Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:19:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525059.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_SRR10525059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:19:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,994
Mapped reads	1,511,416 / 91.21%
Unmapped reads	145,578 / 8.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,031 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	186,513 / 11.26%
Duplication rate	9.51%
Clipped reads	1,513,947 / 91.37%

2.2. ACGT Content

Number/percentage of A's	22,857,353 / 25.77%
Number/percentage of C's	17,393,909 / 19.61%
Number/percentage of T's	27,769,558 / 31.31%
Number/percentage of G's	20,659,862 / 23.29%
Number/percentage of N's	9,002 / 0.01%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2989

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

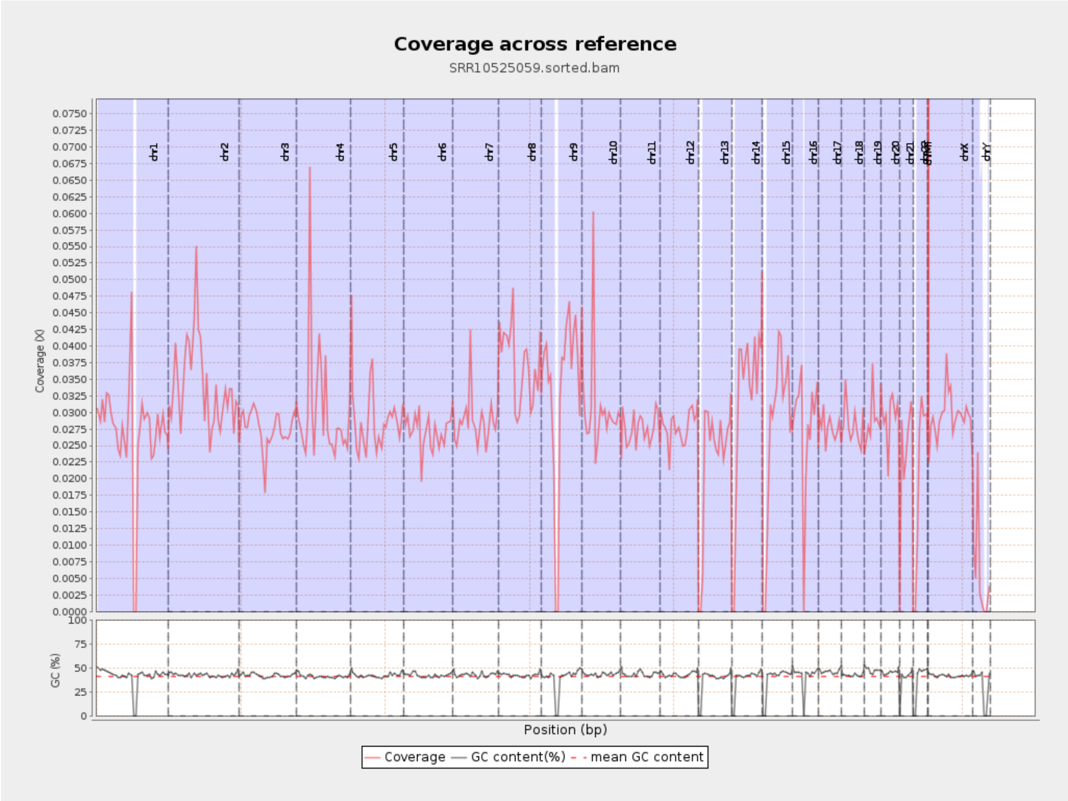
General error rate	0.5%
Mismatches	427,227
Insertions	5,833
Mapped reads with at least one insertion	0.38%
Deletions	17,249
Mapped reads with at least one deletion	1.13%
Homopolymer indels	45.07%

2.6. Chromosome stats

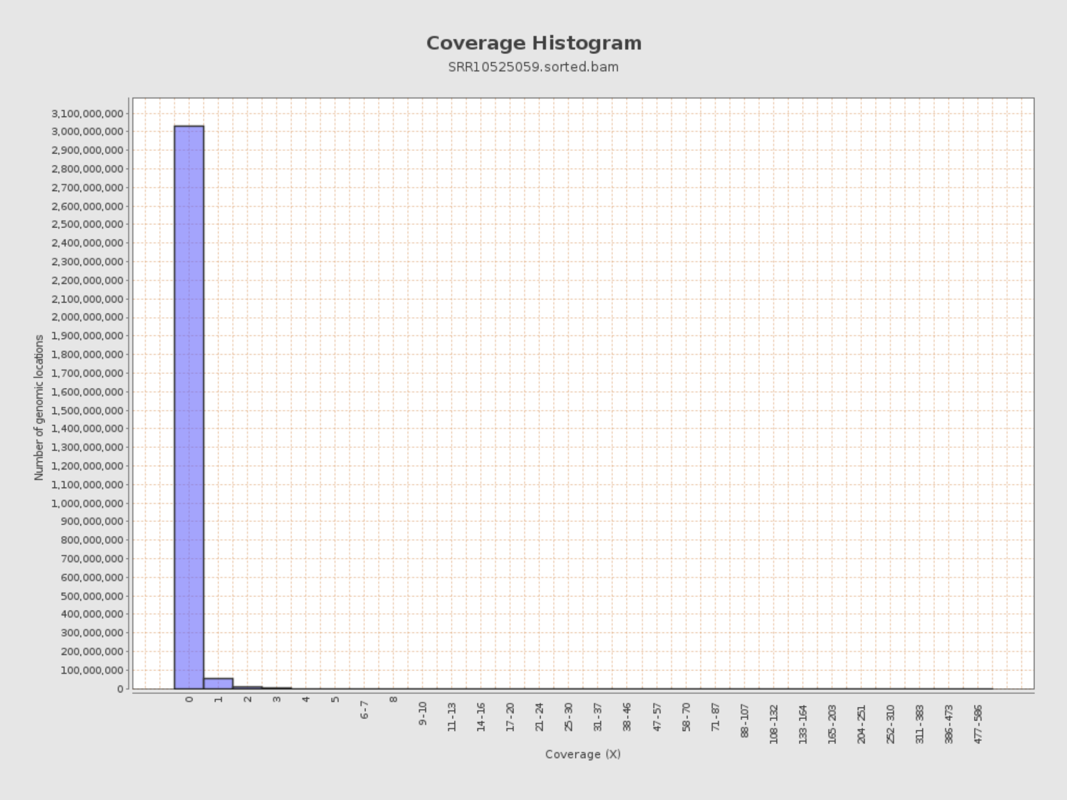
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6699209	0.0269	0.4869
chr2	243199373	8289151	0.0341	0.3848
chr3	198022430	5456547	0.0276	0.2105
chr4	191154276	5757049	0.0301	0.2807
chr5	180915260	5139334	0.0284	0.2138
chr6	171115067	4651436	0.0272	0.2207
chr7	159138663	4566031	0.0287	0.2992

chr8	146364022	5458709	0.0373	0.382
chr9	141213431	4697352	0.0333	0.2645
chr10	135534747	4141506	0.0306	0.3573
chr11	135006516	3734413	0.0277	0.2531
chr12	133851895	3715543	0.0278	0.2186
chr13	115169878	2593318	0.0225	0.1911
chr14	107349540	3385802	0.0315	0.2281
chr15	102531392	2821267	0.0275	0.2095
chr16	90354753	2491202	0.0276	0.2242
chr17	81195210	2246548	0.0277	0.2223
chr18	78077248	2181704	0.0279	0.4112
chr19	59128983	1712530	0.029	0.3558
chr20	63025520	1842345	0.0292	0.2264
chr21	48129895	1155248	0.024	0.2513
chr22	51304566	1050360	0.0205	0.1827
chrMT	16571	18502	1.1165	1.2552
chrX	155270560	4576201	0.0295	0.2324
chrY	59373566	335983	0.0057	0.2336

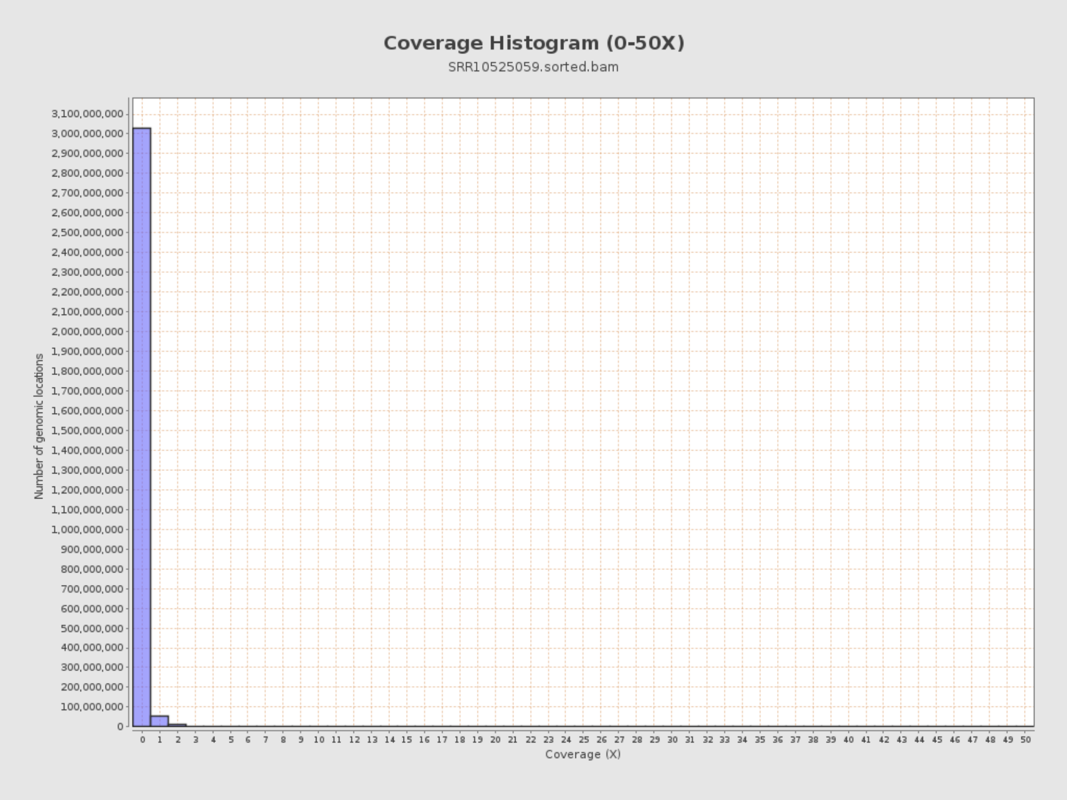
3. Results : Coverage across reference



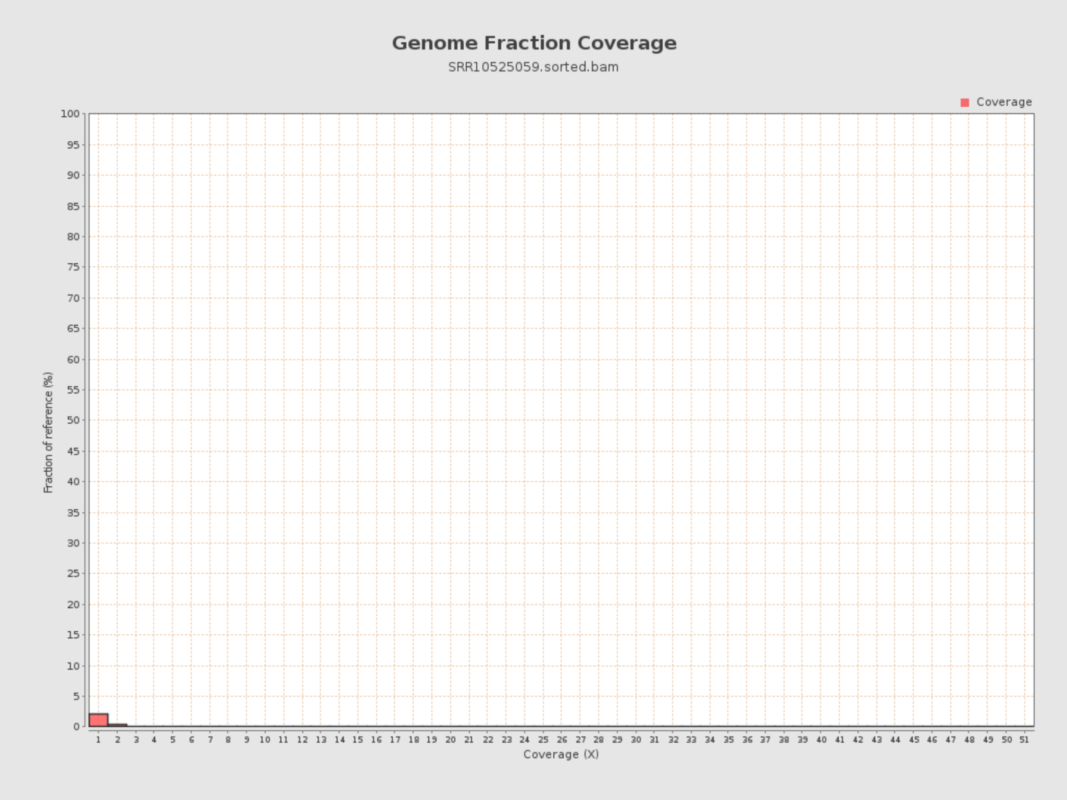
4. Results : Coverage Histogram



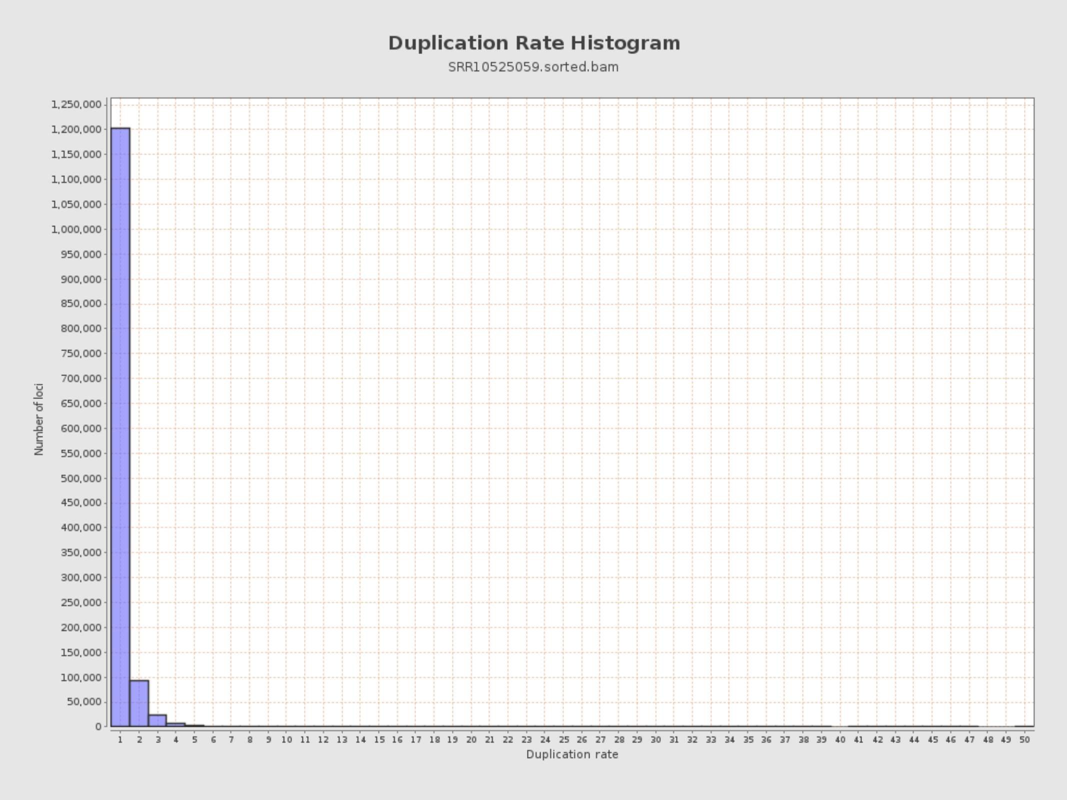
5. Results : Coverage Histogram (0-50X)



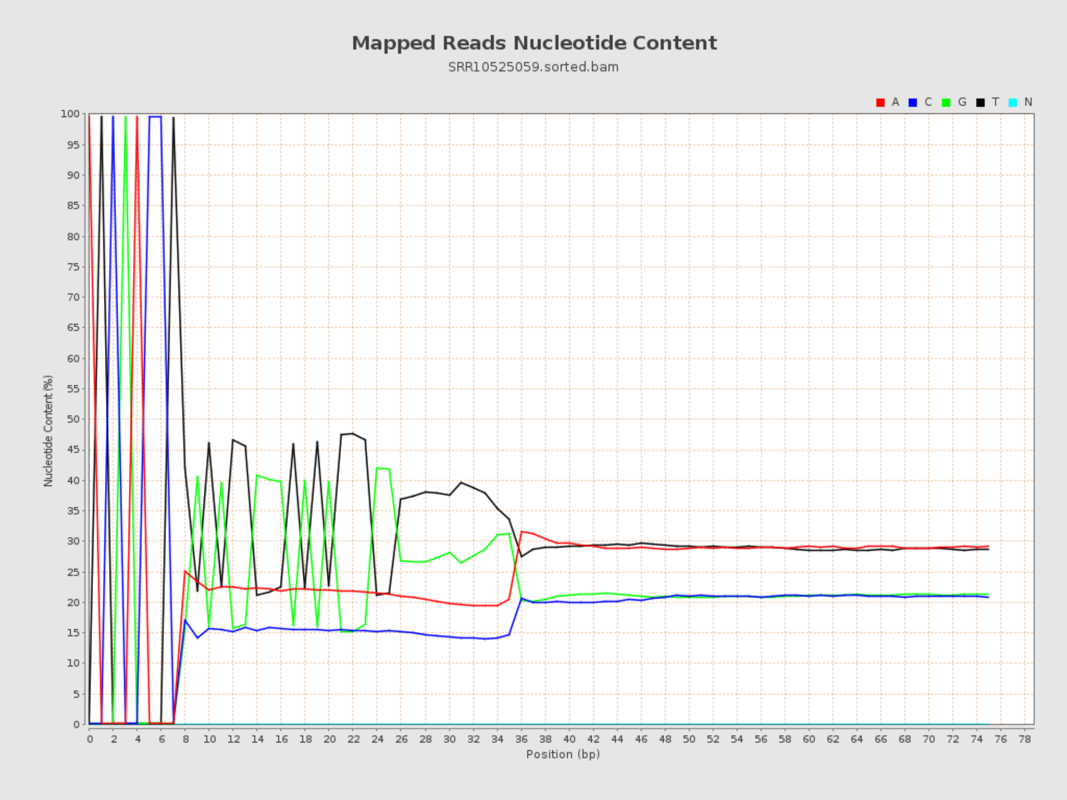
6. Results : Genome Fraction Coverage



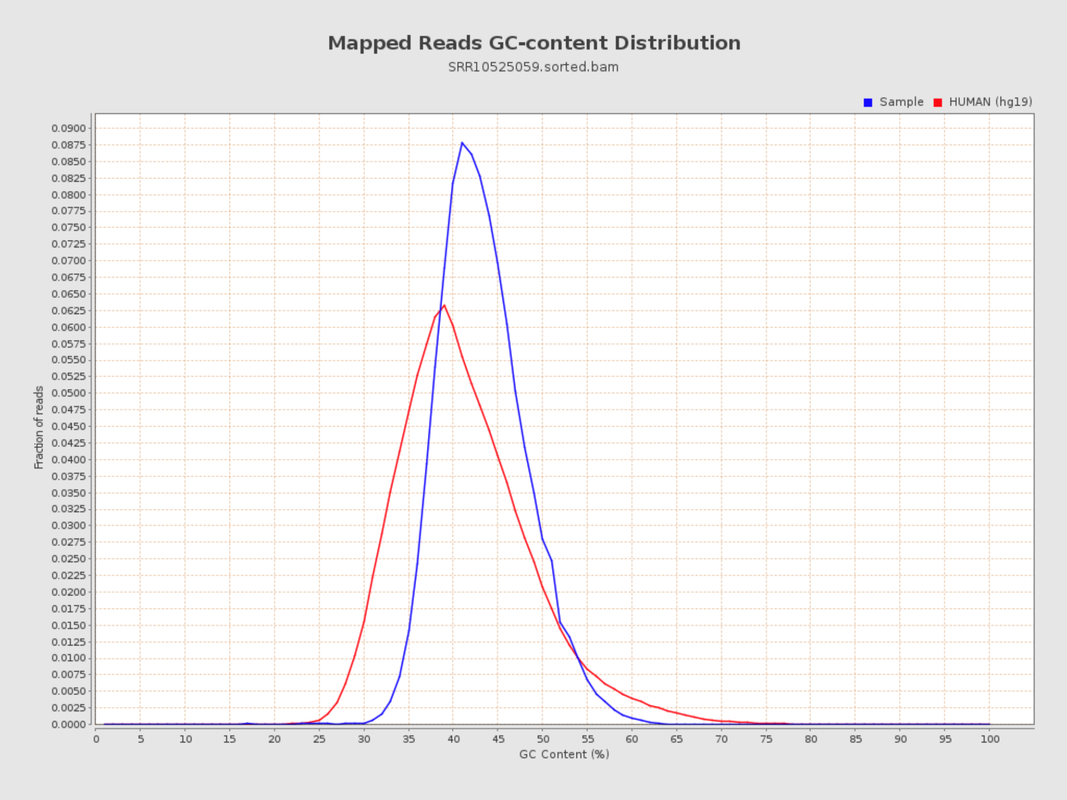
7. Results : Duplication Rate Histogram



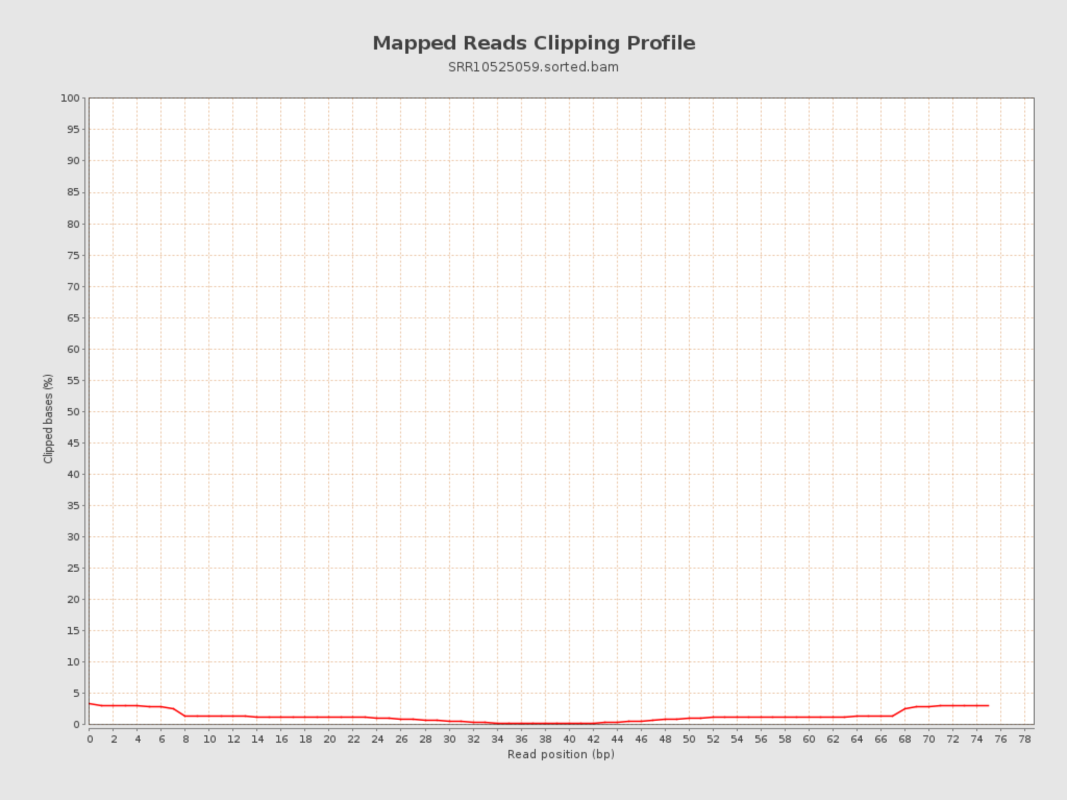
8. Results : Mapped Reads Nucleotide Content



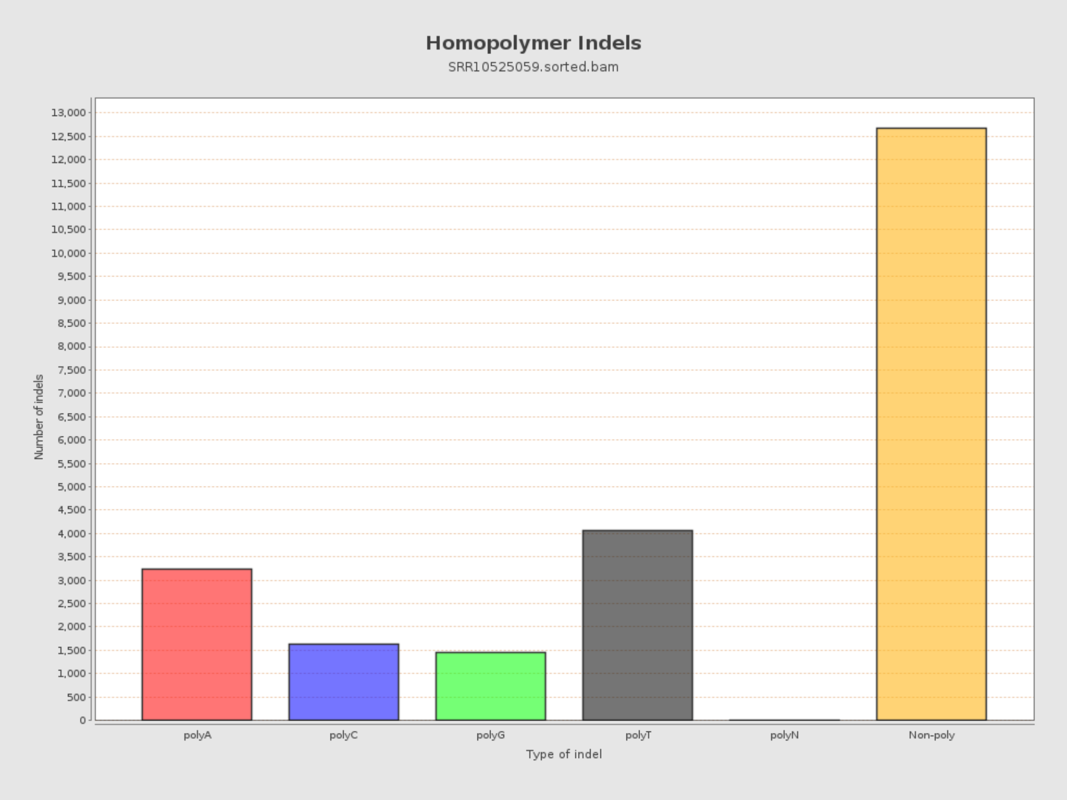
9. Results : Mapped Reads GC-content Distribution



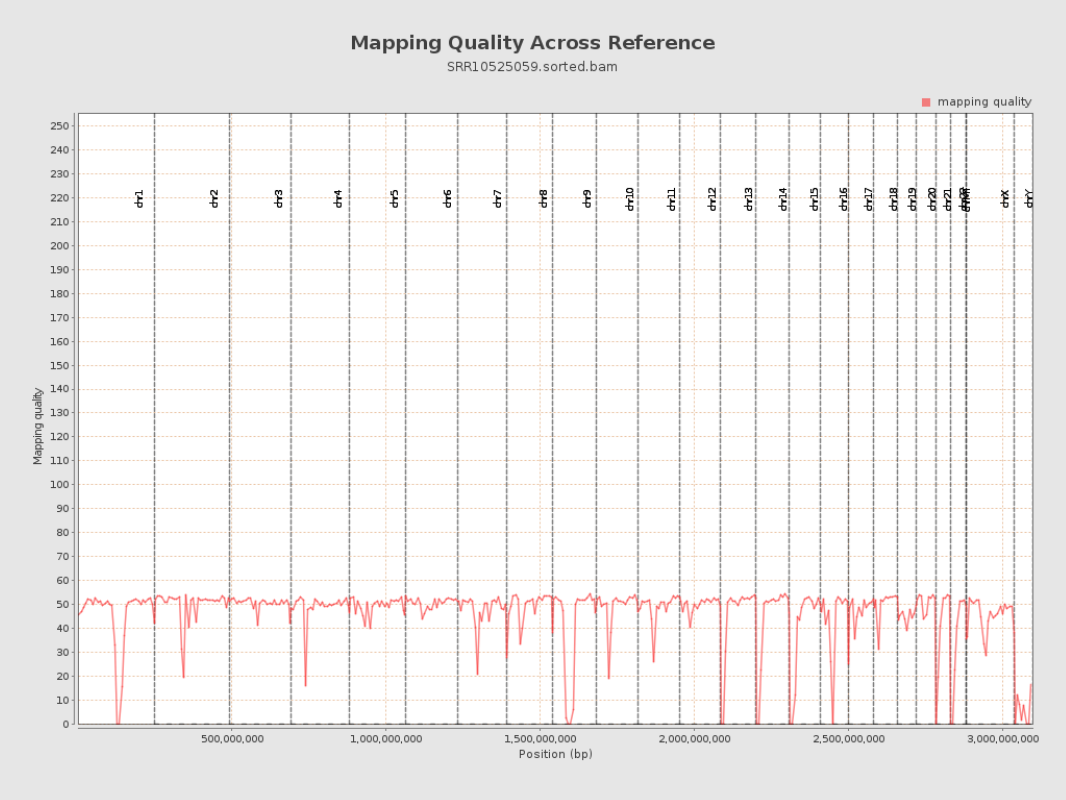
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram