Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:52:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068111.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_SRR6068111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:52:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,309,051
Mapped reads	3,646,913 / 84.63%
Unmapped reads	662,138 / 15.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,647 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	365,306 / 8.48%
Duplication rate	8.37%
Clipped reads	1,573,491 / 36.52%

2.2. ACGT Content

Number/percentage of A's	67,438,693 / 27.81%
Number/percentage of C's	43,798,286 / 18.06%
Number/percentage of T's	78,443,027 / 32.35%
Number/percentage of G's	52,784,145 / 21.77%
Number/percentage of N's	29,240 / 0.01%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0784

Standard Deviation	0.8017

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Mismatches and indels

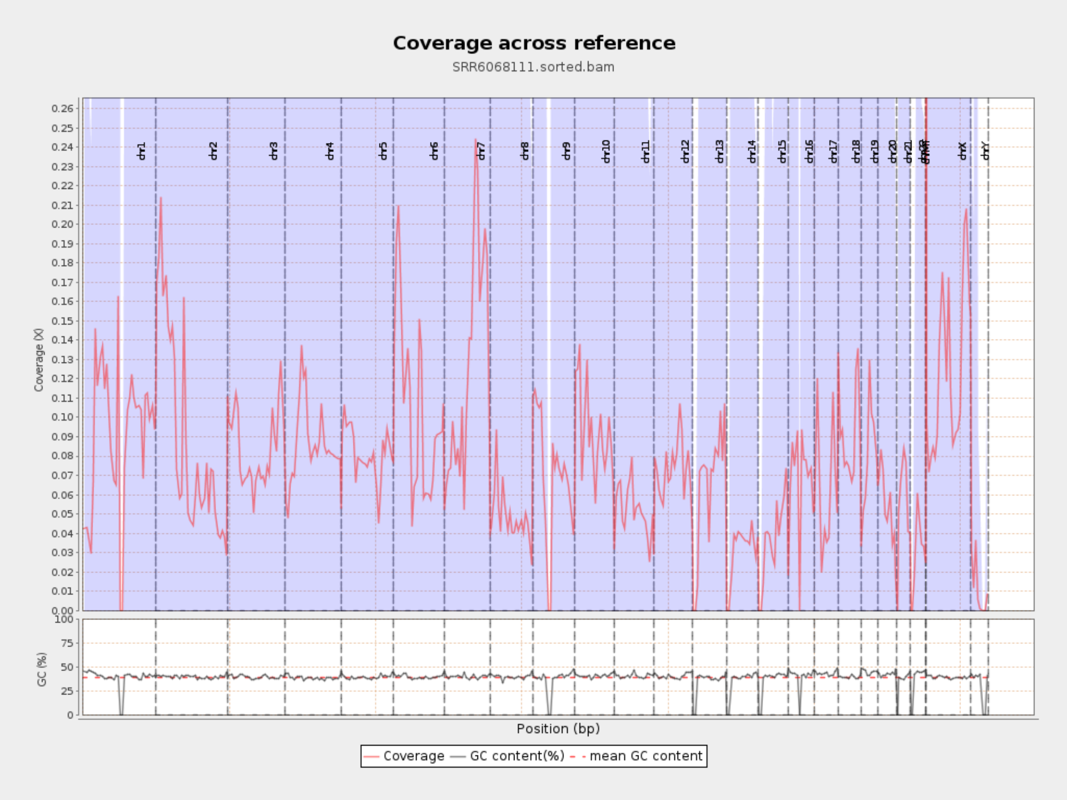
General error rate	0.56%
Mismatches	1,327,658
Insertions	16,872
Mapped reads with at least one insertion	0.46%
Deletions	61,987
Mapped reads with at least one deletion	1.68%
Homopolymer indels	45.29%

2.6. Chromosome stats

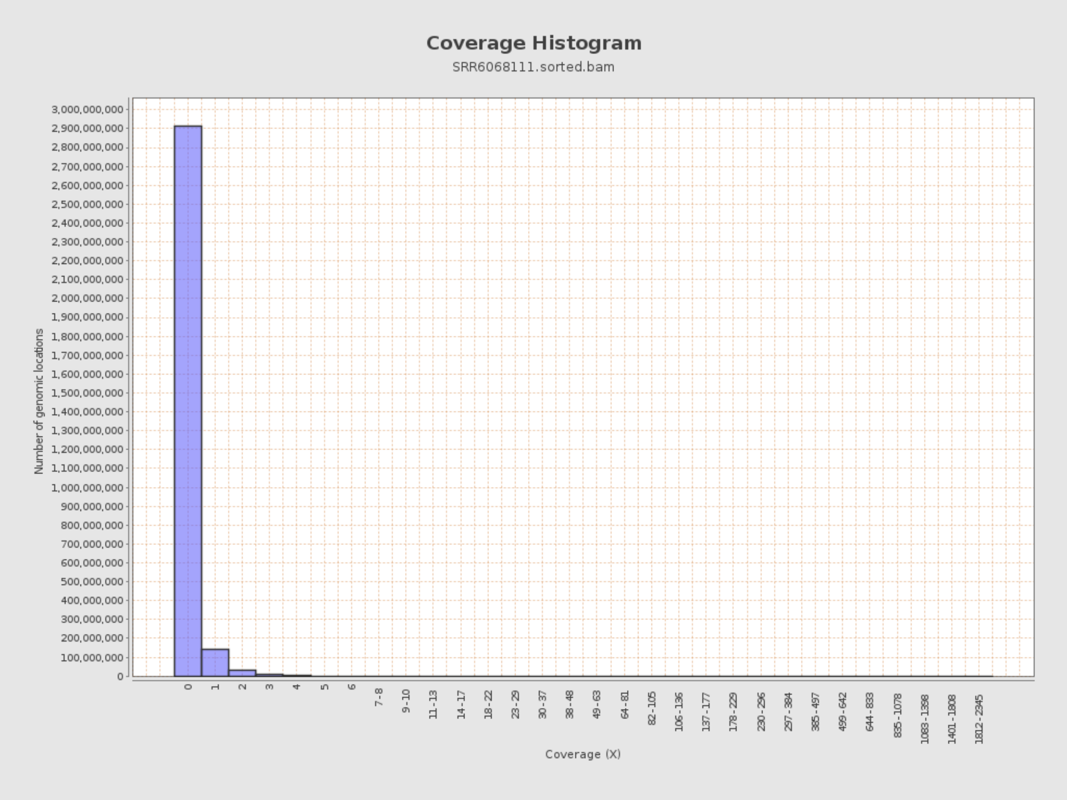
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22620054	0.0908	1.9779
chr2	243199373	21847775	0.0898	0.7666
chr3	198022430	16612540	0.0839	0.3646
chr4	191154276	16600259	0.0868	0.3976
chr5	180915260	14665381	0.0811	0.362
chr6	171115067	17998081	0.1052	0.4792
chr7	159138663	20138407	0.1265	0.7492

chr8	146364022	7112368	0.0486	1.2494
chr9	141213431	9739283	0.069	0.6128
chr10	135534747	12617405	0.0931	0.6013
chr11	135006516	7126552	0.0528	0.412
chr12	133851895	9840203	0.0735	0.3743
chr13	115169878	7424697	0.0645	0.3252
chr14	107349540	3370299	0.0314	0.3008
chr15	102531392	3769498	0.0368	0.2621
chr16	90354753	6022133	0.0666	0.372
chr17	81195210	5281396	0.065	0.3628
chr18	78077248	7177570	0.0919	0.985
chr19	59128983	4826442	0.0816	1.2625
chr20	63025520	3446640	0.0547	0.3209
chr21	48129895	2672091	0.0555	0.3288
chr22	51304566	1539155	0.03	0.2133
chrMT	16571	168755	10.1838	6.9326
chrX	155270560	19335956	0.1245	0.5207
chrY	59373566	650618	0.011	0.3607

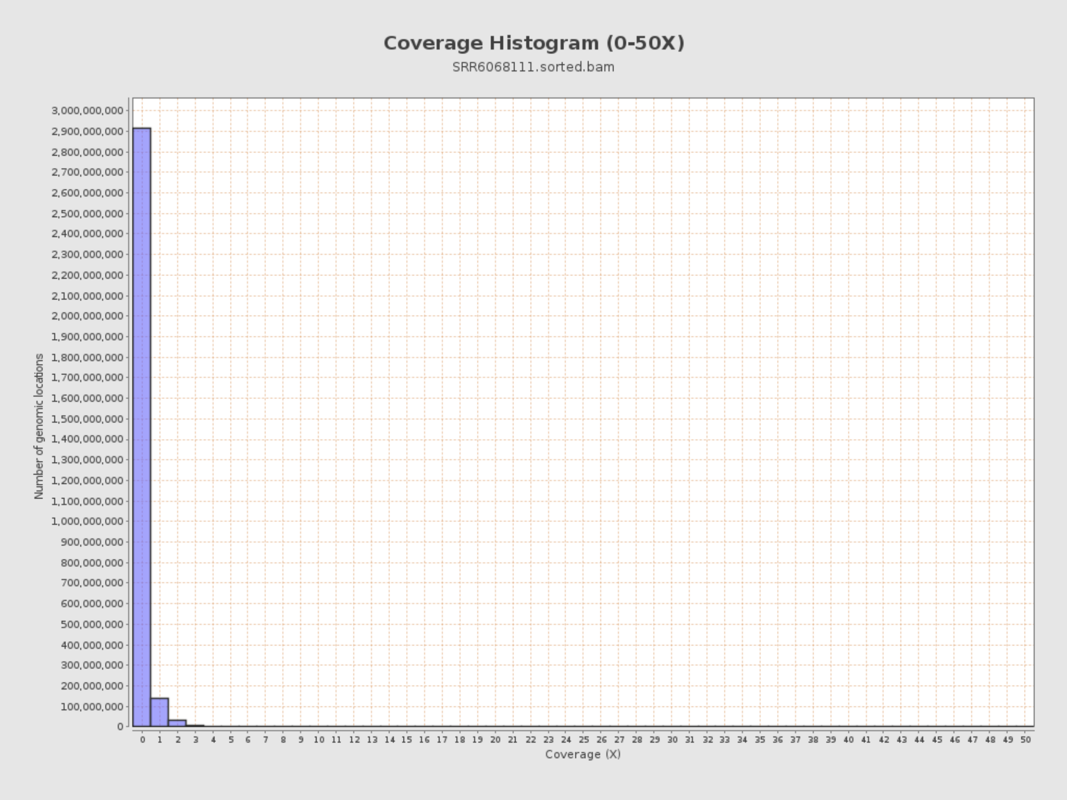
3. Results : Coverage across reference



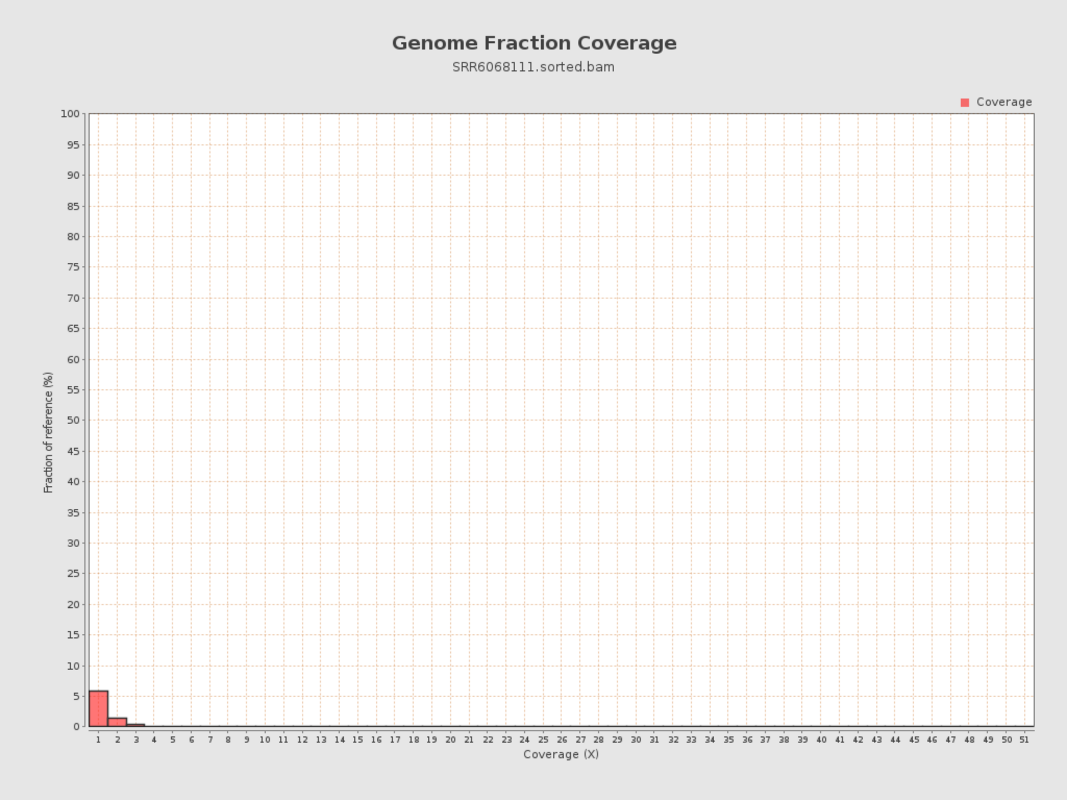
4. Results : Coverage Histogram



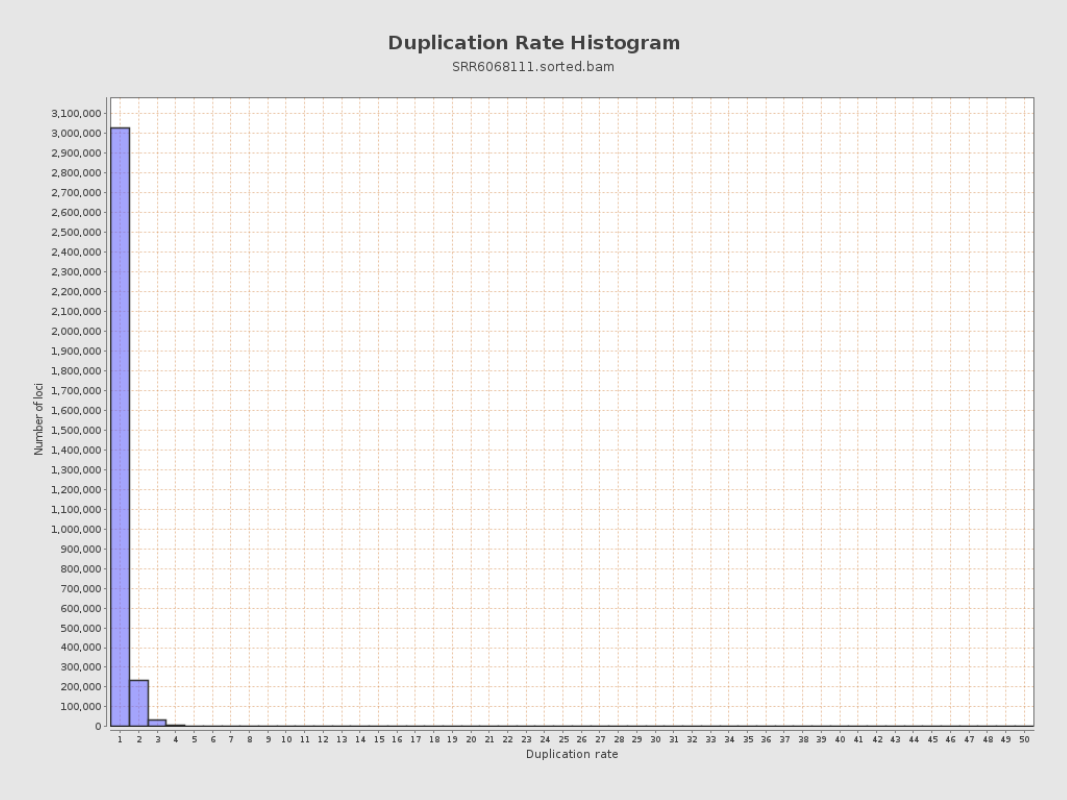
5. Results : Coverage Histogram (0-50X)



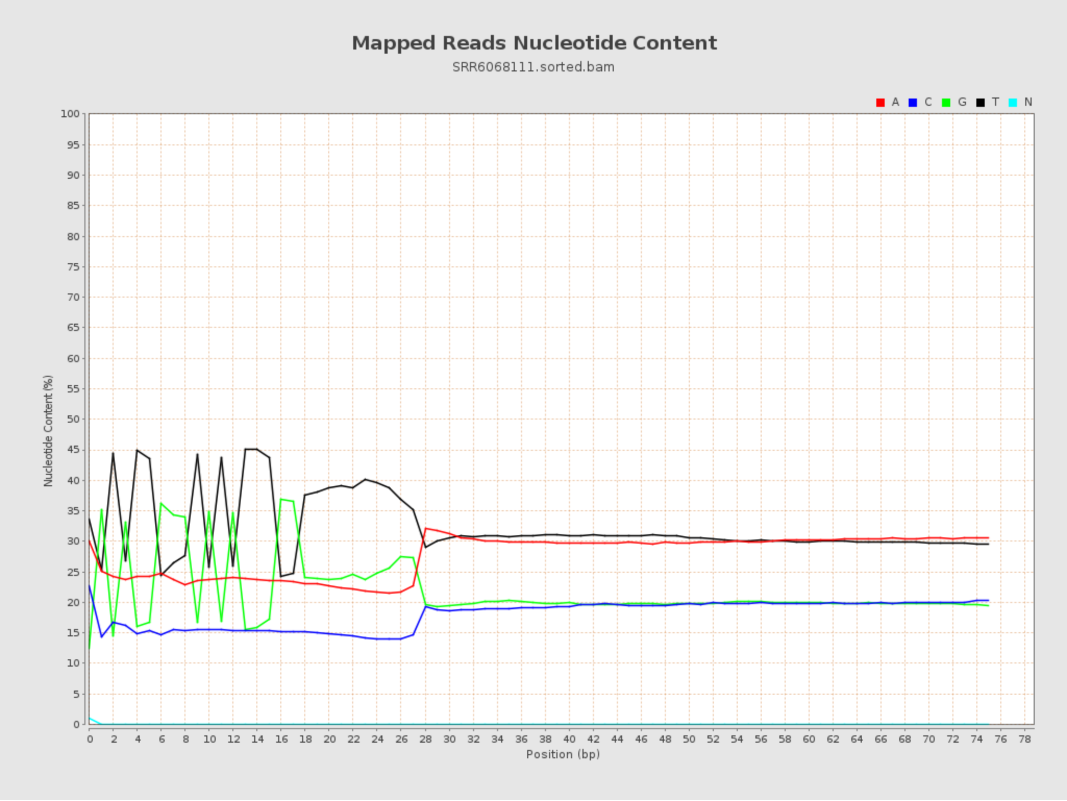
6. Results : Genome Fraction Coverage



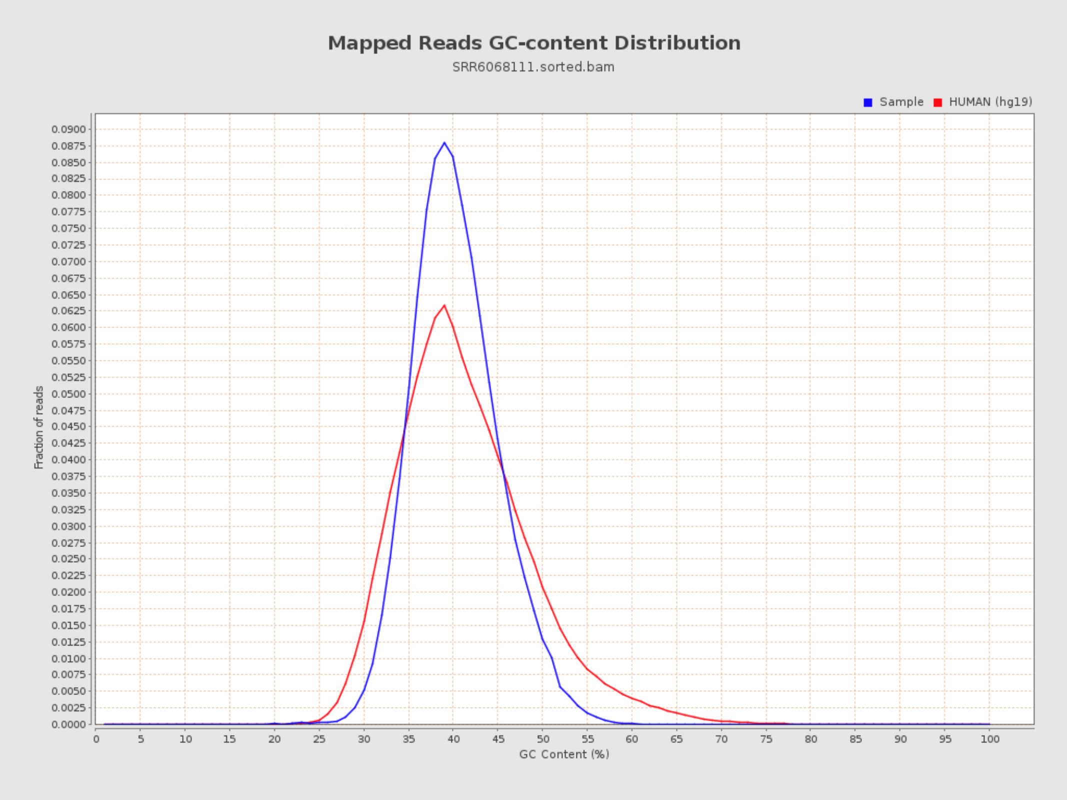
7. Results : Duplication Rate Histogram



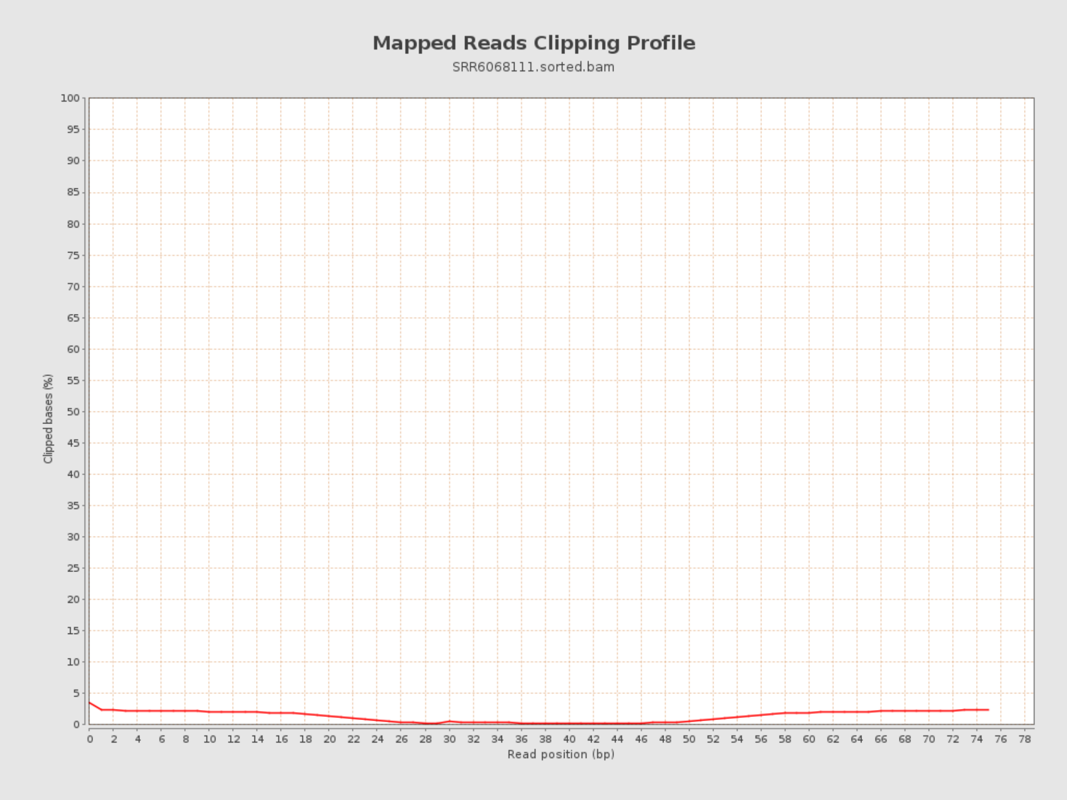
8. Results : Mapped Reads Nucleotide Content



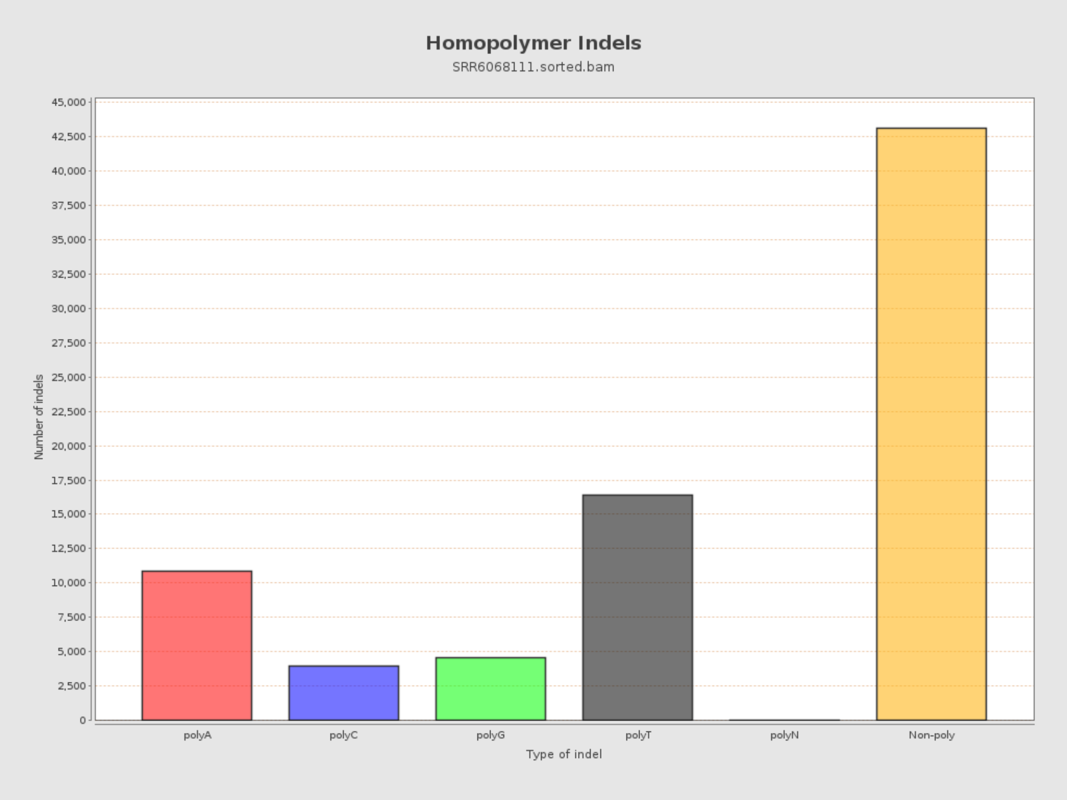
9. Results : Mapped Reads GC-content Distribution



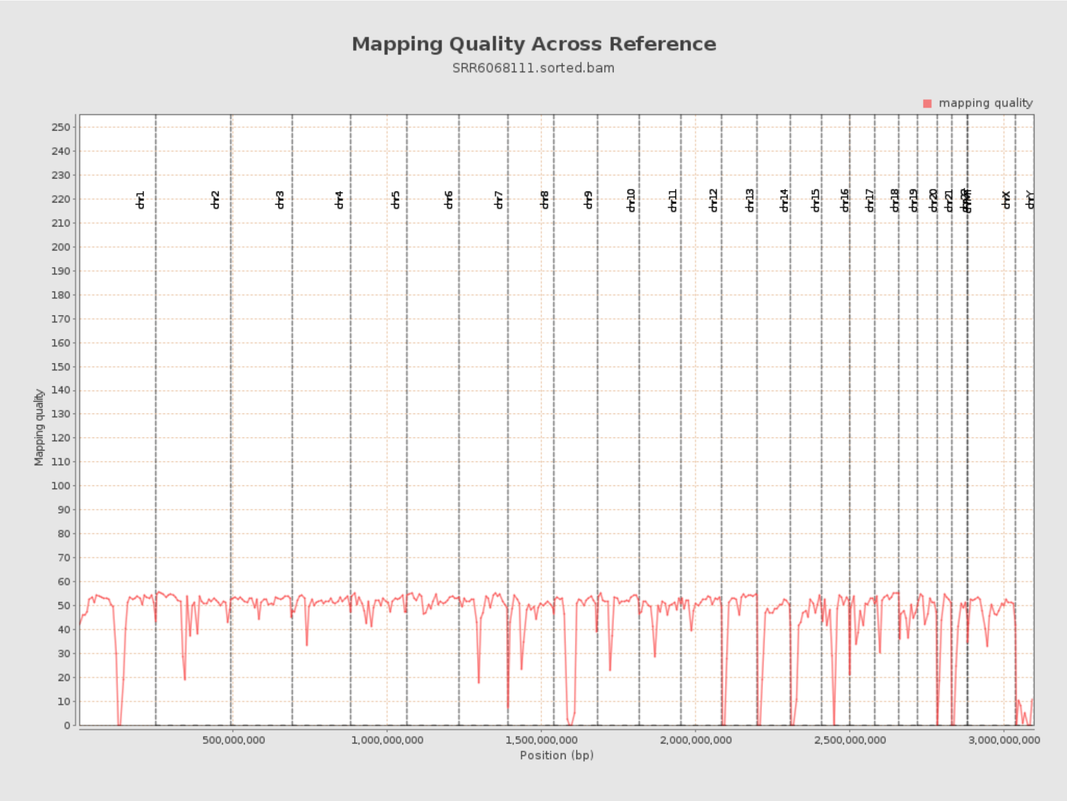
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram