Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:04:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524310.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_SRR10524310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:04:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,651,198
Mapped reads	1,501,363 / 90.93%
Unmapped reads	149,835 / 9.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,318 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	43,841 / 2.66%
Duplication rate	1.98%
Clipped reads	1,503,869 / 91.08%

2.2. ACGT Content

Number/percentage of A's	21,661,685 / 25.09%
Number/percentage of C's	15,438,750 / 17.88%
Number/percentage of T's	27,092,824 / 31.38%
Number/percentage of G's	22,142,175 / 25.64%
Number/percentage of N's	11,905 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.2717

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

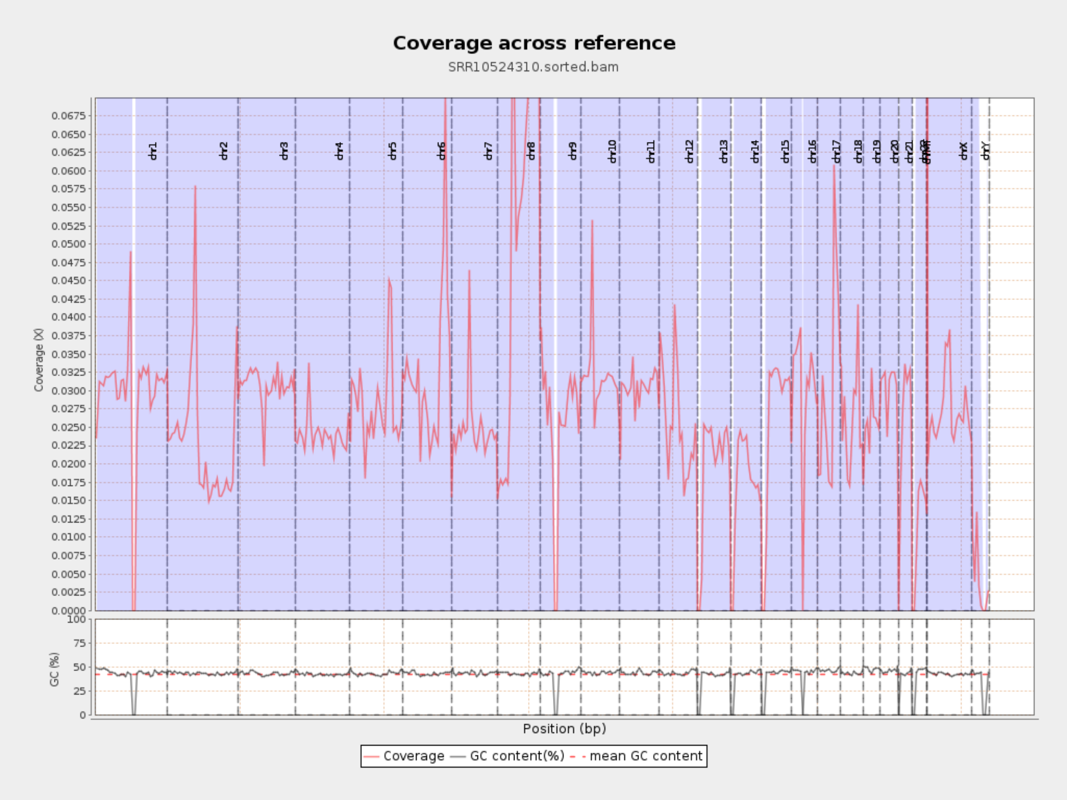
General error rate	0.52%
Mismatches	442,342
Insertions	5,441
Mapped reads with at least one insertion	0.36%
Deletions	14,040
Mapped reads with at least one deletion	0.93%
Homopolymer indels	40.97%

2.6. Chromosome stats

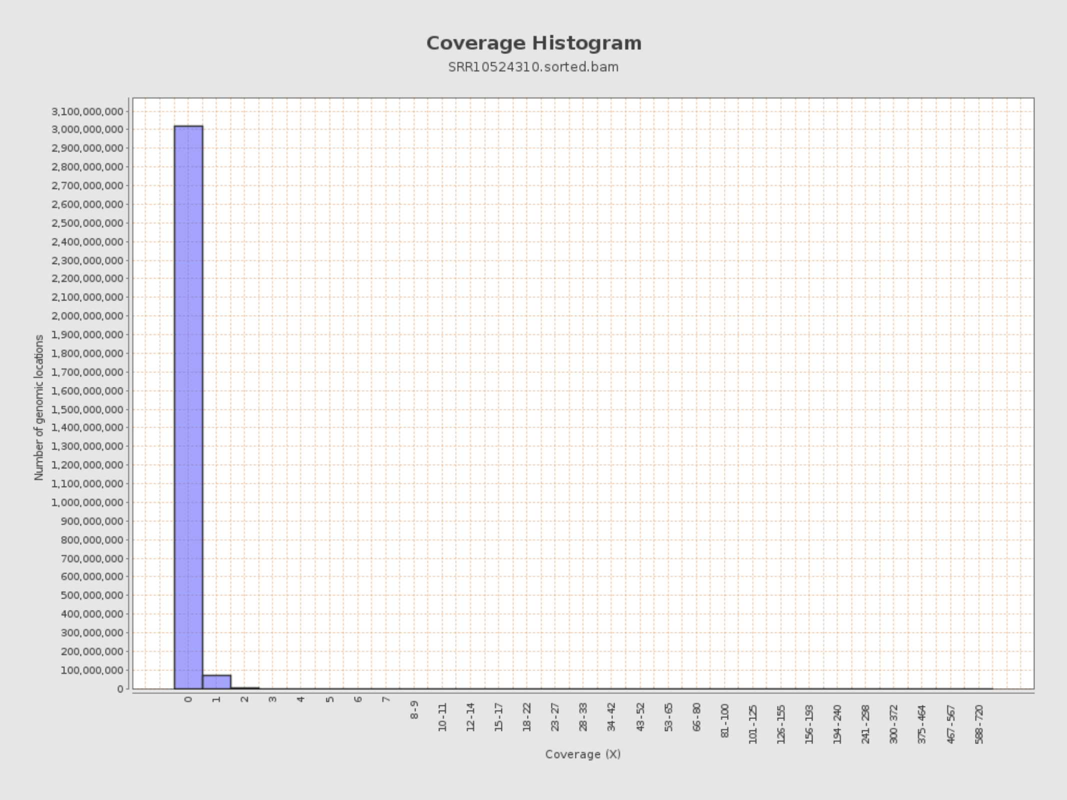
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7324518	0.0294	0.5098
chr2	243199373	5573565	0.0229	0.3394
chr3	198022430	6069968	0.0307	0.1909
chr4	191154276	4605567	0.0241	0.1796
chr5	180915260	5126359	0.0283	0.1821
chr6	171115067	5520426	0.0323	0.2073
chr7	159138663	3995368	0.0251	0.357

chr8	146364022	8989986	0.0614	0.3334
chr9	141213431	3606042	0.0255	0.2131
chr10	135534747	4351790	0.0321	0.2669
chr11	135006516	4119117	0.0305	0.2284
chr12	133851895	3414744	0.0255	0.174
chr13	115169878	2229027	0.0194	0.1489
chr14	107349540	1828738	0.017	0.1513
chr15	102531392	2631727	0.0257	0.1737
chr16	90354753	2658372	0.0294	0.1953
chr17	81195210	2513538	0.031	0.2073
chr18	78077248	2042645	0.0262	0.3701
chr19	59128983	1520889	0.0257	0.3579
chr20	63025520	1915412	0.0304	0.1905
chr21	48129895	1241462	0.0258	0.182
chr22	51304566	593316	0.0116	0.1175
chrMT	16571	16899	1.0198	1.115
chrX	155270560	4242401	0.0273	0.2015
chrY	59373566	237690	0.004	0.11

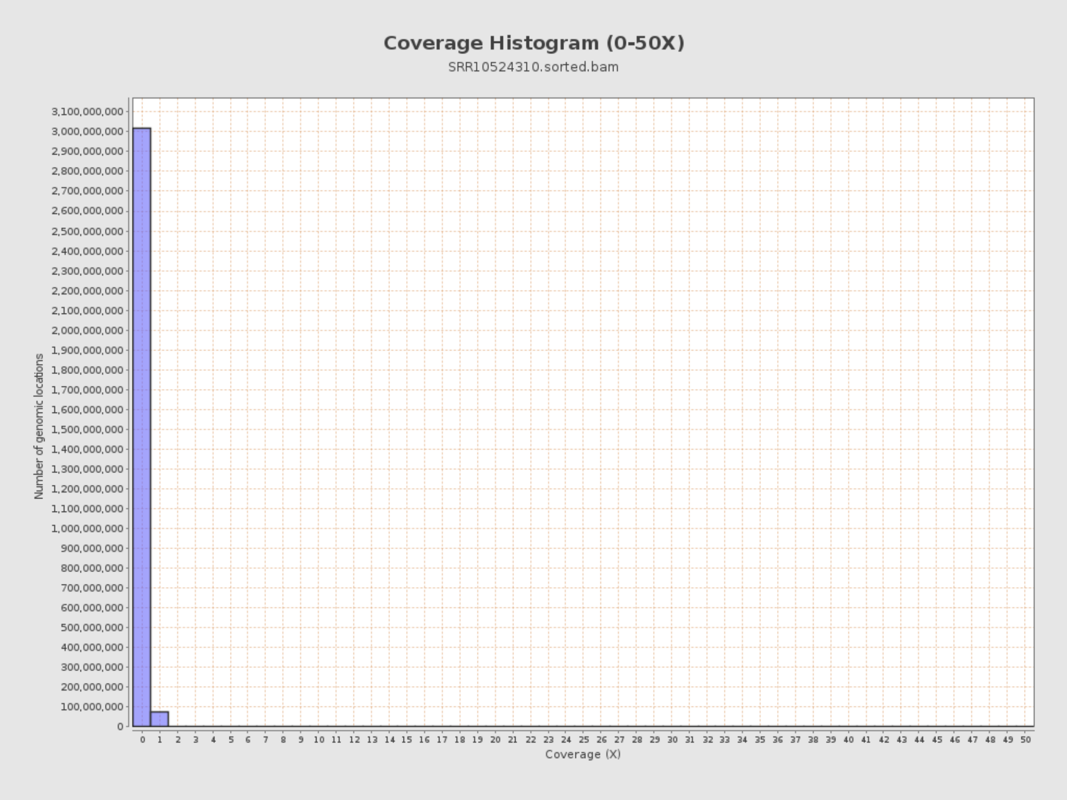
3. Results : Coverage across reference



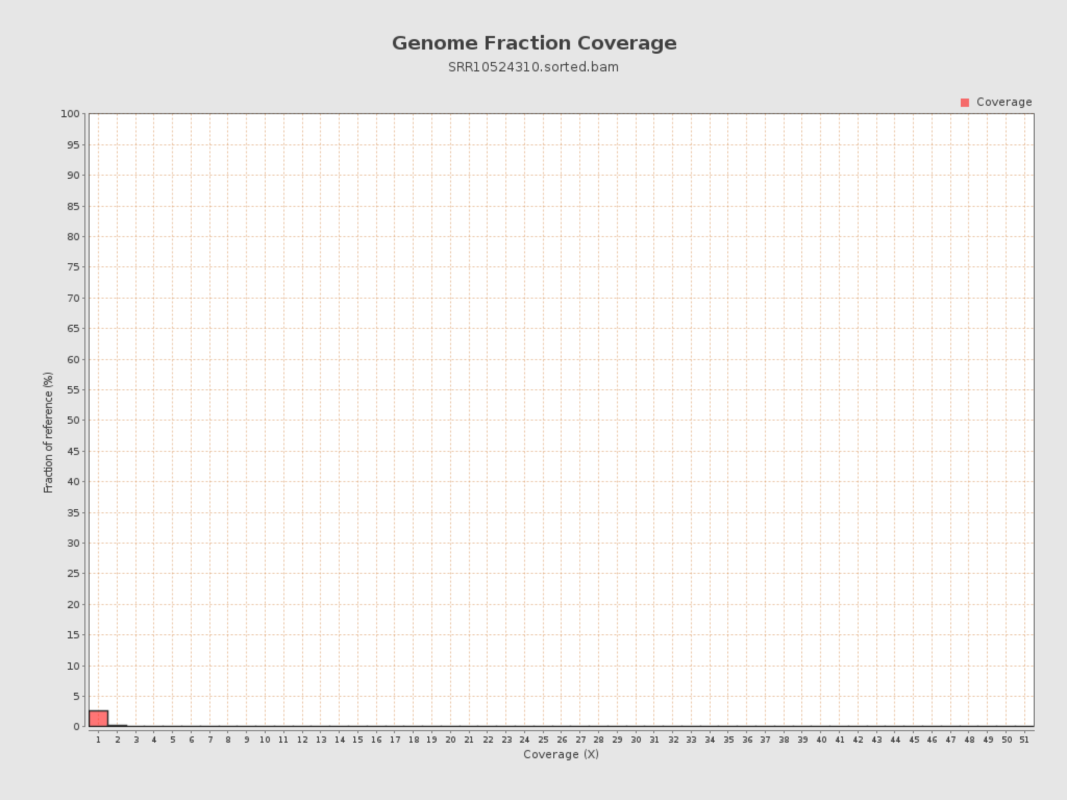
4. Results : Coverage Histogram



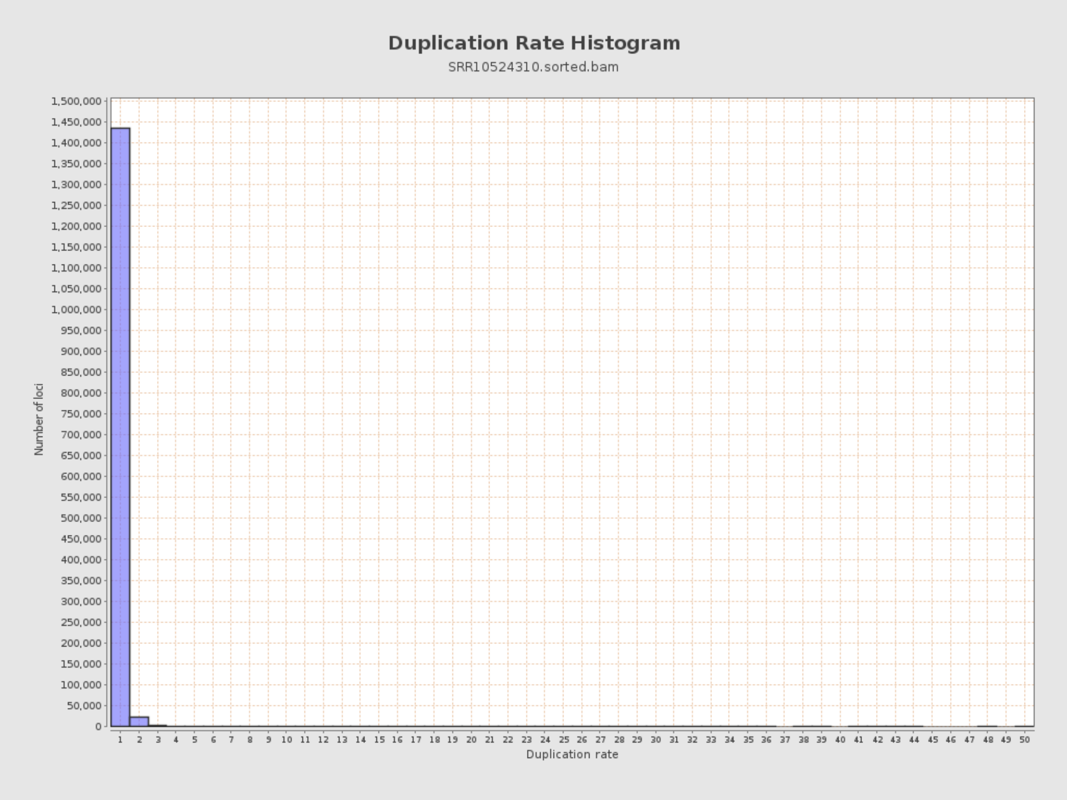
5. Results : Coverage Histogram (0-50X)



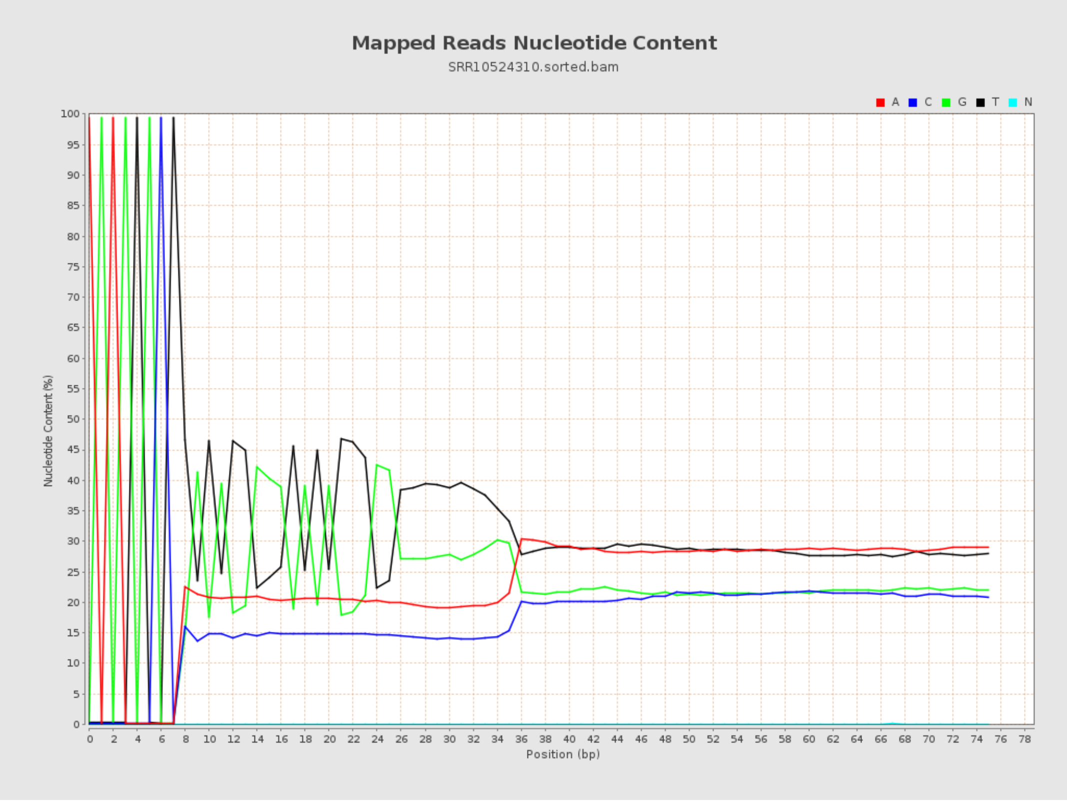
6. Results : Genome Fraction Coverage



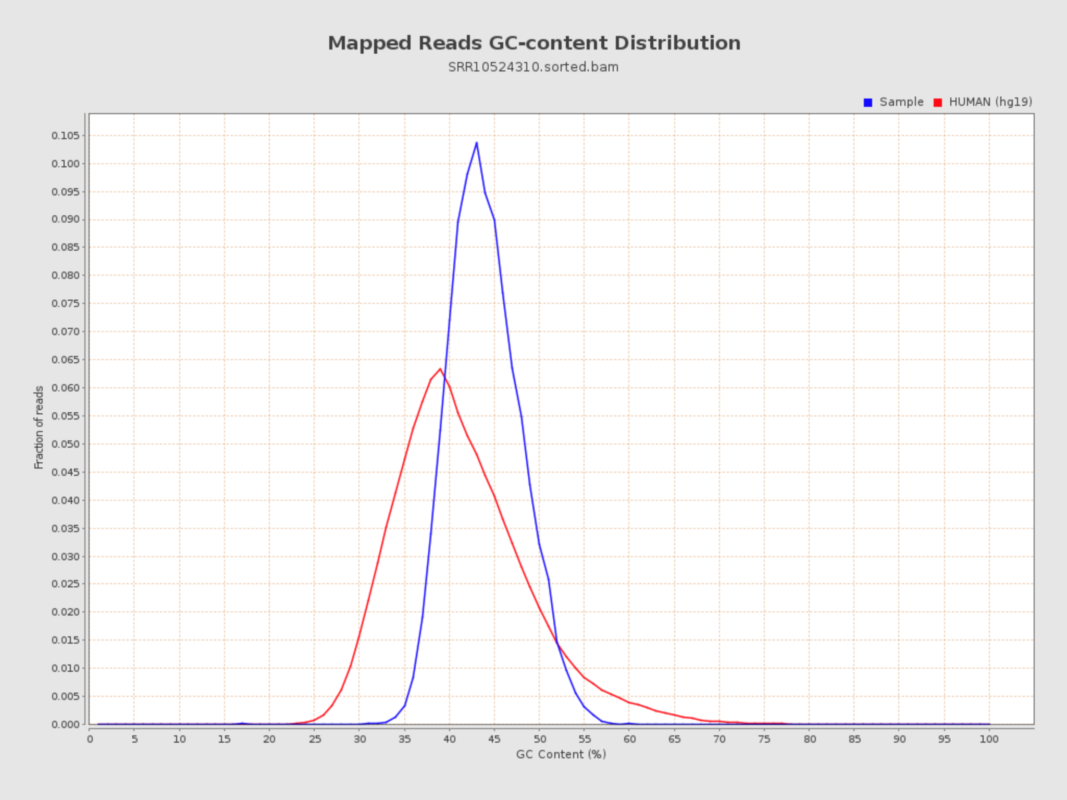
7. Results : Duplication Rate Histogram



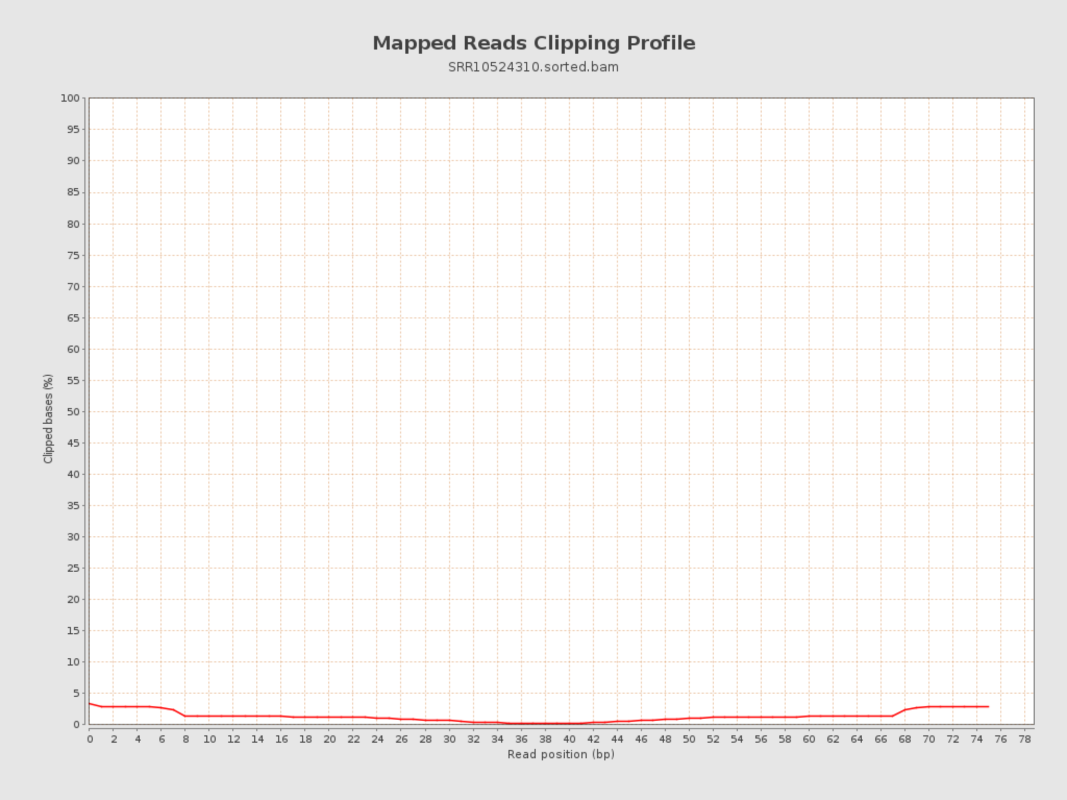
8. Results : Mapped Reads Nucleotide Content



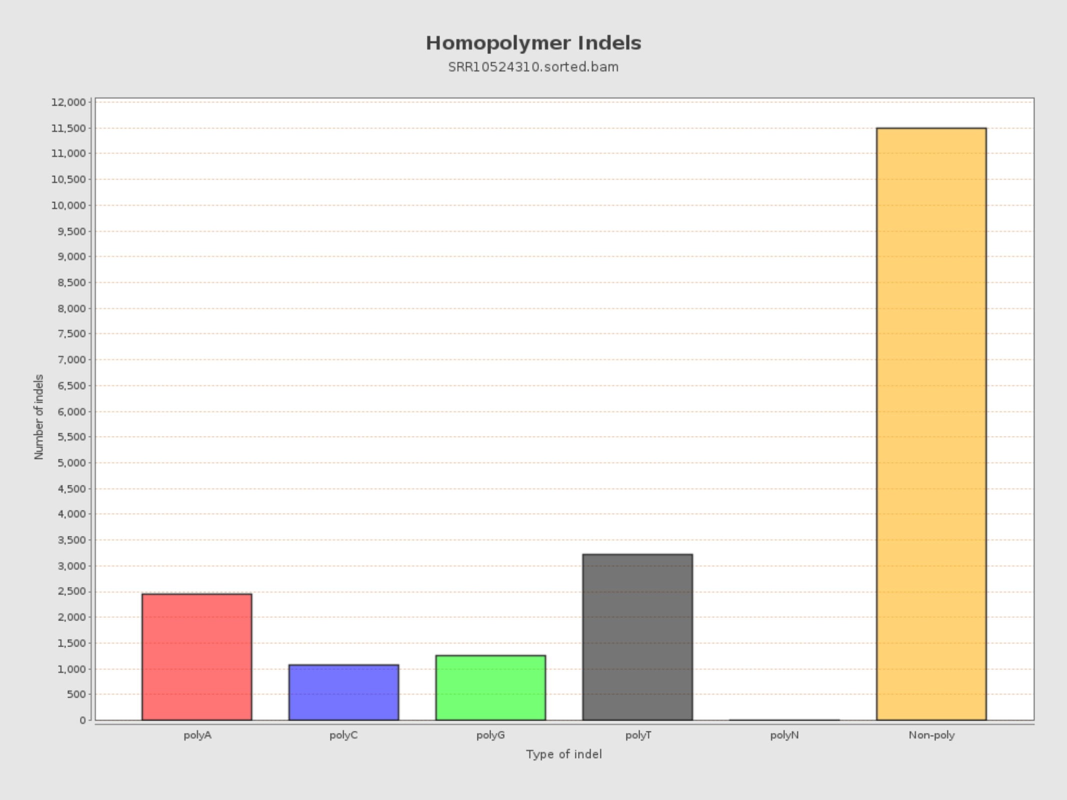
9. Results : Mapped Reads GC-content Distribution



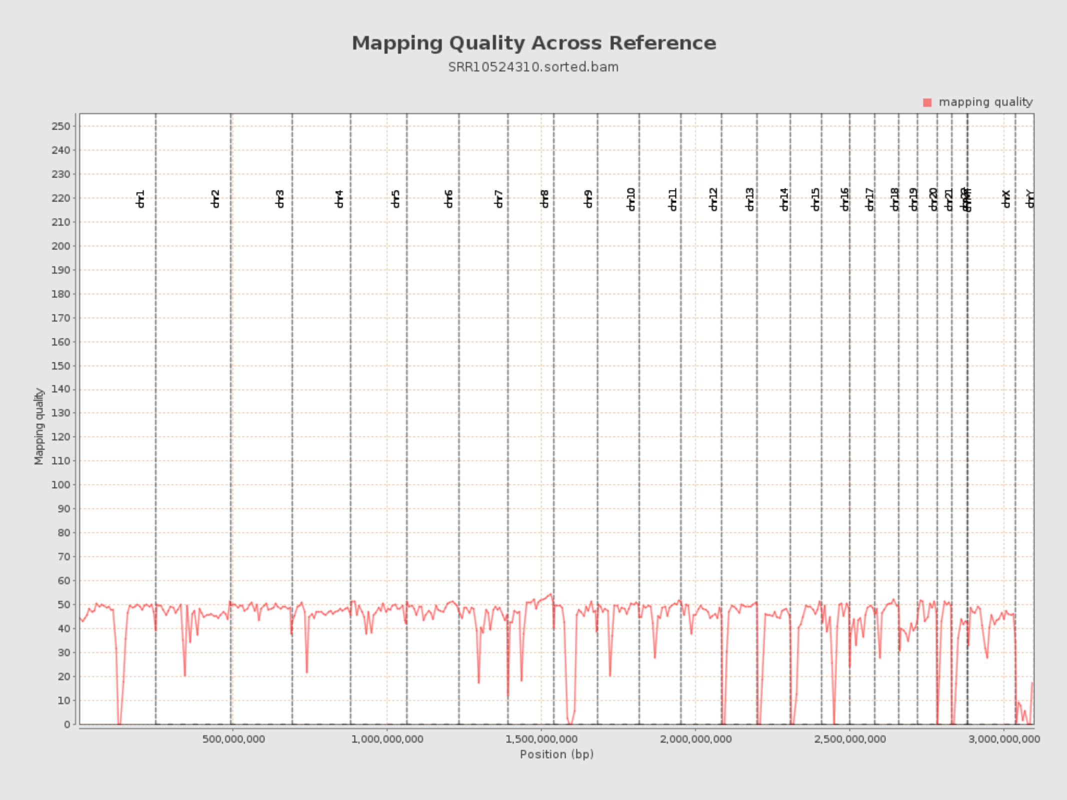
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram