Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:21:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053608.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_SRR053608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:21:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,307,358
Mapped reads	4,650,384 / 63.64%
Unmapped reads	2,656,974 / 36.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	140 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,007,725 / 13.79%
Duplication rate	15.81%
Clipped reads	637,212 / 8.72%

2.2. ACGT Content

Number/percentage of A's	65,904,726 / 30.3%
Number/percentage of C's	42,575,186 / 19.58%
Number/percentage of T's	64,577,331 / 29.69%
Number/percentage of G's	44,327,904 / 20.38%
Number/percentage of N's	108,310 / 0.05%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0703

Standard Deviation	0.8943

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

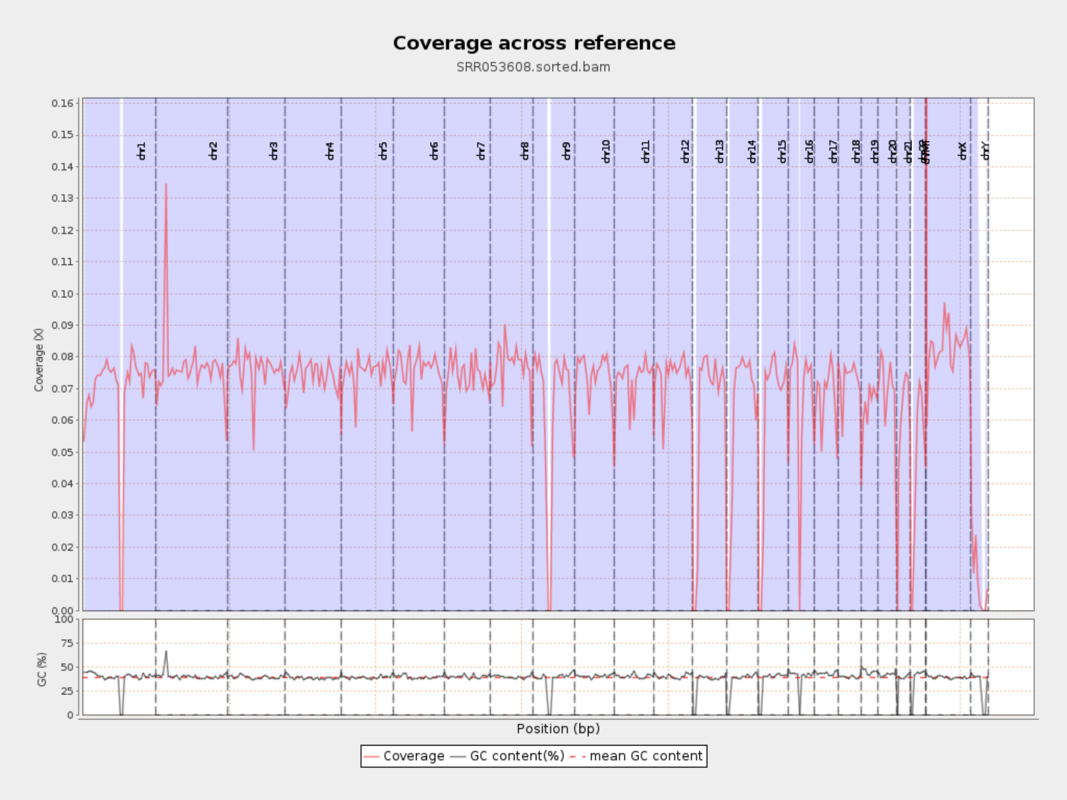
General error rate	0.77%
Mismatches	1,665,257
Insertions	11,400
Mapped reads with at least one insertion	0.24%
Deletions	32,948
Mapped reads with at least one deletion	0.71%
Homopolymer indels	45.85%

2.6. Chromosome stats

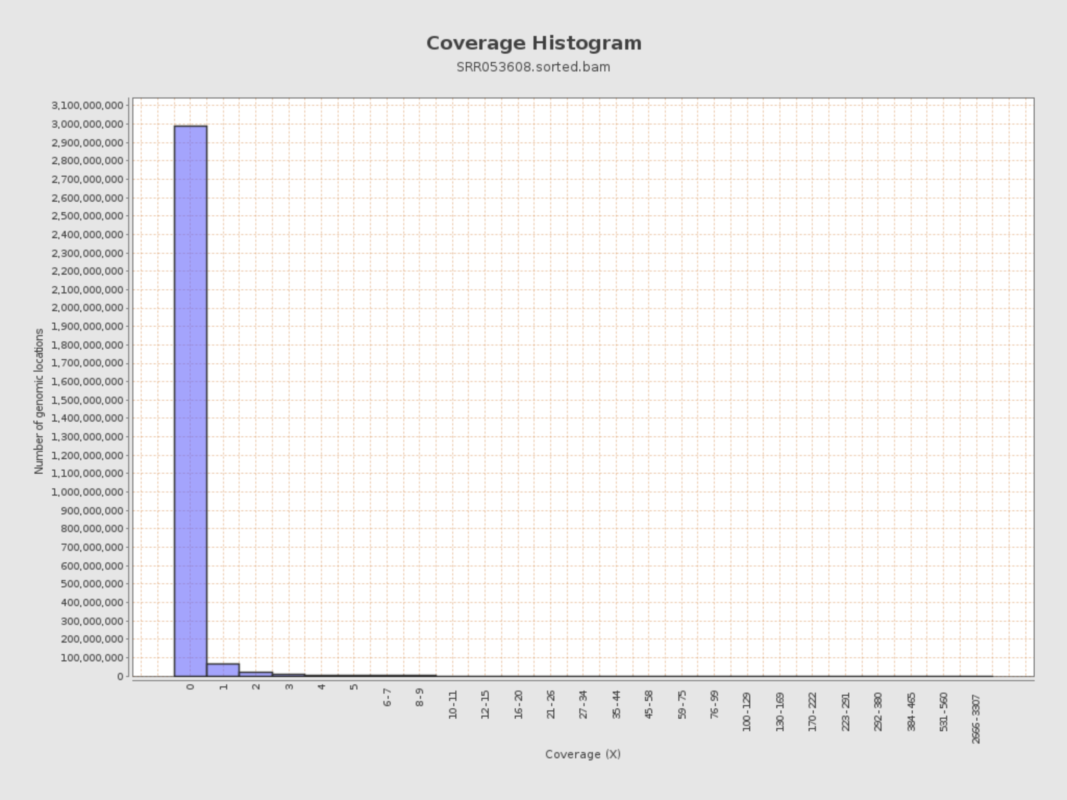
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17118201	0.0687	0.6272
chr2	243199373	18656874	0.0767	2.4511
chr3	198022430	15070865	0.0761	0.5888
chr4	191154276	14208655	0.0743	0.6016
chr5	180915260	13596738	0.0752	0.5904
chr6	171115067	13028129	0.0761	0.6289
chr7	159138663	11769189	0.074	0.6665

chr8	146364022	11255378	0.0769	0.6537
chr9	141213431	8943435	0.0633	0.5561
chr10	135534747	10143064	0.0748	0.6084
chr11	135006516	9837392	0.0729	0.6359
chr12	133851895	9968969	0.0745	0.5928
chr13	115169878	7162791	0.0622	0.5427
chr14	107349540	6639204	0.0618	0.5901
chr15	102531392	6171940	0.0602	0.5122
chr16	90354753	5952547	0.0659	0.5556
chr17	81195210	5533944	0.0682	0.5614
chr18	78077248	5697079	0.073	0.6407
chr19	59128983	3817994	0.0646	0.5959
chr20	63025520	4447554	0.0706	0.5665
chr21	48129895	2777781	0.0577	0.5342
chr22	51304566	2288597	0.0446	0.4298
chrMT	16571	54745	3.3037	5.5317
chrX	155270560	12843624	0.0827	0.6613
chrY	59373566	556719	0.0094	0.1927

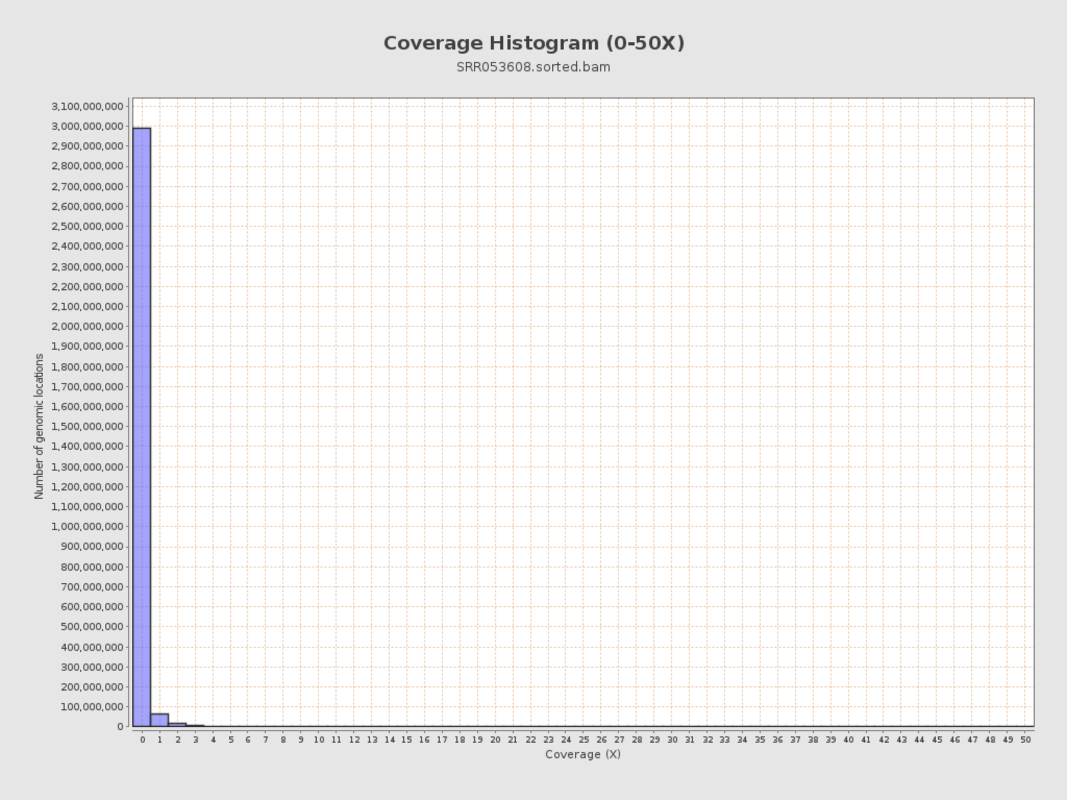
3. Results : Coverage across reference



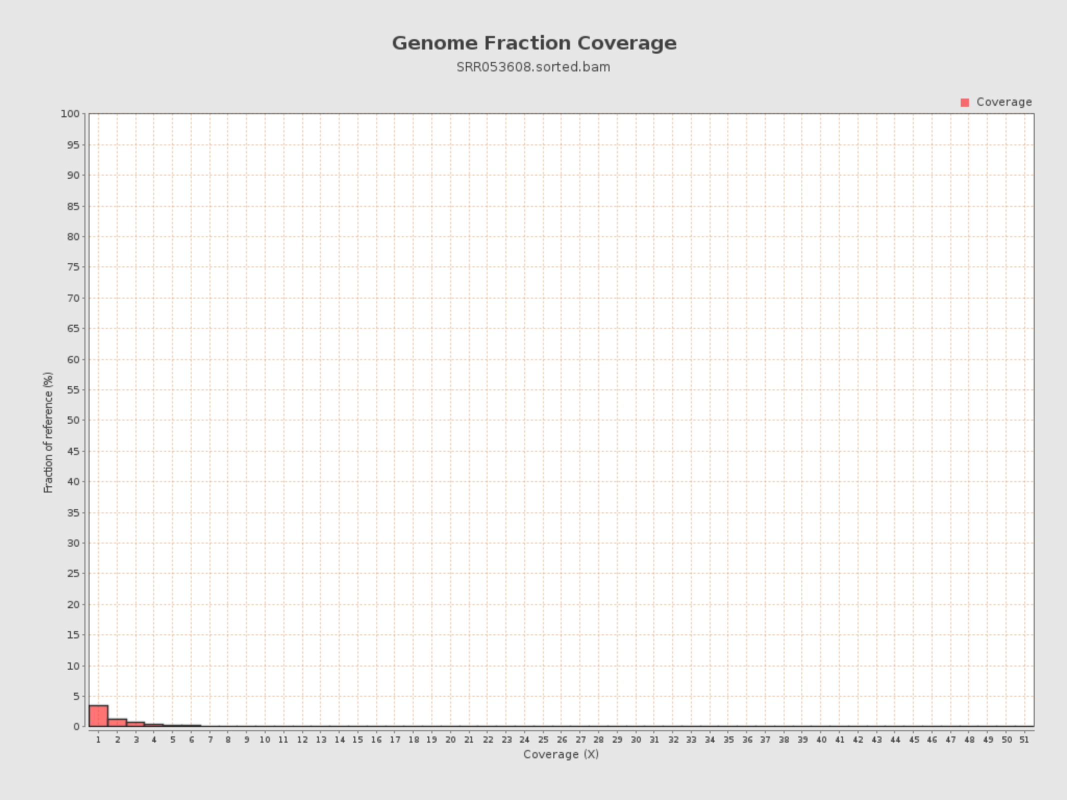
4. Results : Coverage Histogram



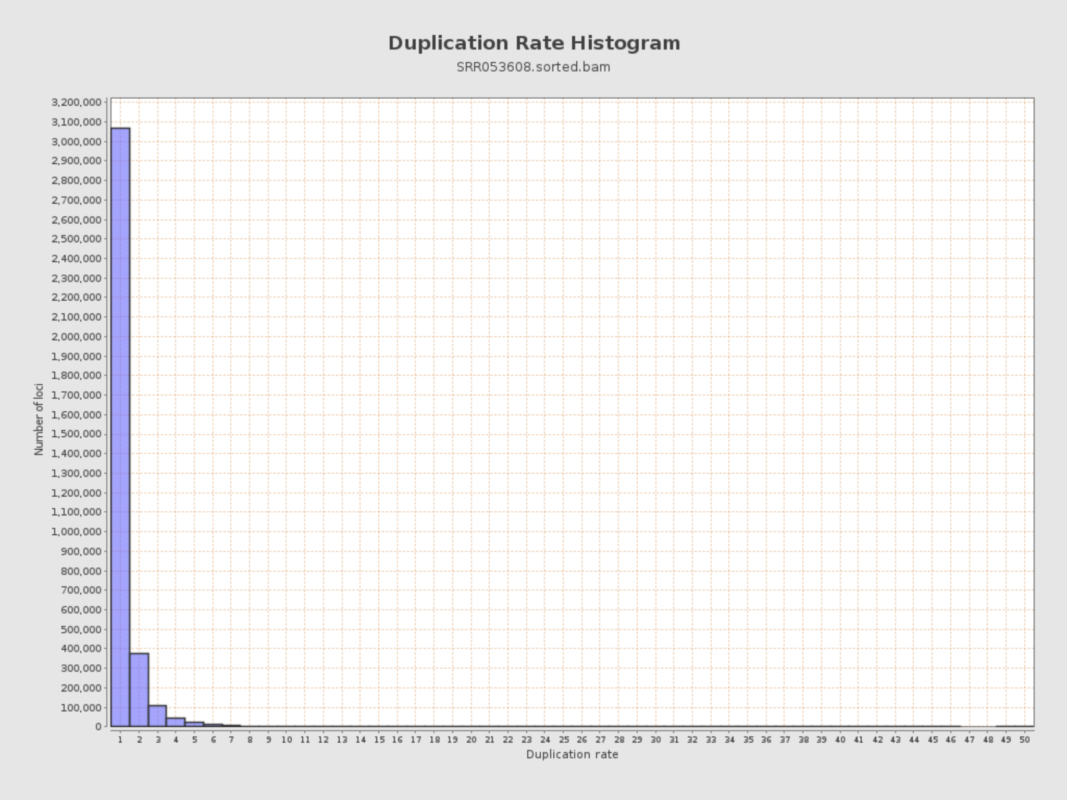
5. Results : Coverage Histogram (0-50X)



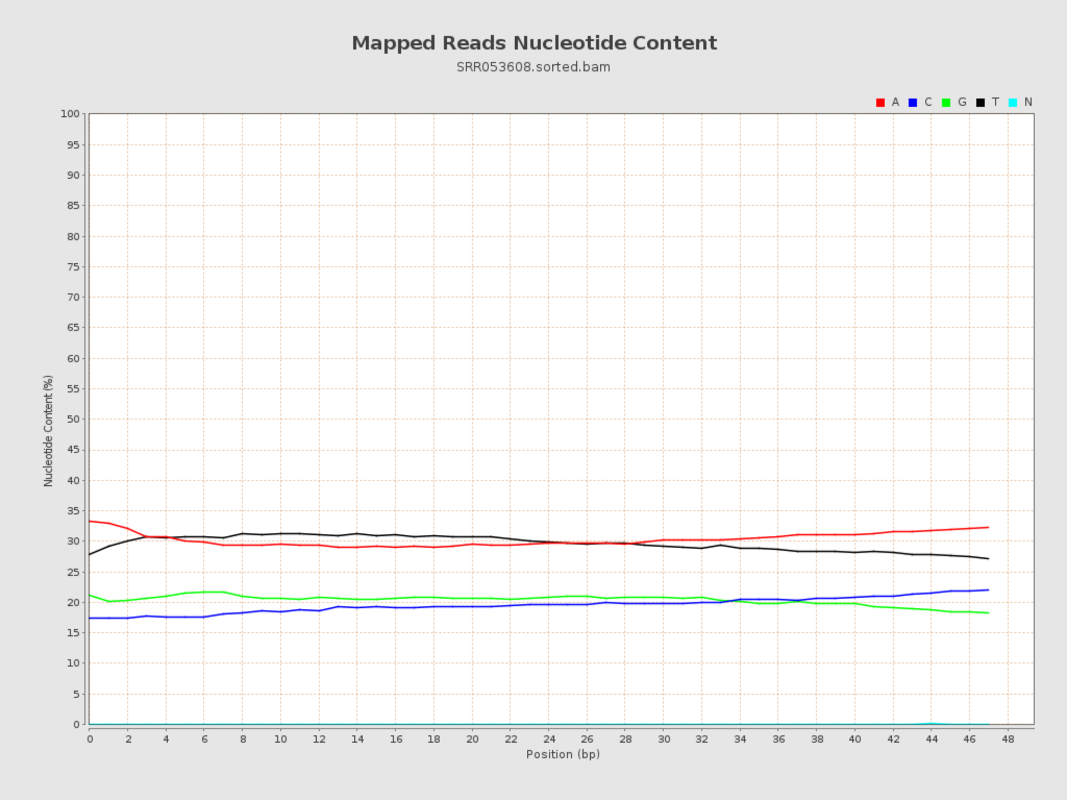
6. Results : Genome Fraction Coverage



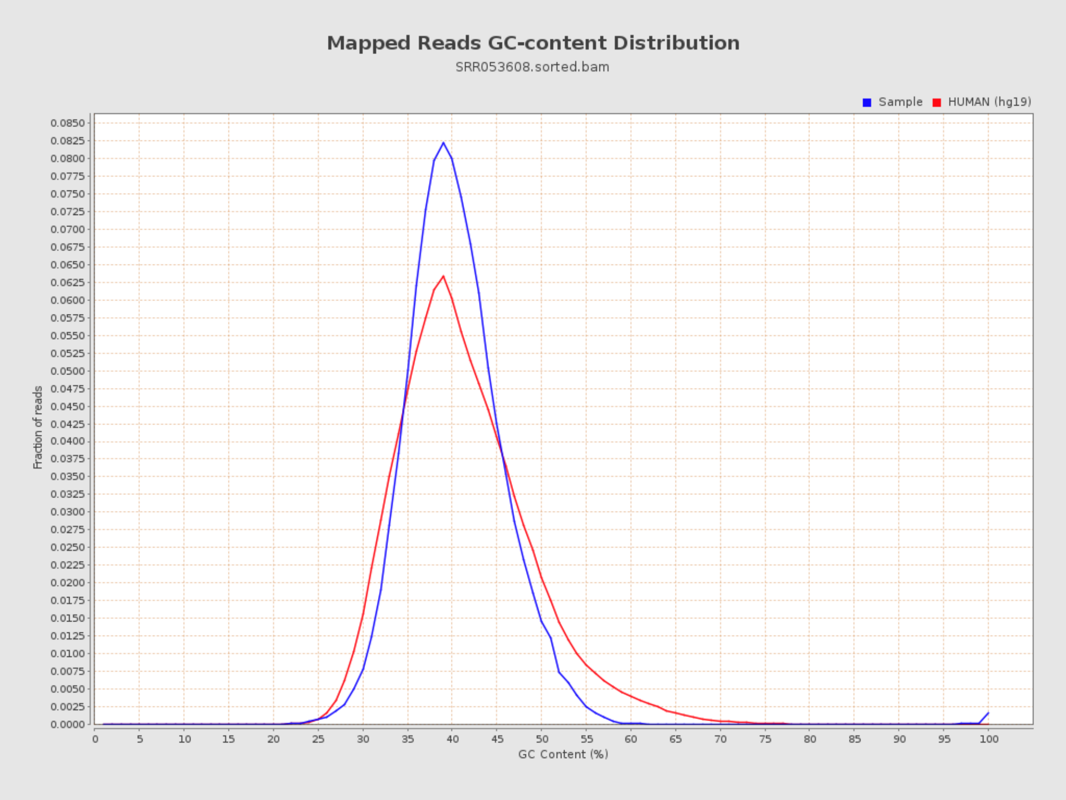
7. Results : Duplication Rate Histogram



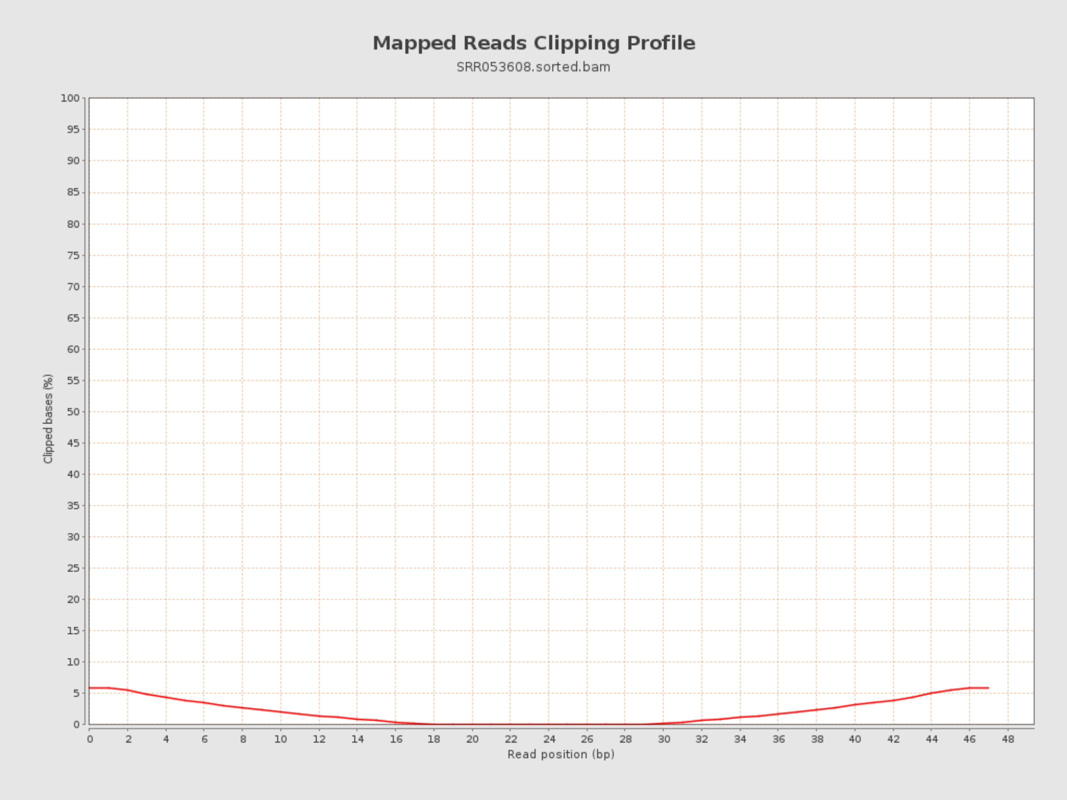
8. Results : Mapped Reads Nucleotide Content



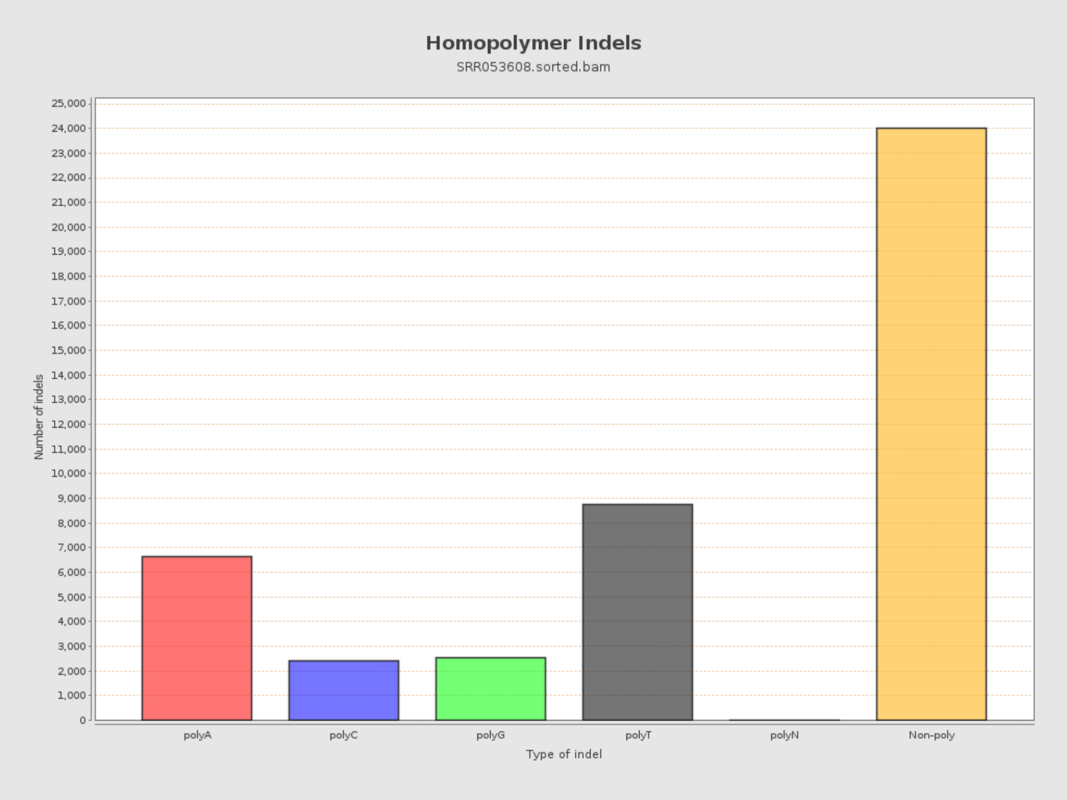
9. Results : Mapped Reads GC-content Distribution



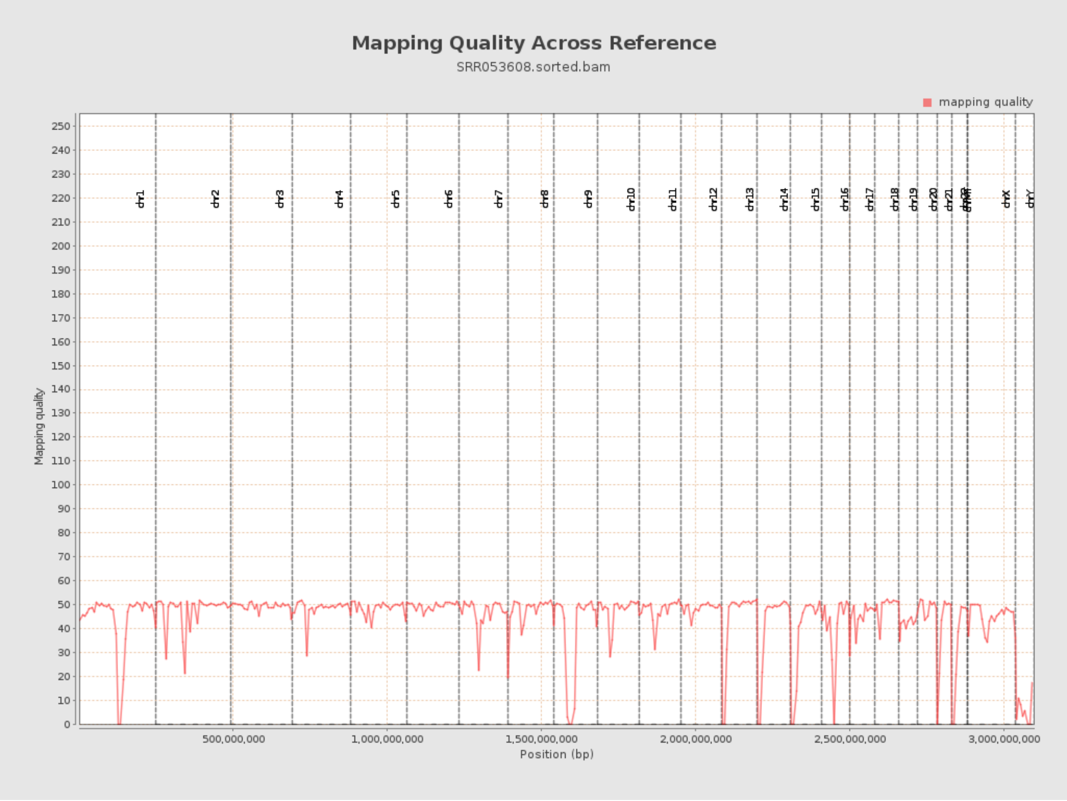
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram