Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:38:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525094.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_SRR10525094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:38:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	931,289
Mapped reads	798,858 / 85.78%
Unmapped reads	132,431 / 14.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,850 / 2.45%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	18,637 / 2%
Duplication rate	1.41%
Clipped reads	820,151 / 88.07%

2.2. ACGT Content

Number/percentage of A's	15,967,574 / 26.14%
Number/percentage of C's	11,931,150 / 19.53%
Number/percentage of T's	18,510,951 / 30.31%
Number/percentage of G's	14,666,166 / 24.01%
Number/percentage of N's	2,149 / 0%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2318

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

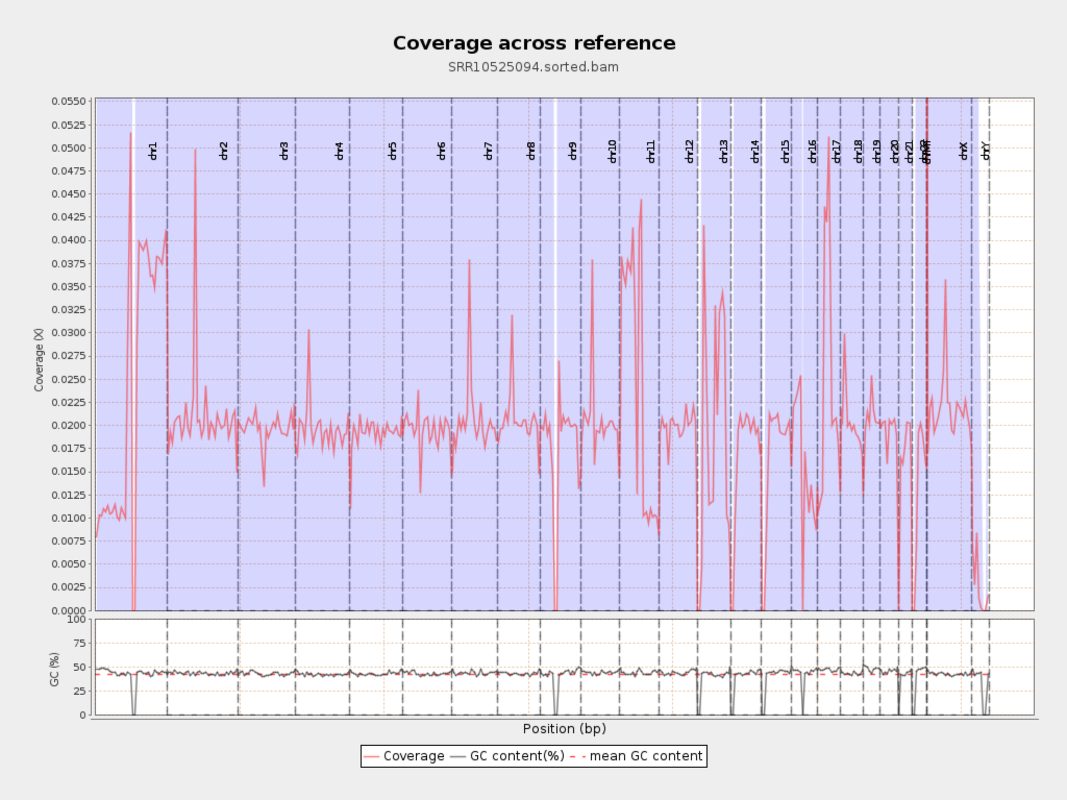
General error rate	0.75%
Mismatches	445,412
Insertions	5,652
Mapped reads with at least one insertion	0.7%
Deletions	14,274
Mapped reads with at least one deletion	1.76%
Homopolymer indels	42.81%

2.6. Chromosome stats

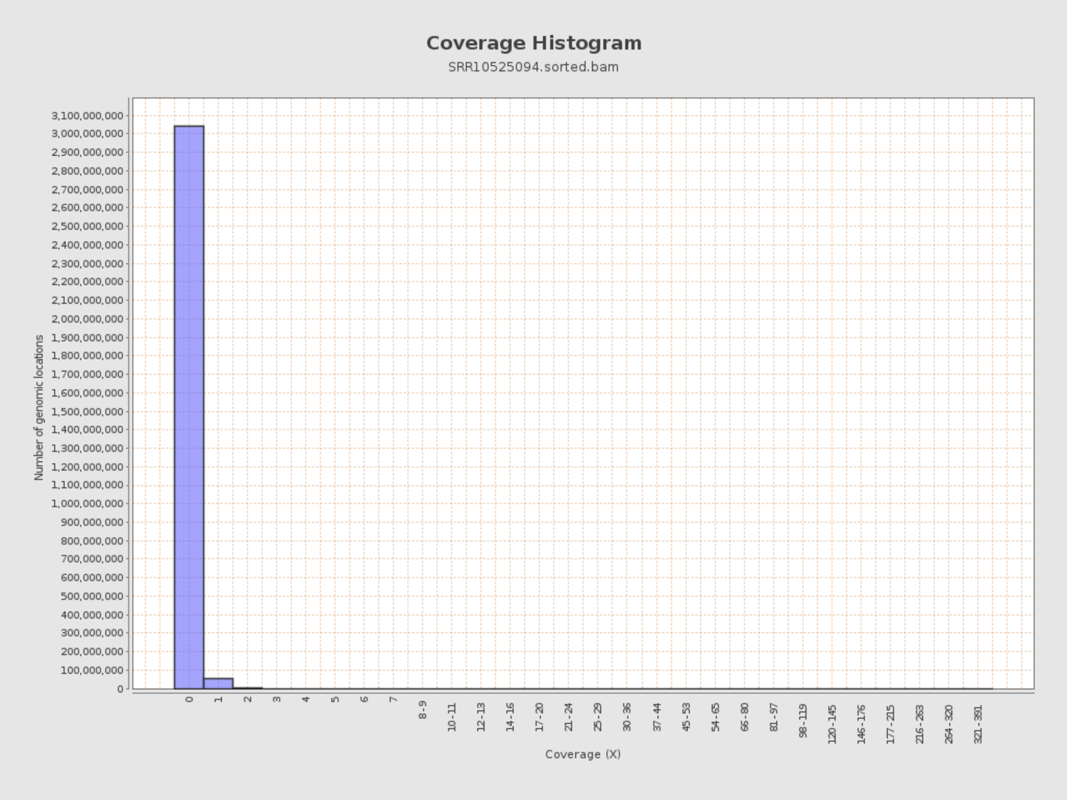
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5880243	0.0236	0.3903
chr2	243199373	5106287	0.021	0.3056
chr3	198022430	3882010	0.0196	0.1483
chr4	191154276	3758091	0.0197	0.1567
chr5	180915260	3496683	0.0193	0.1468
chr6	171115067	3331443	0.0195	0.1581
chr7	159138663	3286245	0.0207	0.2901

chr8	146364022	3017012	0.0206	0.272
chr9	141213431	2475429	0.0175	0.2187
chr10	135534747	2796810	0.0206	0.2372
chr11	135006516	3376002	0.025	0.2823
chr12	133851895	2660936	0.0199	0.149
chr13	115169878	2148977	0.0187	0.1435
chr14	107349540	1785730	0.0166	0.1496
chr15	102531392	1680236	0.0164	0.1338
chr16	90354753	1380353	0.0153	0.1424
chr17	81195210	1998374	0.0246	0.1908
chr18	78077248	1597870	0.0205	0.3699
chr19	59128983	1230647	0.0208	0.2845
chr20	63025520	1207287	0.0192	0.1489
chr21	48129895	776572	0.0161	0.141
chr22	51304566	658265	0.0128	0.1184
chrMT	16571	2449	0.1478	0.4106
chrX	155270560	3419981	0.022	0.1929
chrY	59373566	148421	0.0025	0.0742

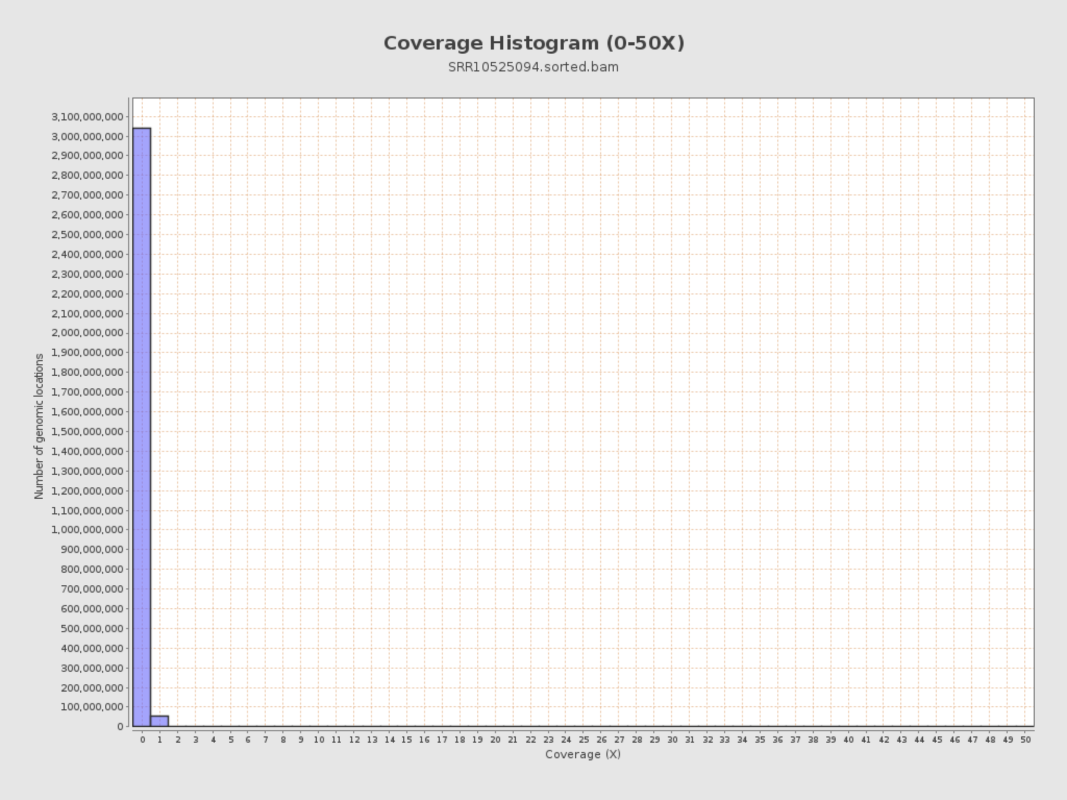
3. Results : Coverage across reference



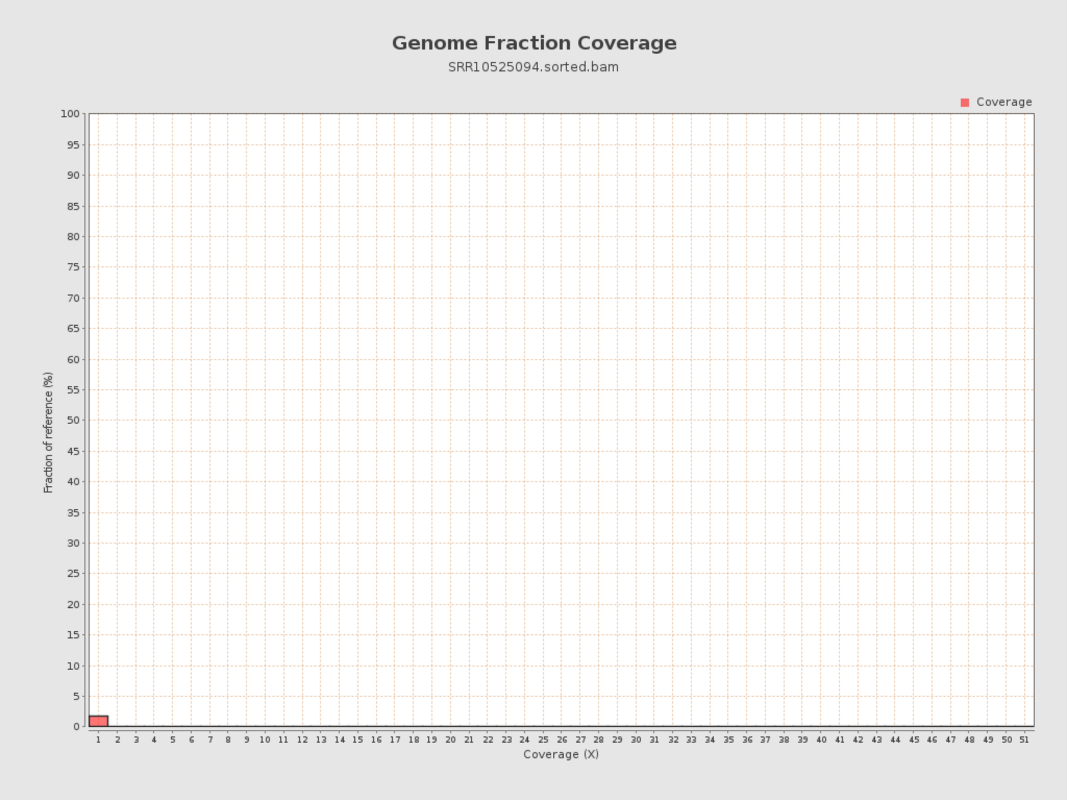
4. Results : Coverage Histogram



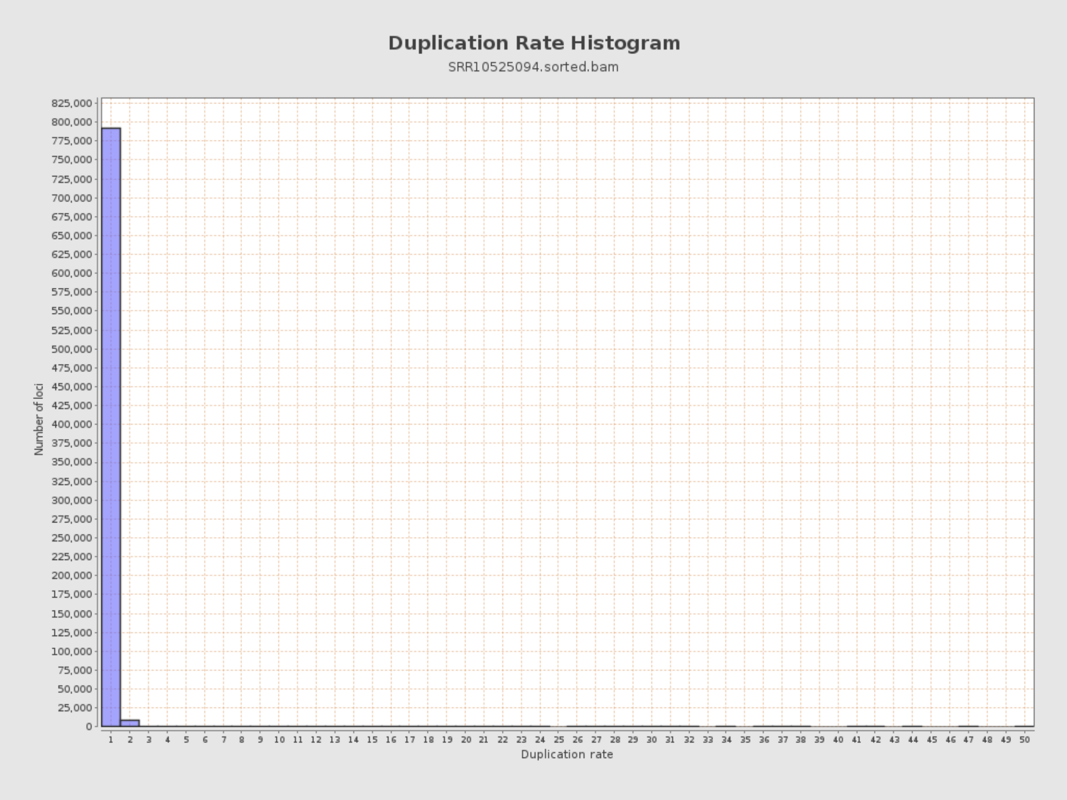
5. Results : Coverage Histogram (0-50X)



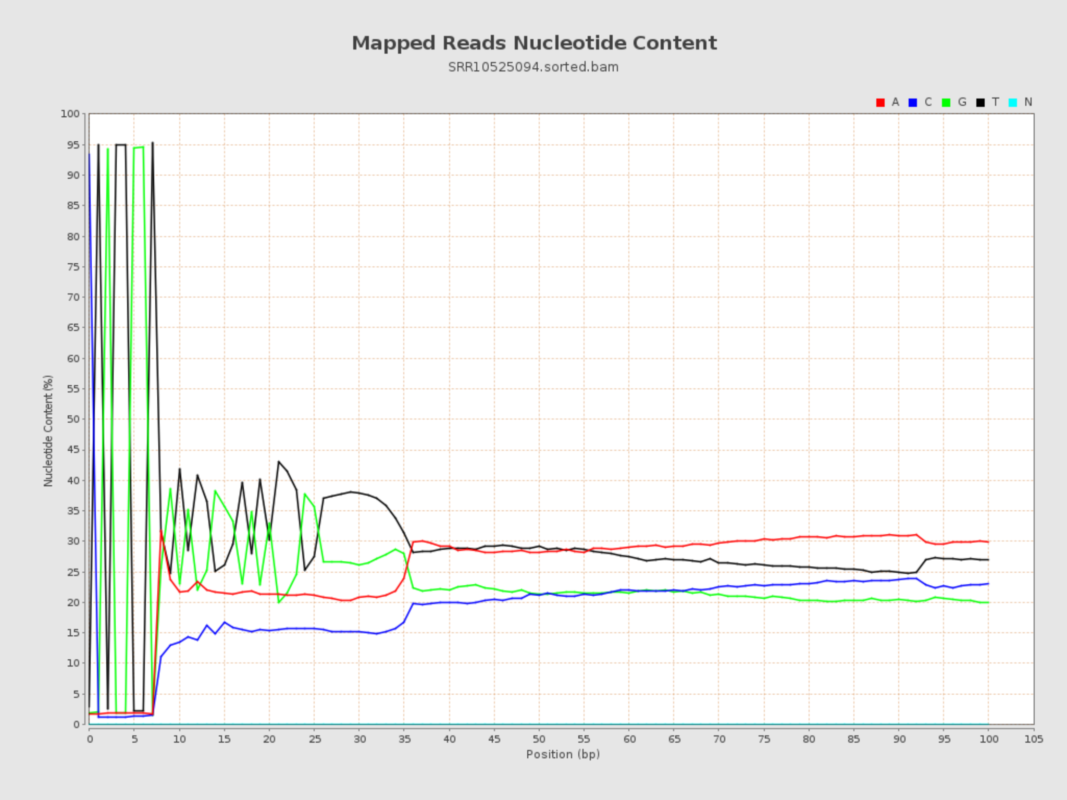
6. Results : Genome Fraction Coverage



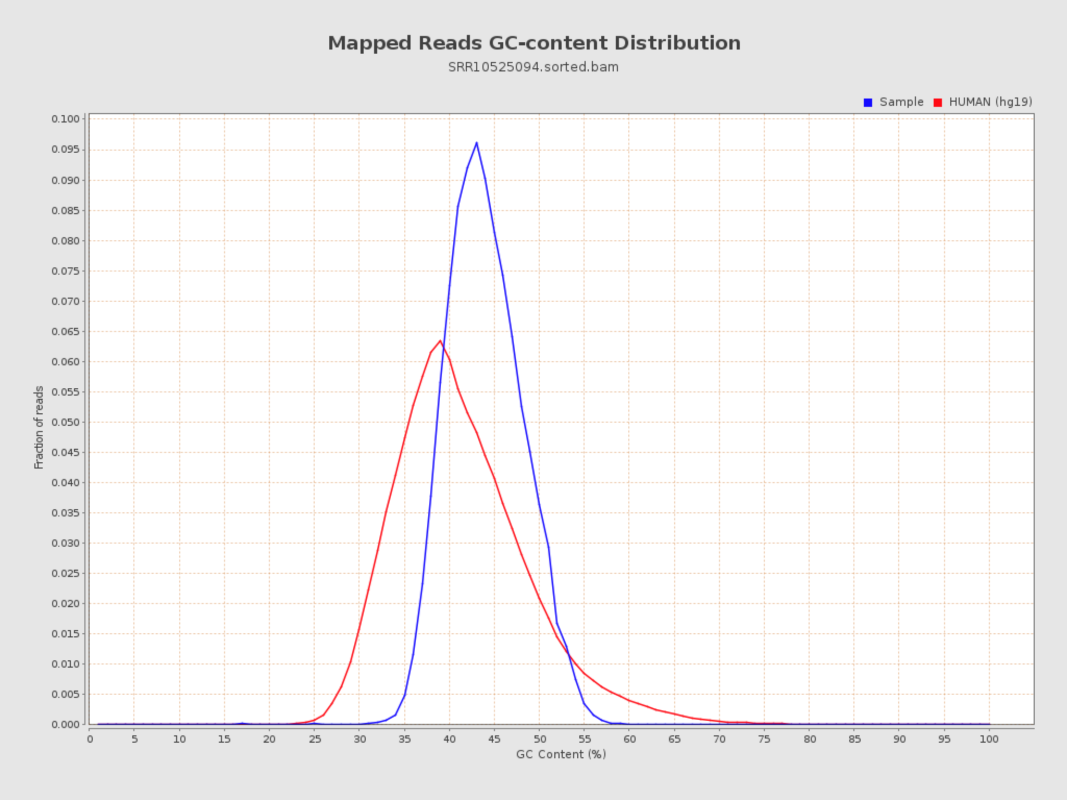
7. Results : Duplication Rate Histogram



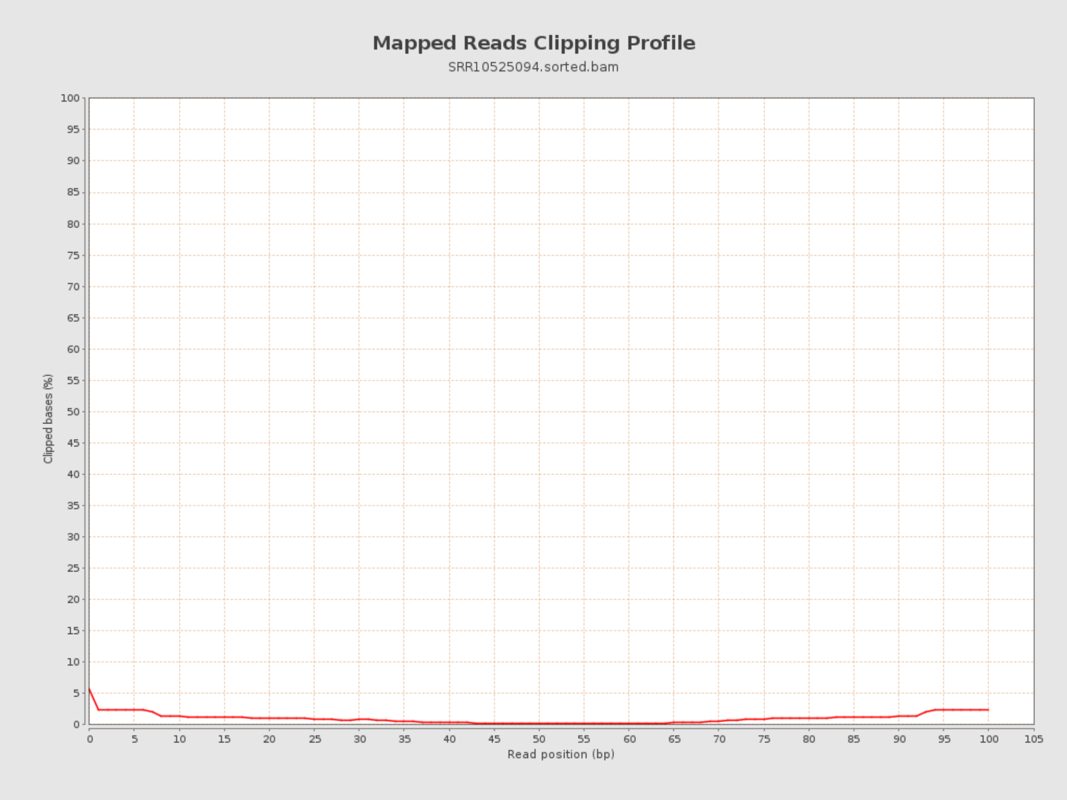
8. Results : Mapped Reads Nucleotide Content



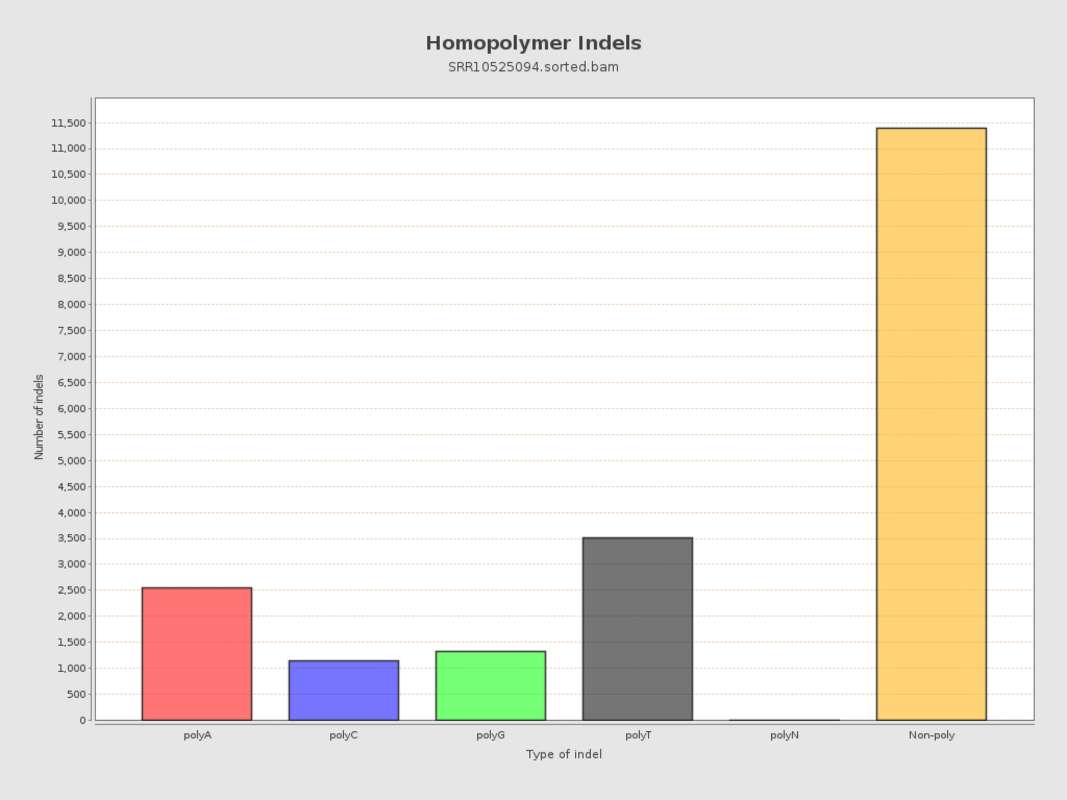
9. Results : Mapped Reads GC-content Distribution



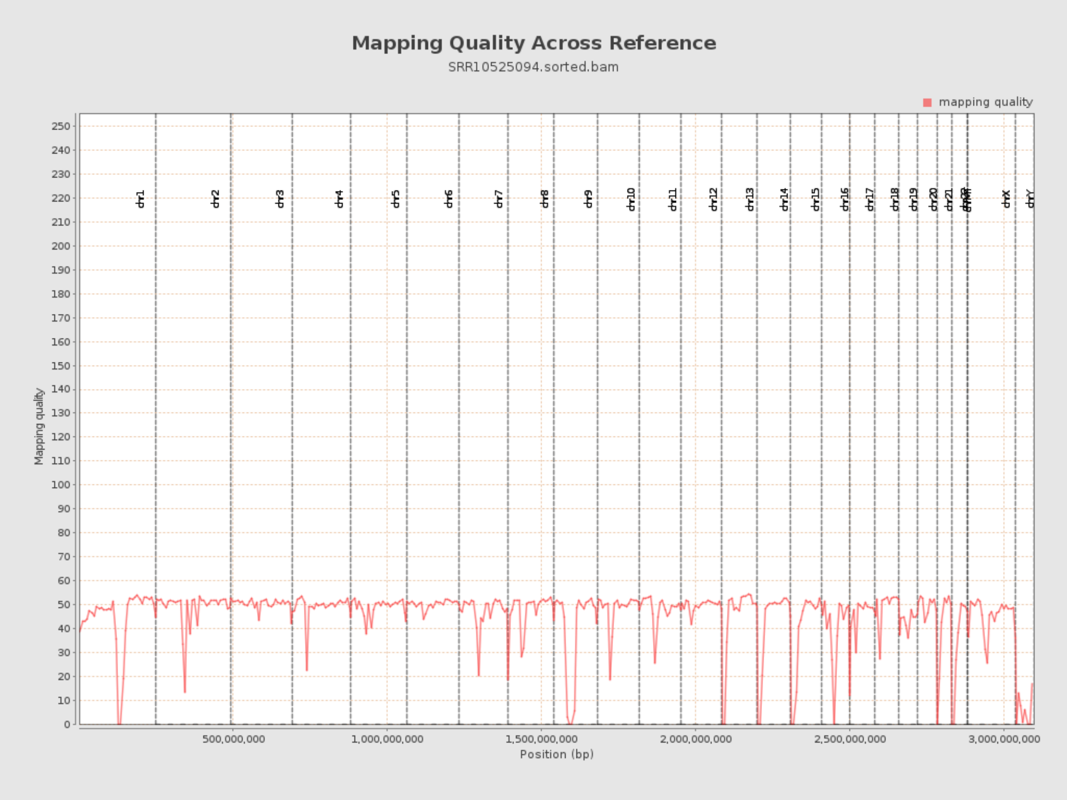
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram