Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:54:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524768.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_SRR10524768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:54:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,478,836
Mapped reads	1,338,912 / 90.54%
Unmapped reads	139,924 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,267 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	47,182 / 3.19%
Duplication rate	2.65%
Clipped reads	1,340,279 / 90.63%

2.2. ACGT Content

Number/percentage of A's	19,016,620 / 24.83%
Number/percentage of C's	14,810,111 / 19.34%
Number/percentage of T's	24,209,013 / 31.61%
Number/percentage of G's	18,547,483 / 24.22%
Number/percentage of N's	9,958 / 0.01%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2268

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

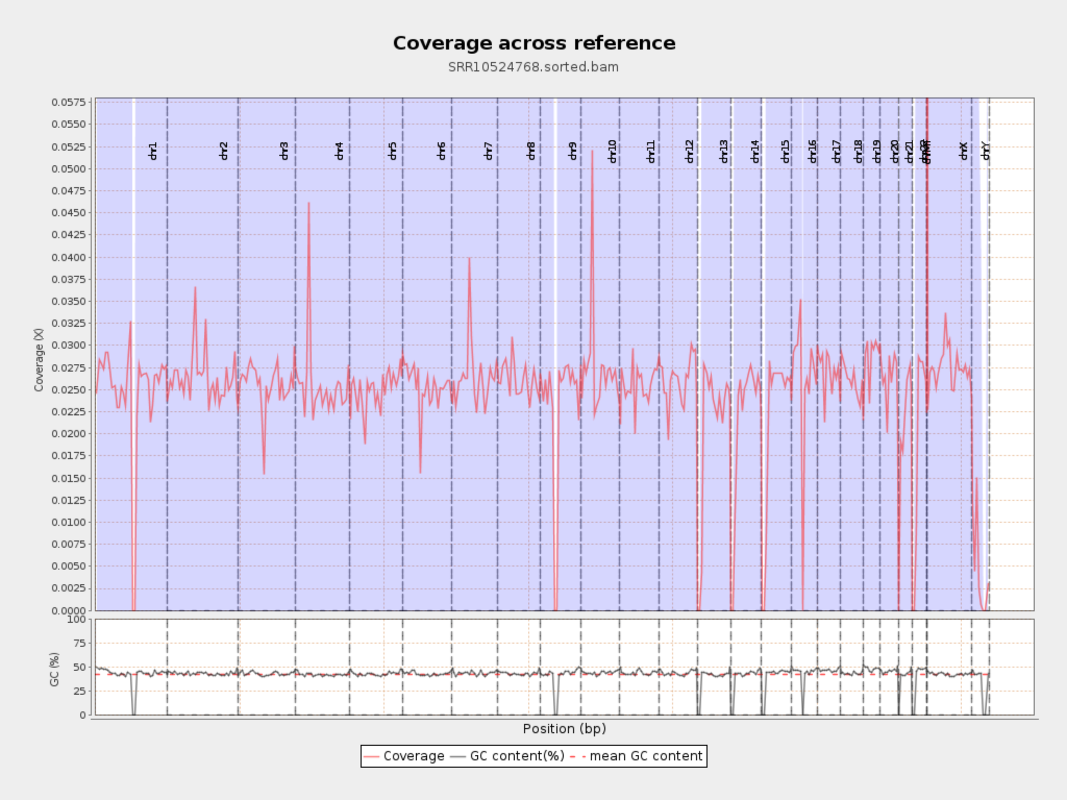
General error rate	0.53%
Mismatches	392,192
Insertions	5,541
Mapped reads with at least one insertion	0.41%
Deletions	15,218
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.28%

2.6. Chromosome stats

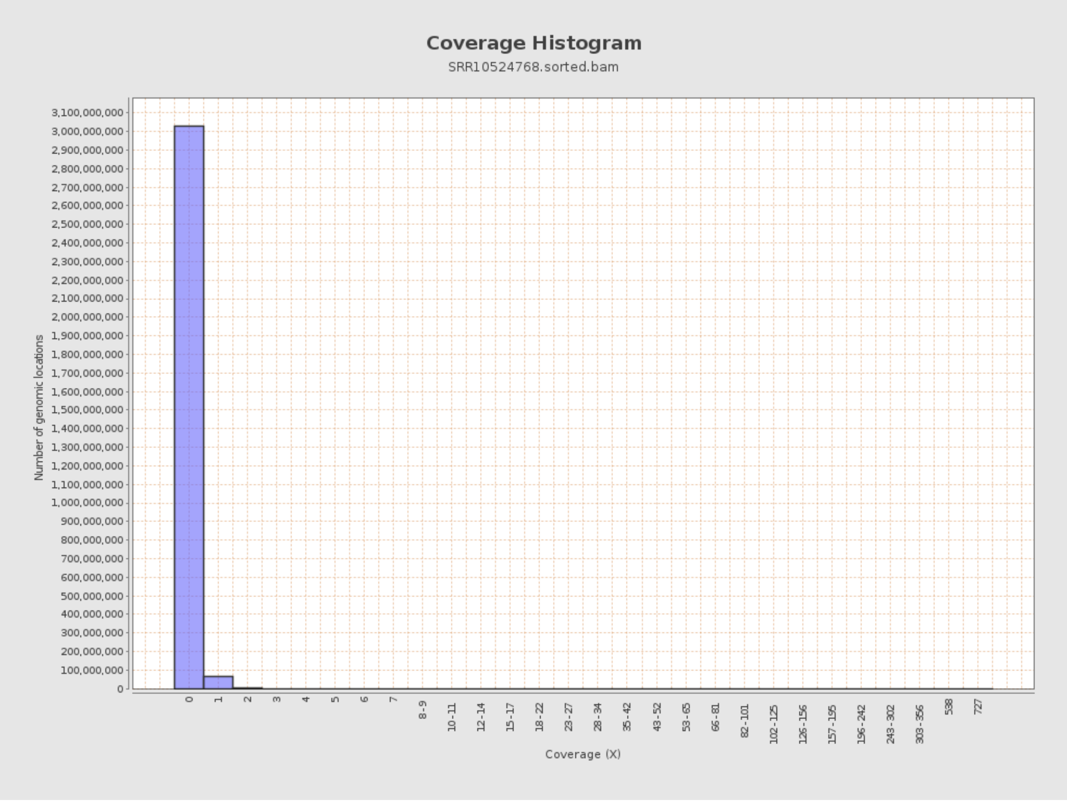
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6125882	0.0246	0.3037
chr2	243199373	6425264	0.0264	0.356
chr3	198022430	5045084	0.0255	0.1765
chr4	191154276	4890028	0.0256	0.1966
chr5	180915260	4540718	0.0251	0.1723
chr6	171115067	4335617	0.0253	0.189
chr7	159138663	4215580	0.0265	0.2833

chr8	146364022	3820803	0.0261	0.2062
chr9	141213431	3227325	0.0229	0.1922
chr10	135534747	3745436	0.0276	0.2682
chr11	135006516	3455189	0.0256	0.2042
chr12	133851895	3484100	0.026	0.1783
chr13	115169878	2367506	0.0206	0.157
chr14	107349540	2285080	0.0213	0.1647
chr15	102531392	2201335	0.0215	0.1602
chr16	90354753	2322679	0.0257	0.1926
chr17	81195210	2186731	0.0269	0.1861
chr18	78077248	2037858	0.0261	0.2893
chr19	59128983	1694897	0.0287	0.2482
chr20	63025520	1656744	0.0263	0.1855
chr21	48129895	1001018	0.0208	0.1718
chr22	51304566	974726	0.019	0.1513
chrMT	16571	44298	2.6732	2.1724
chrX	155270560	4274001	0.0275	0.1938
chrY	59373566	259797	0.0044	0.1317

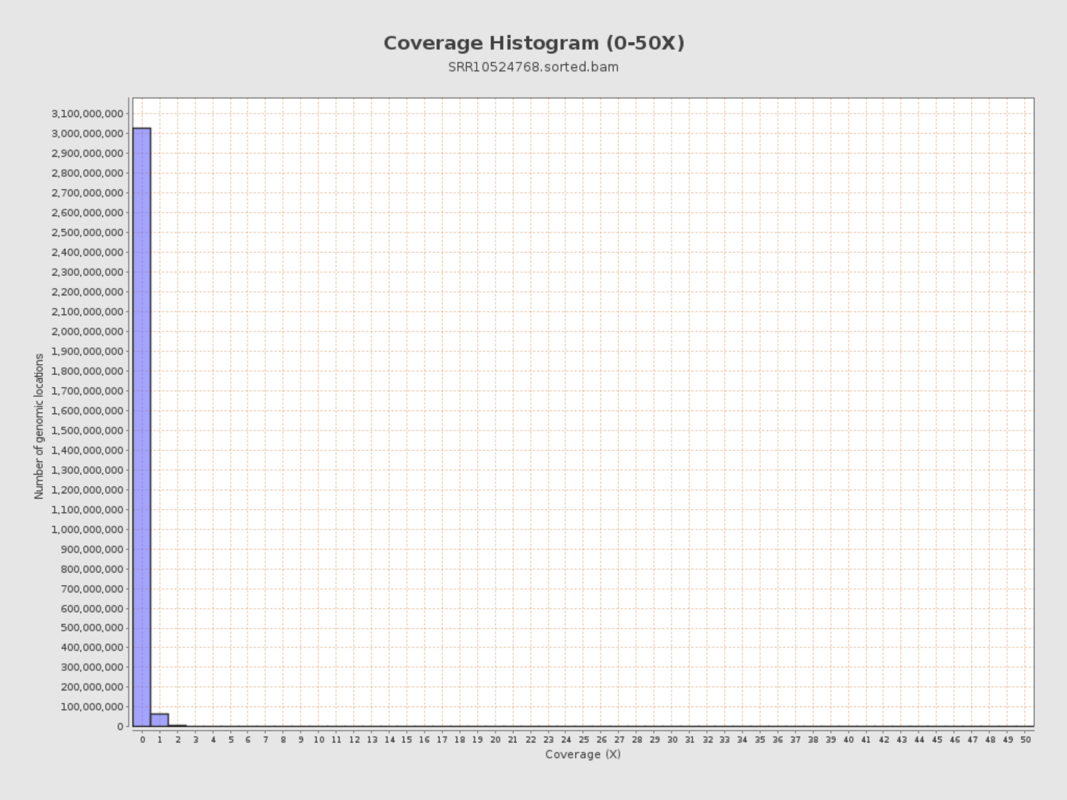
3. Results : Coverage across reference



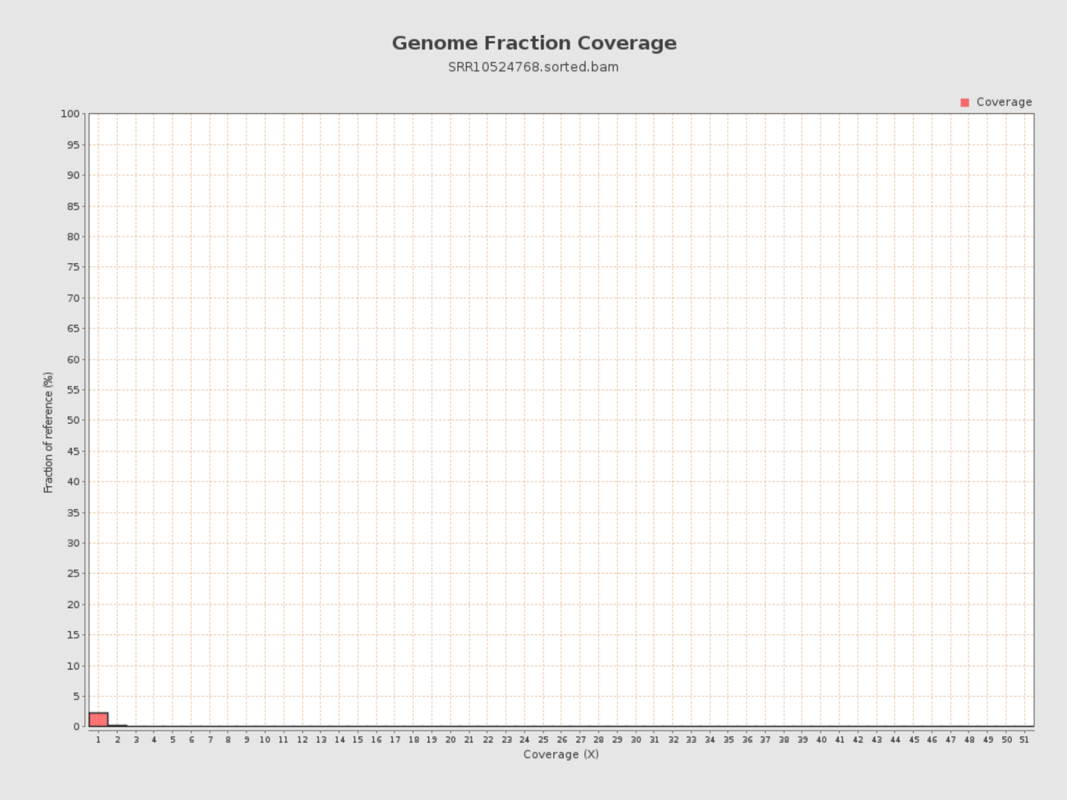
4. Results : Coverage Histogram



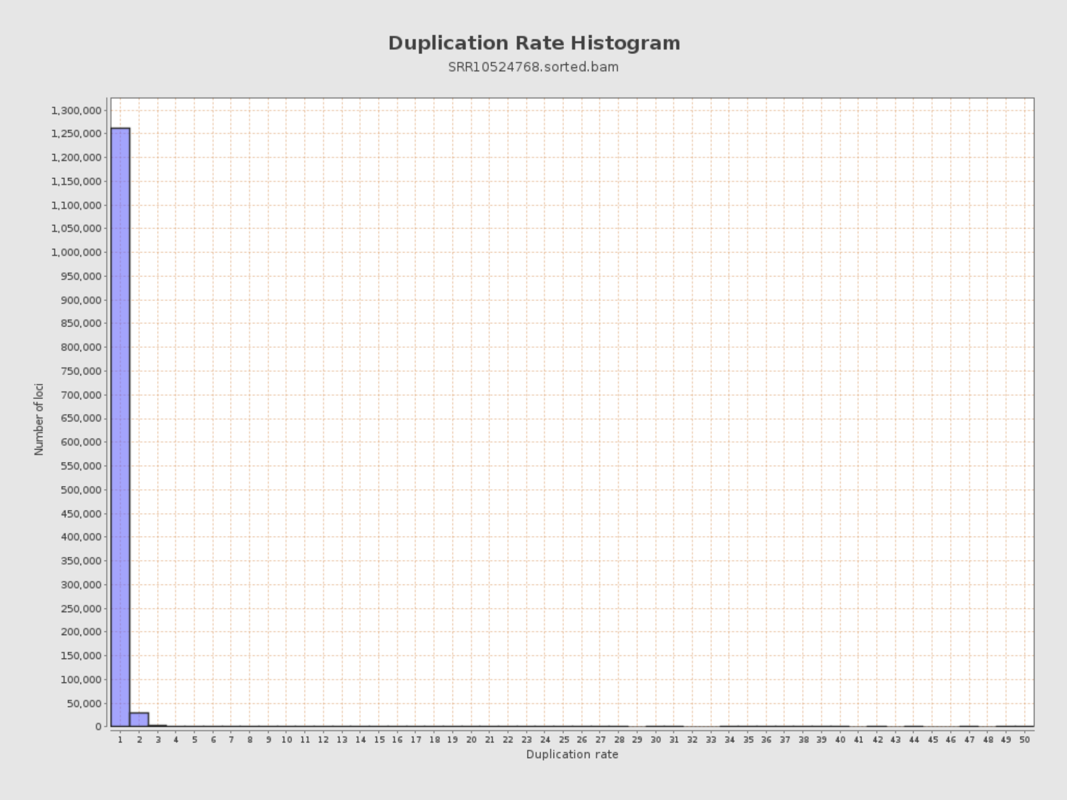
5. Results : Coverage Histogram (0-50X)



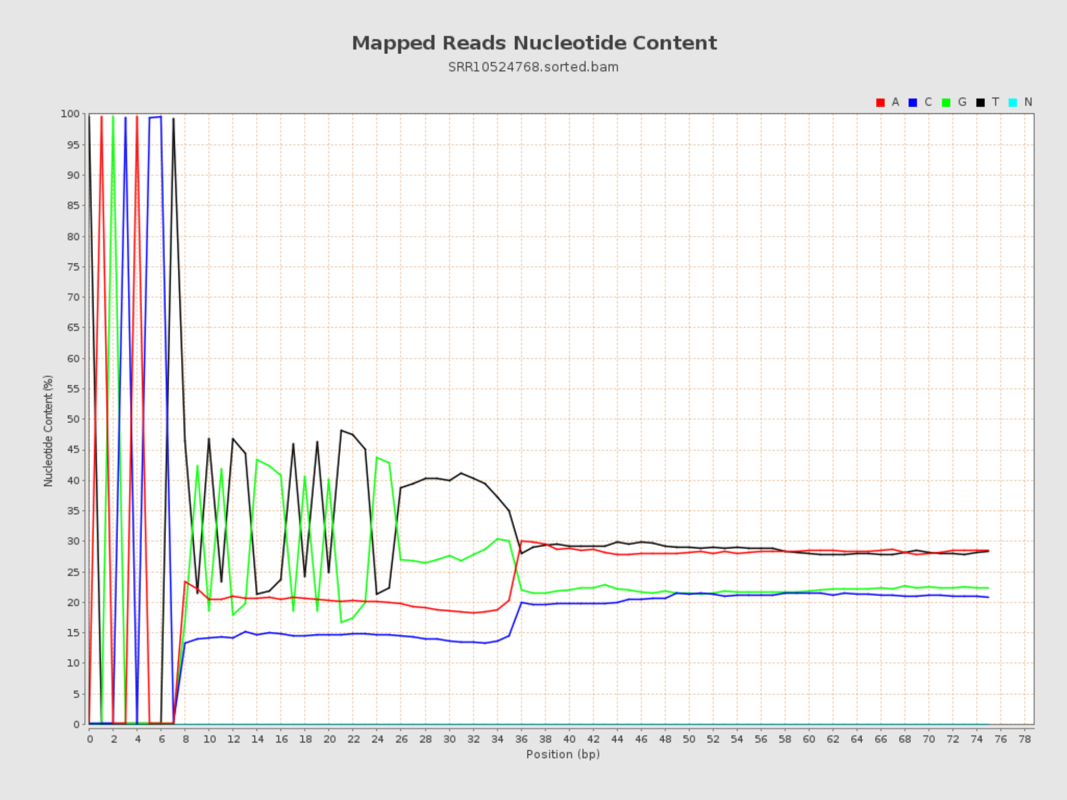
6. Results : Genome Fraction Coverage



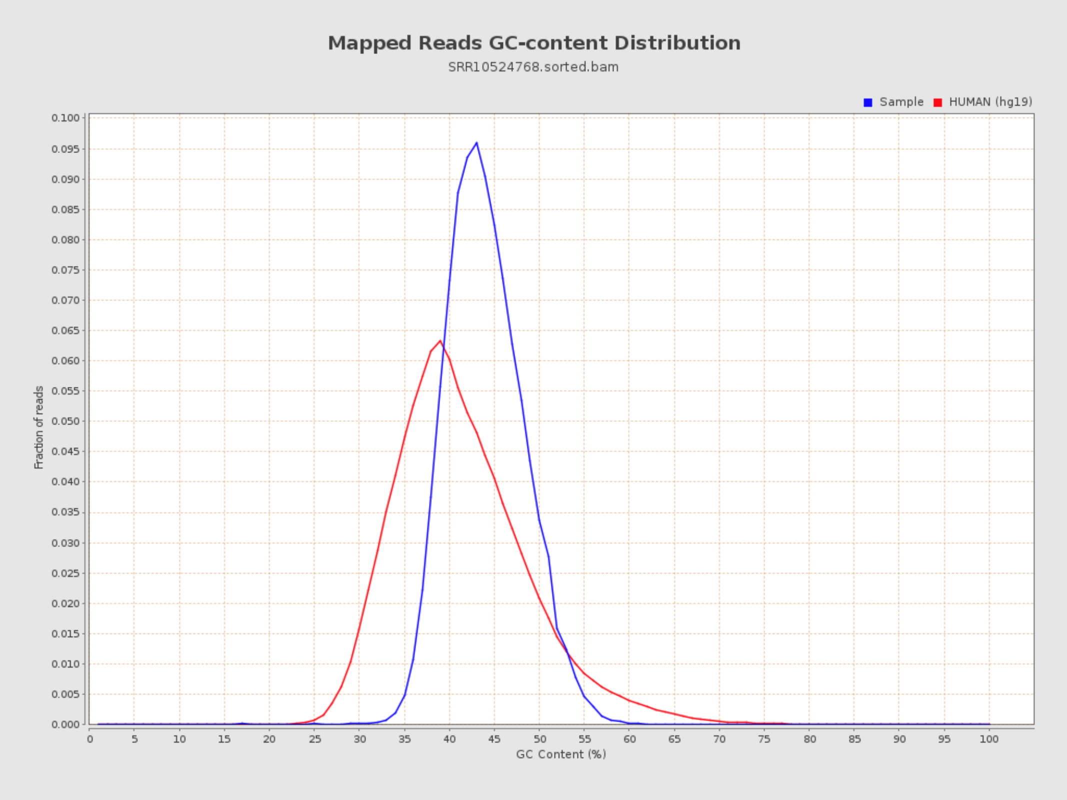
7. Results : Duplication Rate Histogram



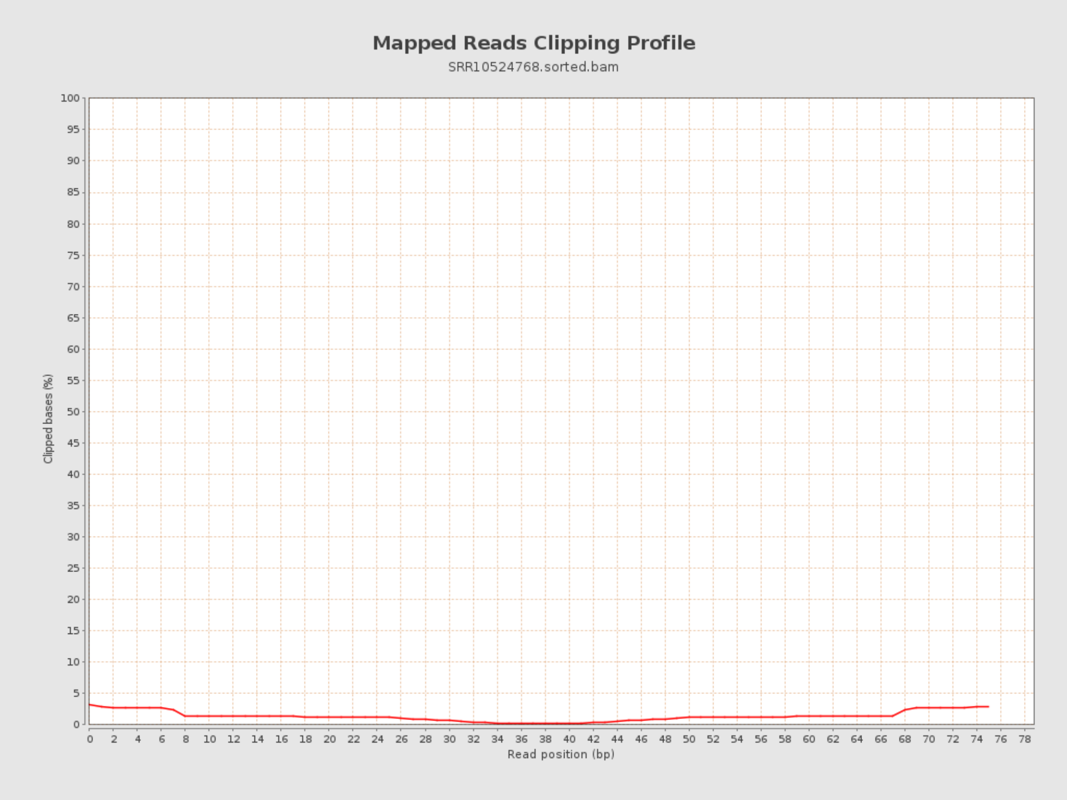
8. Results : Mapped Reads Nucleotide Content



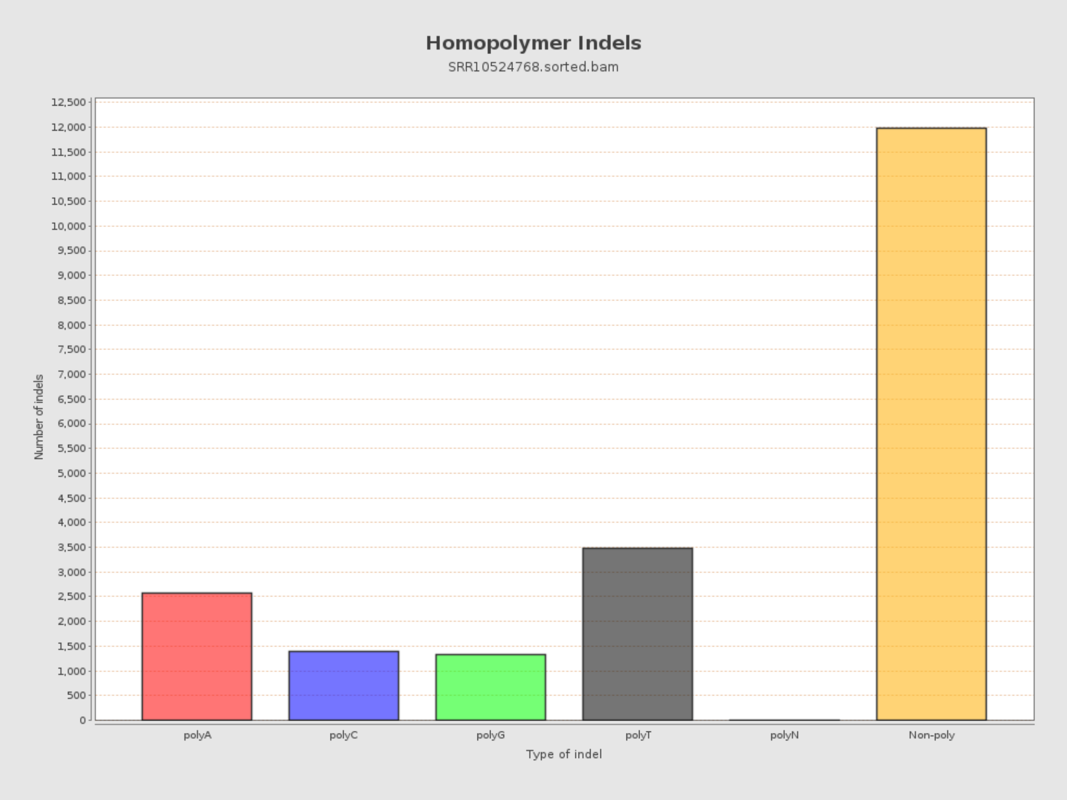
9. Results : Mapped Reads GC-content Distribution



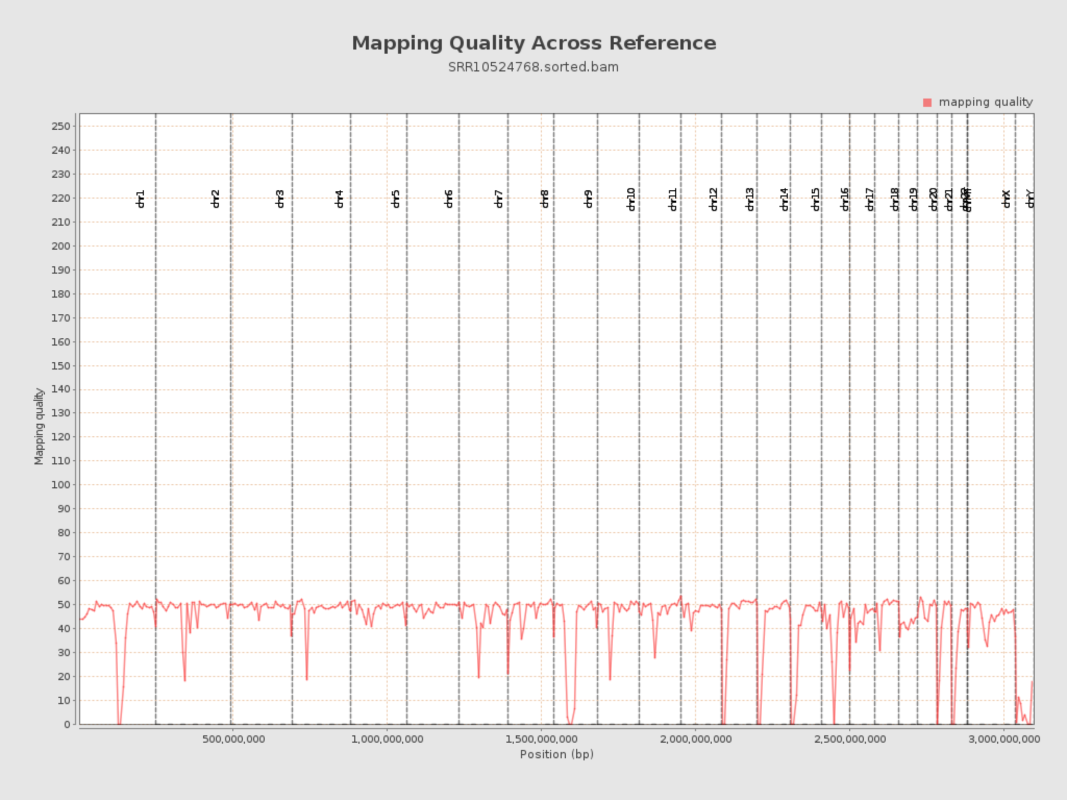
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram