Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:36:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524320.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_SRR10524320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:36:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,210,377
Mapped reads	2,913,258 / 90.75%
Unmapped reads	297,119 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,372 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	138,443 / 4.31%
Duplication rate	3.38%
Clipped reads	2,919,625 / 90.94%

2.2. ACGT Content

Number/percentage of A's	41,970,427 / 24.97%
Number/percentage of C's	31,488,252 / 18.74%
Number/percentage of T's	54,076,625 / 32.17%
Number/percentage of G's	40,513,151 / 24.1%
Number/percentage of N's	23,111 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.4678

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Mismatches and indels

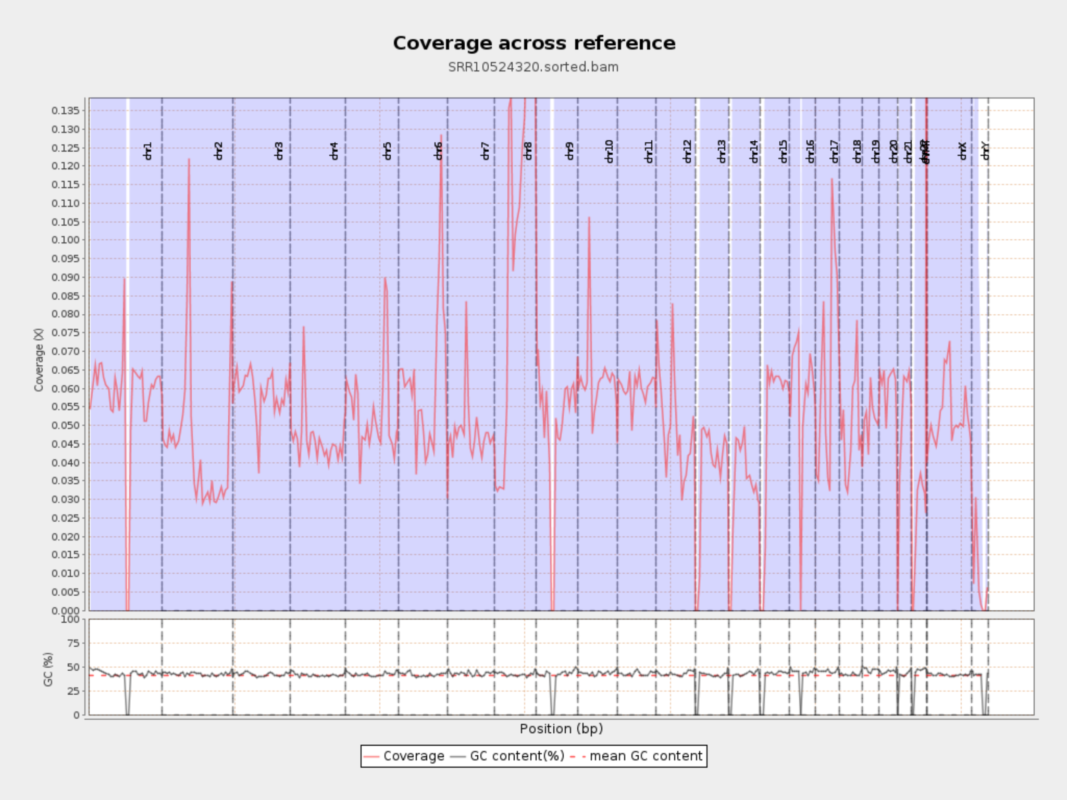
General error rate	0.53%
Mismatches	866,935
Insertions	11,733
Mapped reads with at least one insertion	0.4%
Deletions	27,871
Mapped reads with at least one deletion	0.95%
Homopolymer indels	41.28%

2.6. Chromosome stats

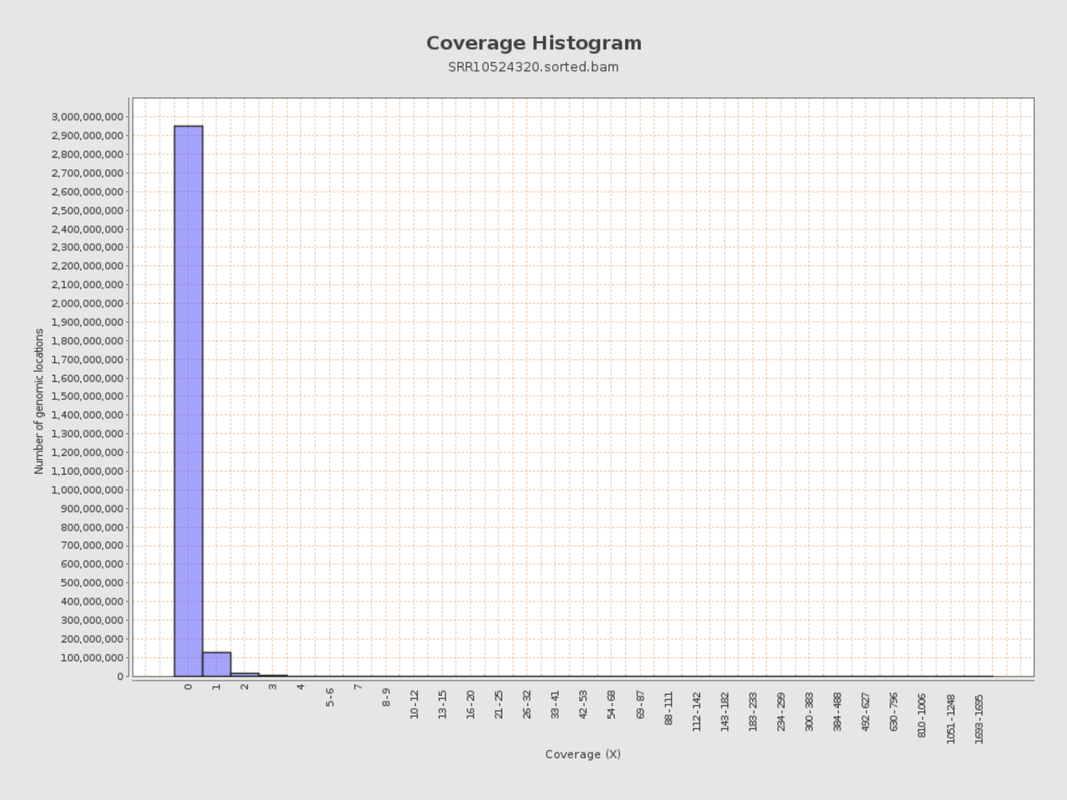
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14307157	0.0574	0.8927
chr2	243199373	10911507	0.0449	0.7233
chr3	198022430	11656141	0.0589	0.2818
chr4	191154276	8782892	0.0459	0.2996
chr5	180915260	9730297	0.0538	0.2657
chr6	171115067	10587019	0.0619	0.3239
chr7	159138663	7743301	0.0487	0.5767

chr8	146364022	17402391	0.1189	0.5542
chr9	141213431	6907136	0.0489	0.3444
chr10	135534747	8544358	0.063	0.4625
chr11	135006516	8097012	0.06	0.3689
chr12	133851895	6706254	0.0501	0.264
chr13	115169878	4237438	0.0368	0.2197
chr14	107349540	3554619	0.0331	0.2276
chr15	102531392	5153375	0.0503	0.2641
chr16	90354753	5316354	0.0588	0.3029
chr17	81195210	5273534	0.0649	0.3295
chr18	78077248	3983893	0.051	0.6298
chr19	59128983	3067122	0.0519	0.5883
chr20	63025520	3846530	0.061	0.2976
chr21	48129895	2419845	0.0503	0.2888
chr22	51304566	1214897	0.0237	0.1748
chrMT	16571	9429	0.569	0.8665
chrX	155270560	8161323	0.0526	0.3068
chrY	59373566	502443	0.0085	0.2273

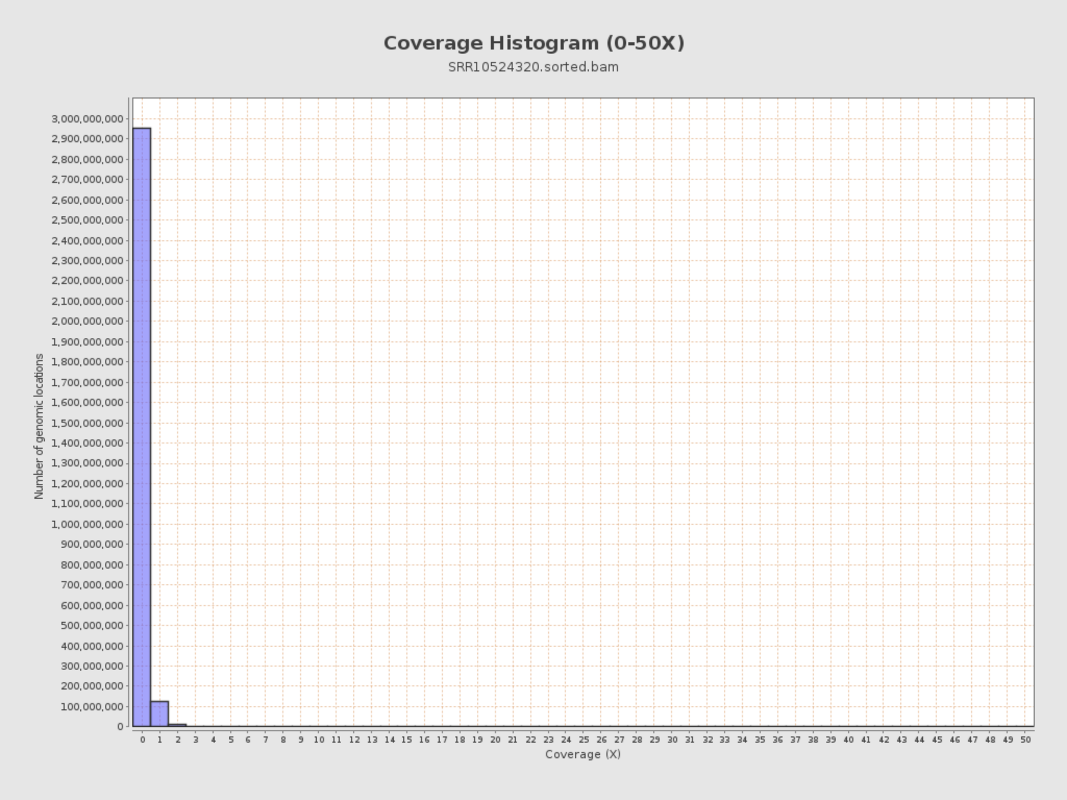
3. Results : Coverage across reference



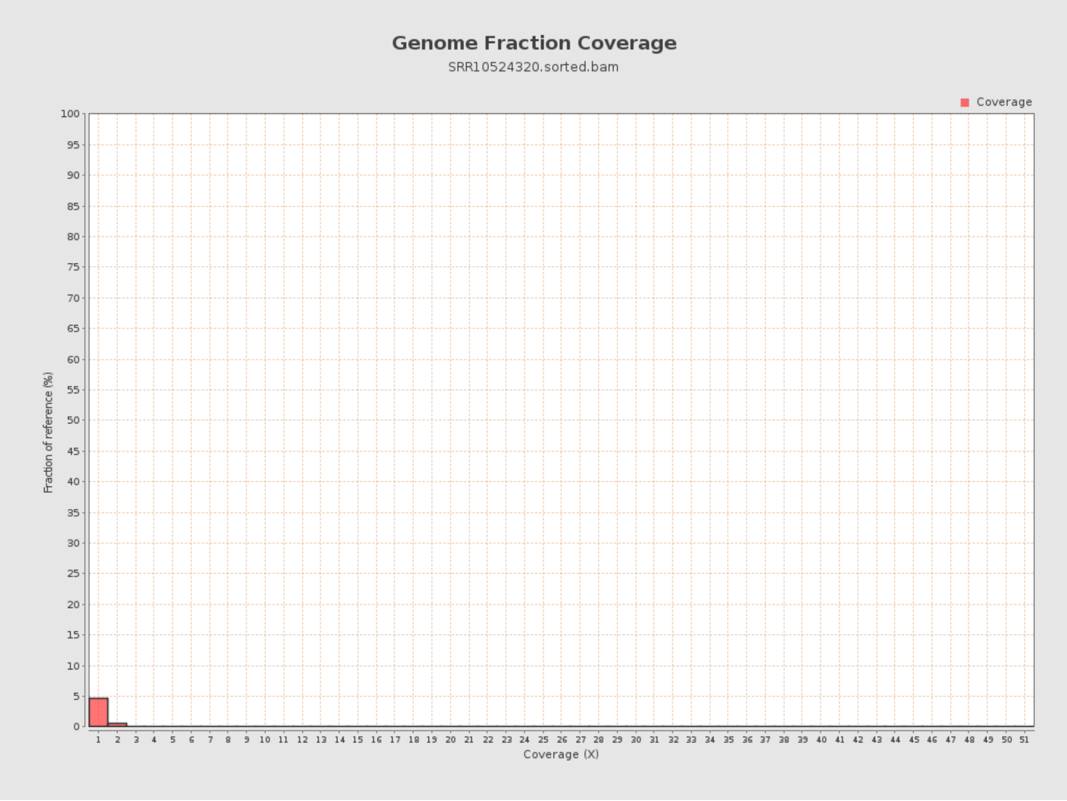
4. Results : Coverage Histogram



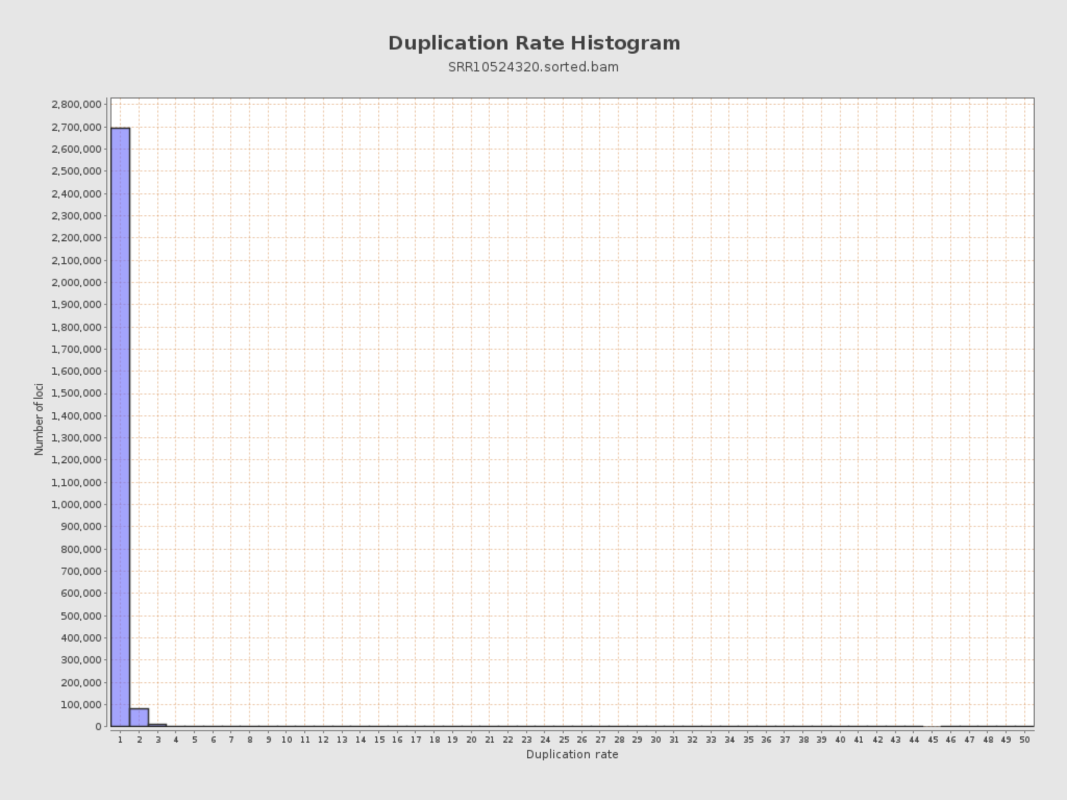
5. Results : Coverage Histogram (0-50X)



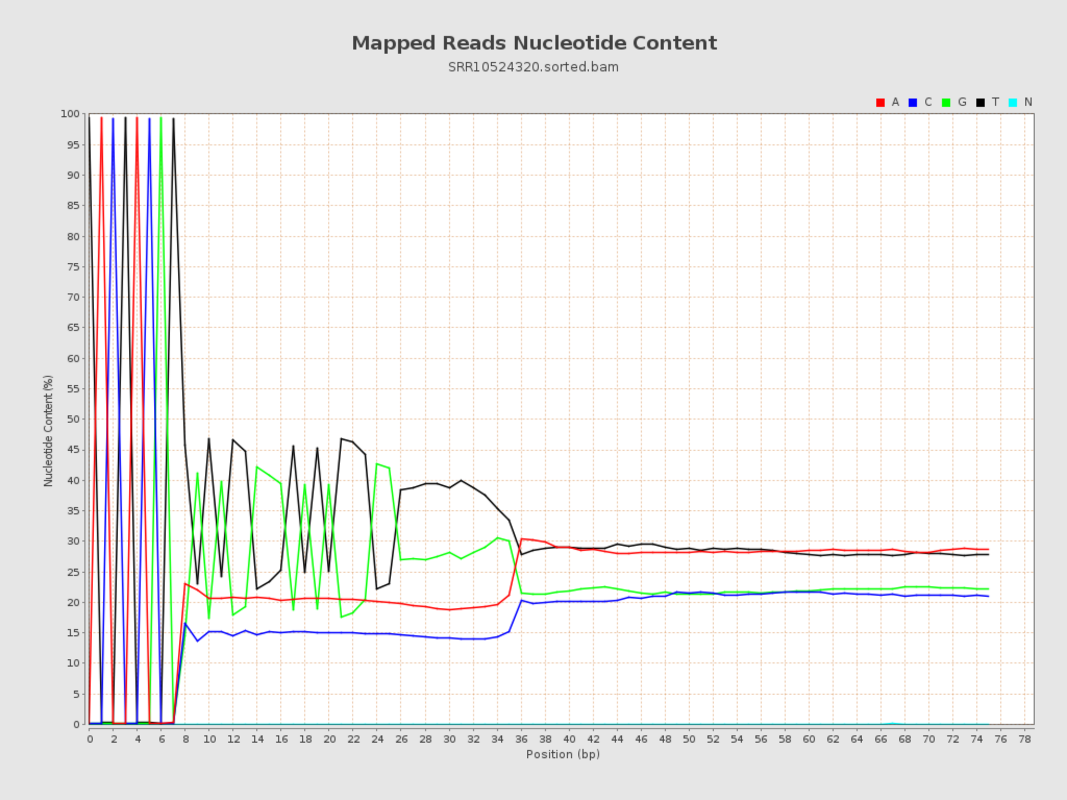
6. Results : Genome Fraction Coverage



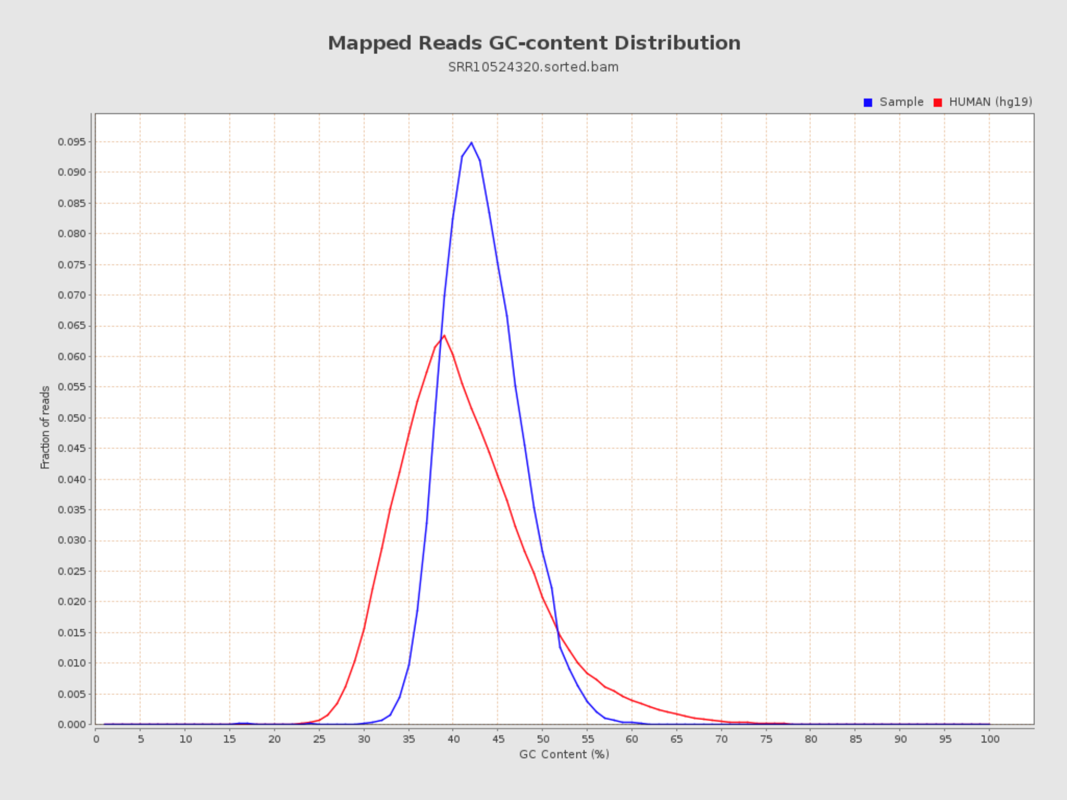
7. Results : Duplication Rate Histogram



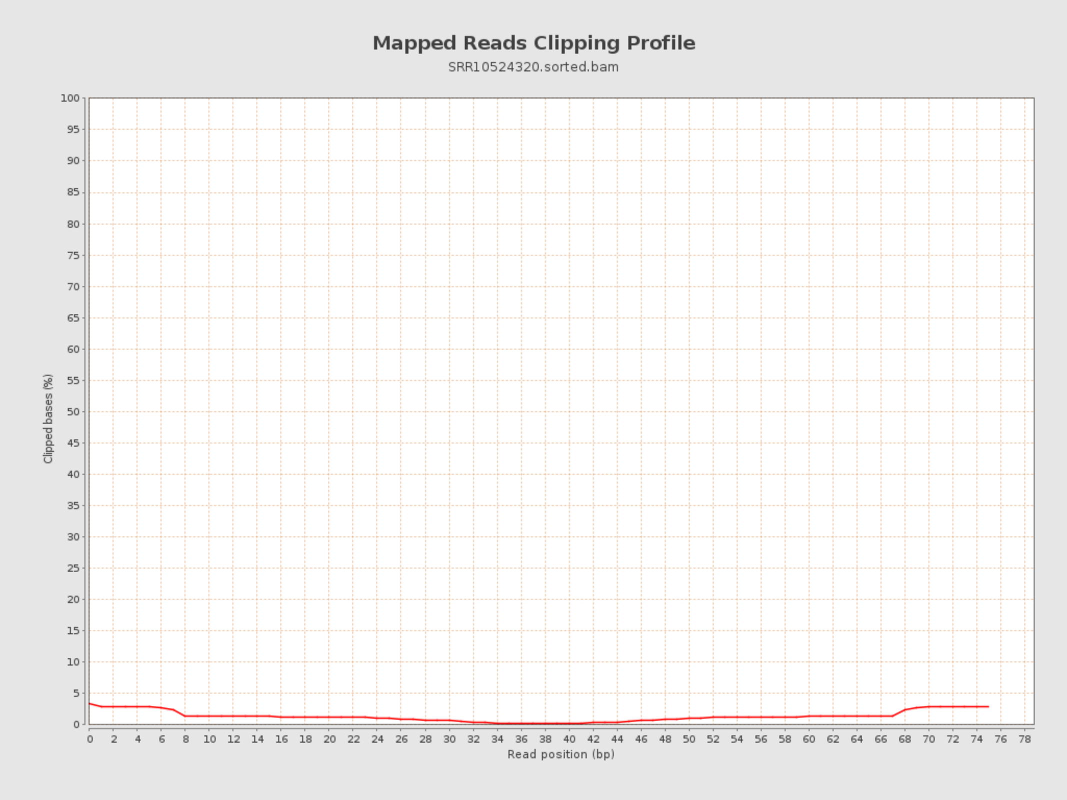
8. Results : Mapped Reads Nucleotide Content



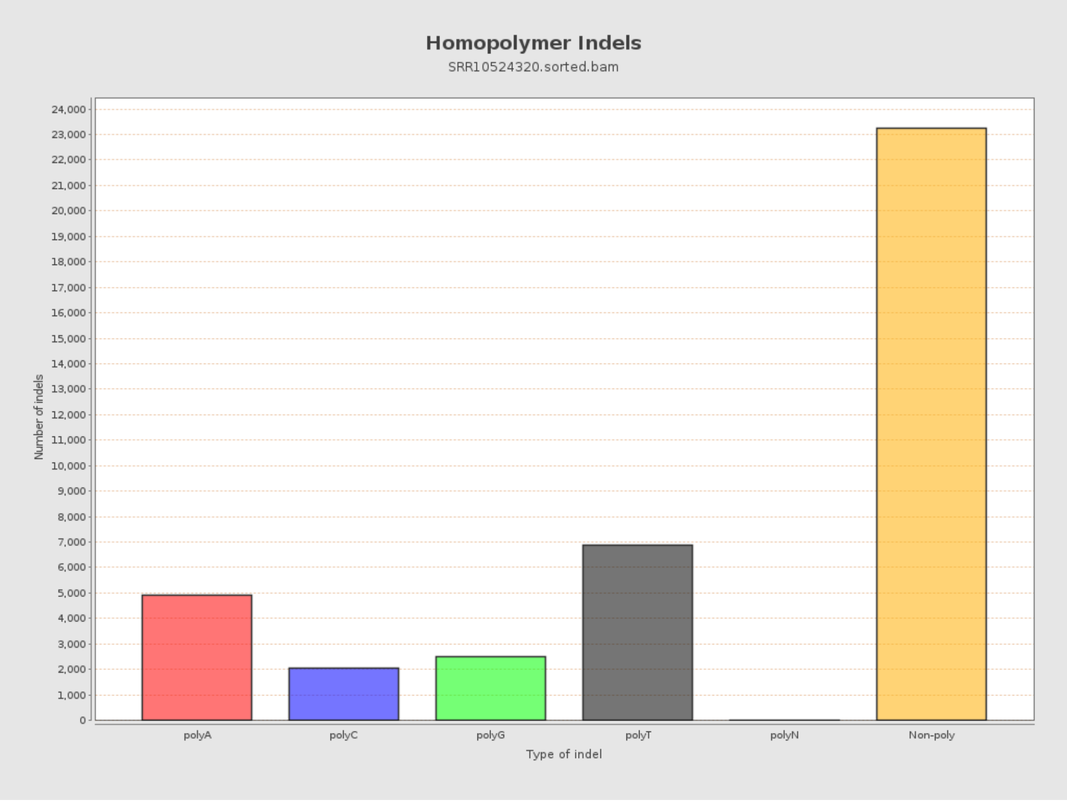
9. Results : Mapped Reads GC-content Distribution



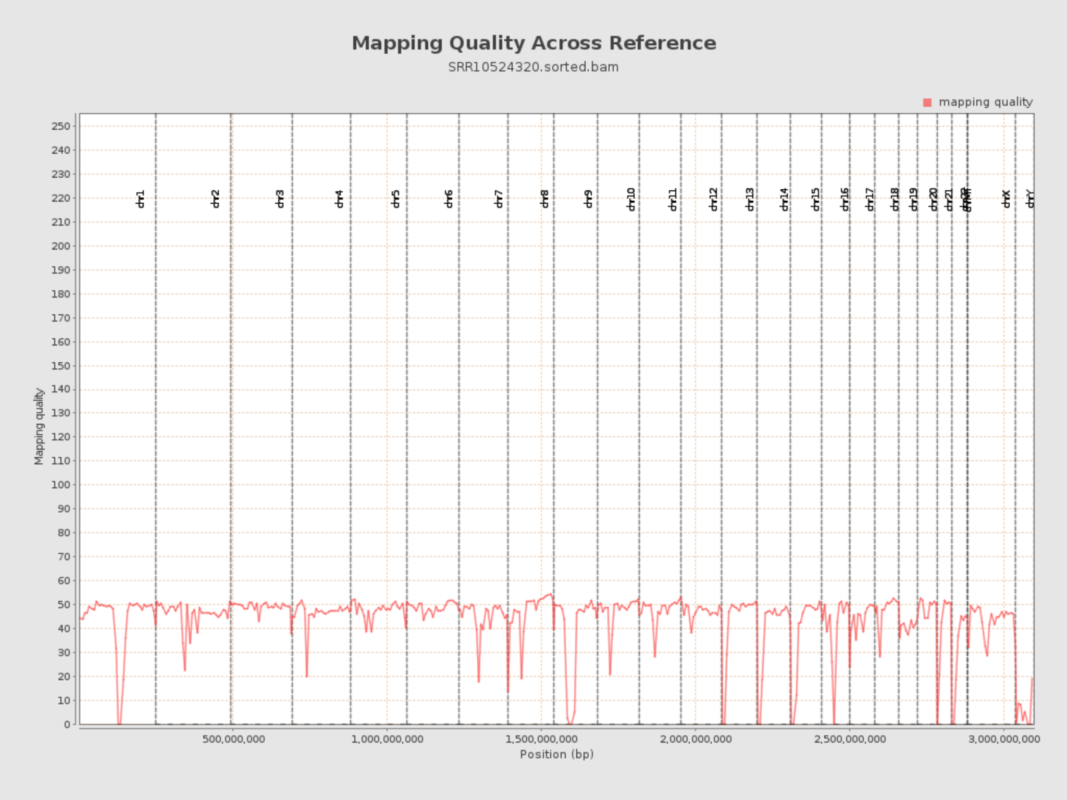
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram