Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:46:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524668.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_SRR10524668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:46:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,570,202
Mapped reads	1,457,874 / 92.85%
Unmapped reads	112,328 / 7.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,479 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	52,829 / 3.36%
Duplication rate	2.66%
Clipped reads	1,462,395 / 93.13%

2.2. ACGT Content

Number/percentage of A's	21,171,878 / 24.46%
Number/percentage of C's	16,358,671 / 18.9%
Number/percentage of T's	27,519,072 / 31.79%
Number/percentage of G's	21,506,590 / 24.84%
Number/percentage of N's	11,782 / 0.01%
GC Percentage	43.74%

2.3. Coverage

Mean	0.028

Standard Deviation	0.266

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

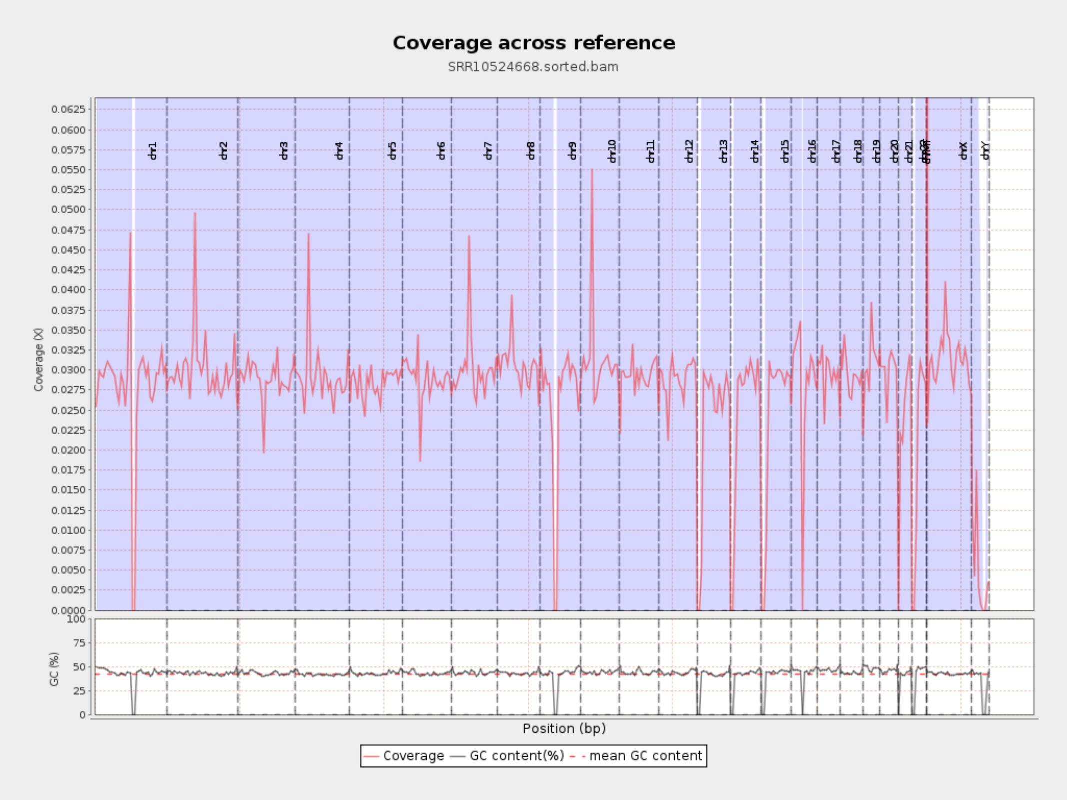
General error rate	0.51%
Mismatches	432,048
Insertions	5,375
Mapped reads with at least one insertion	0.37%
Deletions	15,767
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.4%

2.6. Chromosome stats

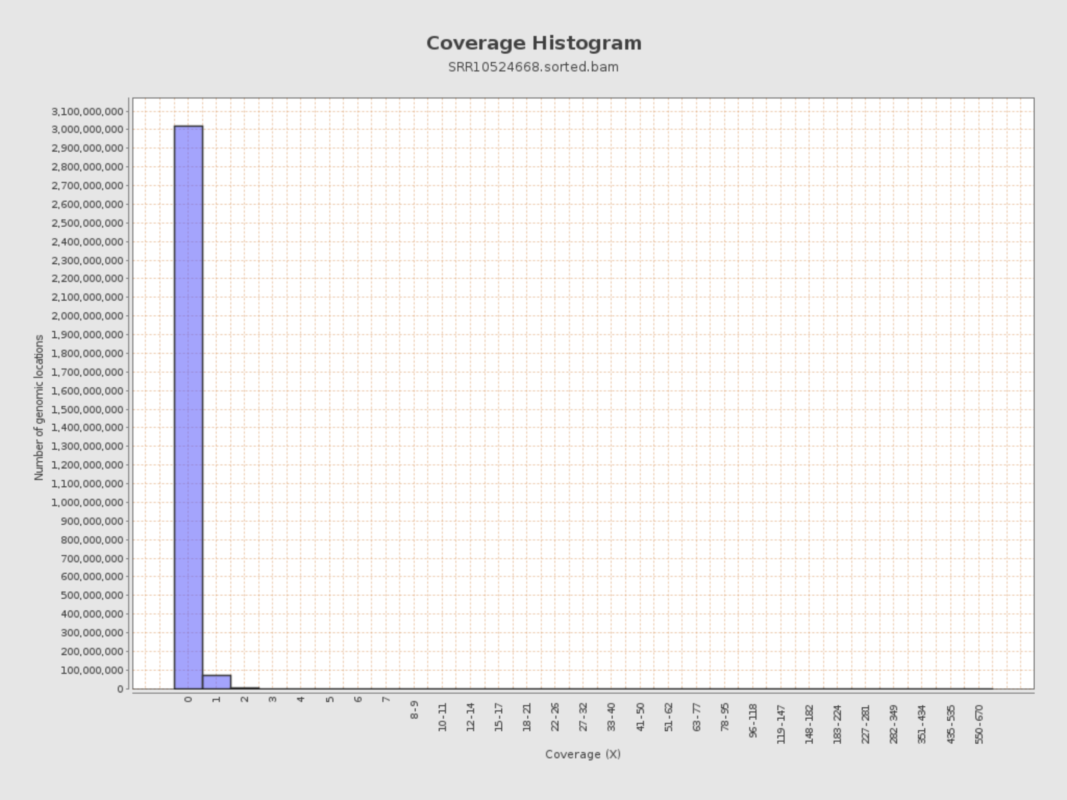
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6908362	0.0277	0.4606
chr2	243199373	7342502	0.0302	0.3578
chr3	198022430	5712294	0.0288	0.1833
chr4	191154276	5600154	0.0293	0.2077
chr5	180915260	5166121	0.0286	0.1829
chr6	171115067	4939211	0.0289	0.2022
chr7	159138663	4805993	0.0302	0.3232

chr8	146364022	4485772	0.0306	0.2849
chr9	141213431	3620407	0.0256	0.2205
chr10	135534747	4255937	0.0314	0.2758
chr11	135006516	3977283	0.0295	0.2401
chr12	133851895	3866384	0.0289	0.1854
chr13	115169878	2651548	0.023	0.1647
chr14	107349540	2586123	0.0241	0.173
chr15	102531392	2433654	0.0237	0.1671
chr16	90354753	2514365	0.0278	0.1989
chr17	81195210	2394260	0.0295	0.1964
chr18	78077248	2298970	0.0294	0.3951
chr19	59128983	1837469	0.0311	0.3516
chr20	63025520	1862382	0.0295	0.1891
chr21	48129895	1144365	0.0238	0.1878
chr22	51304566	1023242	0.0199	0.1522
chrMT	16571	9186	0.5543	0.8455
chrX	155270560	4871755	0.0314	0.2082
chrY	59373566	285318	0.0048	0.1653

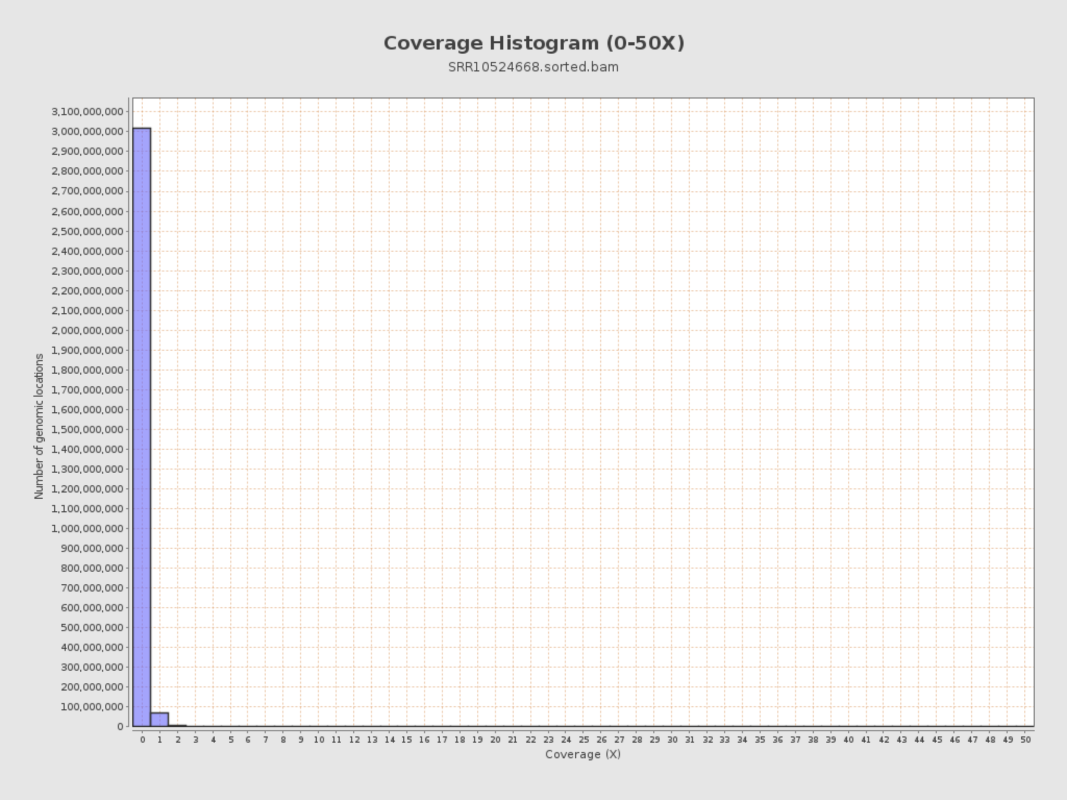
3. Results : Coverage across reference



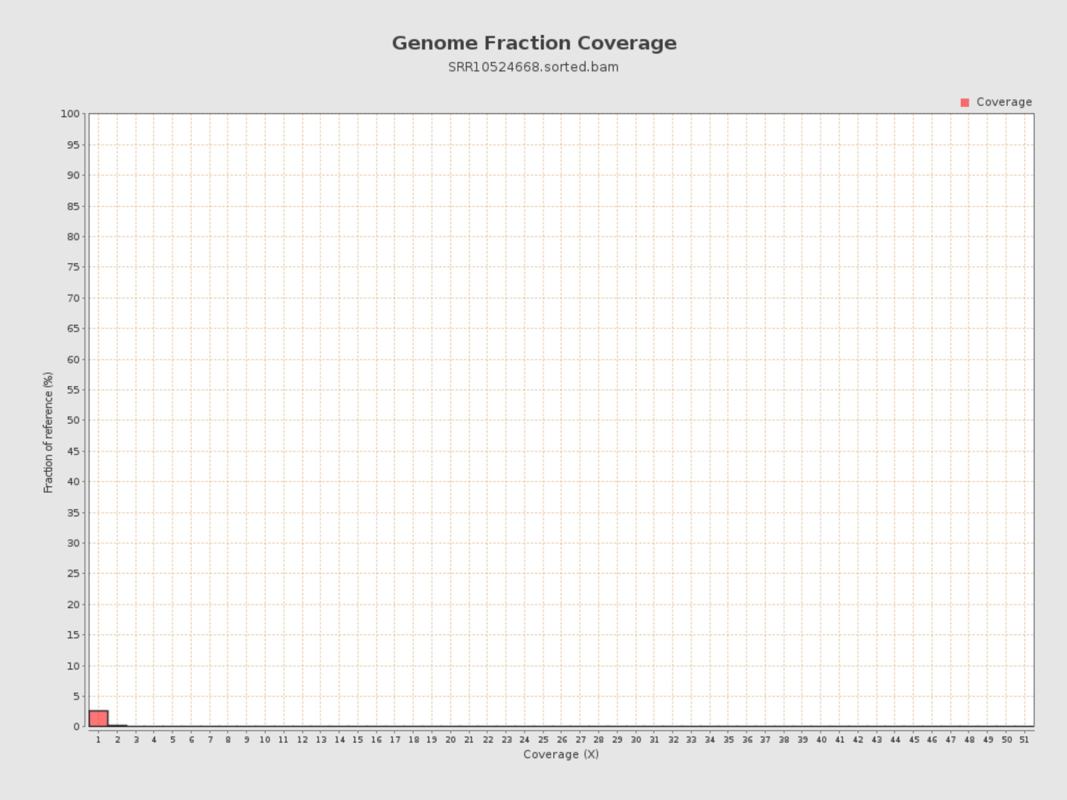
4. Results : Coverage Histogram



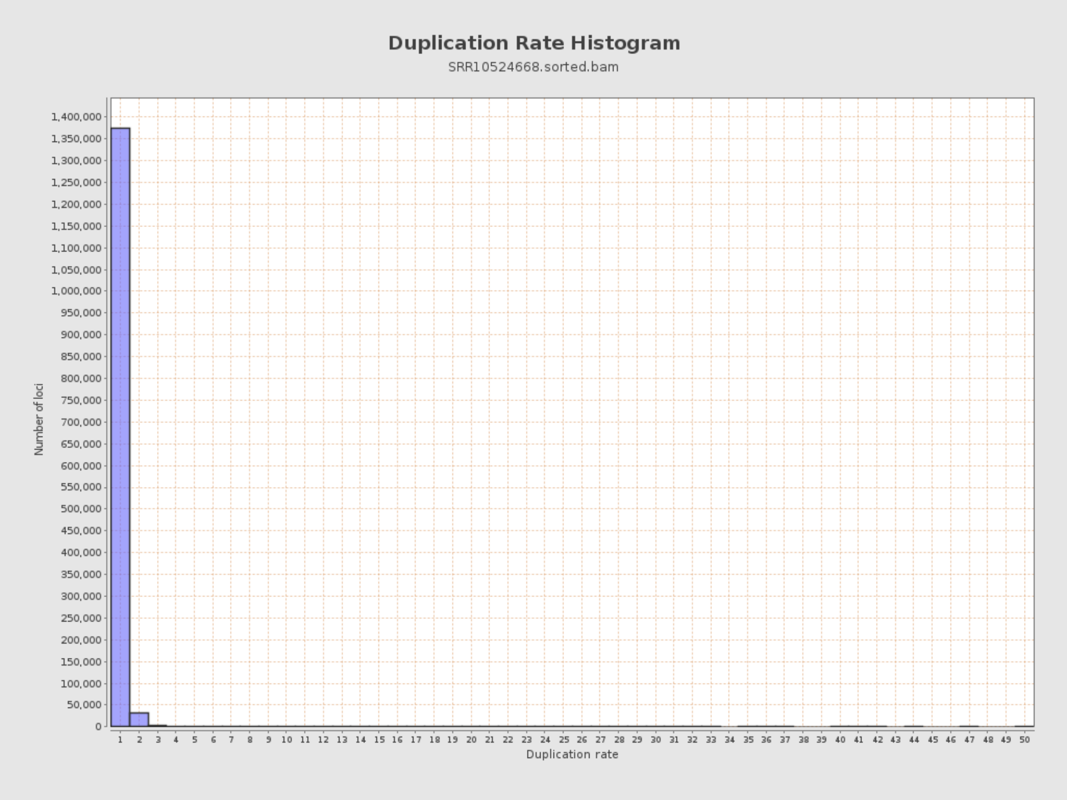
5. Results : Coverage Histogram (0-50X)



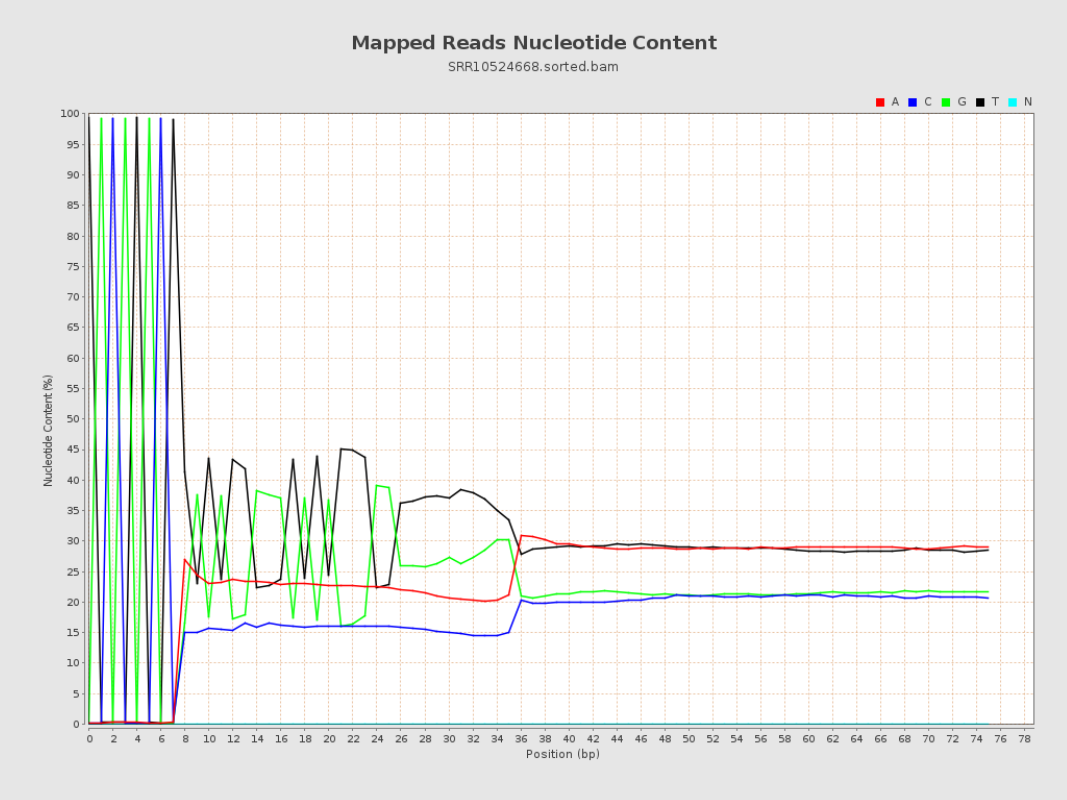
6. Results : Genome Fraction Coverage



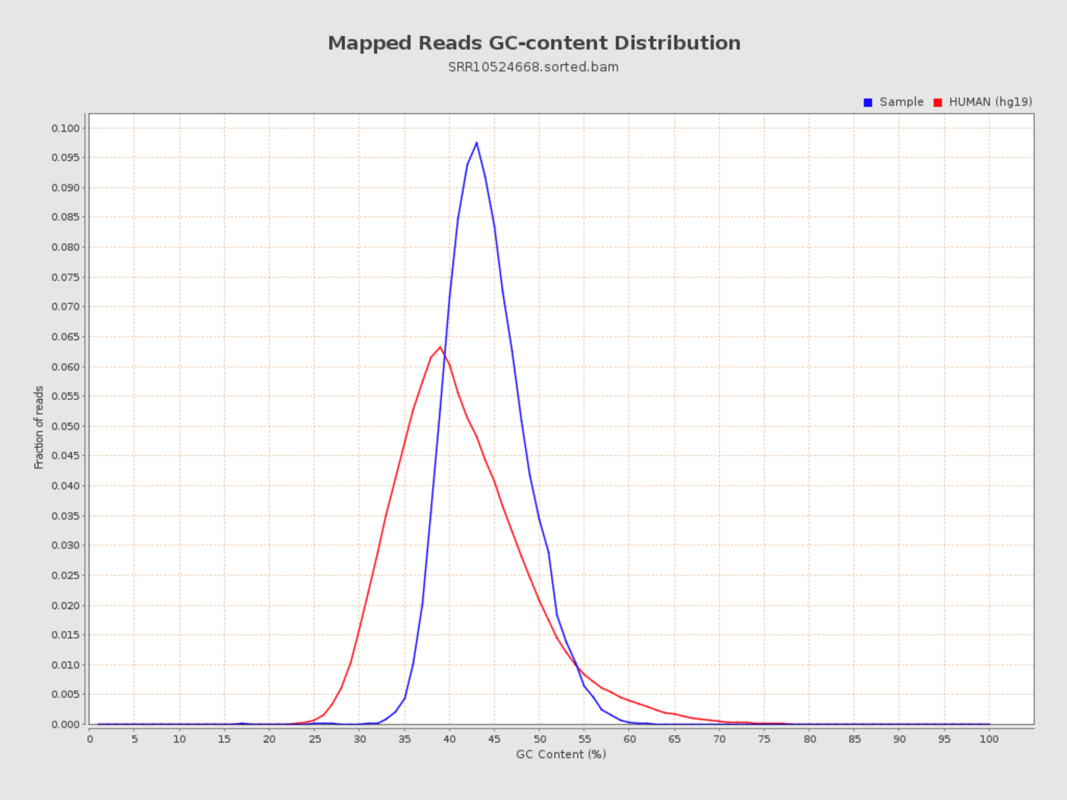
7. Results : Duplication Rate Histogram



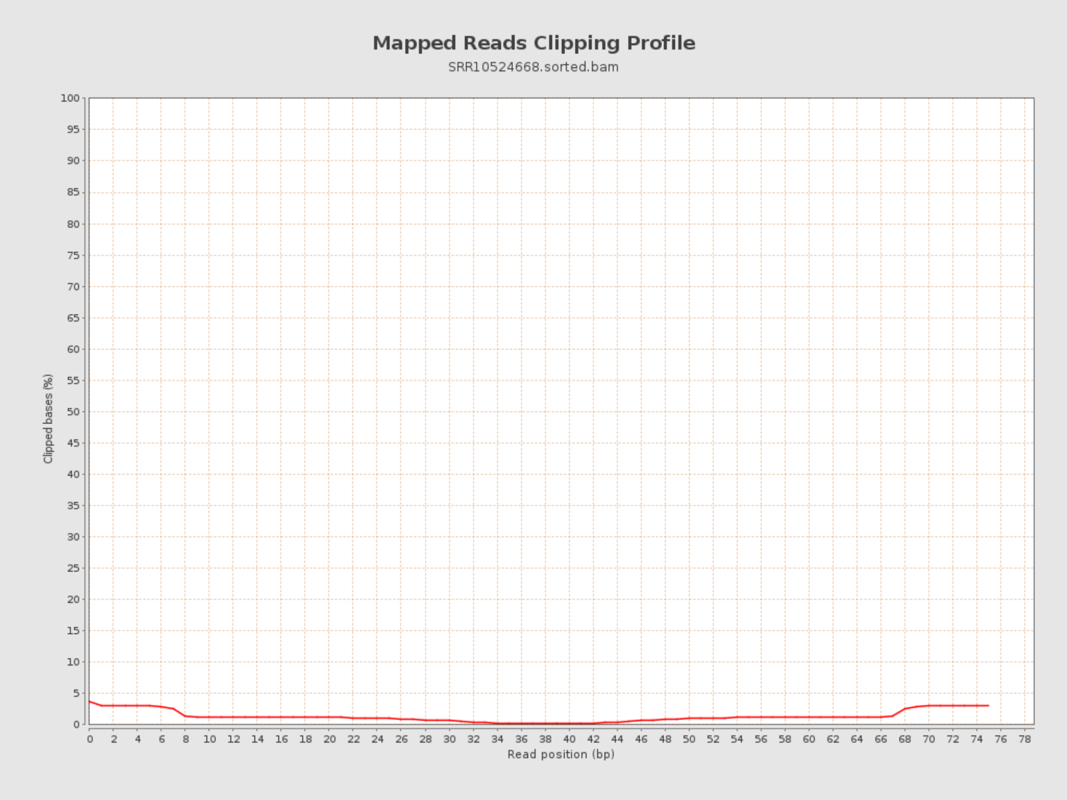
8. Results : Mapped Reads Nucleotide Content



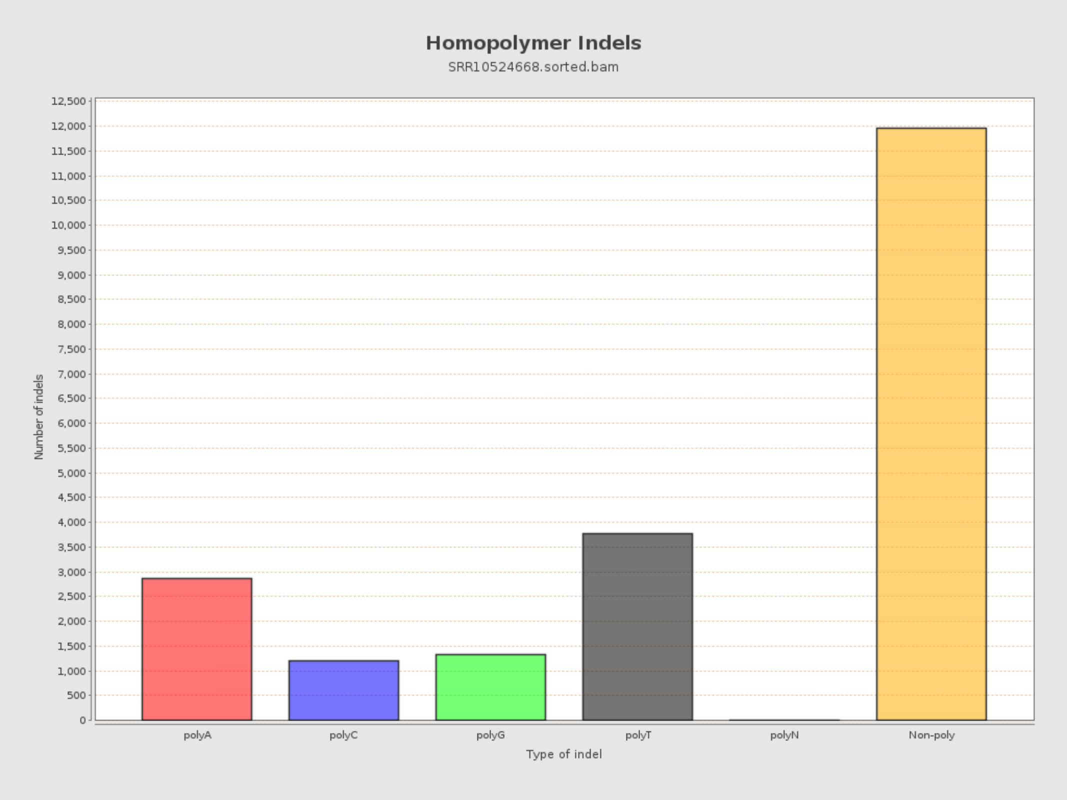
9. Results : Mapped Reads GC-content Distribution



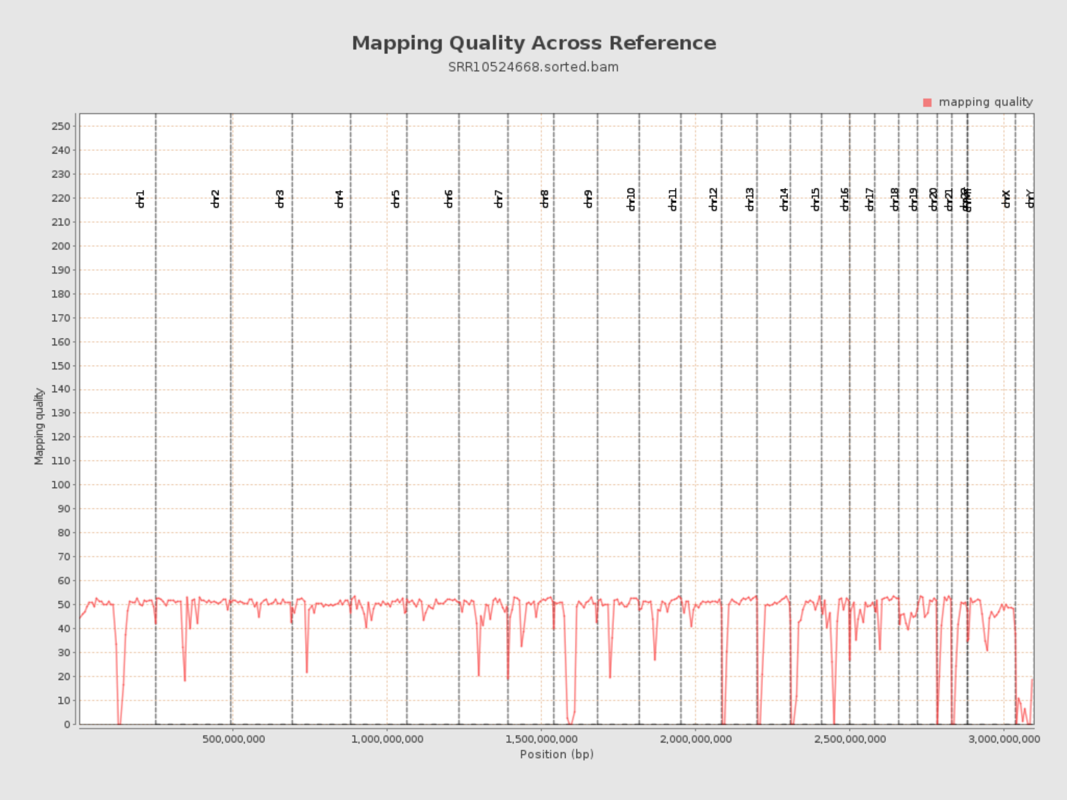
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram