Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:49:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524721.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_SRR10524721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524721.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:49:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	201,866
Mapped reads	188,138 / 93.2%
Unmapped reads	13,728 / 6.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	684 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	2,010 / 1%
Duplication rate	0.84%
Clipped reads	188,204 / 93.23%

2.2. ACGT Content

Number/percentage of A's	3,056,704 / 26.91%
Number/percentage of C's	2,156,167 / 18.98%
Number/percentage of T's	3,430,861 / 30.2%
Number/percentage of G's	2,715,061 / 23.9%
Number/percentage of N's	1,626 / 0.01%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0037

Standard Deviation	0.0669

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

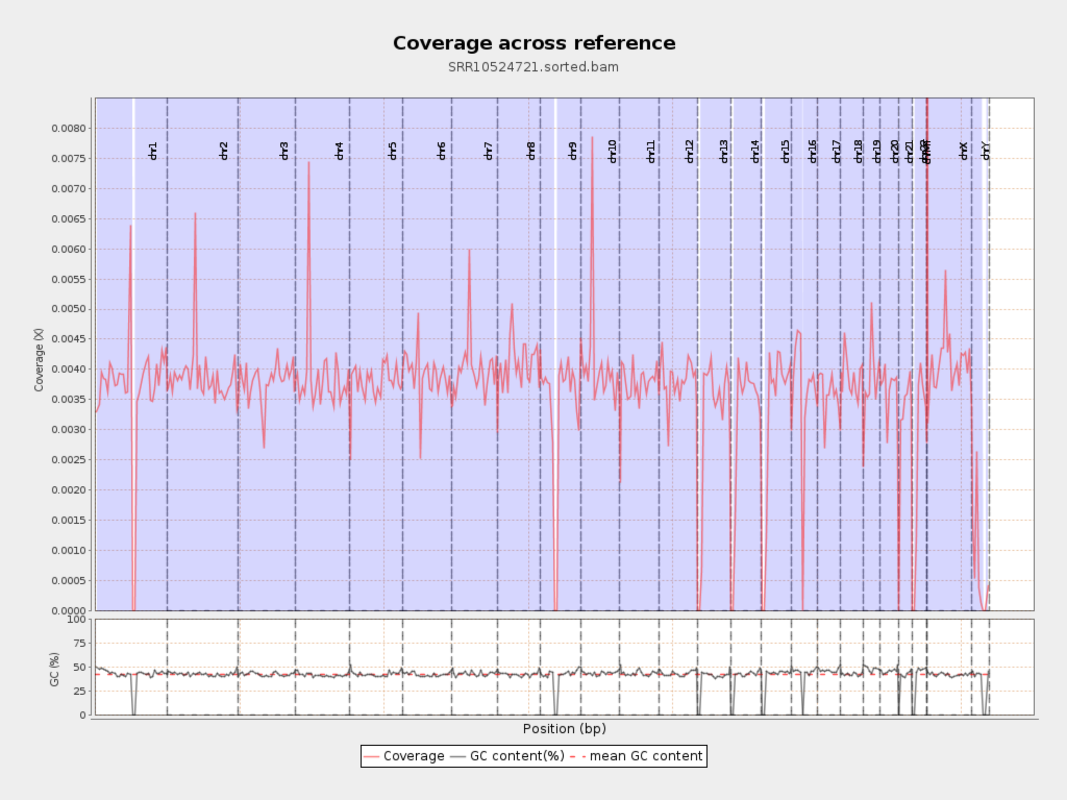
General error rate	0.51%
Mismatches	55,916
Insertions	928
Mapped reads with at least one insertion	0.49%
Deletions	2,109
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.57%

2.6. Chromosome stats

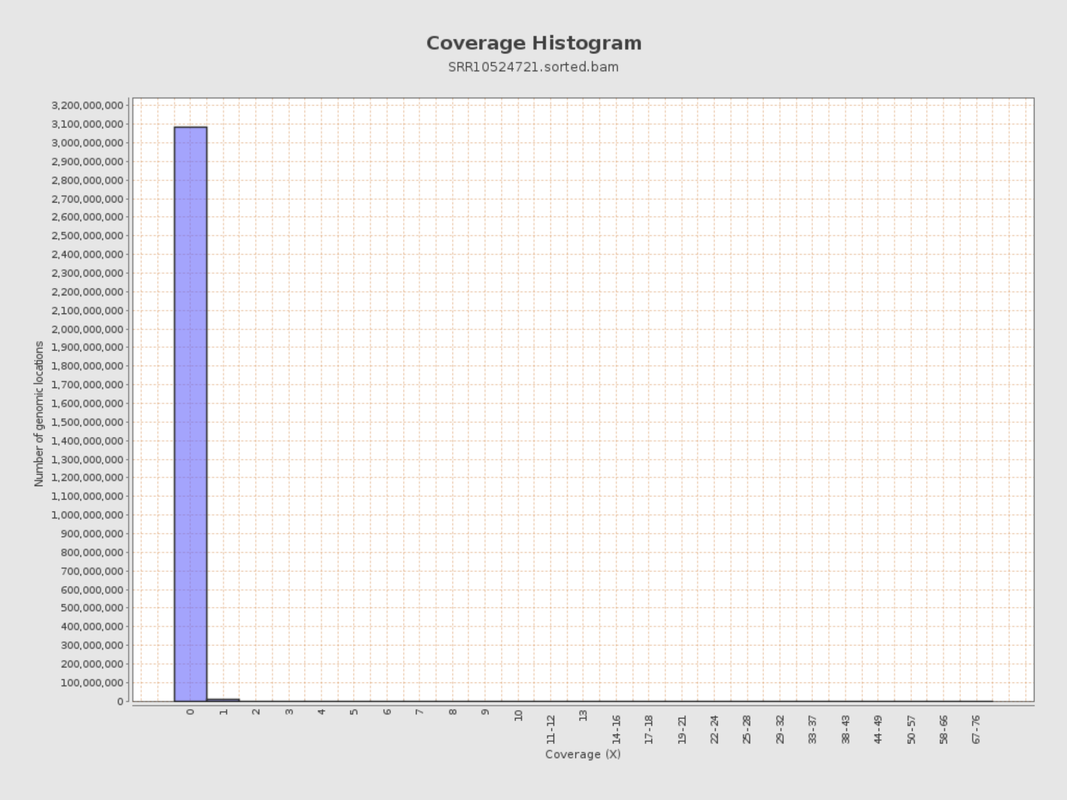
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	913888	0.0037	0.0837
chr2	243199373	948634	0.0039	0.0725
chr3	198022430	753510	0.0038	0.0626
chr4	191154276	745409	0.0039	0.0652
chr5	180915260	692586	0.0038	0.0628
chr6	171115067	667511	0.0039	0.065
chr7	159138663	640657	0.004	0.0717

chr8	146364022	602583	0.0041	0.0746
chr9	141213431	468408	0.0033	0.062
chr10	135534747	555797	0.0041	0.0727
chr11	135006516	510873	0.0038	0.0647
chr12	133851895	511202	0.0038	0.0627
chr13	115169878	357931	0.0031	0.0564
chr14	107349540	332716	0.0031	0.0565
chr15	102531392	327358	0.0032	0.0572
chr16	90354753	320319	0.0035	0.0607
chr17	81195210	290855	0.0036	0.0615
chr18	78077248	301289	0.0039	0.0822
chr19	59128983	228940	0.0039	0.0752
chr20	63025520	229860	0.0036	0.0617
chr21	48129895	152107	0.0032	0.0586
chr22	51304566	131002	0.0026	0.0513
chrMT	16571	3010	0.1816	0.4315
chrX	155270560	637931	0.0041	0.0657
chrY	59373566	39465	0.0007	0.0377

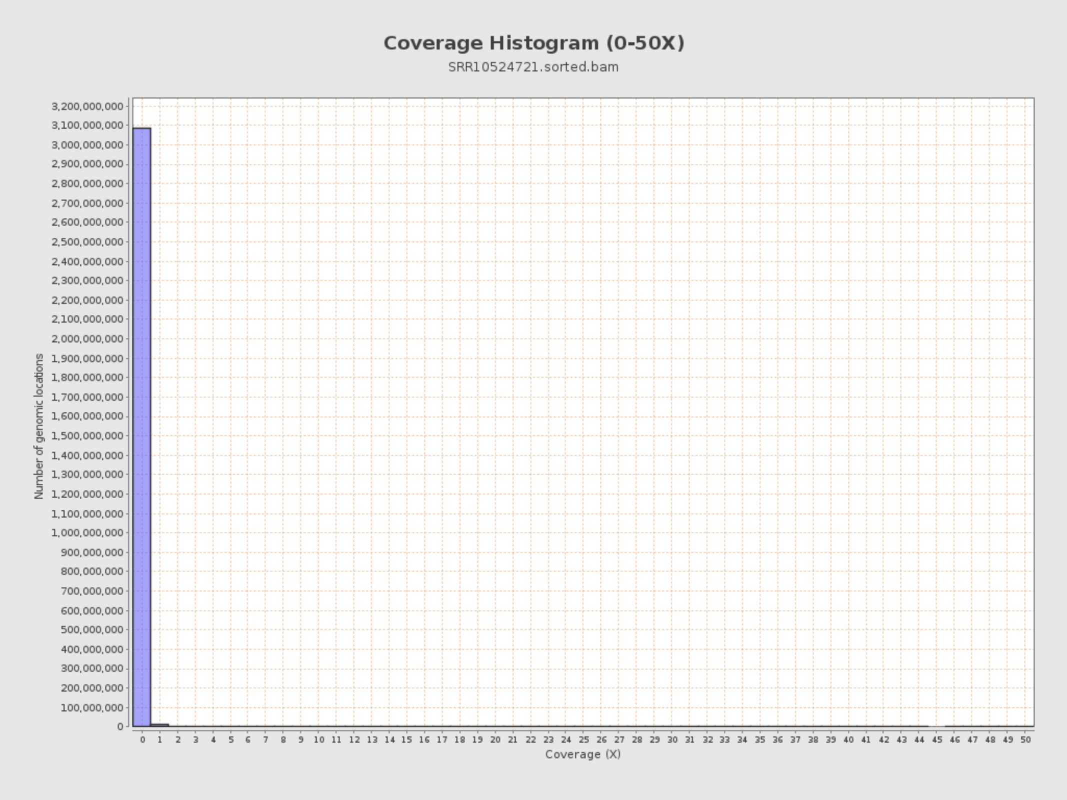
3. Results : Coverage across reference



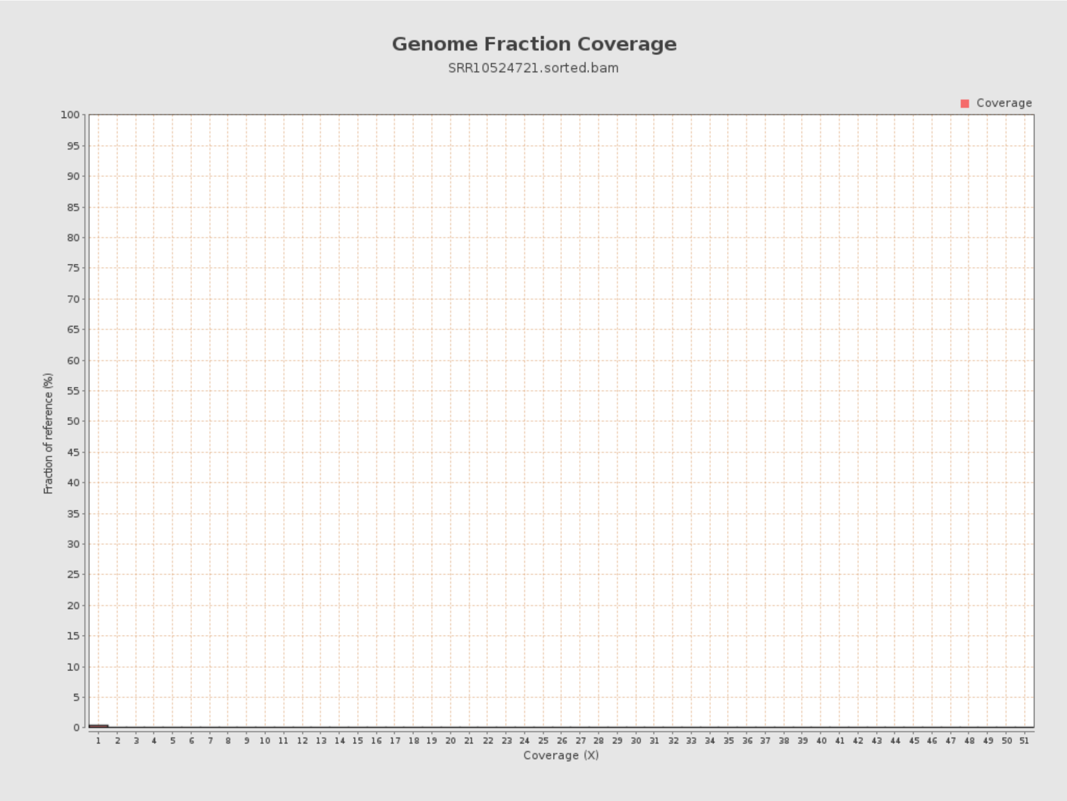
4. Results : Coverage Histogram



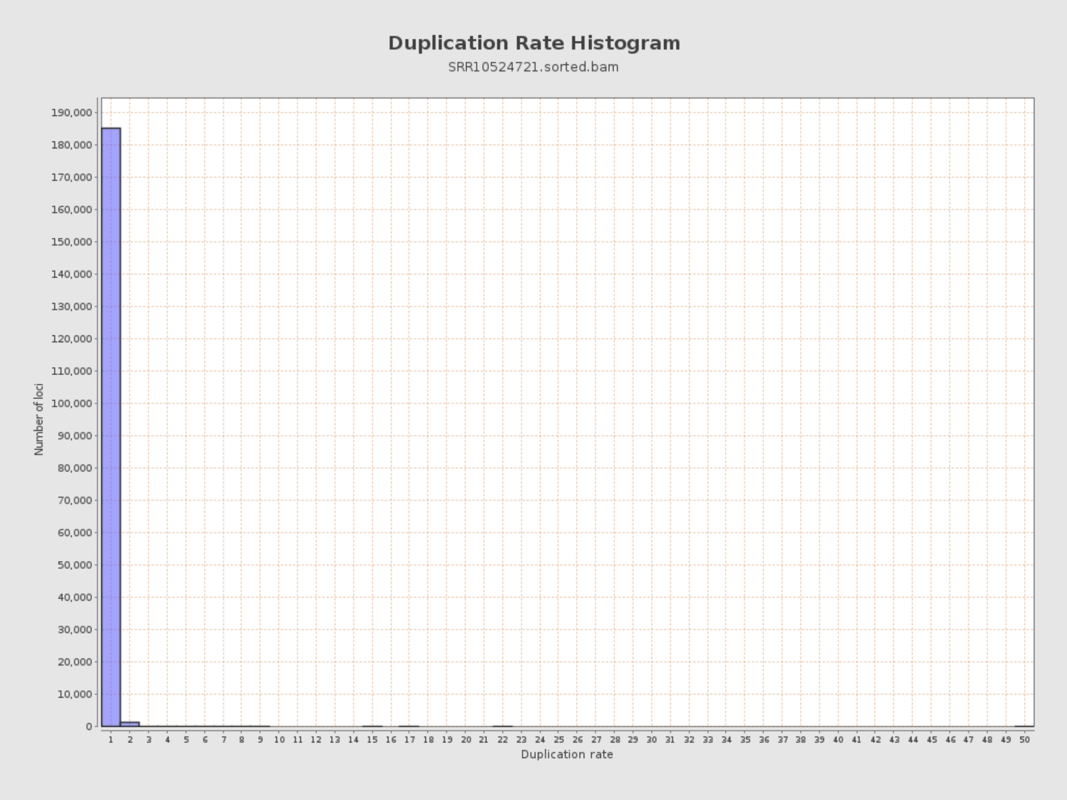
5. Results : Coverage Histogram (0-50X)



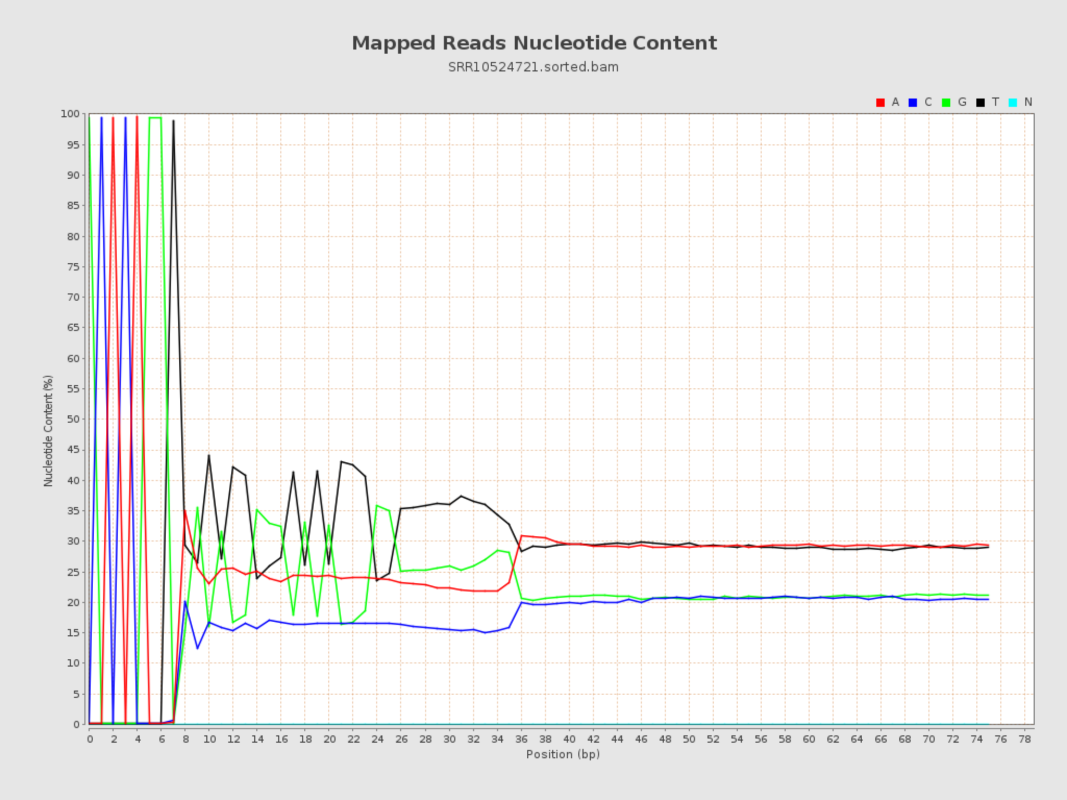
6. Results : Genome Fraction Coverage



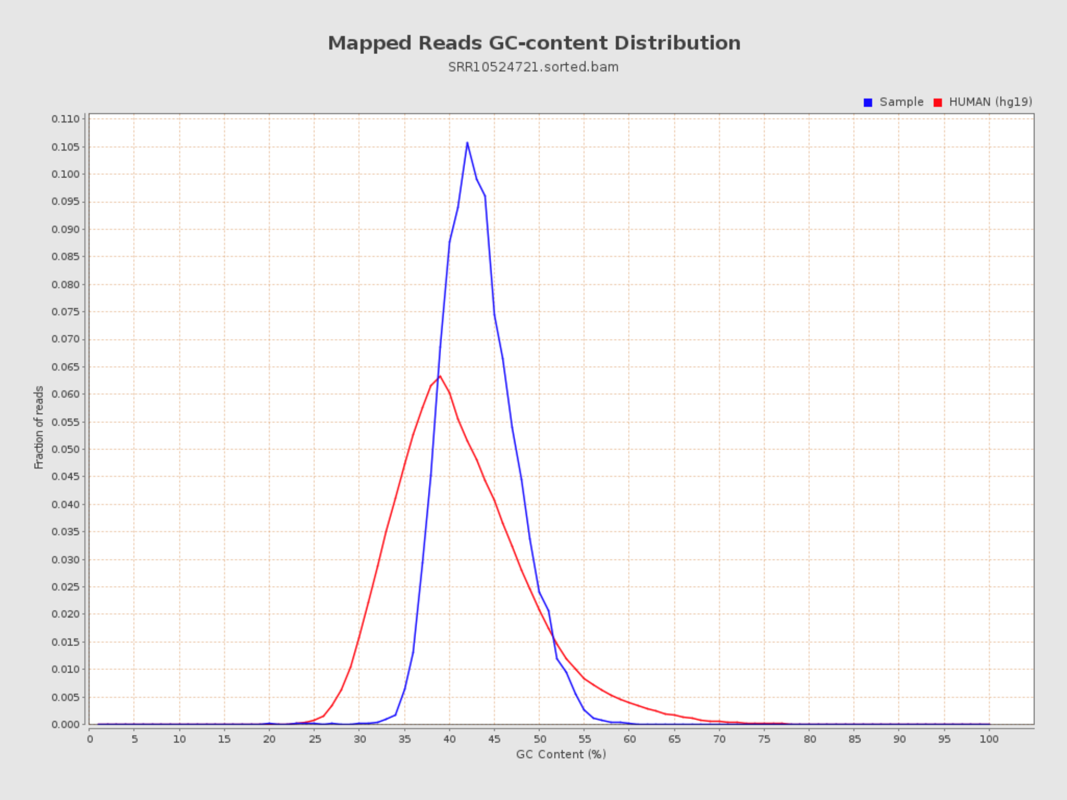
7. Results : Duplication Rate Histogram



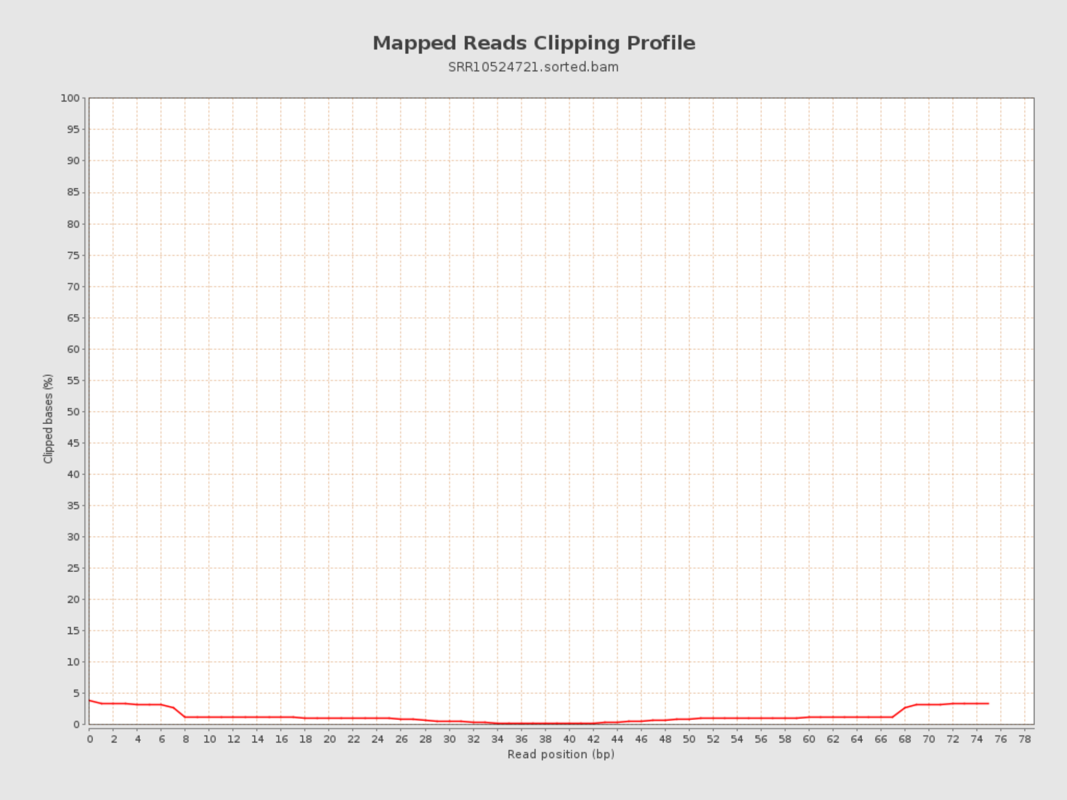
8. Results : Mapped Reads Nucleotide Content



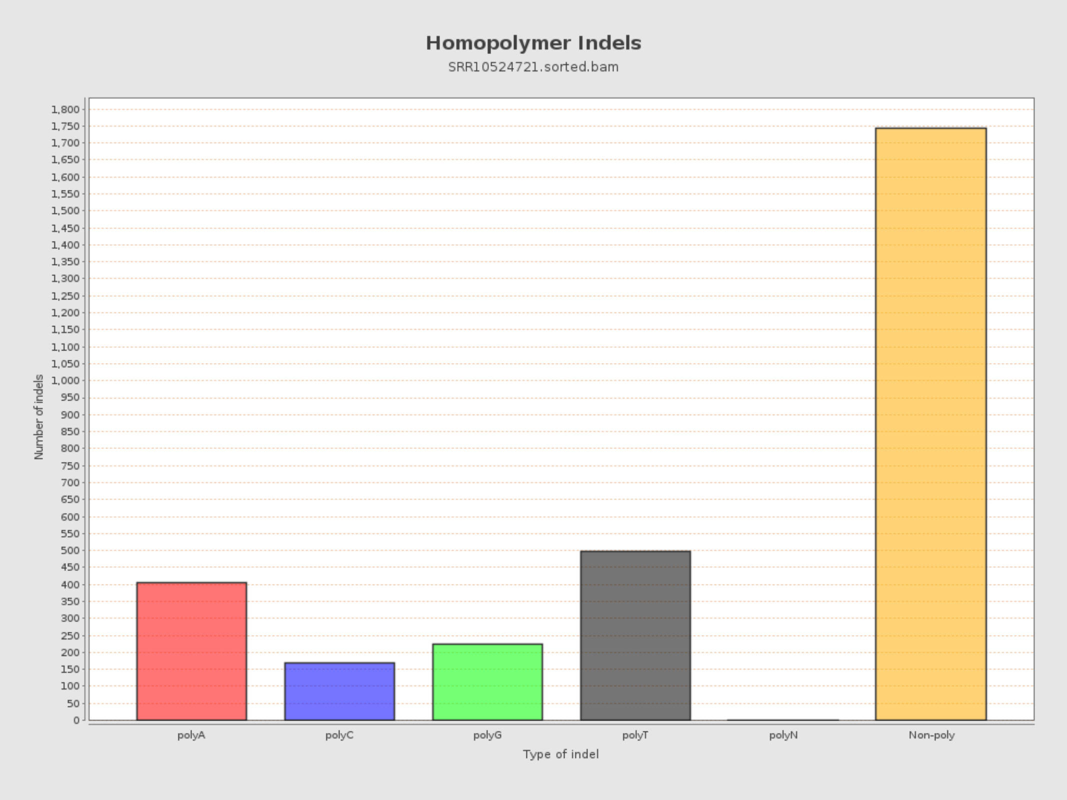
9. Results : Mapped Reads GC-content Distribution



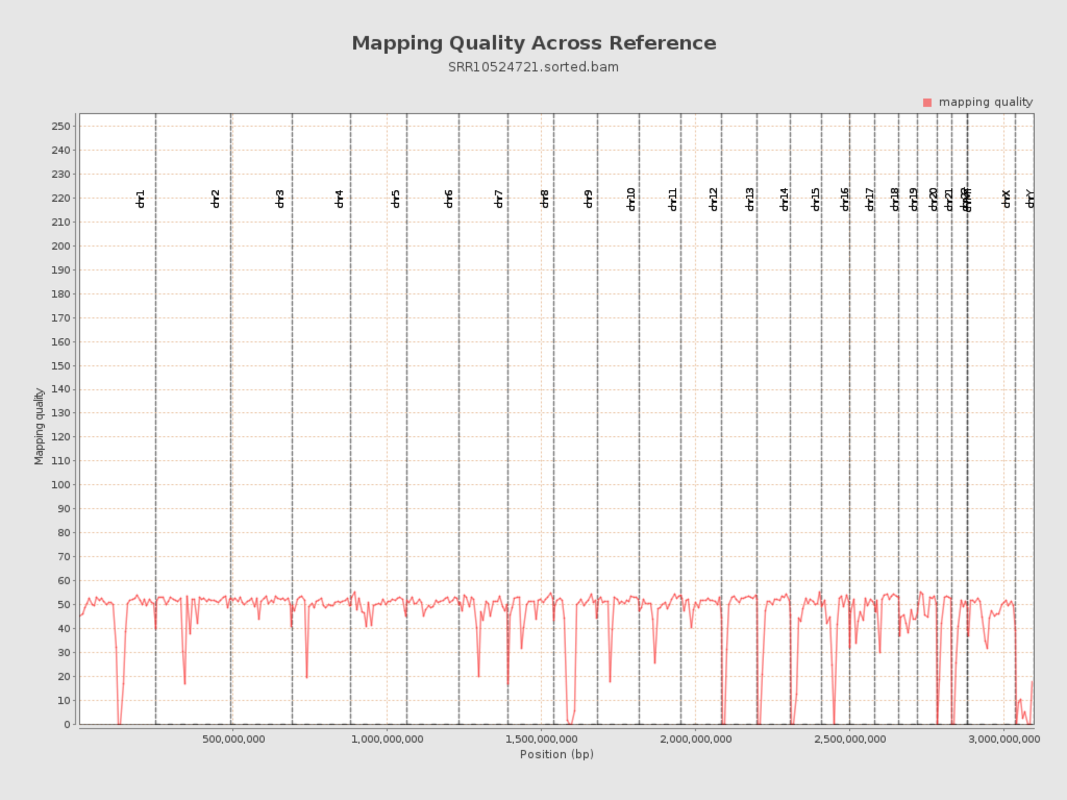
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram