

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:50:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082758.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_SRR3082758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:50:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,408,153
Mapped reads	3,801,238 / 86.23%
Unmapped reads	606,915 / 13.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,747 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	215,295 / 4.88%
Duplication rate	4.55%
Clipped reads	1,606,378 / 36.44%

2.2. ACGT Content

Number/percentage of A's	72,648,095 / 28.34%
Number/percentage of C's	46,094,117 / 17.98%
Number/percentage of T's	83,728,849 / 32.66%
Number/percentage of G's	53,860,705 / 21.01%
Number/percentage of N's	14,327 / 0.01%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0828

Standard Deviation	0.5948
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2.4. Mapping Quality

Mean Mapping Quality	47.08
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2.5. Mismatches and indels

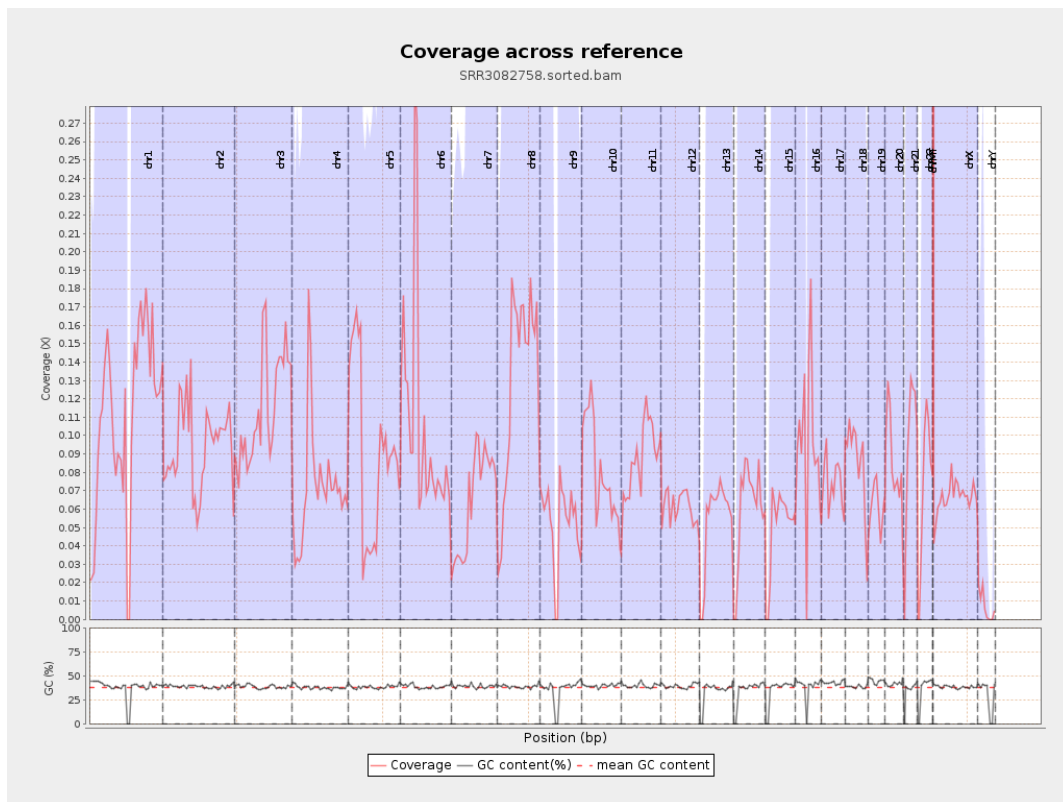
General error rate	0.89%
Mismatches	2,257,616
Insertions	20,480
Mapped reads with at least one insertion	0.53%
Deletions	57,833
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.02%

2.6. Chromosome stats

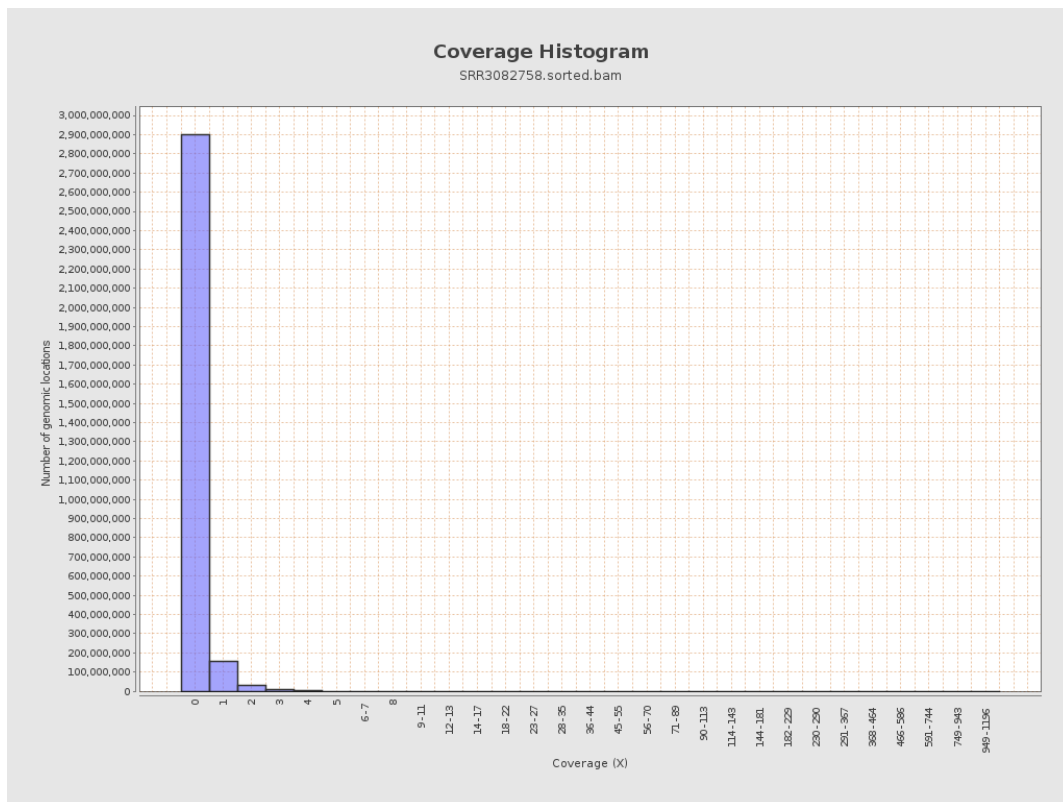
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27548198	0.1105	1.1245
chr2	243199373	23013337	0.0946	0.7192
chr3	198022430	22574331	0.114	0.4194
chr4	191154276	13889892	0.0727	0.3415
chr5	180915260	16179468	0.0894	0.3749
chr6	171115067	18089732	0.1057	0.5887
chr7	159138663	10302271	0.0647	0.4718

chr8	146364022	18994448	0.1298	0.8207
chr9	141213431	7523787	0.0533	0.5397
chr10	135534747	10954258	0.0808	0.4931
chr11	135006516	11824094	0.0876	0.5338
chr12	133851895	8132653	0.0608	0.3125
chr13	115169878	6176021	0.0536	0.2854
chr14	107349540	6573774	0.0612	0.3401
chr15	102531392	5050443	0.0493	0.2714
chr16	90354753	8615462	0.0954	0.4456
chr17	81195210	6052532	0.0745	0.4575
chr18	78077248	6793892	0.087	1.1751
chr19	59128983	3665633	0.062	0.7239
chr20	63025520	5499423	0.0873	0.3782
chr21	48129895	4472214	0.0929	0.3921
chr22	51304566	3673224	0.0716	0.3263
chrMT	16571	162851	9.8275	5.8358
chrX	155270560	10262629	0.0661	0.3813
chrY	59373566	419528	0.0071	0.1373

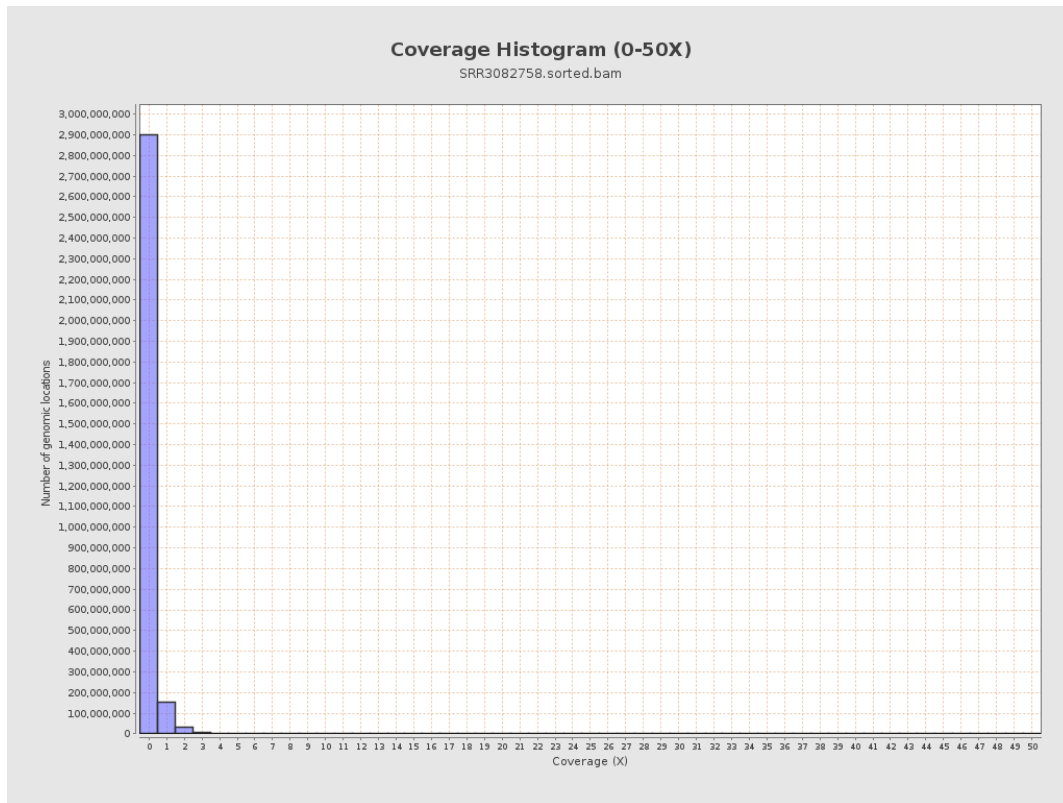
3. Results : Coverage across reference



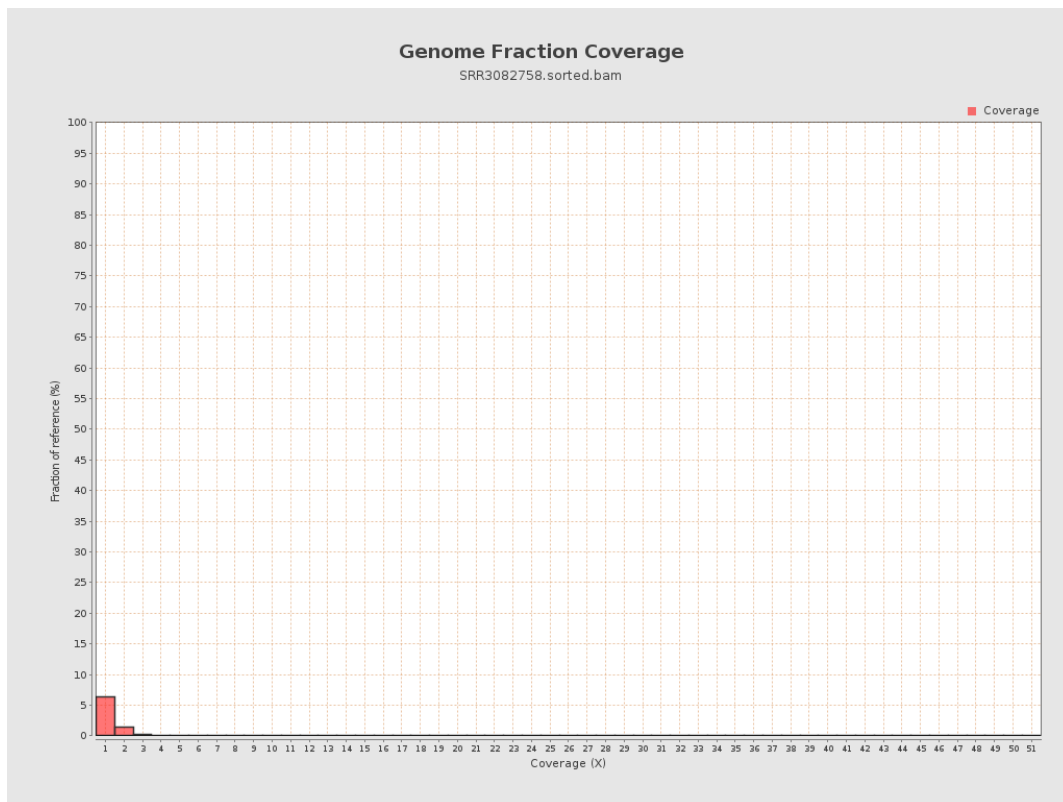
4. Results : Coverage Histogram



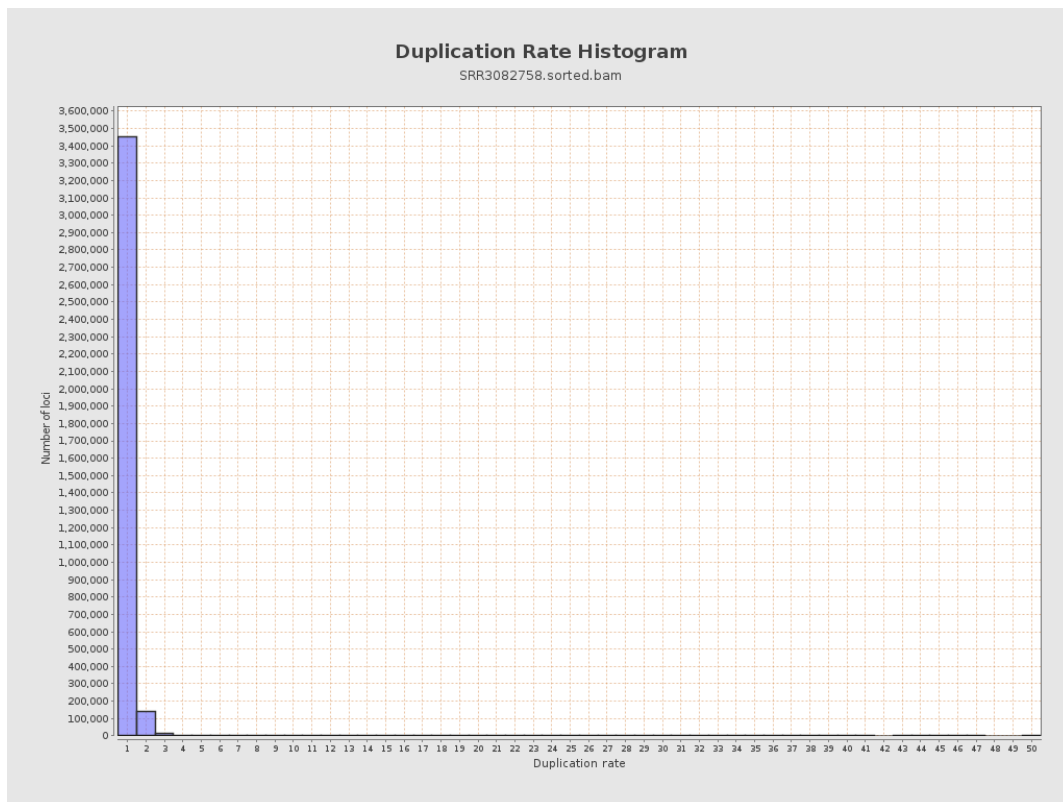
5. Results : Coverage Histogram (0-50X)



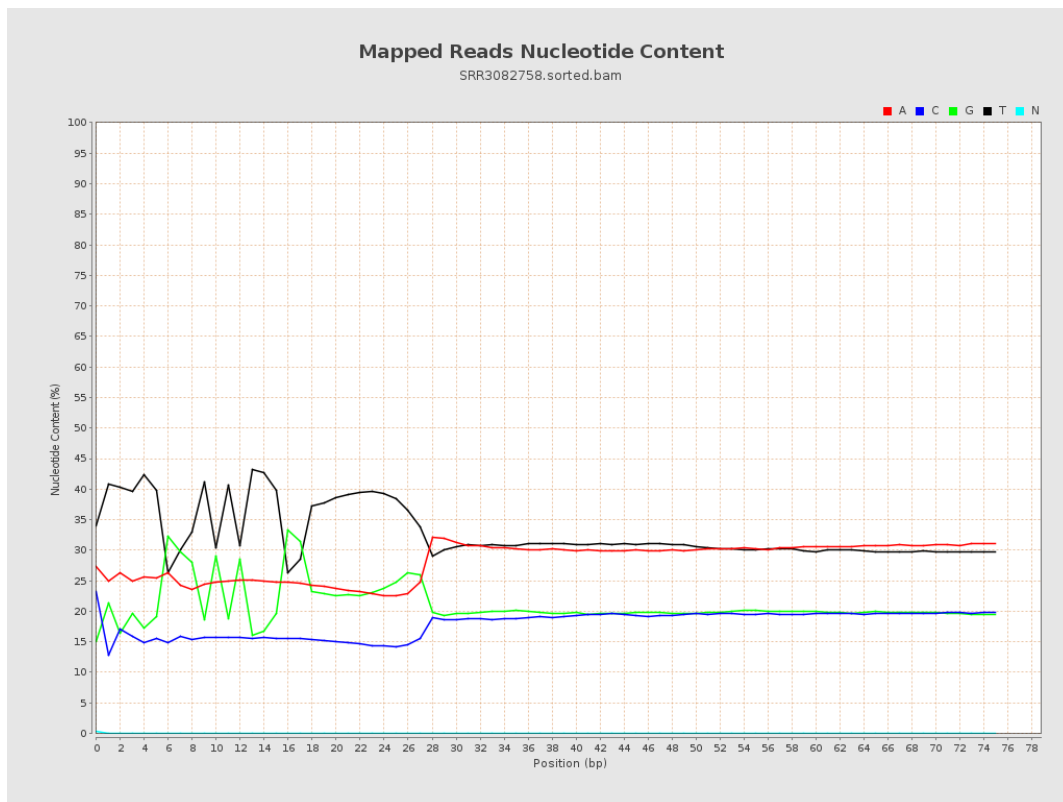
6. Results : Genome Fraction Coverage



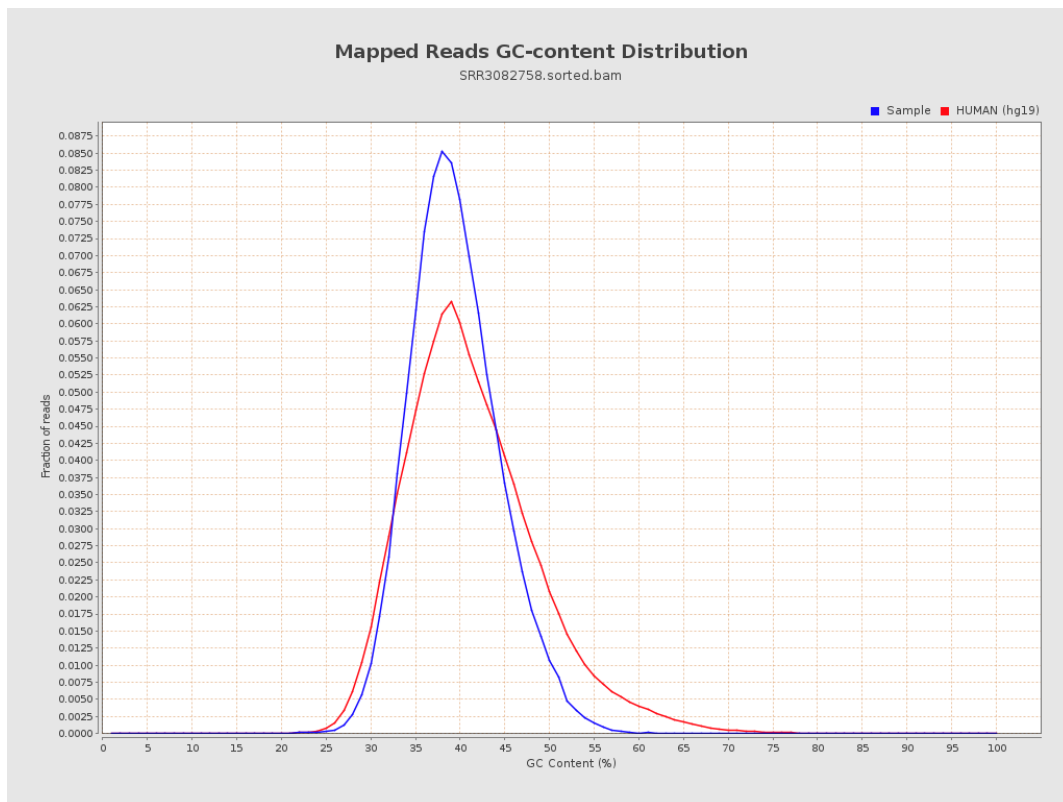
7. Results : Duplication Rate Histogram



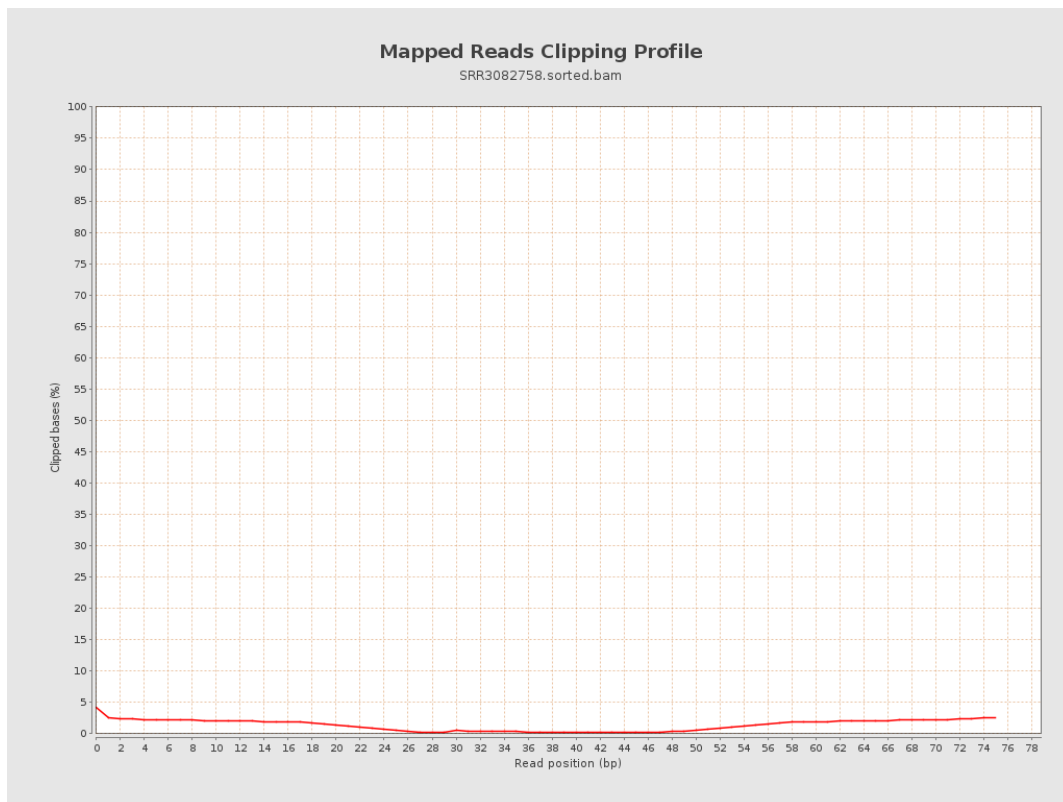
8. Results : Mapped Reads Nucleotide Content



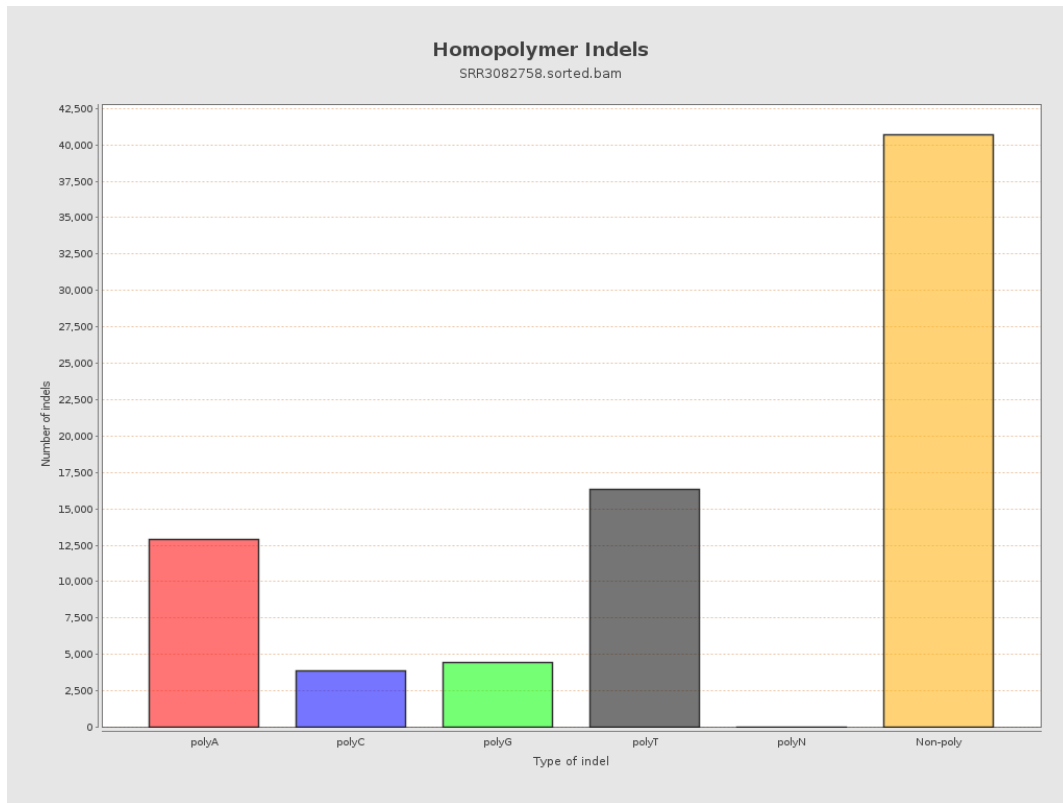
9. Results : Mapped Reads GC-content Distribution



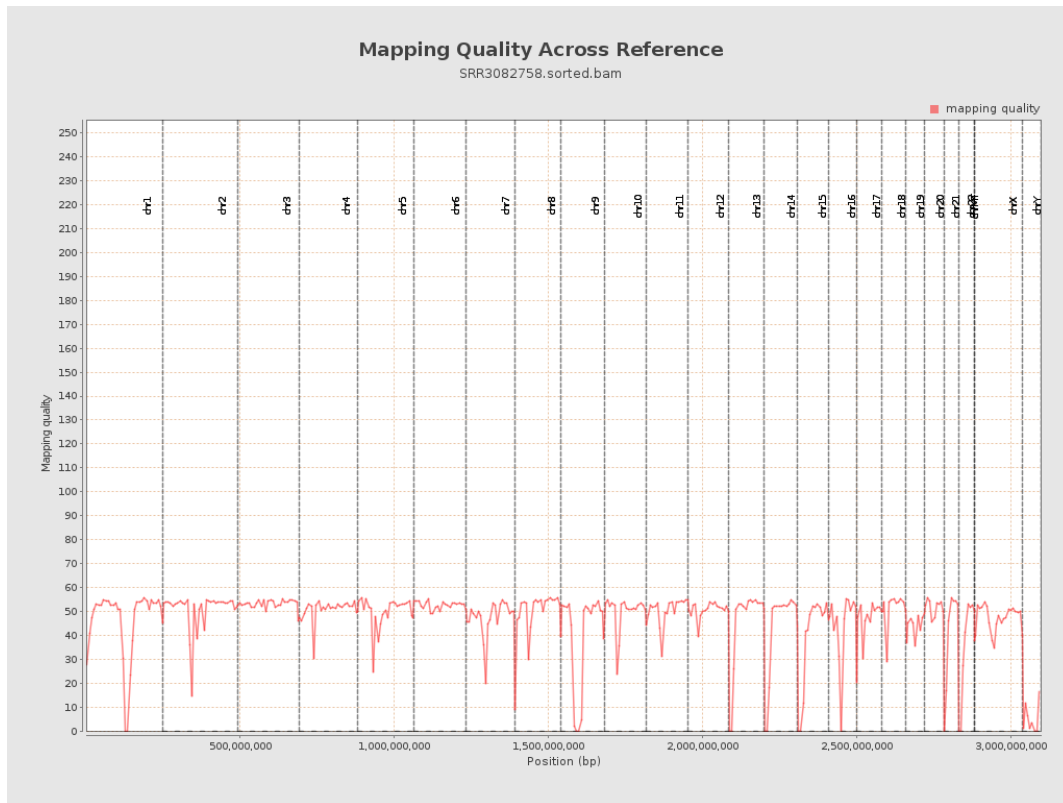
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

