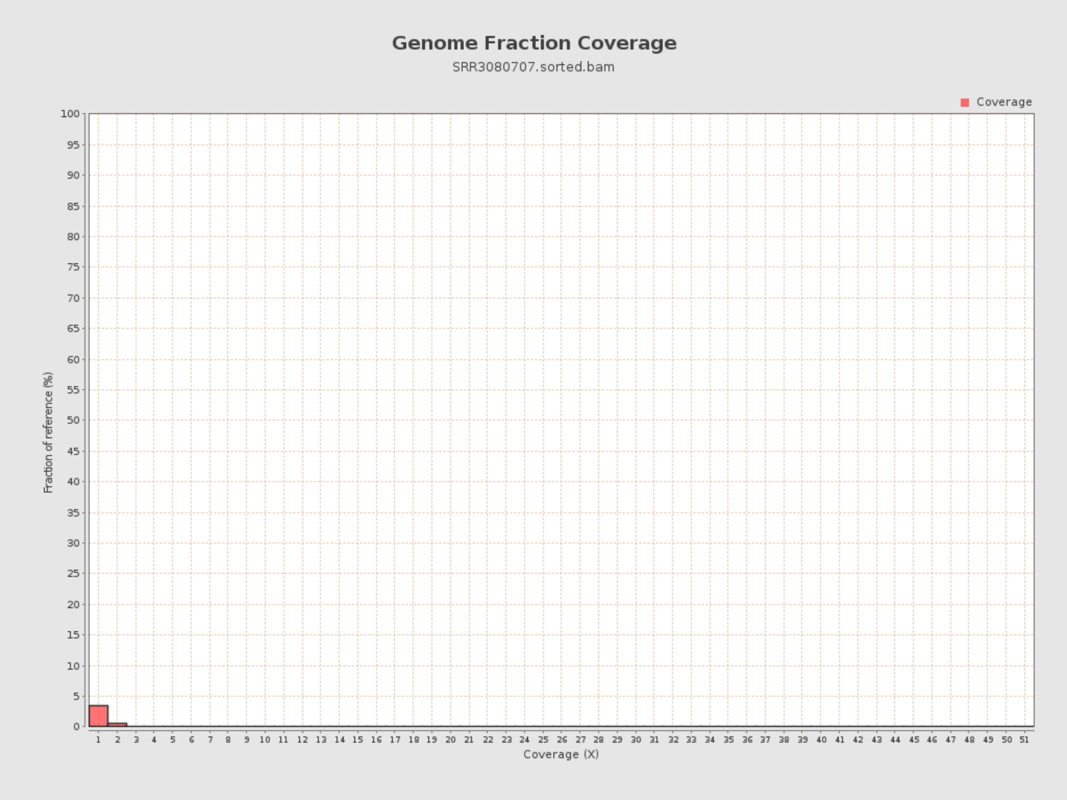
4. Results : Coverage Histogram



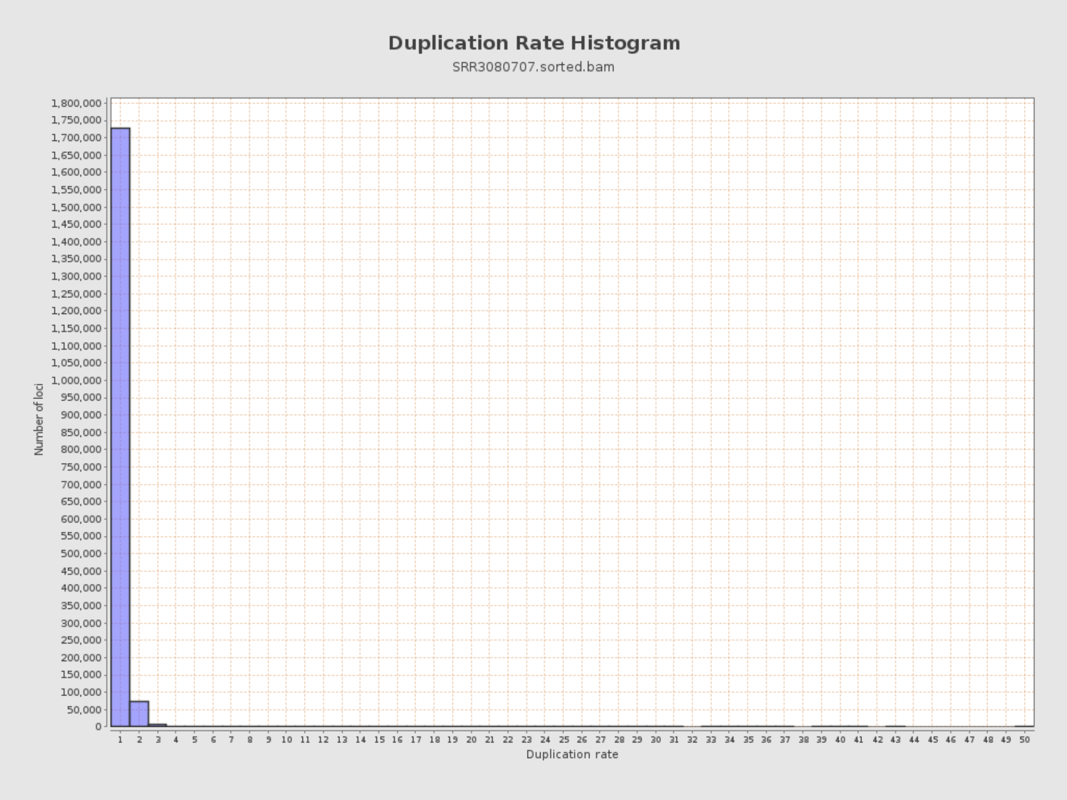
5. Results : Coverage Histogram (0-50X)



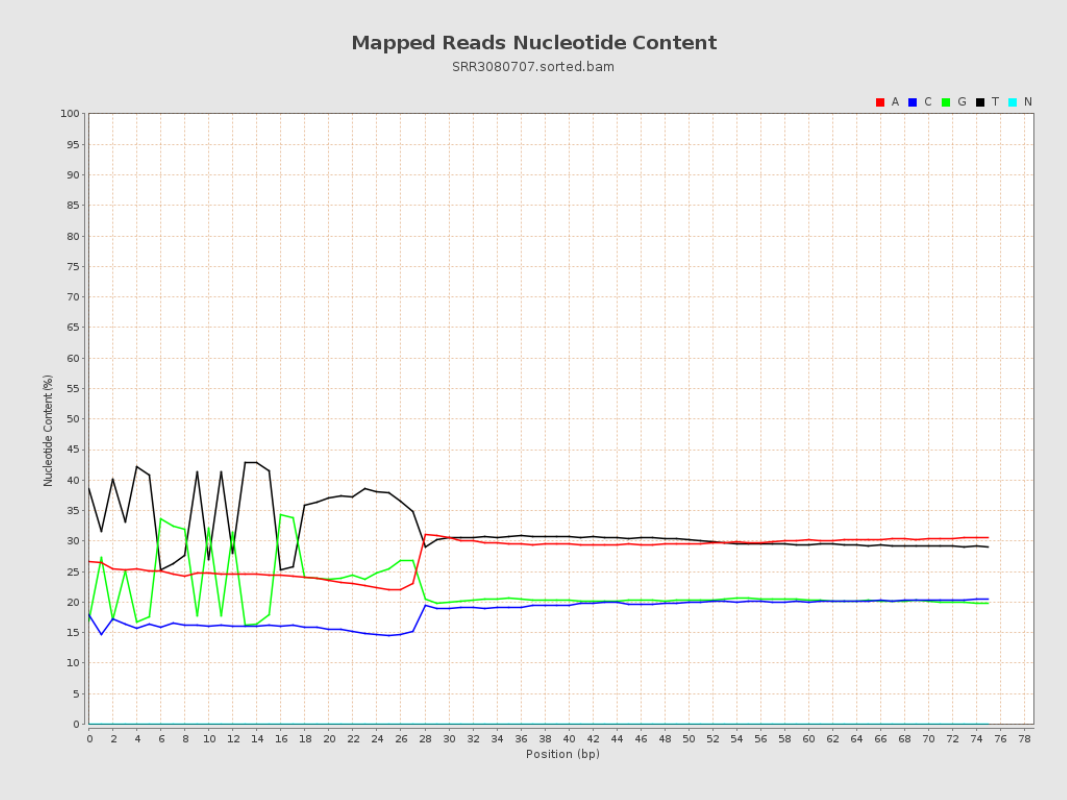
6. Results : Genome Fraction Coverage



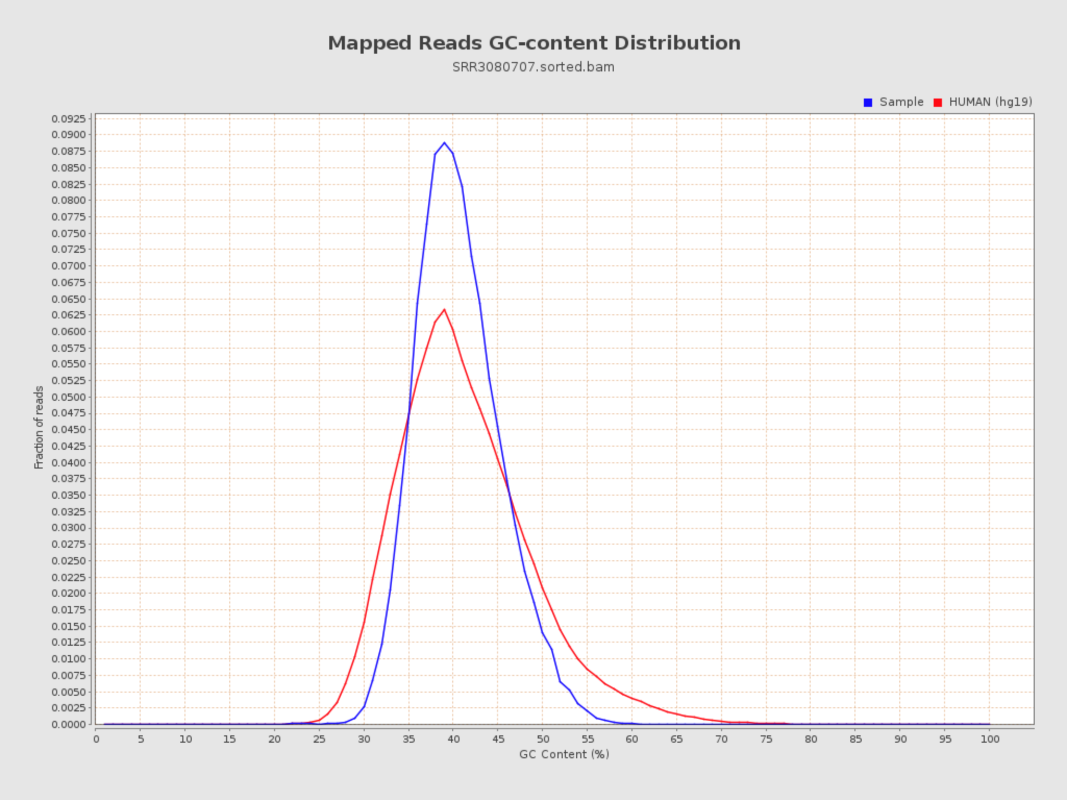
7. Results : Duplication Rate Histogram



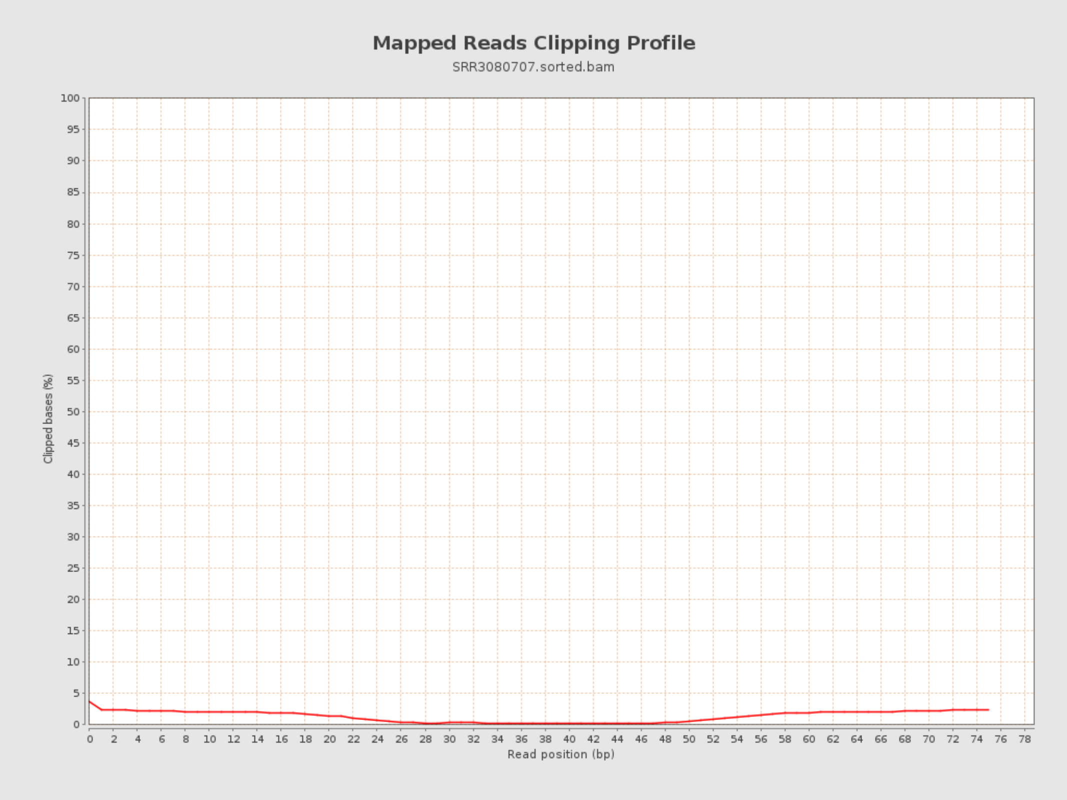
8. Results : Mapped Reads Nucleotide Content



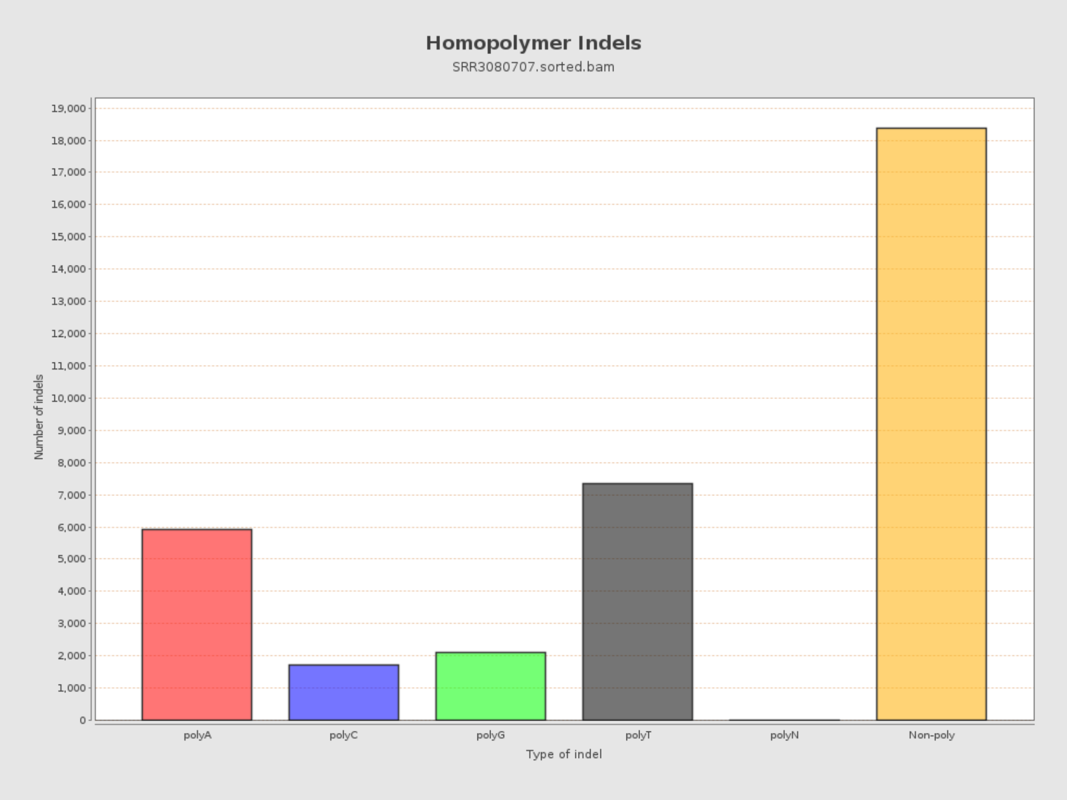
9. Results : Mapped Reads GC-content Distribution



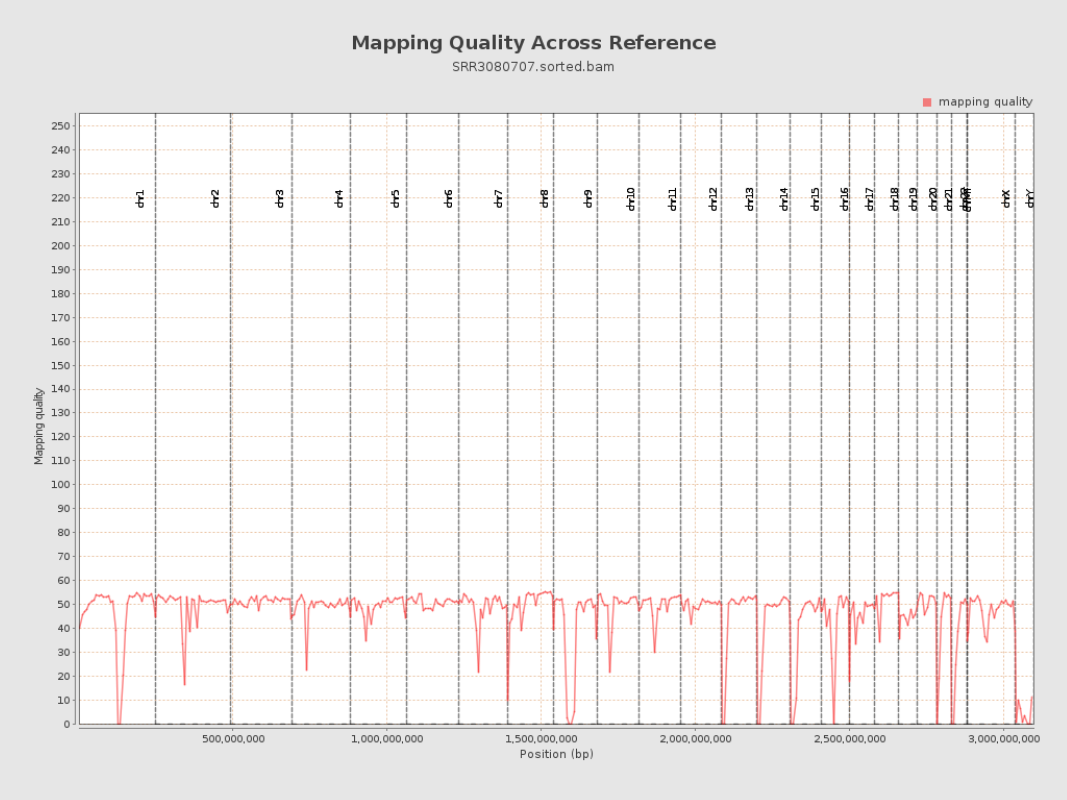
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram