Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:35:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525042.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_SRR10525042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:35:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	684,436
Mapped reads	623,879 / 91.15%
Unmapped reads	60,557 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,534 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	12,038 / 1.76%
Duplication rate	1.4%
Clipped reads	624,975 / 91.31%

2.2. ACGT Content

Number/percentage of A's	9,128,263 / 25.38%
Number/percentage of C's	6,423,108 / 17.86%
Number/percentage of T's	11,247,752 / 31.27%
Number/percentage of G's	9,172,298 / 25.5%
Number/percentage of N's	389 / 0%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0116

Standard Deviation	0.134

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

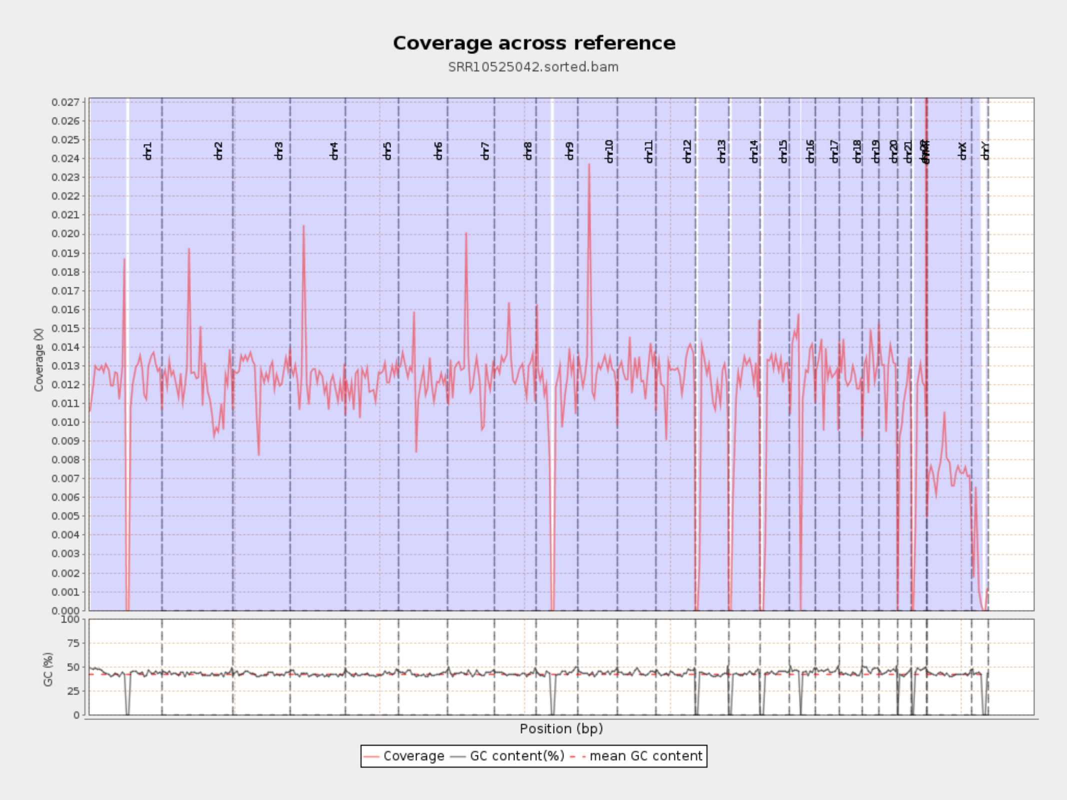
General error rate	0.5%
Mismatches	174,535
Insertions	2,450
Mapped reads with at least one insertion	0.39%
Deletions	6,850
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.97%

2.6. Chromosome stats

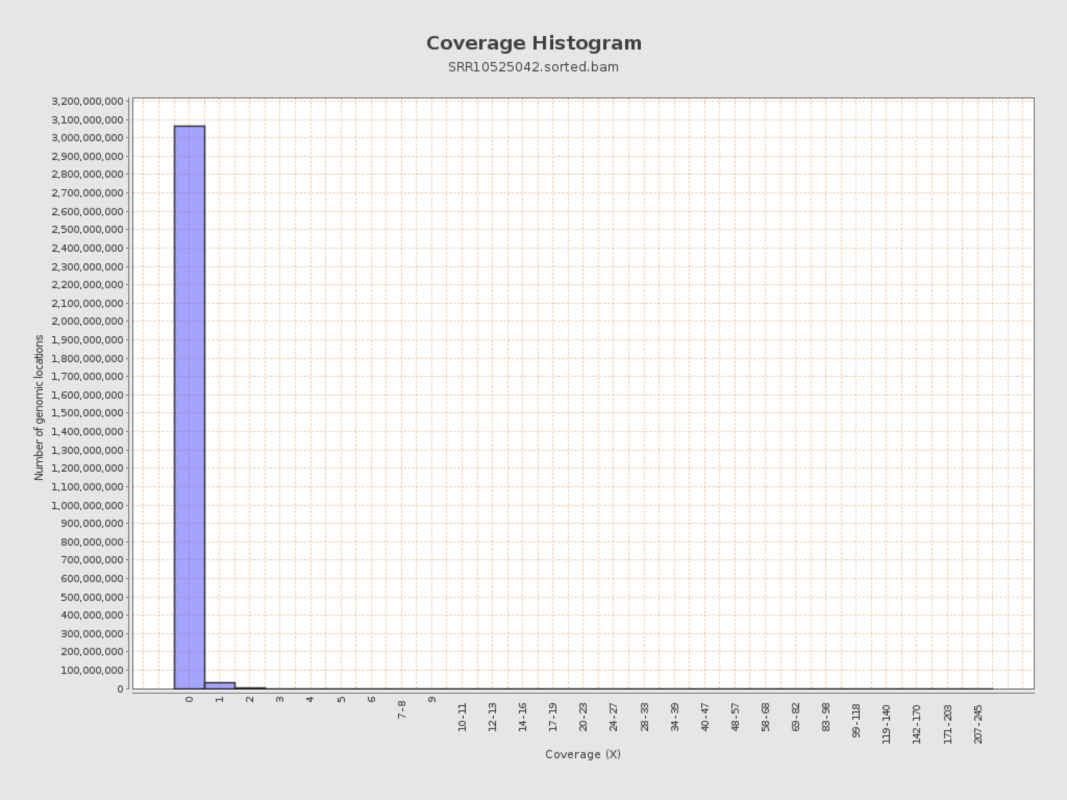
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2970812	0.0119	0.2051
chr2	243199373	2956104	0.0122	0.1451
chr3	198022430	2479895	0.0125	0.1172
chr4	191154276	2375695	0.0124	0.1225
chr5	180915260	2203983	0.0122	0.1148
chr6	171115067	2115603	0.0124	0.1251
chr7	159138663	2018084	0.0127	0.1589

chr8	146364022	1893279	0.0129	0.138
chr9	141213431	1502527	0.0106	0.1181
chr10	135534747	1807124	0.0133	0.147
chr11	135006516	1719892	0.0127	0.1321
chr12	133851895	1687344	0.0126	0.1173
chr13	115169878	1186960	0.0103	0.1055
chr14	107349540	1130577	0.0105	0.1079
chr15	102531392	1076552	0.0105	0.108
chr16	90354753	1112267	0.0123	0.1192
chr17	81195210	1017957	0.0125	0.1207
chr18	78077248	982748	0.0126	0.173
chr19	59128983	771806	0.0131	0.1501
chr20	63025520	800230	0.0127	0.1183
chr21	48129895	480854	0.01	0.1087
chr22	51304566	433654	0.0085	0.0949
chrMT	16571	5662	0.3417	0.6182
chrX	155270560	1154240	0.0074	0.0951
chrY	59373566	99490	0.0017	0.0605

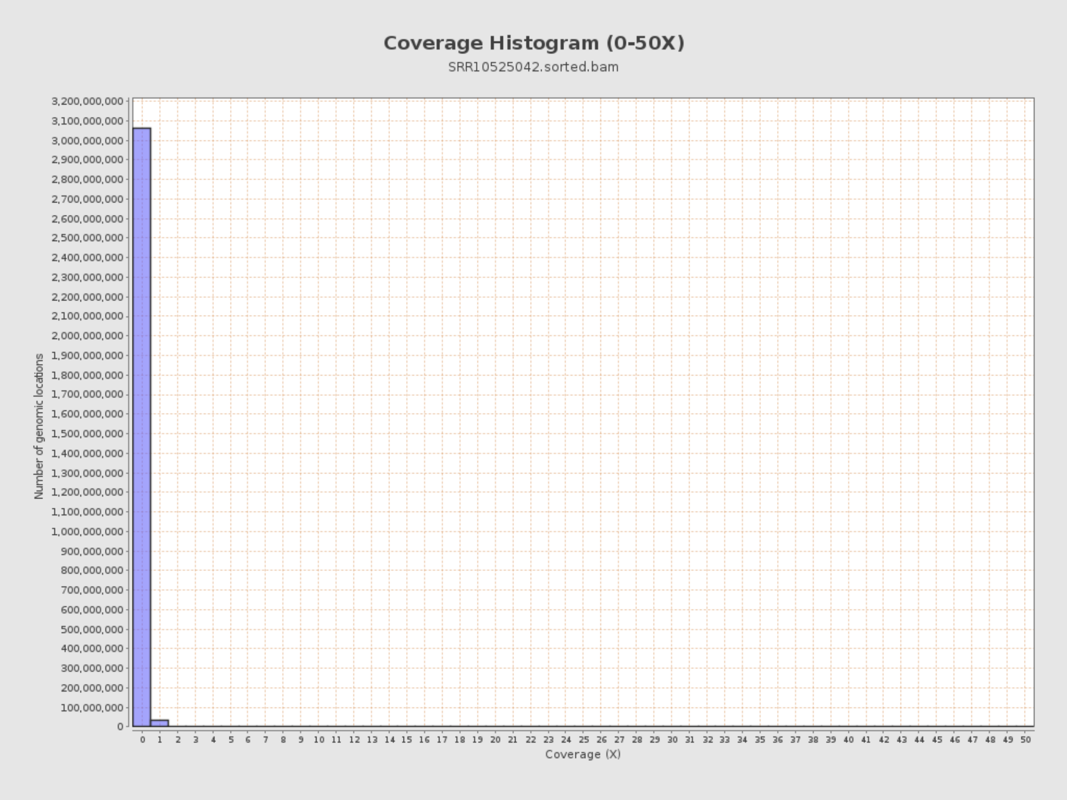
3. Results : Coverage across reference



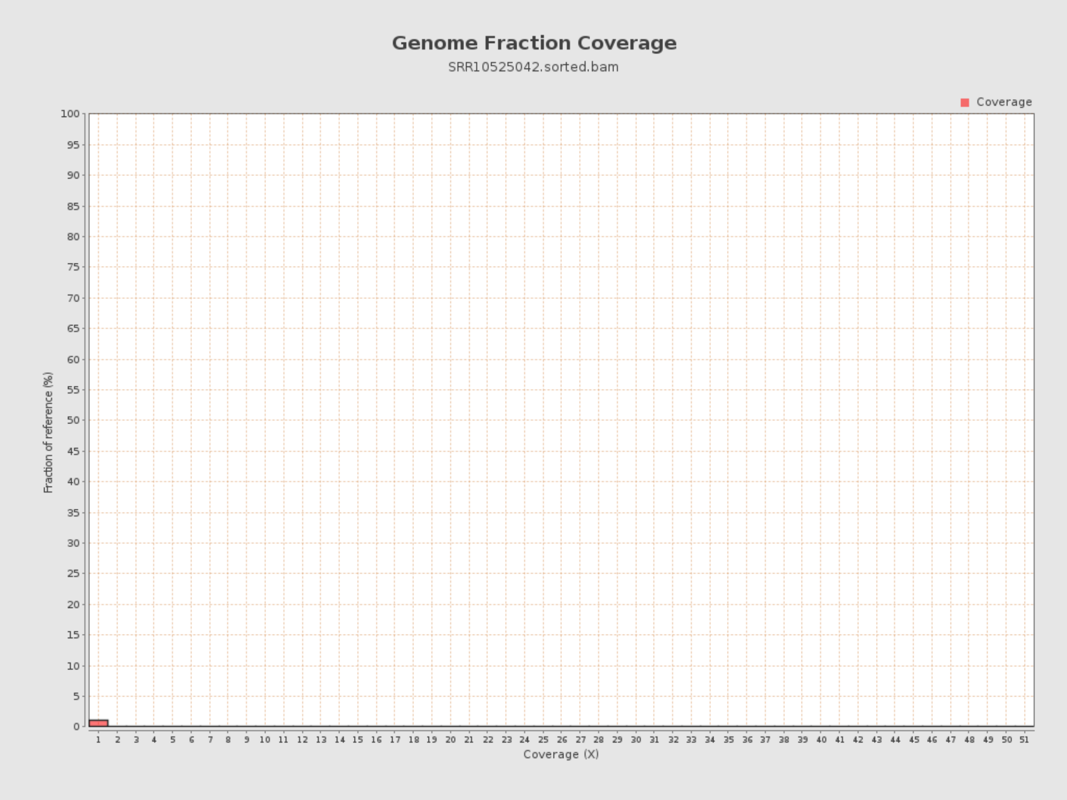
4. Results : Coverage Histogram



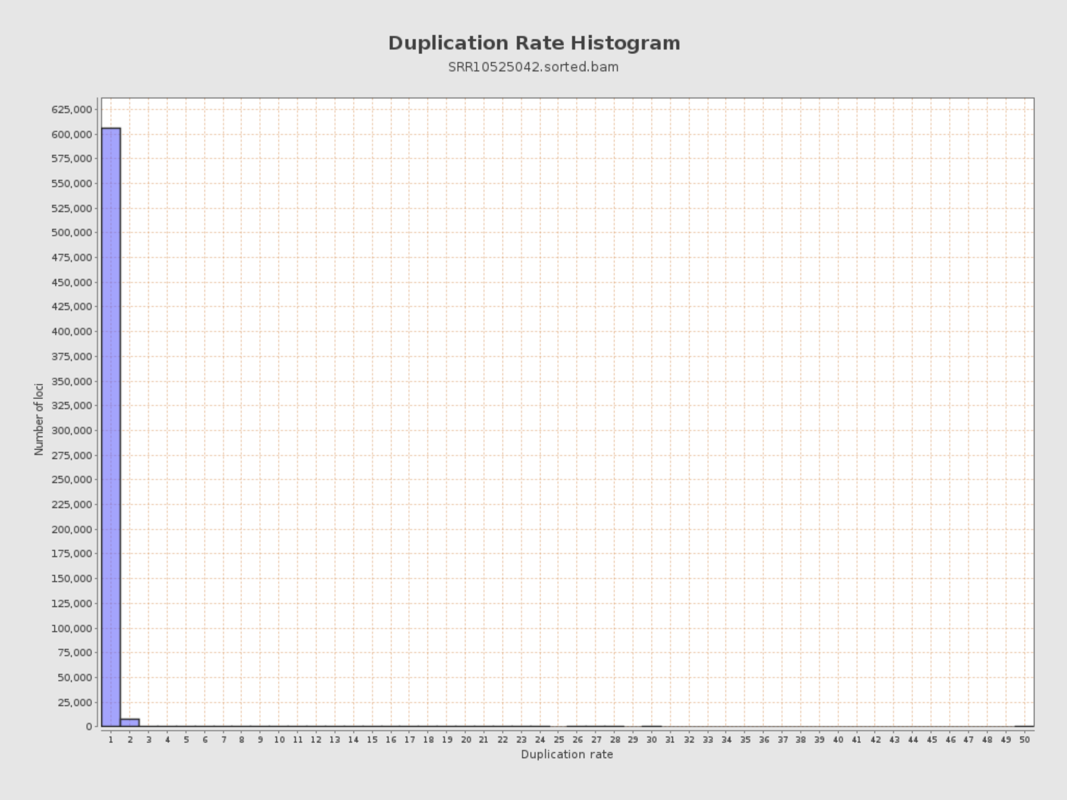
5. Results : Coverage Histogram (0-50X)



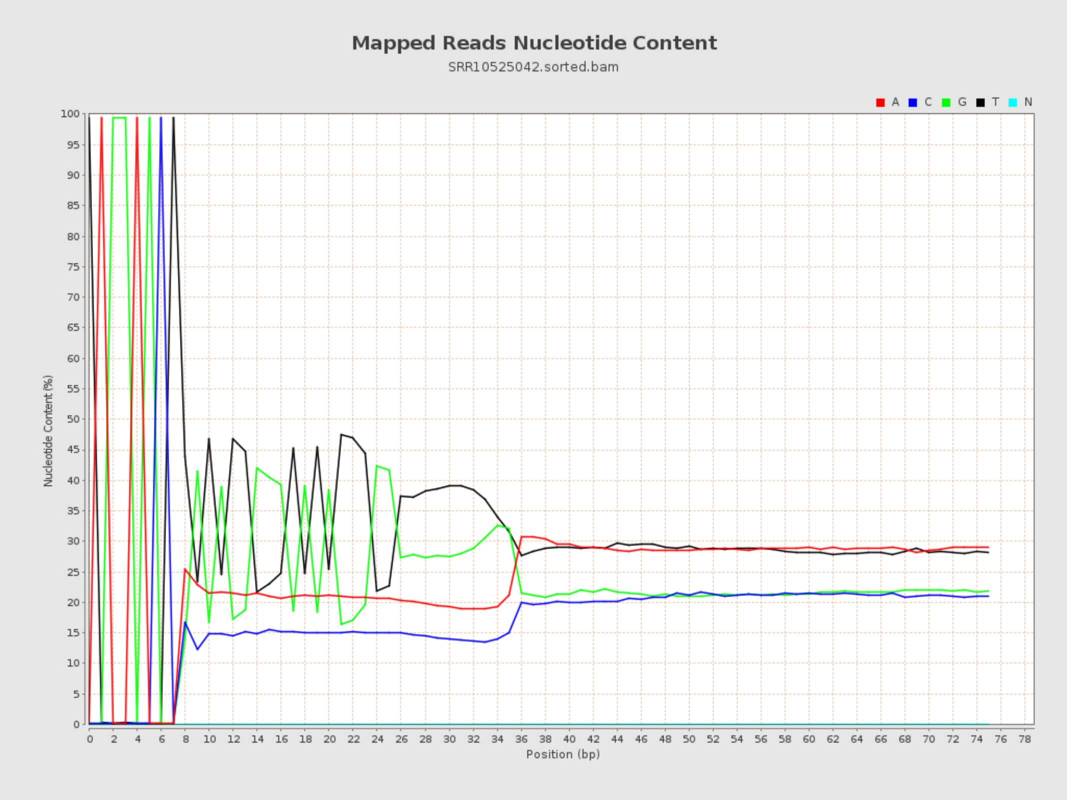
6. Results : Genome Fraction Coverage



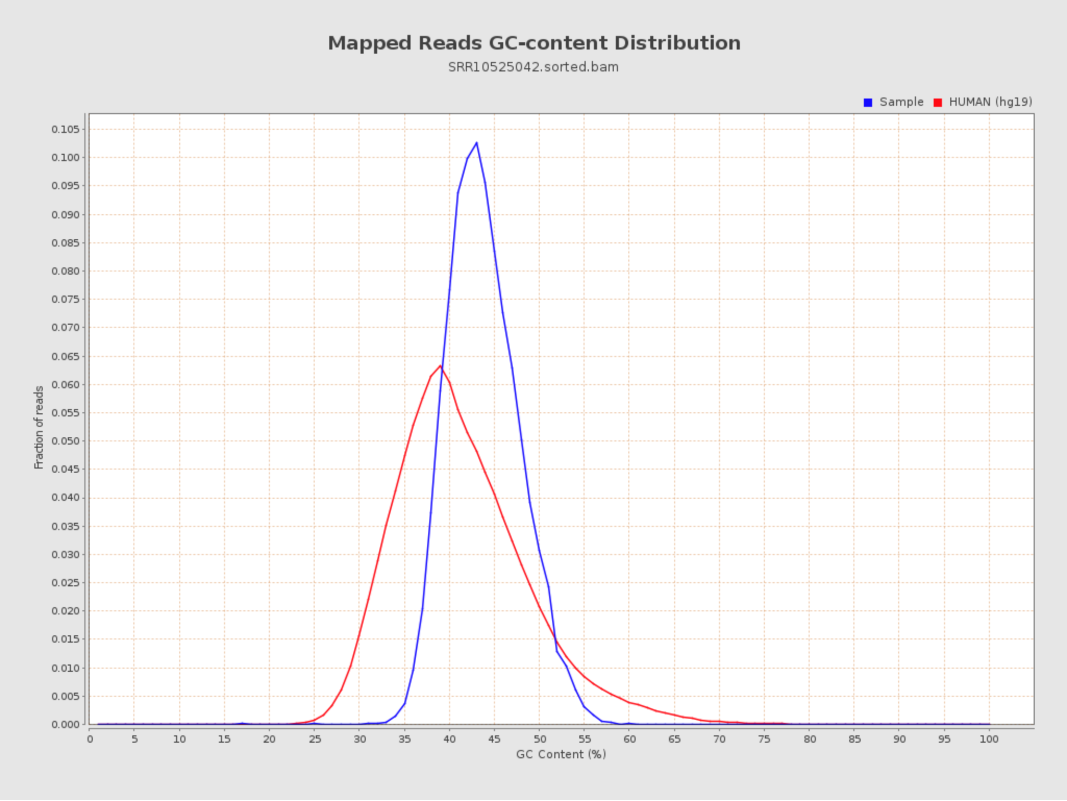
7. Results : Duplication Rate Histogram



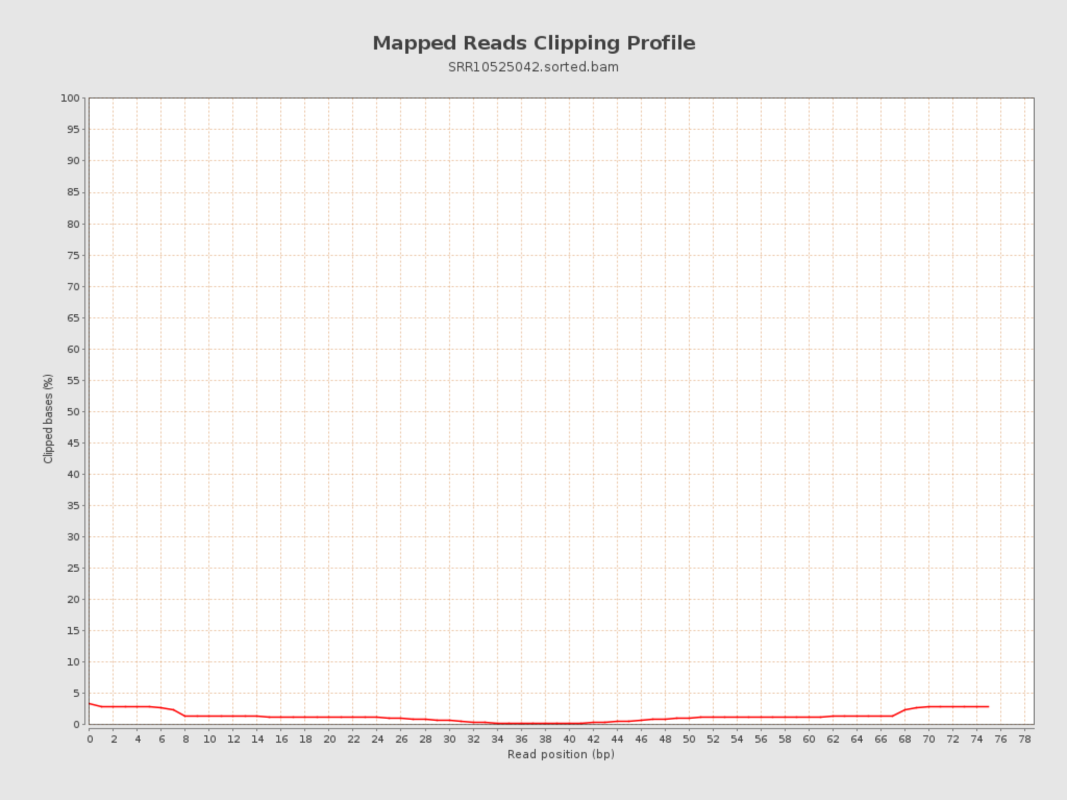
8. Results : Mapped Reads Nucleotide Content



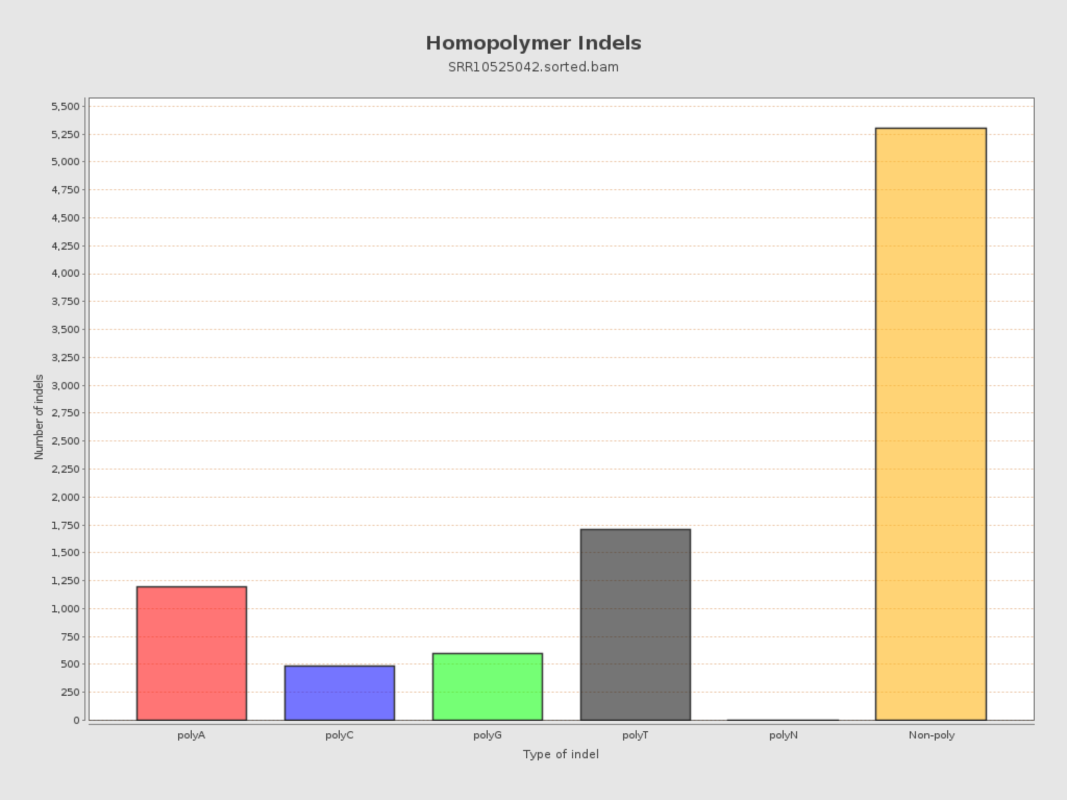
9. Results : Mapped Reads GC-content Distribution



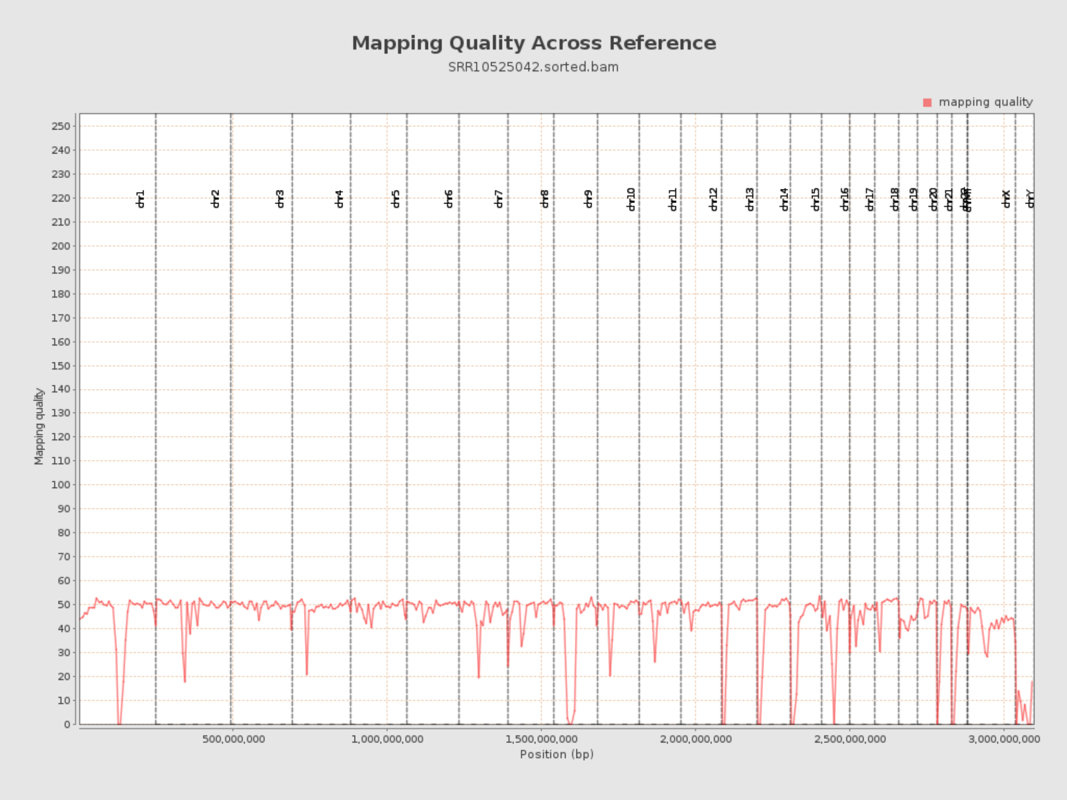
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram