Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:00:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080668.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_SRR3080668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:59:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,730,724
Mapped reads	1,570,873 / 90.76%
Unmapped reads	159,851 / 9.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,791 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	61,444 / 3.55%
Duplication rate	3.17%
Clipped reads	759,796 / 43.9%

2.2. ACGT Content

Number/percentage of A's	27,661,876 / 26.78%
Number/percentage of C's	19,200,263 / 18.59%
Number/percentage of T's	32,475,068 / 31.44%
Number/percentage of G's	23,946,245 / 23.18%
Number/percentage of N's	4,191 / 0%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.2981

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

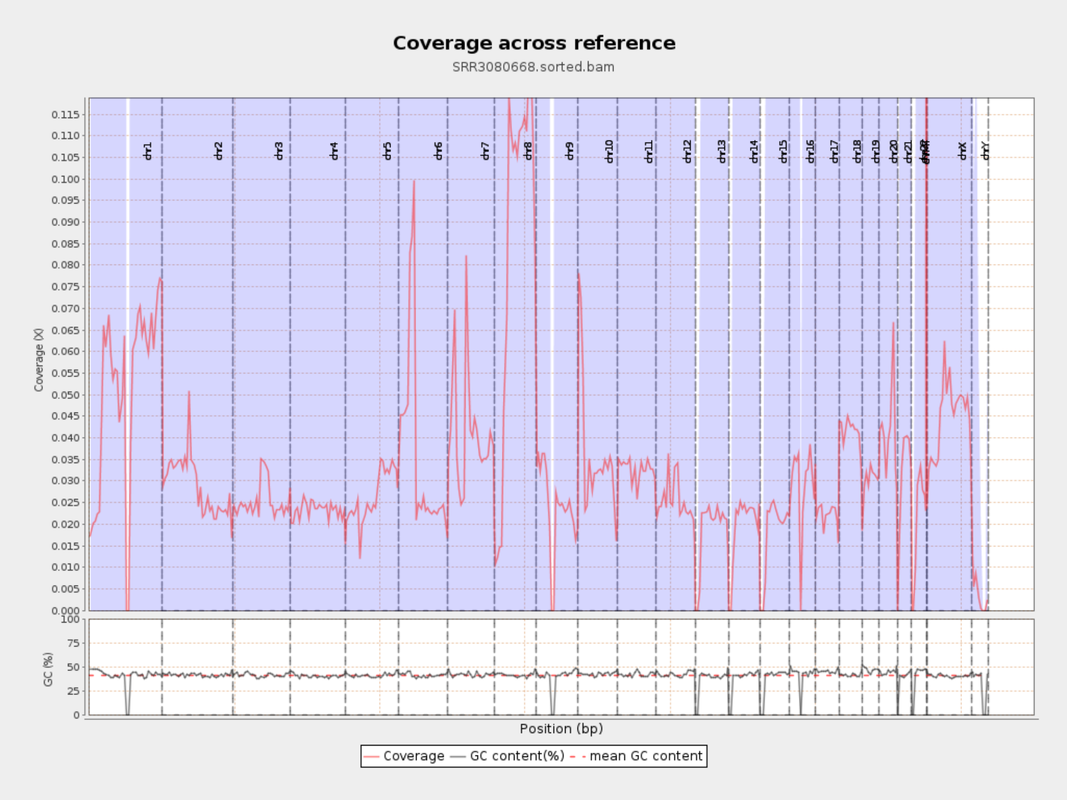
General error rate	0.71%
Mismatches	722,610
Insertions	7,806
Mapped reads with at least one insertion	0.49%
Deletions	23,822
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.35%

2.6. Chromosome stats

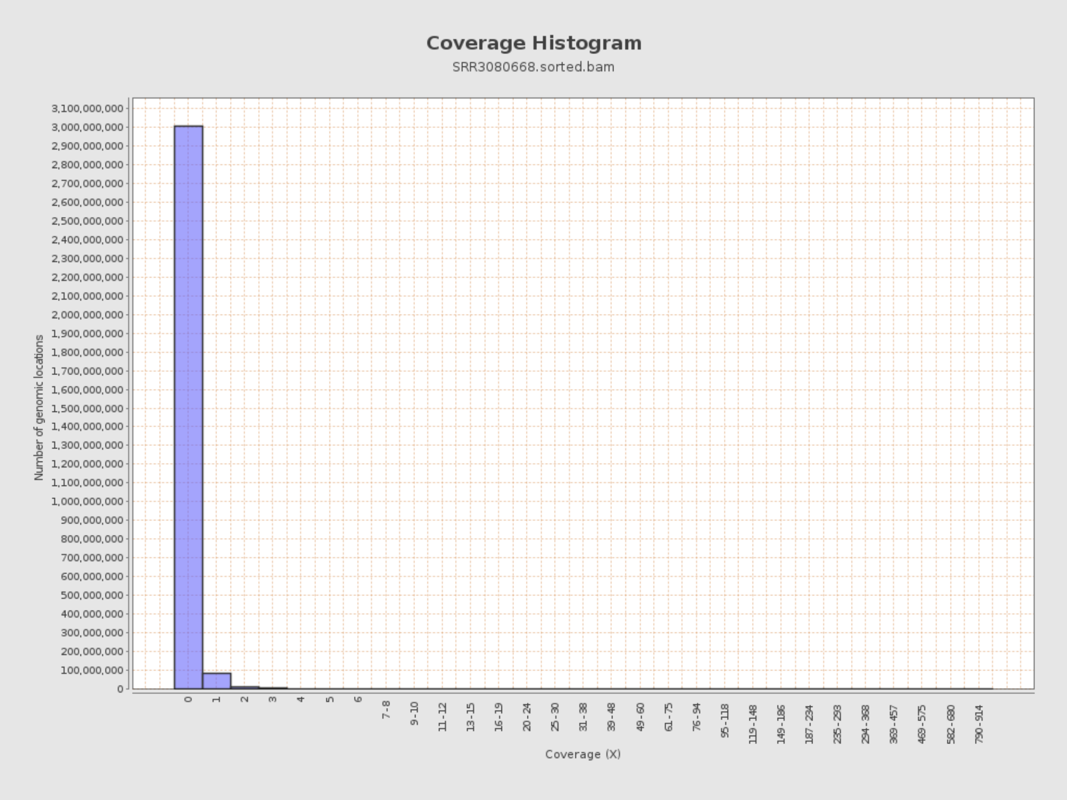
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12716572	0.051	0.382
chr2	243199373	7034096	0.0289	0.4482
chr3	198022430	5004938	0.0253	0.1759
chr4	191154276	4458787	0.0233	0.1751
chr5	180915260	4793462	0.0265	0.1805
chr6	171115067	6269349	0.0366	0.2917
chr7	159138663	6704672	0.0421	0.6408

chr8	146364022	12417507	0.0848	0.384
chr9	141213431	3359509	0.0238	0.2263
chr10	135534747	4956727	0.0366	0.2366
chr11	135006516	4370877	0.0324	0.2287
chr12	133851895	3399301	0.0254	0.1804
chr13	115169878	2124654	0.0184	0.1504
chr14	107349540	2072065	0.0193	0.1582
chr15	102531392	1862021	0.0182	0.1599
chr16	90354753	2635396	0.0292	0.1946
chr17	81195210	1783784	0.022	0.1743
chr18	78077248	3255115	0.0417	0.341
chr19	59128983	1802929	0.0305	0.2577
chr20	63025520	2622860	0.0416	0.2305
chr21	48129895	1497410	0.0311	0.2002
chr22	51304566	1026348	0.02	0.1558
chrMT	16571	8986	0.5423	0.8671
chrX	155270560	6930999	0.0446	0.2531
chrY	59373566	217257	0.0037	0.0735

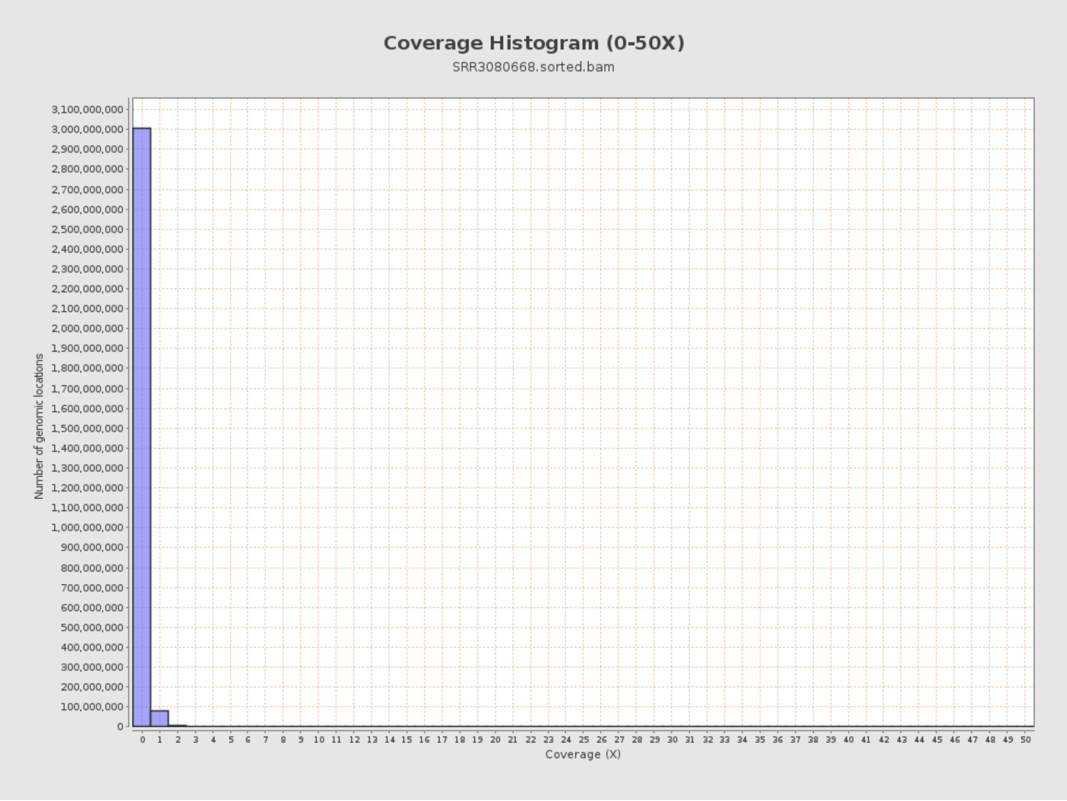
3. Results : Coverage across reference



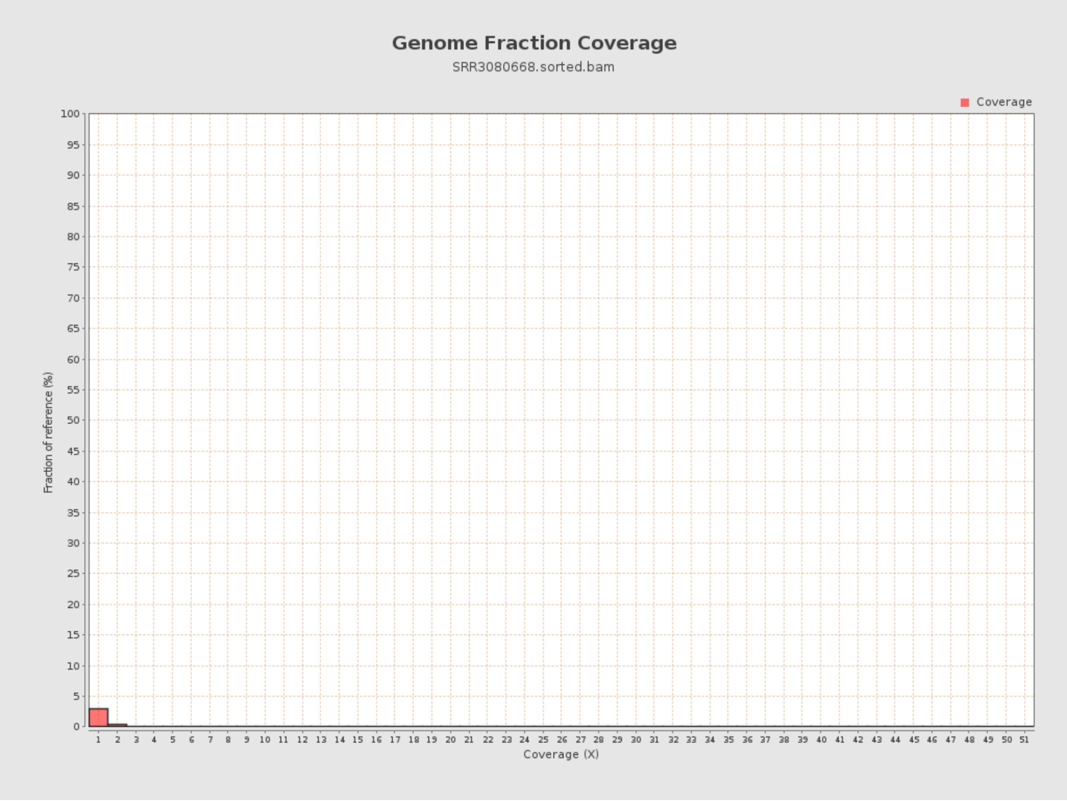
4. Results : Coverage Histogram



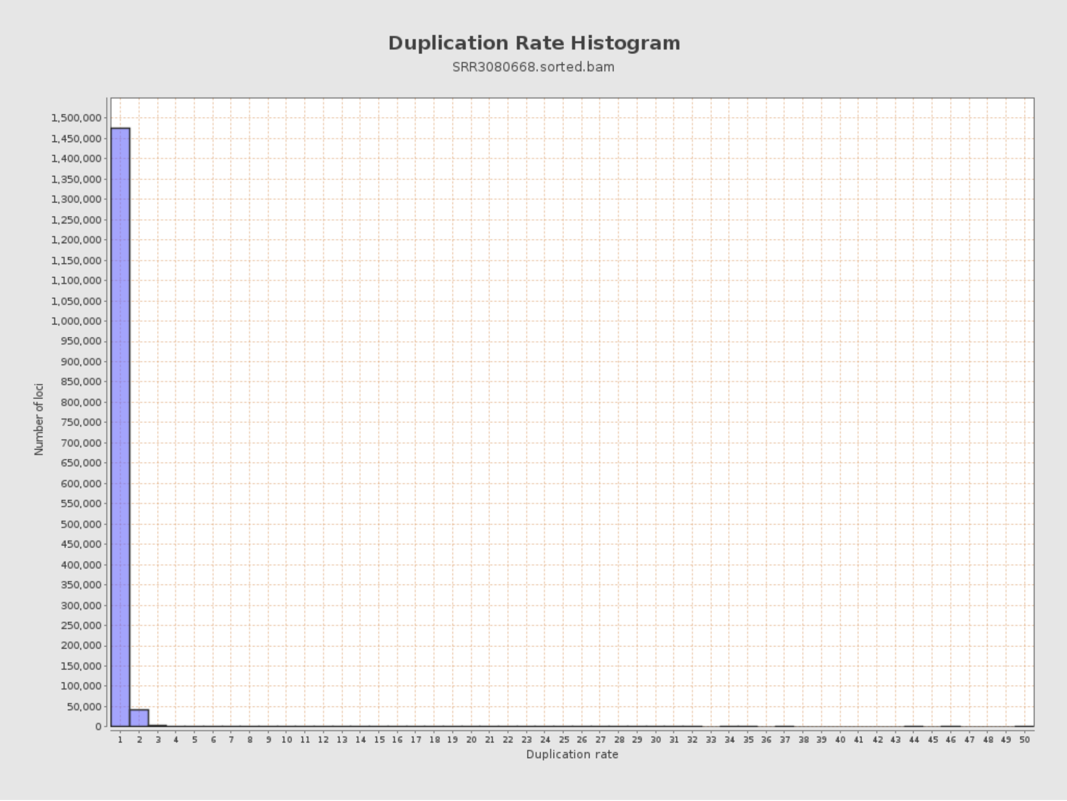
5. Results : Coverage Histogram (0-50X)



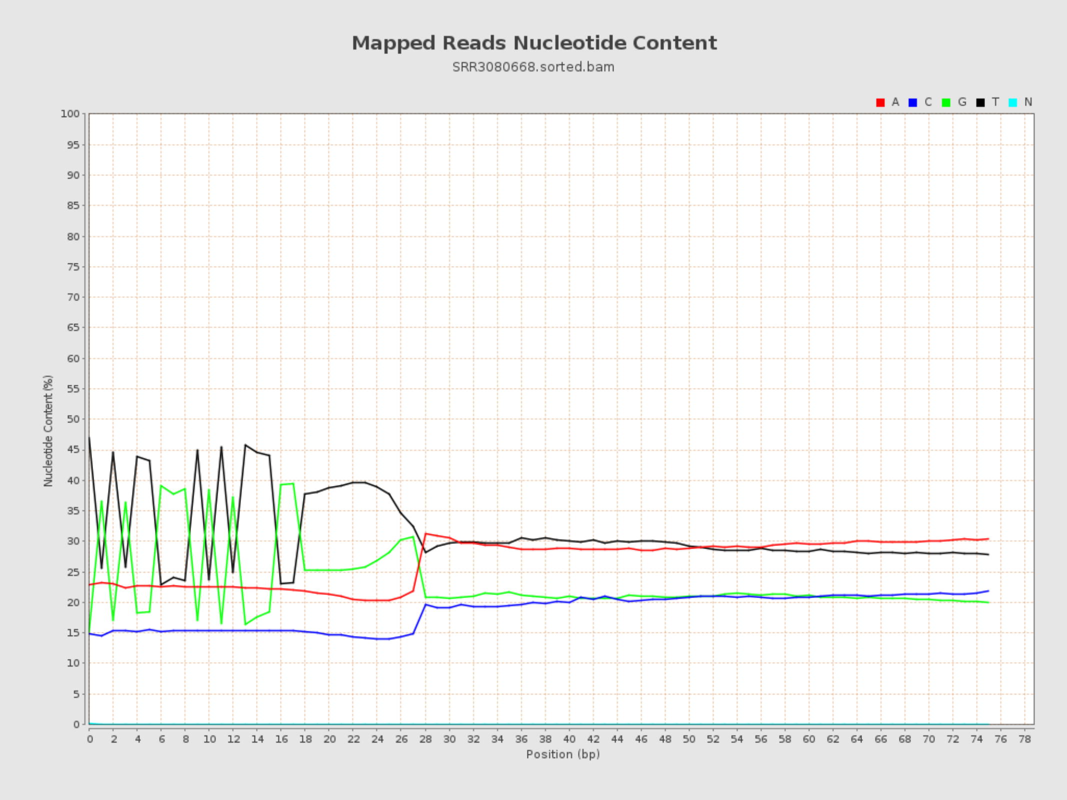
6. Results : Genome Fraction Coverage



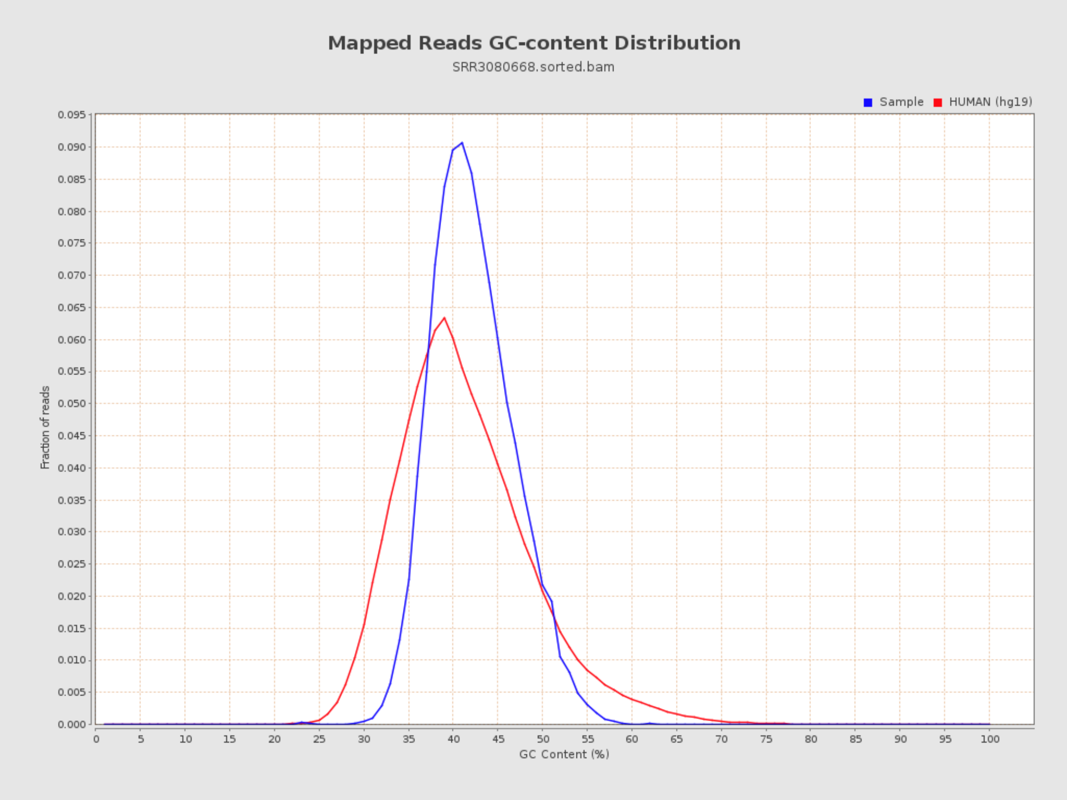
7. Results : Duplication Rate Histogram



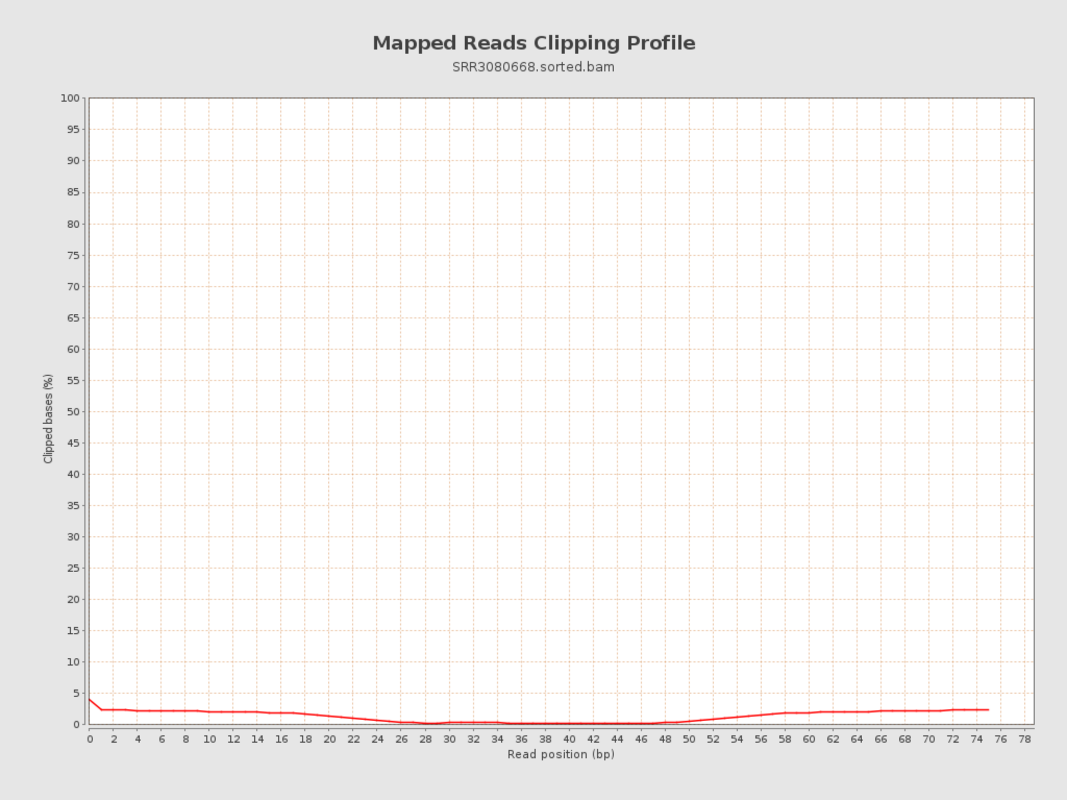
8. Results : Mapped Reads Nucleotide Content



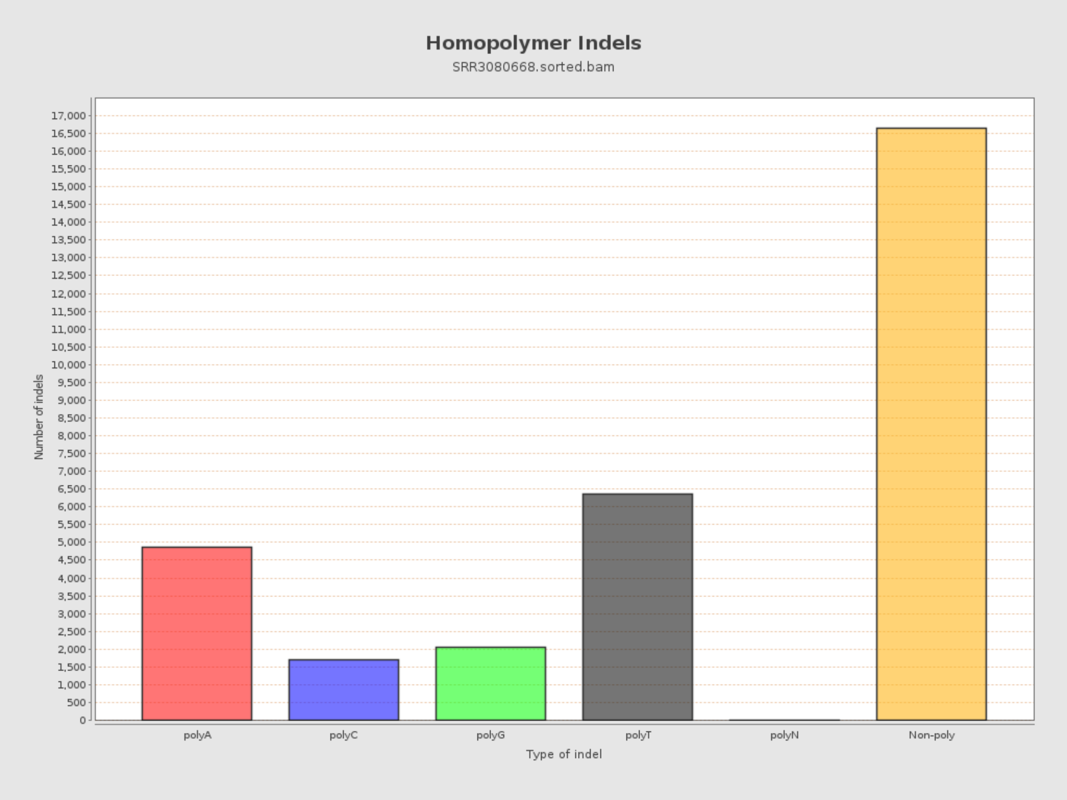
9. Results : Mapped Reads GC-content Distribution



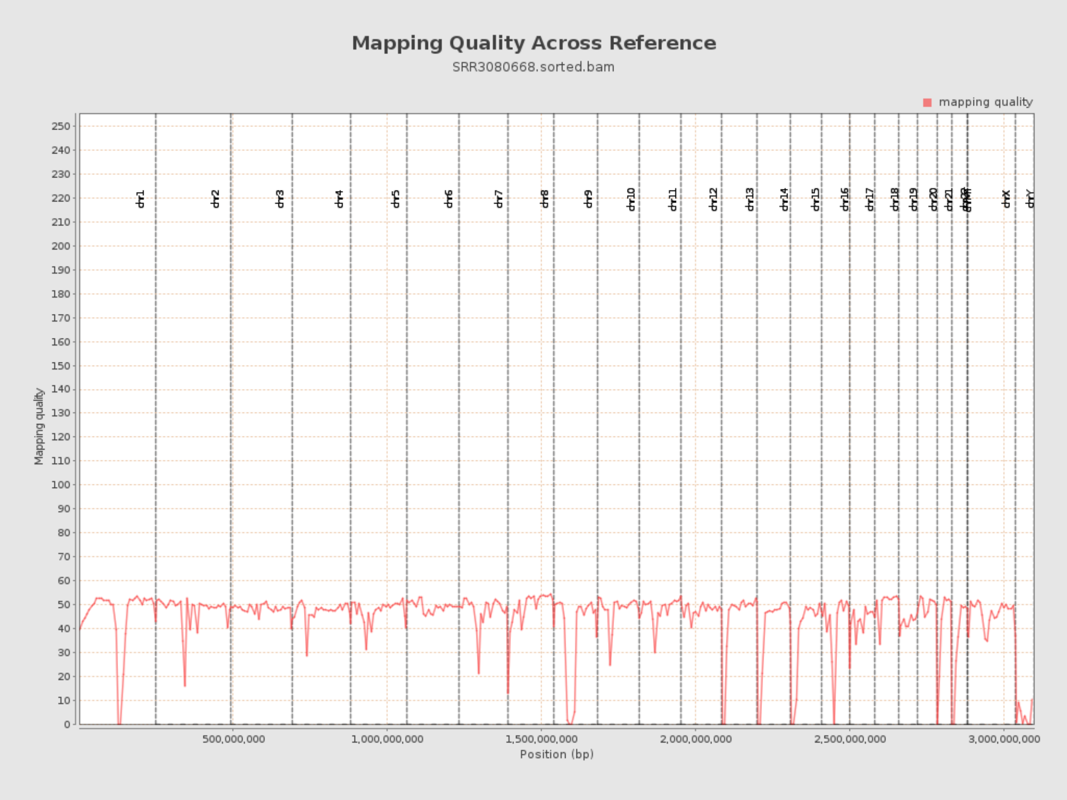
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram