Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:00:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525054.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_SRR10525054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:00:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,218,319
Mapped reads	953,608 / 78.27%
Unmapped reads	264,711 / 21.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,724 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	46,411 / 3.81%
Duplication rate	4.02%
Clipped reads	952,914 / 78.22%

2.2. ACGT Content

Number/percentage of A's	13,649,255 / 24.83%
Number/percentage of C's	10,880,645 / 19.8%
Number/percentage of T's	18,082,269 / 32.9%
Number/percentage of G's	12,343,128 / 22.46%
Number/percentage of N's	5,384 / 0.01%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1929

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

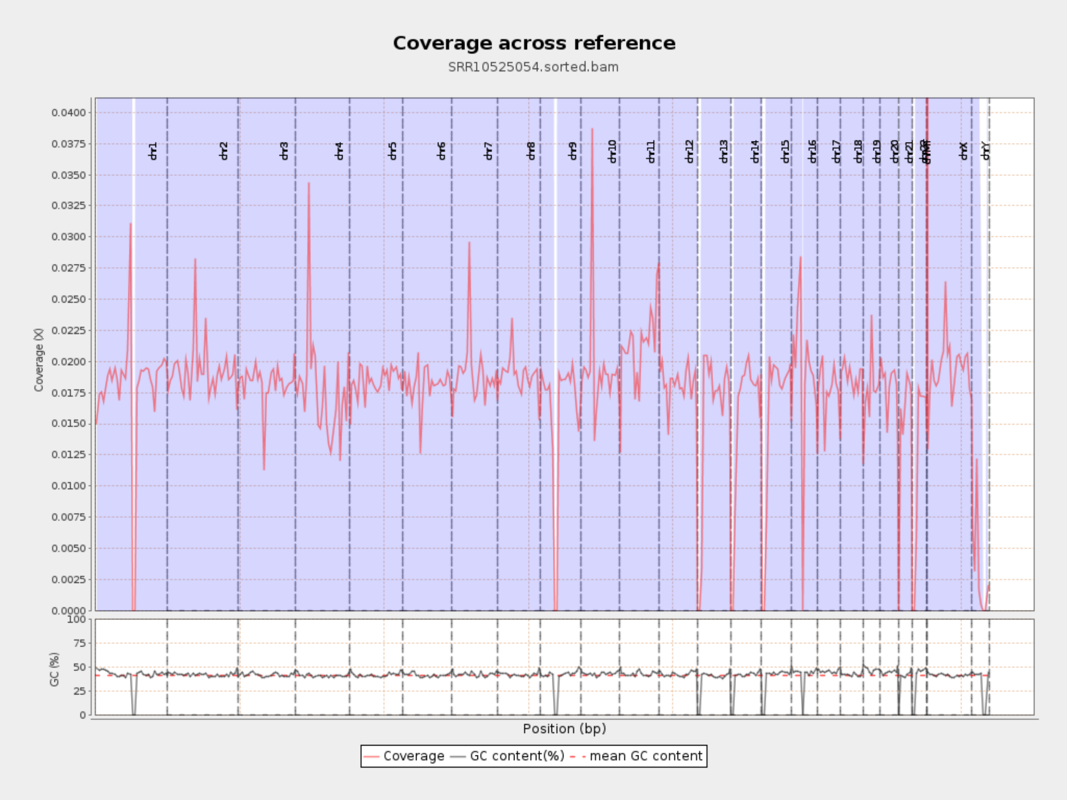
General error rate	0.51%
Mismatches	272,217
Insertions	4,520
Mapped reads with at least one insertion	0.47%
Deletions	11,151
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.06%

2.6. Chromosome stats

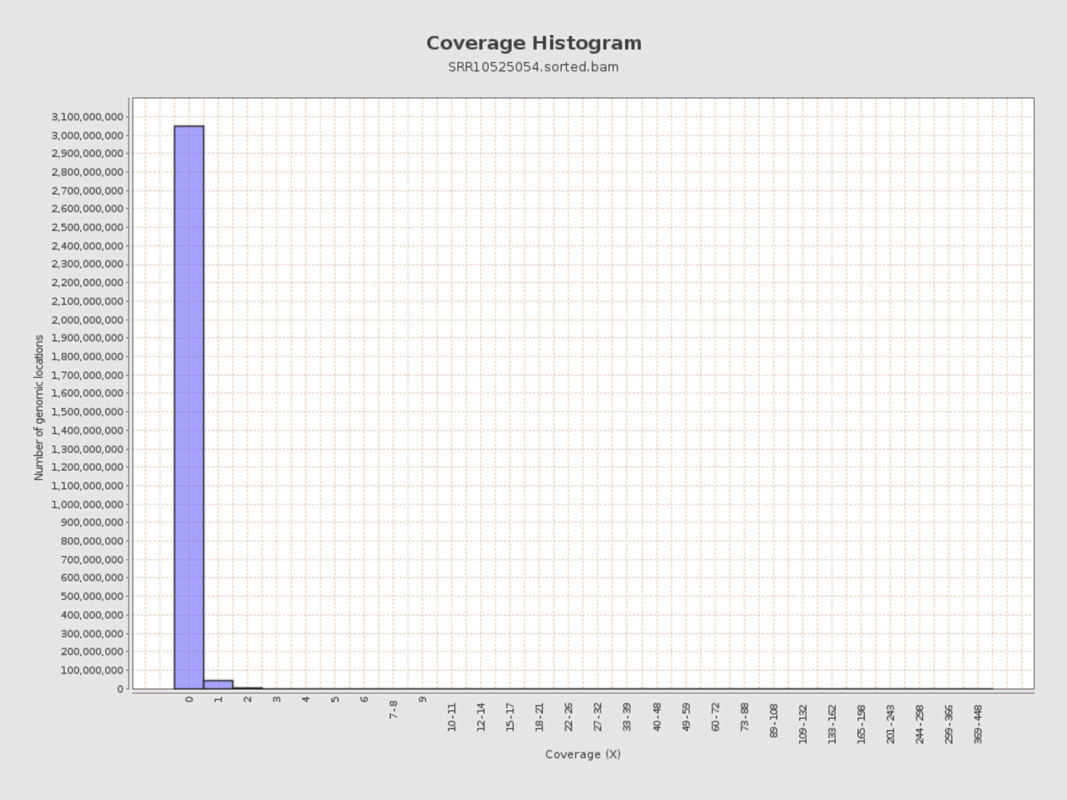
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4445472	0.0178	0.3384
chr2	243199373	4687476	0.0193	0.2286
chr3	198022430	3608540	0.0182	0.1467
chr4	191154276	3382898	0.0177	0.1581
chr5	180915260	3349796	0.0185	0.1481
chr6	171115067	3093545	0.0181	0.1571
chr7	159138663	3051603	0.0192	0.219

chr8	146364022	2778436	0.019	0.2098
chr9	141213431	2236845	0.0158	0.1566
chr10	135534747	2646878	0.0195	0.2115
chr11	135006516	2867533	0.0212	0.1773
chr12	133851895	2440292	0.0182	0.1508
chr13	115169878	1778749	0.0154	0.1349
chr14	107349540	1643330	0.0153	0.1368
chr15	102531392	1583120	0.0154	0.1351
chr16	90354753	1695535	0.0188	0.1611
chr17	81195210	1436694	0.0177	0.1489
chr18	78077248	1470139	0.0188	0.2291
chr19	59128983	1059080	0.0179	0.2399
chr20	63025520	1138836	0.0181	0.1485
chr21	48129895	735466	0.0153	0.1511
chr22	51304566	611001	0.0119	0.1188
chrMT	16571	31824	1.9205	1.6557
chrX	155270560	3020172	0.0195	0.1619
chrY	59373566	185250	0.0031	0.1192

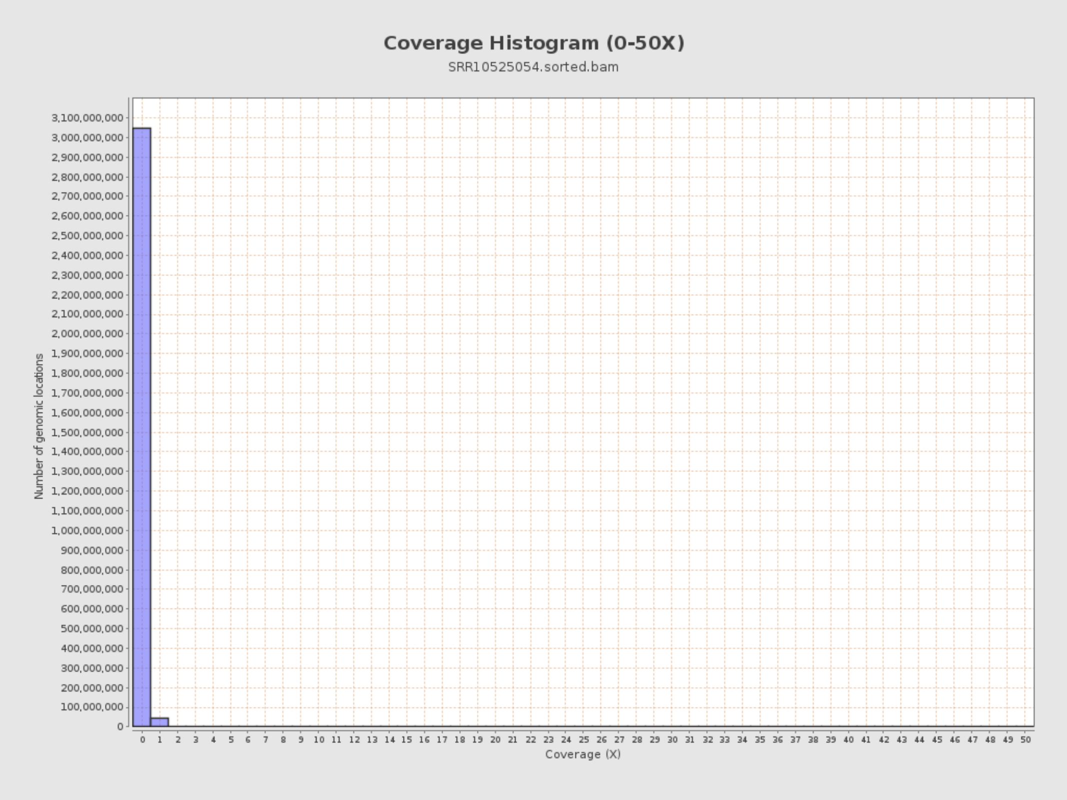
3. Results : Coverage across reference



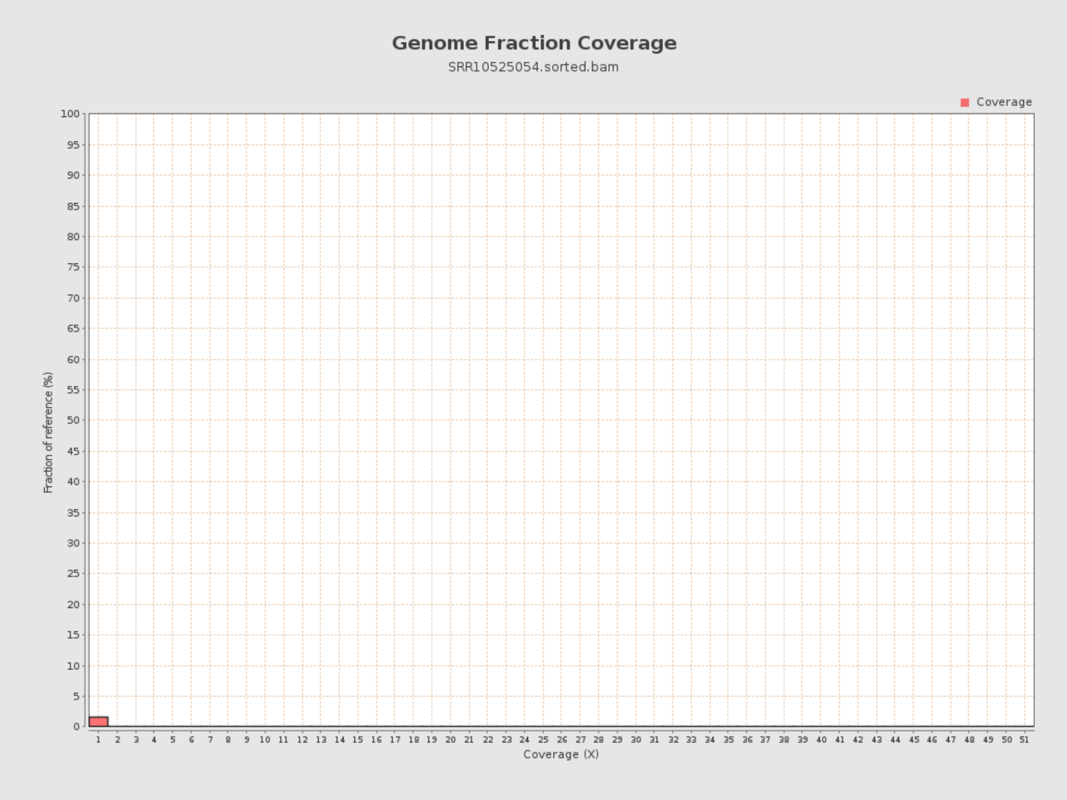
4. Results : Coverage Histogram



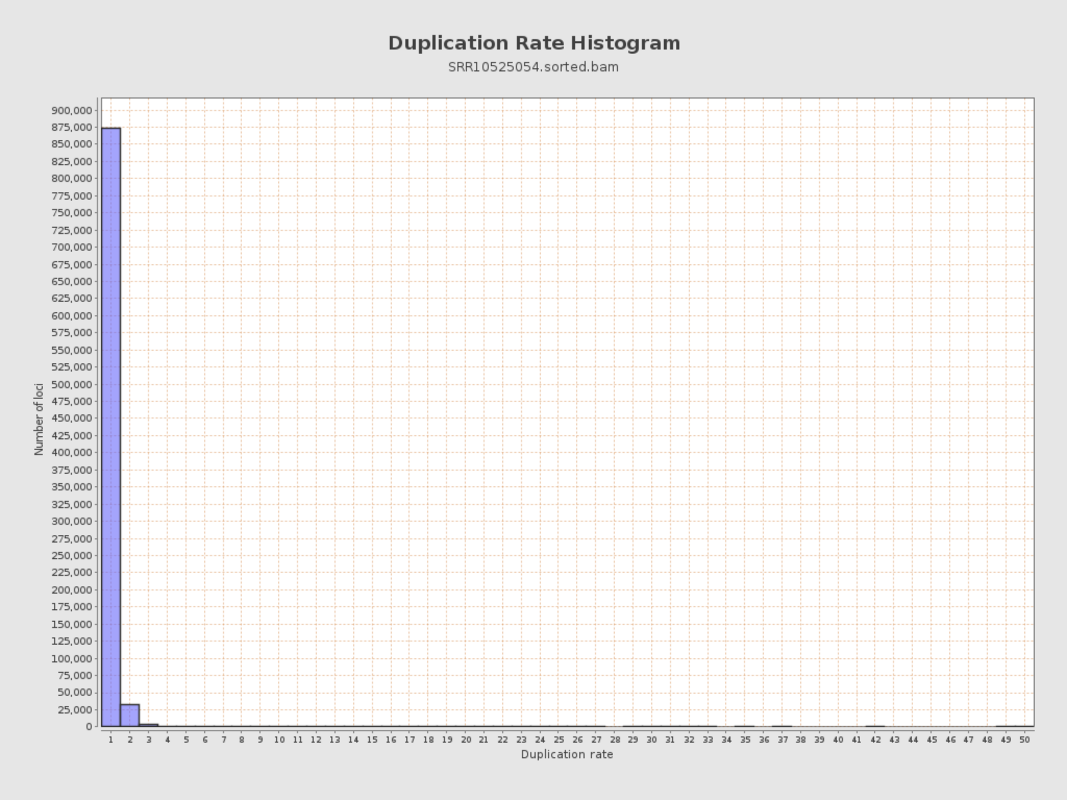
5. Results : Coverage Histogram (0-50X)



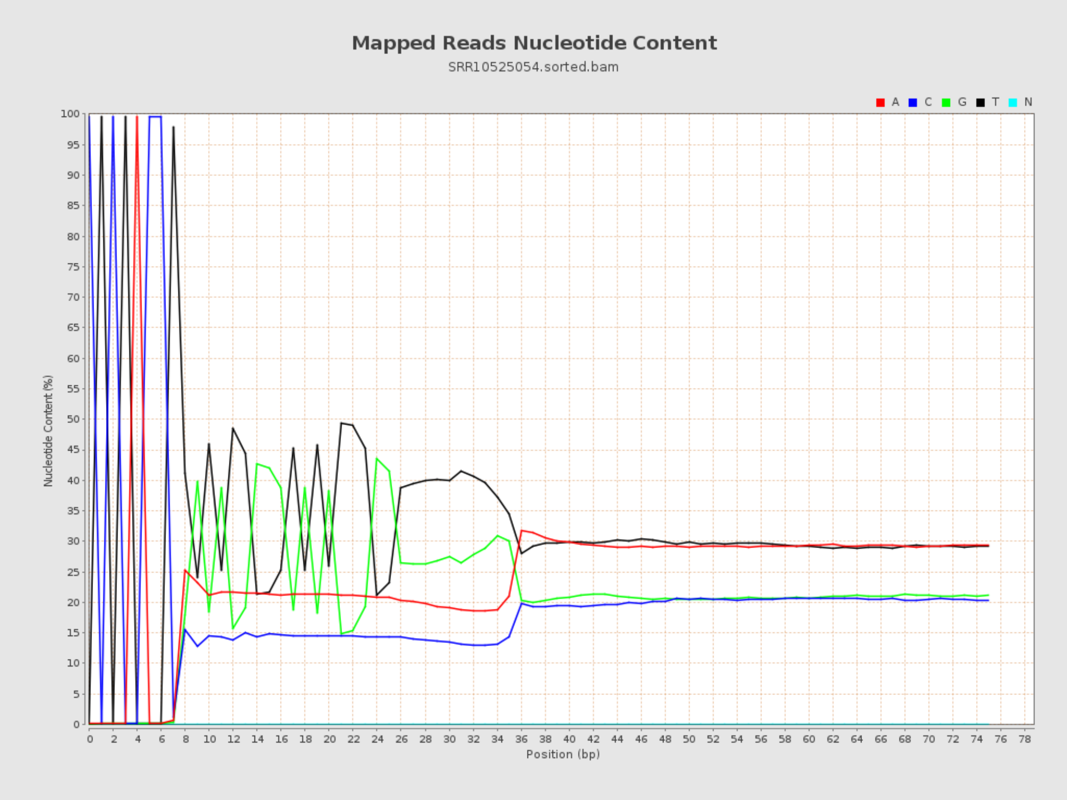
6. Results : Genome Fraction Coverage



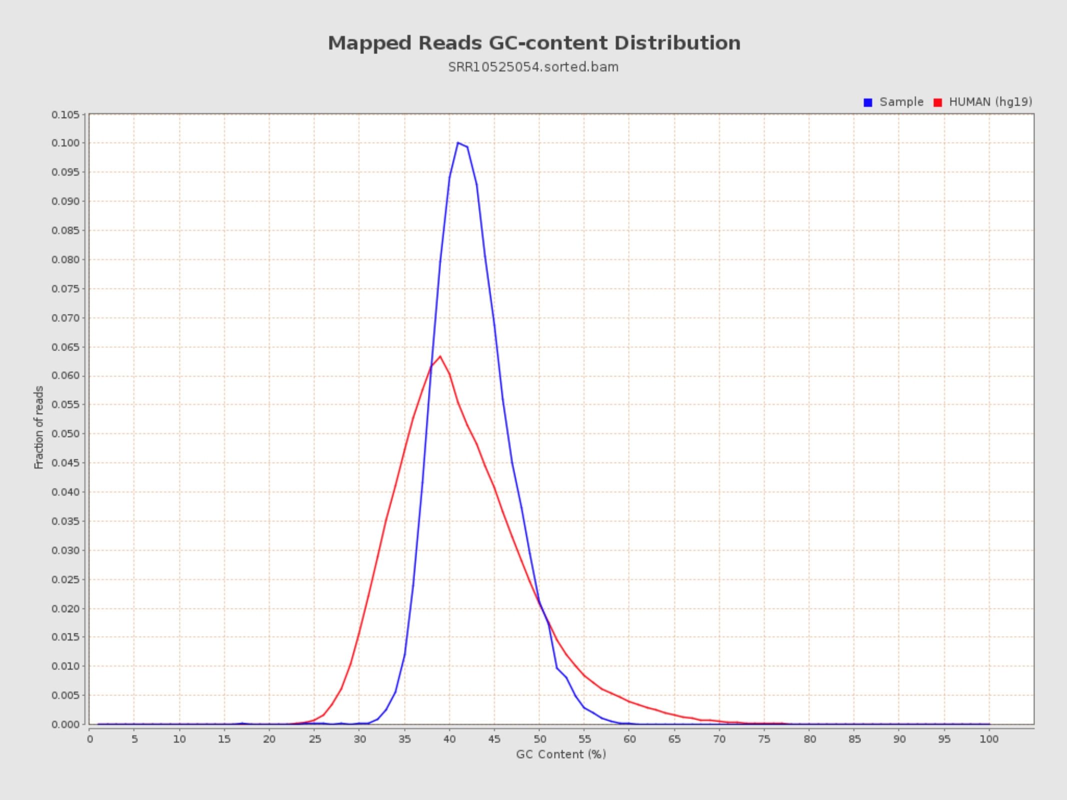
7. Results : Duplication Rate Histogram



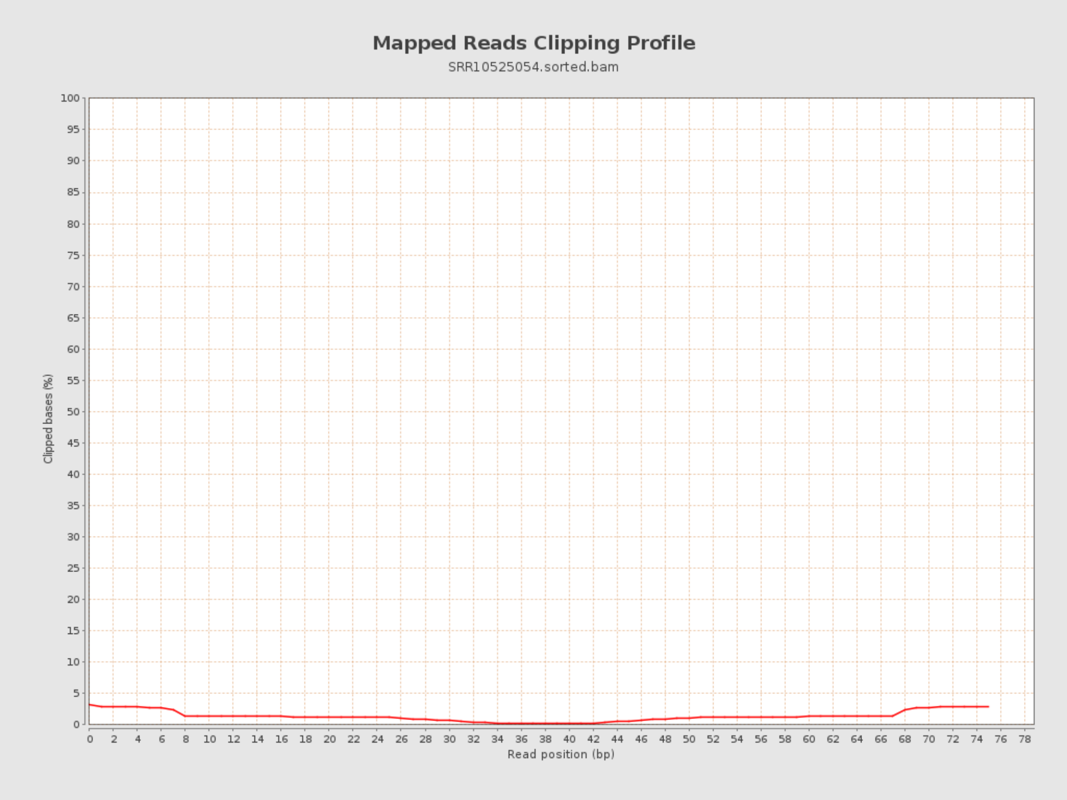
8. Results : Mapped Reads Nucleotide Content



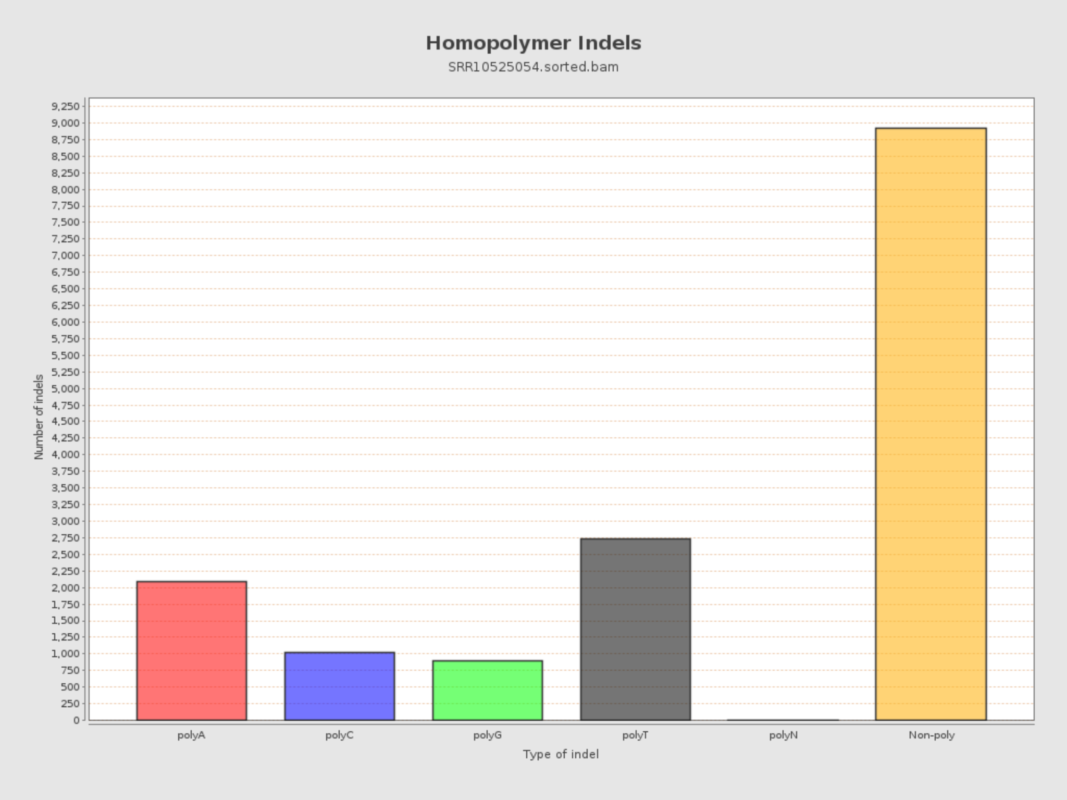
9. Results : Mapped Reads GC-content Distribution



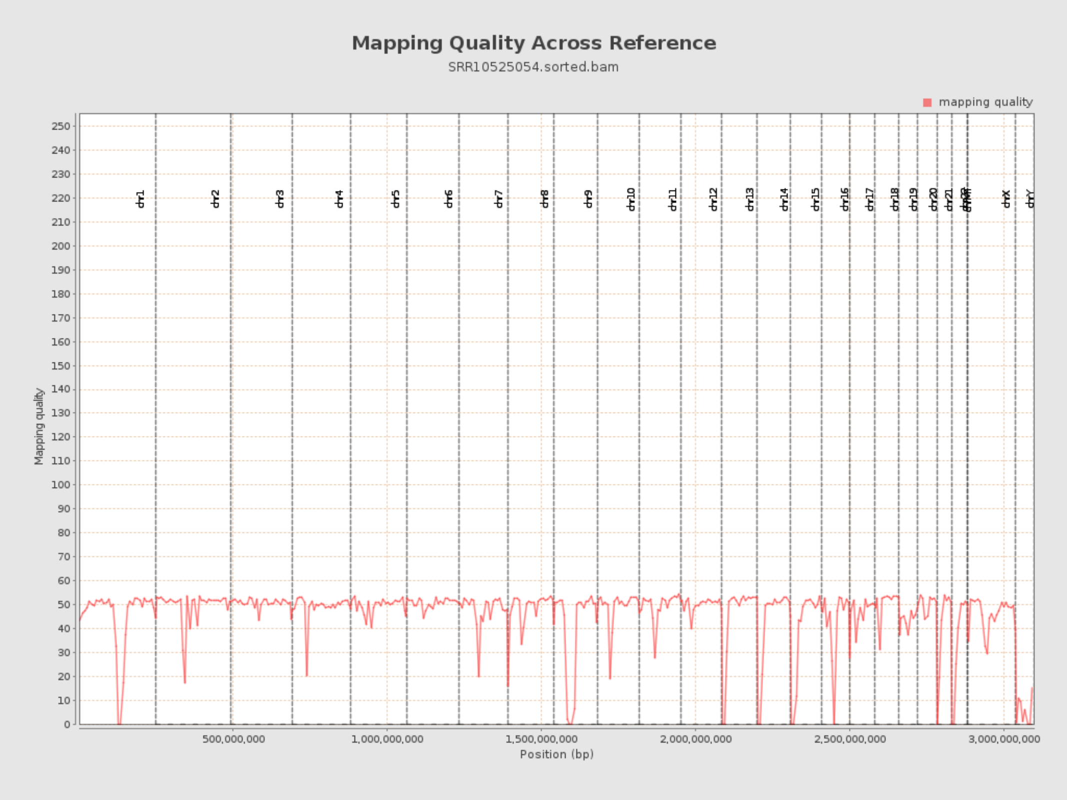
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram