Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 07:28:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524513.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_SRR10524513 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524513.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 07:28:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524513.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,310,285
Mapped reads	2,115,791 / 91.58%
Unmapped reads	194,494 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,492 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	203,144 / 8.79%
Duplication rate	7.38%
Clipped reads	2,119,462 / 91.74%

2.2. ACGT Content

Number/percentage of A's	29,156,347 / 23.74%
Number/percentage of C's	22,942,181 / 18.68%
Number/percentage of T's	39,590,310 / 32.24%
Number/percentage of G's	31,118,439 / 25.34%
Number/percentage of N's	1,710 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.359

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

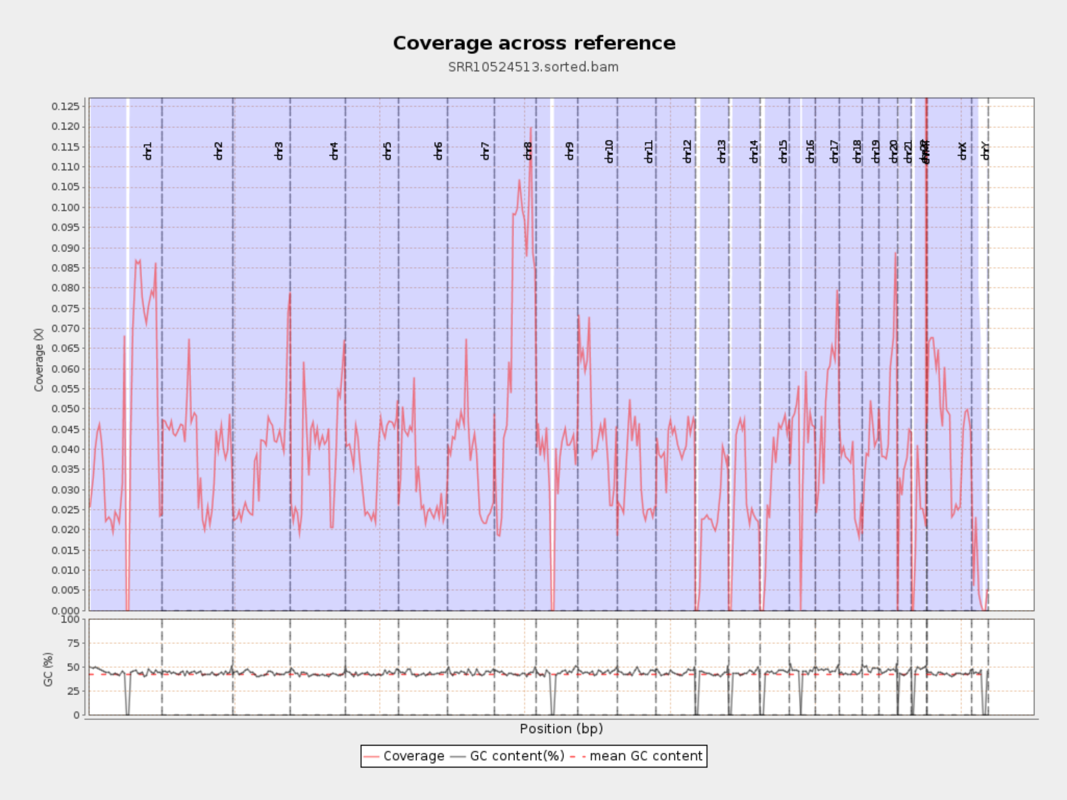
General error rate	0.51%
Mismatches	611,652
Insertions	7,633
Mapped reads with at least one insertion	0.36%
Deletions	21,569
Mapped reads with at least one deletion	1.01%
Homopolymer indels	43.5%

2.6. Chromosome stats

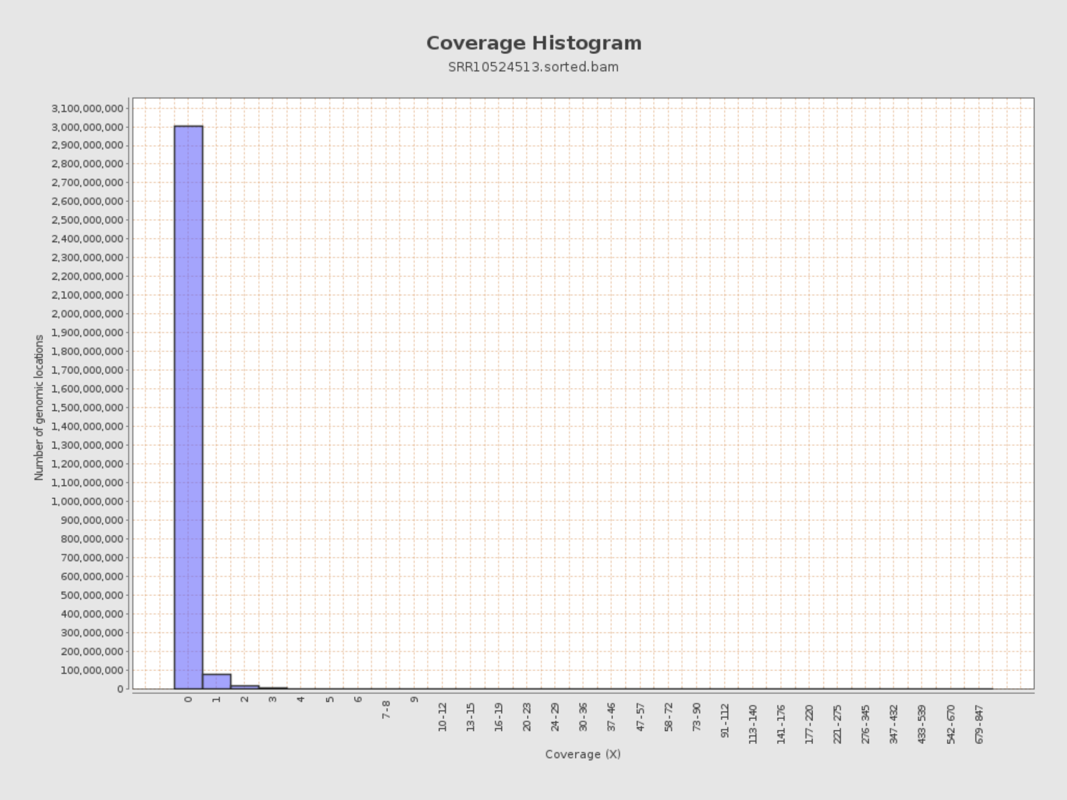
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11712318	0.047	0.6419
chr2	243199373	9884539	0.0406	0.4471
chr3	198022430	7333431	0.037	0.2403
chr4	191154276	7542120	0.0395	0.2878
chr5	180915260	6825718	0.0377	0.2418
chr6	171115067	5488528	0.0321	0.2738
chr7	159138663	5996654	0.0377	0.4321

chr8	146364022	10601709	0.0724	0.4178
chr9	141213431	5030006	0.0356	0.2856
chr10	135534747	6429789	0.0474	0.3833
chr11	135006516	4395604	0.0326	0.3028
chr12	133851895	5586501	0.0417	0.2574
chr13	115169878	2609235	0.0227	0.191
chr14	107349540	3022222	0.0282	0.2128
chr15	102531392	3246063	0.0317	0.2234
chr16	90354753	3883128	0.043	0.2764
chr17	81195210	4273907	0.0526	0.303
chr18	78077248	2578737	0.033	0.4869
chr19	59128983	2417421	0.0409	0.4426
chr20	63025520	3377723	0.0536	0.2973
chr21	48129895	1604169	0.0333	0.2542
chr22	51304566	1032805	0.0201	0.1795
chrMT	16571	246048	14.8481	8.6862
chrX	155270560	7316166	0.0471	0.2909
chrY	59373566	410449	0.0069	0.1731

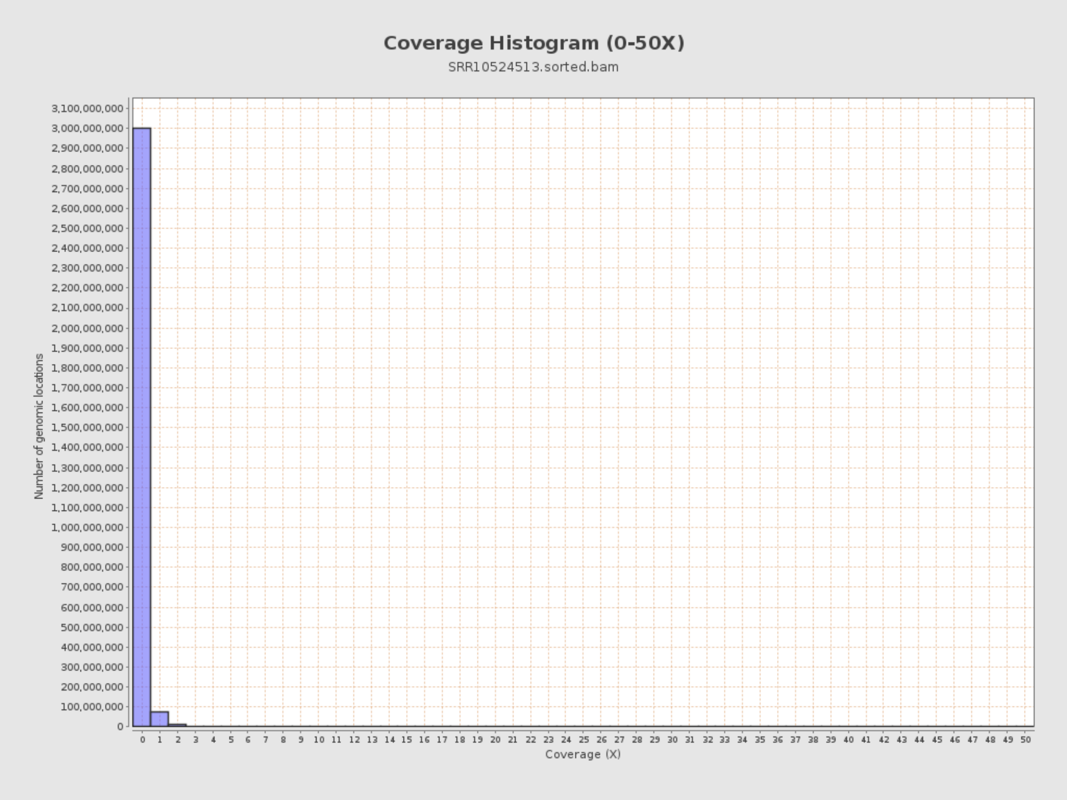
3. Results : Coverage across reference



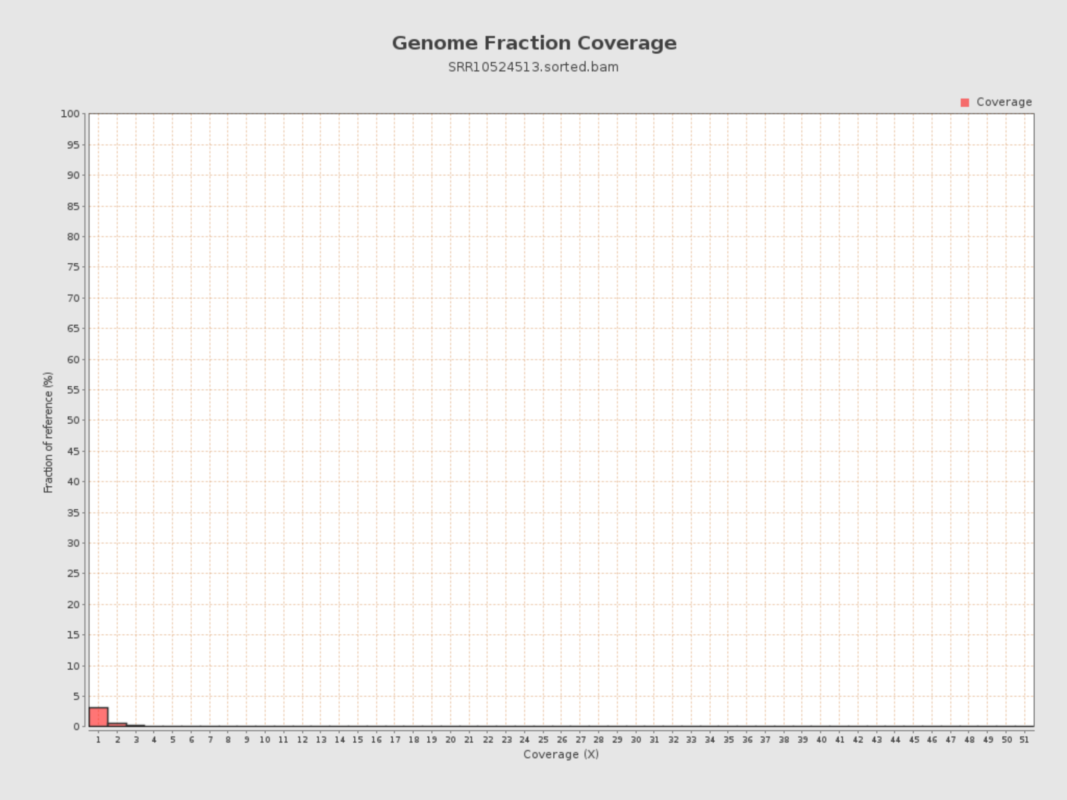
4. Results : Coverage Histogram



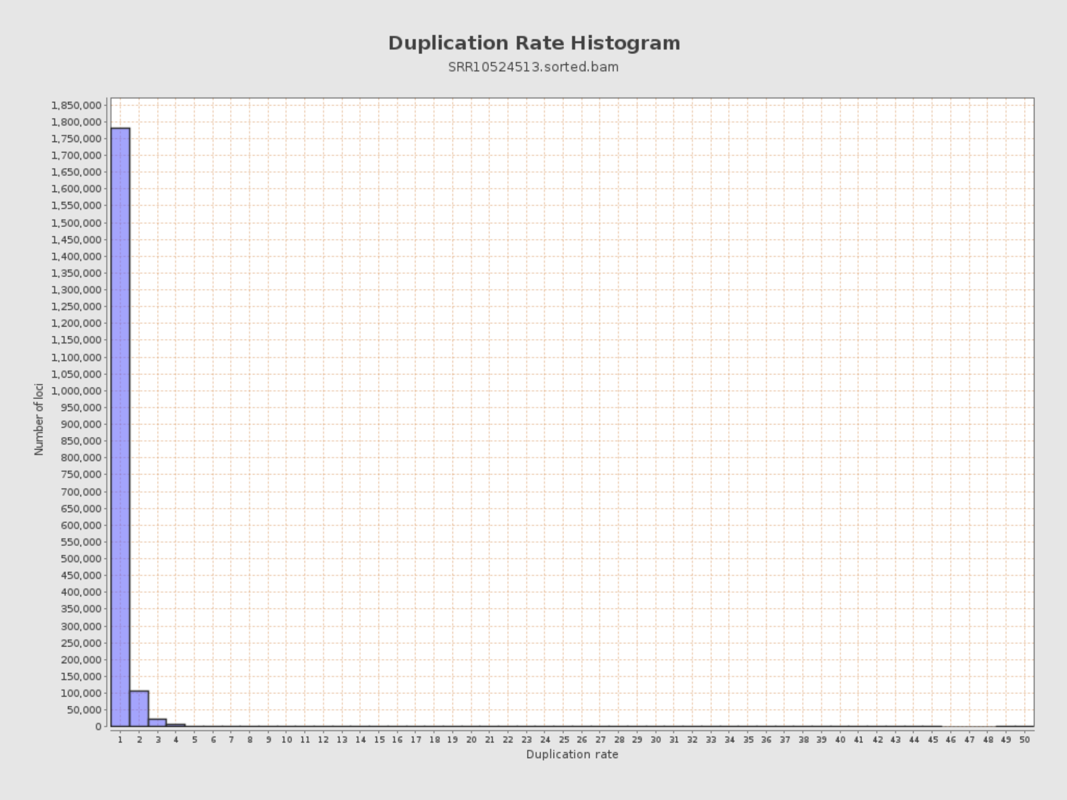
5. Results : Coverage Histogram (0-50X)



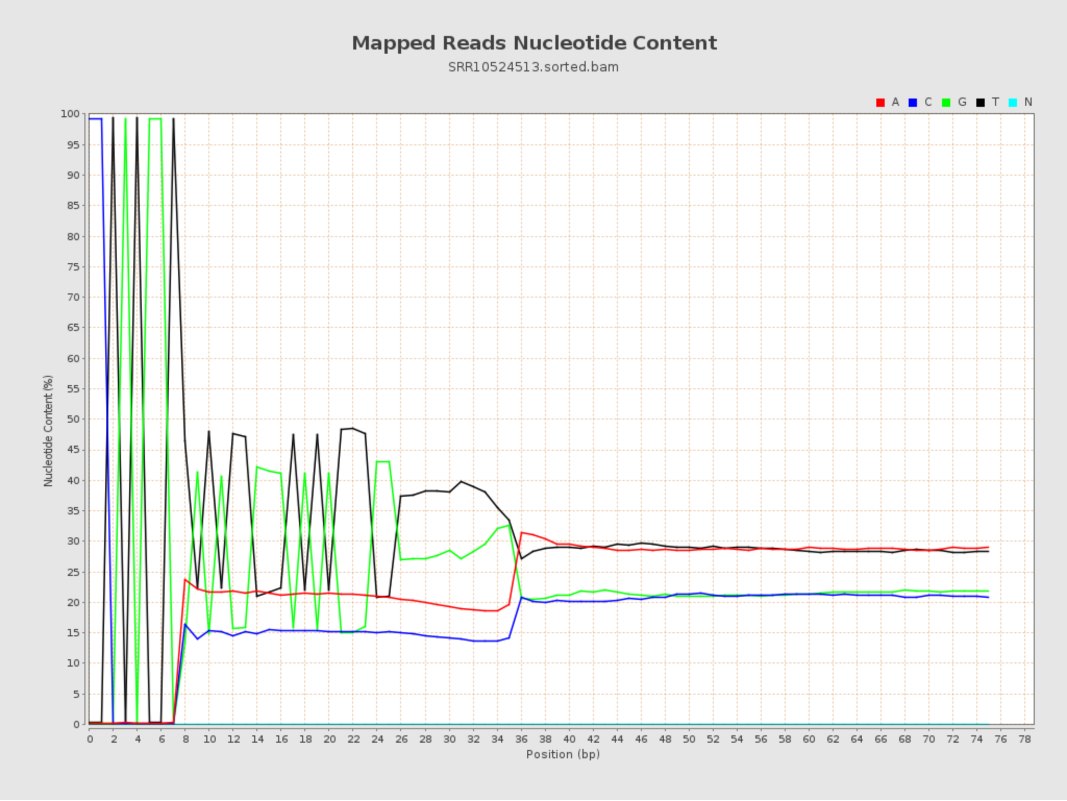
6. Results : Genome Fraction Coverage



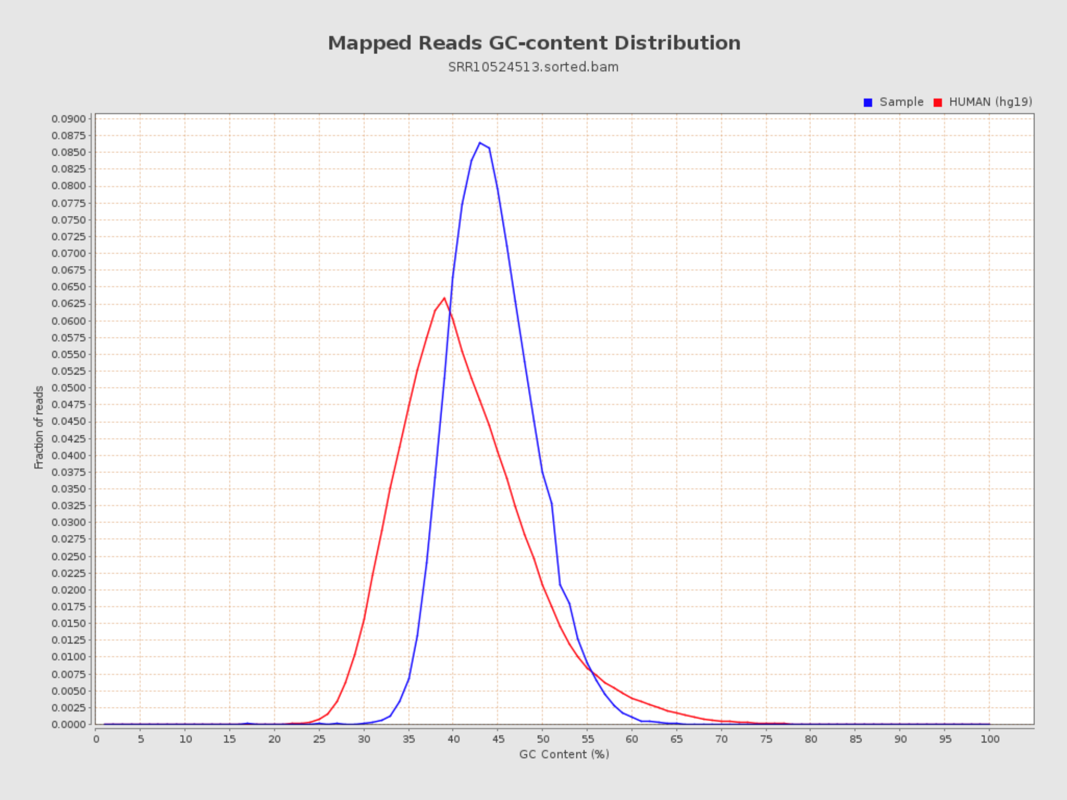
7. Results : Duplication Rate Histogram



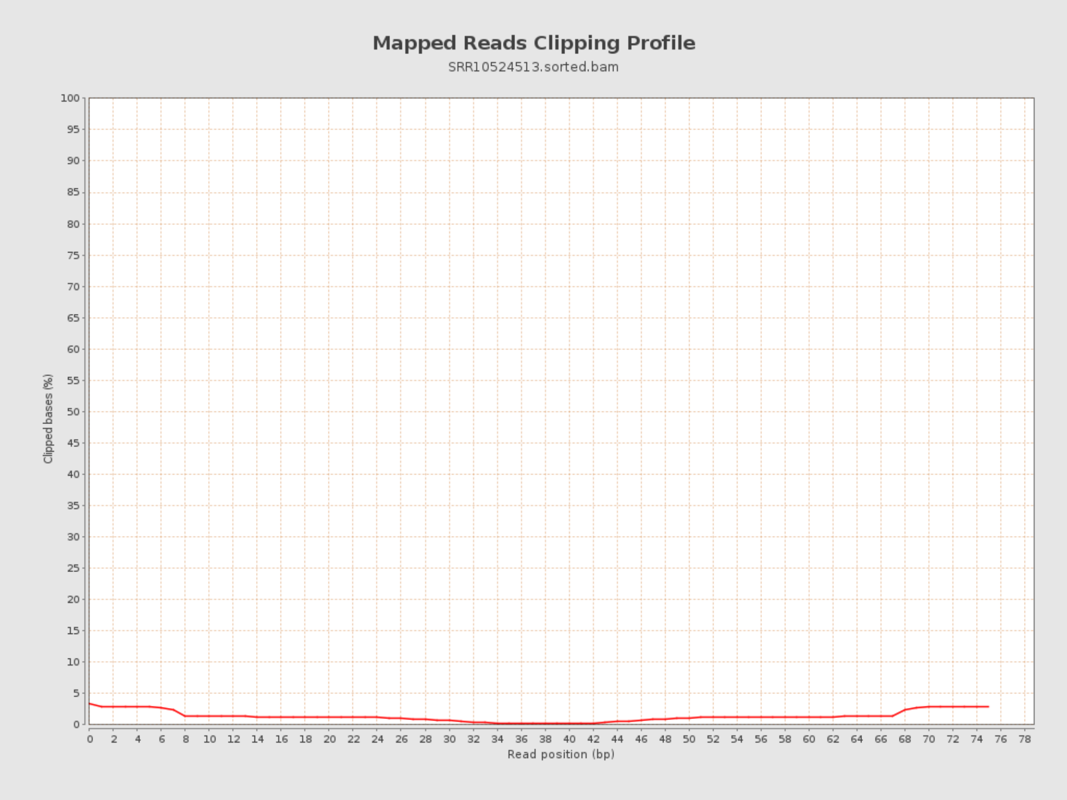
8. Results : Mapped Reads Nucleotide Content



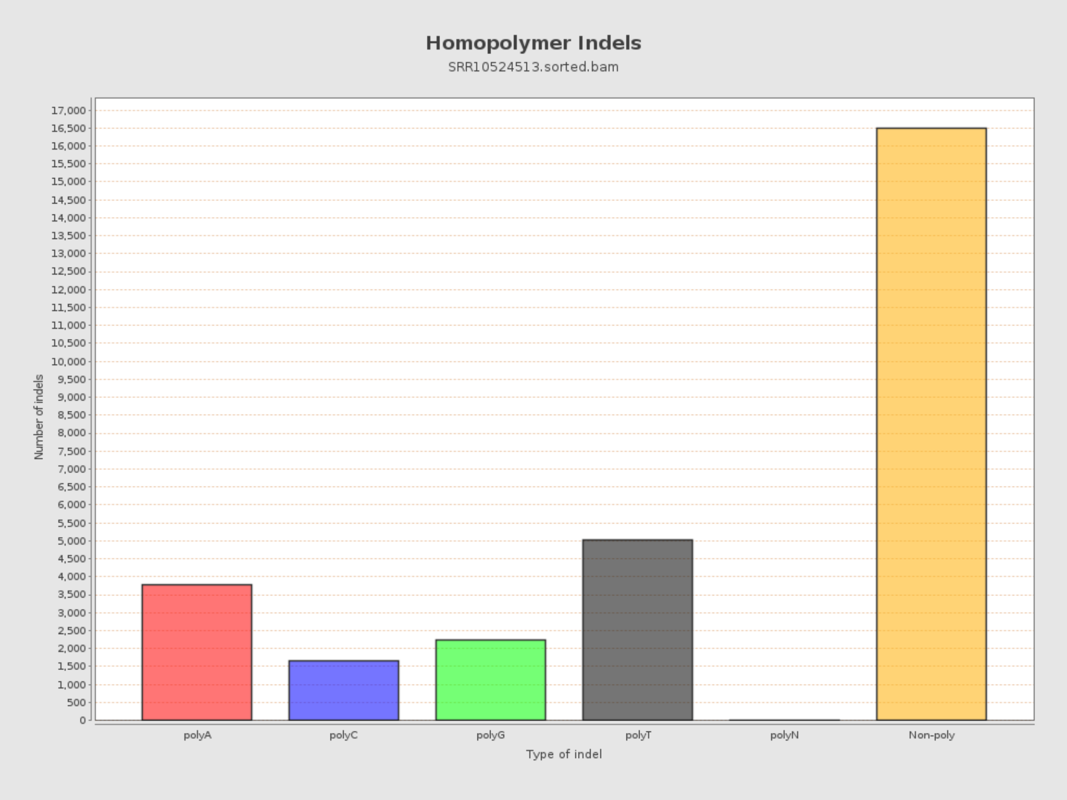
9. Results : Mapped Reads GC-content Distribution



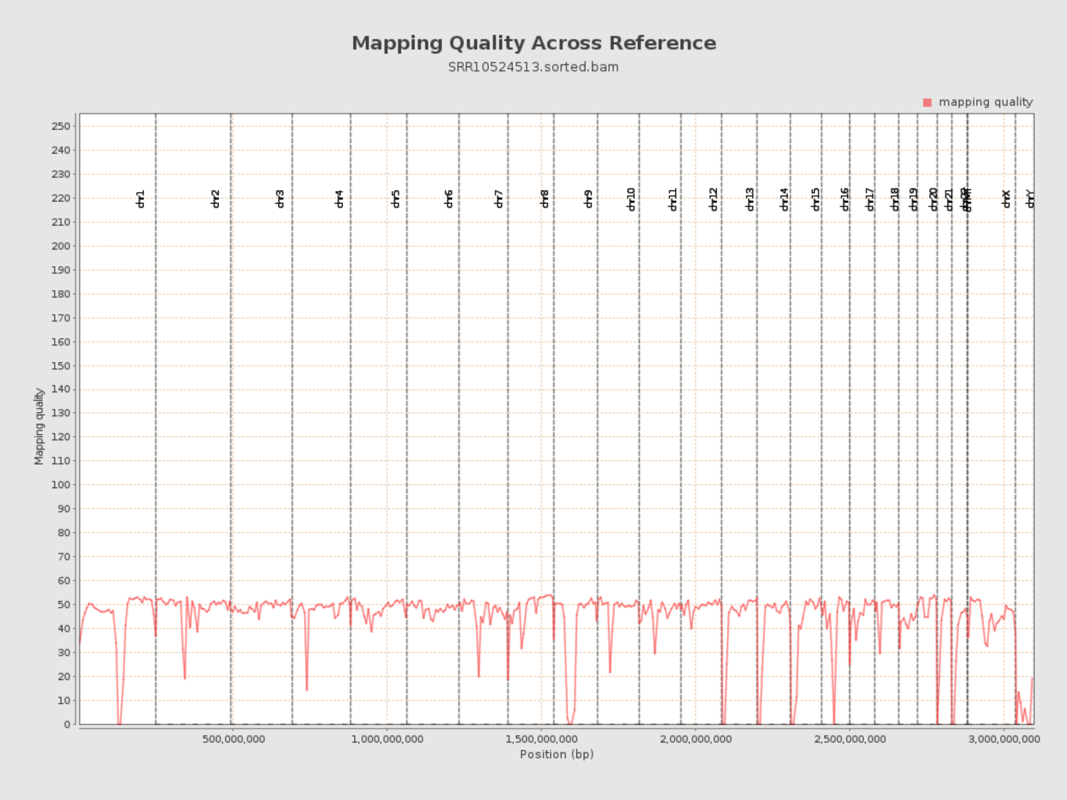
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram