Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:02:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549056.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_SRR1549056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:02:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,176,977
Mapped reads	2,785,281 / 87.67%
Unmapped reads	391,696 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	84,088 / 2.65%
Duplication rate	2.02%
Clipped reads	241,130 / 7.59%

2.2. ACGT Content

Number/percentage of A's	30,544,654 / 27.75%
Number/percentage of C's	24,103,430 / 21.9%
Number/percentage of T's	31,212,584 / 28.36%
Number/percentage of G's	24,197,278 / 21.99%
Number/percentage of N's	914 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0356
Standard Deviation	0.3452

2.4. Mapping Quality

Mean Mapping Quality	36.77

2.5. Mismatches and indels

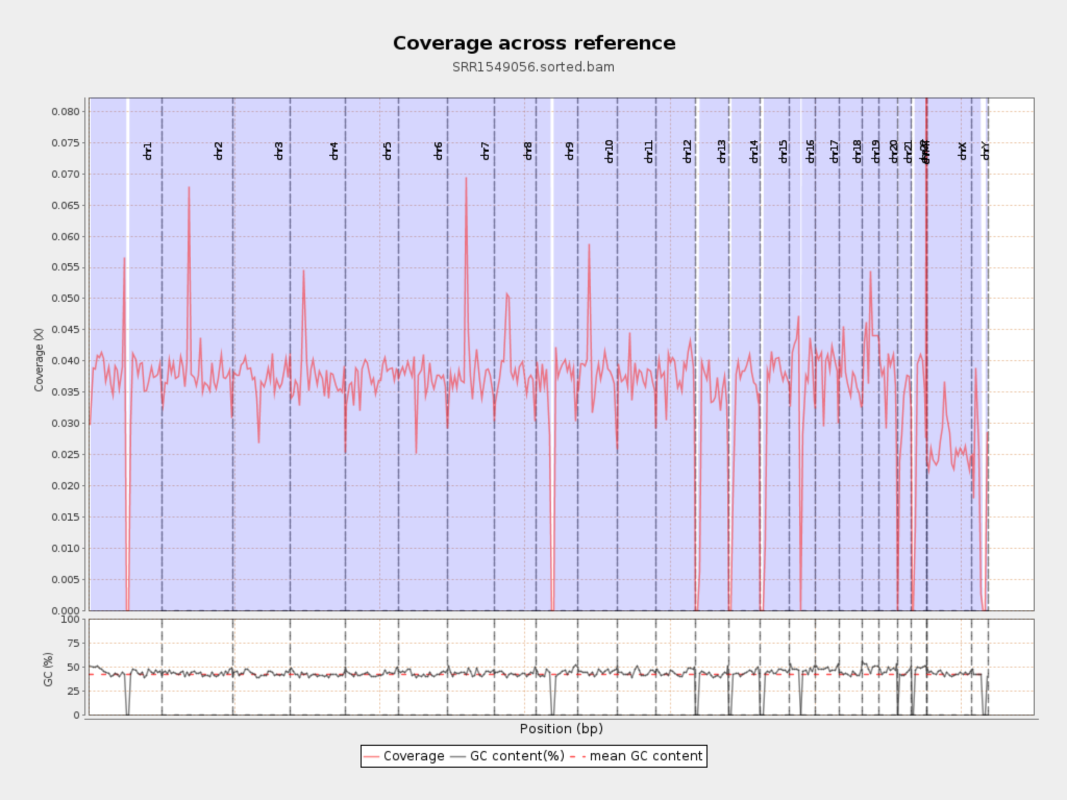
General error rate	0.31%
Mismatches	336,946
Insertions	3,711
Mapped reads with at least one insertion	0.13%
Deletions	8,607
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.4%

2.6. Chromosome stats

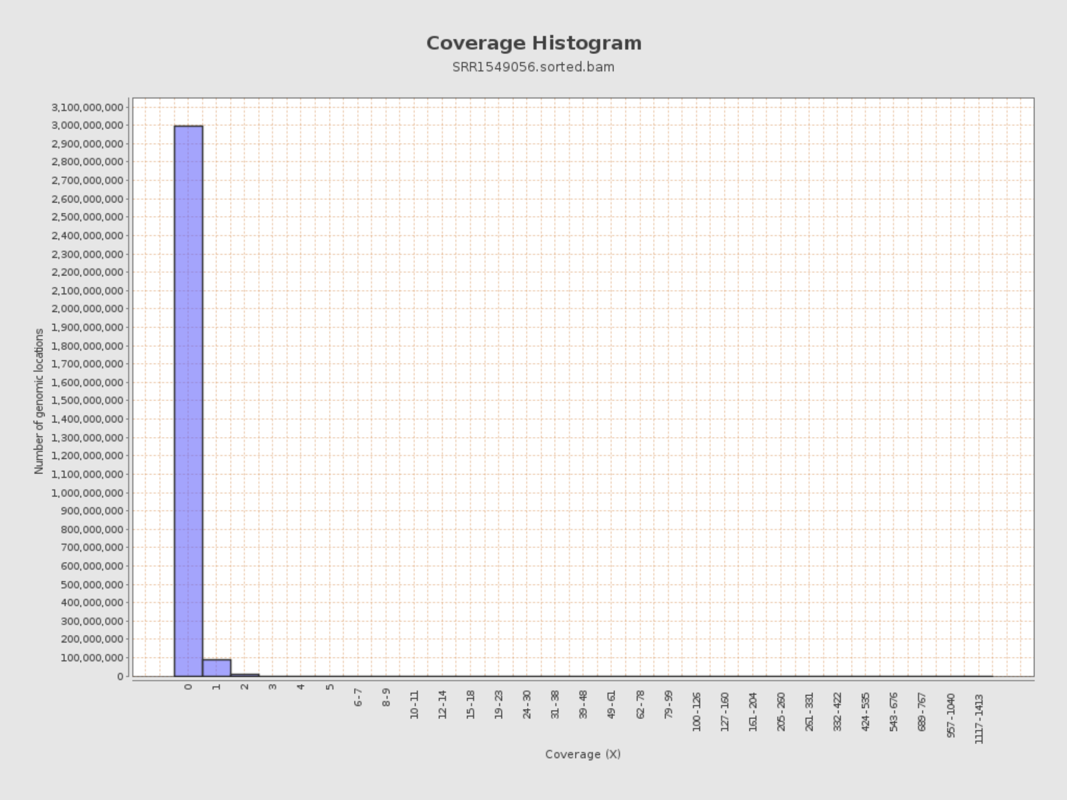
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8972727	0.036	0.5436
chr2	243199373	9374109	0.0385	0.335
chr3	198022430	7392530	0.0373	0.2087
chr4	191154276	7171503	0.0375	0.2255
chr5	180915260	6748479	0.0373	0.2119
chr6	171115067	6352859	0.0371	0.2156
chr7	159138663	6193238	0.0389	0.4244
chr8	146364022	5636652	0.0385	0.7276

chr9	141213431	4698675	0.0333	0.3454
chr10	135534747	5247823	0.0387	0.2885
chr11	135006516	5043224	0.0374	0.2647
chr12	133851895	5135164	0.0384	0.2191
chr13	115169878	3447375	0.0299	0.1849
chr14	107349540	3403536	0.0317	0.2234
chr15	102531392	3187831	0.0311	0.1914
chr16	90354753	3231800	0.0358	0.2272
chr17	81195210	3151207	0.0388	0.2197
chr18	78077248	2921952	0.0374	0.5877
chr19	59128983	2601482	0.044	0.5397
chr20	63025520	2342657	0.0372	0.2175
chr21	48129895	1411180	0.0293	0.2249
chr22	51304566	1364478	0.0266	0.2152
chrMT	16571	3693	0.2229	0.5566
chrX	155270560	4023332	0.0259	0.2181
chrY	59373566	1012594	0.0171	0.1972

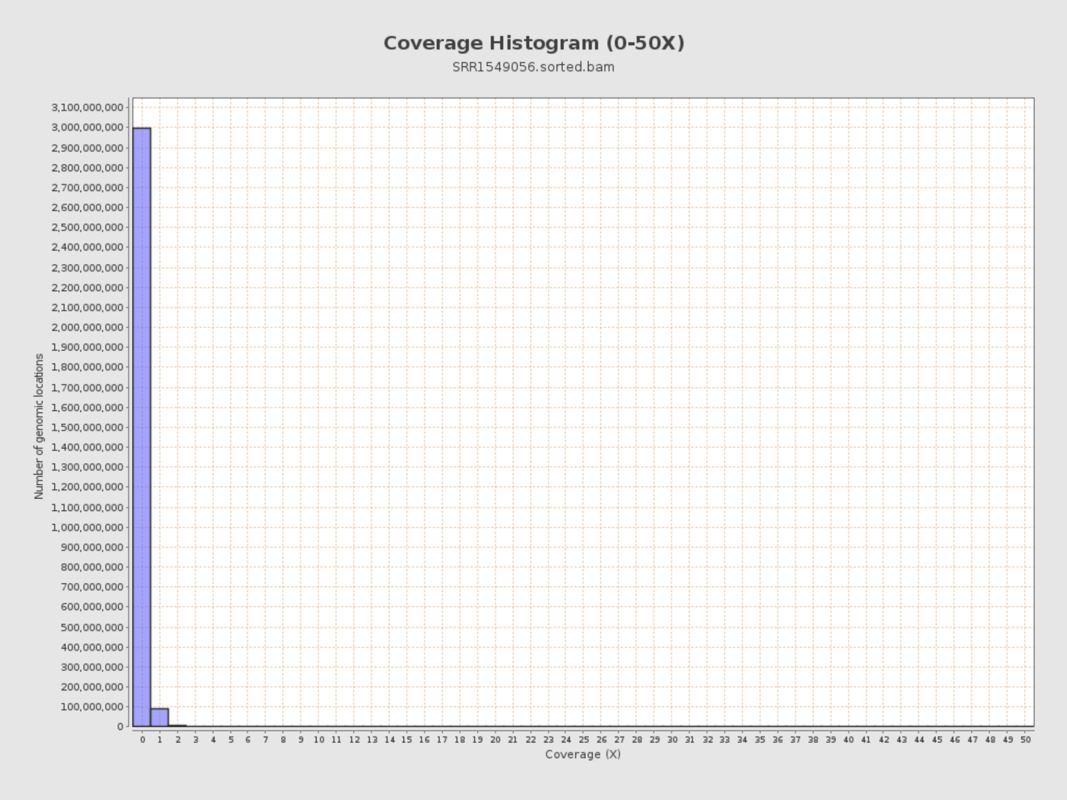
3. Results : Coverage across reference



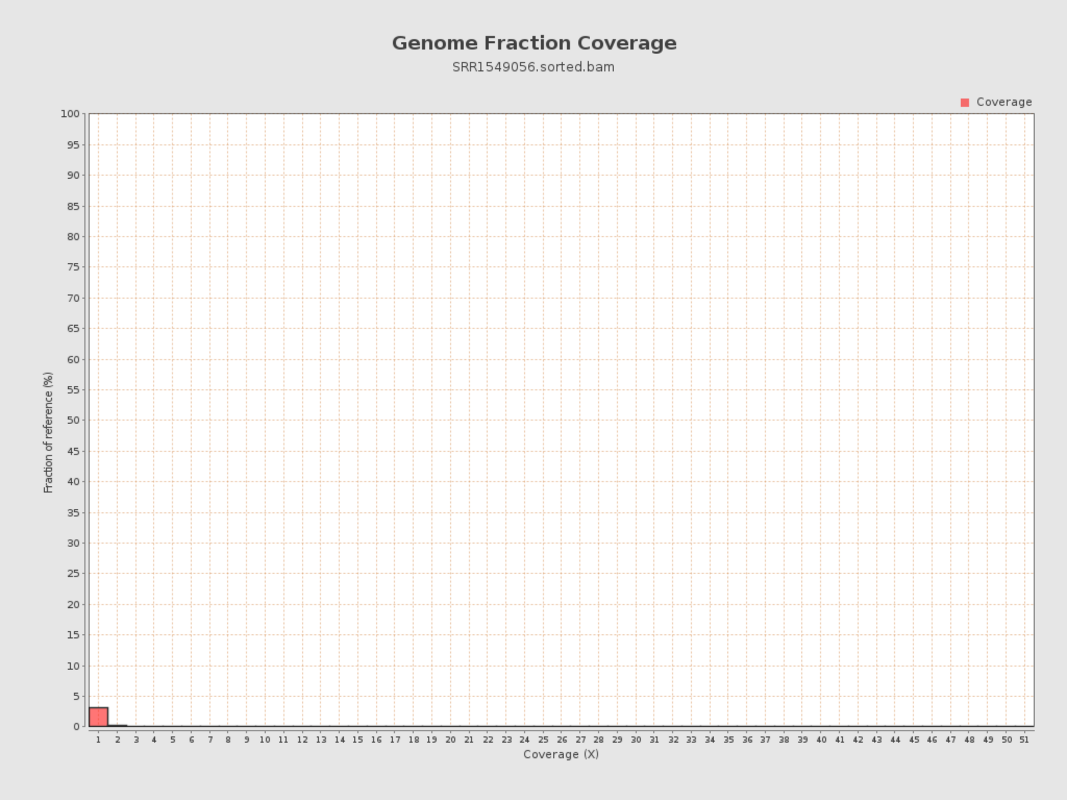
4. Results : Coverage Histogram



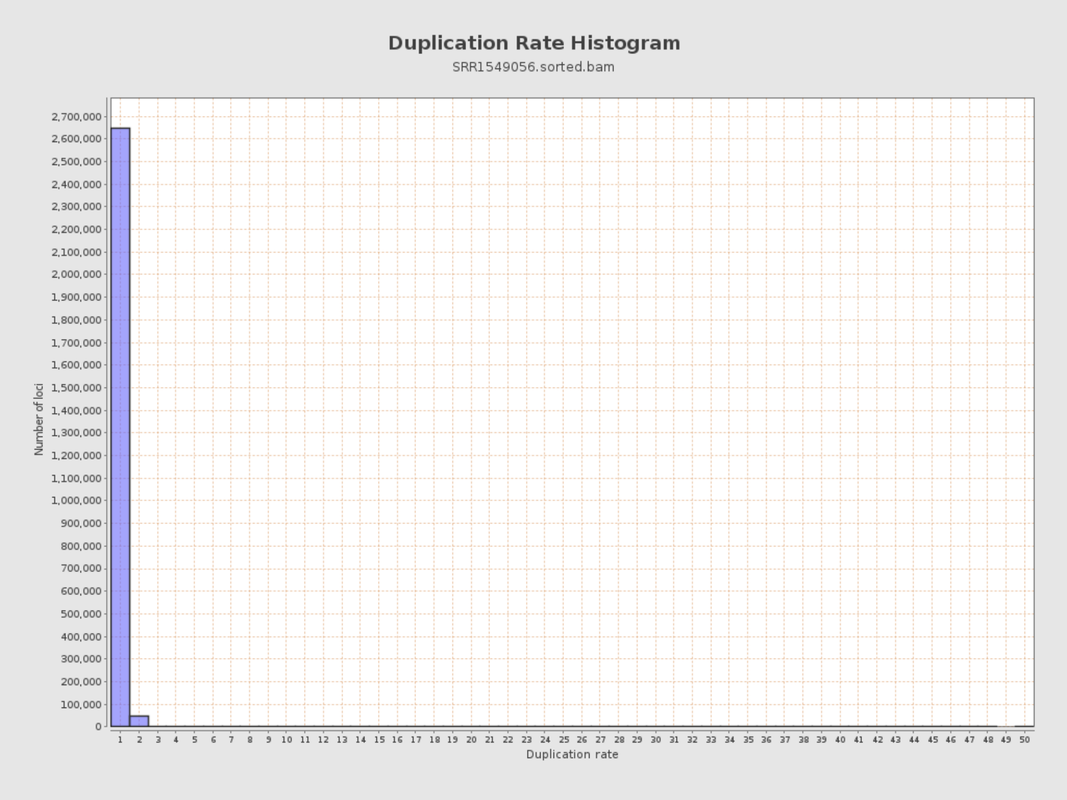
5. Results : Coverage Histogram (0-50X)



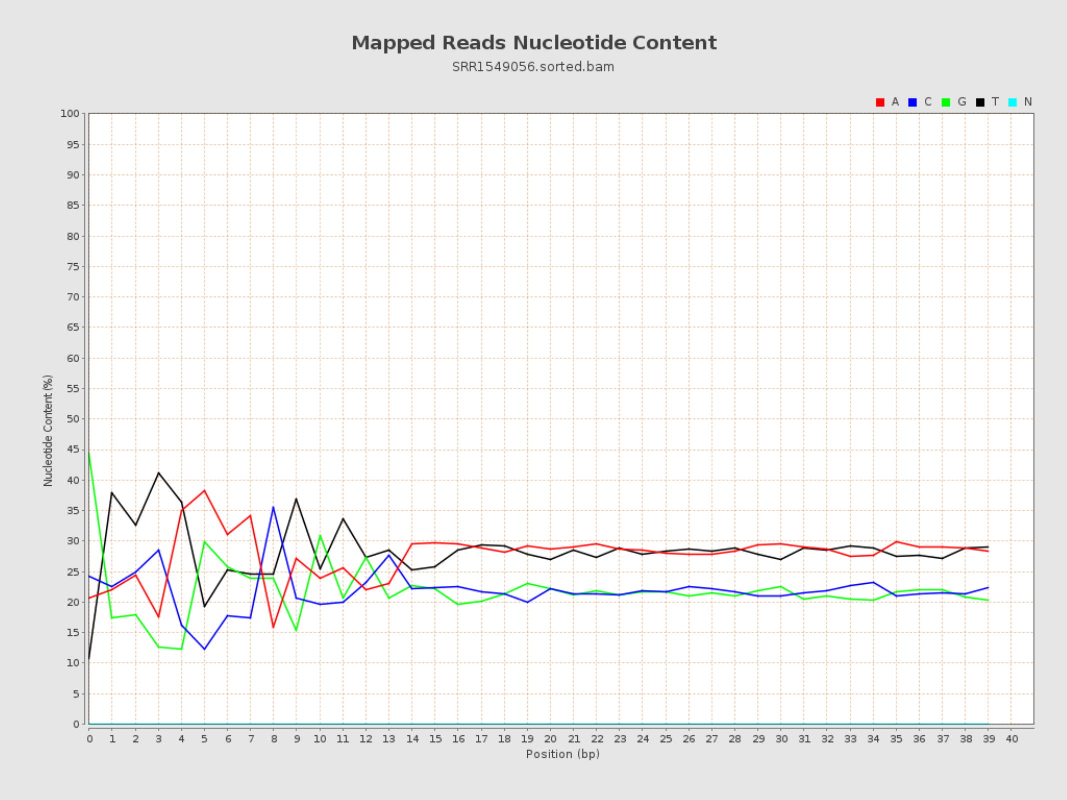
6. Results : Genome Fraction Coverage



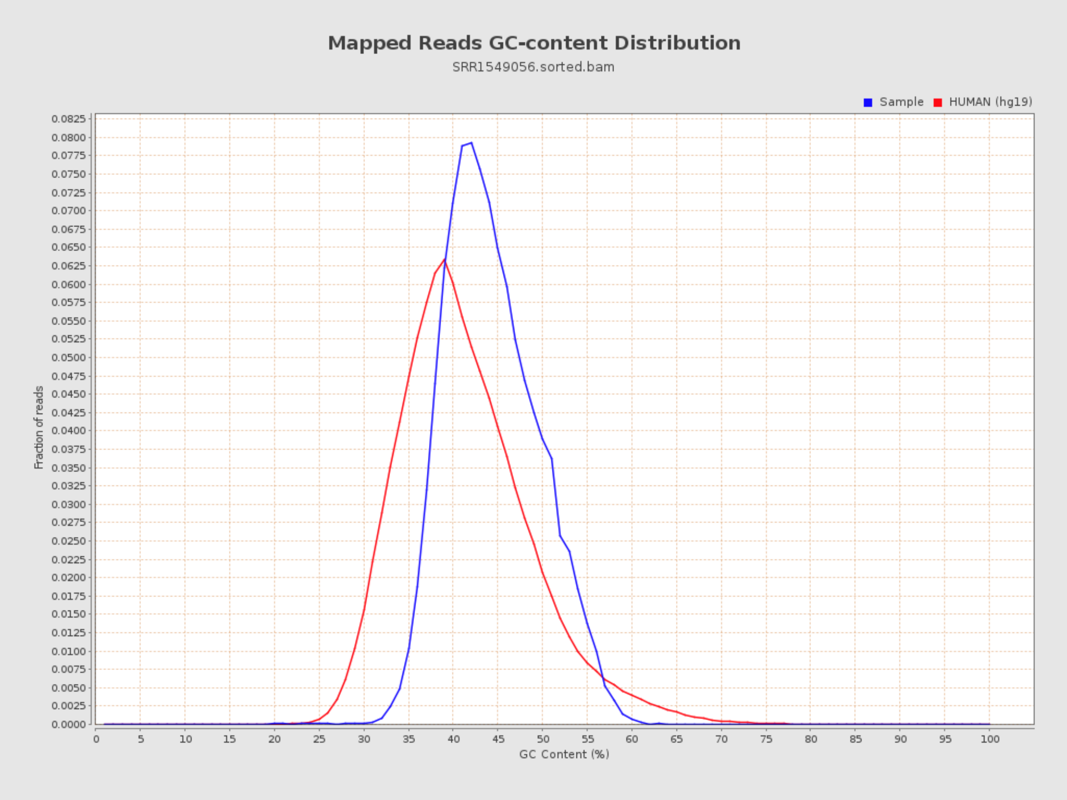
7. Results : Duplication Rate Histogram



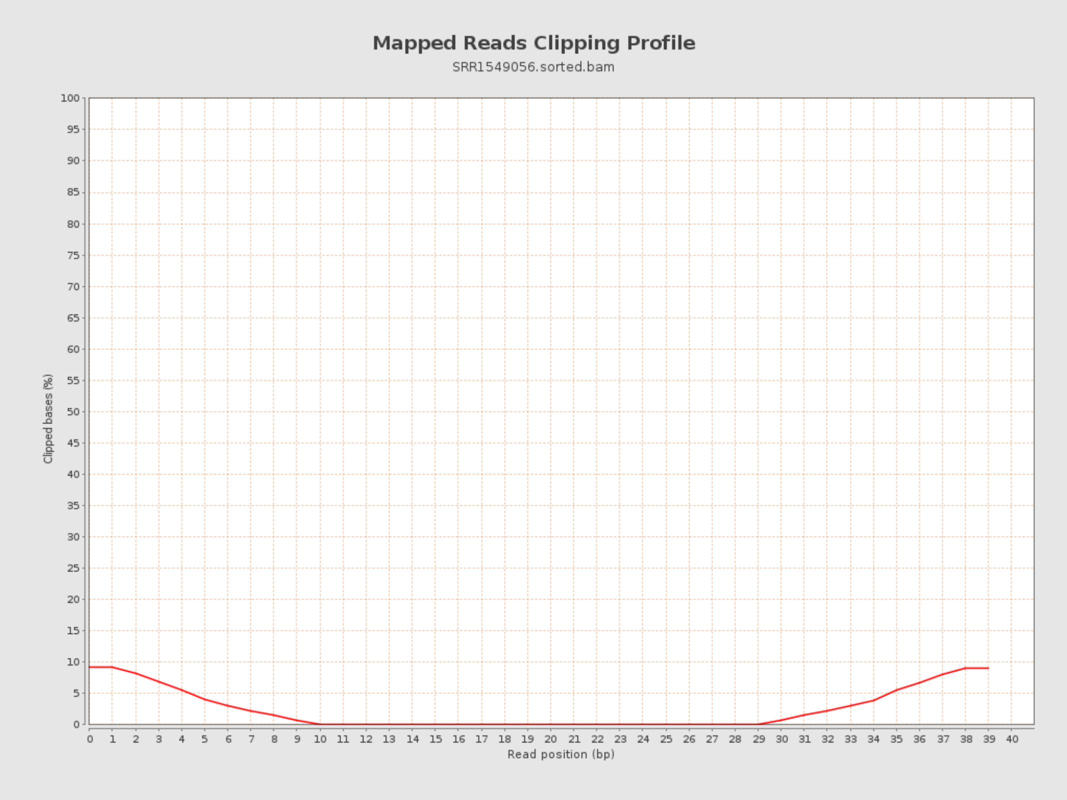
8. Results : Mapped Reads Nucleotide Content



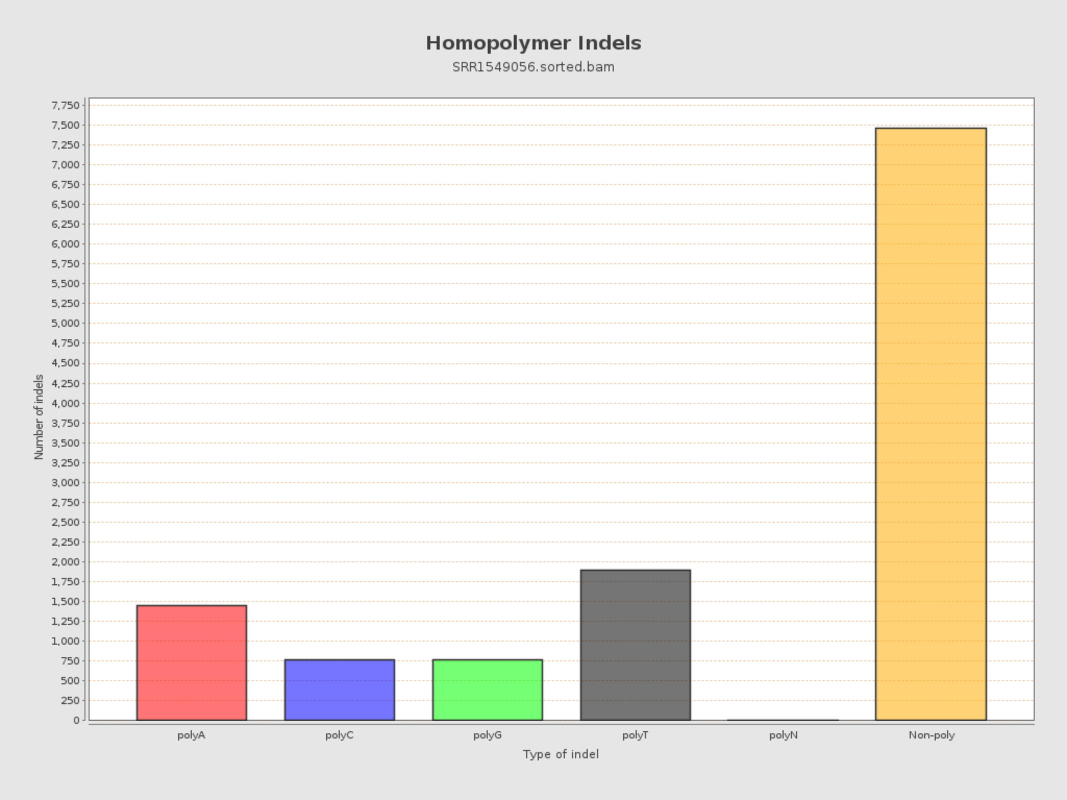
9. Results : Mapped Reads GC-content Distribution



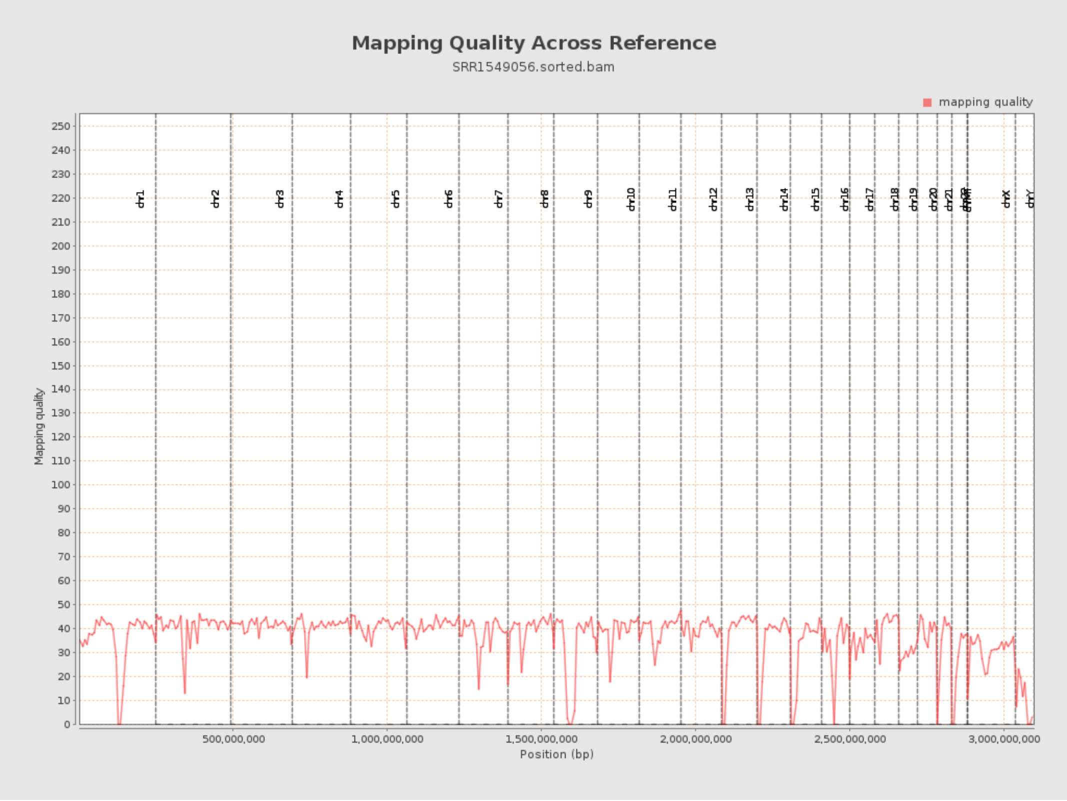
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram