Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:55:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524819.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_SRR10524819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:55:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,674,530
Mapped reads	1,506,878 / 89.99%
Unmapped reads	167,652 / 10.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,291 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	47,821 / 2.86%
Duplication rate	2.34%
Clipped reads	1,508,975 / 90.11%

2.2. ACGT Content

Number/percentage of A's	20,315,754 / 23.83%
Number/percentage of C's	14,855,812 / 17.43%
Number/percentage of T's	28,301,398 / 33.2%
Number/percentage of G's	21,754,361 / 25.52%
Number/percentage of N's	10,110 / 0.01%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2357

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

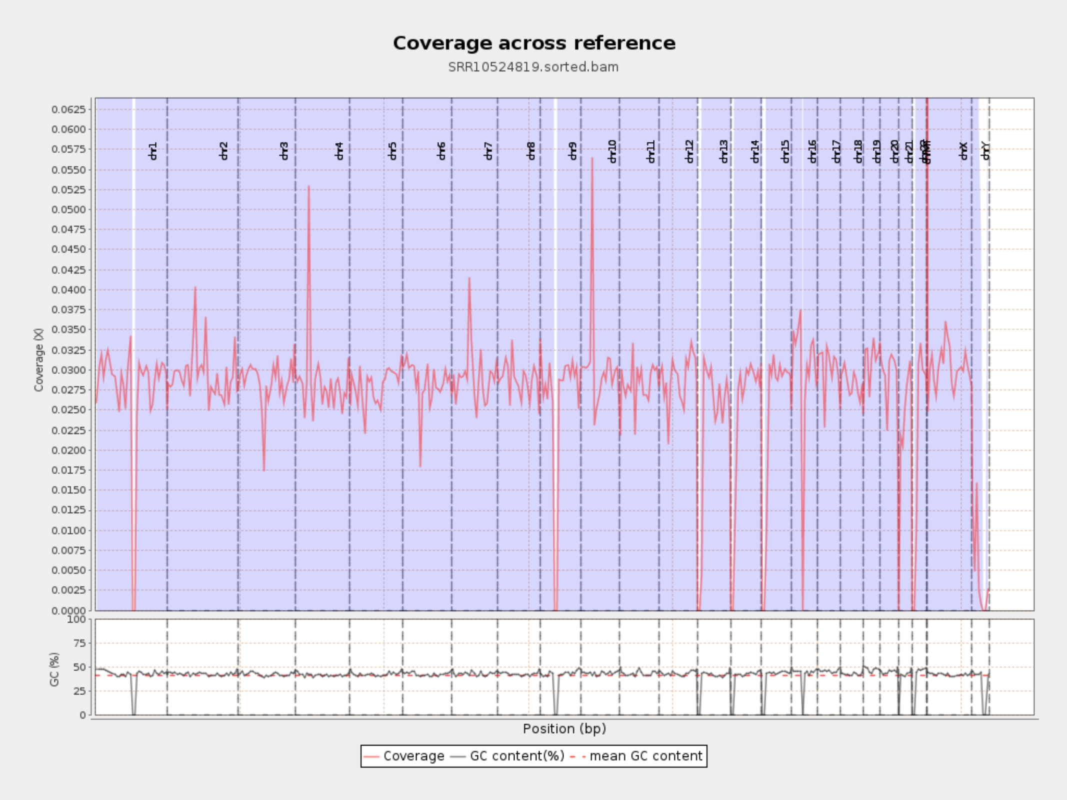
General error rate	0.53%
Mismatches	438,763
Insertions	5,721
Mapped reads with at least one insertion	0.38%
Deletions	16,906
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.62%

2.6. Chromosome stats

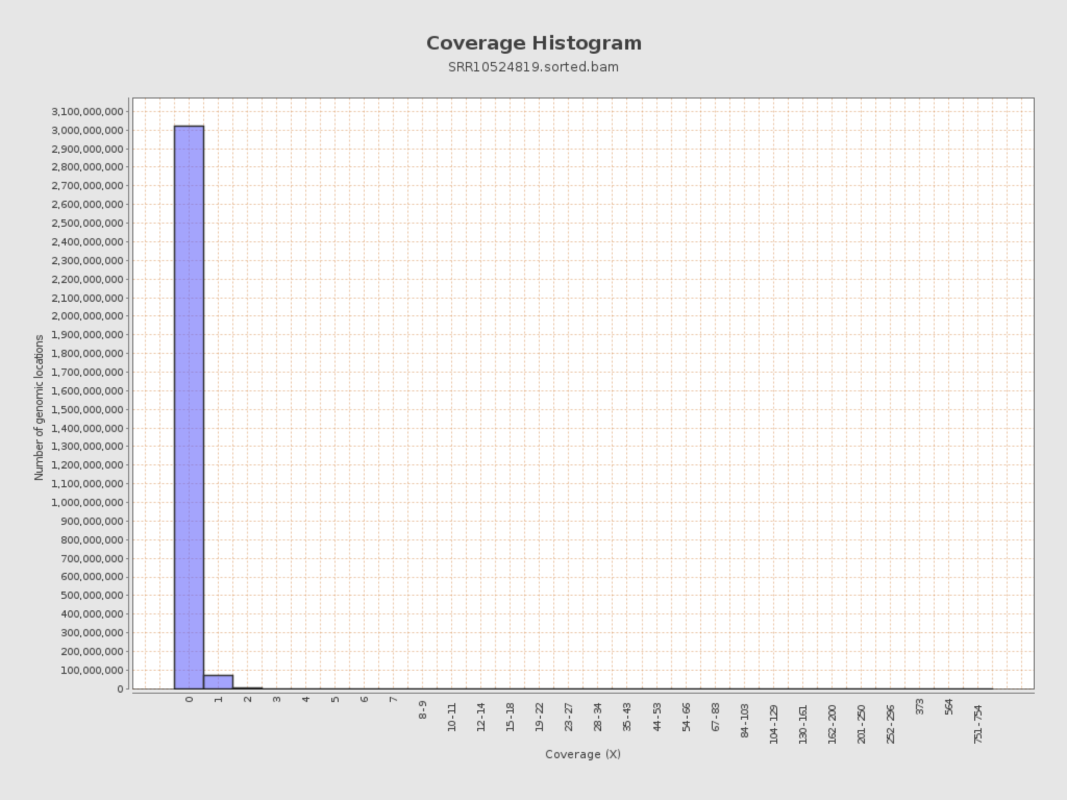
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6808210	0.0273	0.2776
chr2	243199373	7155266	0.0294	0.3778
chr3	198022430	5627016	0.0284	0.185
chr4	191154276	5478464	0.0287	0.2139
chr5	180915260	5095839	0.0282	0.1827
chr6	171115067	4859326	0.0284	0.2023
chr7	159138663	4659148	0.0293	0.2895

chr8	146364022	4208380	0.0288	0.208
chr9	141213431	3635230	0.0257	0.2117
chr10	135534747	4143416	0.0306	0.2906
chr11	135006516	3834045	0.0284	0.2178
chr12	133851895	3869568	0.0289	0.1874
chr13	115169878	2630608	0.0228	0.1654
chr14	107349540	2576619	0.024	0.175
chr15	102531392	2465691	0.024	0.1751
chr16	90354753	2618135	0.029	0.2042
chr17	81195210	2454789	0.0302	0.1968
chr18	78077248	2215899	0.0284	0.3139
chr19	59128983	1850187	0.0313	0.2458
chr20	63025520	1841576	0.0292	0.1976
chr21	48129895	1119454	0.0233	0.1842
chr22	51304566	1086417	0.0212	0.1605
chrMT	16571	40404	2.4382	2.0983
chrX	155270560	4713839	0.0304	0.2056
chrY	59373566	277458	0.0047	0.1308

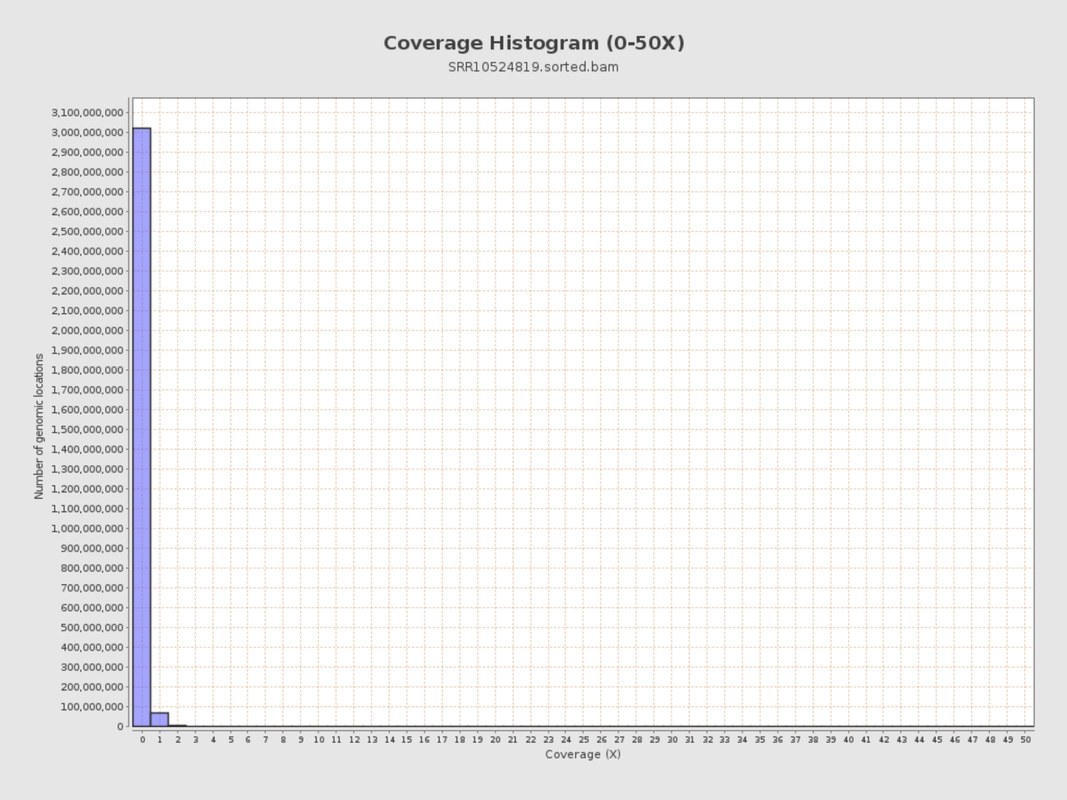
3. Results : Coverage across reference



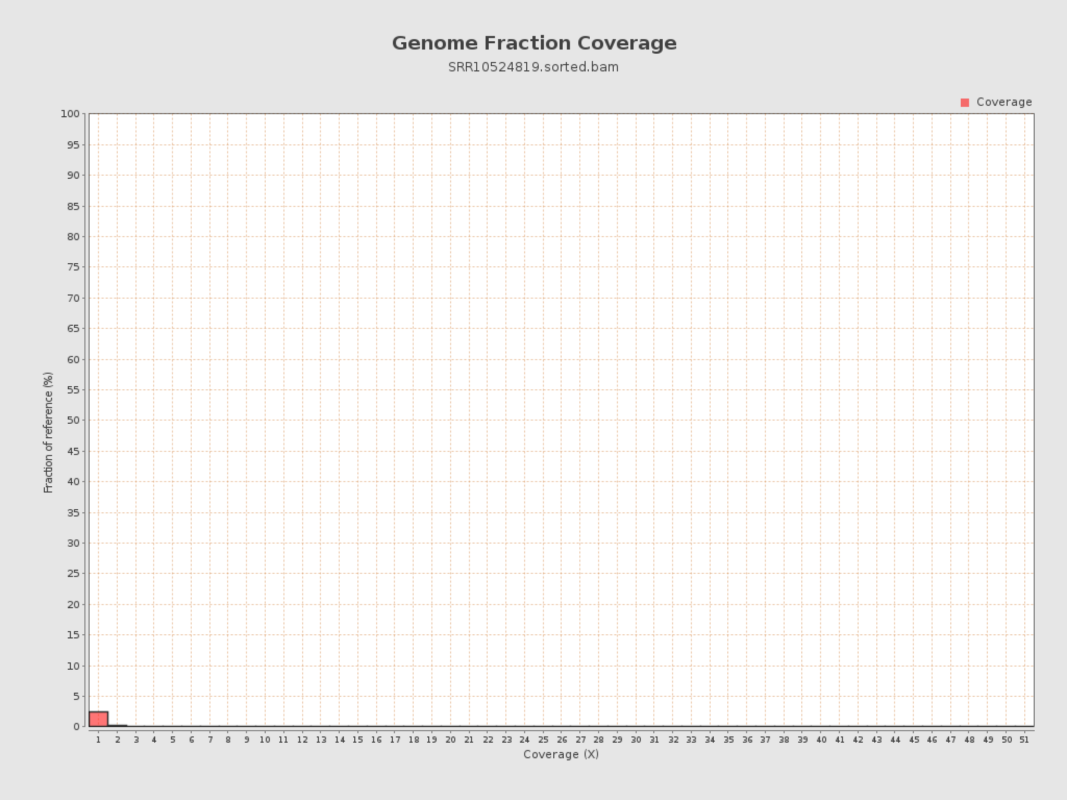
4. Results : Coverage Histogram



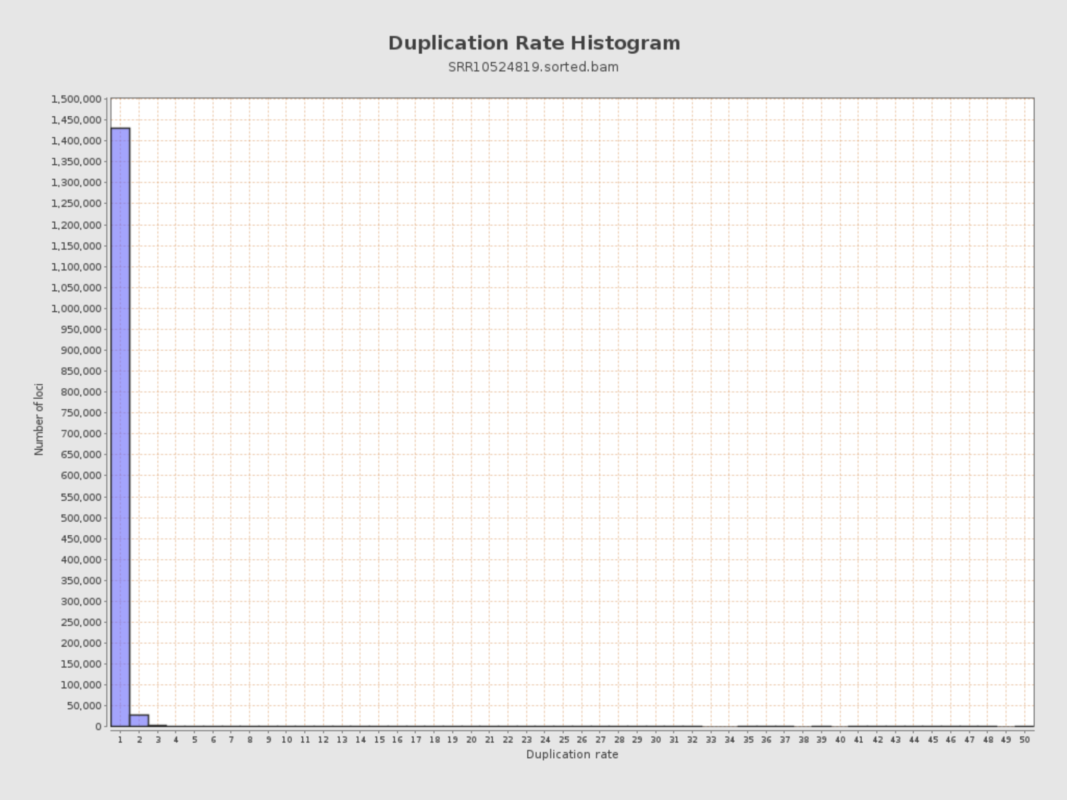
5. Results : Coverage Histogram (0-50X)



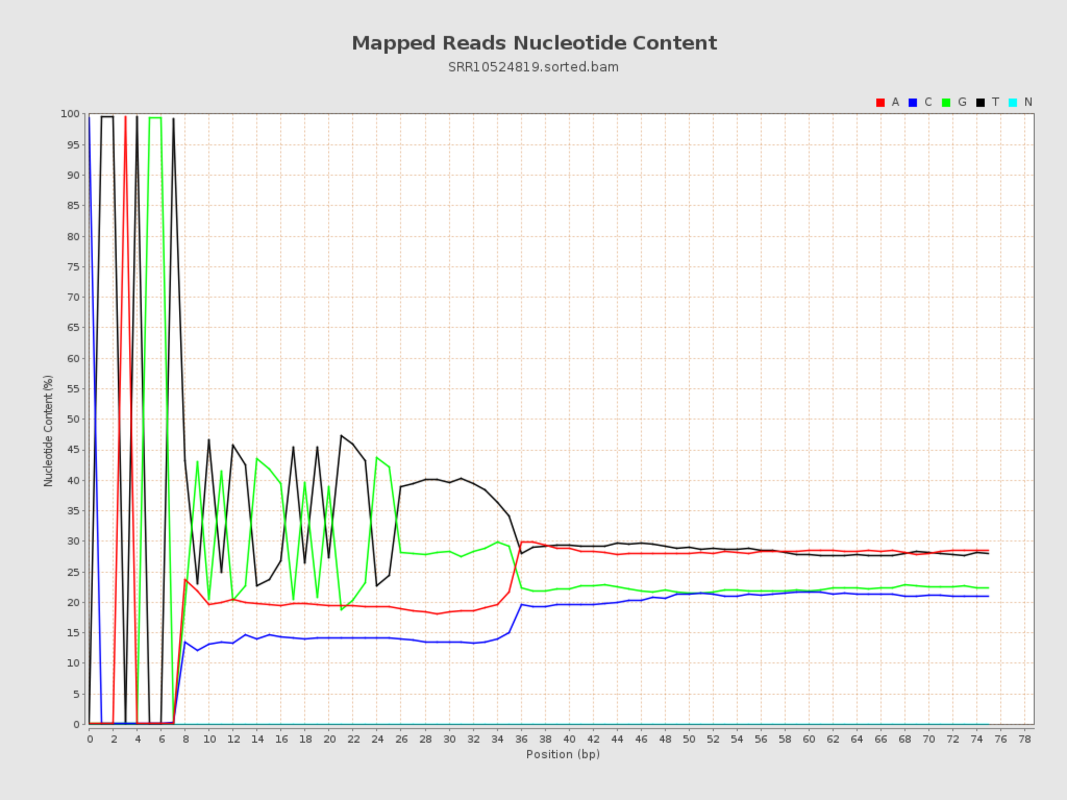
6. Results : Genome Fraction Coverage



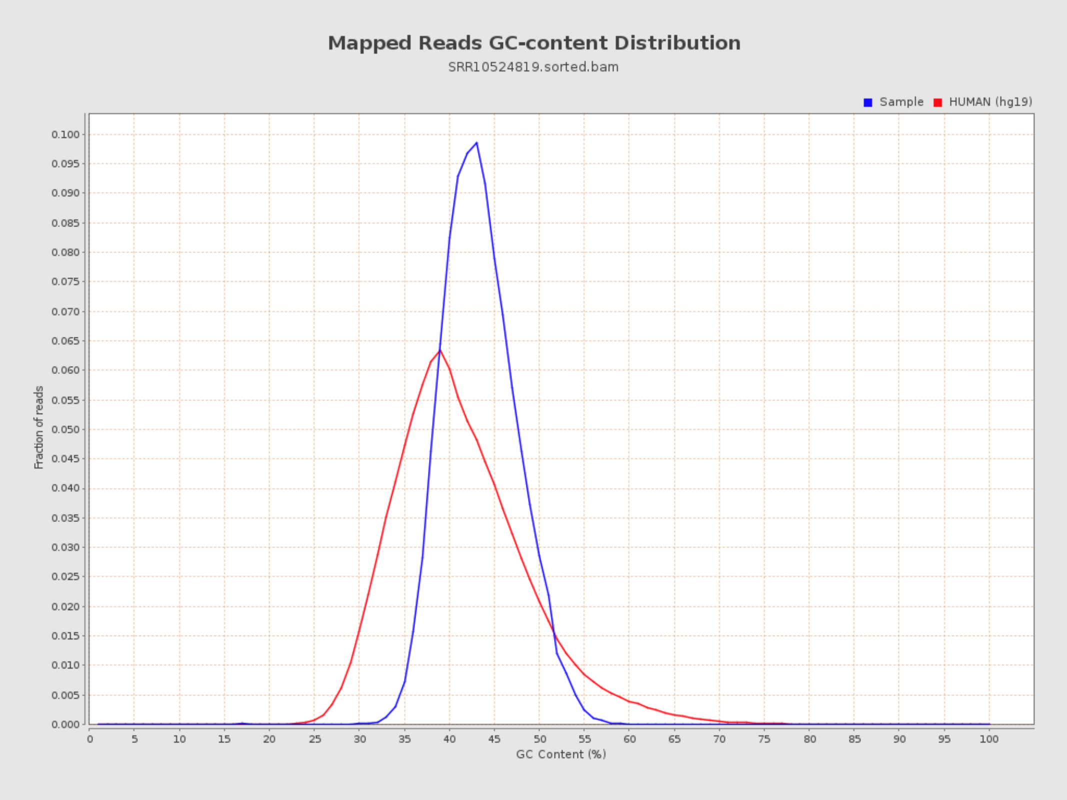
7. Results : Duplication Rate Histogram



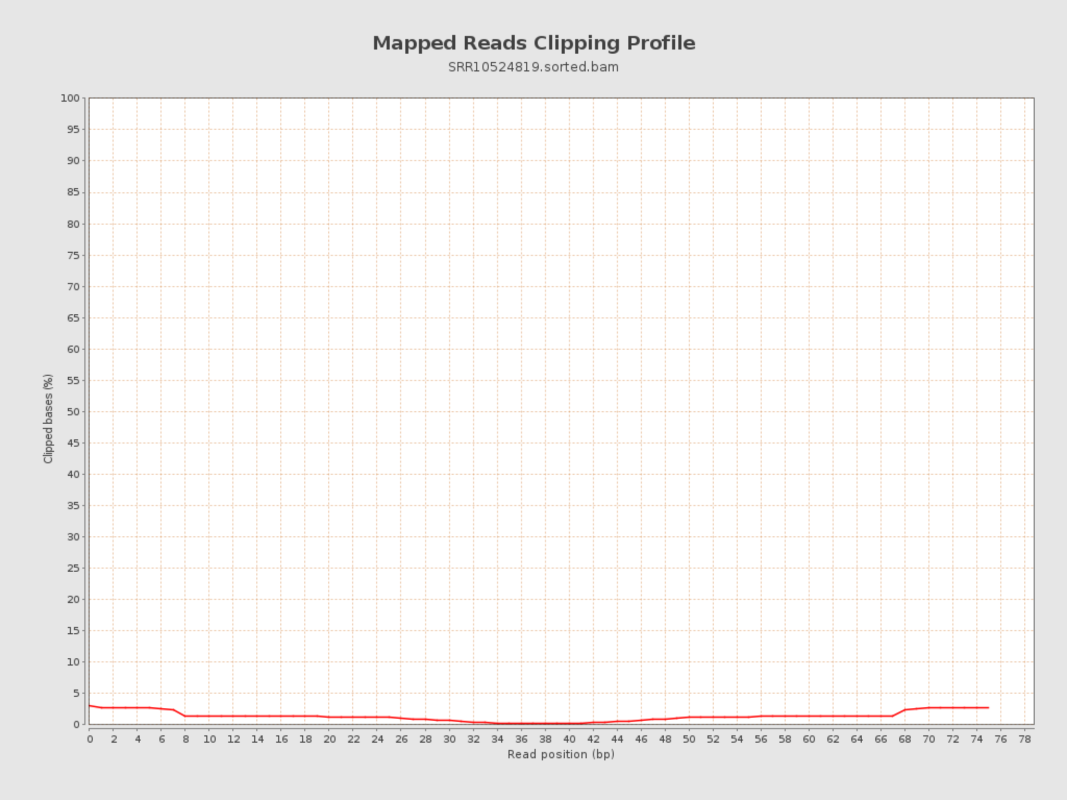
8. Results : Mapped Reads Nucleotide Content



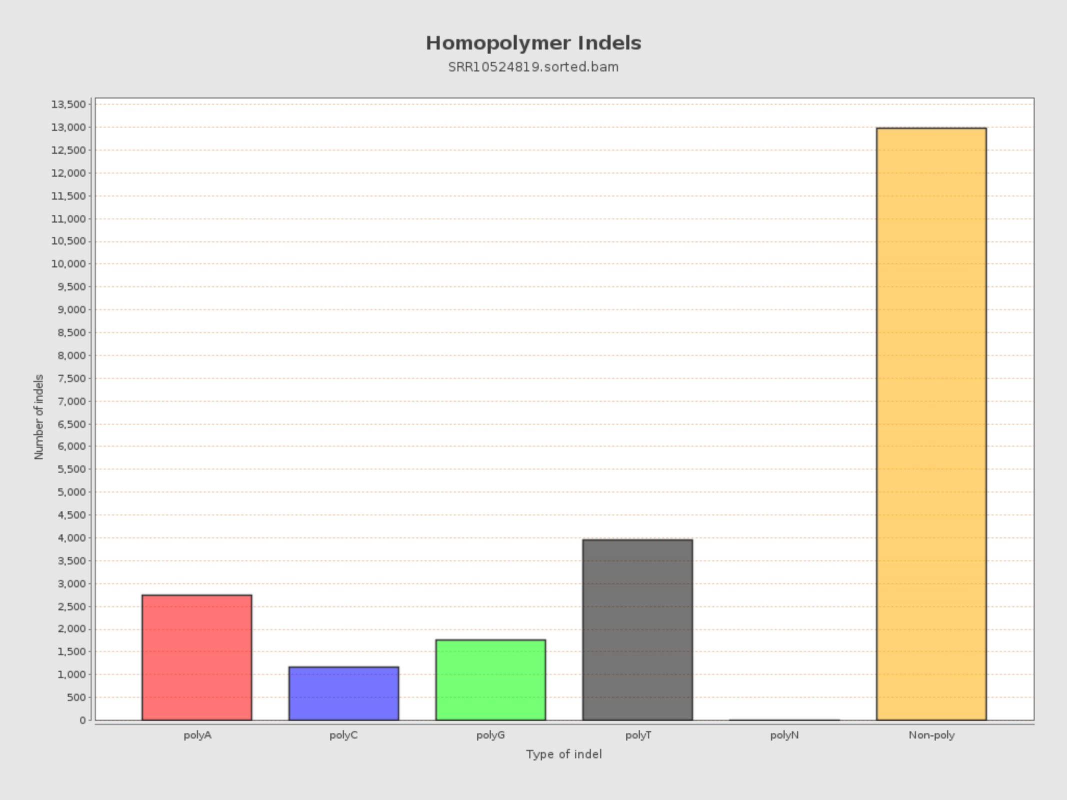
9. Results : Mapped Reads GC-content Distribution



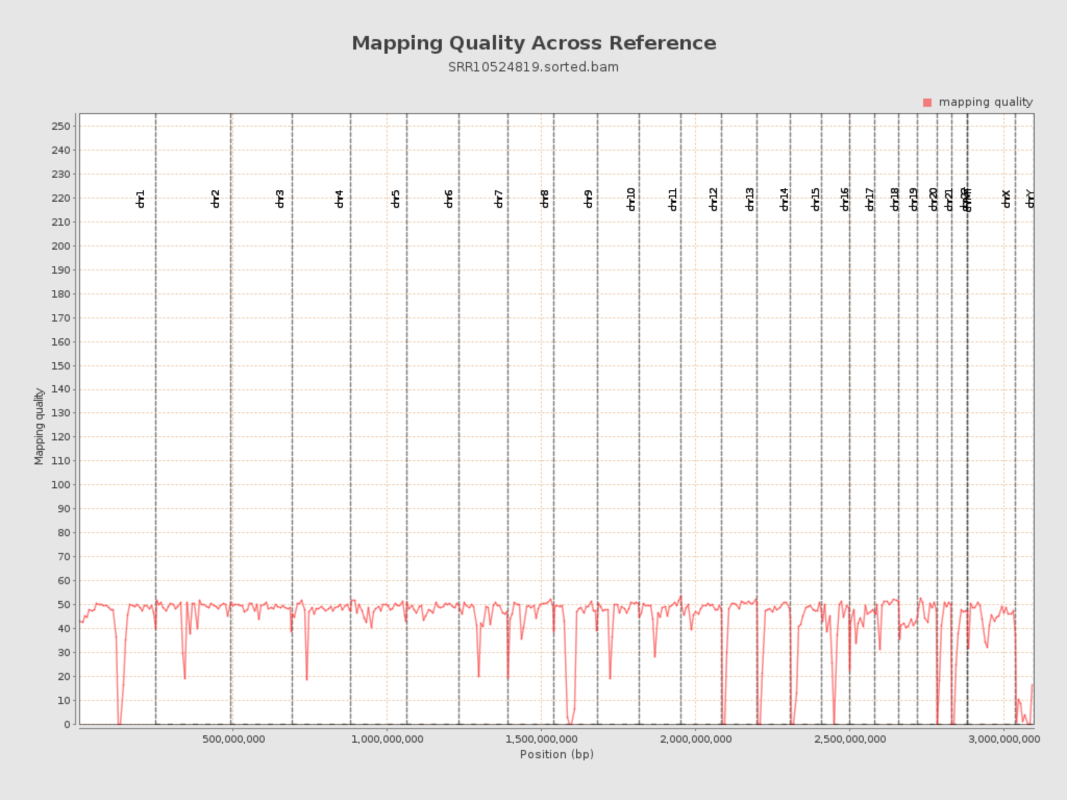
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram