Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080758.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_SRR3080758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:35:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,646,970
Mapped reads	3,529,754 / 75.96%
Unmapped reads	1,117,216 / 24.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,502 / 0.63%
Read min/max/mean length	30 / 66 / 66.21
Duplicated reads (estimated)	449,886 / 9.68%
Duplication rate	9.09%
Clipped reads	515,584 / 11.1%

2.2. ACGT Content

Number/percentage of A's	71,377,769 / 31.62%
Number/percentage of C's	45,149,787 / 20%
Number/percentage of T's	58,227,545 / 25.8%
Number/percentage of G's	50,876,429 / 22.54%
Number/percentage of N's	73,790 / 0.03%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0729

Standard Deviation	0.5016

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

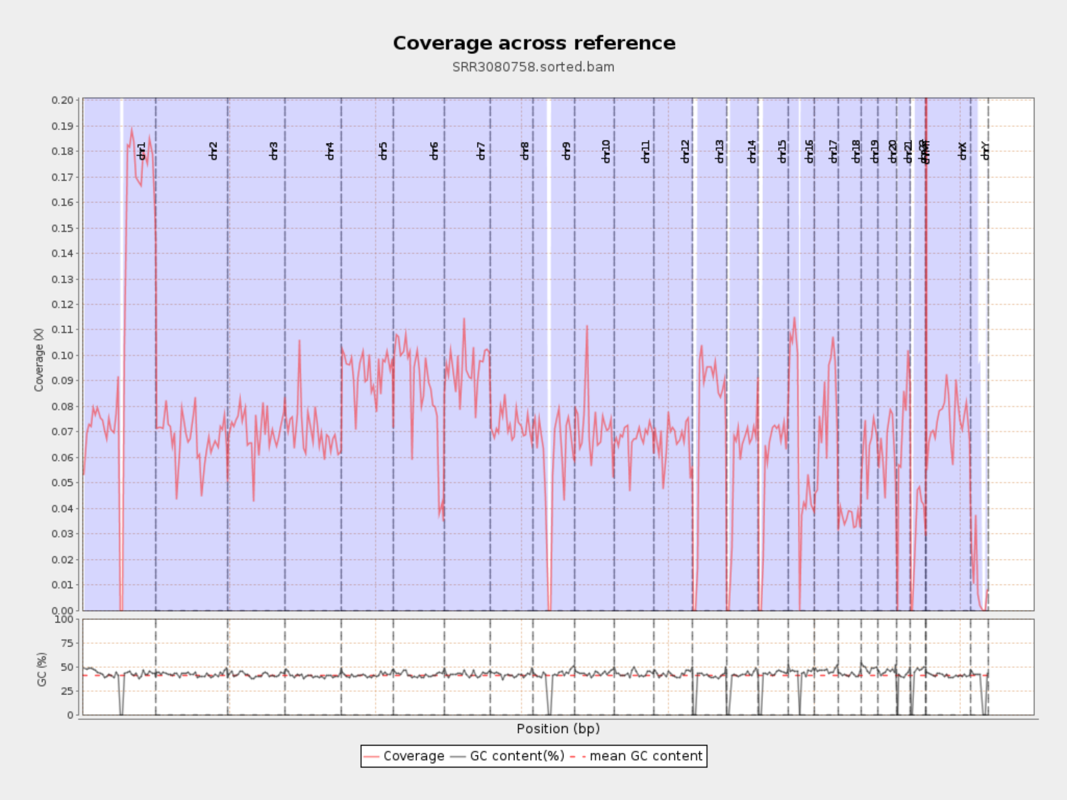
General error rate	0.7%
Mismatches	1,557,814
Insertions	16,556
Mapped reads with at least one insertion	0.46%
Deletions	43,144
Mapped reads with at least one deletion	1.21%
Homopolymer indels	44.09%

2.6. Chromosome stats

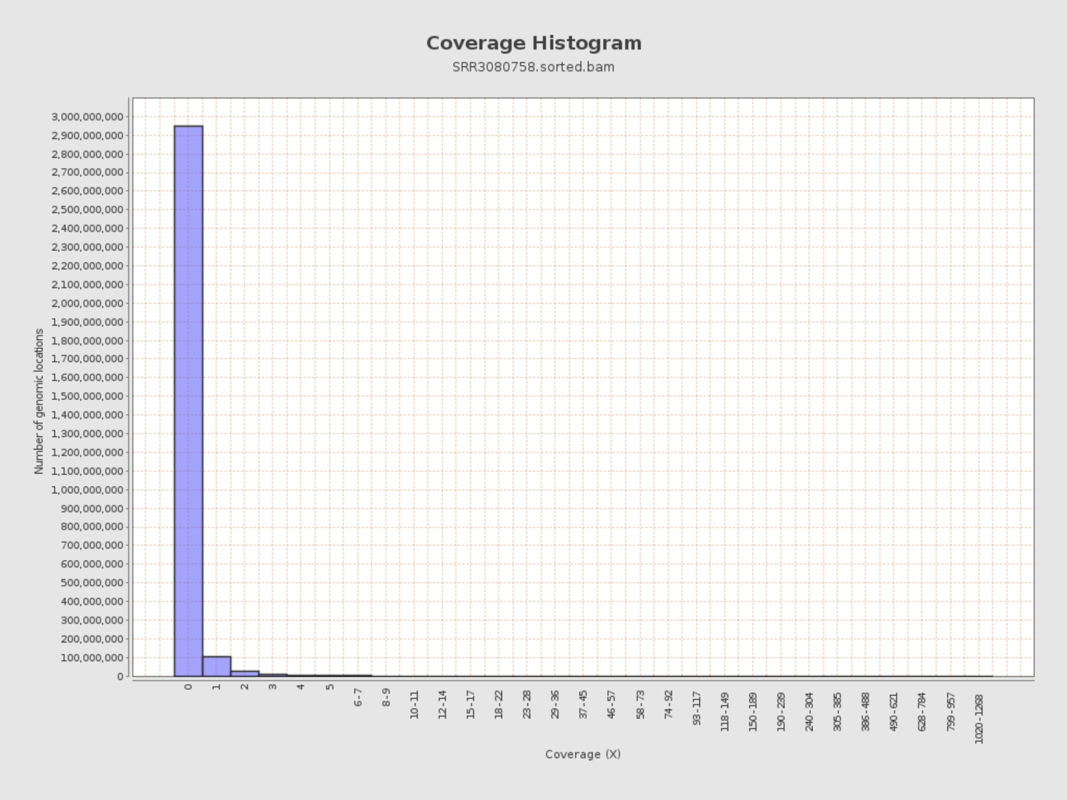
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27929850	0.1121	0.711
chr2	243199373	16471305	0.0677	0.4595
chr3	198022430	13945599	0.0704	0.3933
chr4	191154276	13492942	0.0706	0.4444
chr5	180915260	16873715	0.0933	0.4613
chr6	171115067	14841323	0.0867	0.5155
chr7	159138663	15119457	0.095	0.5975

chr8	146364022	10610078	0.0725	0.8731
chr9	141213431	8265072	0.0585	0.3893
chr10	135534747	9788472	0.0722	0.5751
chr11	135006516	9126458	0.0676	0.4223
chr12	133851895	8934114	0.0667	0.3871
chr13	115169878	8888743	0.0772	0.419
chr14	107349540	6040676	0.0563	0.3855
chr15	102531392	5631740	0.0549	0.3478
chr16	90354753	5705138	0.0631	0.4052
chr17	81195210	6359605	0.0783	0.4271
chr18	78077248	2823796	0.0362	0.4399
chr19	59128983	3830814	0.0648	0.6062
chr20	63025520	4010210	0.0636	0.3909
chr21	48129895	3375518	0.0701	0.4529
chr22	51304566	1585278	0.0309	0.256
chrMT	16571	33151	2.0005	2.3322
chrX	155270560	11481688	0.0739	0.4144
chrY	59373566	621717	0.0105	0.2757

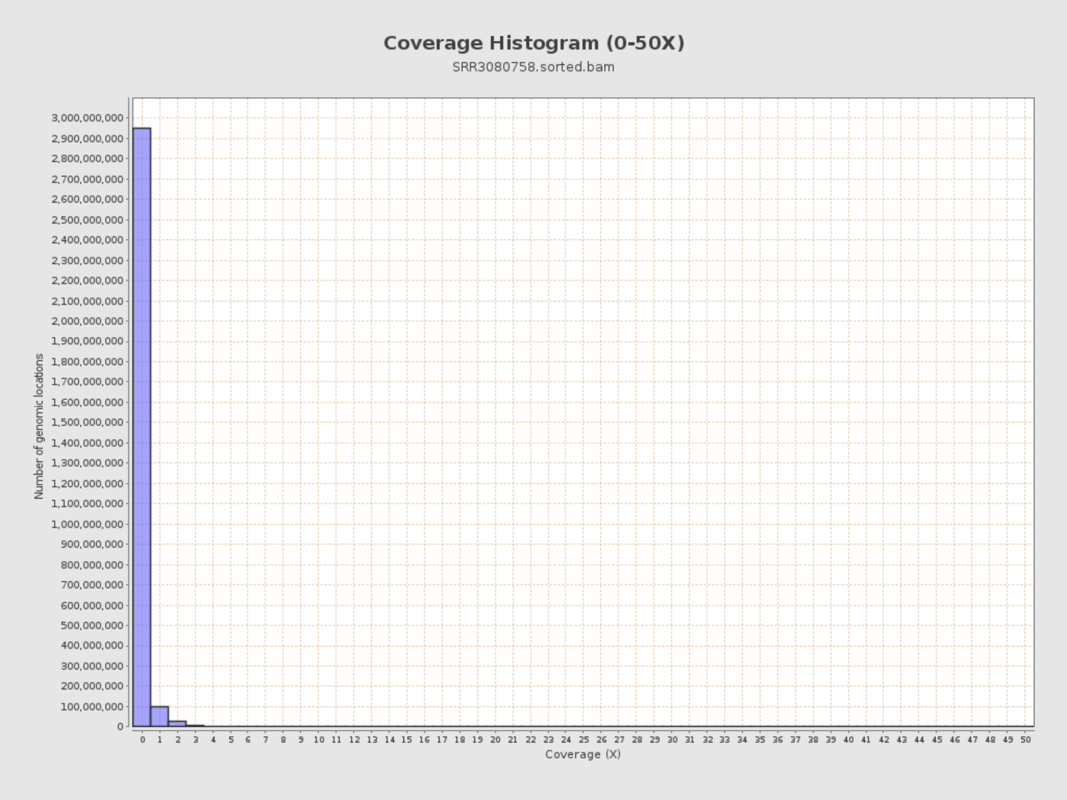
3. Results : Coverage across reference



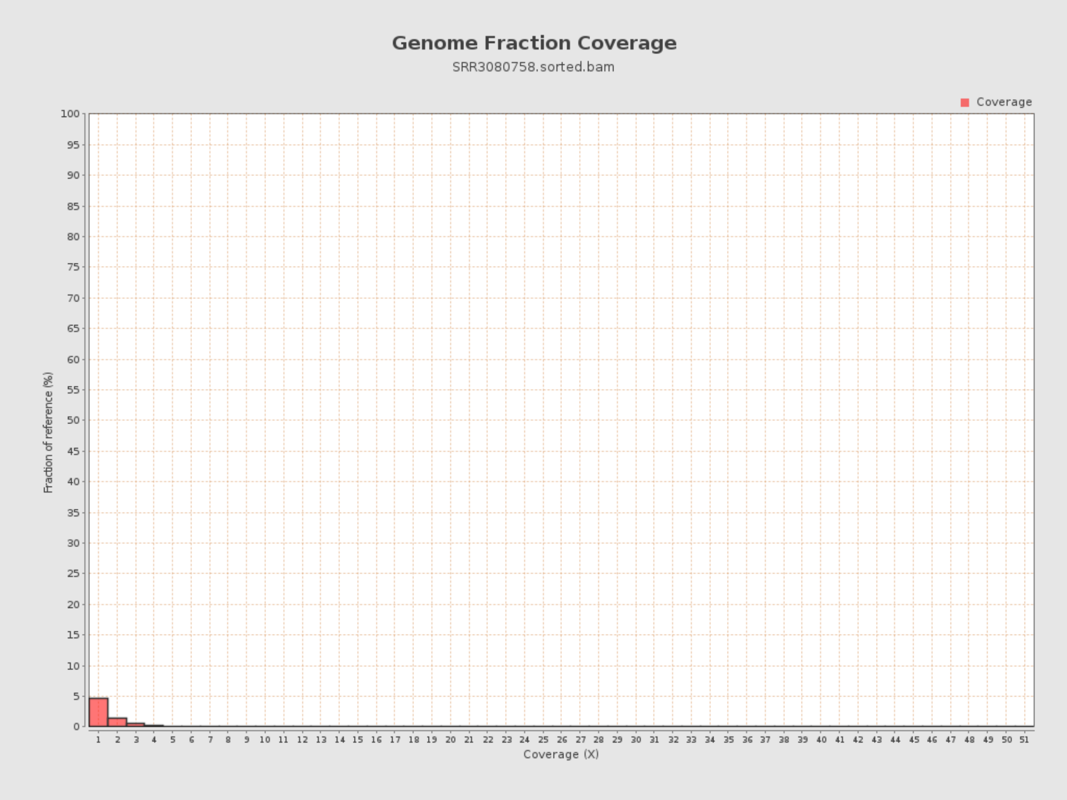
4. Results : Coverage Histogram



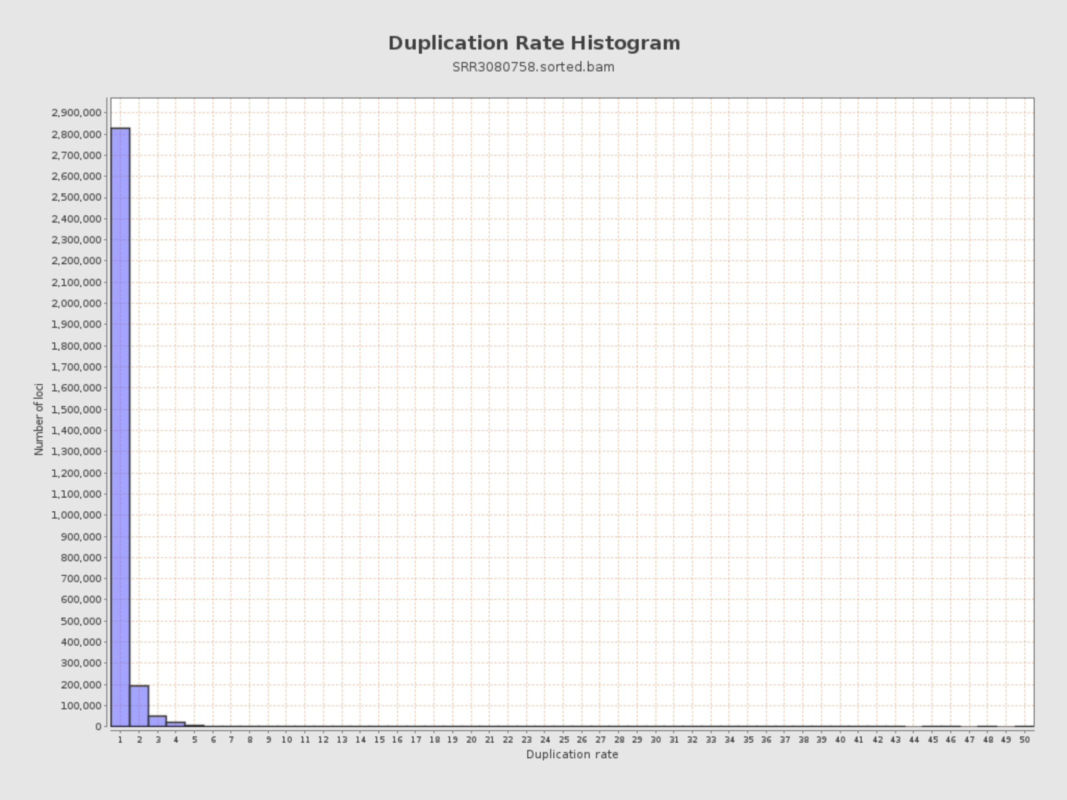
5. Results : Coverage Histogram (0-50X)



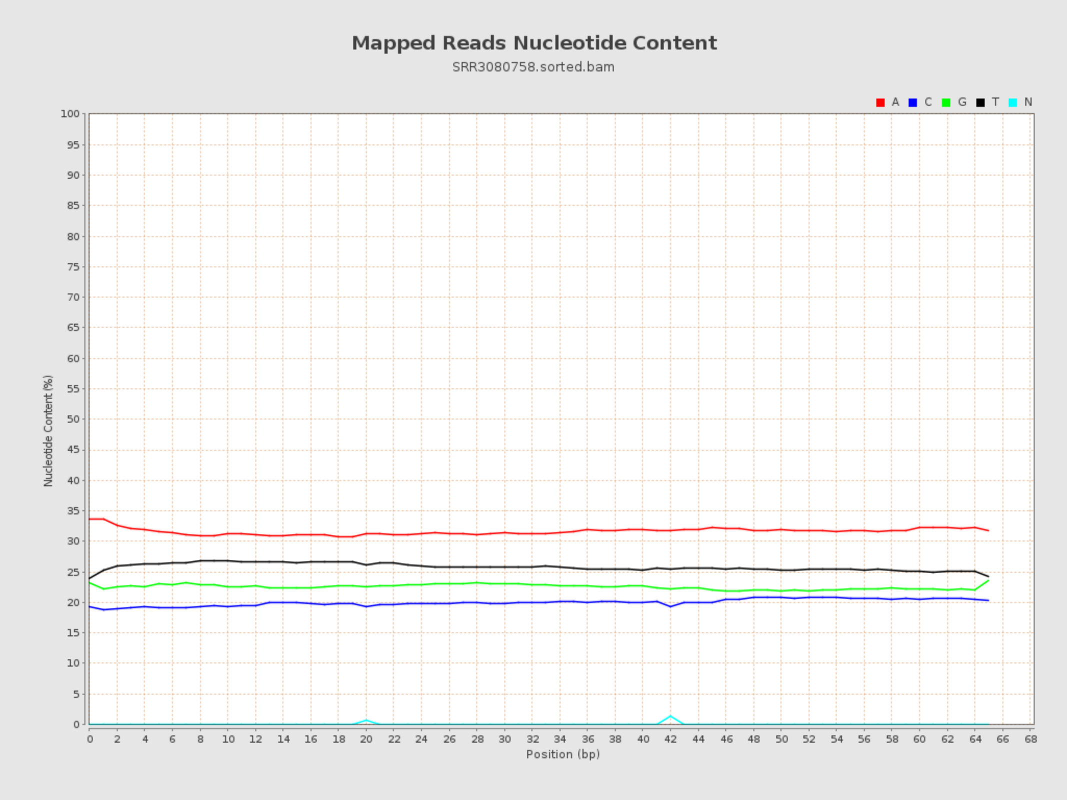
6. Results : Genome Fraction Coverage



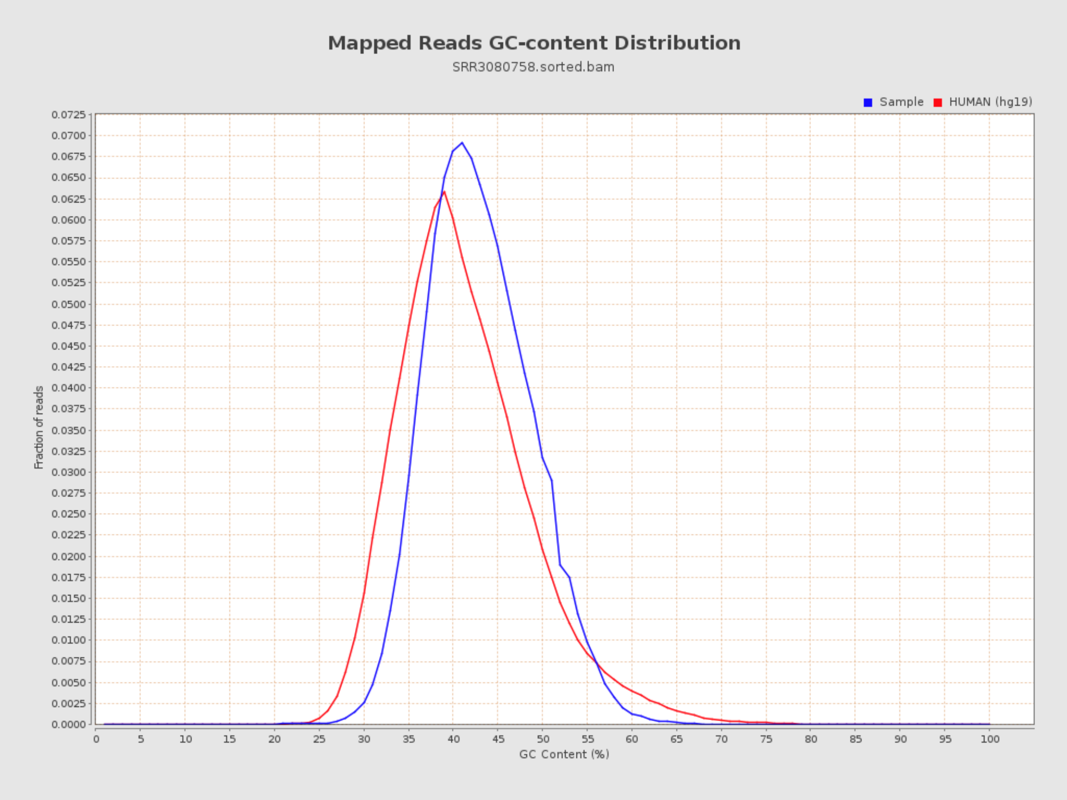
7. Results : Duplication Rate Histogram



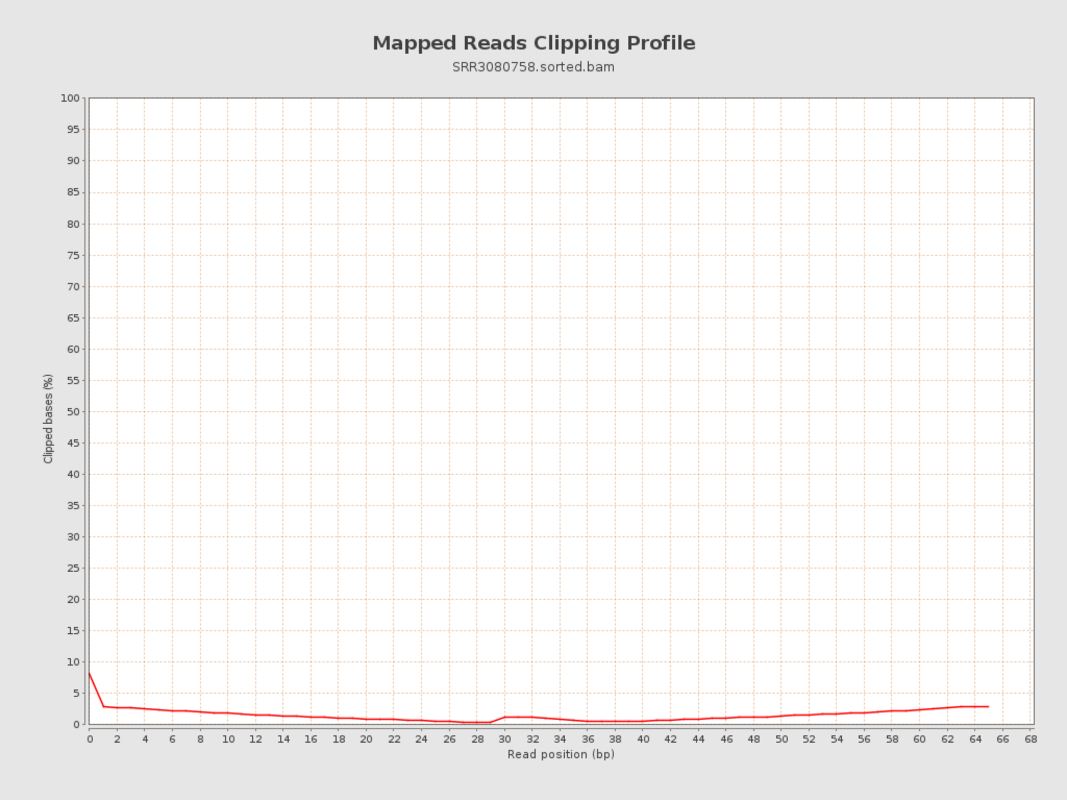
8. Results : Mapped Reads Nucleotide Content



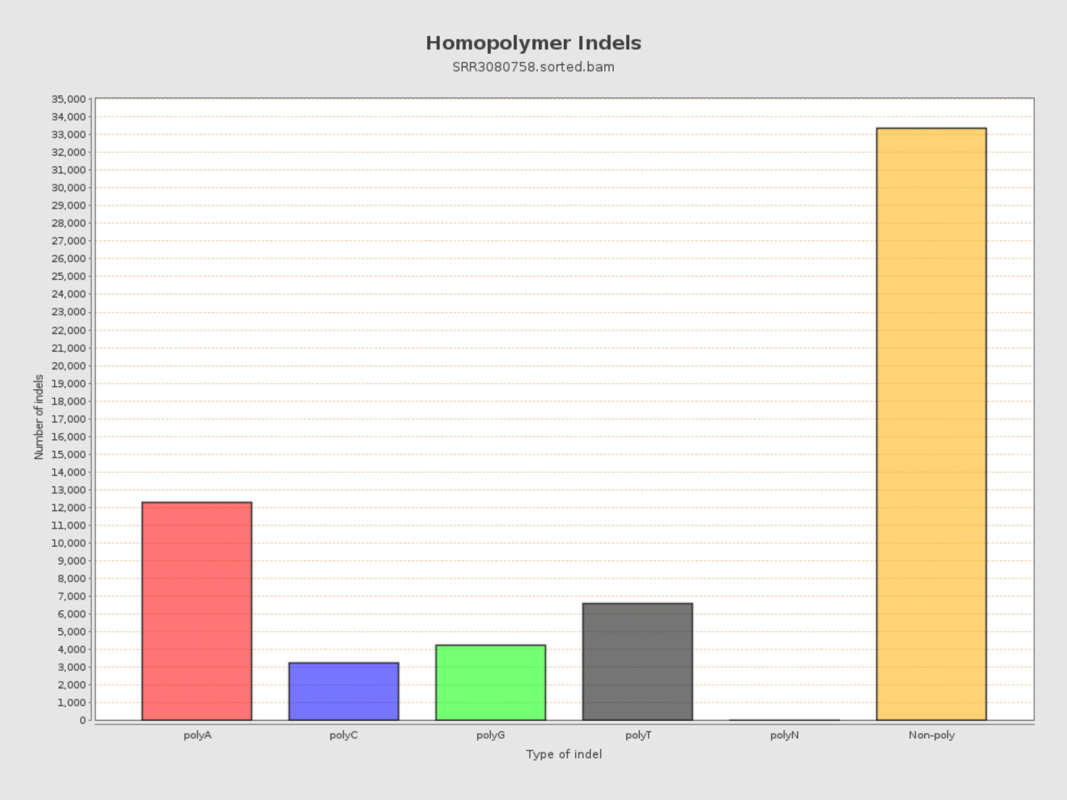
9. Results : Mapped Reads GC-content Distribution



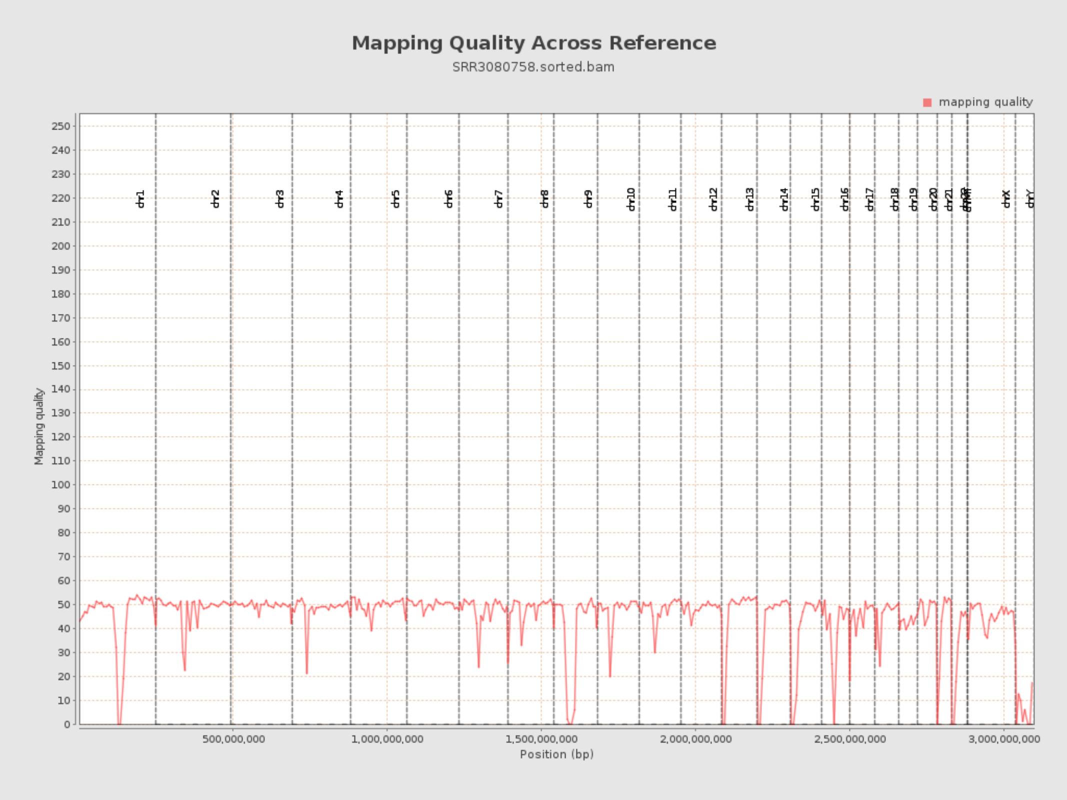
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram