Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:45:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068157.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_SRR6068157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:45:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,948,605
Mapped reads	4,604,578 / 93.05%
Unmapped reads	344,027 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,665 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	484,278 / 9.79%
Duplication rate	8.51%
Clipped reads	2,415,623 / 48.81%

2.2. ACGT Content

Number/percentage of A's	76,466,769 / 25.81%
Number/percentage of C's	53,576,977 / 18.09%
Number/percentage of T's	96,206,774 / 32.48%
Number/percentage of G's	69,948,558 / 23.61%
Number/percentage of N's	33,590 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0957

Standard Deviation	1.2265

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

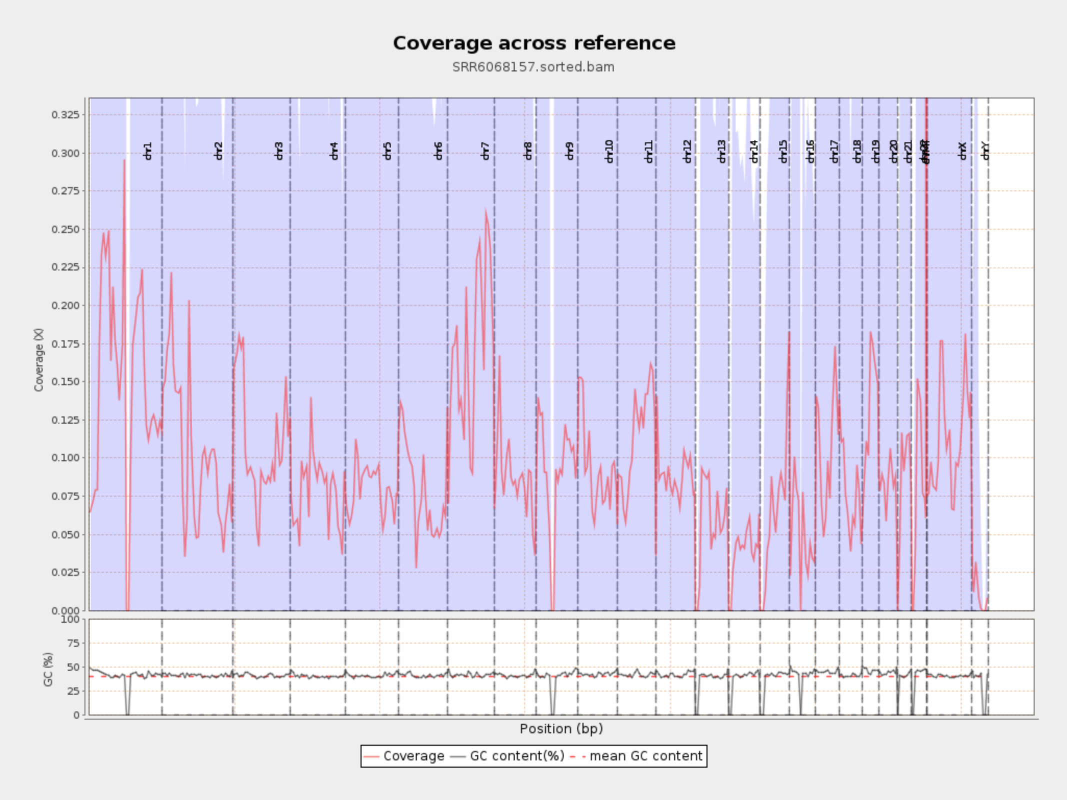
General error rate	0.56%
Mismatches	1,621,665
Insertions	18,115
Mapped reads with at least one insertion	0.39%
Deletions	73,131
Mapped reads with at least one deletion	1.57%
Homopolymer indels	44.66%

2.6. Chromosome stats

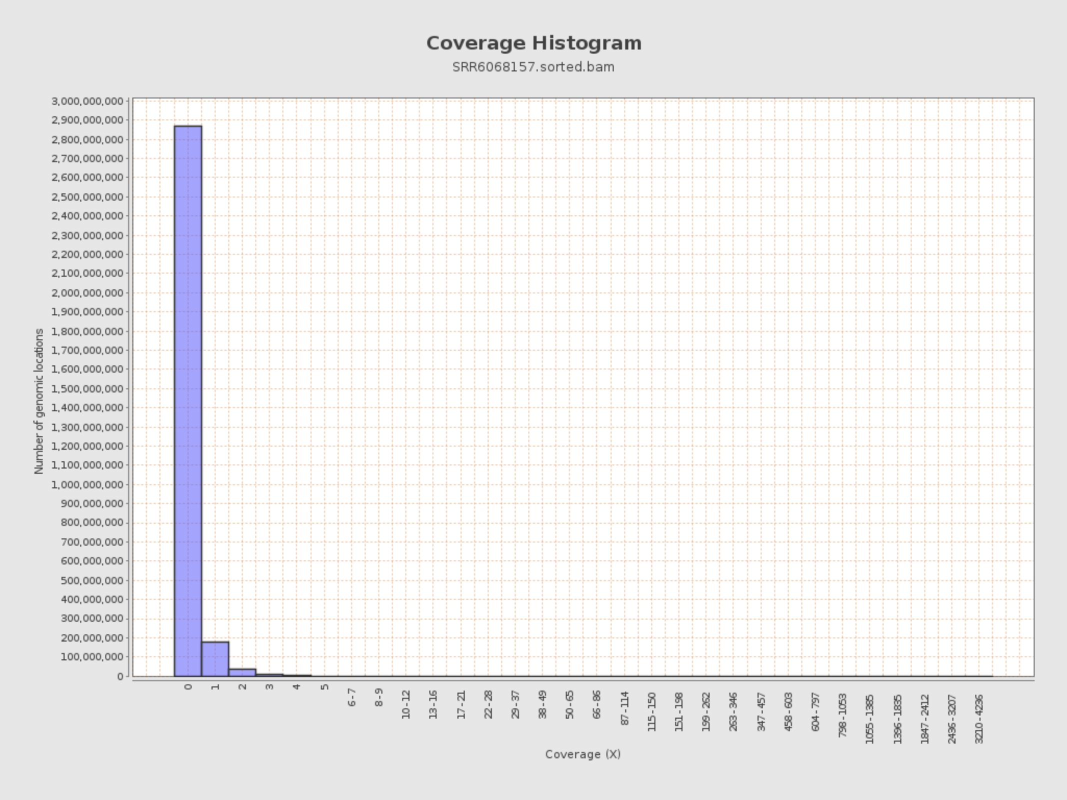
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37916432	0.1521	3.3122
chr2	243199373	25312299	0.1041	1.6518
chr3	198022430	21705899	0.1096	0.4159
chr4	191154276	14879177	0.0778	0.378
chr5	180915260	14349533	0.0793	0.3613
chr6	171115067	13446412	0.0786	0.5587
chr7	159138663	27550063	0.1731	1.4277

chr8	146364022	12806445	0.0875	0.9487
chr9	141213431	12859989	0.0911	0.6966
chr10	135534747	12823248	0.0946	0.5894
chr11	135006516	15184859	0.1125	0.6237
chr12	133851895	11965121	0.0894	0.4056
chr13	115169878	6598385	0.0573	0.3518
chr14	107349540	4041670	0.0376	0.3194
chr15	102531392	6523598	0.0636	0.3779
chr16	90354753	4491226	0.0497	0.3557
chr17	81195210	8603464	0.106	0.4599
chr18	78077248	6073357	0.0778	1.2991
chr19	59128983	7841616	0.1326	1.8364
chr20	63025520	5212199	0.0827	0.3916
chr21	48129895	4120603	0.0856	0.3832
chr22	51304566	3824335	0.0745	0.3377
chrMT	16571	146642	8.8493	5.5534
chrX	155270560	17504942	0.1127	0.5225
chrY	59373566	578893	0.0098	0.2632

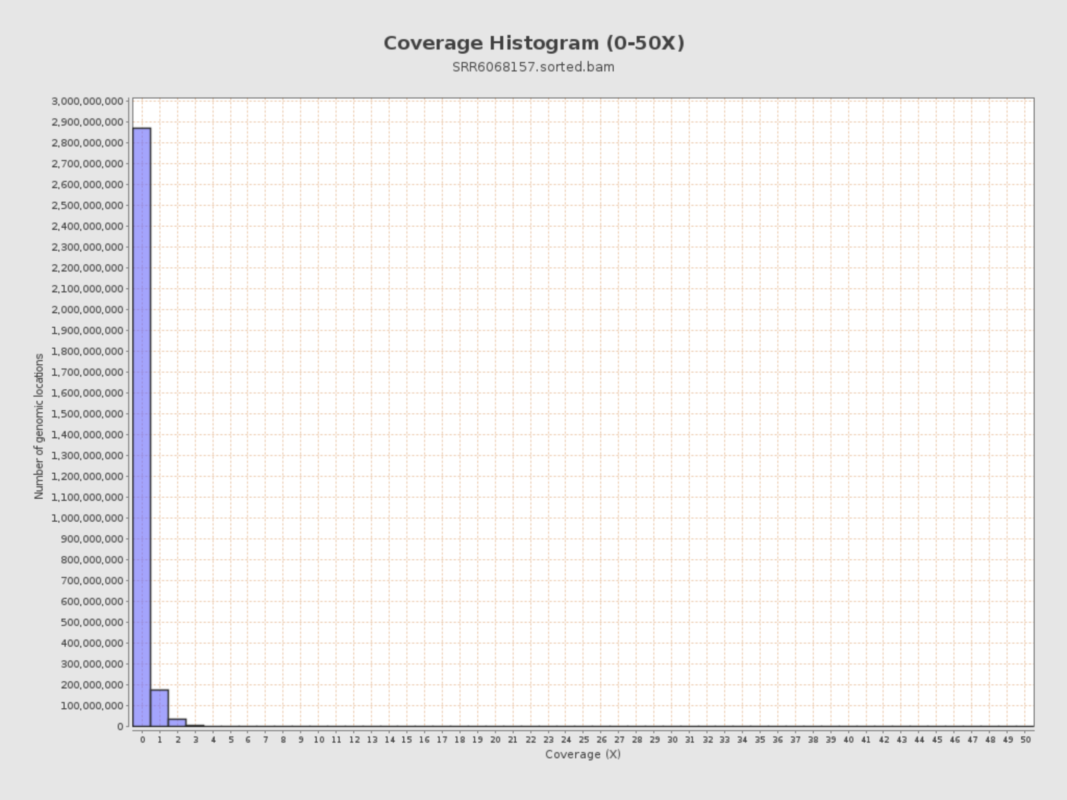
3. Results : Coverage across reference



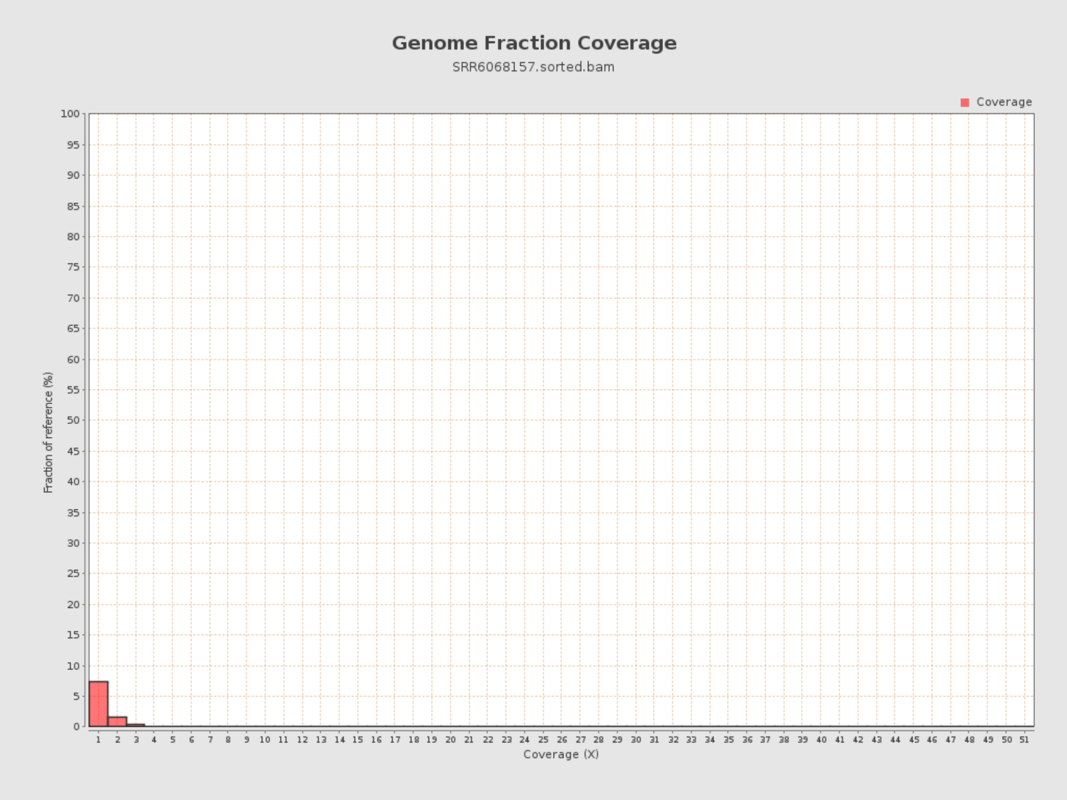
4. Results : Coverage Histogram



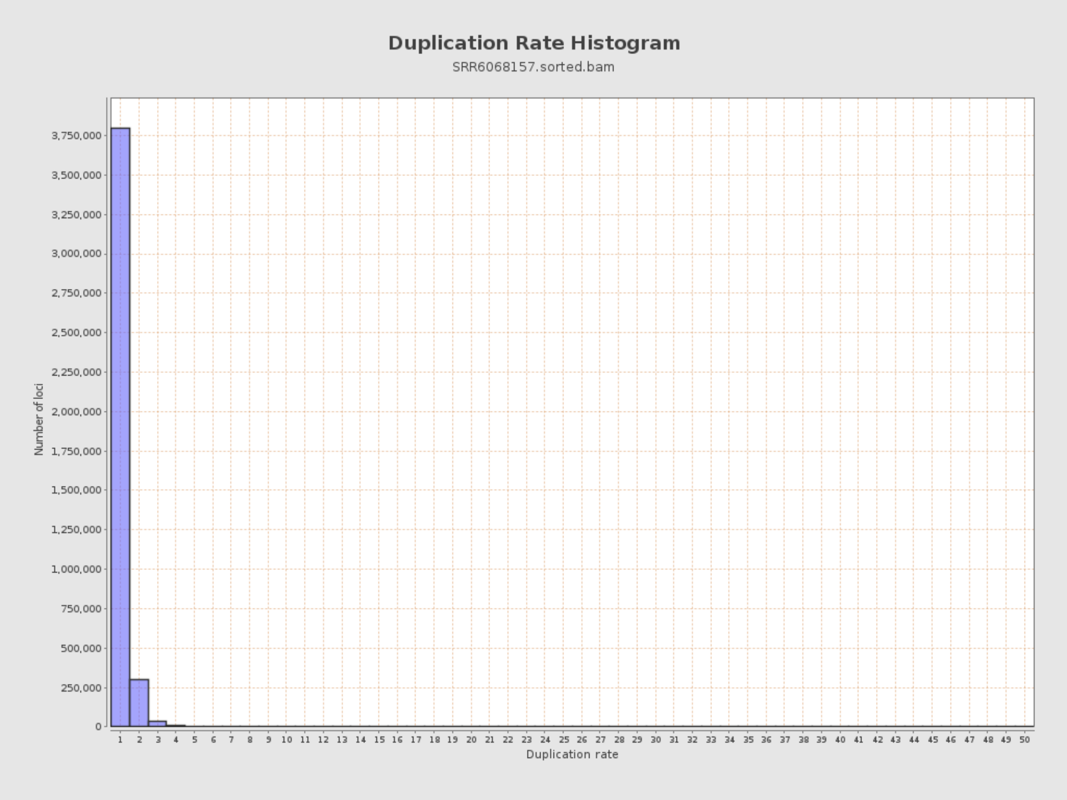
5. Results : Coverage Histogram (0-50X)



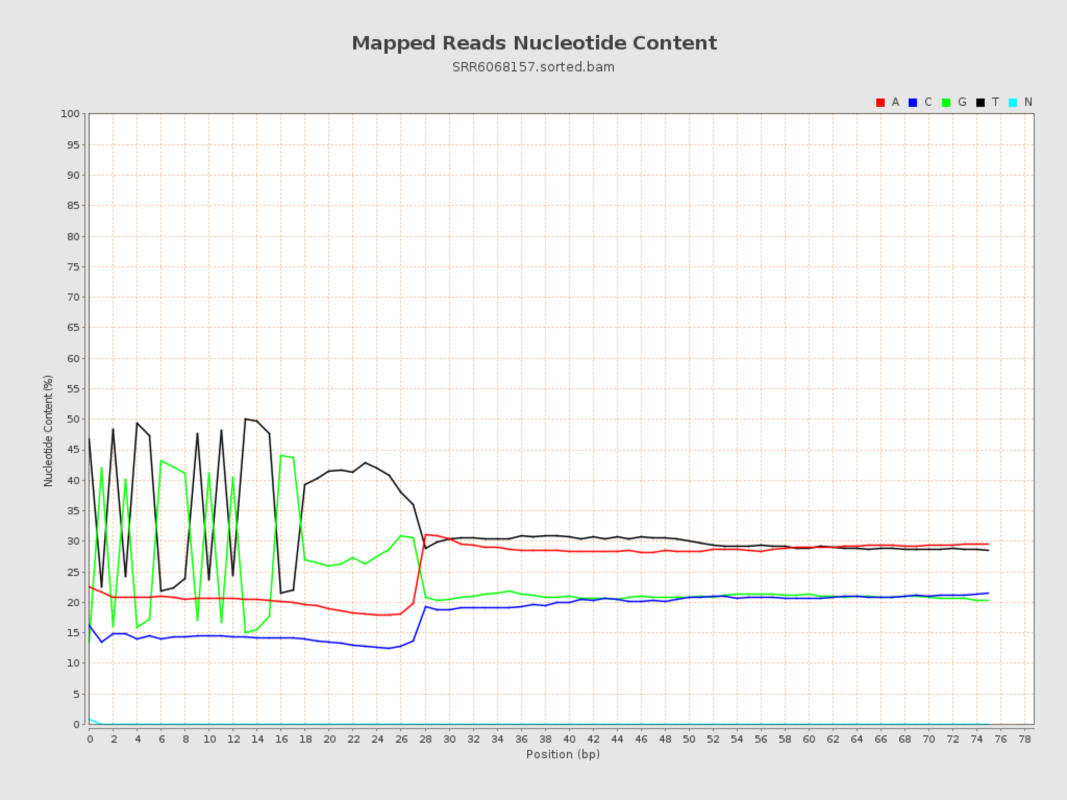
6. Results : Genome Fraction Coverage



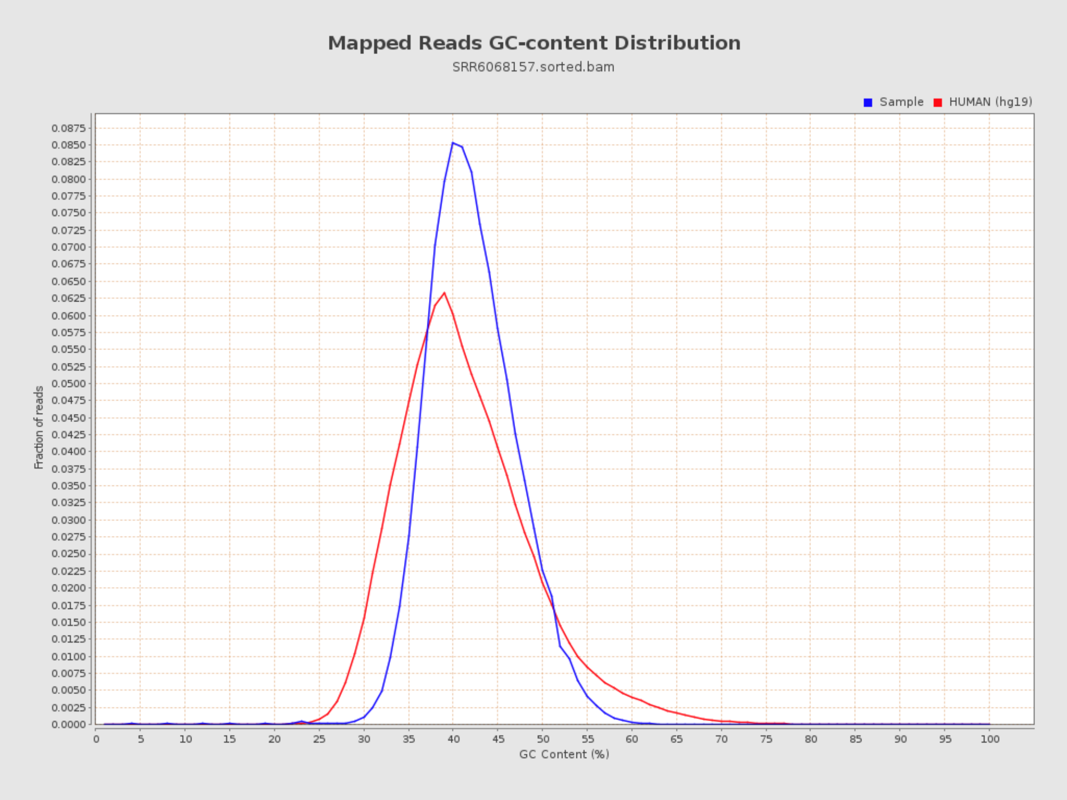
7. Results : Duplication Rate Histogram



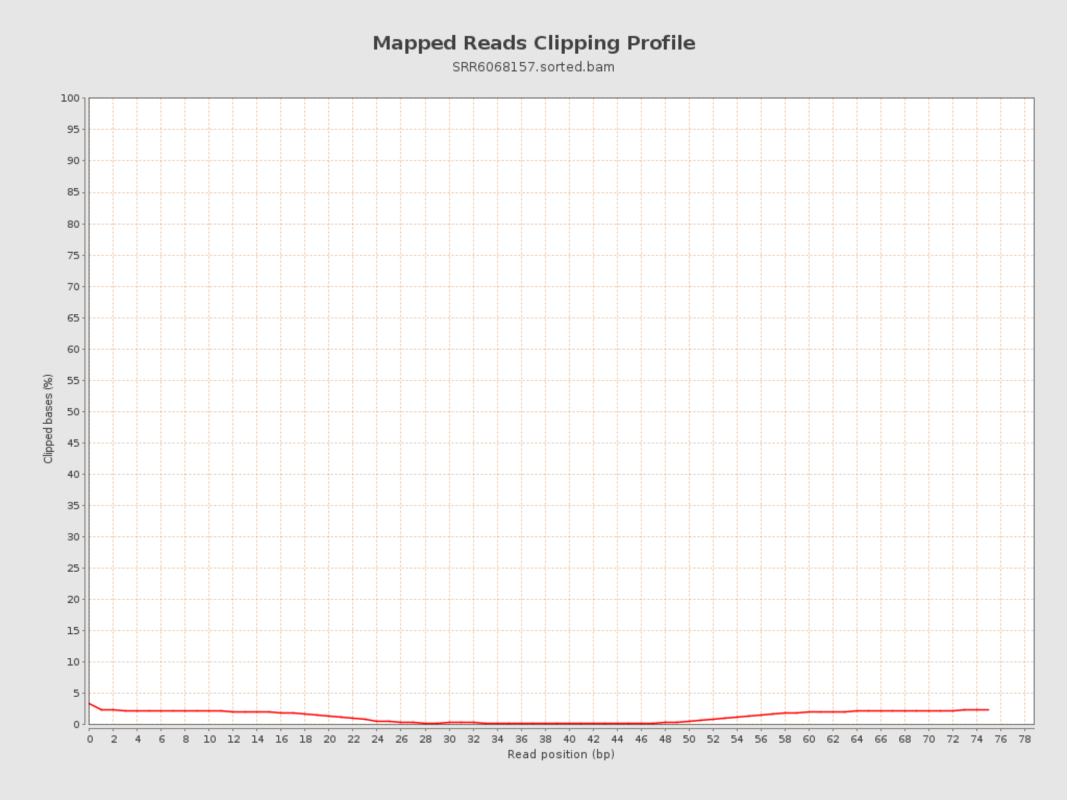
8. Results : Mapped Reads Nucleotide Content



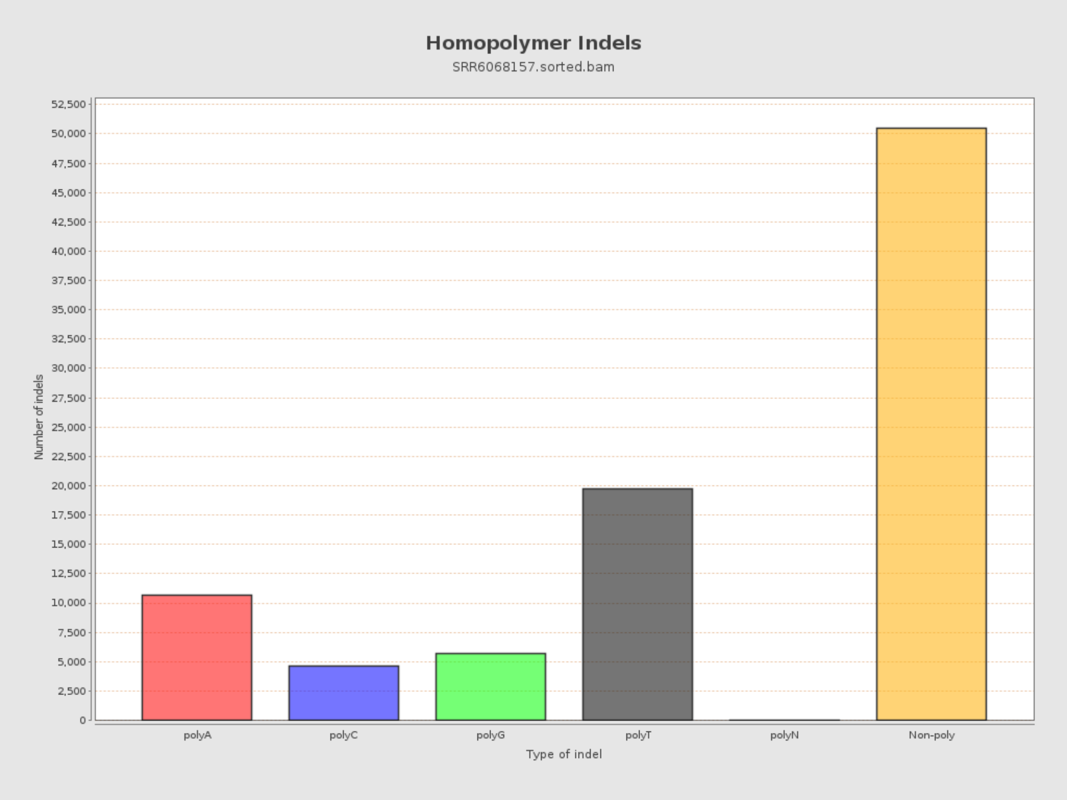
9. Results : Mapped Reads GC-content Distribution



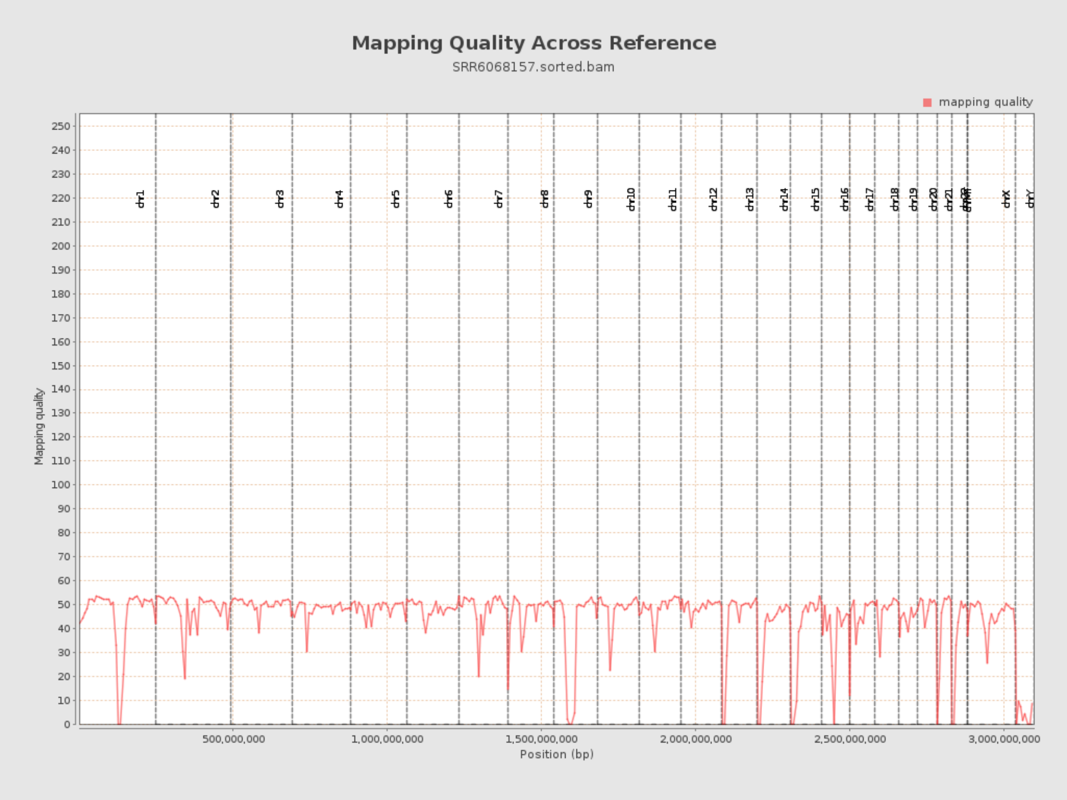
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram