Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 20:56:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524282.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_SRR10524282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 20:56:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,390,179
Mapped reads	2,220,018 / 92.88%
Unmapped reads	170,161 / 7.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,001 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	124,441 / 5.21%
Duplication rate	4.19%
Clipped reads	2,222,077 / 92.97%

2.2. ACGT Content

Number/percentage of A's	32,817,423 / 25.19%
Number/percentage of C's	24,066,547 / 18.47%
Number/percentage of T's	42,062,016 / 32.28%
Number/percentage of G's	31,327,748 / 24.04%
Number/percentage of N's	17,336 / 0.01%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.4107

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

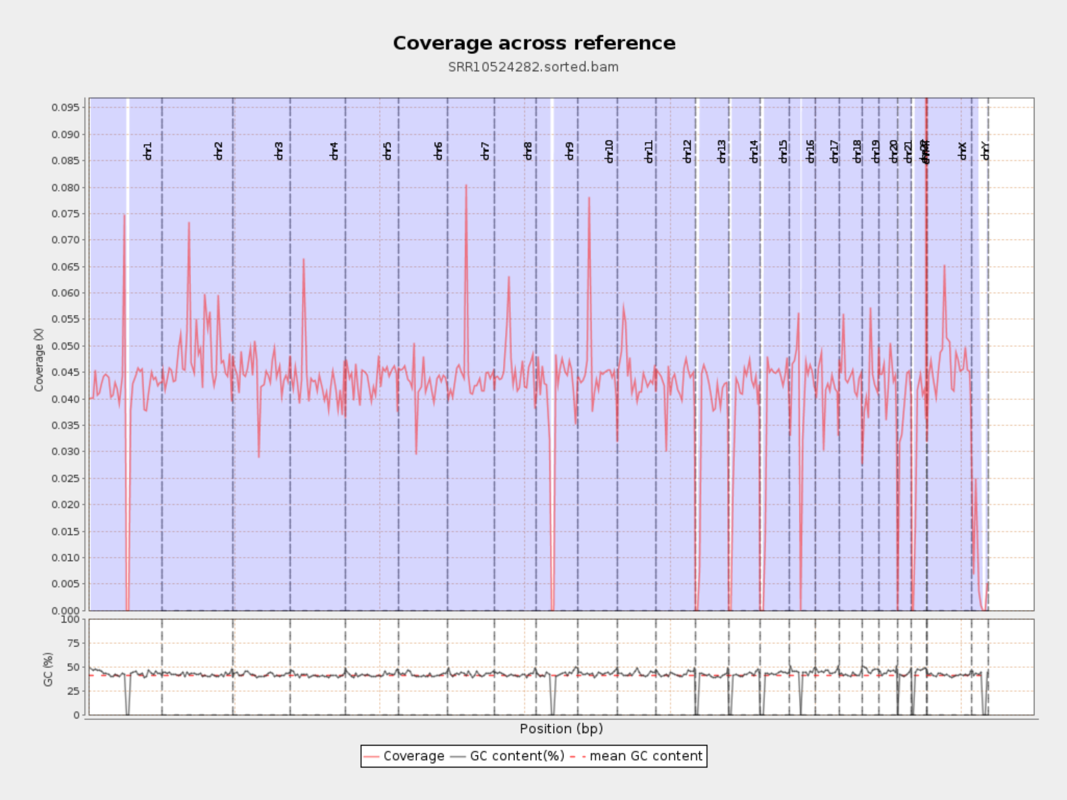
General error rate	0.5%
Mismatches	628,467
Insertions	9,825
Mapped reads with at least one insertion	0.44%
Deletions	24,547
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.84%

2.6. Chromosome stats

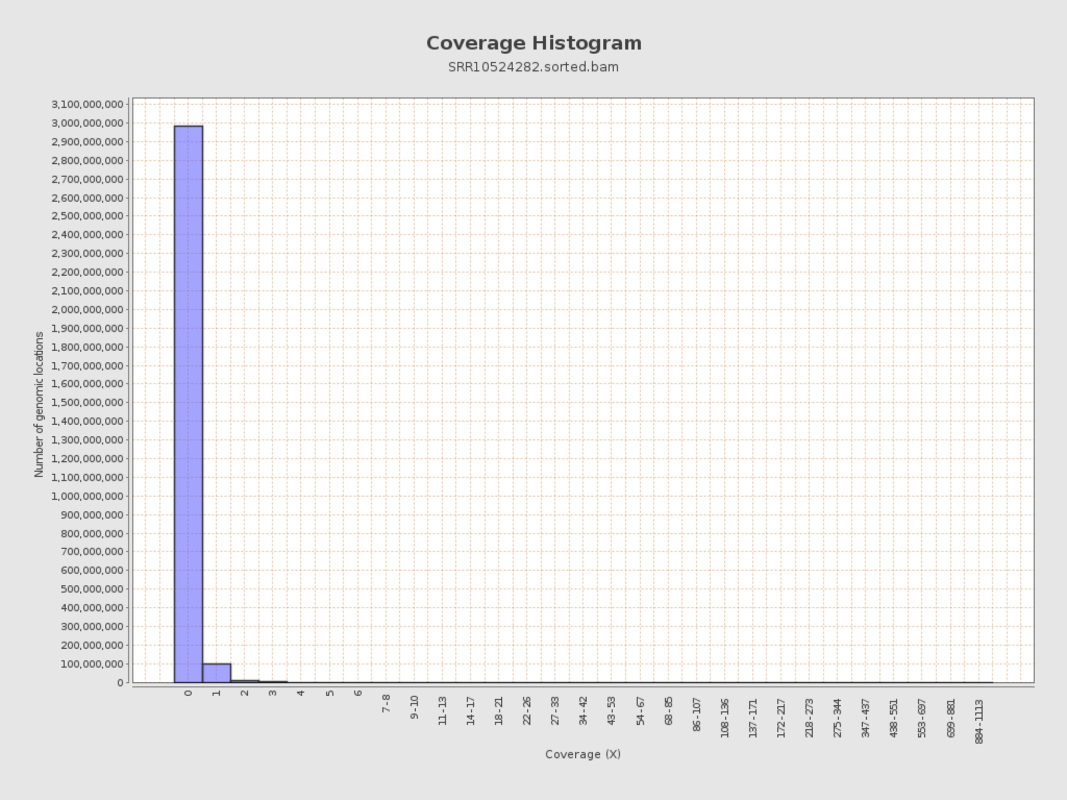
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10166019	0.0408	0.8315
chr2	243199373	11788994	0.0485	0.424
chr3	198022430	8834859	0.0446	0.2364
chr4	191154276	8246815	0.0431	0.2689
chr5	180915260	7942663	0.0439	0.2371
chr6	171115067	7400221	0.0432	0.2638
chr7	159138663	7171362	0.0451	0.6045

chr8	146364022	6696835	0.0458	0.4028
chr9	141213431	5469892	0.0387	0.3449
chr10	135534747	6186110	0.0456	0.3613
chr11	135006516	6062835	0.0449	0.3563
chr12	133851895	5751646	0.043	0.241
chr13	115169878	4035633	0.035	0.214
chr14	107349540	3897623	0.0363	0.2326
chr15	102531392	3729466	0.0364	0.2144
chr16	90354753	3717666	0.0411	0.2575
chr17	81195210	3361715	0.0414	0.2554
chr18	78077248	3508284	0.0449	0.7336
chr19	59128983	2505160	0.0424	0.565
chr20	63025520	2738576	0.0435	0.239
chr21	48129895	1690654	0.0351	0.2404
chr22	51304566	1501365	0.0293	0.1907
chrMT	16571	284218	17.1515	10.0911
chrX	155270560	7231430	0.0466	0.2893
chrY	59373566	409485	0.0069	0.1866

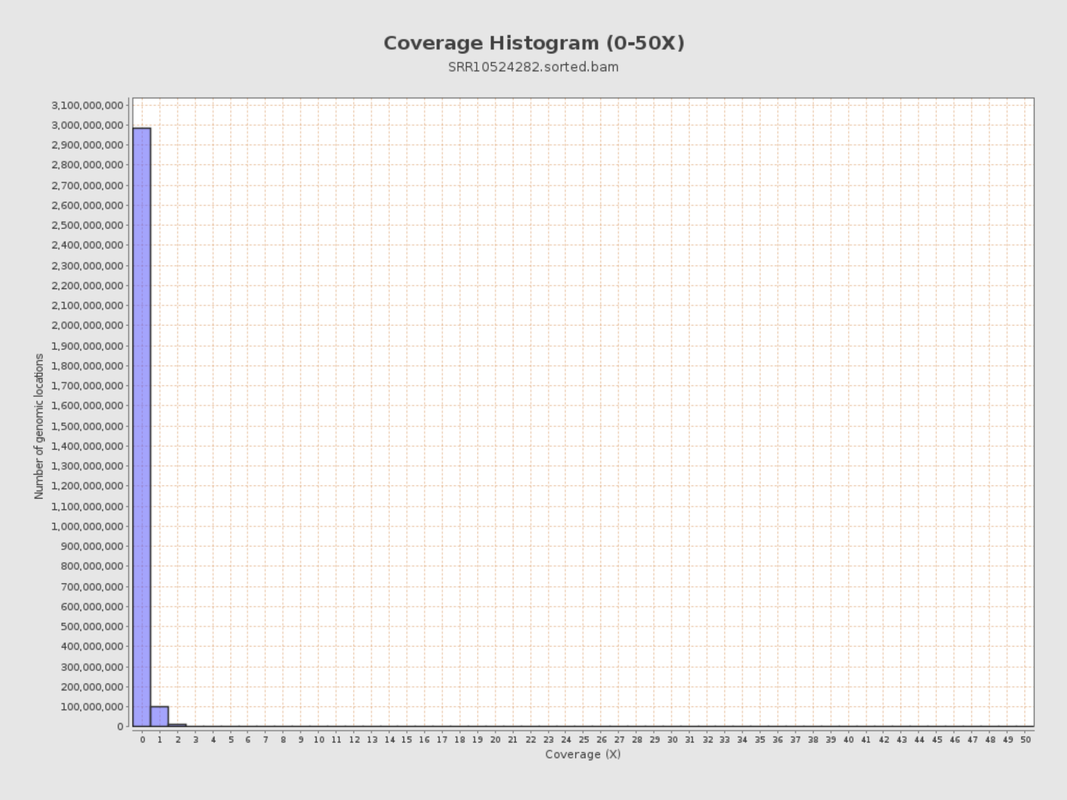
3. Results : Coverage across reference



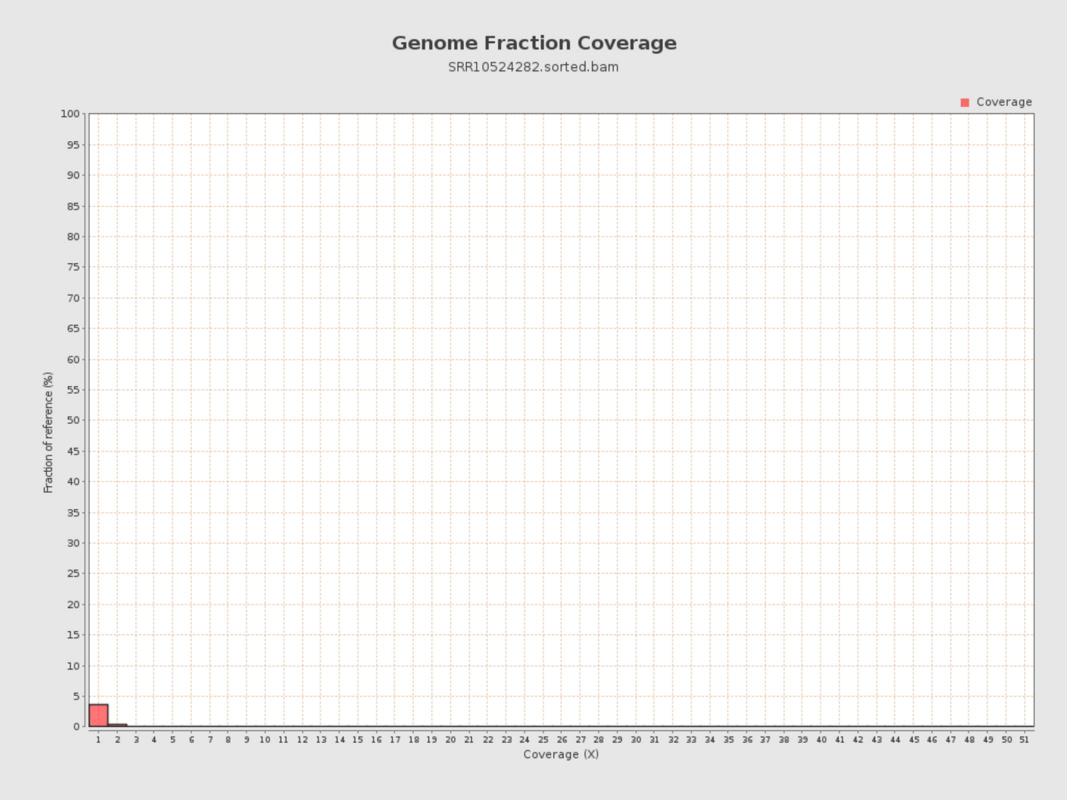
4. Results : Coverage Histogram



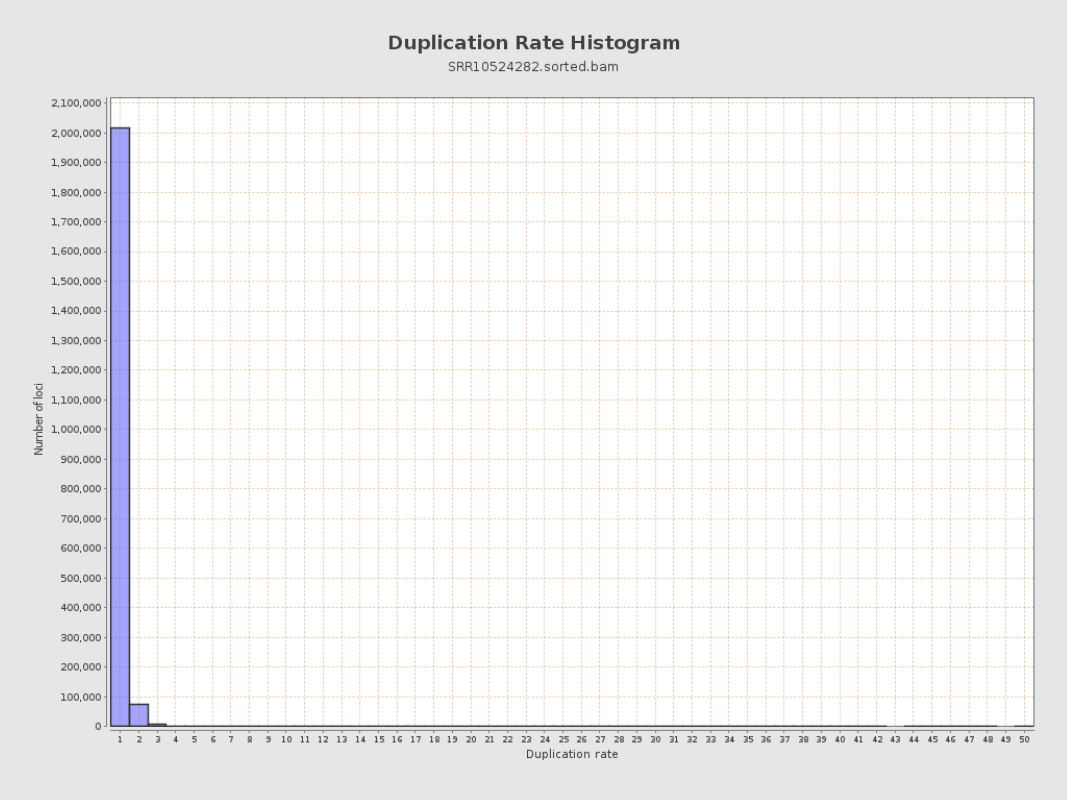
5. Results : Coverage Histogram (0-50X)



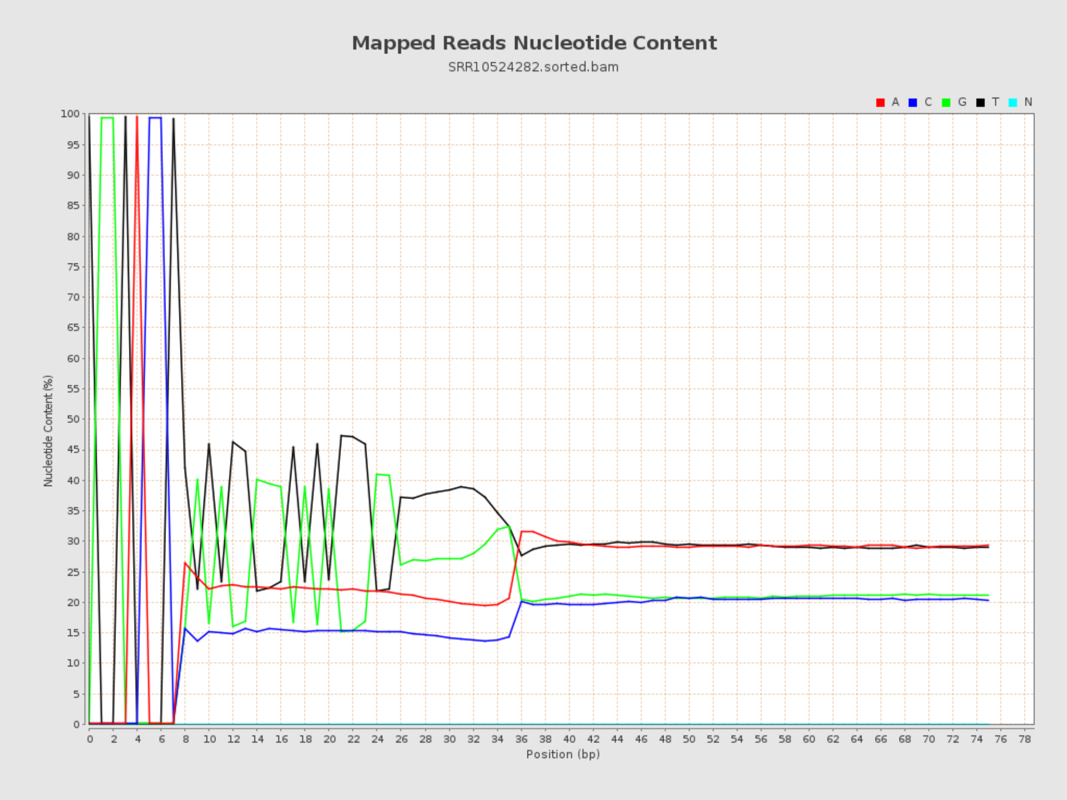
6. Results : Genome Fraction Coverage



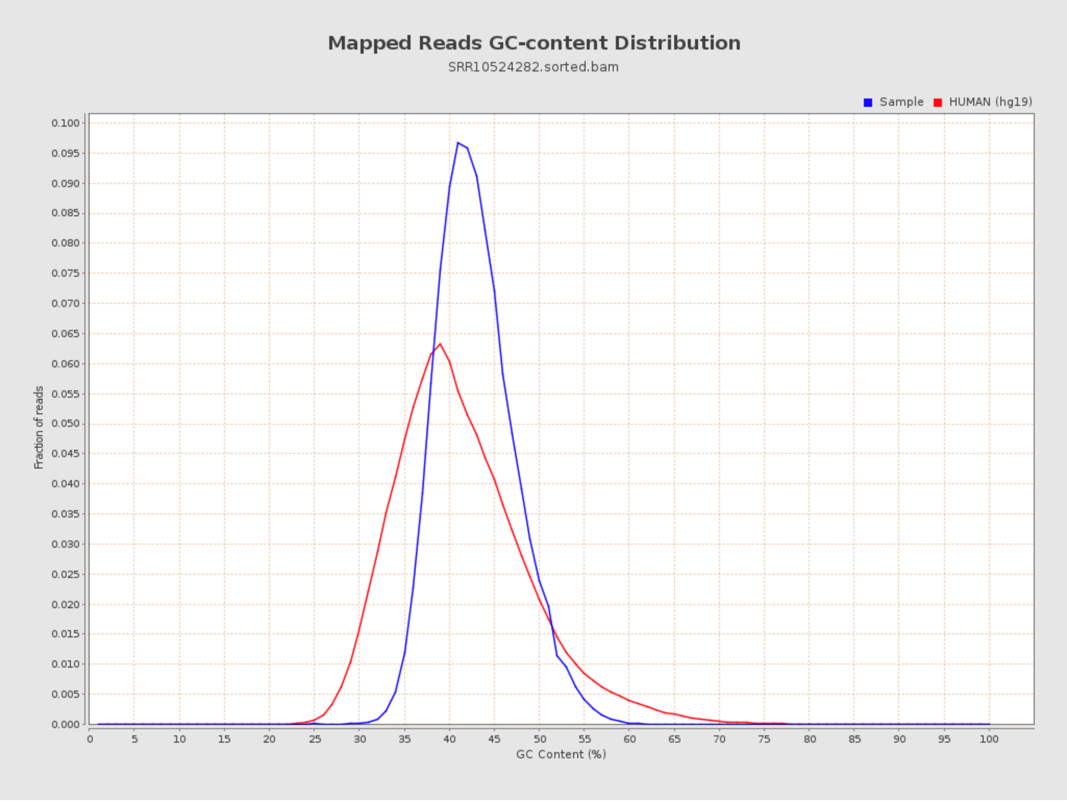
7. Results : Duplication Rate Histogram



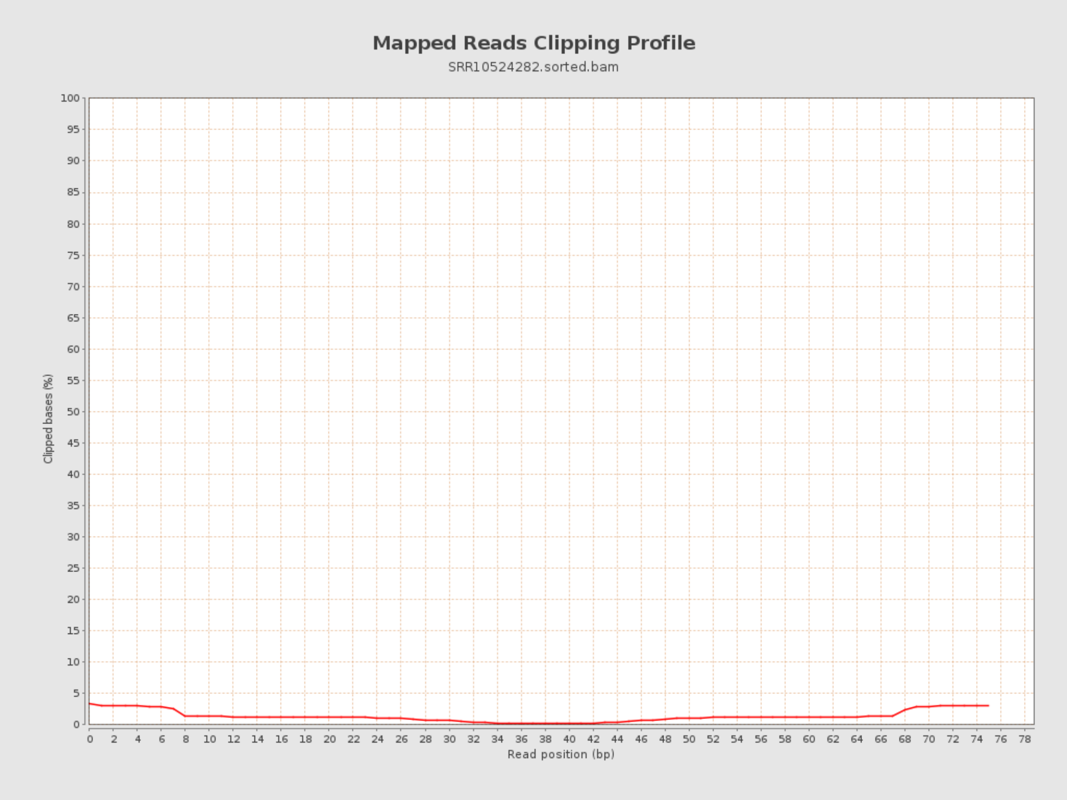
8. Results : Mapped Reads Nucleotide Content



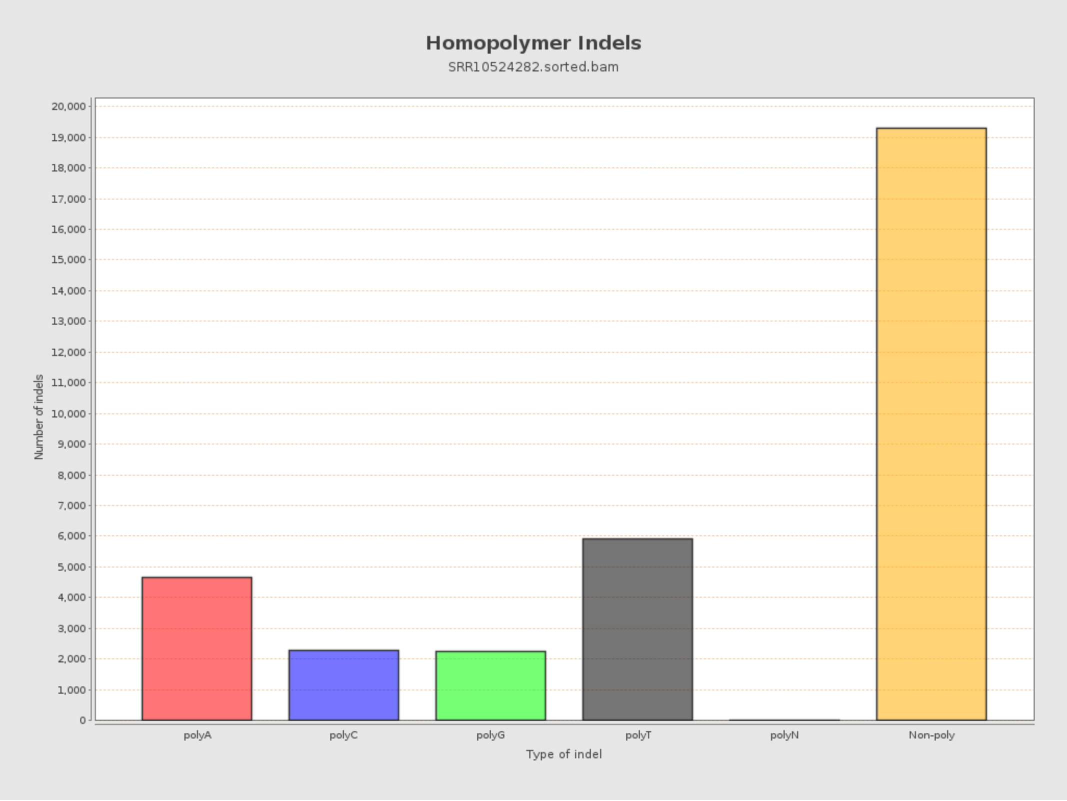
9. Results : Mapped Reads GC-content Distribution



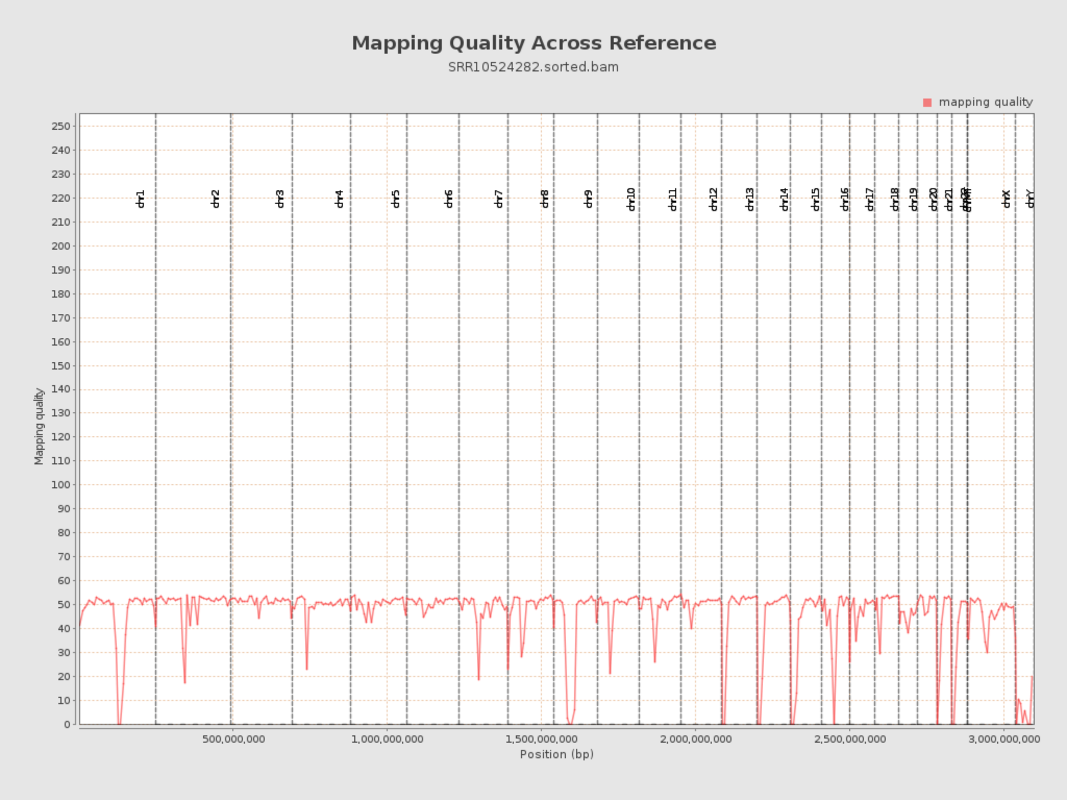
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram