Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:45:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525118.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_SRR10525118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:45:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,126,609
Mapped reads	1,031,786 / 91.58%
Unmapped reads	94,823 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,638 / 2.45%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	28,436 / 2.52%
Duplication rate	1.7%
Clipped reads	1,057,438 / 93.86%

2.2. ACGT Content

Number/percentage of A's	21,218,404 / 27.15%
Number/percentage of C's	15,933,303 / 20.39%
Number/percentage of T's	23,407,327 / 29.95%
Number/percentage of G's	17,583,277 / 22.5%
Number/percentage of N's	2,828 / 0%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2837

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

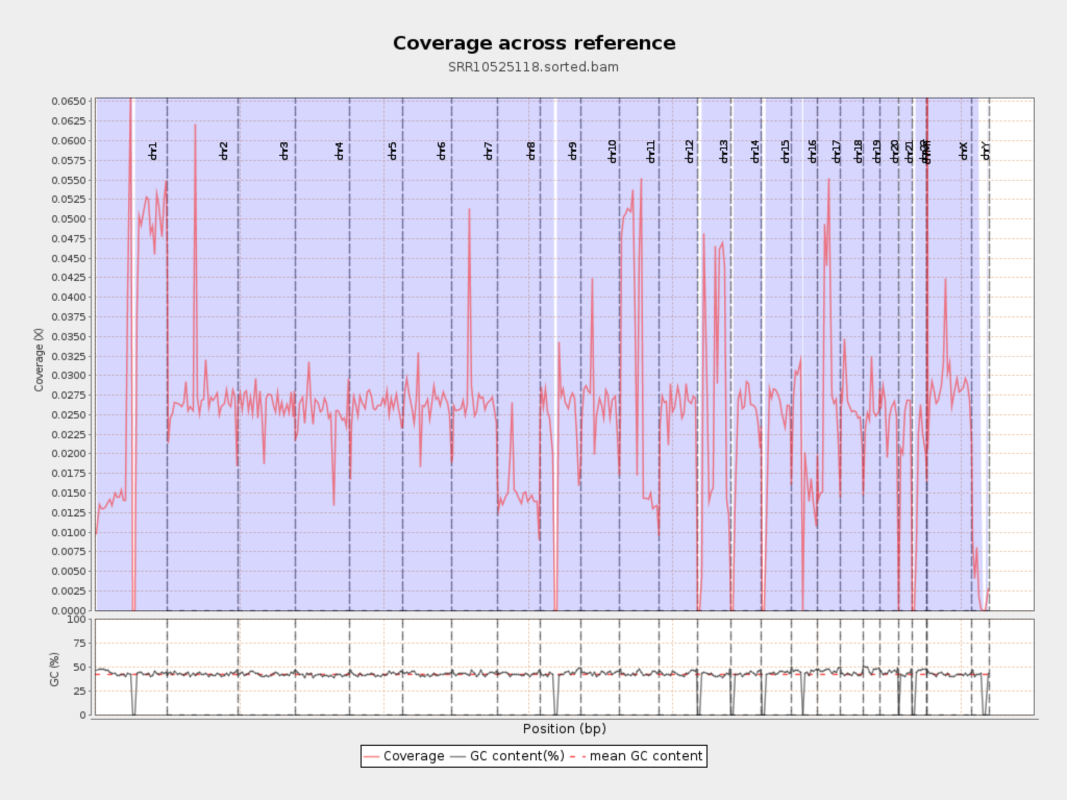
General error rate	0.73%
Mismatches	556,029
Insertions	7,126
Mapped reads with at least one insertion	0.68%
Deletions	17,408
Mapped reads with at least one deletion	1.67%
Homopolymer indels	41.39%

2.6. Chromosome stats

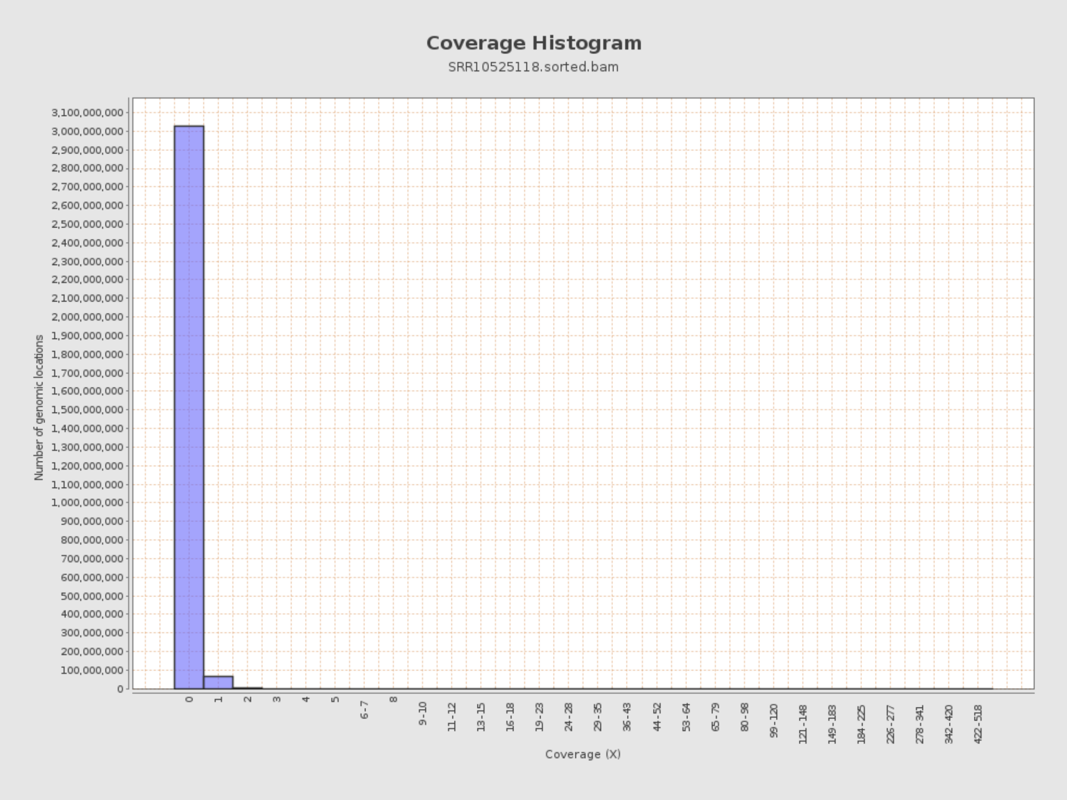
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7773441	0.0312	0.4739
chr2	243199373	6701713	0.0276	0.3827
chr3	198022430	5199153	0.0263	0.1735
chr4	191154276	4825731	0.0252	0.1755
chr5	180915260	4757984	0.0263	0.1772
chr6	171115067	4513229	0.0264	0.1932
chr7	159138663	4334612	0.0272	0.4088

chr8	146364022	2200479	0.015	0.3434
chr9	141213431	3261027	0.0231	0.2585
chr10	135534747	3617506	0.0267	0.2732
chr11	135006516	4394104	0.0325	0.3503
chr12	133851895	3504152	0.0262	0.1752
chr13	115169878	2838662	0.0246	0.1689
chr14	107349540	2361985	0.022	0.1768
chr15	102531392	2220672	0.0217	0.1574
chr16	90354753	1727670	0.0191	0.1606
chr17	81195210	2341127	0.0288	0.2124
chr18	78077248	2060666	0.0264	0.4194
chr19	59128983	1500873	0.0254	0.3598
chr20	63025520	1557072	0.0247	0.1699
chr21	48129895	1020182	0.0212	0.1651
chr22	51304566	806973	0.0157	0.1337
chrMT	16571	3298	0.199	0.5187
chrX	155270560	4475112	0.0288	0.2354
chrY	59373566	177493	0.003	0.0724

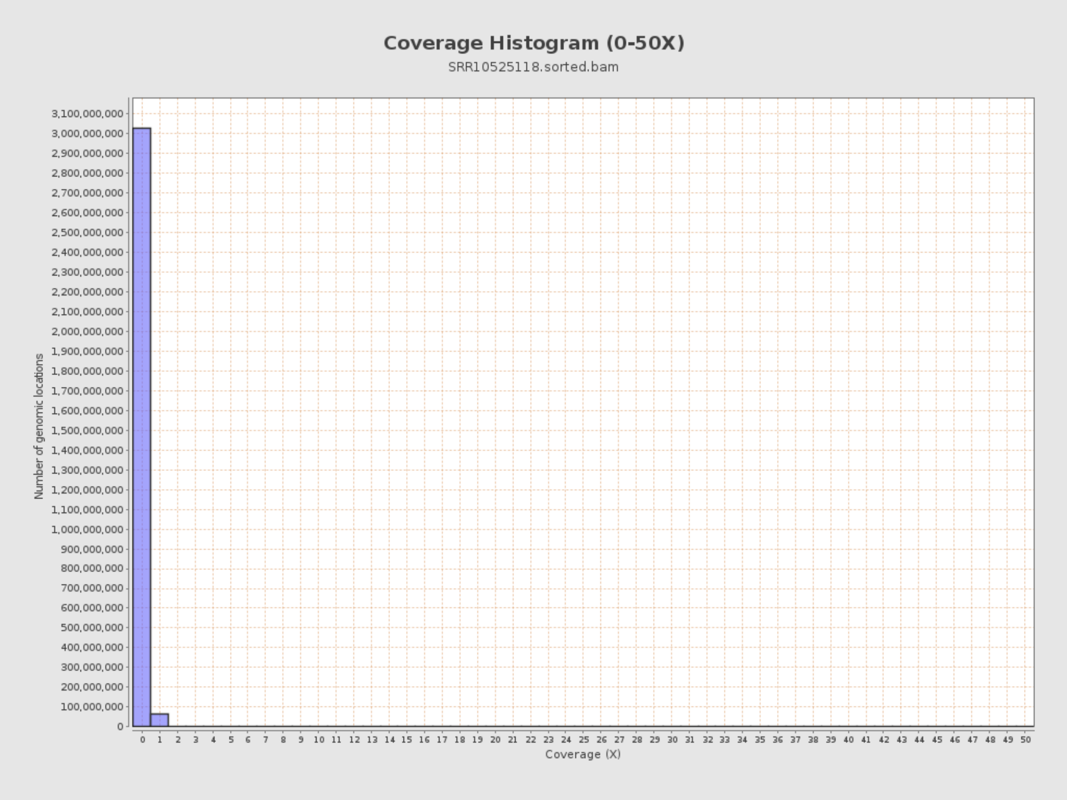
3. Results : Coverage across reference



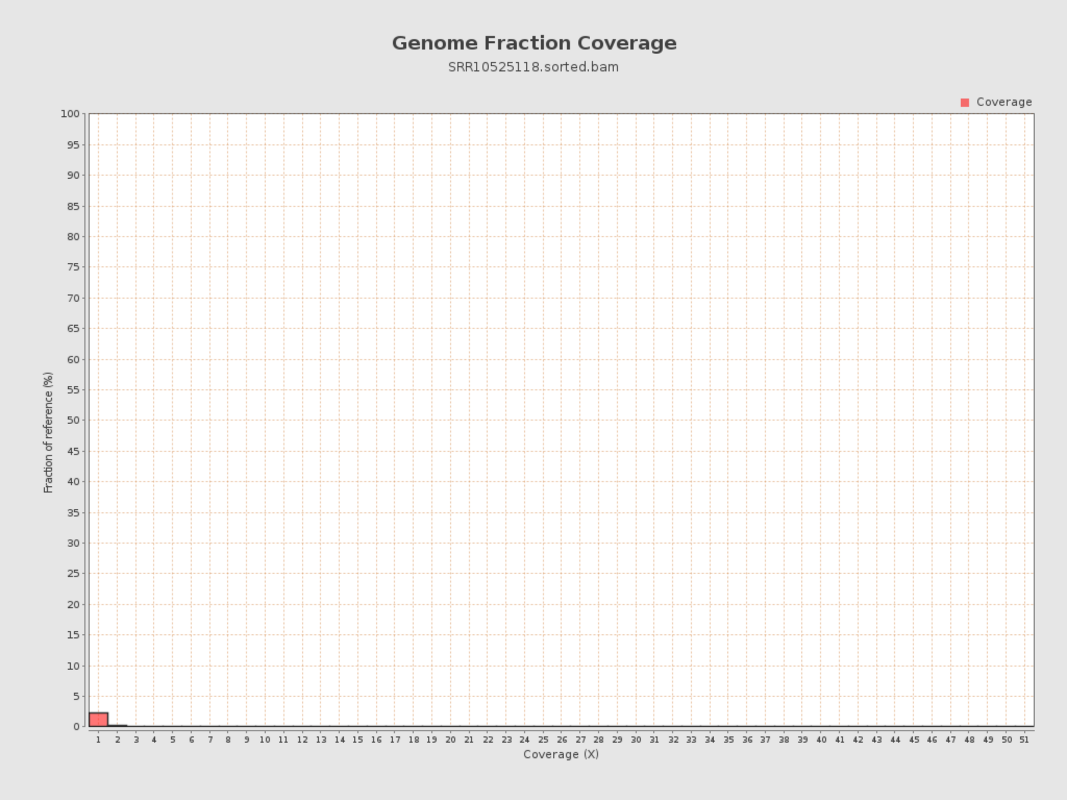
4. Results : Coverage Histogram



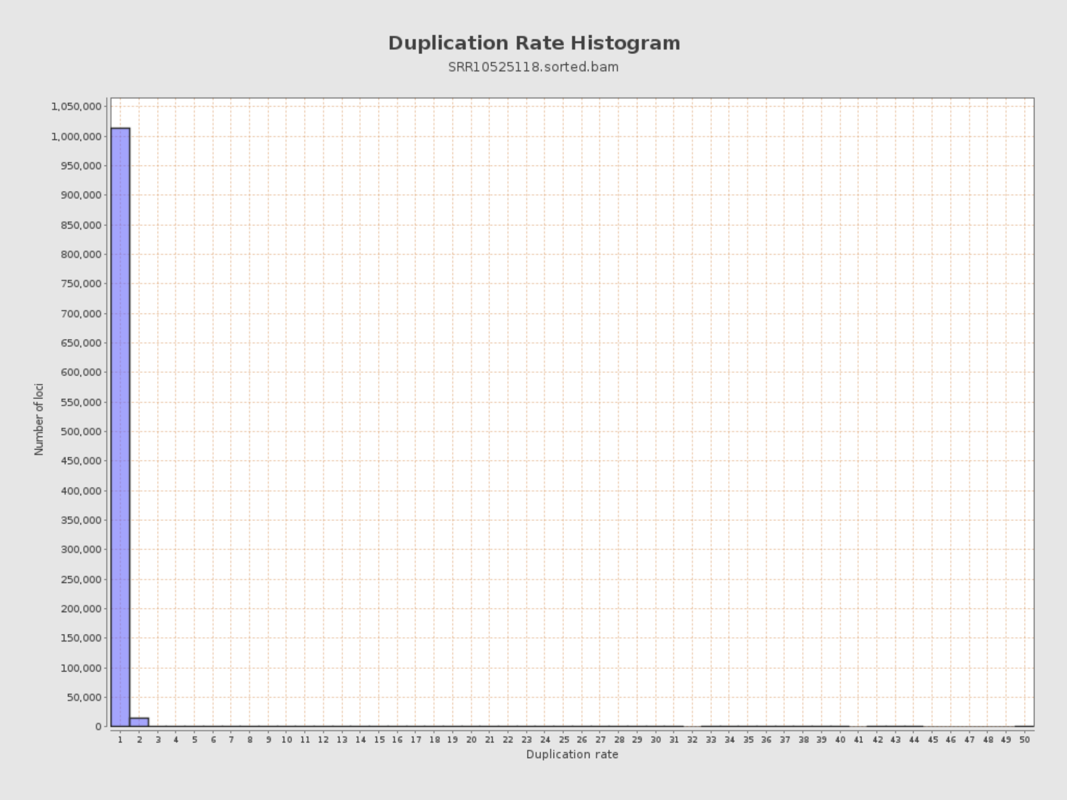
5. Results : Coverage Histogram (0-50X)



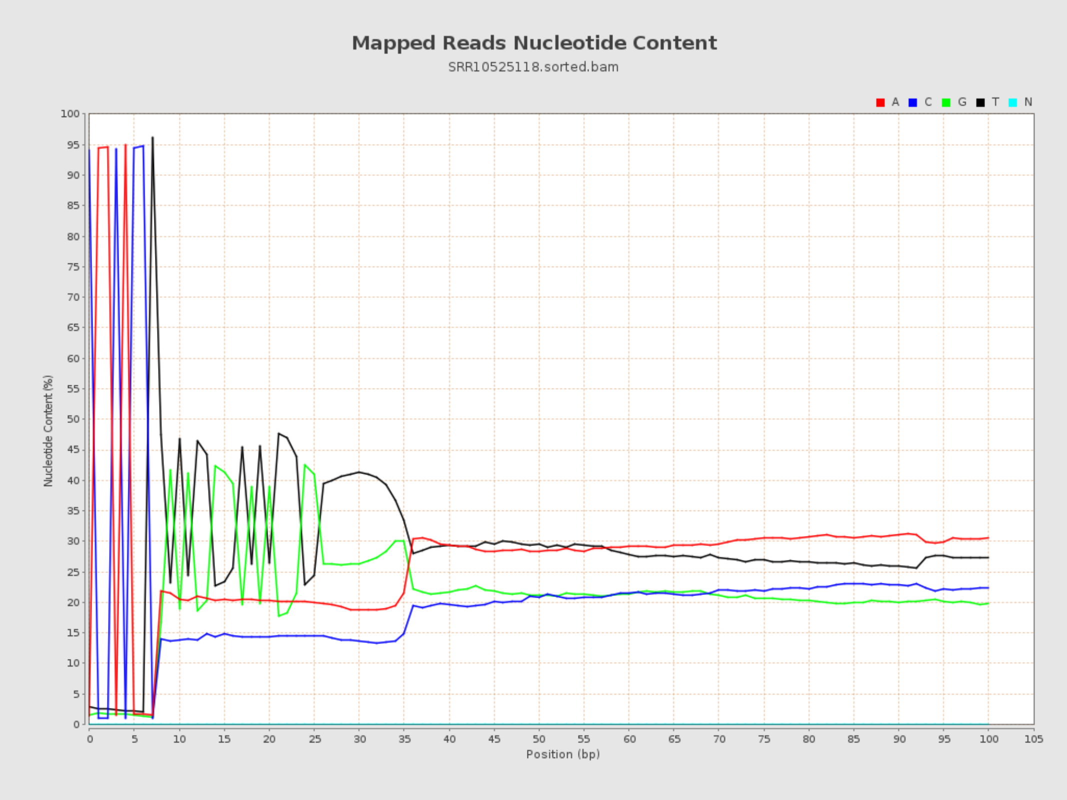
6. Results : Genome Fraction Coverage



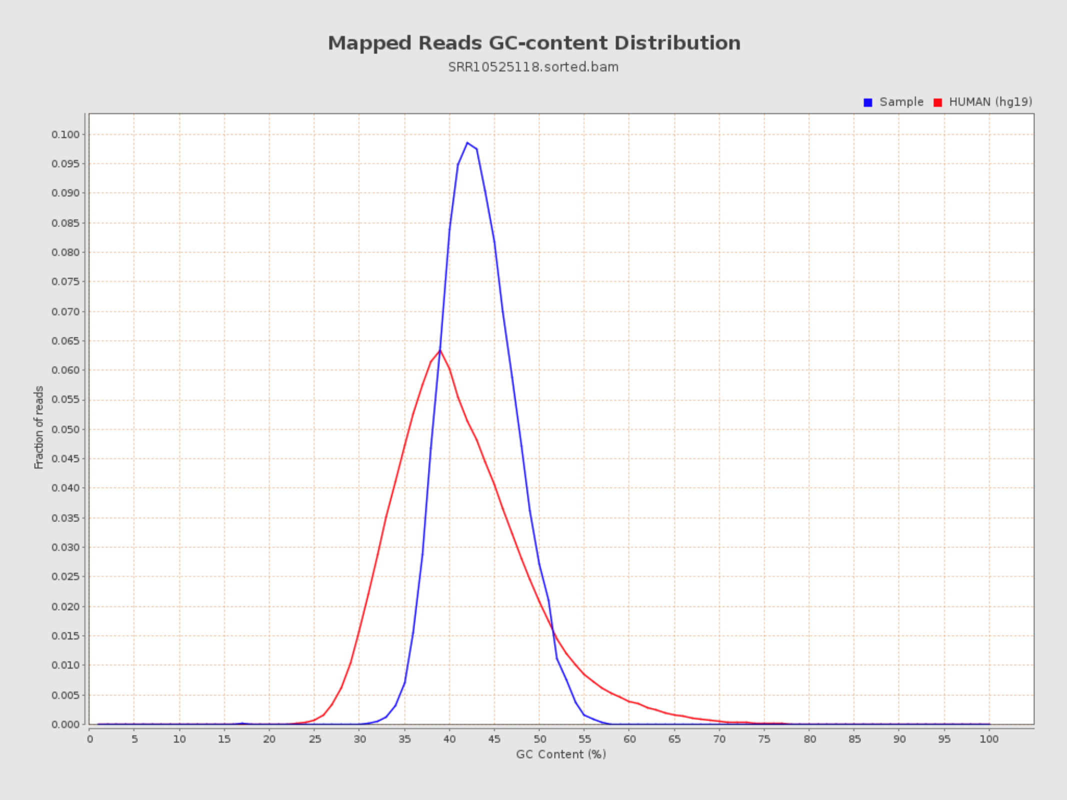
7. Results : Duplication Rate Histogram



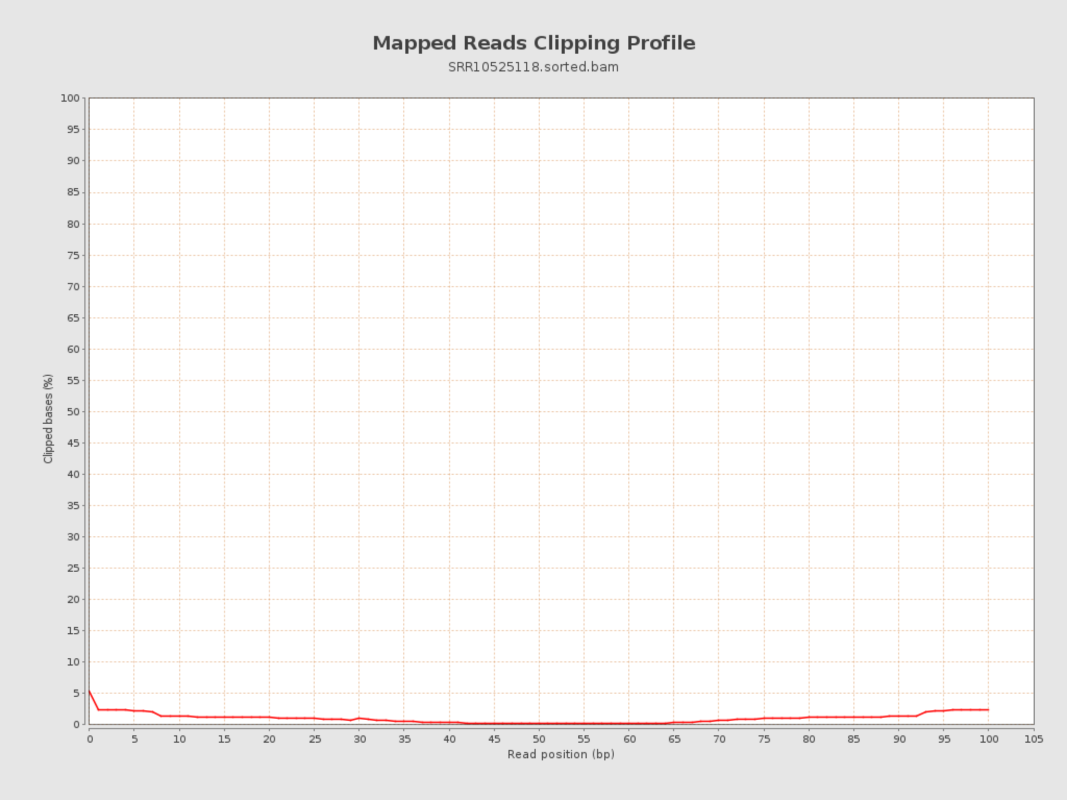
8. Results : Mapped Reads Nucleotide Content



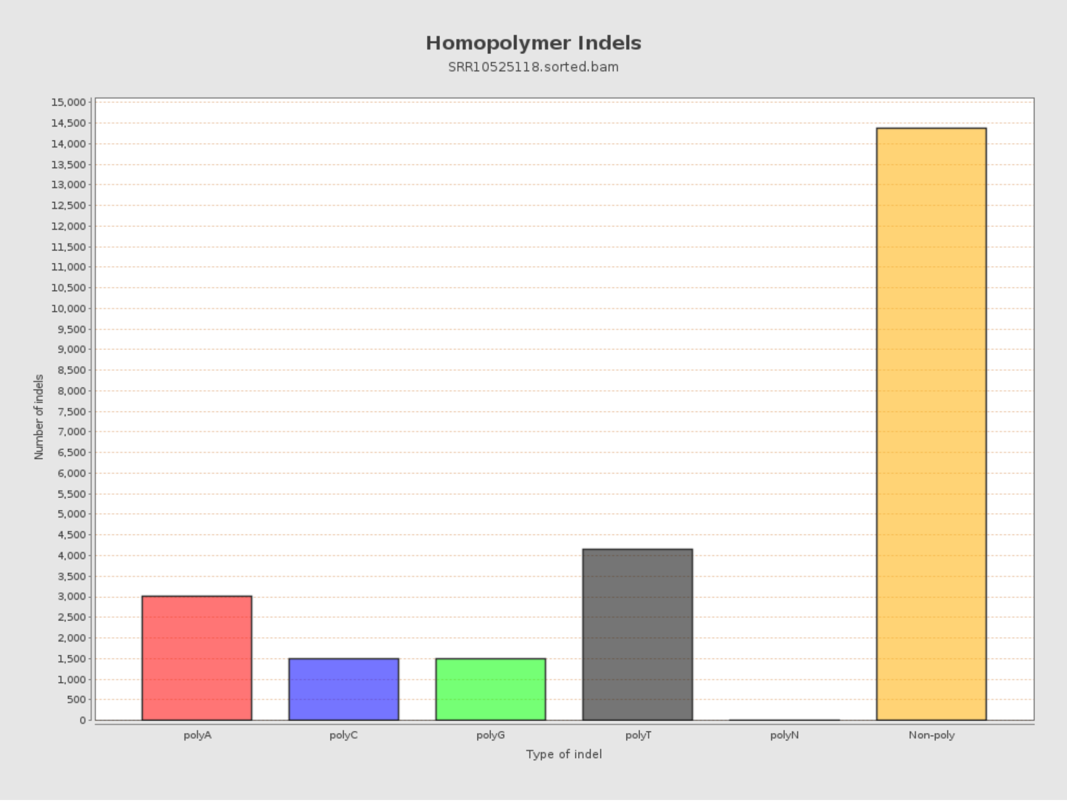
9. Results : Mapped Reads GC-content Distribution



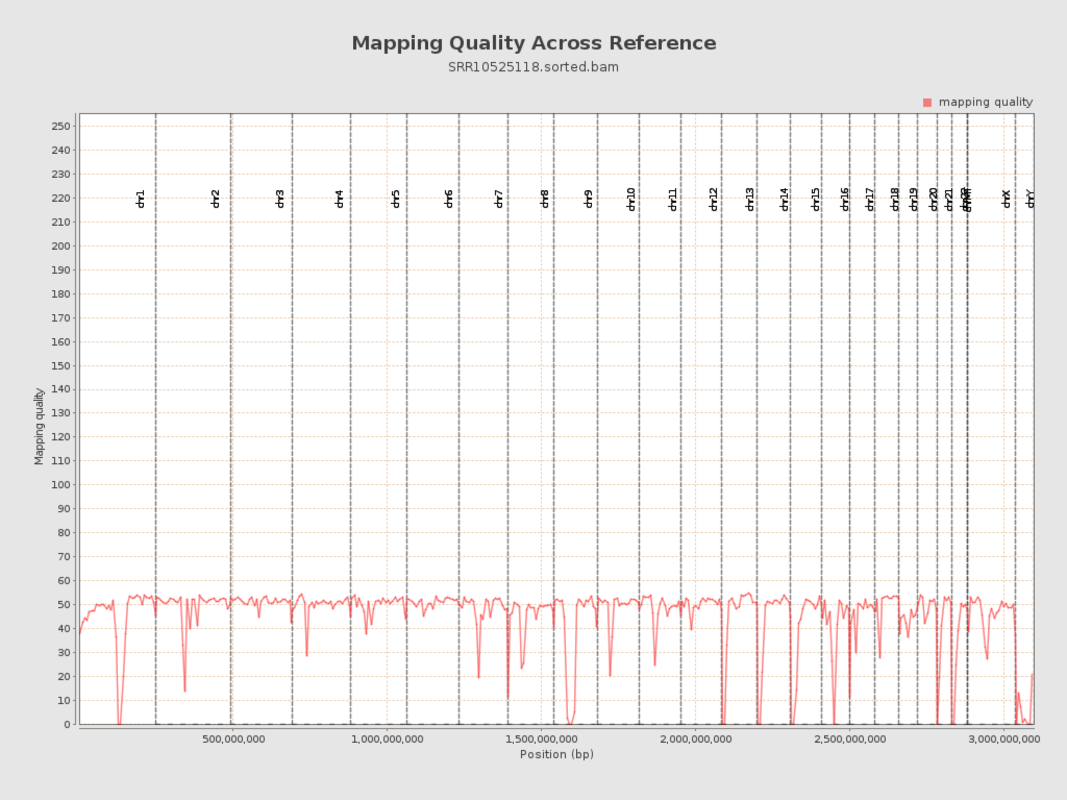
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram