Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:35:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524601.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_SRR10524601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:35:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	991,427
Mapped reads	920,859 / 92.88%
Unmapped reads	70,568 / 7.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,944 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	30,525 / 3.08%
Duplication rate	2.57%
Clipped reads	921,797 / 92.98%

2.2. ACGT Content

Number/percentage of A's	13,190,973 / 24.68%
Number/percentage of C's	9,828,103 / 18.39%
Number/percentage of T's	17,283,875 / 32.34%
Number/percentage of G's	13,141,638 / 24.59%
Number/percentage of N's	350 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1785

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

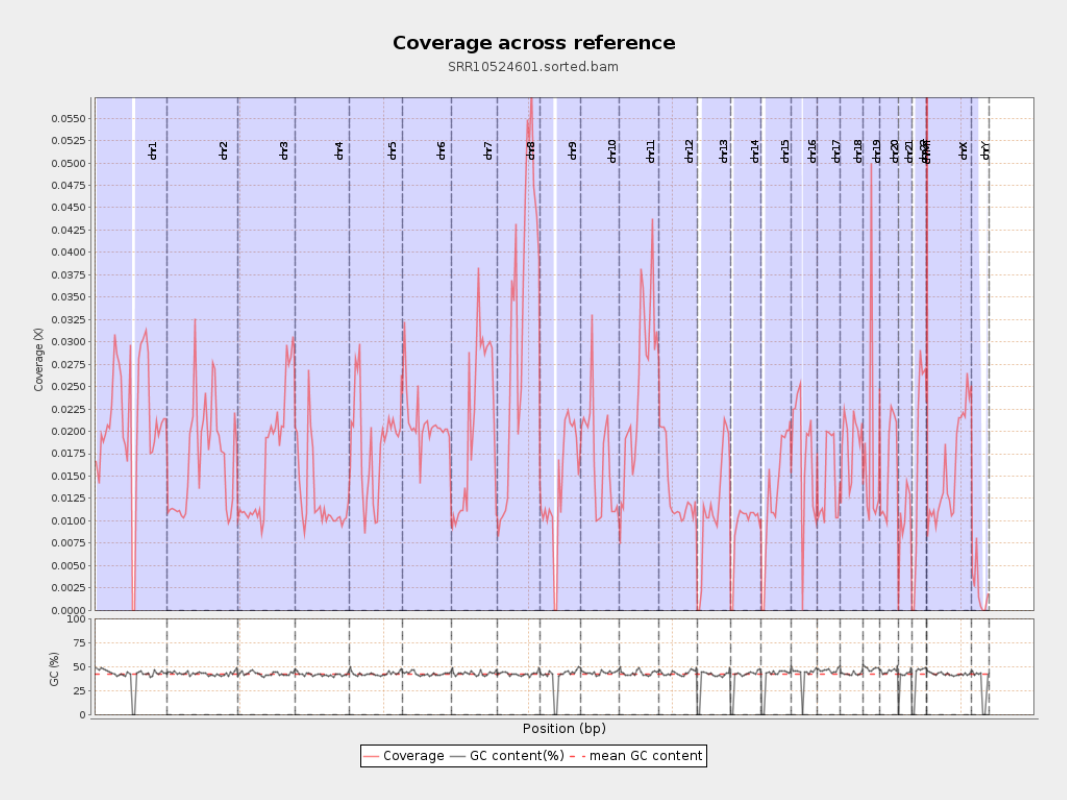
General error rate	0.47%
Mismatches	247,575
Insertions	2,912
Mapped reads with at least one insertion	0.32%
Deletions	9,375
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.87%

2.6. Chromosome stats

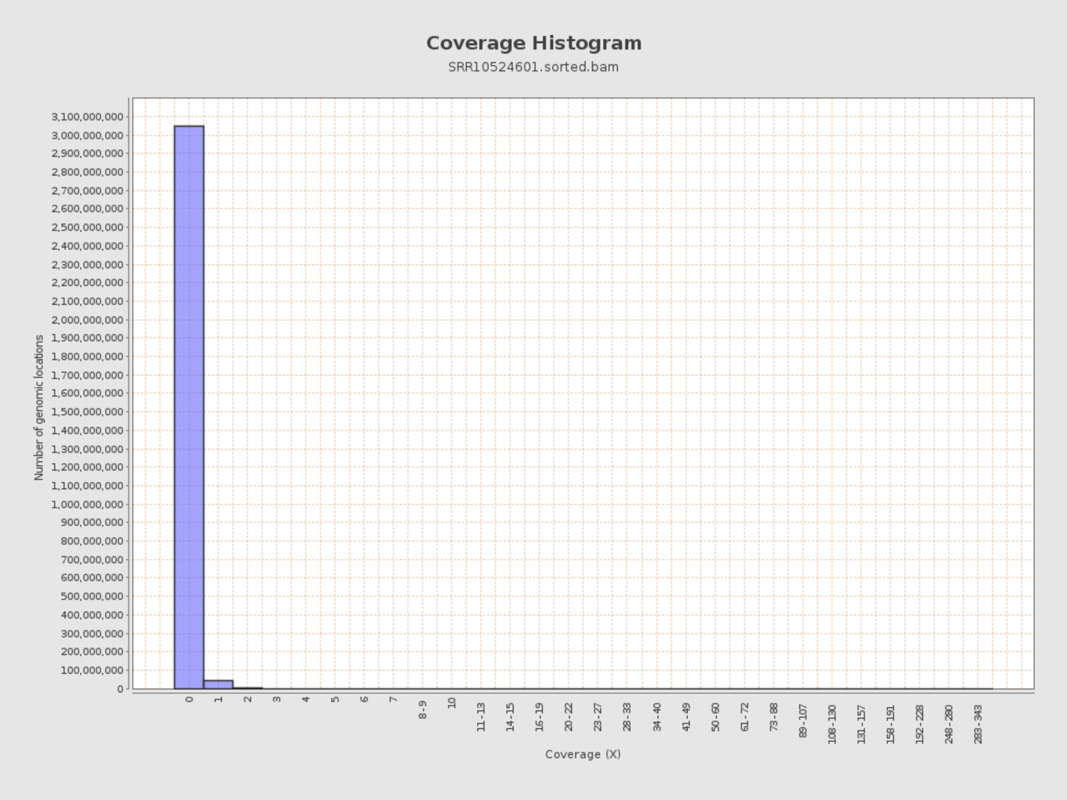
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5255322	0.0211	0.2834
chr2	243199373	4101890	0.0169	0.1977
chr3	198022430	3362973	0.017	0.1394
chr4	191154276	2432765	0.0127	0.1356
chr5	180915260	3399324	0.0188	0.1468
chr6	171115067	3571155	0.0209	0.1626
chr7	159138663	3307989	0.0208	0.2314

chr8	146364022	4721924	0.0323	0.2294
chr9	141213431	1964797	0.0139	0.1658
chr10	135534747	2311742	0.0171	0.1811
chr11	135006516	3374137	0.025	0.1925
chr12	133851895	1787214	0.0134	0.127
chr13	115169878	1336429	0.0116	0.118
chr14	107349540	979435	0.0091	0.1052
chr15	102531392	1329959	0.013	0.1259
chr16	90354753	1566076	0.0173	0.1478
chr17	81195210	1158045	0.0143	0.1292
chr18	78077248	1462304	0.0187	0.2356
chr19	59128983	1057970	0.0179	0.2148
chr20	63025520	1012014	0.0161	0.1386
chr21	48129895	478562	0.0099	0.1158
chr22	51304566	909503	0.0177	0.1429
chrMT	16571	3767	0.2273	0.5056
chrX	155270560	2442073	0.0157	0.1489
chrY	59373566	133582	0.0022	0.0741

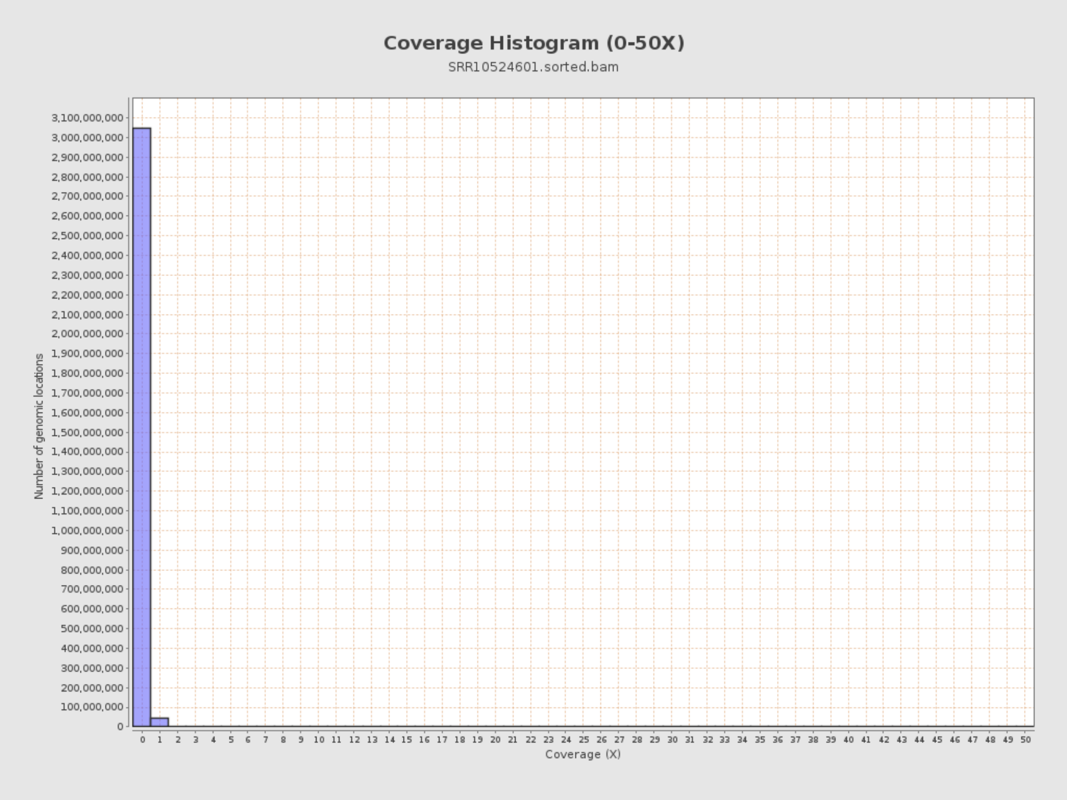
3. Results : Coverage across reference



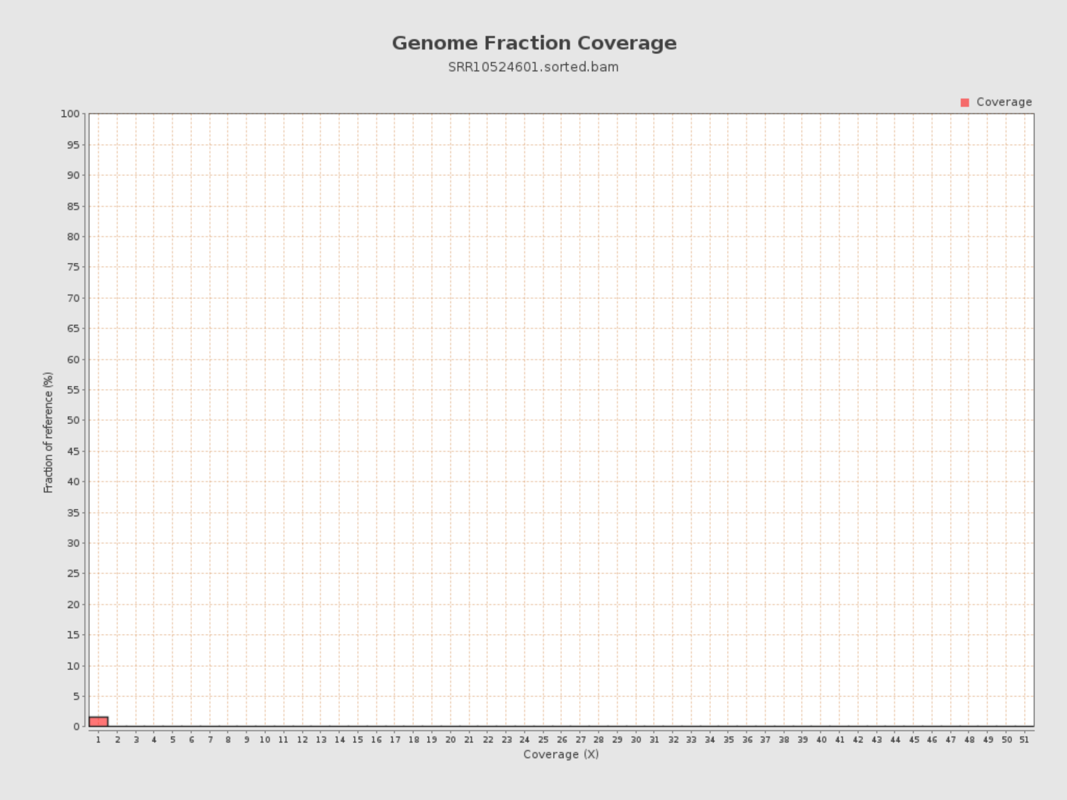
4. Results : Coverage Histogram



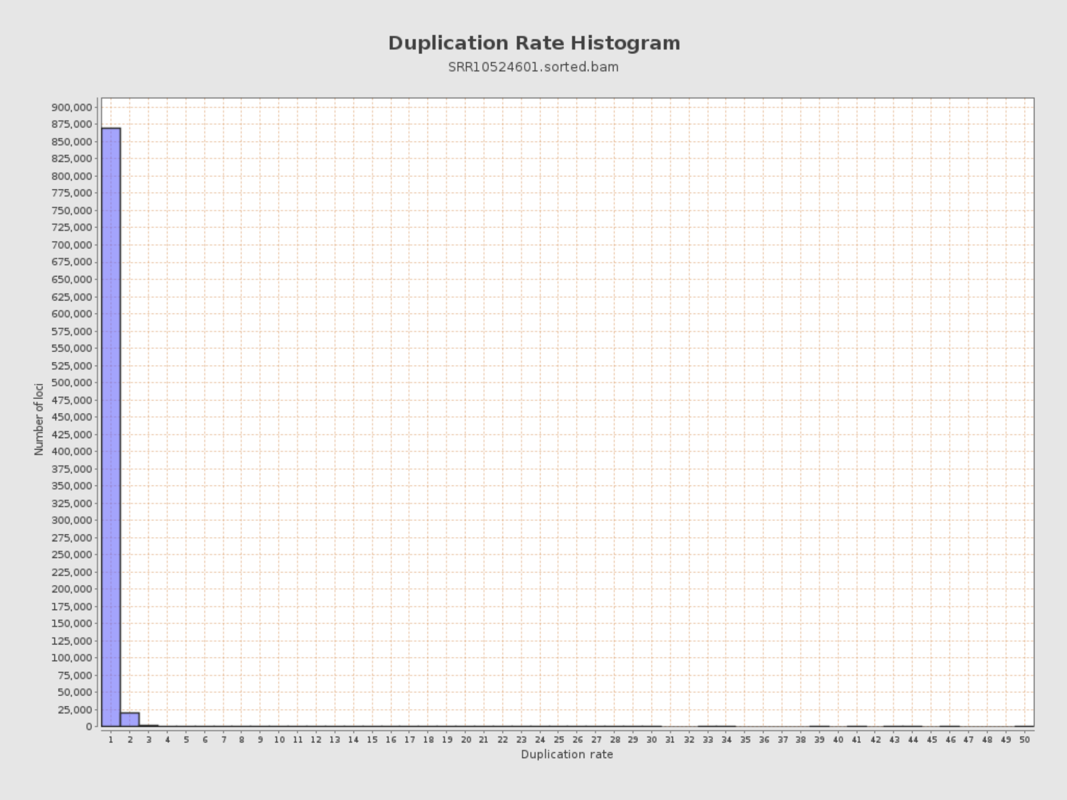
5. Results : Coverage Histogram (0-50X)



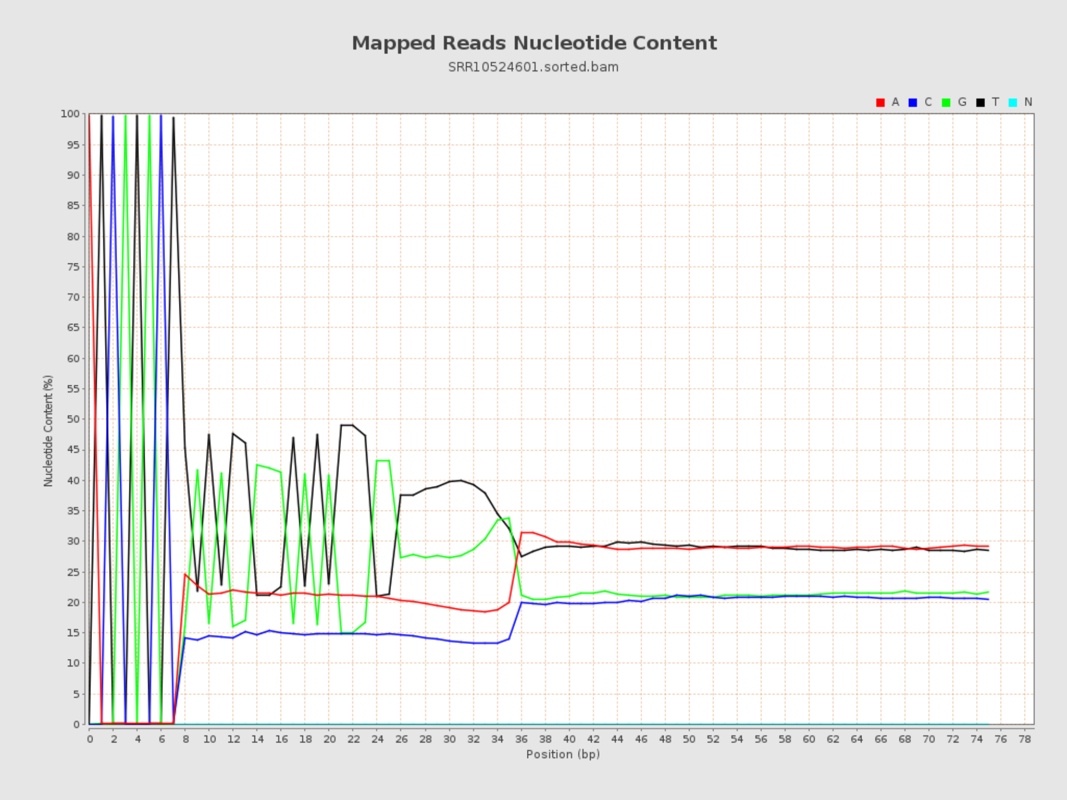
6. Results : Genome Fraction Coverage



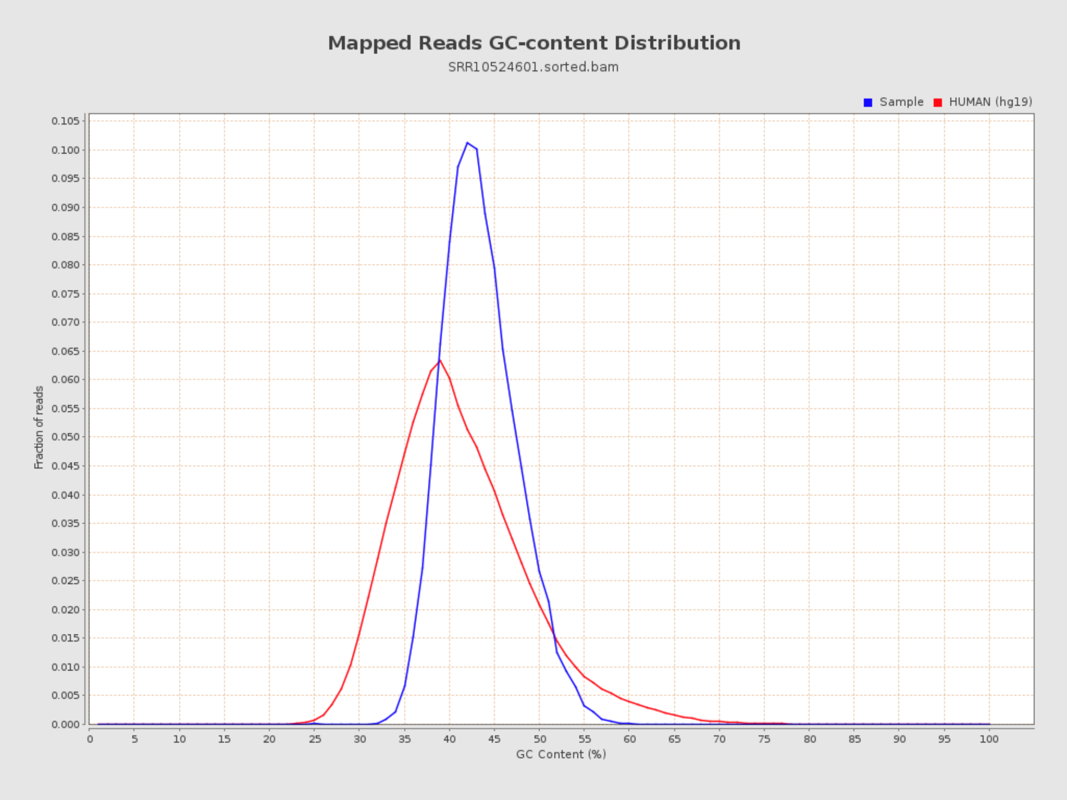
7. Results : Duplication Rate Histogram



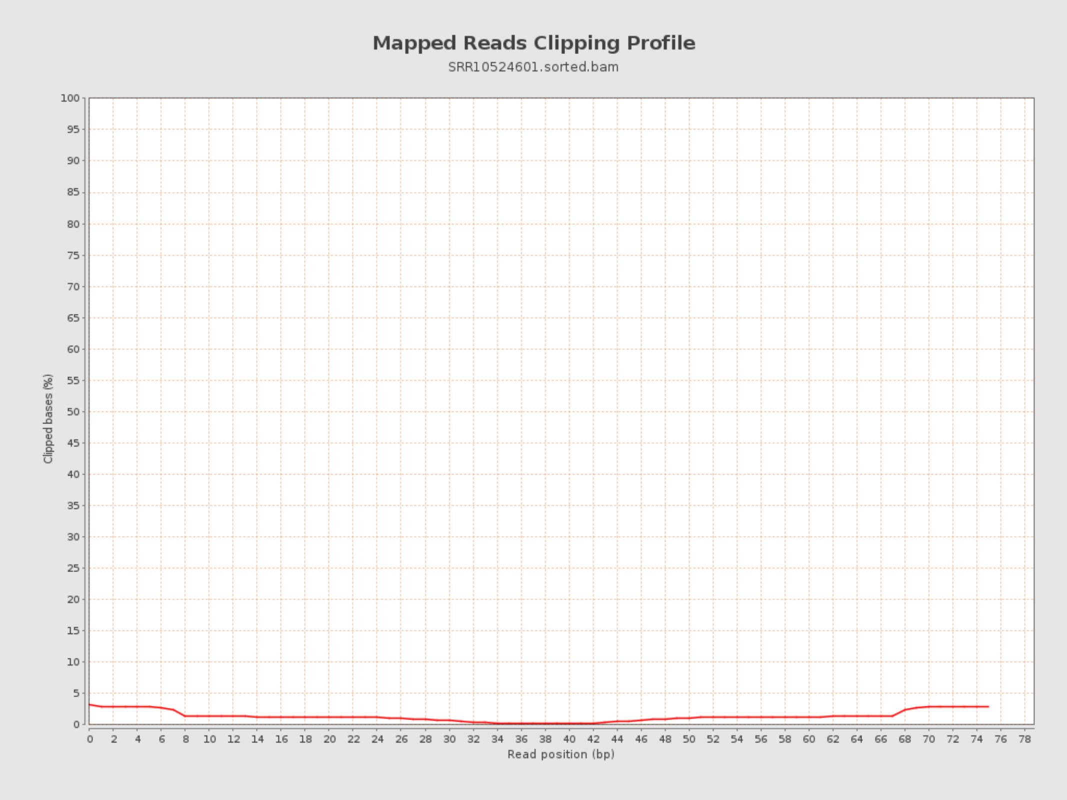
8. Results : Mapped Reads Nucleotide Content



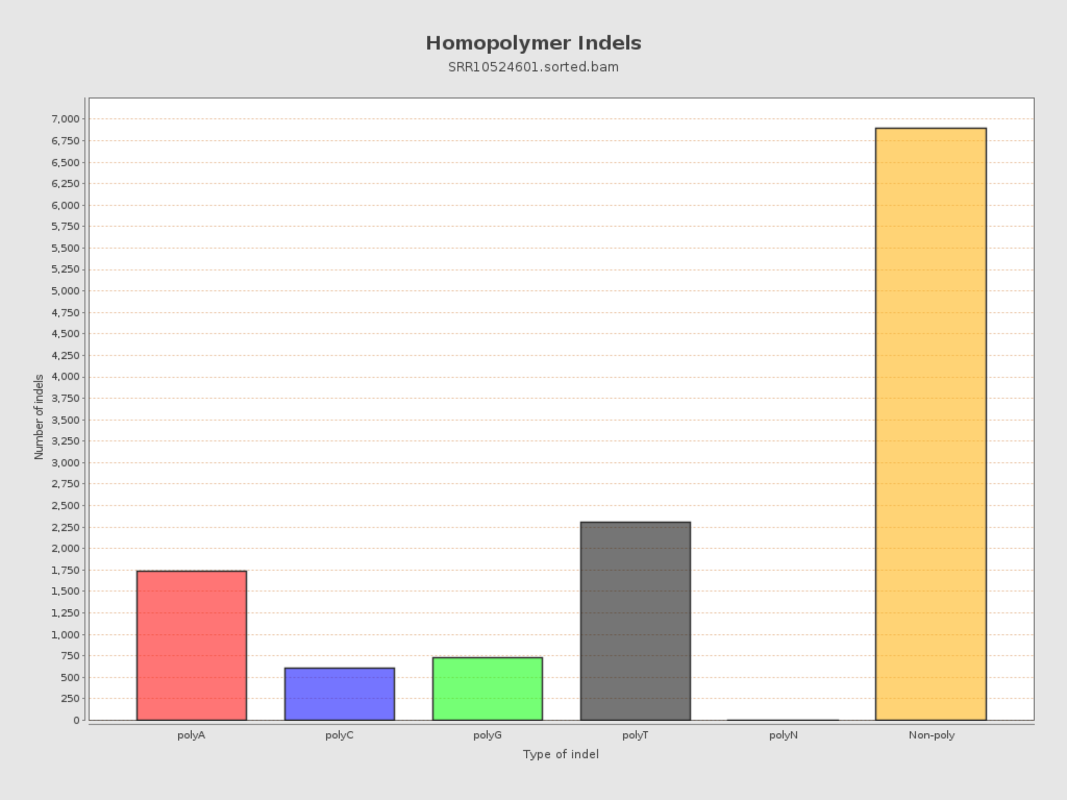
9. Results : Mapped Reads GC-content Distribution



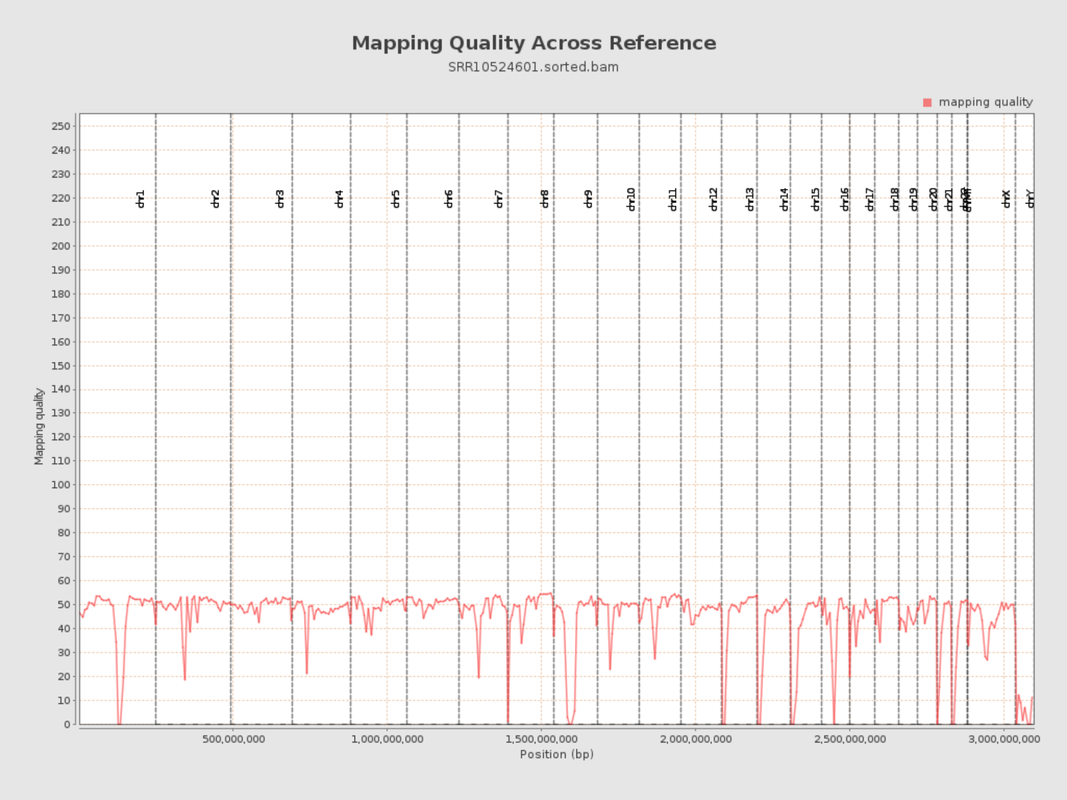
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram