Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:57:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525006.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_SRR10525006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525006.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:57:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,652,577
Mapped reads	1,512,688 / 91.54%
Unmapped reads	139,889 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,180 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	45,577 / 2.76%
Duplication rate	2.13%
Clipped reads	1,514,659 / 91.65%

2.2. ACGT Content

Number/percentage of A's	21,256,137 / 24.33%
Number/percentage of C's	16,319,042 / 18.68%
Number/percentage of T's	27,997,944 / 32.05%
Number/percentage of G's	21,794,475 / 24.95%
Number/percentage of N's	990 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2581

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

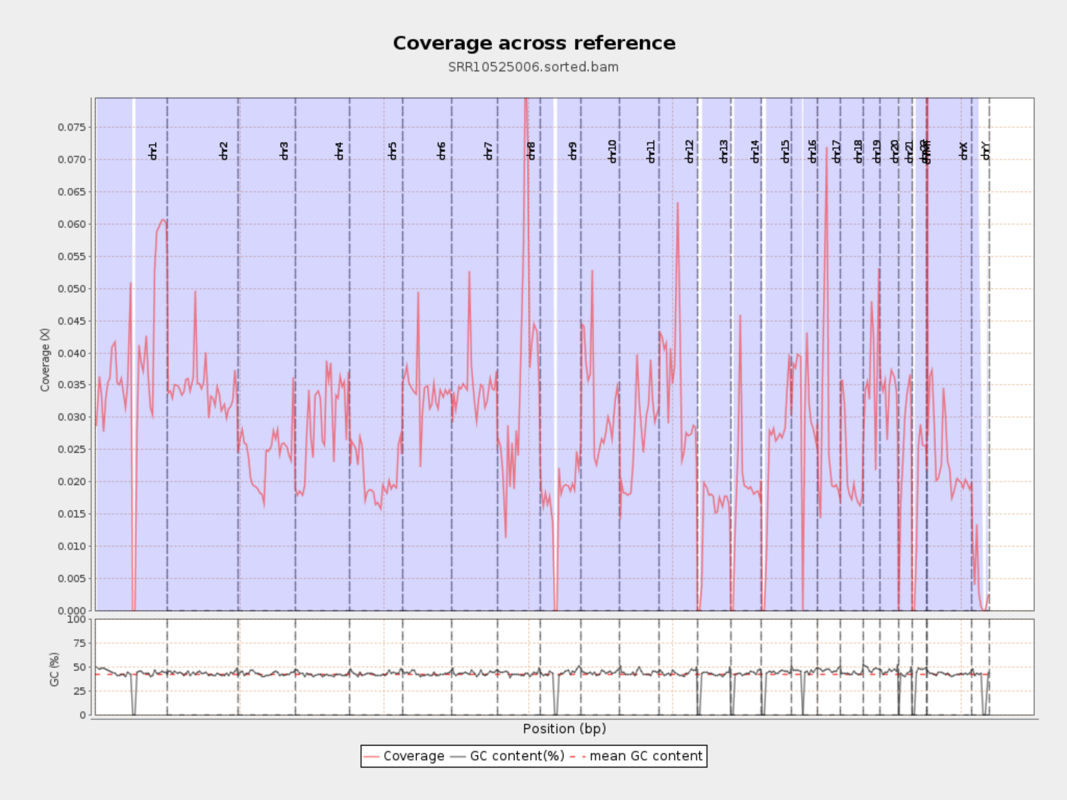
General error rate	0.51%
Mismatches	431,622
Insertions	5,654
Mapped reads with at least one insertion	0.37%
Deletions	16,859
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.9%

2.6. Chromosome stats

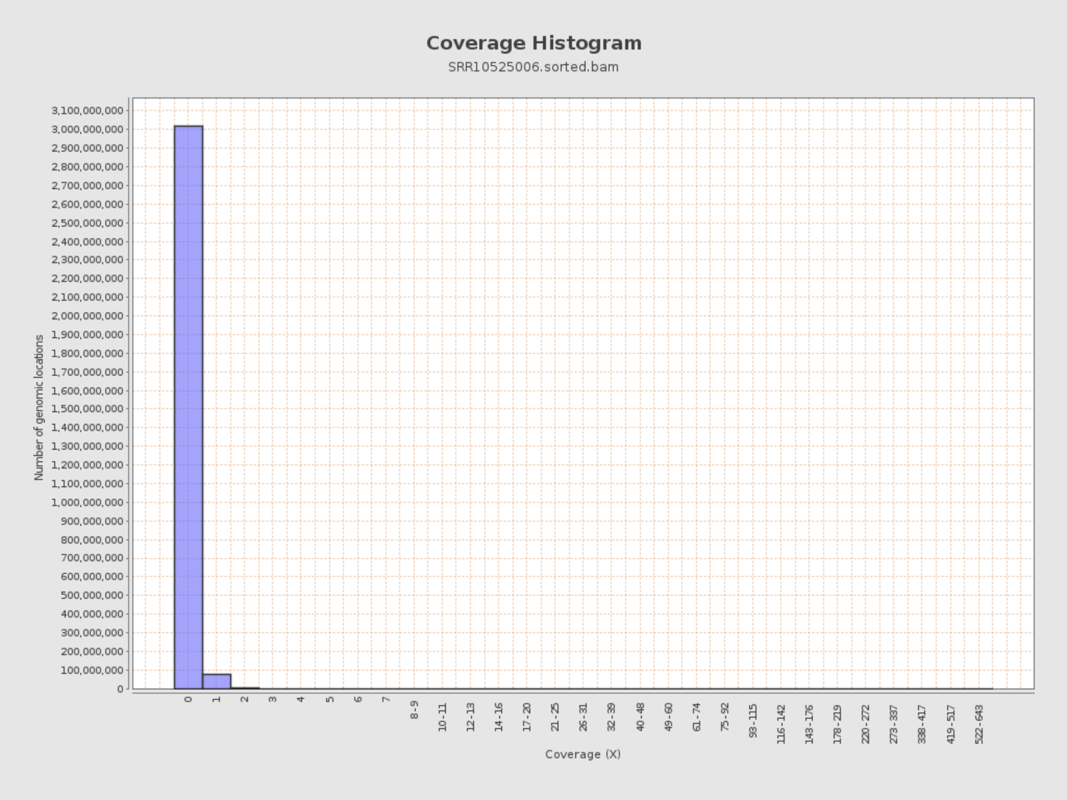
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9442868	0.0379	0.4911
chr2	243199373	8368202	0.0344	0.3035
chr3	198022430	4802301	0.0243	0.1685
chr4	191154276	5599076	0.0293	0.1972
chr5	180915260	3785357	0.0209	0.1579
chr6	171115067	5837934	0.0341	0.2641
chr7	159138663	5540164	0.0348	0.3476

chr8	146364022	5325211	0.0364	0.2576
chr9	141213431	2396333	0.017	0.1845
chr10	135534747	4425436	0.0327	0.2544
chr11	135006516	3652053	0.0271	0.2233
chr12	133851895	4742682	0.0354	0.2034
chr13	115169878	1674375	0.0145	0.1303
chr14	107349540	1990850	0.0185	0.15
chr15	102531392	2439907	0.0238	0.1779
chr16	90354753	2826926	0.0313	0.1986
chr17	81195210	2362448	0.0291	0.2449
chr18	78077248	1707519	0.0219	0.2846
chr19	59128983	2229616	0.0377	0.3091
chr20	63025520	2134064	0.0339	0.199
chr21	48129895	1240785	0.0258	0.1798
chr22	51304566	933335	0.0182	0.1434
chrMT	16571	8707	0.5254	0.7837
chrX	155270560	3695127	0.0238	0.1882
chrY	59373566	235762	0.004	0.1032

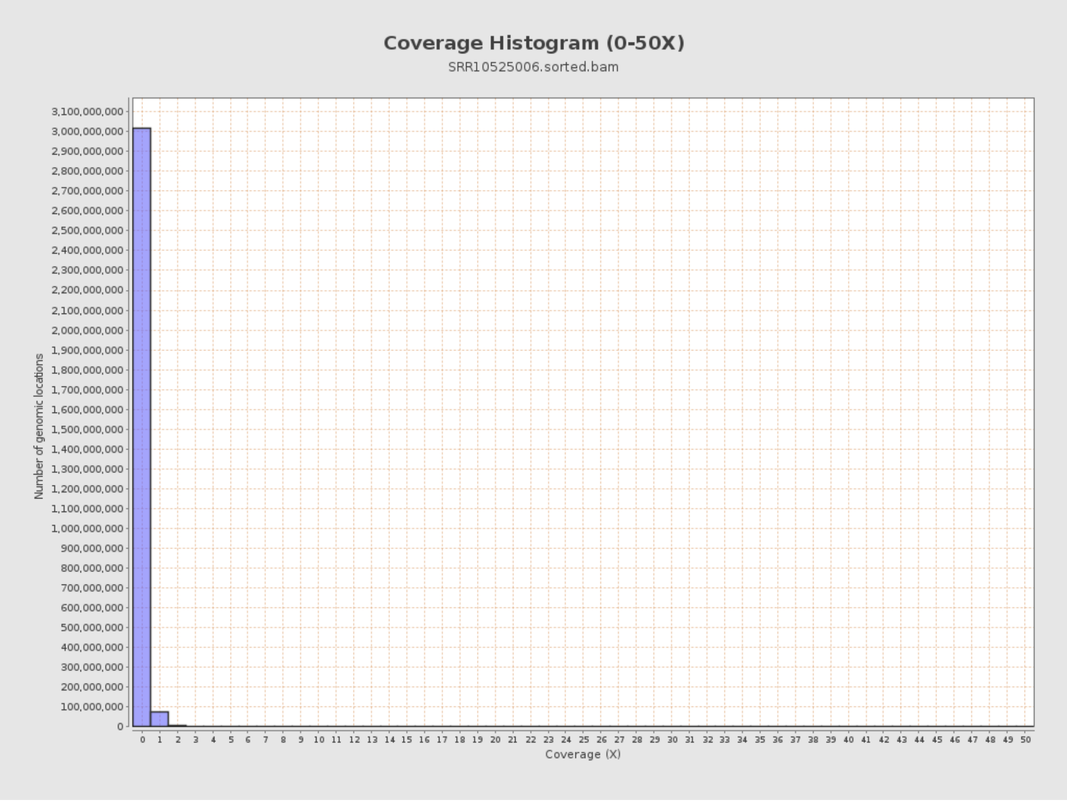
3. Results : Coverage across reference



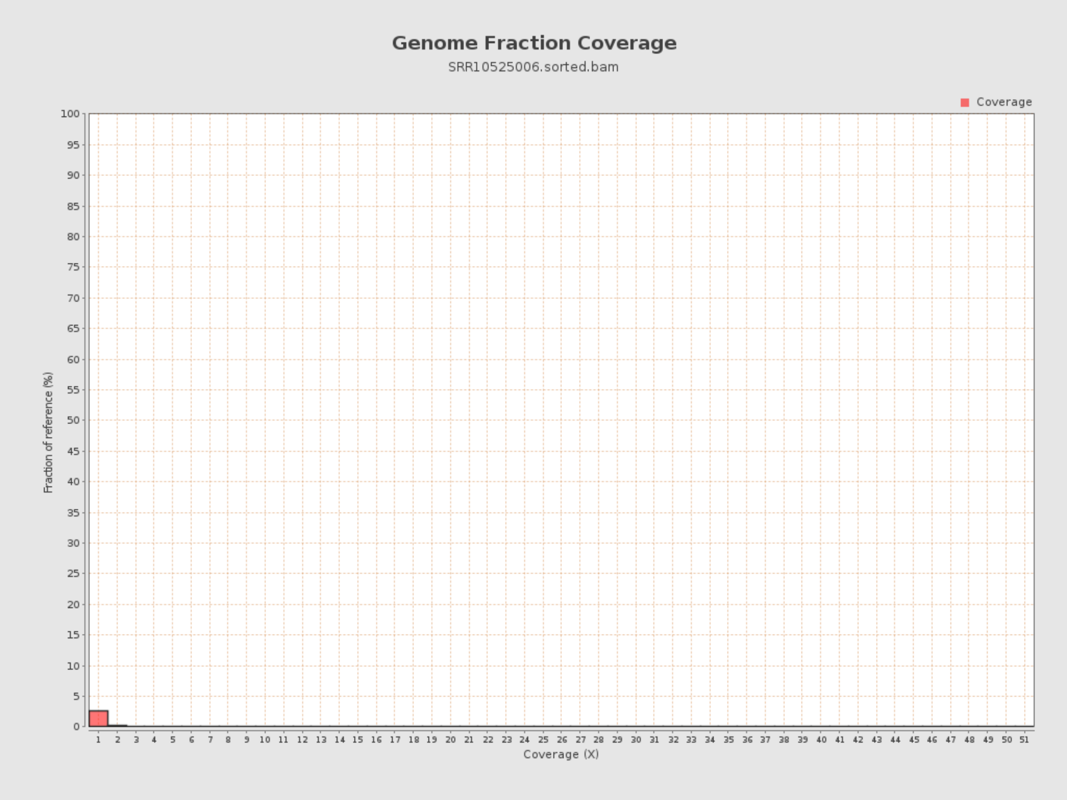
4. Results : Coverage Histogram



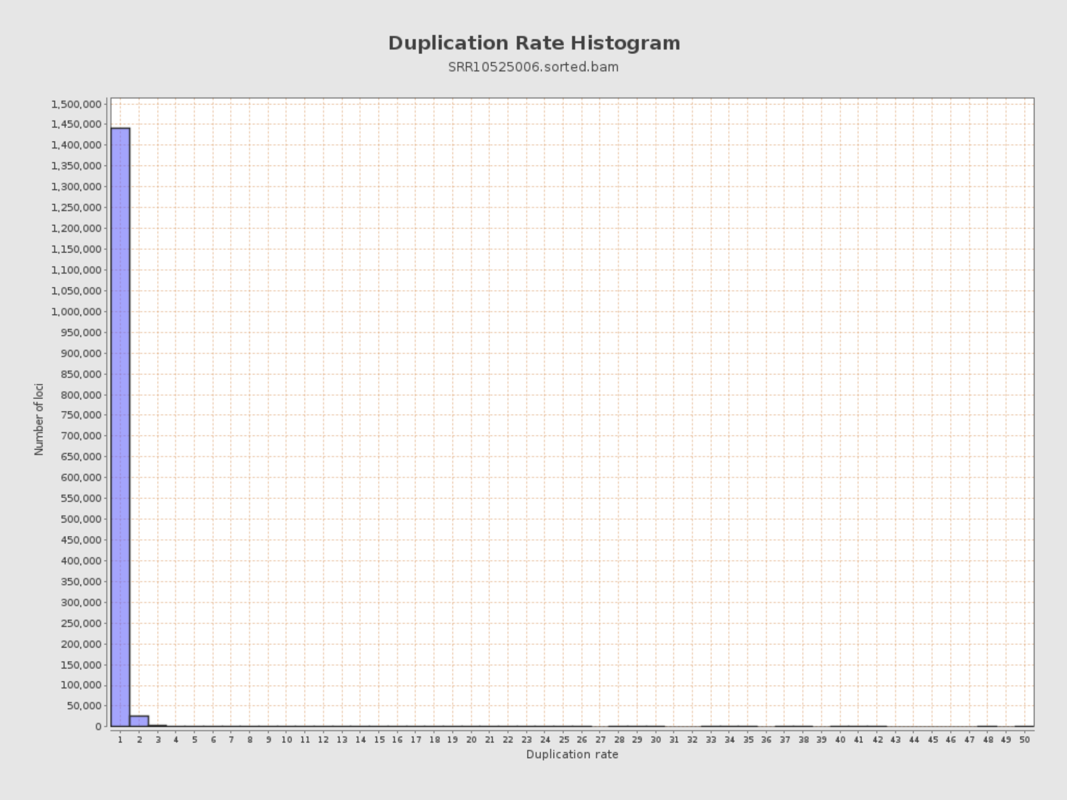
5. Results : Coverage Histogram (0-50X)



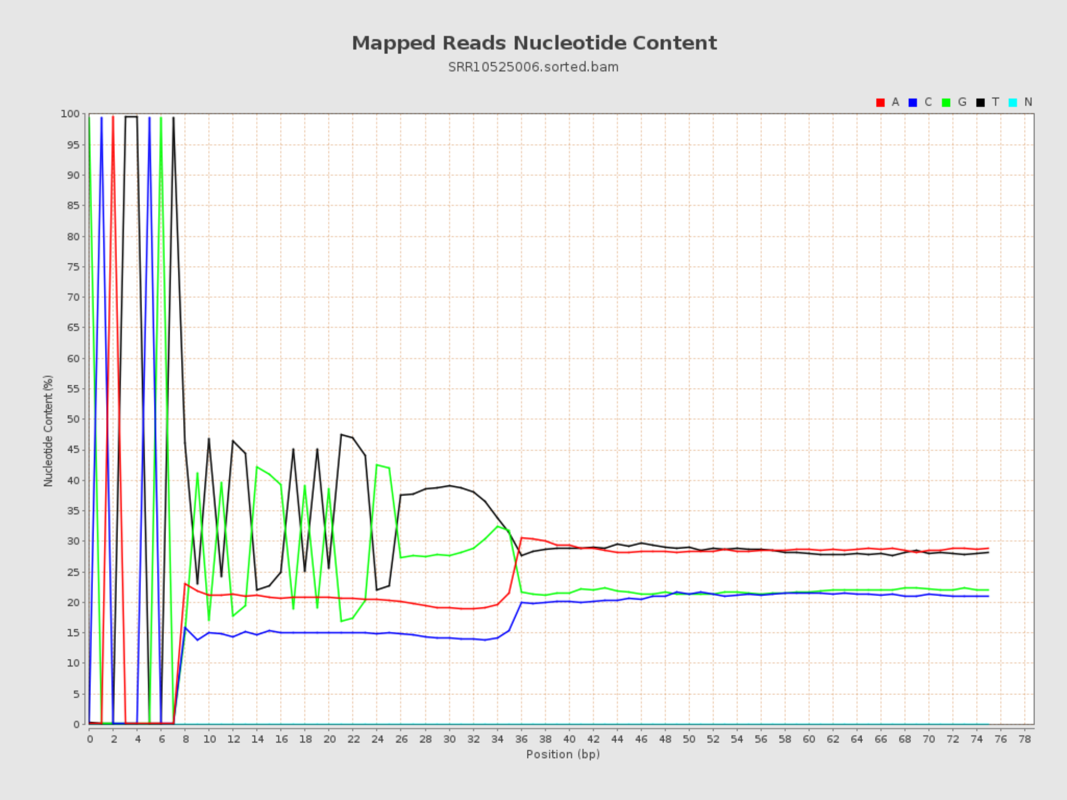
6. Results : Genome Fraction Coverage



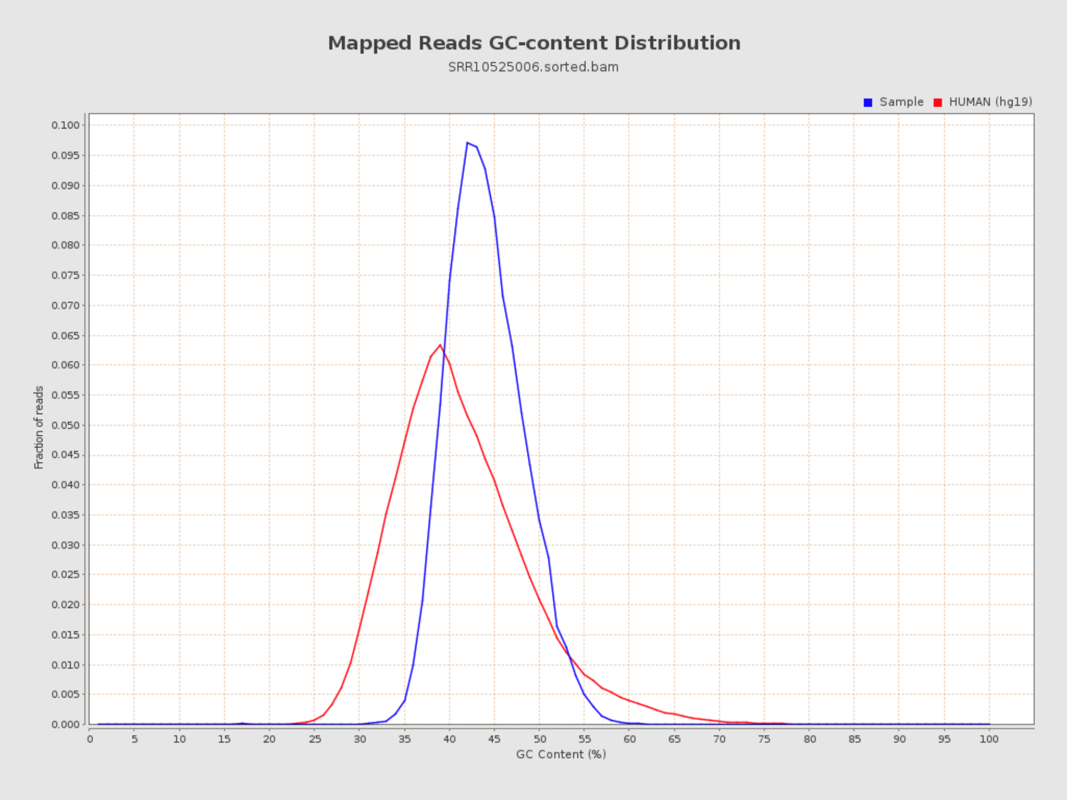
7. Results : Duplication Rate Histogram



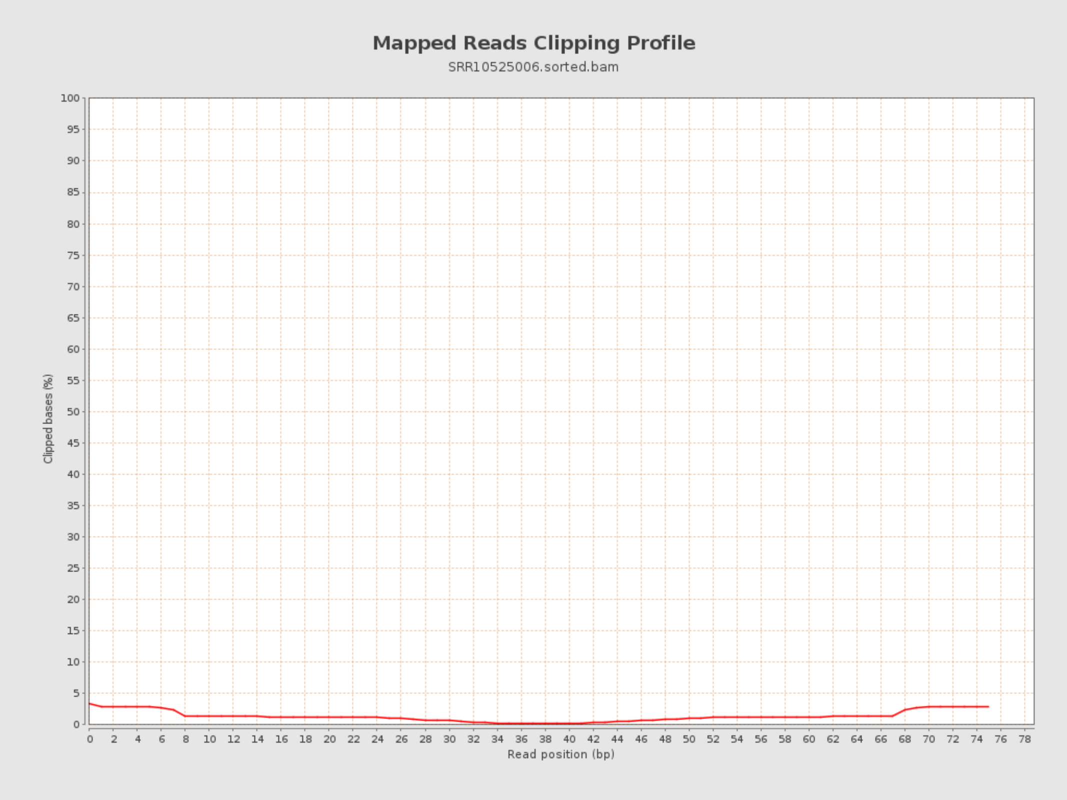
8. Results : Mapped Reads Nucleotide Content



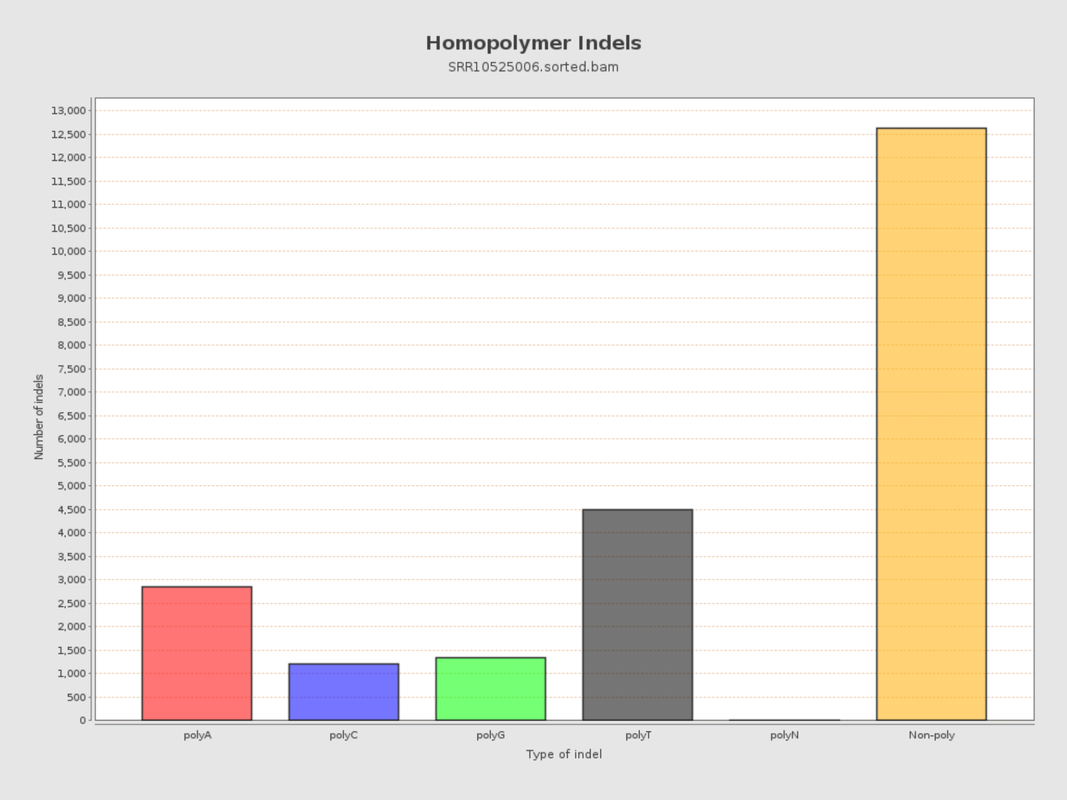
9. Results : Mapped Reads GC-content Distribution



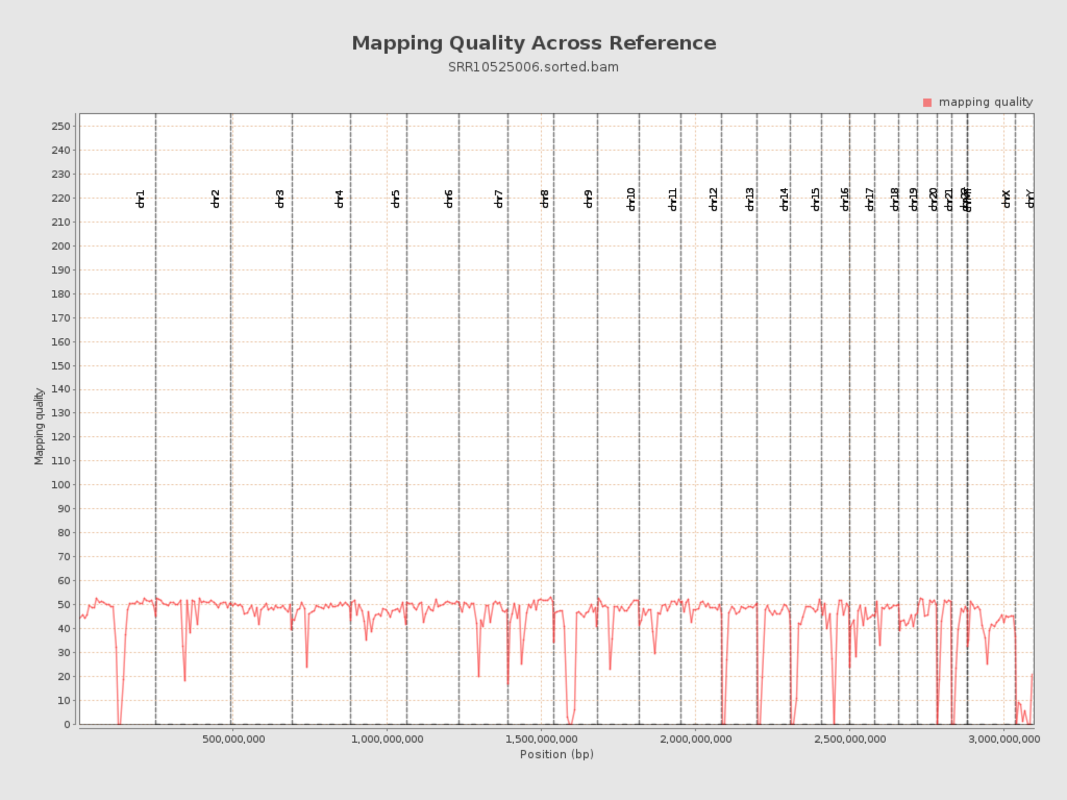
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram