Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:39:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524715.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_SRR10524715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524715.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:39:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,123,513
Mapped reads	1,038,751 / 92.46%
Unmapped reads	84,762 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,668 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	34,345 / 3.06%
Duplication rate	2.4%
Clipped reads	1,041,087 / 92.66%

2.2. ACGT Content

Number/percentage of A's	15,399,550 / 25.22%
Number/percentage of C's	11,918,785 / 19.52%
Number/percentage of T's	19,074,236 / 31.23%
Number/percentage of G's	14,671,361 / 24.02%
Number/percentage of N's	7,879 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2126

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

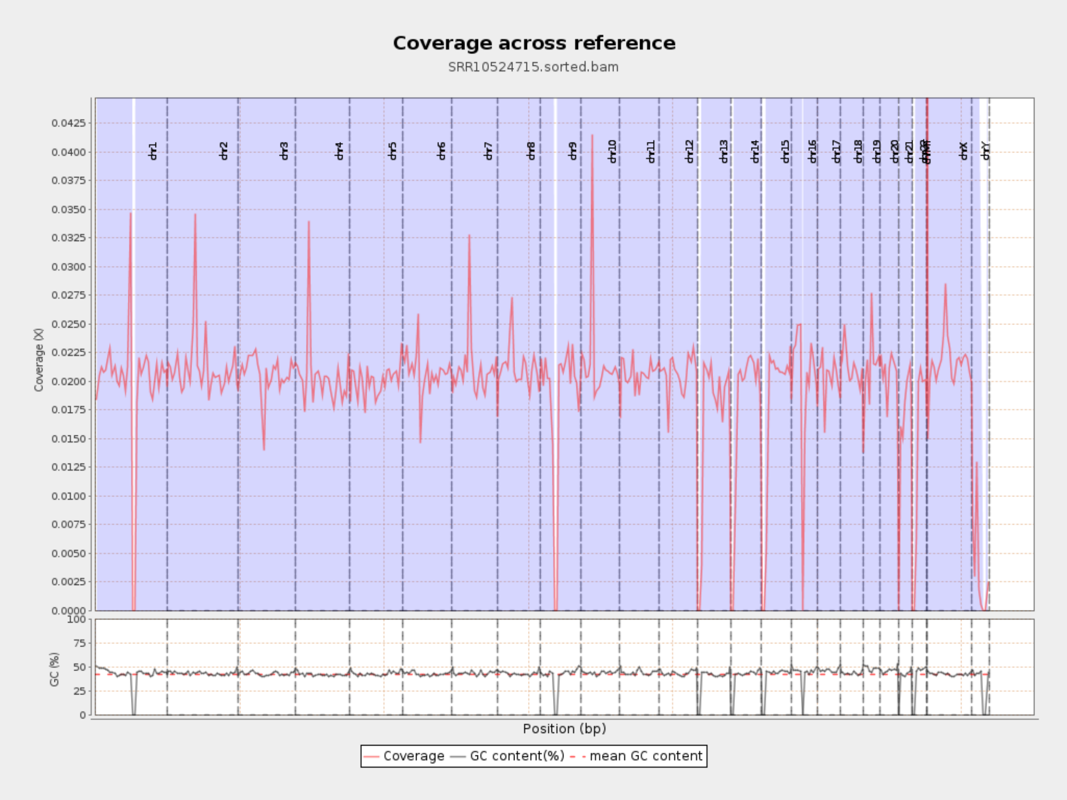
General error rate	0.51%
Mismatches	305,712
Insertions	3,937
Mapped reads with at least one insertion	0.38%
Deletions	11,445
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.19%

2.6. Chromosome stats

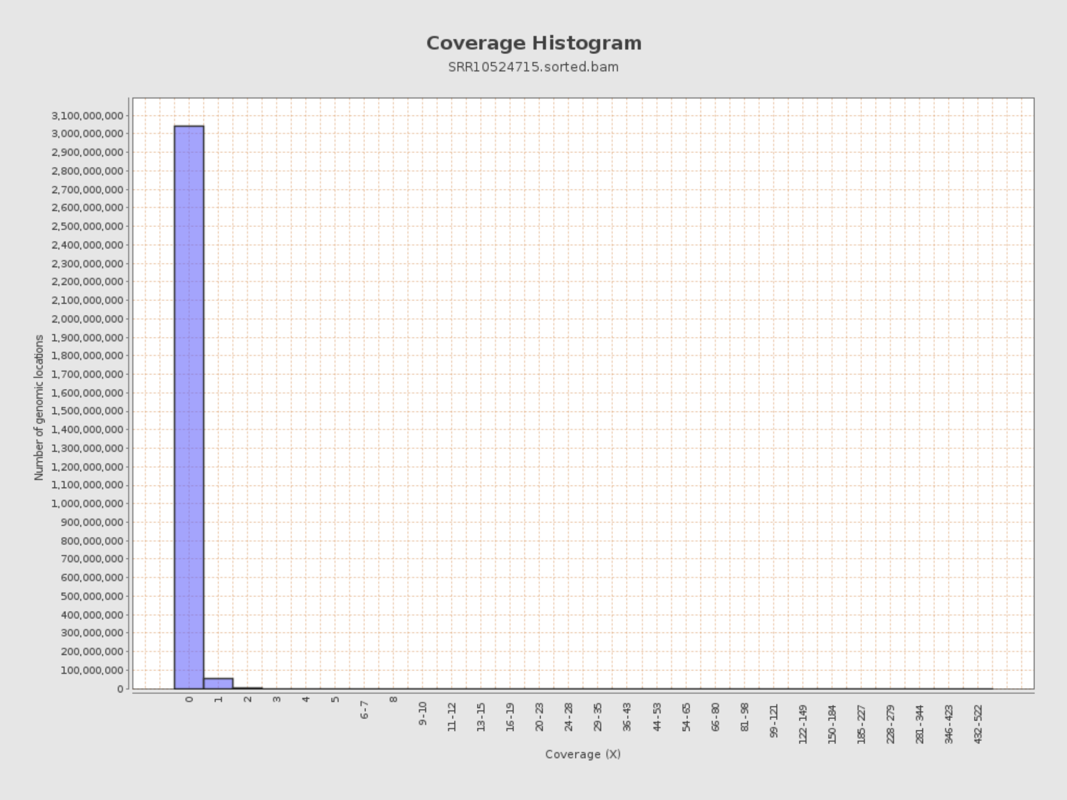
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4931816	0.0198	0.3688
chr2	243199373	5172680	0.0213	0.2778
chr3	198022430	4073031	0.0206	0.1528
chr4	191154276	3910713	0.0205	0.1672
chr5	180915260	3634967	0.0201	0.1514
chr6	171115067	3554991	0.0208	0.1699
chr7	159138663	3365998	0.0212	0.2439

chr8	146364022	3113960	0.0213	0.2302
chr9	141213431	2575925	0.0182	0.1768
chr10	135534747	2959314	0.0218	0.2199
chr11	135006516	2790124	0.0207	0.1842
chr12	133851895	2766046	0.0207	0.1543
chr13	115169878	1893983	0.0164	0.137
chr14	107349540	1854611	0.0173	0.1454
chr15	102531392	1750198	0.0171	0.1384
chr16	90354753	1775121	0.0196	0.1573
chr17	81195210	1657104	0.0204	0.1577
chr18	78077248	1660447	0.0213	0.3107
chr19	59128983	1265148	0.0214	0.2959
chr20	63025520	1297281	0.0206	0.1545
chr21	48129895	796262	0.0165	0.1533
chr22	51304566	711091	0.0139	0.1257
chrMT	16571	4820	0.2909	0.627
chrX	155270560	3372733	0.0217	0.1673
chrY	59373566	201674	0.0034	0.1337

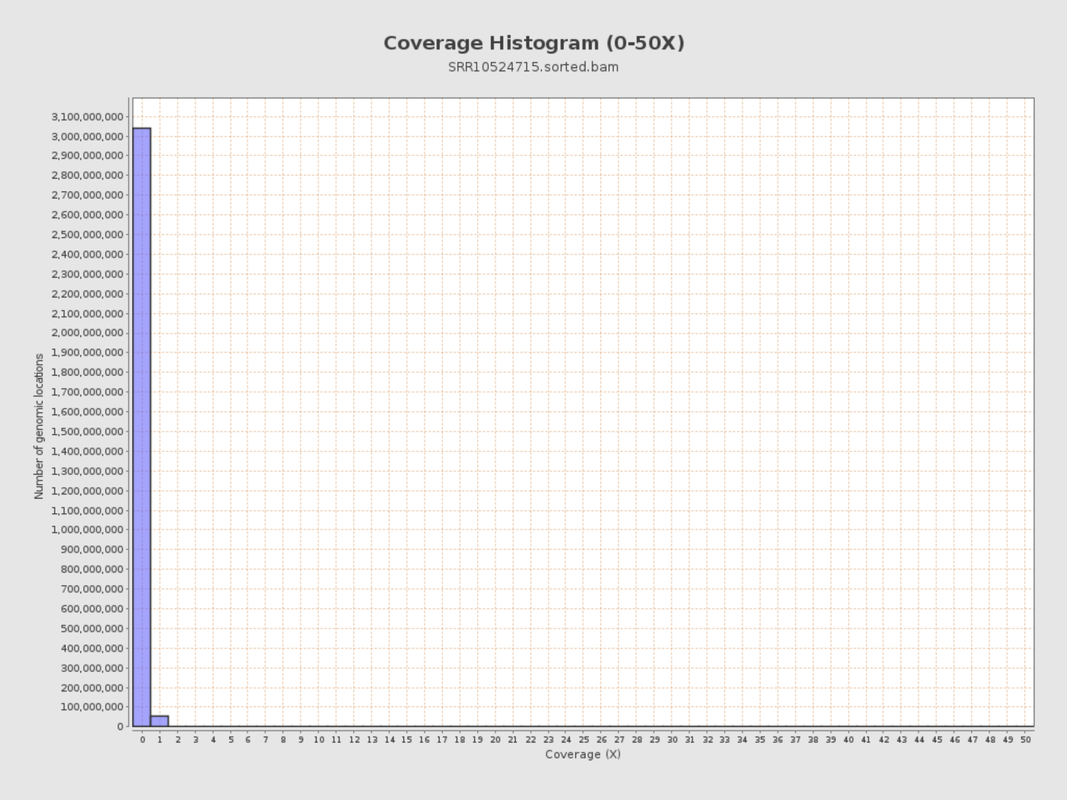
3. Results : Coverage across reference



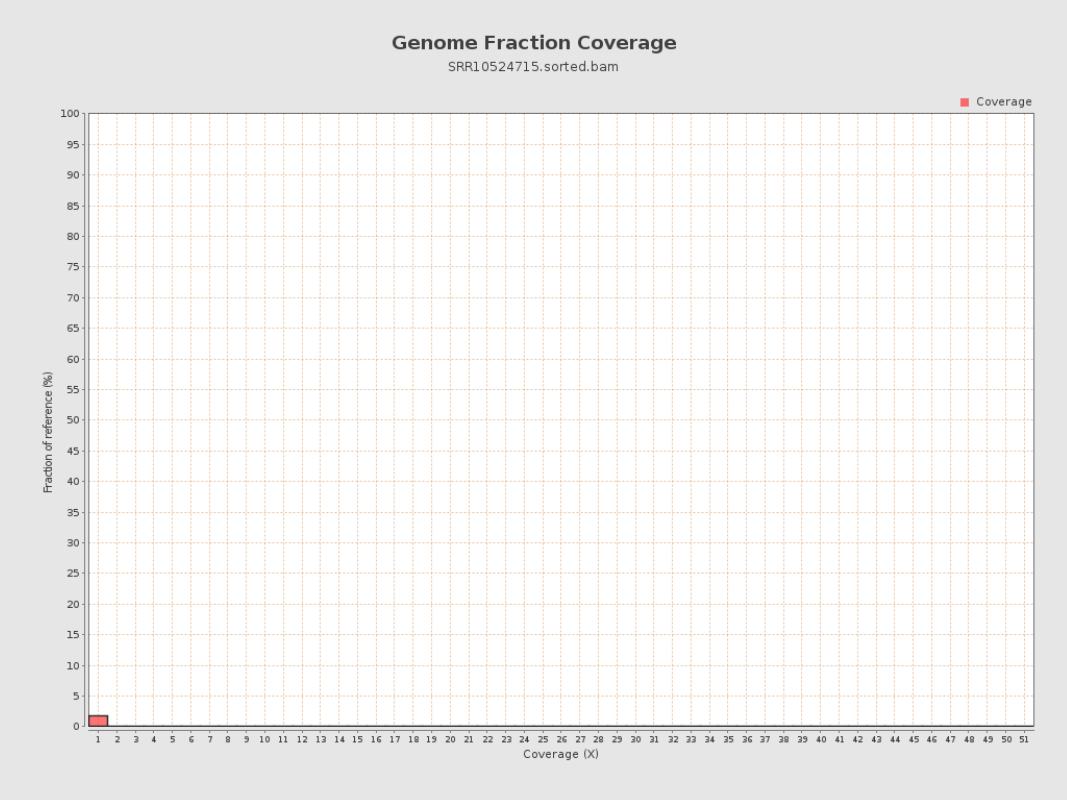
4. Results : Coverage Histogram



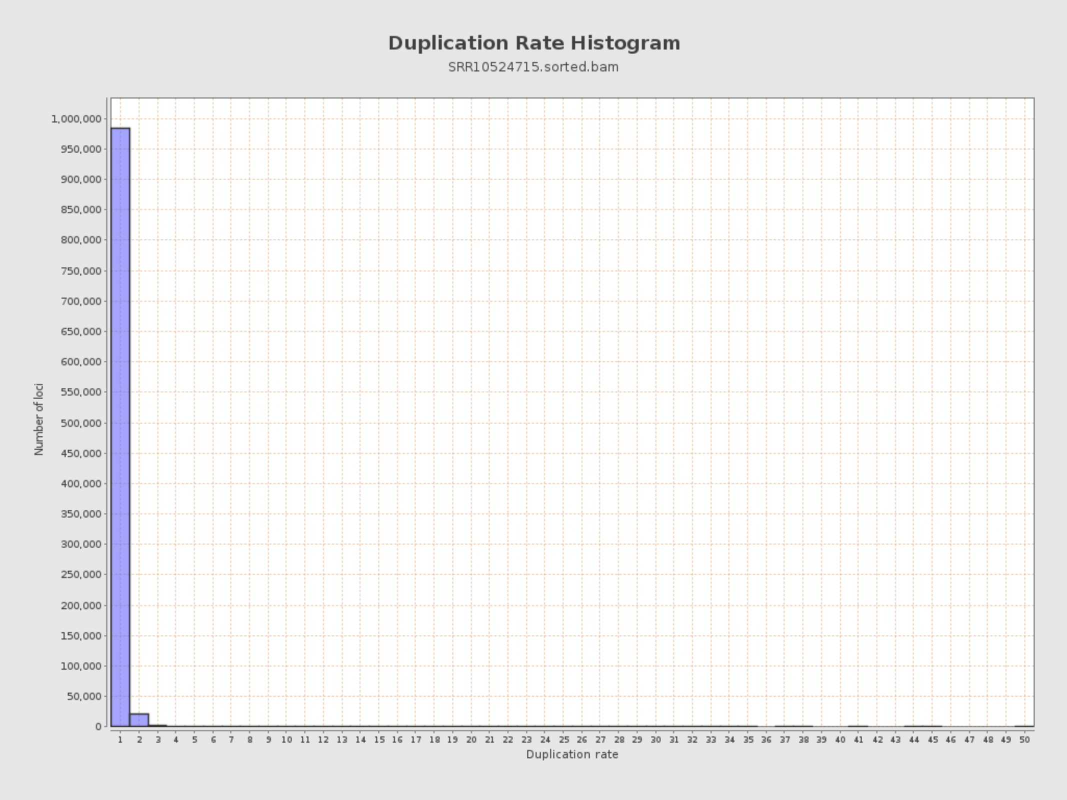
5. Results : Coverage Histogram (0-50X)



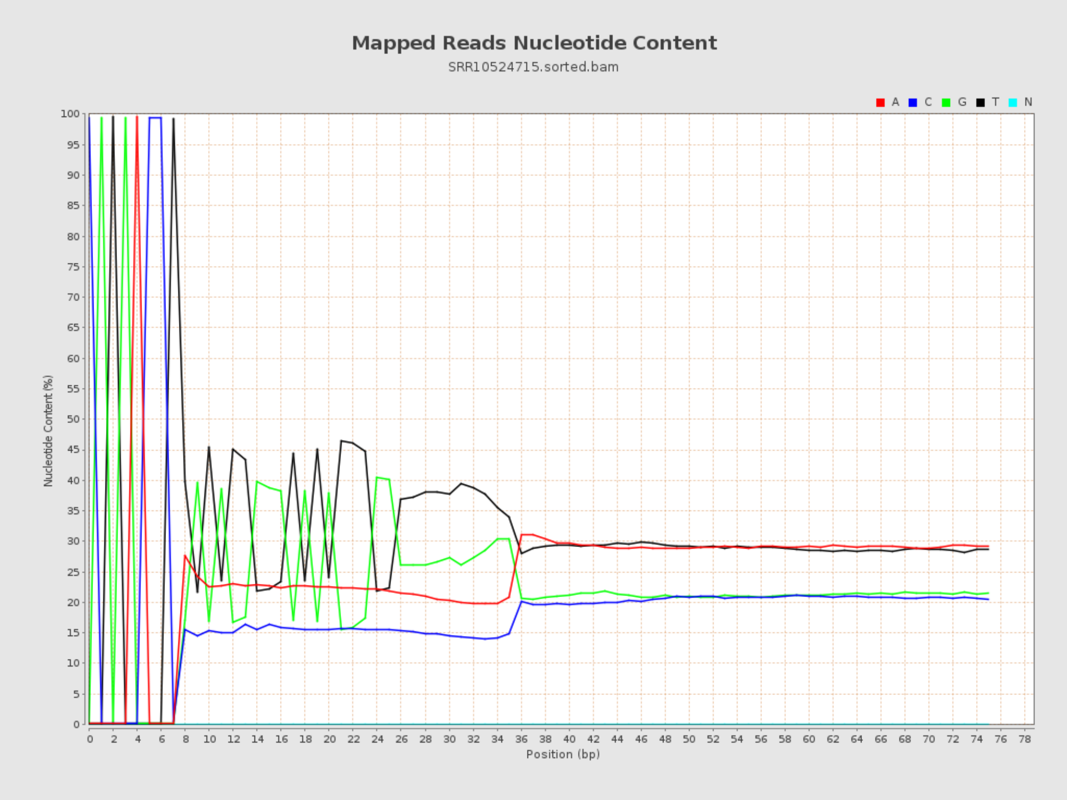
6. Results : Genome Fraction Coverage



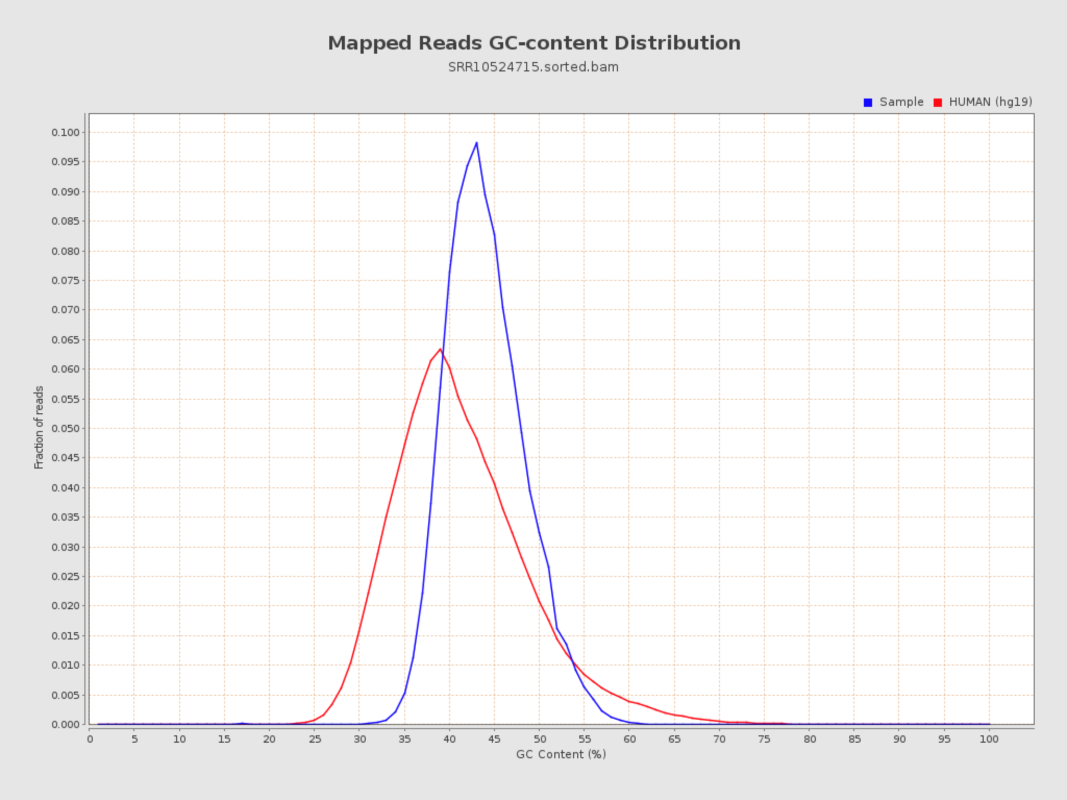
7. Results : Duplication Rate Histogram



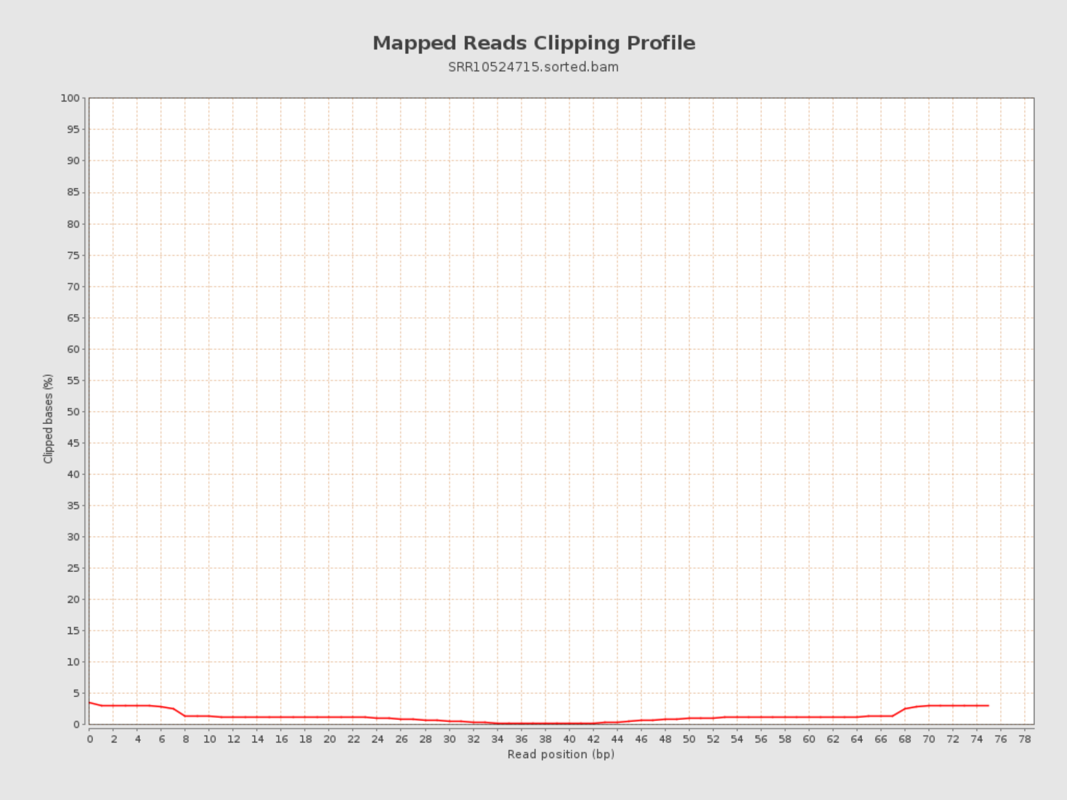
8. Results : Mapped Reads Nucleotide Content



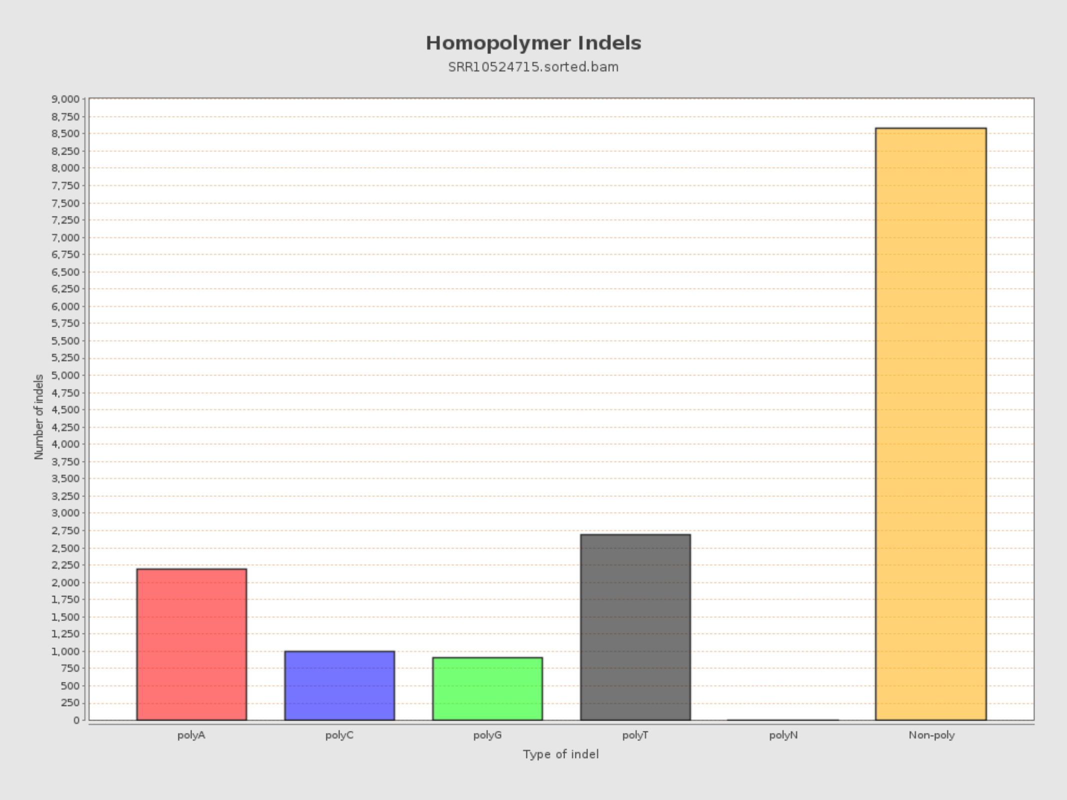
9. Results : Mapped Reads GC-content Distribution



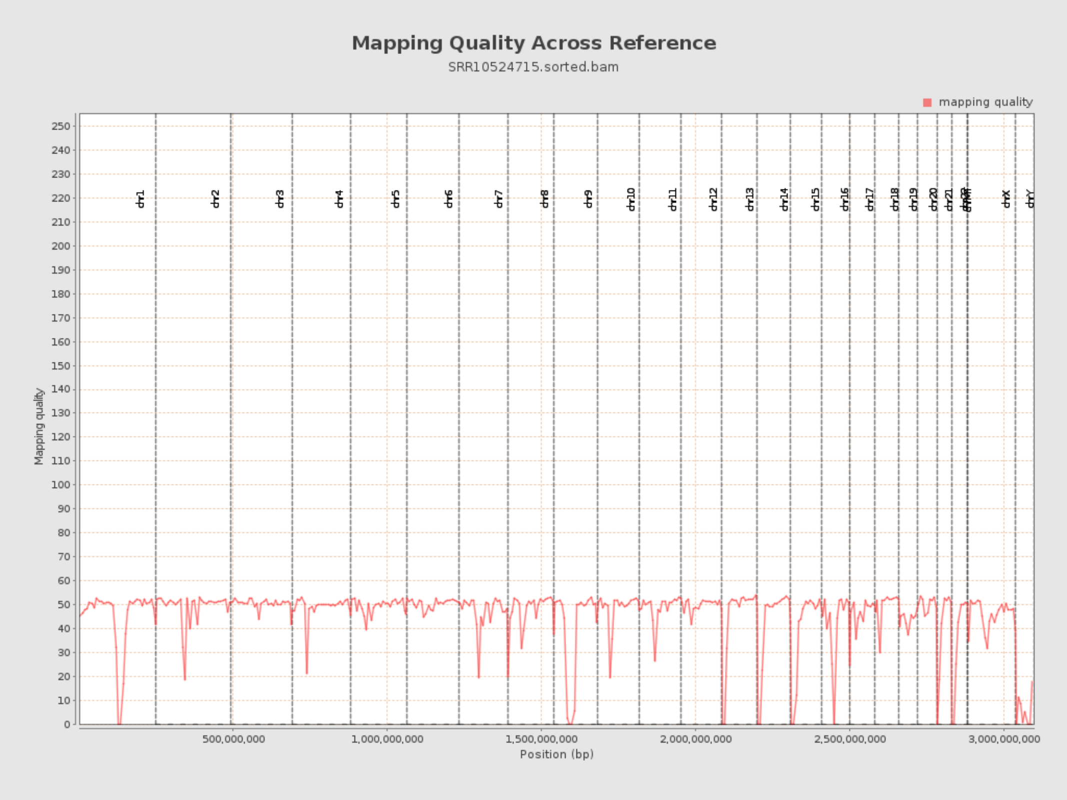
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram