Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524598.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_SRR10524598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:24:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,674,959
Mapped reads	1,560,027 / 93.14%
Unmapped reads	114,932 / 6.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,164 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	67,819 / 4.05%
Duplication rate	3.35%
Clipped reads	1,558,998 / 93.08%

2.2. ACGT Content

Number/percentage of A's	23,290,529 / 25.69%
Number/percentage of C's	15,869,228 / 17.5%
Number/percentage of T's	28,524,744 / 31.46%
Number/percentage of G's	22,986,944 / 25.35%
Number/percentage of N's	574 / 0%
GC Percentage	42.85%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.263

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

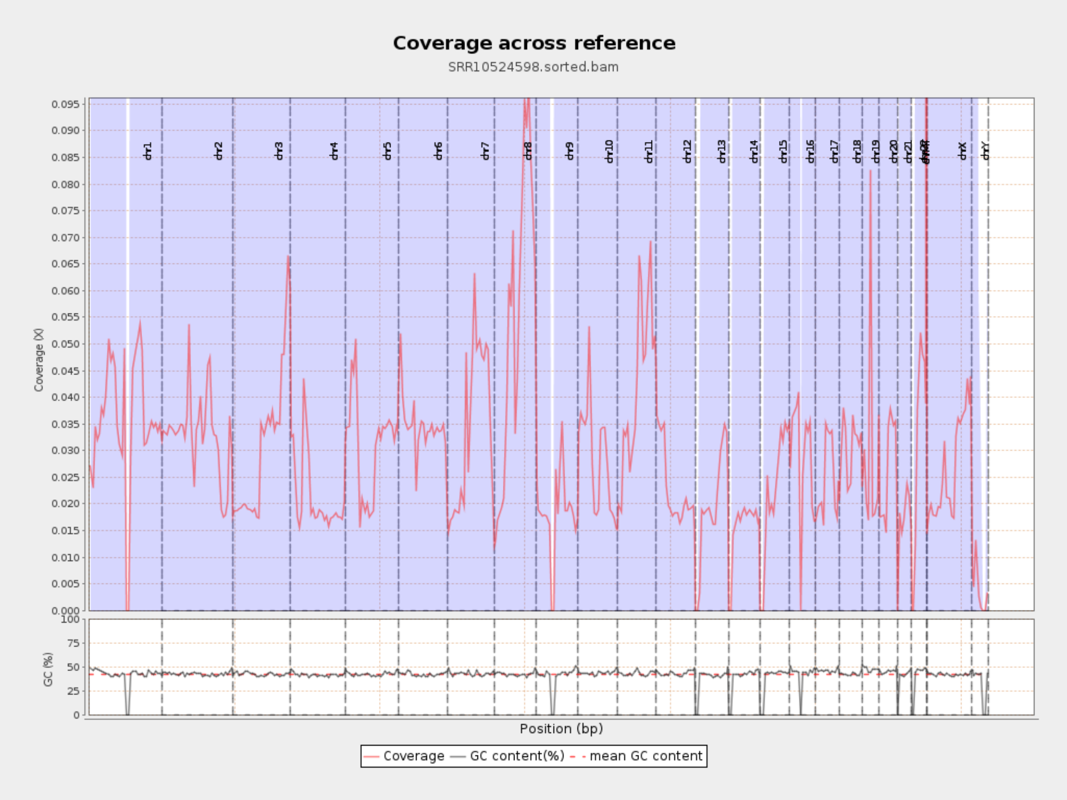
General error rate	0.47%
Mismatches	419,669
Insertions	5,678
Mapped reads with at least one insertion	0.36%
Deletions	17,301
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.33%

2.6. Chromosome stats

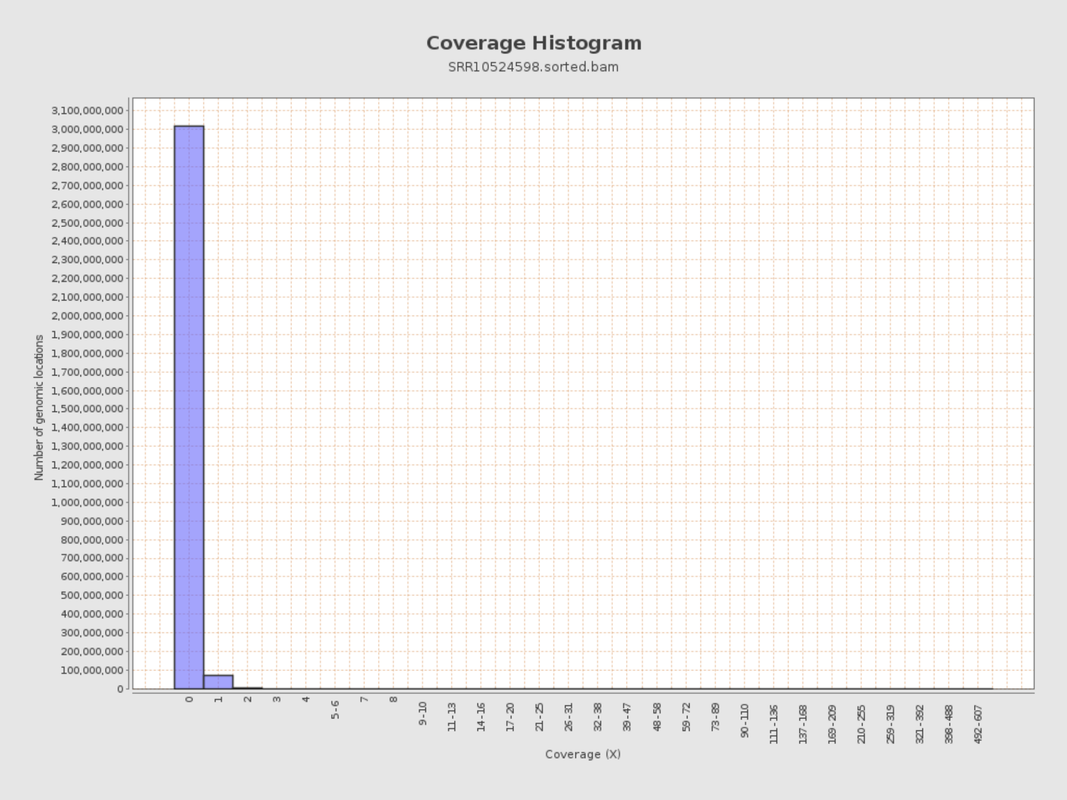
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8926964	0.0358	0.4599
chr2	243199373	8078186	0.0332	0.2946
chr3	198022430	6041073	0.0305	0.1949
chr4	191154276	4075045	0.0213	0.1839
chr5	180915260	5612397	0.031	0.1958
chr6	171115067	5934914	0.0347	0.2208
chr7	159138663	5506818	0.0346	0.3472

chr8	146364022	8023922	0.0548	0.3403
chr9	141213431	2548878	0.018	0.2211
chr10	135534747	3885263	0.0287	0.2581
chr11	135006516	5678952	0.0421	0.2813
chr12	133851895	3032484	0.0227	0.1718
chr13	115169878	2230824	0.0194	0.1561
chr14	107349540	1658557	0.0155	0.1425
chr15	102531392	2274627	0.0222	0.1744
chr16	90354753	2602207	0.0288	0.1983
chr17	81195210	1994621	0.0246	0.1779
chr18	78077248	2420991	0.031	0.3765
chr19	59128983	1746718	0.0295	0.3258
chr20	63025520	1669840	0.0265	0.186
chr21	48129895	813722	0.0169	0.1594
chr22	51304566	1602937	0.0312	0.197
chrMT	16571	8375	0.5054	0.8126
chrX	155270560	4112386	0.0265	0.2034
chrY	59373566	220731	0.0037	0.1069

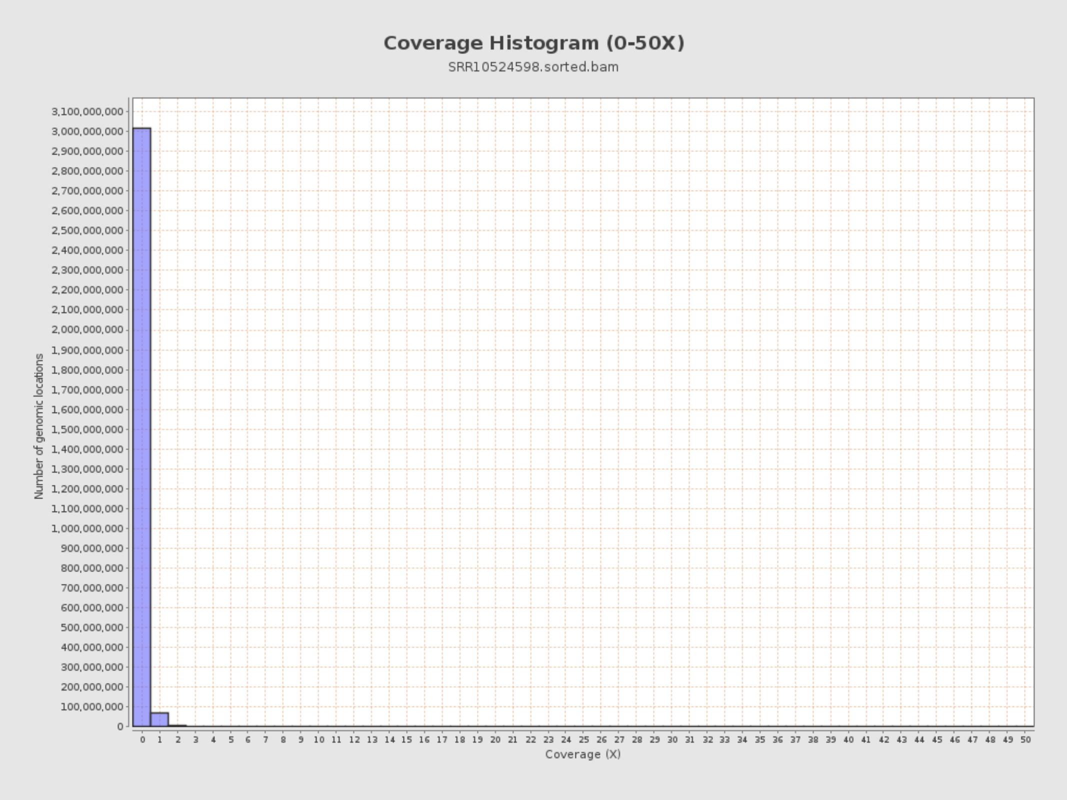
3. Results : Coverage across reference



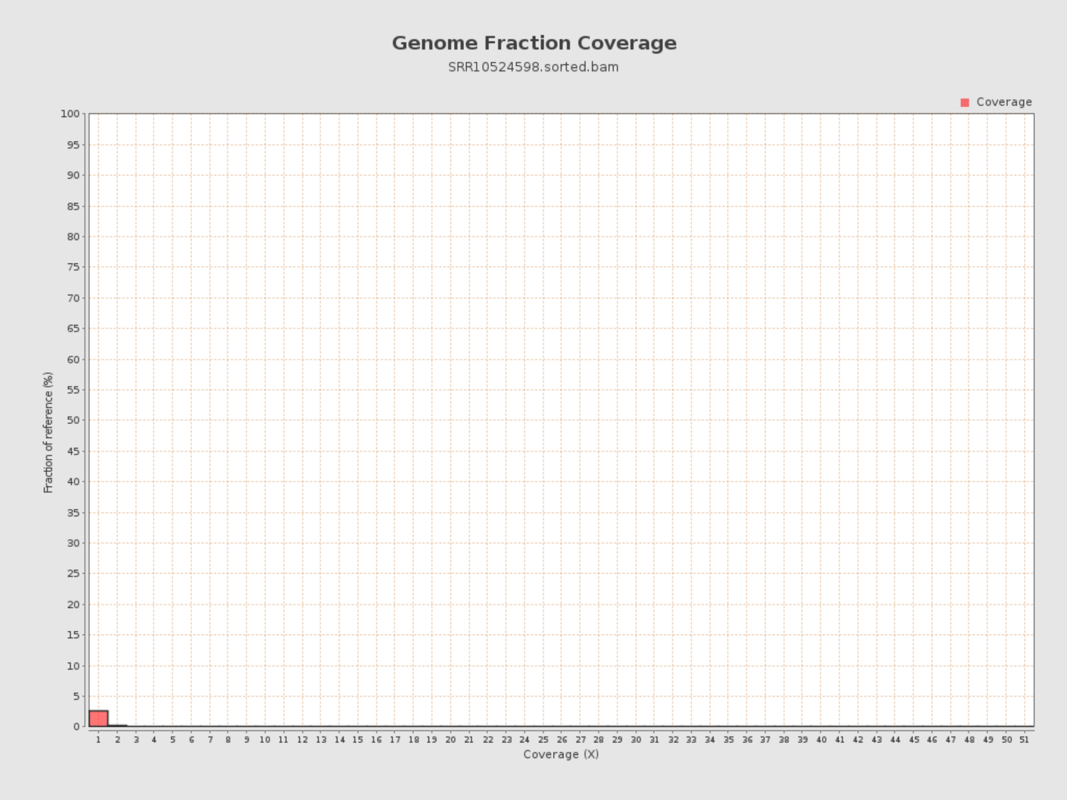
4. Results : Coverage Histogram



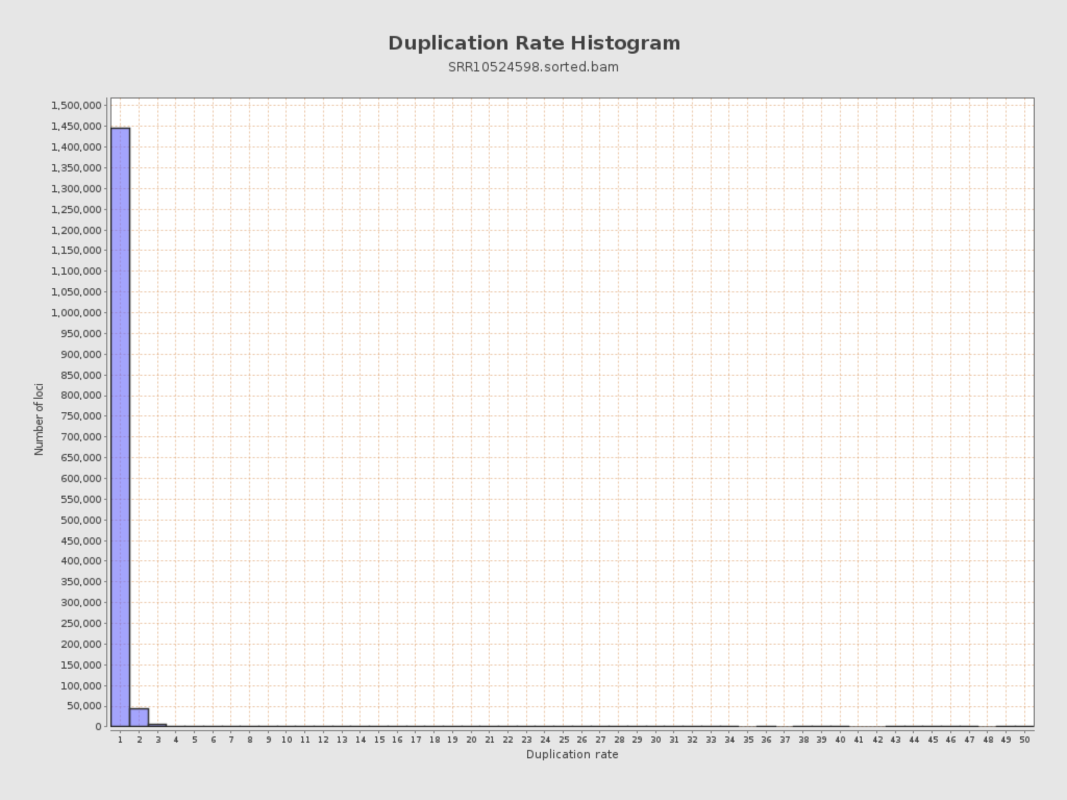
5. Results : Coverage Histogram (0-50X)



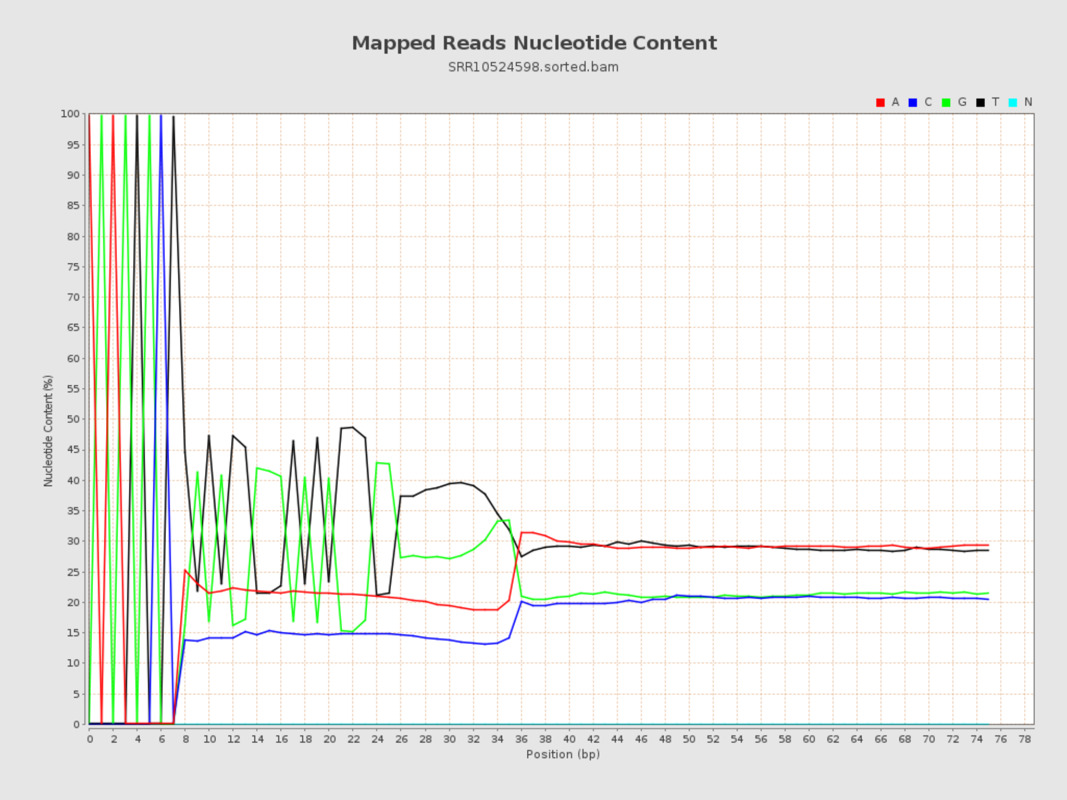
6. Results : Genome Fraction Coverage



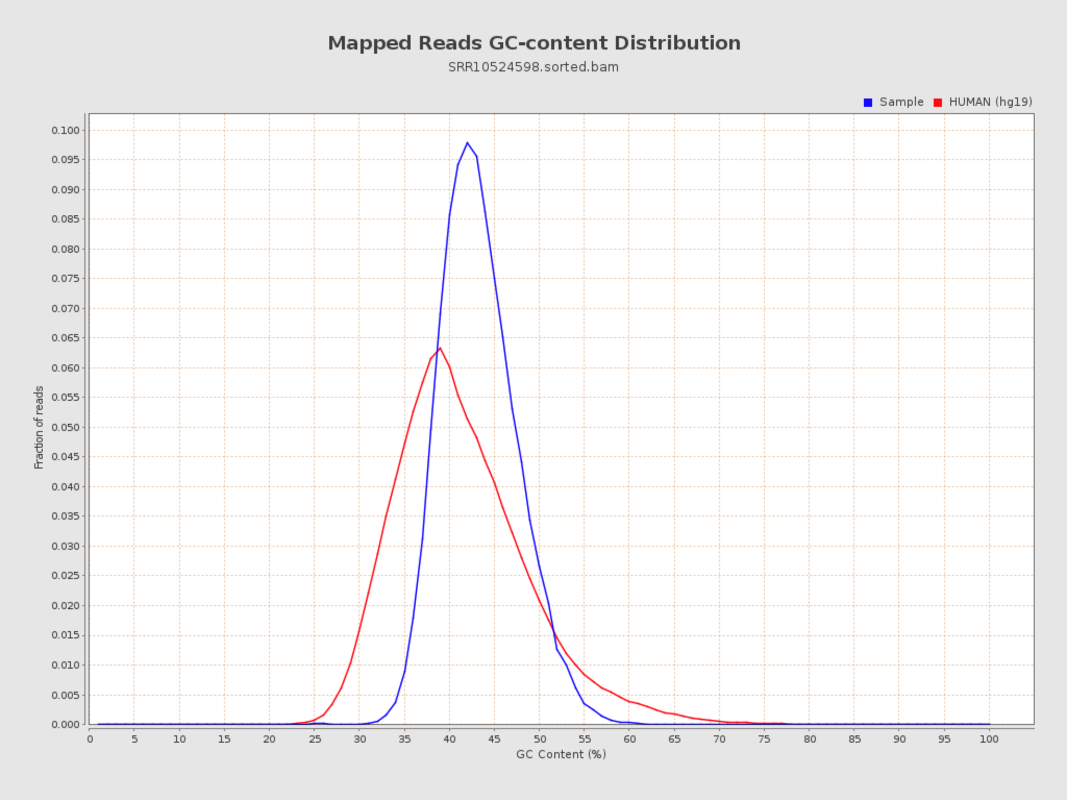
7. Results : Duplication Rate Histogram



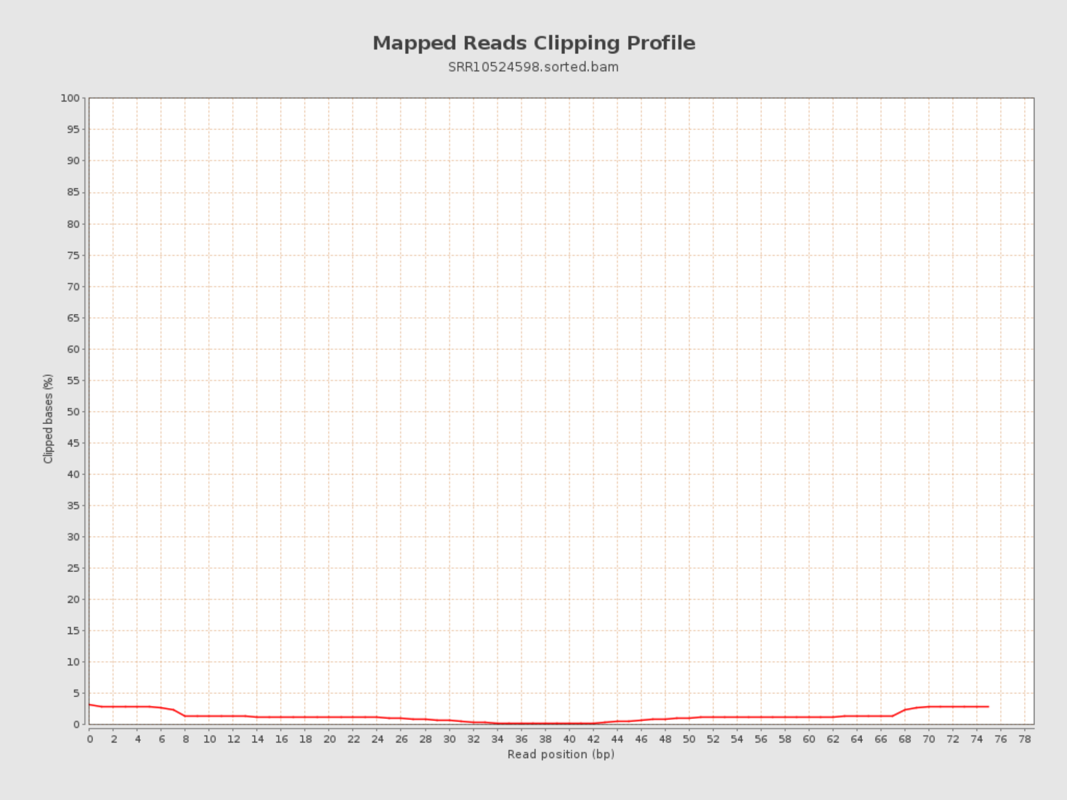
8. Results : Mapped Reads Nucleotide Content



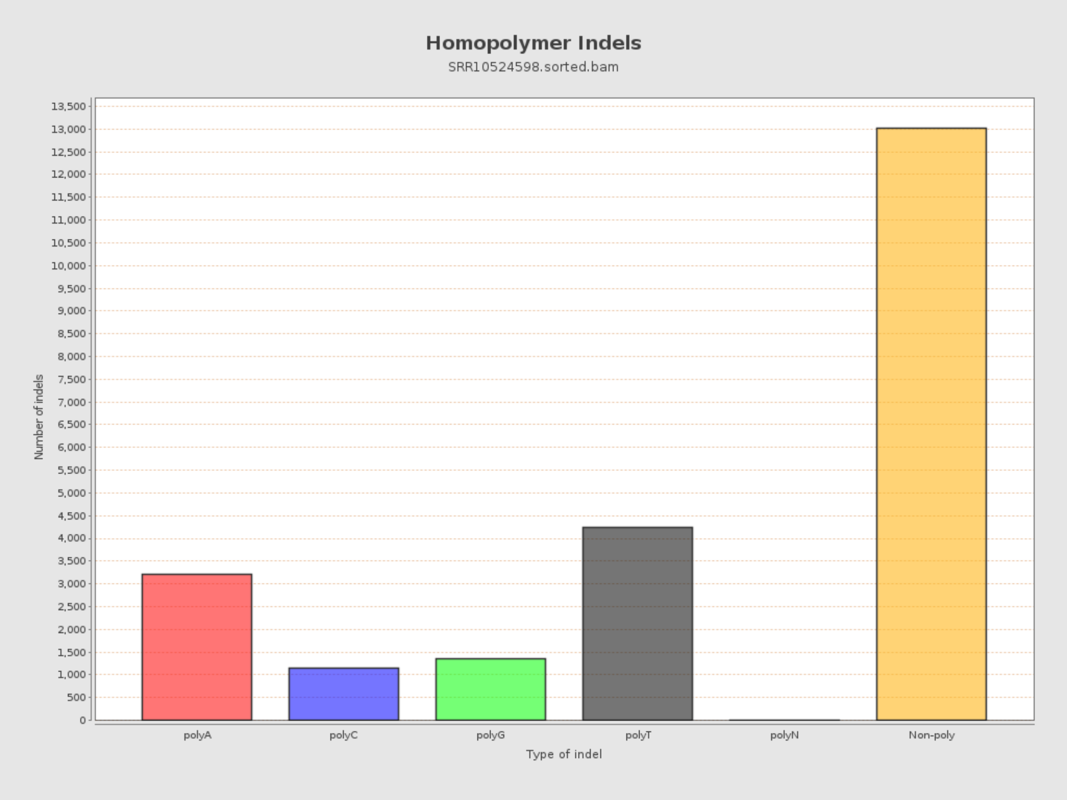
9. Results : Mapped Reads GC-content Distribution



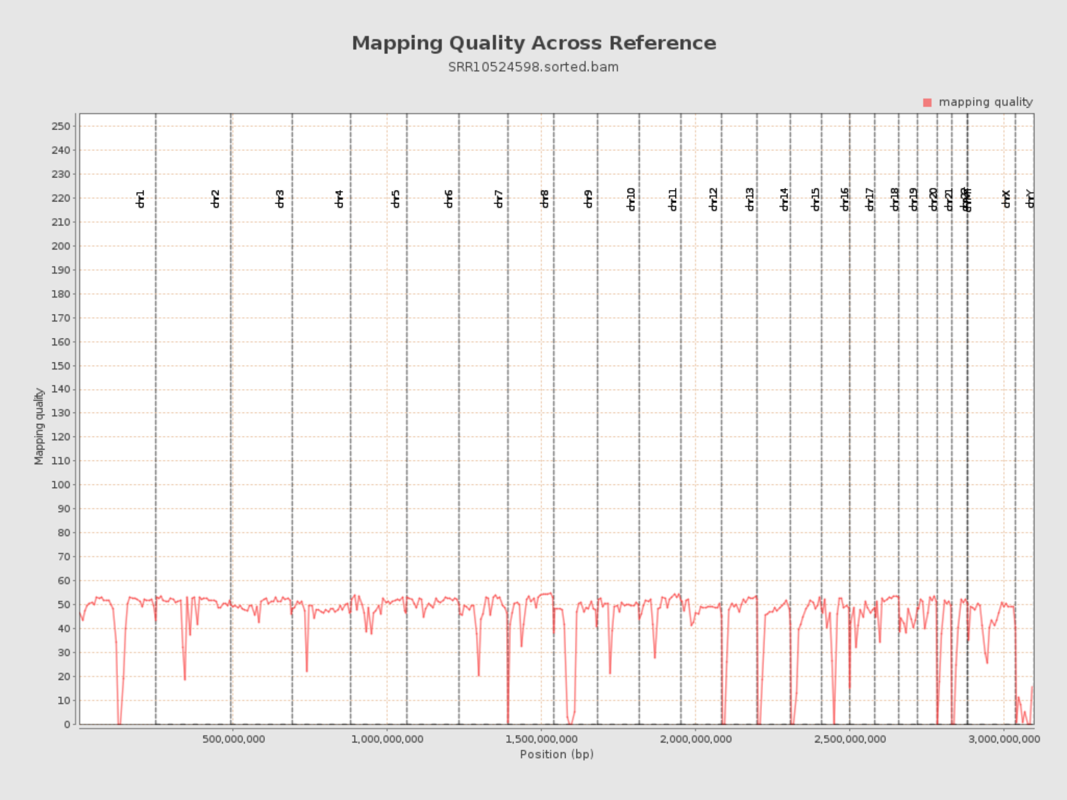
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram