Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:27:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524409.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_SRR10524409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524409.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:27:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,009,328
Mapped reads	1,850,865 / 92.11%
Unmapped reads	158,463 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,413 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	85,886 / 4.27%
Duplication rate	3.49%
Clipped reads	1,853,617 / 92.25%

2.2. ACGT Content

Number/percentage of A's	26,962,113 / 24.97%
Number/percentage of C's	19,038,761 / 17.64%
Number/percentage of T's	35,640,947 / 33.01%
Number/percentage of G's	26,301,922 / 24.36%
Number/percentage of N's	13,938 / 0.01%
GC Percentage	42%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.342

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

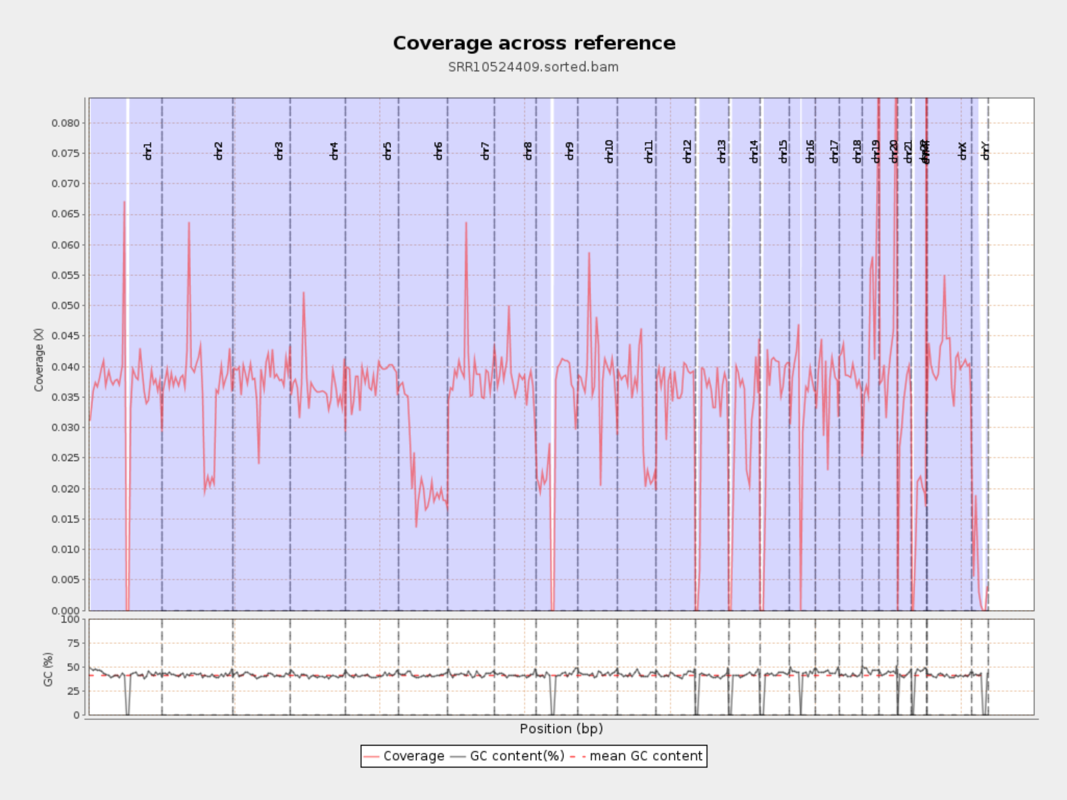
General error rate	0.5%
Mismatches	526,933
Insertions	7,243
Mapped reads with at least one insertion	0.39%
Deletions	19,586
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.16%

2.6. Chromosome stats

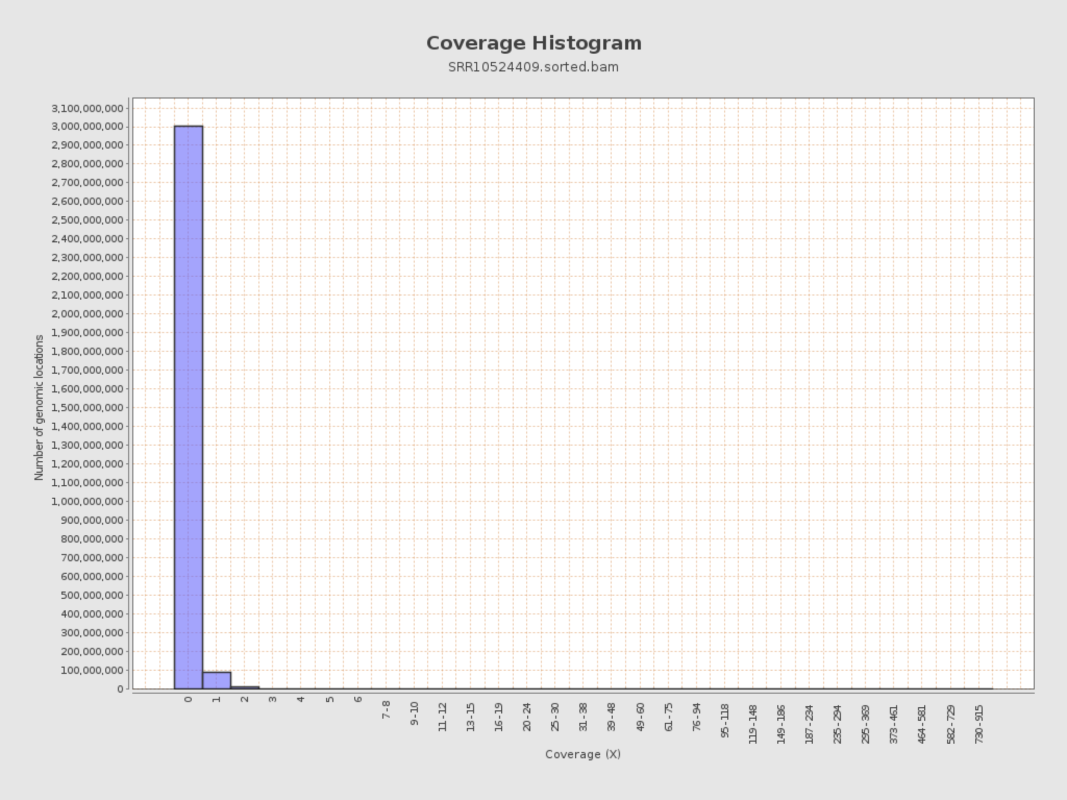
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8987841	0.0361	0.7296
chr2	243199373	8896964	0.0366	0.3842
chr3	198022430	7572928	0.0382	0.2162
chr4	191154276	7000950	0.0366	0.2401
chr5	180915260	6891690	0.0381	0.2174
chr6	171115067	3952415	0.0231	0.1892
chr7	159138663	6256835	0.0393	0.4787

chr8	146364022	5618468	0.0384	0.3118
chr9	141213431	4068288	0.0288	0.2524
chr10	135534747	5310241	0.0392	0.3006
chr11	135006516	4489309	0.0333	0.2654
chr12	133851895	4988200	0.0373	0.2224
chr13	115169878	3532435	0.0307	0.1936
chr14	107349540	3086396	0.0288	0.1932
chr15	102531392	3321032	0.0324	0.1994
chr16	90354753	3134240	0.0347	0.2167
chr17	81195210	2946131	0.0363	0.2335
chr18	78077248	3070862	0.0393	0.4497
chr19	59128983	2948264	0.0499	0.5068
chr20	63025520	2986030	0.0474	0.2495
chr21	48129895	1491286	0.031	0.2148
chr22	51304566	743131	0.0145	0.1328
chrMT	16571	3689	0.2226	0.5086
chrX	155270560	6368719	0.041	0.2525
chrY	59373566	322205	0.0054	0.1466

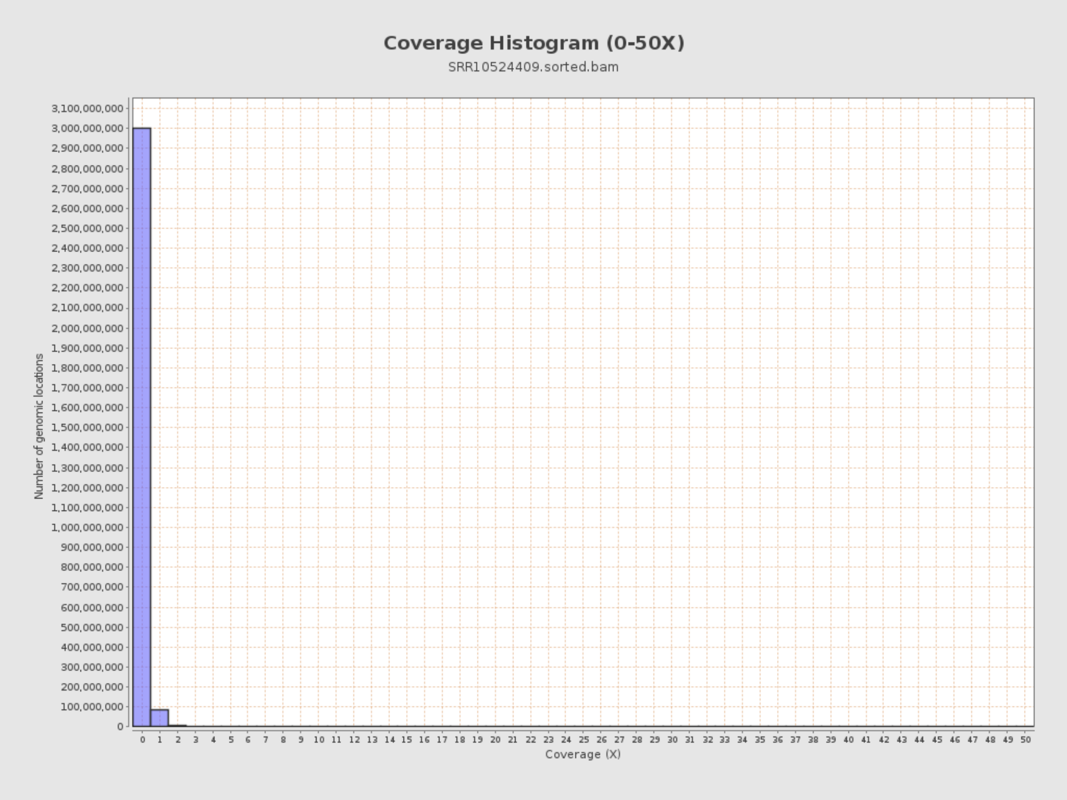
3. Results : Coverage across reference



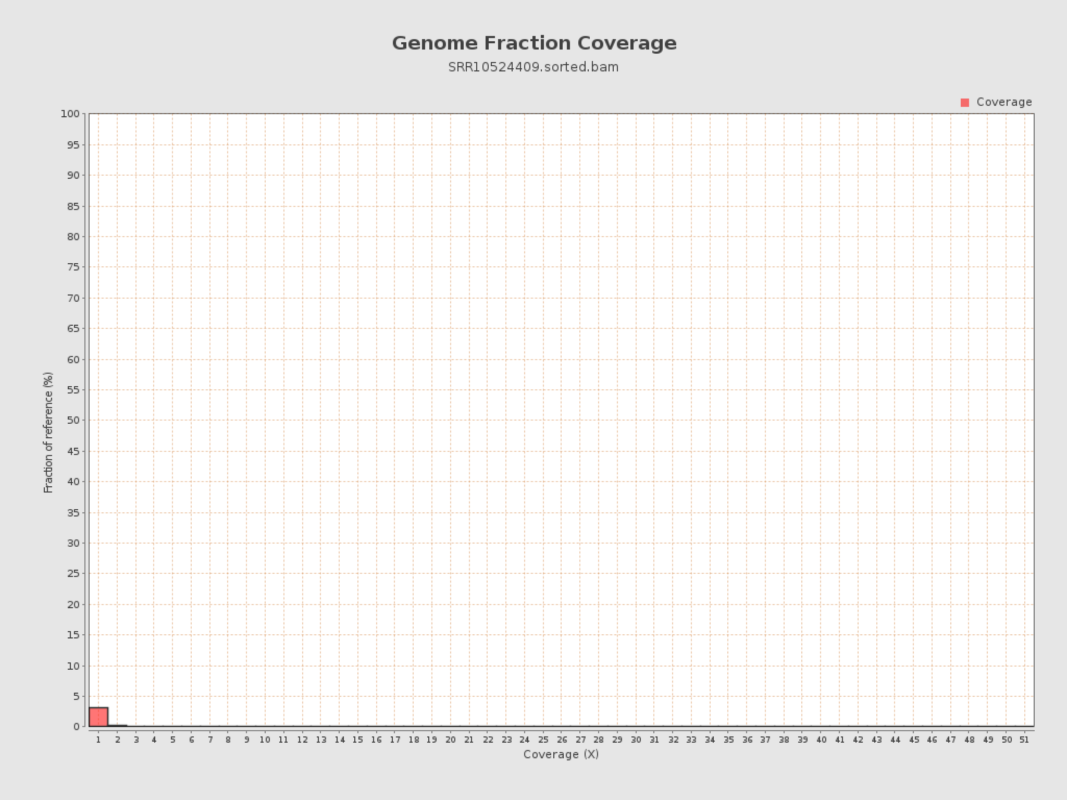
4. Results : Coverage Histogram



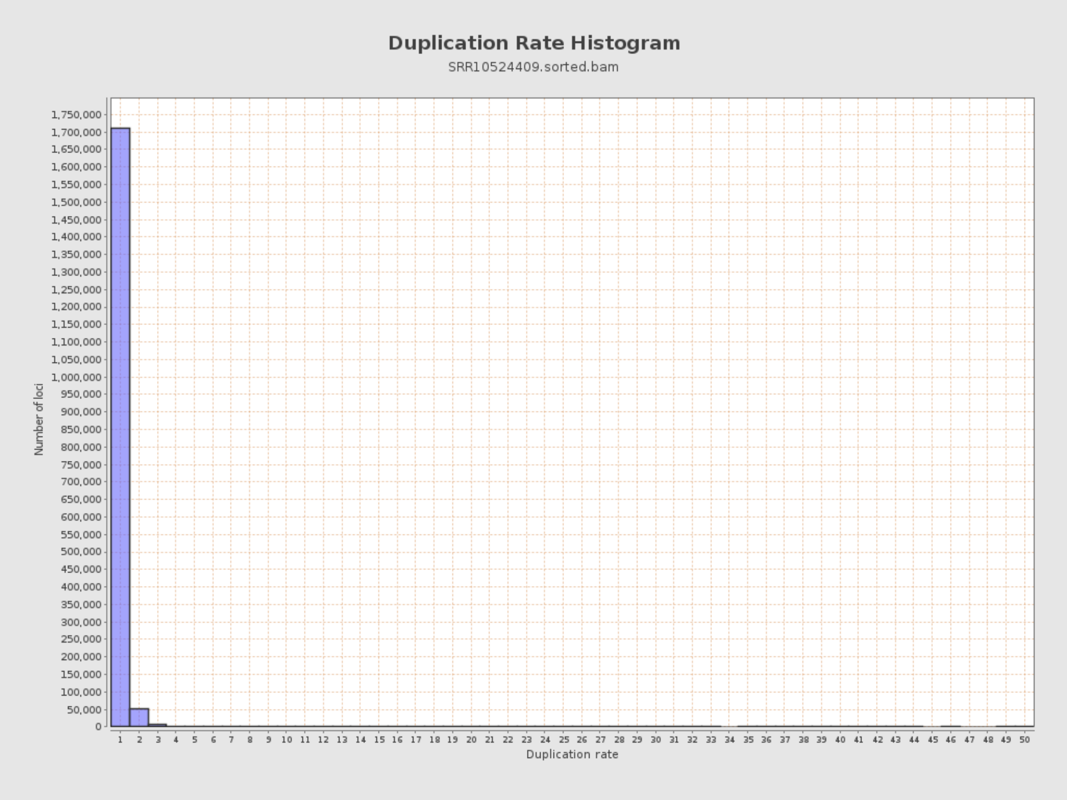
5. Results : Coverage Histogram (0-50X)



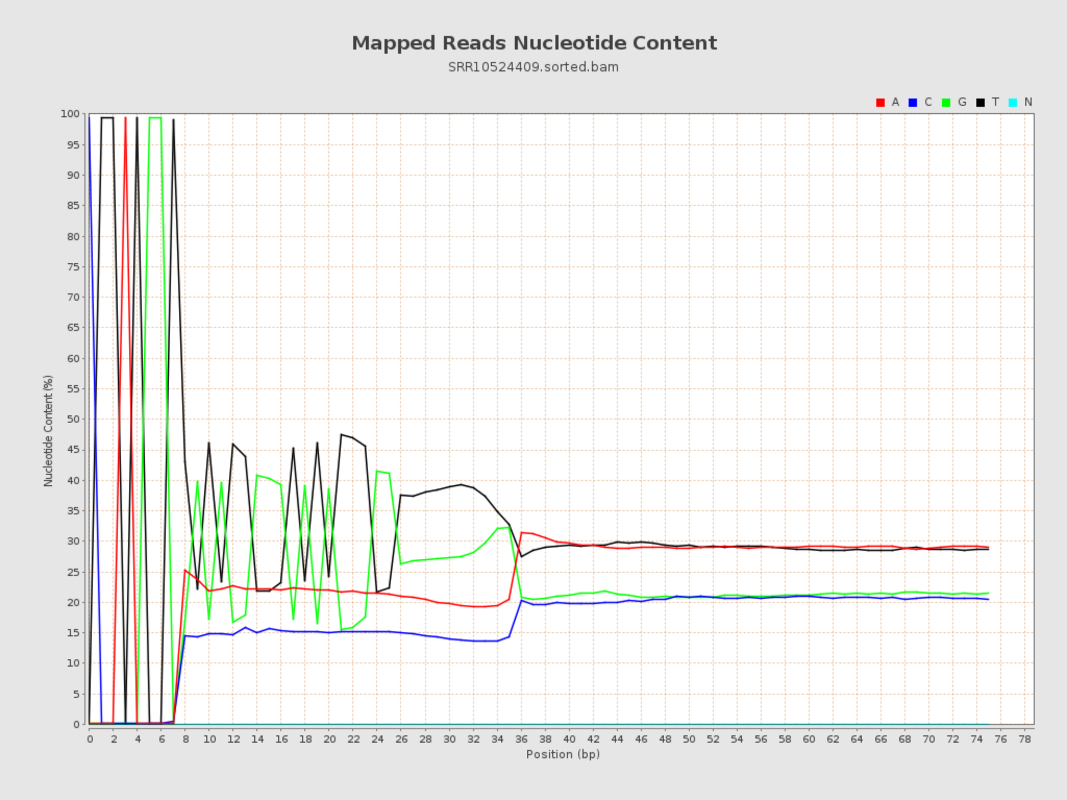
6. Results : Genome Fraction Coverage



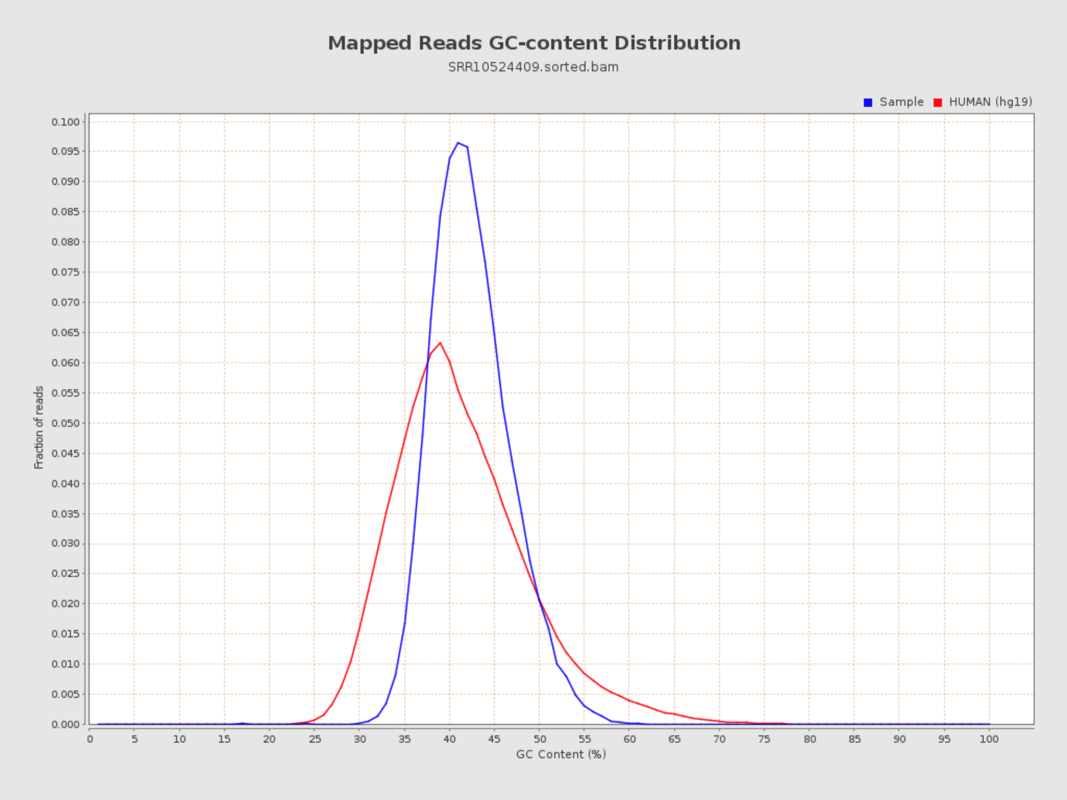
7. Results : Duplication Rate Histogram



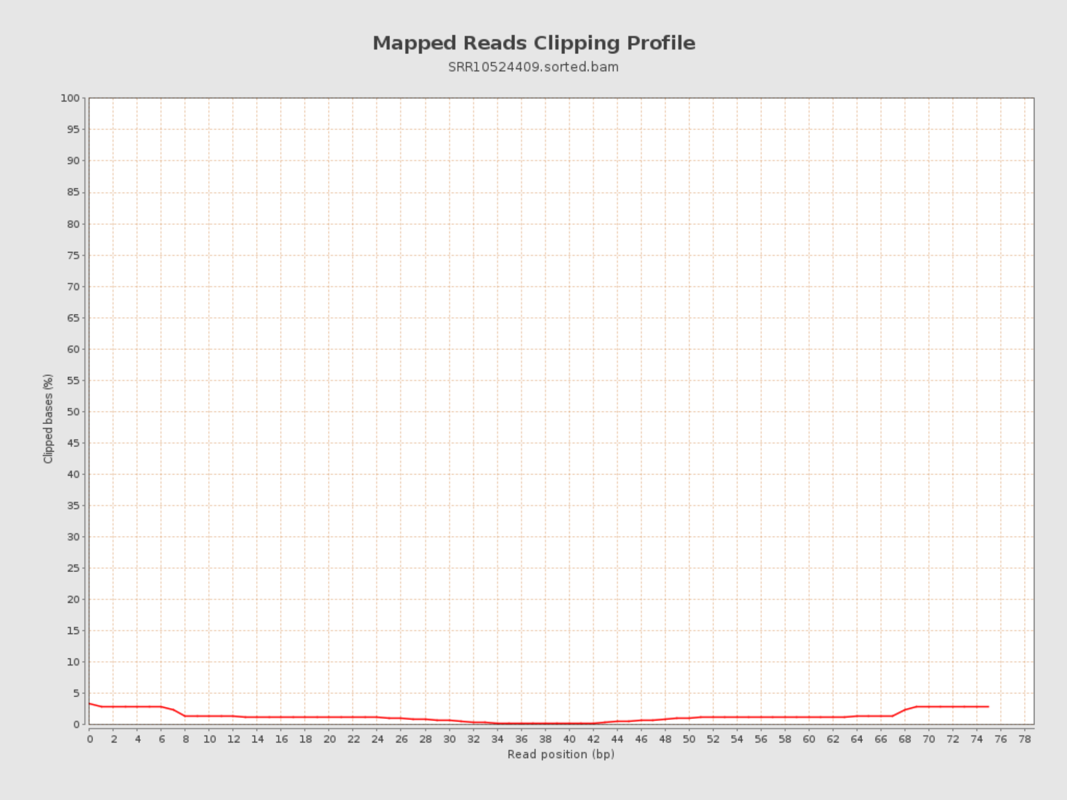
8. Results : Mapped Reads Nucleotide Content



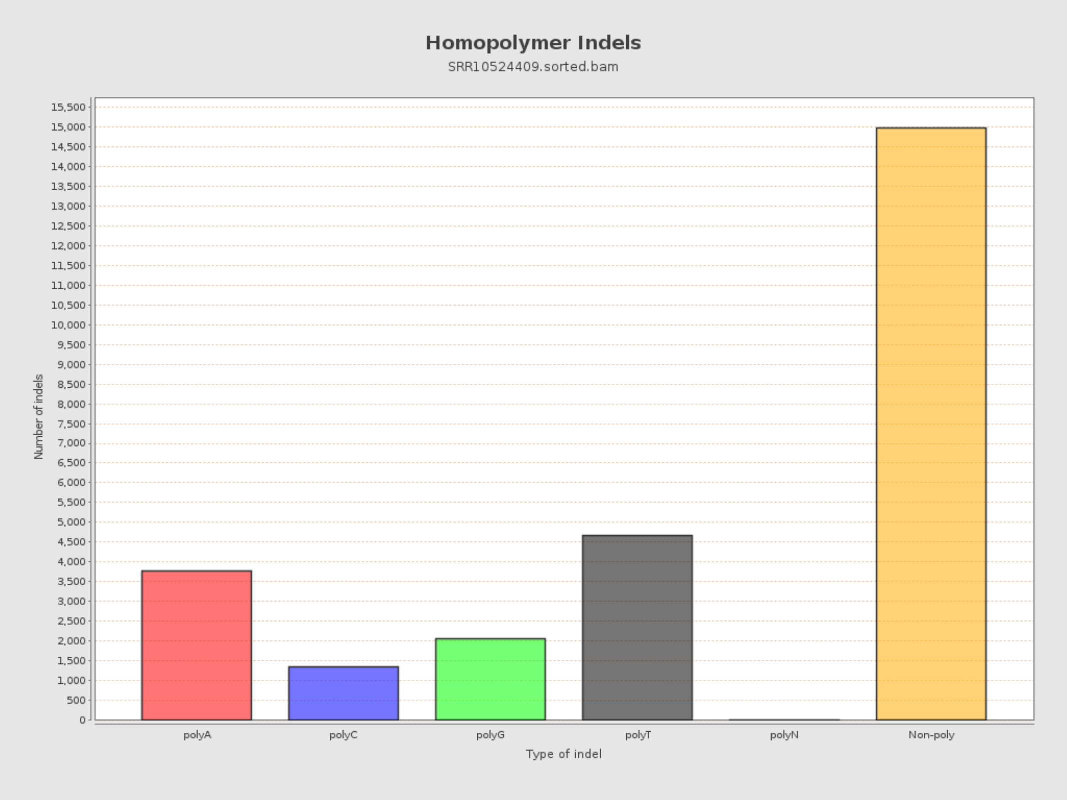
9. Results : Mapped Reads GC-content Distribution



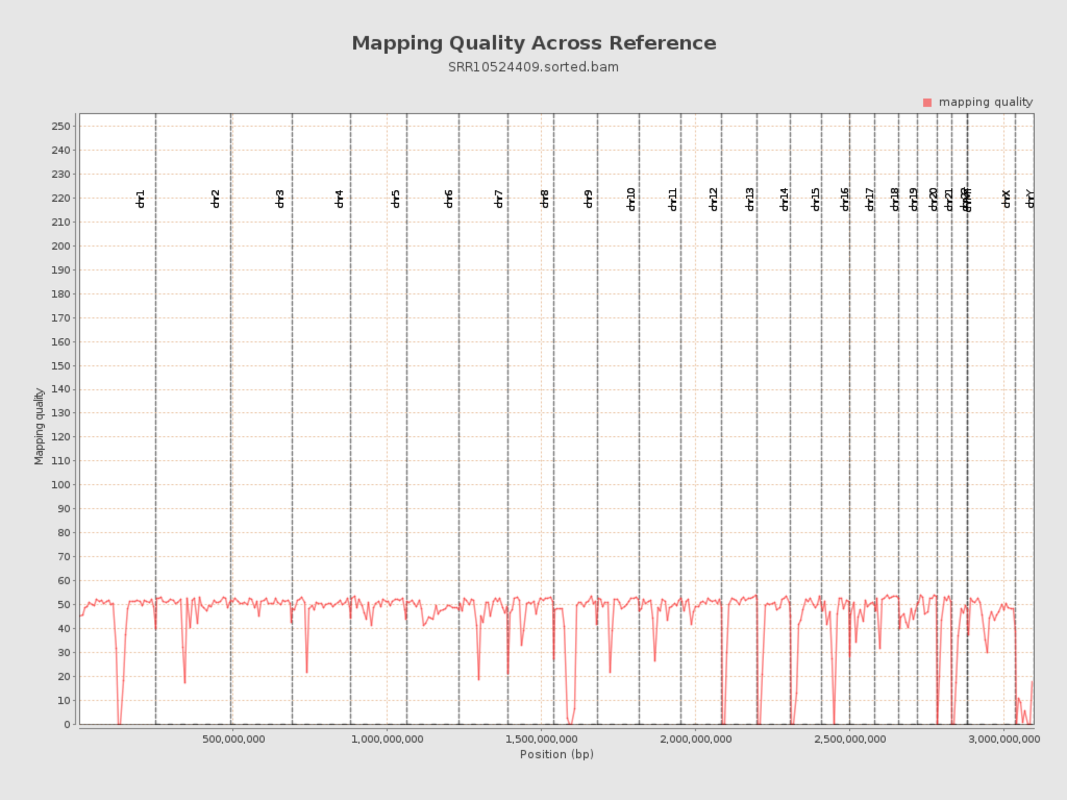
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram