Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:39:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524889.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_SRR10524889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524889.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:39:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	743,327
Mapped reads	661,373 / 88.97%
Unmapped reads	81,954 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,244 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	12,532 / 1.69%
Duplication rate	1.35%
Clipped reads	662,482 / 89.12%

2.2. ACGT Content

Number/percentage of A's	10,789,461 / 27.14%
Number/percentage of C's	7,398,760 / 18.61%
Number/percentage of T's	12,566,843 / 31.61%
Number/percentage of G's	8,998,030 / 22.63%
Number/percentage of N's	815 / 0%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0128

Standard Deviation	0.1536

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

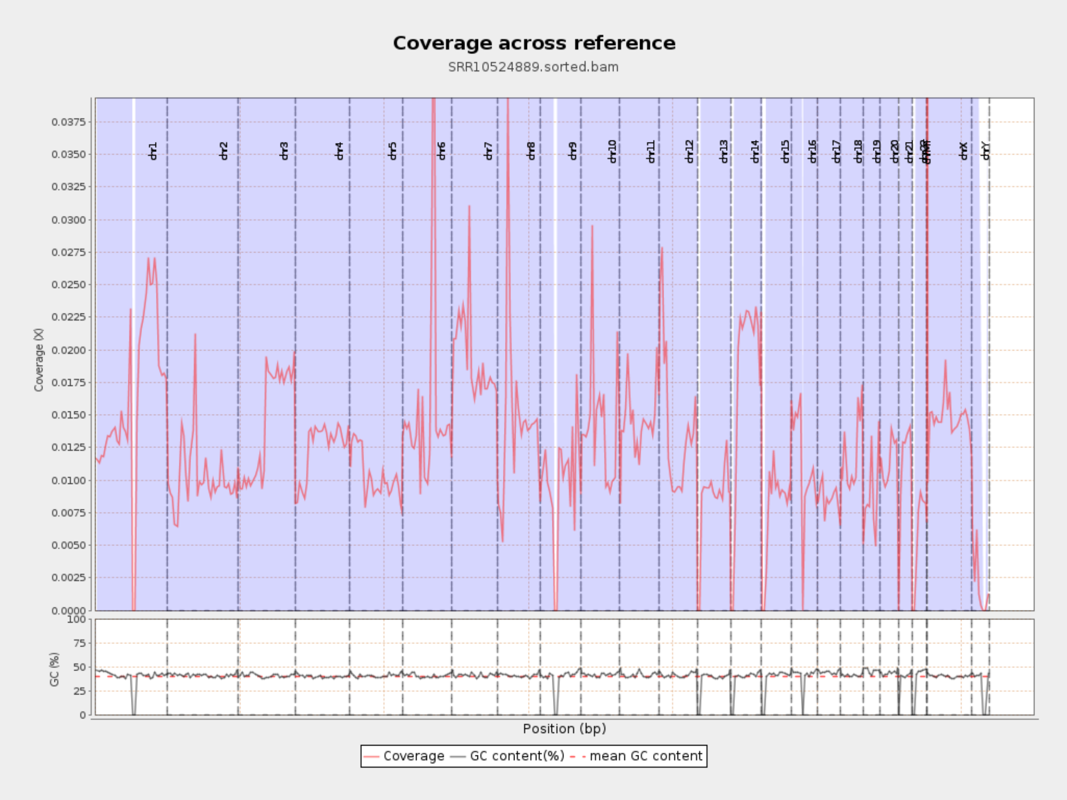
General error rate	0.5%
Mismatches	192,941
Insertions	2,904
Mapped reads with at least one insertion	0.44%
Deletions	8,062
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.21%

2.6. Chromosome stats

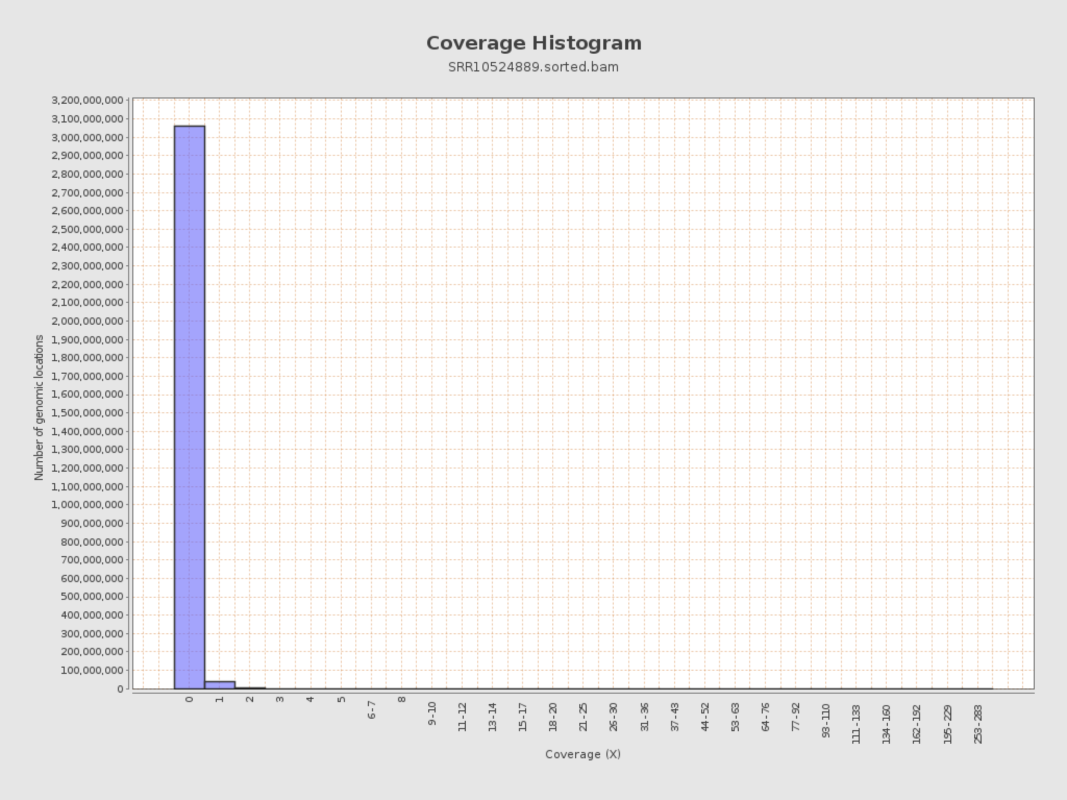
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4084484	0.0164	0.2509
chr2	243199373	2500562	0.0103	0.1473
chr3	198022430	2841718	0.0144	0.125
chr4	191154276	2386853	0.0125	0.117
chr5	180915260	1877686	0.0104	0.1052
chr6	171115067	2698087	0.0158	0.1367
chr7	159138663	3098533	0.0195	0.2596

chr8	146364022	2185202	0.0149	0.1511
chr9	141213431	1387056	0.0098	0.1196
chr10	135534747	1942662	0.0143	0.1834
chr11	135006516	1954495	0.0145	0.1372
chr12	133851895	1900587	0.0142	0.1235
chr13	115169878	985911	0.0086	0.0956
chr14	107349540	1921111	0.0179	0.1398
chr15	102531392	788662	0.0077	0.0908
chr16	90354753	993083	0.011	0.1144
chr17	81195210	699496	0.0086	0.0978
chr18	78077248	927804	0.0119	0.1936
chr19	59128983	530880	0.009	0.1754
chr20	63025520	712658	0.0113	0.1101
chr21	48129895	540424	0.0112	0.1126
chr22	51304566	301291	0.0059	0.0794
chrMT	16571	87167	5.2602	3.3651
chrX	155270560	2303606	0.0148	0.131
chrY	59373566	117036	0.002	0.0633

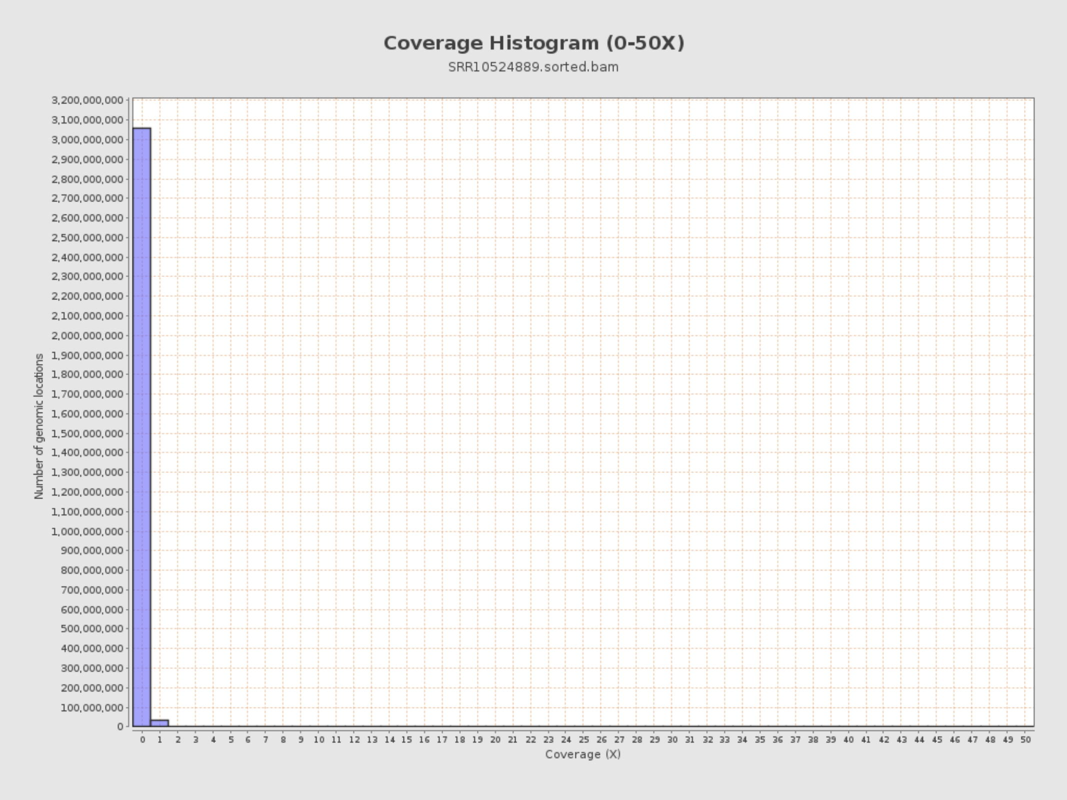
3. Results : Coverage across reference



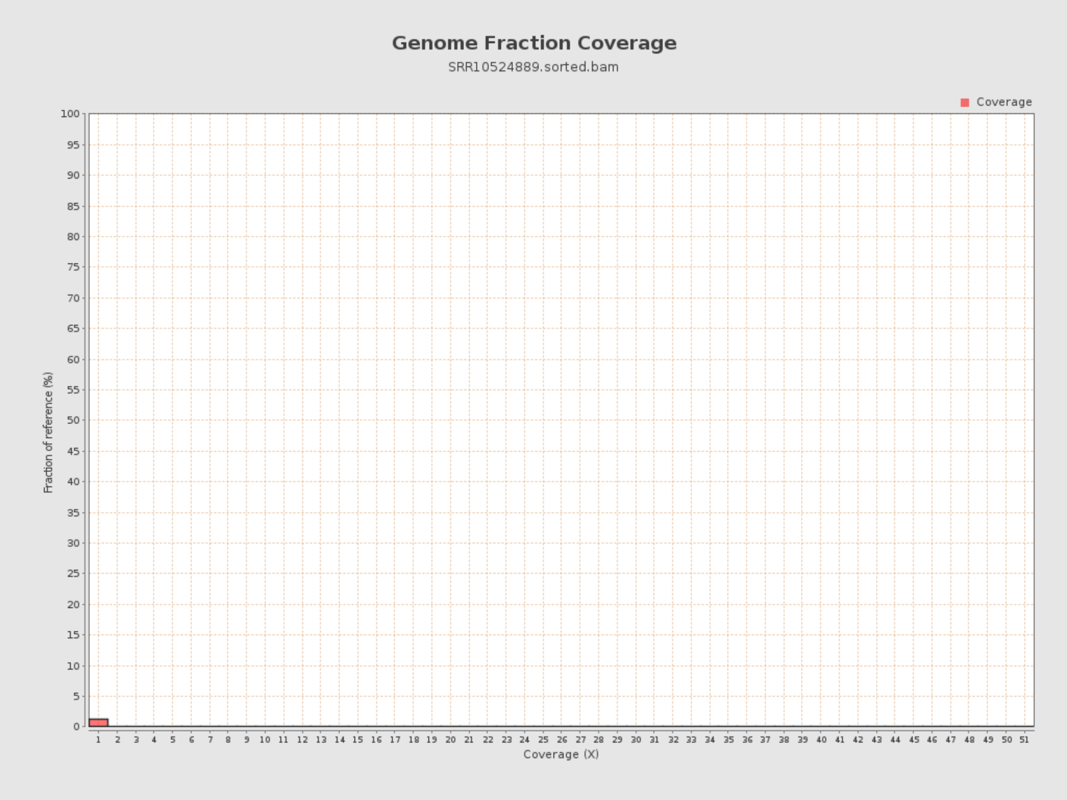
4. Results : Coverage Histogram



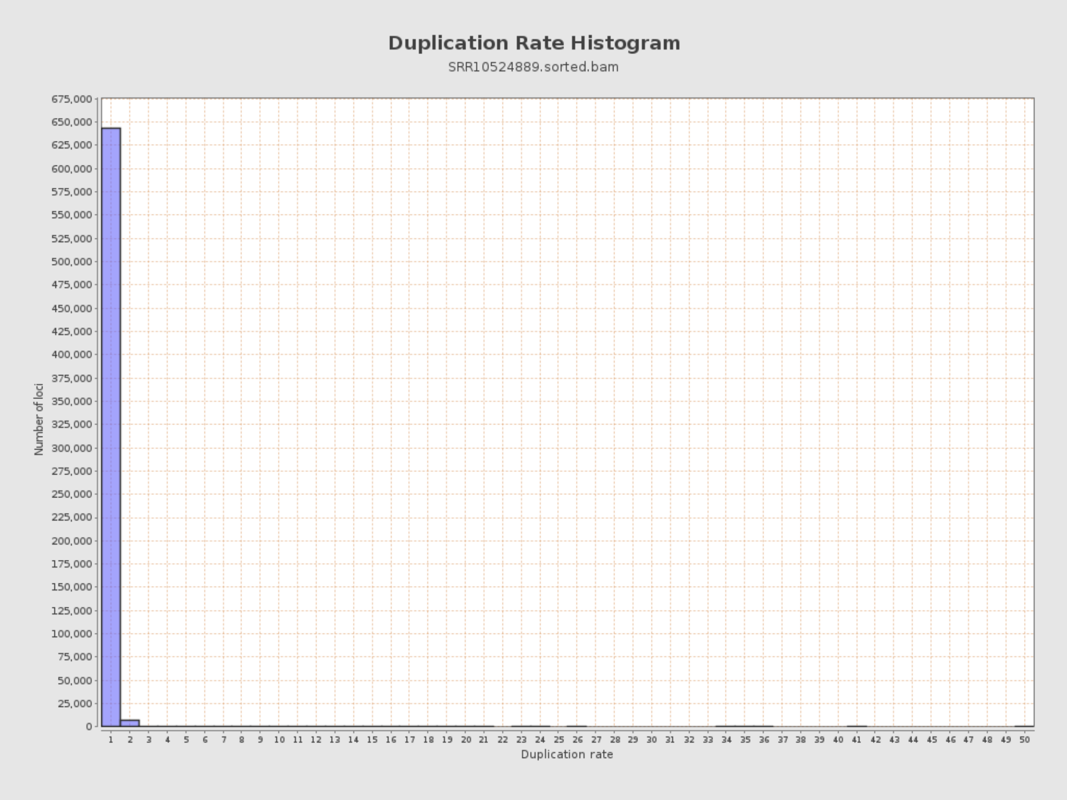
5. Results : Coverage Histogram (0-50X)



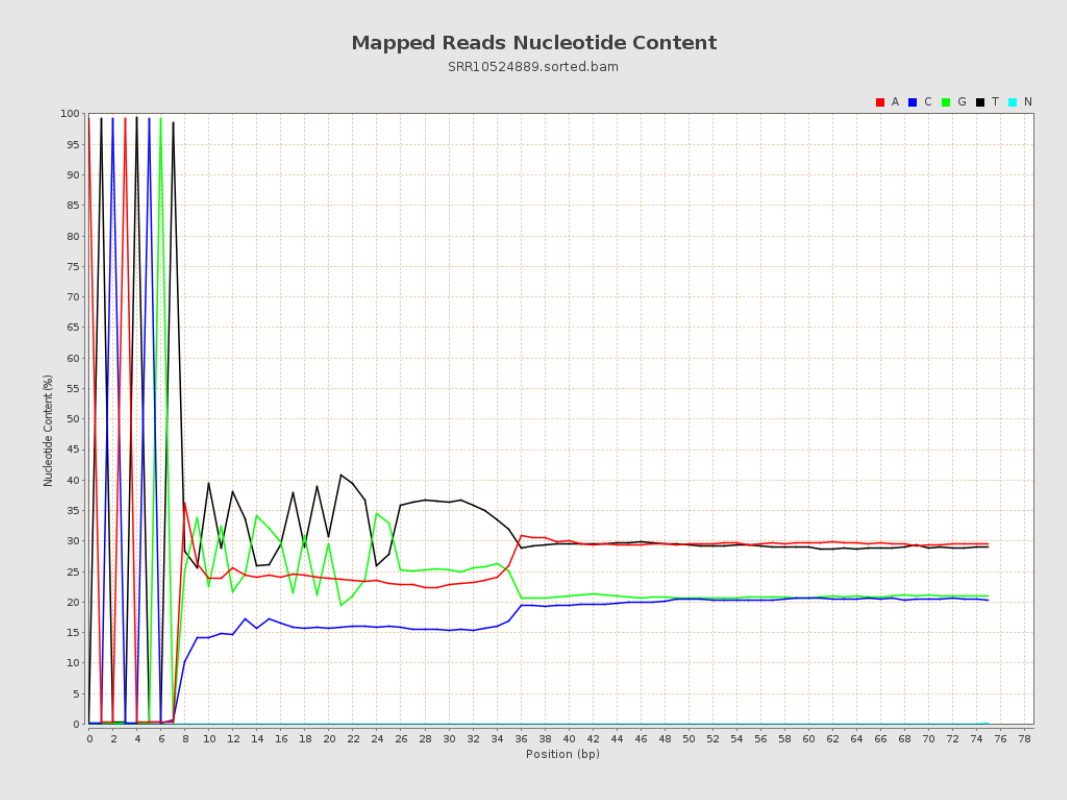
6. Results : Genome Fraction Coverage



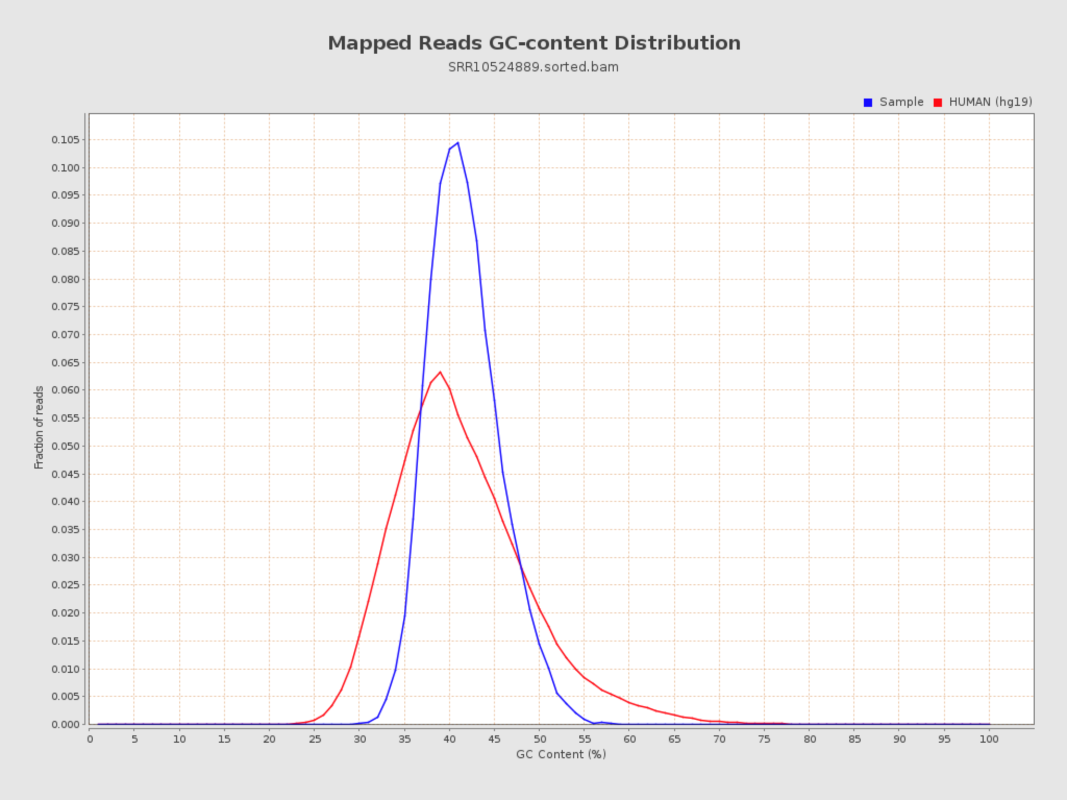
7. Results : Duplication Rate Histogram



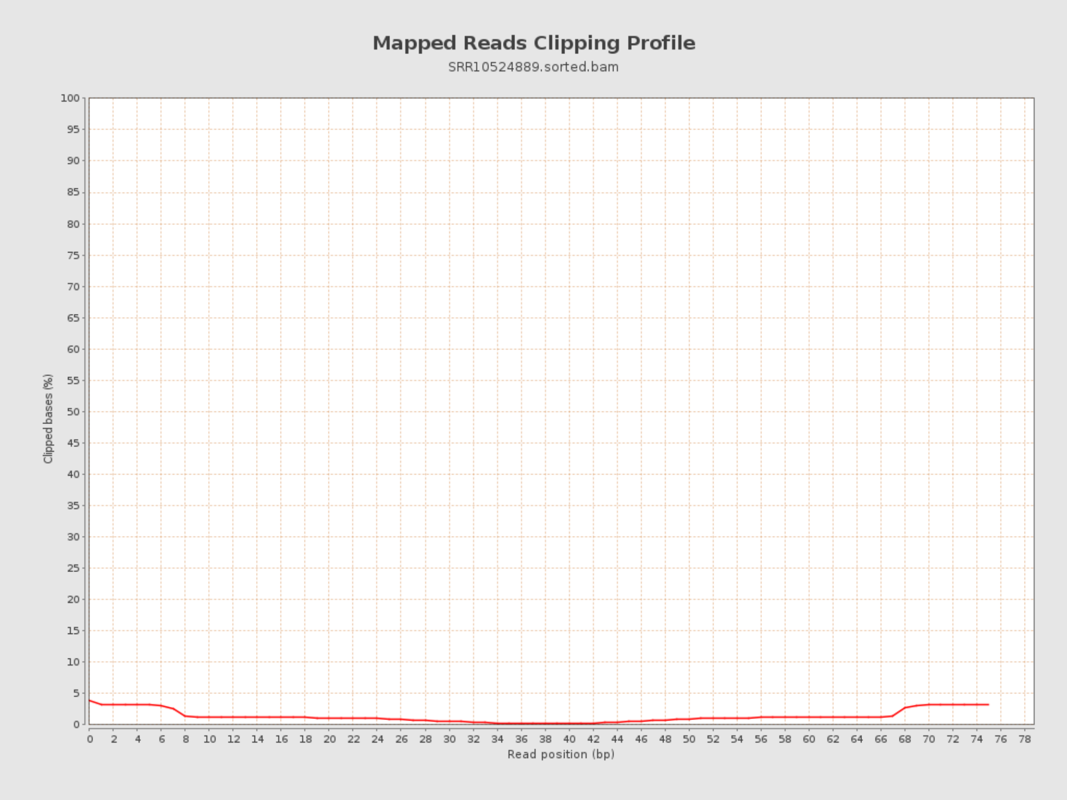
8. Results : Mapped Reads Nucleotide Content



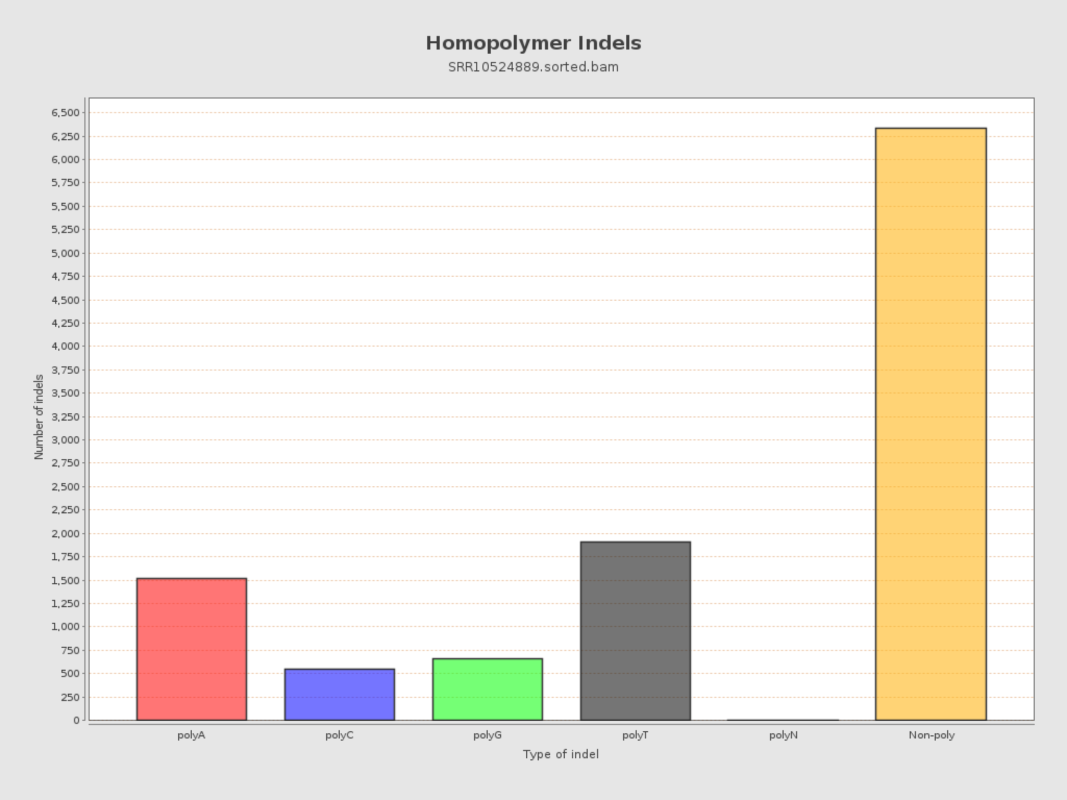
9. Results : Mapped Reads GC-content Distribution



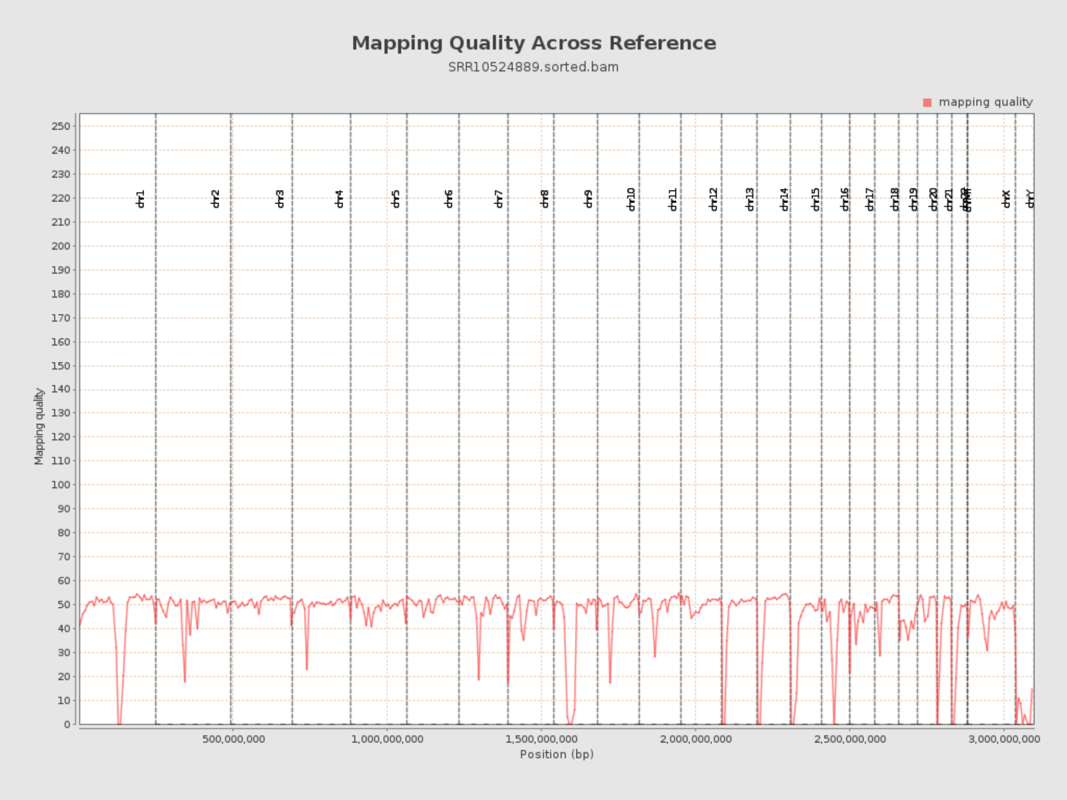
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram