Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:41:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525139.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_SRR10525139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:41:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	965,829
Mapped reads	834,155 / 86.37%
Unmapped reads	131,674 / 13.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,920 / 2.06%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	20,544 / 2.13%
Duplication rate	1.46%
Clipped reads	852,448 / 88.26%

2.2. ACGT Content

Number/percentage of A's	16,335,916 / 25.95%
Number/percentage of C's	12,217,030 / 19.41%
Number/percentage of T's	20,115,960 / 31.96%
Number/percentage of G's	14,273,468 / 22.68%
Number/percentage of N's	2,431 / 0%
GC Percentage	42.09%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2402

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

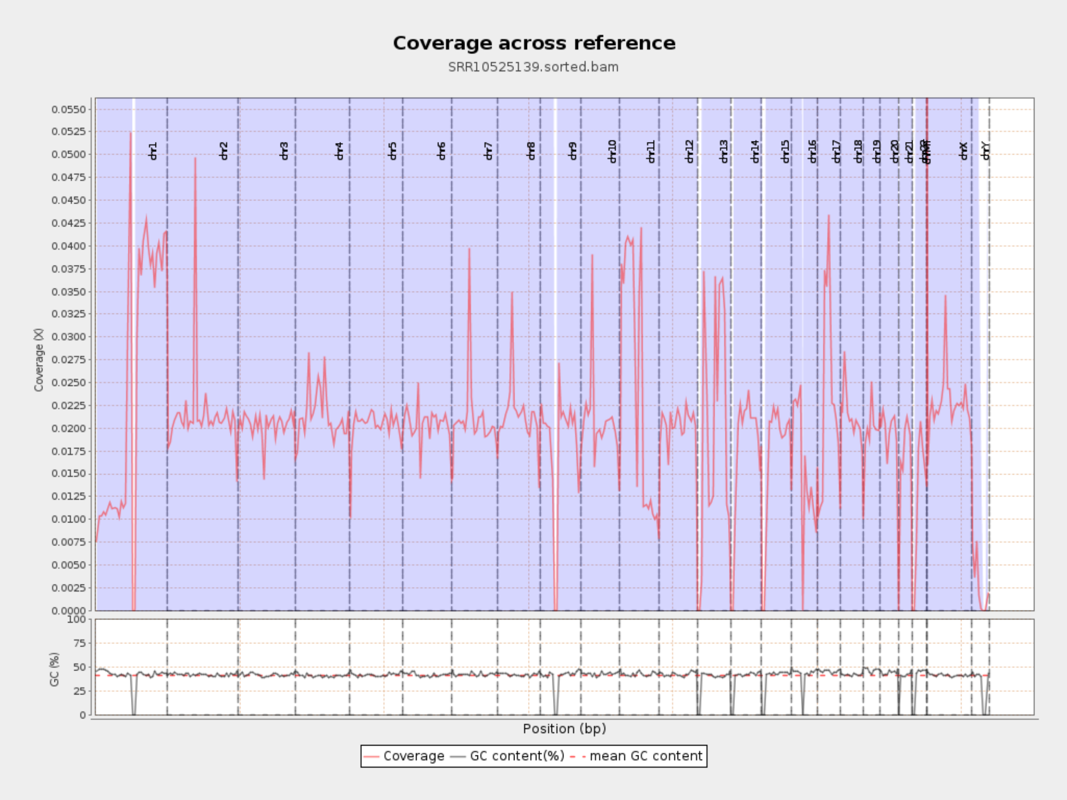
General error rate	0.82%
Mismatches	503,407
Insertions	5,491
Mapped reads with at least one insertion	0.65%
Deletions	15,064
Mapped reads with at least one deletion	1.78%
Homopolymer indels	43.41%

2.6. Chromosome stats

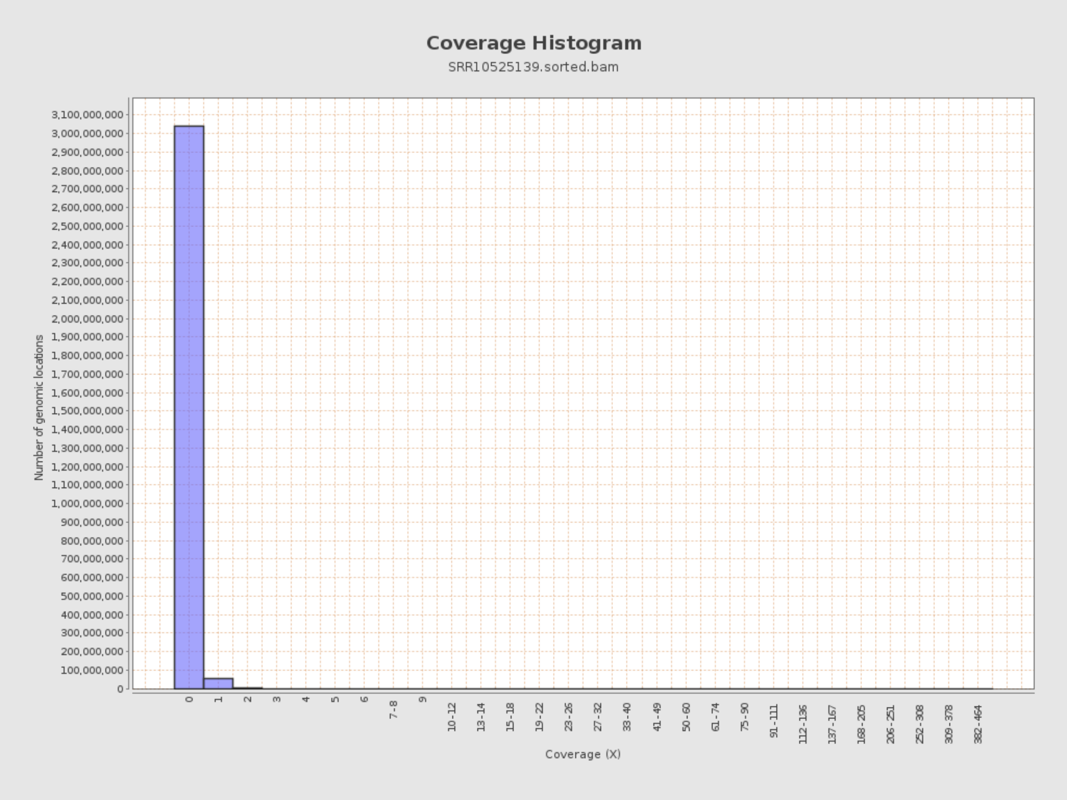
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6060709	0.0243	0.4035
chr2	243199373	5262024	0.0216	0.3312
chr3	198022430	4041303	0.0204	0.1511
chr4	191154276	4098233	0.0214	0.1615
chr5	180915260	3719492	0.0206	0.1525
chr6	171115067	3495198	0.0204	0.1672
chr7	159138663	3370222	0.0212	0.3334

chr8	146364022	3157538	0.0216	0.2989
chr9	141213431	2556698	0.0181	0.2225
chr10	135534747	2835213	0.0209	0.2487
chr11	135006516	3404535	0.0252	0.2521
chr12	133851895	2728106	0.0204	0.1521
chr13	115169878	2234810	0.0194	0.1476
chr14	107349540	1872636	0.0174	0.1526
chr15	102531392	1719491	0.0168	0.1363
chr16	90354753	1371929	0.0152	0.1425
chr17	81195210	1861194	0.0229	0.1795
chr18	78077248	1668197	0.0214	0.3424
chr19	59128983	1173992	0.0199	0.2935
chr20	63025520	1219504	0.0193	0.1486
chr21	48129895	783322	0.0163	0.1414
chr22	51304566	633284	0.0123	0.1162
chrMT	16571	1372	0.0828	0.2977
chrX	155270560	3548176	0.0229	0.1965
chrY	59373566	153391	0.0026	0.0719

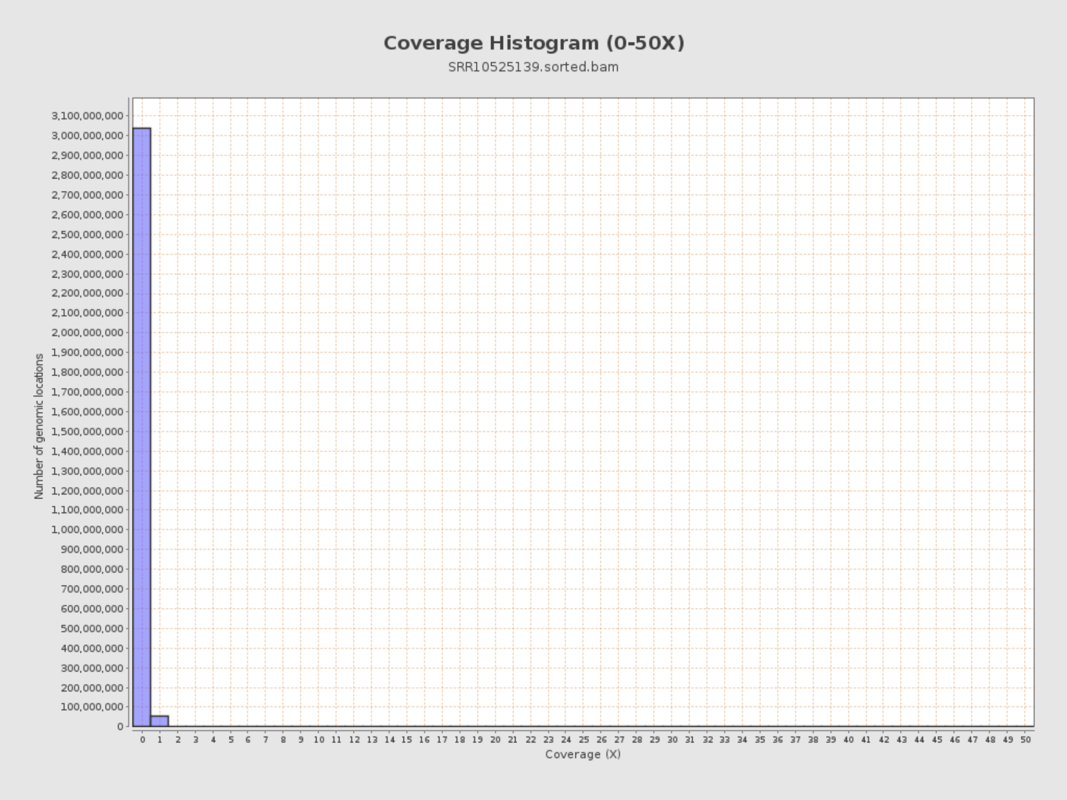
3. Results : Coverage across reference



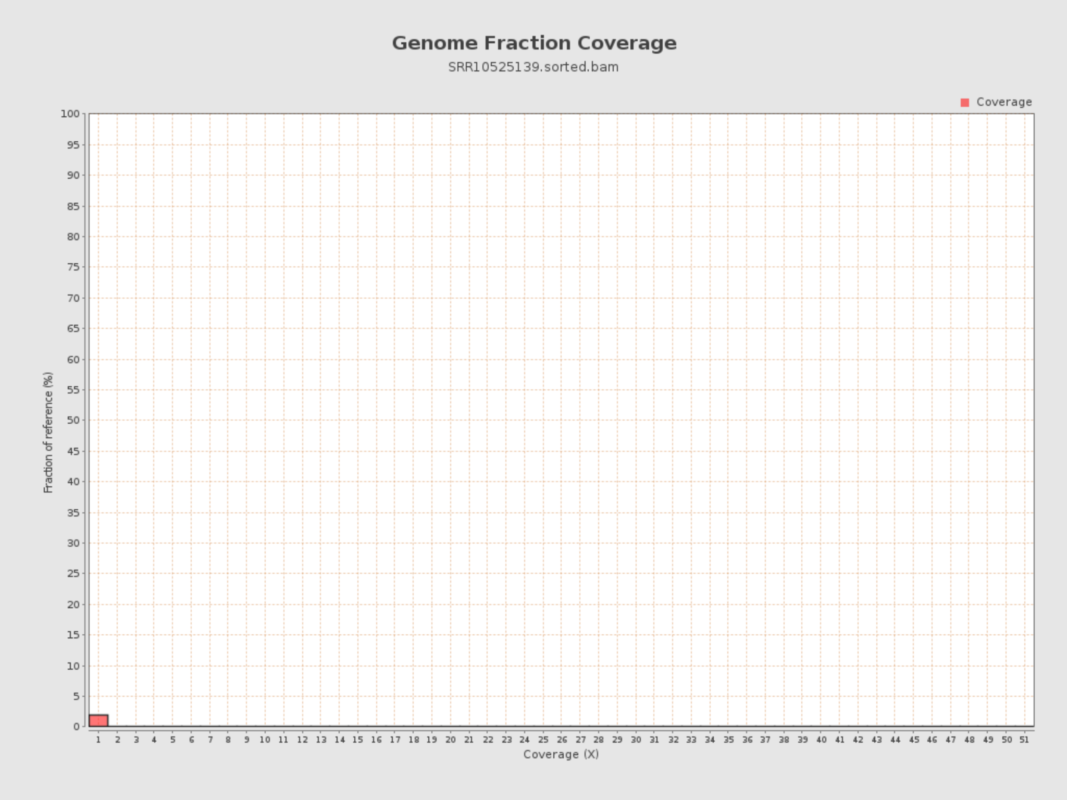
4. Results : Coverage Histogram



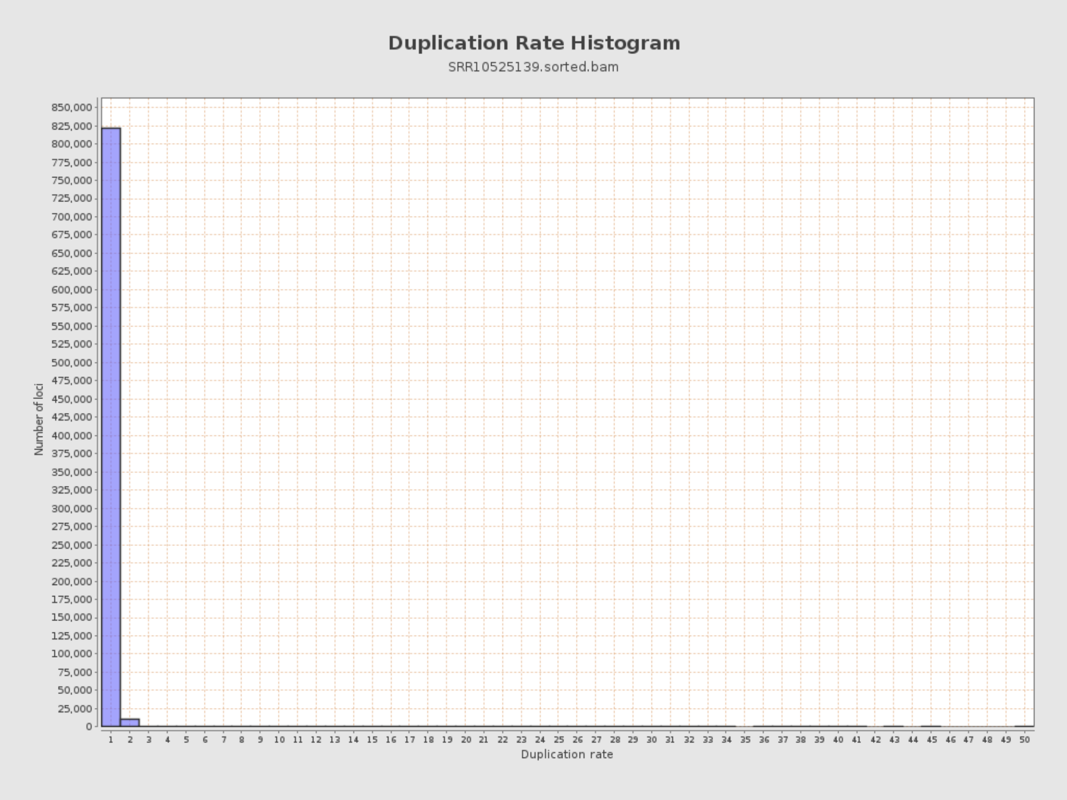
5. Results : Coverage Histogram (0-50X)



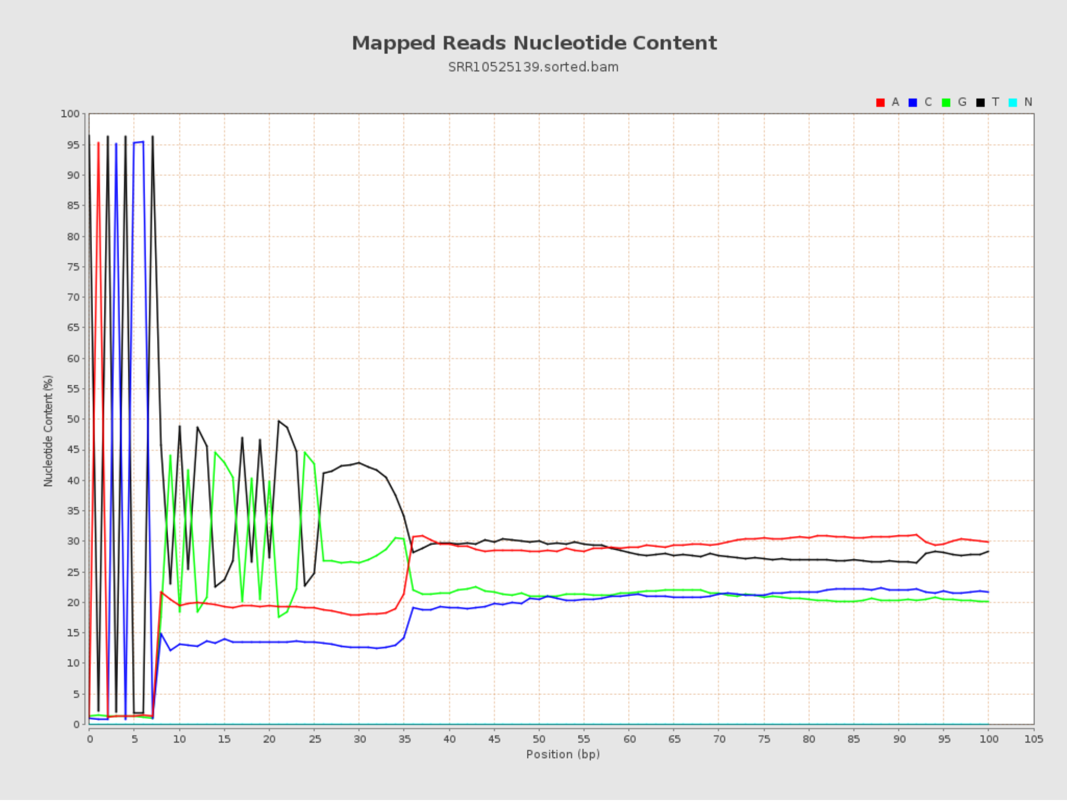
6. Results : Genome Fraction Coverage



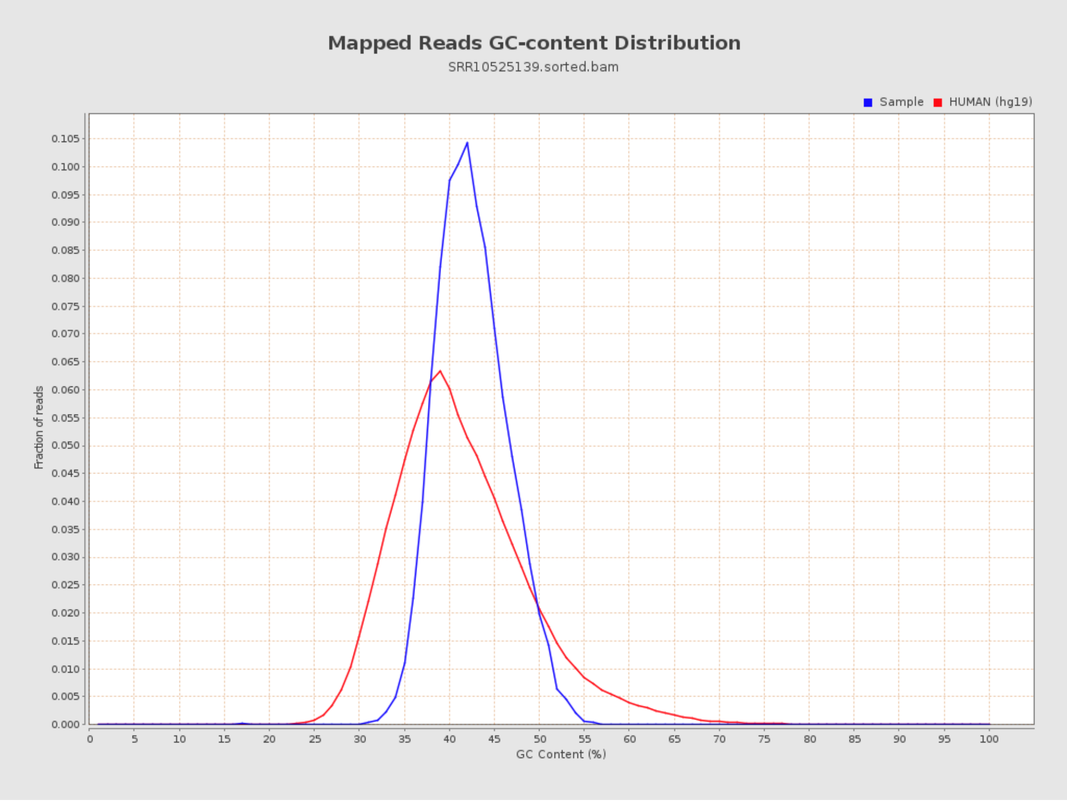
7. Results : Duplication Rate Histogram



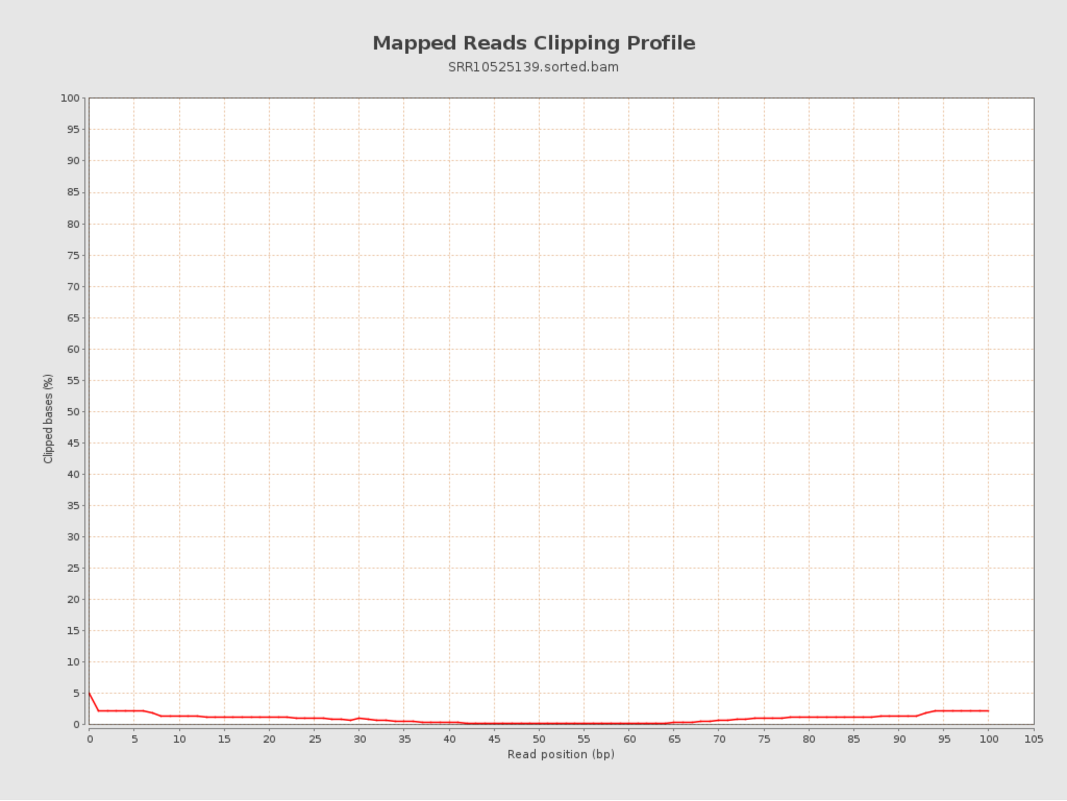
8. Results : Mapped Reads Nucleotide Content



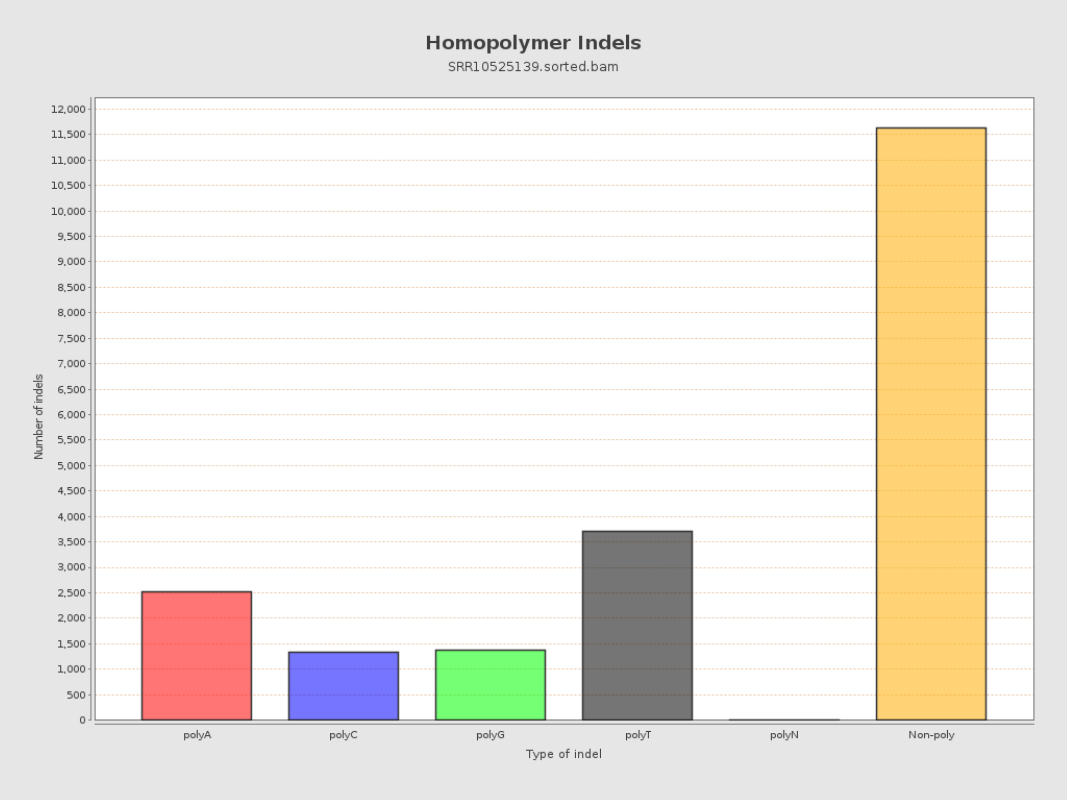
9. Results : Mapped Reads GC-content Distribution



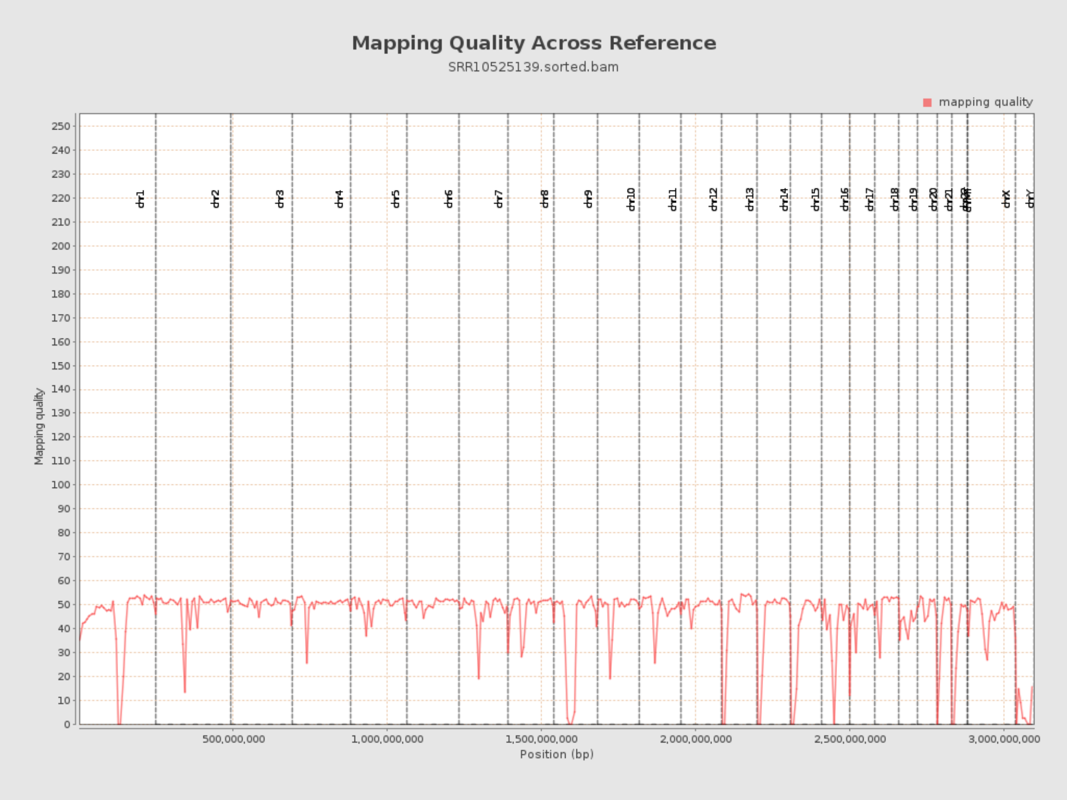
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram