Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525111.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_SRR10525111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:27:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,080,209
Mapped reads	1,876,714 / 90.22%
Unmapped reads	203,495 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,054 / 2.84%
Read min/max/mean length	30 / 101 / 102.05
Duplicated reads (estimated)	63,529 / 3.05%
Duplication rate	1.97%
Clipped reads	1,934,309 / 92.99%

2.2. ACGT Content

Number/percentage of A's	37,224,290 / 25.82%
Number/percentage of C's	28,174,641 / 19.54%
Number/percentage of T's	44,327,209 / 30.75%
Number/percentage of G's	34,432,377 / 23.88%
Number/percentage of N's	5,775 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.4835

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

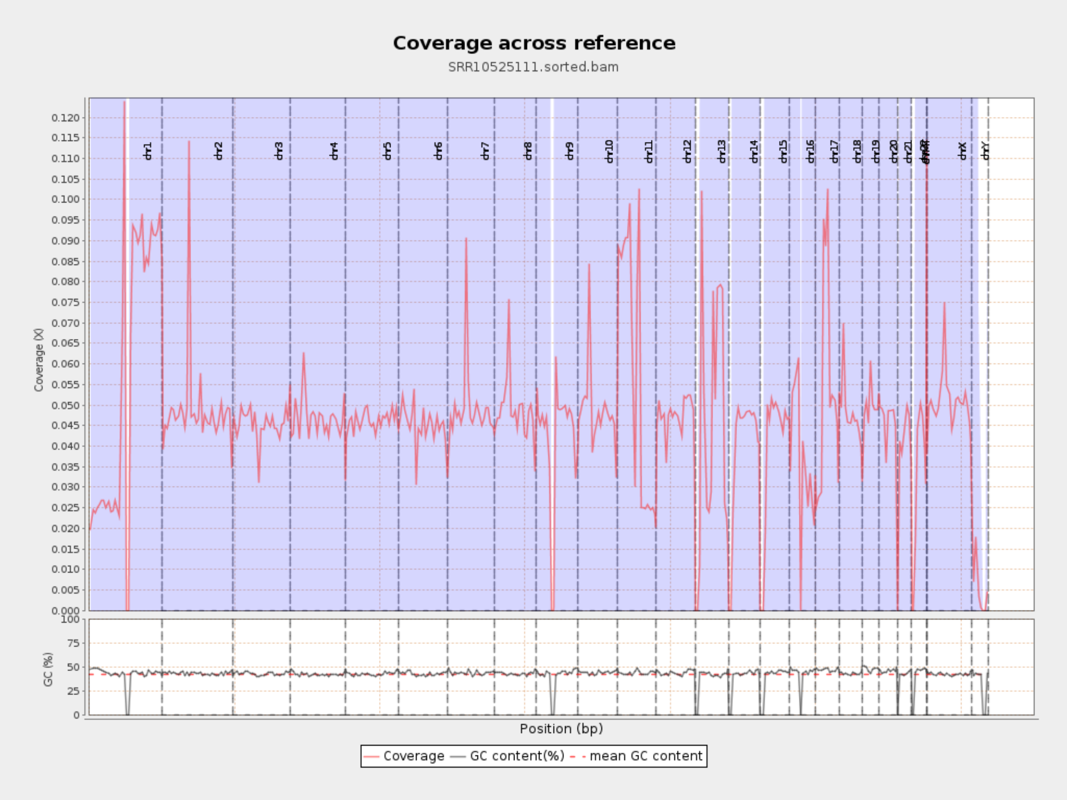
General error rate	0.77%
Mismatches	1,093,862
Insertions	11,881
Mapped reads with at least one insertion	0.62%
Deletions	34,468
Mapped reads with at least one deletion	1.81%
Homopolymer indels	42.67%

2.6. Chromosome stats

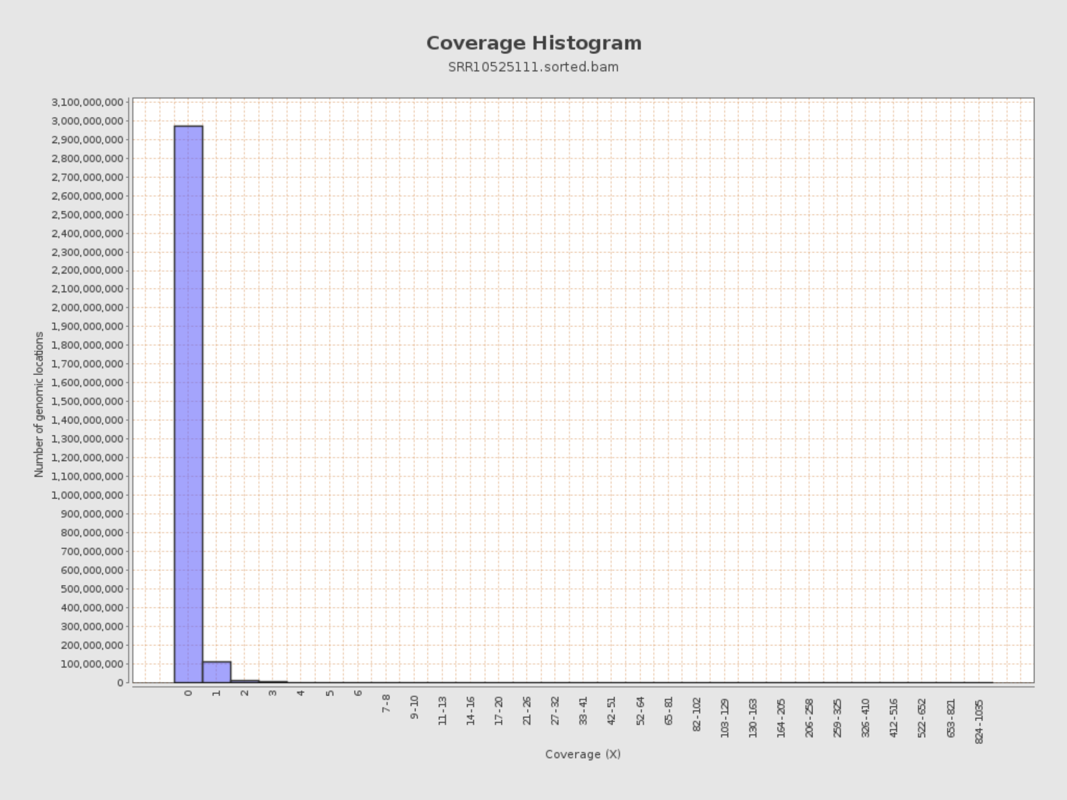
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13980332	0.0561	0.8926
chr2	243199373	11912281	0.049	0.6645
chr3	198022430	8992987	0.0454	0.238
chr4	191154276	8951202	0.0468	0.2595
chr5	180915260	8373311	0.0463	0.2438
chr6	171115067	7729090	0.0452	0.2678
chr7	159138663	7875073	0.0495	0.6716

chr8	146364022	7131874	0.0487	0.6029
chr9	141213431	5869983	0.0416	0.4297
chr10	135534747	6616131	0.0488	0.4598
chr11	135006516	7877758	0.0584	0.5727
chr12	133851895	6353701	0.0475	0.244
chr13	115169878	5128288	0.0445	0.2356
chr14	107349540	4220384	0.0393	0.265
chr15	102531392	4006947	0.0391	0.221
chr16	90354753	3329897	0.0369	0.254
chr17	81195210	4503818	0.0555	0.3353
chr18	78077248	3820237	0.0489	0.8069
chr19	59128983	2929680	0.0495	0.65
chr20	63025520	2862570	0.0454	0.2479
chr21	48129895	1879242	0.039	0.2409
chr22	51304566	1591831	0.031	0.1947
chrMT	16571	1898	0.1145	0.3606
chrX	155270560	7935830	0.0511	0.3495
chrY	59373566	350114	0.0059	0.1354

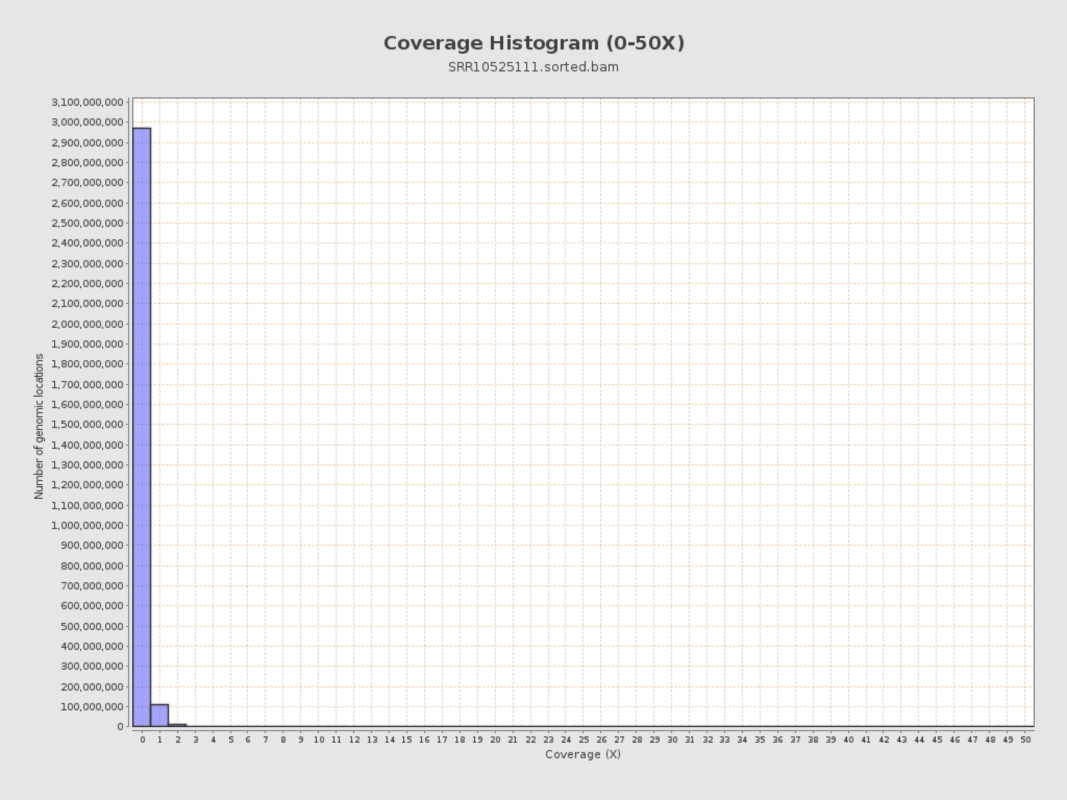
3. Results : Coverage across reference



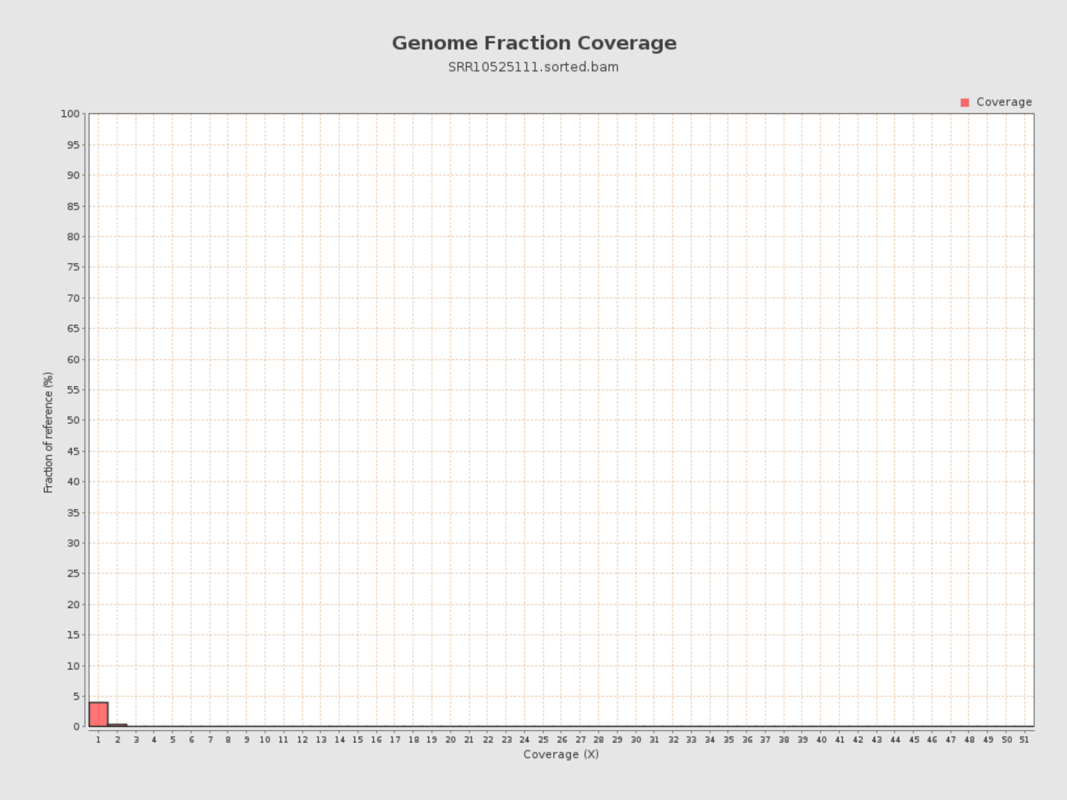
4. Results : Coverage Histogram



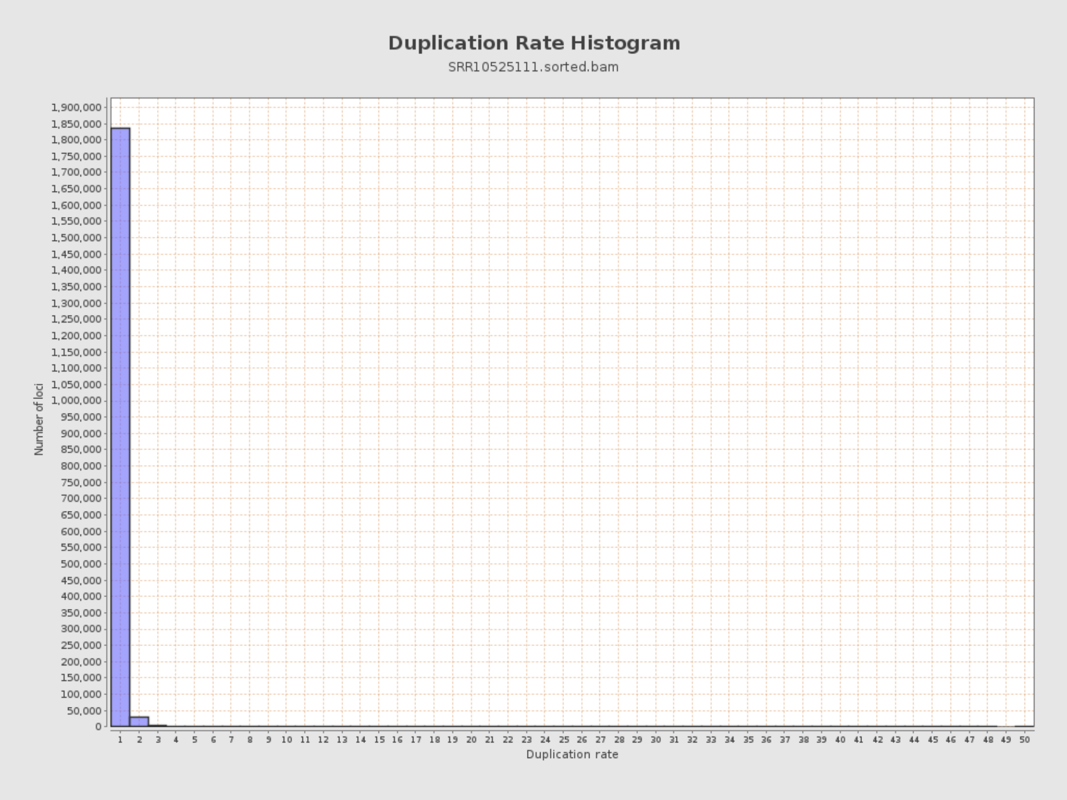
5. Results : Coverage Histogram (0-50X)



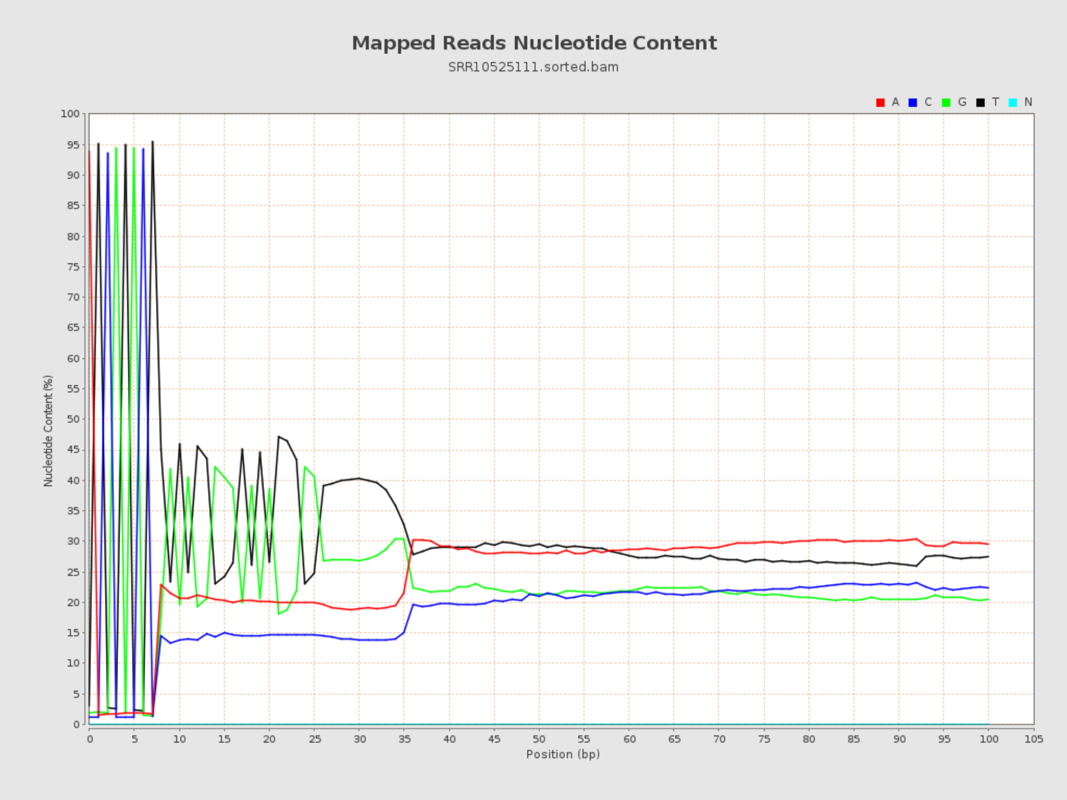
6. Results : Genome Fraction Coverage



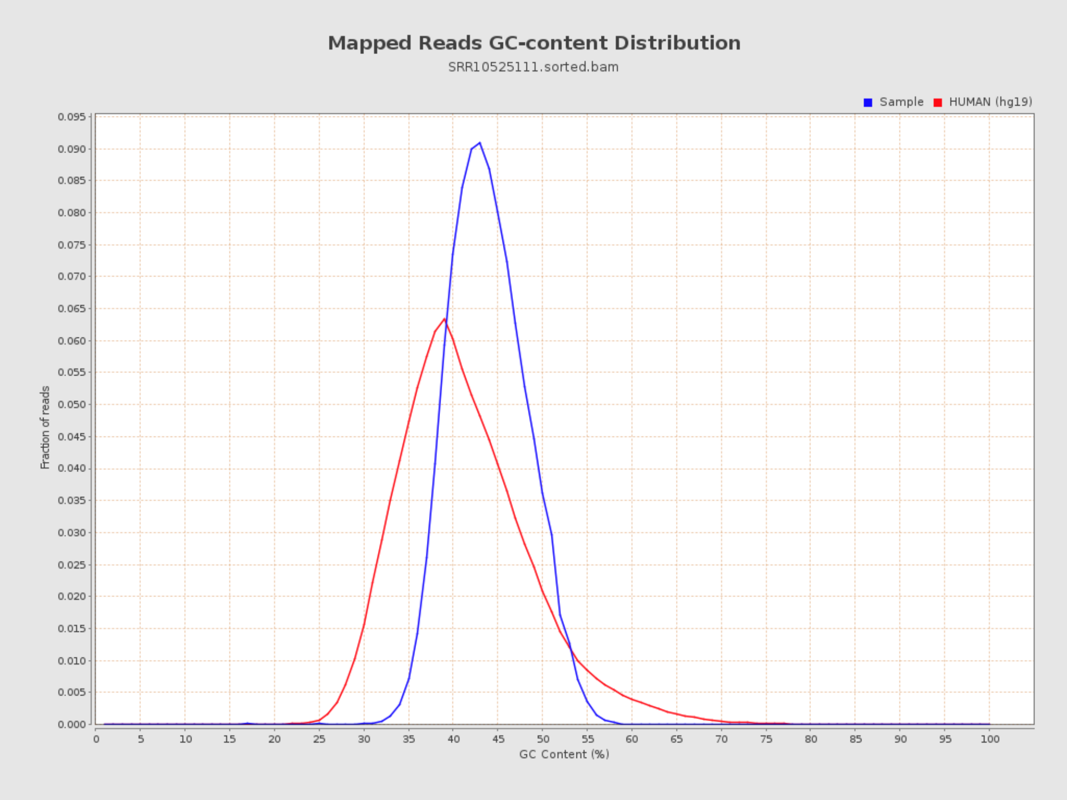
7. Results : Duplication Rate Histogram



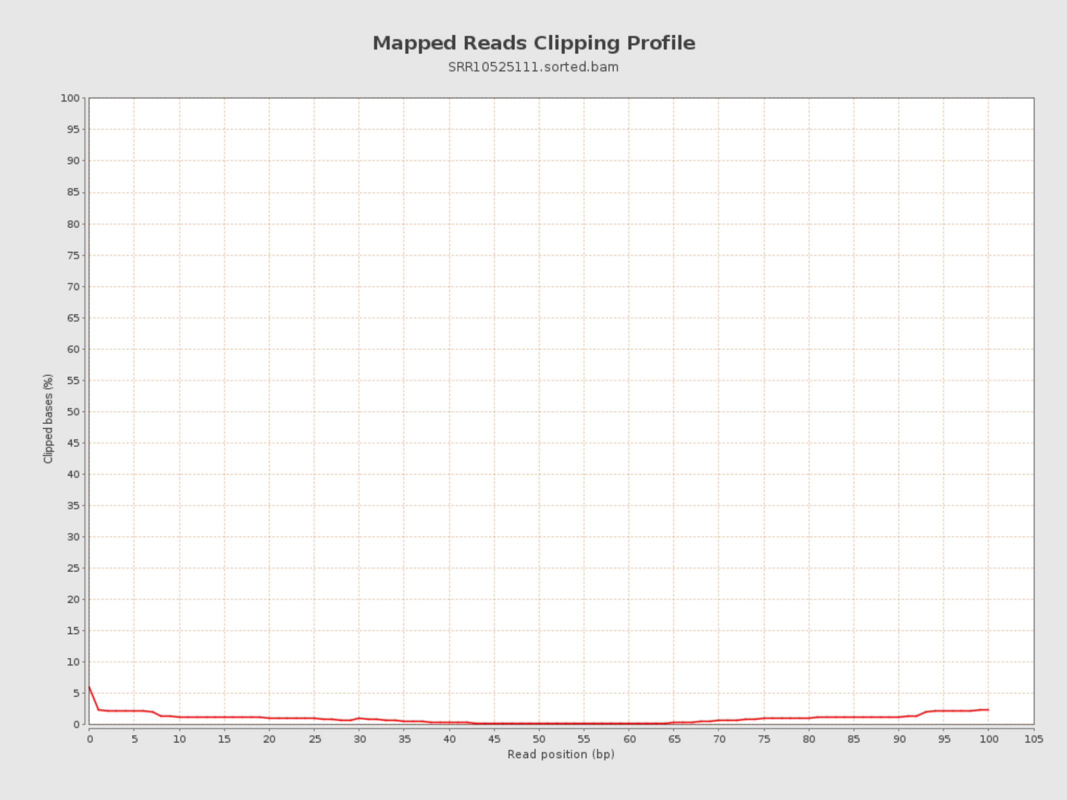
8. Results : Mapped Reads Nucleotide Content



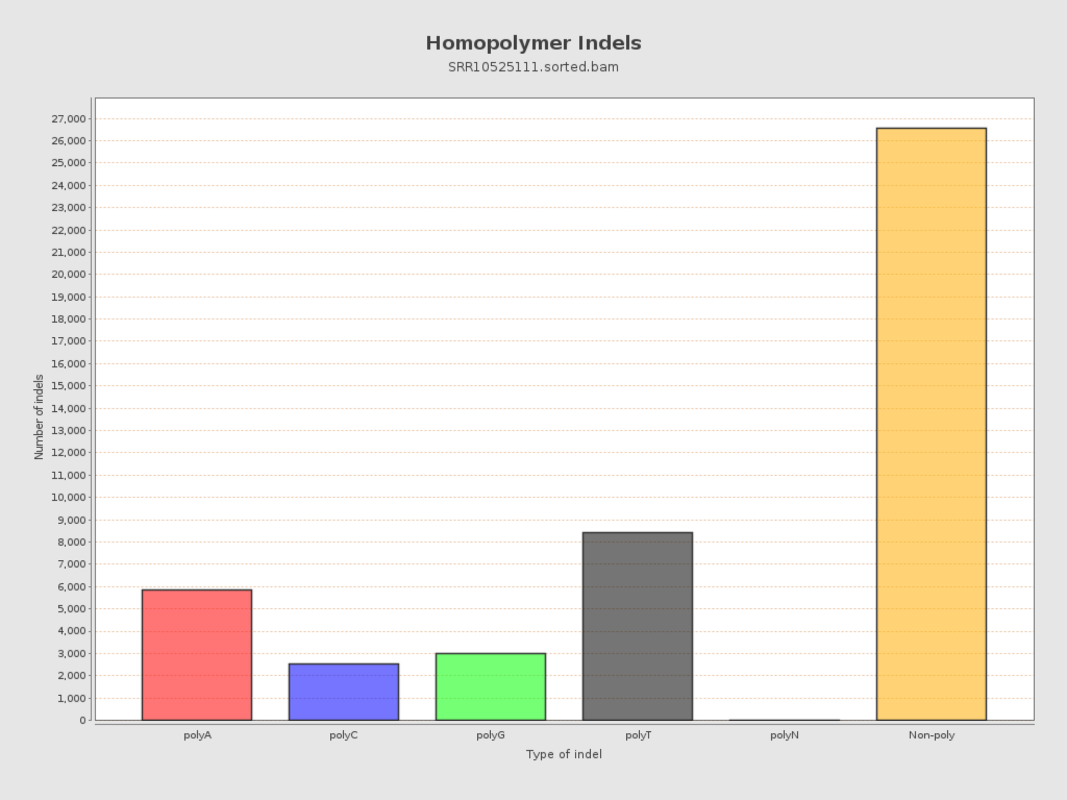
9. Results : Mapped Reads GC-content Distribution



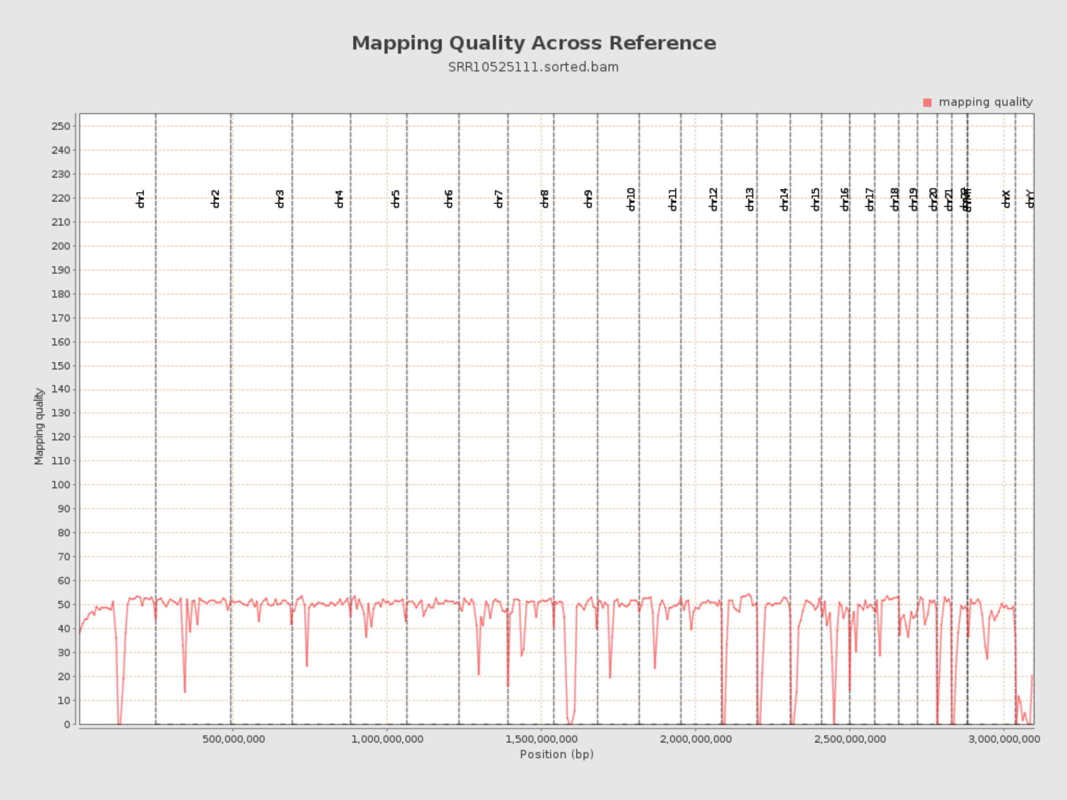
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram