Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:14:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068164.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_SRR6068164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:14:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,869,338
Mapped reads	1,612,694 / 86.27%
Unmapped reads	256,644 / 13.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,715 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	129,579 / 6.93%
Duplication rate	6.68%
Clipped reads	676,533 / 36.19%

2.2. ACGT Content

Number/percentage of A's	31,402,193 / 28.77%
Number/percentage of C's	20,636,093 / 18.91%
Number/percentage of T's	33,986,027 / 31.14%
Number/percentage of G's	22,975,153 / 21.05%
Number/percentage of N's	137,179 / 0.13%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.3539

2.4. Mapping Quality

Mean Mapping Quality	47.58

2.5. Mismatches and indels

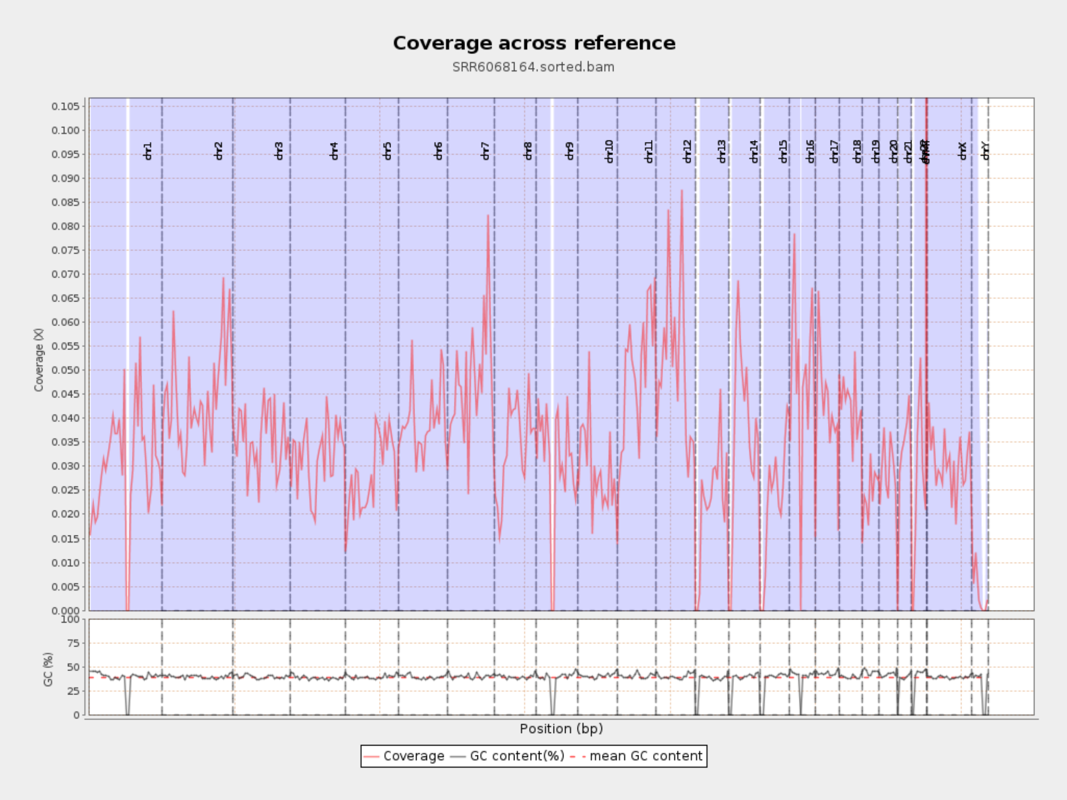
General error rate	0.85%
Mismatches	911,022
Insertions	7,734
Mapped reads with at least one insertion	0.48%
Deletions	26,067
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.18%

2.6. Chromosome stats

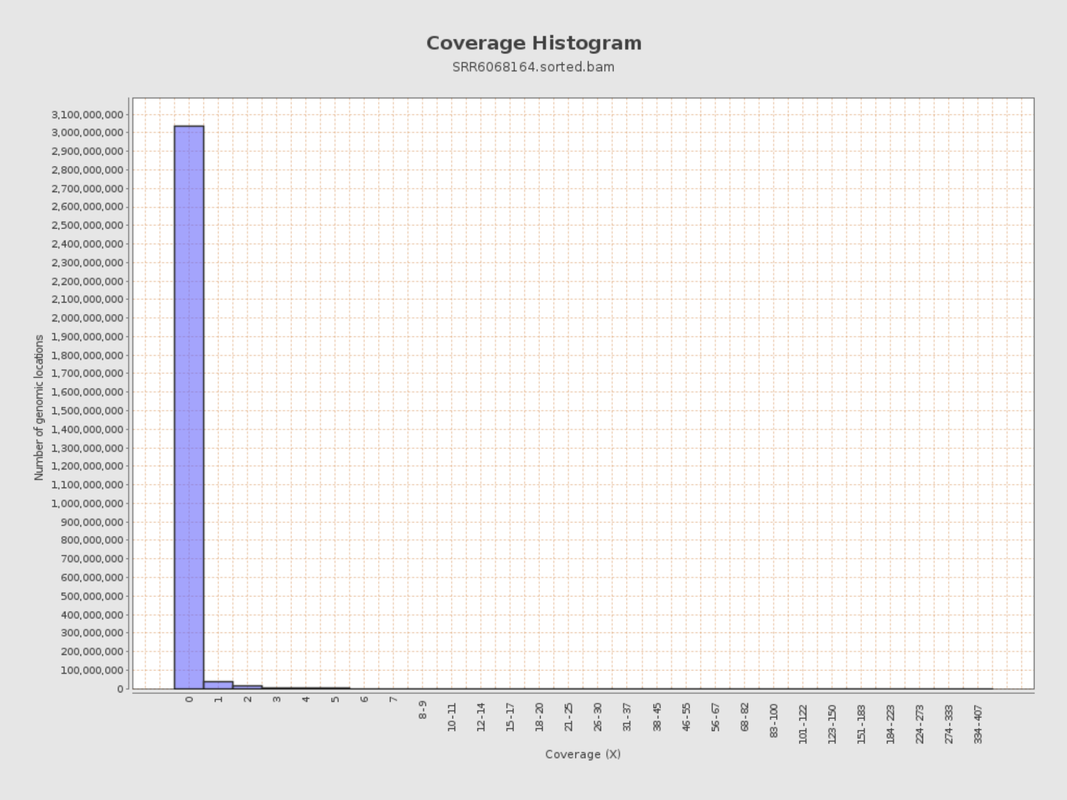
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7601486	0.0305	0.4417
chr2	243199373	10763046	0.0443	0.3891
chr3	198022430	7085759	0.0358	0.3037
chr4	191154276	6131963	0.0321	0.2919
chr5	180915260	5087613	0.0281	0.2706
chr6	171115067	6735059	0.0394	0.3492
chr7	159138663	7665791	0.0482	0.4411

chr8	146364022	5035805	0.0344	0.3829
chr9	141213431	4332559	0.0307	0.3365
chr10	135534747	3991216	0.0294	0.3821
chr11	135006516	6659363	0.0493	0.4187
chr12	133851895	6958809	0.052	0.3781
chr13	115169878	2560188	0.0222	0.2428
chr14	107349540	3994855	0.0372	0.3234
chr15	102531392	2347350	0.0229	0.2426
chr16	90354753	4396435	0.0487	0.3651
chr17	81195210	3433817	0.0423	0.3565
chr18	78077248	3347380	0.0429	0.5442
chr19	59128983	1454463	0.0246	0.334
chr20	63025520	1811888	0.0287	0.2795
chr21	48129895	1542348	0.032	0.2922
chr22	51304566	1260170	0.0246	0.2518
chrMT	16571	9622	0.5807	1.0844
chrX	155270560	4747428	0.0306	0.2921
chrY	59373566	228550	0.0038	0.1086

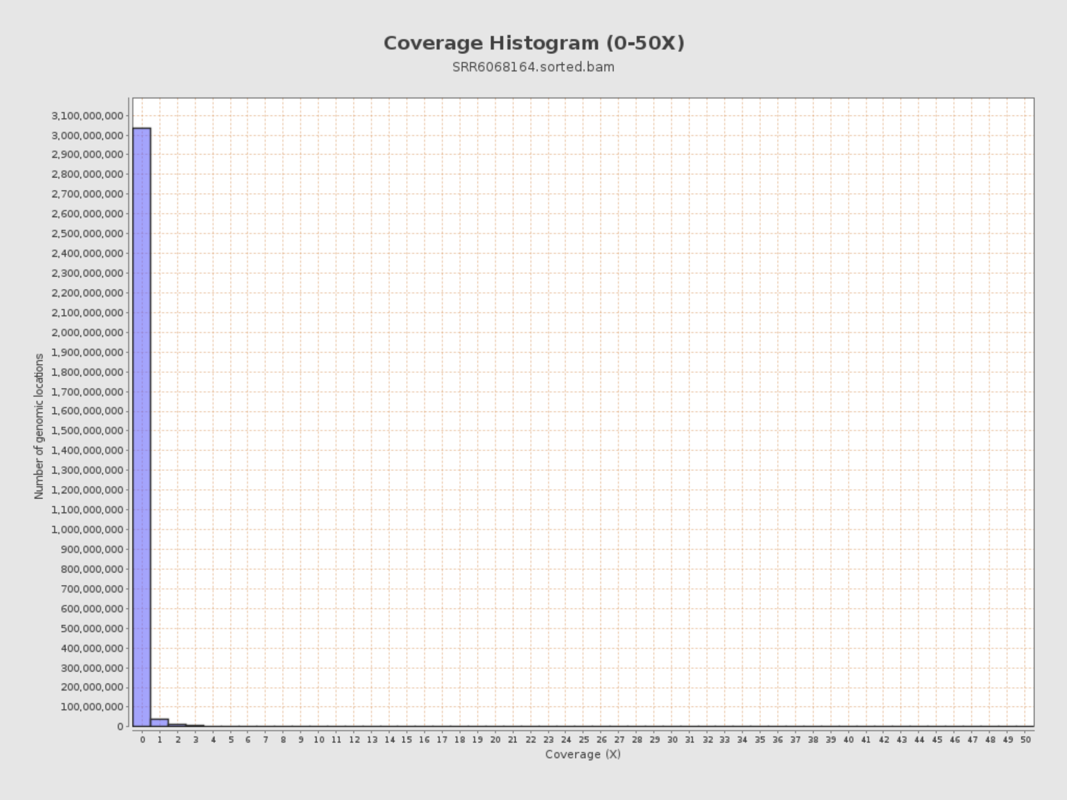
3. Results : Coverage across reference



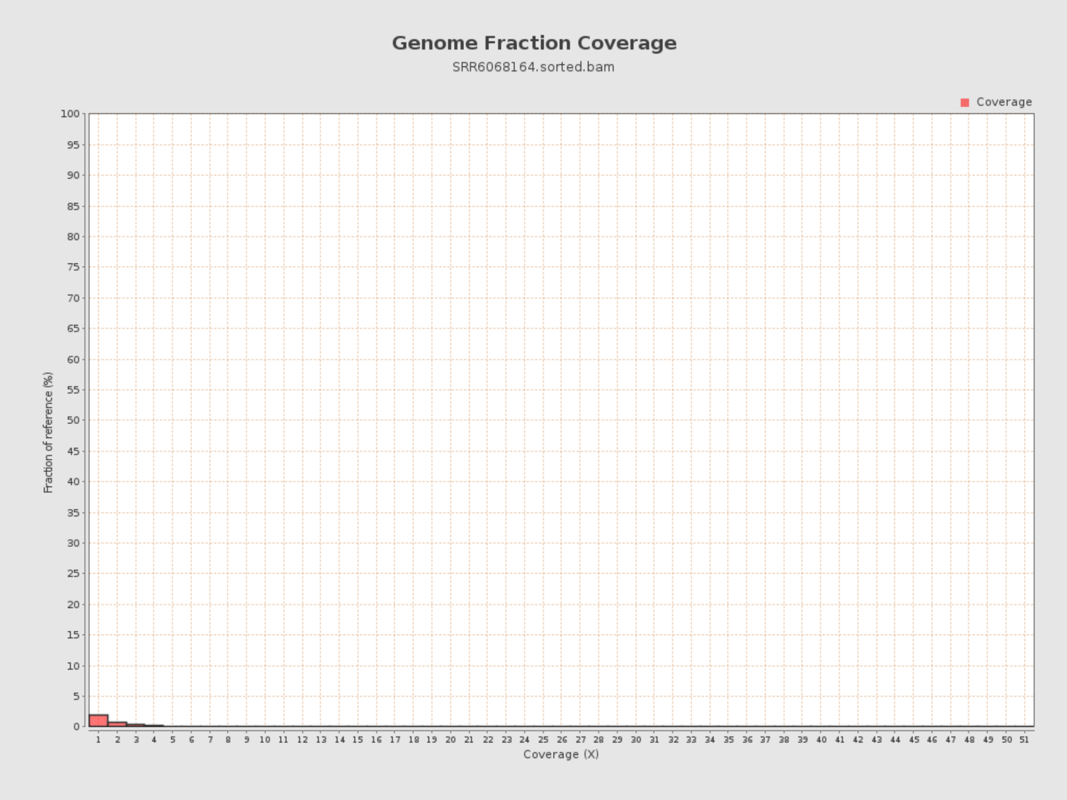
4. Results : Coverage Histogram



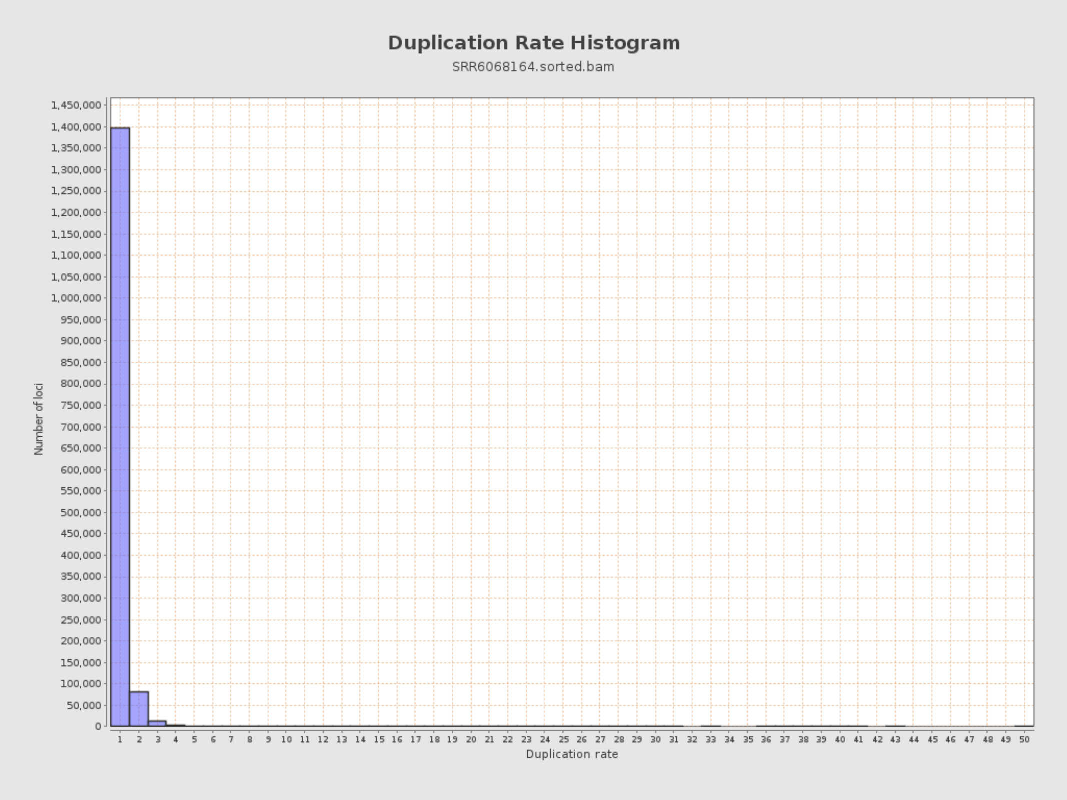
5. Results : Coverage Histogram (0-50X)



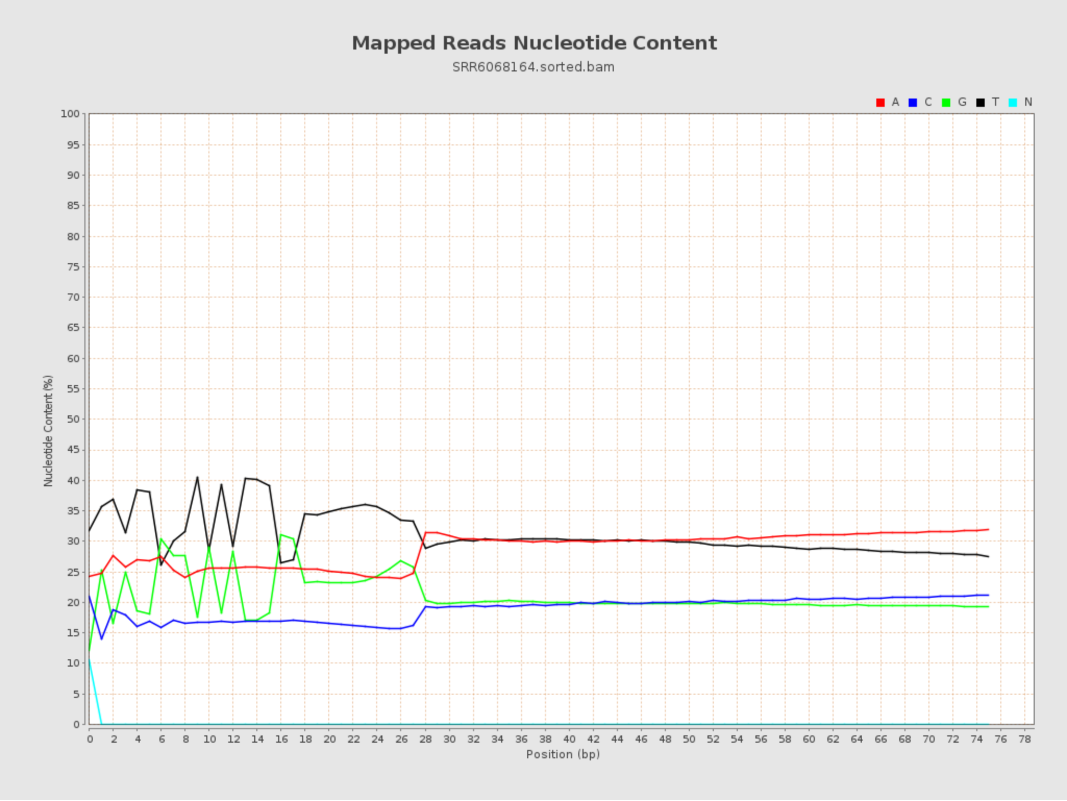
6. Results : Genome Fraction Coverage



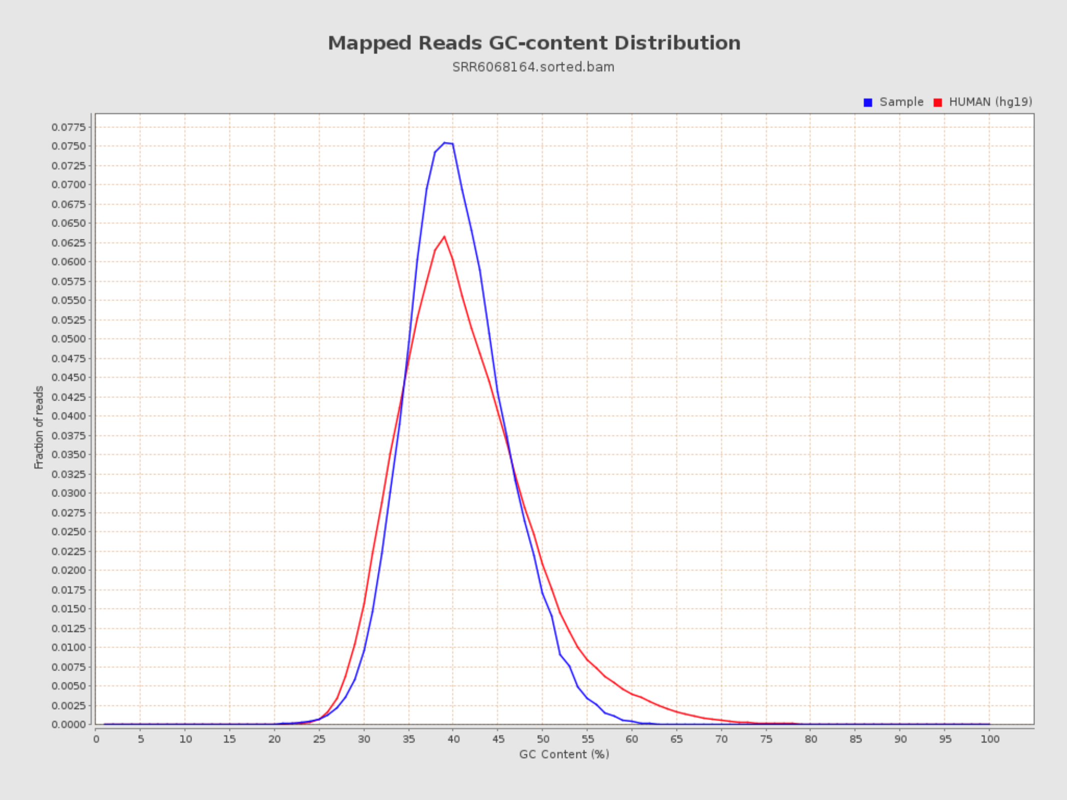
7. Results : Duplication Rate Histogram



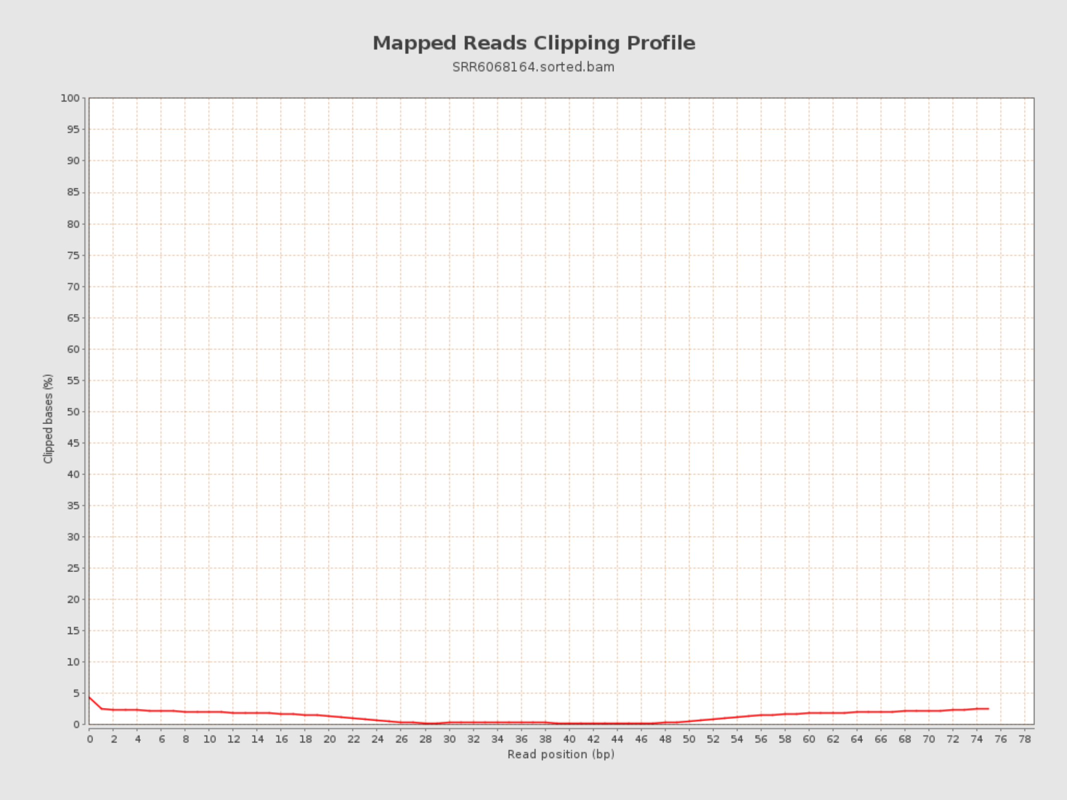
8. Results : Mapped Reads Nucleotide Content



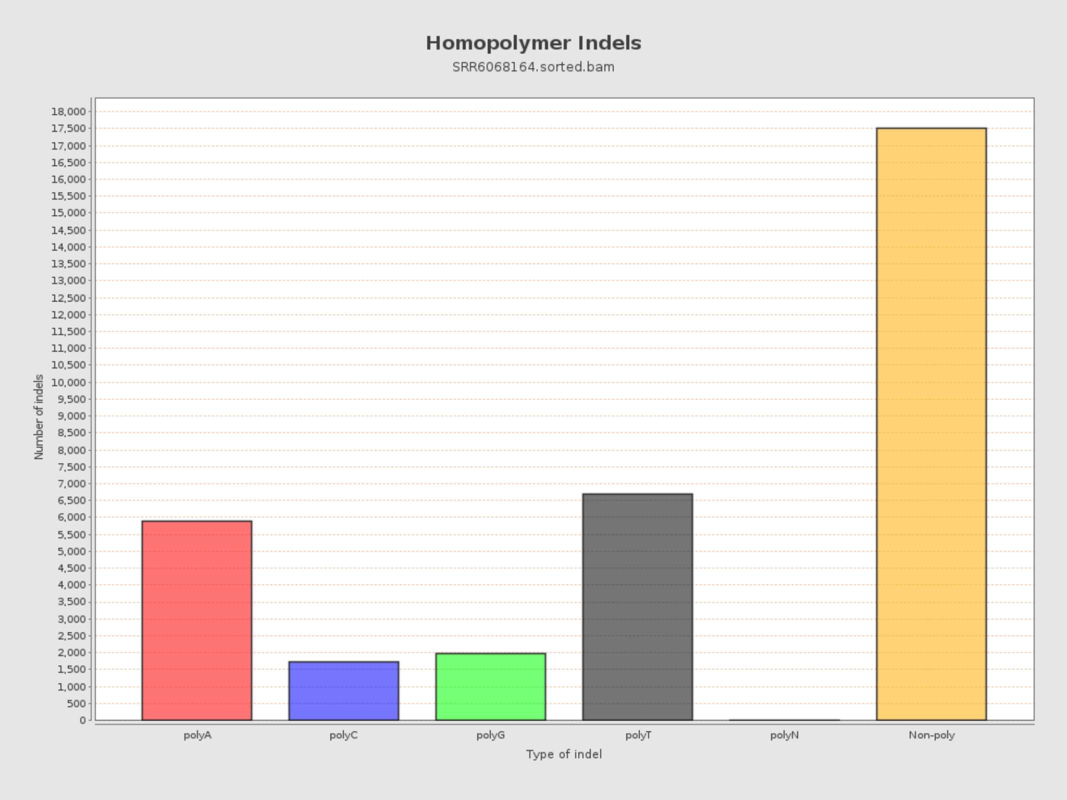
9. Results : Mapped Reads GC-content Distribution



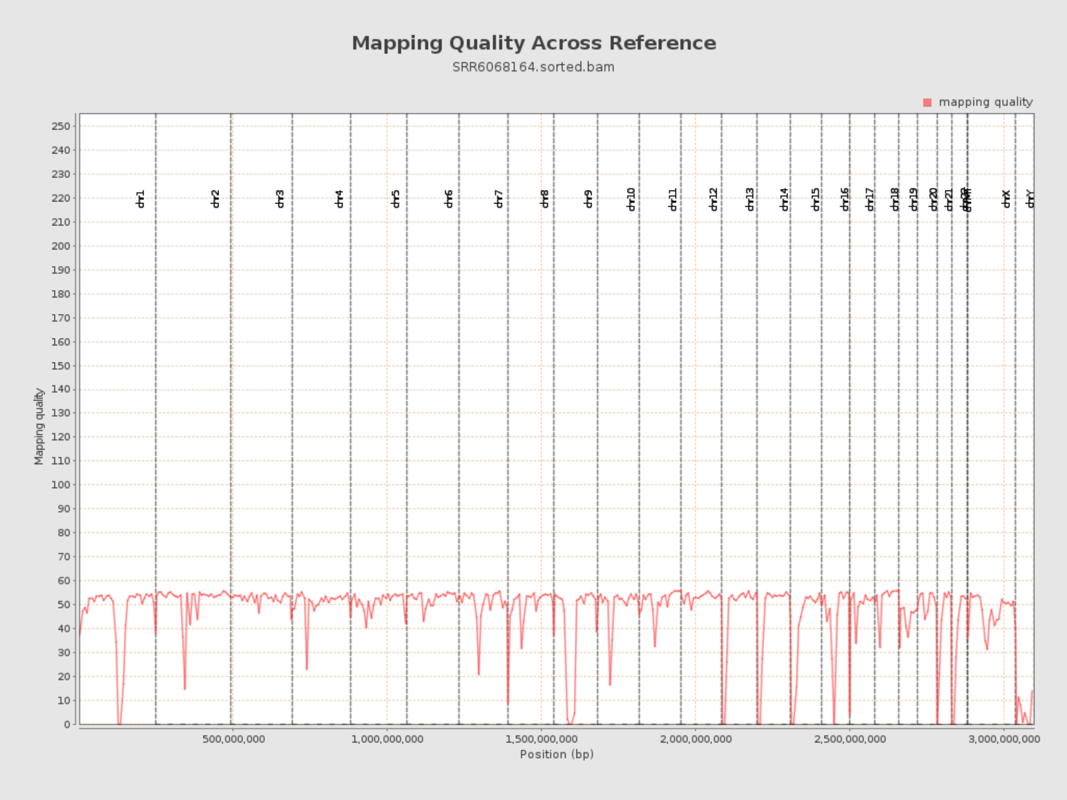
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram