Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:23:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525076.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_SRR10525076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:23:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	760,766
Mapped reads	705,078 / 92.68%
Unmapped reads	55,688 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,411 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,545 / 3.23%
Duplication rate	2.91%
Clipped reads	706,662 / 92.89%

2.2. ACGT Content

Number/percentage of A's	9,958,350 / 24.13%
Number/percentage of C's	7,366,181 / 17.85%
Number/percentage of T's	13,587,700 / 32.92%
Number/percentage of G's	10,359,836 / 25.1%
Number/percentage of N's	4,558 / 0.01%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1481

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

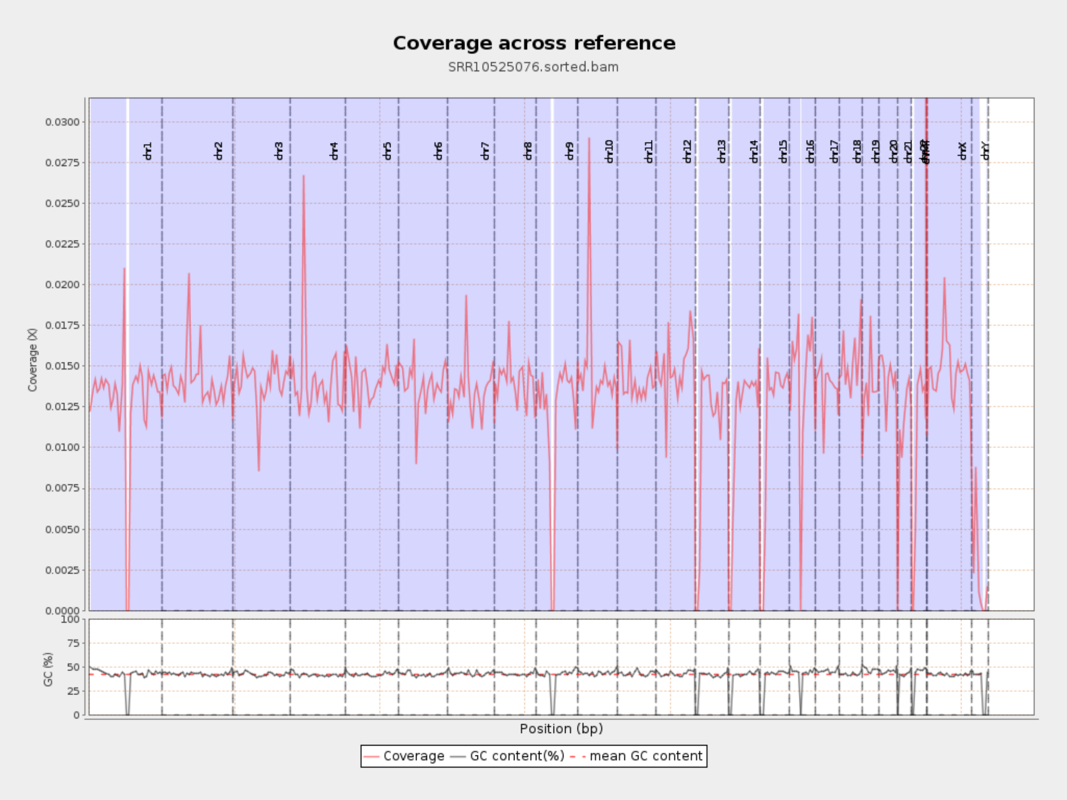
General error rate	0.48%
Mismatches	192,441
Insertions	2,440
Mapped reads with at least one insertion	0.34%
Deletions	7,869
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.96%

2.6. Chromosome stats

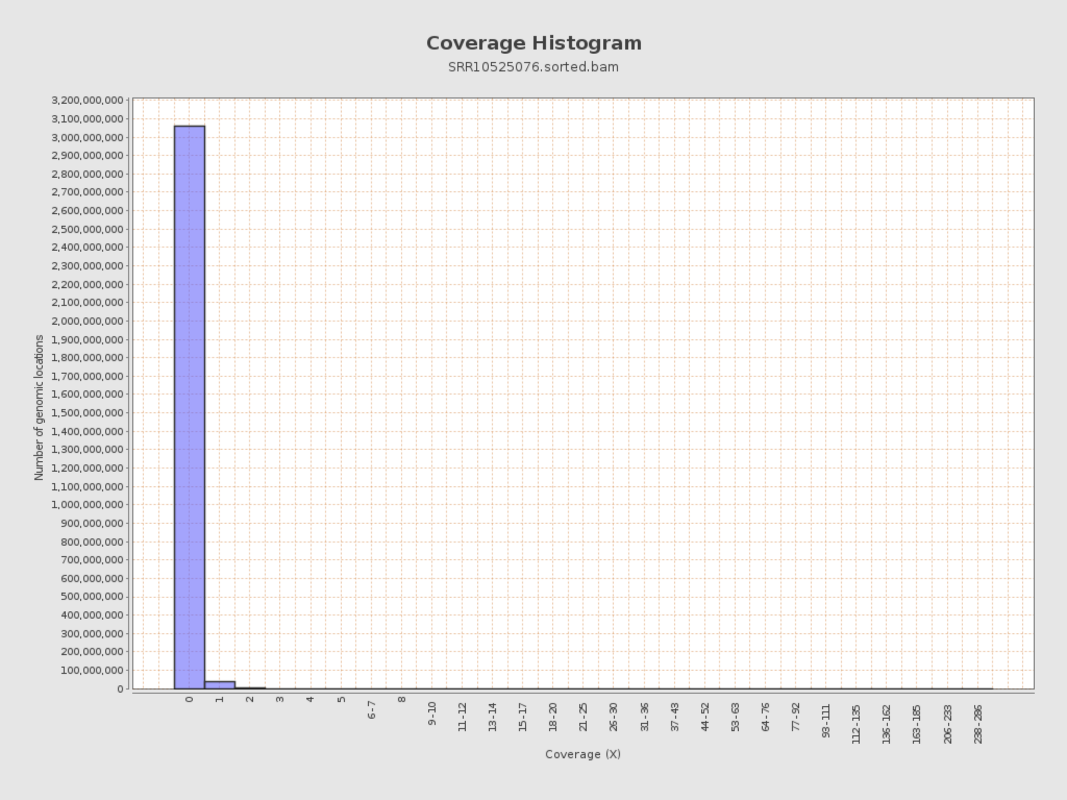
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3211277	0.0129	0.2212
chr2	243199373	3467092	0.0143	0.1745
chr3	198022430	2773138	0.014	0.1259
chr4	191154276	2691984	0.0141	0.1362
chr5	180915260	2562945	0.0142	0.1261
chr6	171115067	2380662	0.0139	0.131
chr7	159138663	2151383	0.0135	0.1609

chr8	146364022	2064062	0.0141	0.1513
chr9	141213431	1676286	0.0119	0.1294
chr10	135534747	1995795	0.0147	0.1701
chr11	135006516	1891614	0.014	0.1388
chr12	133851895	1992255	0.0149	0.1307
chr13	115169878	1287171	0.0112	0.1123
chr14	107349540	1212569	0.0113	0.1141
chr15	102531392	1177196	0.0115	0.1138
chr16	90354753	1280653	0.0142	0.1308
chr17	81195210	1117056	0.0138	0.1287
chr18	78077248	1189978	0.0152	0.188
chr19	59128983	813439	0.0138	0.1733
chr20	63025520	896726	0.0142	0.1289
chr21	48129895	526142	0.0109	0.1189
chr22	51304566	493992	0.0096	0.1045
chrMT	16571	10876	0.6563	0.8776
chrX	155270560	2290768	0.0148	0.1351
chrY	59373566	134391	0.0023	0.0846

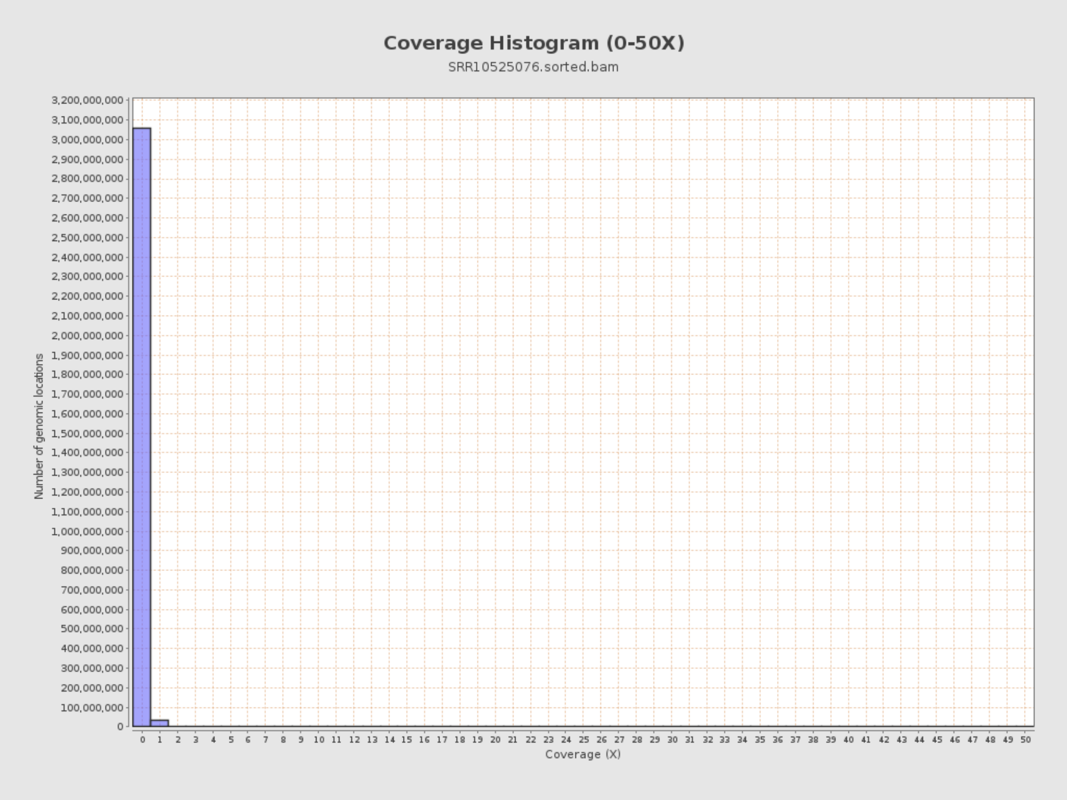
3. Results : Coverage across reference



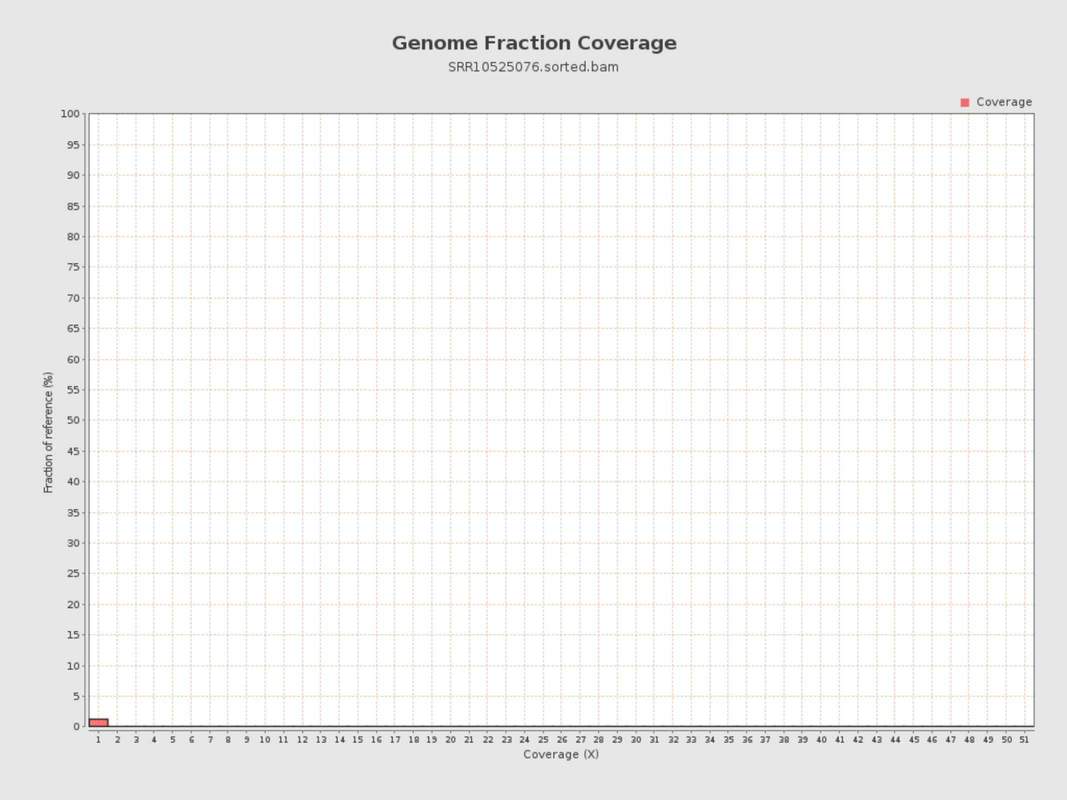
4. Results : Coverage Histogram



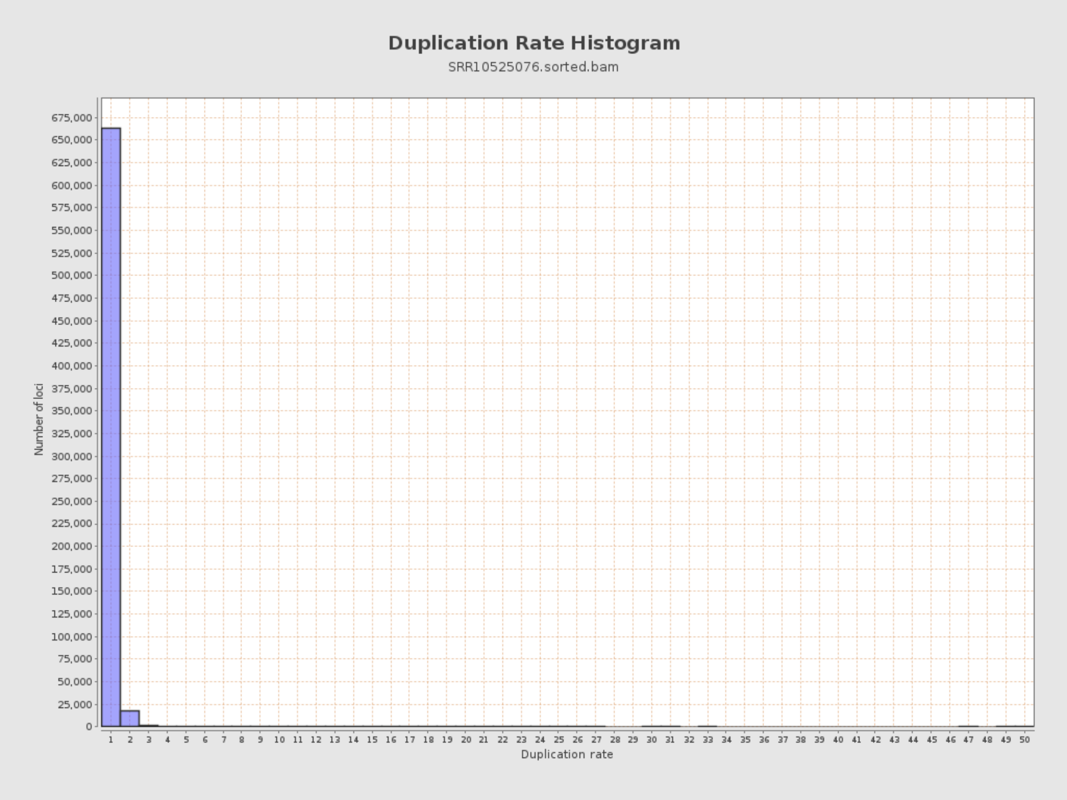
5. Results : Coverage Histogram (0-50X)



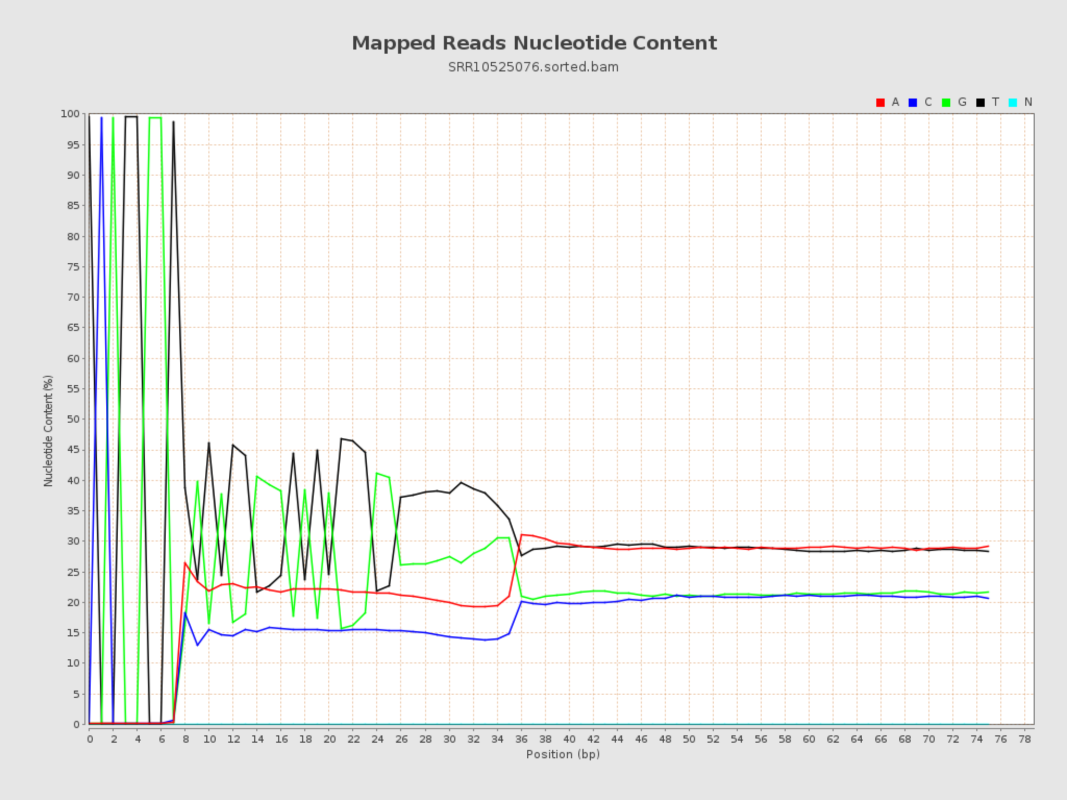
6. Results : Genome Fraction Coverage



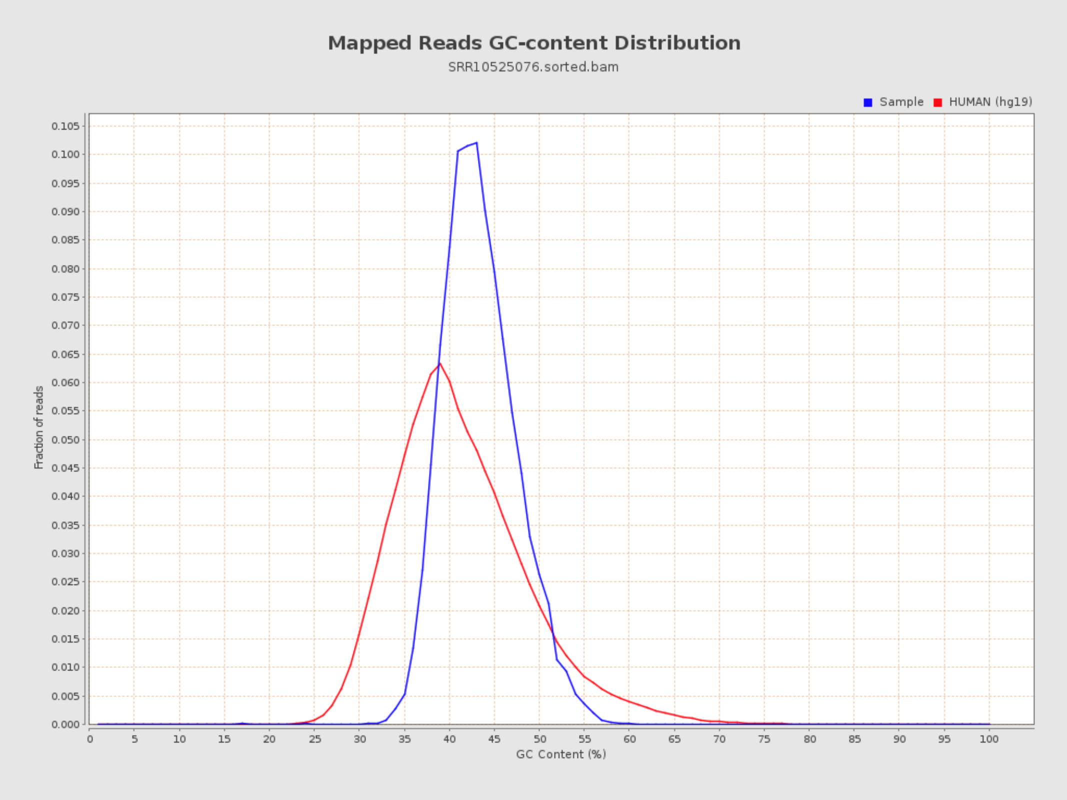
7. Results : Duplication Rate Histogram



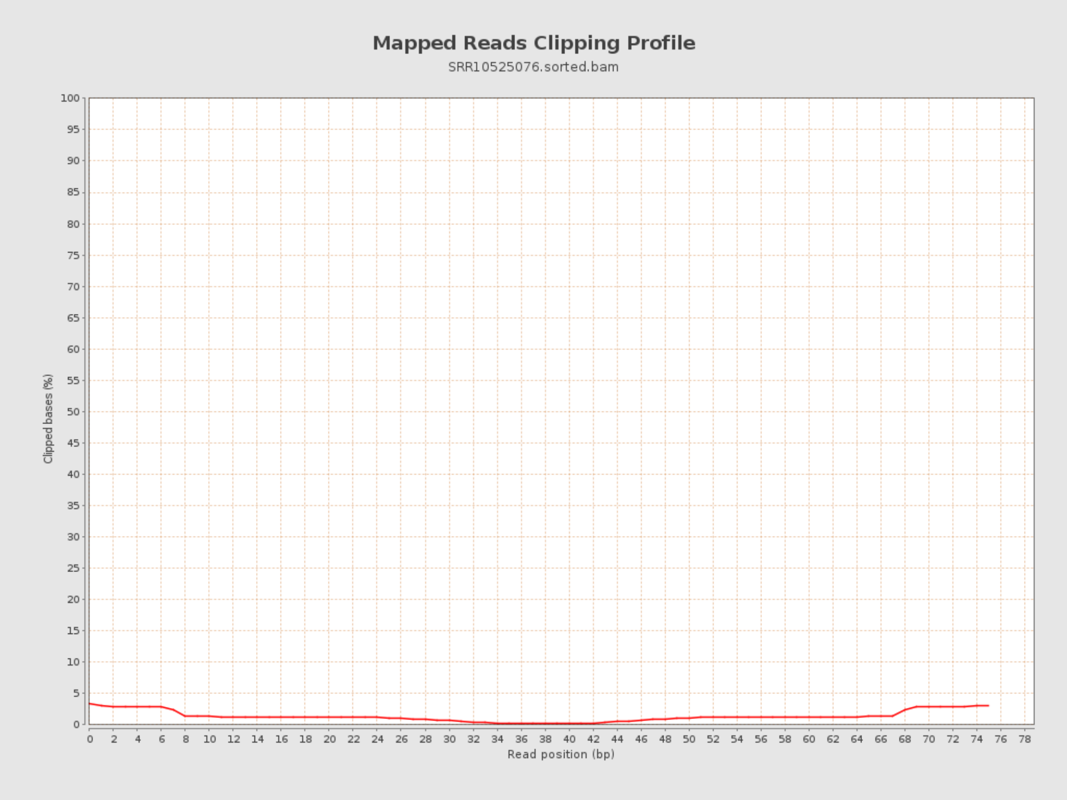
8. Results : Mapped Reads Nucleotide Content



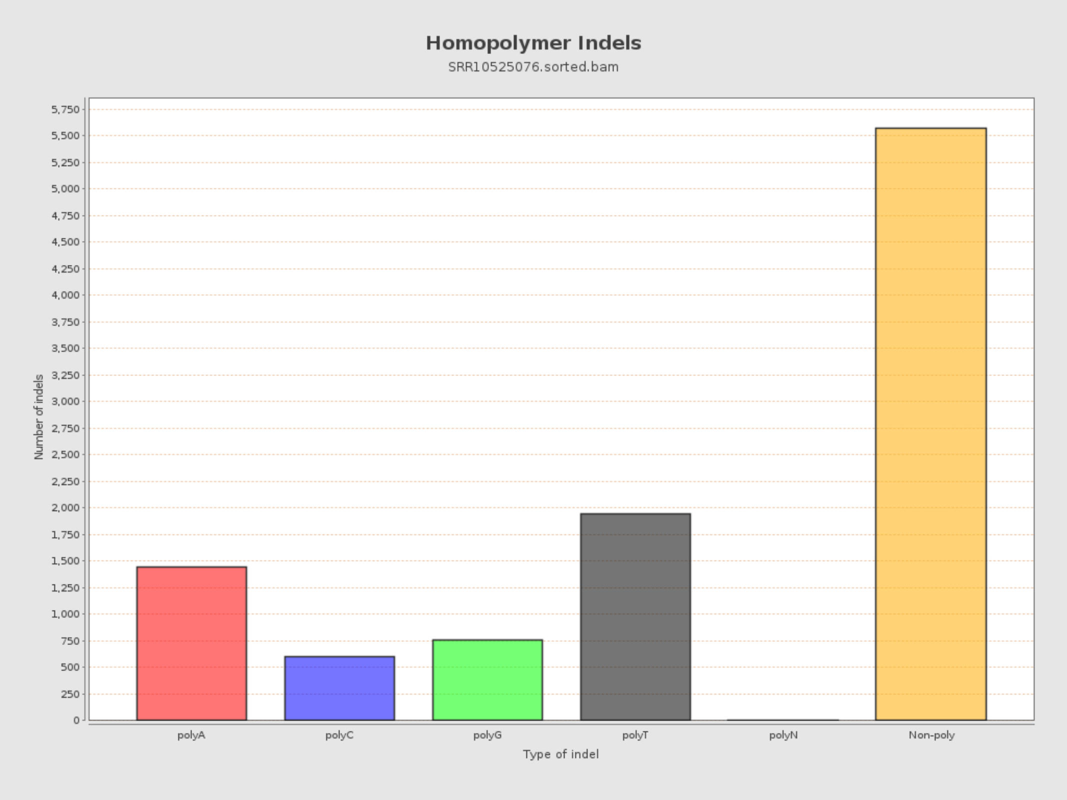
9. Results : Mapped Reads GC-content Distribution



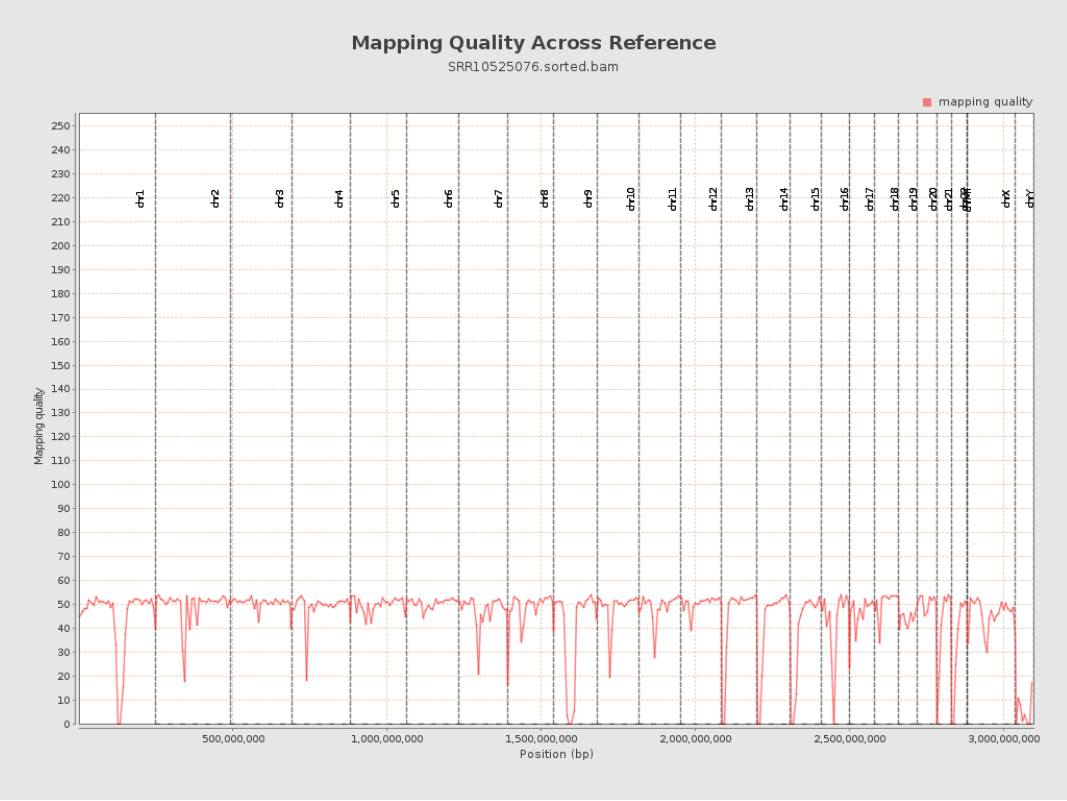
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram