Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 07:39:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524516.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_SRR10524516 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524516.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 07:39:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524516.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,396,990
Mapped reads	1,264,580 / 90.52%
Unmapped reads	132,410 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,557 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	71,475 / 5.12%
Duplication rate	4.44%
Clipped reads	1,266,037 / 90.63%

2.2. ACGT Content

Number/percentage of A's	18,574,538 / 25.34%
Number/percentage of C's	12,462,407 / 17%
Number/percentage of T's	23,641,480 / 32.25%
Number/percentage of G's	18,624,997 / 25.41%
Number/percentage of N's	1,014 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2479

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

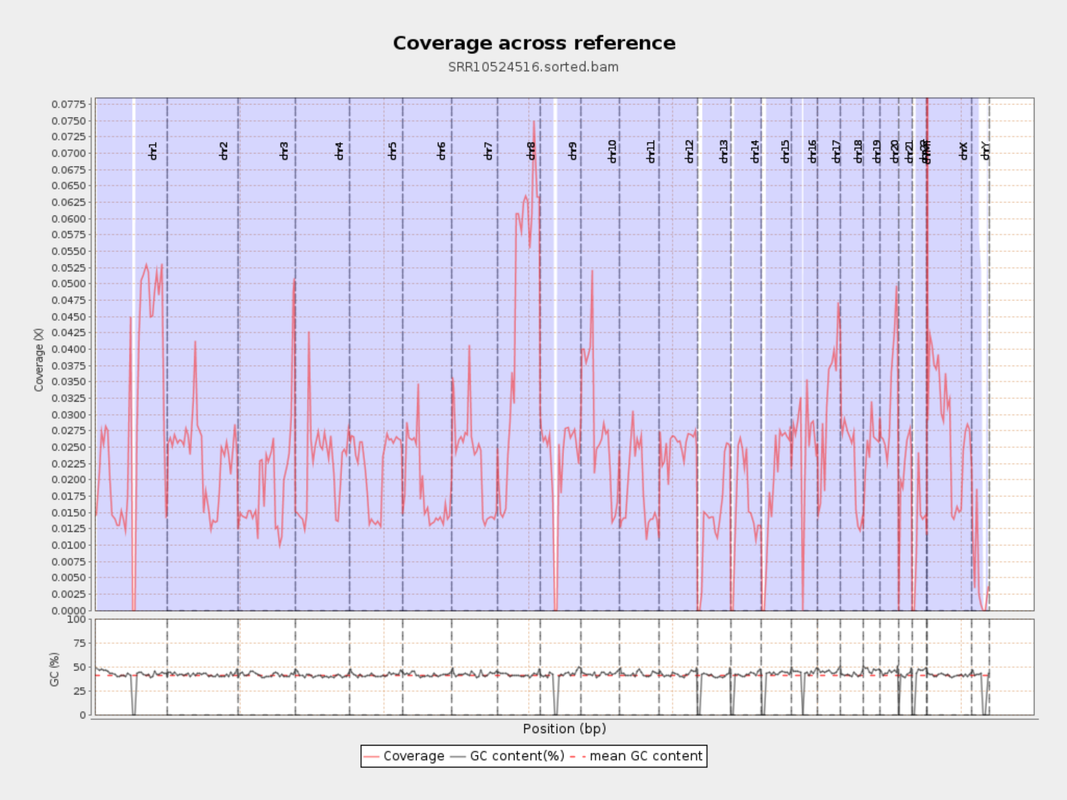
General error rate	0.53%
Mismatches	378,780
Insertions	5,090
Mapped reads with at least one insertion	0.4%
Deletions	13,541
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.94%

2.6. Chromosome stats

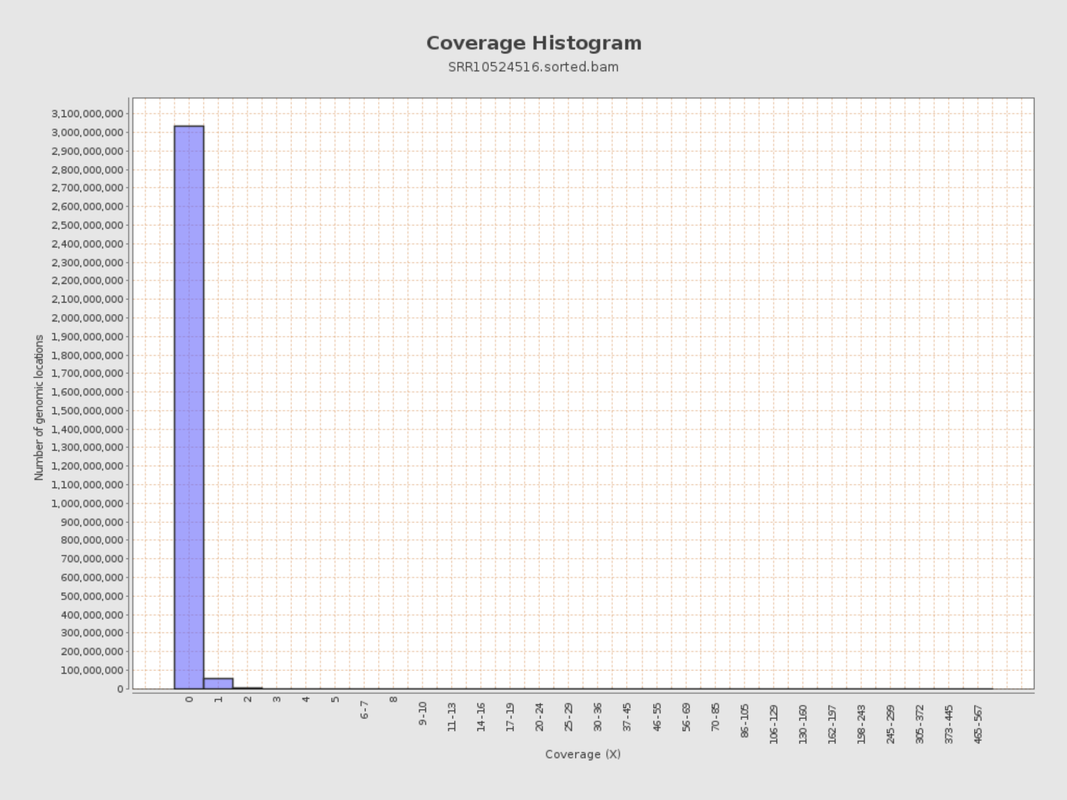
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7252590	0.0291	0.4566
chr2	243199373	5763174	0.0237	0.3045
chr3	198022430	3836709	0.0194	0.1567
chr4	191154276	4216067	0.0221	0.2025
chr5	180915260	3976448	0.022	0.1675
chr6	171115067	3194402	0.0187	0.1837
chr7	159138663	3684166	0.0232	0.2831

chr8	146364022	6691801	0.0457	0.2869
chr9	141213431	3172355	0.0225	0.2025
chr10	135534747	3928425	0.029	0.2704
chr11	135006516	2506998	0.0186	0.2093
chr12	133851895	3382961	0.0253	0.1799
chr13	115169878	1637680	0.0142	0.1348
chr14	107349540	1673180	0.0156	0.1434
chr15	102531392	1946662	0.019	0.1553
chr16	90354753	2269333	0.0251	0.1878
chr17	81195210	2558745	0.0315	0.2083
chr18	78077248	1749311	0.0224	0.3458
chr19	59128983	1505648	0.0255	0.3055
chr20	63025520	2064270	0.0328	0.2088
chr21	48129895	1016542	0.0211	0.1826
chr22	51304566	611915	0.0119	0.1246
chrMT	16571	8758	0.5285	0.9626
chrX	155270560	4390442	0.0283	0.2012
chrY	59373566	288505	0.0049	0.1615

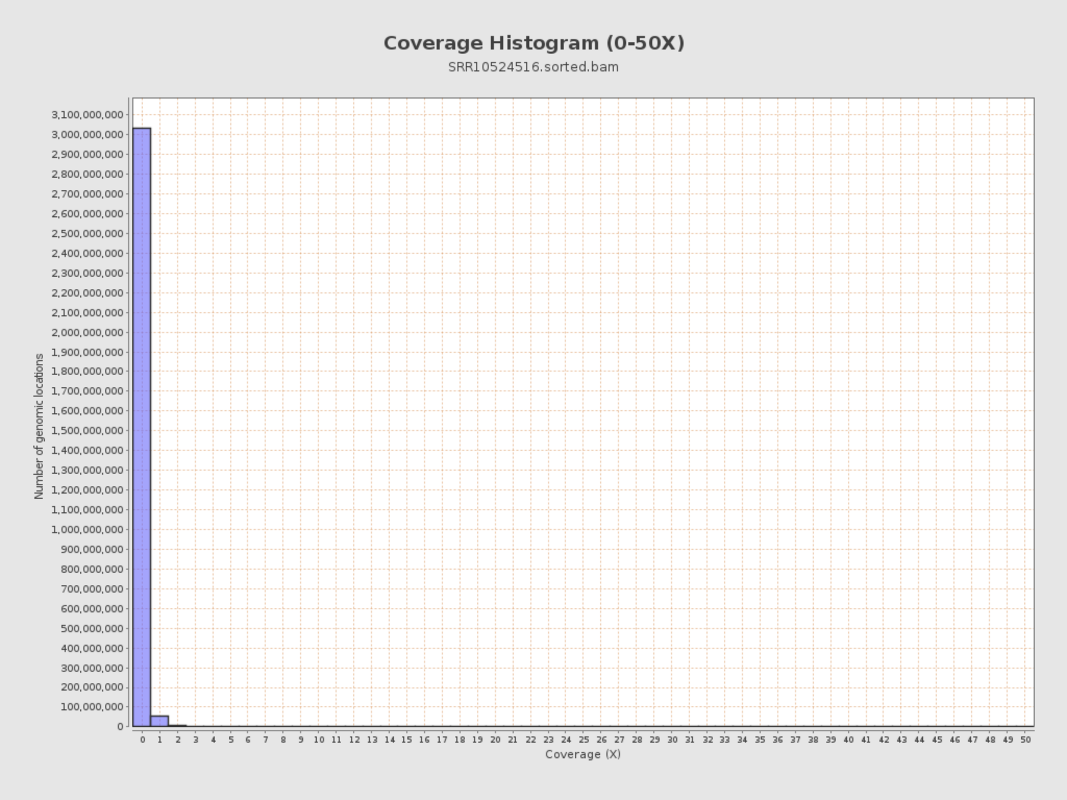
3. Results : Coverage across reference



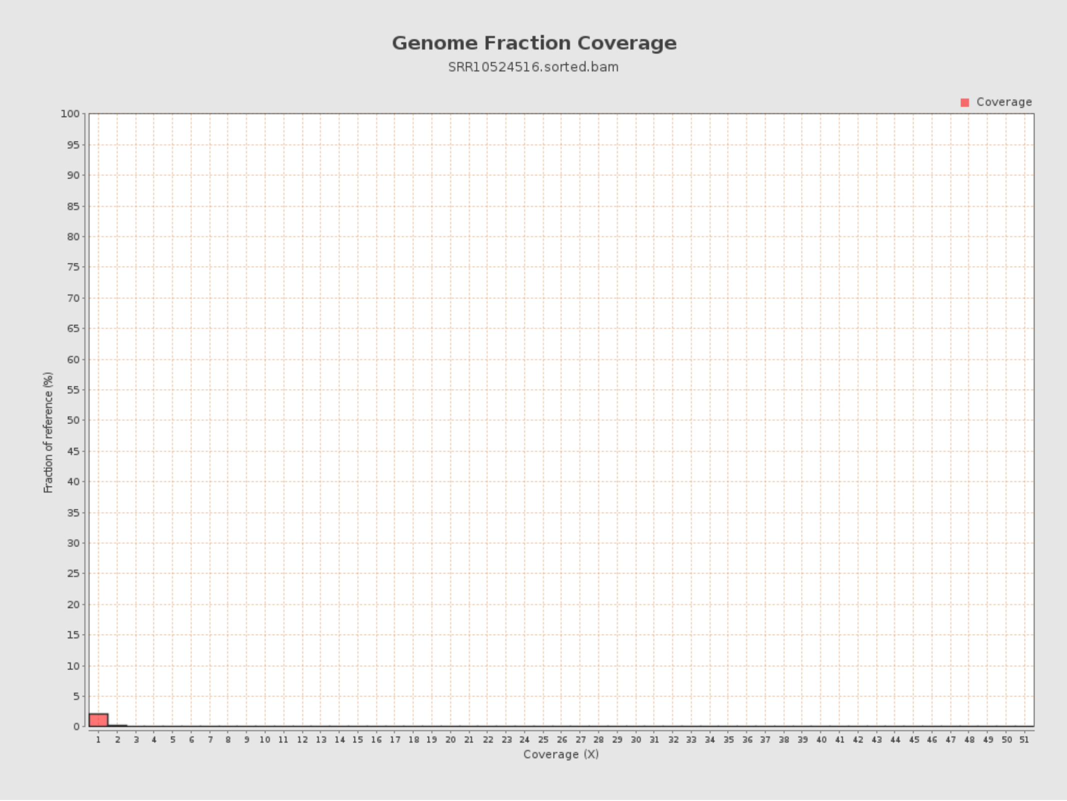
4. Results : Coverage Histogram



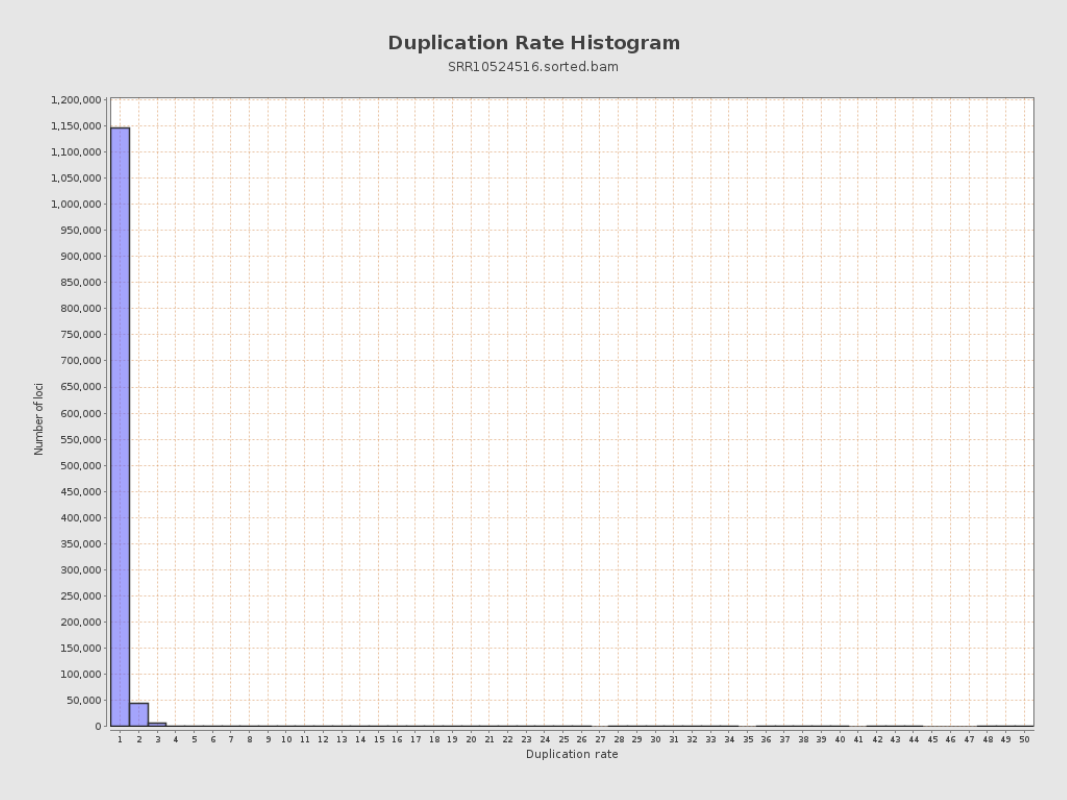
5. Results : Coverage Histogram (0-50X)



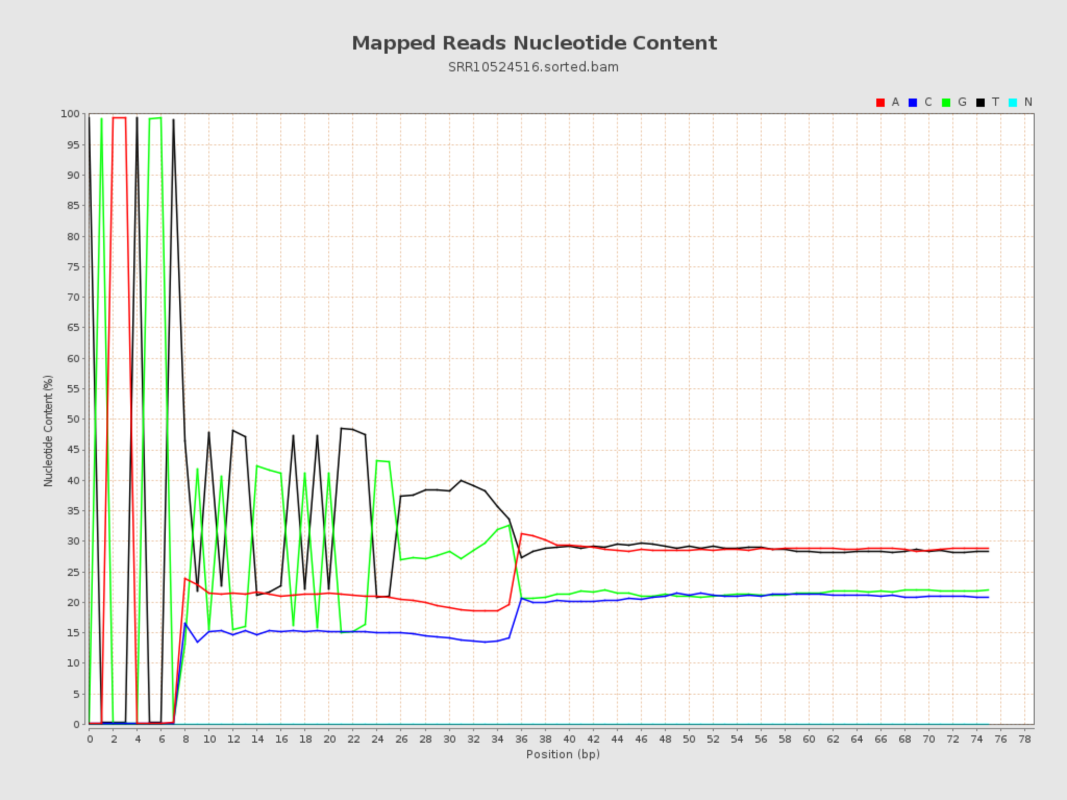
6. Results : Genome Fraction Coverage



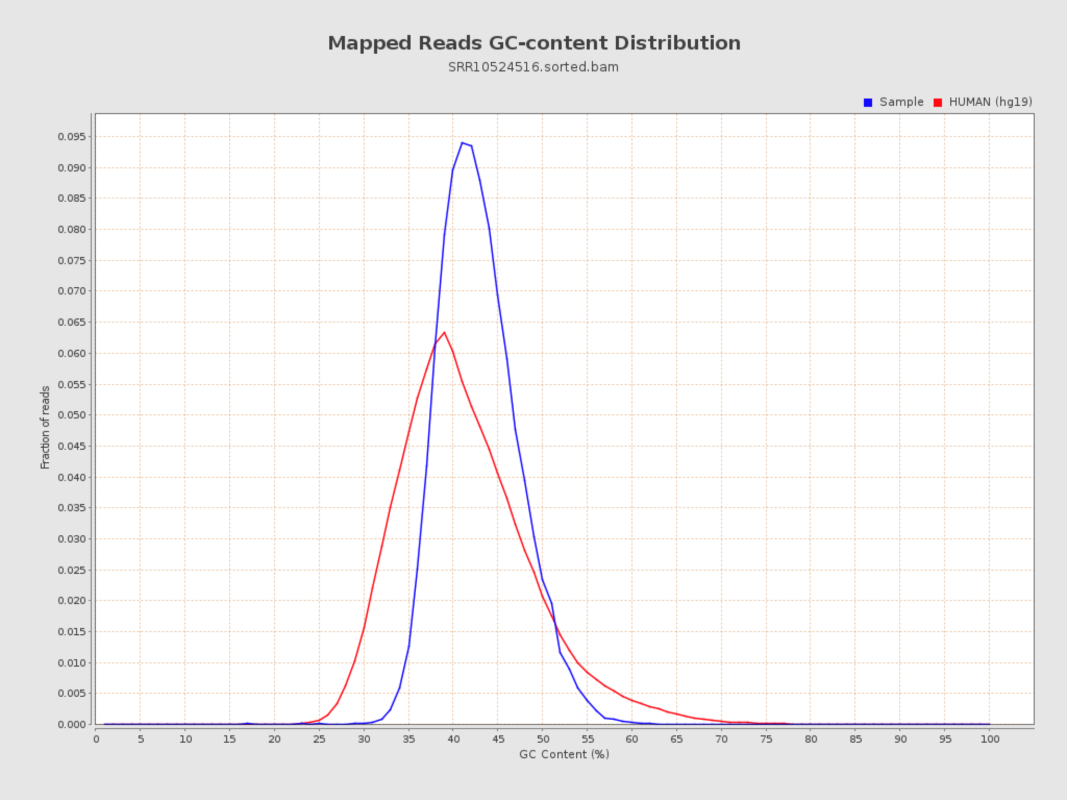
7. Results : Duplication Rate Histogram



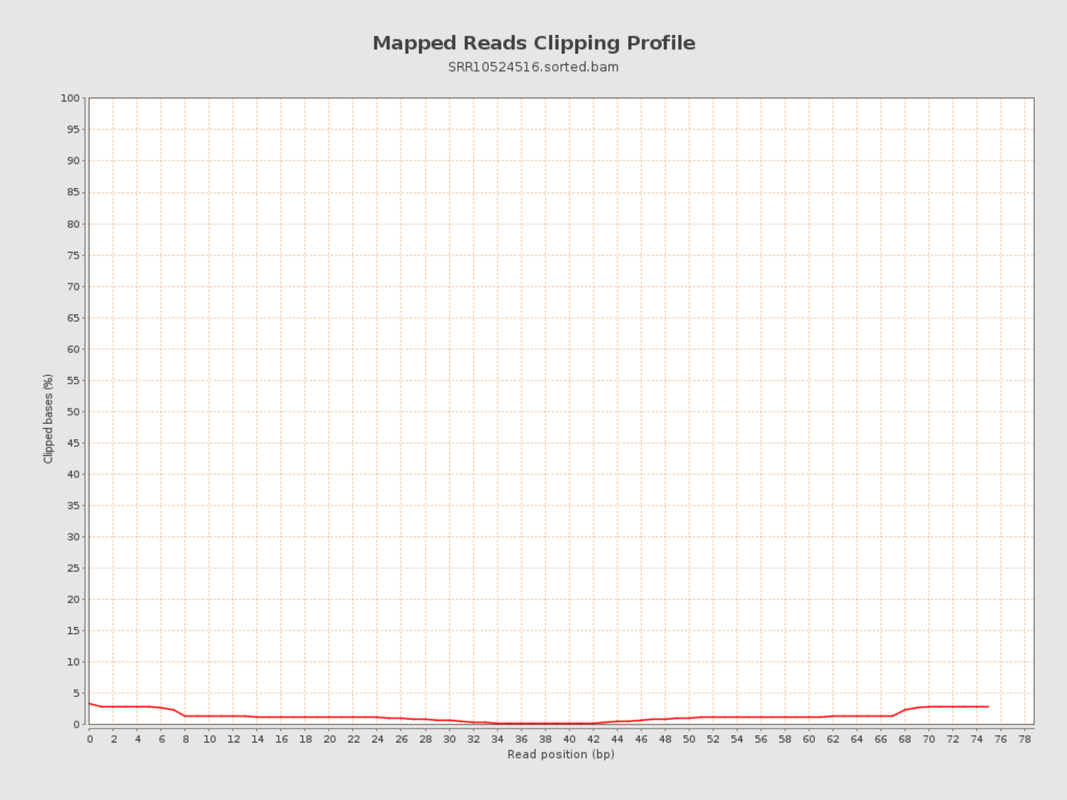
8. Results : Mapped Reads Nucleotide Content



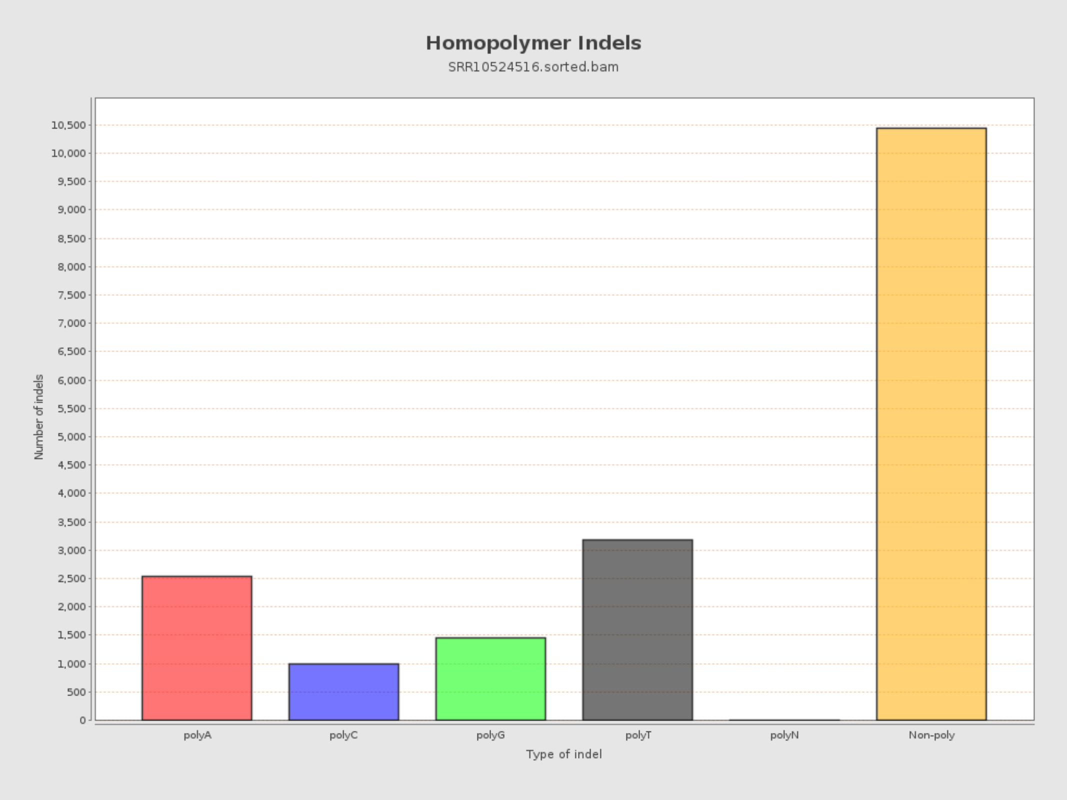
9. Results : Mapped Reads GC-content Distribution



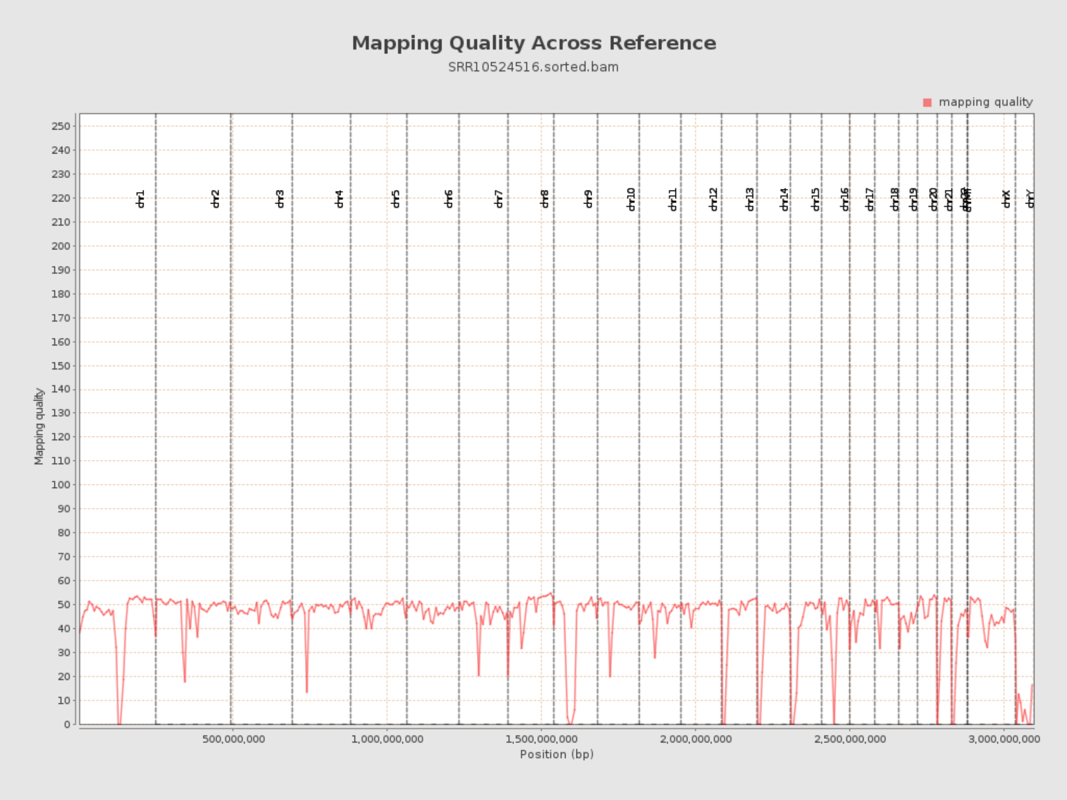
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram