Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:58:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524619.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_SRR10524619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524619.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:58:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,720,063
Mapped reads	1,598,599 / 92.94%
Unmapped reads	121,464 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,706 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	72,640 / 4.22%
Duplication rate	3.55%
Clipped reads	1,596,884 / 92.84%

2.2. ACGT Content

Number/percentage of A's	23,071,119 / 24.76%
Number/percentage of C's	18,732,922 / 20.11%
Number/percentage of T's	30,064,068 / 32.27%
Number/percentage of G's	21,304,592 / 22.87%
Number/percentage of N's	572 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2622

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

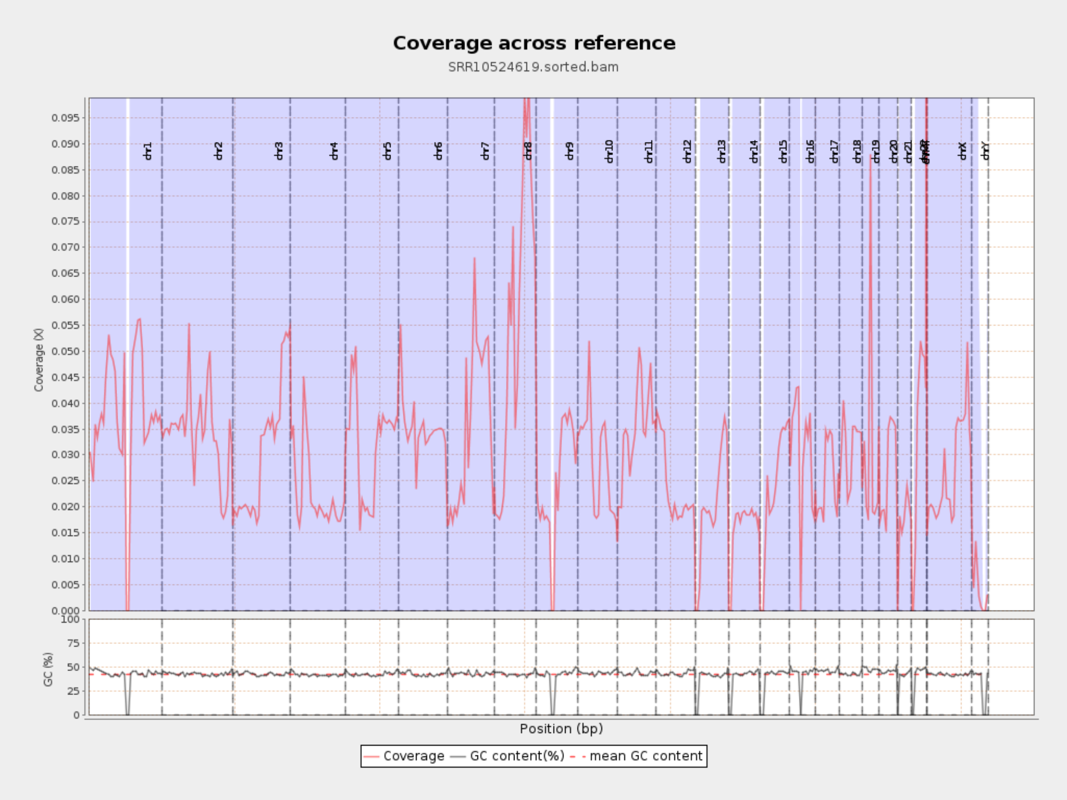
General error rate	0.49%
Mismatches	440,429
Insertions	6,680
Mapped reads with at least one insertion	0.42%
Deletions	17,400
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.21%

2.6. Chromosome stats

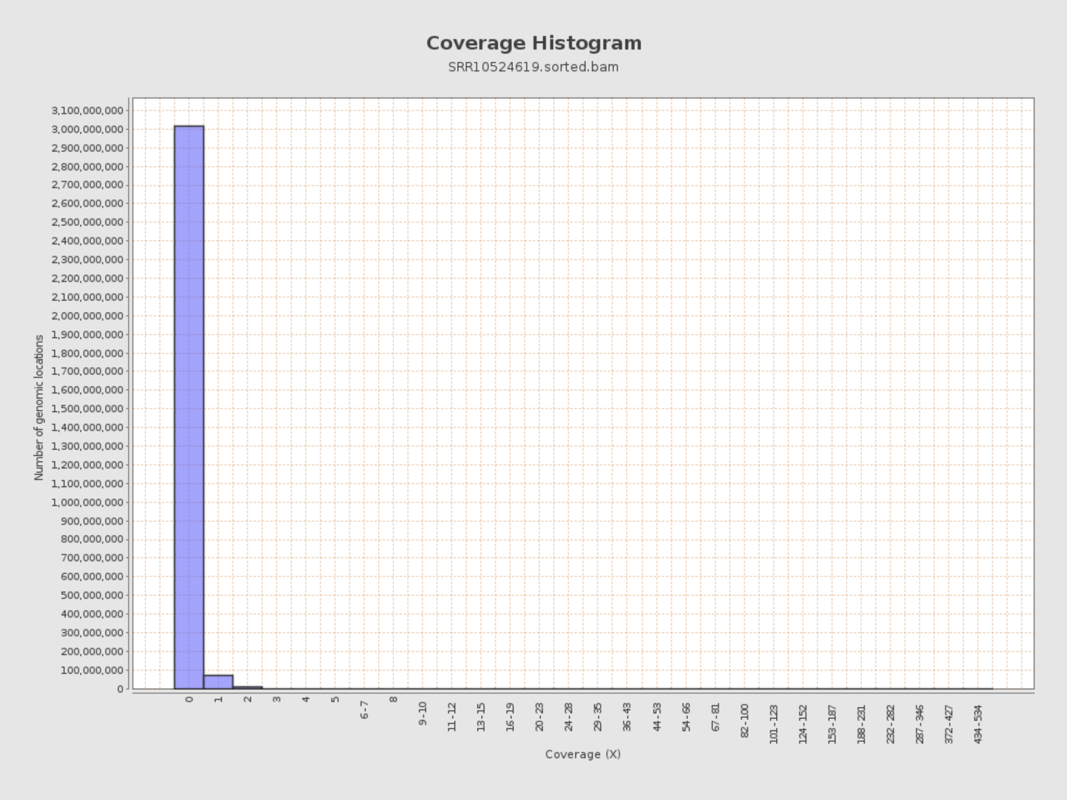
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9386438	0.0377	0.427
chr2	243199373	8380857	0.0345	0.3095
chr3	198022430	6013198	0.0304	0.1947
chr4	191154276	4303693	0.0225	0.1887
chr5	180915260	5820221	0.0322	0.2003
chr6	171115067	6044327	0.0353	0.2258
chr7	159138663	5743914	0.0361	0.3557

chr8	146364022	8242511	0.0563	0.3445
chr9	141213431	3420154	0.0242	0.2439
chr10	135534747	3931209	0.029	0.2524
chr11	135006516	4710136	0.0349	0.2688
chr12	133851895	3130799	0.0234	0.1755
chr13	115169878	2318784	0.0201	0.1599
chr14	107349540	1698828	0.0158	0.1478
chr15	102531392	2381789	0.0232	0.1768
chr16	90354753	2744669	0.0304	0.2029
chr17	81195210	2034240	0.0251	0.1818
chr18	78077248	2487755	0.0319	0.3858
chr19	59128983	1820975	0.0308	0.3144
chr20	63025520	1716146	0.0272	0.1873
chr21	48129895	821153	0.0171	0.1558
chr22	51304566	1643513	0.032	0.2001
chrMT	16571	4511	0.2722	0.5521
chrX	155270560	4178277	0.0269	0.2071
chrY	59373566	224150	0.0038	0.105

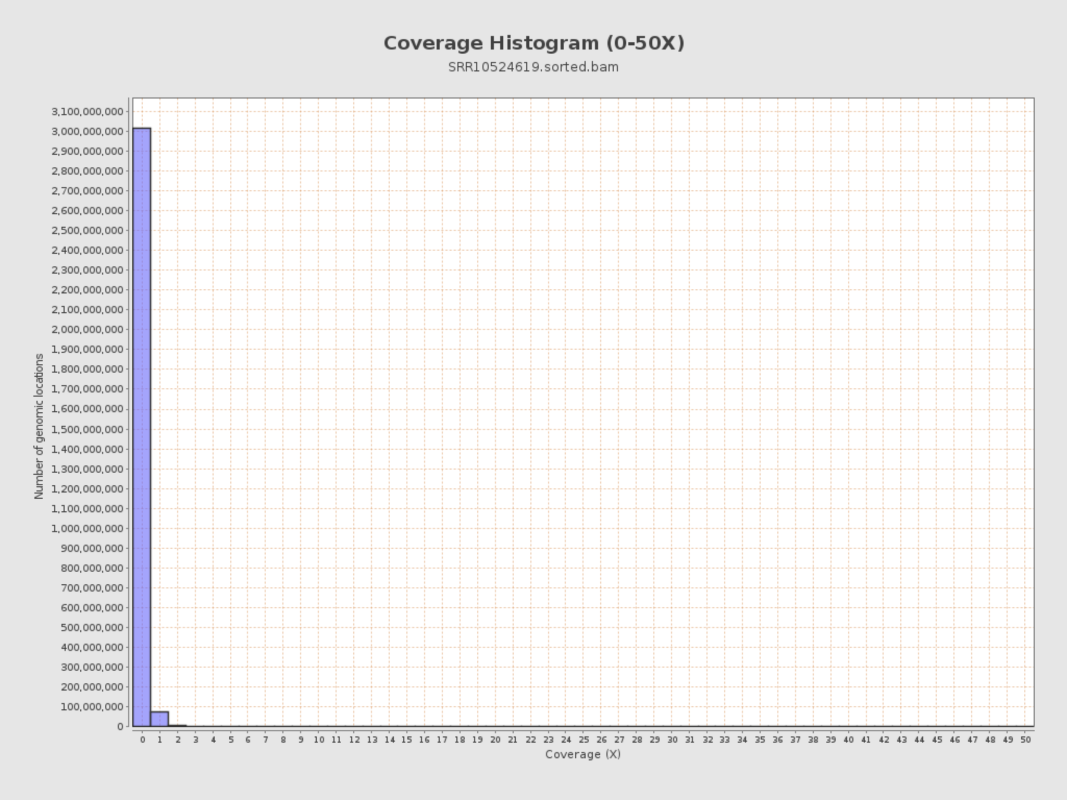
3. Results : Coverage across reference



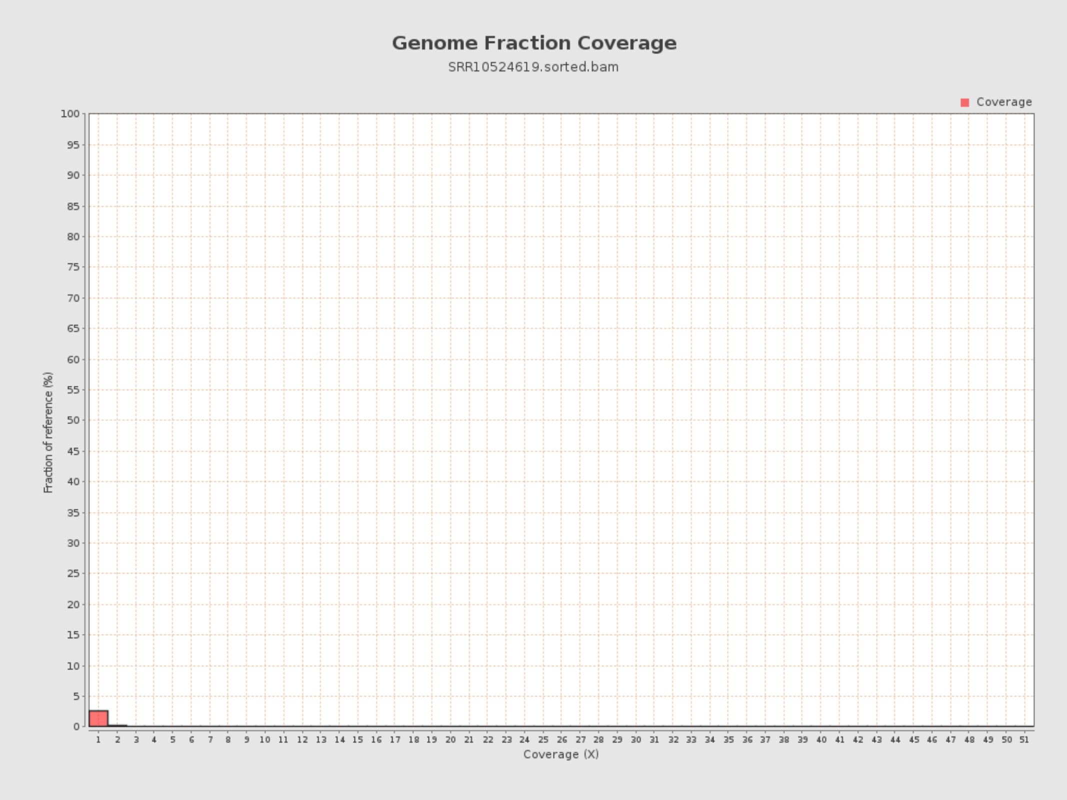
4. Results : Coverage Histogram



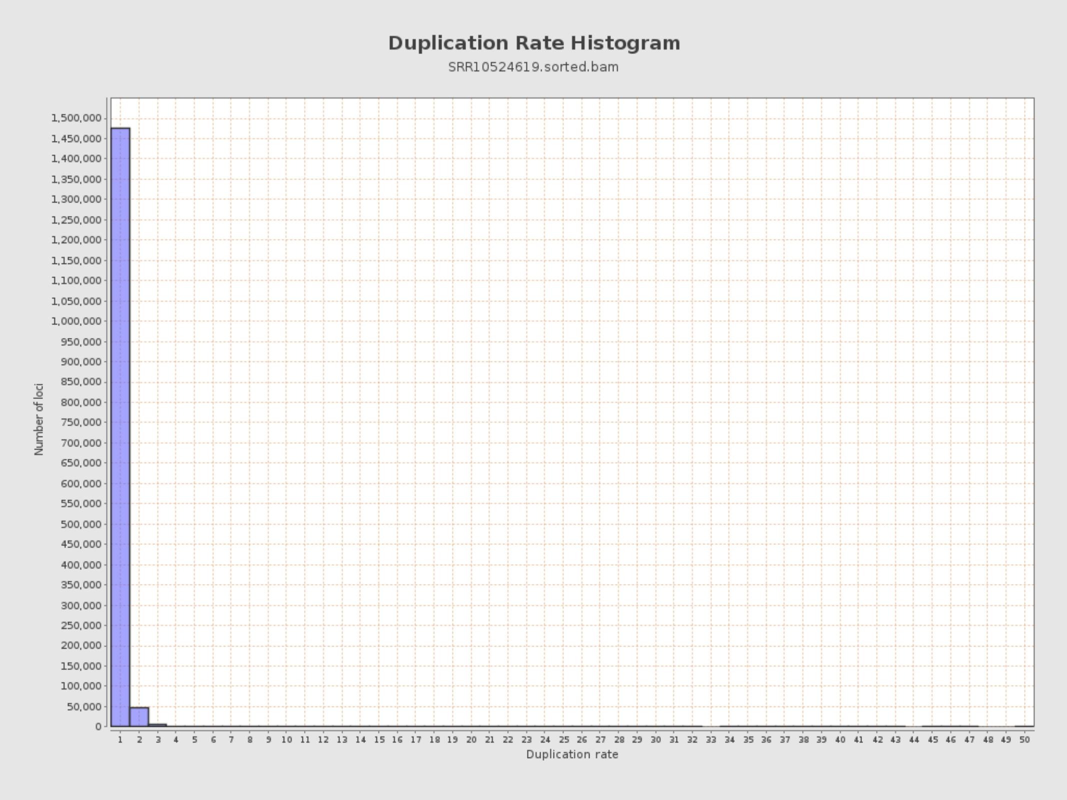
5. Results : Coverage Histogram (0-50X)



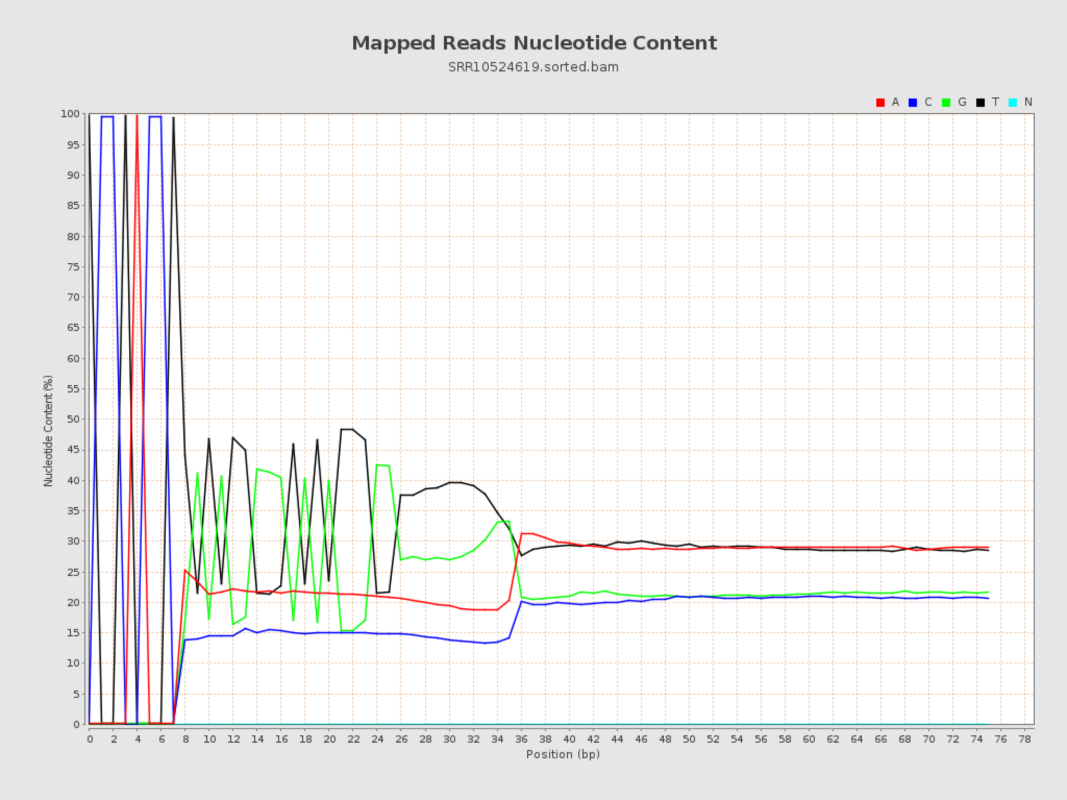
6. Results : Genome Fraction Coverage



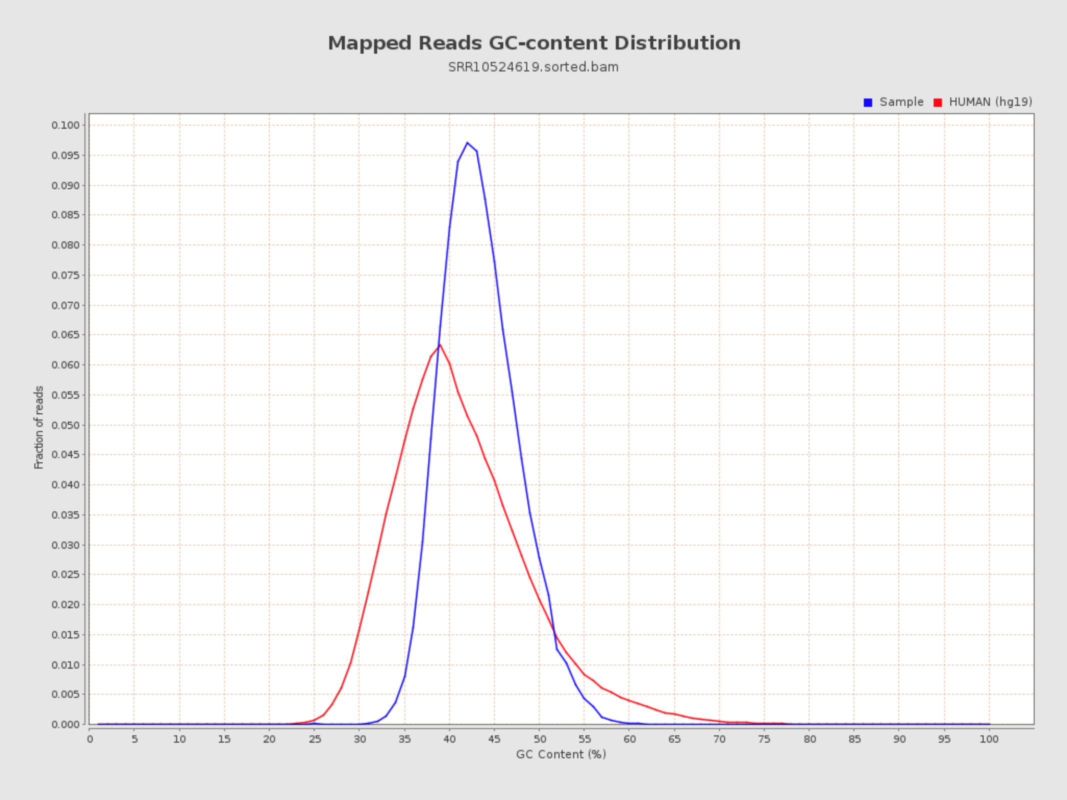
7. Results : Duplication Rate Histogram



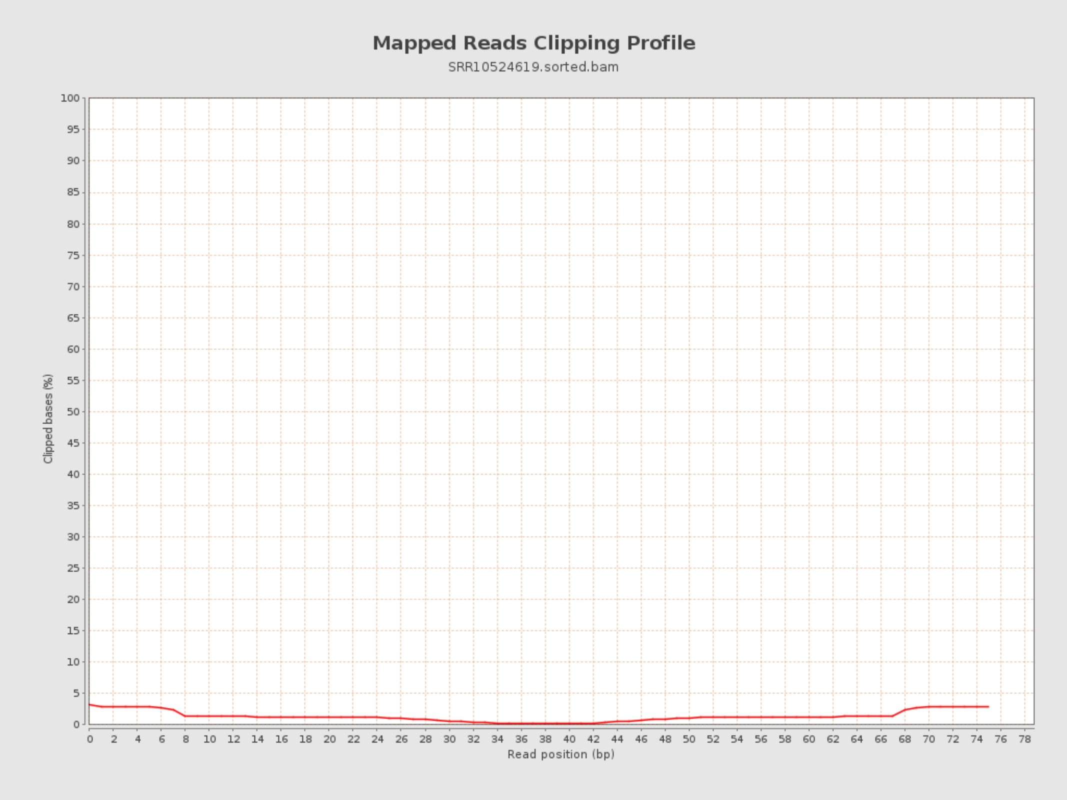
8. Results : Mapped Reads Nucleotide Content



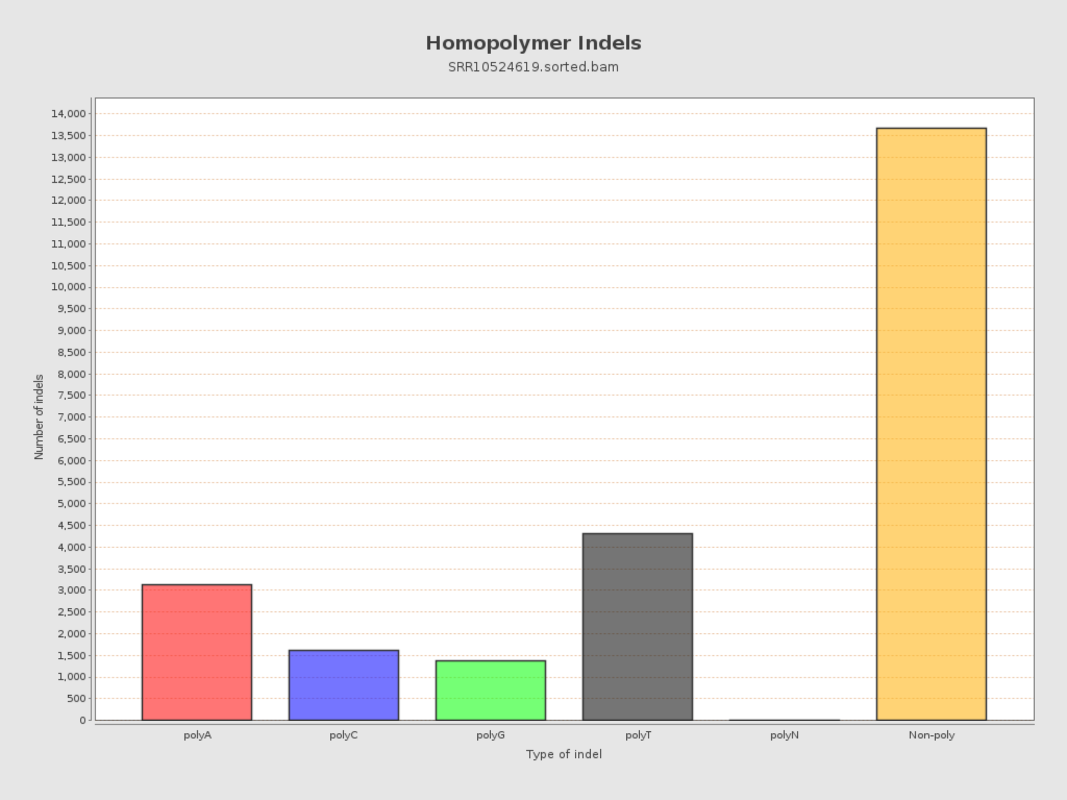
9. Results : Mapped Reads GC-content Distribution



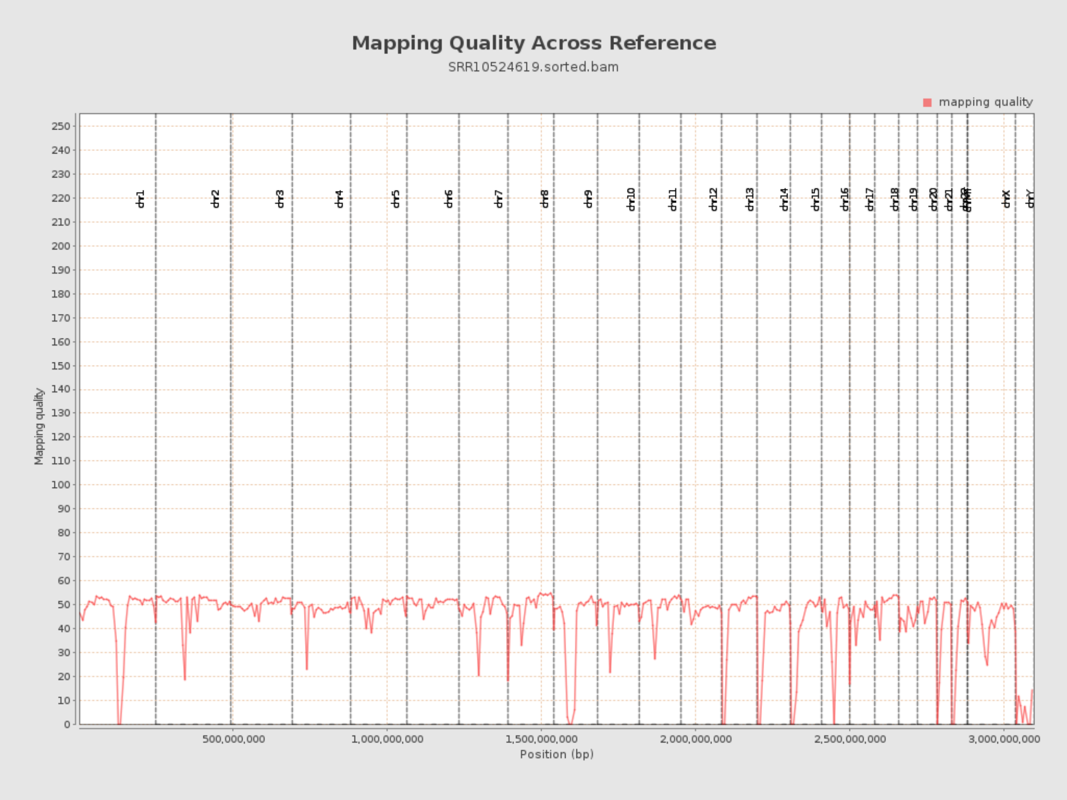
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram