Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:56:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524462.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_SRR10524462 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524462.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:56:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524462.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,945,054
Mapped reads	2,716,634 / 92.24%
Unmapped reads	228,420 / 7.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,237 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	162,441 / 5.52%
Duplication rate	4.52%
Clipped reads	2,713,538 / 92.14%

2.2. ACGT Content

Number/percentage of A's	40,680,065 / 25.69%
Number/percentage of C's	29,342,599 / 18.53%
Number/percentage of T's	50,792,927 / 32.07%
Number/percentage of G's	37,540,247 / 23.71%
Number/percentage of N's	3,226 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.4289

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

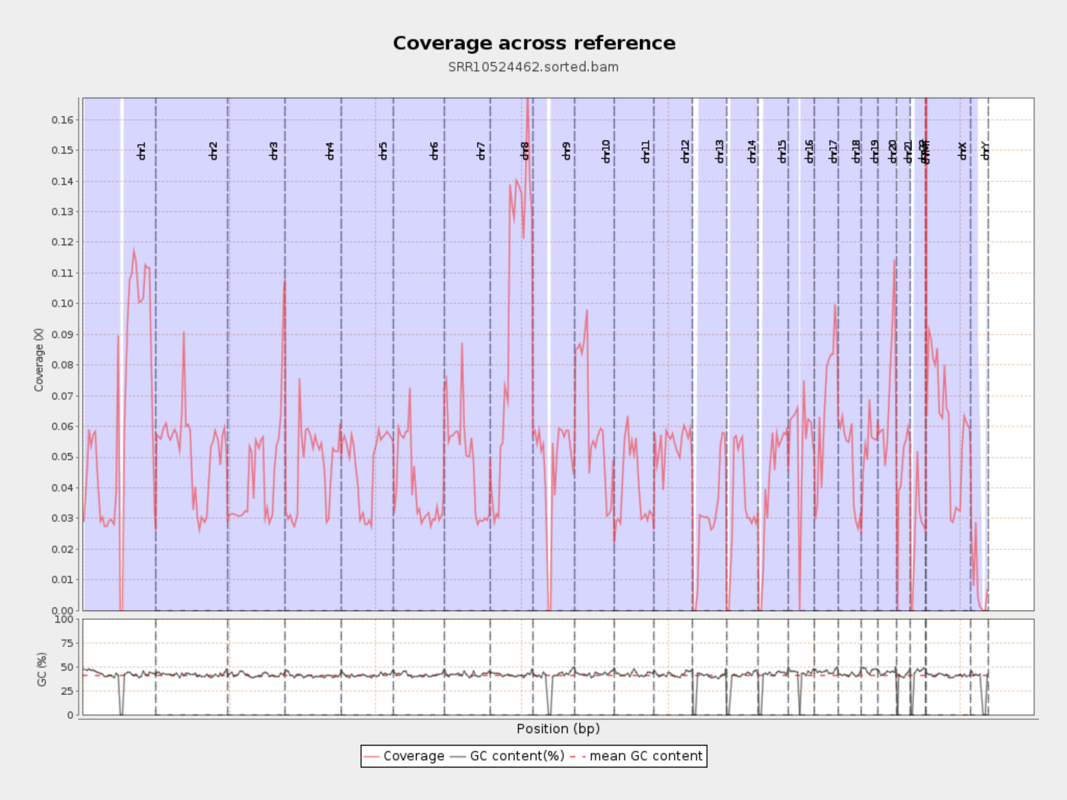
General error rate	0.48%
Mismatches	741,266
Insertions	10,542
Mapped reads with at least one insertion	0.39%
Deletions	29,417
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.05%

2.6. Chromosome stats

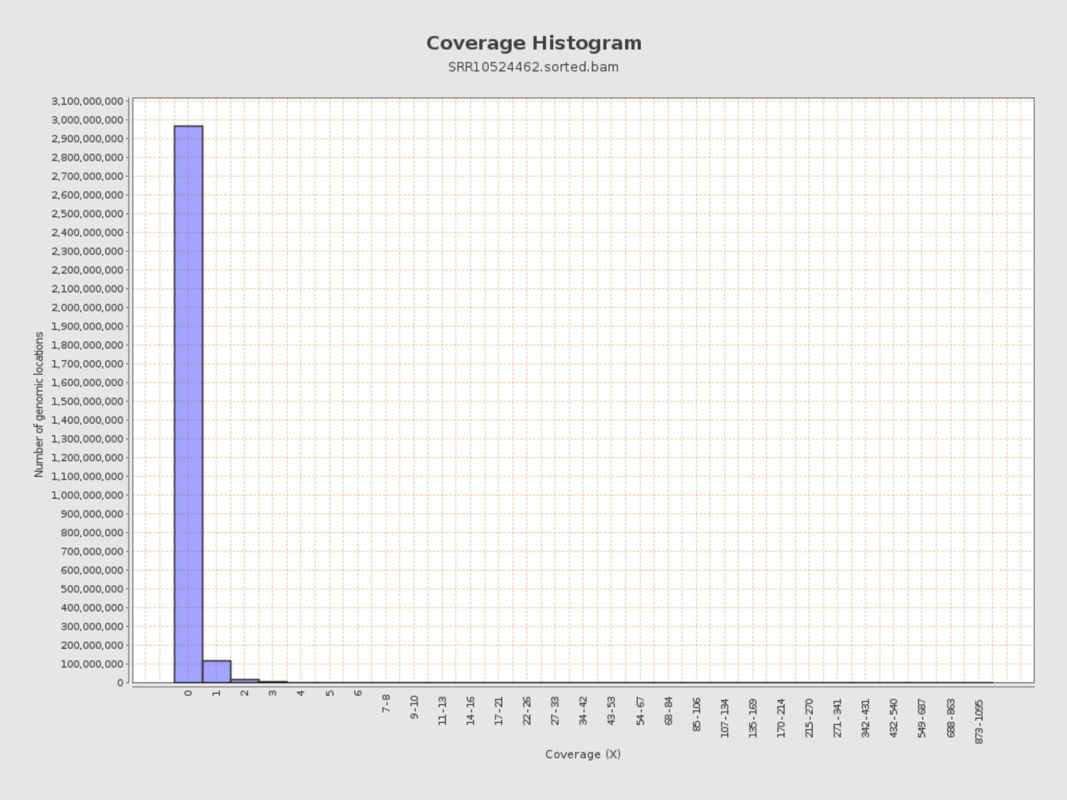
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15594148	0.0626	0.826
chr2	243199373	12632166	0.0519	0.4826
chr3	198022430	8722339	0.044	0.247
chr4	191154276	8987721	0.047	0.3037
chr5	180915260	8614154	0.0476	0.2568
chr6	171115067	6889051	0.0403	0.3199
chr7	159138663	7881472	0.0495	0.58

chr8	146364022	14564336	0.0995	0.4533
chr9	141213431	6685996	0.0473	0.3737
chr10	135534747	8281040	0.0611	0.4357
chr11	135006516	5383304	0.0399	0.4009
chr12	133851895	7302513	0.0546	0.2735
chr13	115169878	3570839	0.031	0.2095
chr14	107349540	3758730	0.035	0.2272
chr15	102531392	4147661	0.0405	0.2555
chr16	90354753	4925808	0.0545	0.3004
chr17	81195210	5465081	0.0673	0.329
chr18	78077248	3786137	0.0485	0.6819
chr19	59128983	3188406	0.0539	0.5611
chr20	63025520	4499615	0.0714	0.3189
chr21	48129895	2191573	0.0455	0.2814
chr22	51304566	1278670	0.0249	0.1821
chrMT	16571	70855	4.2758	3.1752
chrX	155270560	9482875	0.0611	0.3409
chrY	59373566	505151	0.0085	0.2098

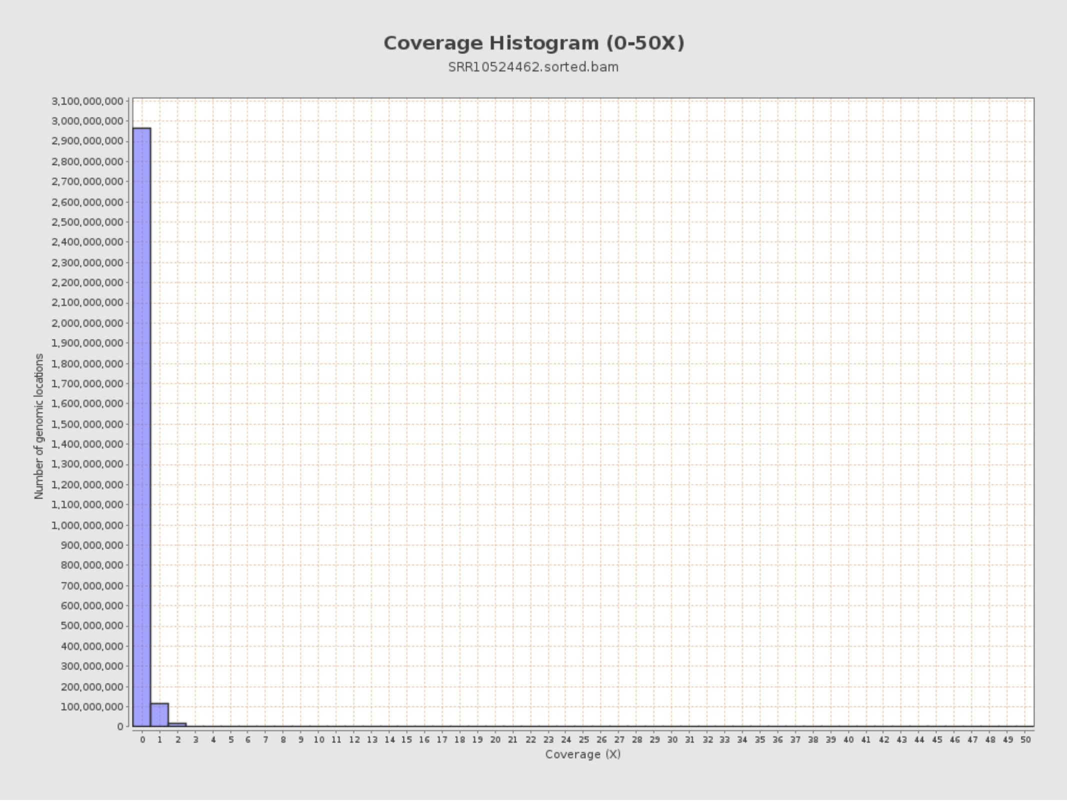
3. Results : Coverage across reference



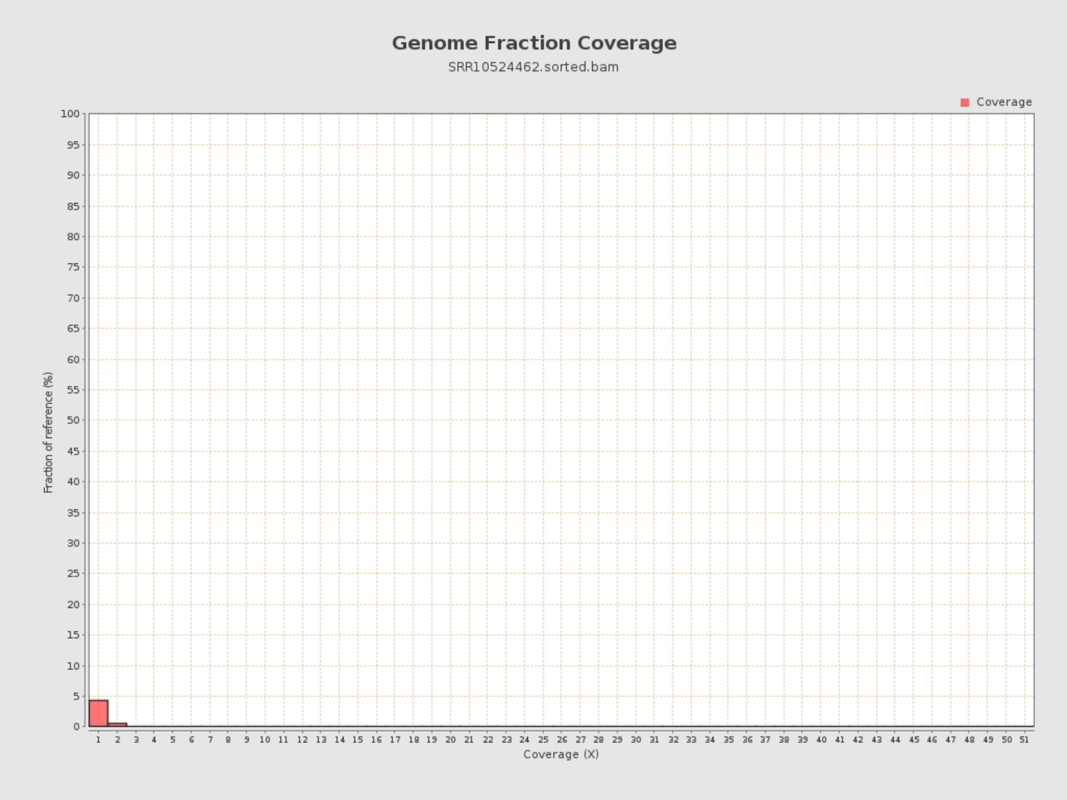
4. Results : Coverage Histogram



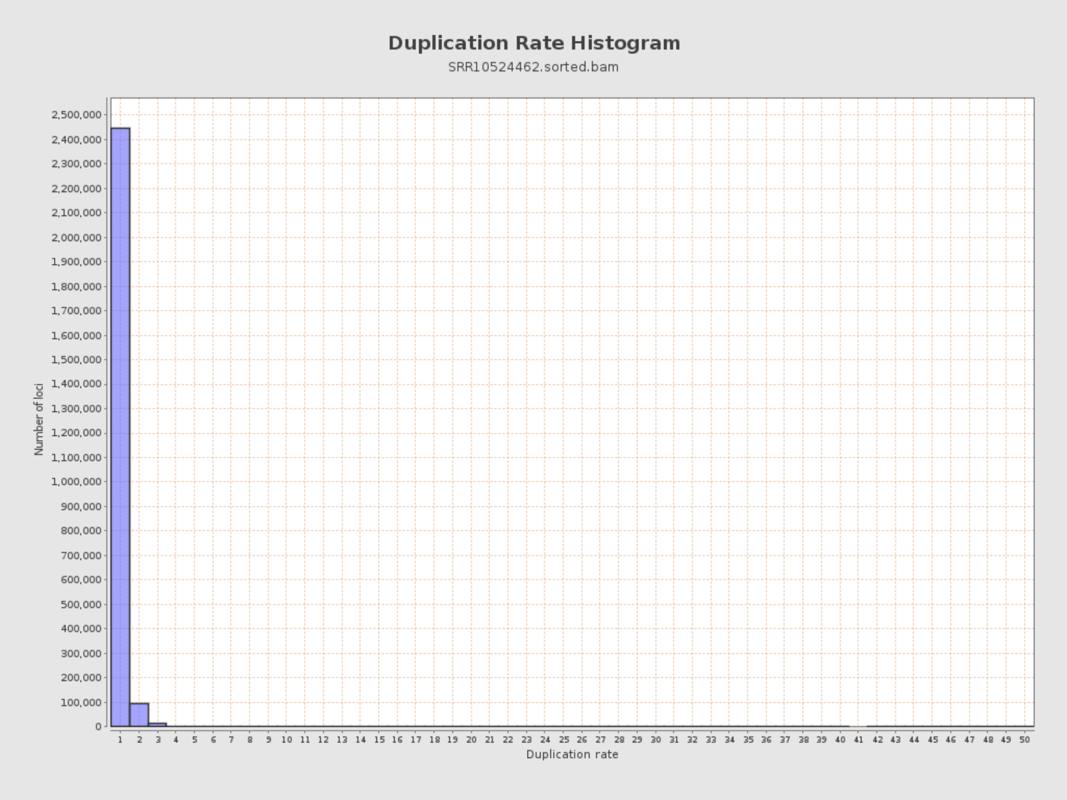
5. Results : Coverage Histogram (0-50X)



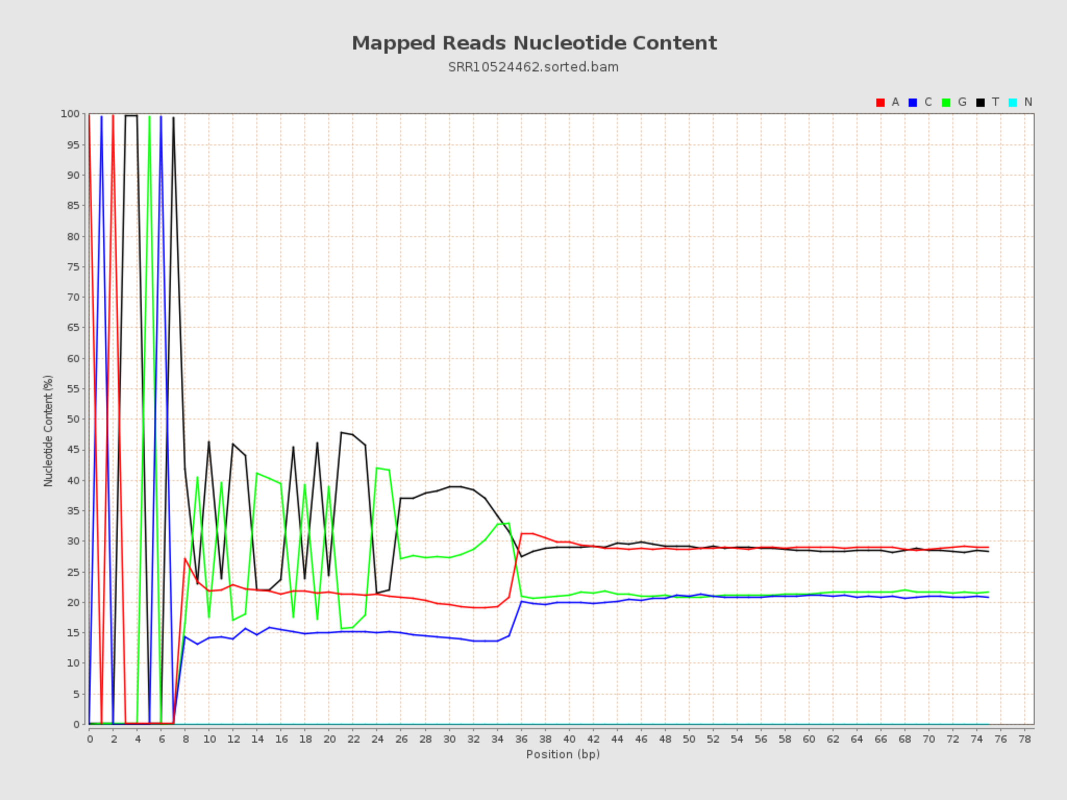
6. Results : Genome Fraction Coverage



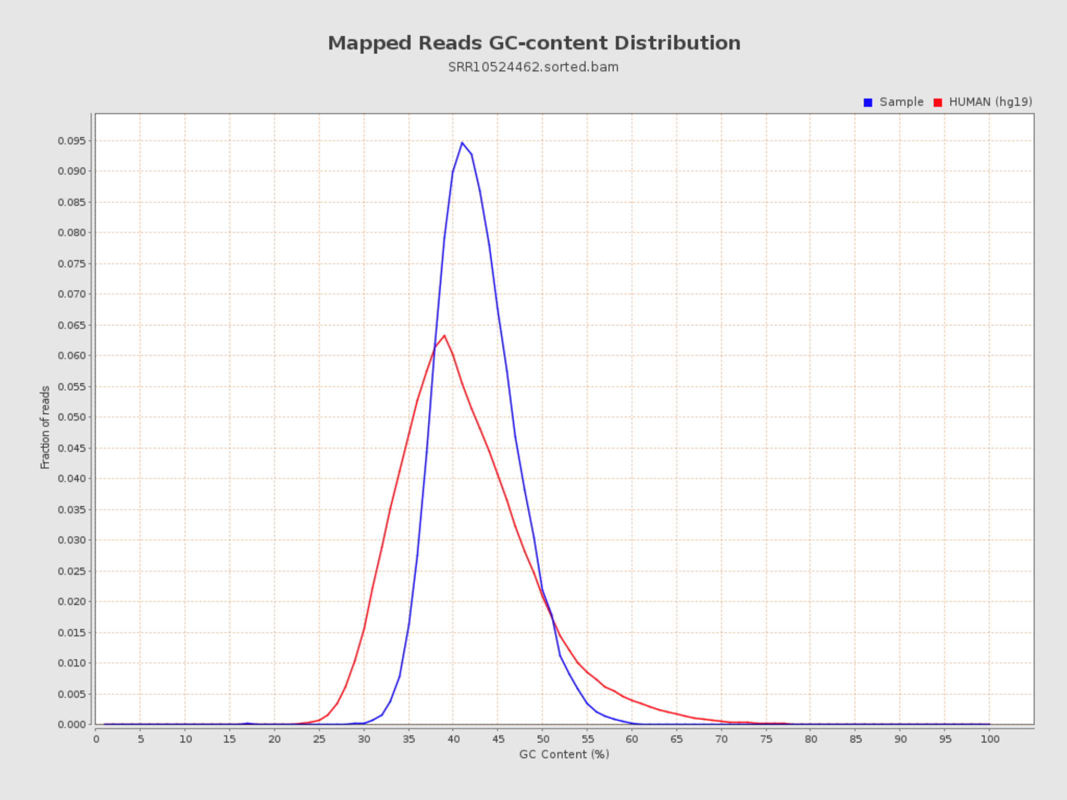
7. Results : Duplication Rate Histogram



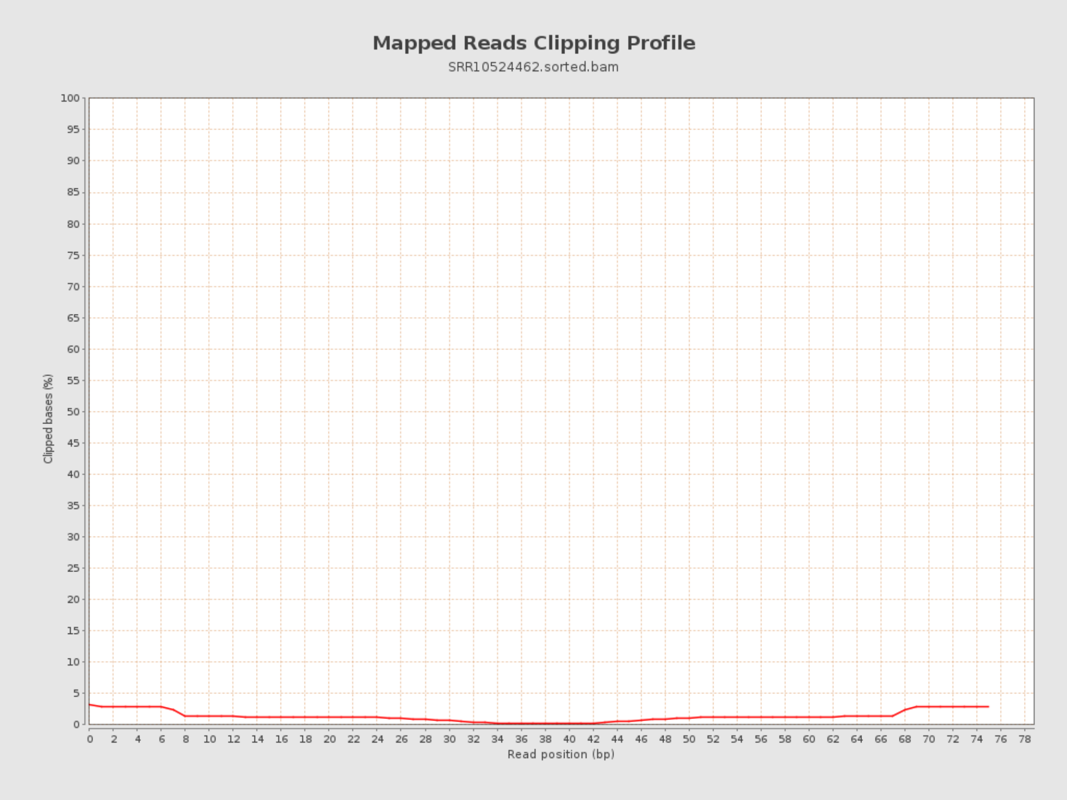
8. Results : Mapped Reads Nucleotide Content



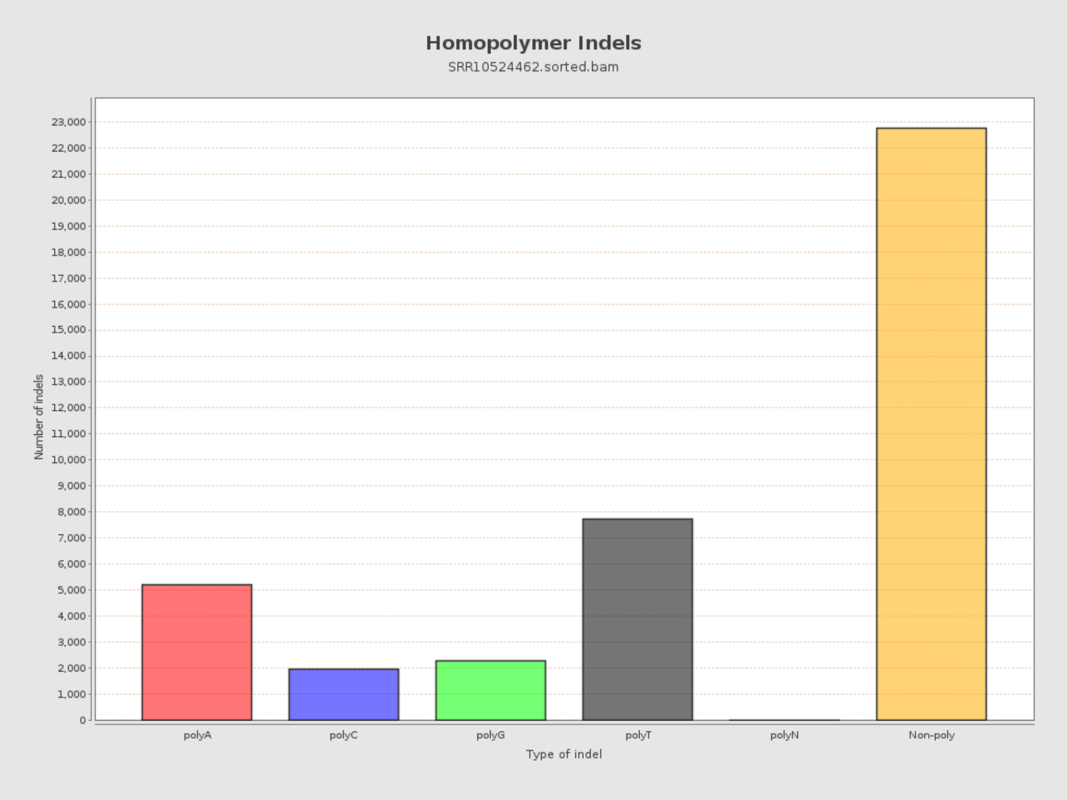
9. Results : Mapped Reads GC-content Distribution



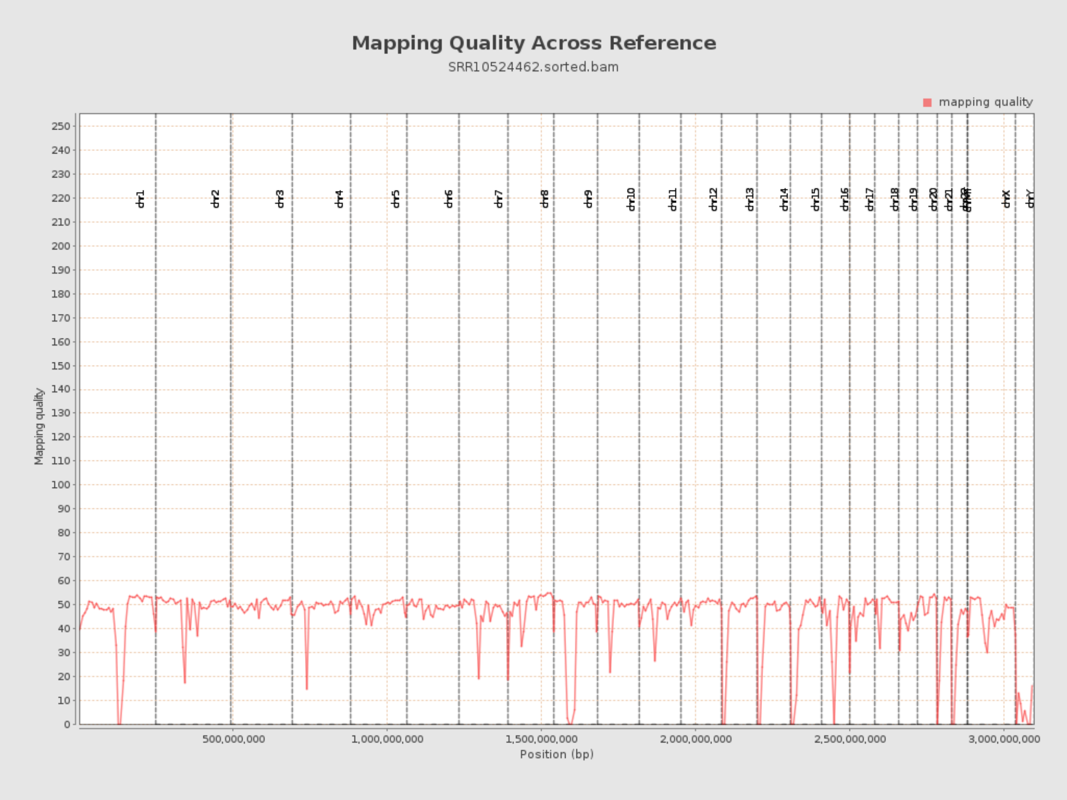
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram