Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:59:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549000.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_SRR1549000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549000.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:59:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,038,593
Mapped reads	7,812,070 / 86.43%
Unmapped reads	1,226,523 / 13.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	689,628 / 7.63%
Duplication rate	8.12%
Clipped reads	378,005 / 4.18%

2.2. ACGT Content

Number/percentage of A's	93,308,077 / 30.08%
Number/percentage of C's	61,431,156 / 19.8%
Number/percentage of T's	93,476,821 / 30.13%
Number/percentage of G's	61,990,381 / 19.98%
Number/percentage of N's	3,169 / 0%
GC Percentage	39.79%

2.3. Coverage

Mean	0.1002
Standard Deviation	0.8526

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

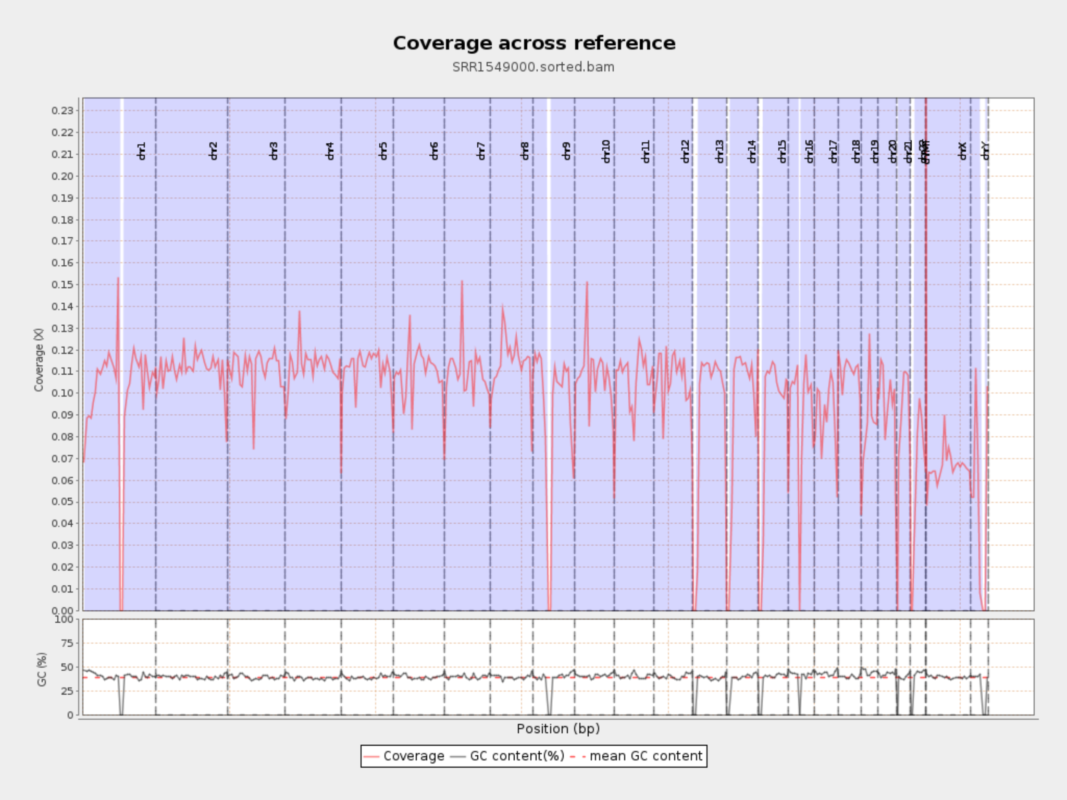
General error rate	0.29%
Mismatches	888,740
Insertions	9,377
Mapped reads with at least one insertion	0.12%
Deletions	26,783
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.11%

2.6. Chromosome stats

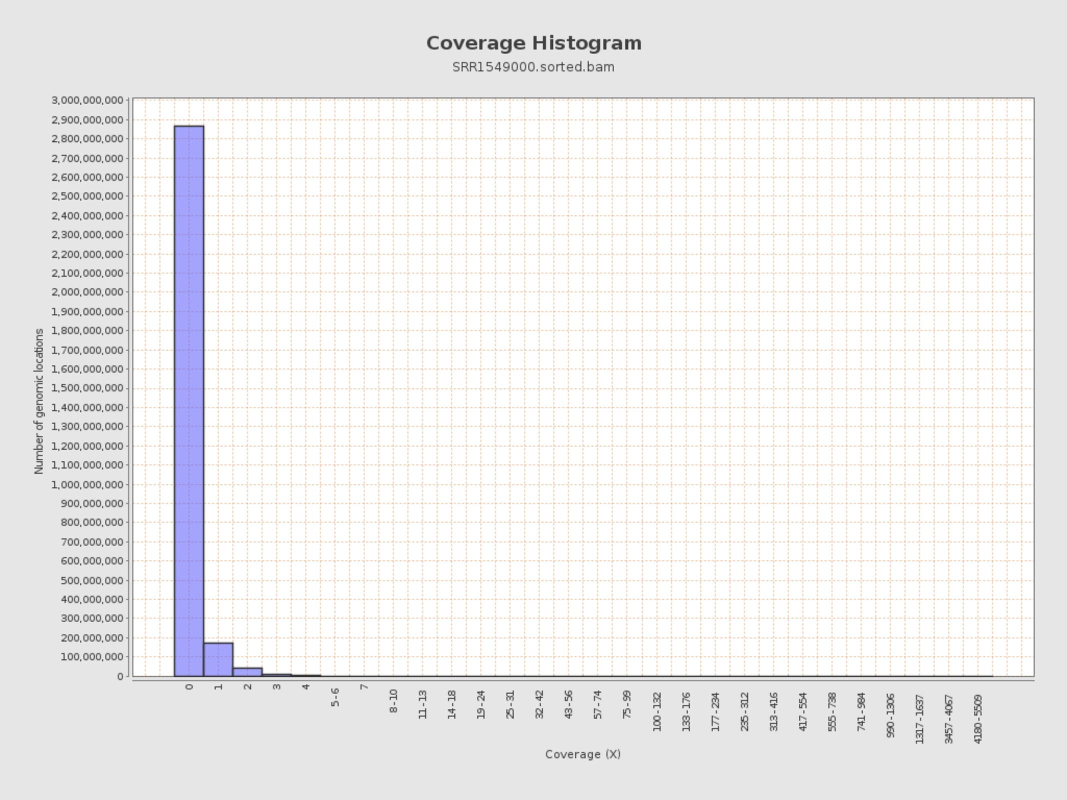
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25051408	0.1005	1.2548
chr2	243199373	27095576	0.1114	0.5519
chr3	198022430	22045327	0.1113	0.4251
chr4	191154276	21583027	0.1129	0.4701
chr5	180915260	20124566	0.1112	0.4319
chr6	171115067	18898184	0.1104	0.4895
chr7	159138663	17453237	0.1097	0.8095
chr8	146364022	16737616	0.1144	2.7247

chr9	141213431	12979132	0.0919	0.5081
chr10	135534747	14794138	0.1092	0.6172
chr11	135006516	14413220	0.1068	0.5327
chr12	133851895	14279640	0.1067	0.4339
chr13	115169878	10461854	0.0908	0.3809
chr14	107349540	9769971	0.091	0.4498
chr15	102531392	8788997	0.0857	0.3691
chr16	90354753	8021937	0.0888	0.4118
chr17	81195210	7416327	0.0913	0.4136
chr18	78077248	8630998	0.1105	1.0117
chr19	59128983	5164338	0.0873	0.9698
chr20	63025520	6140994	0.0974	0.421
chr21	48129895	4091153	0.085	0.4469
chr22	51304566	3062032	0.0597	0.3293
chrMT	16571	5562	0.3356	0.7691
chrX	155270560	10283647	0.0662	0.407
chrY	59373566	2951225	0.0497	0.5645

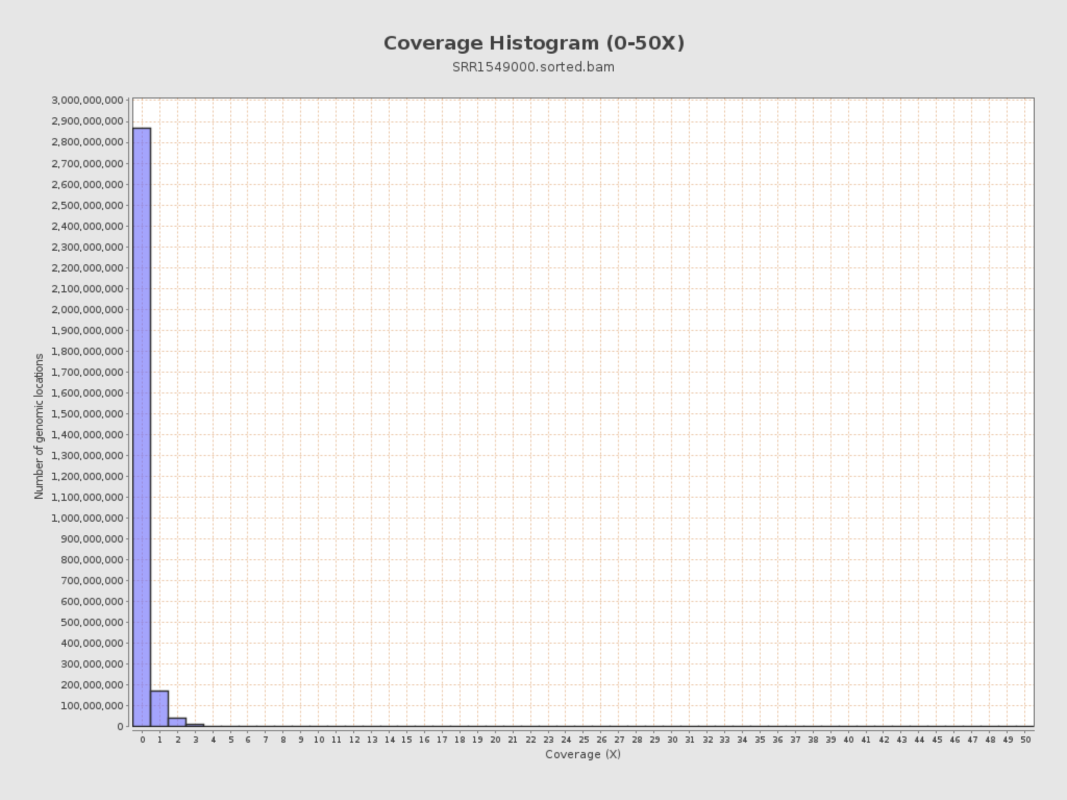
3. Results : Coverage across reference



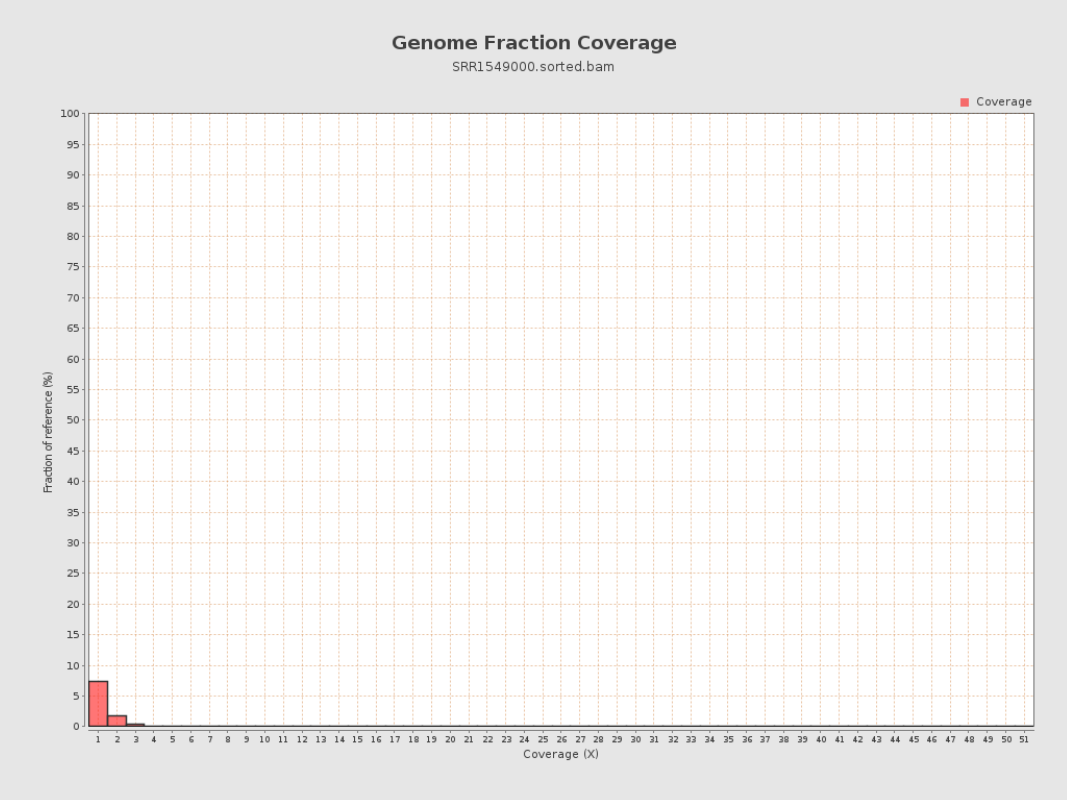
4. Results : Coverage Histogram



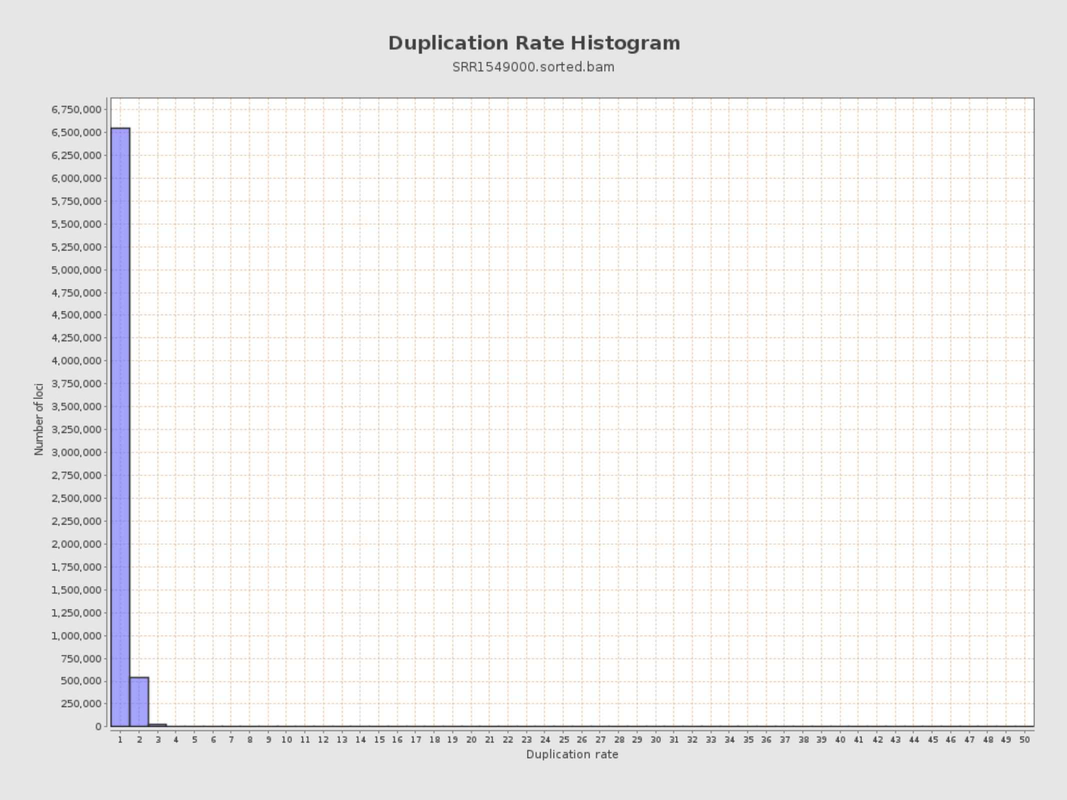
5. Results : Coverage Histogram (0-50X)



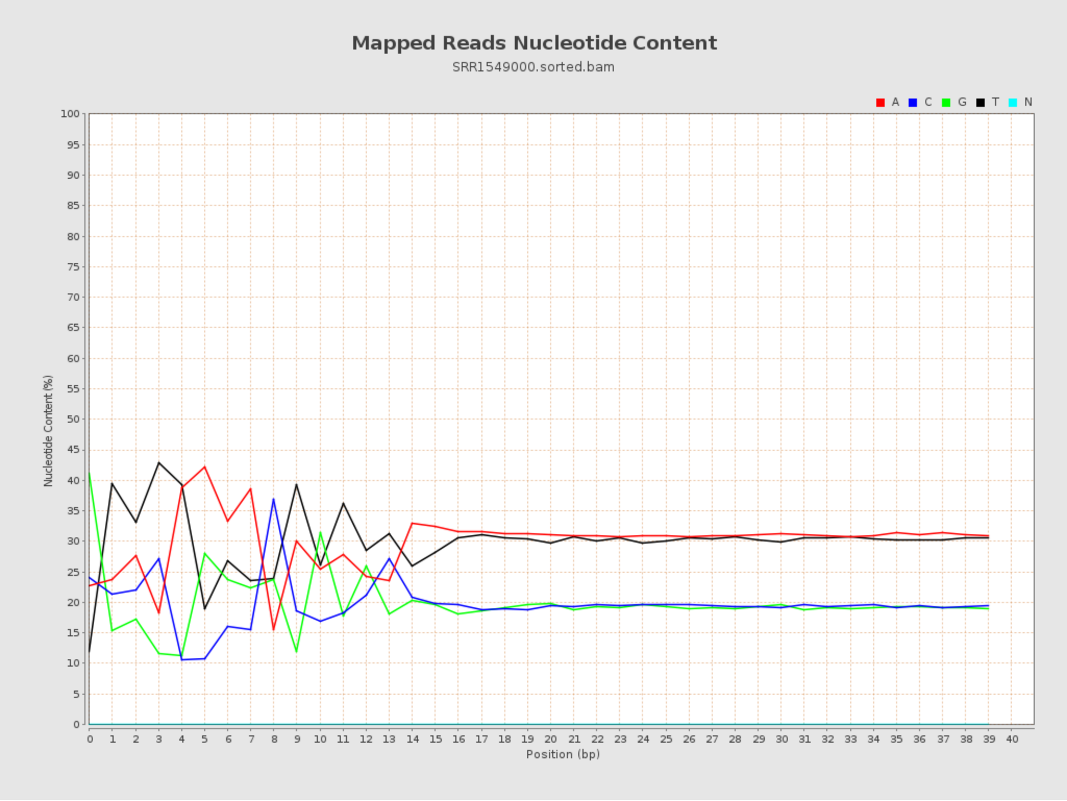
6. Results : Genome Fraction Coverage



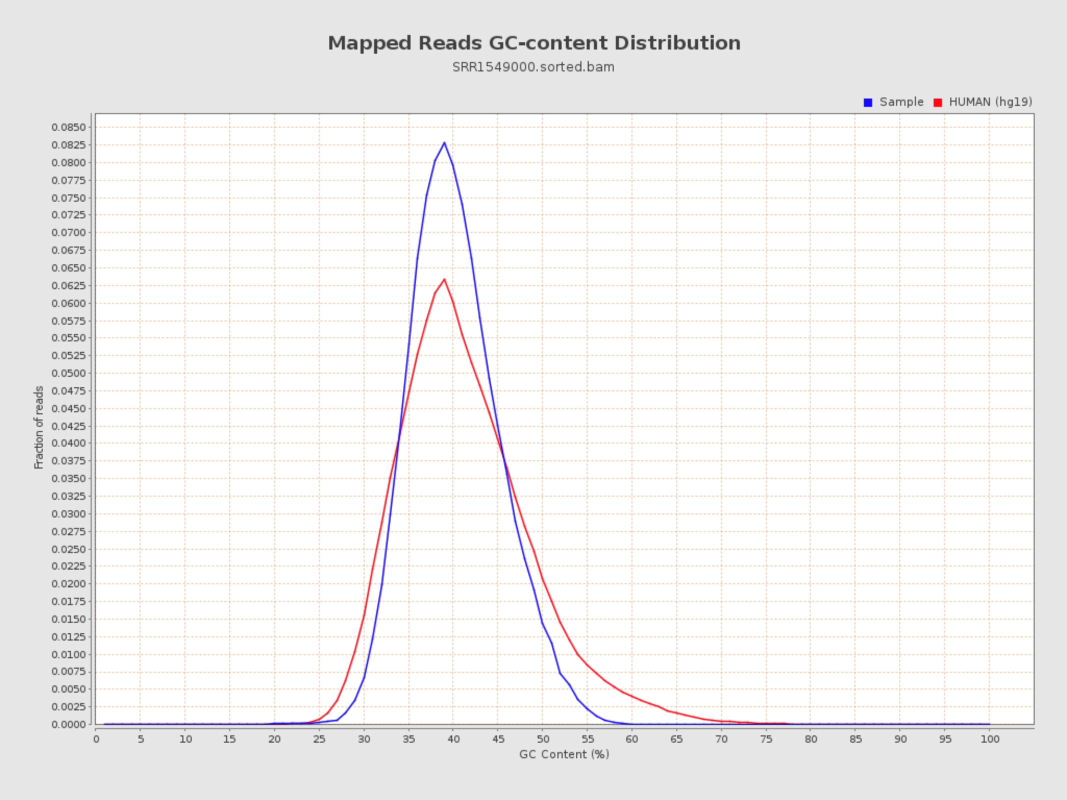
7. Results : Duplication Rate Histogram



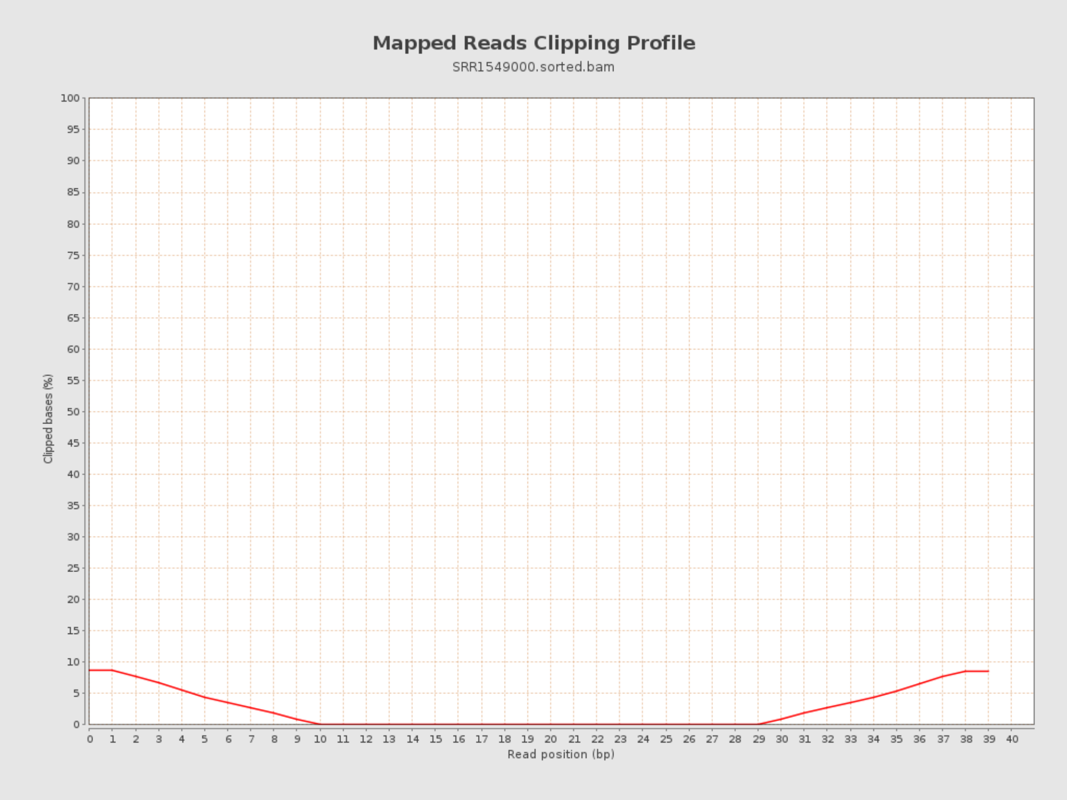
8. Results : Mapped Reads Nucleotide Content



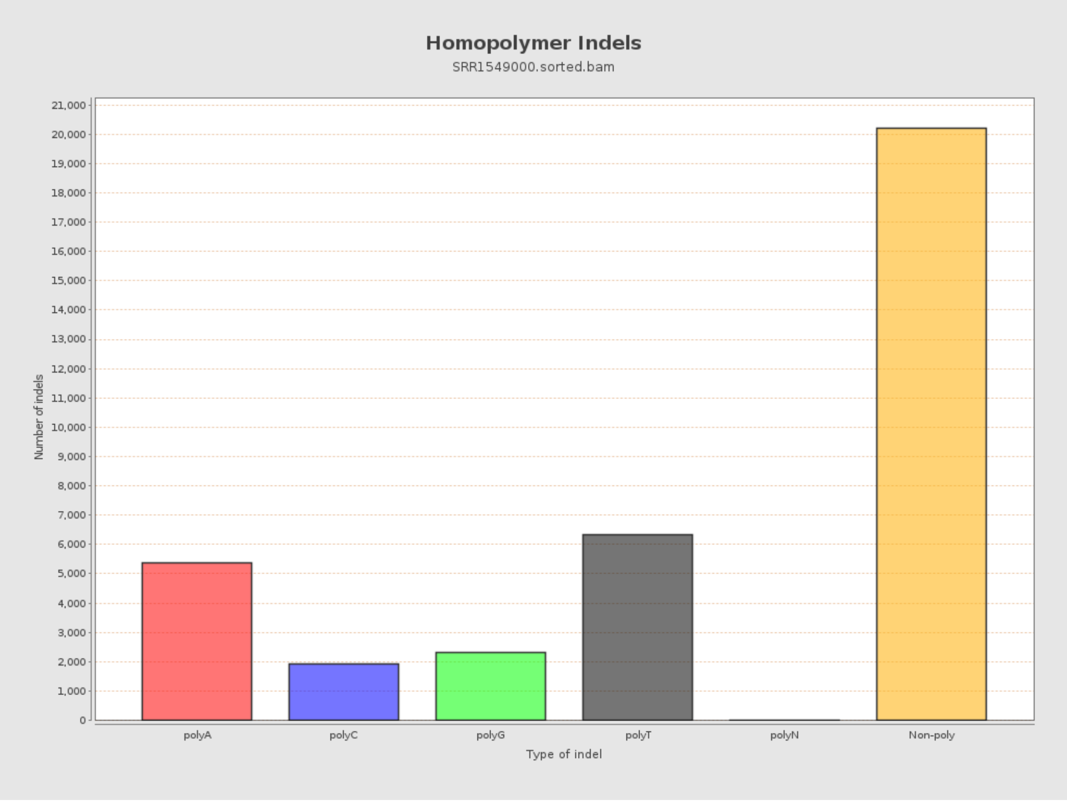
9. Results : Mapped Reads GC-content Distribution



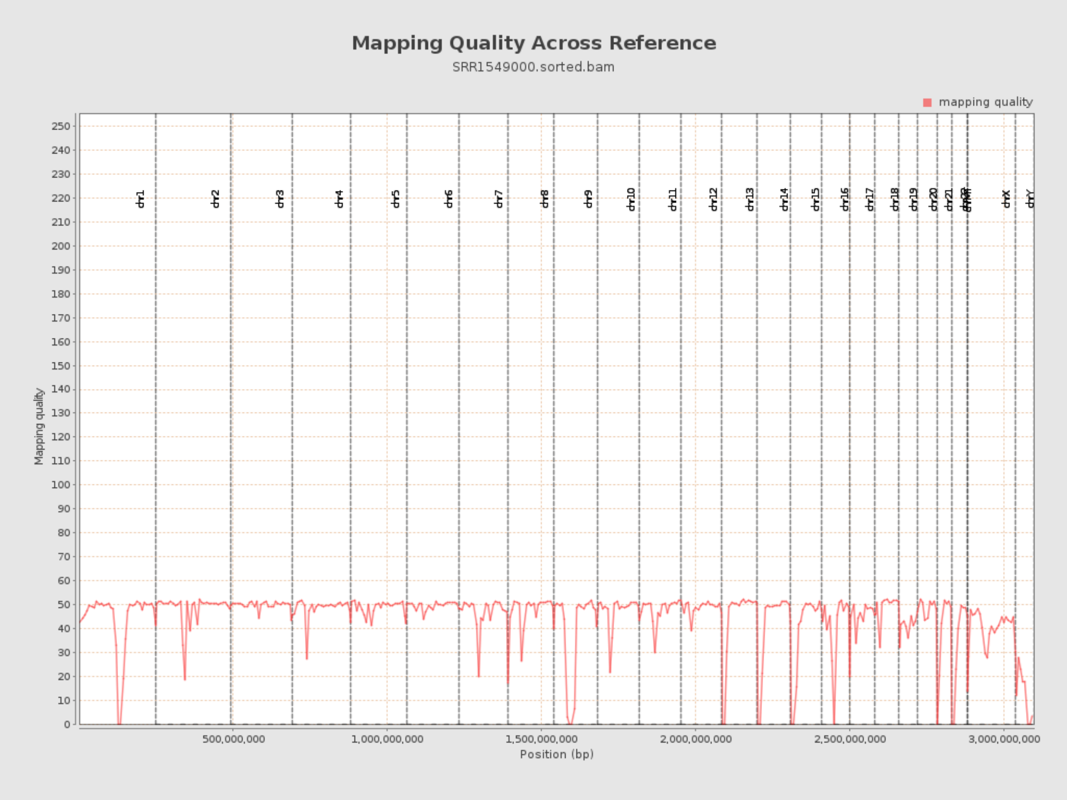
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram