Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:36:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525196.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_SRR10525196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525196.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:36:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	841,876
Mapped reads	762,498 / 90.57%
Unmapped reads	79,378 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,000 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	18,381 / 2.18%
Duplication rate	1.73%
Clipped reads	763,239 / 90.66%

2.2. ACGT Content

Number/percentage of A's	11,116,549 / 25.4%
Number/percentage of C's	7,909,337 / 18.07%
Number/percentage of T's	14,259,824 / 32.59%
Number/percentage of G's	10,473,662 / 23.93%
Number/percentage of N's	1,033 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1645

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

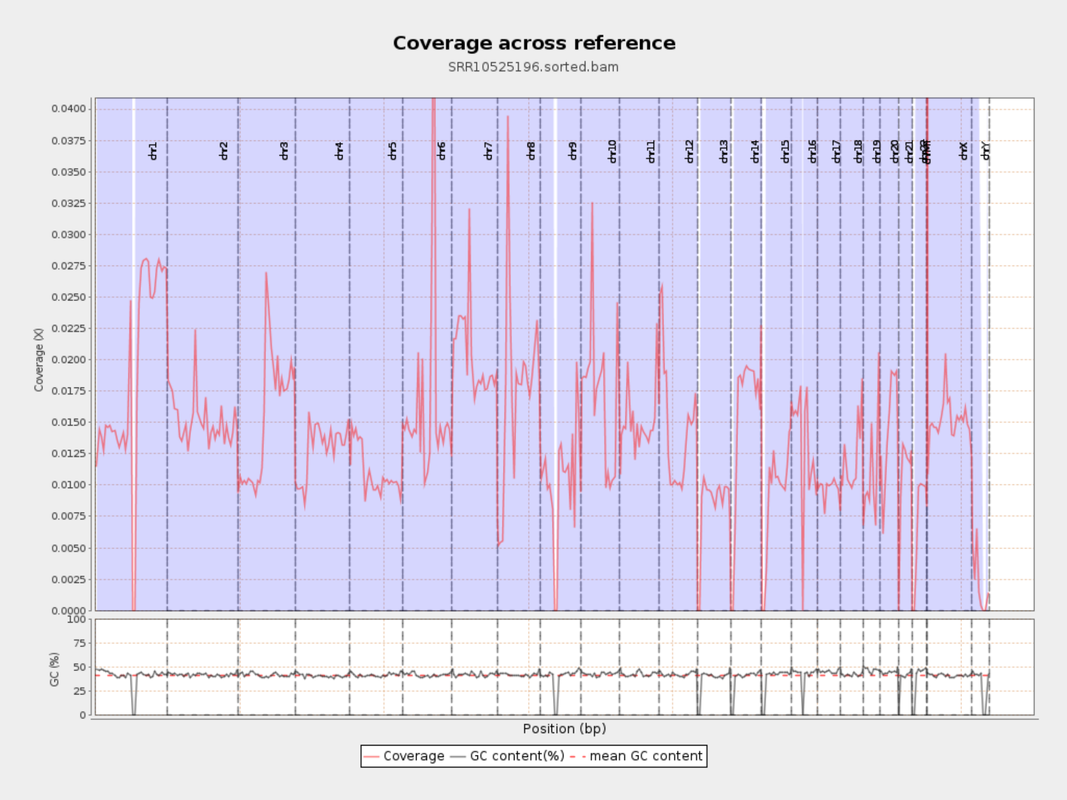
General error rate	0.54%
Mismatches	230,854
Insertions	2,713
Mapped reads with at least one insertion	0.35%
Deletions	8,741
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.35%

2.6. Chromosome stats

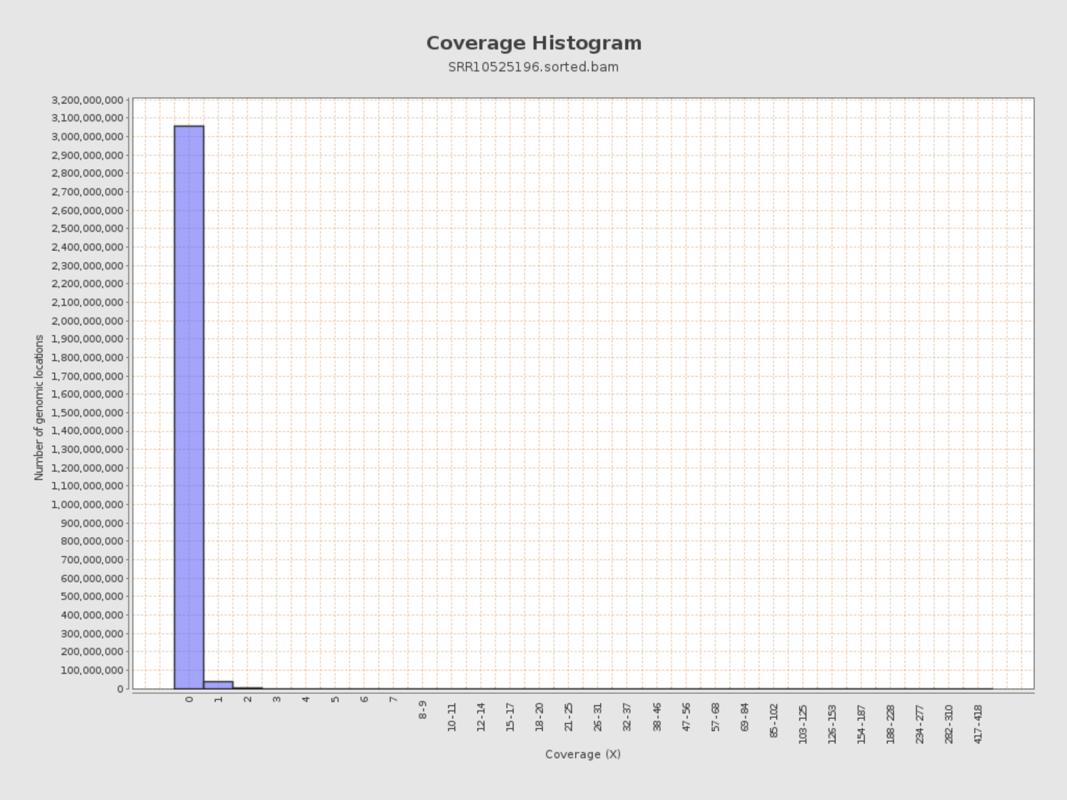
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4655251	0.0187	0.2591
chr2	243199373	3684635	0.0152	0.216
chr3	198022430	3052266	0.0154	0.1308
chr4	191154276	2476050	0.013	0.1222
chr5	180915260	1999035	0.011	0.1096
chr6	171115067	2902181	0.017	0.1478
chr7	159138663	3234256	0.0203	0.2692

chr8	146364022	2587958	0.0177	0.1589
chr9	141213431	1460309	0.0103	0.1237
chr10	135534747	2346571	0.0173	0.1904
chr11	135006516	2026869	0.015	0.1418
chr12	133851895	1960703	0.0146	0.1281
chr13	115169878	964700	0.0084	0.0961
chr14	107349540	1646133	0.0153	0.1306
chr15	102531392	927168	0.009	0.1024
chr16	90354753	1172426	0.013	0.126
chr17	81195210	788454	0.0097	0.1044
chr18	78077248	937875	0.012	0.1916
chr19	59128983	650759	0.011	0.1818
chr20	63025520	907904	0.0144	0.1267
chr21	48129895	521254	0.0108	0.1143
chr22	51304566	356789	0.007	0.0868
chrMT	16571	25636	1.547	1.4583
chrX	155270560	2366207	0.0152	0.1353
chrY	59373566	122733	0.0021	0.0671

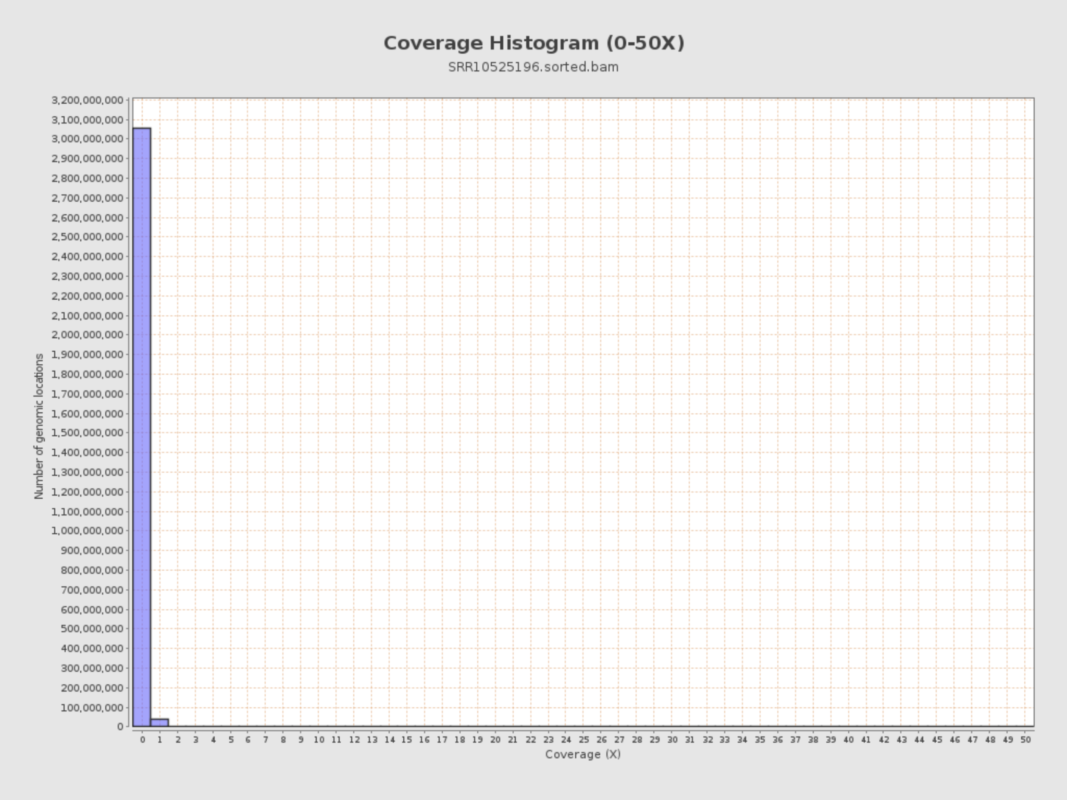
3. Results : Coverage across reference



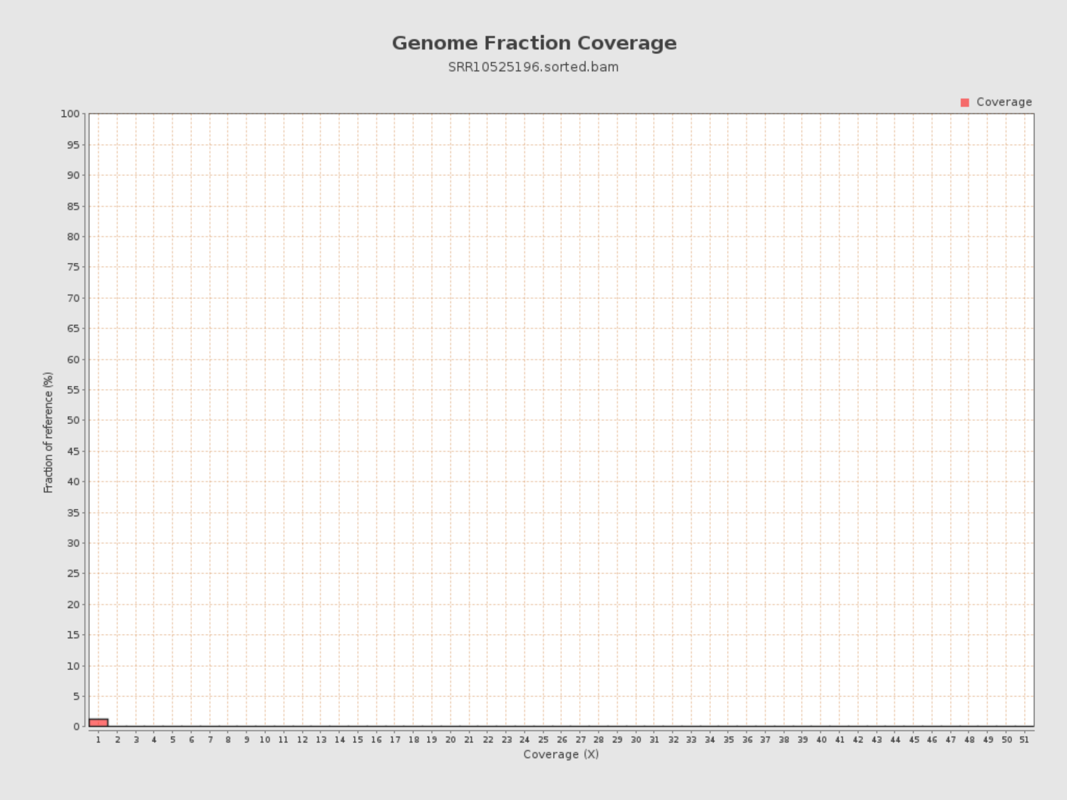
4. Results : Coverage Histogram



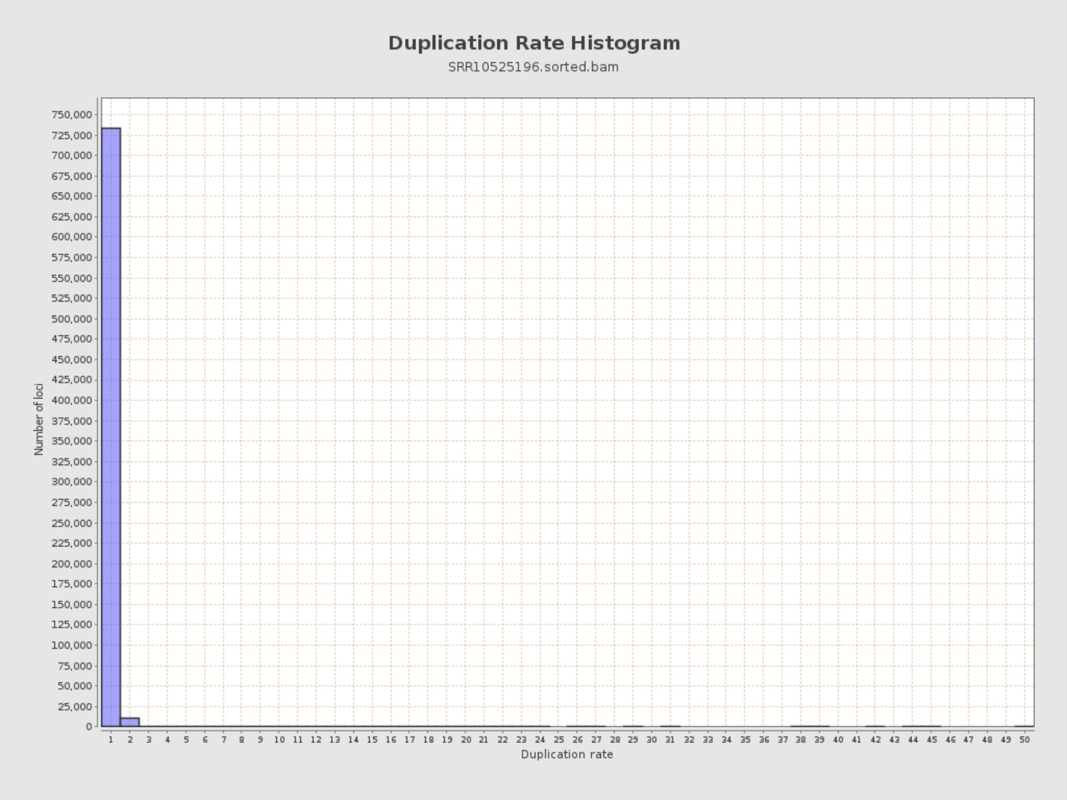
5. Results : Coverage Histogram (0-50X)



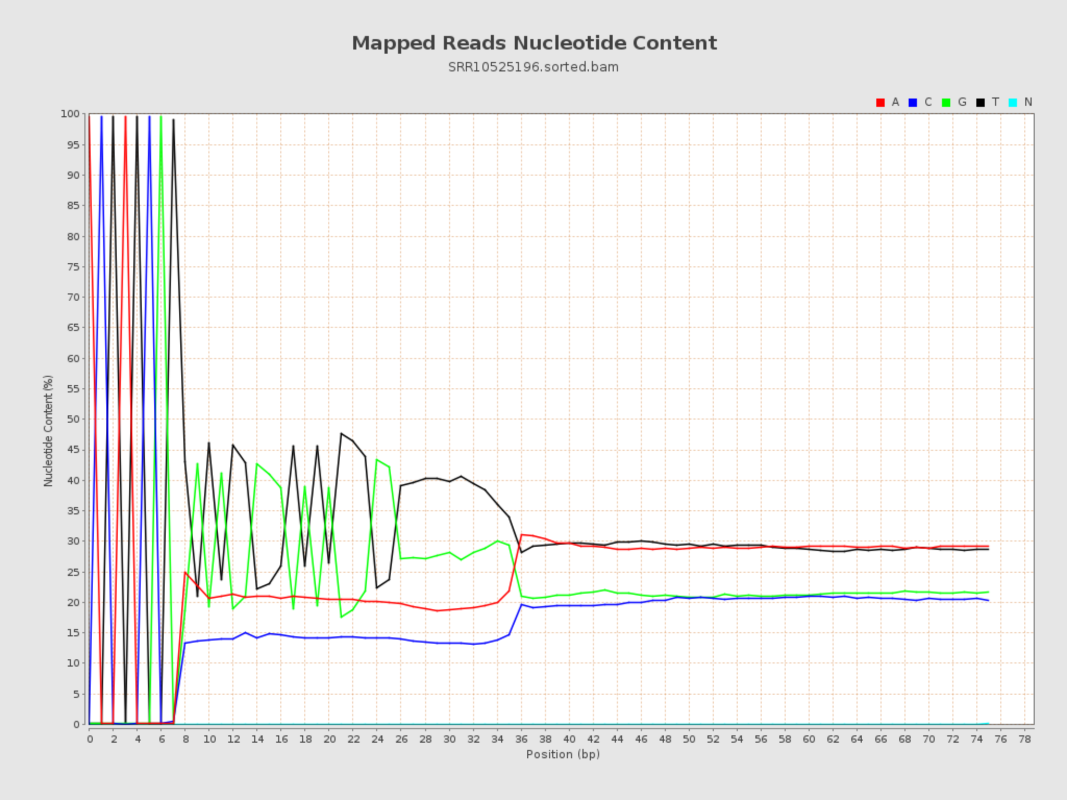
6. Results : Genome Fraction Coverage



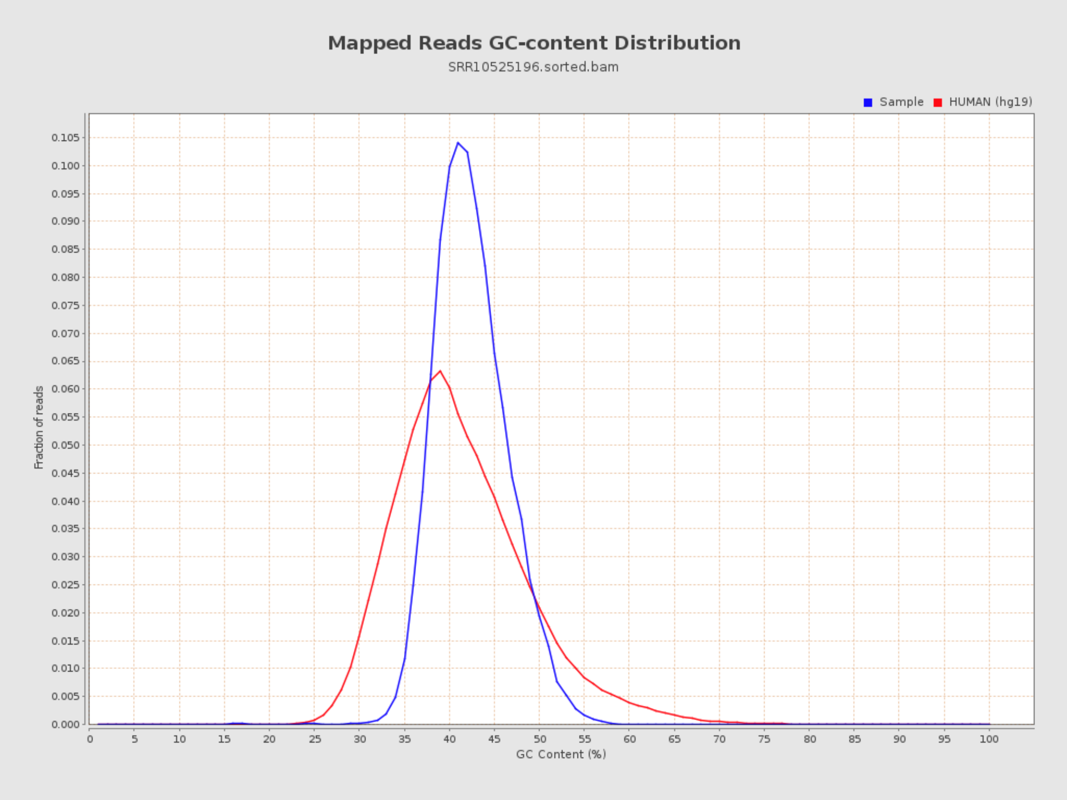
7. Results : Duplication Rate Histogram



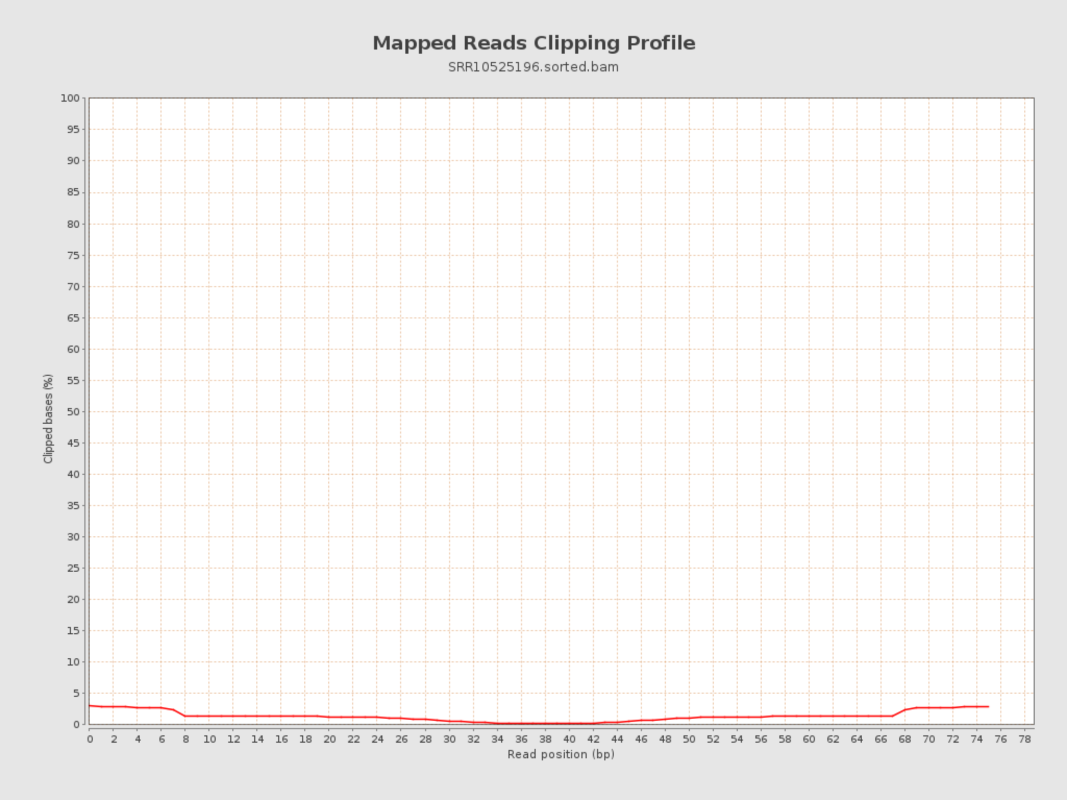
8. Results : Mapped Reads Nucleotide Content



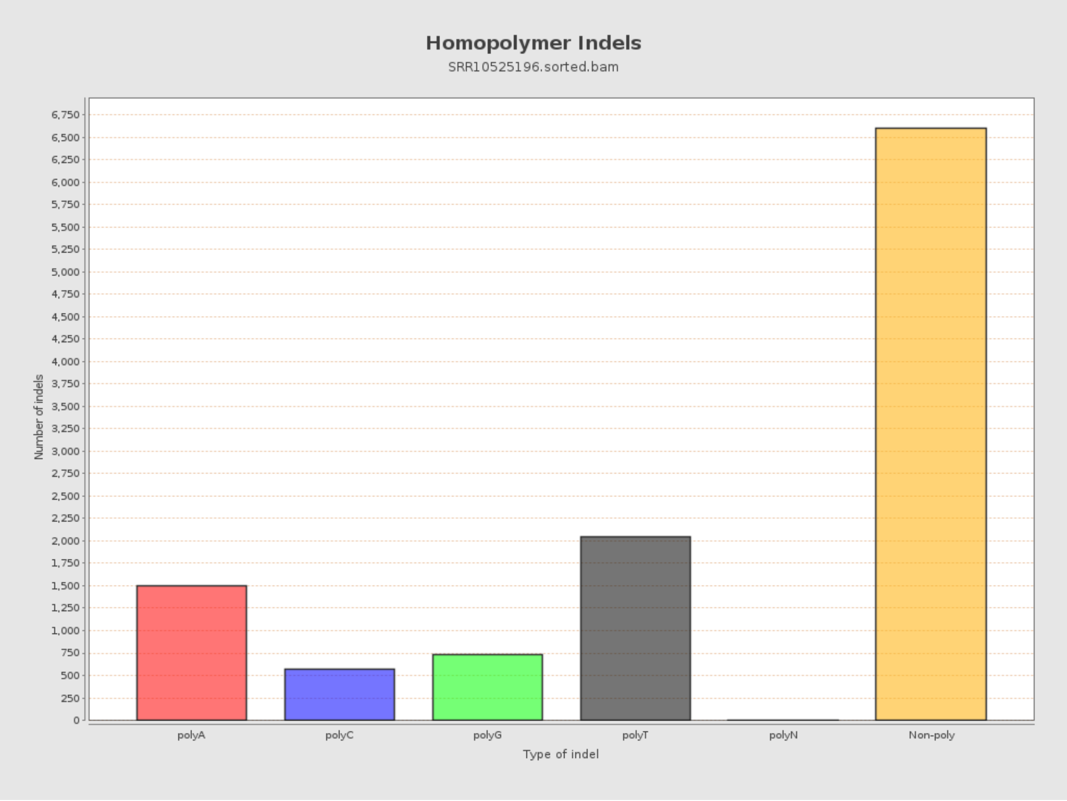
9. Results : Mapped Reads GC-content Distribution



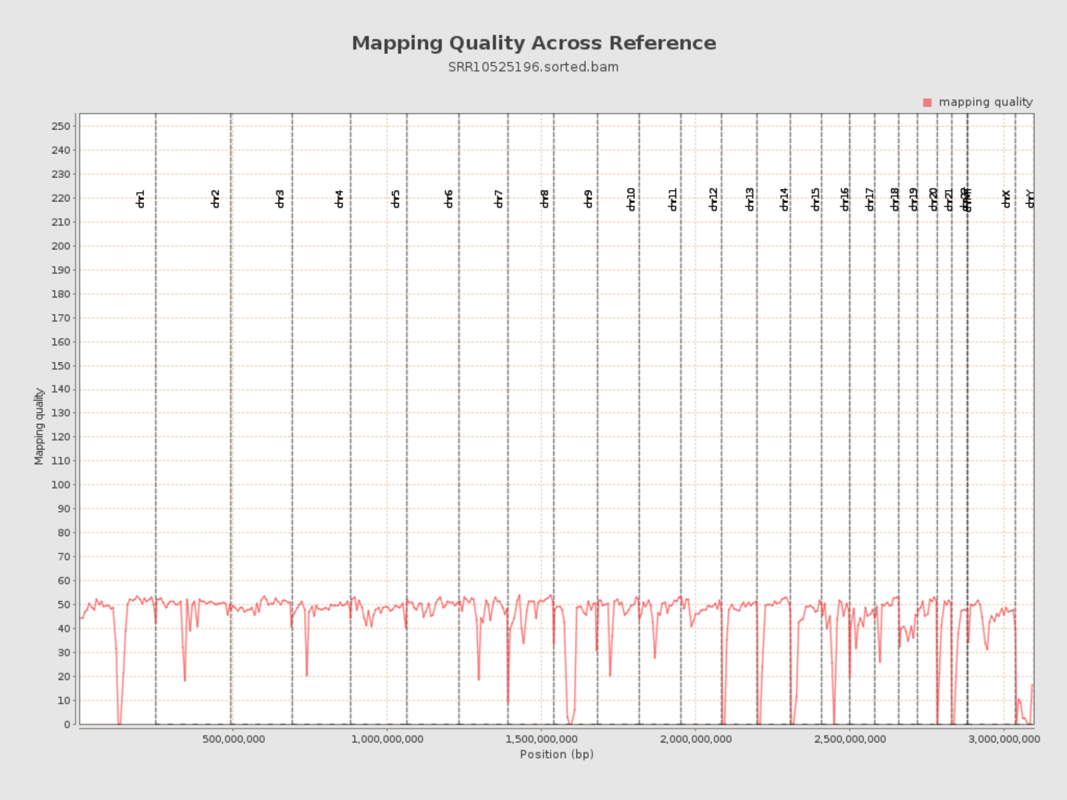
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram