Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:01:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524467.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_SRR10524467 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524467.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:01:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524467.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,449,375
Mapped reads	2,242,560 / 91.56%
Unmapped reads	206,815 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,186 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	122,291 / 4.99%
Duplication rate	4.13%
Clipped reads	2,242,856 / 91.57%

2.2. ACGT Content

Number/percentage of A's	33,611,832 / 25.75%
Number/percentage of C's	24,144,140 / 18.49%
Number/percentage of T's	41,842,376 / 32.05%
Number/percentage of G's	30,951,543 / 23.71%
Number/percentage of N's	2,864 / 0%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.3685

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

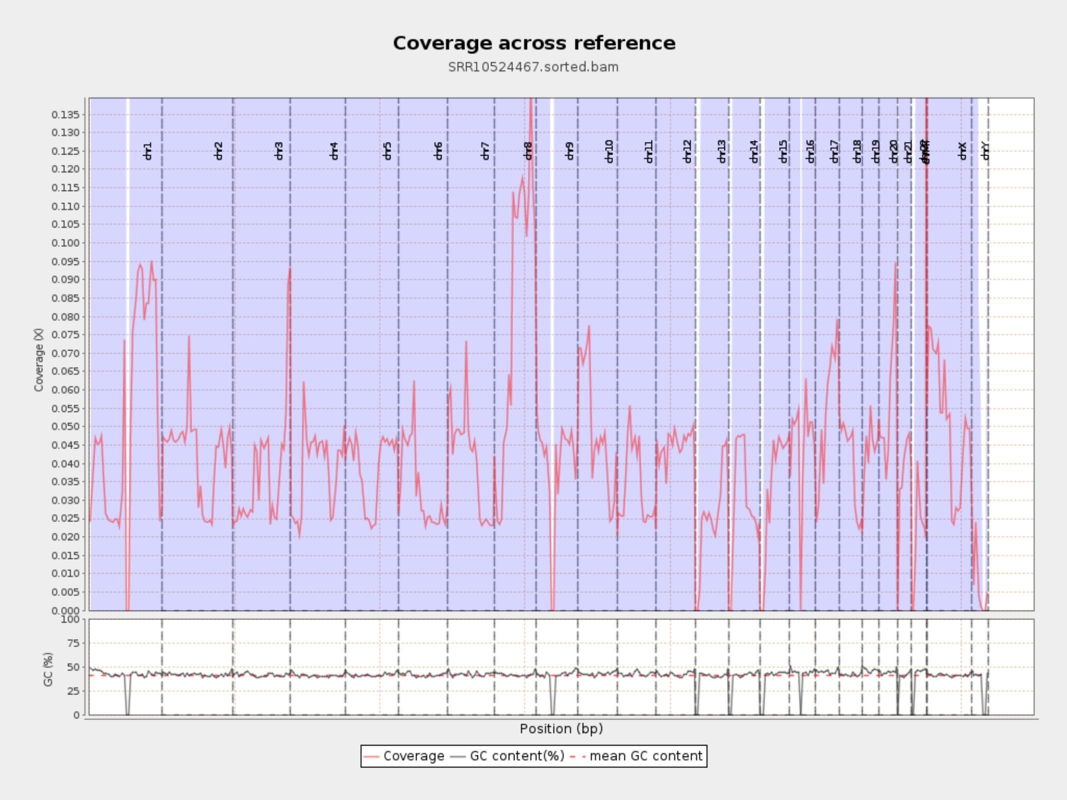
General error rate	0.48%
Mismatches	607,459
Insertions	8,915
Mapped reads with at least one insertion	0.4%
Deletions	23,454
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.84%

2.6. Chromosome stats

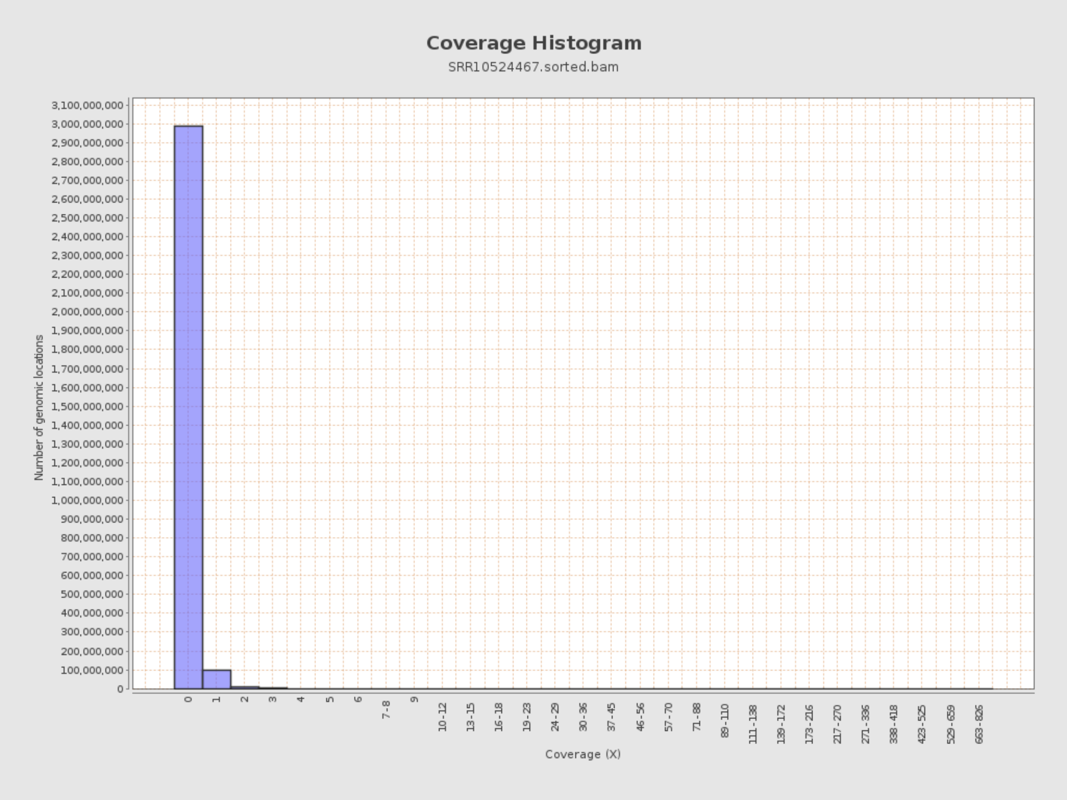
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12806912	0.0514	0.6772
chr2	243199373	10397858	0.0428	0.4356
chr3	198022430	7247449	0.0366	0.2215
chr4	191154276	7347742	0.0384	0.265
chr5	180915260	7033392	0.0389	0.2277
chr6	171115067	5669824	0.0331	0.2844
chr7	159138663	6525770	0.041	0.5071

chr8	146364022	12084979	0.0826	0.3974
chr9	141213431	5478550	0.0388	0.3209
chr10	135534747	6743824	0.0498	0.3726
chr11	135006516	4586280	0.034	0.3512
chr12	133851895	6048897	0.0452	0.2462
chr13	115169878	2922433	0.0254	0.1868
chr14	107349540	3168087	0.0295	0.2051
chr15	102531392	3393388	0.0331	0.2302
chr16	90354753	4093842	0.0453	0.2675
chr17	81195210	4456029	0.0549	0.2862
chr18	78077248	3138812	0.0402	0.5677
chr19	59128983	2625879	0.0444	0.4712
chr20	63025520	3636212	0.0577	0.2798
chr21	48129895	1764113	0.0367	0.2399
chr22	51304566	1017504	0.0198	0.1603
chrMT	16571	10626	0.6412	0.9747
chrX	155270560	7973990	0.0514	0.3046
chrY	59373566	420706	0.0071	0.1836

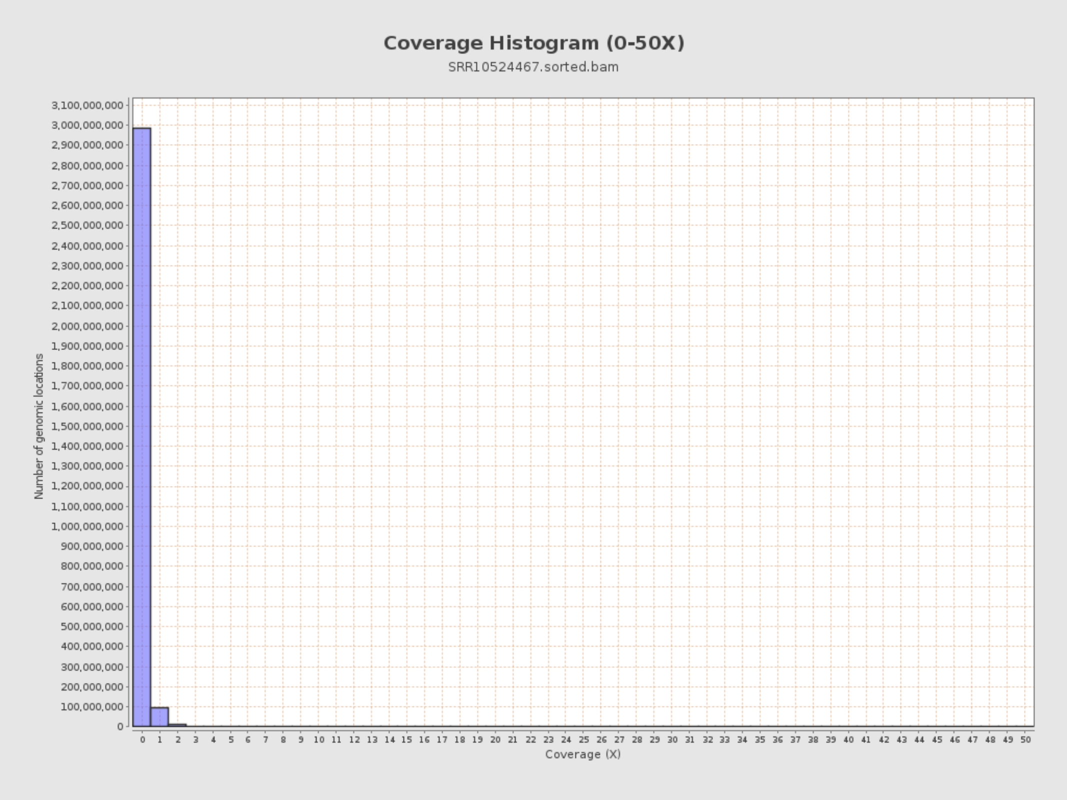
3. Results : Coverage across reference



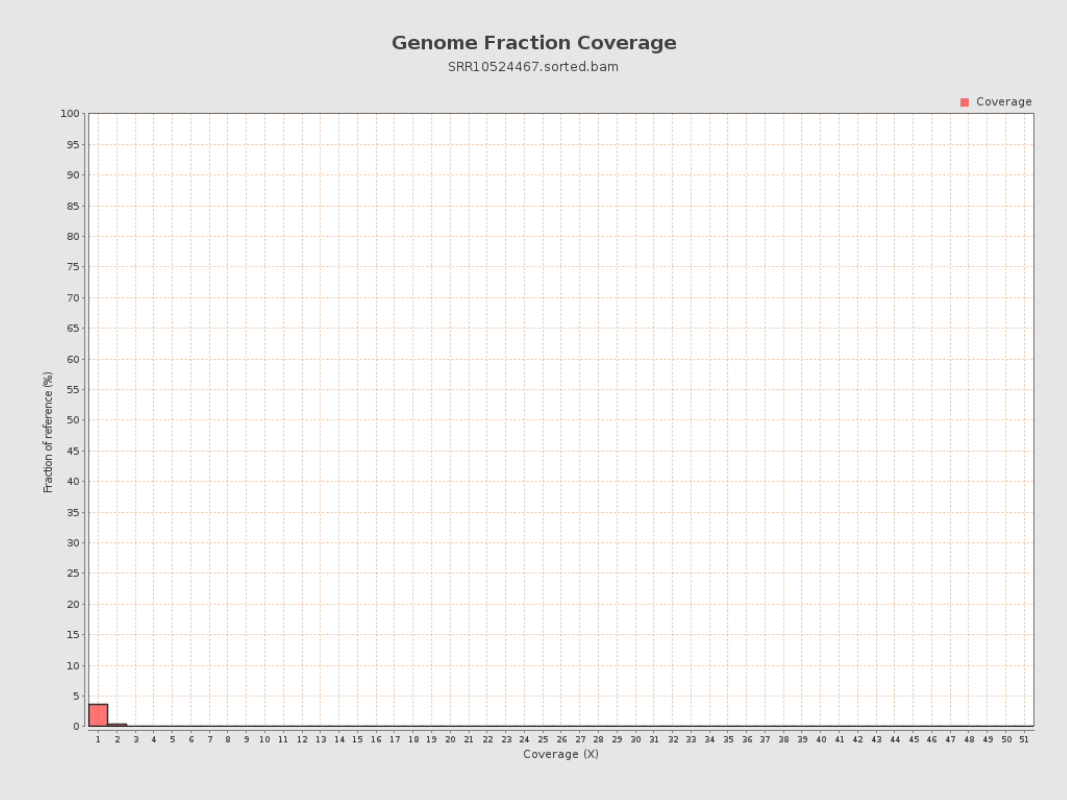
4. Results : Coverage Histogram



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



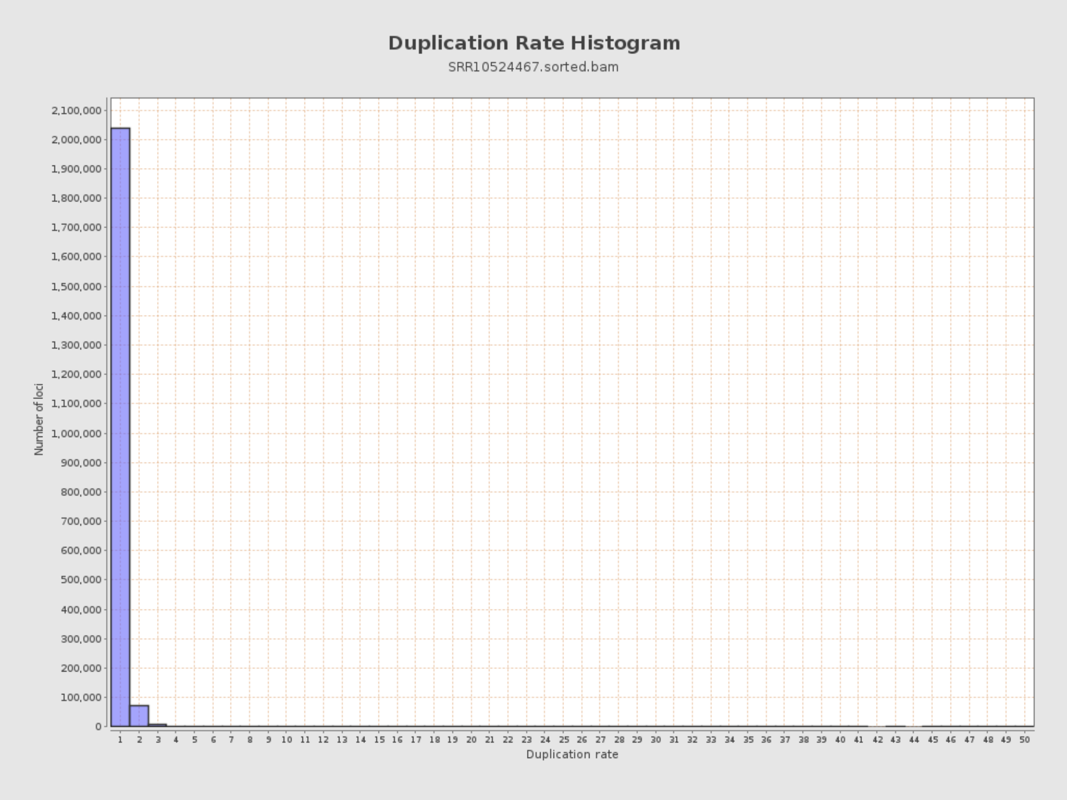
6. Results : Genome Fraction Coverage



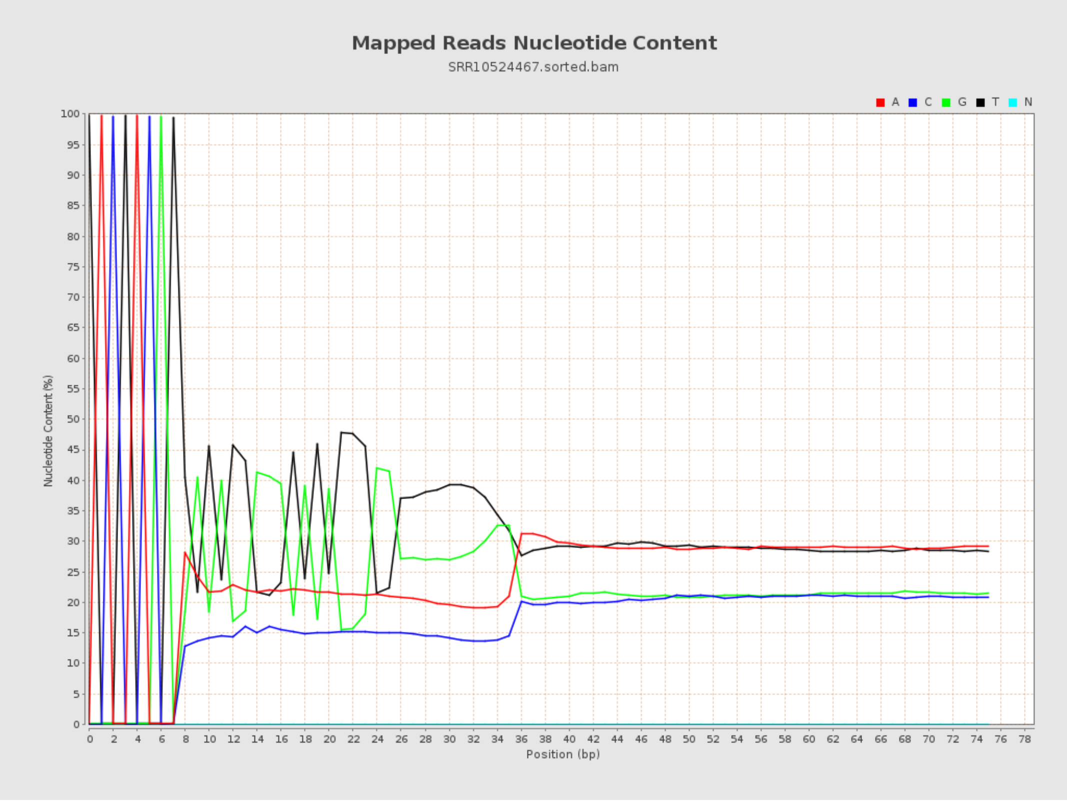
Genome Fraction Coverage

SRR10524467.sorted.bam

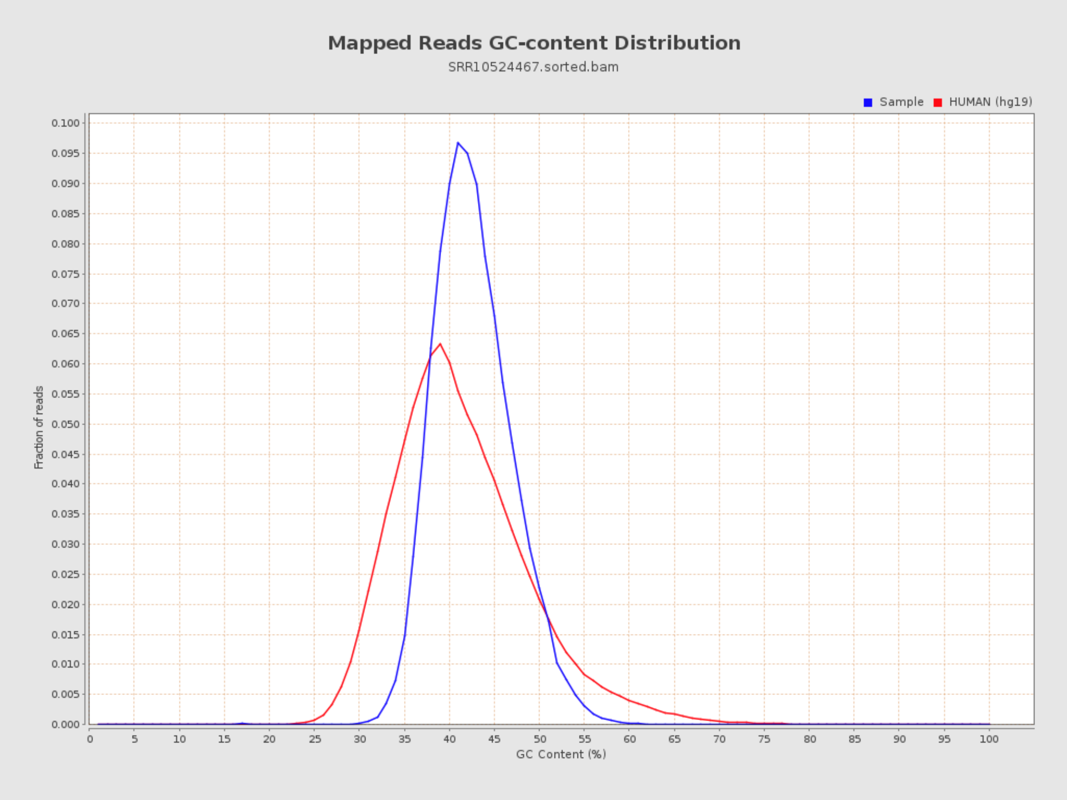
7. Results : Duplication Rate Histogram



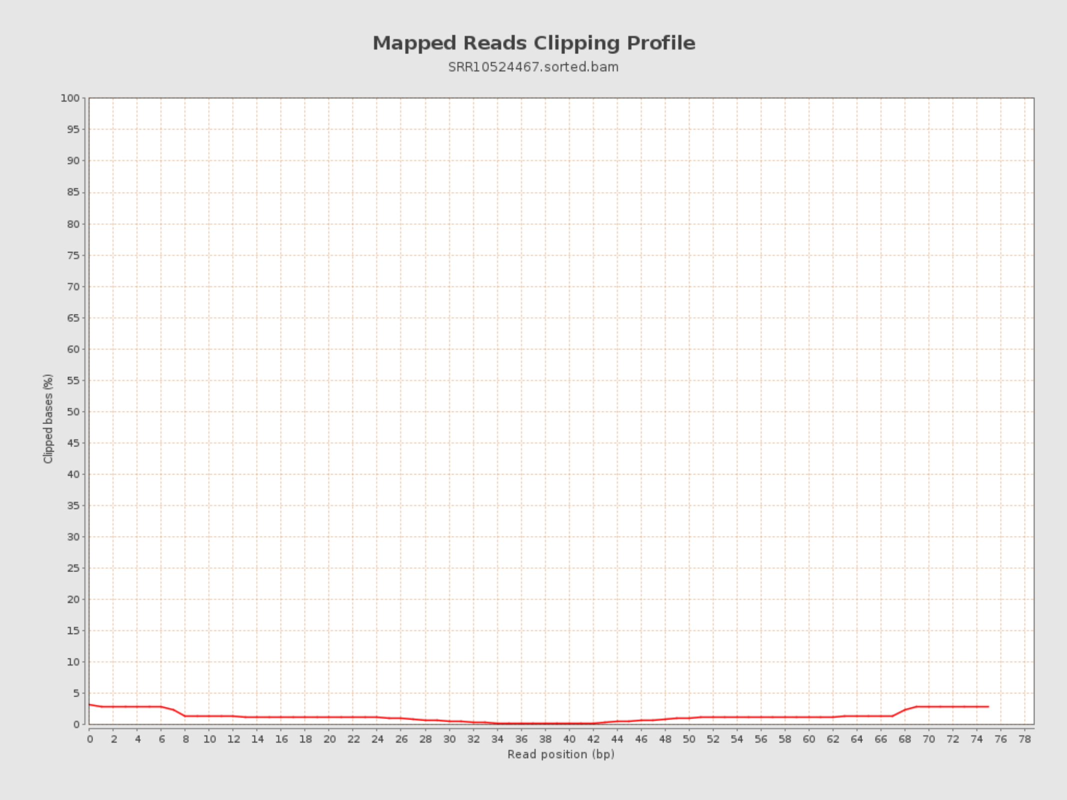
8. Results : Mapped Reads Nucleotide Content



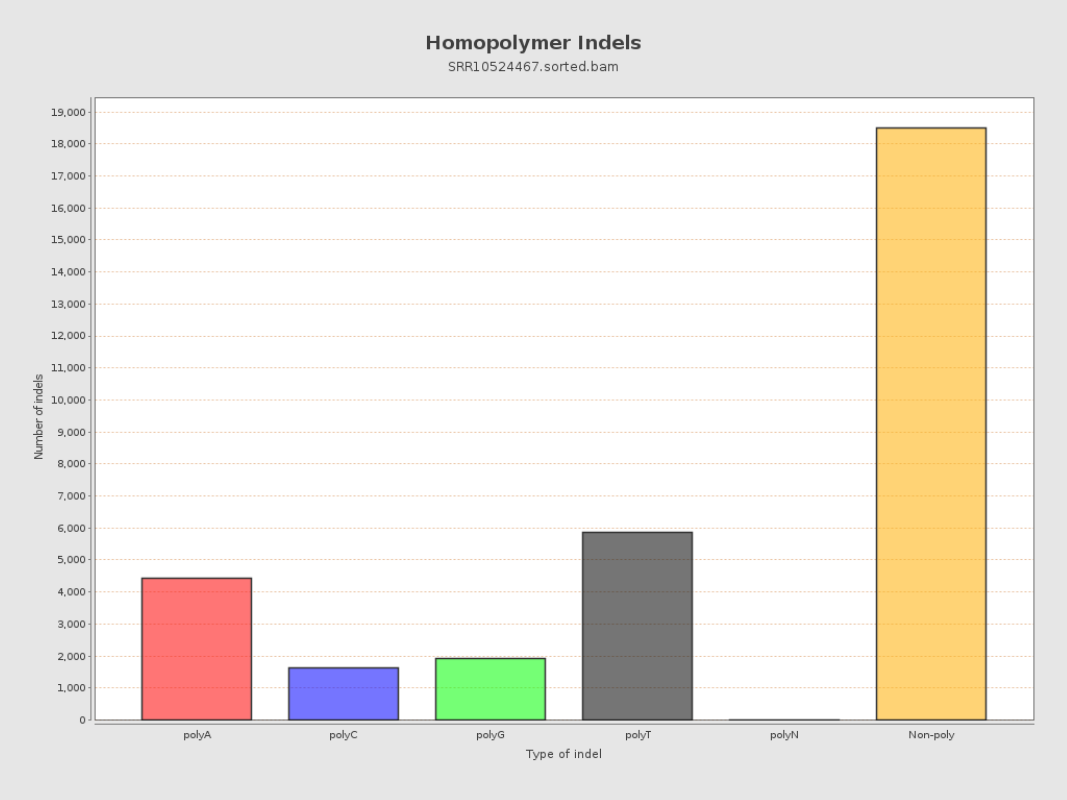
9. Results : Mapped Reads GC-content Distribution



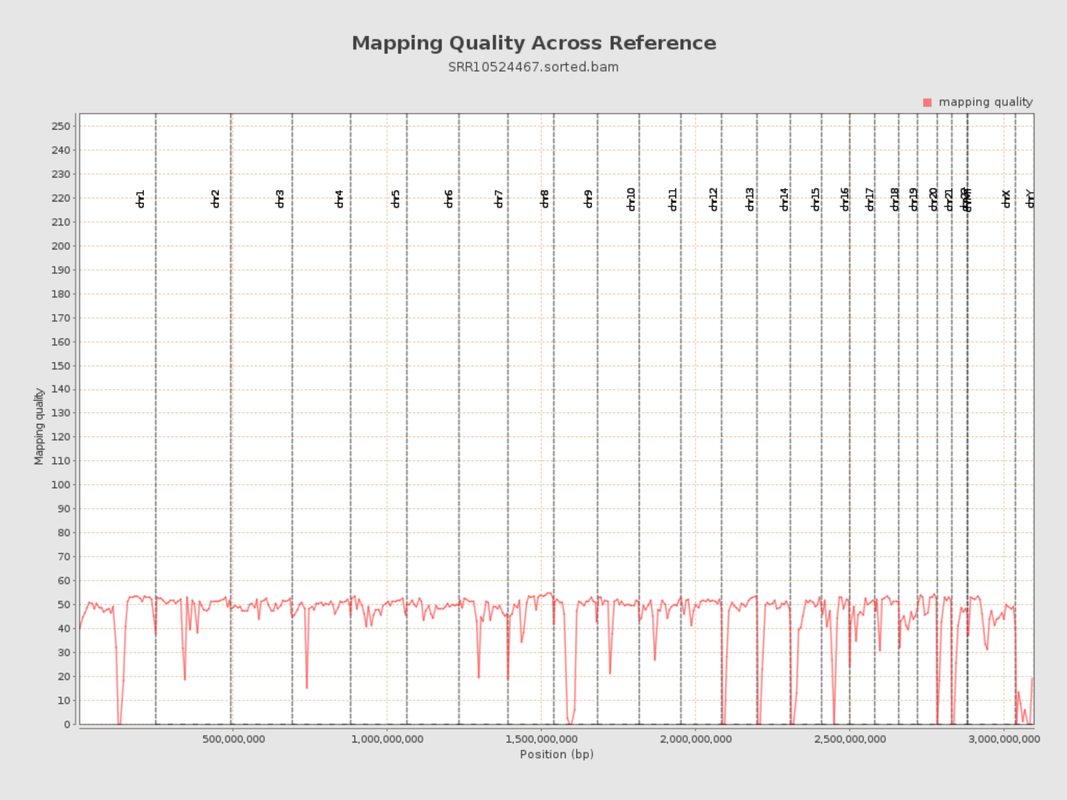
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram