Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:15:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524624.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_SRR10524624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:15:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,850,388
Mapped reads	1,722,017 / 93.06%
Unmapped reads	128,371 / 6.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,924 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	78,072 / 4.22%
Duplication rate	3.5%
Clipped reads	1,719,191 / 92.91%

2.2. ACGT Content

Number/percentage of A's	24,065,229 / 23.99%
Number/percentage of C's	19,289,024 / 19.23%
Number/percentage of T's	33,243,091 / 33.14%
Number/percentage of G's	23,726,744 / 23.65%
Number/percentage of N's	605 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.2827

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

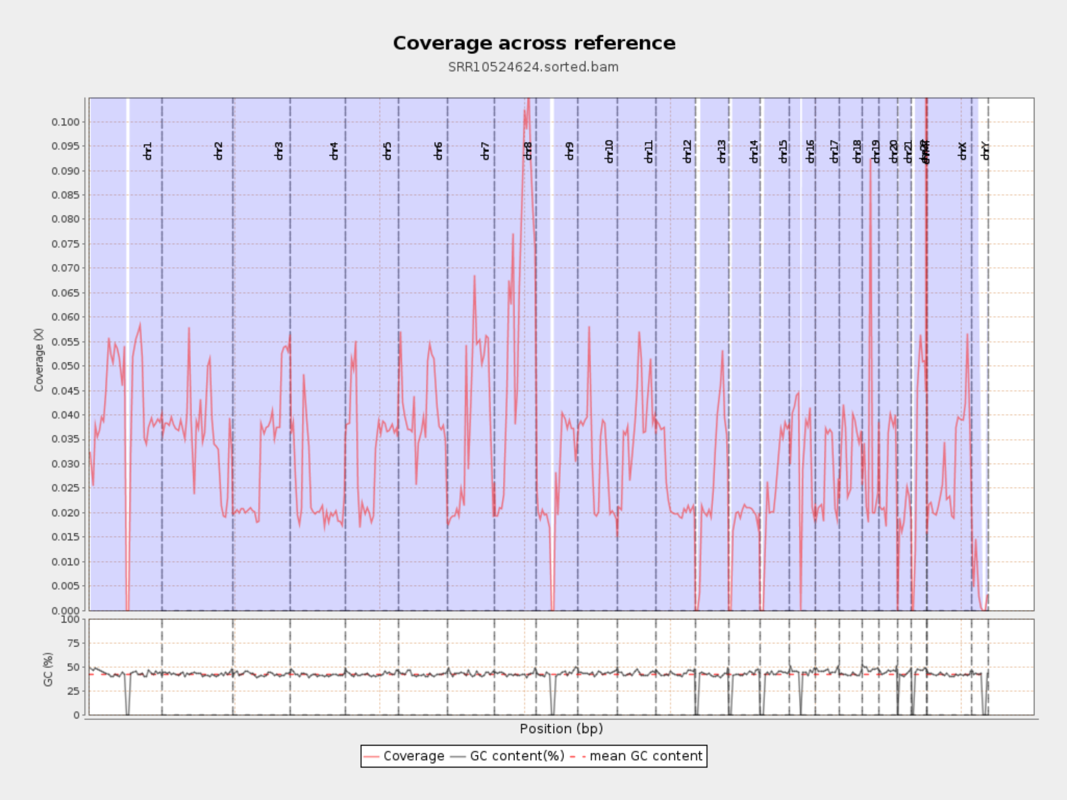
General error rate	0.48%
Mismatches	470,861
Insertions	7,011
Mapped reads with at least one insertion	0.41%
Deletions	19,185
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.27%

2.6. Chromosome stats

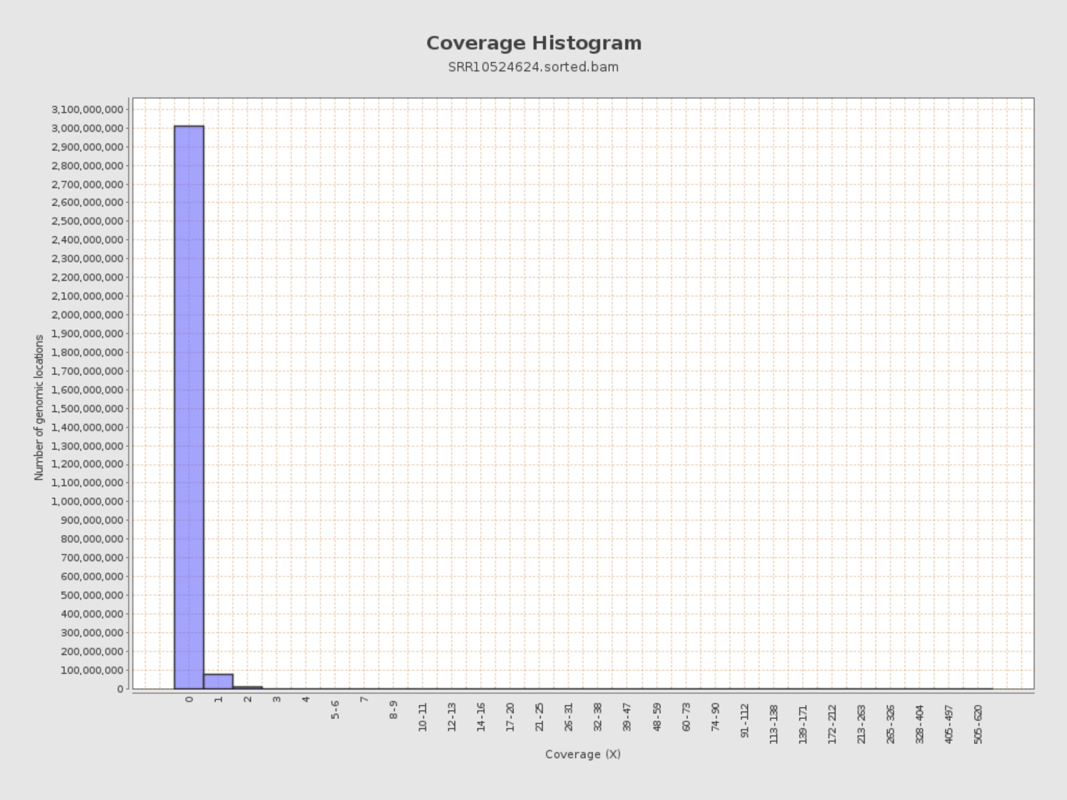
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10248324	0.0411	0.4867
chr2	243199373	8828624	0.0363	0.3222
chr3	198022430	6294052	0.0318	0.1984
chr4	191154276	4541915	0.0238	0.1976
chr5	180915260	6031291	0.0333	0.2043
chr6	171115067	6992205	0.0409	0.2395
chr7	159138663	6044770	0.038	0.3861

chr8	146364022	8820952	0.0603	0.3808
chr9	141213431	3572304	0.0253	0.2493
chr10	135534747	4244929	0.0313	0.2781
chr11	135006516	5085007	0.0377	0.2756
chr12	133851895	3302271	0.0247	0.1802
chr13	115169878	2972976	0.0258	0.1795
chr14	107349540	1859457	0.0173	0.1541
chr15	102531392	2474375	0.0241	0.1856
chr16	90354753	2921103	0.0323	0.212
chr17	81195210	2164996	0.0267	0.1912
chr18	78077248	2671294	0.0342	0.4082
chr19	59128983	1934009	0.0327	0.344
chr20	63025520	1850093	0.0294	0.1948
chr21	48129895	878703	0.0183	0.1697
chr22	51304566	1763624	0.0344	0.2073
chrMT	16571	51493	3.1074	2.4632
chrX	155270560	4558327	0.0294	0.2189
chrY	59373566	250167	0.0042	0.1208

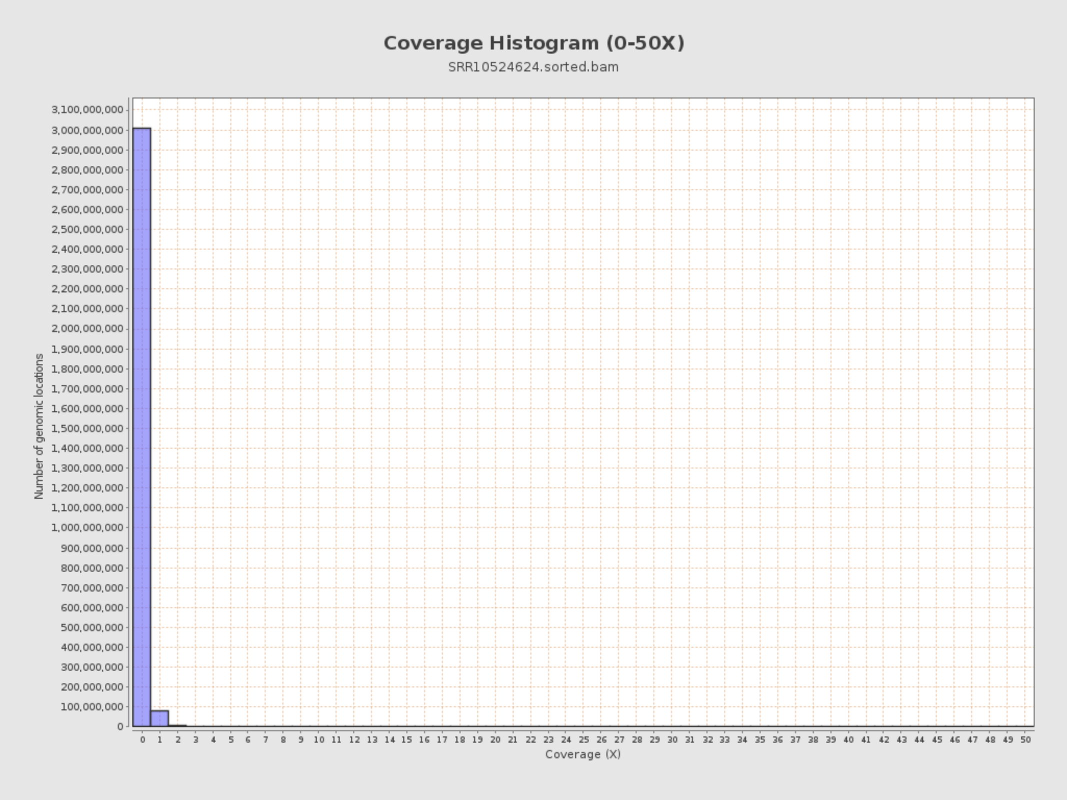
3. Results : Coverage across reference



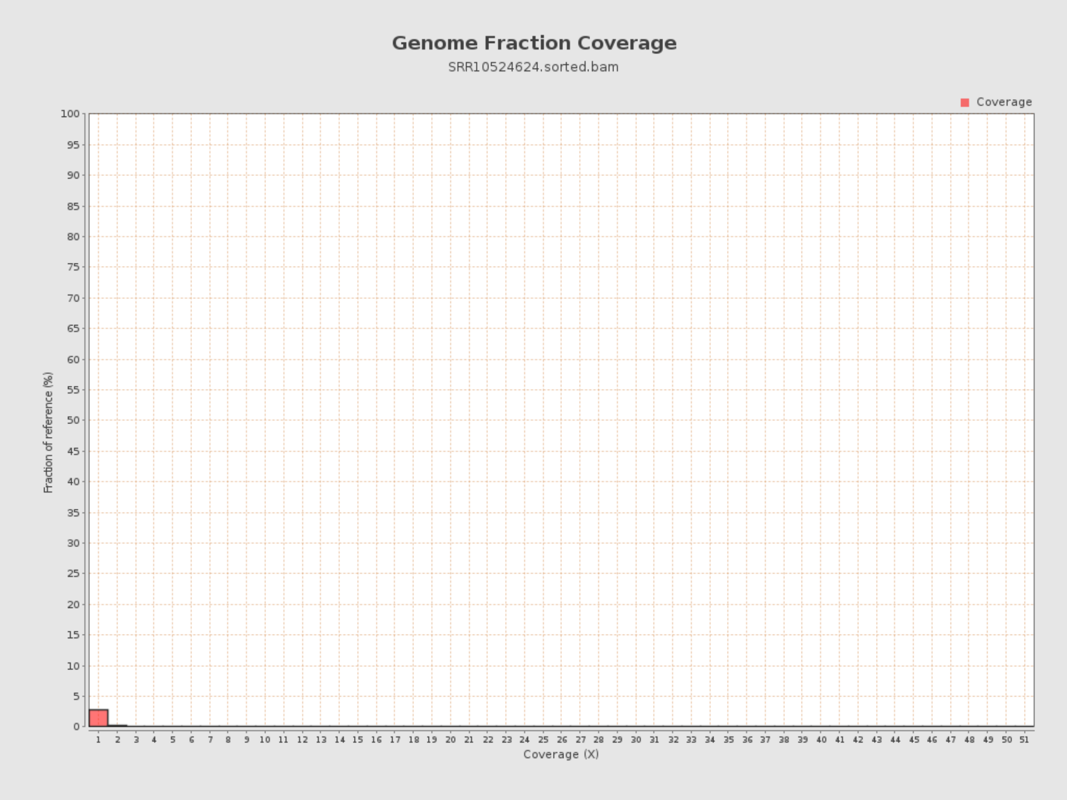
4. Results : Coverage Histogram



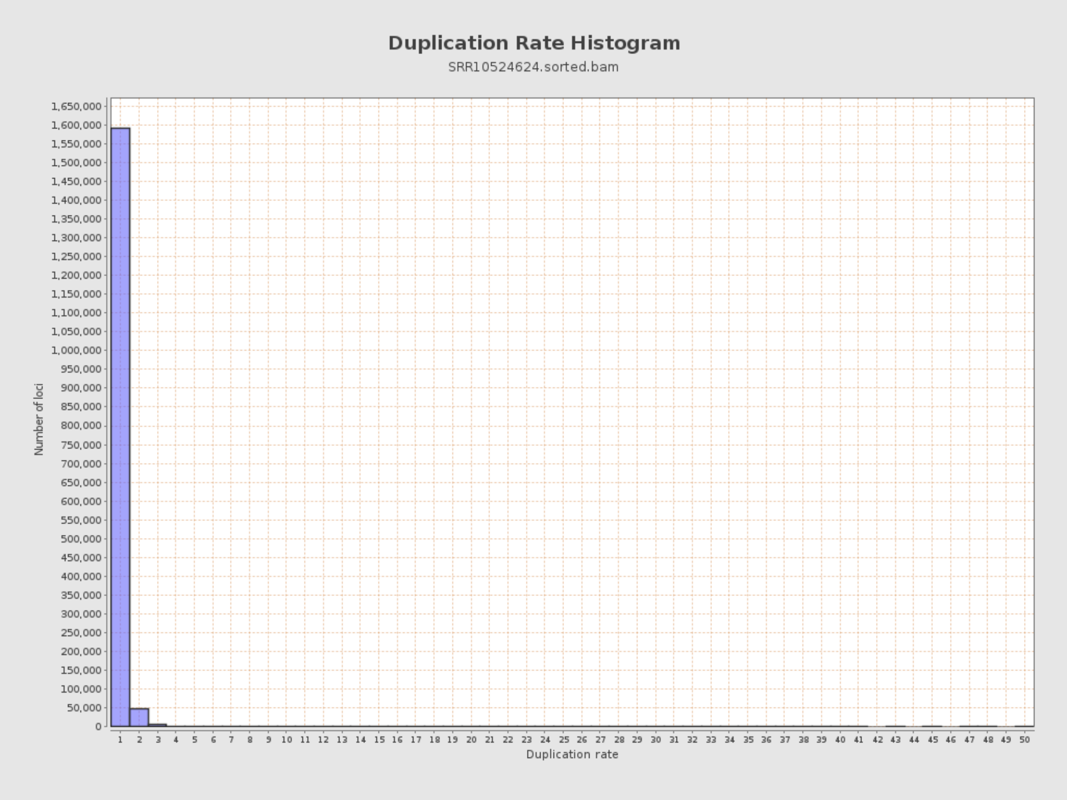
5. Results : Coverage Histogram (0-50X)



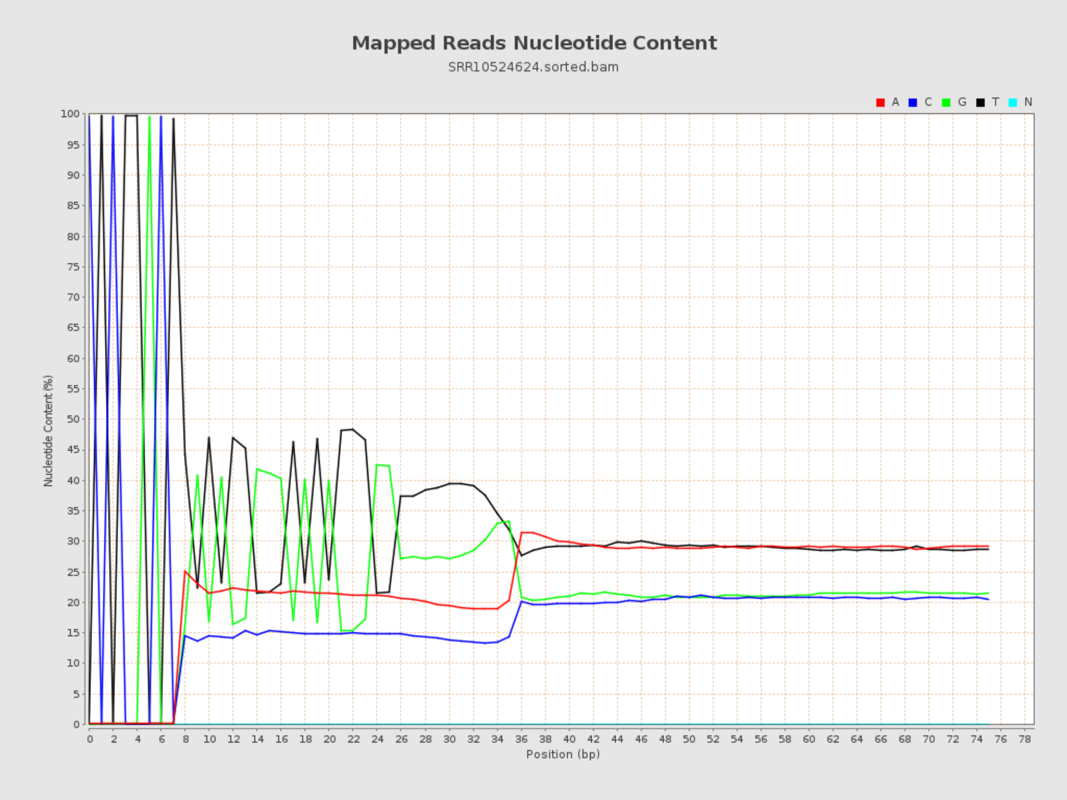
6. Results : Genome Fraction Coverage



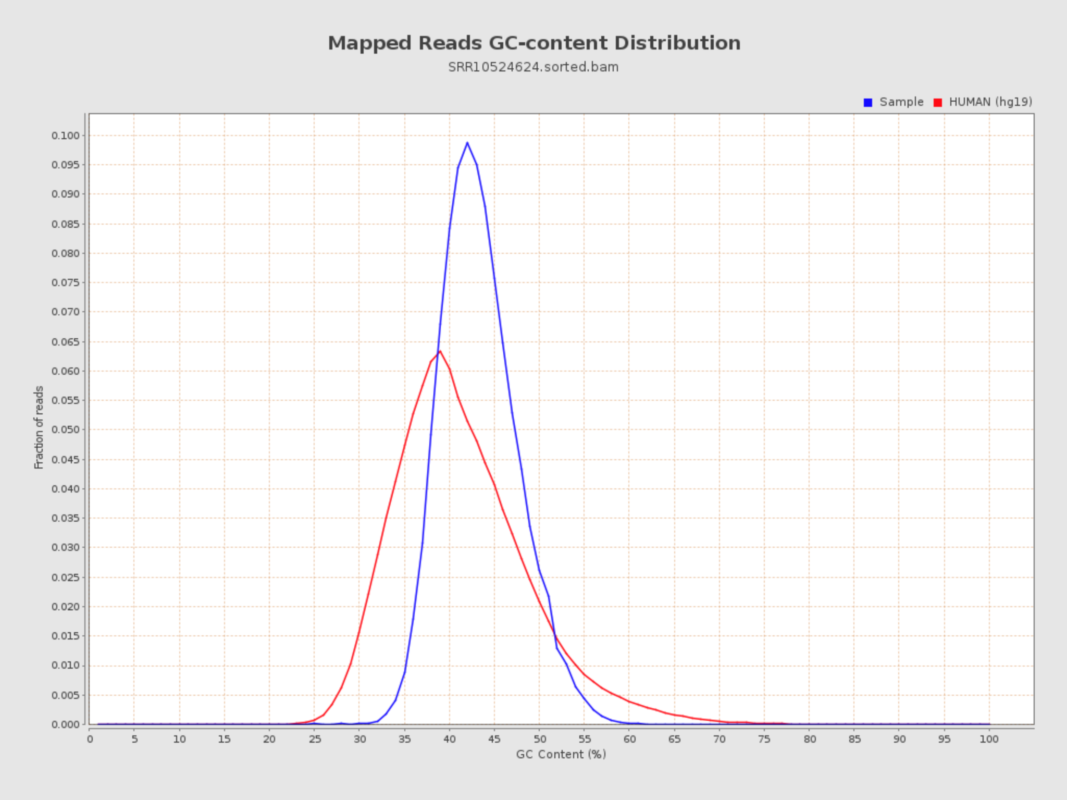
7. Results : Duplication Rate Histogram



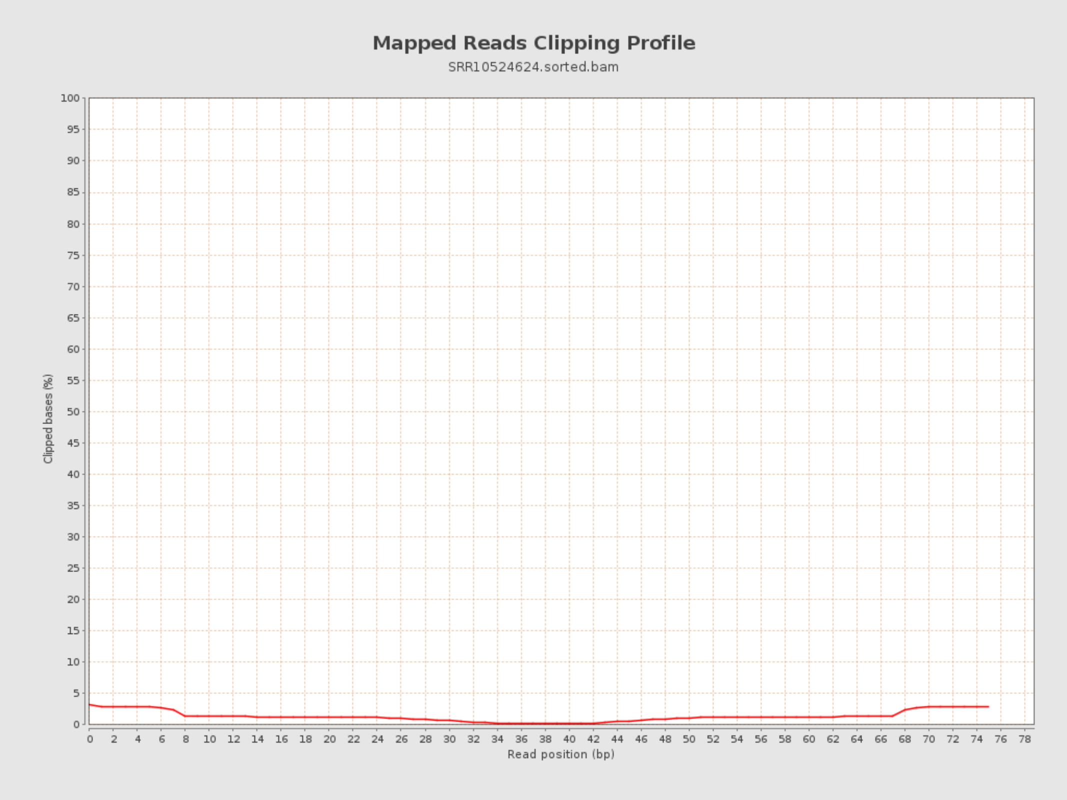
8. Results : Mapped Reads Nucleotide Content



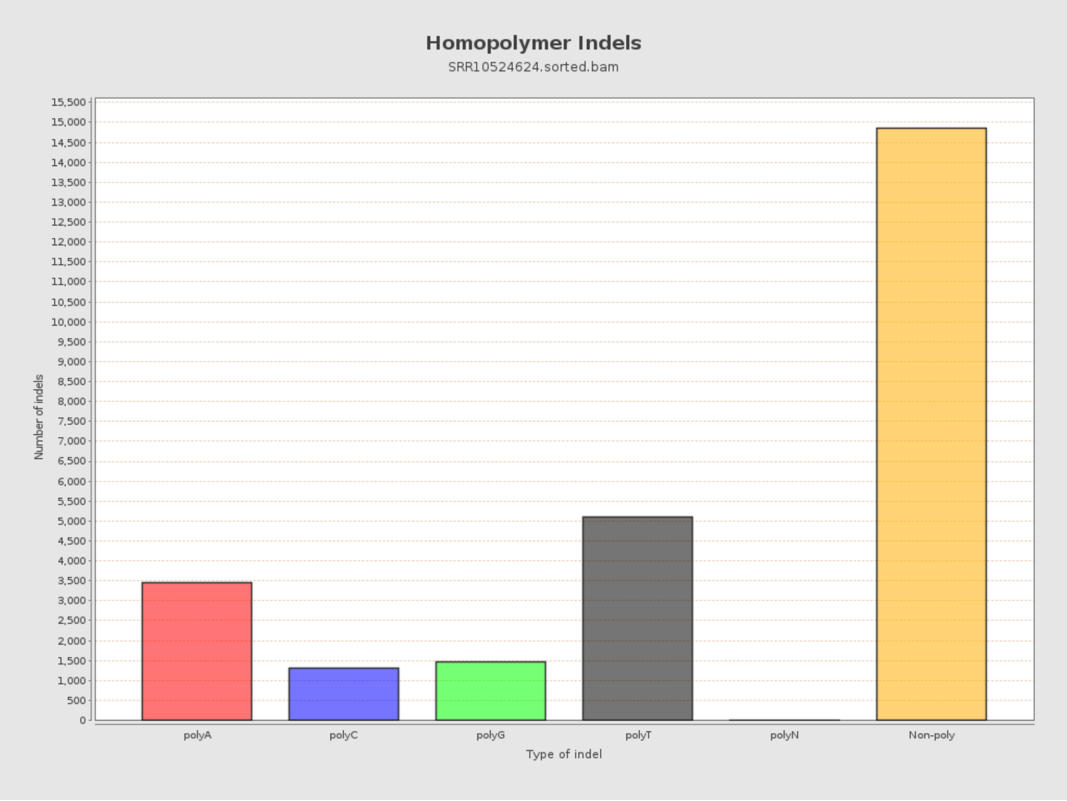
9. Results : Mapped Reads GC-content Distribution



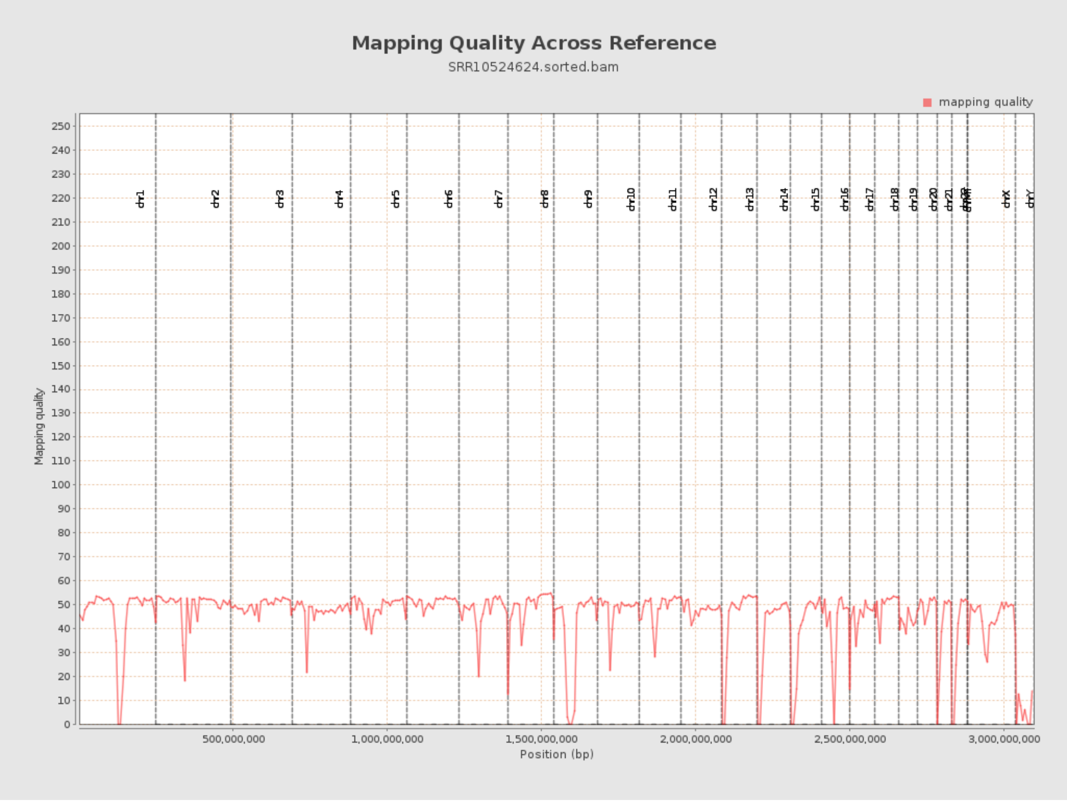
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram