Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:47:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525142.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_SRR10525142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:47:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	794,769
Mapped reads	706,870 / 88.94%
Unmapped reads	87,899 / 11.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,748 / 2.99%
Read min/max/mean length	30 / 101 / 102.11
Duplicated reads (estimated)	17,267 / 2.17%
Duplication rate	1.41%
Clipped reads	729,850 / 91.83%

2.2. ACGT Content

Number/percentage of A's	13,984,415 / 25.98%
Number/percentage of C's	10,558,513 / 19.61%
Number/percentage of T's	16,444,153 / 30.55%
Number/percentage of G's	12,842,948 / 23.86%
Number/percentage of N's	2,210 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.2237

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

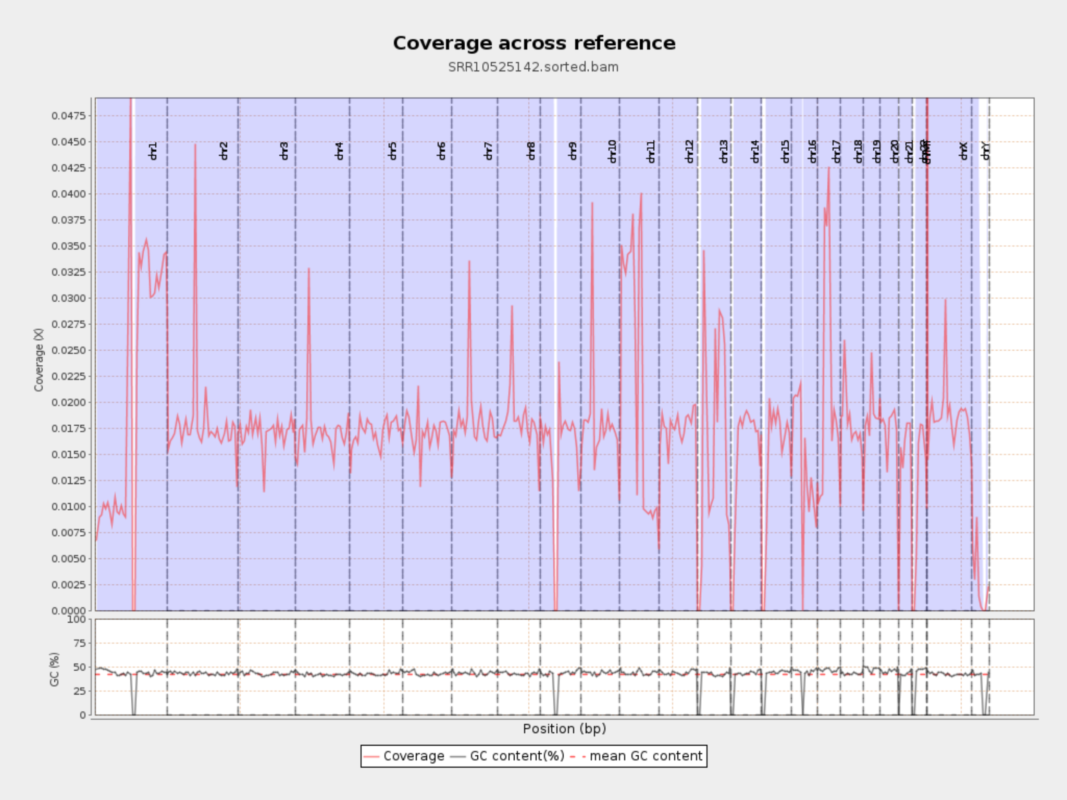
General error rate	0.79%
Mismatches	416,143
Insertions	5,086
Mapped reads with at least one insertion	0.71%
Deletions	11,705
Mapped reads with at least one deletion	1.63%
Homopolymer indels	41.55%

2.6. Chromosome stats

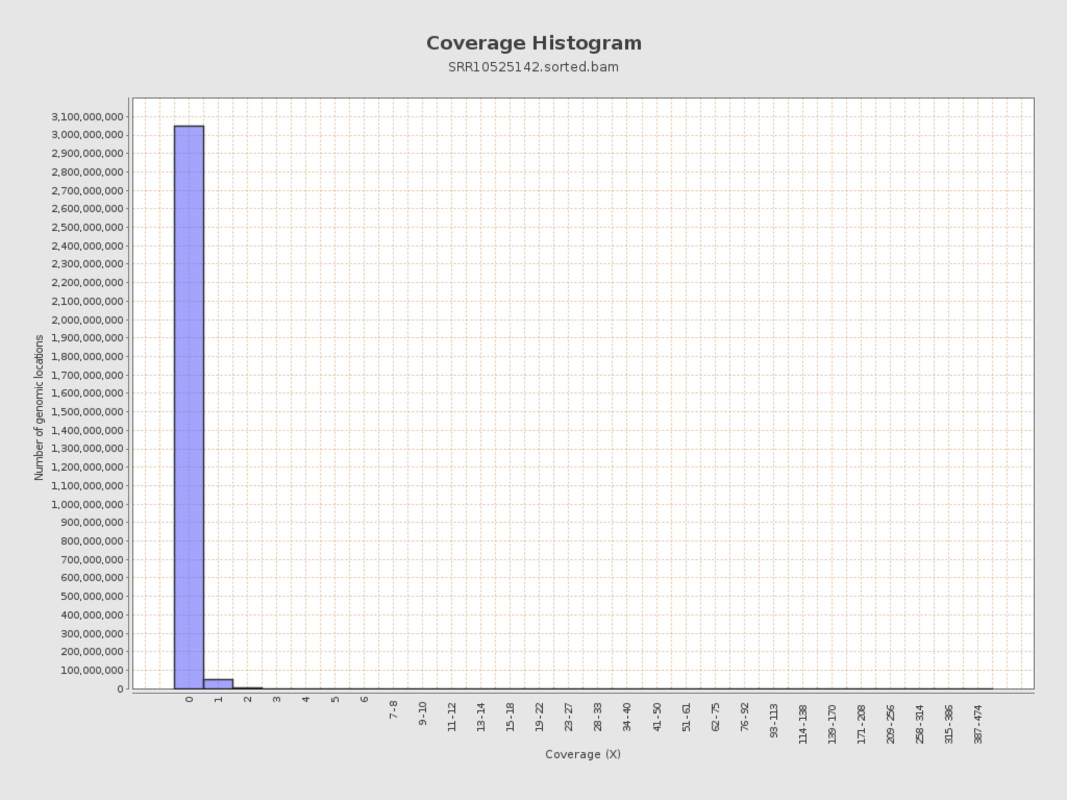
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5138308	0.0206	0.4147
chr2	243199373	4379874	0.018	0.2834
chr3	198022430	3389905	0.0171	0.1382
chr4	191154276	3341719	0.0175	0.1539
chr5	180915260	3122636	0.0173	0.1388
chr6	171115067	2923997	0.0171	0.1504
chr7	159138663	2932261	0.0184	0.2677

chr8	146364022	2686190	0.0184	0.2686
chr9	141213431	2143463	0.0152	0.1934
chr10	135534747	2478251	0.0183	0.2386
chr11	135006516	3070430	0.0227	0.2502
chr12	133851895	2356310	0.0176	0.1386
chr13	115169878	1819856	0.0158	0.1311
chr14	107349540	1590123	0.0148	0.1406
chr15	102531392	1489523	0.0145	0.125
chr16	90354753	1252449	0.0139	0.1359
chr17	81195210	1750454	0.0216	0.1757
chr18	78077248	1417357	0.0182	0.3274
chr19	59128983	1106422	0.0187	0.2852
chr20	63025520	1081937	0.0172	0.1409
chr21	48129895	697093	0.0145	0.1347
chr22	51304566	573763	0.0112	0.1097
chrMT	16571	12609	0.7609	0.9509
chrX	155270560	2943204	0.019	0.173
chrY	59373566	155201	0.0026	0.0805

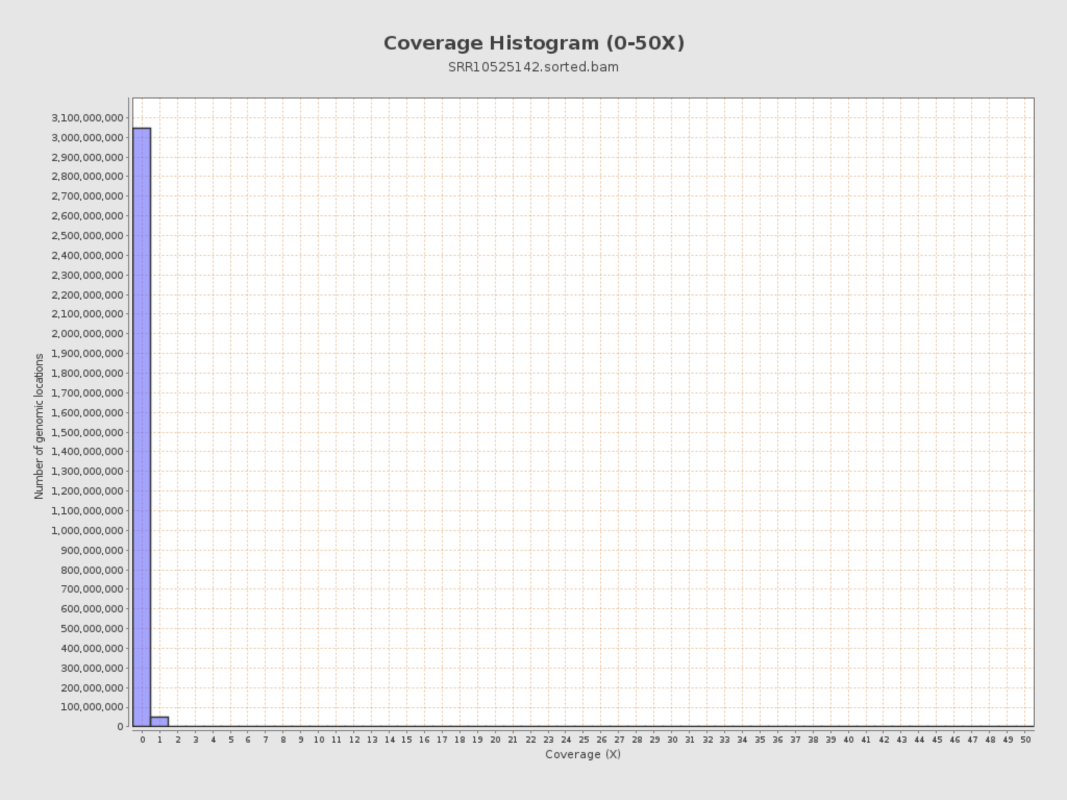
3. Results : Coverage across reference



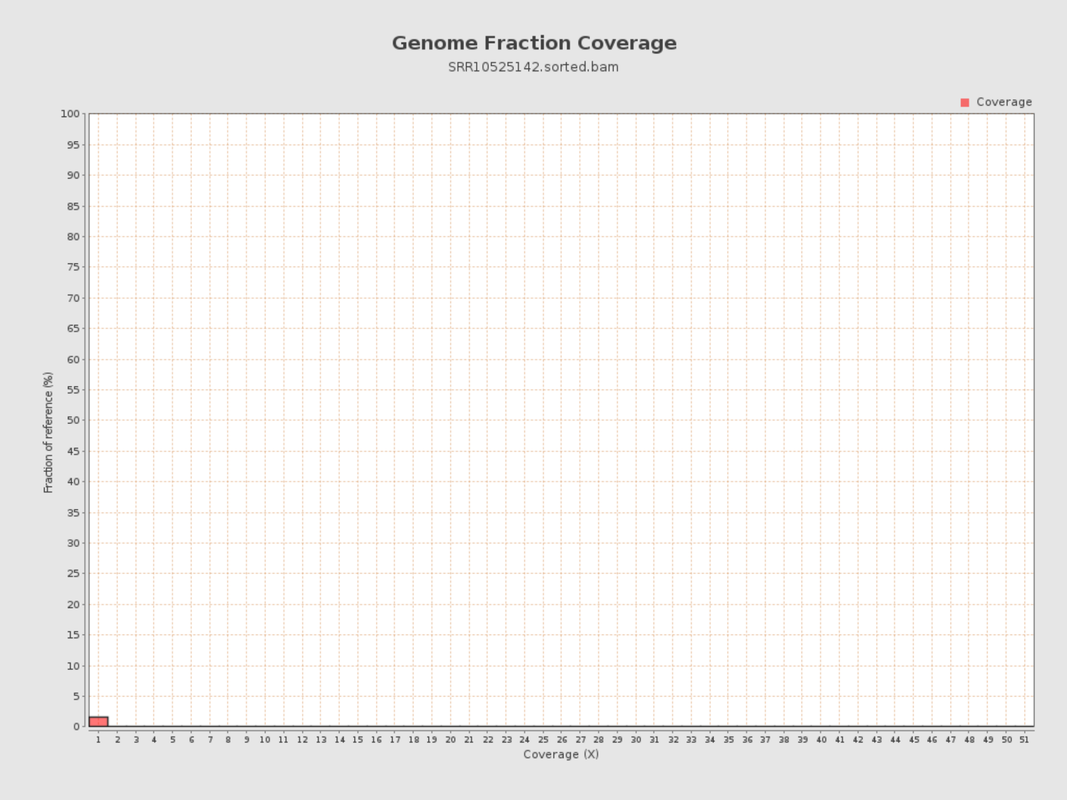
4. Results : Coverage Histogram



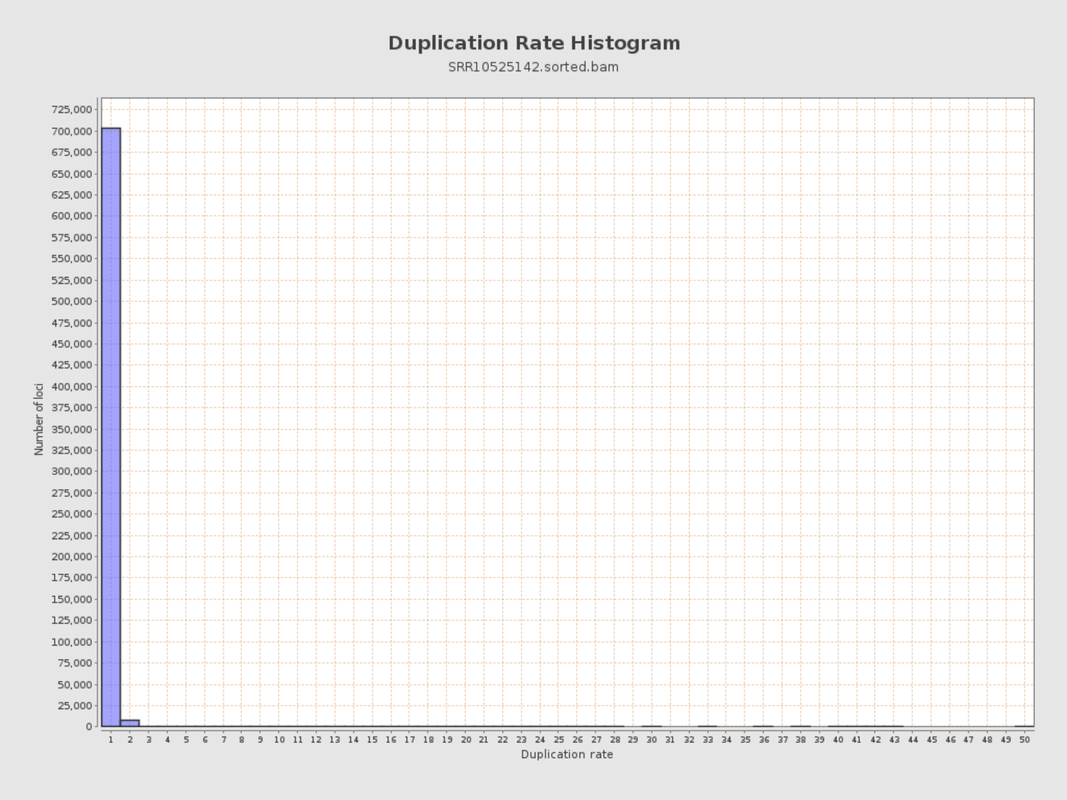
5. Results : Coverage Histogram (0-50X)



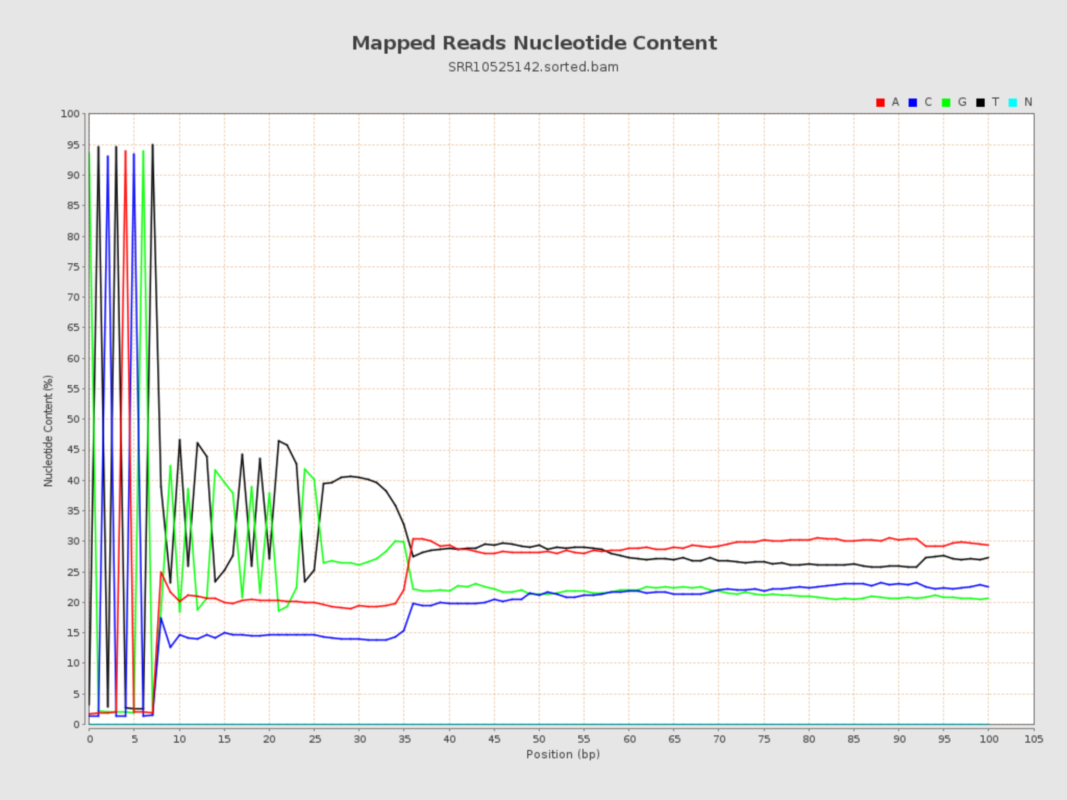
6. Results : Genome Fraction Coverage



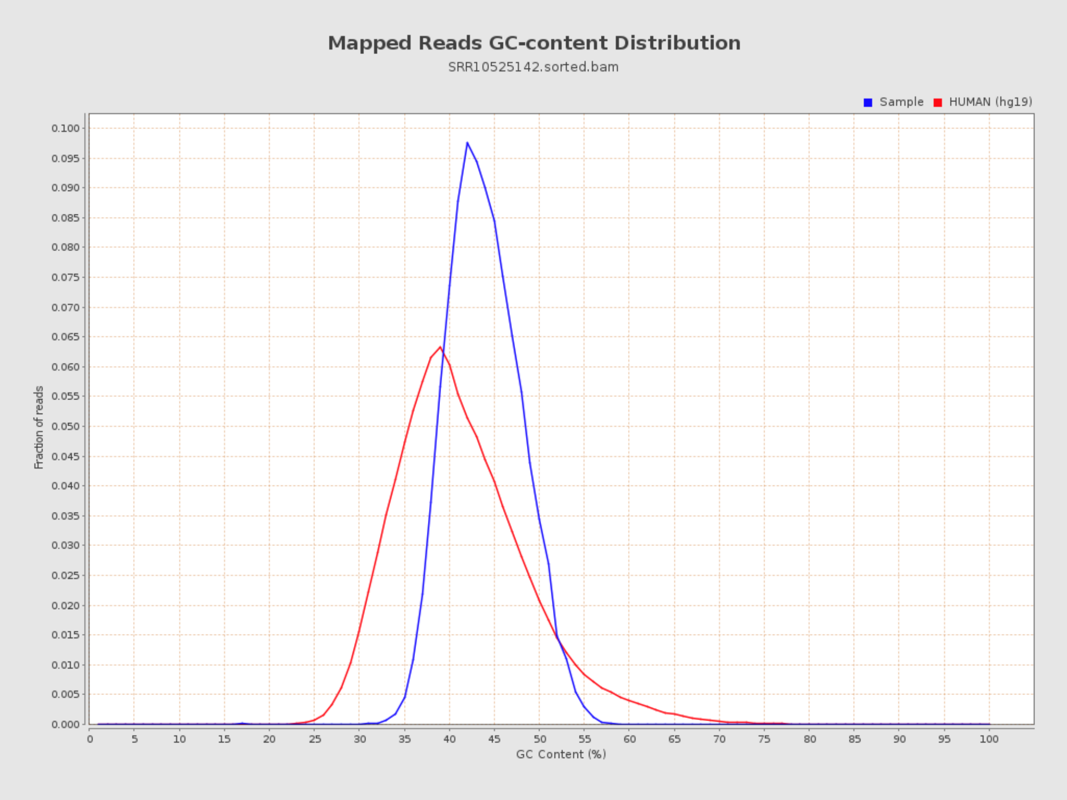
7. Results : Duplication Rate Histogram



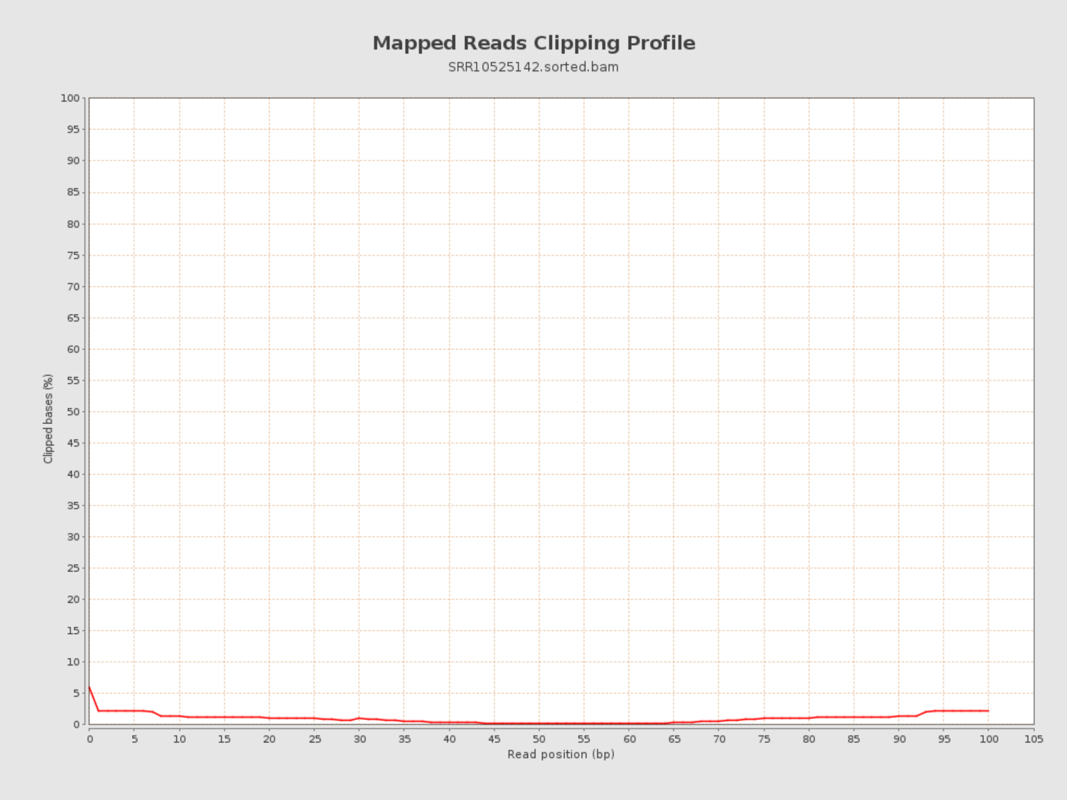
8. Results : Mapped Reads Nucleotide Content



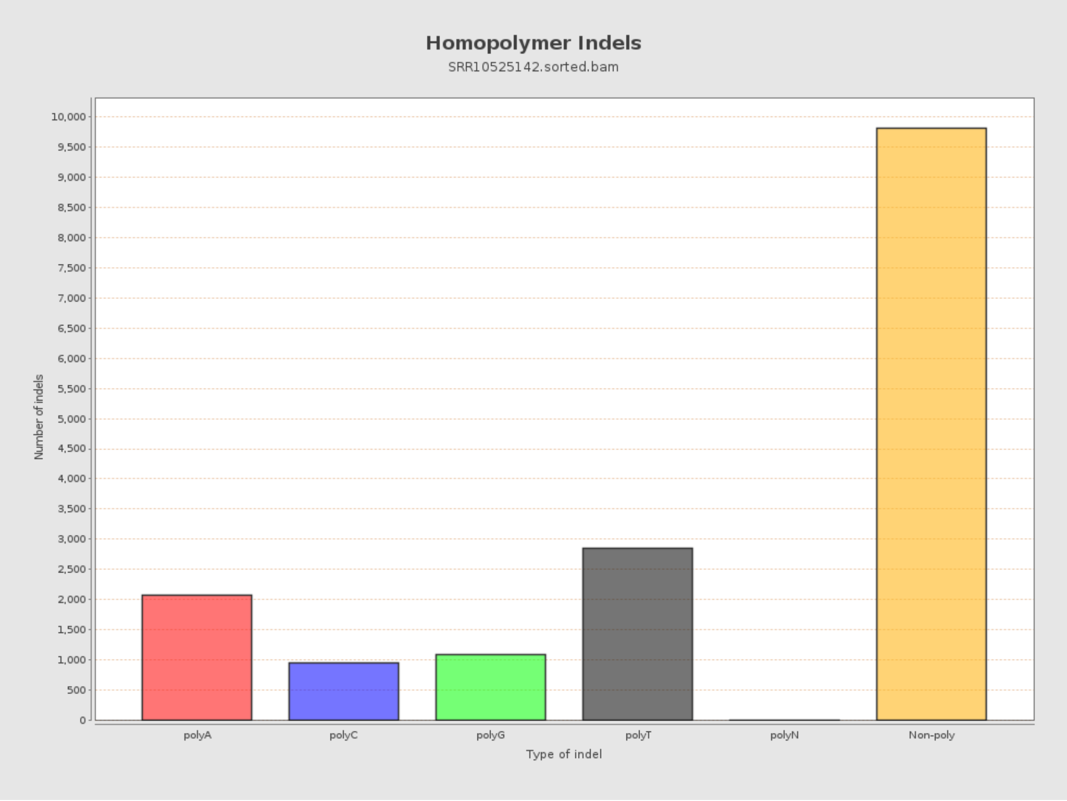
9. Results : Mapped Reads GC-content Distribution



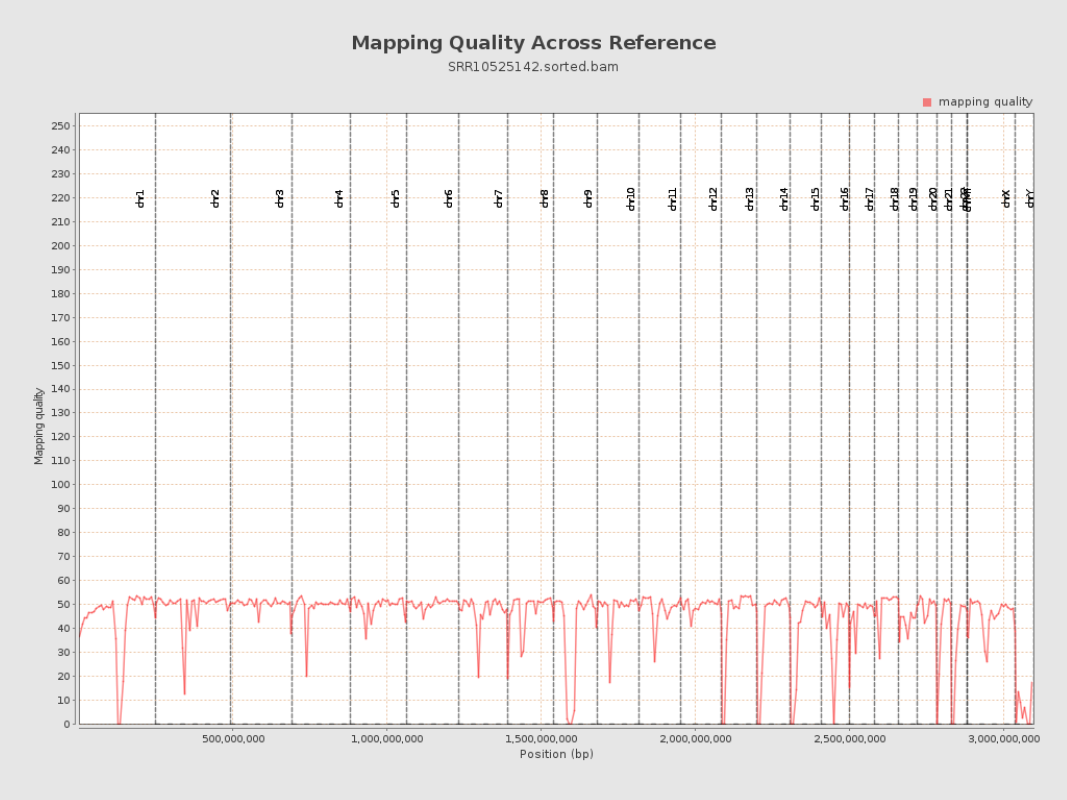
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram