Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:56:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080684.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_SRR3080684 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080684.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:56:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080684.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,227,567
Mapped reads	1,136,947 / 92.62%
Unmapped reads	90,620 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,614 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	36,299 / 2.96%
Duplication rate	2.8%
Clipped reads	499,396 / 40.68%

2.2. ACGT Content

Number/percentage of A's	20,942,541 / 27.6%
Number/percentage of C's	13,881,497 / 18.3%
Number/percentage of T's	24,189,882 / 31.88%
Number/percentage of G's	16,849,505 / 22.21%
Number/percentage of N's	3,729 / 0%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2039

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

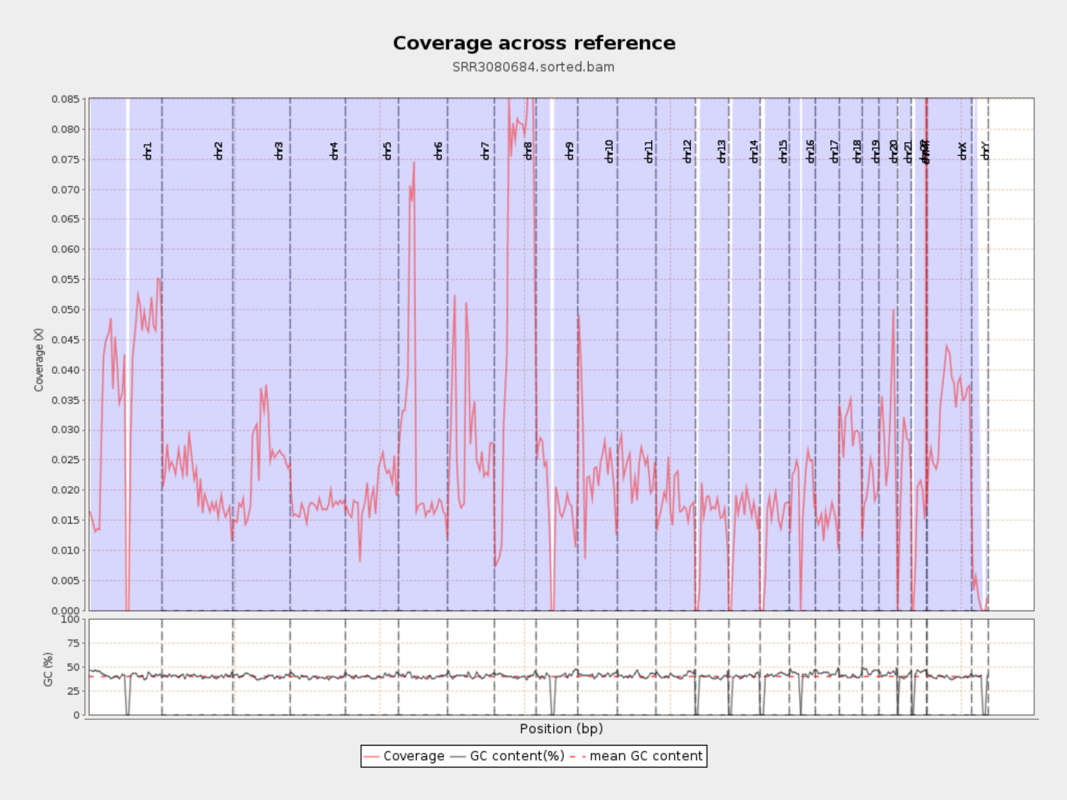
General error rate	0.69%
Mismatches	510,227
Insertions	5,769
Mapped reads with at least one insertion	0.5%
Deletions	17,290
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.67%

2.6. Chromosome stats

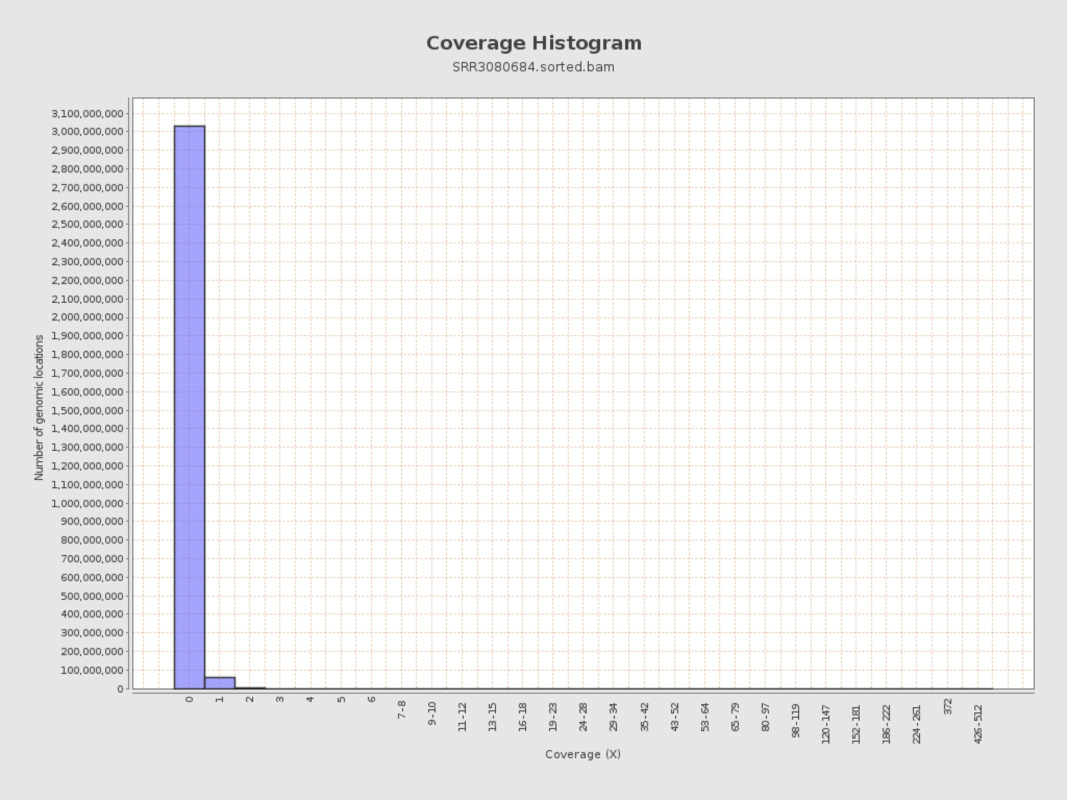
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9265462	0.0372	0.2419
chr2	243199373	5074556	0.0209	0.2704
chr3	198022430	4821505	0.0243	0.1708
chr4	191154276	3308725	0.0173	0.1463
chr5	180915260	3524186	0.0195	0.1525
chr6	171115067	4728107	0.0276	0.21
chr7	159138663	4657822	0.0293	0.3493

chr8	146364022	8887819	0.0607	0.2956
chr9	141213431	2465392	0.0175	0.163
chr10	135534747	3378580	0.0249	0.1821
chr11	135006516	3170458	0.0235	0.1763
chr12	133851895	2373104	0.0177	0.1456
chr13	115169878	1629496	0.0141	0.1312
chr14	107349540	1543666	0.0144	0.1335
chr15	102531392	1396601	0.0136	0.1318
chr16	90354753	1822783	0.0202	0.1583
chr17	81195210	1203542	0.0148	0.1356
chr18	78077248	2366997	0.0303	0.2312
chr19	59128983	1200135	0.0203	0.1742
chr20	63025520	1904661	0.0302	0.1927
chr21	48129895	1087487	0.0226	0.1672
chr22	51304566	690389	0.0135	0.1259
chrMT	16571	14676	0.8856	1.1284
chrX	155270560	5234037	0.0337	0.2076
chrY	59373566	145074	0.0024	0.0573

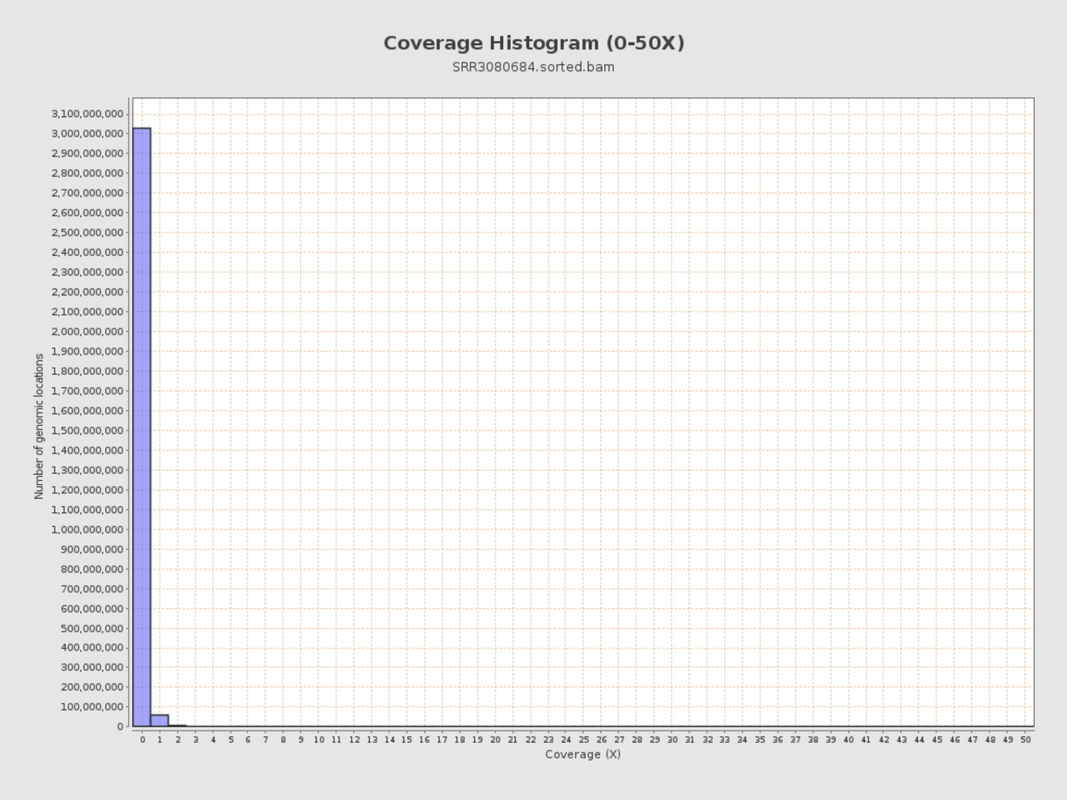
3. Results : Coverage across reference



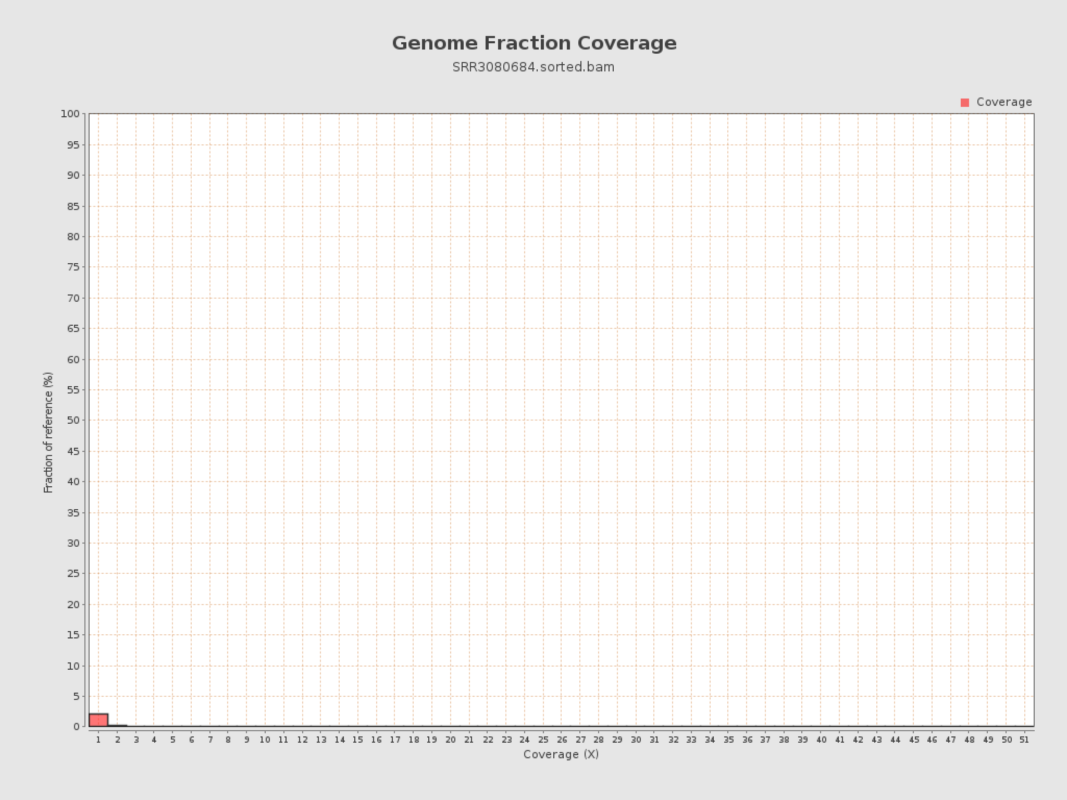
4. Results : Coverage Histogram



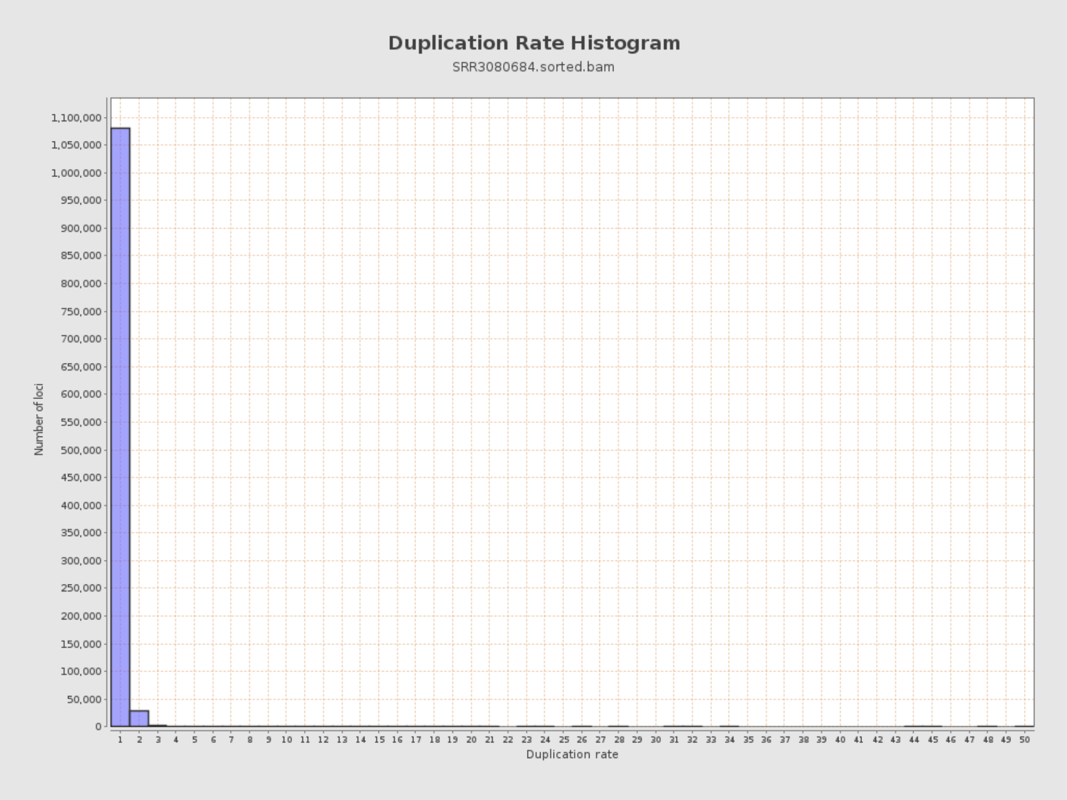
5. Results : Coverage Histogram (0-50X)



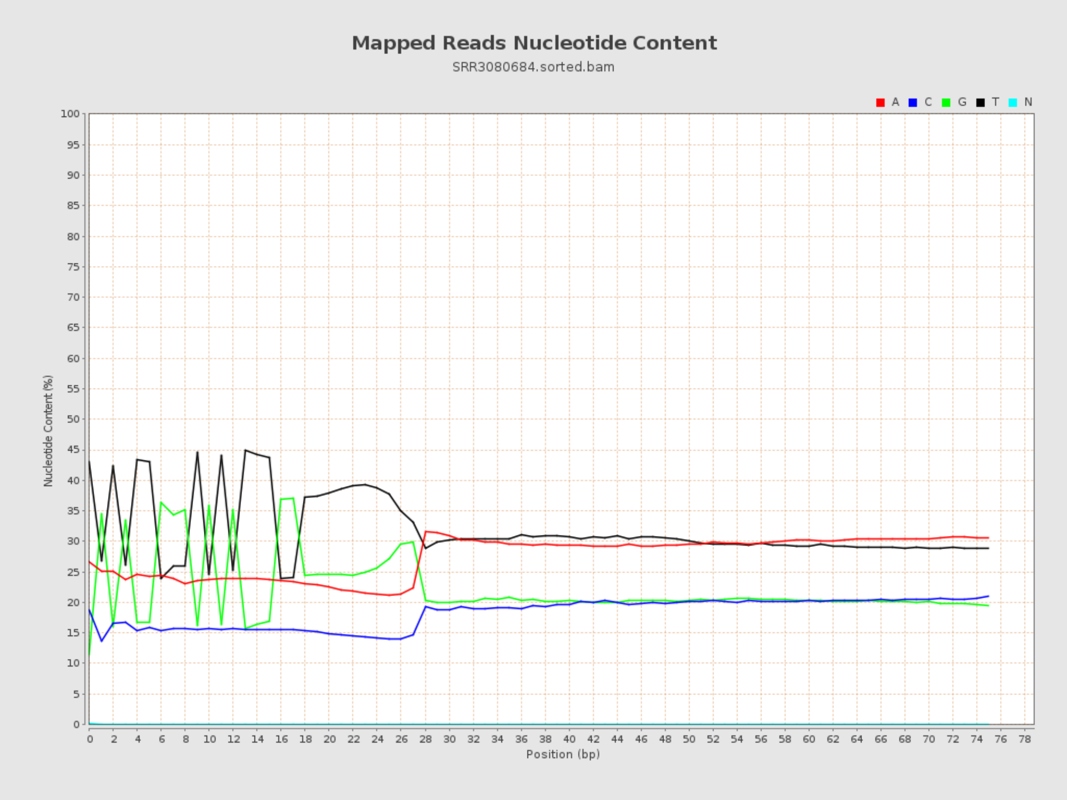
6. Results : Genome Fraction Coverage



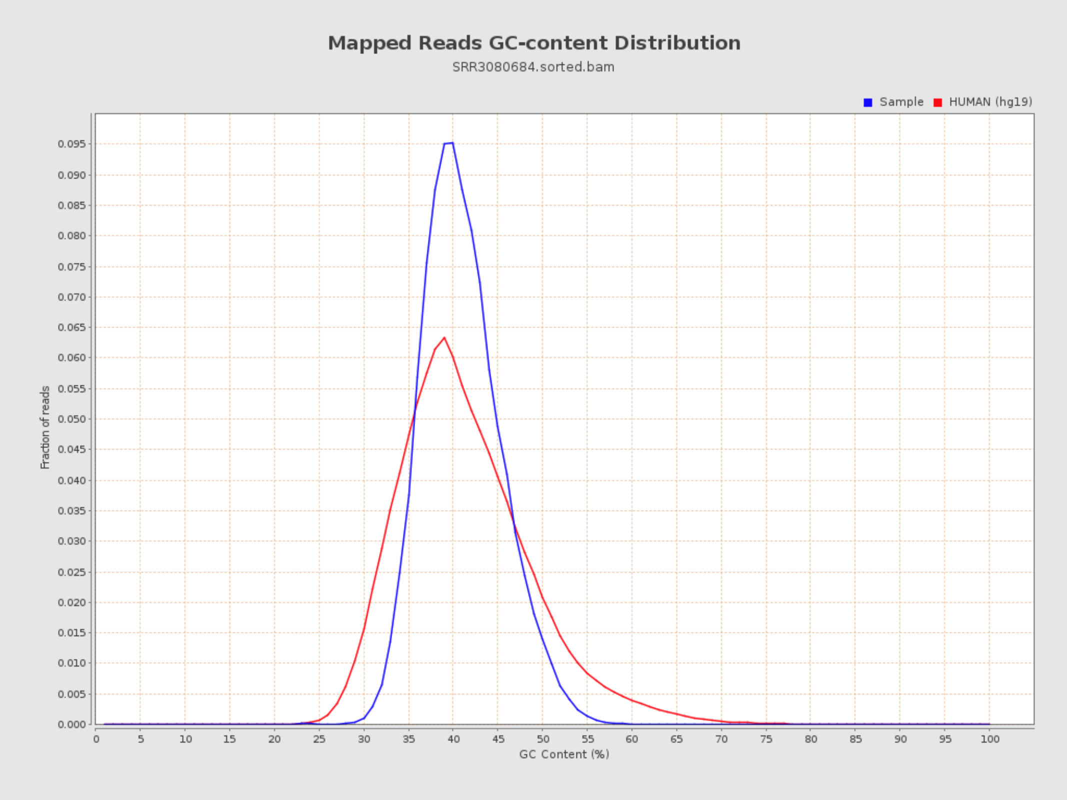
7. Results : Duplication Rate Histogram



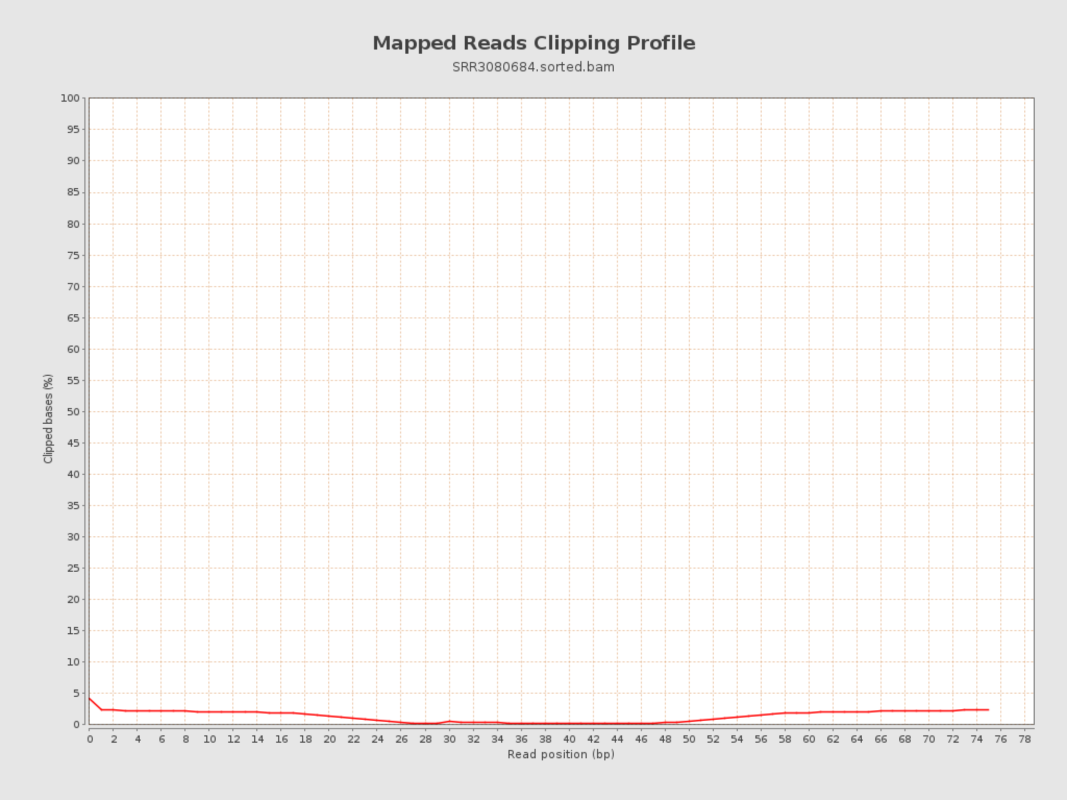
8. Results : Mapped Reads Nucleotide Content



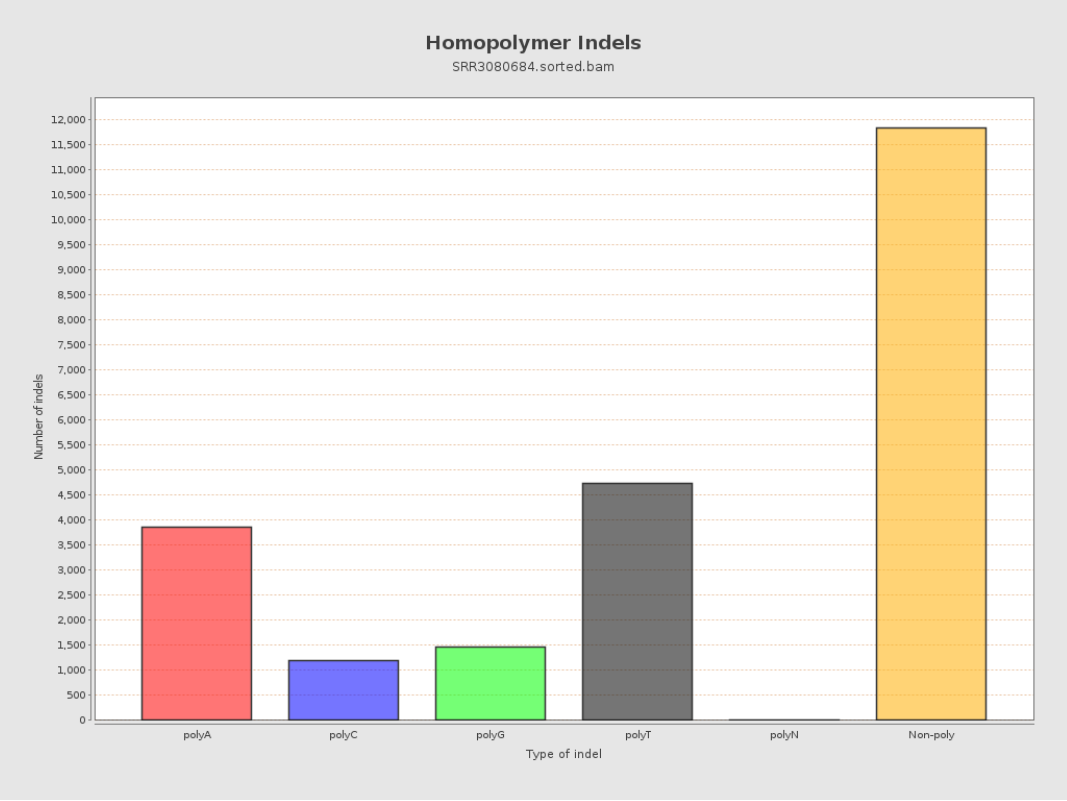
9. Results : Mapped Reads GC-content Distribution



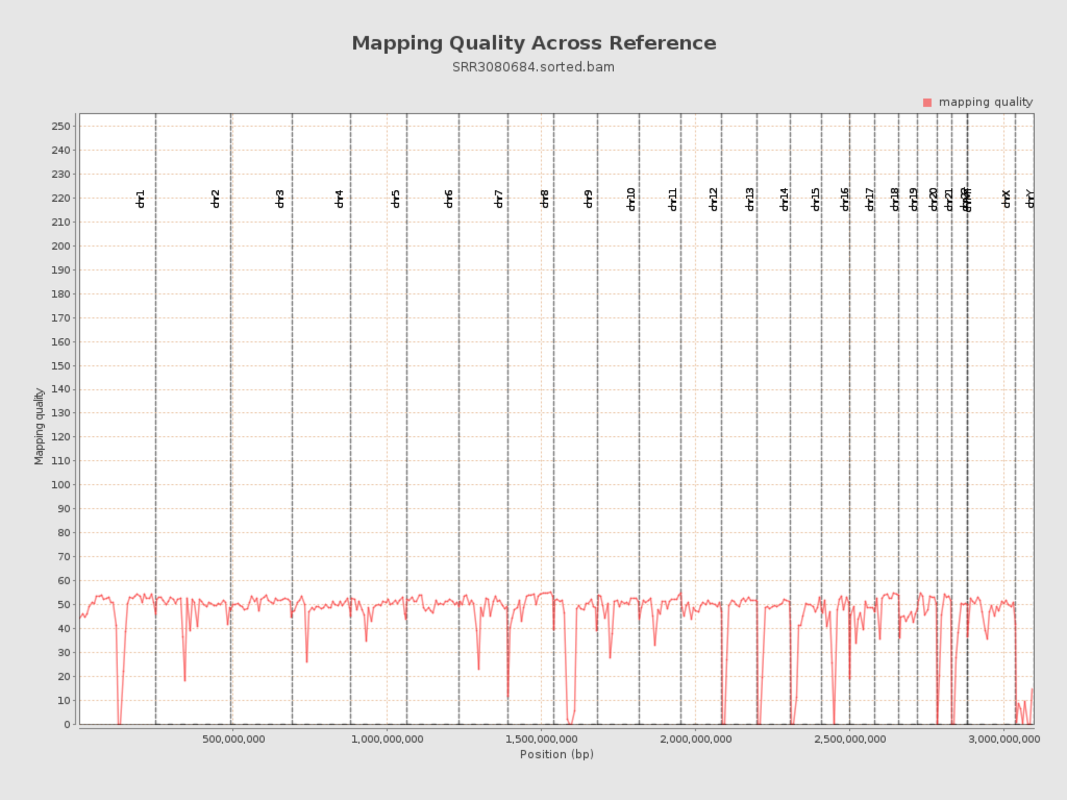
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram