Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:55:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524589.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_SRR10524589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524589.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:55:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,502,287
Mapped reads	1,386,076 / 92.26%
Unmapped reads	116,211 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,107 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	47,904 / 3.19%
Duplication rate	2.46%
Clipped reads	1,388,421 / 92.42%

2.2. ACGT Content

Number/percentage of A's	19,762,725 / 24.46%
Number/percentage of C's	15,804,083 / 19.56%
Number/percentage of T's	25,373,001 / 31.41%
Number/percentage of G's	19,841,037 / 24.56%
Number/percentage of N's	1,585 / 0%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.251

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

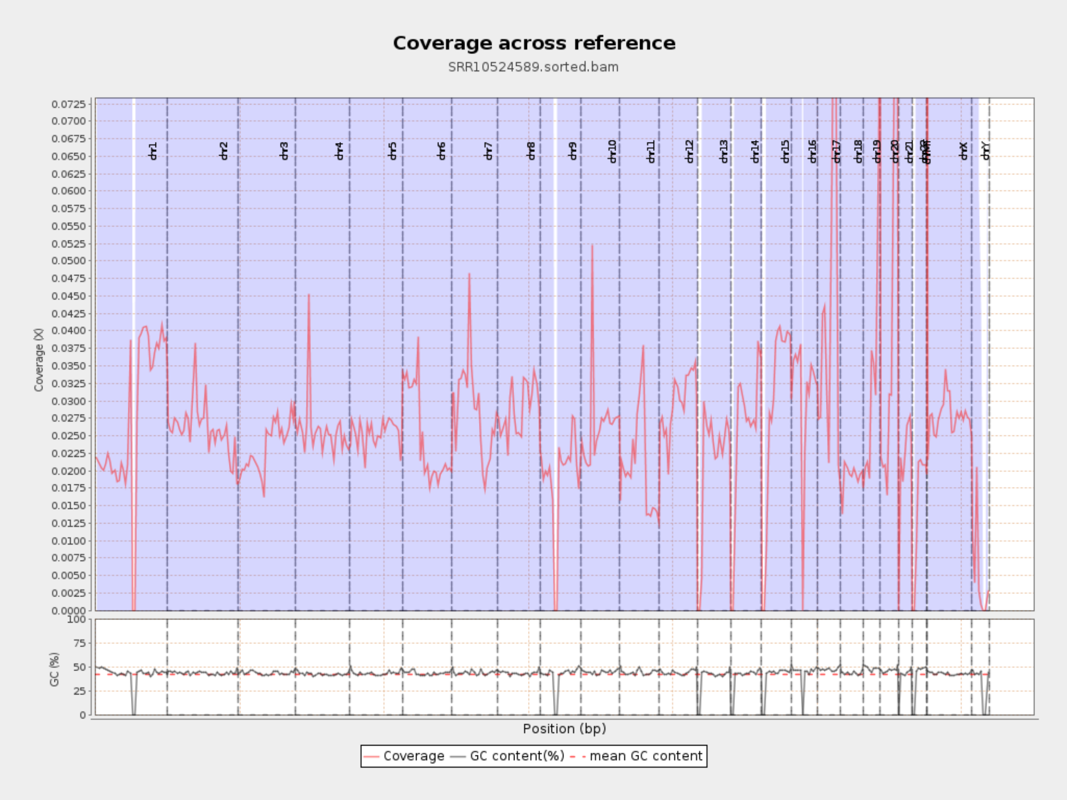
General error rate	0.52%
Mismatches	407,487
Insertions	5,458
Mapped reads with at least one insertion	0.39%
Deletions	16,325
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.76%

2.6. Chromosome stats

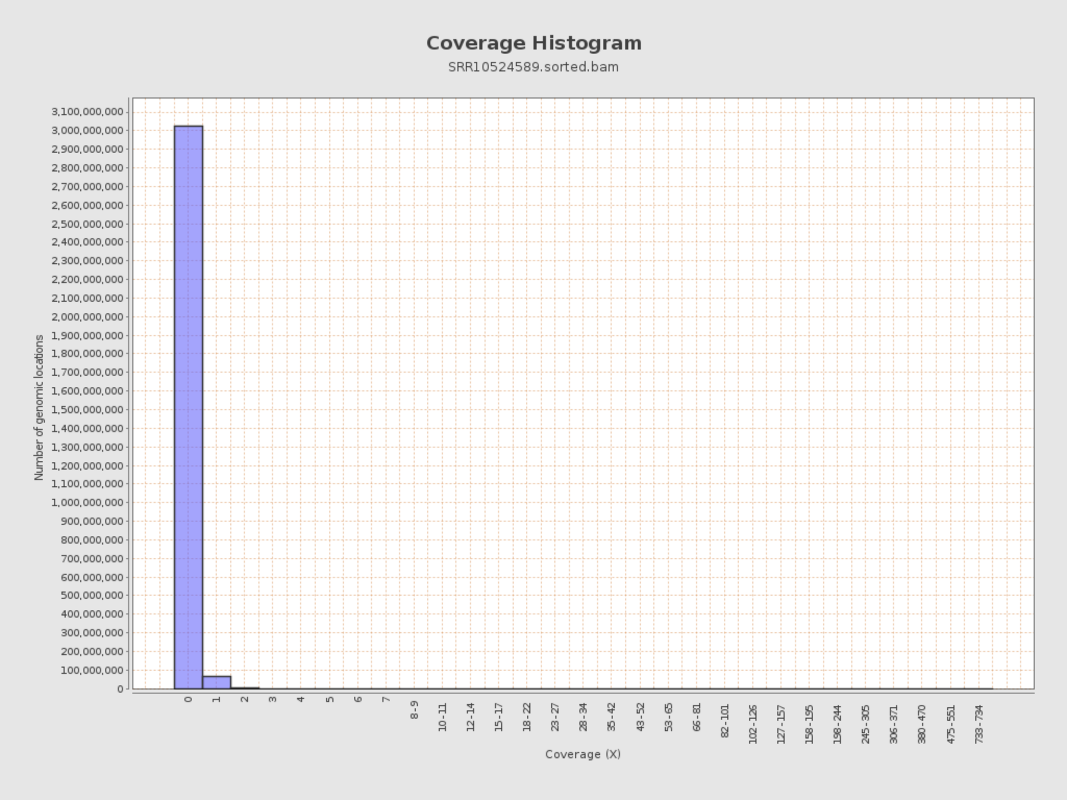
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6799980	0.0273	0.3801
chr2	243199373	6353324	0.0261	0.3499
chr3	198022430	4618788	0.0233	0.165
chr4	191154276	4943917	0.0259	0.2015
chr5	180915260	4605662	0.0255	0.1721
chr6	171115067	4264110	0.0249	0.1979
chr7	159138663	4583090	0.0288	0.3339

chr8	146364022	4240460	0.029	0.3109
chr9	141213431	2673643	0.0189	0.1816
chr10	135534747	3624016	0.0267	0.2647
chr11	135006516	2843560	0.0211	0.1944
chr12	133851895	3988883	0.0298	0.1869
chr13	115169878	2420759	0.021	0.1566
chr14	107349540	2721404	0.0254	0.1745
chr15	102531392	2977622	0.029	0.1857
chr16	90354753	2750276	0.0304	0.1982
chr17	81195210	3546559	0.0437	0.2341
chr18	78077248	1486567	0.019	0.2982
chr19	59128983	2086205	0.0353	0.3118
chr20	63025520	2670115	0.0424	0.2287
chr21	48129895	1023606	0.0213	0.1881
chr22	51304566	761125	0.0148	0.1316
chrMT	16571	200861	12.1212	7.5967
chrX	155270560	4329818	0.0279	0.1926
chrY	59373566	294792	0.005	0.2171

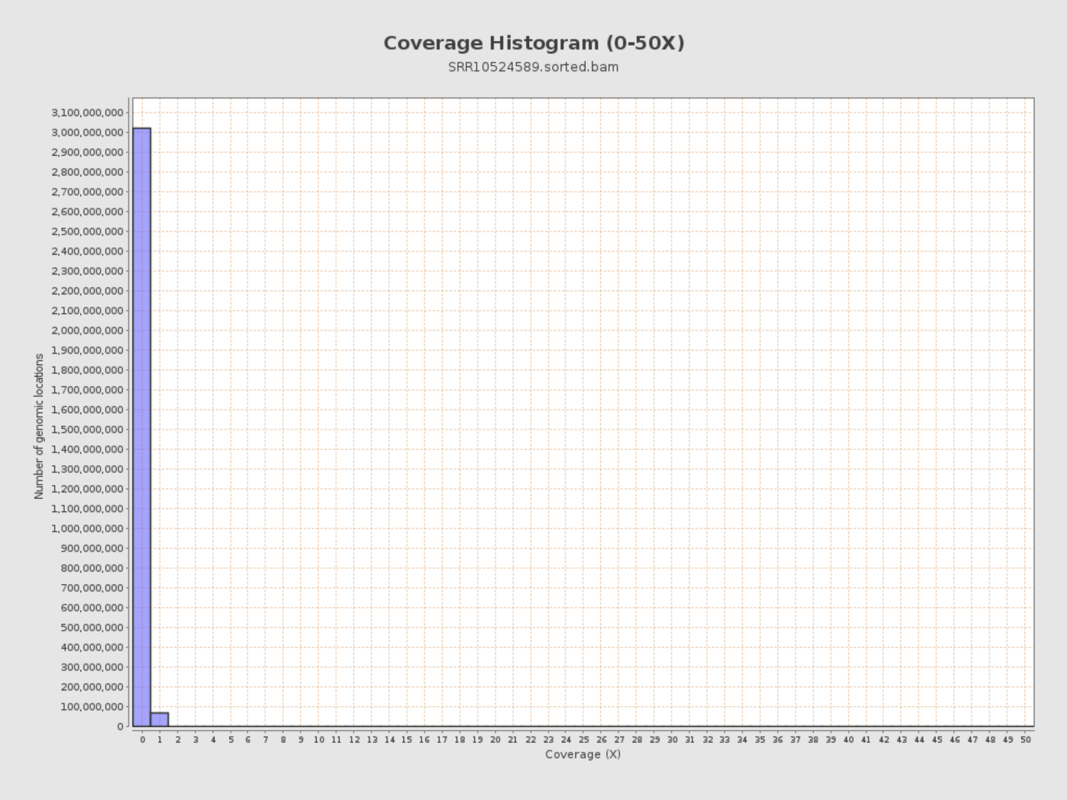
3. Results : Coverage across reference



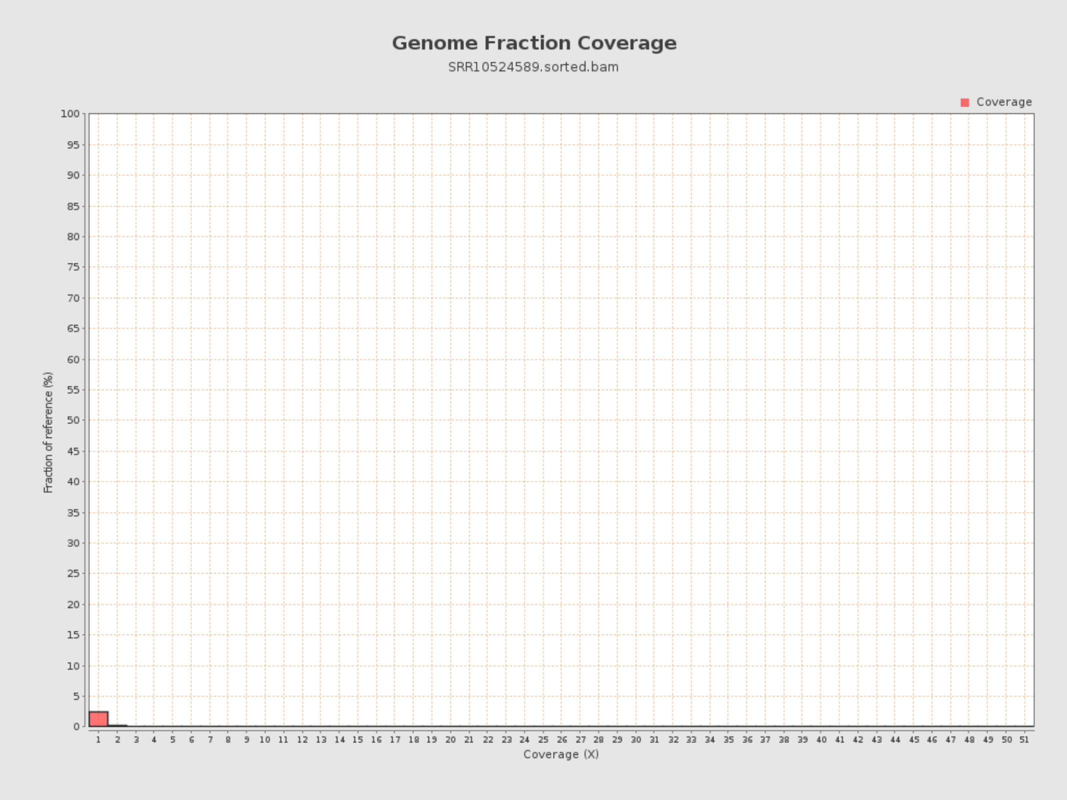
4. Results : Coverage Histogram



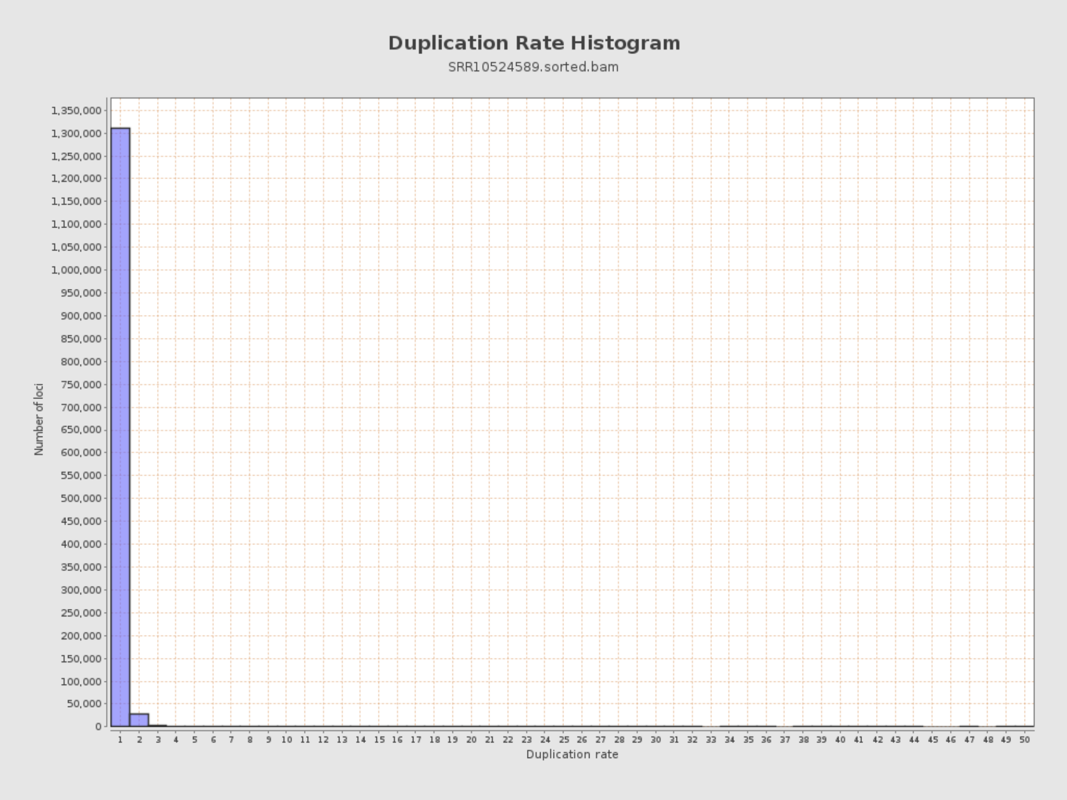
5. Results : Coverage Histogram (0-50X)



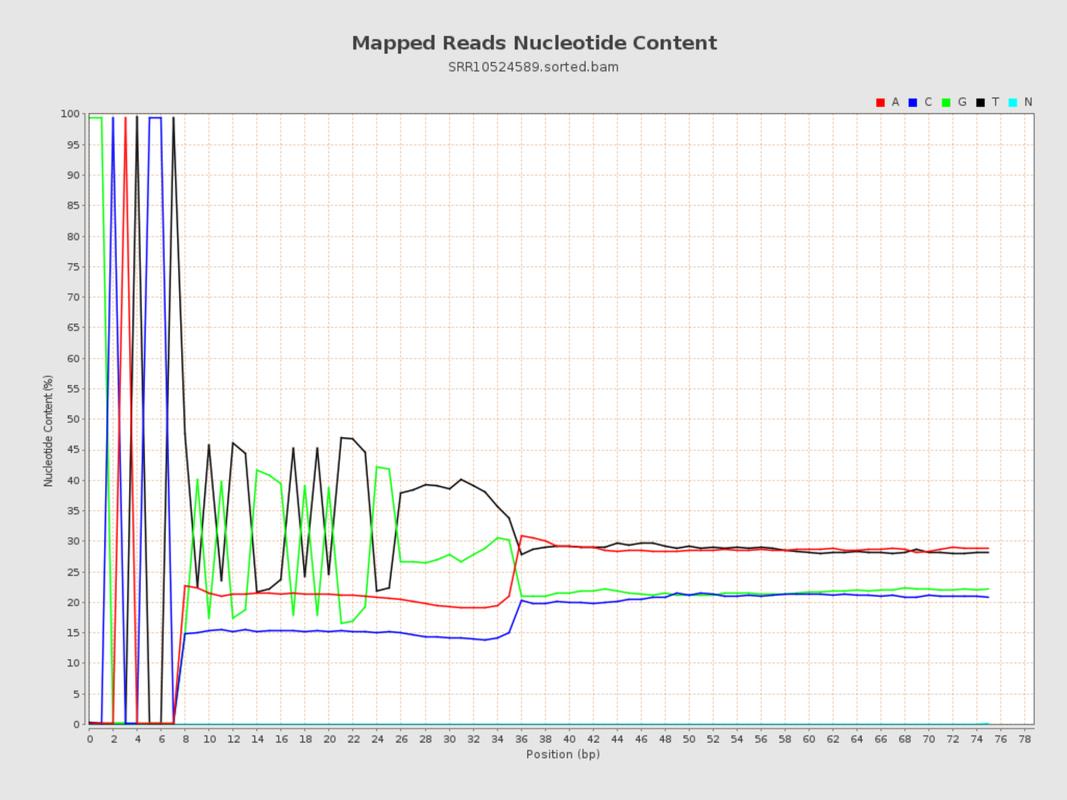
6. Results : Genome Fraction Coverage



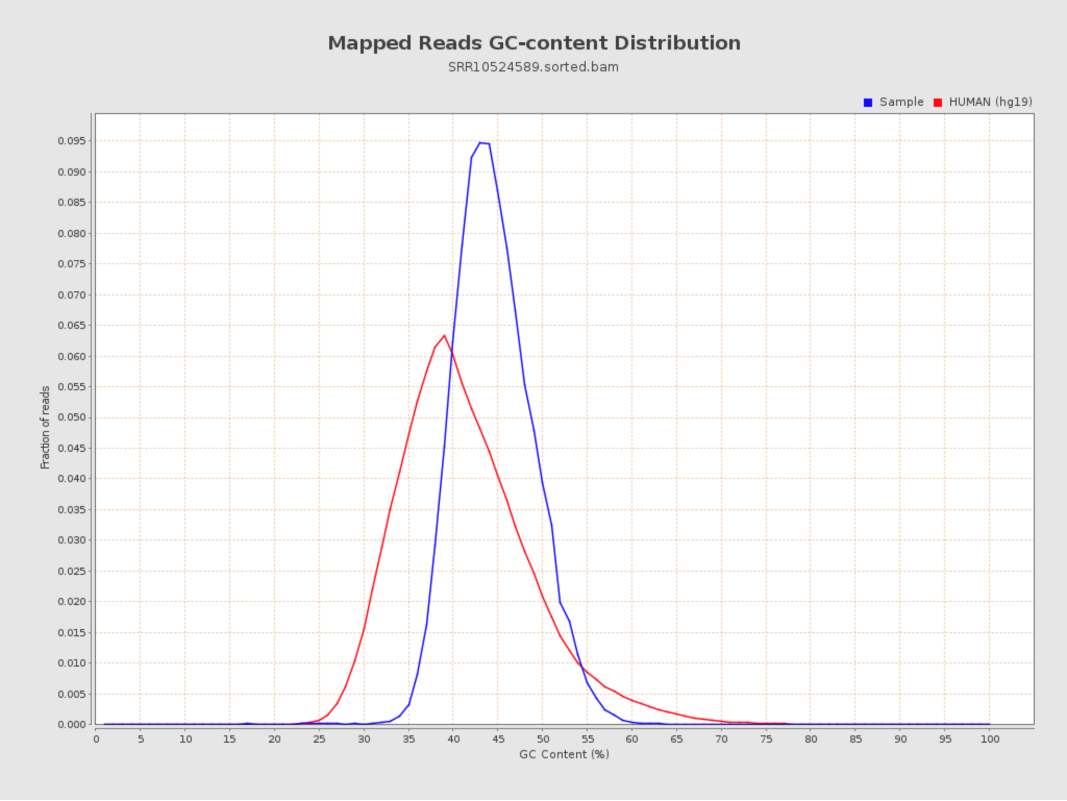
7. Results : Duplication Rate Histogram



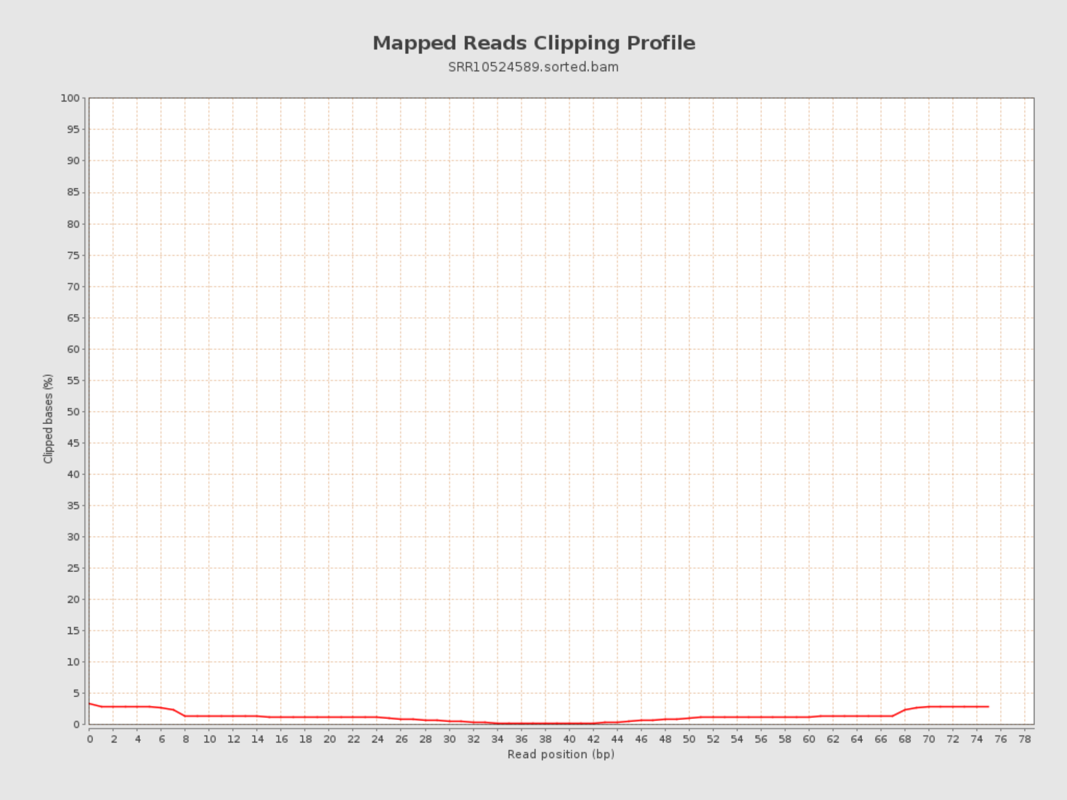
8. Results : Mapped Reads Nucleotide Content



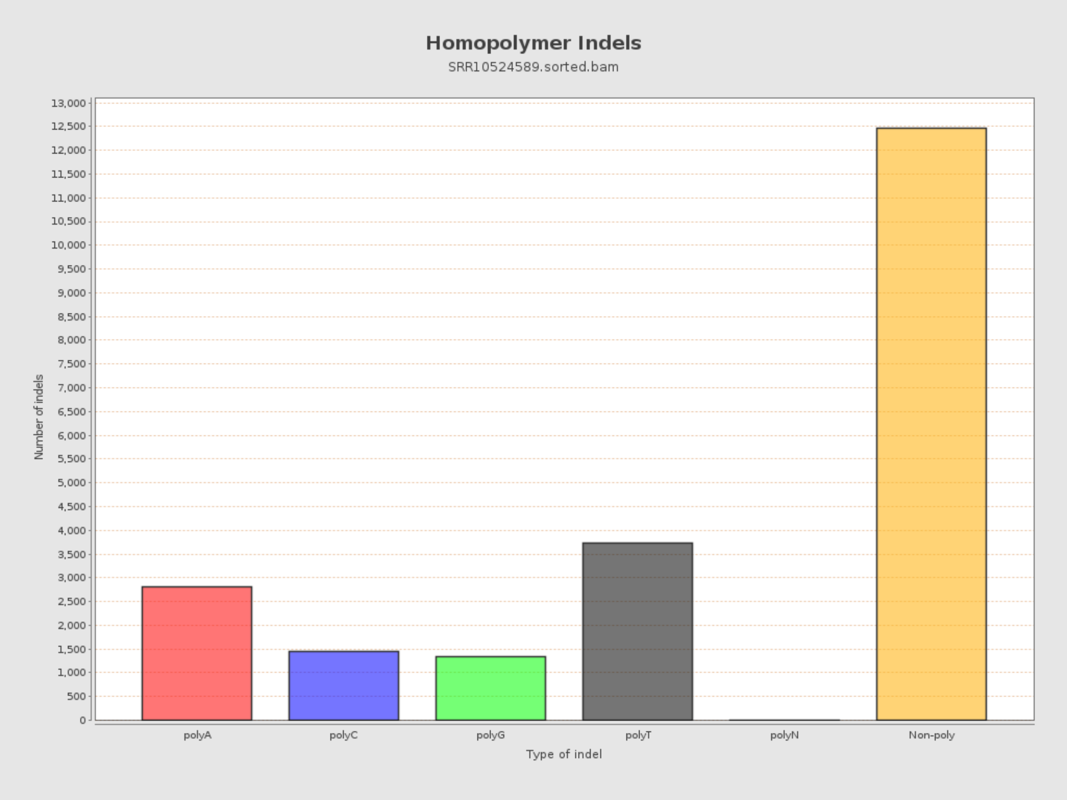
9. Results : Mapped Reads GC-content Distribution



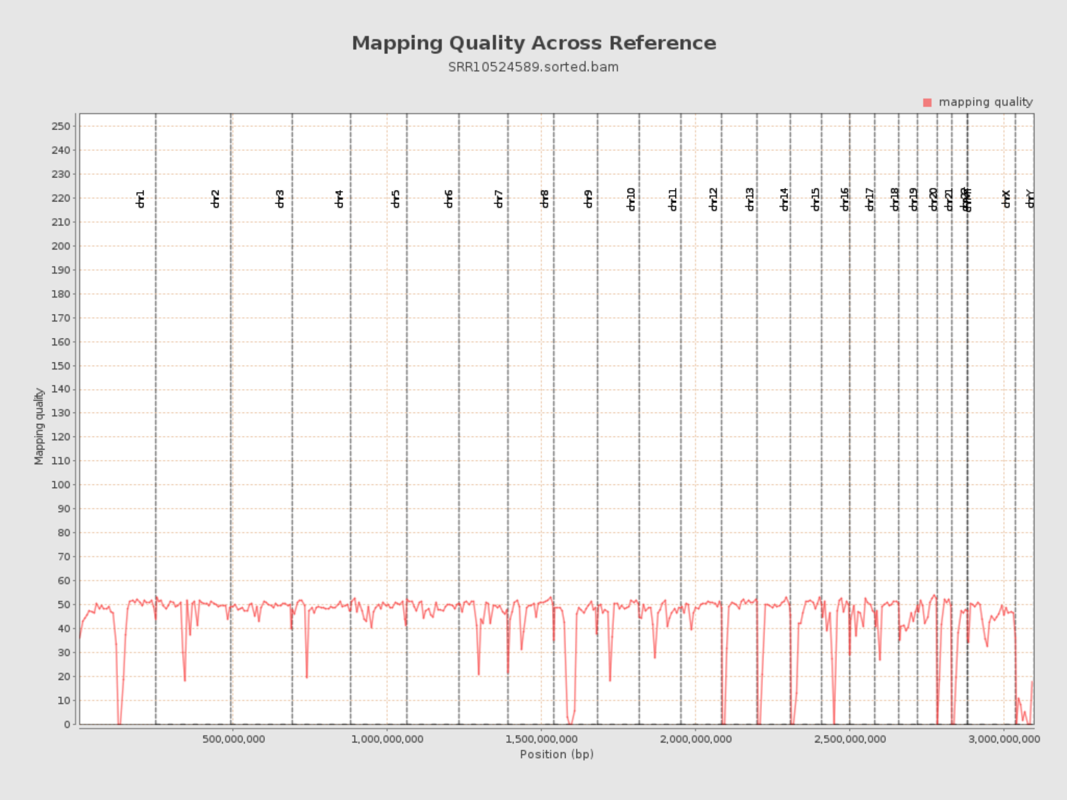
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram