Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:38:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525138.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_SRR10525138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:38:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,148,378
Mapped reads	1,029,841 / 89.68%
Unmapped reads	118,537 / 10.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,810 / 2.77%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	24,486 / 2.13%
Duplication rate	1.46%
Clipped reads	1,061,071 / 92.4%

2.2. ACGT Content

Number/percentage of A's	20,495,850 / 26.21%
Number/percentage of C's	16,036,181 / 20.51%
Number/percentage of T's	23,190,359 / 29.66%
Number/percentage of G's	18,473,873 / 23.62%
Number/percentage of N's	3,075 / 0%
GC Percentage	44.13%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2581

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

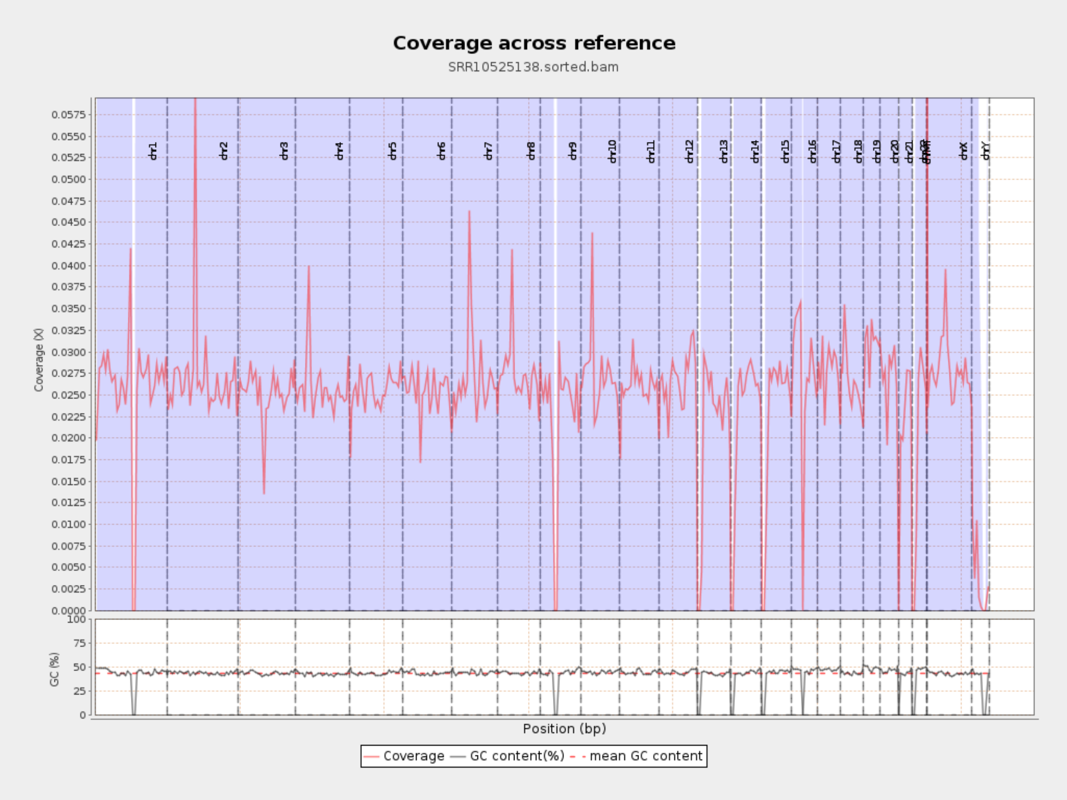
General error rate	0.76%
Mismatches	581,501
Insertions	6,819
Mapped reads with at least one insertion	0.65%
Deletions	18,112
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.99%

2.6. Chromosome stats

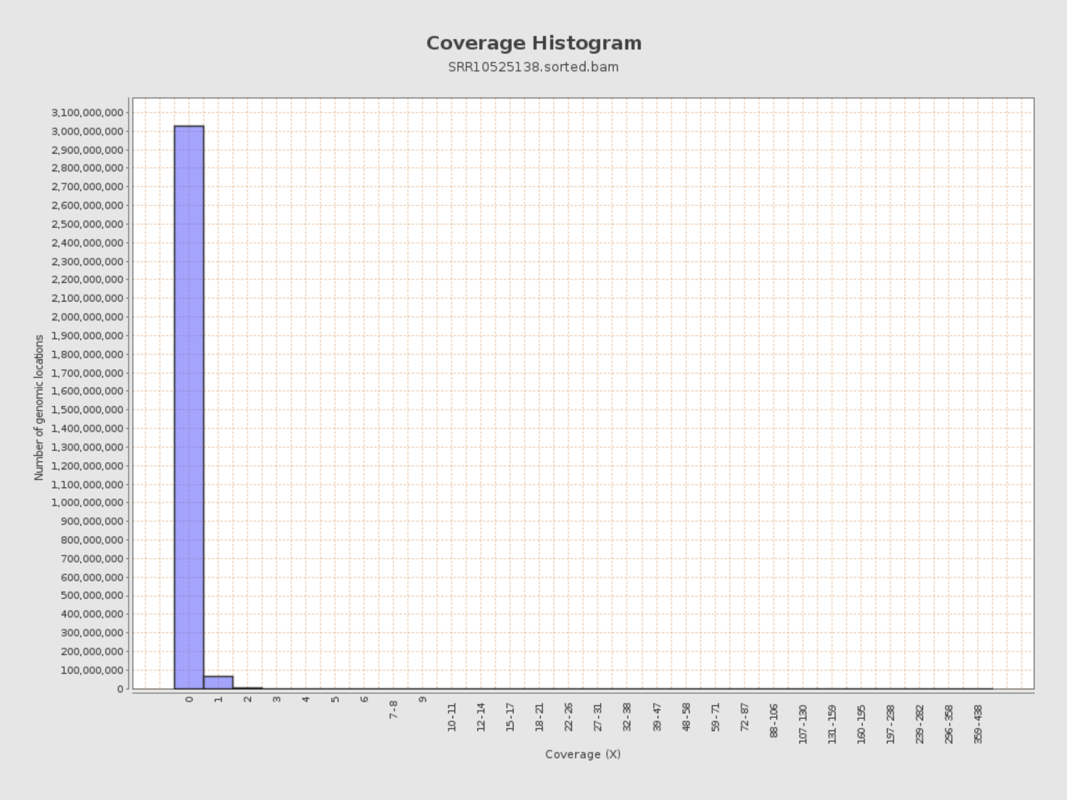
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6398746	0.0257	0.3643
chr2	243199373	6616099	0.0272	0.3883
chr3	198022430	4981990	0.0252	0.1689
chr4	191154276	4977765	0.026	0.1881
chr5	180915260	4665855	0.0258	0.1724
chr6	171115067	4348788	0.0254	0.1845
chr7	159138663	4323621	0.0272	0.3461

chr8	146364022	4023831	0.0275	0.3551
chr9	141213431	3159981	0.0224	0.2463
chr10	135534747	3714949	0.0274	0.2576
chr11	135006516	3541899	0.0262	0.2469
chr12	133851895	3581584	0.0268	0.1758
chr13	115169878	2416860	0.021	0.1539
chr14	107349540	2393356	0.0223	0.1769
chr15	102531392	2261075	0.0221	0.1582
chr16	90354753	2422018	0.0268	0.1878
chr17	81195210	2254061	0.0278	0.2003
chr18	78077248	2077303	0.0266	0.4071
chr19	59128983	1816130	0.0307	0.2974
chr20	63025520	1679805	0.0267	0.1785
chr21	48129895	1033597	0.0215	0.1673
chr22	51304566	977367	0.0191	0.1476
chrMT	16571	2392	0.1443	0.3882
chrX	155270560	4362376	0.0281	0.213
chrY	59373566	199980	0.0034	0.0928

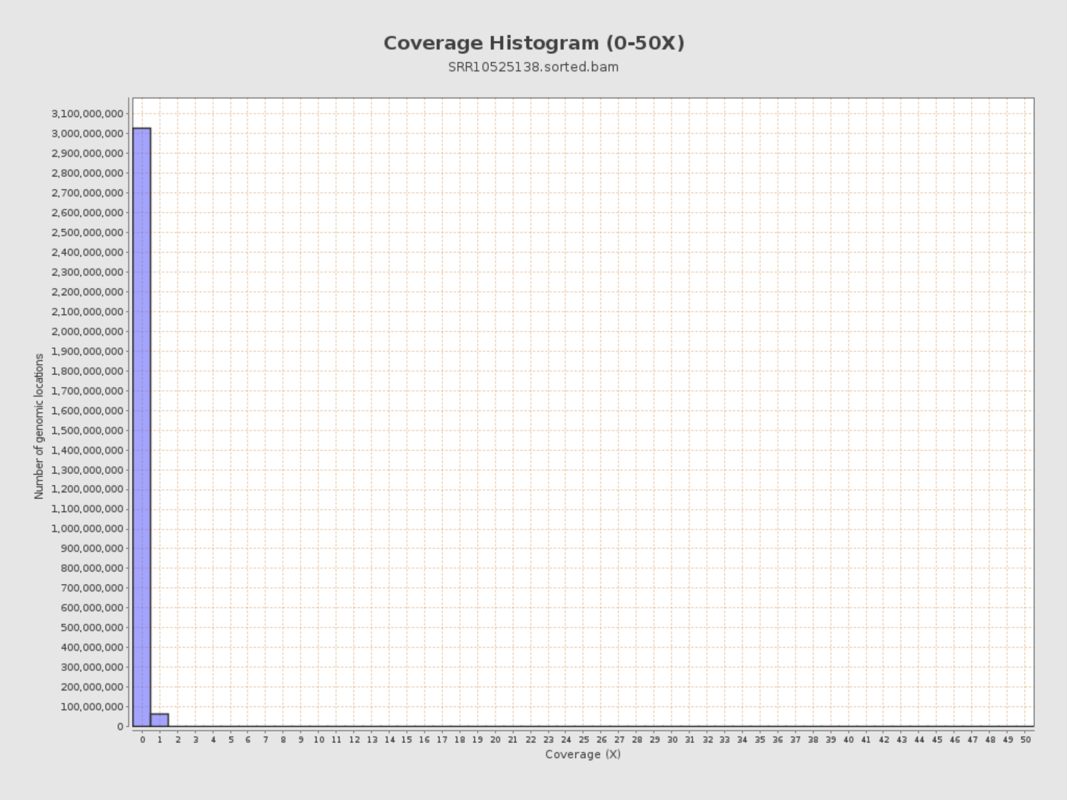
3. Results : Coverage across reference



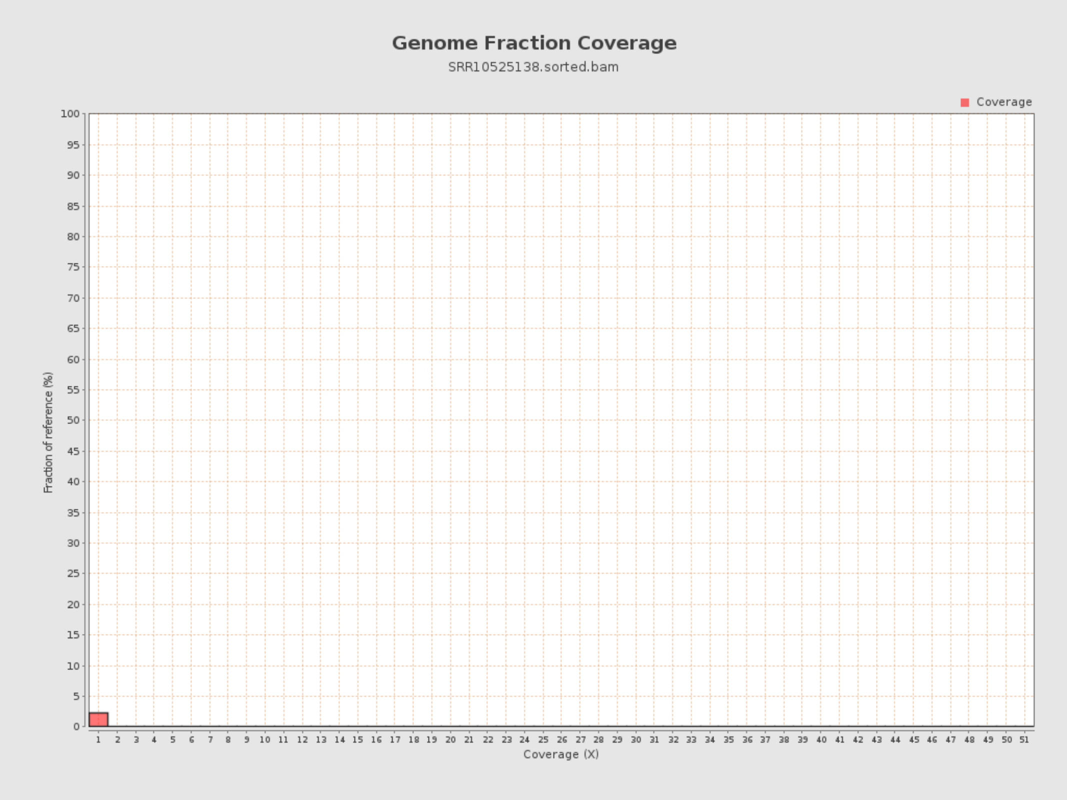
4. Results : Coverage Histogram



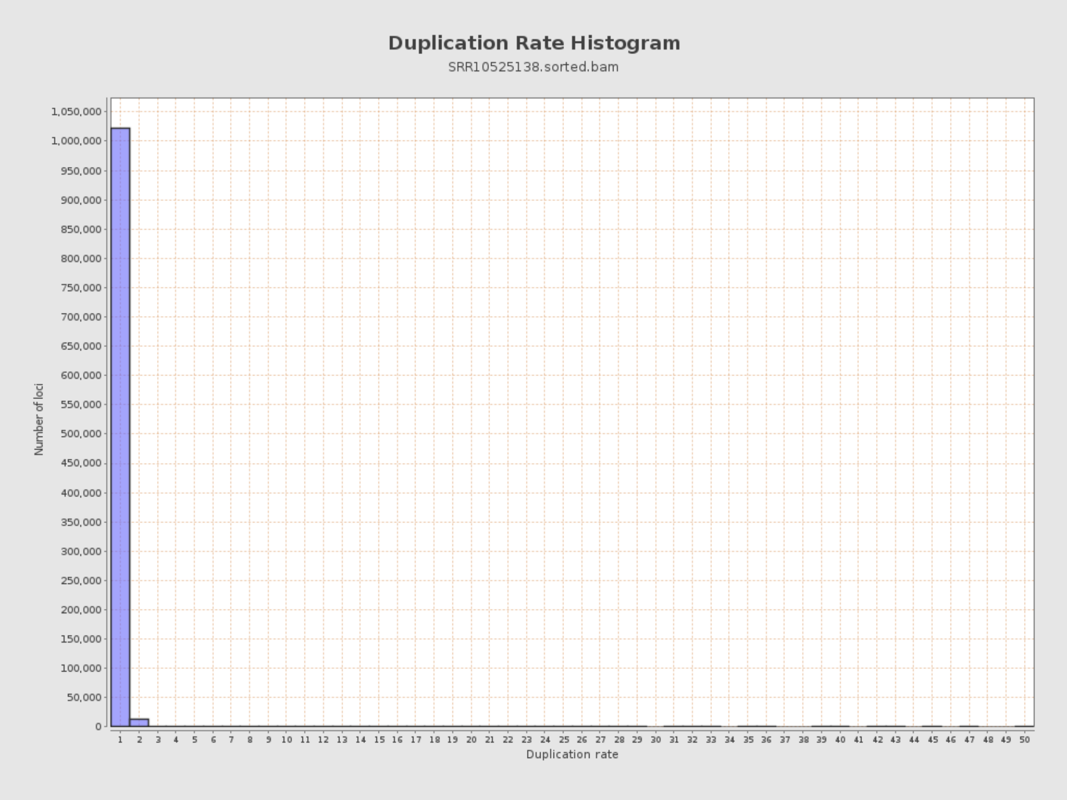
5. Results : Coverage Histogram (0-50X)



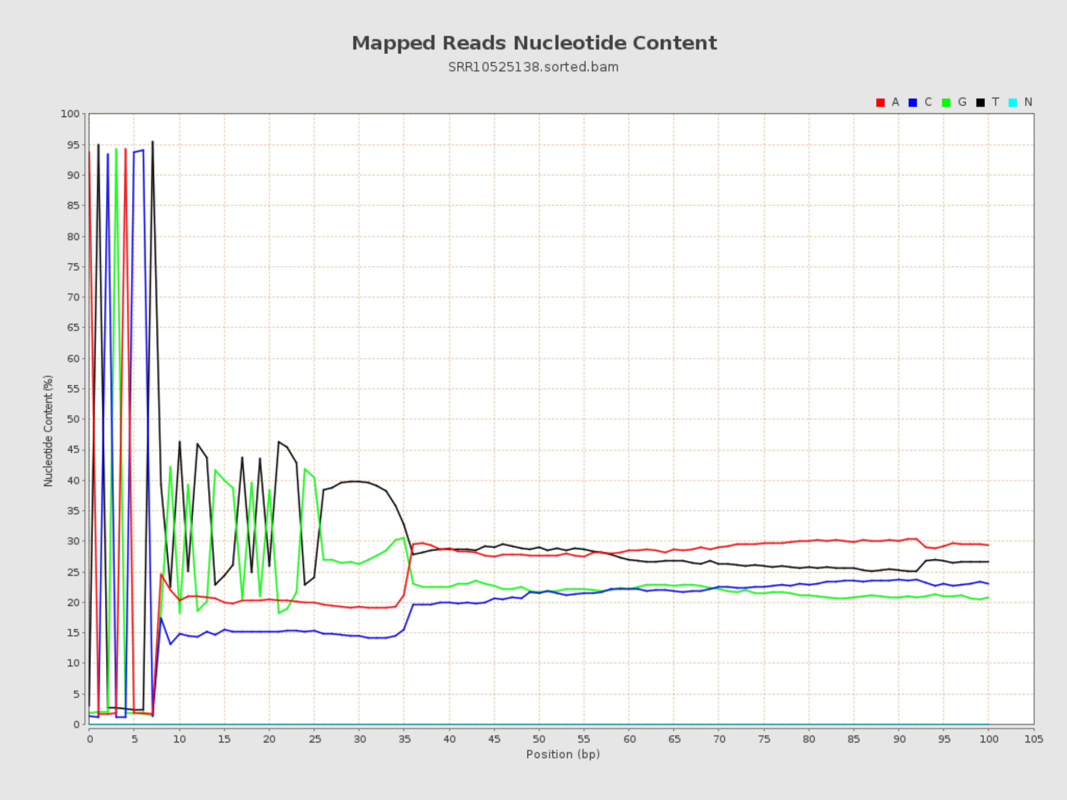
6. Results : Genome Fraction Coverage



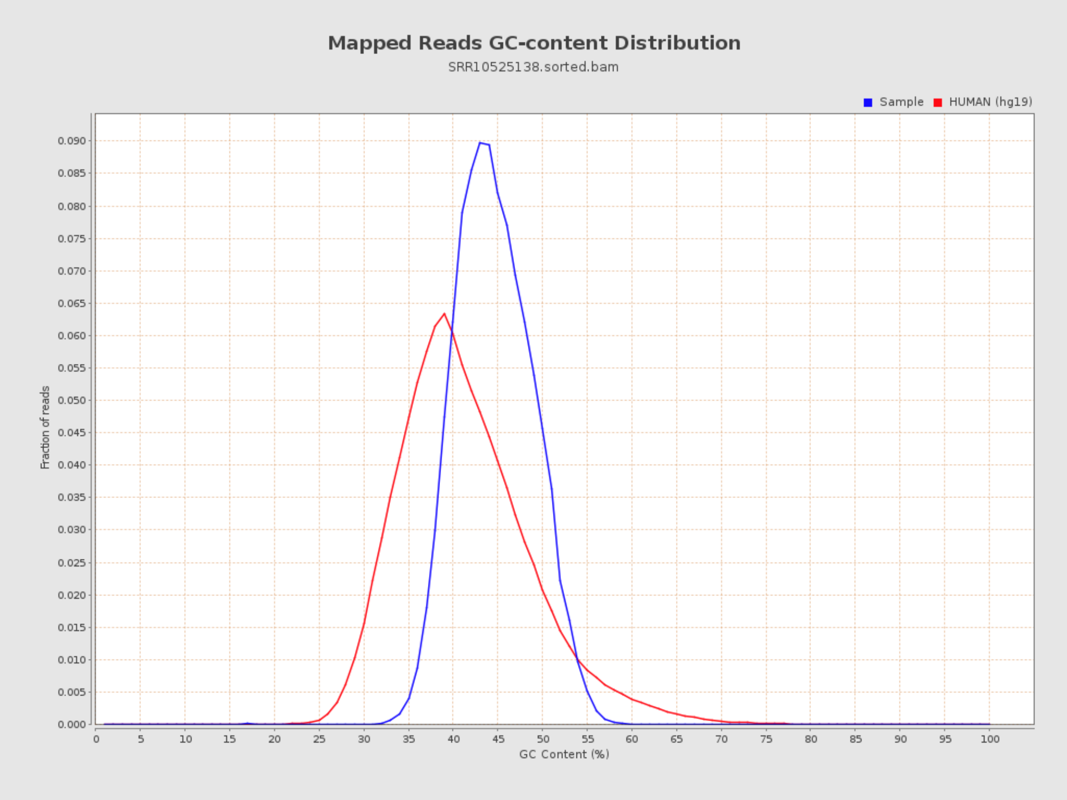
7. Results : Duplication Rate Histogram



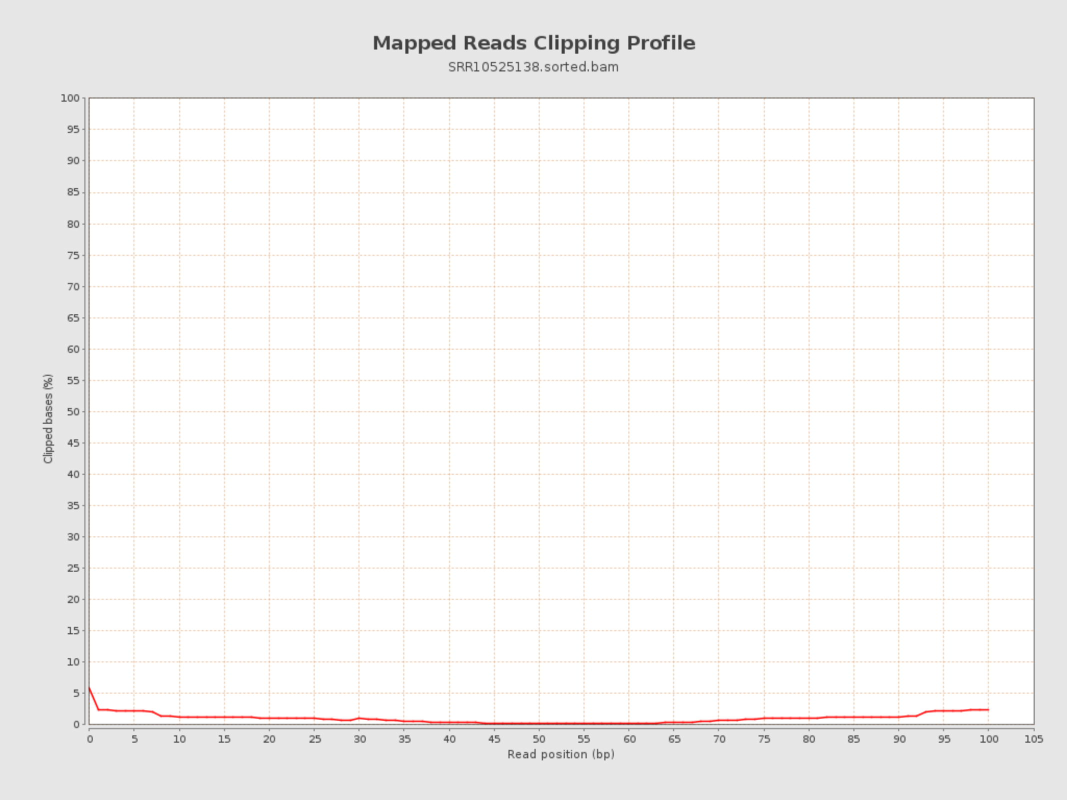
8. Results : Mapped Reads Nucleotide Content



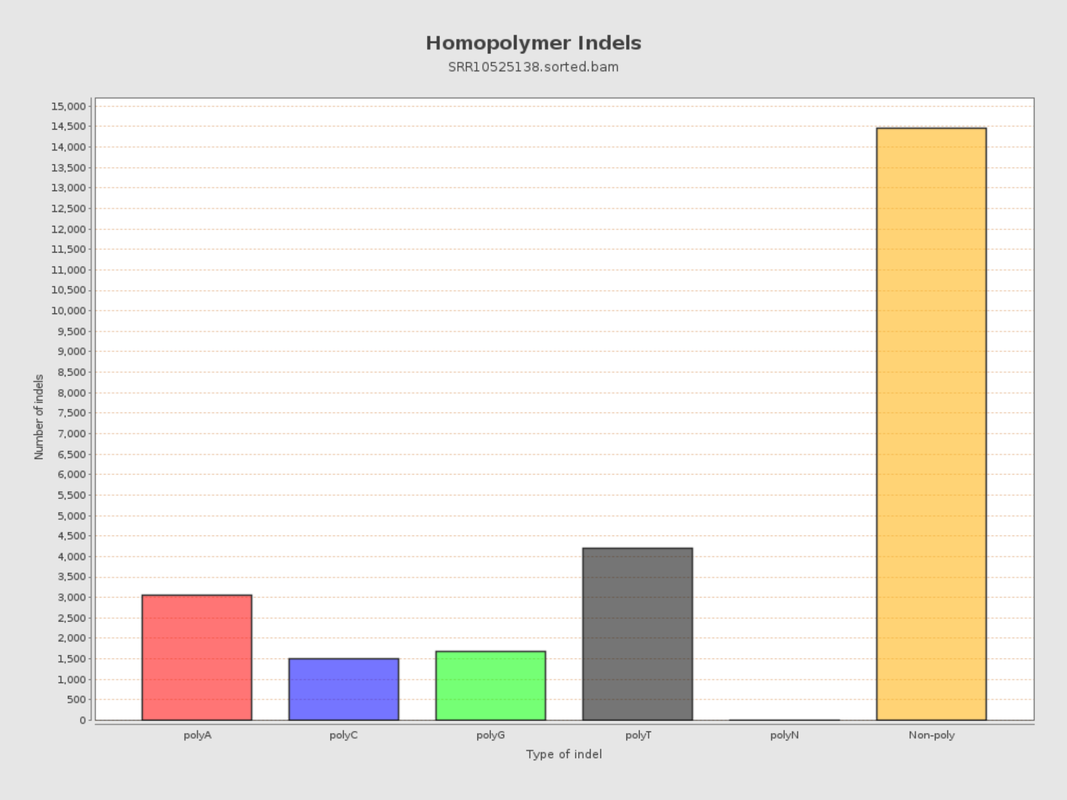
9. Results : Mapped Reads GC-content Distribution



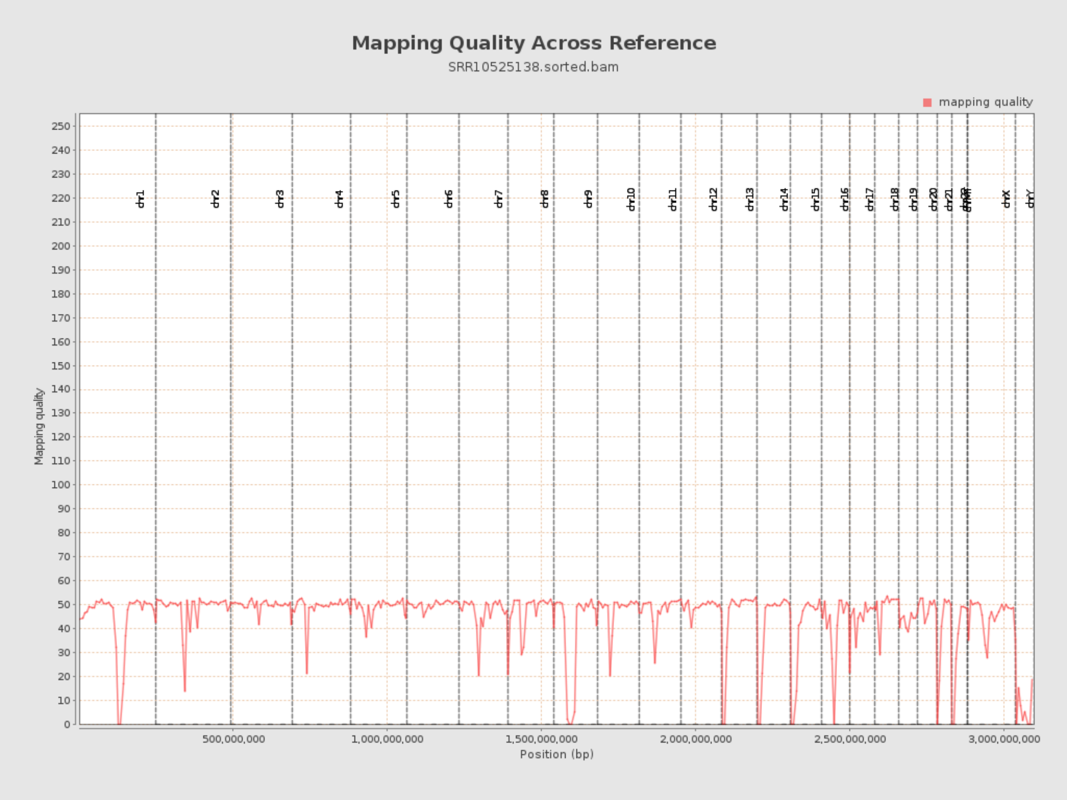
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram