Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:06:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085118.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_SRR3085118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:06:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,076,111
Mapped reads	1,834,775 / 88.38%
Unmapped reads	241,336 / 11.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,652 / 1.28%
Read min/max/mean length	30 / 76 / 76.45
Duplicated reads (estimated)	68,596 / 3.3%
Duplication rate	2.16%
Clipped reads	899,445 / 43.32%

2.2. ACGT Content

Number/percentage of A's	34,579,427 / 28.49%
Number/percentage of C's	22,969,993 / 18.92%
Number/percentage of T's	36,624,834 / 30.17%
Number/percentage of G's	27,184,869 / 22.4%
Number/percentage of N's	20,360 / 0.02%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0392

Standard Deviation	0.5187

2.4. Mapping Quality

Mean Mapping Quality	43.39

2.5. Mismatches and indels

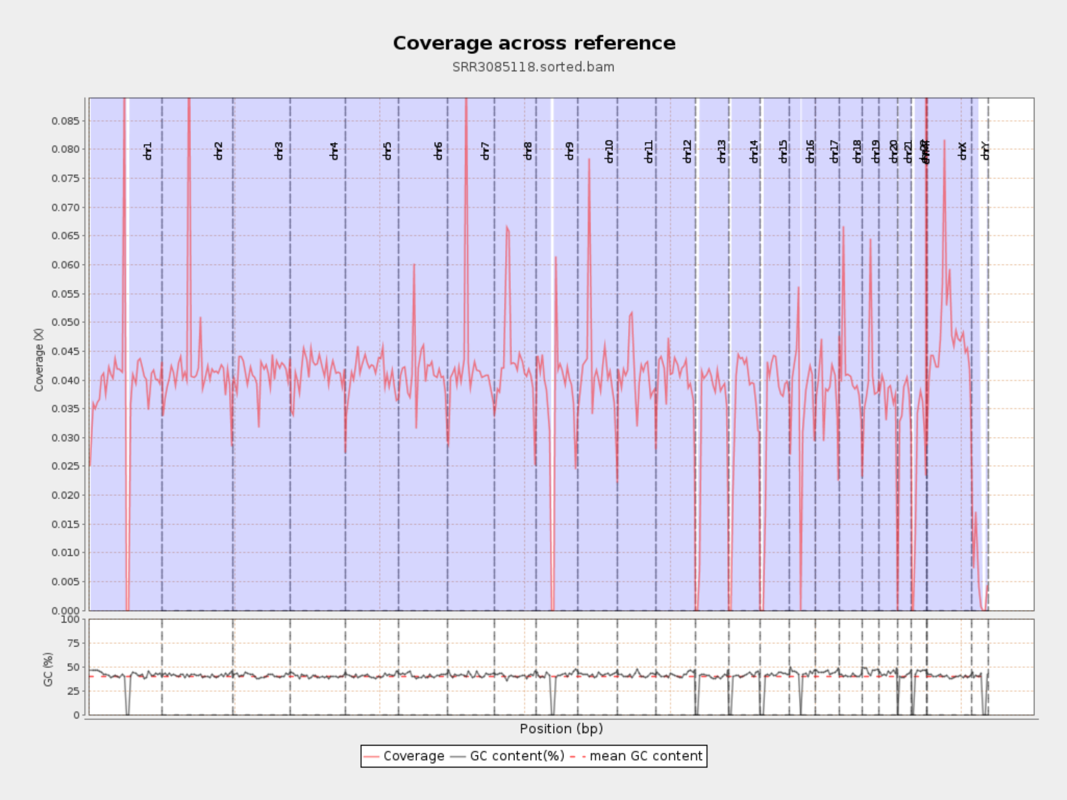
General error rate	0.91%
Mismatches	1,084,436
Insertions	10,187
Mapped reads with at least one insertion	0.55%
Deletions	24,461
Mapped reads with at least one deletion	1.32%
Homopolymer indels	44.52%

2.6. Chromosome stats

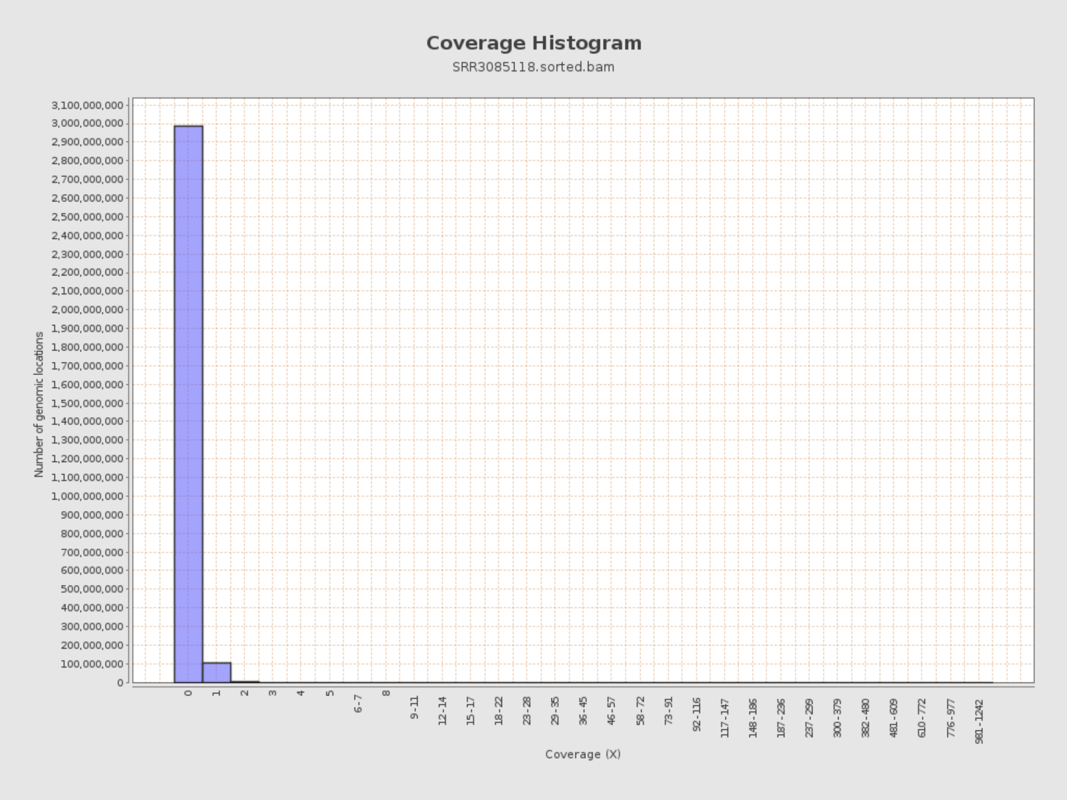
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9666394	0.0388	1.0854
chr2	243199373	10421091	0.0428	0.5641
chr3	198022430	8154259	0.0412	0.2168
chr4	191154276	7905598	0.0414	0.233
chr5	180915260	7458296	0.0412	0.2217
chr6	171115067	7074671	0.0413	0.3042
chr7	159138663	6883006	0.0433	0.7335

chr8	146364022	6290395	0.043	0.7967
chr9	141213431	5097004	0.0361	0.4437
chr10	135534747	5697471	0.042	0.4388
chr11	135006516	5513721	0.0408	0.434
chr12	133851895	5477187	0.0409	0.2302
chr13	115169878	3781302	0.0328	0.1911
chr14	107349540	3637312	0.0339	0.2382
chr15	102531392	3393004	0.0331	0.2086
chr16	90354753	3298802	0.0365	0.2641
chr17	81195210	3070014	0.0378	0.2627
chr18	78077248	3291669	0.0422	0.918
chr19	59128983	2411398	0.0408	0.7999
chr20	63025520	2324019	0.0369	0.2176
chr21	48129895	1570843	0.0326	0.2114
chr22	51304566	1224579	0.0239	0.162
chrMT	16571	15428	0.931	1.0779
chrX	155270560	7430921	0.0479	0.3065
chrY	59373566	331491	0.0056	0.1338

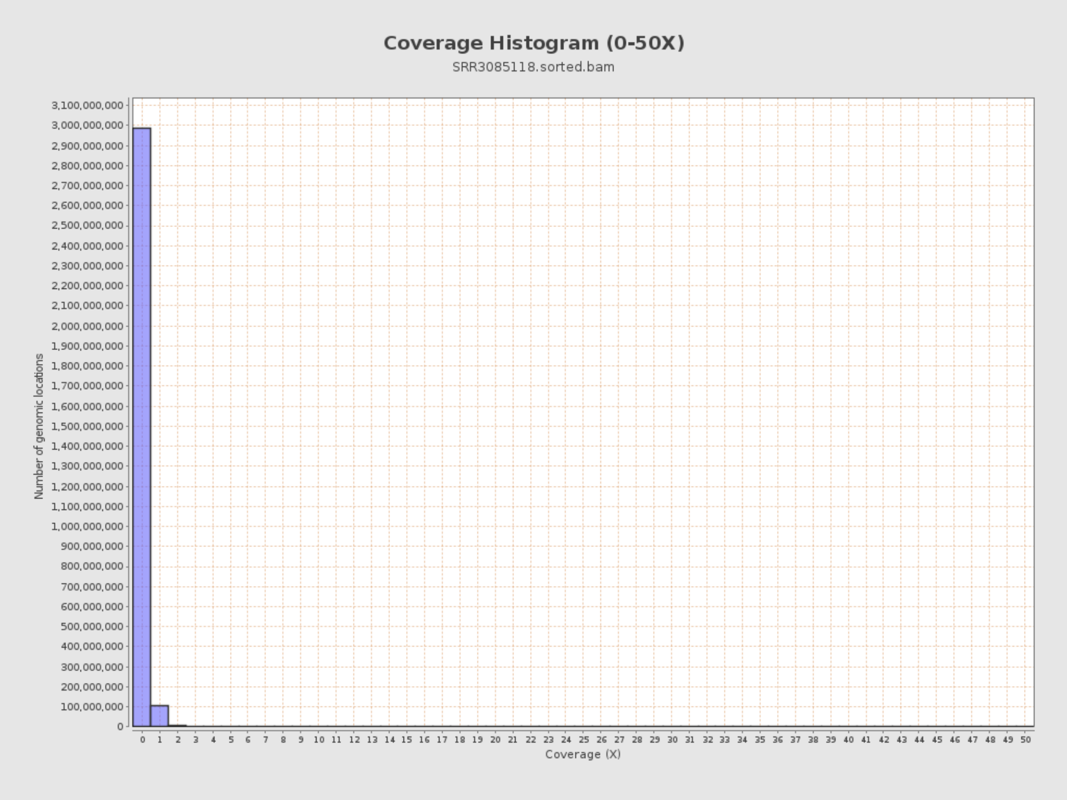
3. Results : Coverage across reference



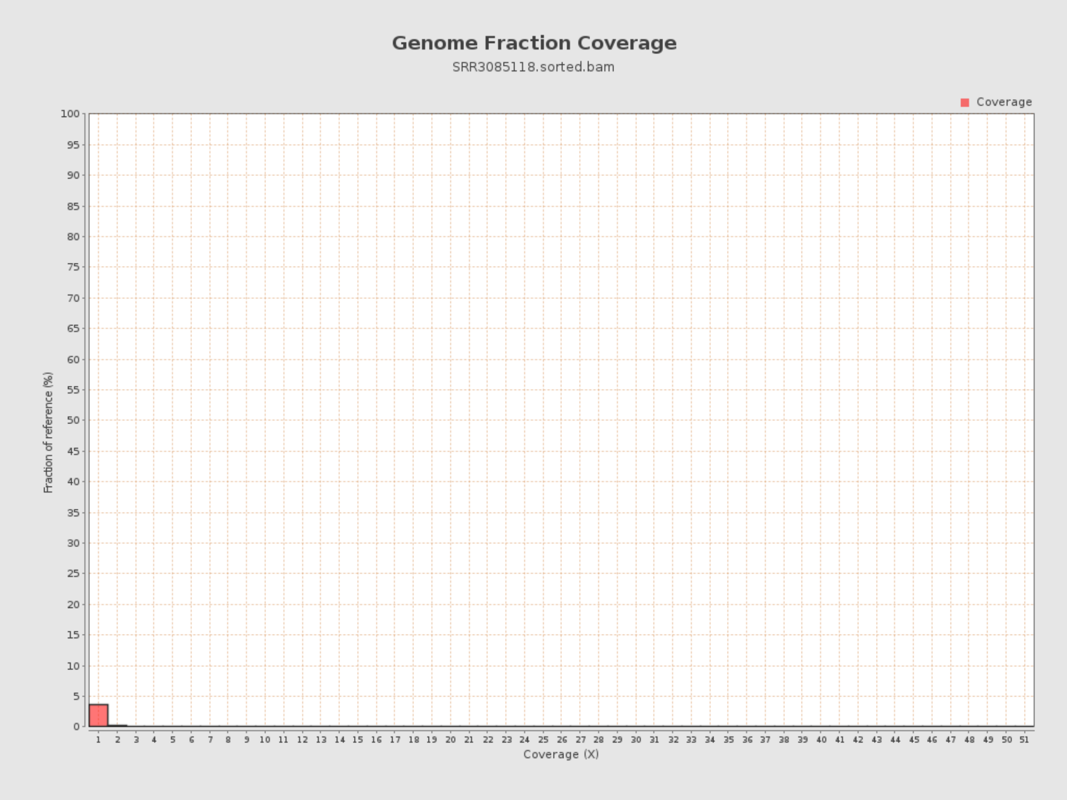
4. Results : Coverage Histogram



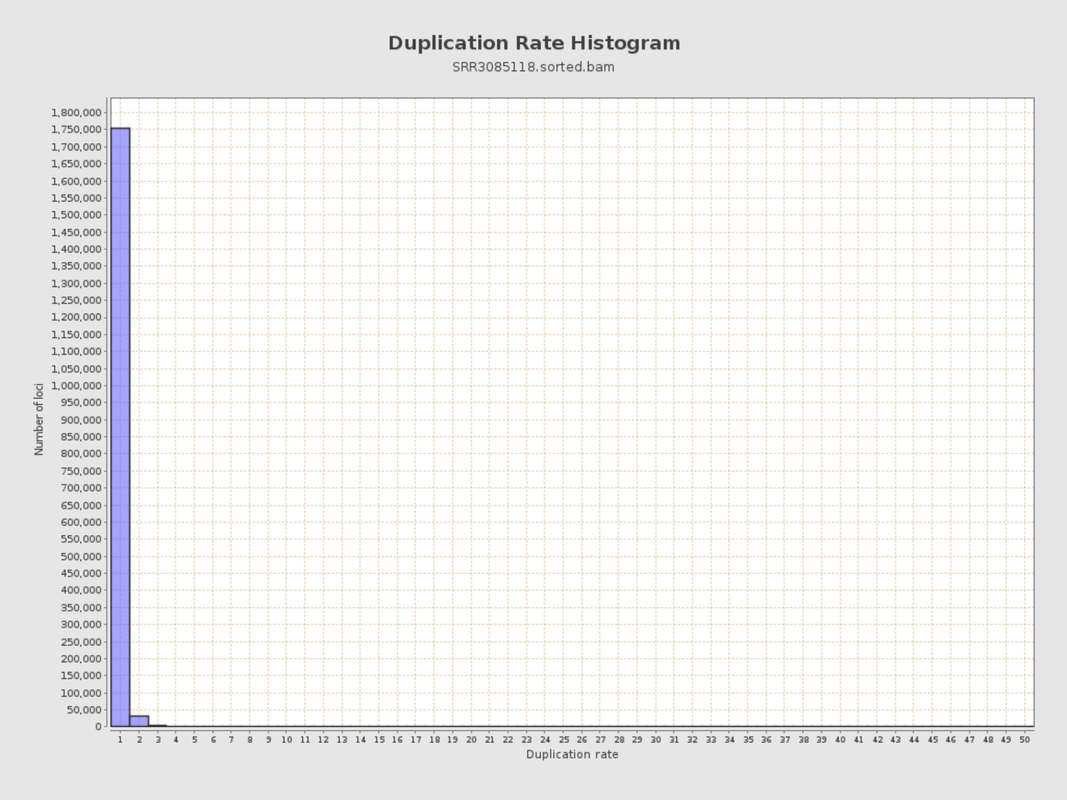
5. Results : Coverage Histogram (0-50X)



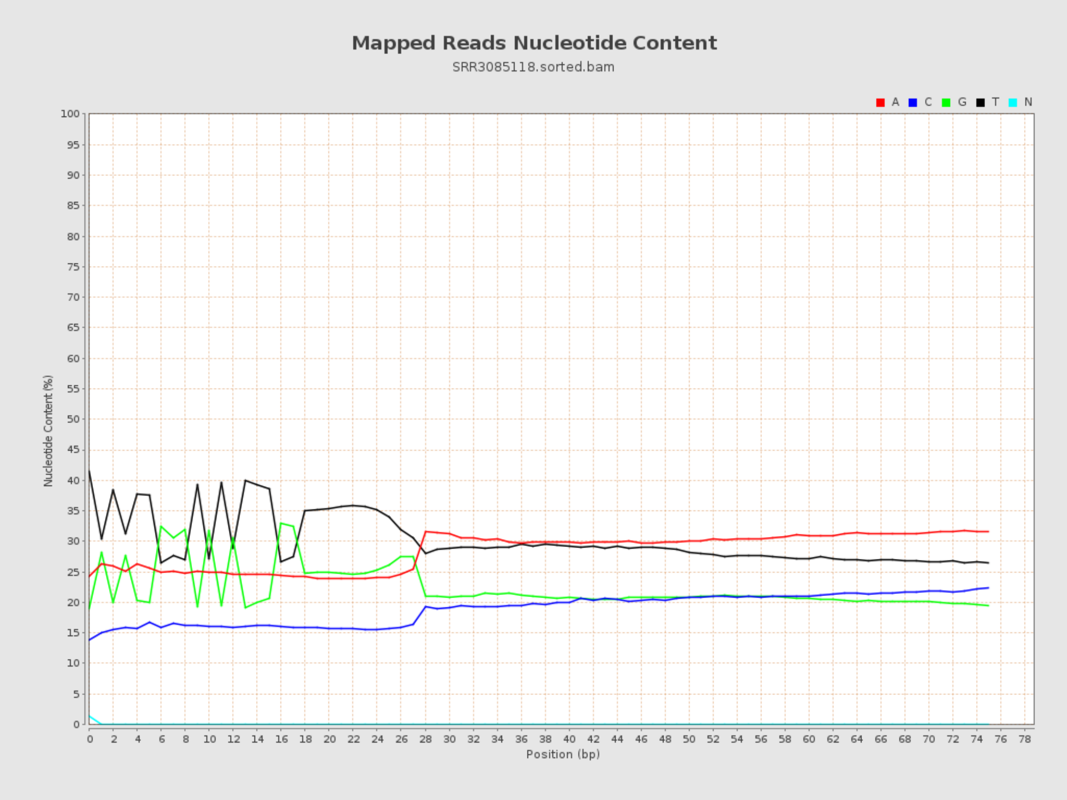
6. Results : Genome Fraction Coverage



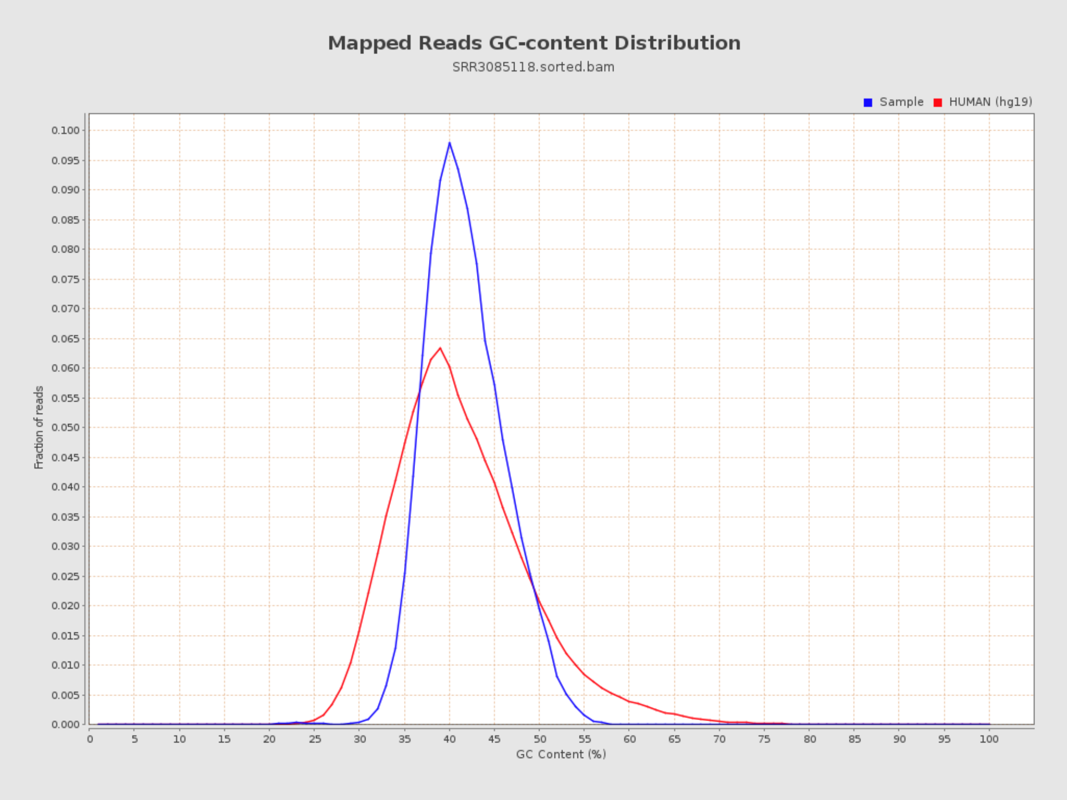
7. Results : Duplication Rate Histogram



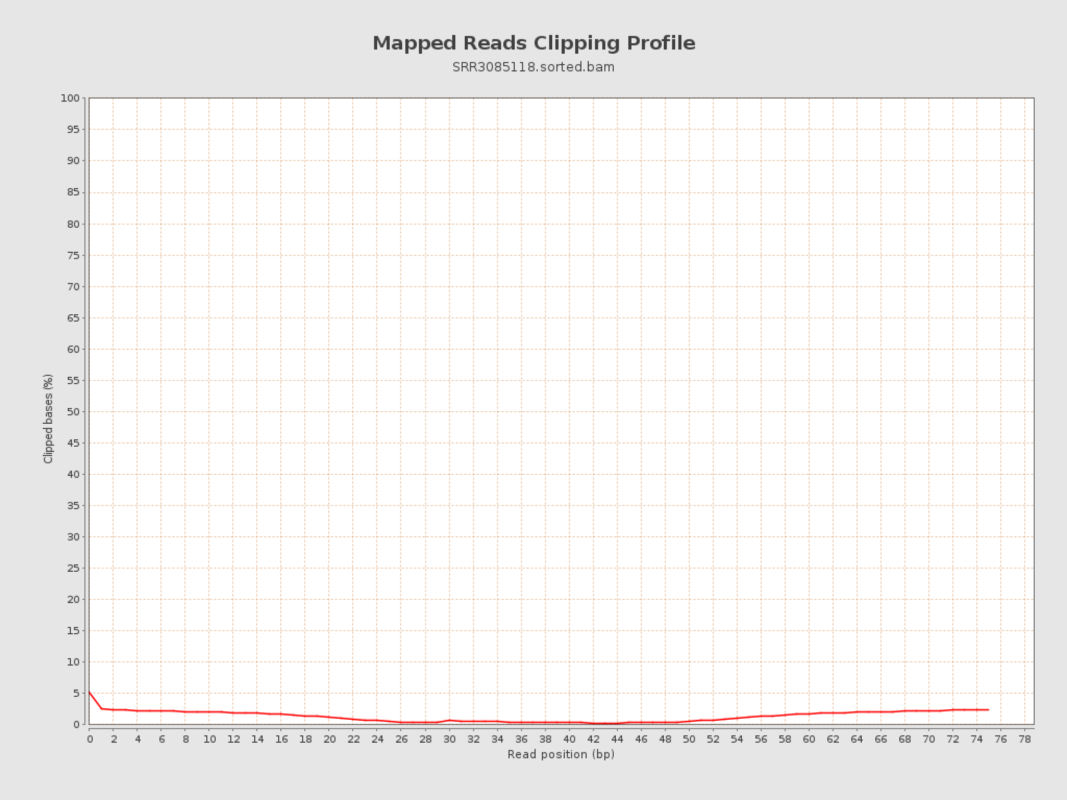
8. Results : Mapped Reads Nucleotide Content



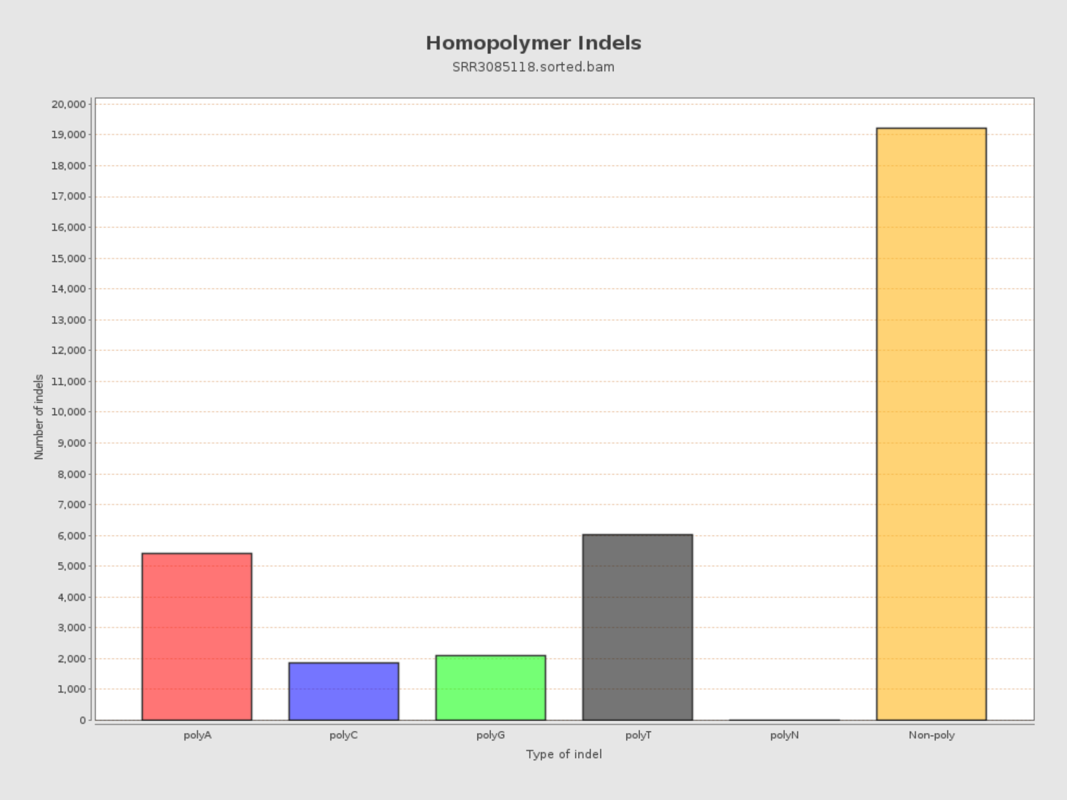
9. Results : Mapped Reads GC-content Distribution



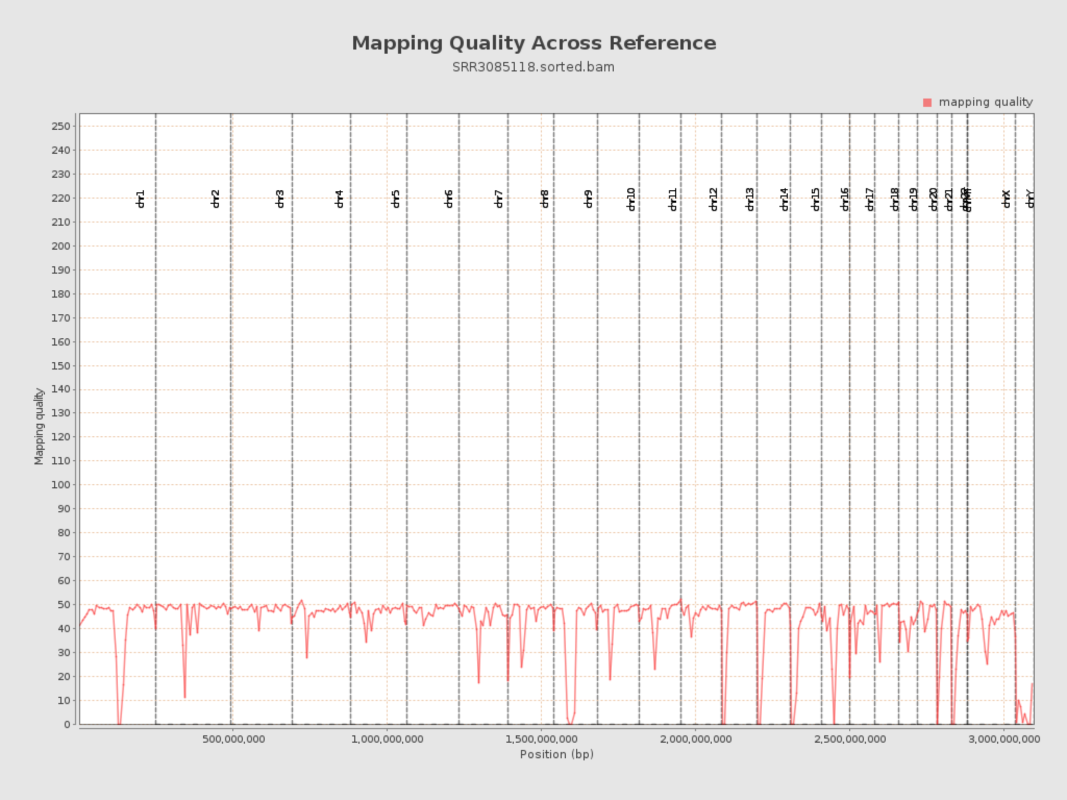
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram