Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:48:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525068.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_SRR10525068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:48:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,637,036
Mapped reads	1,469,068 / 89.74%
Unmapped reads	167,968 / 10.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,465 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	82,586 / 5.04%
Duplication rate	4.57%
Clipped reads	1,469,253 / 89.75%

2.2. ACGT Content

Number/percentage of A's	21,411,436 / 25.08%
Number/percentage of C's	15,532,363 / 18.19%
Number/percentage of T's	27,952,346 / 32.74%
Number/percentage of G's	20,468,109 / 23.97%
Number/percentage of N's	8,901 / 0.01%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2692

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

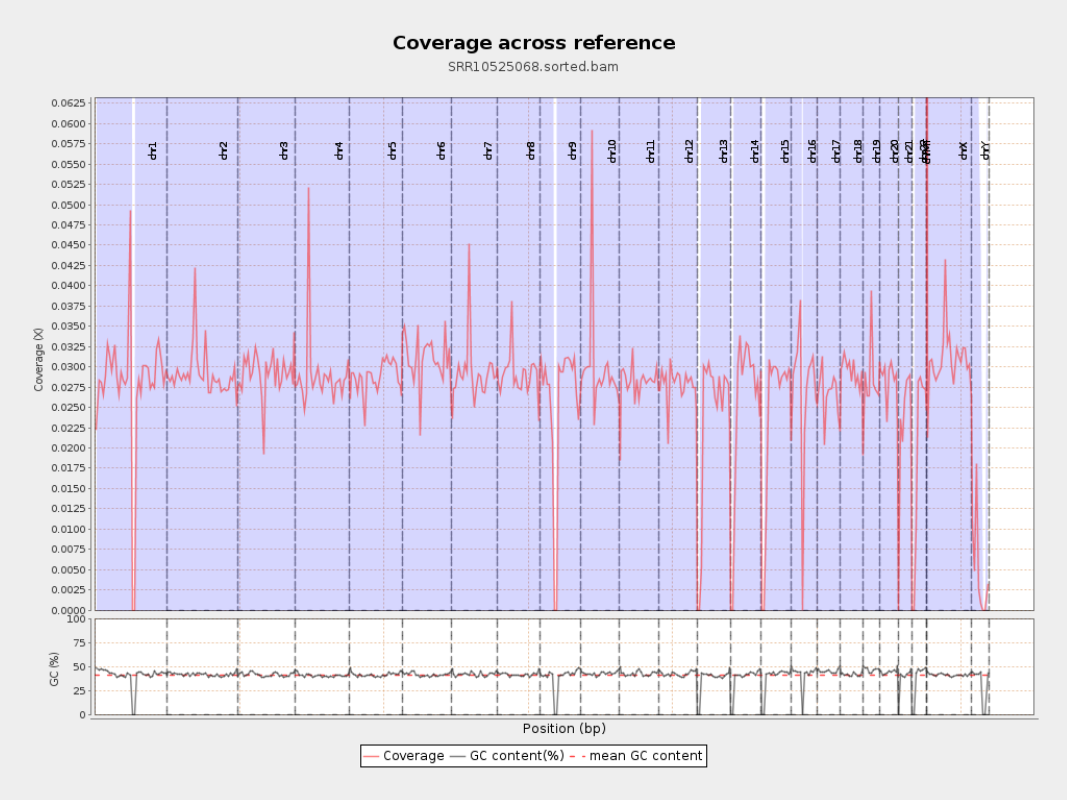
General error rate	0.5%
Mismatches	419,452
Insertions	5,784
Mapped reads with at least one insertion	0.39%
Deletions	17,512
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.62%

2.6. Chromosome stats

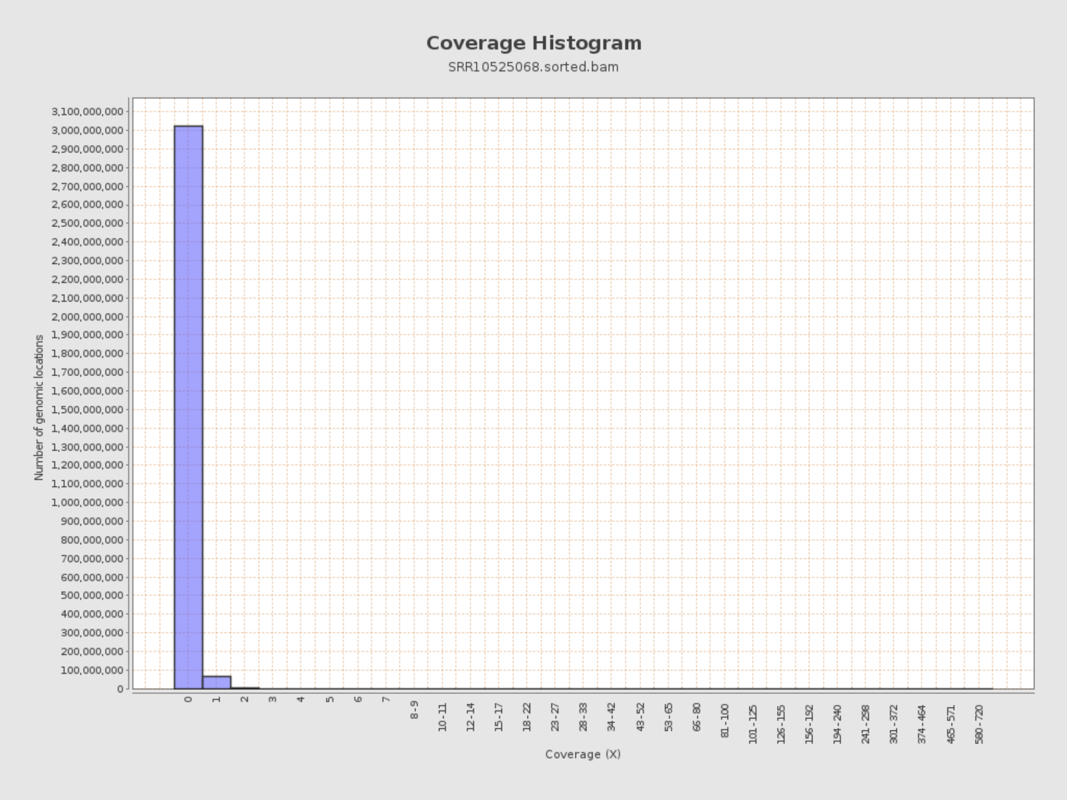
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6913186	0.0277	0.5076
chr2	243199373	7086206	0.0291	0.322
chr3	198022430	5772525	0.0292	0.1904
chr4	191154276	5547616	0.029	0.2127
chr5	180915260	5229061	0.0289	0.1894
chr6	171115067	5318265	0.0311	0.2185
chr7	159138663	4658939	0.0293	0.3074

chr8	146364022	4255503	0.0291	0.2833
chr9	141213431	3597751	0.0255	0.2208
chr10	135534747	4078178	0.0301	0.2939
chr11	135006516	3817801	0.0283	0.2214
chr12	133851895	3730723	0.0279	0.1905
chr13	115169878	2695957	0.0234	0.1712
chr14	107349540	2676027	0.0249	0.1795
chr15	102531392	2442455	0.0238	0.1721
chr16	90354753	2407549	0.0266	0.1974
chr17	81195210	2164117	0.0267	0.191
chr18	78077248	2305708	0.0295	0.3492
chr19	59128983	1692185	0.0286	0.355
chr20	63025520	1788892	0.0284	0.1926
chr21	48129895	1110763	0.0231	0.1925
chr22	51304566	994858	0.0194	0.1537
chrMT	16571	15640	0.9438	1.0866
chrX	155270560	4815929	0.031	0.2163
chrY	59373566	285401	0.0048	0.1656

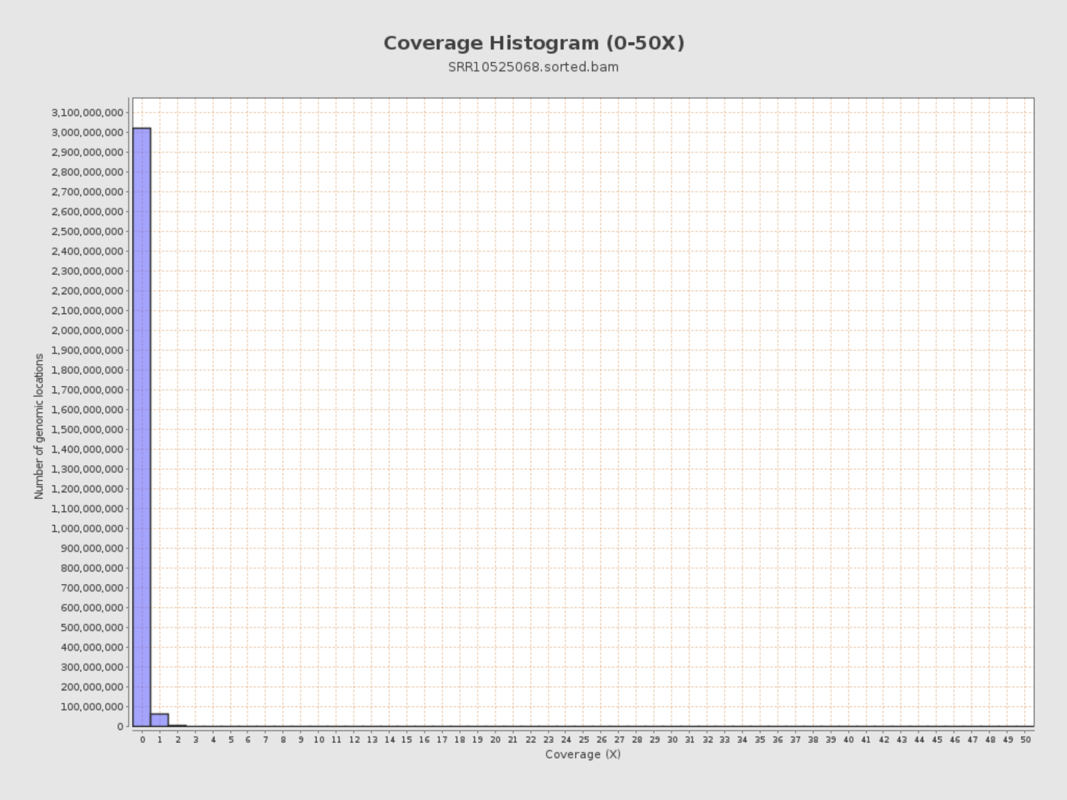
3. Results : Coverage across reference



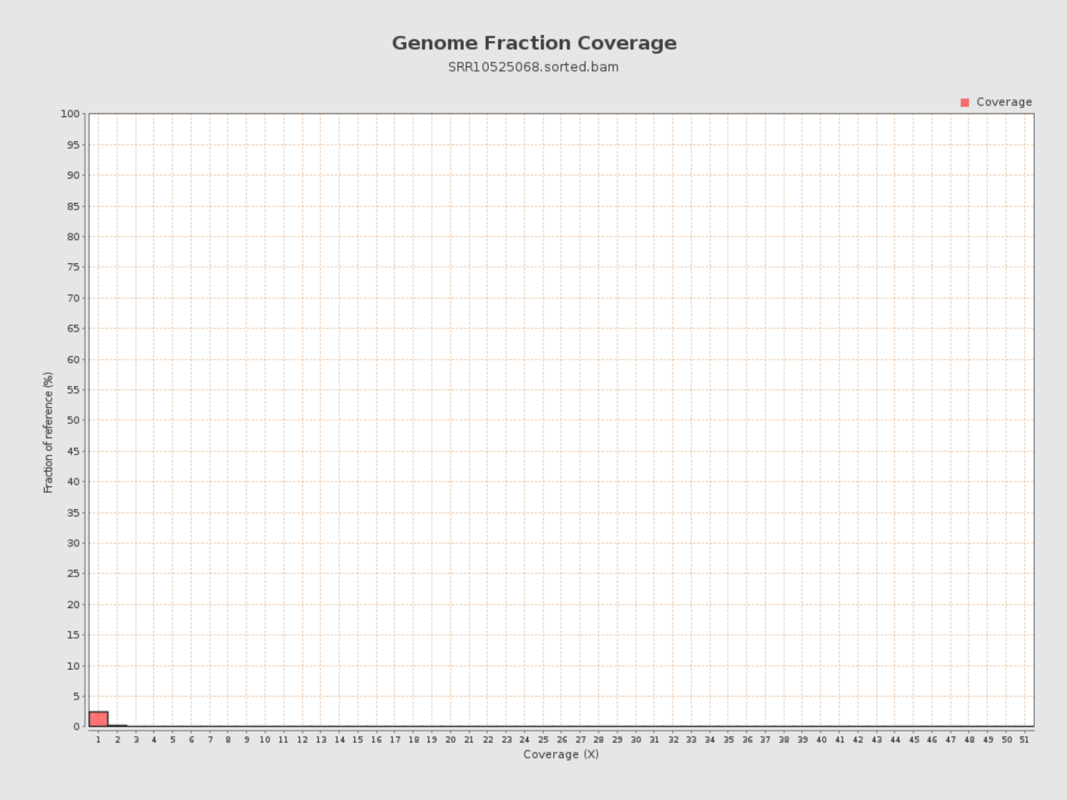
4. Results : Coverage Histogram



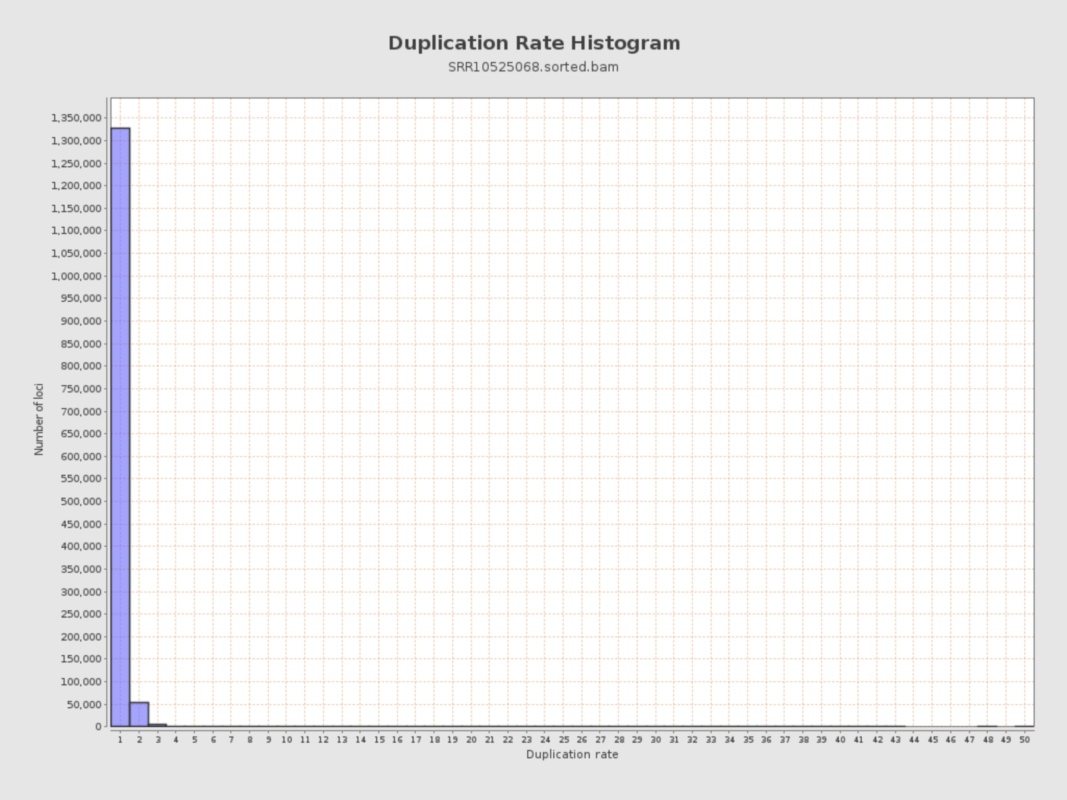
5. Results : Coverage Histogram (0-50X)



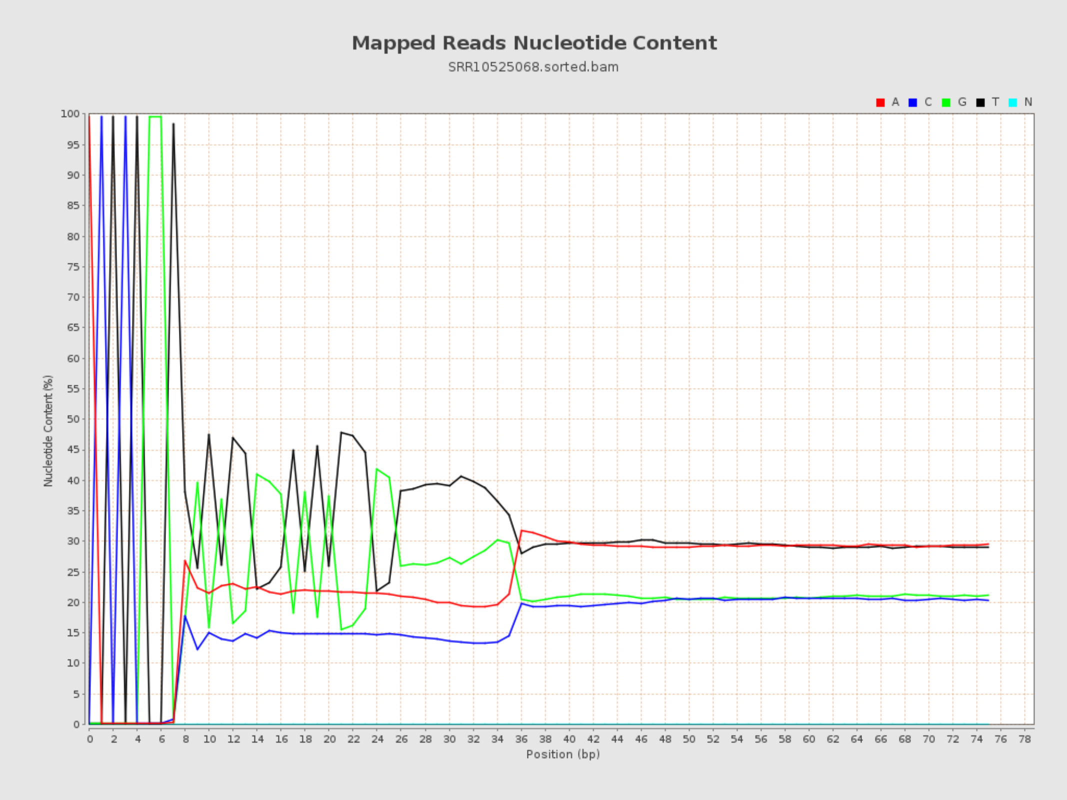
6. Results : Genome Fraction Coverage



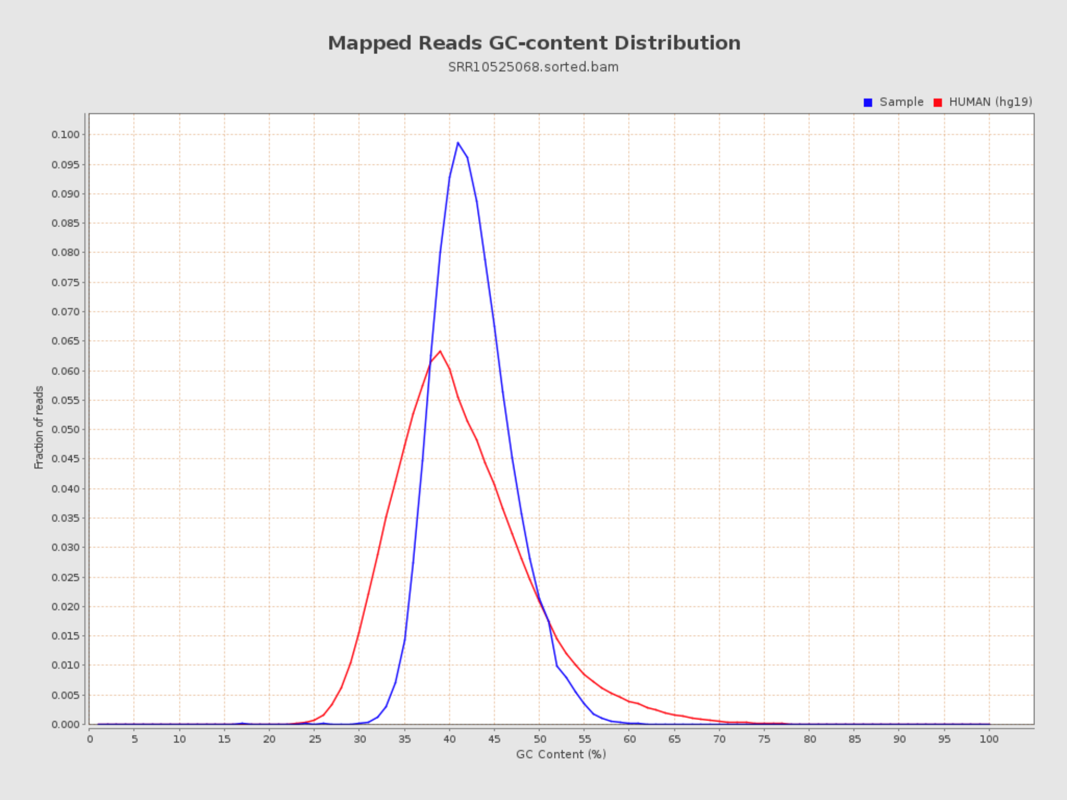
7. Results : Duplication Rate Histogram



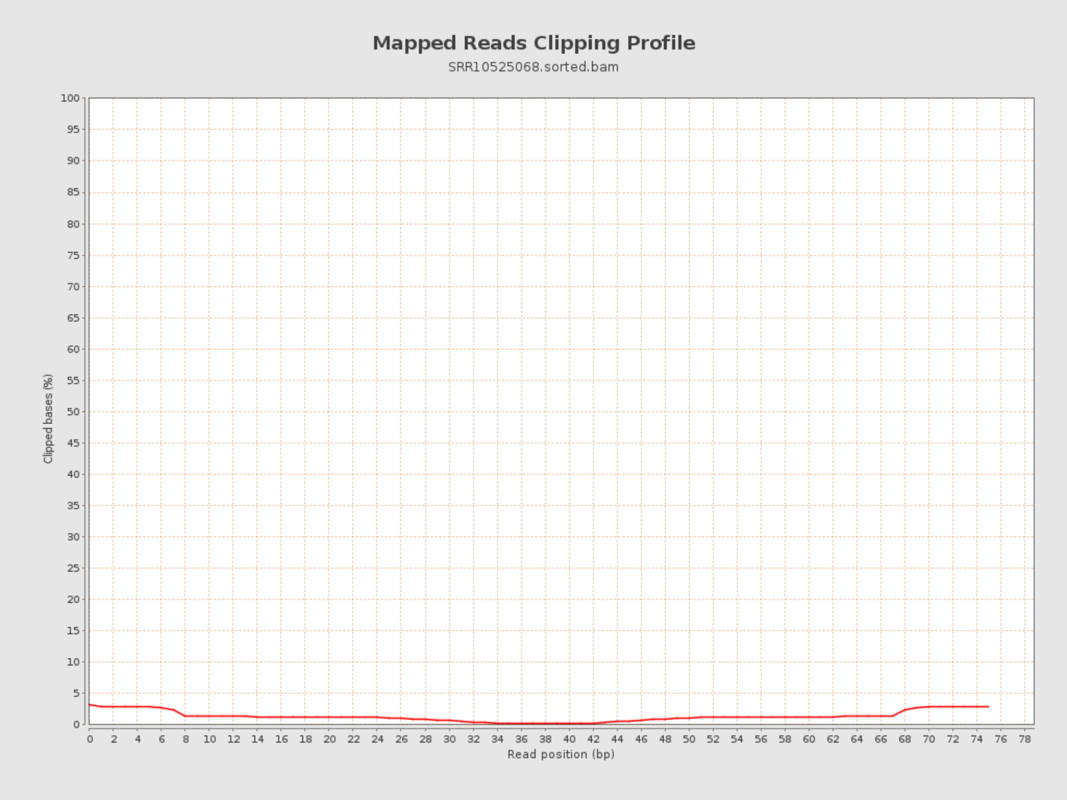
8. Results : Mapped Reads Nucleotide Content



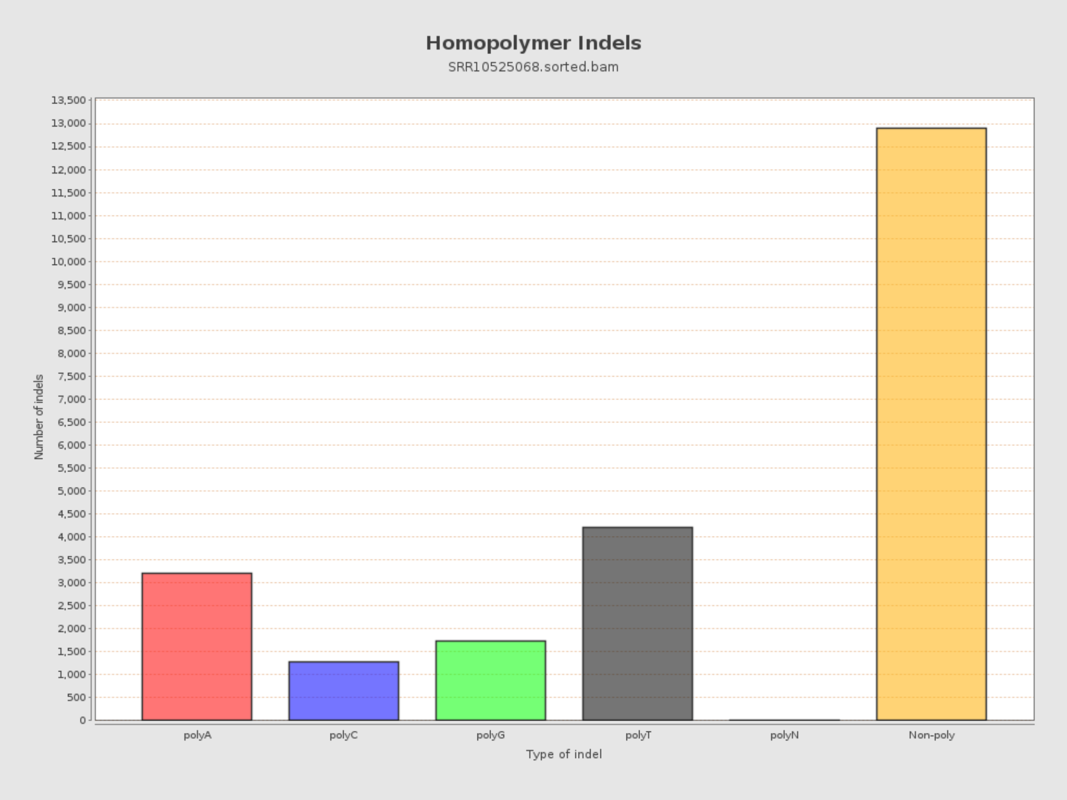
9. Results : Mapped Reads GC-content Distribution



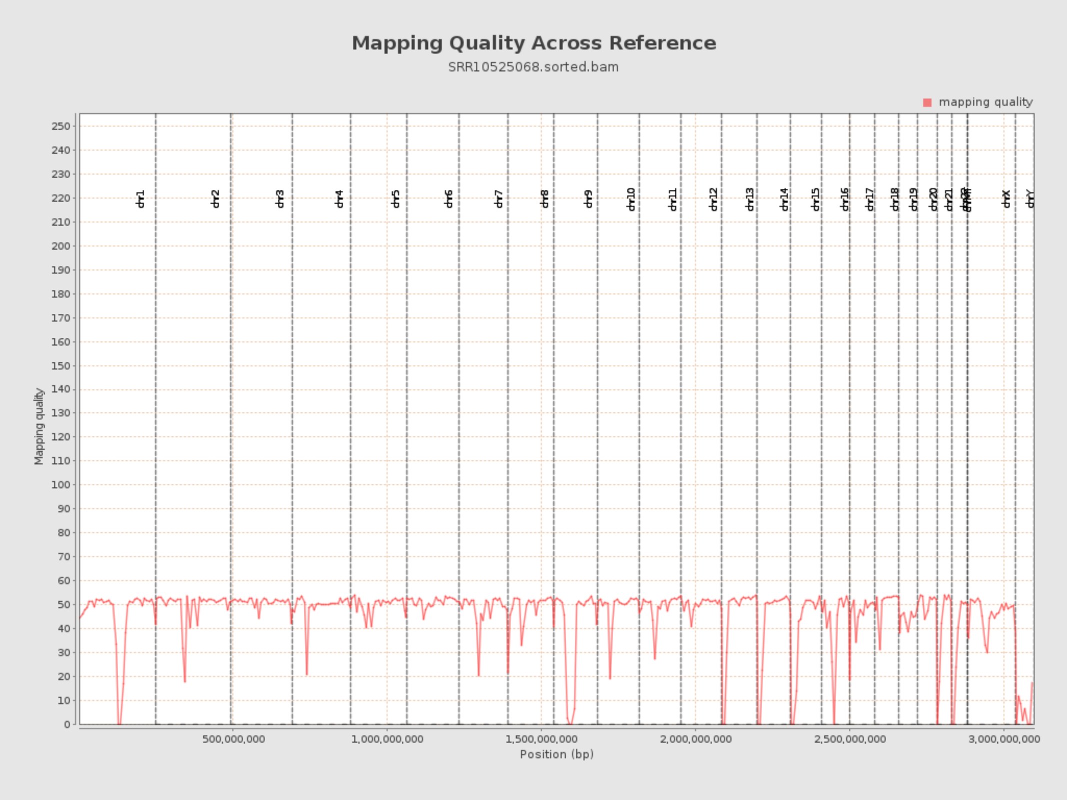
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram