Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:13:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548939.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_SRR1548939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548939.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:12:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,371,643
Mapped reads	2,947,682 / 87.43%
Unmapped reads	423,961 / 12.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	78,238 / 2.32%
Duplication rate	1.55%
Clipped reads	266,937 / 7.92%

2.2. ACGT Content

Number/percentage of A's	33,895,153 / 29.11%
Number/percentage of C's	24,269,464 / 20.85%
Number/percentage of T's	34,053,925 / 29.25%
Number/percentage of G's	24,203,617 / 20.79%
Number/percentage of N's	939 / 0%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0376
Standard Deviation	0.4829

2.4. Mapping Quality

Mean Mapping Quality	37.51

2.5. Mismatches and indels

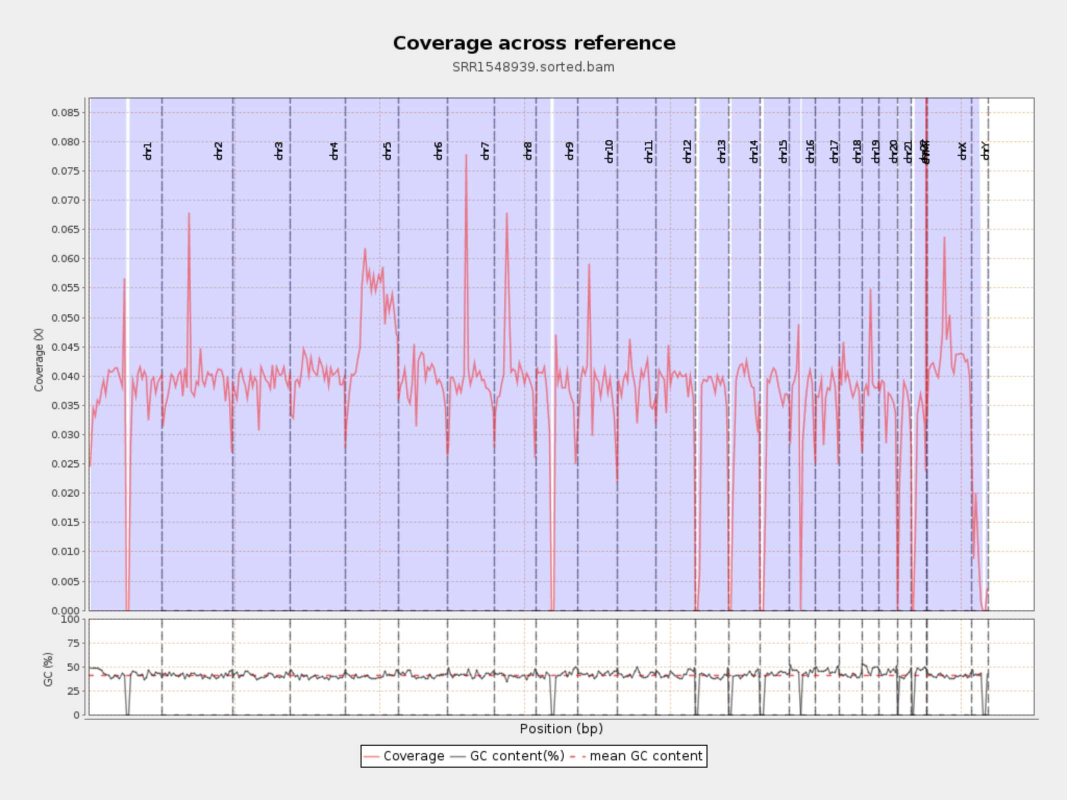
General error rate	0.34%
Mismatches	386,805
Insertions	4,344
Mapped reads with at least one insertion	0.15%
Deletions	9,794
Mapped reads with at least one deletion	0.33%
Homopolymer indels	38.79%

2.6. Chromosome stats

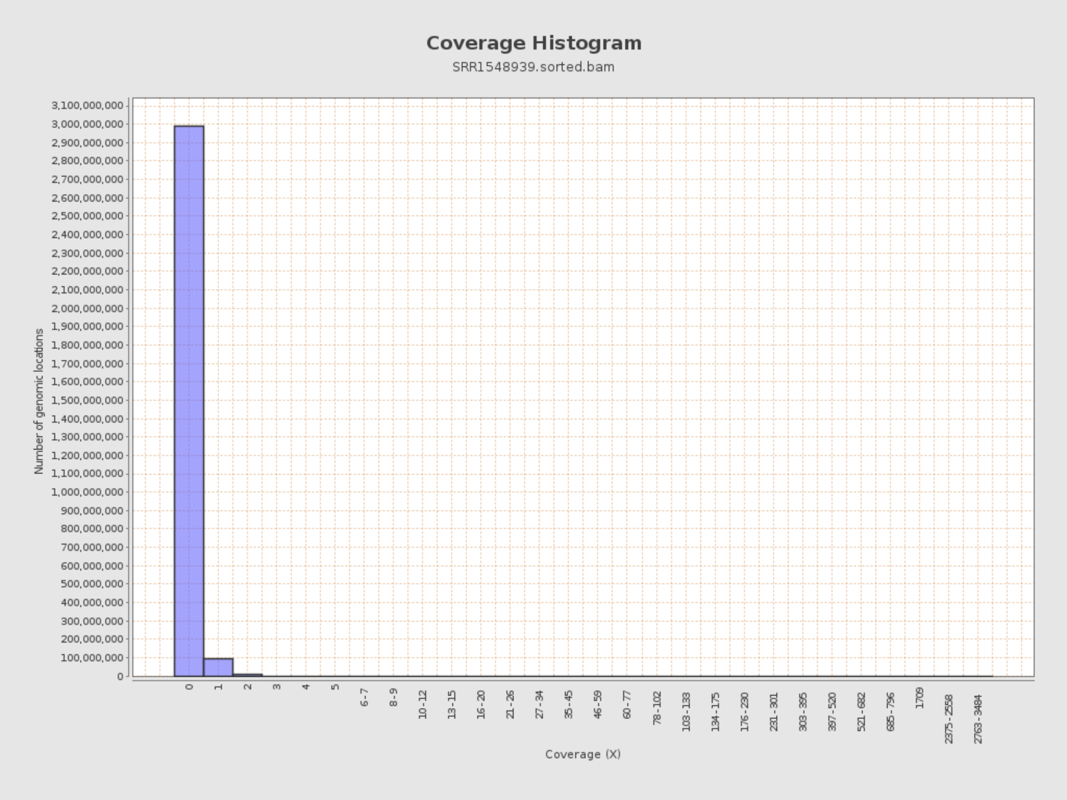
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8977198	0.036	0.5165
chr2	243199373	9606771	0.0395	0.3321
chr3	198022430	7741220	0.0391	0.2138
chr4	191154276	7662285	0.0401	0.2242
chr5	180915260	9058404	0.0501	0.2452
chr6	171115067	6706572	0.0392	0.2289
chr7	159138663	6451362	0.0405	0.4665
chr8	146364022	5969273	0.0408	1.6979

chr9	141213431	4792152	0.0339	0.3359
chr10	135534747	5265984	0.0389	0.2888
chr11	135006516	5196493	0.0385	0.3205
chr12	133851895	5227775	0.0391	0.2232
chr13	115169878	3687799	0.032	0.1908
chr14	107349540	3490233	0.0325	0.23
chr15	102531392	3199623	0.0312	0.1908
chr16	90354753	3088389	0.0342	0.2228
chr17	81195210	2909570	0.0358	0.2147
chr18	78077248	3026925	0.0388	0.6017
chr19	59128983	2341501	0.0396	0.5334
chr20	63025520	2207913	0.035	0.2087
chr21	48129895	1422568	0.0296	0.212
chr22	51304566	1211003	0.0236	0.1839
chrMT	16571	3997	0.2412	0.5345
chrX	155270560	6761895	0.0435	0.2688
chrY	59373566	428891	0.0072	0.1147

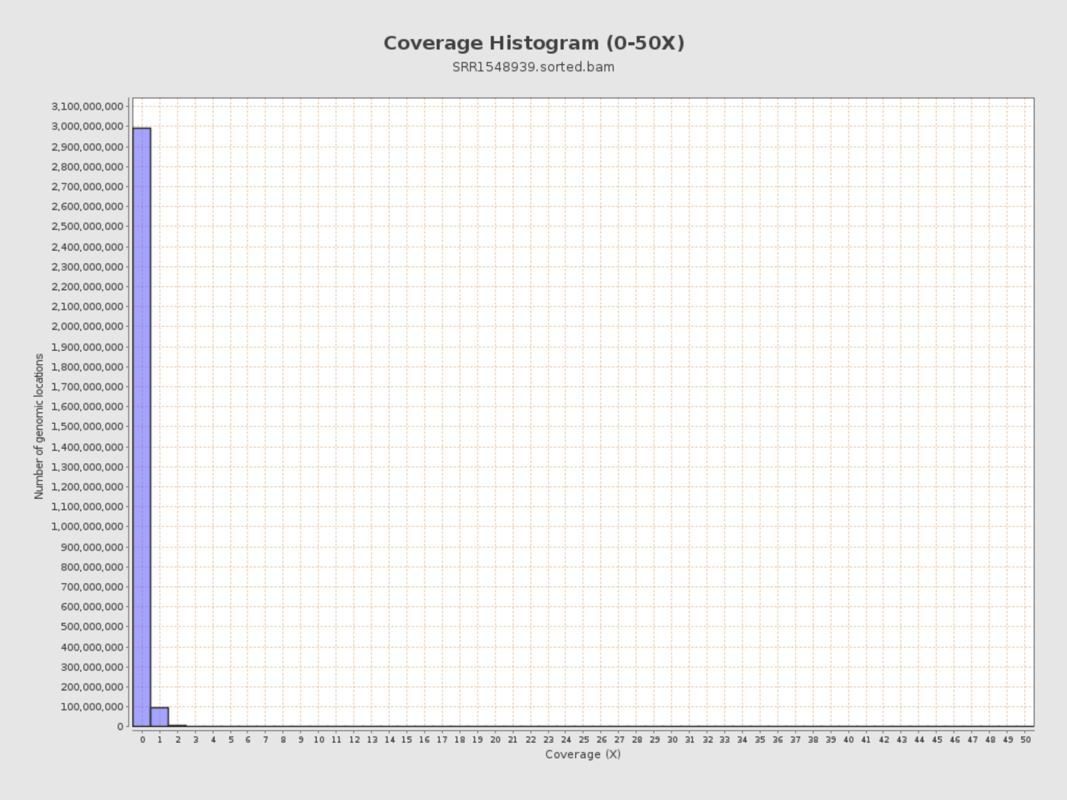
3. Results : Coverage across reference



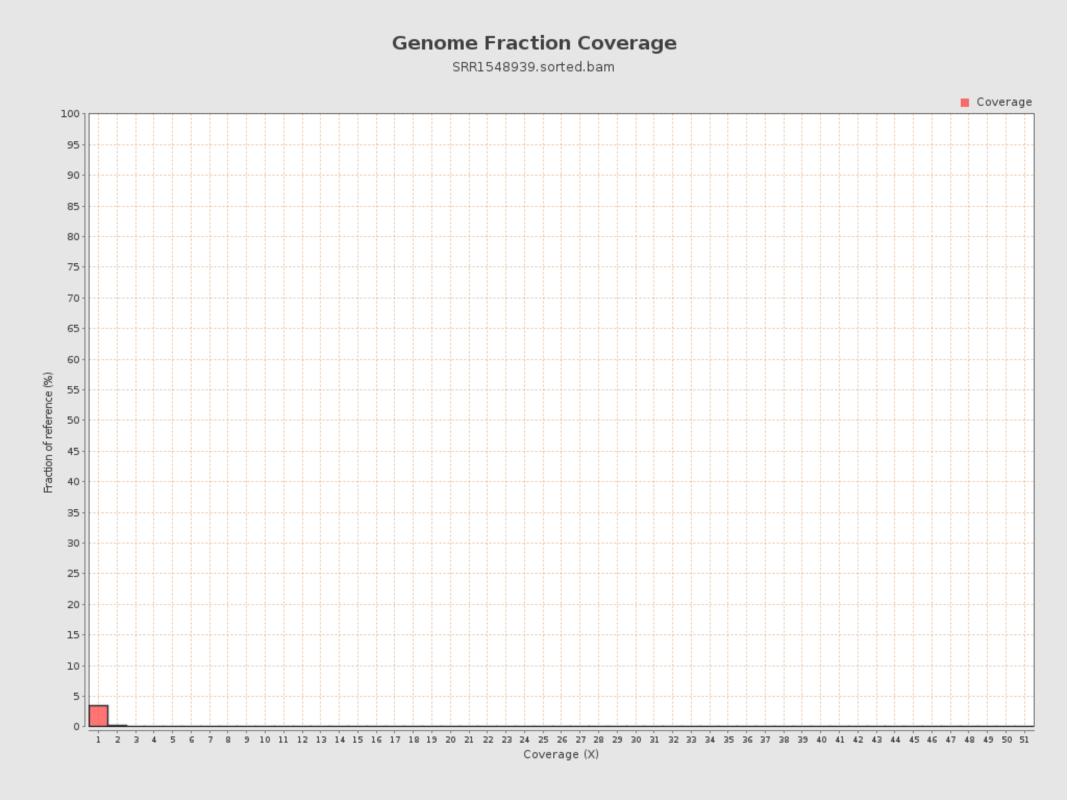
4. Results : Coverage Histogram



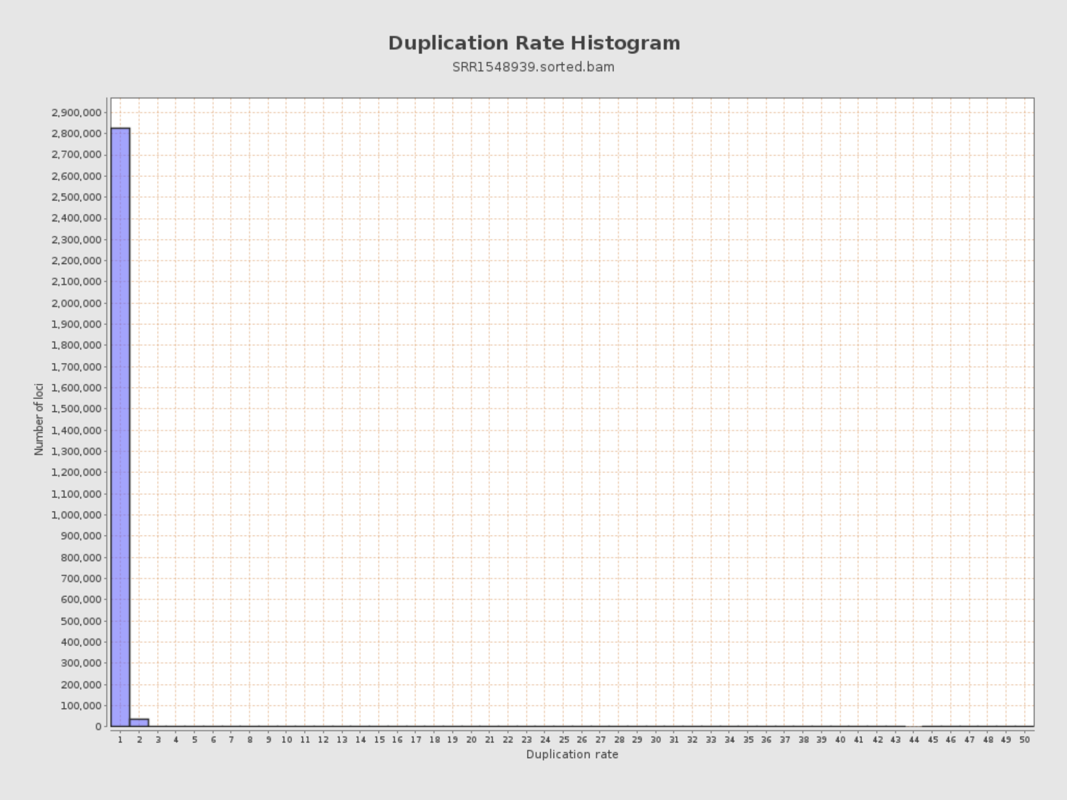
5. Results : Coverage Histogram (0-50X)



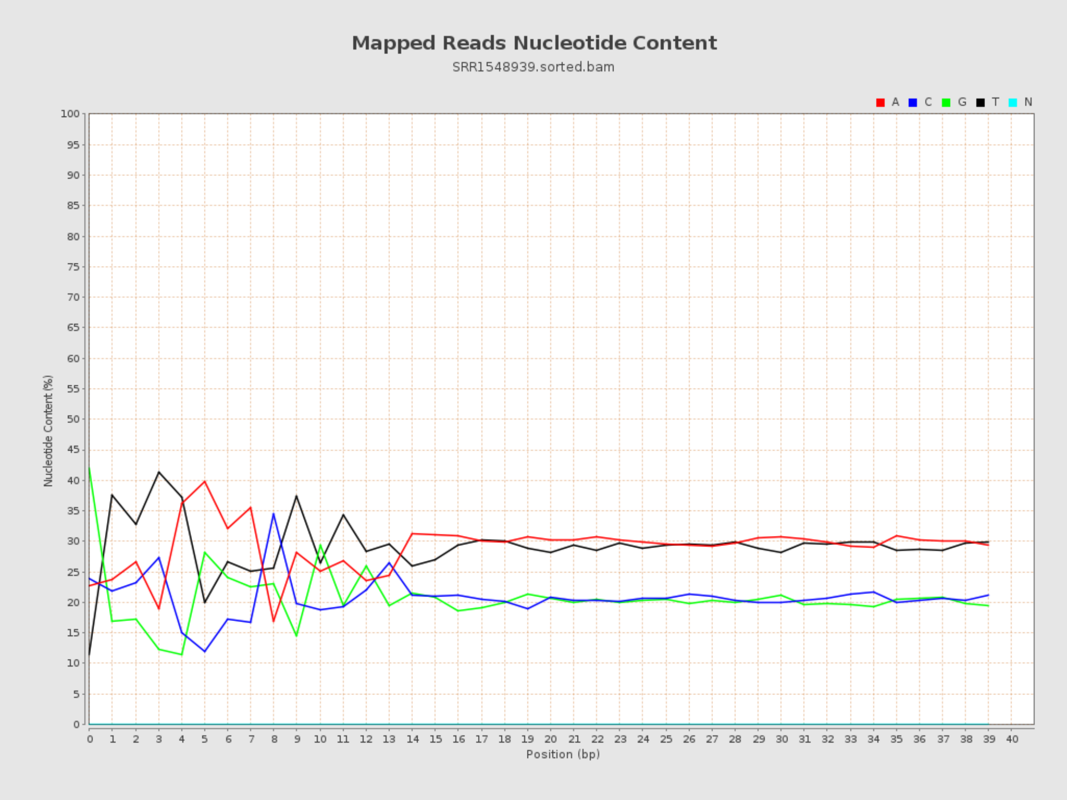
6. Results : Genome Fraction Coverage



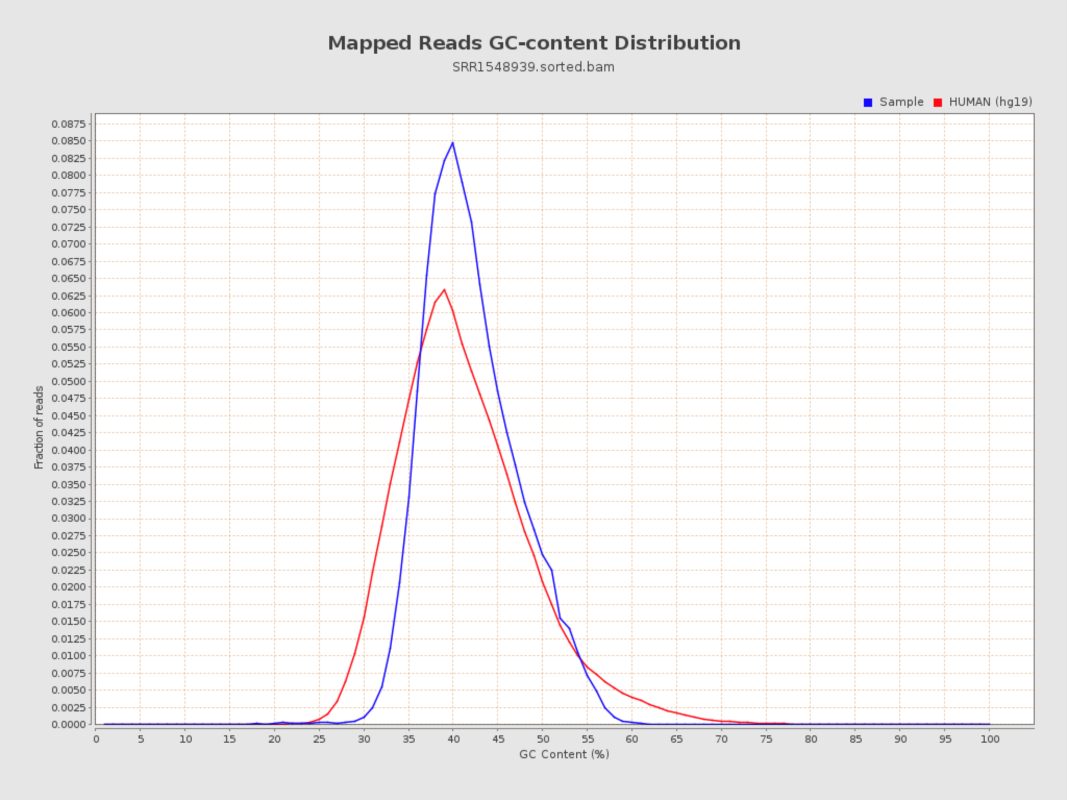
7. Results : Duplication Rate Histogram



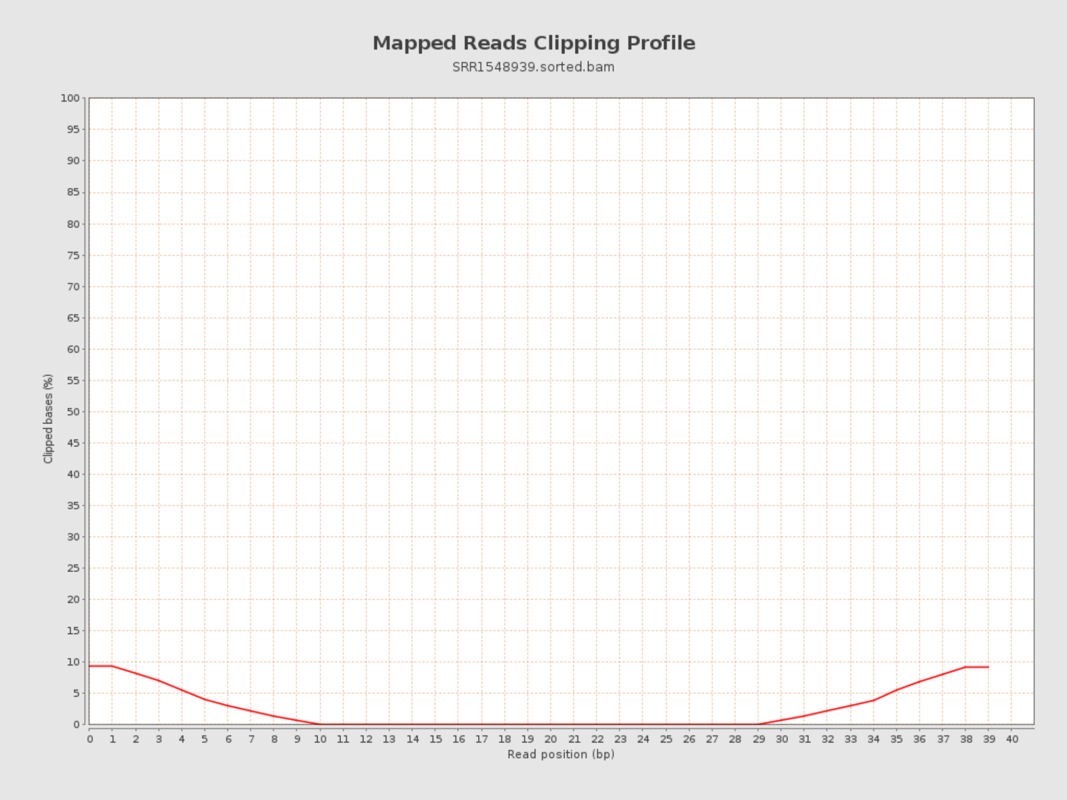
8. Results : Mapped Reads Nucleotide Content



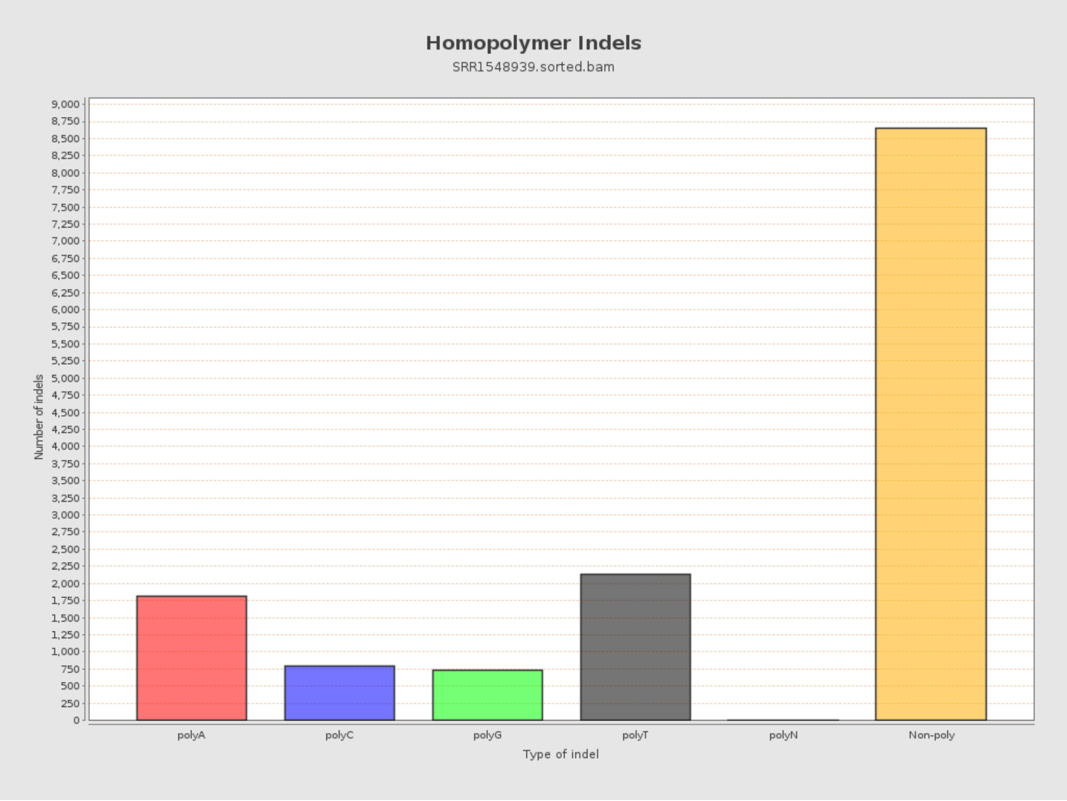
9. Results : Mapped Reads GC-content Distribution



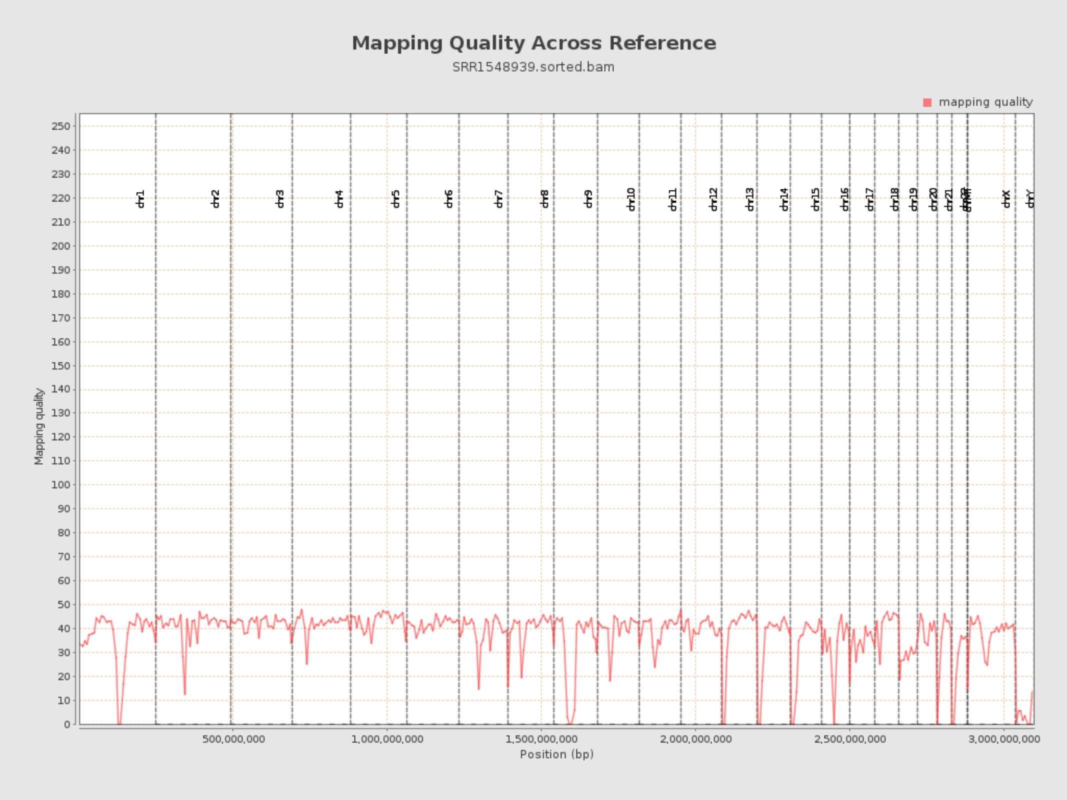
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram