Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:07:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524824.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_SRR10524824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:07:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,593,775
Mapped reads	1,447,774 / 90.84%
Unmapped reads	146,001 / 9.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,362 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	50,487 / 3.17%
Duplication rate	2.65%
Clipped reads	1,451,505 / 91.07%

2.2. ACGT Content

Number/percentage of A's	19,914,590 / 24.03%
Number/percentage of C's	14,795,665 / 17.86%
Number/percentage of T's	25,854,068 / 31.2%
Number/percentage of G's	22,284,689 / 26.89%
Number/percentage of N's	9,962 / 0.01%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2294

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

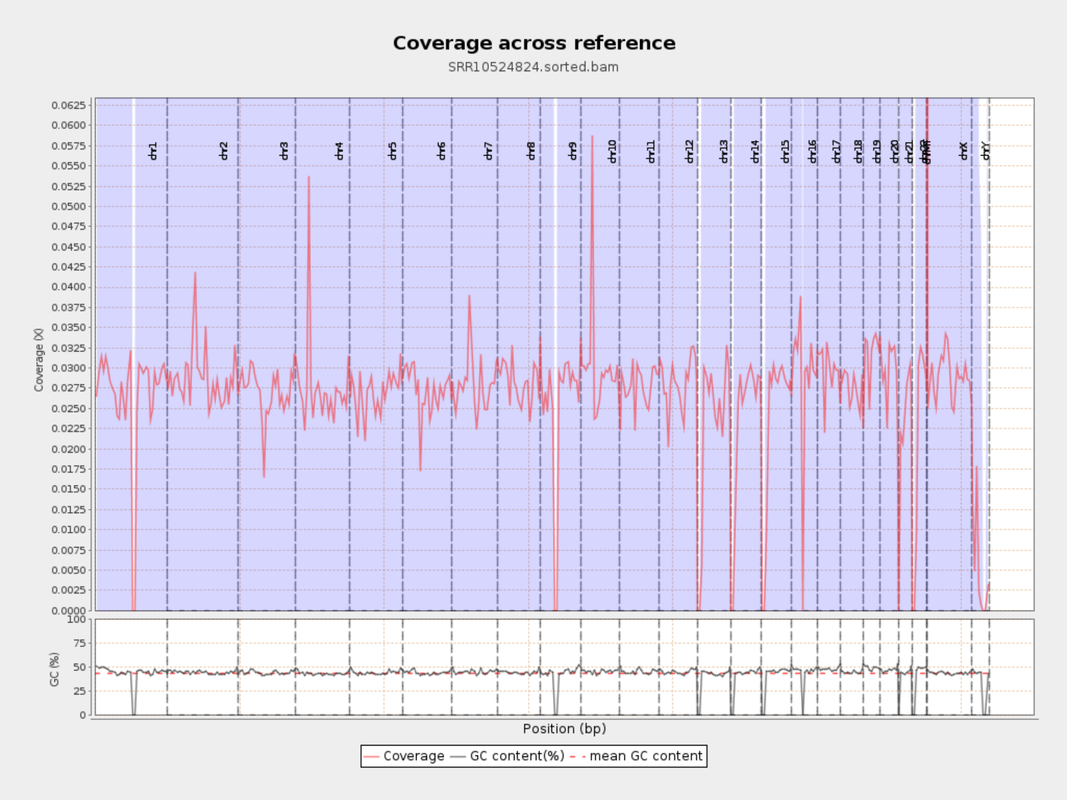
General error rate	0.51%
Mismatches	413,630
Insertions	5,045
Mapped reads with at least one insertion	0.35%
Deletions	15,304
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.59%

2.6. Chromosome stats

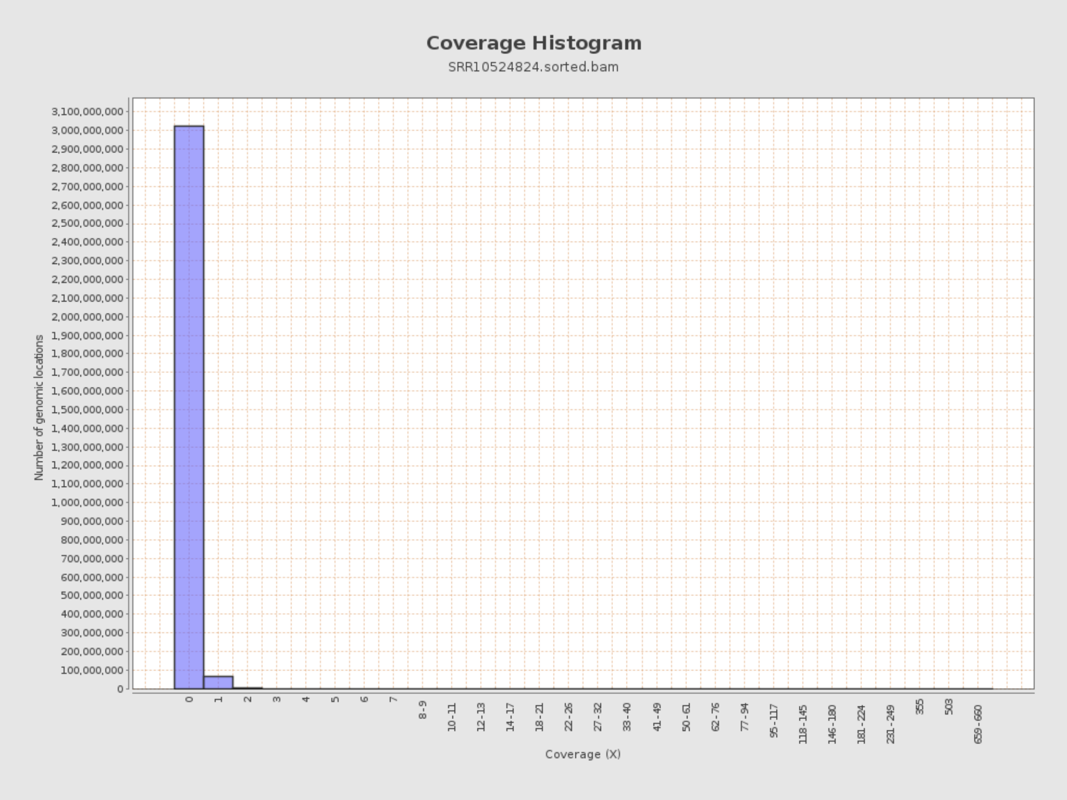
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6591379	0.0264	0.2606
chr2	243199373	7007126	0.0288	0.3568
chr3	198022430	5353601	0.027	0.1817
chr4	191154276	5287974	0.0277	0.2166
chr5	180915260	4884710	0.027	0.1807
chr6	171115067	4651746	0.0272	0.1967
chr7	159138663	4467275	0.0281	0.2698

chr8	146364022	4121601	0.0282	0.2061
chr9	141213431	3525574	0.025	0.2052
chr10	135534747	4107785	0.0303	0.2929
chr11	135006516	3762249	0.0279	0.2134
chr12	133851895	3763284	0.0281	0.1855
chr13	115169878	2615042	0.0227	0.1663
chr14	107349540	2495391	0.0232	0.1722
chr15	102531392	2387121	0.0233	0.17
chr16	90354753	2583726	0.0286	0.2103
chr17	81195210	2417134	0.0298	0.1992
chr18	78077248	2145321	0.0275	0.3054
chr19	59128983	1869966	0.0316	0.2528
chr20	63025520	1857577	0.0295	0.201
chr21	48129895	1106485	0.023	0.1882
chr22	51304566	1080044	0.0211	0.1617
chrMT	16571	11157	0.6733	0.9222
chrX	155270560	4498480	0.029	0.2009
chrY	59373566	292167	0.0049	0.146

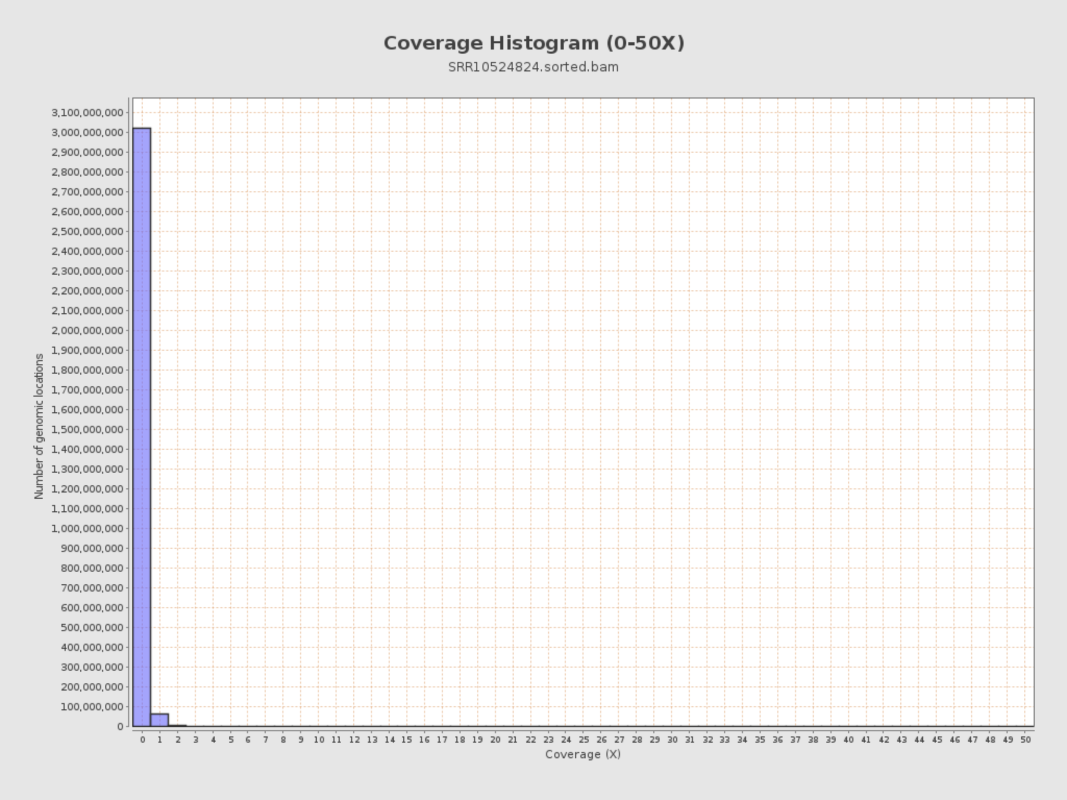
3. Results : Coverage across reference



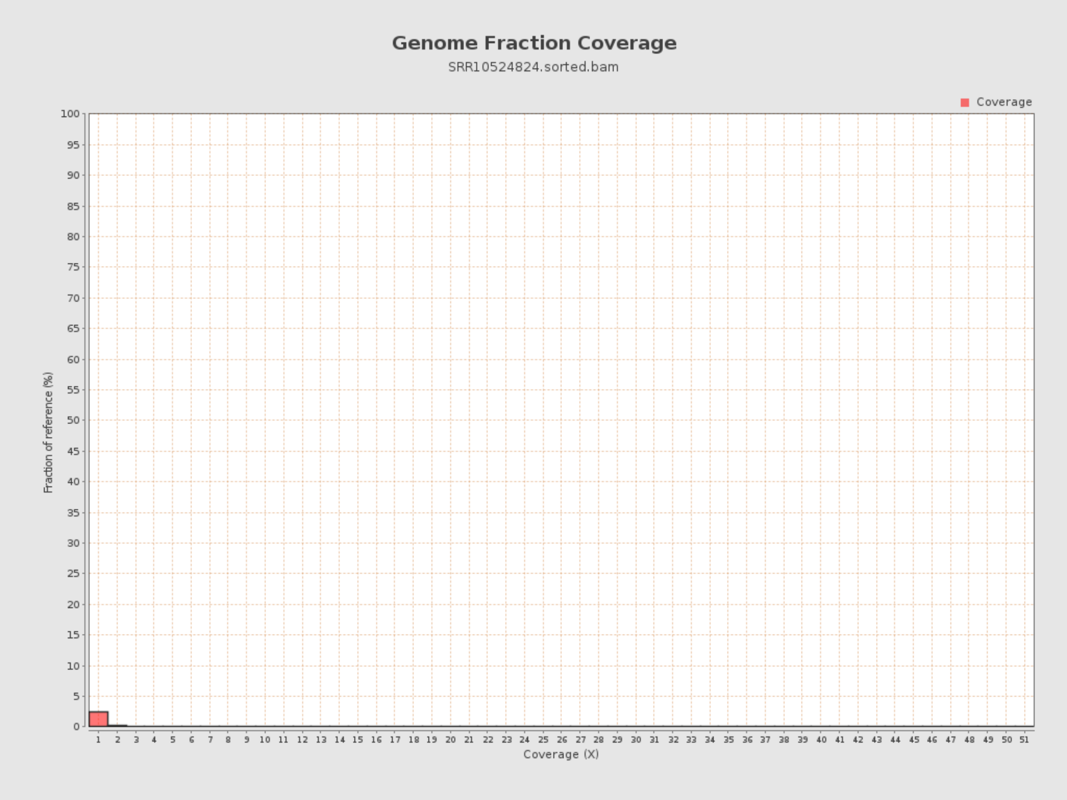
4. Results : Coverage Histogram



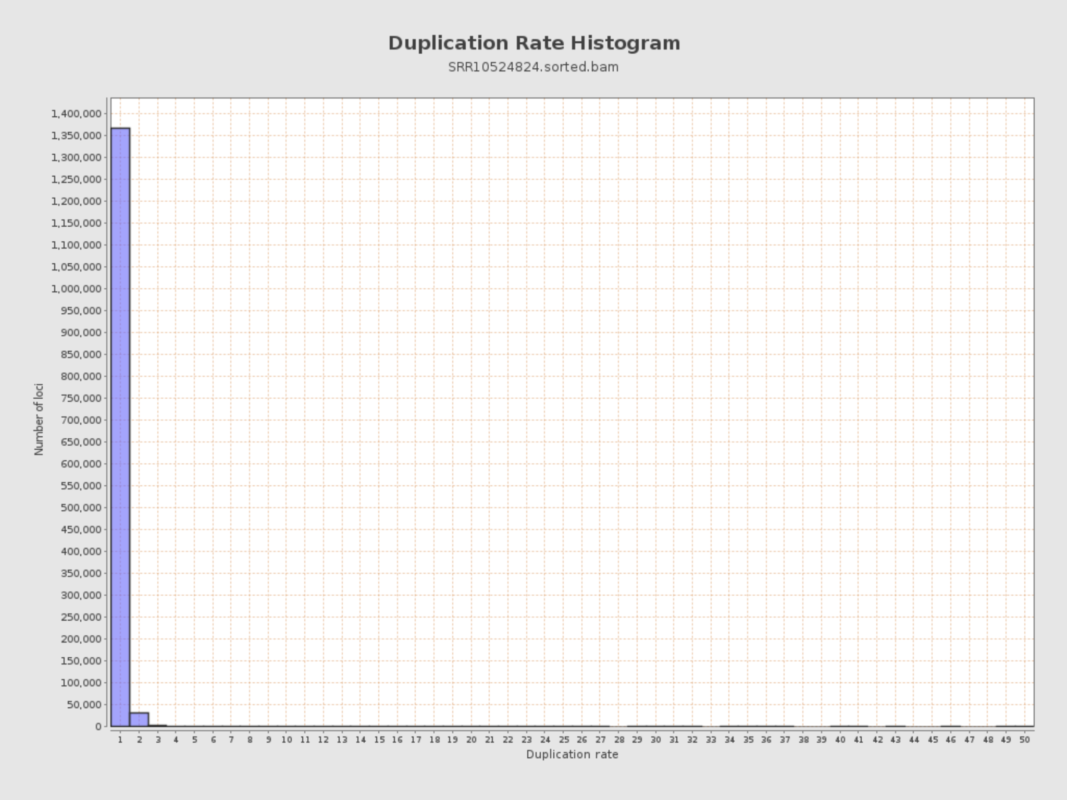
5. Results : Coverage Histogram (0-50X)



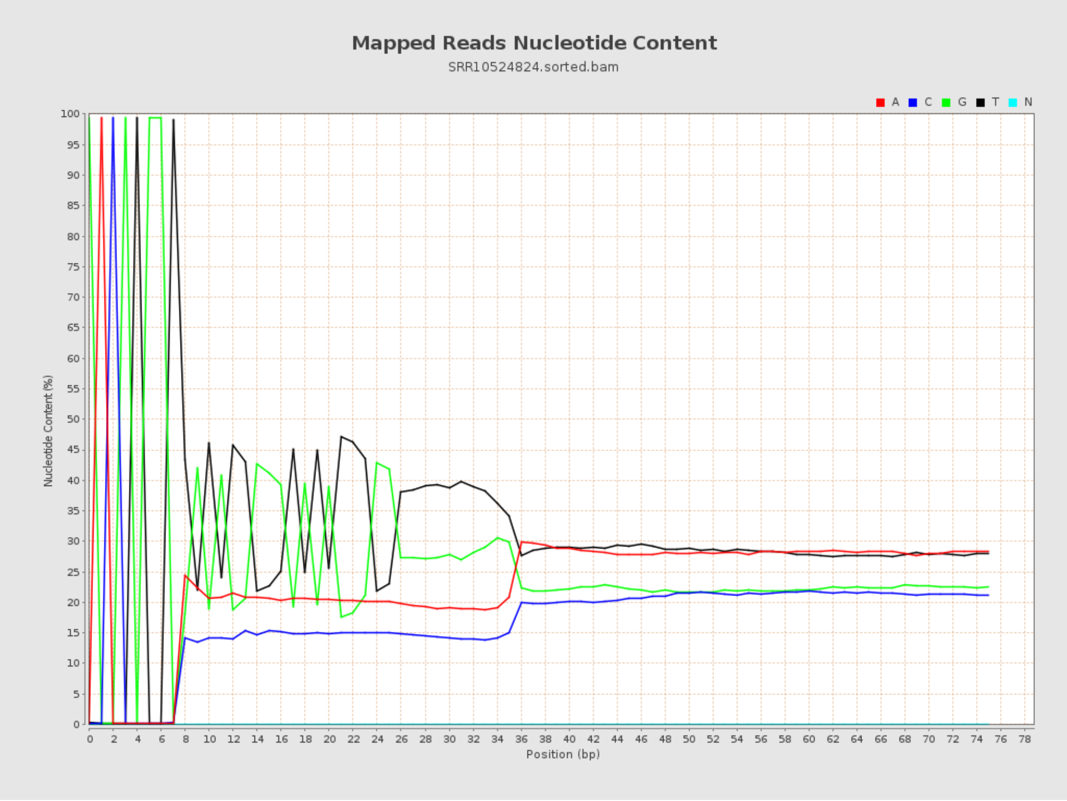
6. Results : Genome Fraction Coverage



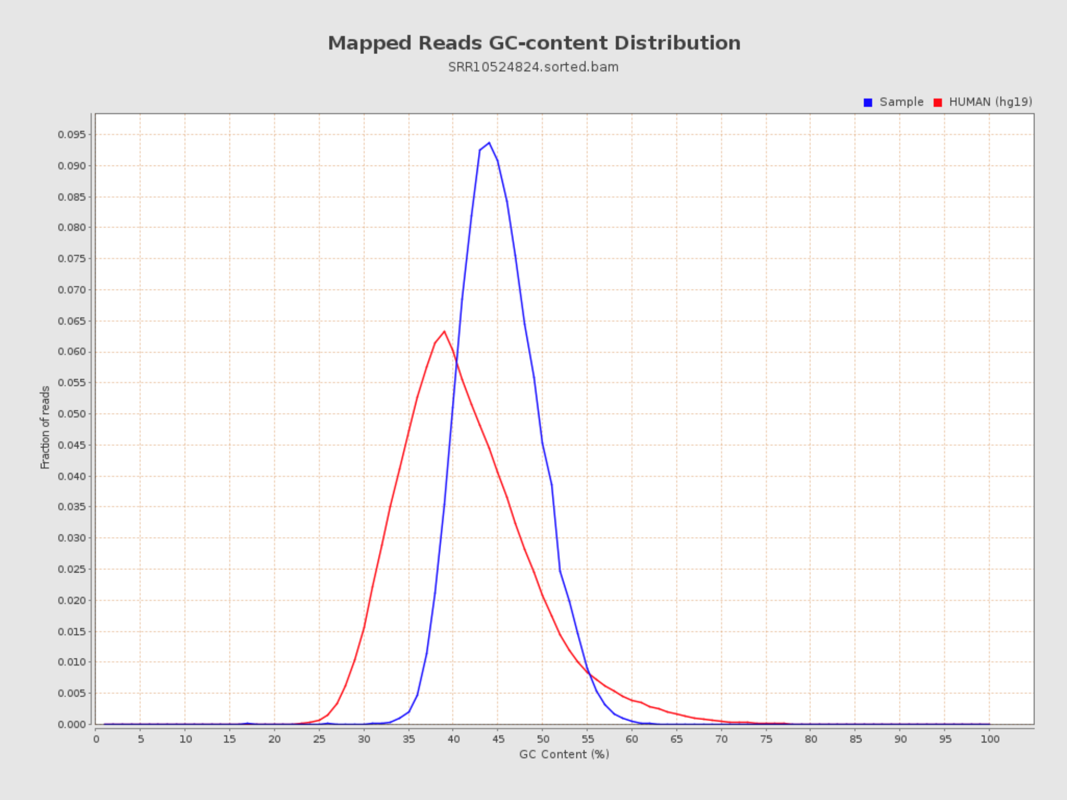
7. Results : Duplication Rate Histogram



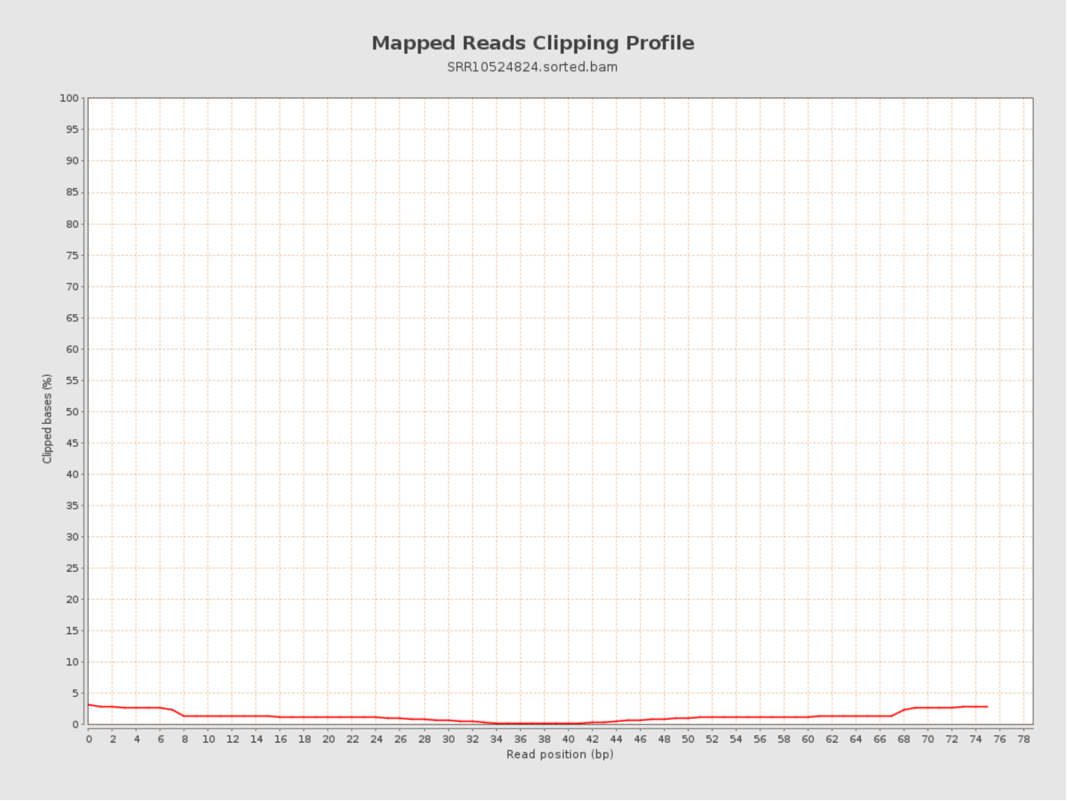
8. Results : Mapped Reads Nucleotide Content



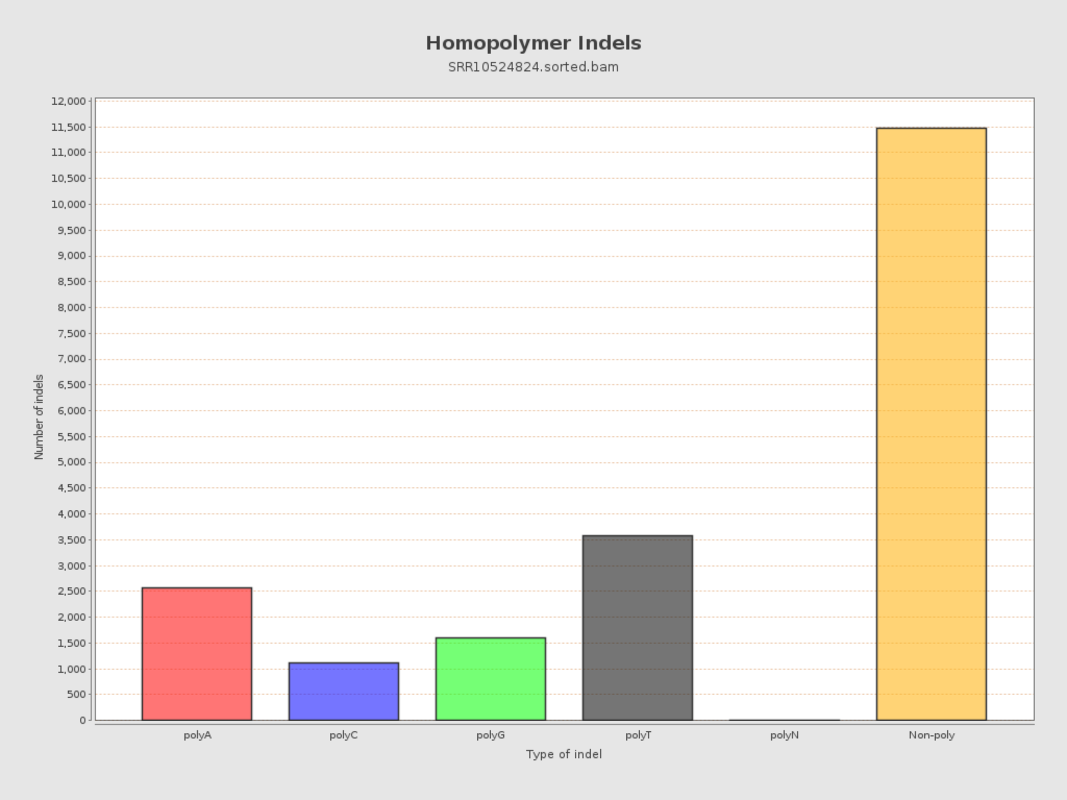
9. Results : Mapped Reads GC-content Distribution



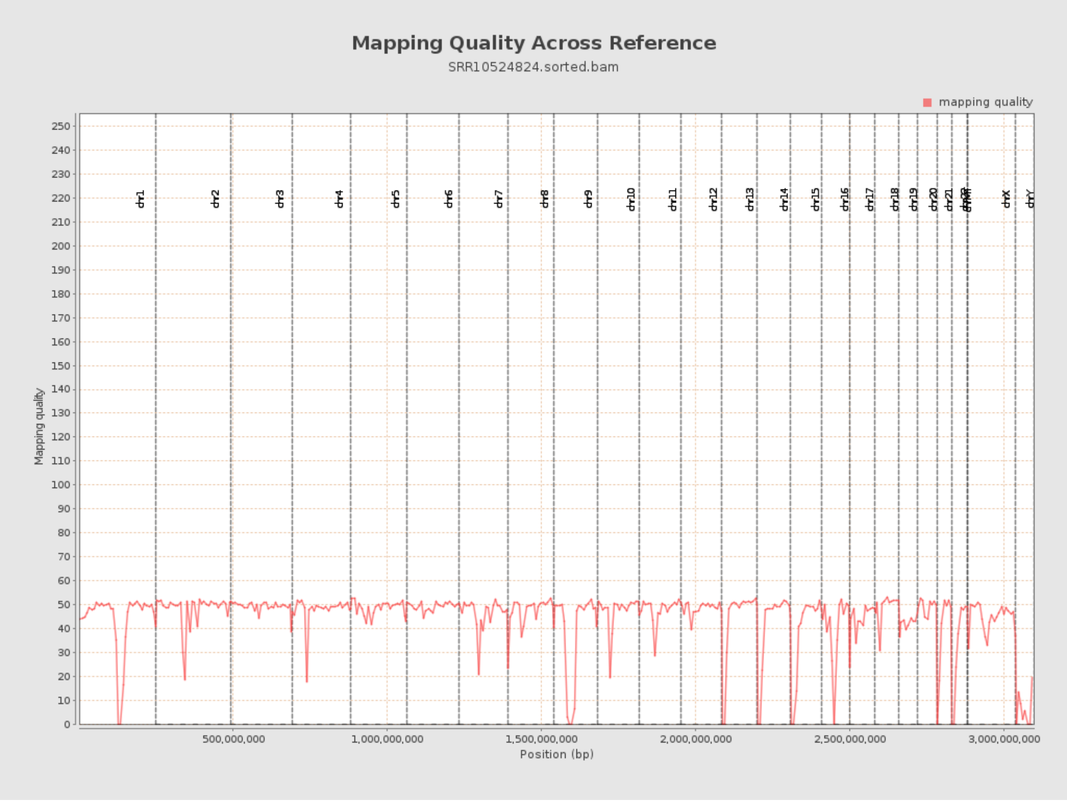
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram