Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:36:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525021.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_SRR10525021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:36:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,437,279
Mapped reads	1,312,853 / 91.34%
Unmapped reads	124,426 / 8.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,527 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	35,173 / 2.45%
Duplication rate	1.86%
Clipped reads	1,313,579 / 91.39%

2.2. ACGT Content

Number/percentage of A's	17,888,774 / 23.64%
Number/percentage of C's	14,699,383 / 19.42%
Number/percentage of T's	24,921,398 / 32.93%
Number/percentage of G's	18,170,523 / 24.01%
Number/percentage of N's	685 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2369

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

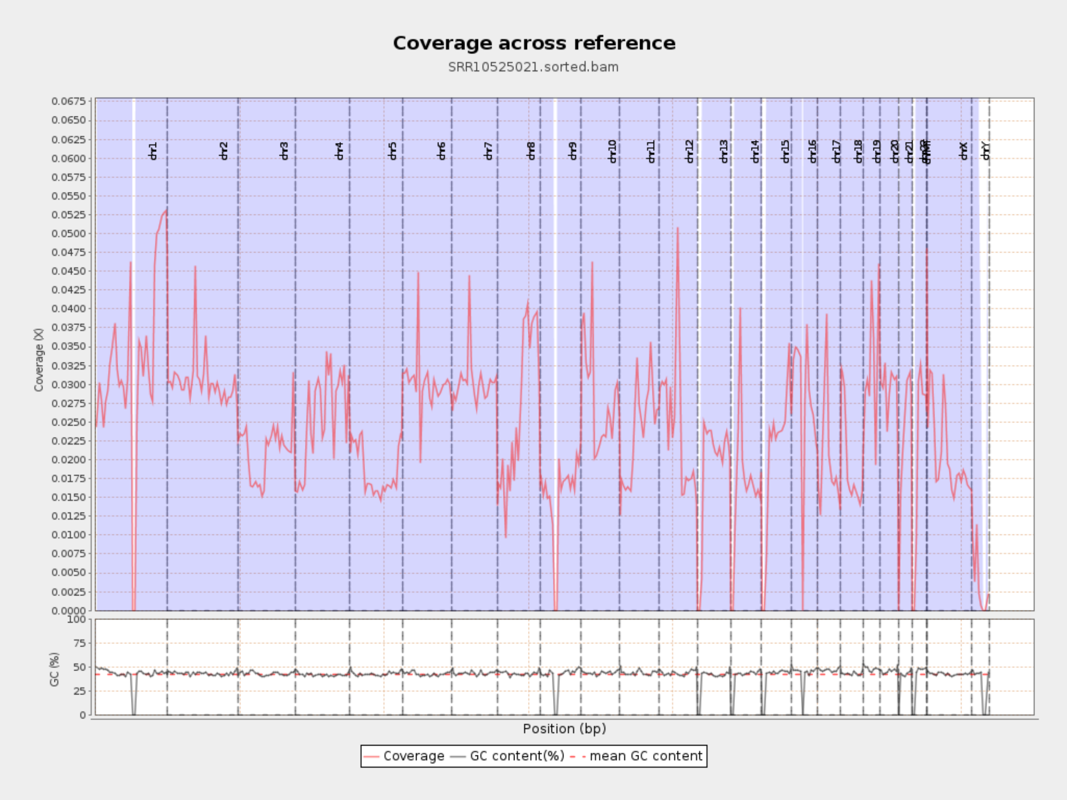
General error rate	0.51%
Mismatches	379,859
Insertions	5,378
Mapped reads with at least one insertion	0.41%
Deletions	15,044
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.03%

2.6. Chromosome stats

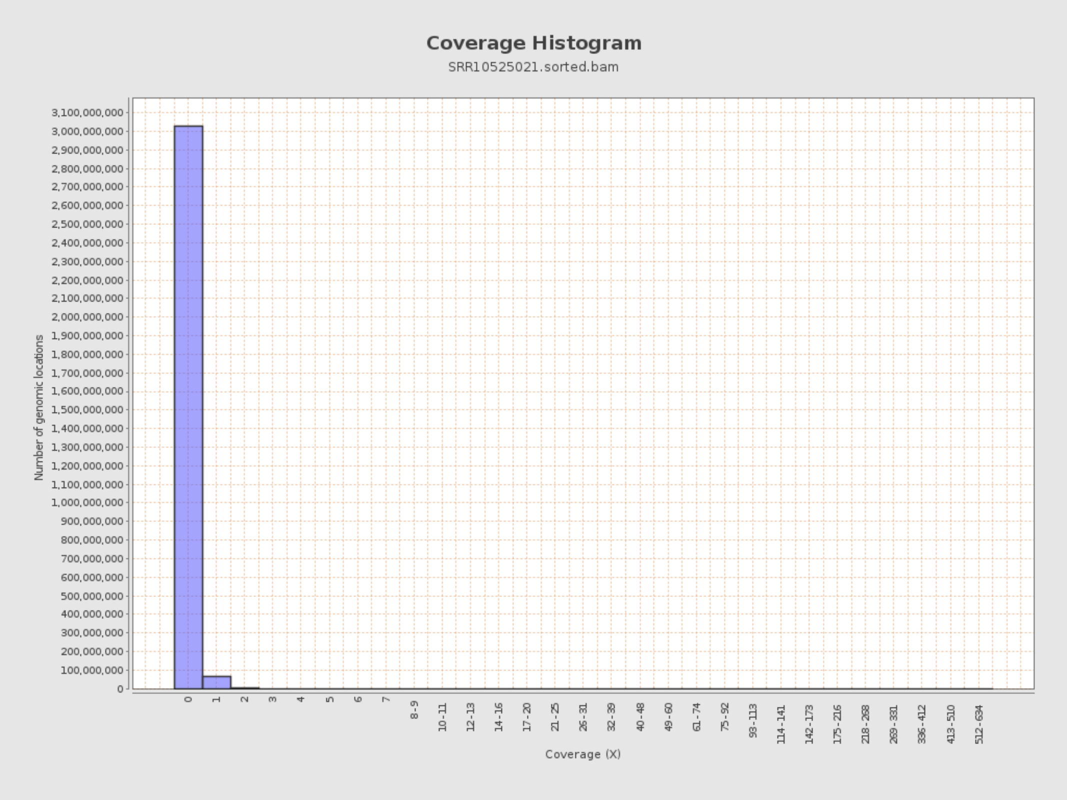
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8214283	0.033	0.4592
chr2	243199373	7407991	0.0305	0.274
chr3	198022430	4205748	0.0212	0.1553
chr4	191154276	4934254	0.0258	0.1811
chr5	180915260	3350169	0.0185	0.1468
chr6	171115067	5165139	0.0302	0.2438
chr7	159138663	4842463	0.0304	0.3071

chr8	146364022	3934023	0.0269	0.2318
chr9	141213431	2127258	0.0151	0.1749
chr10	135534747	3850274	0.0284	0.2321
chr11	135006516	3245393	0.024	0.2085
chr12	133851895	3296468	0.0246	0.169
chr13	115169878	2153773	0.0187	0.1445
chr14	107349540	1763733	0.0164	0.1395
chr15	102531392	2119093	0.0207	0.1598
chr16	90354753	2504275	0.0277	0.182
chr17	81195210	1670106	0.0206	0.1832
chr18	78077248	1518066	0.0194	0.2768
chr19	59128983	1938832	0.0328	0.2829
chr20	63025520	1855191	0.0294	0.1843
chr21	48129895	1110901	0.0231	0.1666
chr22	51304566	1058303	0.0206	0.1516
chrMT	16571	797	0.0481	0.2138
chrX	155270560	3231014	0.0208	0.1755
chrY	59373566	208185	0.0035	0.0943

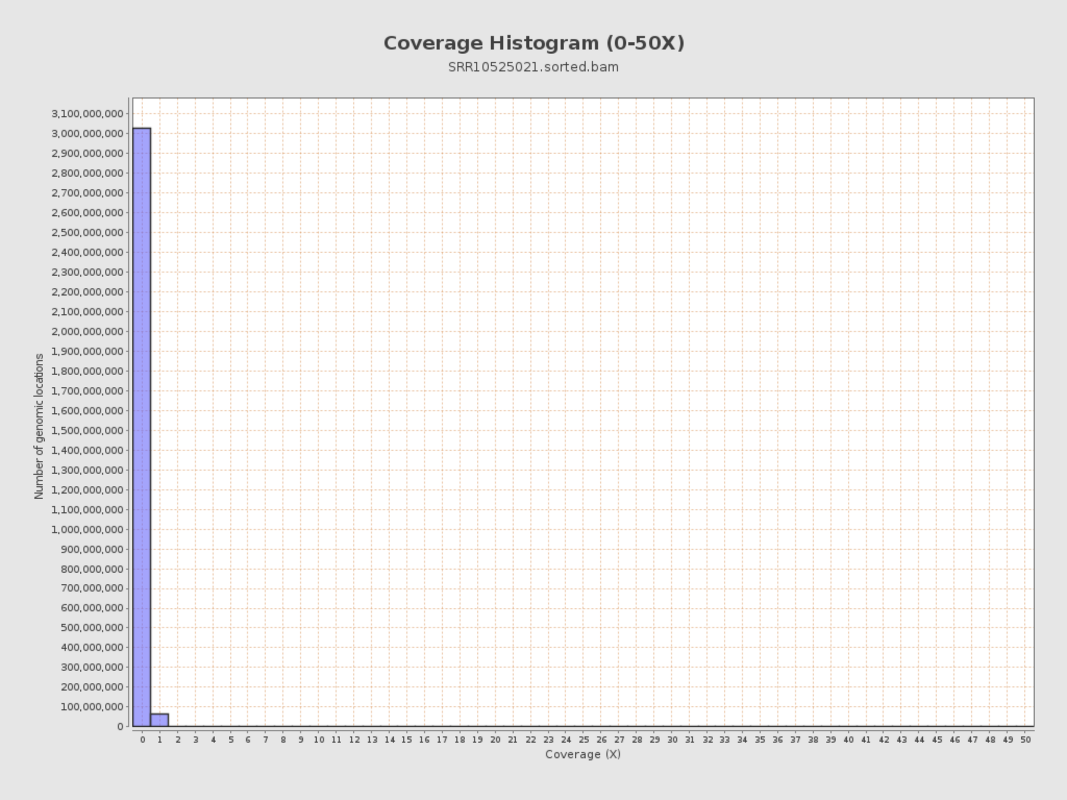
3. Results : Coverage across reference



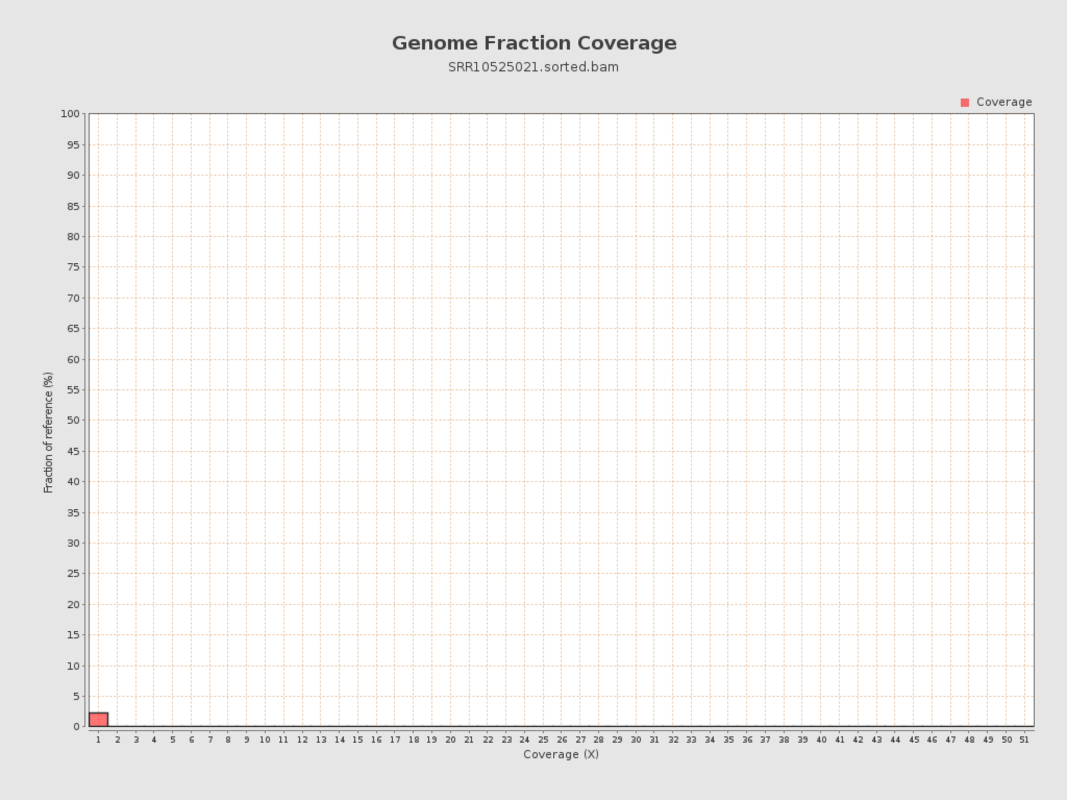
4. Results : Coverage Histogram



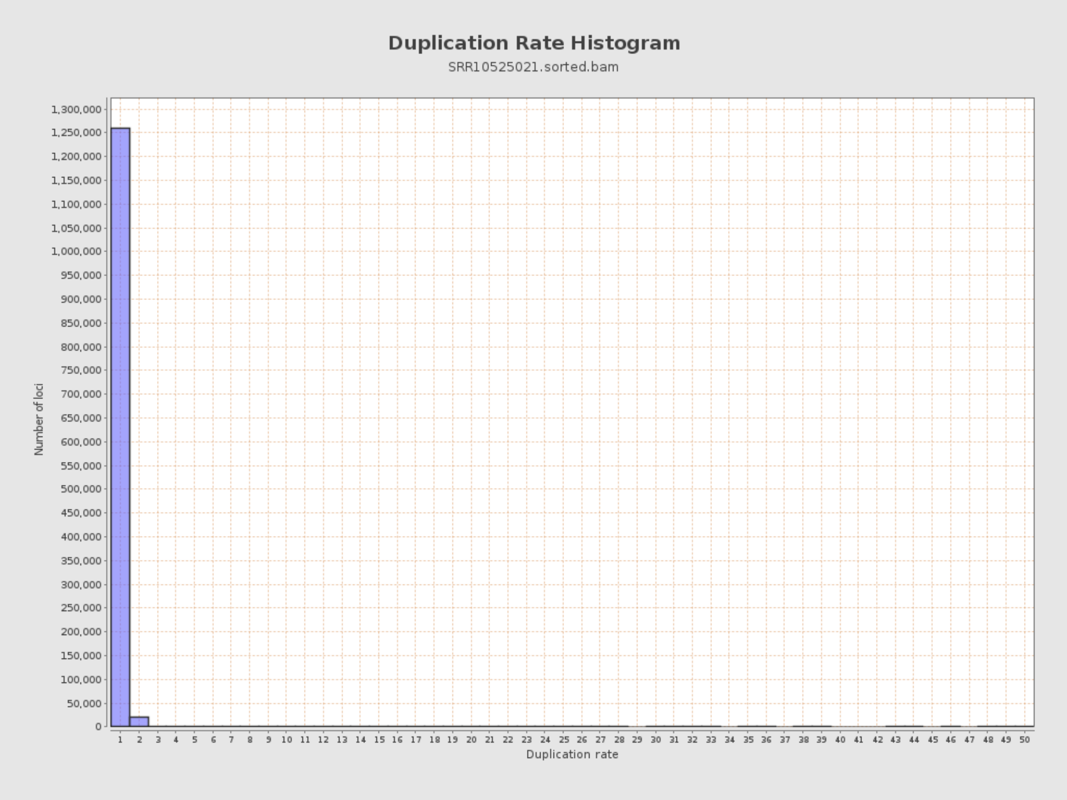
5. Results : Coverage Histogram (0-50X)



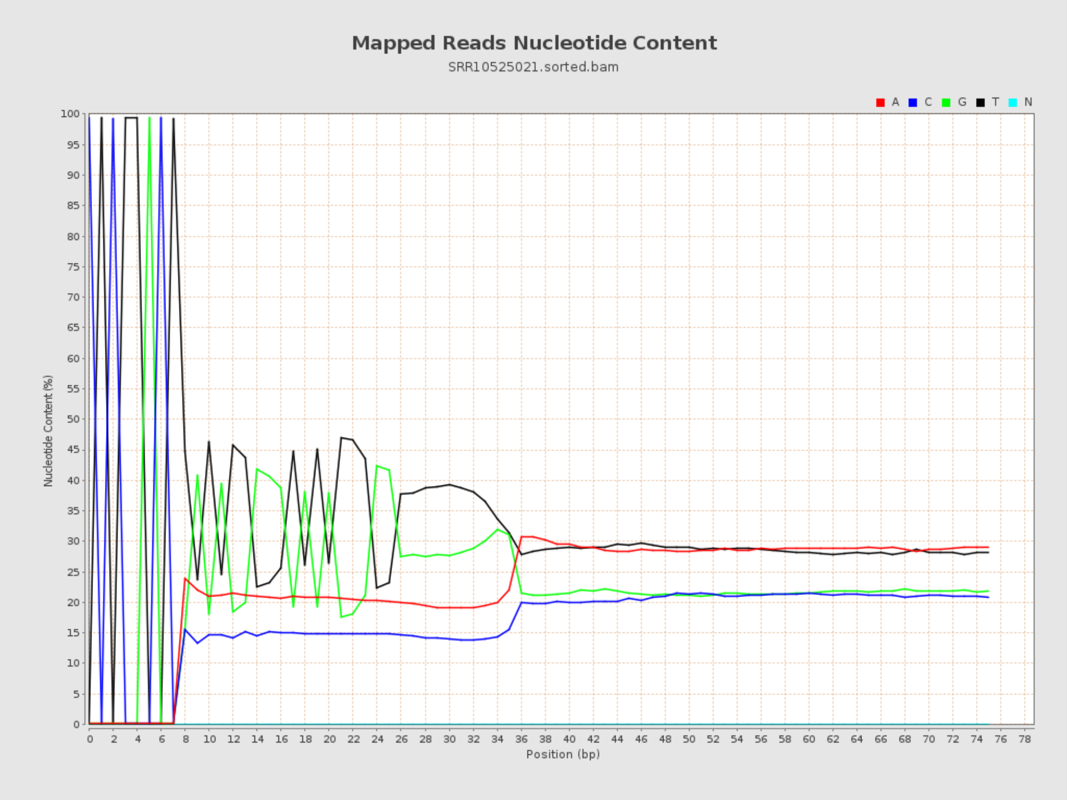
6. Results : Genome Fraction Coverage



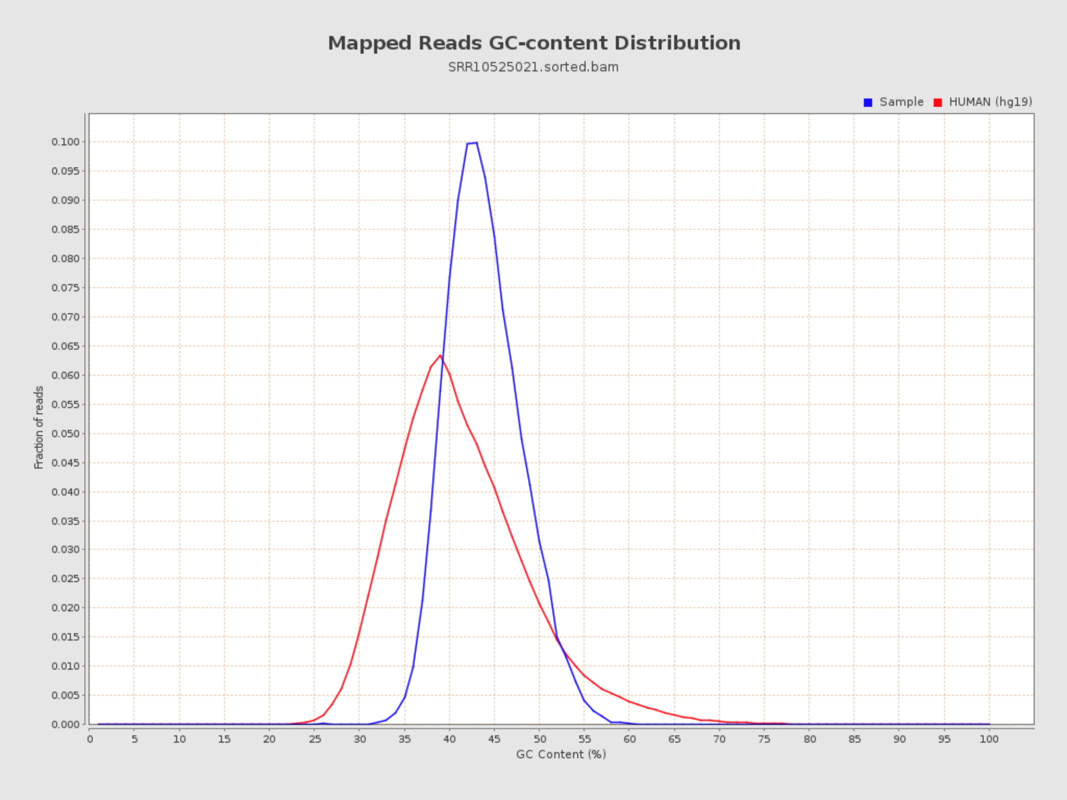
7. Results : Duplication Rate Histogram



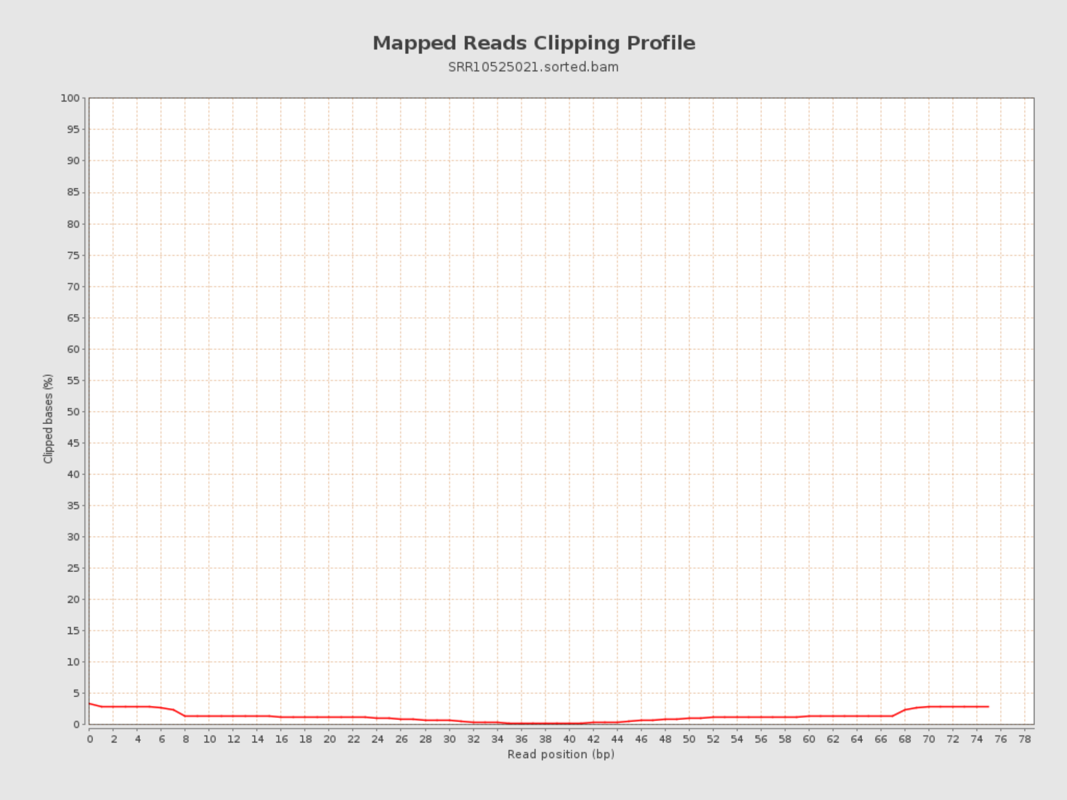
8. Results : Mapped Reads Nucleotide Content



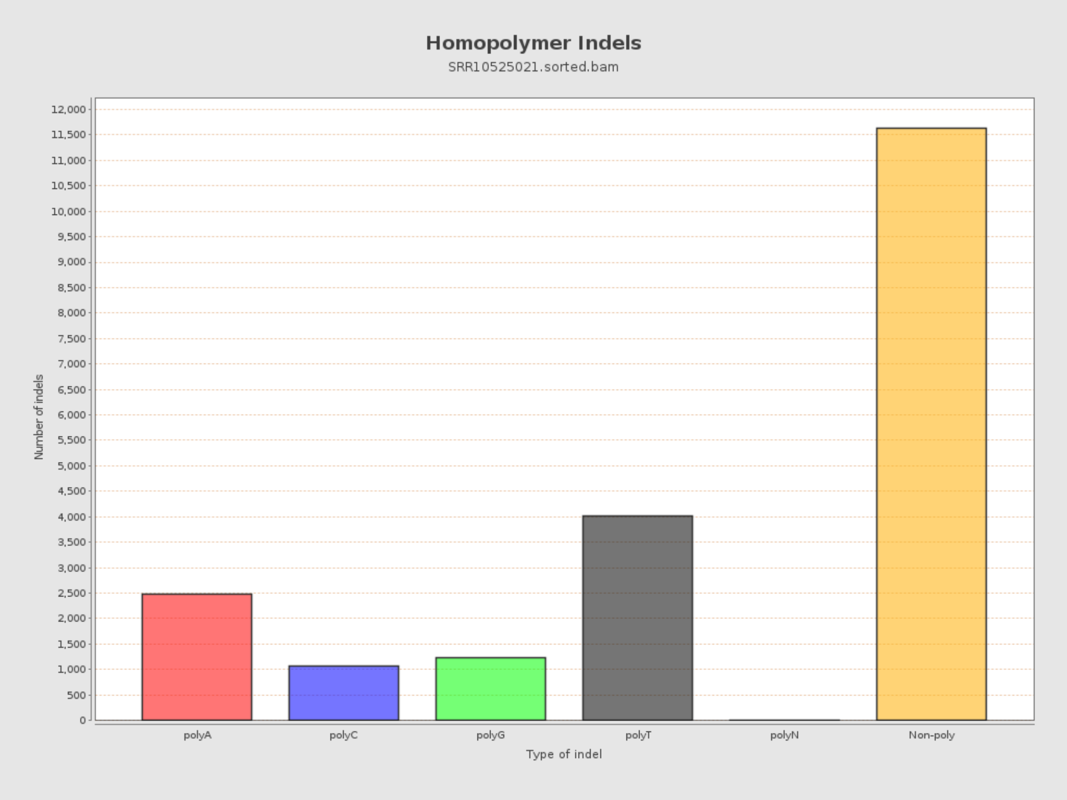
9. Results : Mapped Reads GC-content Distribution



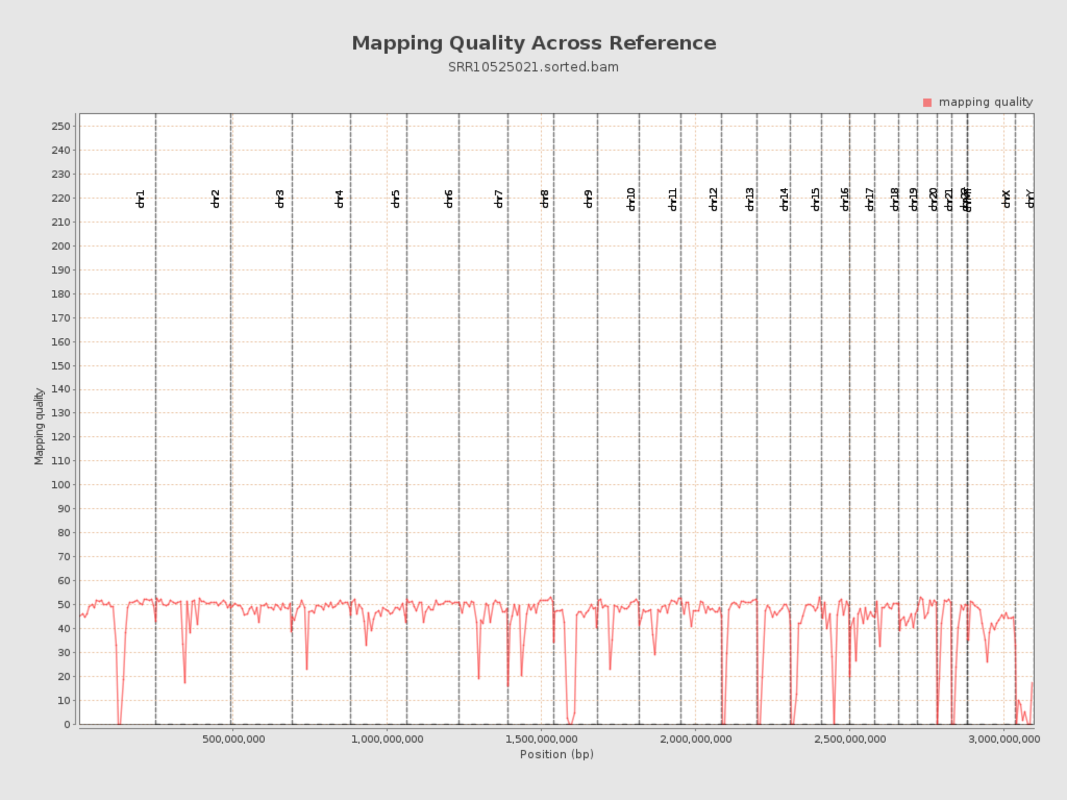
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram