Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:50:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549053.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_SRR1549053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:50:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,822,430
Mapped reads	3,304,657 / 86.45%
Unmapped reads	517,773 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	102,444 / 2.68%
Duplication rate	2.15%
Clipped reads	274,461 / 7.18%

2.2. ACGT Content

Number/percentage of A's	36,914,522 / 28.26%
Number/percentage of C's	27,831,557 / 21.3%
Number/percentage of T's	37,755,760 / 28.9%
Number/percentage of G's	28,142,108 / 21.54%
Number/percentage of N's	1,056 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0422
Standard Deviation	0.3663

2.4. Mapping Quality

Mean Mapping Quality	39.48

2.5. Mismatches and indels

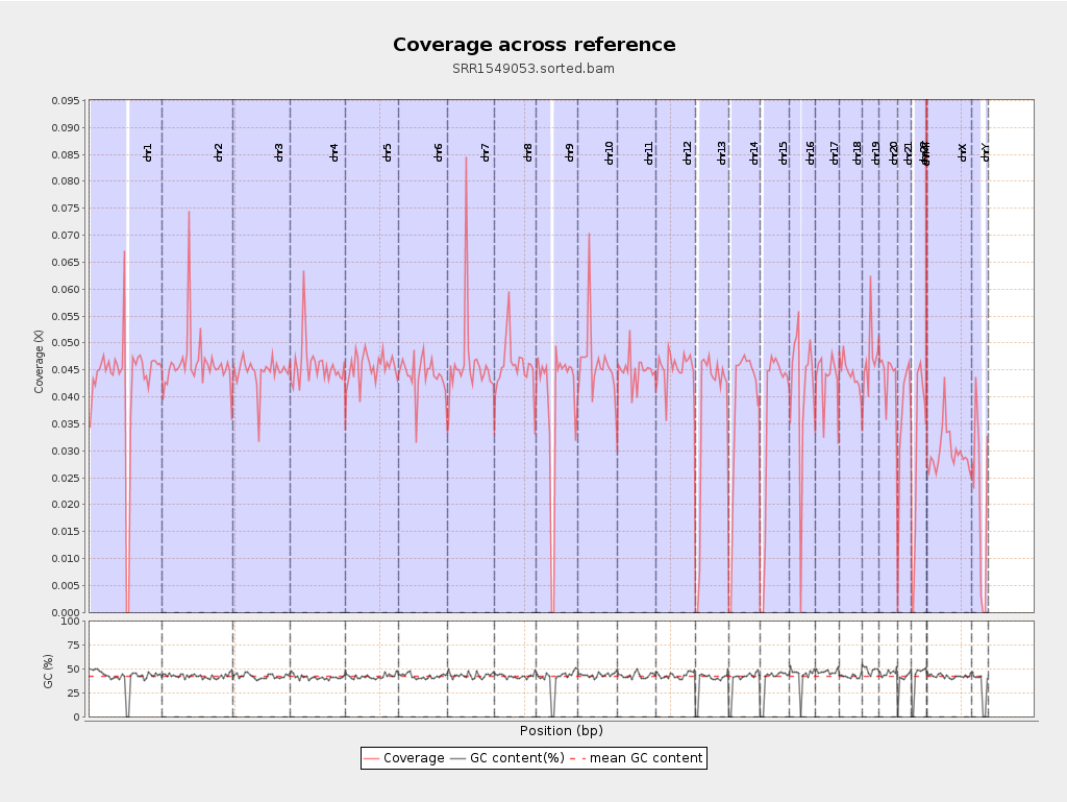
General error rate	0.28%
Mismatches	363,852
Insertions	4,314
Mapped reads with at least one insertion	0.13%
Deletions	9,736
Mapped reads with at least one deletion	0.29%
Homopolymer indels	41.17%

2.6. Chromosome stats

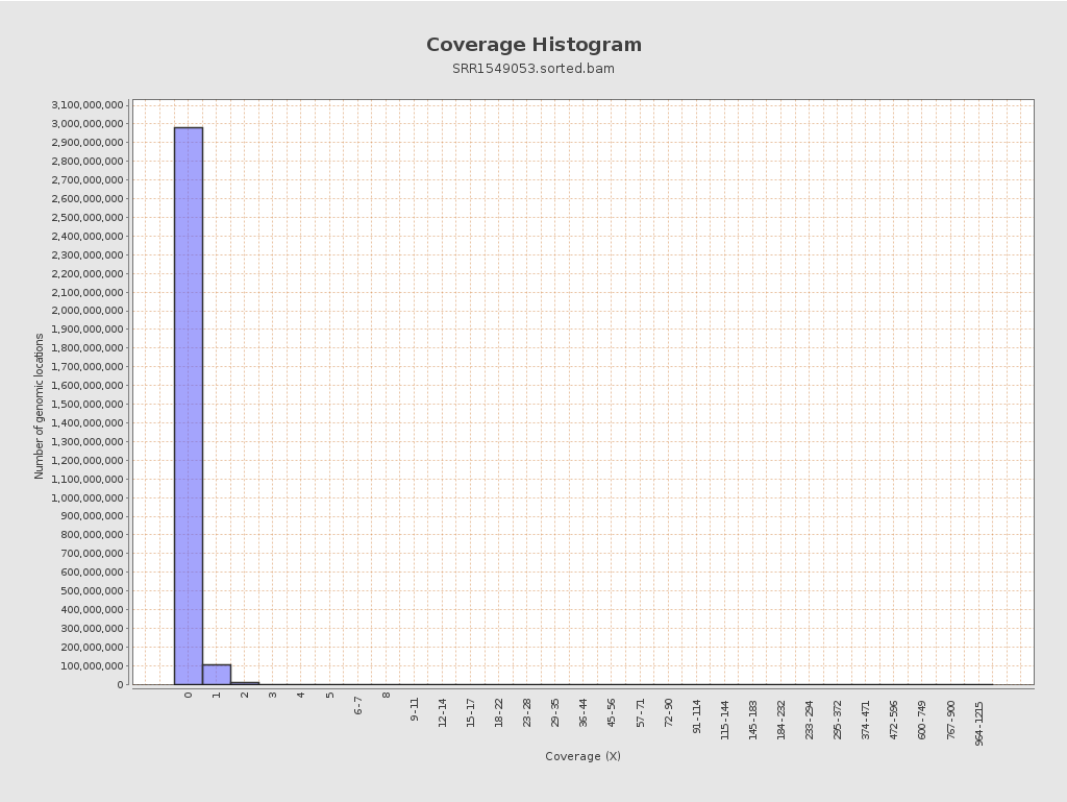
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10648096	0.0427	0.5954
chr2	243199373	11241051	0.0462	0.3547
chr3	198022430	8833322	0.0446	0.2307
chr4	191154276	8745209	0.0457	0.2511
chr5	180915260	8252936	0.0456	0.2351
chr6	171115067	7532812	0.044	0.2398
chr7	159138663	7399139	0.0465	0.5223
chr8	146364022	6686178	0.0457	0.653

chr9	141213431	5525867	0.0391	0.3619
chr10	135534747	6269993	0.0463	0.3227
chr11	135006516	6024997	0.0446	0.2888
chr12	133851895	6059448	0.0453	0.2408
chr13	115169878	4277531	0.0371	0.209
chr14	107349540	4057367	0.0378	0.2596
chr15	102531392	3730441	0.0364	0.2088
chr16	90354753	3776273	0.0418	0.2514
chr17	81195210	3511614	0.0432	0.239
chr18	78077248	3466286	0.0444	0.5967
chr19	59128983	2798514	0.0473	0.5909
chr20	63025520	2756817	0.0437	0.2388
chr21	48129895	1722950	0.0358	0.2527
chr22	51304566	1519681	0.0296	0.2441
chrMT	16571	7582	0.4575	0.8067
chrX	155270560	4635401	0.0299	0.2323
chrY	59373566	1178173	0.0198	0.2138

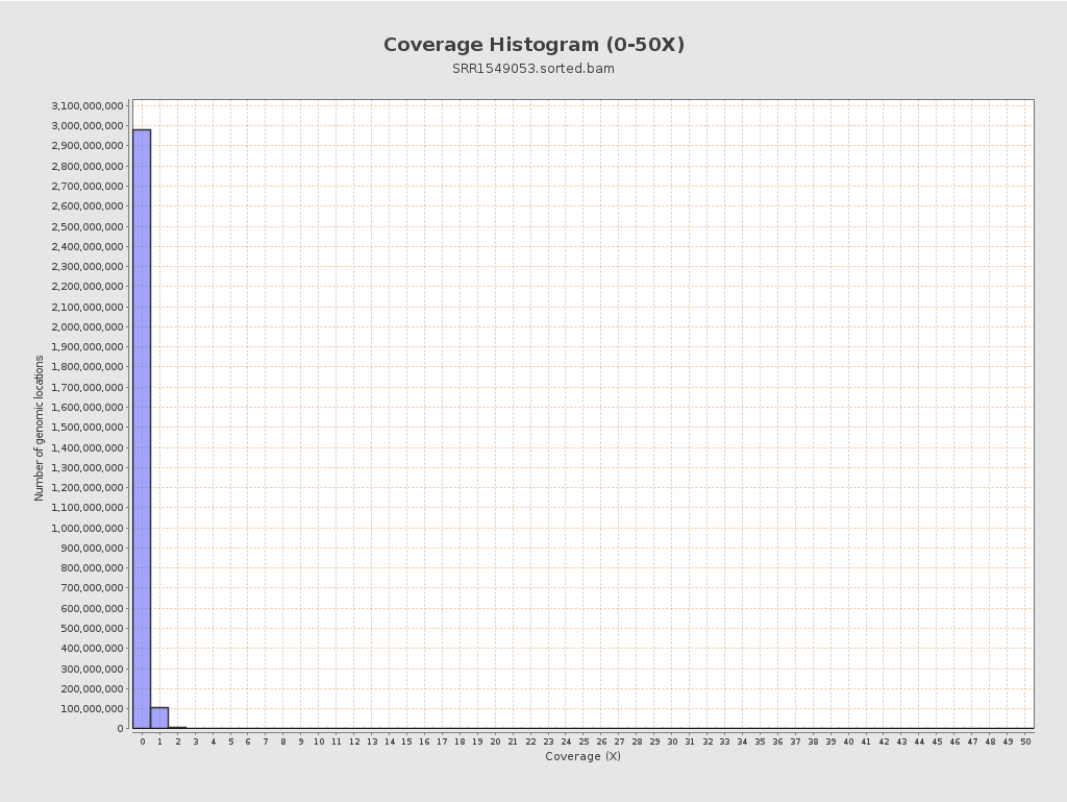
3. Results : Coverage across reference



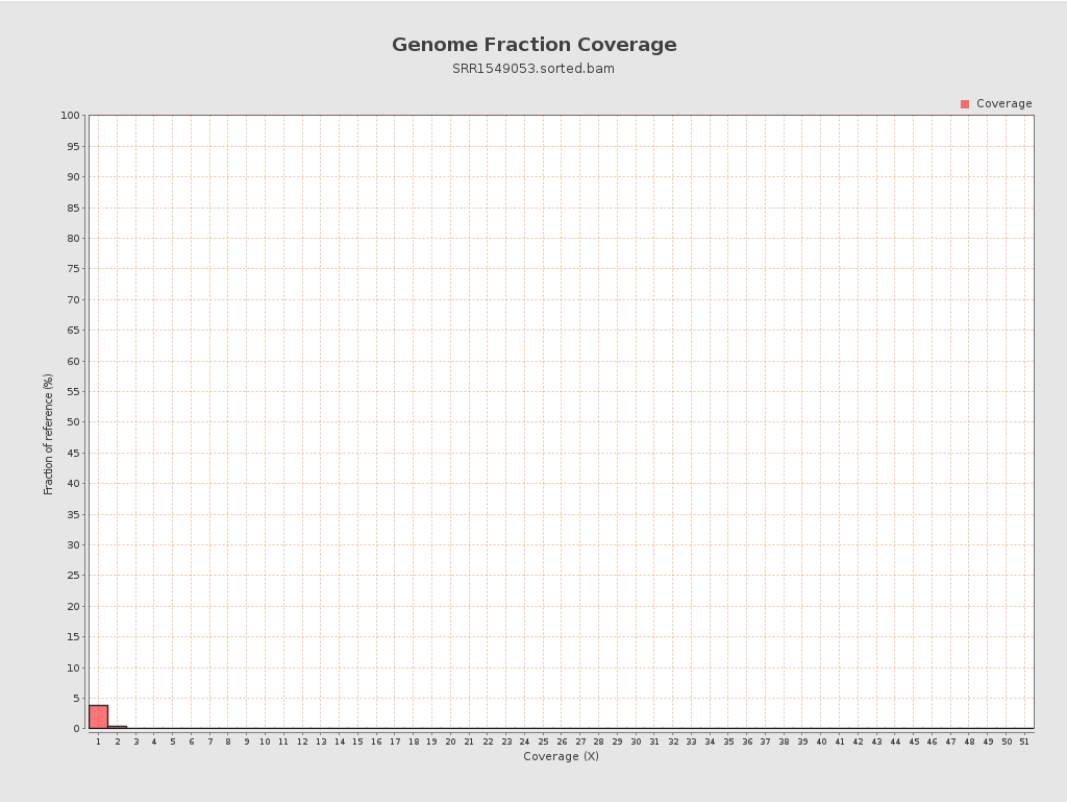
4. Results : Coverage Histogram



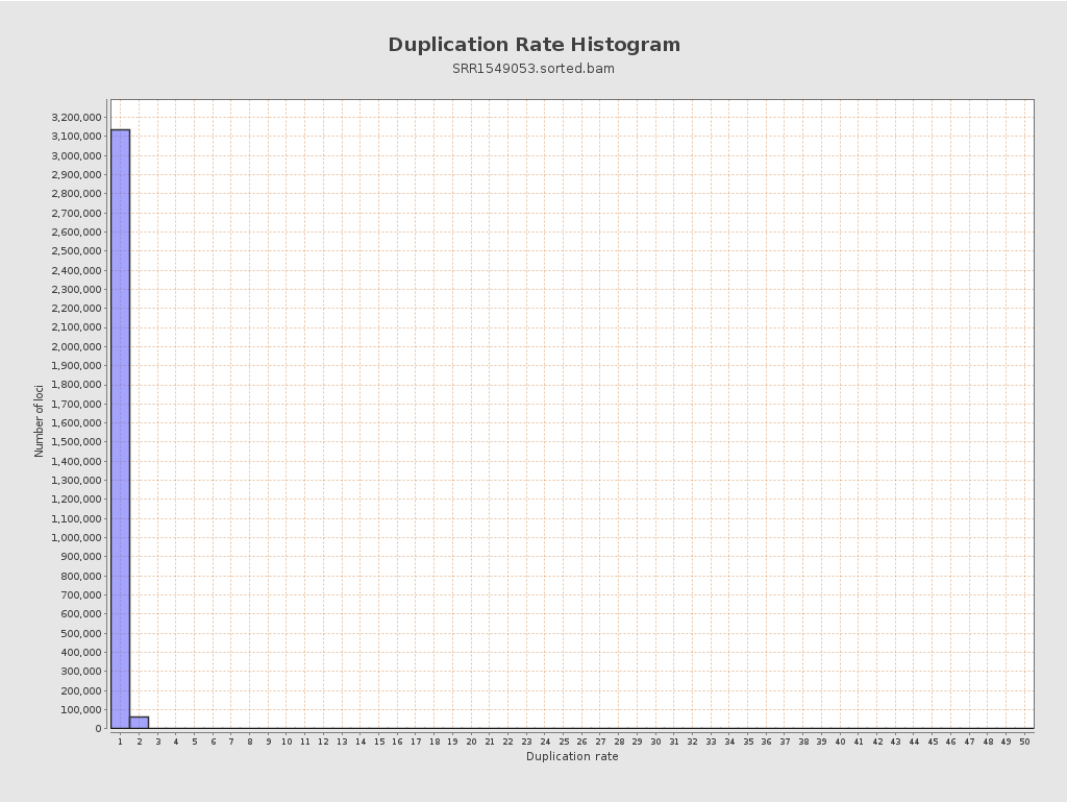
5. Results : Coverage Histogram (0-50X)



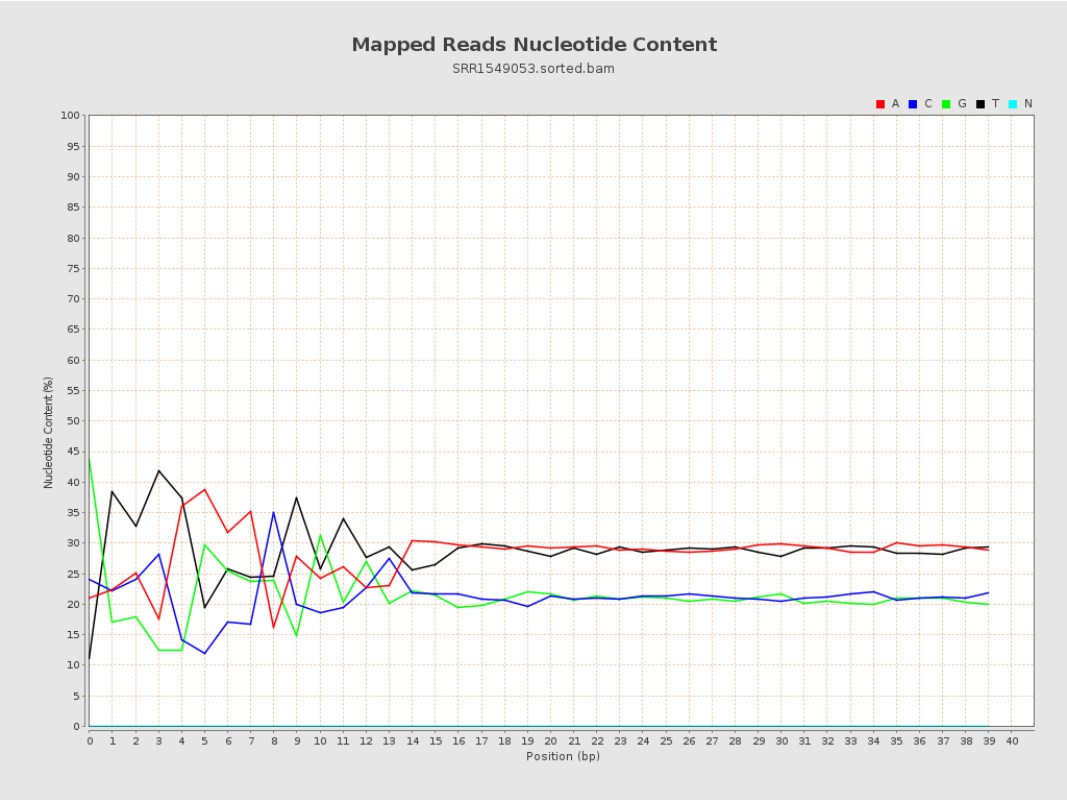
6. Results : Genome Fraction Coverage



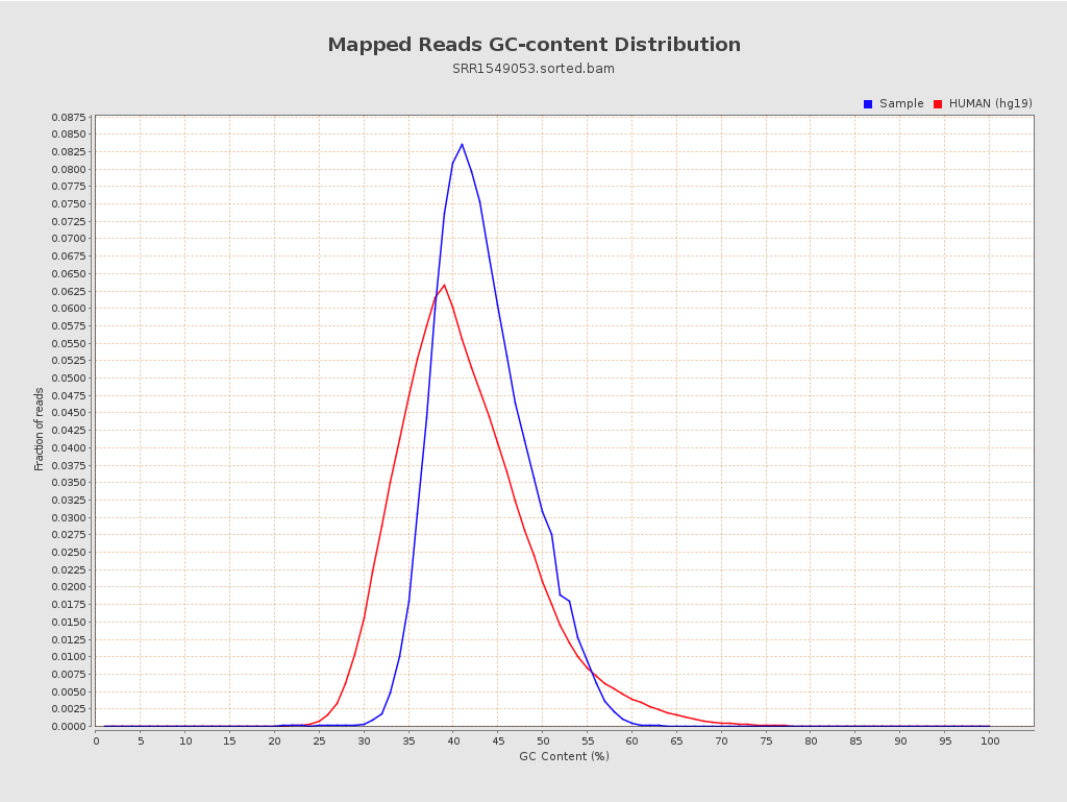
7. Results : Duplication Rate Histogram



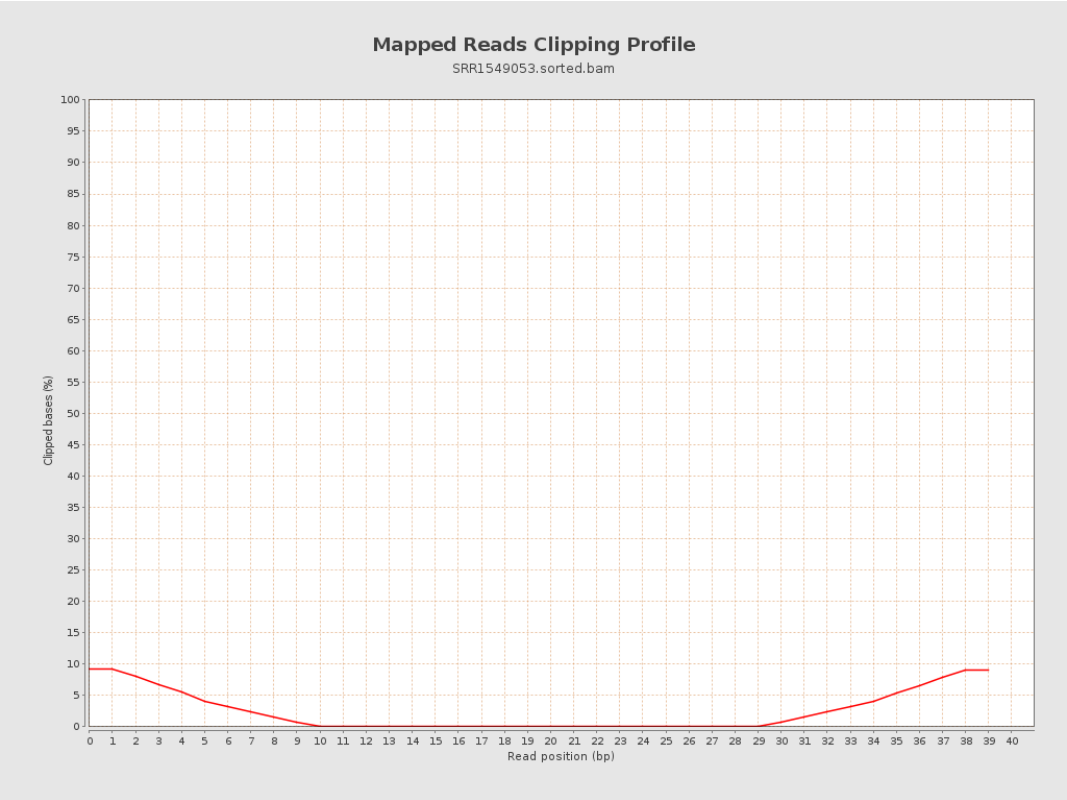
8. Results : Mapped Reads Nucleotide Content



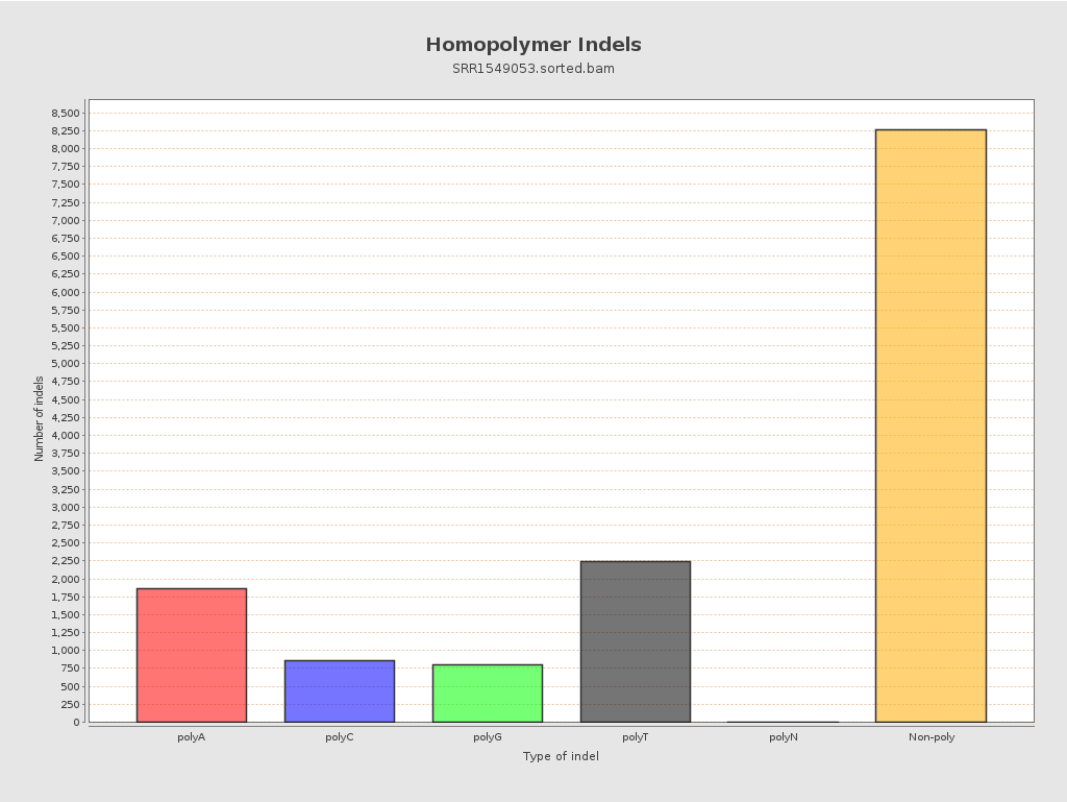
9. Results : Mapped Reads GC-content Distribution



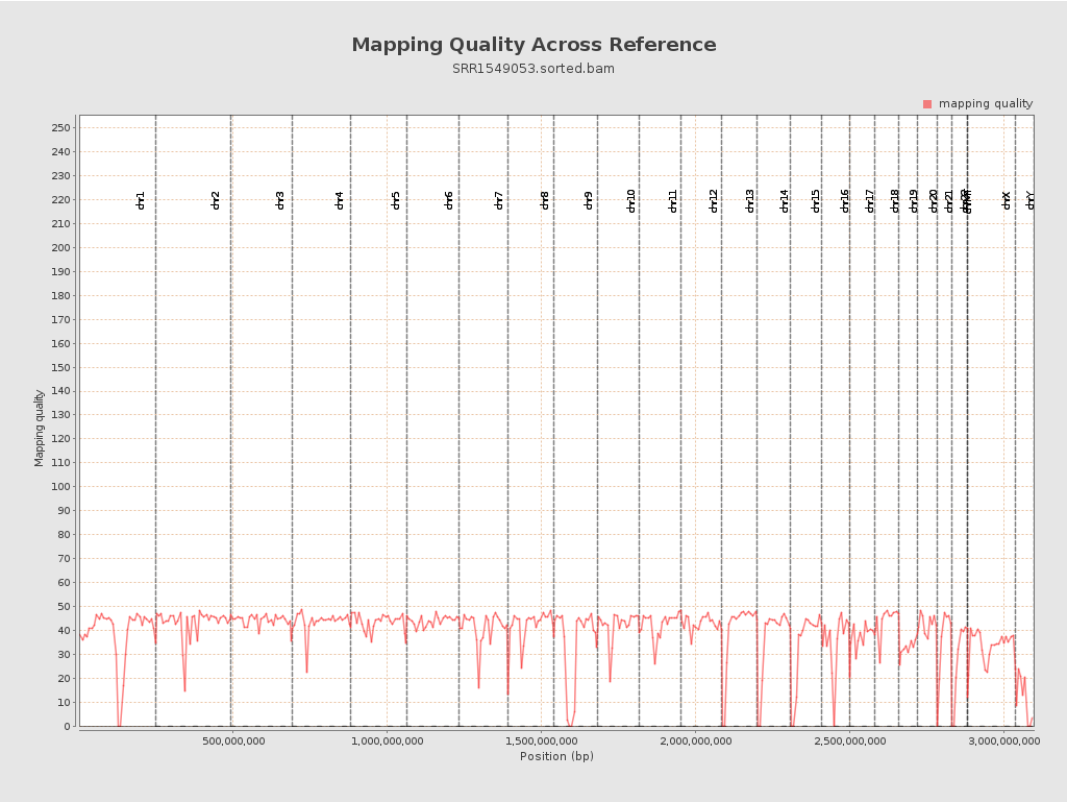
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram