Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:11:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525012.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_SRR10525012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:11:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,876,243
Mapped reads	1,726,064 / 92%
Unmapped reads	150,179 / 8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,082 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	60,978 / 3.25%
Duplication rate	2.54%
Clipped reads	1,727,617 / 92.08%

2.2. ACGT Content

Number/percentage of A's	24,509,358 / 24.48%
Number/percentage of C's	18,725,758 / 18.71%
Number/percentage of T's	32,180,025 / 32.14%
Number/percentage of G's	24,693,684 / 24.67%
Number/percentage of N's	988 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.2986

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

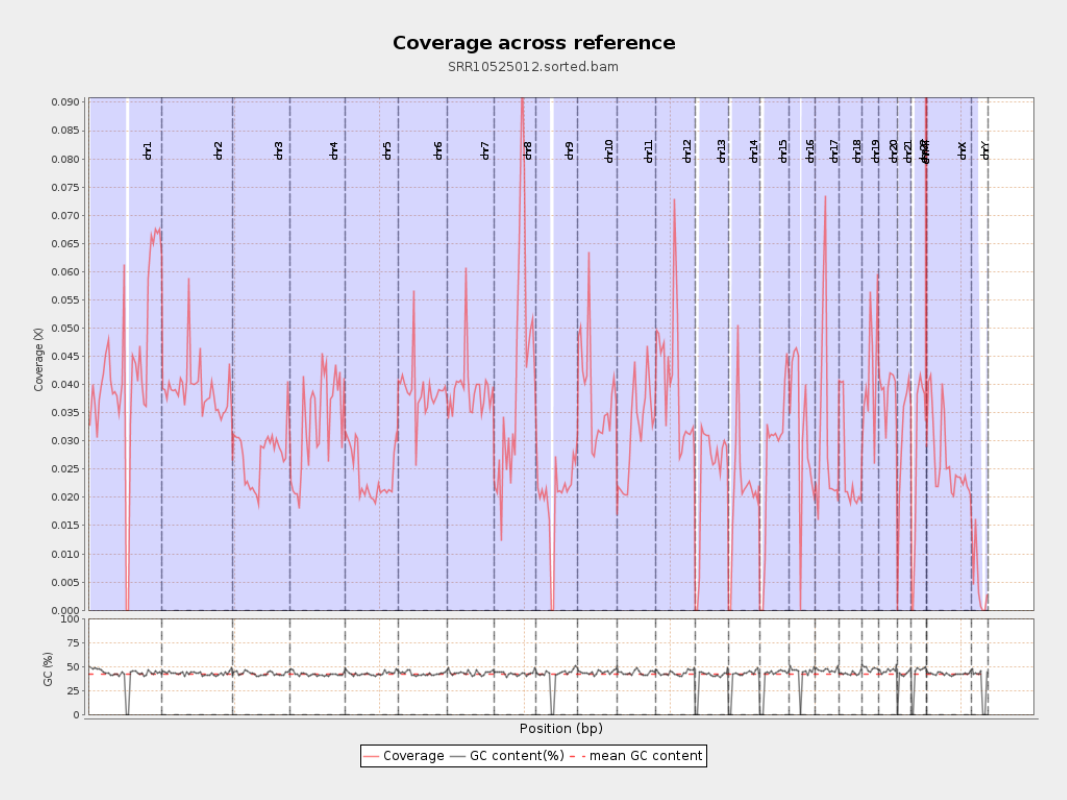
General error rate	0.51%
Mismatches	493,991
Insertions	6,507
Mapped reads with at least one insertion	0.38%
Deletions	20,149
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.28%

2.6. Chromosome stats

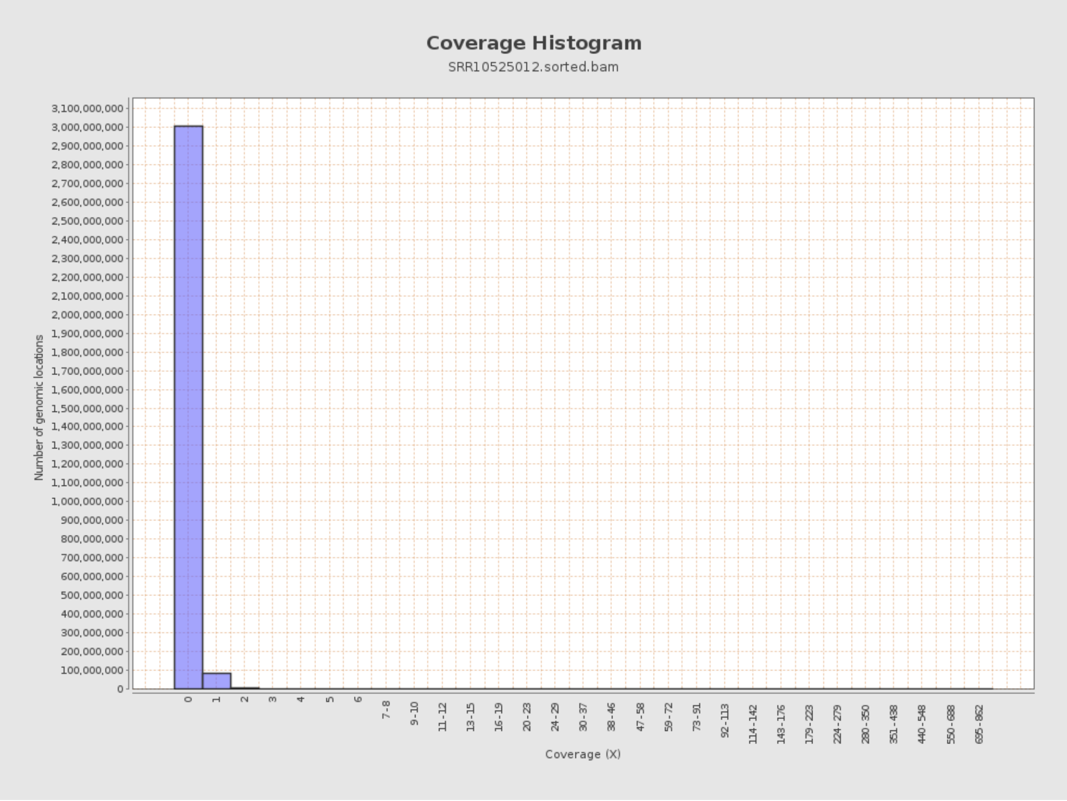
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10618311	0.0426	0.6099
chr2	243199373	9519021	0.0391	0.3272
chr3	198022430	5446293	0.0275	0.1802
chr4	191154276	6333387	0.0331	0.218
chr5	180915260	4335730	0.024	0.1721
chr6	171115067	6651464	0.0389	0.3007
chr7	159138663	6265100	0.0394	0.3837

chr8	146364022	5947539	0.0406	0.2942
chr9	141213431	2779763	0.0197	0.2119
chr10	135534747	5144693	0.038	0.2991
chr11	135006516	4196956	0.0311	0.2522
chr12	133851895	5380610	0.0402	0.2203
chr13	115169878	2769533	0.024	0.1723
chr14	107349540	2271631	0.0212	0.1621
chr15	102531392	2791588	0.0272	0.1878
chr16	90354753	2860442	0.0317	0.2026
chr17	81195210	2585815	0.0318	0.2598
chr18	78077248	1963028	0.0251	0.3691
chr19	59128983	2493100	0.0422	0.3455
chr20	63025520	2449912	0.0389	0.2167
chr21	48129895	1455412	0.0302	0.201
chr22	51304566	1383967	0.027	0.1764
chrMT	16571	30298	1.8284	1.7417
chrX	155270560	4193309	0.027	0.2078
chrY	59373566	275882	0.0046	0.1285

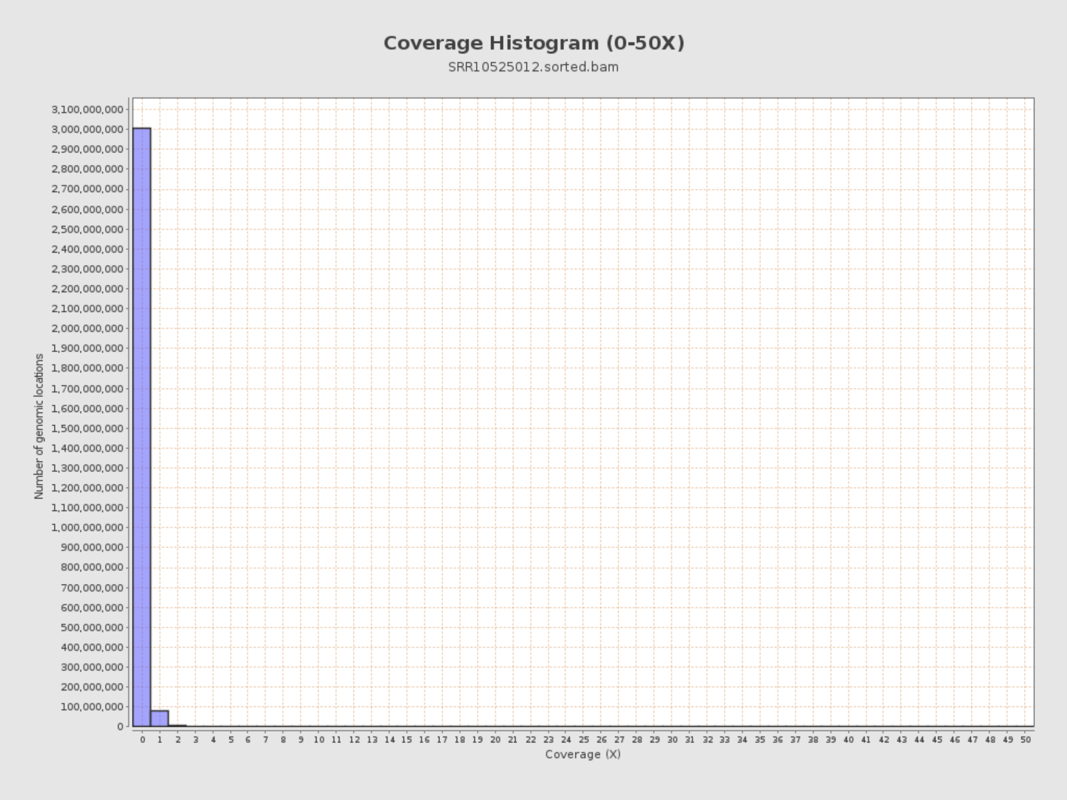
3. Results : Coverage across reference



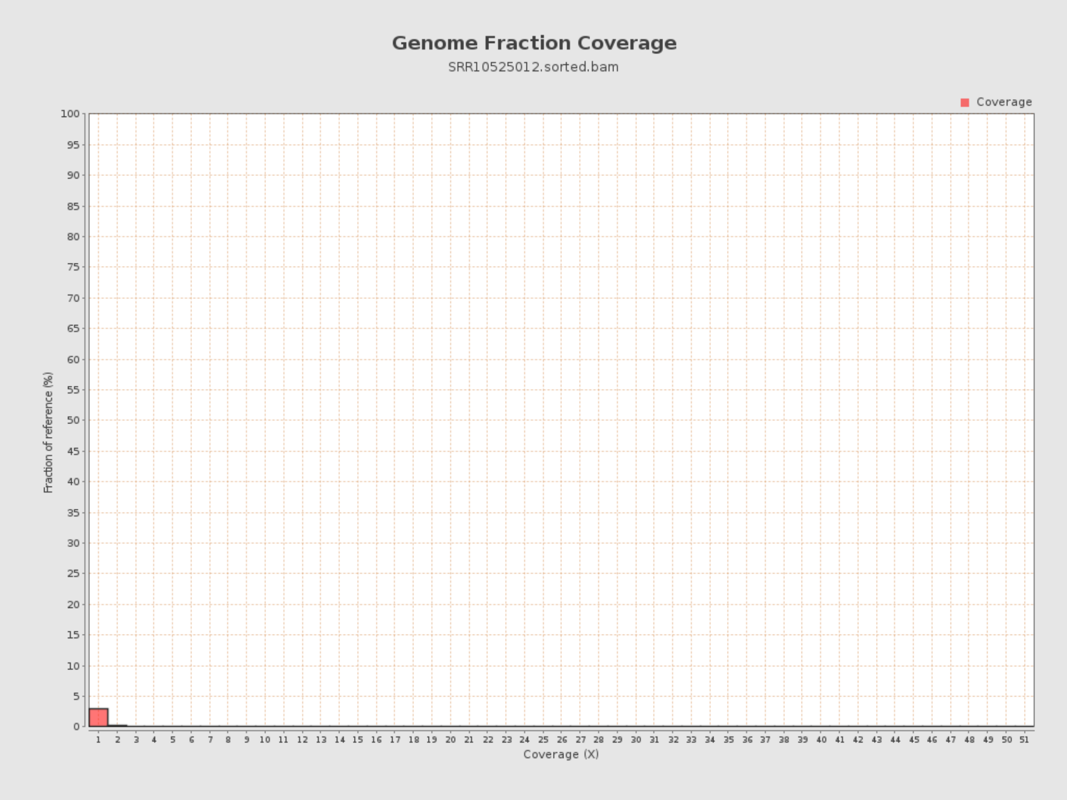
4. Results : Coverage Histogram



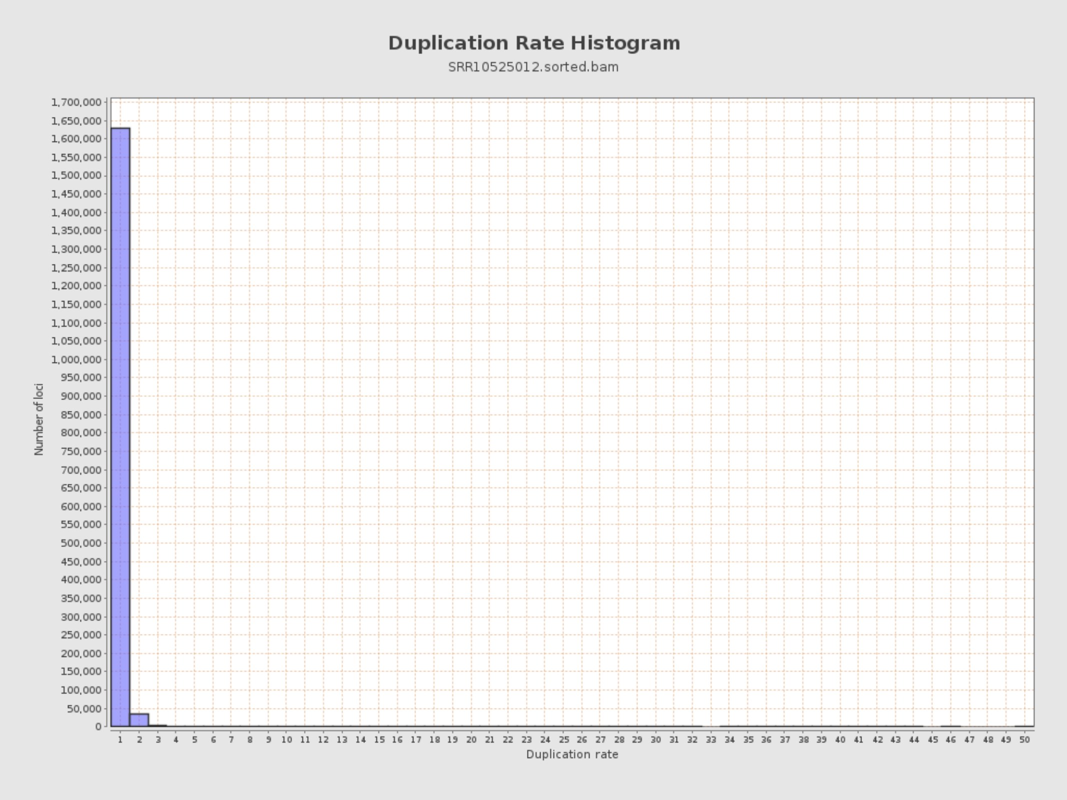
5. Results : Coverage Histogram (0-50X)



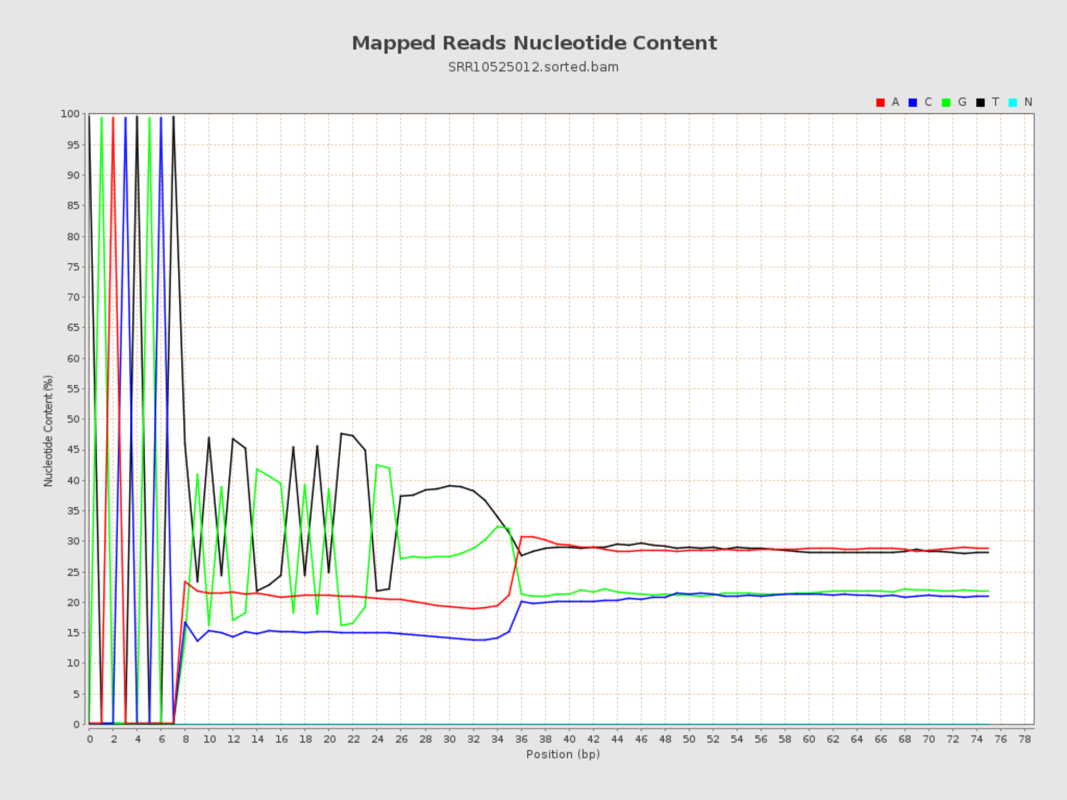
6. Results : Genome Fraction Coverage



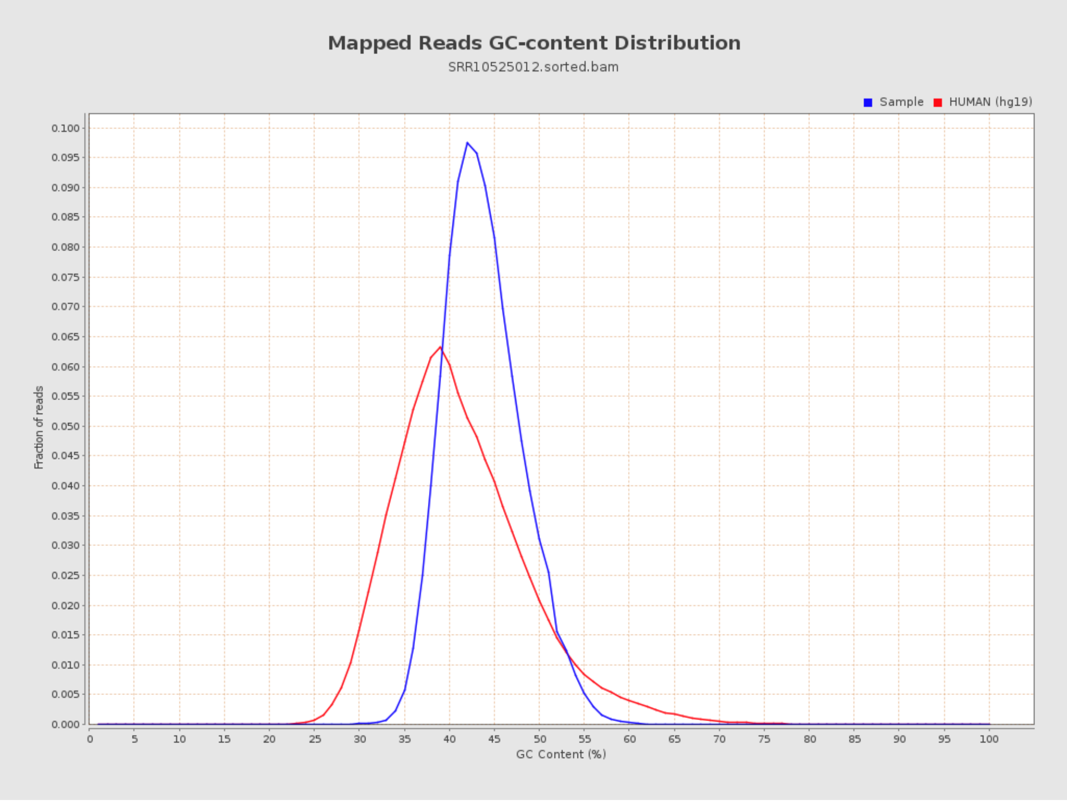
7. Results : Duplication Rate Histogram



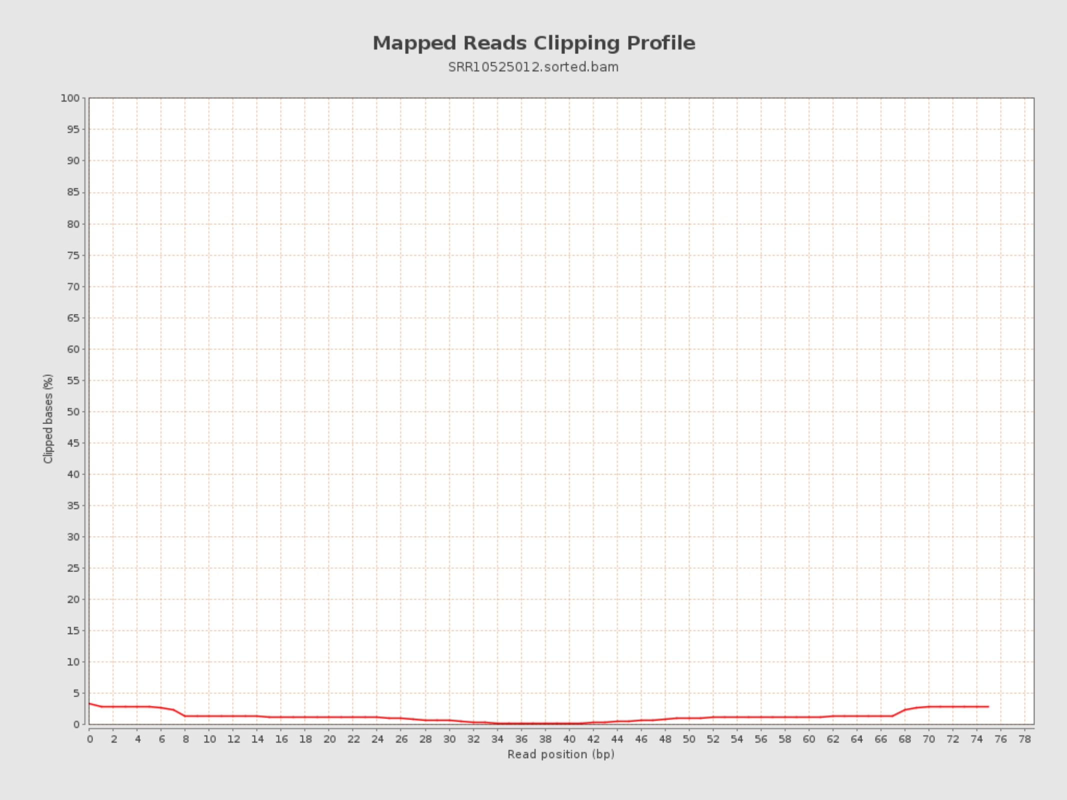
8. Results : Mapped Reads Nucleotide Content



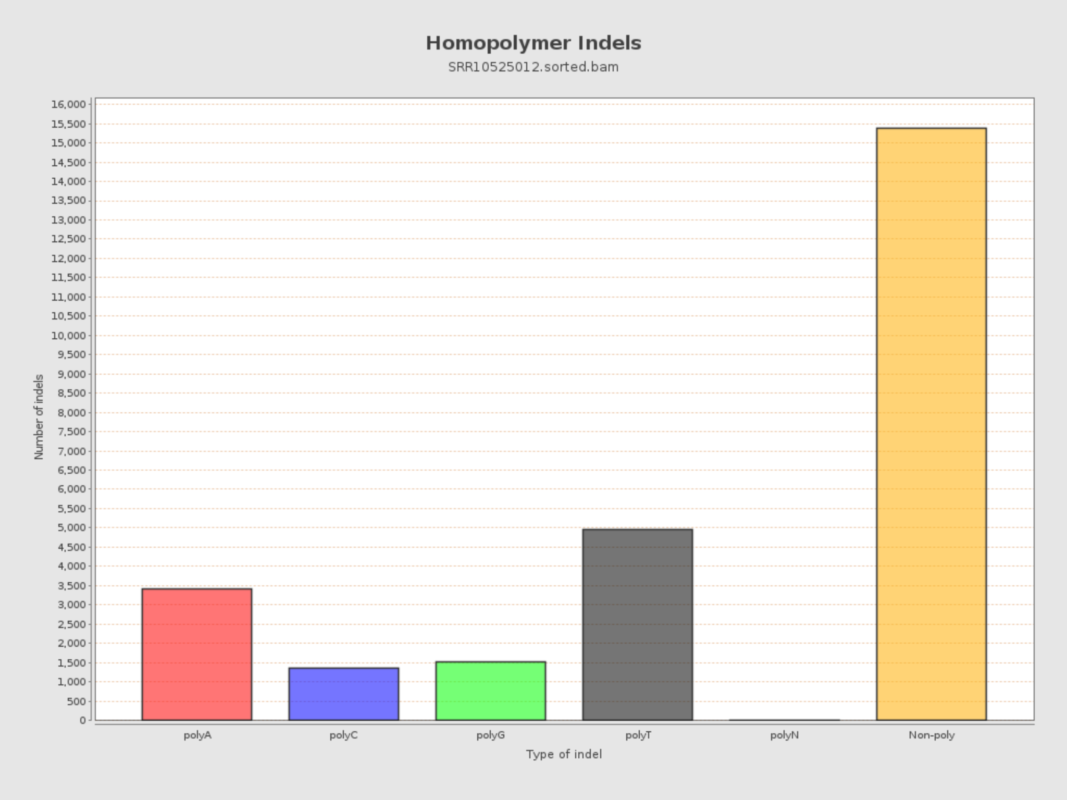
9. Results : Mapped Reads GC-content Distribution



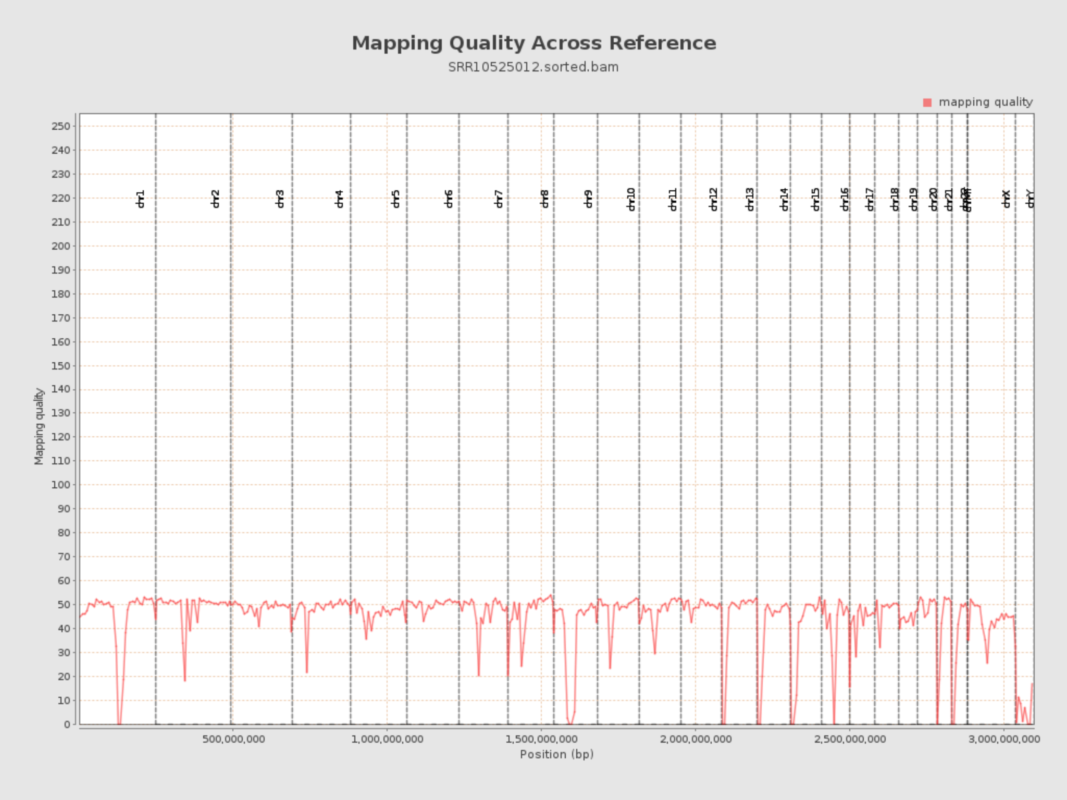
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram