Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:40:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525198.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_SRR10525198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:40:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,308,609
Mapped reads	1,169,116 / 89.34%
Unmapped reads	139,493 / 10.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,180 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	27,930 / 2.13%
Duplication rate	1.63%
Clipped reads	1,168,514 / 89.29%

2.2. ACGT Content

Number/percentage of A's	18,245,705 / 25.46%
Number/percentage of C's	14,644,983 / 20.44%
Number/percentage of T's	22,610,304 / 31.55%
Number/percentage of G's	16,152,058 / 22.54%
Number/percentage of N's	1,697 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.242

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

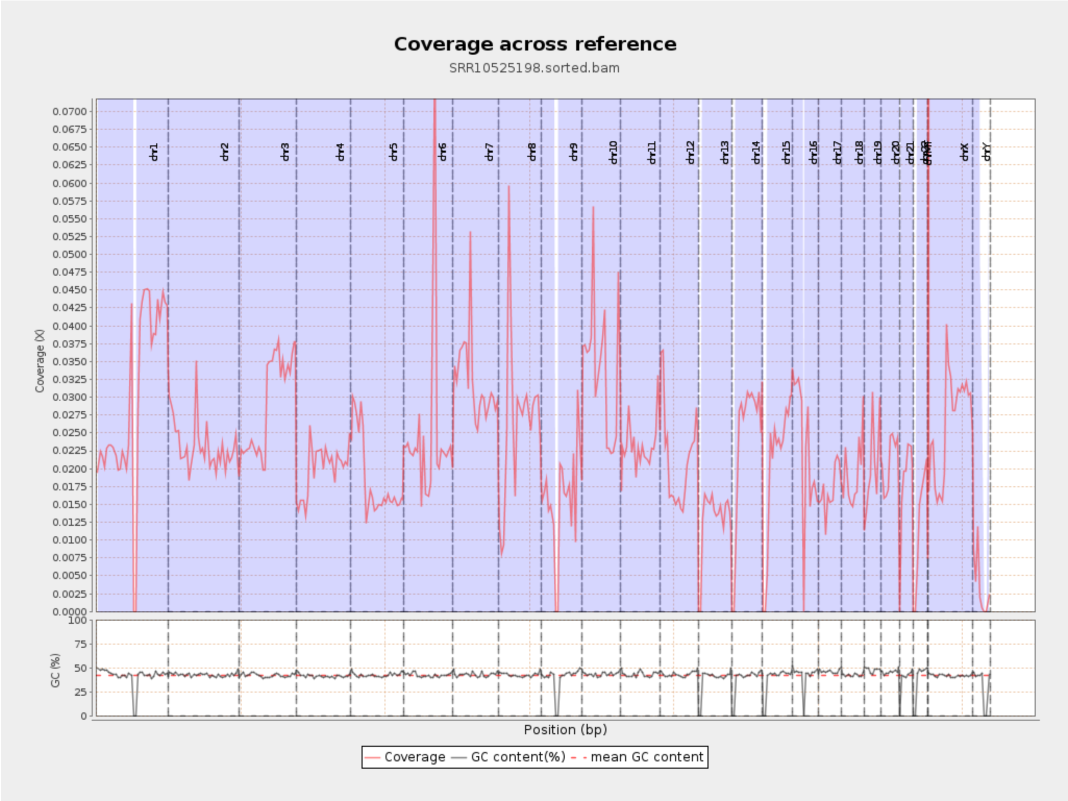
General error rate	0.5%
Mismatches	345,641
Insertions	5,293
Mapped reads with at least one insertion	0.45%
Deletions	14,687
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.5%

2.6. Chromosome stats

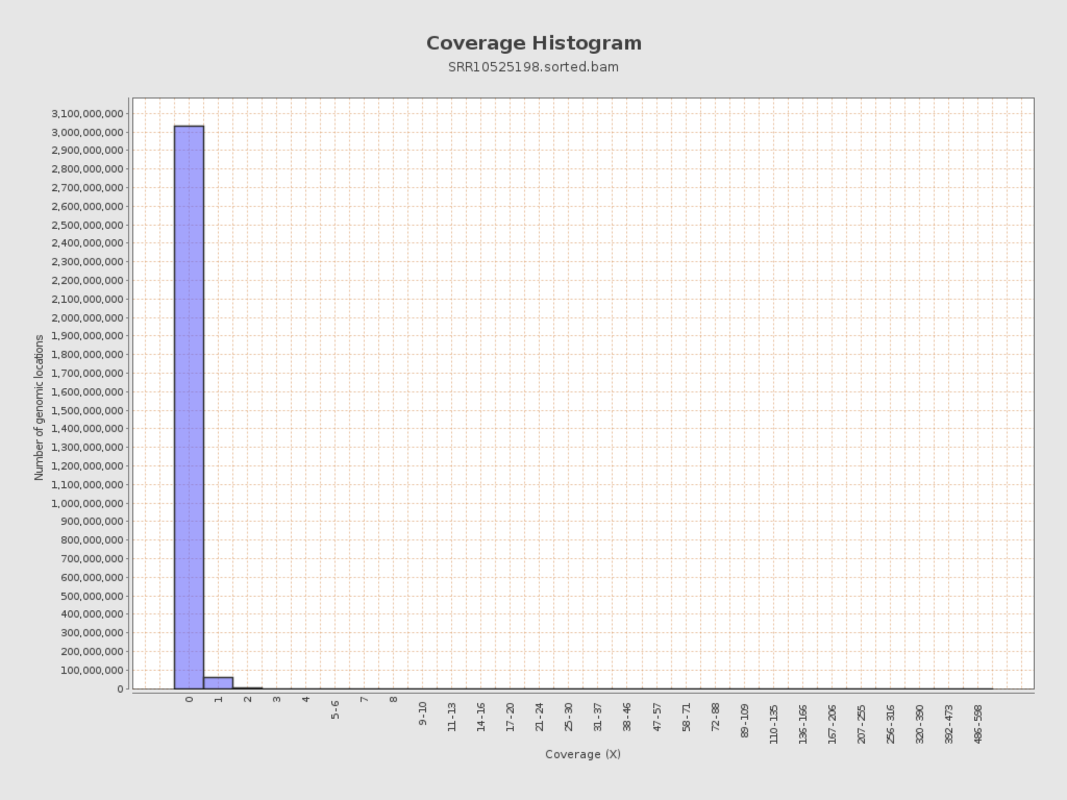
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7375453	0.0296	0.4643
chr2	243199373	5634043	0.0232	0.2474
chr3	198022430	5730914	0.0289	0.1804
chr4	191154276	3847207	0.0201	0.1559
chr5	180915260	3349341	0.0185	0.143
chr6	171115067	4326210	0.0253	0.1796
chr7	159138663	5145569	0.0323	0.4231

chr8	146364022	3926295	0.0268	0.2151
chr9	141213431	2220801	0.0157	0.1691
chr10	135534747	4628989	0.0342	0.2743
chr11	135006516	3132086	0.0232	0.1883
chr12	133851895	2865023	0.0214	0.1555
chr13	115169878	1484001	0.0129	0.1206
chr14	107349540	2574783	0.024	0.1646
chr15	102531392	2084878	0.0203	0.1495
chr16	90354753	2056807	0.0228	0.1711
chr17	81195210	1390628	0.0171	0.1436
chr18	78077248	1470238	0.0188	0.3158
chr19	59128983	1220616	0.0206	0.3191
chr20	63025520	1302306	0.0207	0.1534
chr21	48129895	883801	0.0184	0.1517
chr22	51304566	619587	0.0121	0.1152
chrMT	16571	77844	4.6976	3.3421
chrX	155270560	4124653	0.0266	0.1817
chrY	59373566	206379	0.0035	0.111

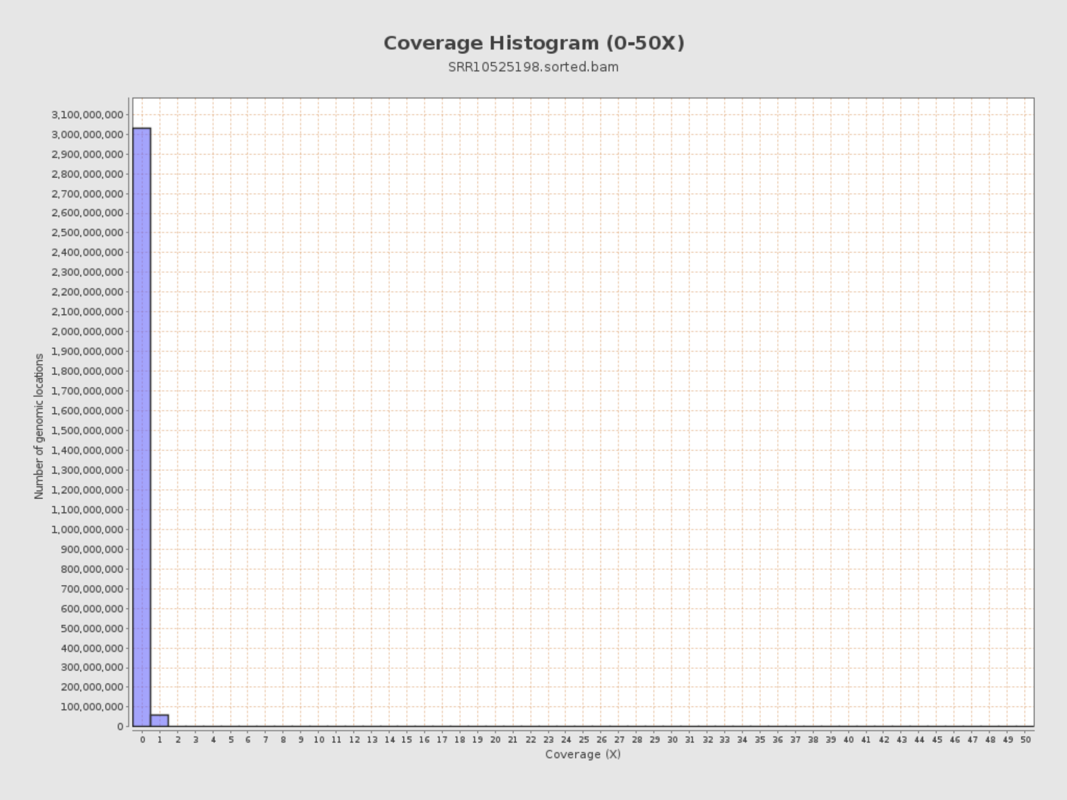
3. Results : Coverage across reference



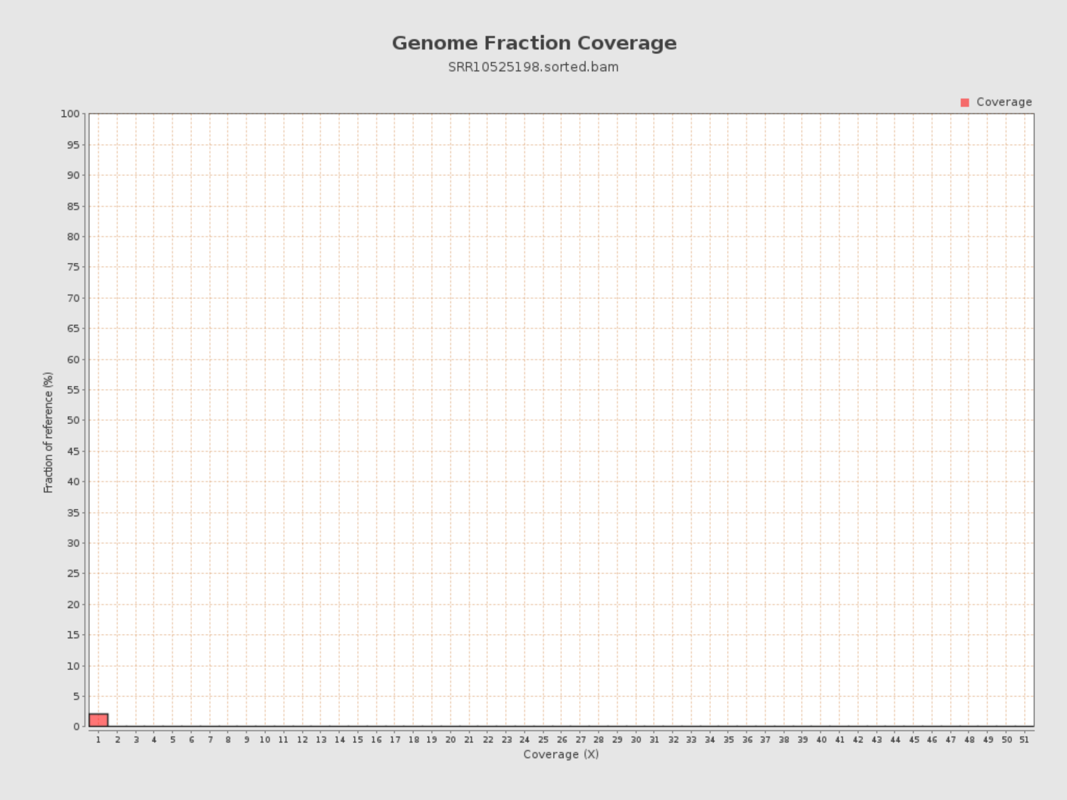
4. Results : Coverage Histogram



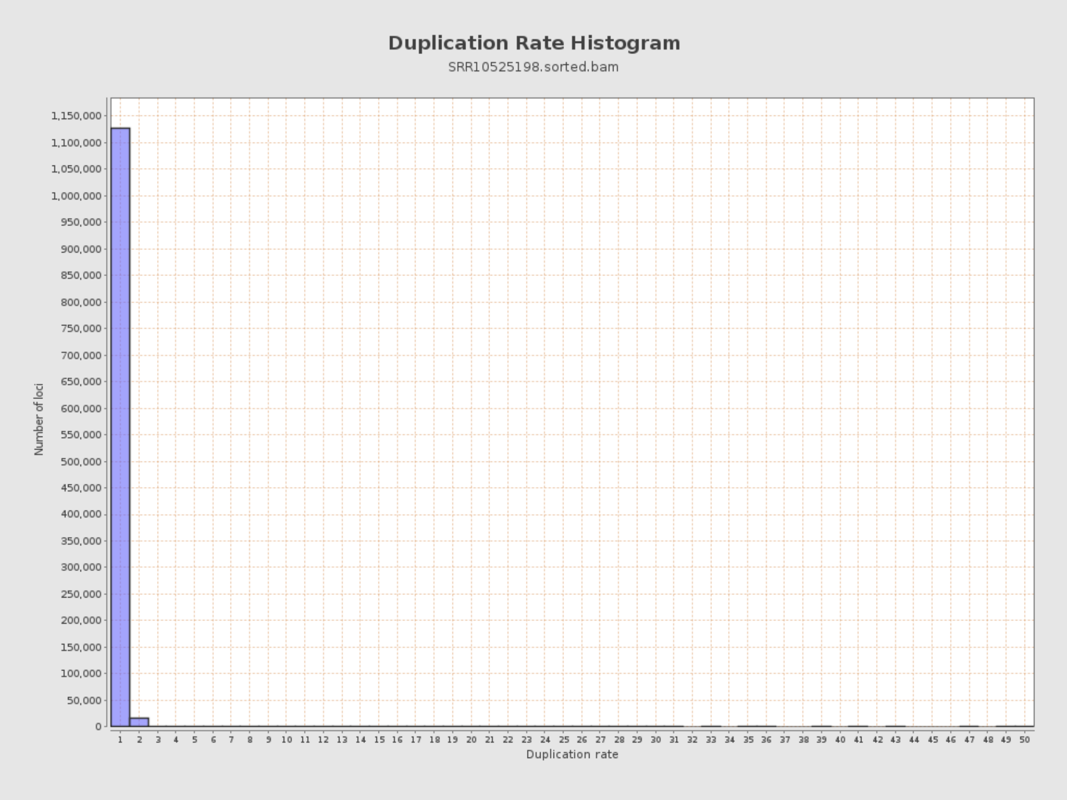
5. Results : Coverage Histogram (0-50X)



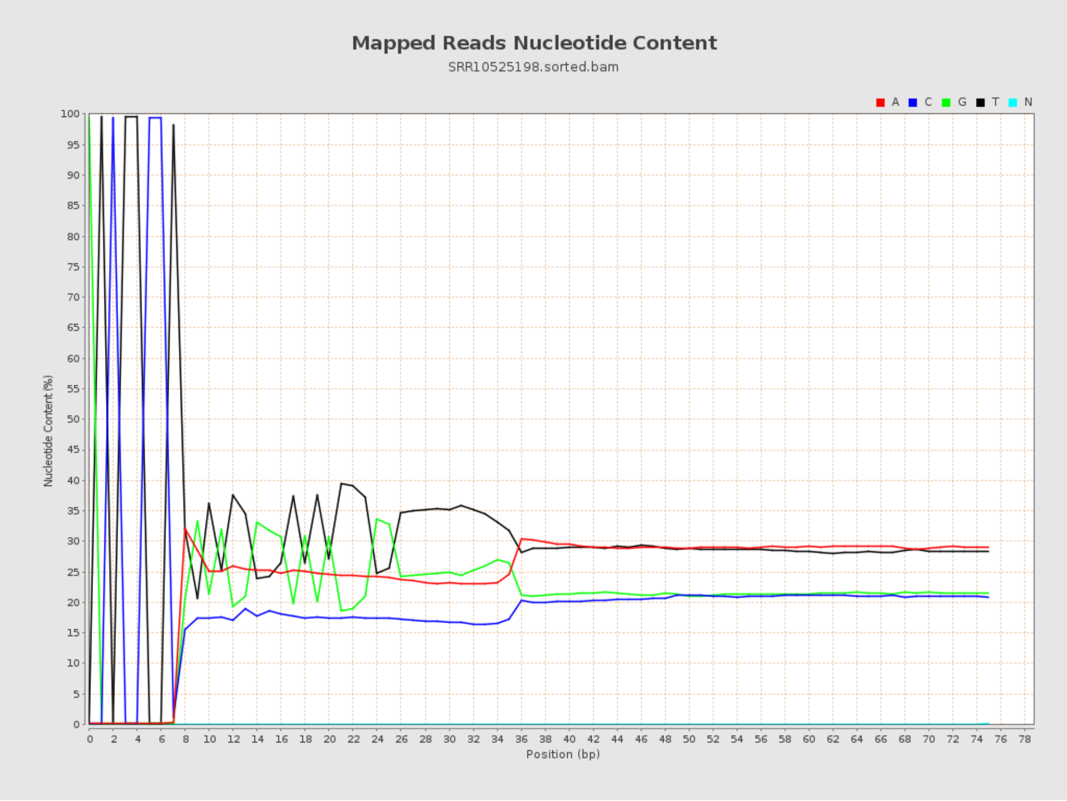
6. Results : Genome Fraction Coverage



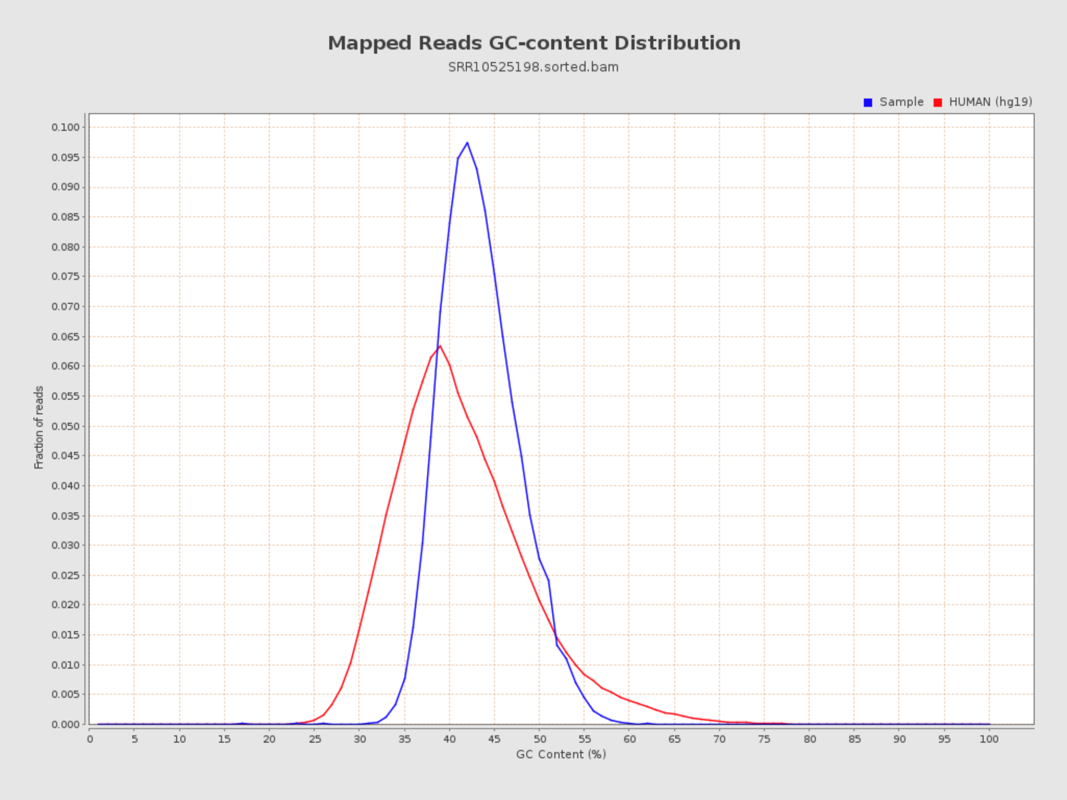
7. Results : Duplication Rate Histogram



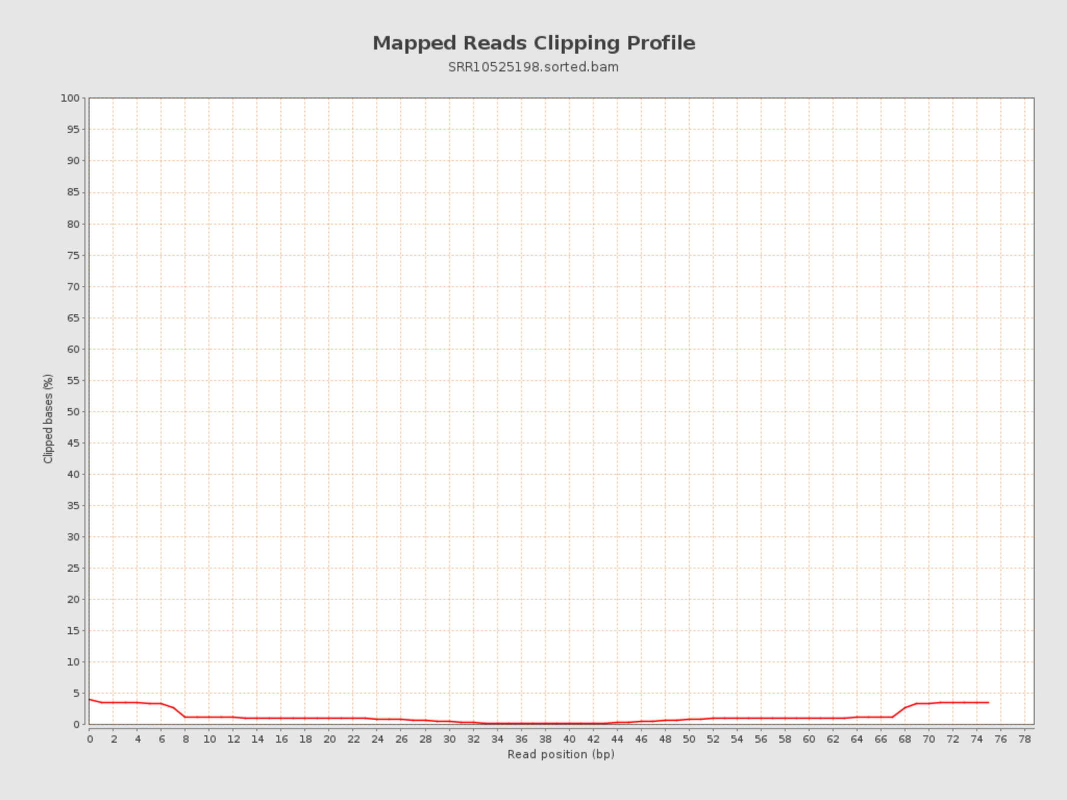
8. Results : Mapped Reads Nucleotide Content



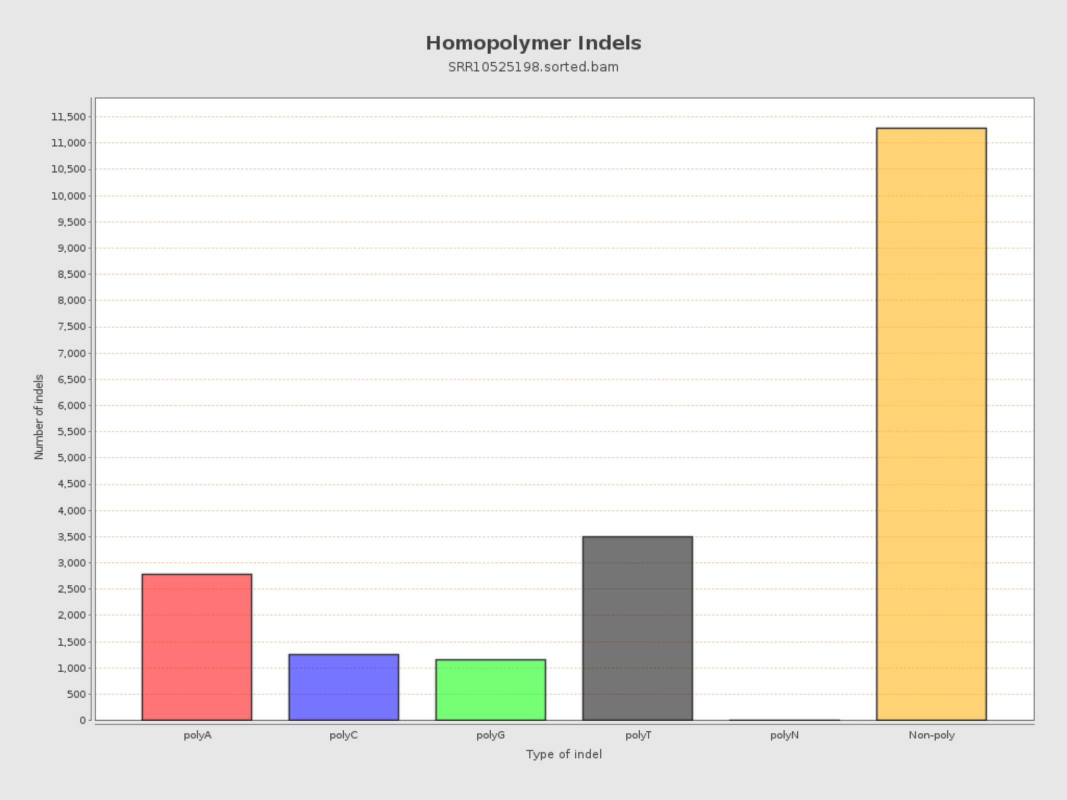
9. Results : Mapped Reads GC-content Distribution



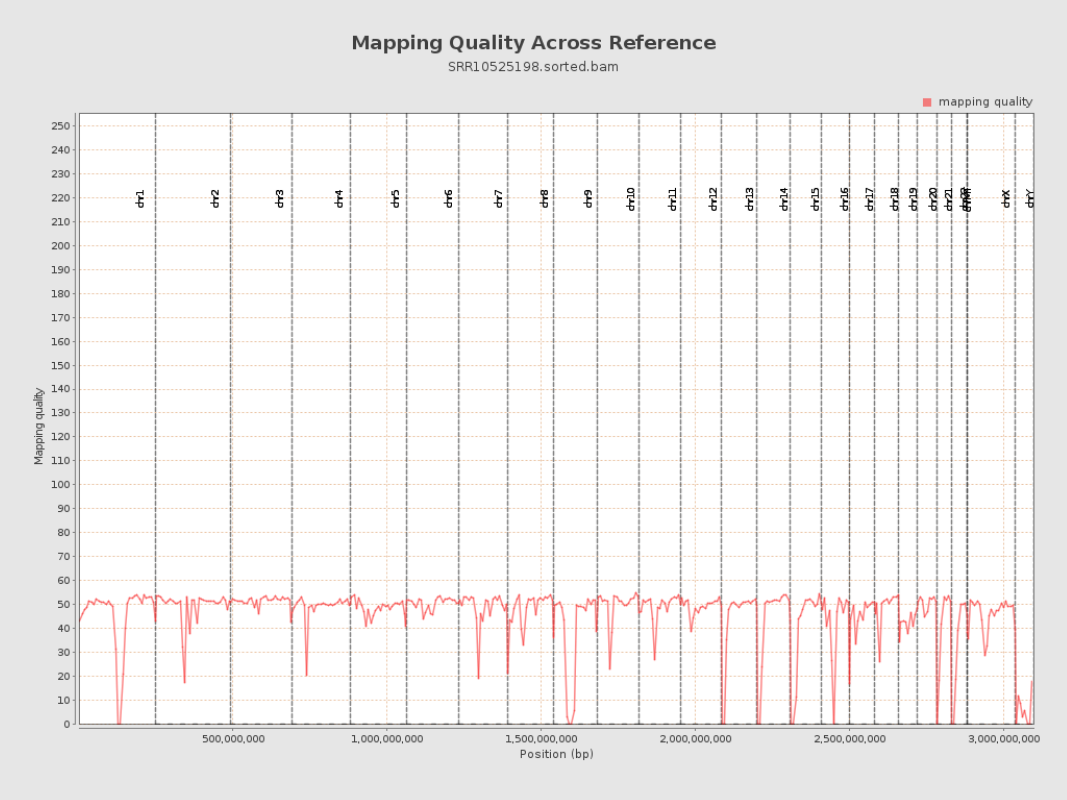
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram