Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:22:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525155.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_SRR10525155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:22:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,309,075
Mapped reads	1,083,273 / 82.75%
Unmapped reads	225,802 / 17.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,008 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	23,078 / 1.76%
Duplication rate	1.51%
Clipped reads	1,083,127 / 82.74%

2.2. ACGT Content

Number/percentage of A's	17,653,123 / 26.39%
Number/percentage of C's	14,318,160 / 21.4%
Number/percentage of T's	20,258,889 / 30.28%
Number/percentage of G's	14,665,150 / 21.92%
Number/percentage of N's	1,705 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2202

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

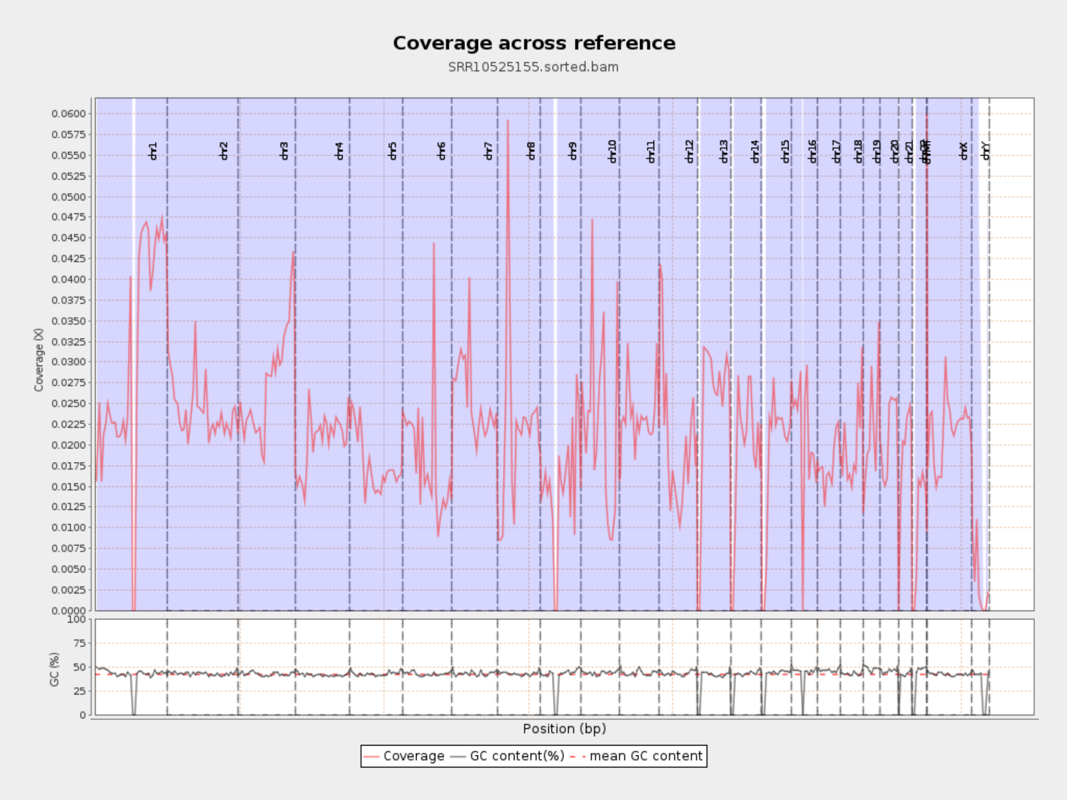
General error rate	0.5%
Mismatches	322,775
Insertions	4,887
Mapped reads with at least one insertion	0.45%
Deletions	13,675
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.09%

2.6. Chromosome stats

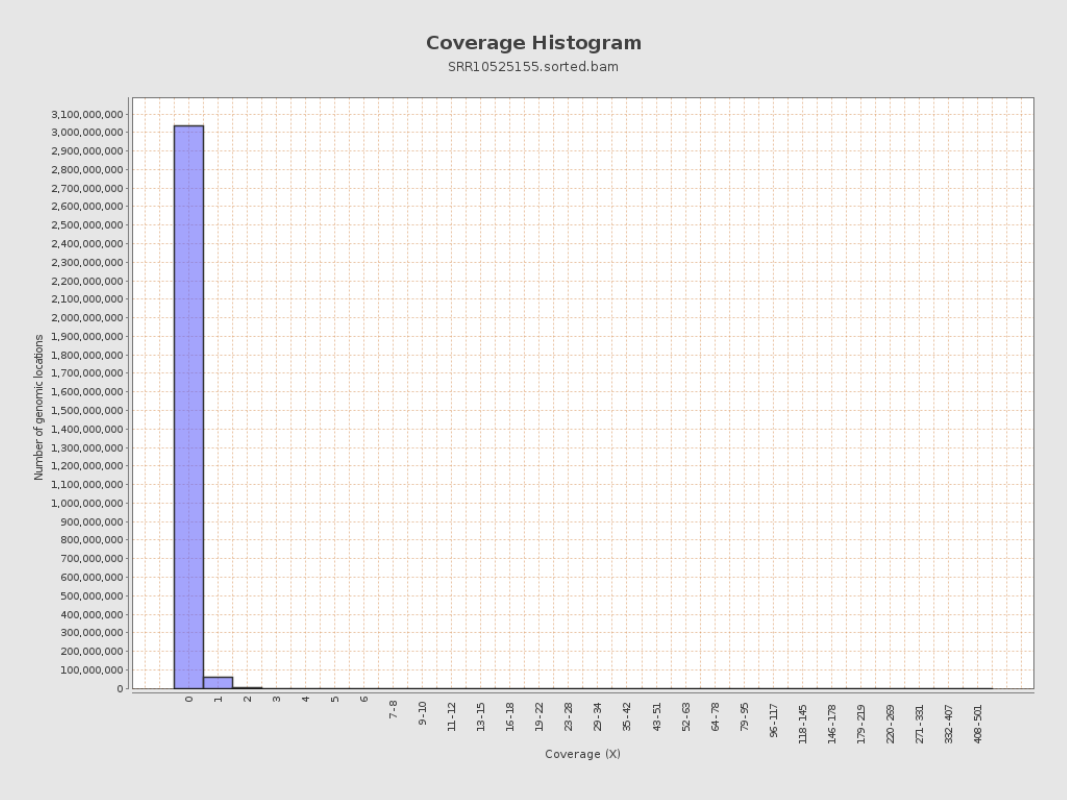
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7582262	0.0304	0.4341
chr2	243199373	5874231	0.0242	0.2345
chr3	198022430	5450024	0.0275	0.1773
chr4	191154276	3943090	0.0206	0.1577
chr5	180915260	3203353	0.0177	0.1399
chr6	171115067	3147069	0.0184	0.1501
chr7	159138663	4097818	0.0257	0.3117

chr8	146364022	3241583	0.0221	0.1784
chr9	141213431	2108017	0.0149	0.1599
chr10	135534747	3072892	0.0227	0.2522
chr11	135006516	3178795	0.0235	0.1773
chr12	133851895	2739587	0.0205	0.152
chr13	115169878	2848696	0.0247	0.1656
chr14	107349540	2013683	0.0188	0.1494
chr15	102531392	1877866	0.0183	0.1437
chr16	90354753	1905779	0.0211	0.1649
chr17	81195210	1437476	0.0177	0.146
chr18	78077248	1537283	0.0197	0.2948
chr19	59128983	1294777	0.0219	0.2904
chr20	63025520	1322779	0.021	0.1564
chr21	48129895	904529	0.0188	0.1525
chr22	51304566	532096	0.0104	0.1064
chrMT	16571	994	0.06	0.2382
chrX	155270560	3408904	0.022	0.163
chrY	59373566	195998	0.0033	0.1003

3. Results : Coverage across reference



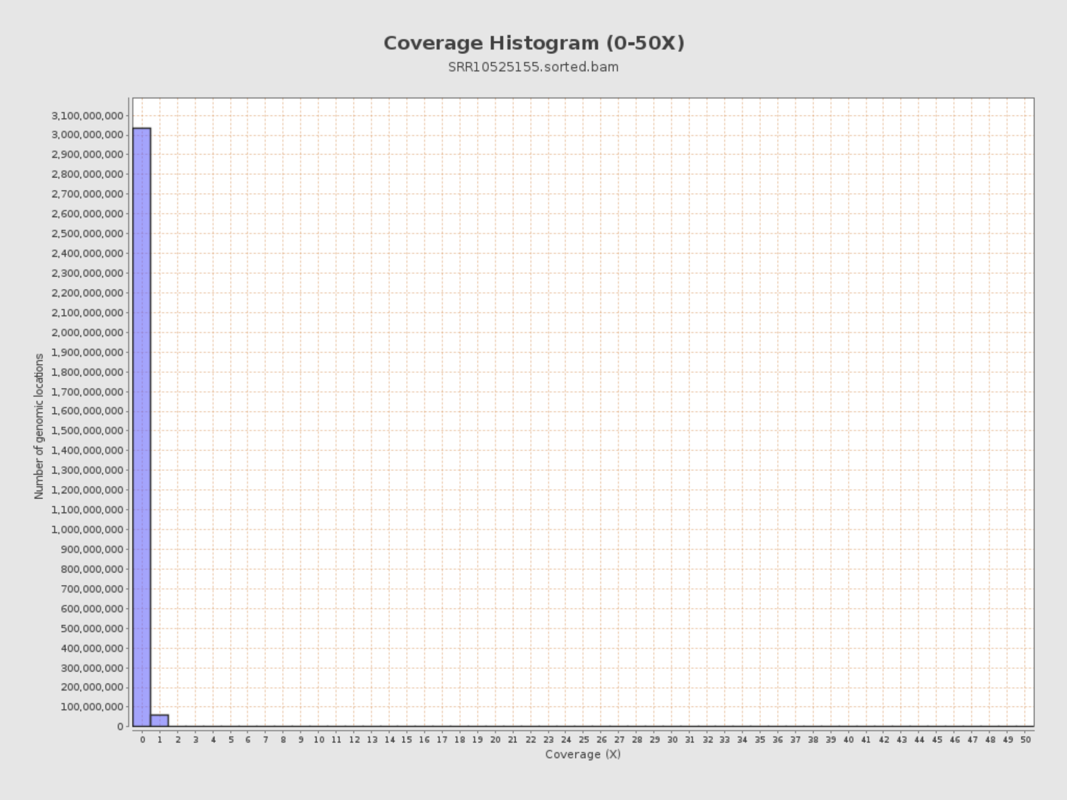
4. Results : Coverage Histogram



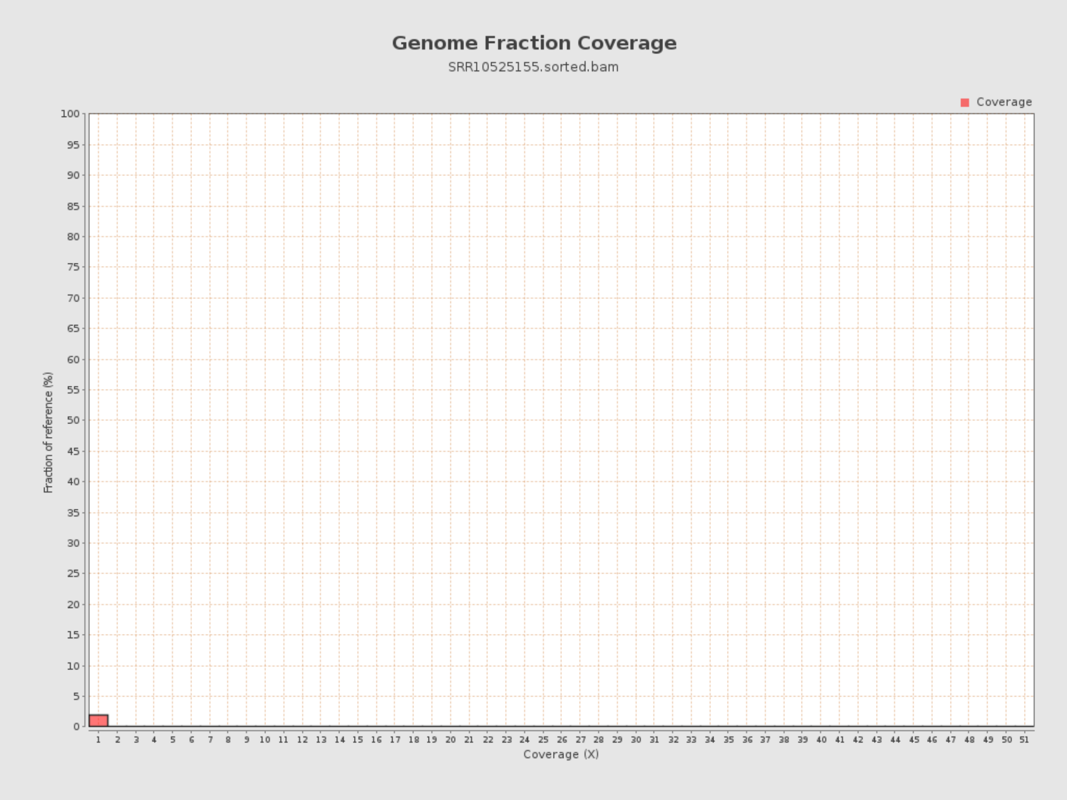
Coverage Histogram

SRR10525155.sorted.bam

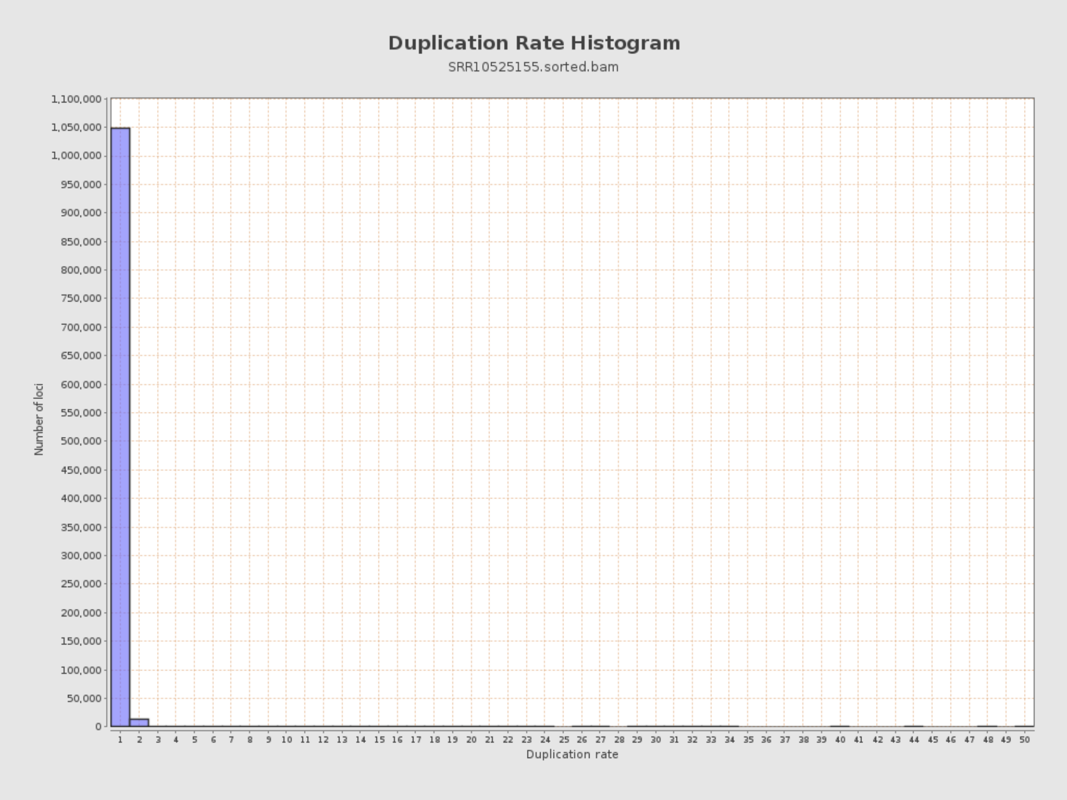
5. Results : Coverage Histogram (0-50X)



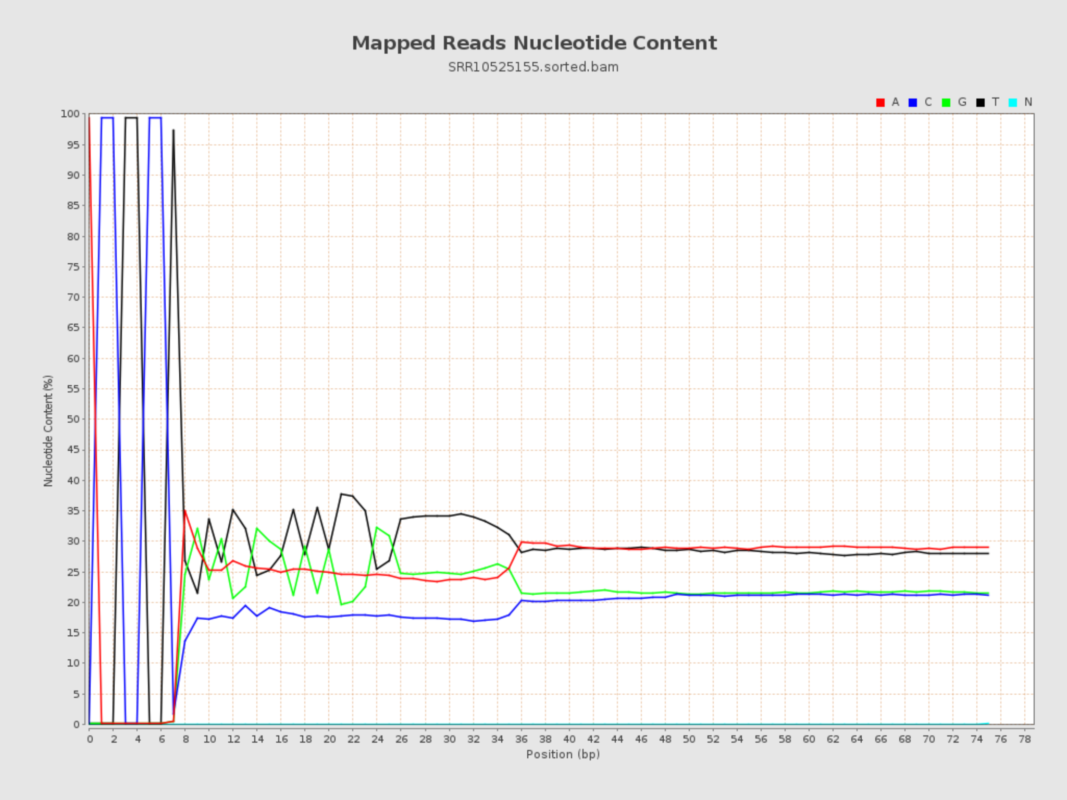
6. Results : Genome Fraction Coverage



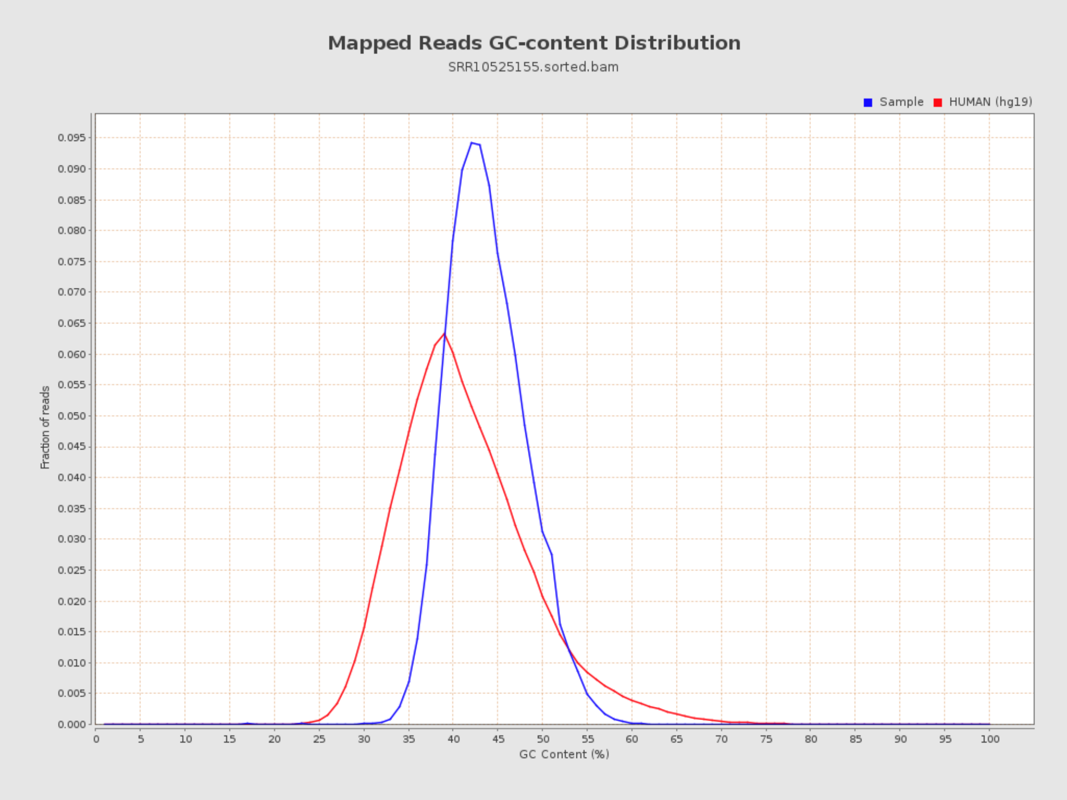
7. Results : Duplication Rate Histogram



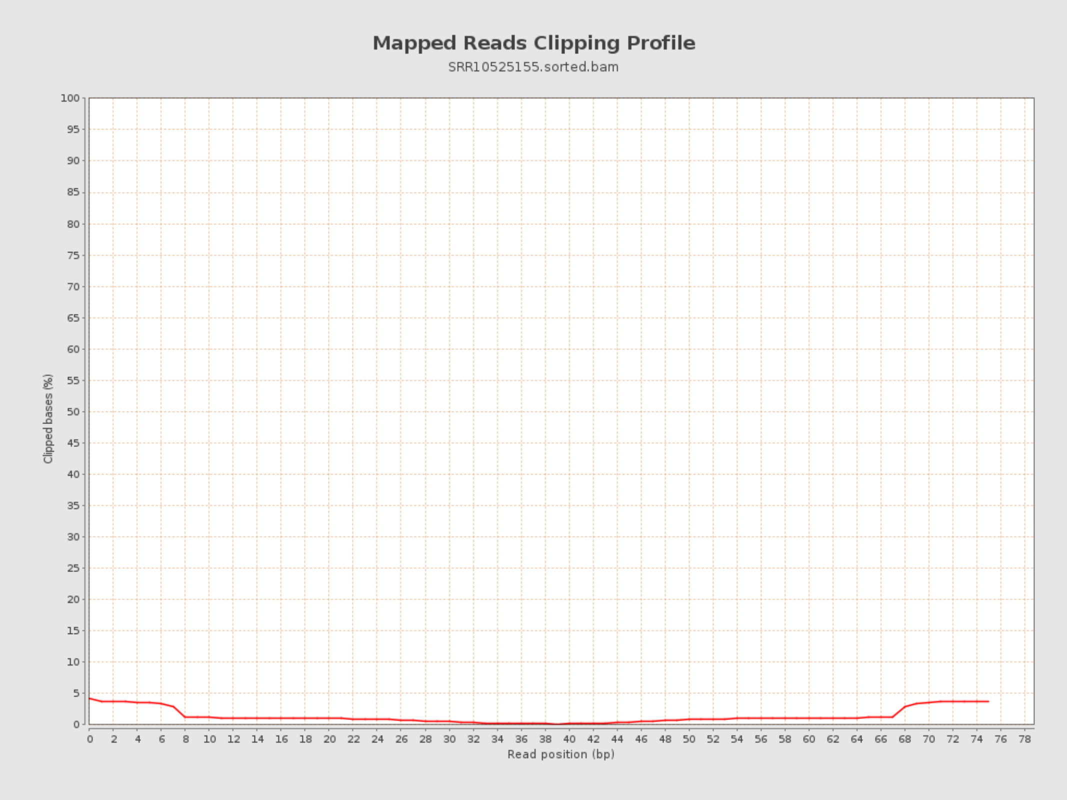
8. Results : Mapped Reads Nucleotide Content



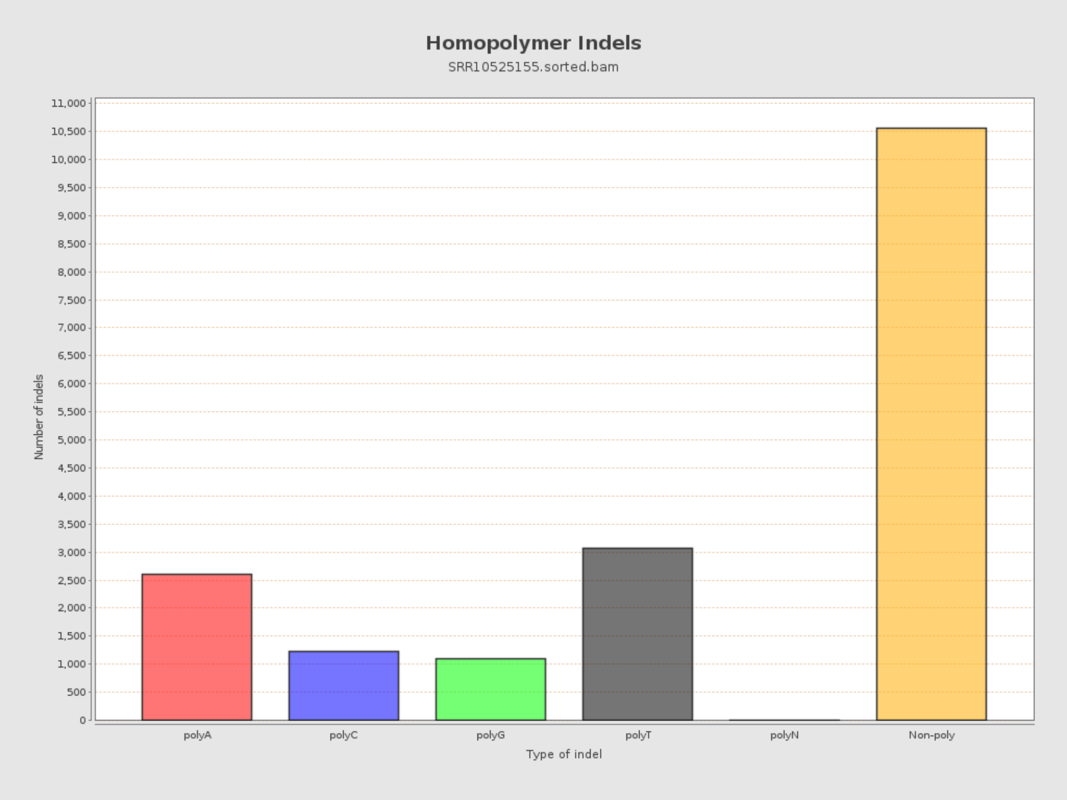
9. Results : Mapped Reads GC-content Distribution



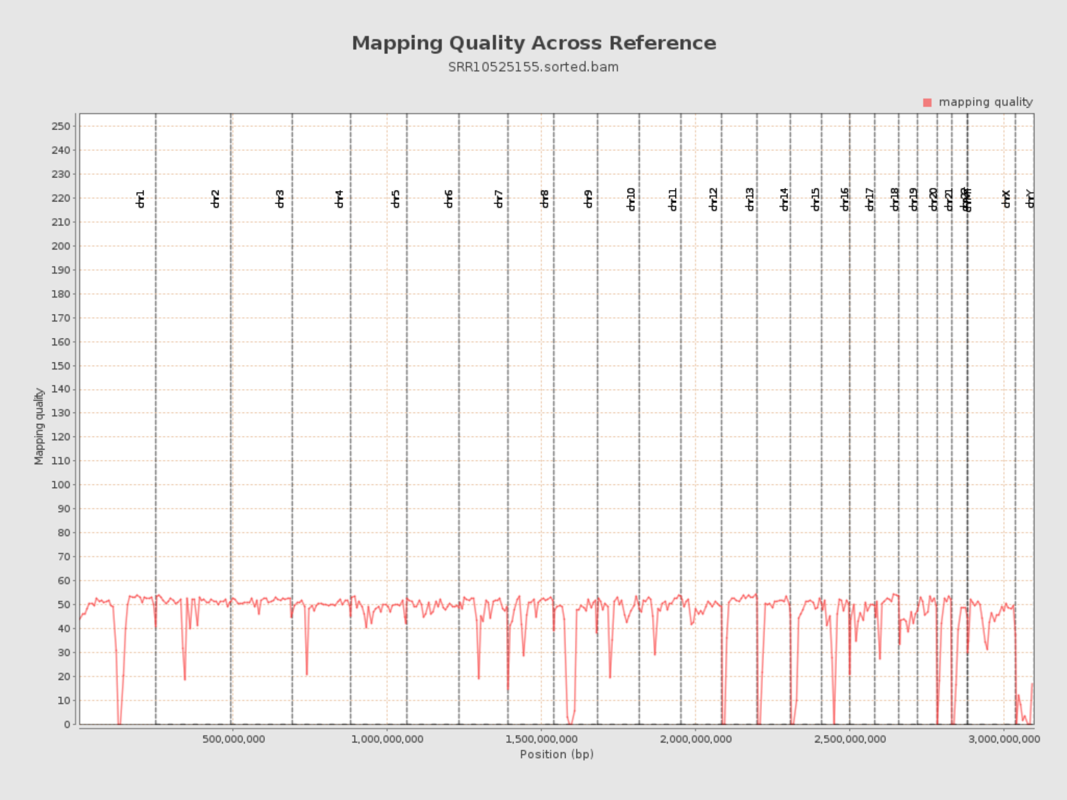
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram