Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:06:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068132.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_SRR6068132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:06:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,429,046
Mapped reads	1,222,167 / 85.52%
Unmapped reads	206,879 / 14.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,758 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	140,959 / 9.86%
Duplication rate	9.37%
Clipped reads	286,581 / 20.05%

2.2. ACGT Content

Number/percentage of A's	25,674,497 / 29.38%
Number/percentage of C's	16,923,967 / 19.37%
Number/percentage of T's	26,912,725 / 30.8%
Number/percentage of G's	17,826,432 / 20.4%
Number/percentage of N's	52,529 / 0.06%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.5001

2.4. Mapping Quality

Mean Mapping Quality	47.94

2.5. Mismatches and indels

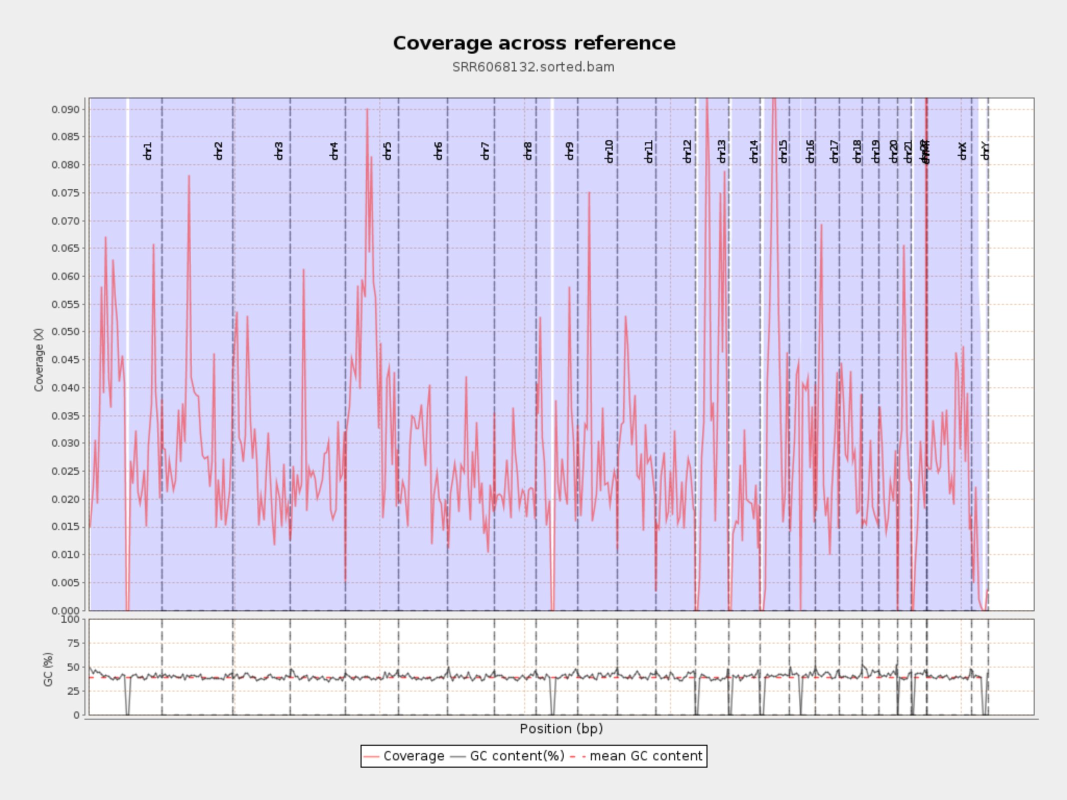
General error rate	0.91%
Mismatches	782,075
Insertions	7,328
Mapped reads with at least one insertion	0.6%
Deletions	21,169
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.04%

2.6. Chromosome stats

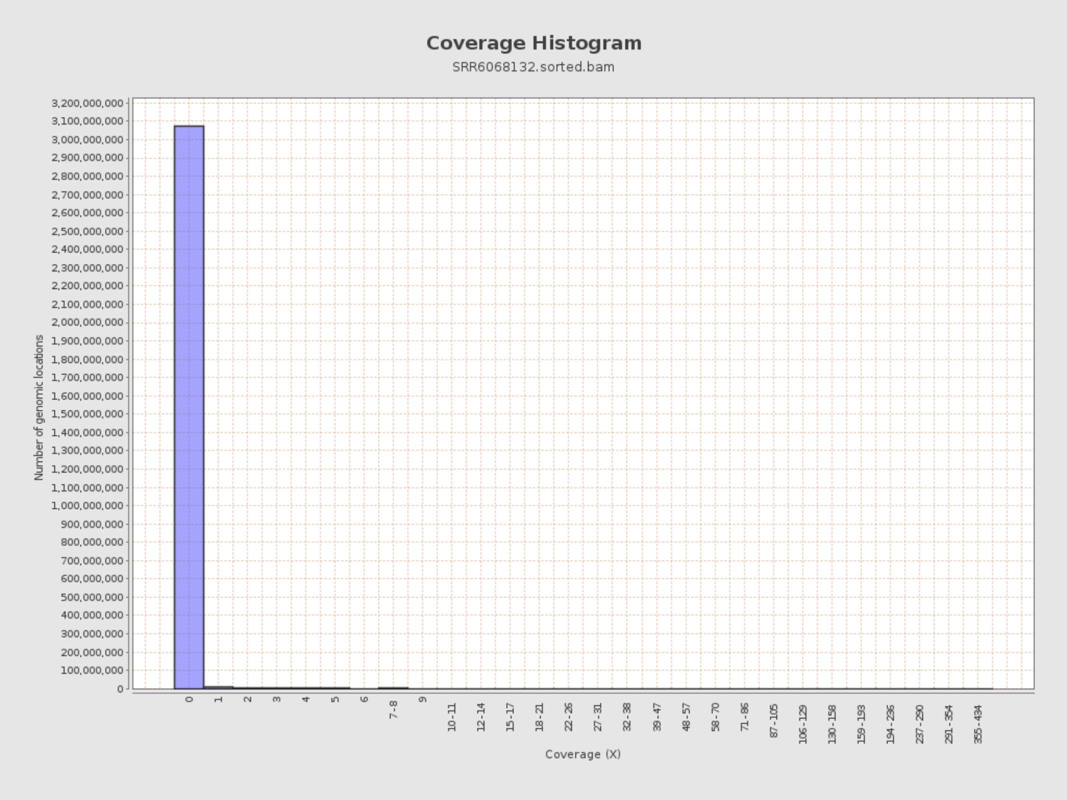
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8356907	0.0335	0.6295
chr2	243199373	7372285	0.0303	0.5188
chr3	198022430	5352617	0.027	0.4601
chr4	191154276	4781486	0.025	0.469
chr5	180915260	8246615	0.0456	0.5959
chr6	171115067	4377053	0.0256	0.4626
chr7	159138663	3537211	0.0222	0.486

chr8	146364022	3200217	0.0219	0.4565
chr9	141213431	3701604	0.0262	0.4567
chr10	135534747	3693381	0.0273	0.5762
chr11	135006516	4096491	0.0303	0.474
chr12	133851895	2794155	0.0209	0.3996
chr13	115169878	4707218	0.0409	0.5708
chr14	107349540	1762600	0.0164	0.3478
chr15	102531392	4125517	0.0402	0.5858
chr16	90354753	2720646	0.0301	0.4833
chr17	81195210	2323519	0.0286	0.4779
chr18	78077248	2401195	0.0308	0.5613
chr19	59128983	1147631	0.0194	0.4681
chr20	63025520	1448302	0.023	0.4145
chr21	48129895	1522929	0.0316	0.508
chr22	51304566	799120	0.0156	0.3359
chrMT	16571	19046	1.1494	2.4925
chrX	155270560	4633988	0.0298	0.4786
chrY	59373566	304388	0.0051	0.2243

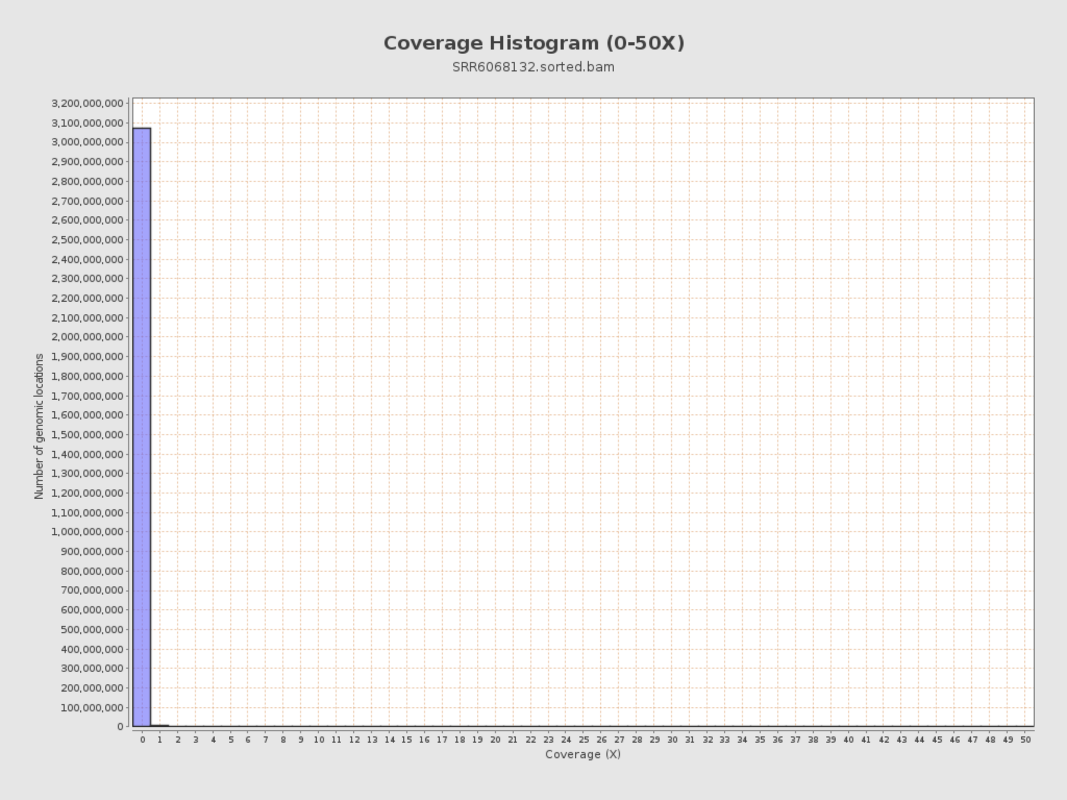
3. Results : Coverage across reference



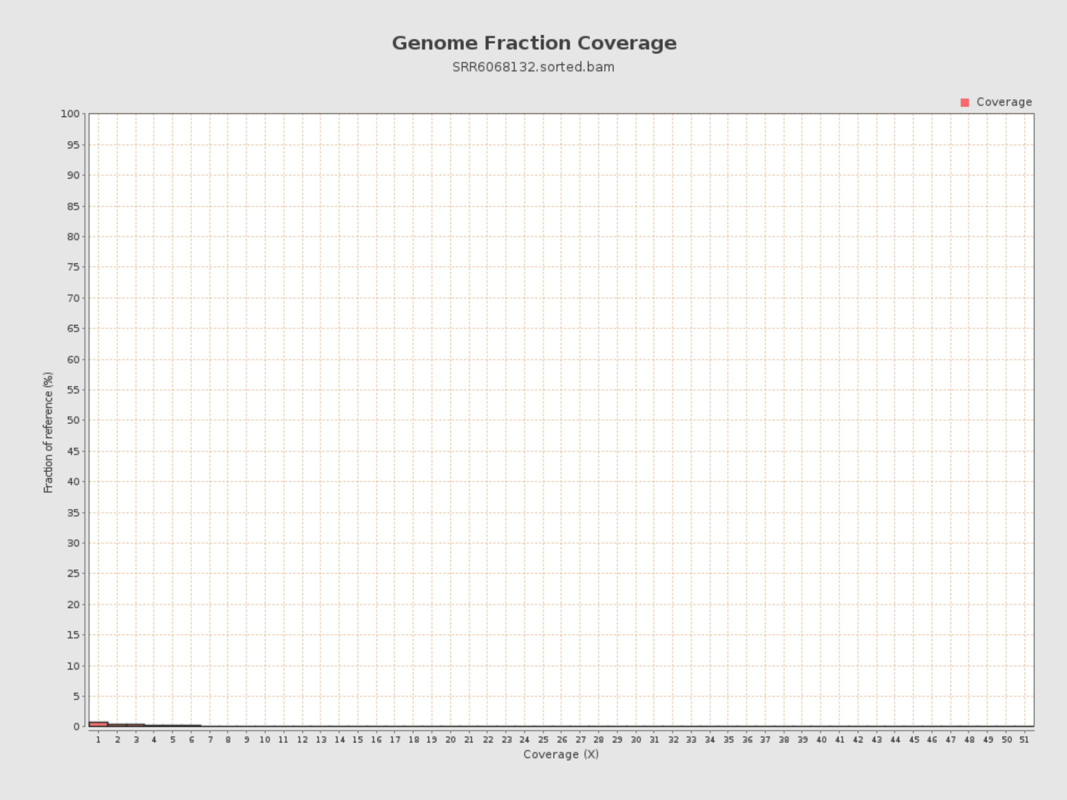
4. Results : Coverage Histogram



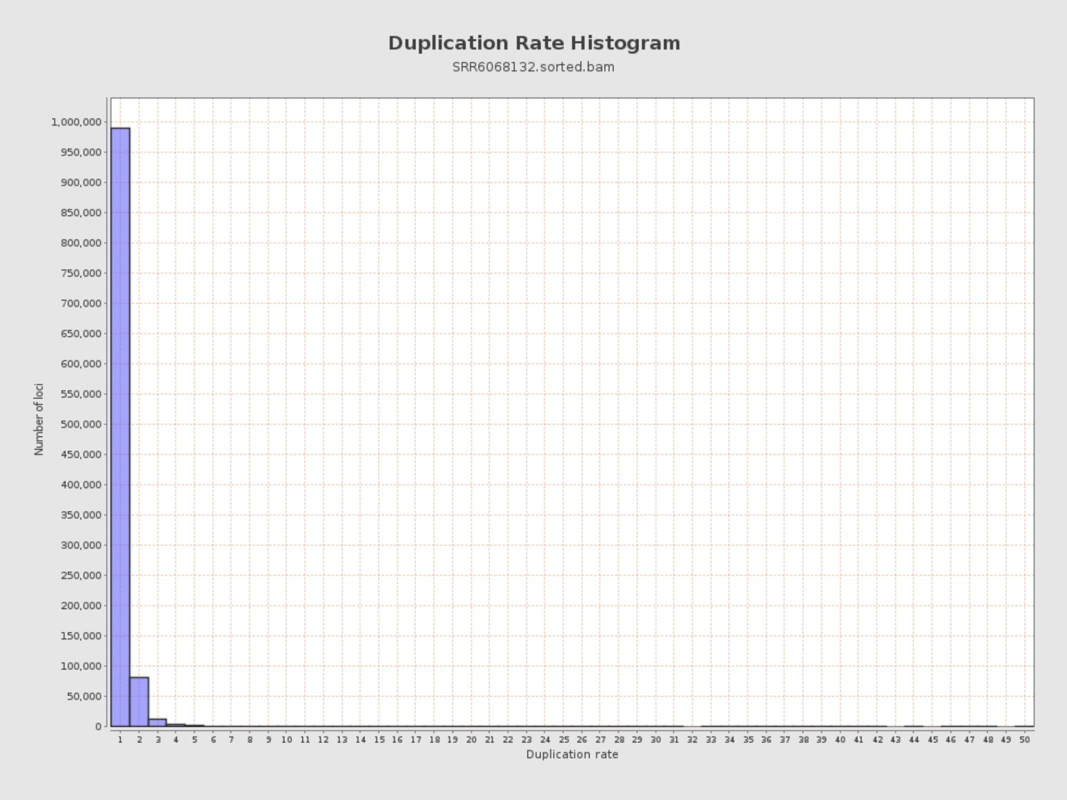
5. Results : Coverage Histogram (0-50X)



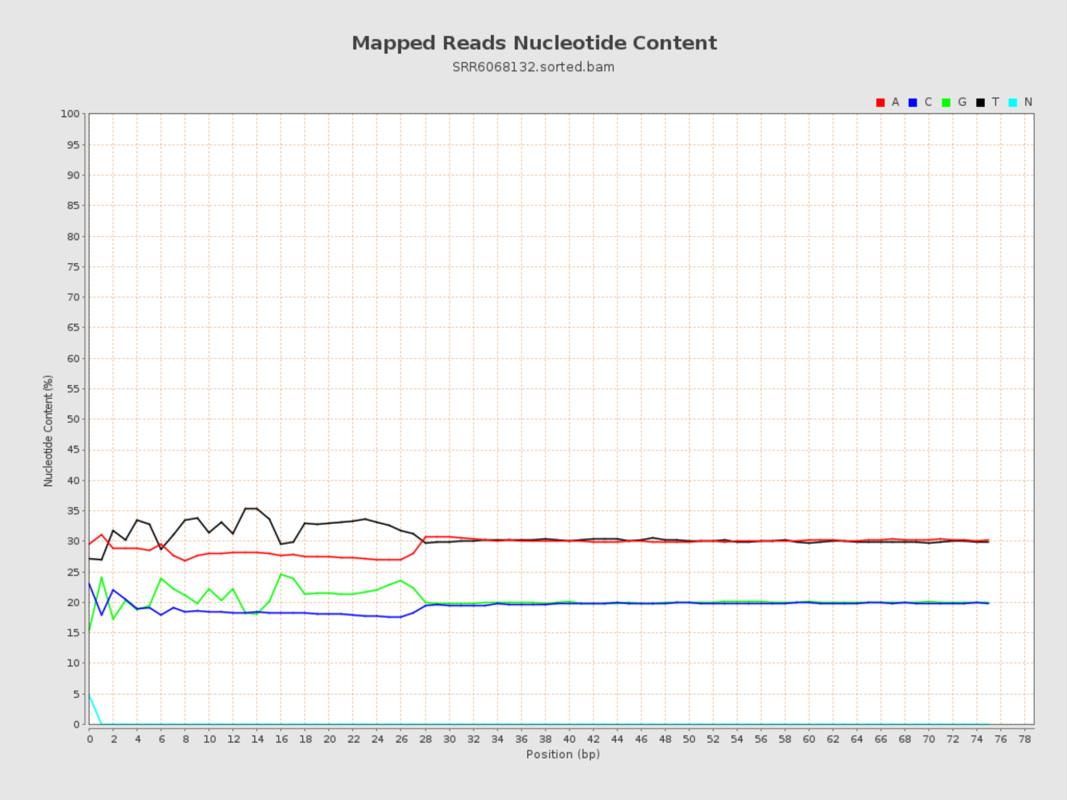
6. Results : Genome Fraction Coverage



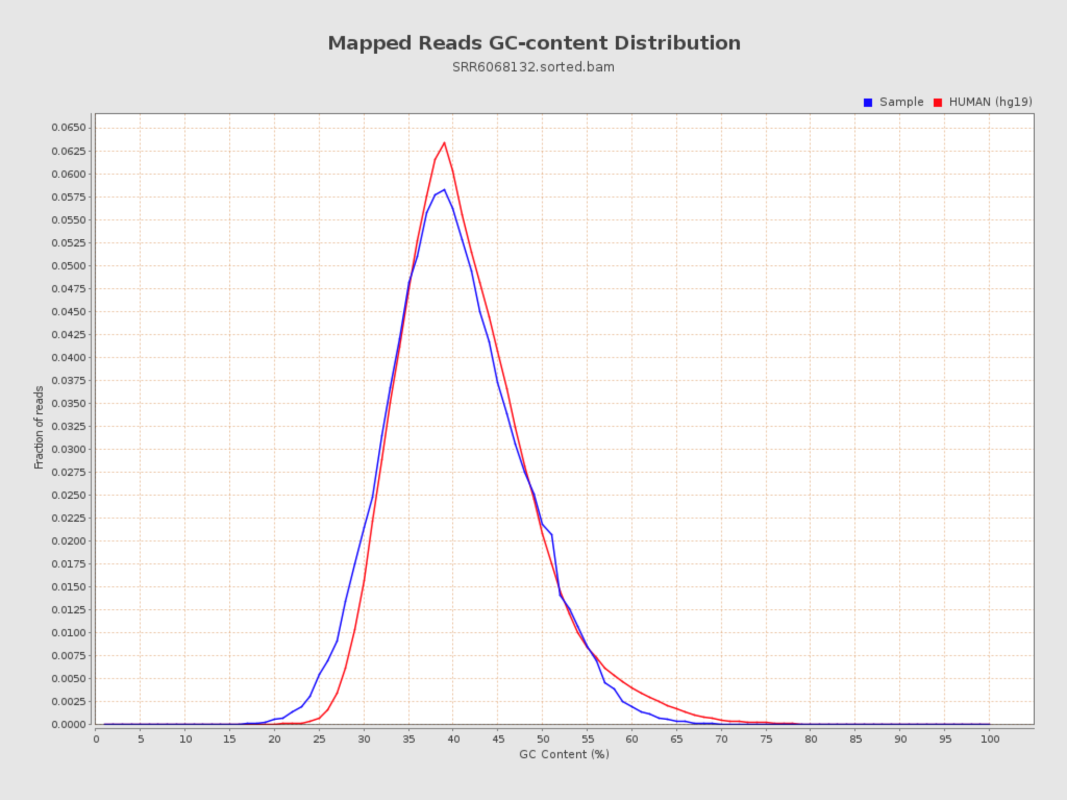
7. Results : Duplication Rate Histogram



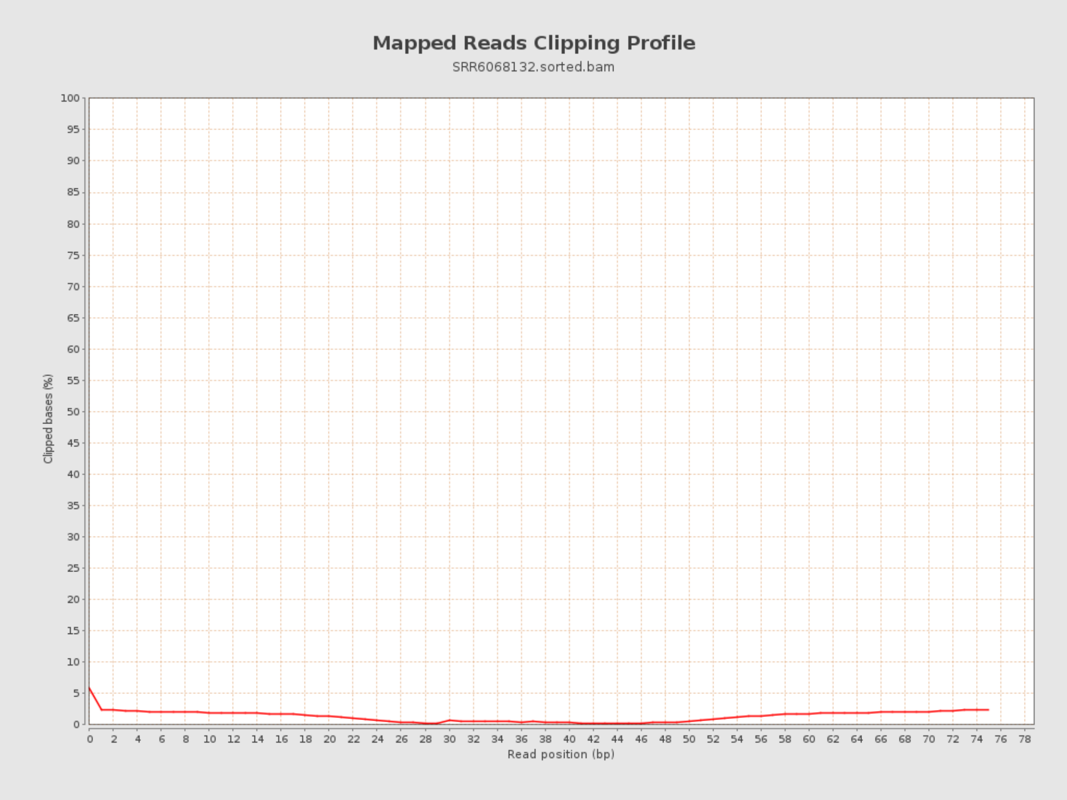
8. Results : Mapped Reads Nucleotide Content



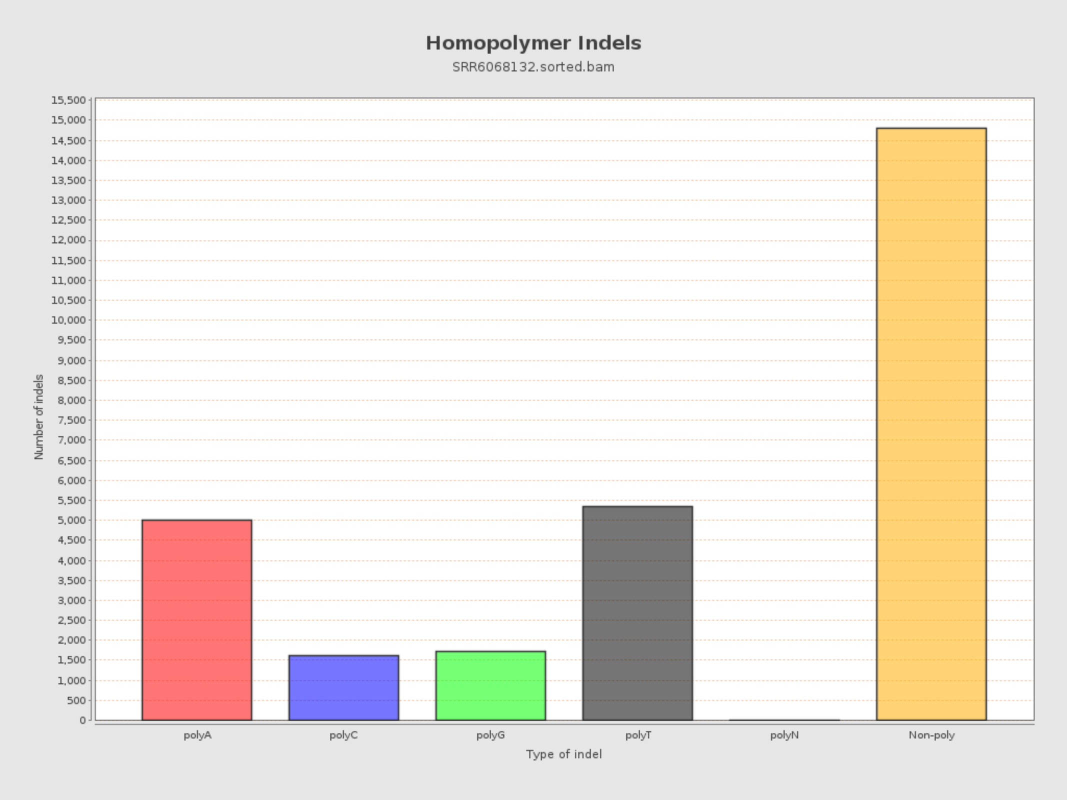
9. Results : Mapped Reads GC-content Distribution



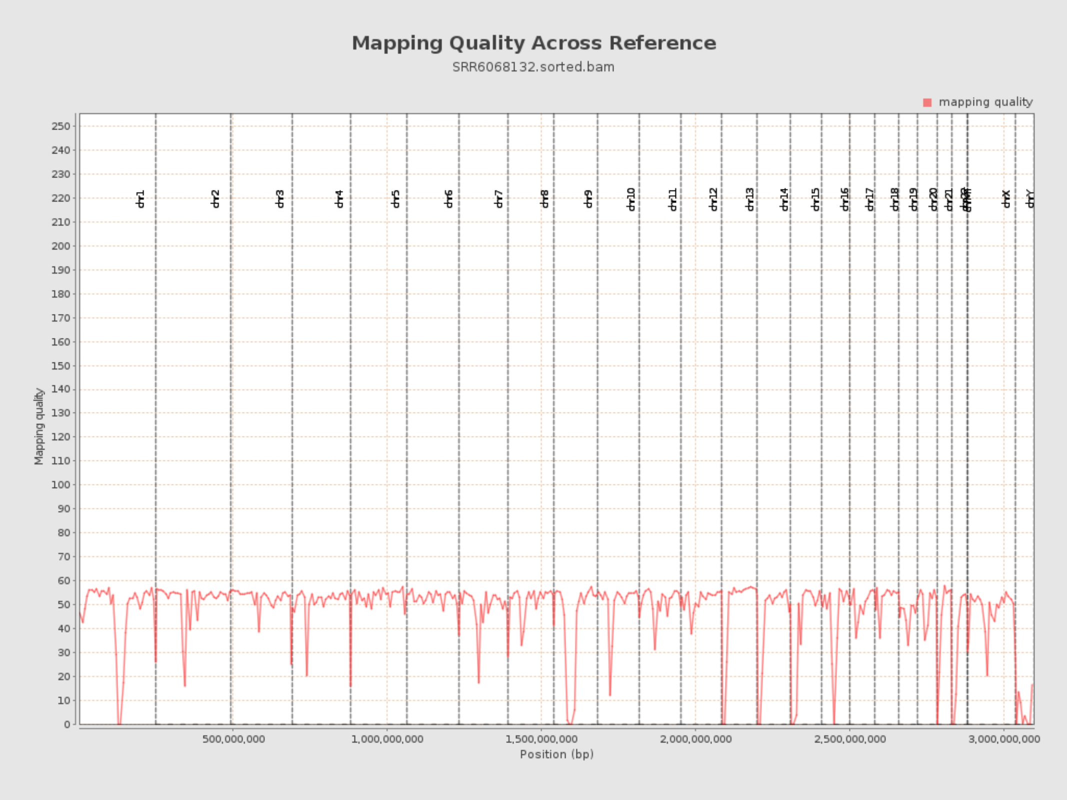
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram