Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:27:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525192.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_SRR10525192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525192.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:27:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,844,058
Mapped reads	1,726,185 / 93.61%
Unmapped reads	117,873 / 6.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,844 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,181 / 3.16%
Duplication rate	2.33%
Clipped reads	1,729,392 / 93.78%

2.2. ACGT Content

Number/percentage of A's	25,559,035 / 24.67%
Number/percentage of C's	19,962,195 / 19.27%
Number/percentage of T's	32,521,589 / 31.39%
Number/percentage of G's	25,551,452 / 24.66%
Number/percentage of N's	2,610 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3284

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

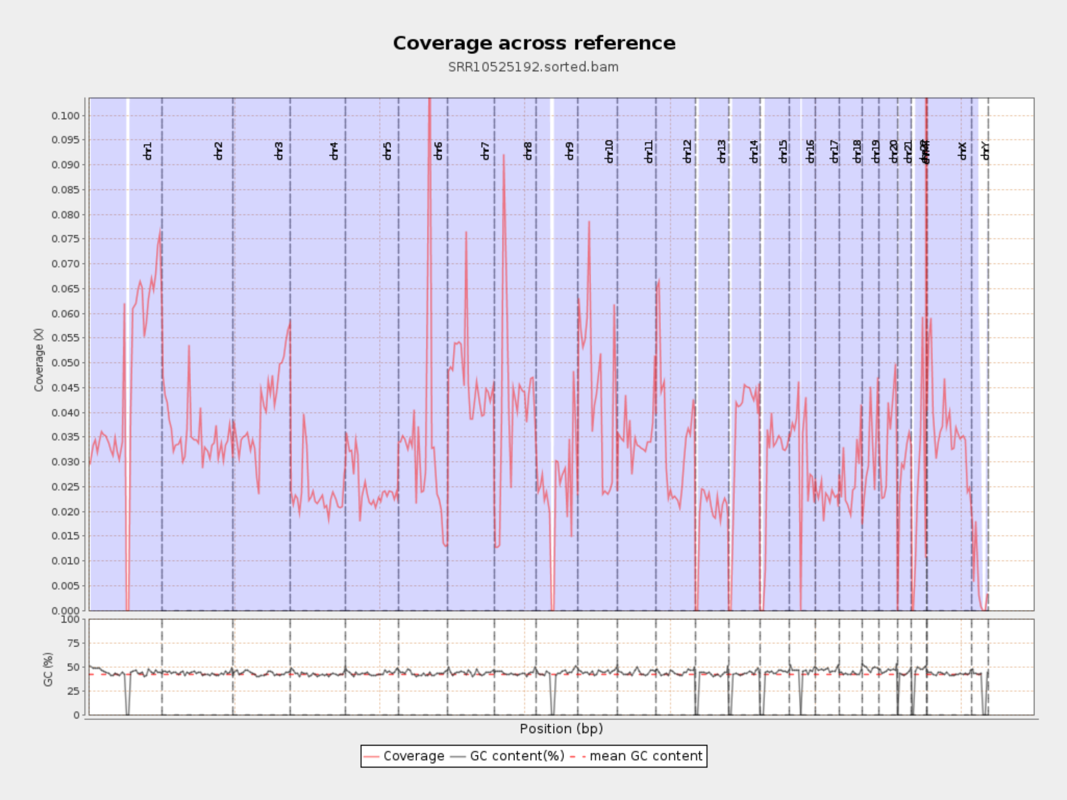
General error rate	0.51%
Mismatches	521,675
Insertions	6,295
Mapped reads with at least one insertion	0.36%
Deletions	21,971
Mapped reads with at least one deletion	1.26%
Homopolymer indels	43.63%

2.6. Chromosome stats

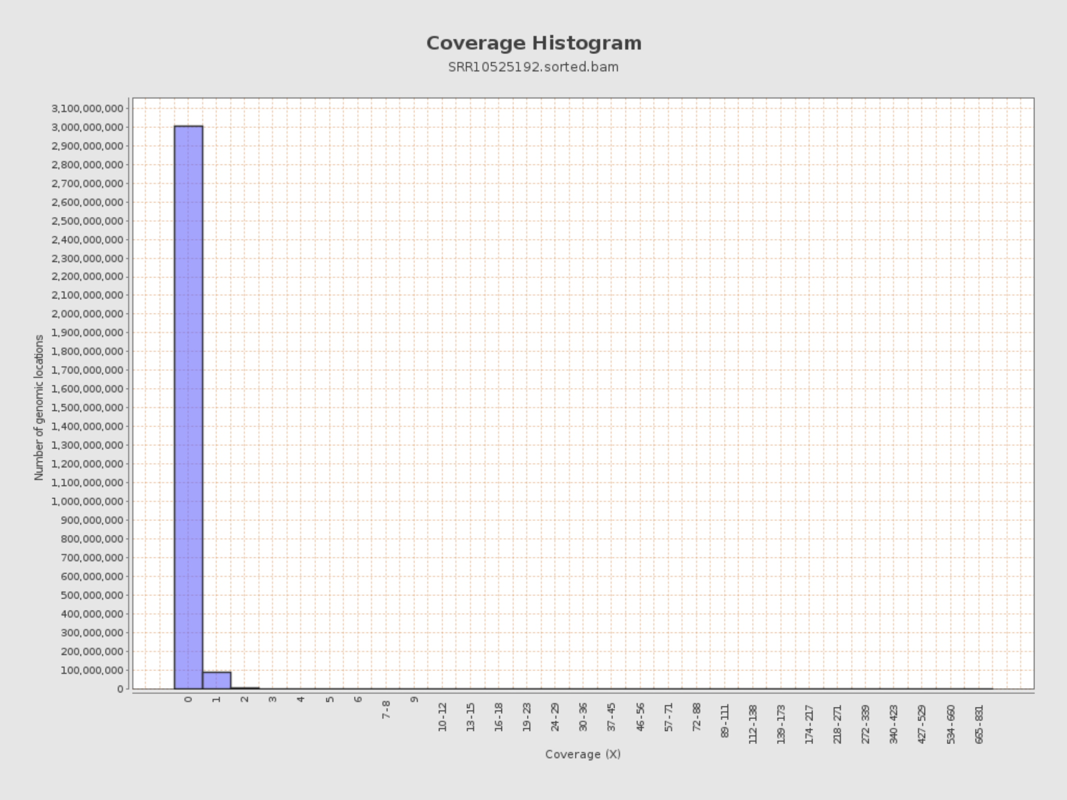
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11301483	0.0453	0.6386
chr2	243199373	8611251	0.0354	0.3793
chr3	198022430	7963100	0.0402	0.2217
chr4	191154276	4477201	0.0234	0.1801
chr5	180915260	4573842	0.0253	0.172
chr6	171115067	5864316	0.0343	0.228
chr7	159138663	7523378	0.0473	0.5888

chr8	146364022	5954072	0.0407	0.2854
chr9	141213431	3448492	0.0244	0.2298
chr10	135534747	6094208	0.045	0.3648
chr11	135006516	4760943	0.0353	0.2583
chr12	133851895	4653465	0.0348	0.2048
chr13	115169878	2203608	0.0191	0.1537
chr14	107349540	3833576	0.0357	0.2104
chr15	102531392	2834715	0.0276	0.1797
chr16	90354753	2789556	0.0309	0.219
chr17	81195210	1861708	0.0229	0.1717
chr18	78077248	2098799	0.0269	0.4463
chr19	59128983	1898639	0.0321	0.4293
chr20	63025520	2166765	0.0344	0.2036
chr21	48129895	1337551	0.0278	0.1939
chr22	51304566	1206284	0.0235	0.1664
chrMT	16571	84401	5.0933	3.3162
chrX	155270560	5760842	0.0371	0.2237
chrY	59373566	330014	0.0056	0.1575

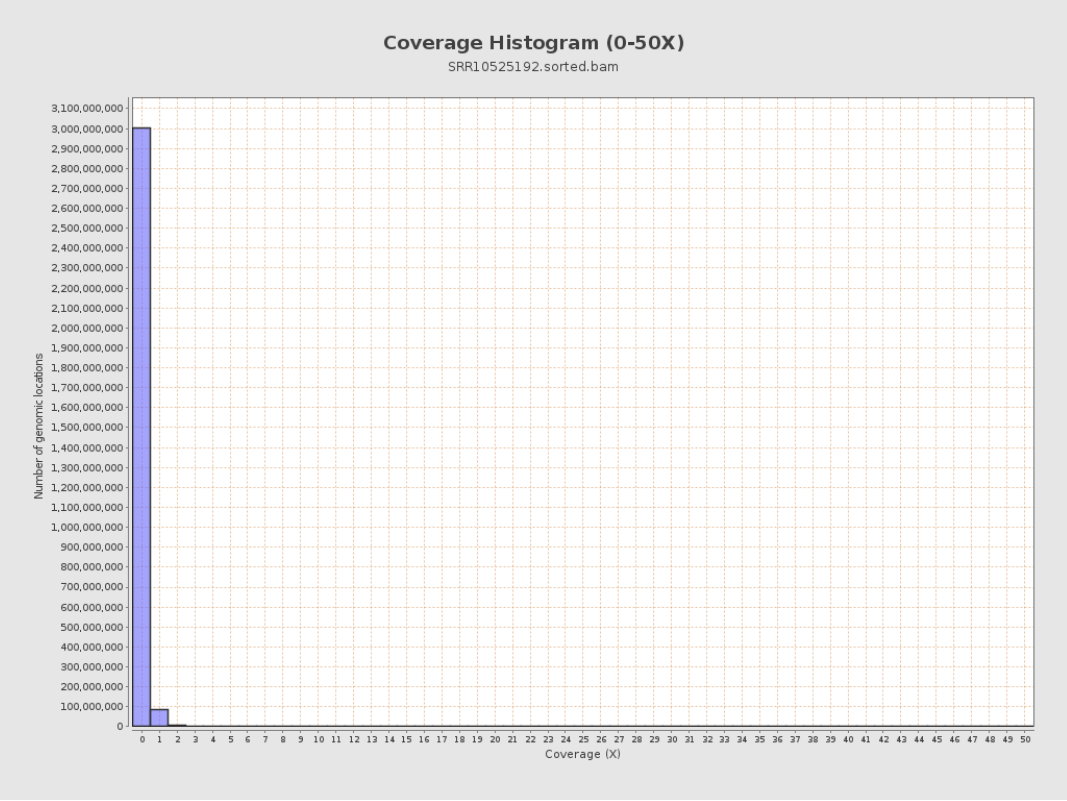
3. Results : Coverage across reference



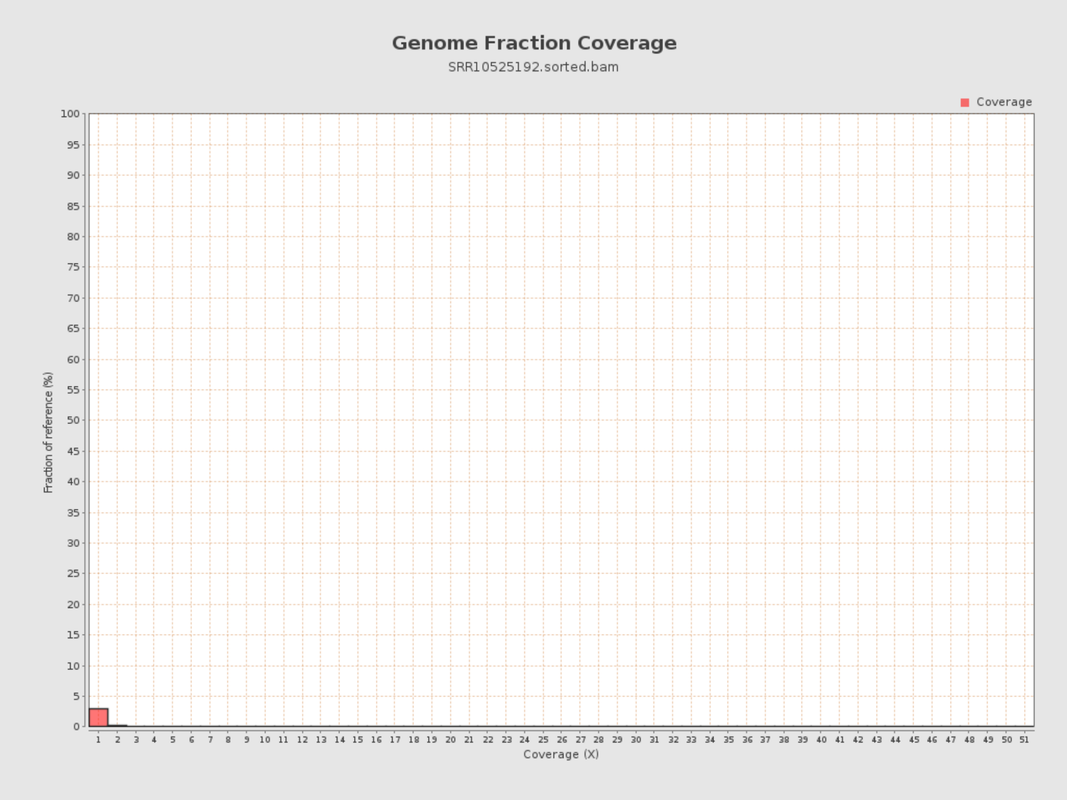
4. Results : Coverage Histogram



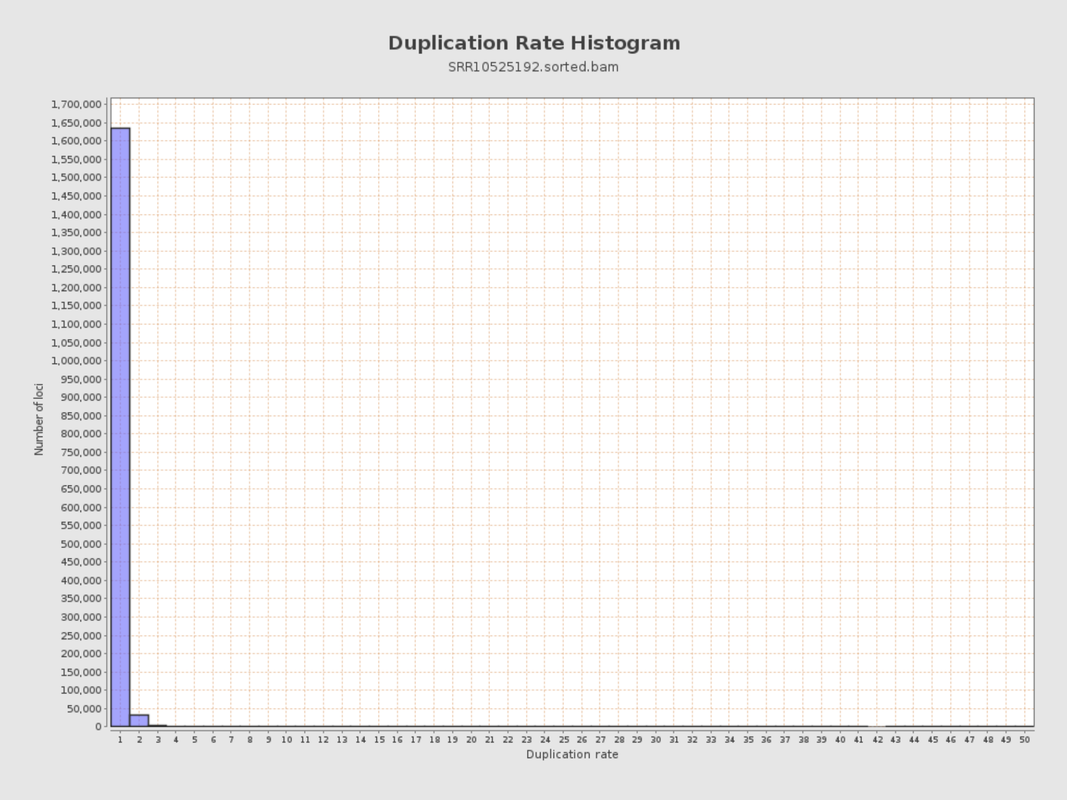
5. Results : Coverage Histogram (0-50X)



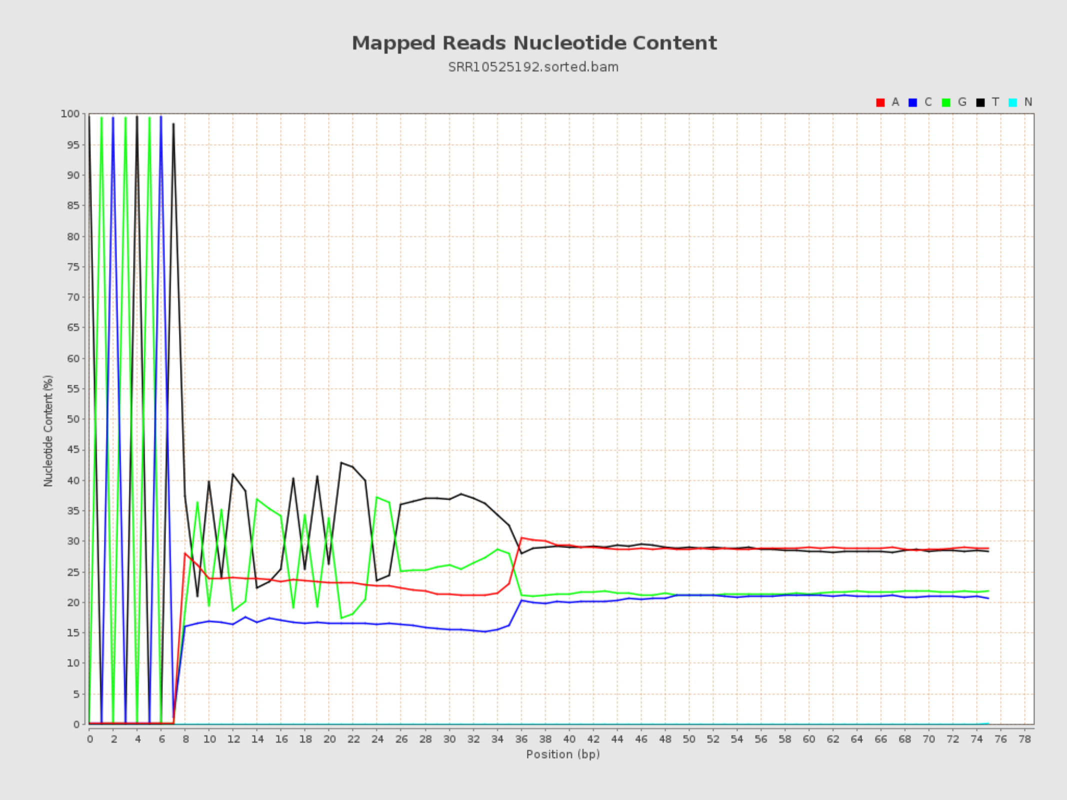
6. Results : Genome Fraction Coverage



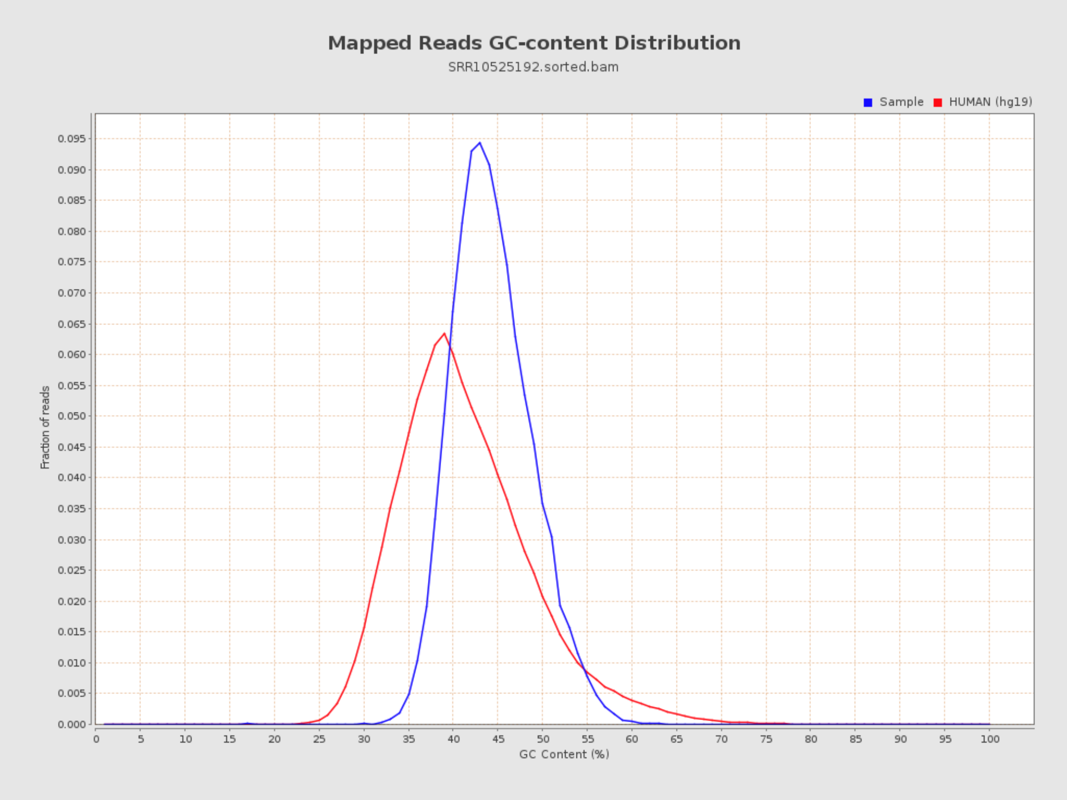
7. Results : Duplication Rate Histogram



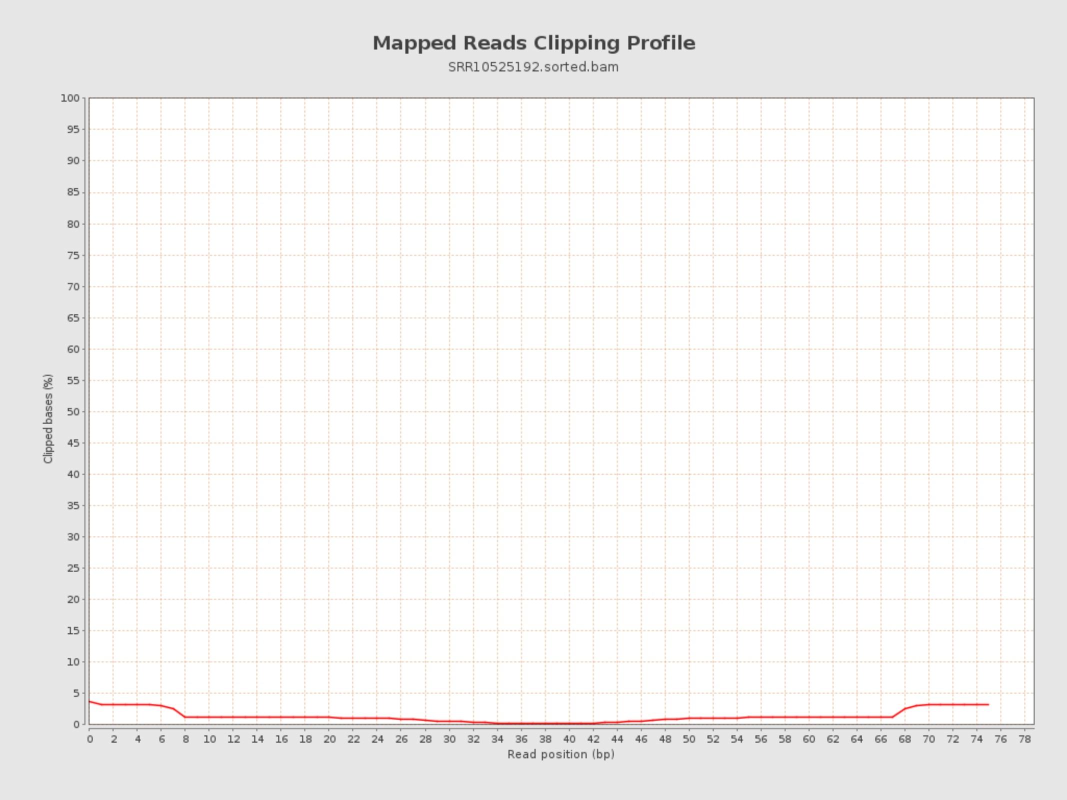
8. Results : Mapped Reads Nucleotide Content



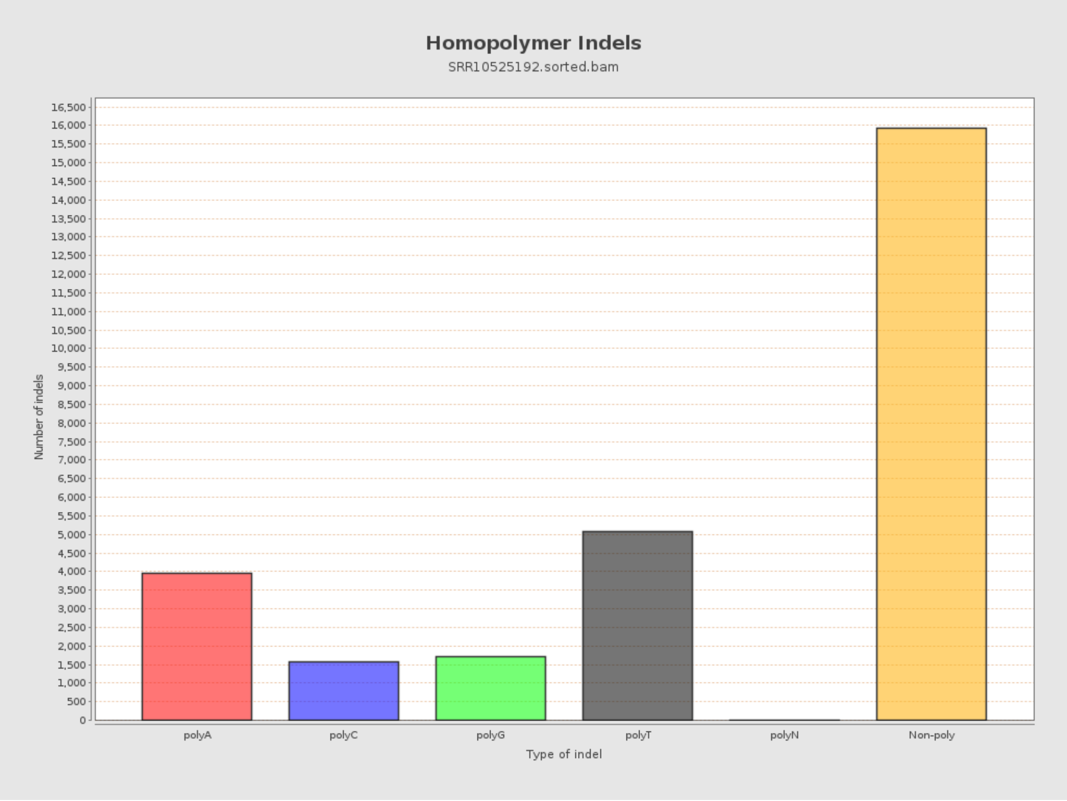
9. Results : Mapped Reads GC-content Distribution



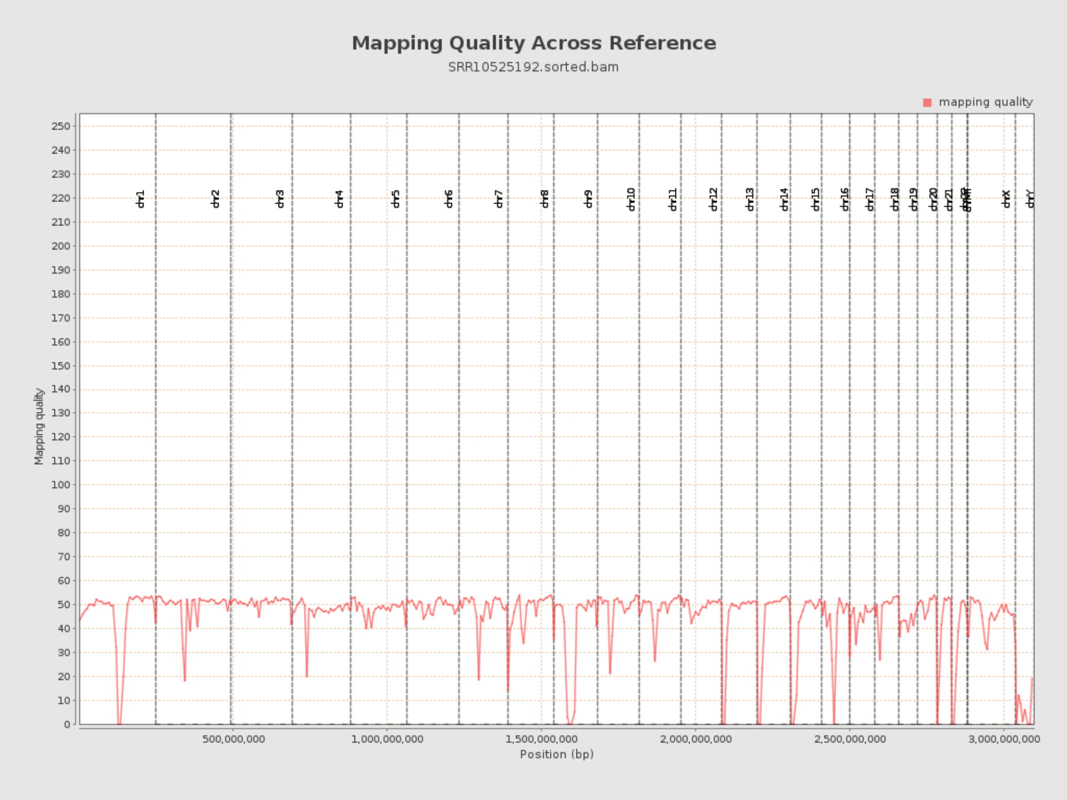
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram