

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:30:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472810.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_SRR3472810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:30:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,334,631
Mapped reads	1,839,221 / 78.78%
Unmapped reads	495,410 / 21.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,936 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	76,199 / 3.26%
Duplication rate	3.1%
Clipped reads	1,037,464 / 44.44%

2.2. ACGT Content

Number/percentage of A's	31,261,475 / 26.66%
Number/percentage of C's	23,894,345 / 20.37%
Number/percentage of T's	34,308,339 / 29.25%
Number/percentage of G's	27,813,462 / 23.72%
Number/percentage of N's	2,922 / 0%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0379

Standard Deviation	0.2982
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2.4. Mapping Quality

Mean Mapping Quality	43.18
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2.5. Mismatches and indels

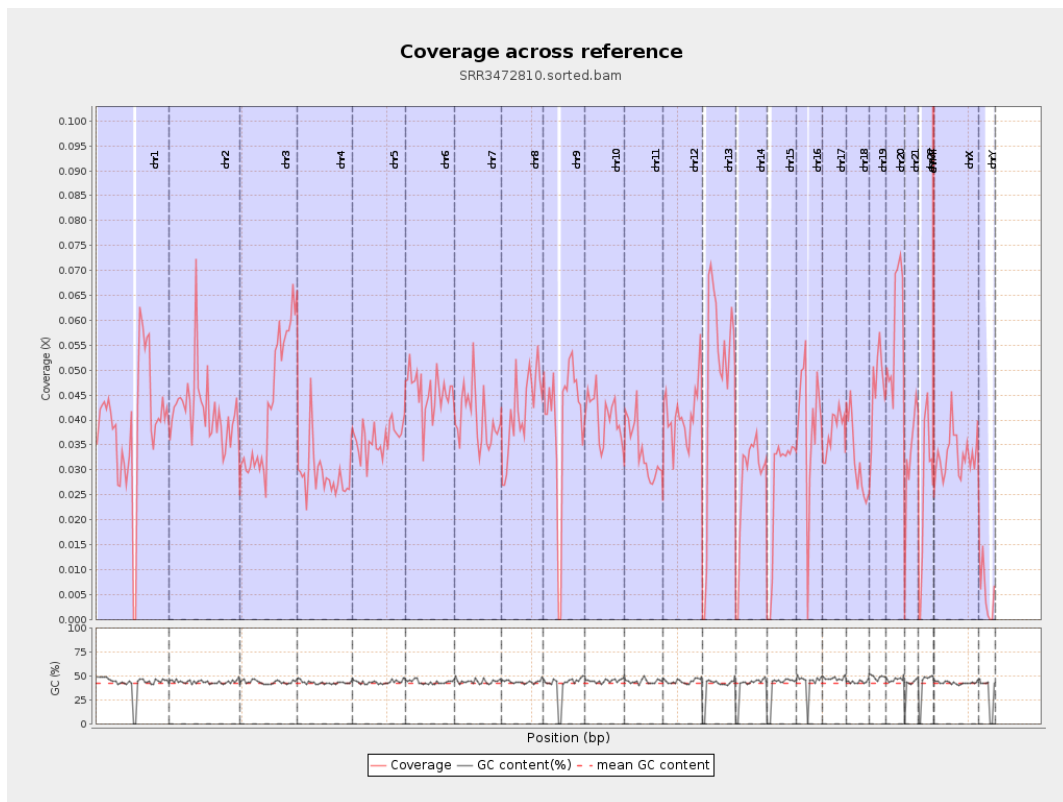
General error rate	0.89%
Mismatches	1,031,999
Insertions	9,190
Mapped reads with at least one insertion	0.5%
Deletions	27,519
Mapped reads with at least one deletion	1.48%
Homopolymer indels	44.89%

2.6. Chromosome stats

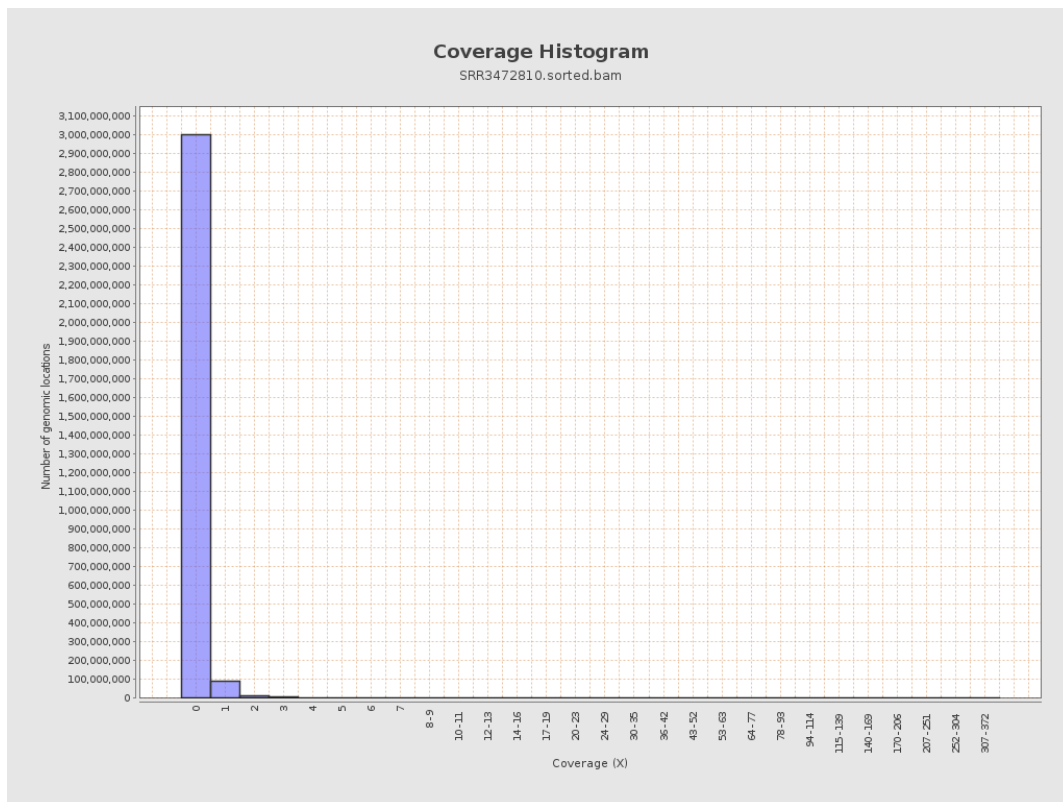
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9670646	0.0388	0.3613
chr2	243199373	10198266	0.0419	0.4007
chr3	198022430	8512480	0.043	0.2446
chr4	191154276	5561158	0.0291	0.2232
chr5	180915260	6557297	0.0362	0.2269
chr6	171115067	7805213	0.0456	0.2705
chr7	159138663	6406174	0.0403	0.3727

chr8	146364022	6083010	0.0416	0.2887
chr9	141213431	5618662	0.0398	0.3294
chr10	135534747	5523129	0.0408	0.2941
chr11	135006516	4538452	0.0336	0.315
chr12	133851895	5515512	0.0412	0.2462
chr13	115169878	5588692	0.0485	0.2633
chr14	107349540	2954919	0.0275	0.2202
chr15	102531392	2756782	0.0269	0.207
chr16	90354753	3594359	0.0398	0.2551
chr17	81195210	3058953	0.0377	0.2495
chr18	78077248	2508374	0.0321	0.5252
chr19	59128983	2751183	0.0465	0.3177
chr20	63025520	3698120	0.0587	0.2949
chr21	48129895	1592409	0.0331	0.246
chr22	51304566	1314080	0.0256	0.1951
chrMT	16571	108583	6.5526	5.0317
chrX	155270560	5105039	0.0329	0.2427
chrY	59373566	308769	0.0052	0.1185

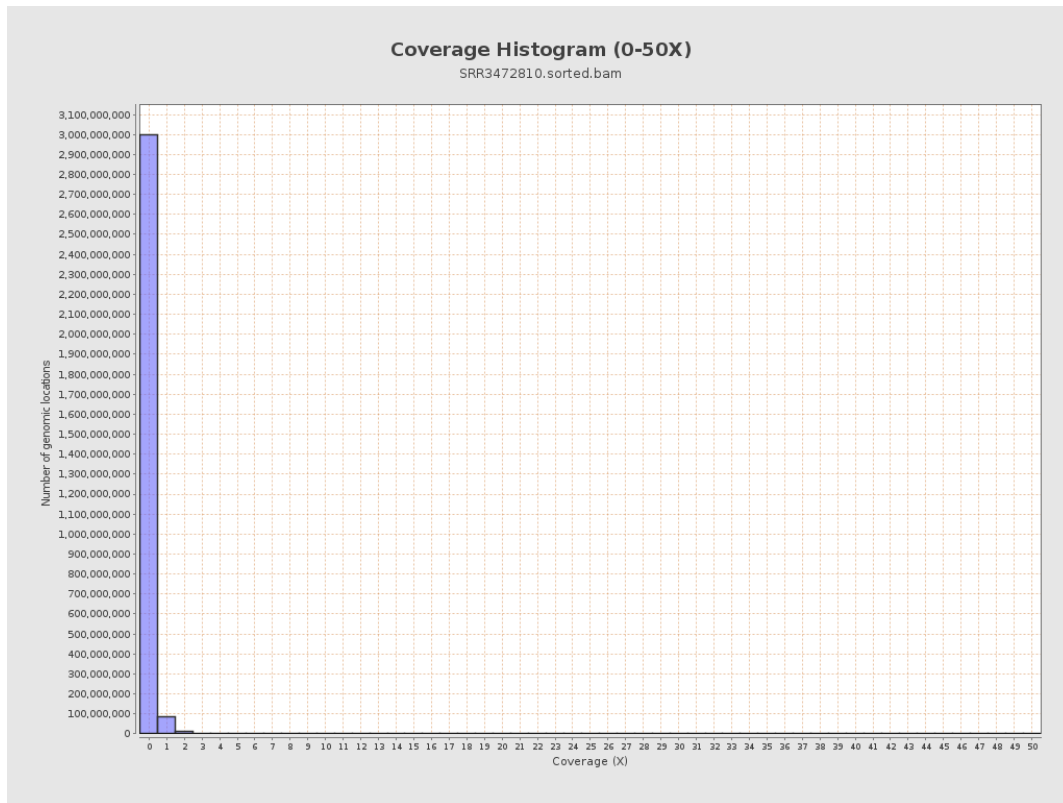
3. Results : Coverage across reference



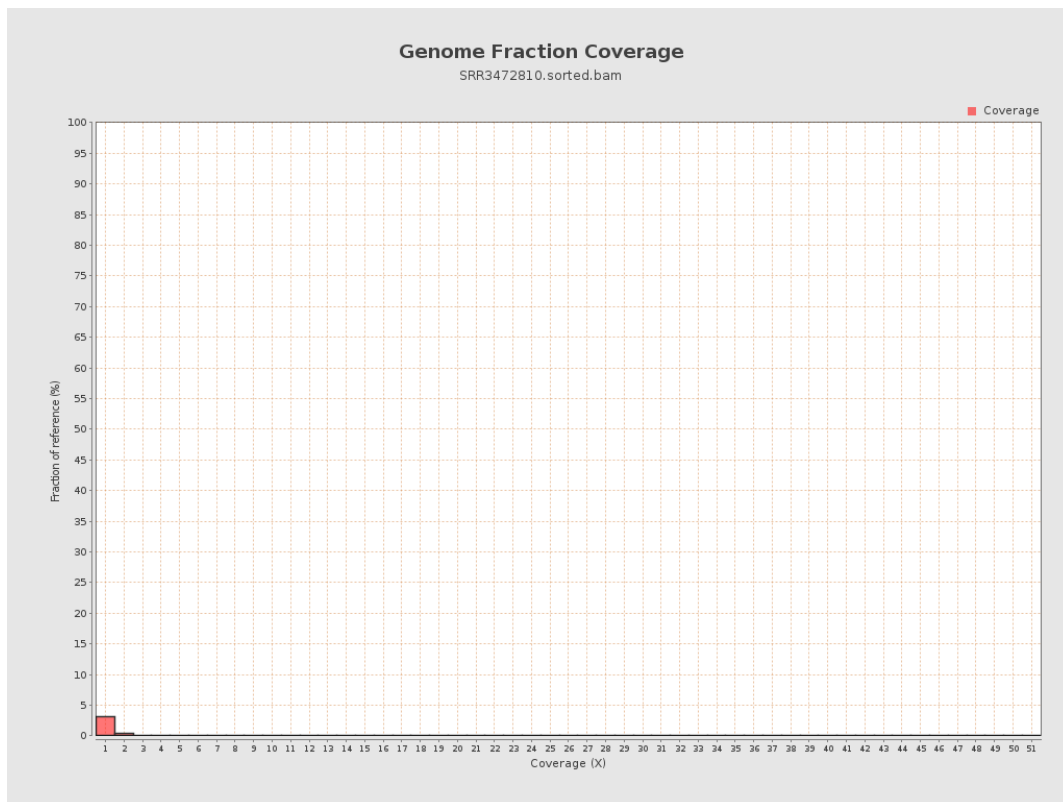
4. Results : Coverage Histogram



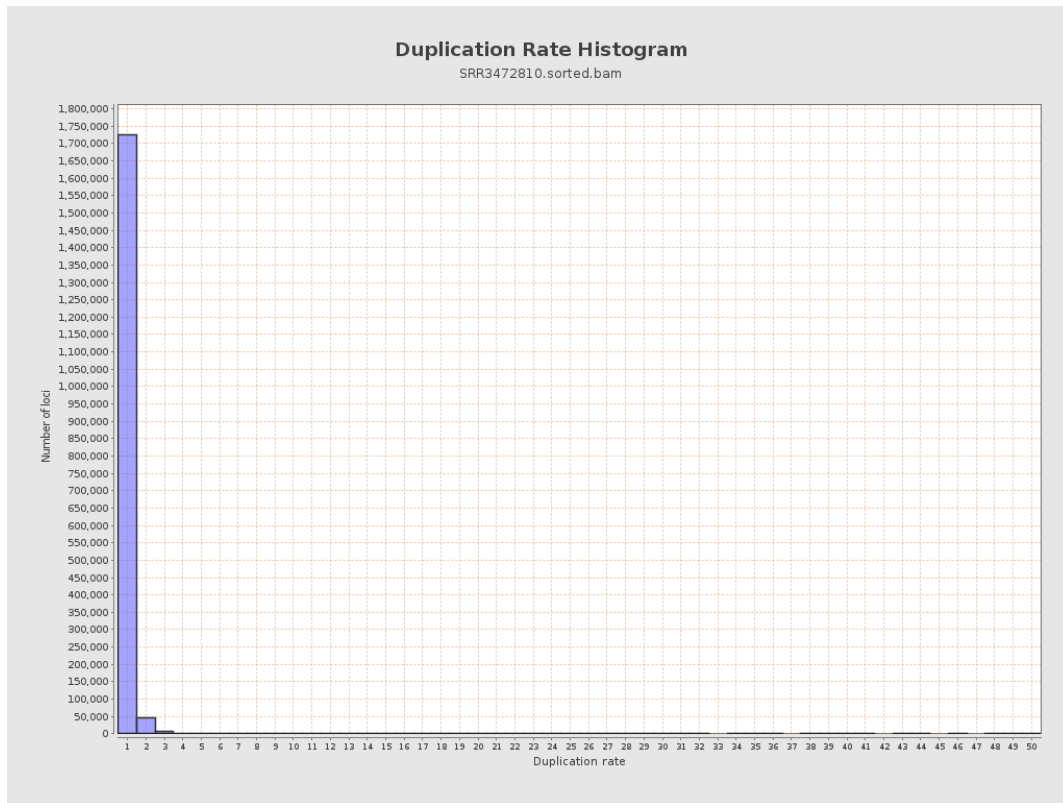
5. Results : Coverage Histogram (0-50X)



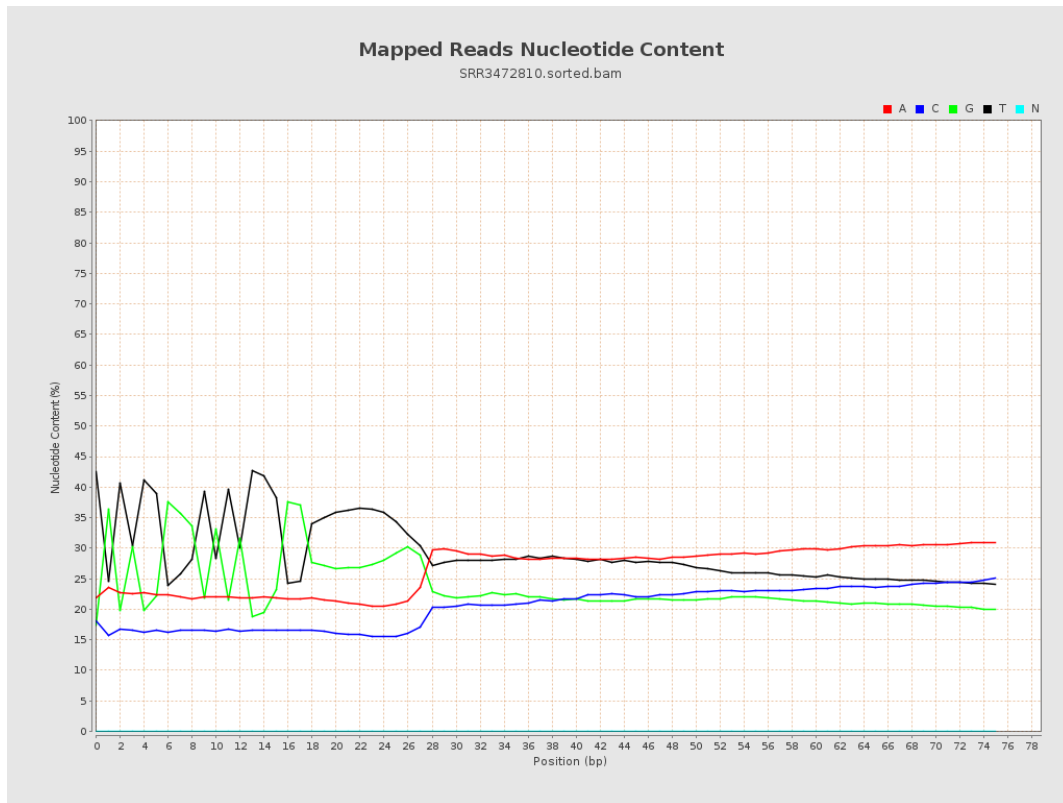
6. Results : Genome Fraction Coverage



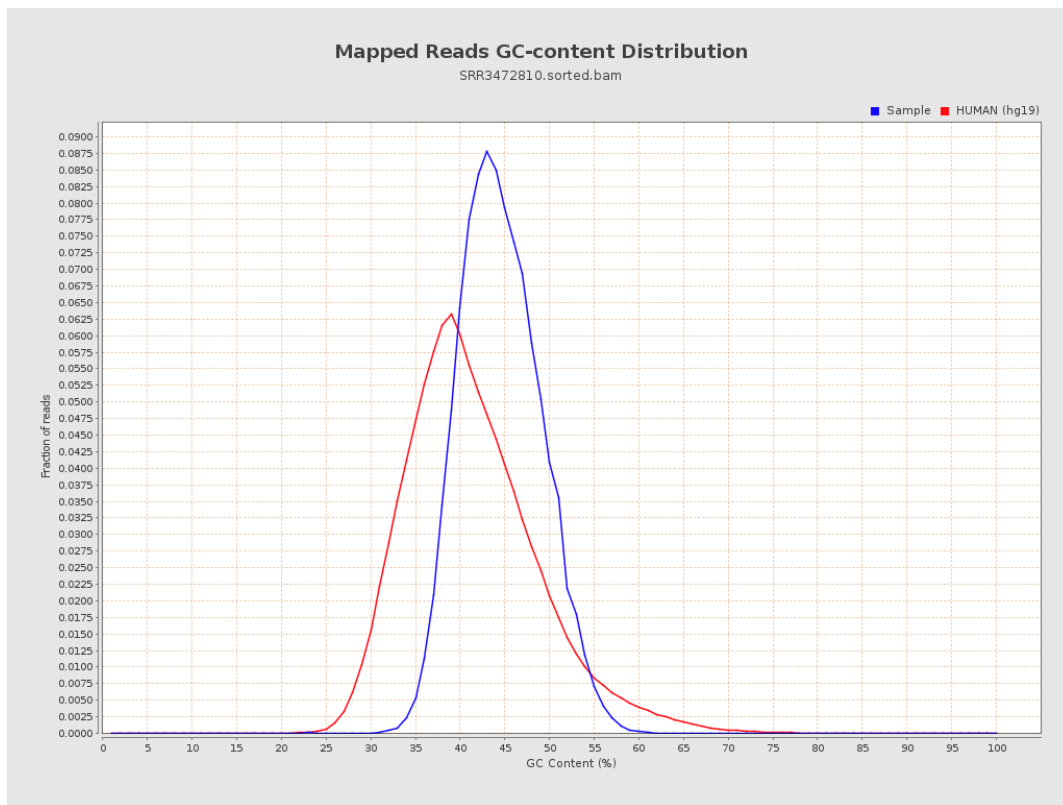
7. Results : Duplication Rate Histogram



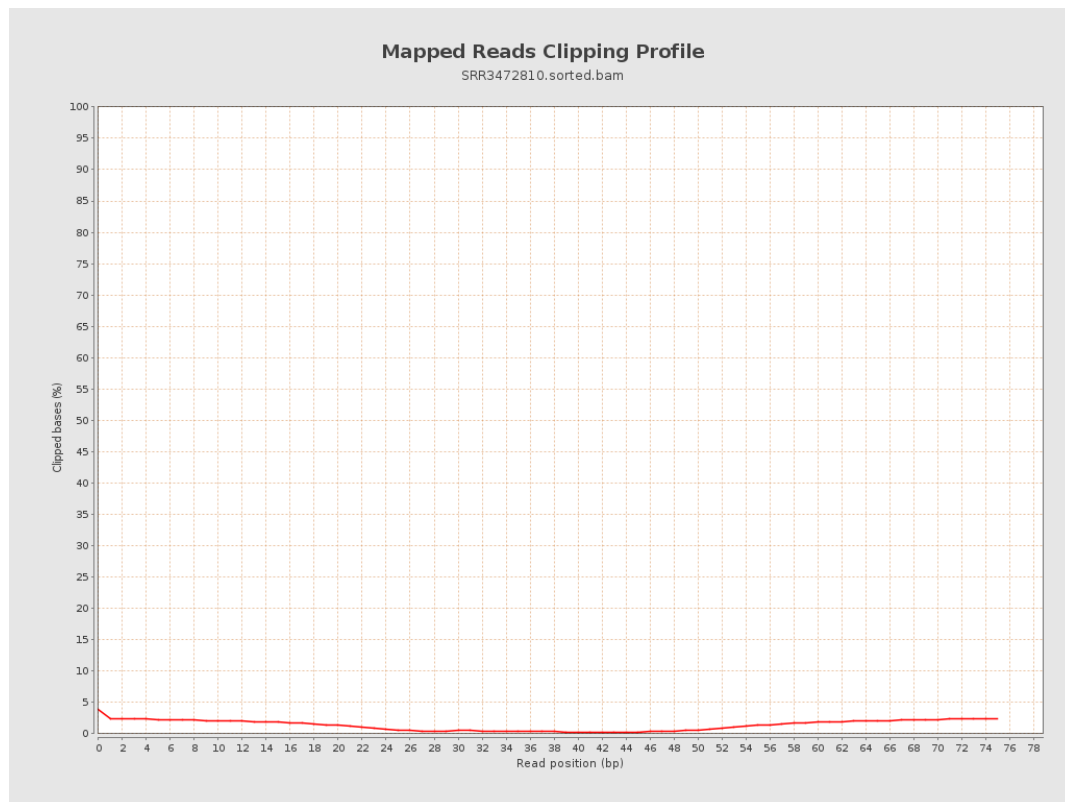
8. Results : Mapped Reads Nucleotide Content



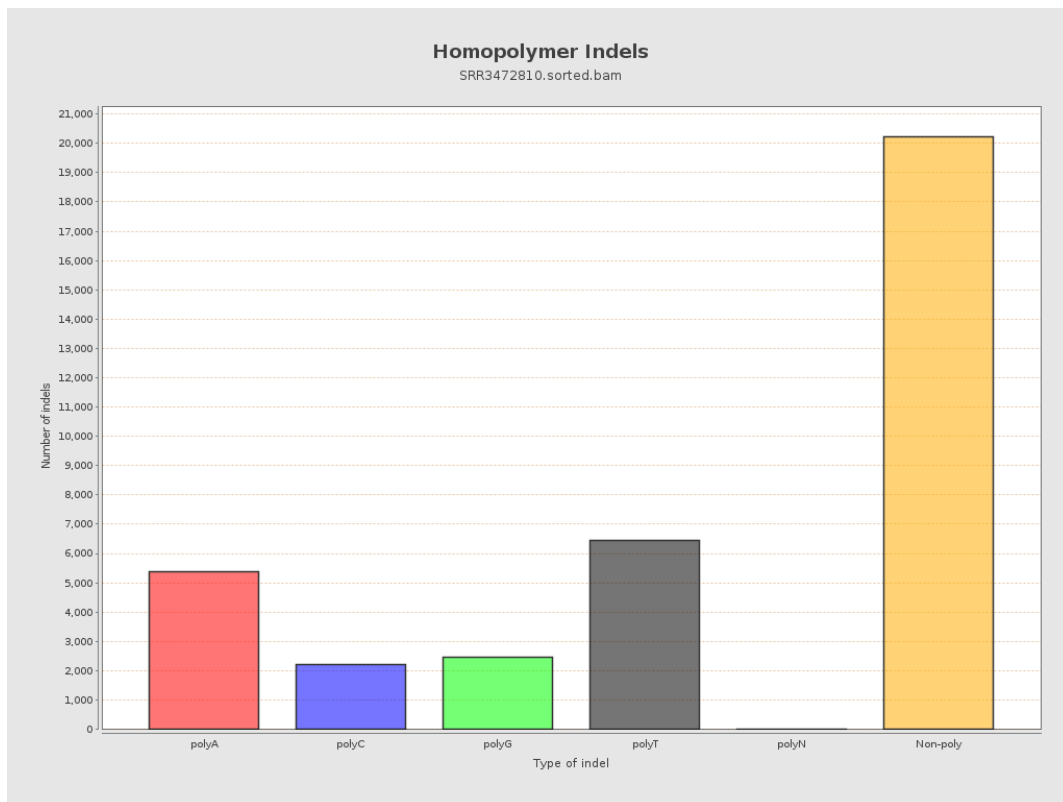
9. Results : Mapped Reads GC-content Distribution



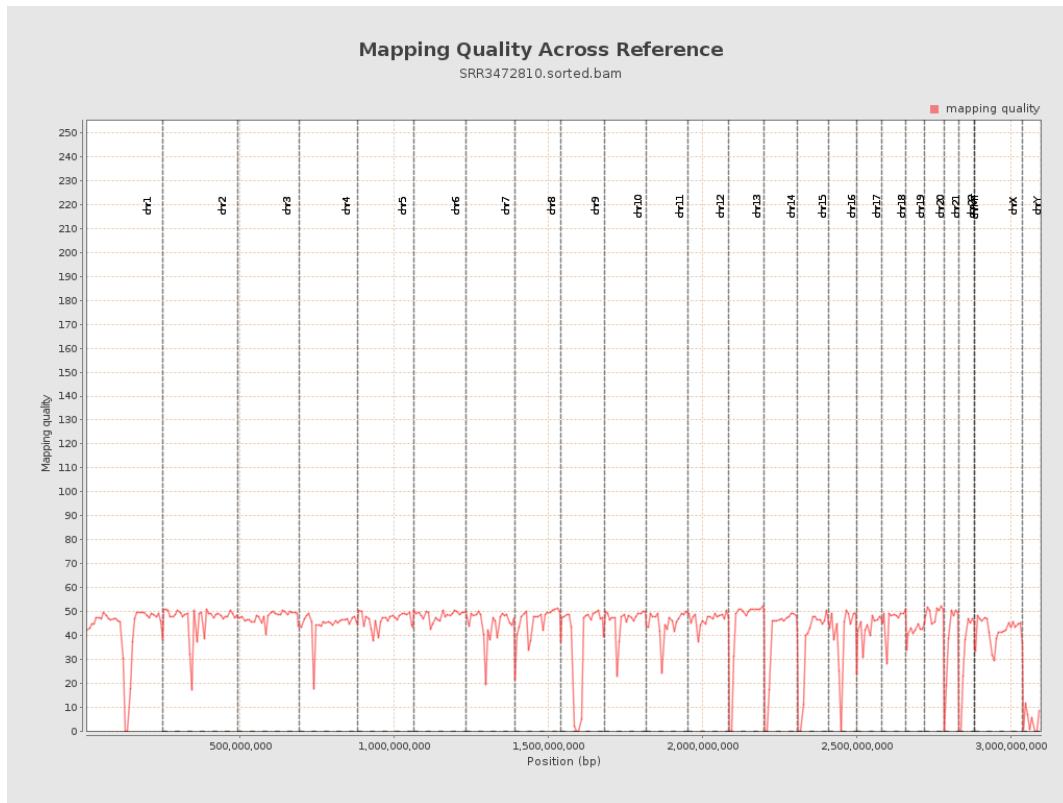
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

