Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:34:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525114.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_SRR10525114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:34:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	699,899
Mapped reads	622,969 / 89.01%
Unmapped reads	76,930 / 10.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,958 / 2.28%
Read min/max/mean length	30 / 101 / 101.83
Duplicated reads (estimated)	13,854 / 1.98%
Duplication rate	1.38%
Clipped reads	638,079 / 91.17%

2.2. ACGT Content

Number/percentage of A's	12,598,488 / 26.74%
Number/percentage of C's	8,921,627 / 18.93%
Number/percentage of T's	14,803,001 / 31.42%
Number/percentage of G's	10,794,399 / 22.91%
Number/percentage of N's	1,765 / 0%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1869

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

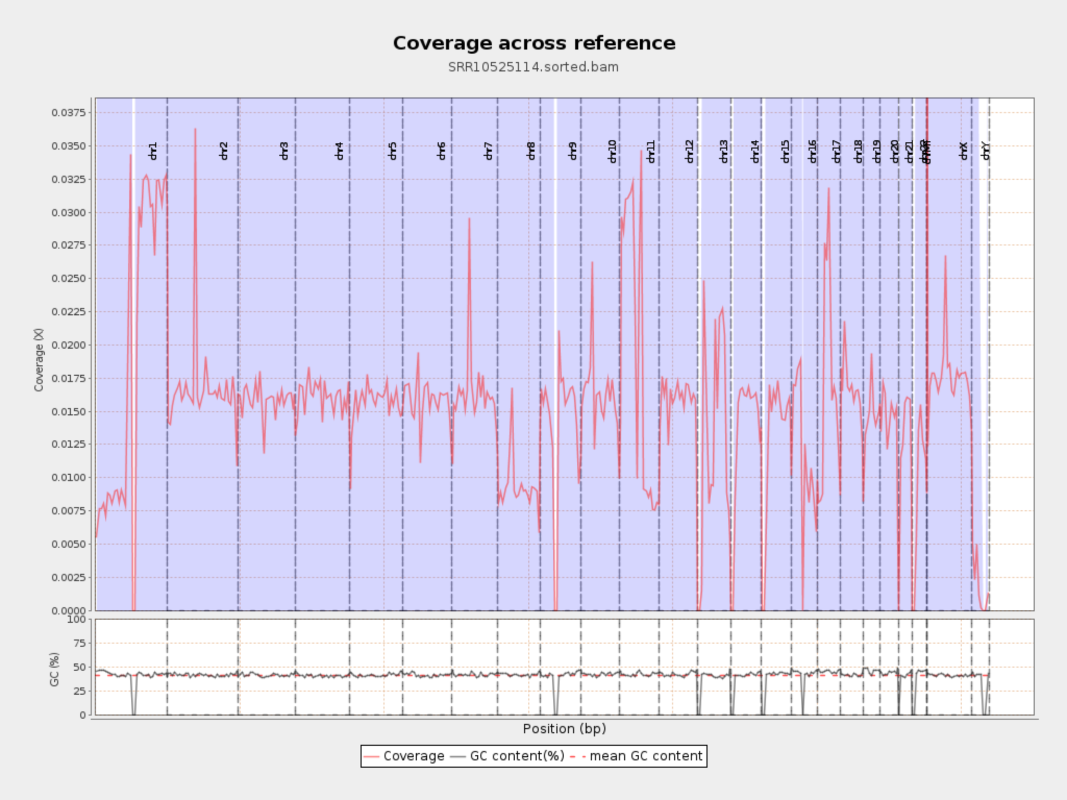
General error rate	0.78%
Mismatches	361,035
Insertions	4,184
Mapped reads with at least one insertion	0.67%
Deletions	10,642
Mapped reads with at least one deletion	1.69%
Homopolymer indels	42.88%

2.6. Chromosome stats

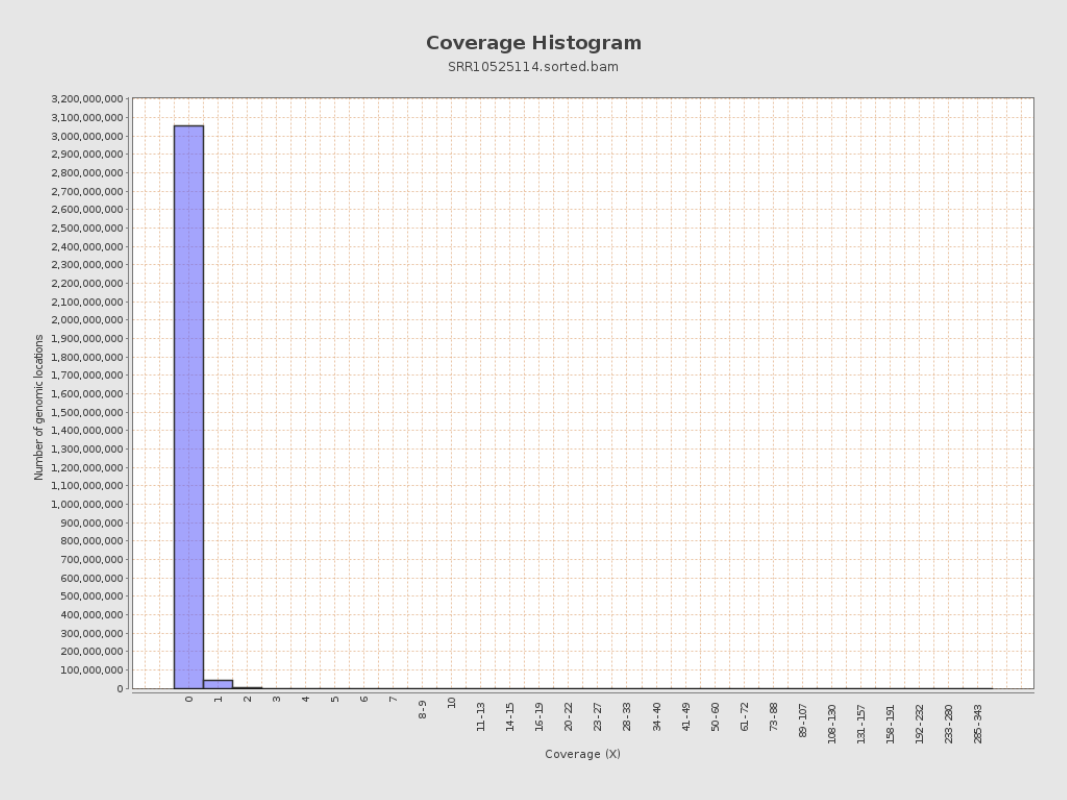
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4636472	0.0186	0.2943
chr2	243199373	4077836	0.0168	0.2399
chr3	198022430	3139750	0.0159	0.1313
chr4	191154276	3076359	0.0161	0.1355
chr5	180915260	2858830	0.0158	0.1324
chr6	171115067	2714492	0.0159	0.1415
chr7	159138663	2632656	0.0165	0.2592

chr8	146364022	1373742	0.0094	0.2159
chr9	141213431	1980484	0.014	0.1776
chr10	135534747	2213660	0.0163	0.1878
chr11	135006516	2648300	0.0196	0.2198
chr12	133851895	2137823	0.016	0.1329
chr13	115169878	1458601	0.0127	0.1176
chr14	107349540	1429955	0.0133	0.1315
chr15	102531392	1313174	0.0128	0.1185
chr16	90354753	1038933	0.0115	0.1179
chr17	81195210	1366457	0.0168	0.1509
chr18	78077248	1314300	0.0168	0.2773
chr19	59128983	873016	0.0148	0.2112
chr20	63025520	908860	0.0144	0.1263
chr21	48129895	608900	0.0127	0.1225
chr22	51304566	473359	0.0092	0.1002
chrMT	16571	2694	0.1626	0.444
chrX	155270560	2755024	0.0177	0.1673
chrY	59373566	103596	0.0017	0.0524

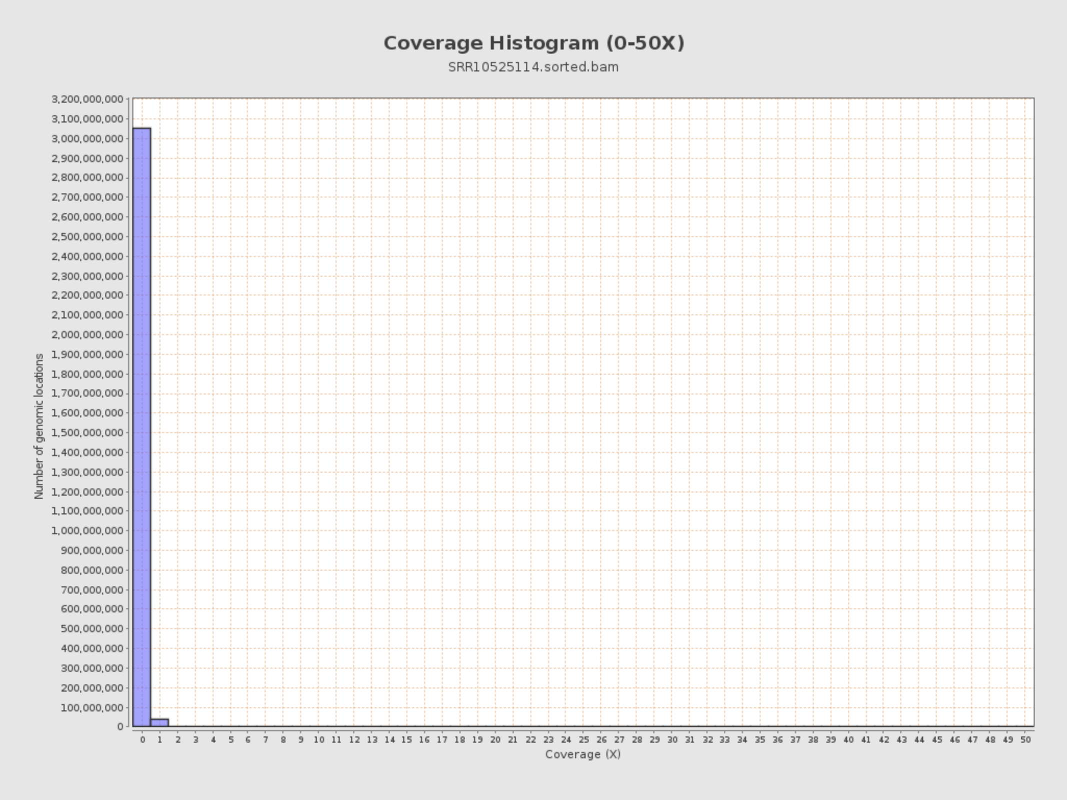
3. Results : Coverage across reference



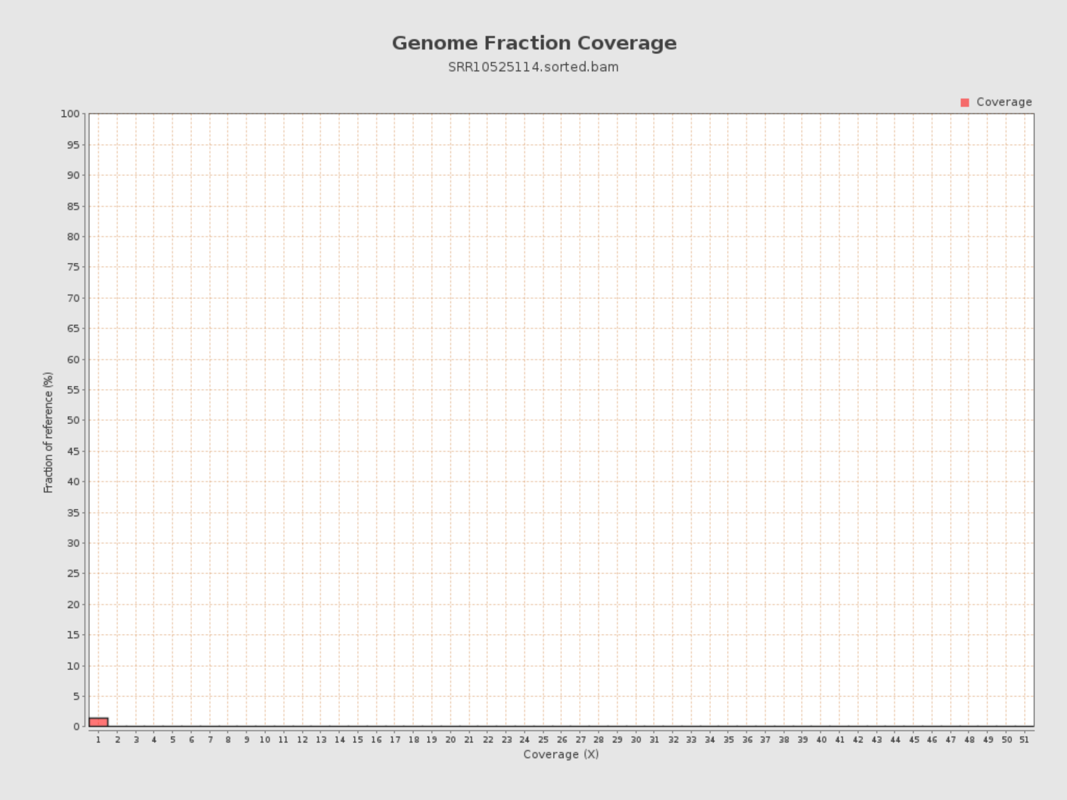
4. Results : Coverage Histogram



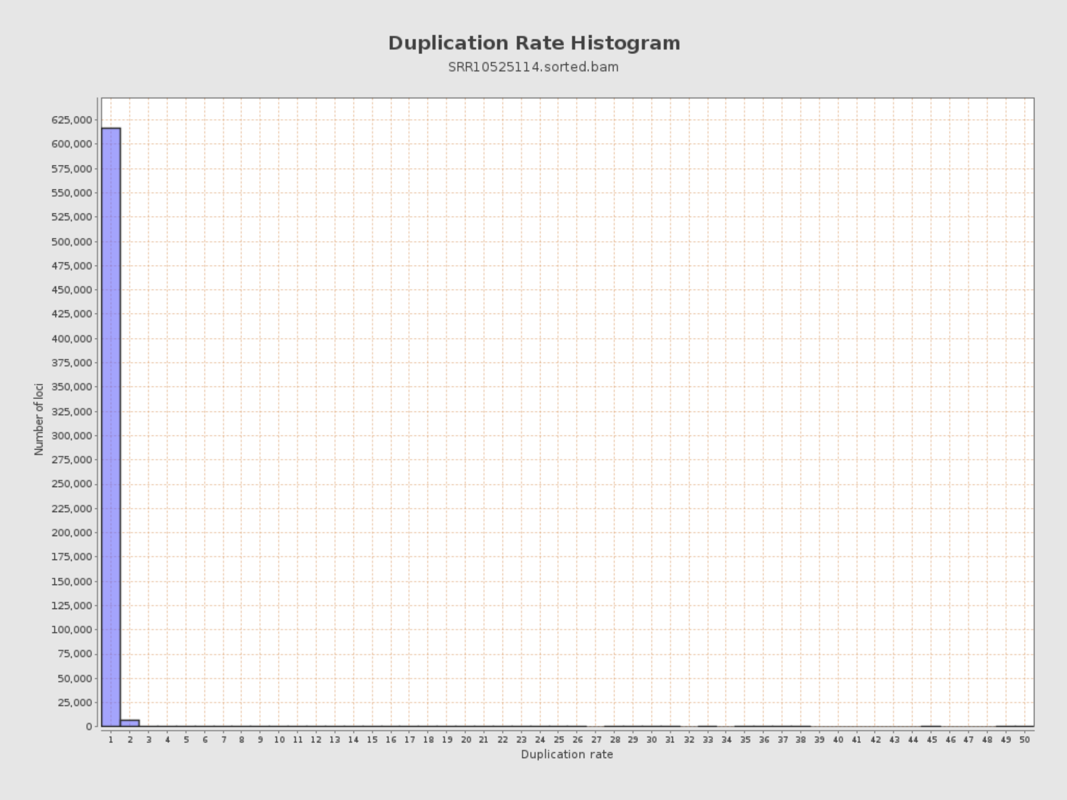
5. Results : Coverage Histogram (0-50X)



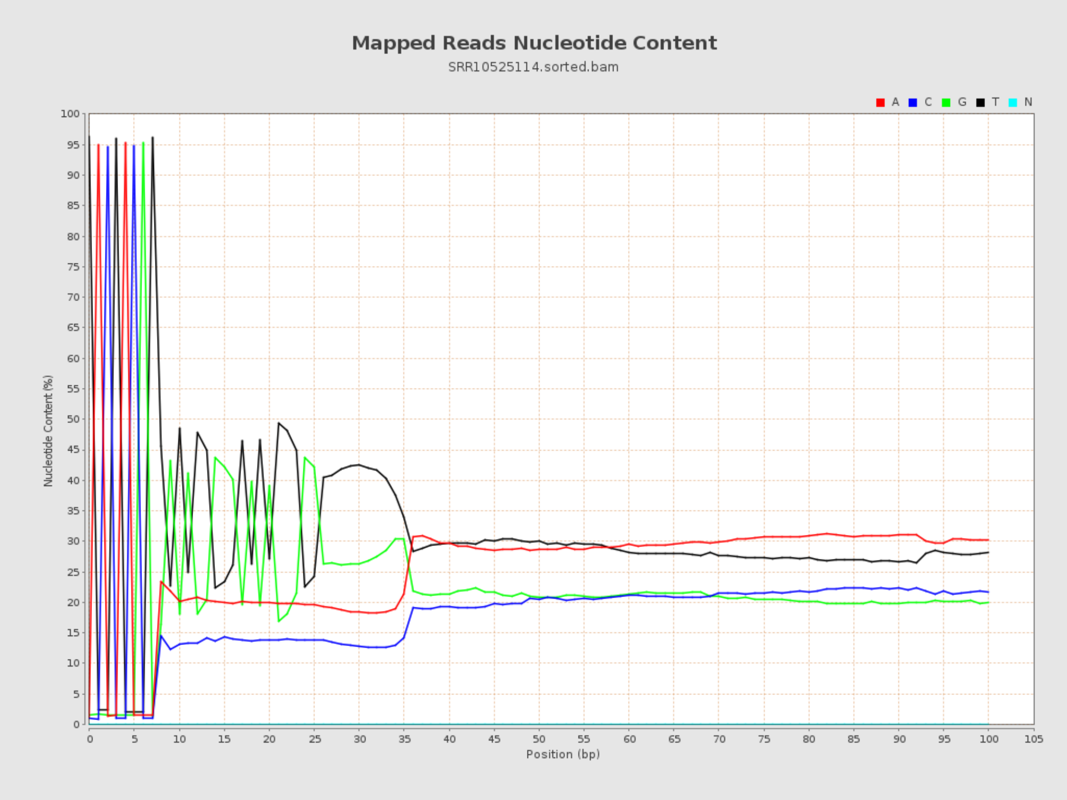
6. Results : Genome Fraction Coverage



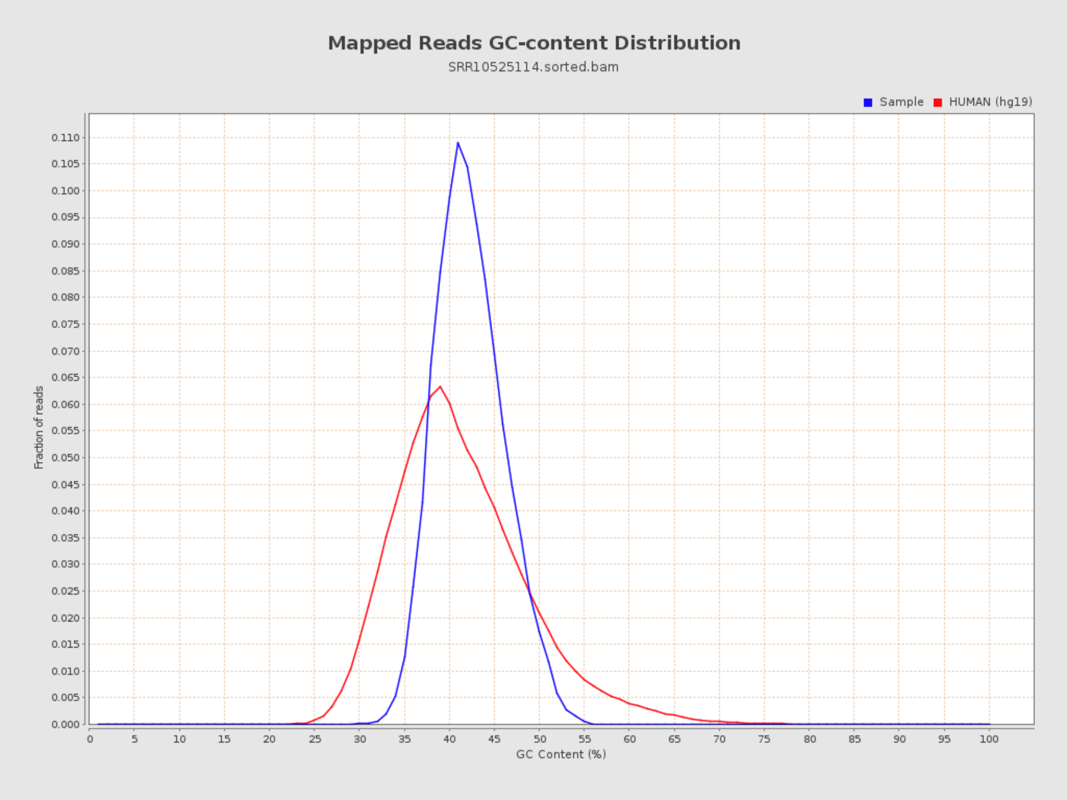
7. Results : Duplication Rate Histogram



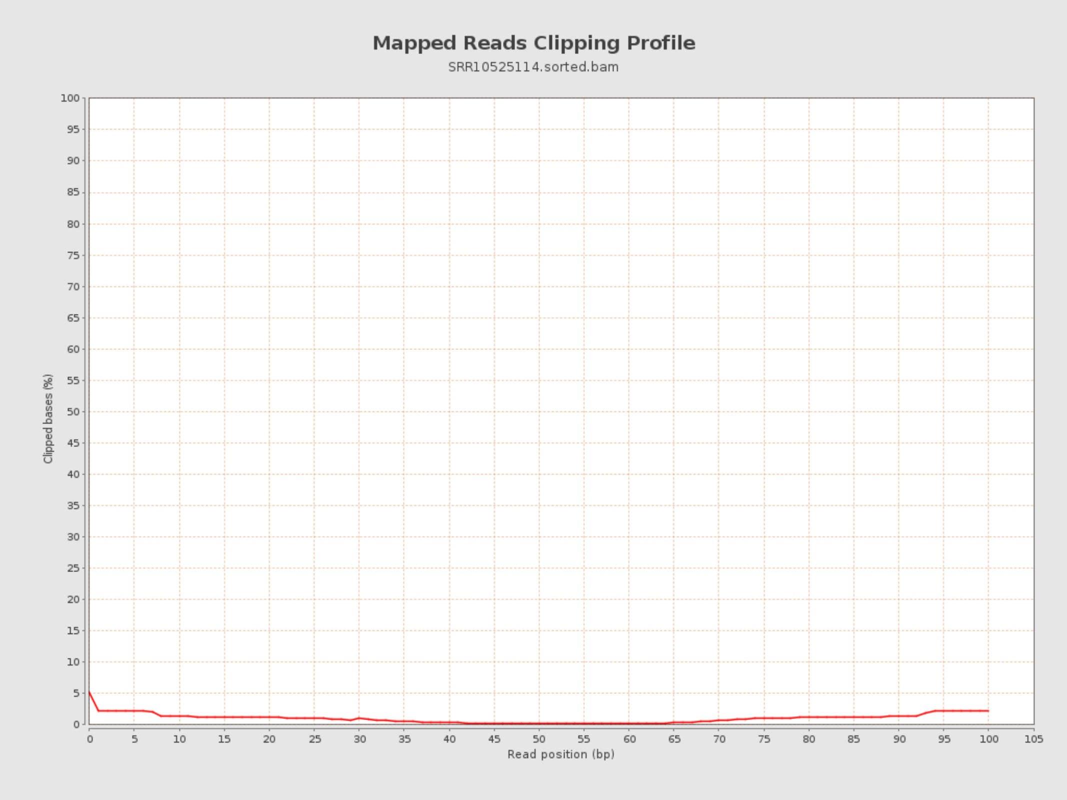
8. Results : Mapped Reads Nucleotide Content



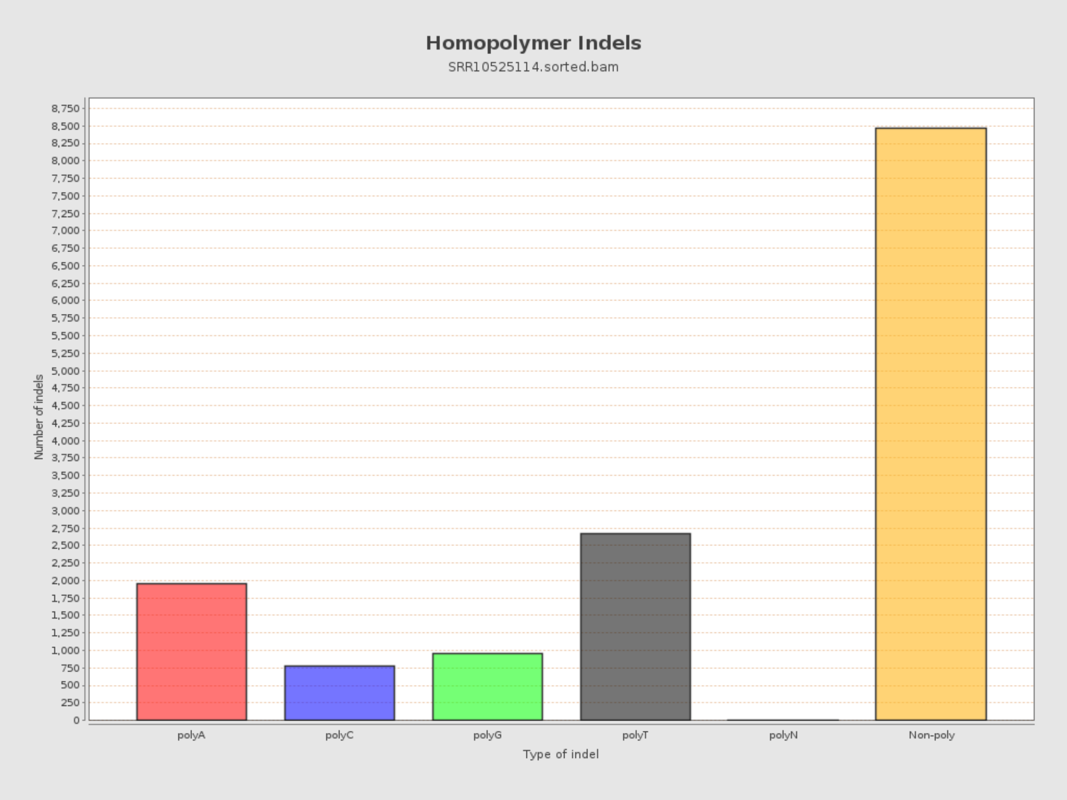
9. Results : Mapped Reads GC-content Distribution



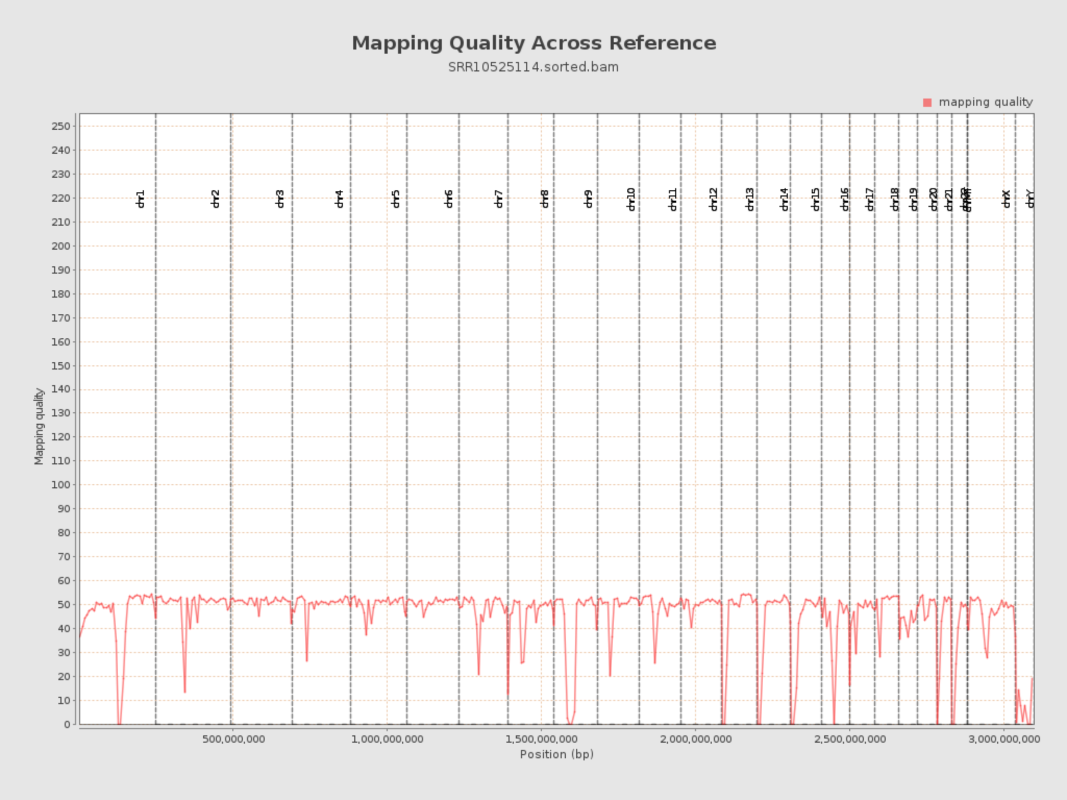
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram