Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068933.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_SRR6068933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068933.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:04:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,321,685
Mapped reads	1,900,995 / 81.88%
Unmapped reads	420,690 / 18.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,010 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	73,813 / 3.18%
Duplication rate	2.81%
Clipped reads	932,801 / 40.18%

2.2. ACGT Content

Number/percentage of A's	33,727,662 / 27.11%
Number/percentage of C's	21,488,414 / 17.27%
Number/percentage of T's	41,170,332 / 33.09%
Number/percentage of G's	27,715,675 / 22.28%
Number/percentage of N's	301,546 / 0.24%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.4216

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

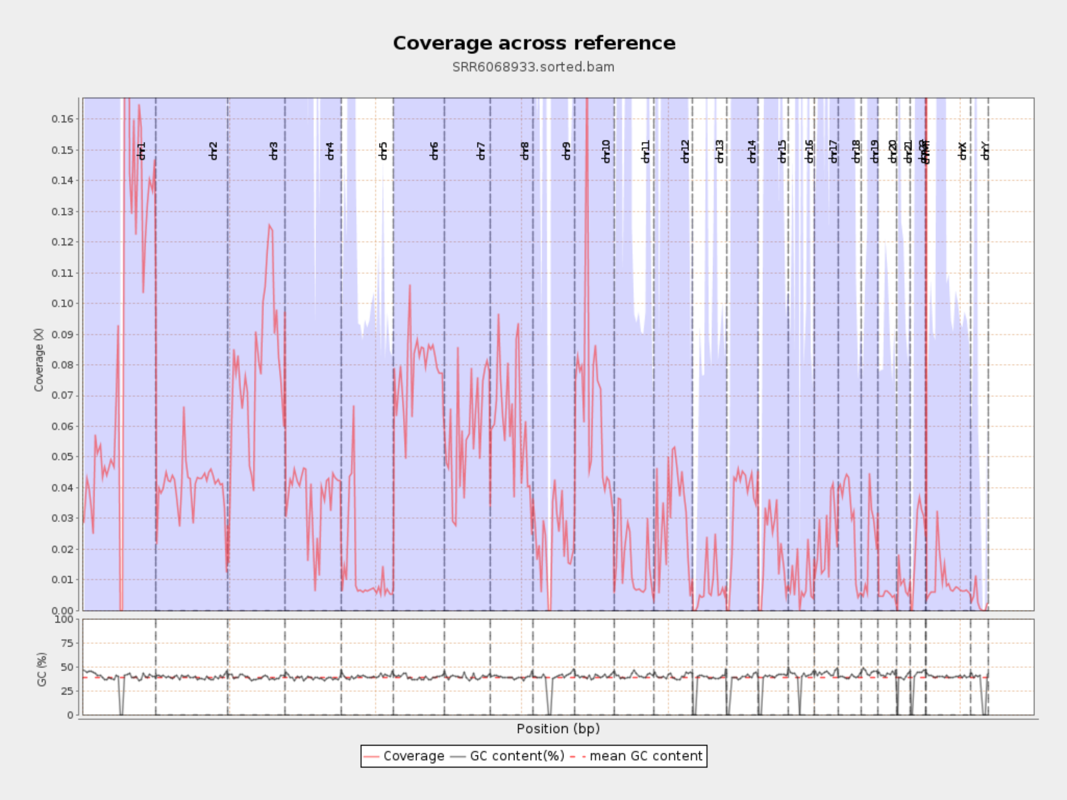
General error rate	0.96%
Mismatches	1,169,514
Insertions	10,782
Mapped reads with at least one insertion	0.56%
Deletions	30,798
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.67%

2.6. Chromosome stats

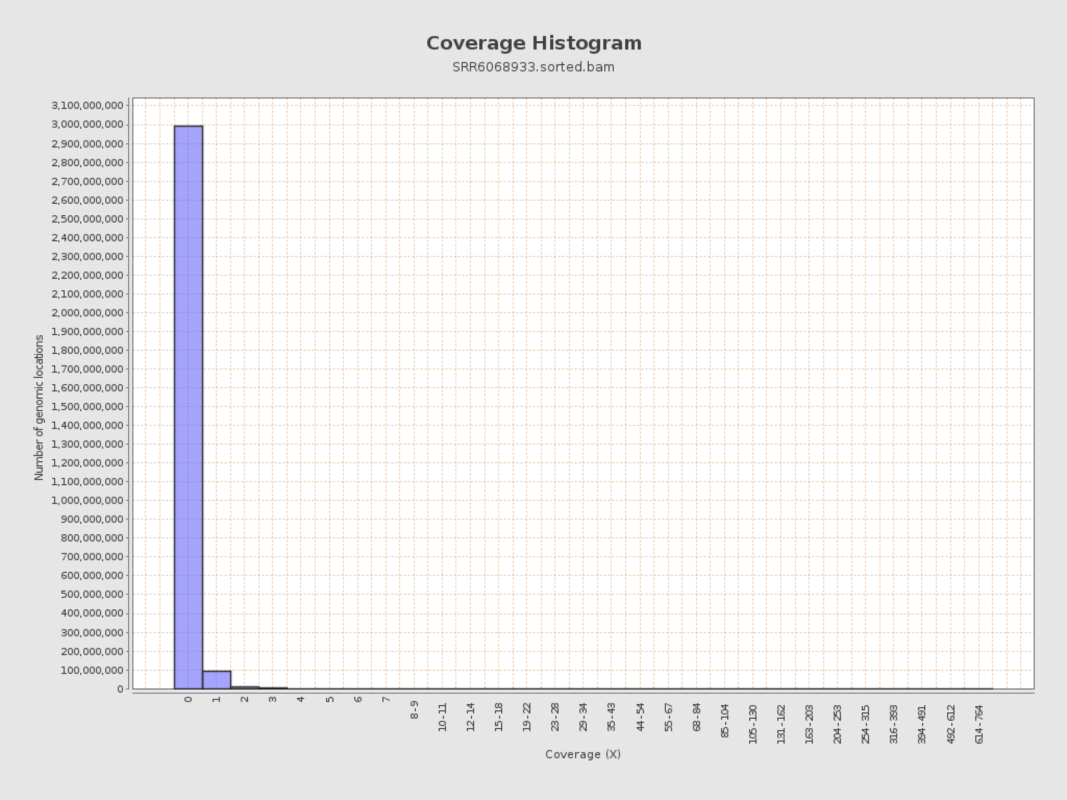
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22766909	0.0913	0.6486
chr2	243199373	9969046	0.041	0.3058
chr3	198022430	15464568	0.0781	0.4229
chr4	191154276	6923729	0.0362	0.2184
chr5	180915260	2380876	0.0132	0.1288
chr6	171115067	13519678	0.079	0.4344
chr7	159138663	9441224	0.0593	0.407

chr8	146364022	8991086	0.0614	0.3812
chr9	141213431	3157590	0.0224	0.2507
chr10	135534747	9170046	0.0677	1.3076
chr11	135006516	2109508	0.0156	0.2321
chr12	133851895	4192190	0.0313	0.2001
chr13	115169878	851290	0.0074	0.0953
chr14	107349540	3745274	0.0349	0.2087
chr15	102531392	1973150	0.0192	0.1548
chr16	90354753	783319	0.0087	0.2001
chr17	81195210	1911878	0.0235	0.1788
chr18	78077248	2356198	0.0302	0.3943
chr19	59128983	1211640	0.0205	0.3418
chr20	63025520	319050	0.0051	0.0854
chr21	48129895	415148	0.0086	0.1158
chr22	51304566	1177596	0.023	0.1702
chrMT	16571	40246	2.4287	2.0339
chrX	155270560	1403272	0.009	0.1338
chrY	59373566	179844	0.003	0.0955

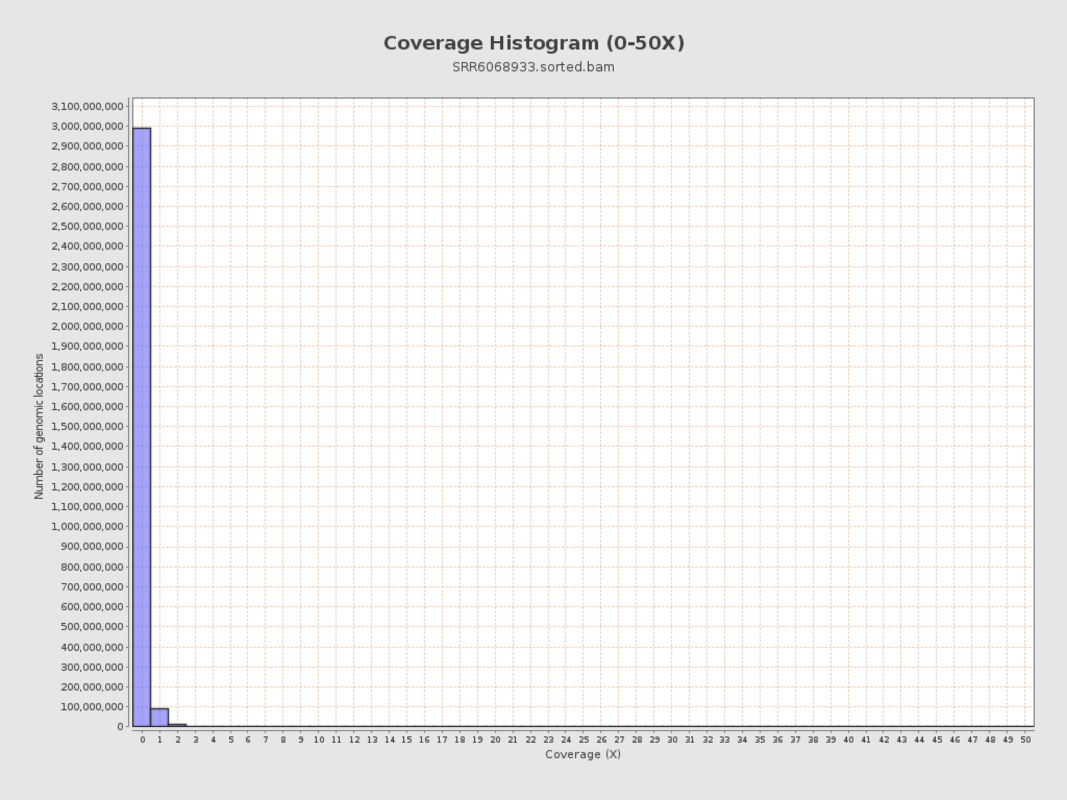
3. Results : Coverage across reference



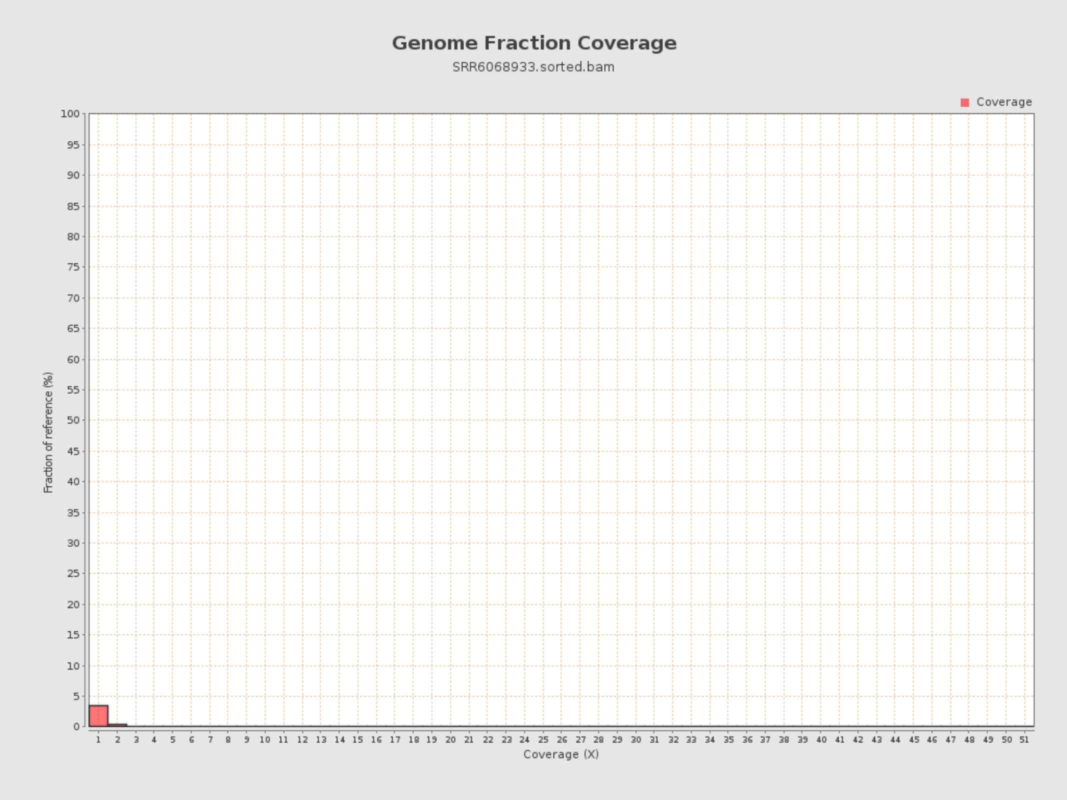
4. Results : Coverage Histogram



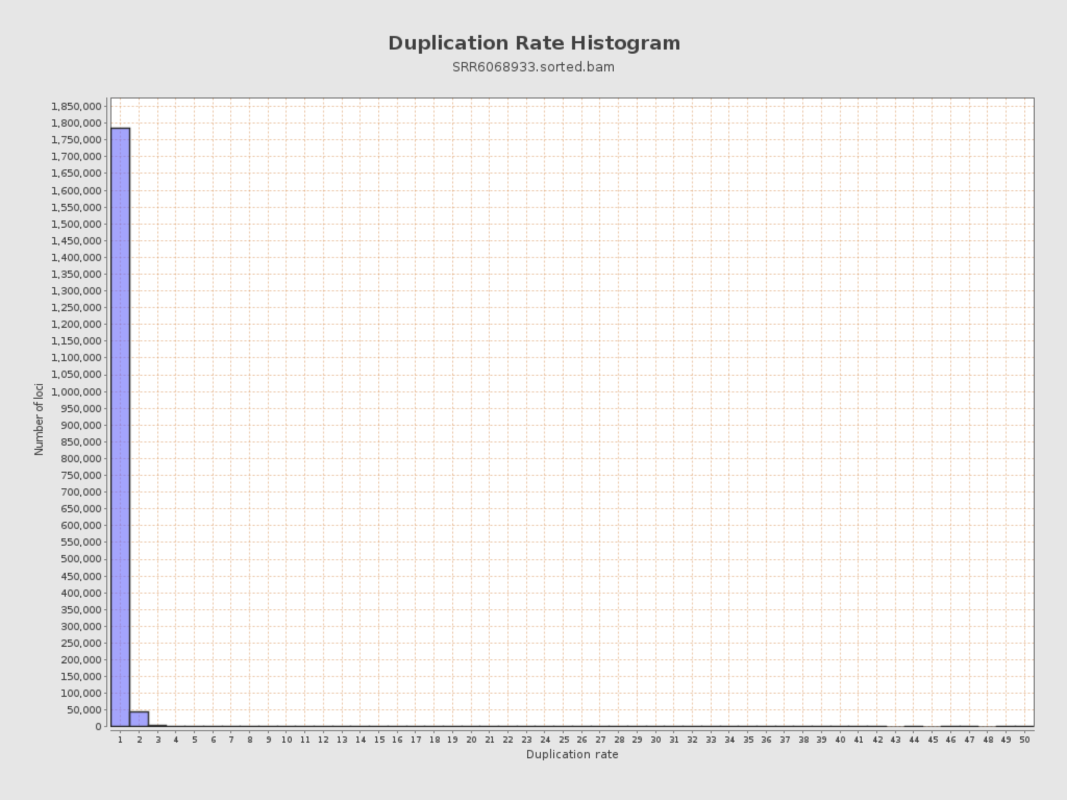
5. Results : Coverage Histogram (0-50X)



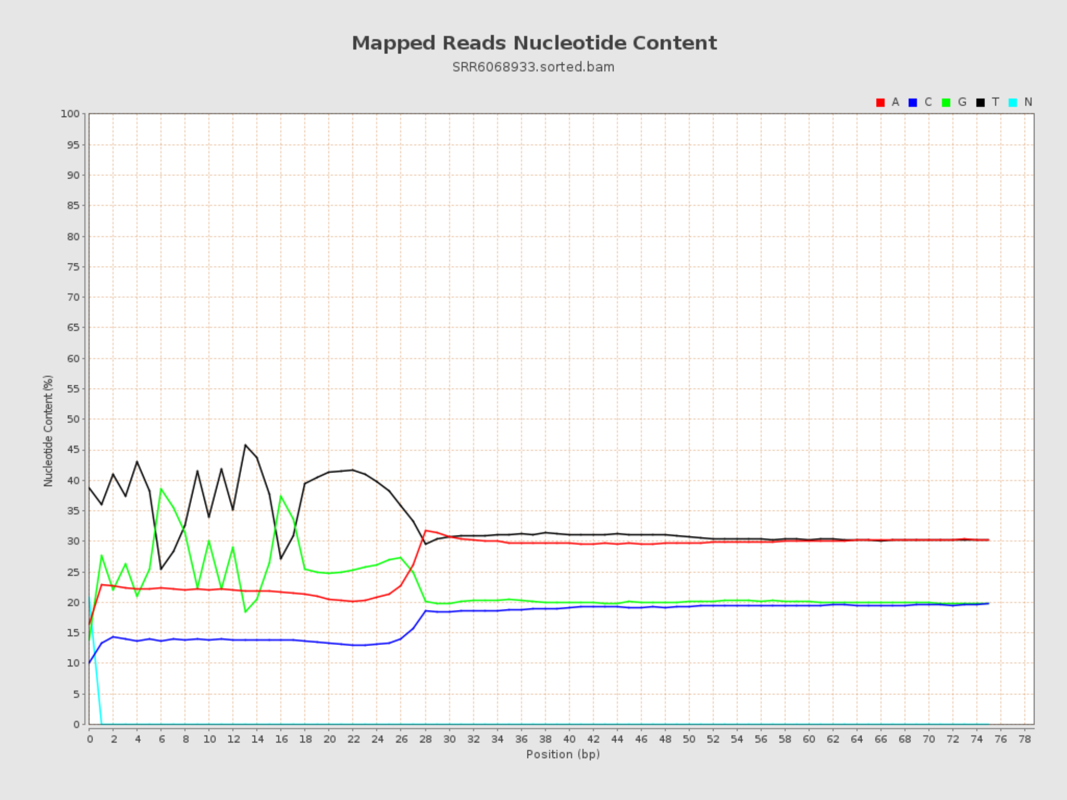
6. Results : Genome Fraction Coverage



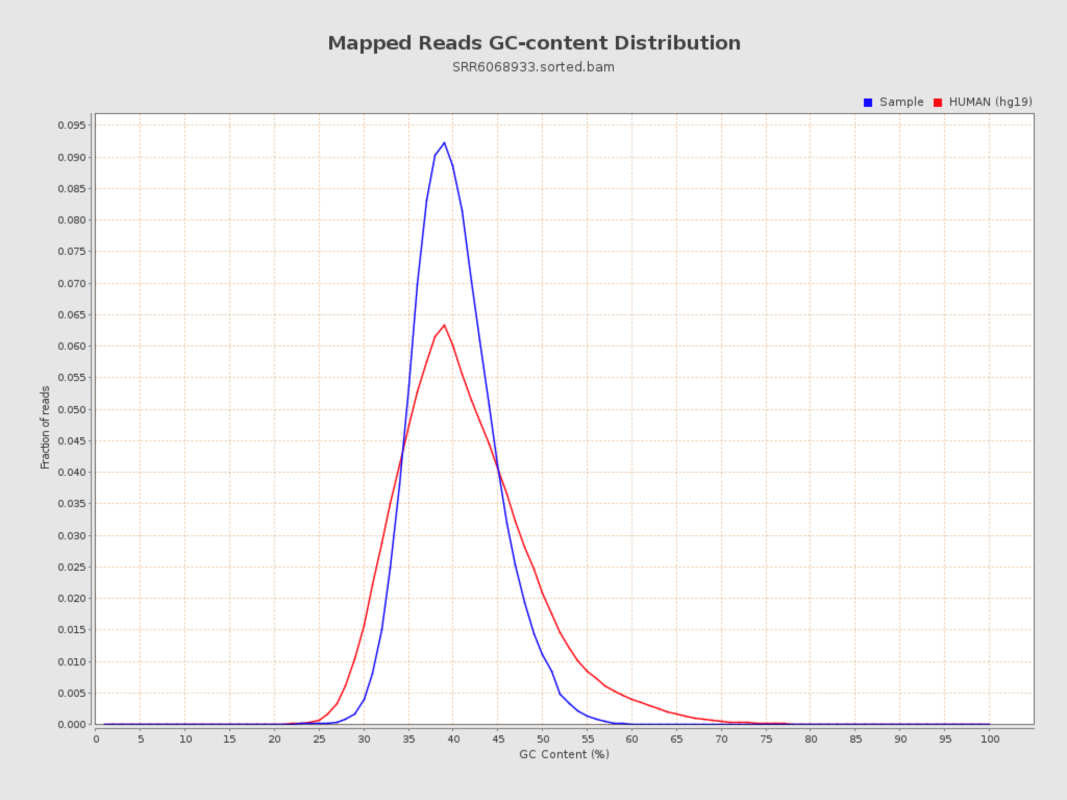
7. Results : Duplication Rate Histogram



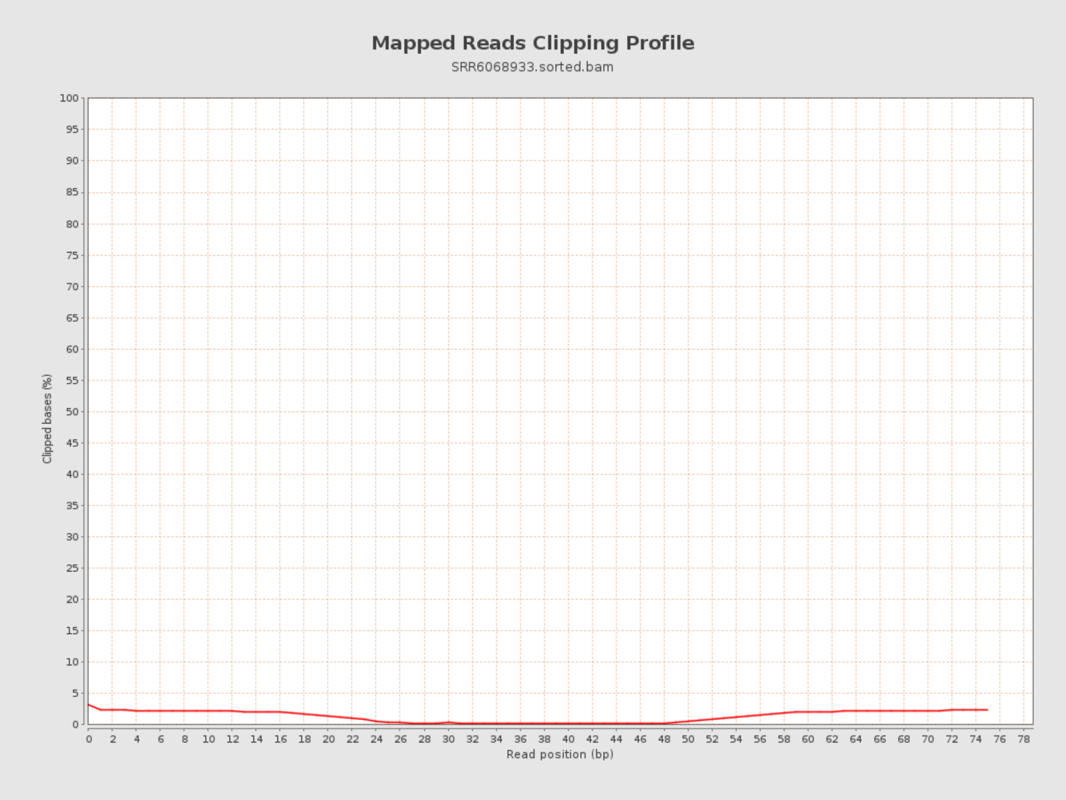
8. Results : Mapped Reads Nucleotide Content



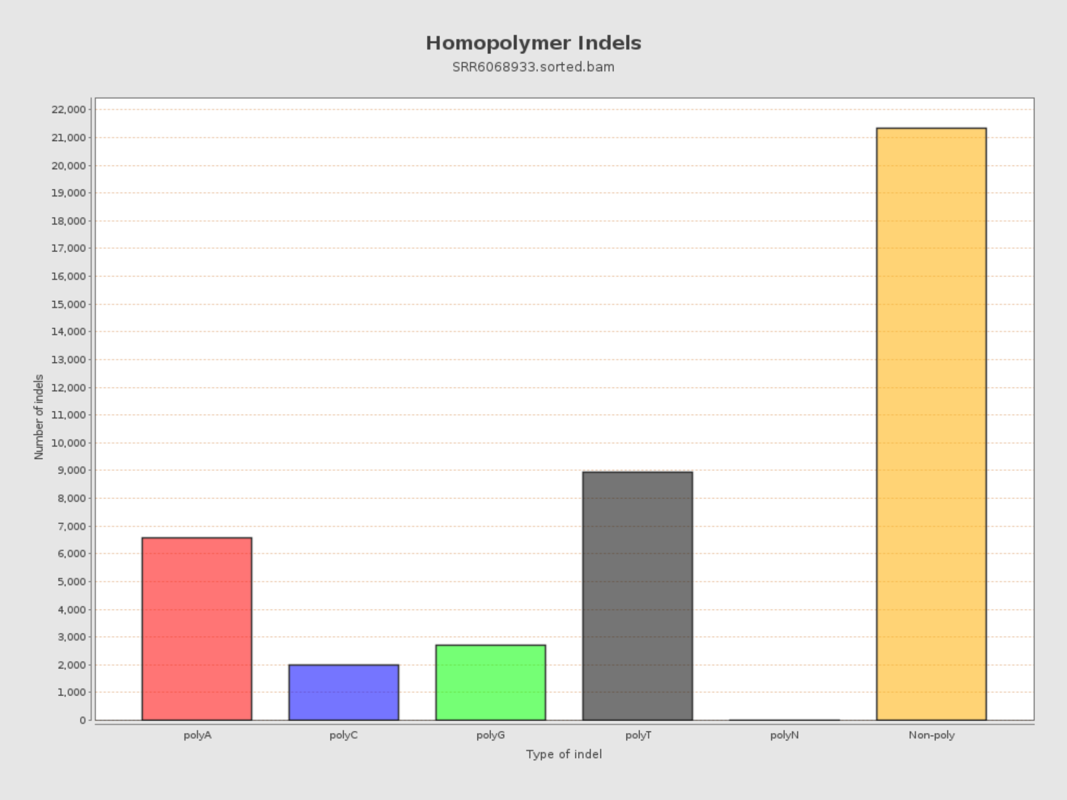
9. Results : Mapped Reads GC-content Distribution



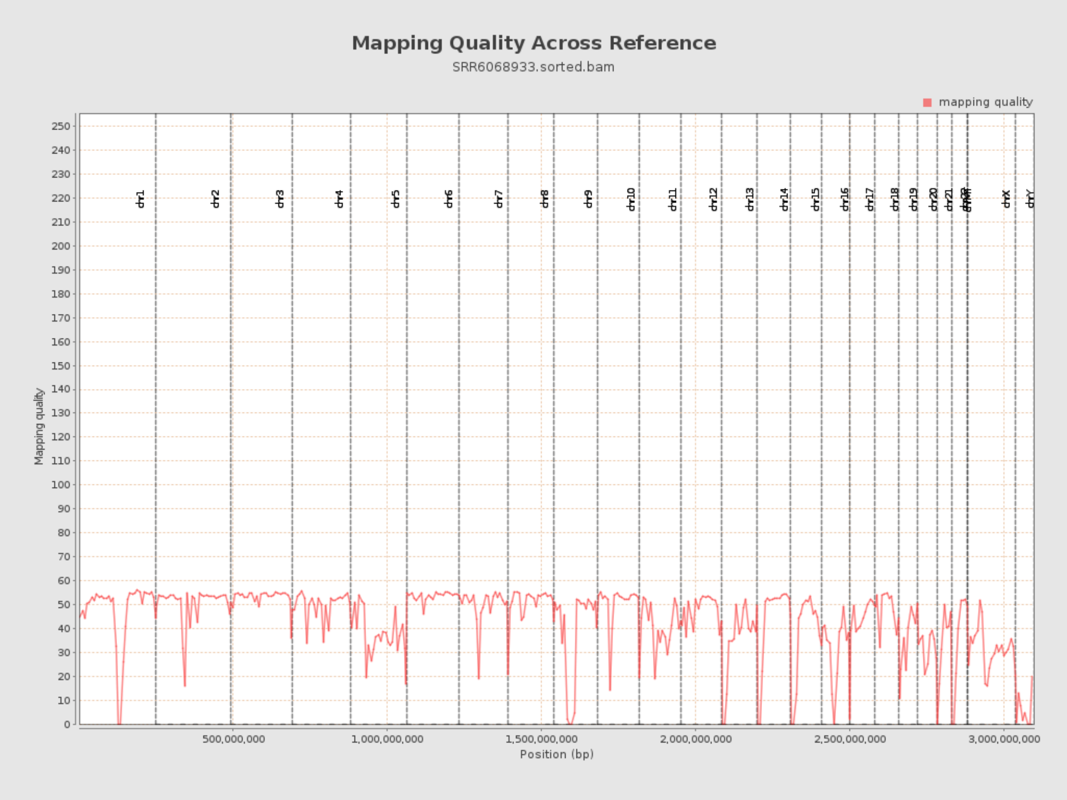
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram