Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:32:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525113.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_SRR10525113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:32:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	688,596
Mapped reads	612,500 / 88.95%
Unmapped reads	76,096 / 11.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,886 / 2.6%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	12,534 / 1.82%
Duplication rate	1.22%
Clipped reads	629,585 / 91.43%

2.2. ACGT Content

Number/percentage of A's	12,196,710 / 26.17%
Number/percentage of C's	9,009,494 / 19.33%
Number/percentage of T's	14,395,924 / 30.89%
Number/percentage of G's	10,997,969 / 23.6%
Number/percentage of N's	1,616 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1831

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

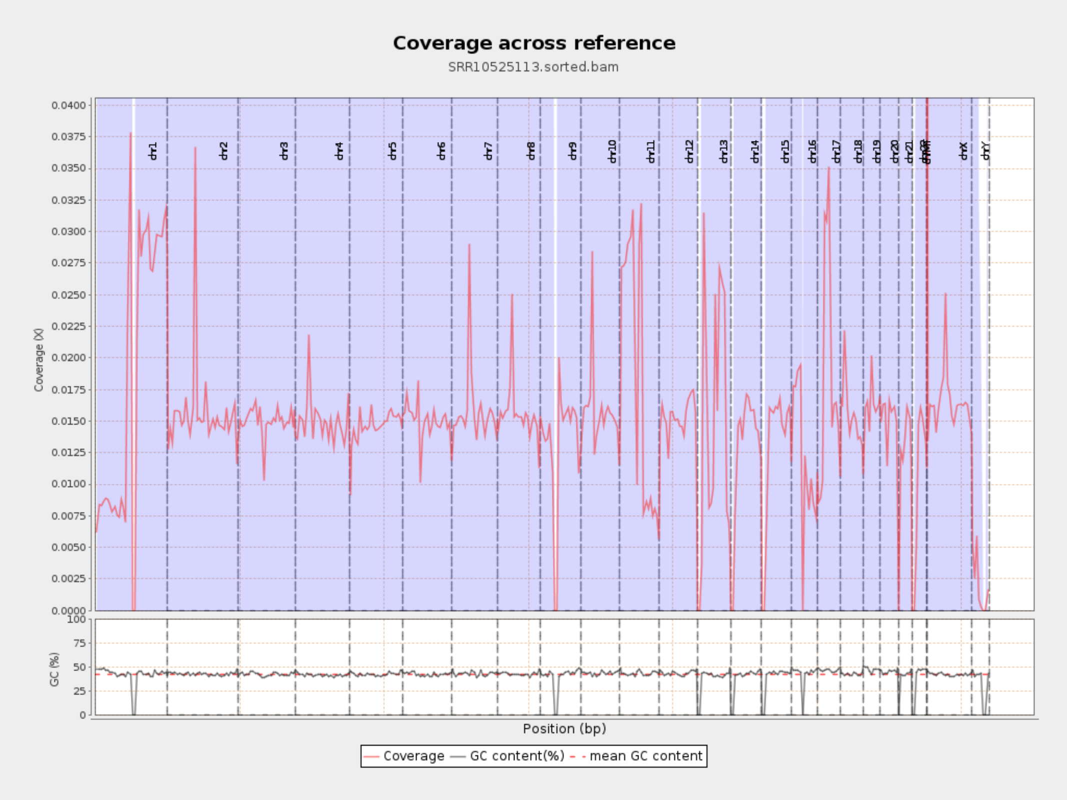
General error rate	0.77%
Mismatches	352,965
Insertions	4,116
Mapped reads with at least one insertion	0.66%
Deletions	10,761
Mapped reads with at least one deletion	1.74%
Homopolymer indels	42.91%

2.6. Chromosome stats

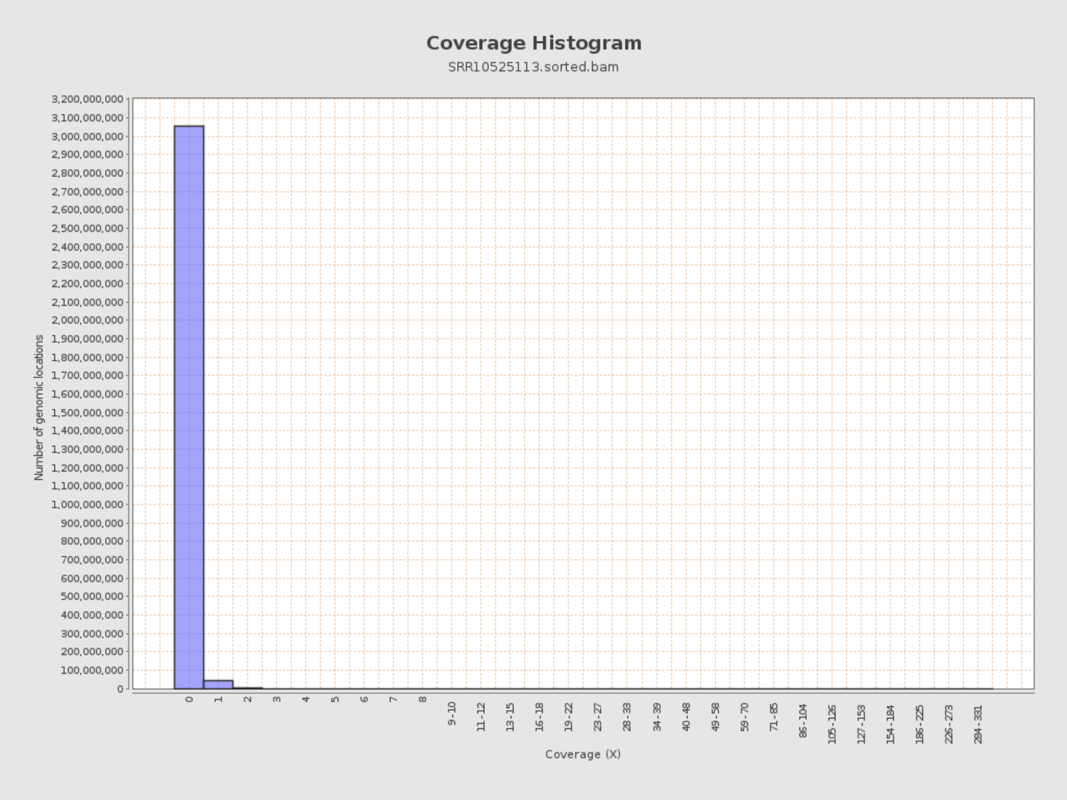
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4534199	0.0182	0.295
chr2	243199373	3817762	0.0157	0.2411
chr3	198022430	2963186	0.015	0.1273
chr4	191154276	2867937	0.015	0.1332
chr5	180915260	2670020	0.0148	0.1276
chr6	171115067	2567170	0.015	0.1361
chr7	159138663	2521119	0.0158	0.2345

chr8	146364022	2290004	0.0156	0.2086
chr9	141213431	1866716	0.0132	0.1675
chr10	135534747	2151512	0.0159	0.1874
chr11	135006516	2526796	0.0187	0.1984
chr12	133851895	2037274	0.0152	0.1289
chr13	115169878	1656141	0.0144	0.125
chr14	107349540	1356836	0.0126	0.1297
chr15	102531392	1307491	0.0128	0.1176
chr16	90354753	1070328	0.0118	0.1191
chr17	81195210	1487550	0.0183	0.1562
chr18	78077248	1217928	0.0156	0.2694
chr19	59128983	959403	0.0162	0.2439
chr20	63025520	942693	0.015	0.1323
chr21	48129895	594751	0.0124	0.1212
chr22	51304566	521368	0.0102	0.1042
chrMT	16571	5215	0.3147	0.646
chrX	155270560	2572292	0.0166	0.1566
chrY	59373566	114681	0.0019	0.0616

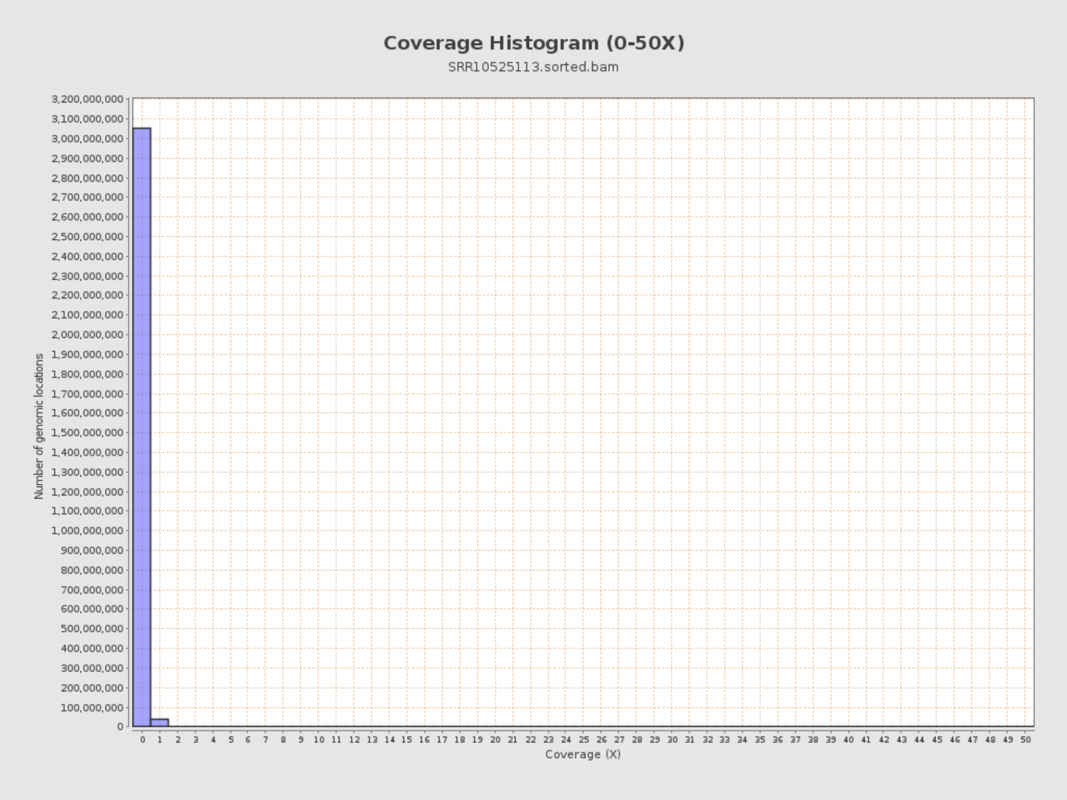
3. Results : Coverage across reference



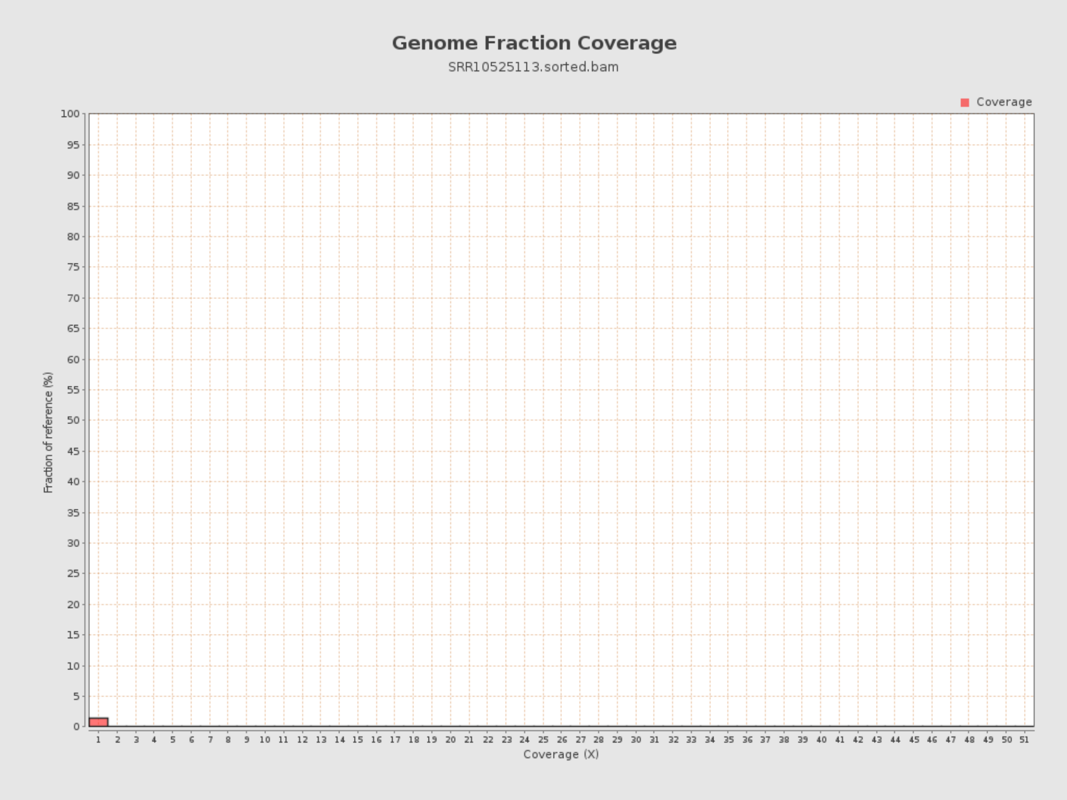
4. Results : Coverage Histogram



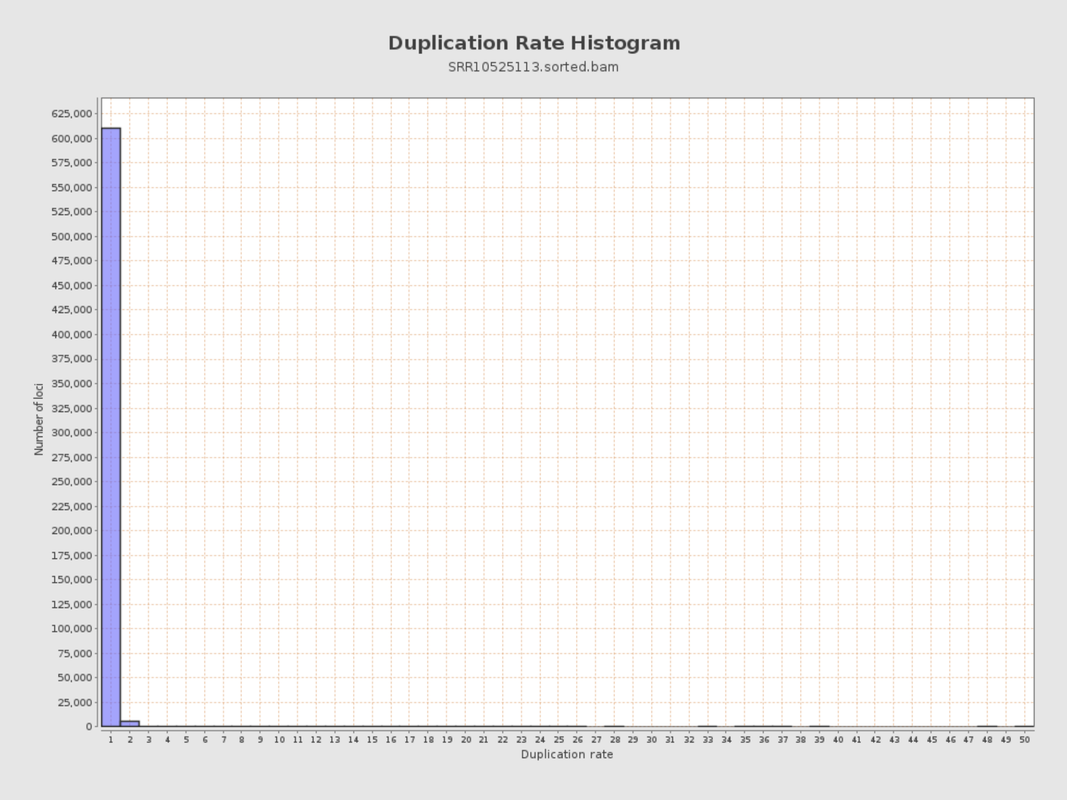
5. Results : Coverage Histogram (0-50X)



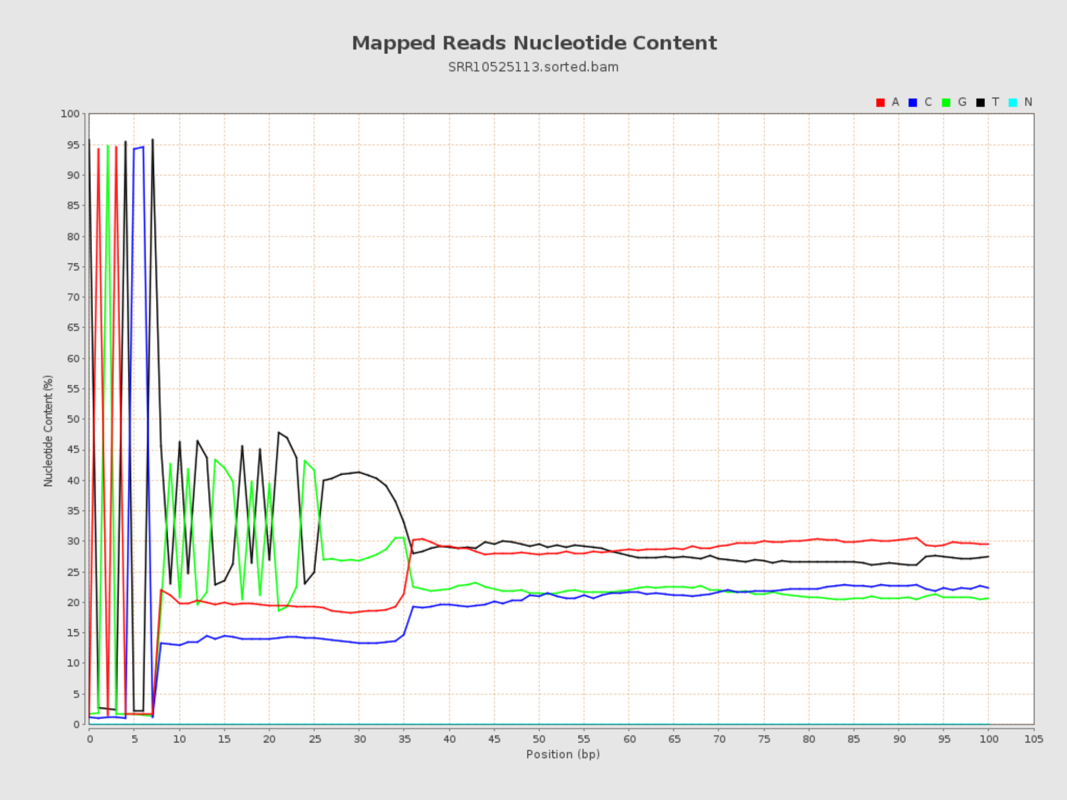
6. Results : Genome Fraction Coverage



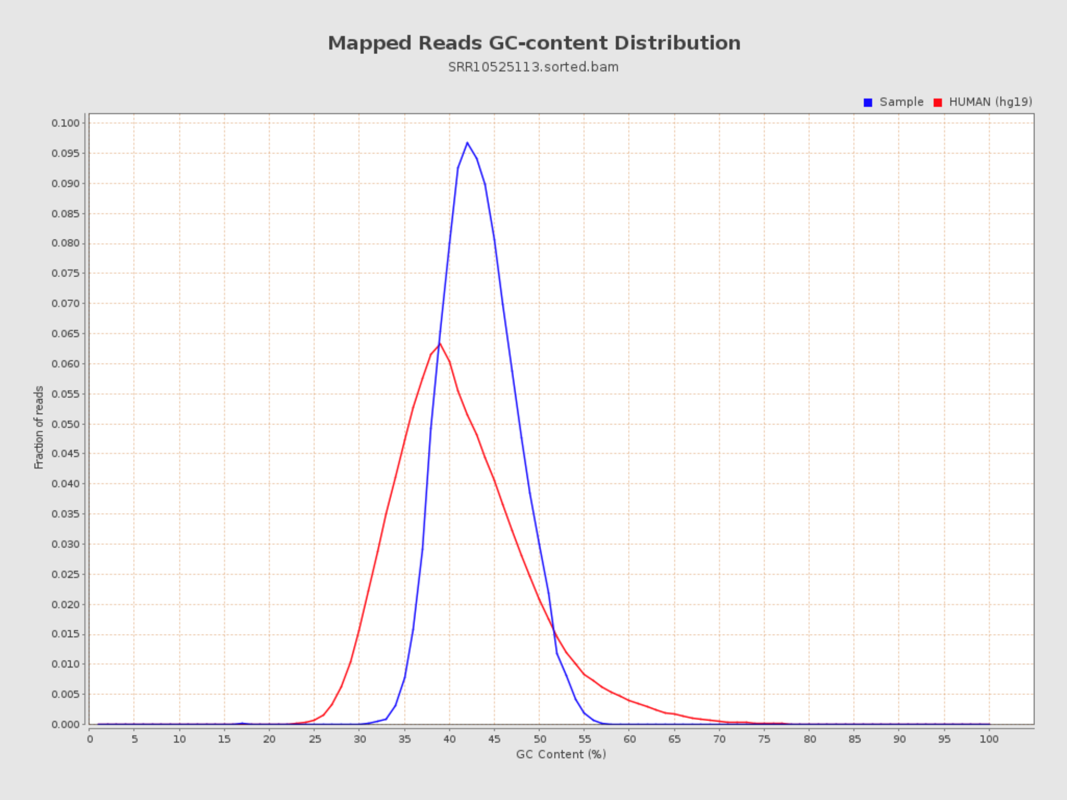
7. Results : Duplication Rate Histogram



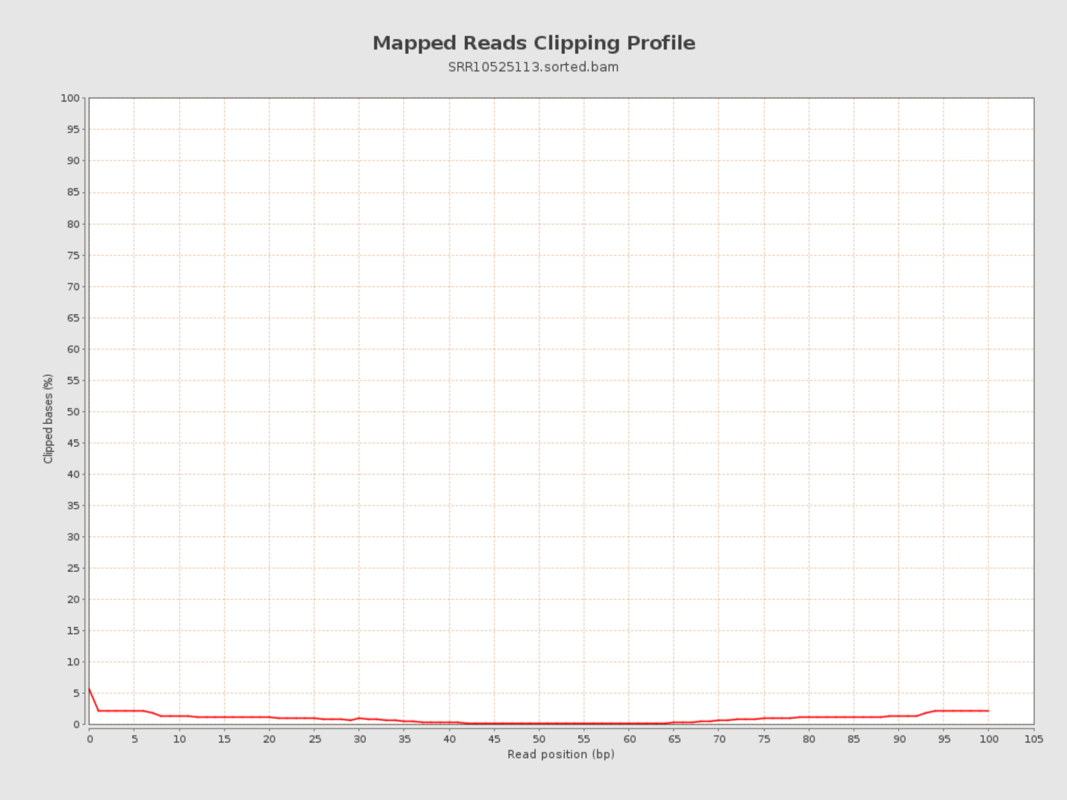
8. Results : Mapped Reads Nucleotide Content



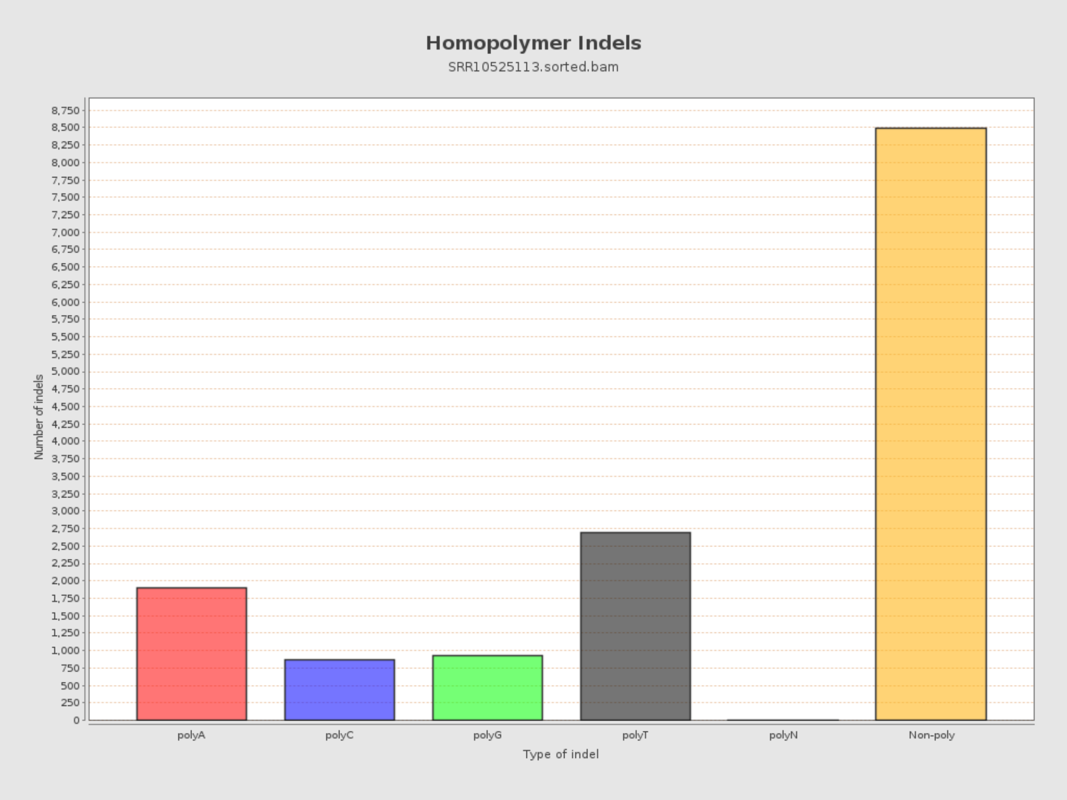
9. Results : Mapped Reads GC-content Distribution



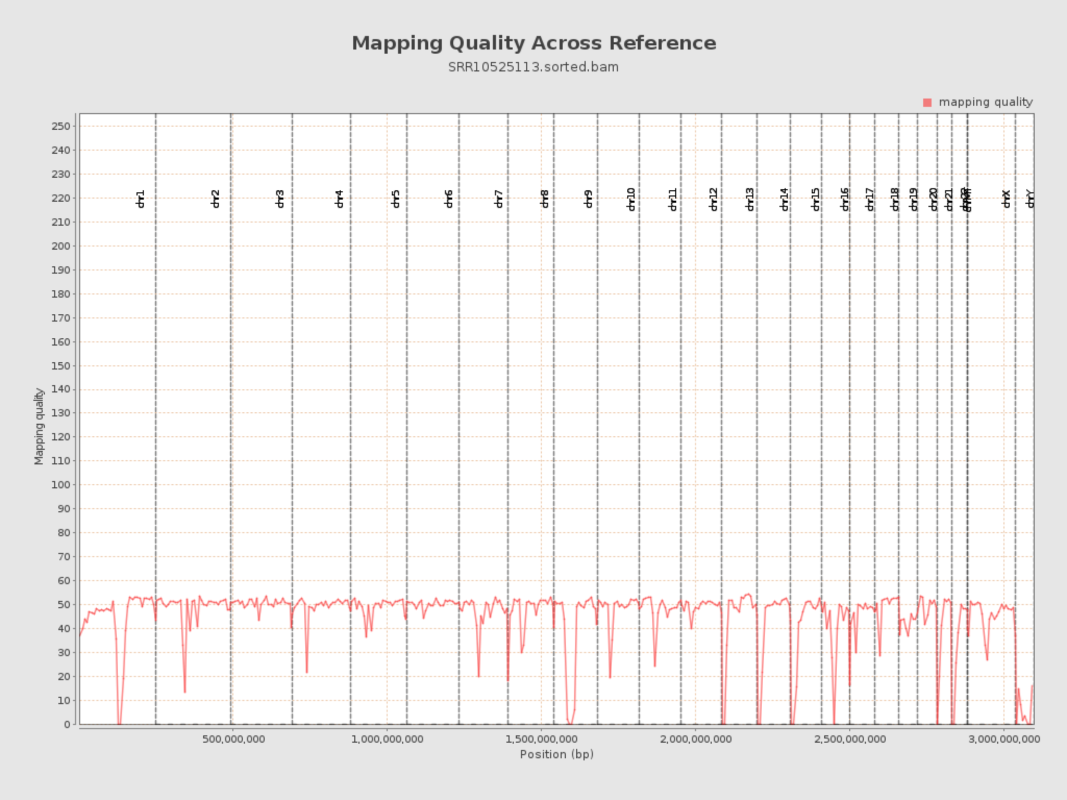
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram