Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:54:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525122.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_SRR10525122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:54:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	953,474
Mapped reads	860,434 / 90.24%
Unmapped reads	93,040 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,388 / 2.56%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	19,970 / 2.09%
Duplication rate	1.39%
Clipped reads	883,525 / 92.66%

2.2. ACGT Content

Number/percentage of A's	17,389,603 / 26.39%
Number/percentage of C's	13,113,481 / 19.9%
Number/percentage of T's	20,025,104 / 30.39%
Number/percentage of G's	15,359,747 / 23.31%
Number/percentage of N's	2,448 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2349

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

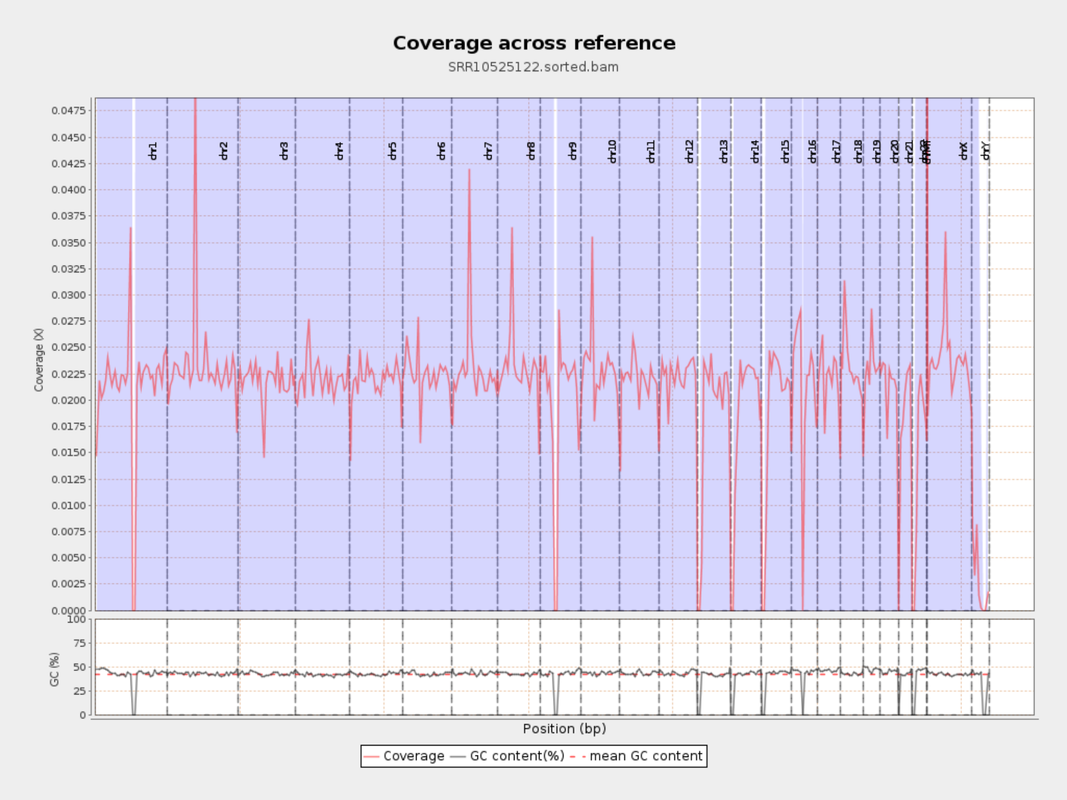
General error rate	0.77%
Mismatches	496,637
Insertions	5,739
Mapped reads with at least one insertion	0.66%
Deletions	15,191
Mapped reads with at least one deletion	1.74%
Homopolymer indels	42.67%

2.6. Chromosome stats

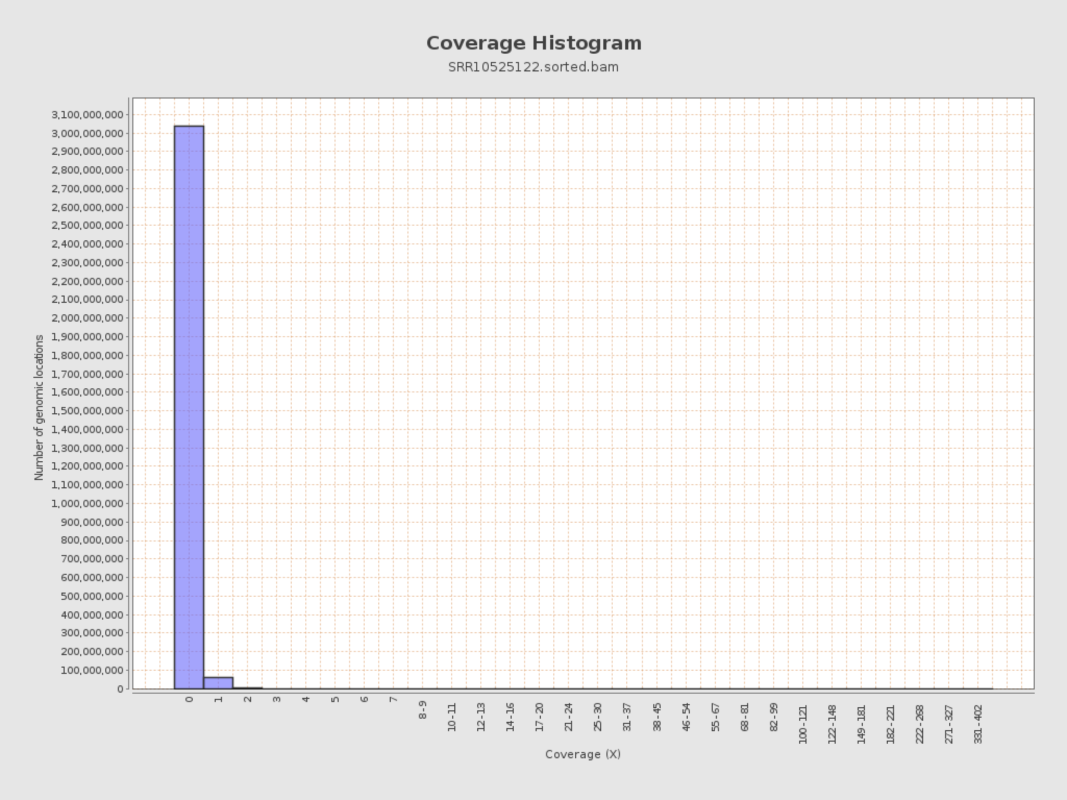
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5260399	0.0211	0.3365
chr2	243199373	5703385	0.0235	0.3432
chr3	198022430	4325661	0.0218	0.1557
chr4	191154276	4230389	0.0221	0.1617
chr5	180915260	3993547	0.0221	0.1591
chr6	171115067	3838078	0.0224	0.1743
chr7	159138663	3670369	0.0231	0.3397

chr8	146364022	3385360	0.0231	0.2993
chr9	141213431	2785994	0.0197	0.2276
chr10	135534747	3125658	0.0231	0.2268
chr11	135006516	2987445	0.0221	0.2229
chr12	133851895	2975691	0.0222	0.1583
chr13	115169878	2079985	0.0181	0.1408
chr14	107349540	1977466	0.0184	0.1603
chr15	102531392	1901507	0.0185	0.144
chr16	90354753	1896111	0.021	0.1634
chr17	81195210	1787340	0.022	0.1767
chr18	78077248	1822520	0.0233	0.3832
chr19	59128983	1371500	0.0232	0.2946
chr20	63025520	1336637	0.0212	0.1558
chr21	48129895	856182	0.0178	0.1479
chr22	51304566	719512	0.014	0.1245
chrMT	16571	2180	0.1316	0.3701
chrX	155270560	3727639	0.024	0.1993
chrY	59373566	155860	0.0026	0.0729

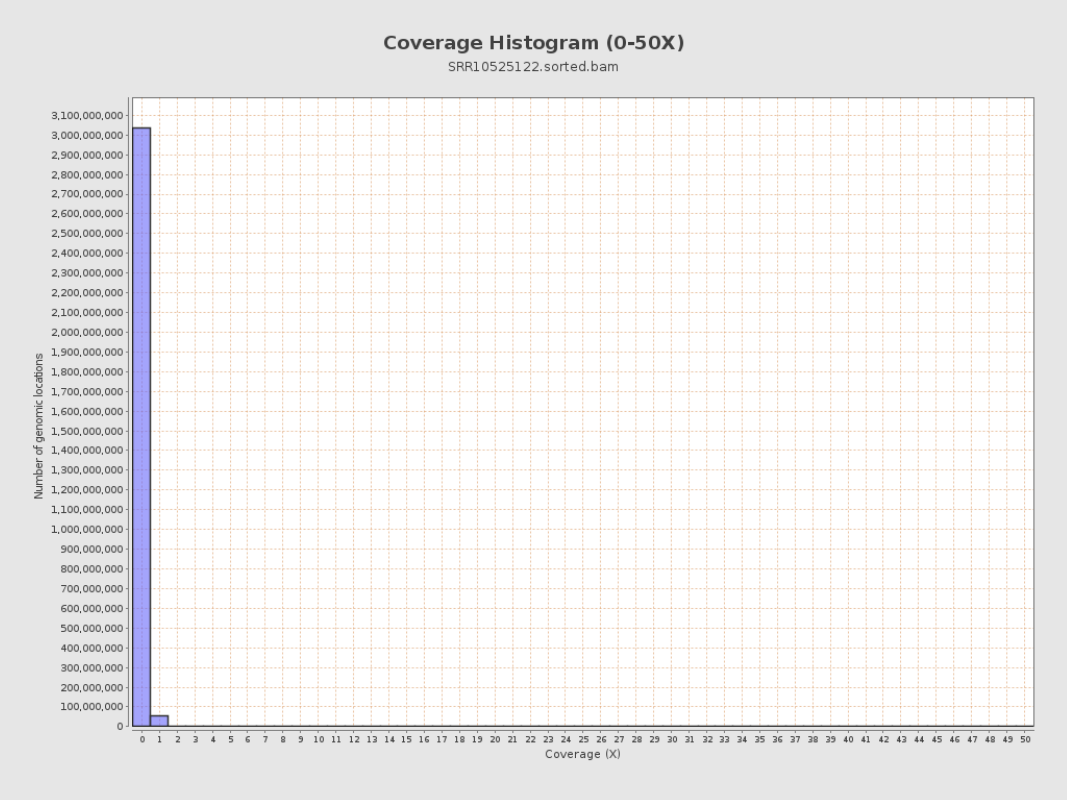
3. Results : Coverage across reference



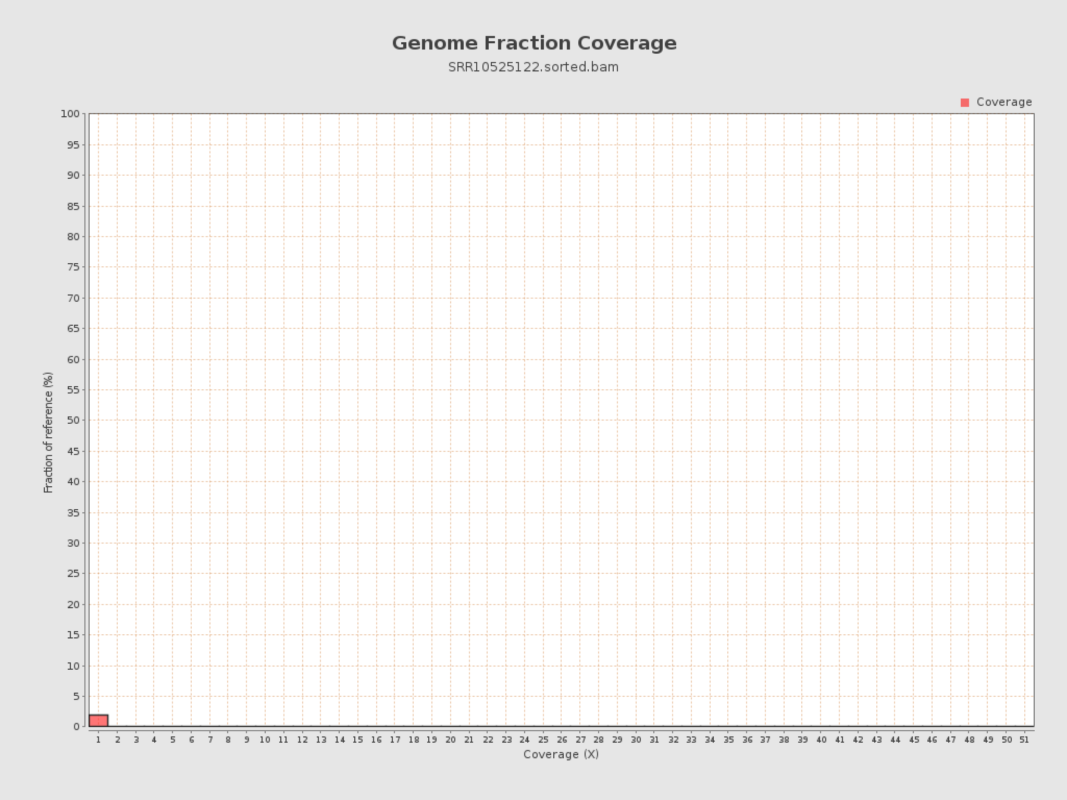
4. Results : Coverage Histogram



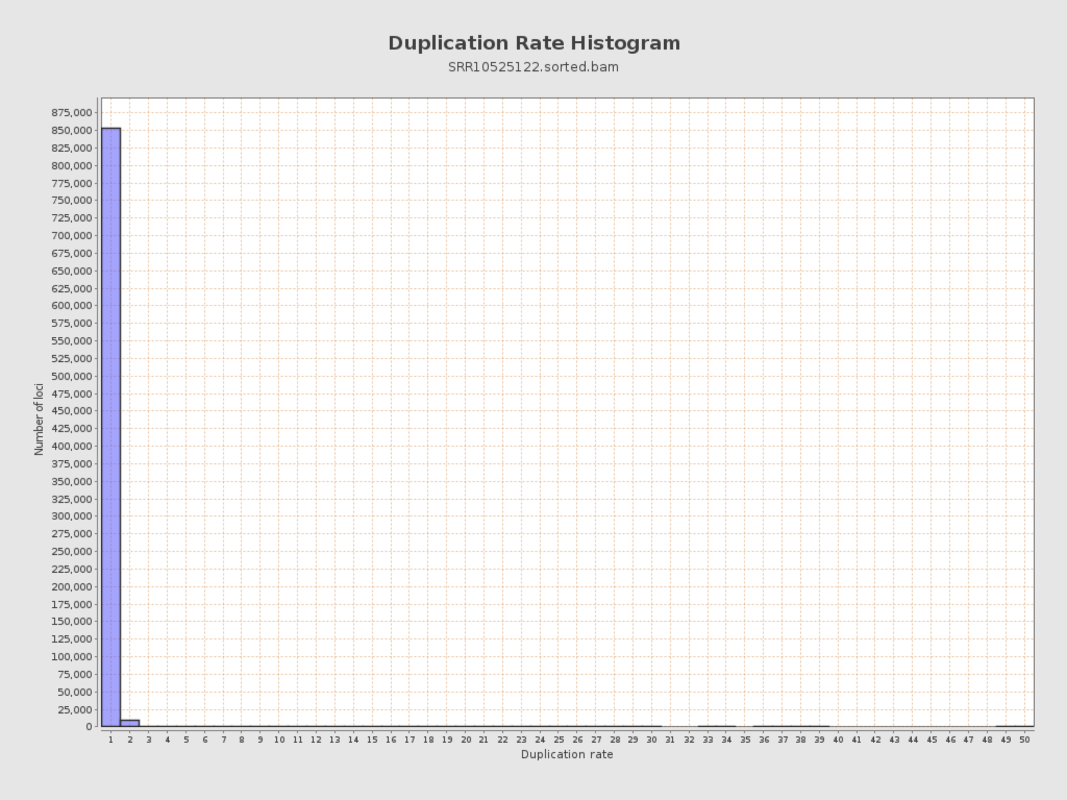
5. Results : Coverage Histogram (0-50X)



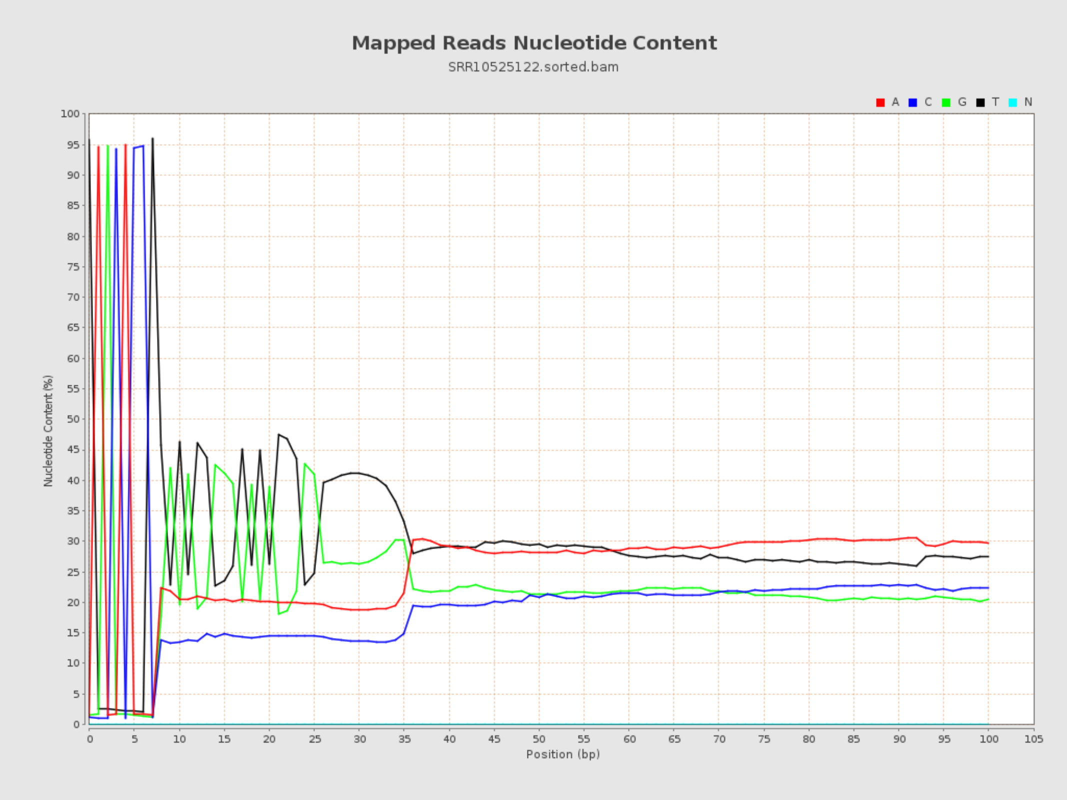
6. Results : Genome Fraction Coverage



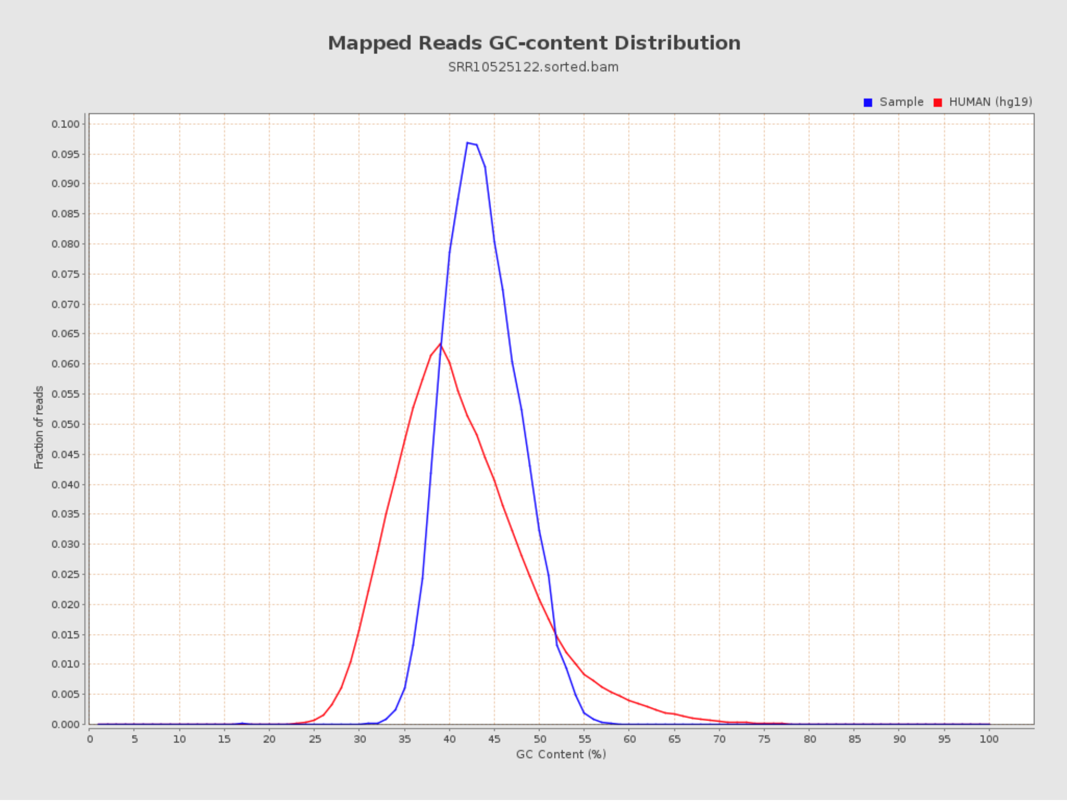
7. Results : Duplication Rate Histogram



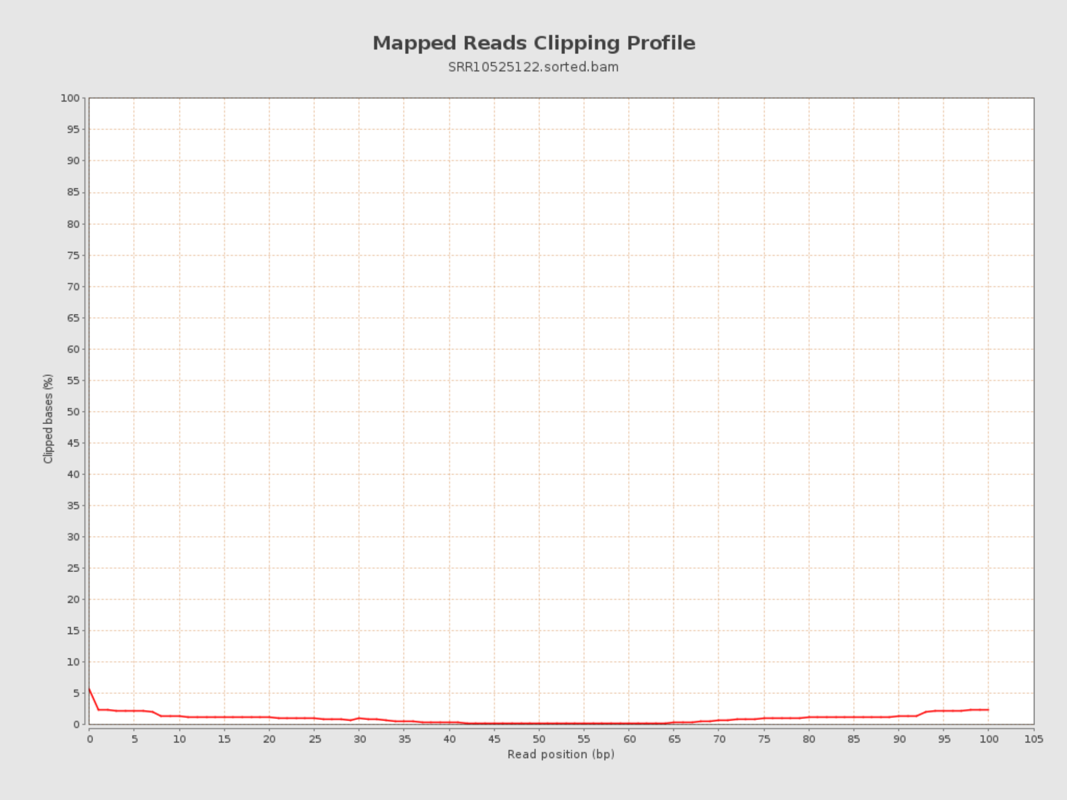
8. Results : Mapped Reads Nucleotide Content



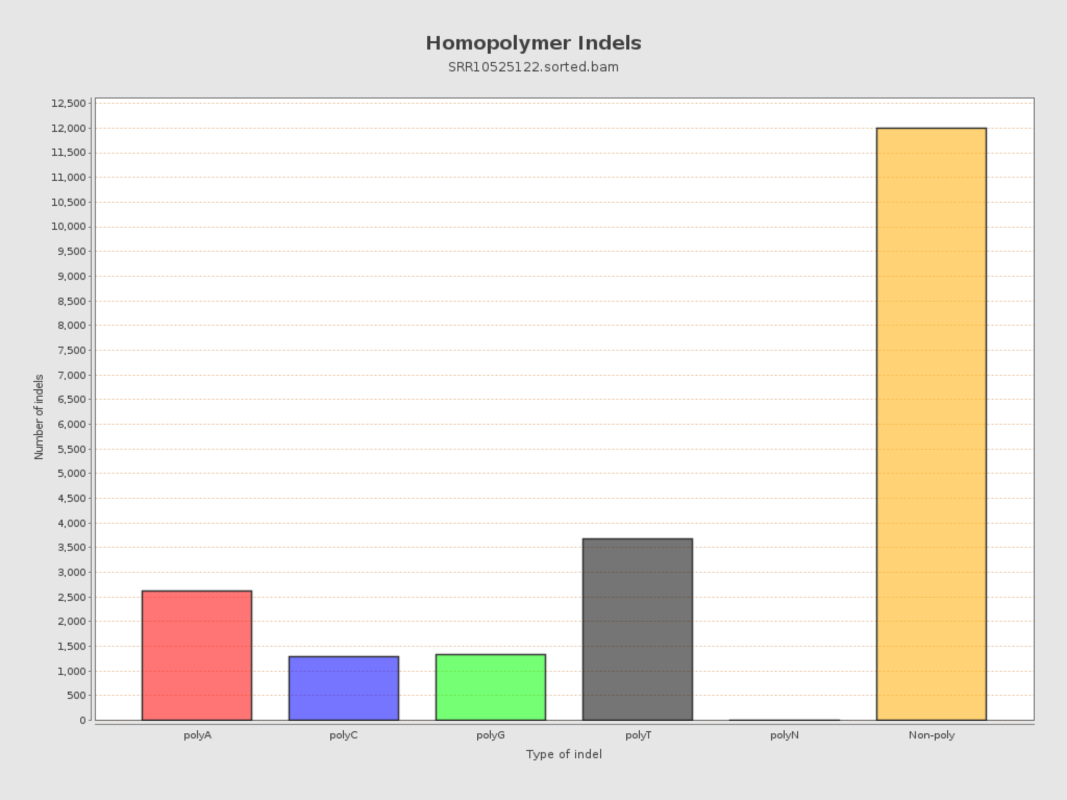
9. Results : Mapped Reads GC-content Distribution



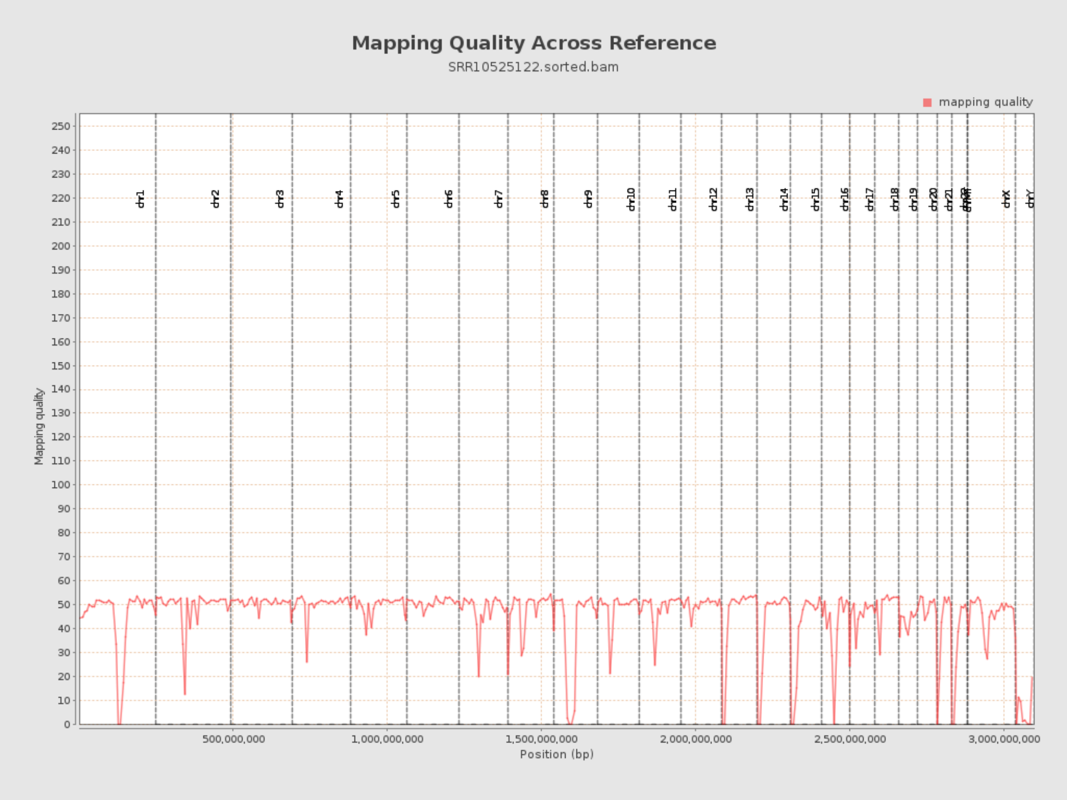
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram