Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:22:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080681.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_SRR3080681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080681.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:22:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,324,307
Mapped reads	1,201,981 / 90.76%
Unmapped reads	122,326 / 9.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,065 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	41,790 / 3.16%
Duplication rate	3.01%
Clipped reads	549,786 / 41.51%

2.2. ACGT Content

Number/percentage of A's	21,699,790 / 27.25%
Number/percentage of C's	14,463,447 / 18.16%
Number/percentage of T's	25,477,775 / 31.99%
Number/percentage of G's	17,991,416 / 22.59%
Number/percentage of N's	3,370 / 0%
GC Percentage	40.75%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2174

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

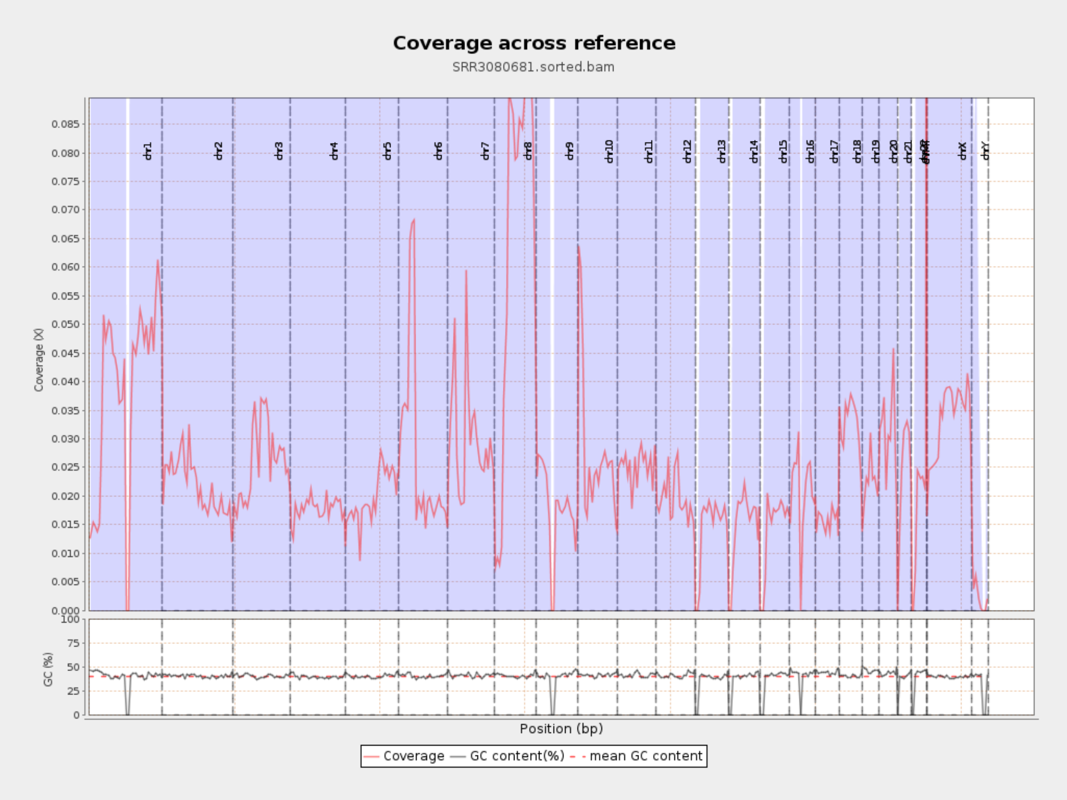
General error rate	0.7%
Mismatches	546,271
Insertions	6,007
Mapped reads with at least one insertion	0.5%
Deletions	18,691
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.87%

2.6. Chromosome stats

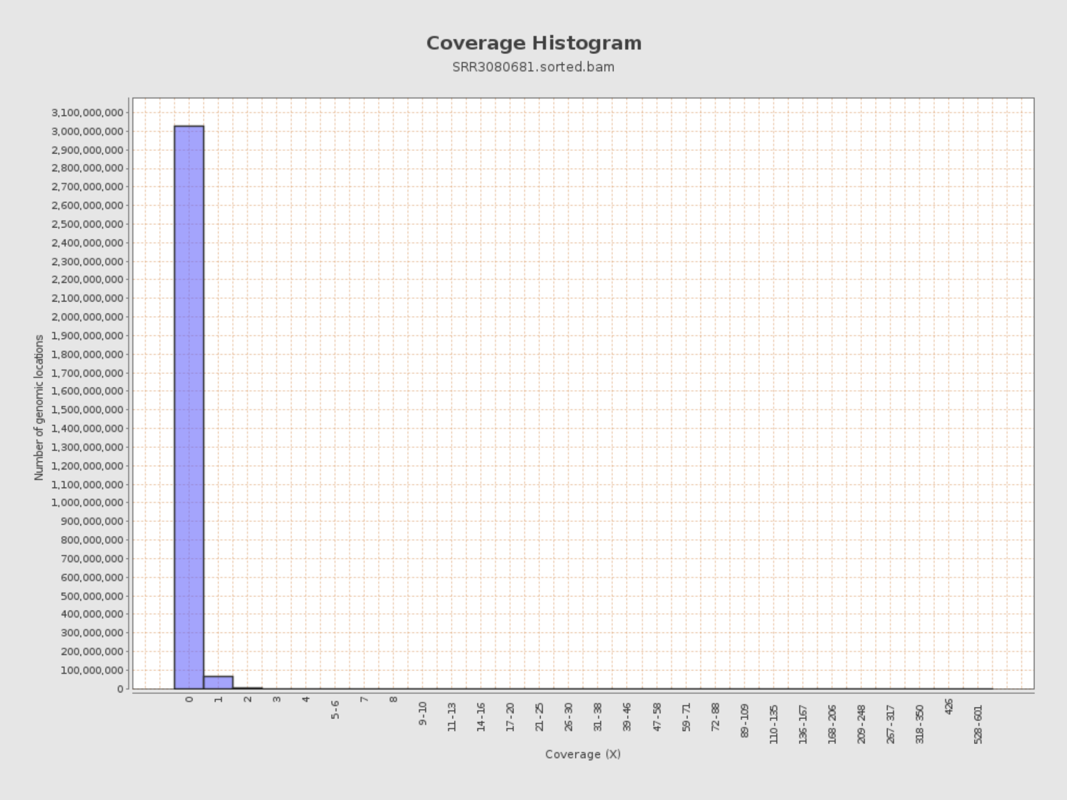
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9632821	0.0386	0.2491
chr2	243199373	5323278	0.0219	0.3077
chr3	198022430	5173320	0.0261	0.1774
chr4	191154276	3406696	0.0178	0.1496
chr5	180915260	3585633	0.0198	0.154
chr6	171115067	4751300	0.0278	0.2102
chr7	159138663	4895112	0.0308	0.4075

chr8	146364022	9504456	0.0649	0.3137
chr9	141213431	2488633	0.0176	0.1618
chr10	135534747	3832007	0.0283	0.1955
chr11	135006516	3392433	0.0251	0.18
chr12	133851895	2583571	0.0193	0.1523
chr13	115169878	1646800	0.0143	0.132
chr14	107349540	1593713	0.0148	0.1366
chr15	102531392	1466458	0.0143	0.1366
chr16	90354753	1898247	0.021	0.1618
chr17	81195210	1269865	0.0156	0.1378
chr18	78077248	2574429	0.033	0.2374
chr19	59128983	1343629	0.0227	0.1832
chr20	63025520	1973789	0.0313	0.1969
chr21	48129895	1153306	0.024	0.1721
chr22	51304566	817476	0.0159	0.138
chrMT	16571	5766	0.348	0.6496
chrX	155270560	5199020	0.0335	0.206
chrY	59373566	153976	0.0026	0.0582

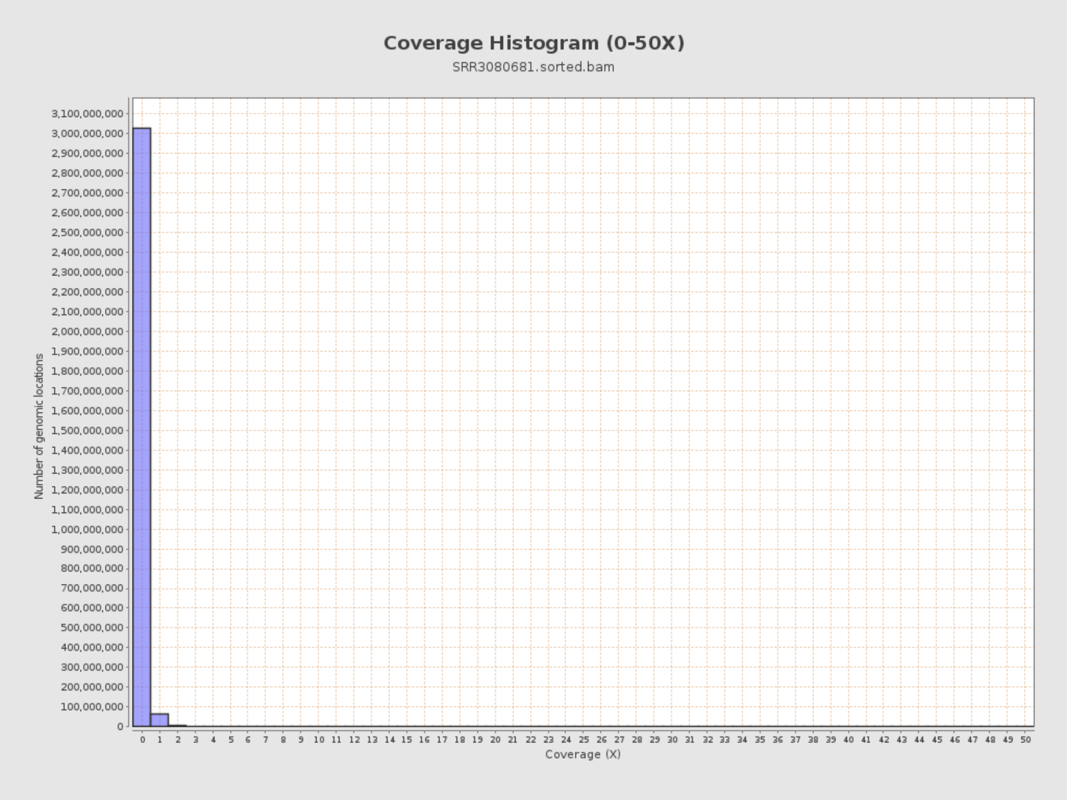
3. Results : Coverage across reference



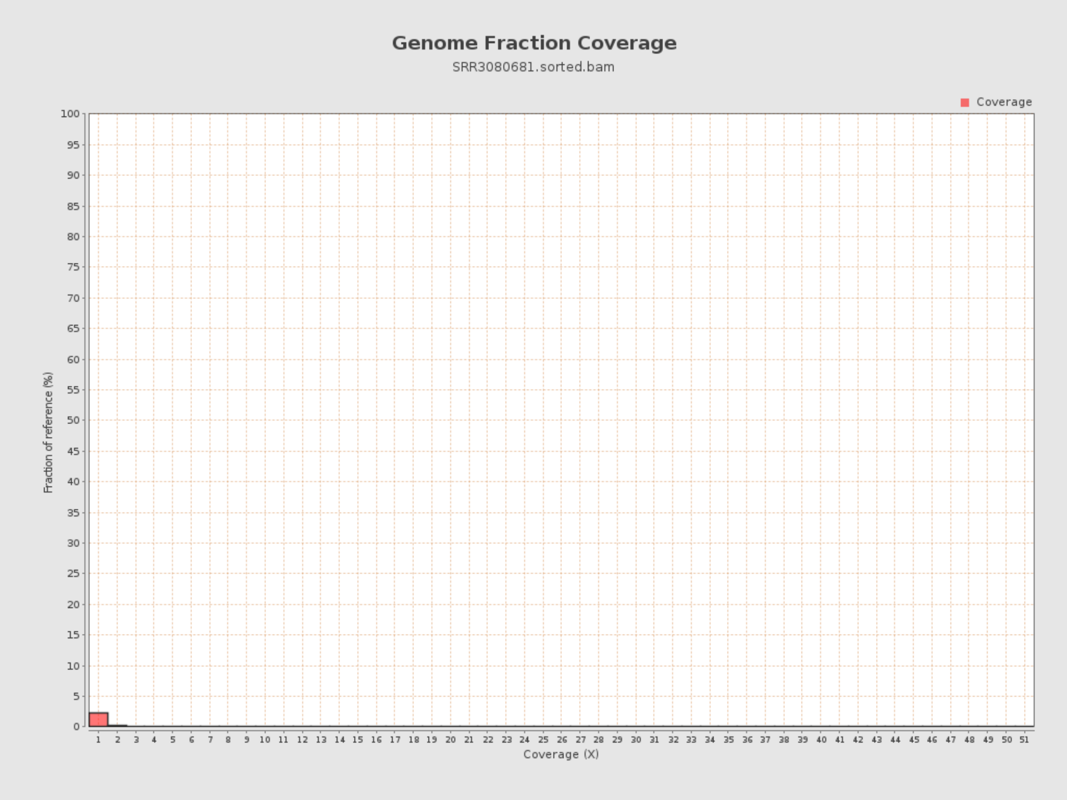
4. Results : Coverage Histogram



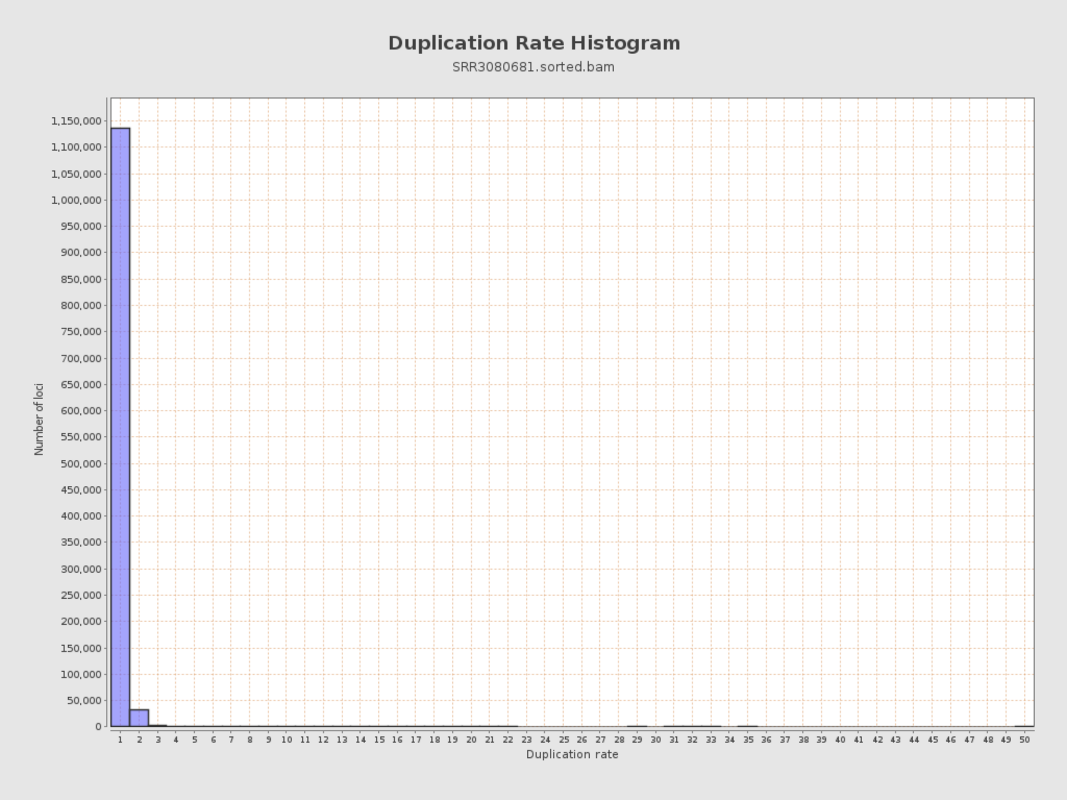
5. Results : Coverage Histogram (0-50X)



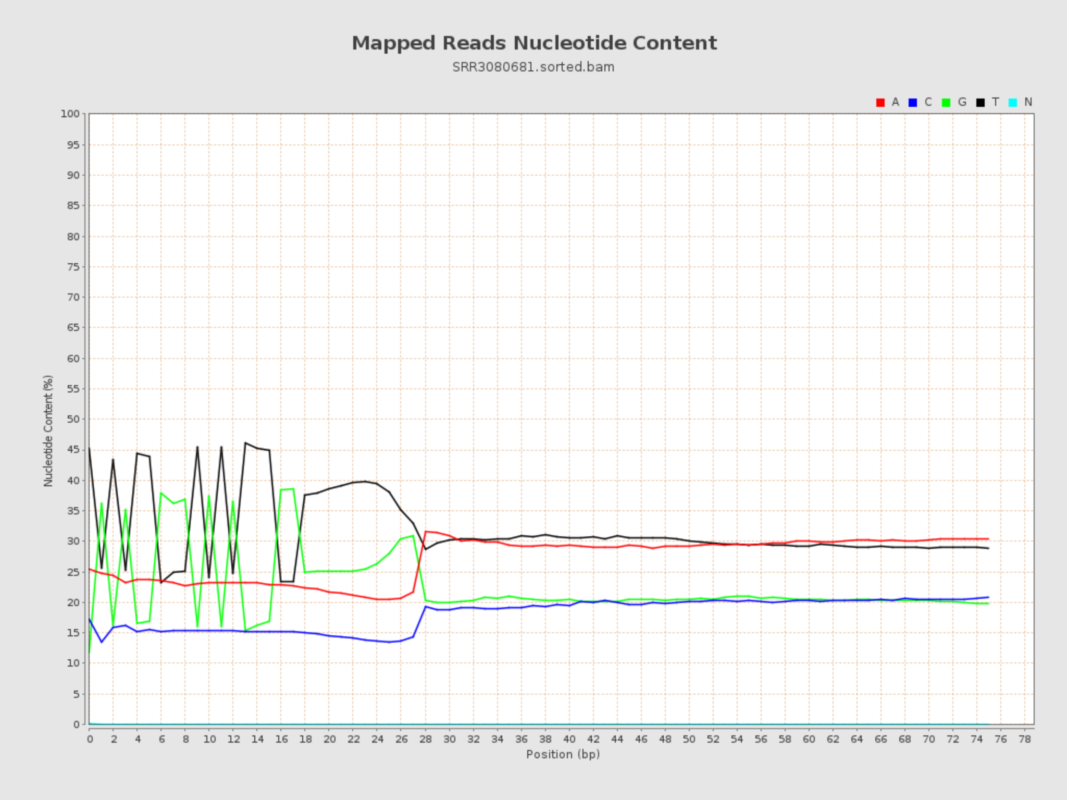
6. Results : Genome Fraction Coverage



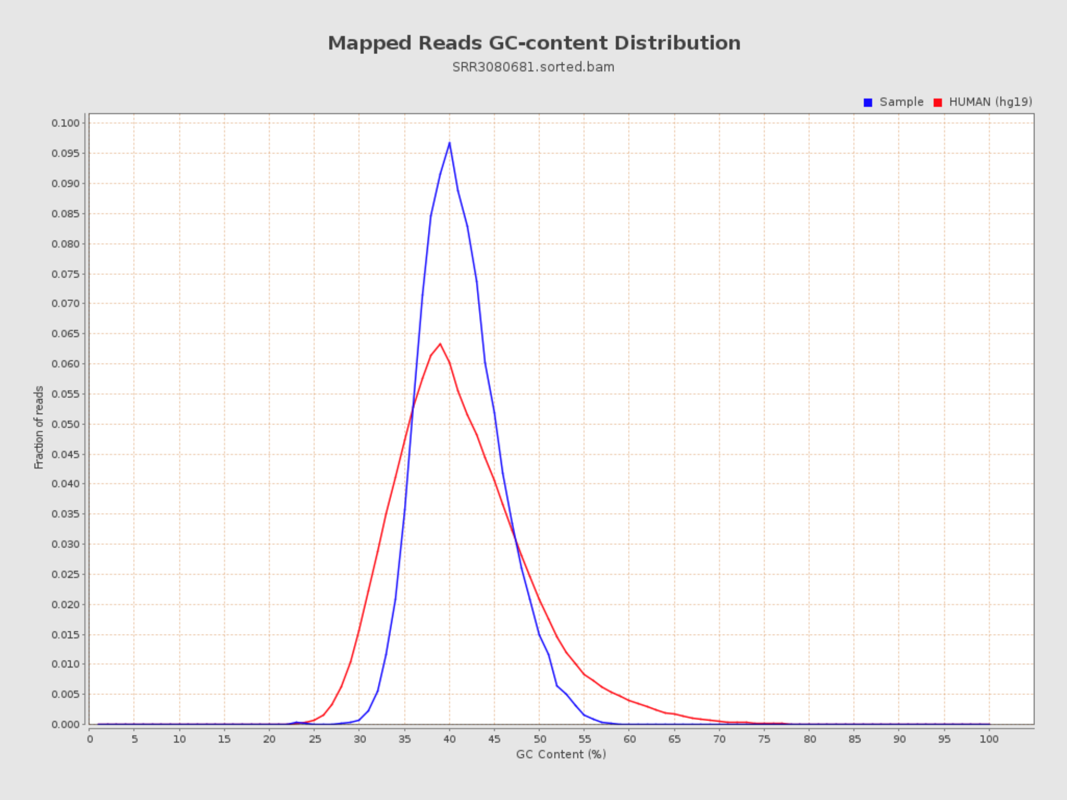
7. Results : Duplication Rate Histogram



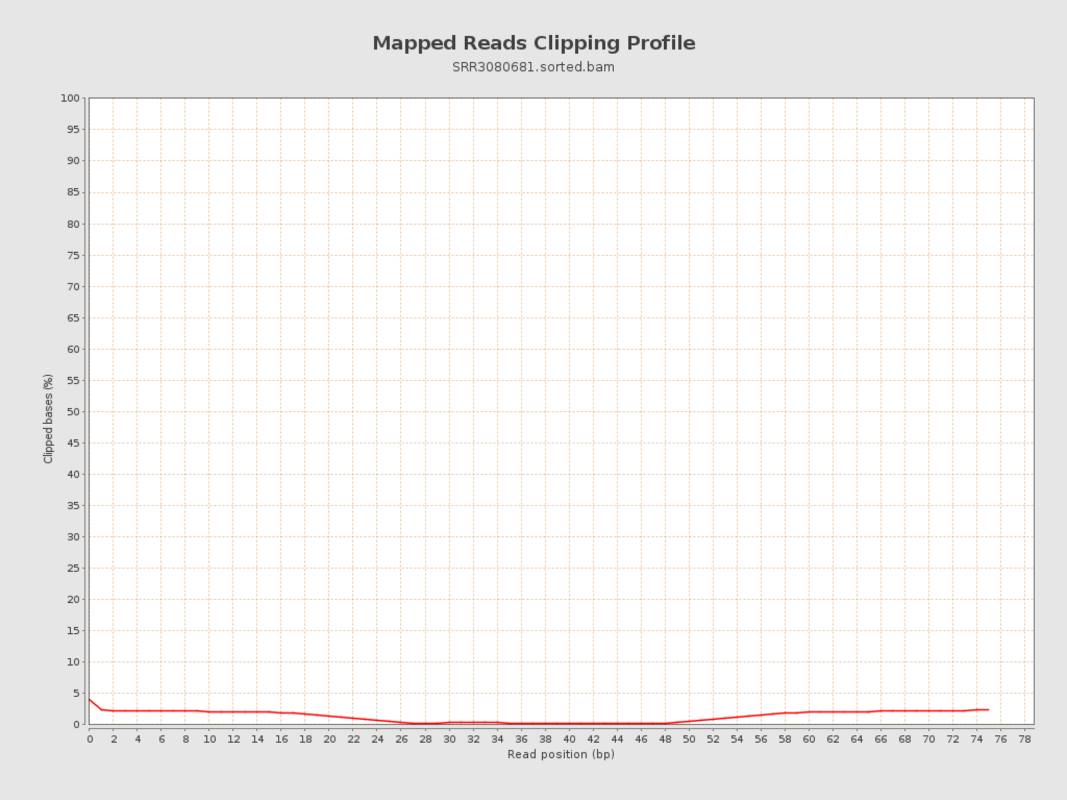
8. Results : Mapped Reads Nucleotide Content



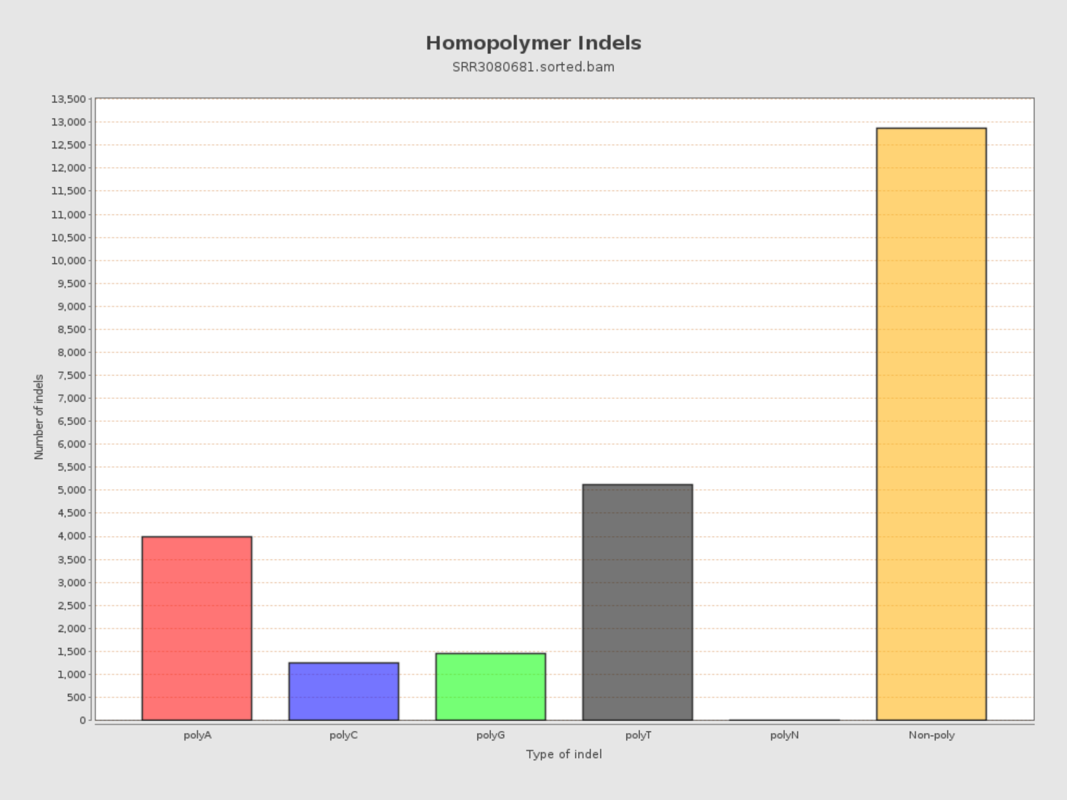
9. Results : Mapped Reads GC-content Distribution



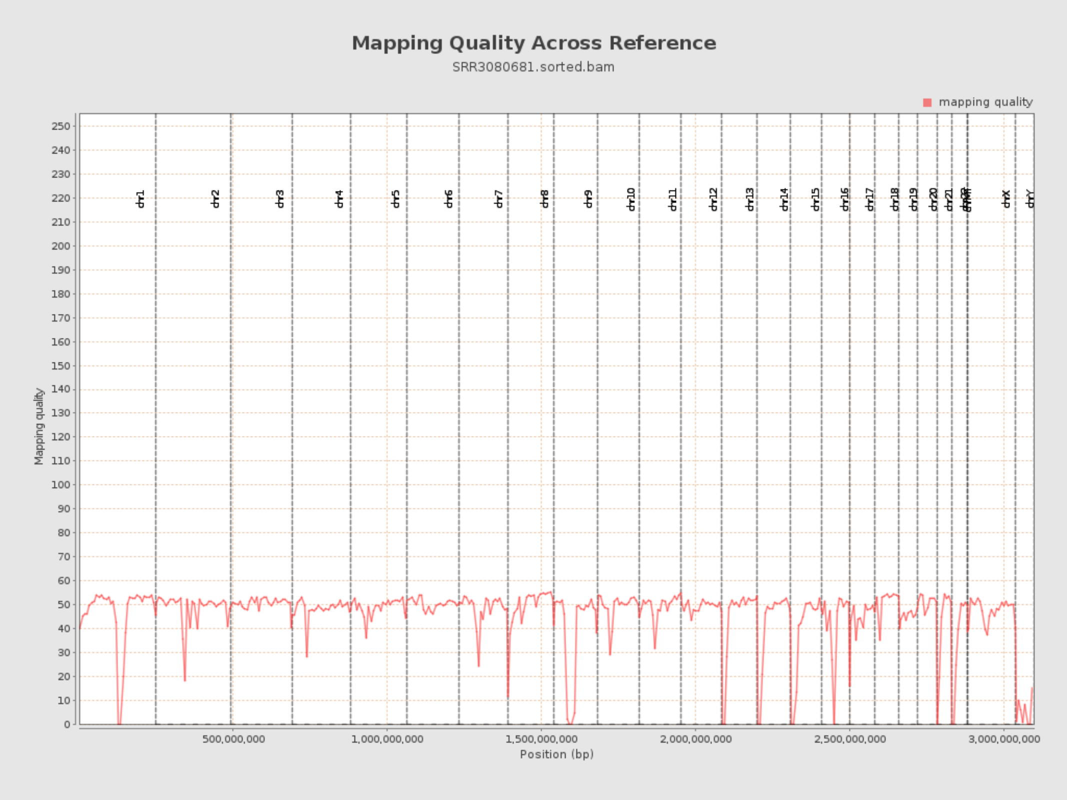
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram