Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:30:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525112.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_SRR10525112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:30:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	818,233
Mapped reads	737,464 / 90.13%
Unmapped reads	80,769 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,987 / 2.69%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	15,932 / 1.95%
Duplication rate	1.3%
Clipped reads	757,826 / 92.62%

2.2. ACGT Content

Number/percentage of A's	14,794,852 / 26.19%
Number/percentage of C's	11,429,852 / 20.23%
Number/percentage of T's	16,947,792 / 30%
Number/percentage of G's	13,320,830 / 23.58%
Number/percentage of N's	2,187 / 0%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.2052

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

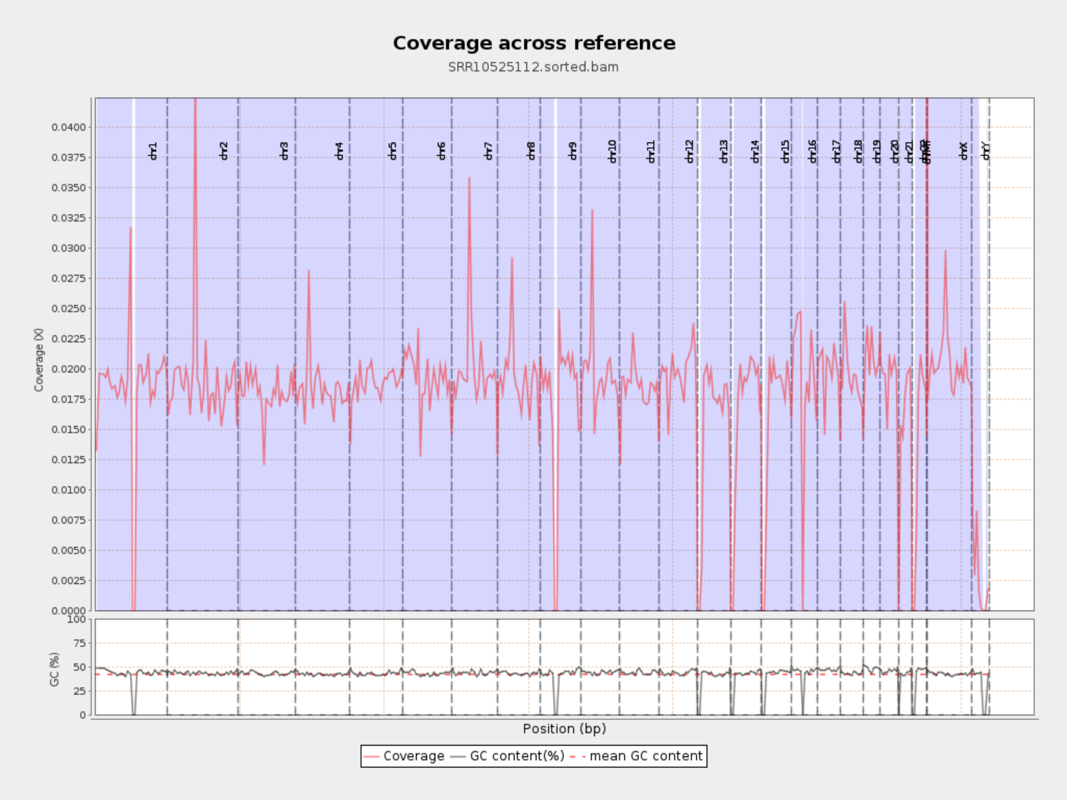
General error rate	0.76%
Mismatches	418,911
Insertions	5,718
Mapped reads with at least one insertion	0.76%
Deletions	13,116
Mapped reads with at least one deletion	1.75%
Homopolymer indels	41.94%

2.6. Chromosome stats

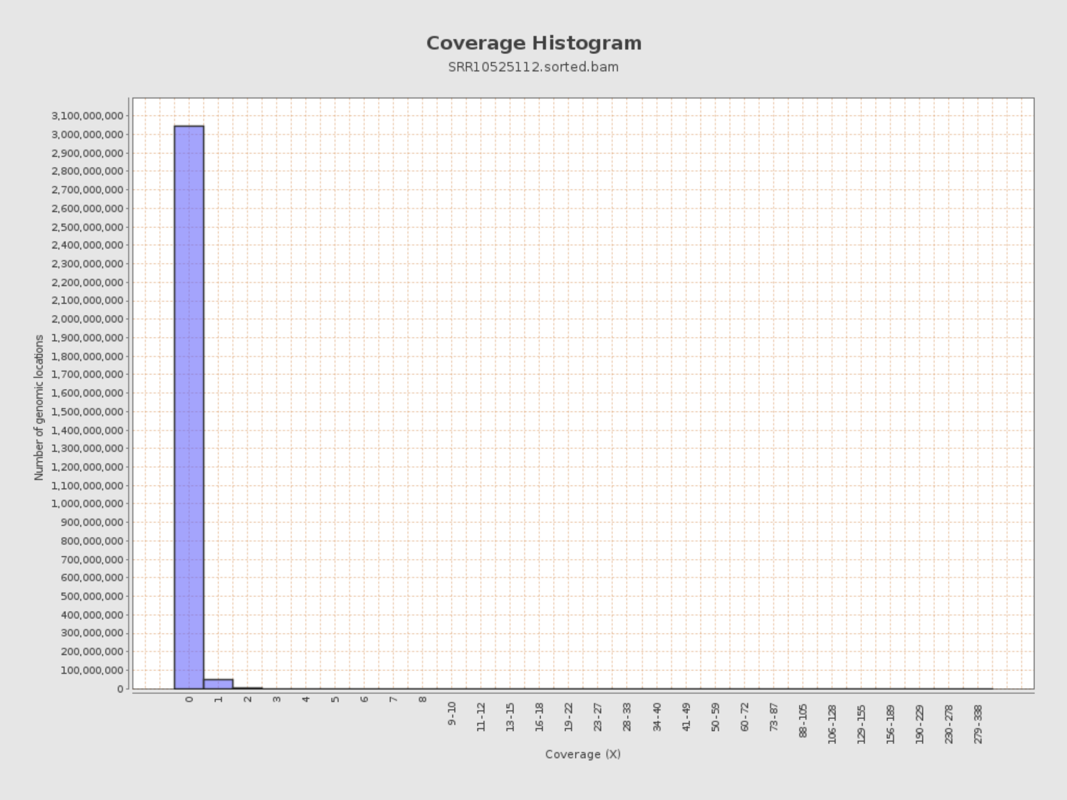
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4535387	0.0182	0.2992
chr2	243199373	4688468	0.0193	0.2865
chr3	198022430	3583198	0.0181	0.141
chr4	191154276	3532572	0.0185	0.1502
chr5	180915260	3436781	0.019	0.1454
chr6	171115067	3288348	0.0192	0.1593
chr7	159138663	3206640	0.0201	0.2957

chr8	146364022	2822322	0.0193	0.2583
chr9	141213431	2463795	0.0174	0.1978
chr10	135534747	2672743	0.0197	0.2086
chr11	135006516	2525708	0.0187	0.1973
chr12	133851895	2636693	0.0197	0.1474
chr13	115169878	1745625	0.0152	0.1284
chr14	107349540	1729272	0.0161	0.1394
chr15	102531392	1614111	0.0157	0.1313
chr16	90354753	1693763	0.0187	0.152
chr17	81195210	1607583	0.0198	0.1649
chr18	78077248	1519197	0.0195	0.2894
chr19	59128983	1238806	0.021	0.2501
chr20	63025520	1202657	0.0191	0.1482
chr21	48129895	750338	0.0156	0.1388
chr22	51304566	673668	0.0131	0.1196
chrMT	16571	2689	0.1623	0.4333
chrX	155270560	3190541	0.0205	0.1742
chrY	59373566	157610	0.0027	0.0773

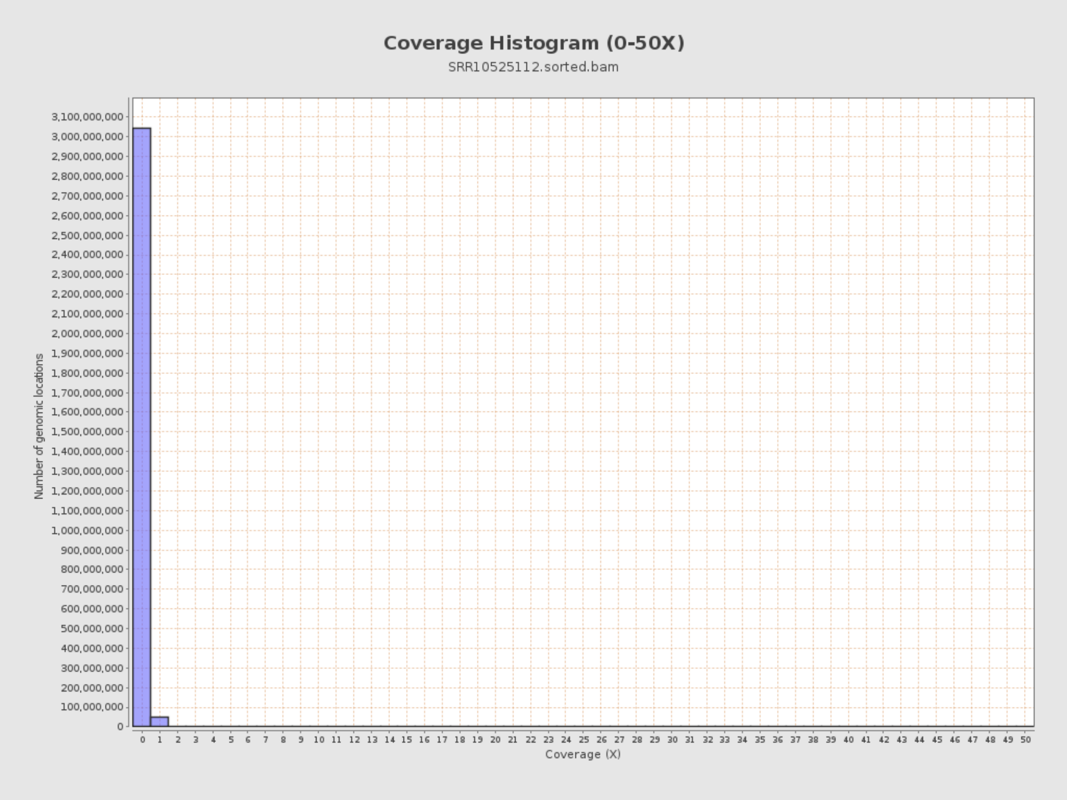
3. Results : Coverage across reference



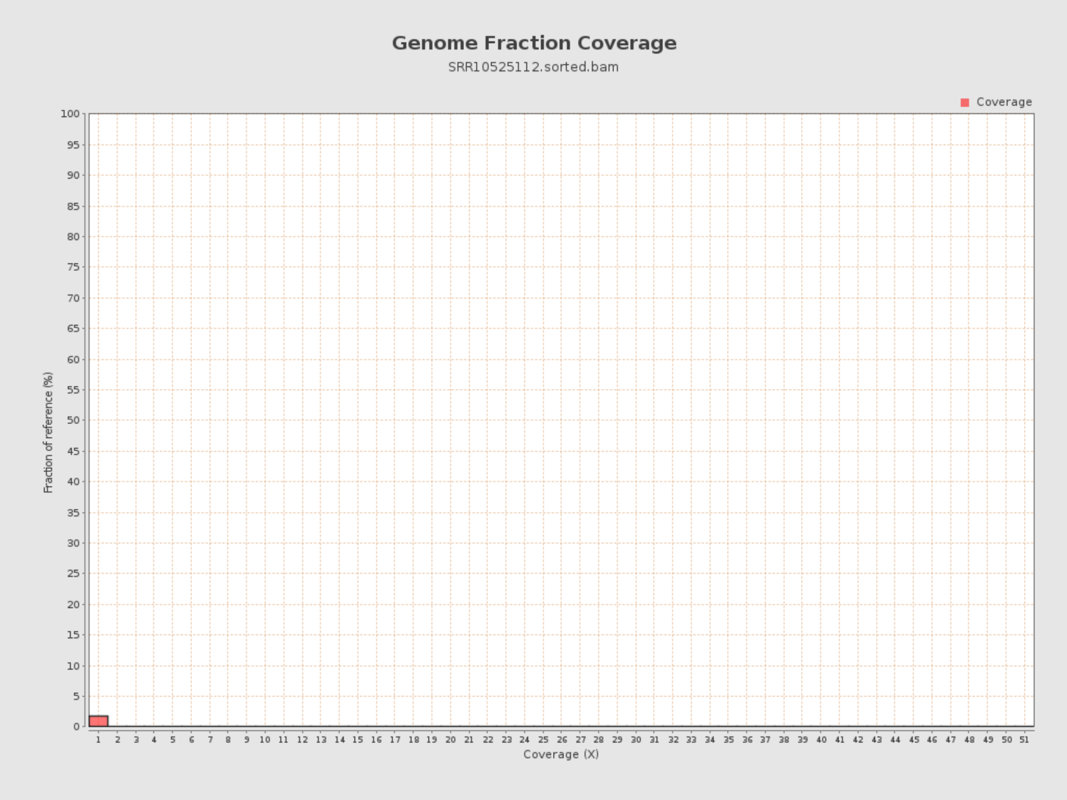
4. Results : Coverage Histogram



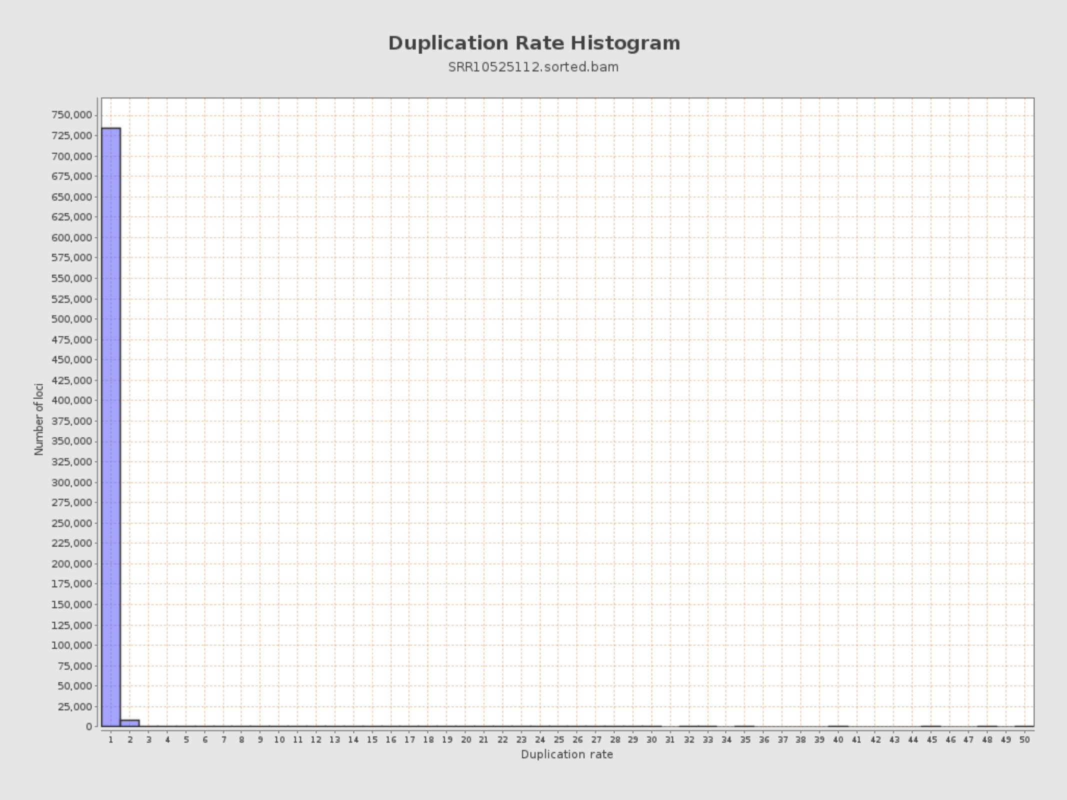
5. Results : Coverage Histogram (0-50X)



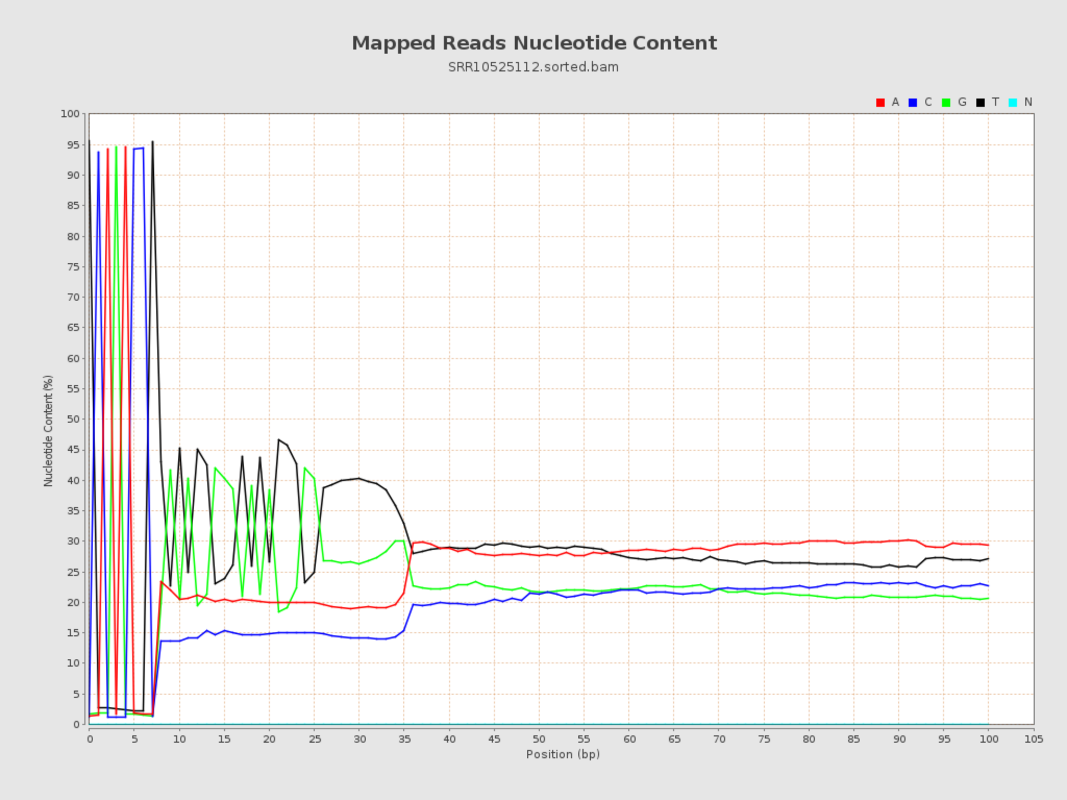
6. Results : Genome Fraction Coverage



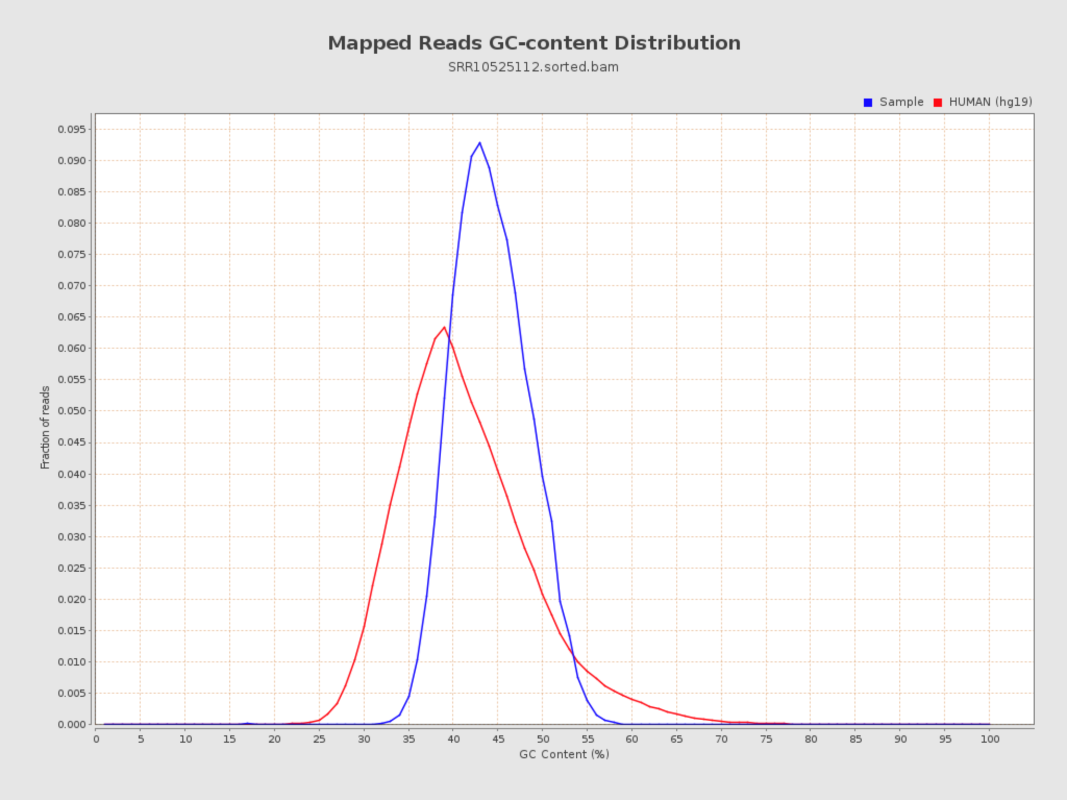
7. Results : Duplication Rate Histogram



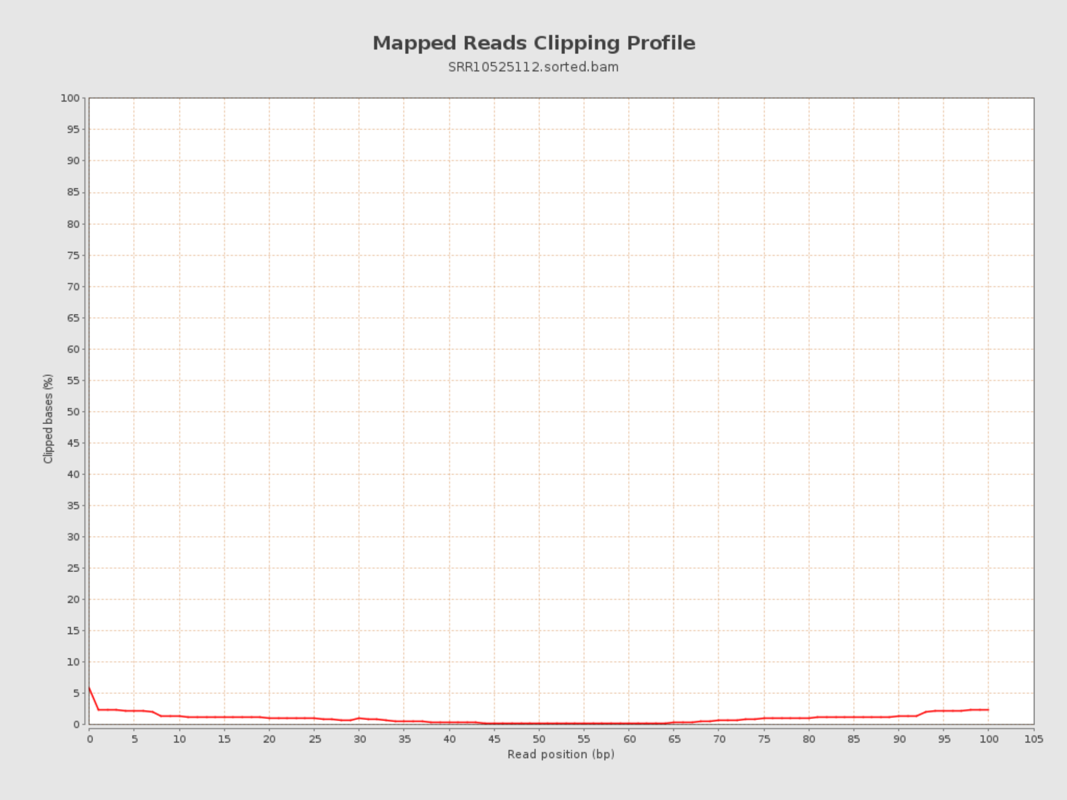
8. Results : Mapped Reads Nucleotide Content



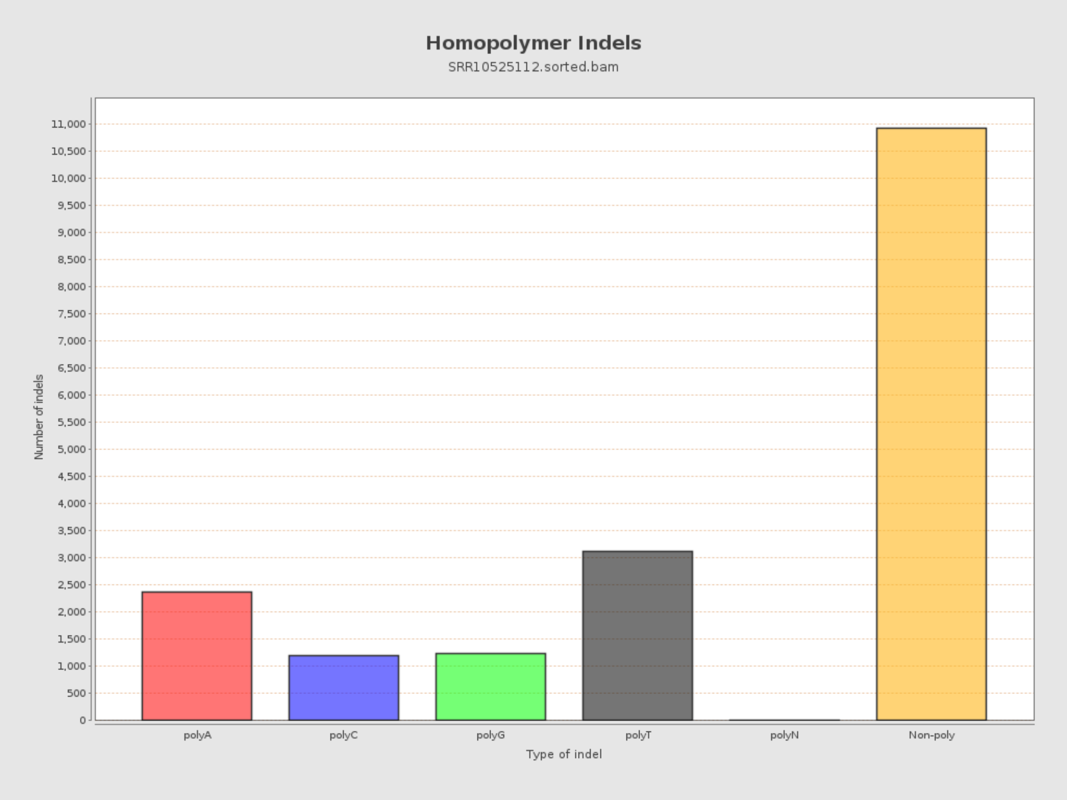
9. Results : Mapped Reads GC-content Distribution



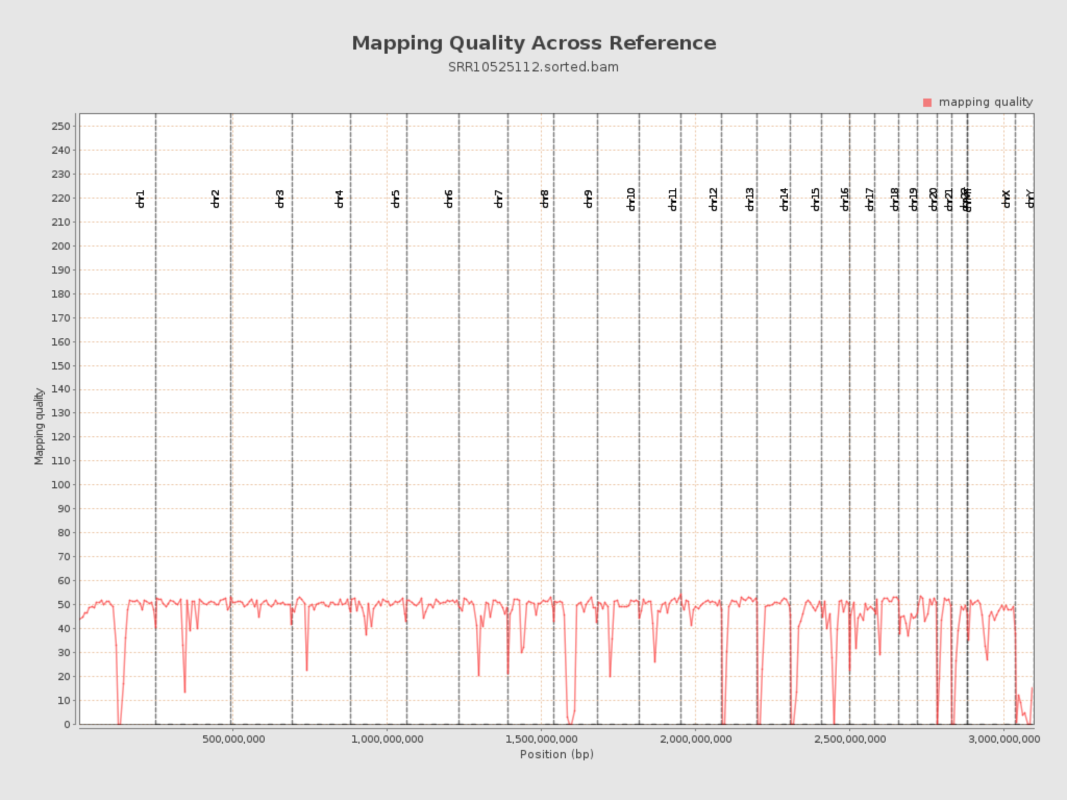
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram