Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:29:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525238.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_SRR10525238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:29:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	373,647
Mapped reads	345,512 / 92.47%
Unmapped reads	28,135 / 7.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,166 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	5,071 / 1.36%
Duplication rate	1.13%
Clipped reads	345,359 / 92.43%

2.2. ACGT Content

Number/percentage of A's	5,360,911 / 26.32%
Number/percentage of C's	3,577,953 / 17.57%
Number/percentage of T's	6,463,525 / 31.74%
Number/percentage of G's	4,962,364 / 24.37%
Number/percentage of N's	462 / 0%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0066

Standard Deviation	0.0943

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

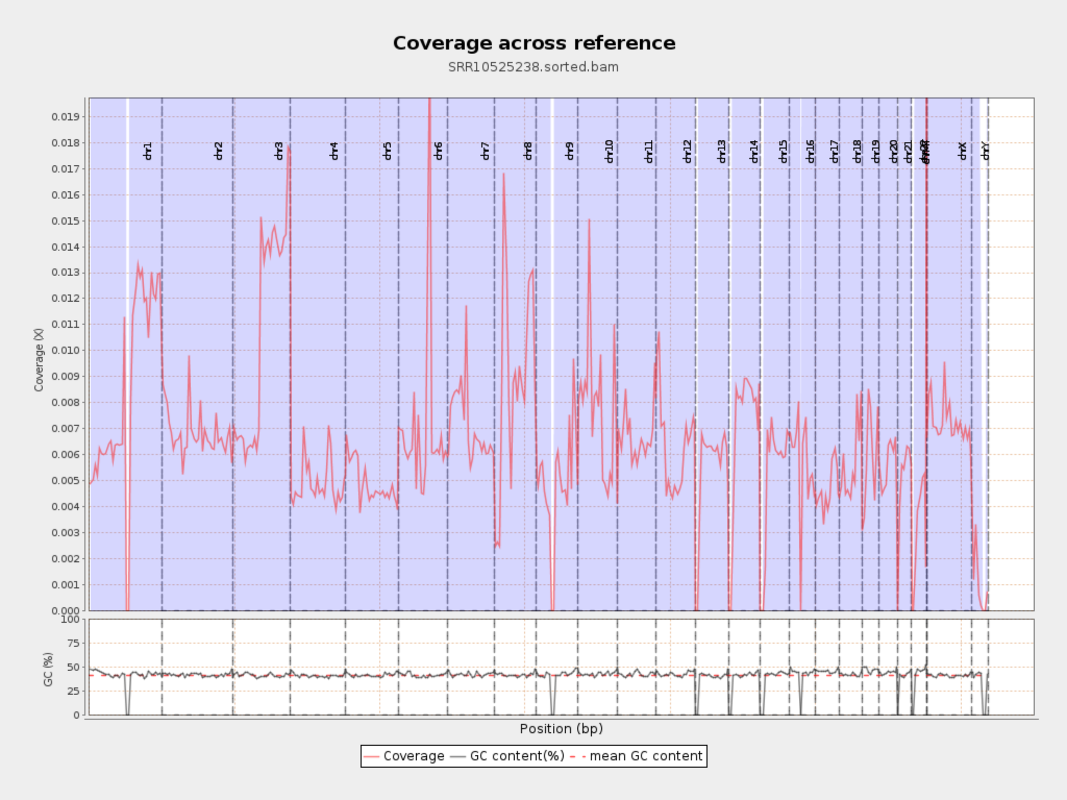
General error rate	0.51%
Mismatches	100,125
Insertions	1,690
Mapped reads with at least one insertion	0.49%
Deletions	4,375
Mapped reads with at least one deletion	1.25%
Homopolymer indels	40.53%

2.6. Chromosome stats

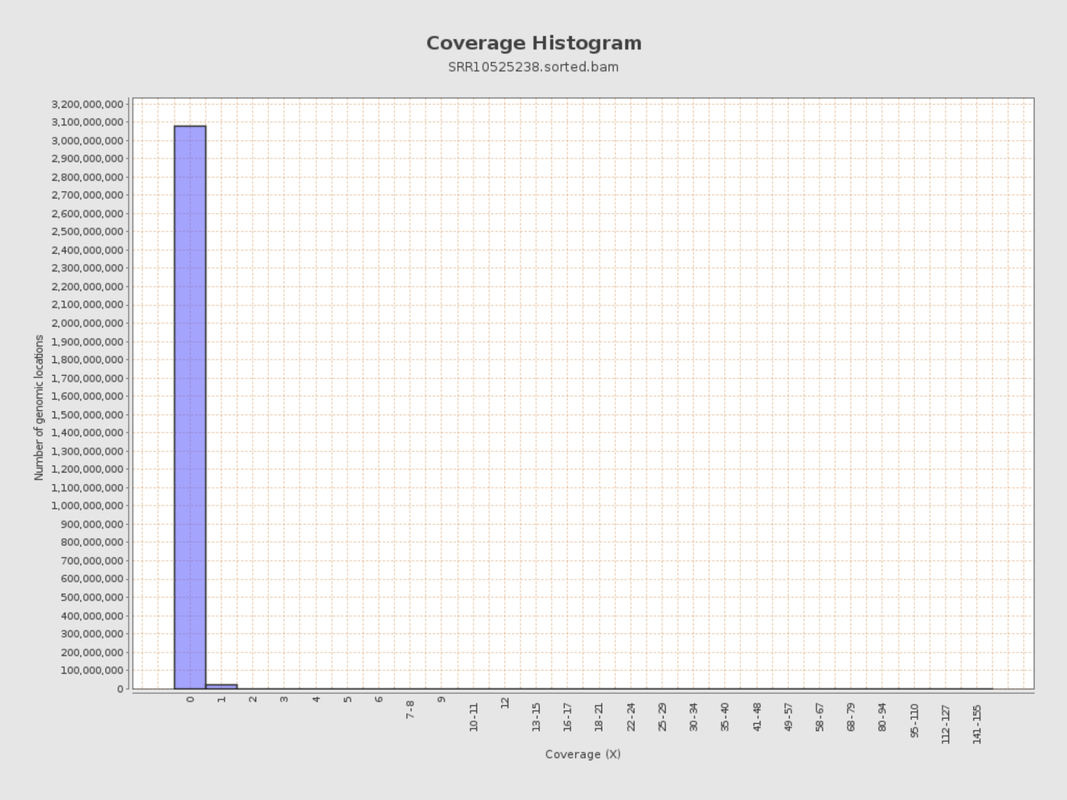
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2098620	0.0084	0.1403
chr2	243199373	1662204	0.0068	0.0997
chr3	198022430	2107542	0.0106	0.1056
chr4	191154276	936699	0.0049	0.073
chr5	180915260	885639	0.0049	0.0715
chr6	171115067	1235713	0.0072	0.0893
chr7	159138663	1142964	0.0072	0.1167

chr8	146364022	1292243	0.0088	0.1089
chr9	141213431	691532	0.0049	0.0758
chr10	135534747	1062875	0.0078	0.1067
chr11	135006516	905421	0.0067	0.088
chr12	133851895	835392	0.0062	0.0811
chr13	115169878	626520	0.0054	0.0753
chr14	107349540	739797	0.0069	0.0854
chr15	102531392	527596	0.0051	0.0737
chr16	90354753	502444	0.0056	0.078
chr17	81195210	377144	0.0046	0.0698
chr18	78077248	438726	0.0056	0.1037
chr19	59128983	356048	0.006	0.1021
chr20	63025520	351883	0.0056	0.0766
chr21	48129895	241183	0.005	0.0727
chr22	51304566	161311	0.0031	0.0574
chrMT	16571	528	0.0319	0.1756
chrX	155270560	1129746	0.0073	0.0886
chrY	59373566	62509	0.0011	0.0419

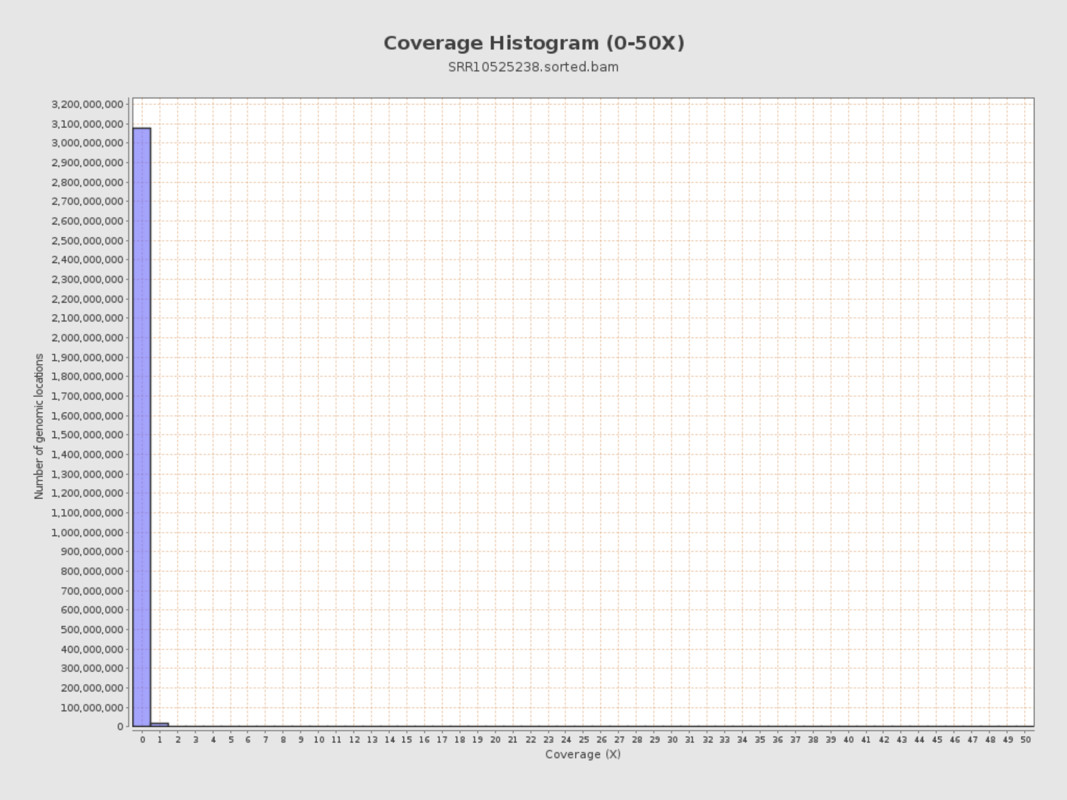
3. Results : Coverage across reference



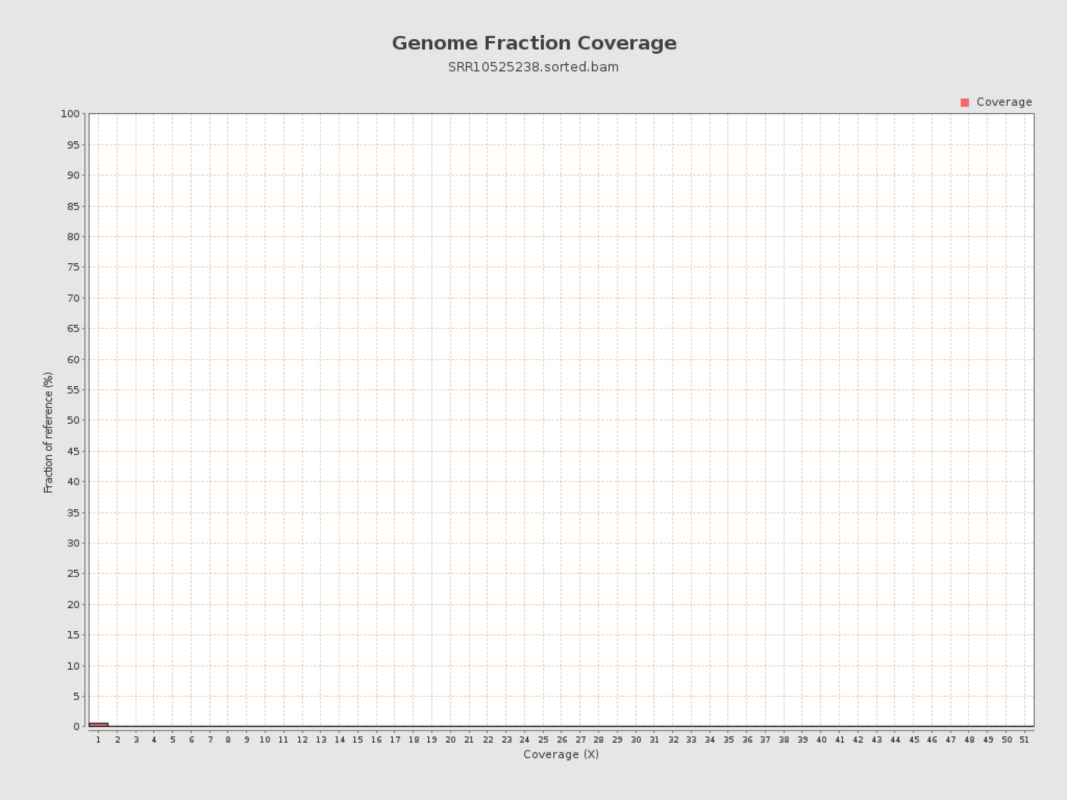
4. Results : Coverage Histogram



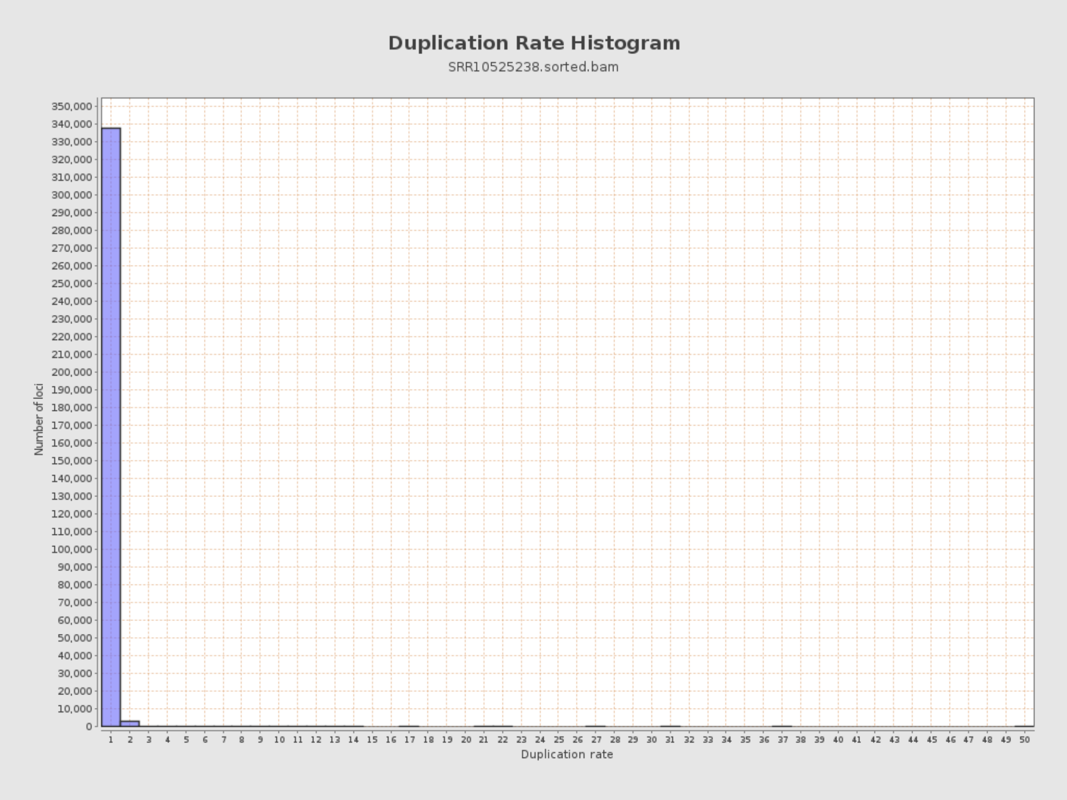
5. Results : Coverage Histogram (0-50X)



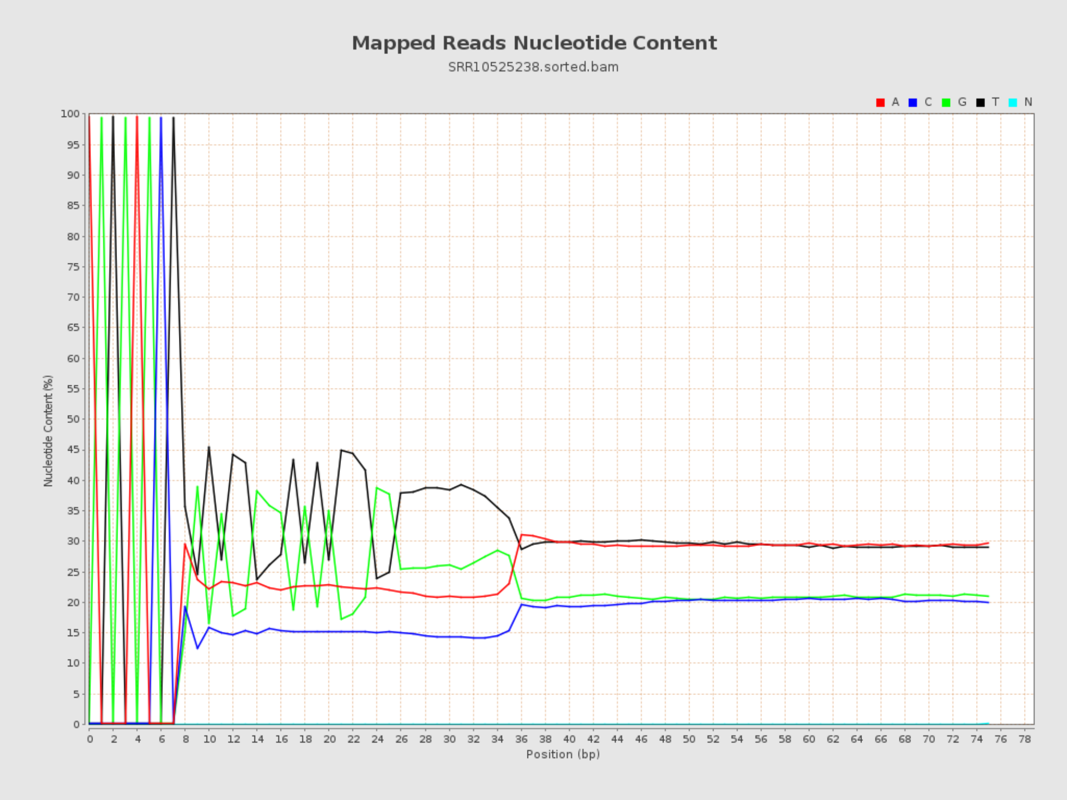
6. Results : Genome Fraction Coverage



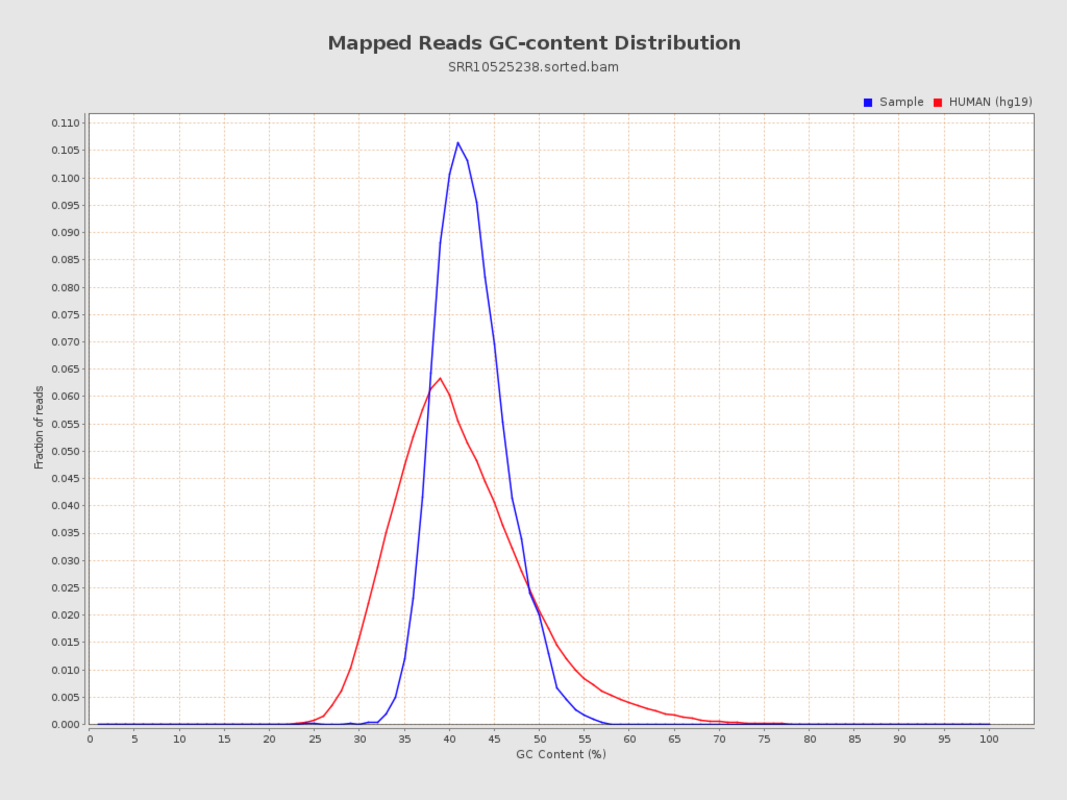
7. Results : Duplication Rate Histogram



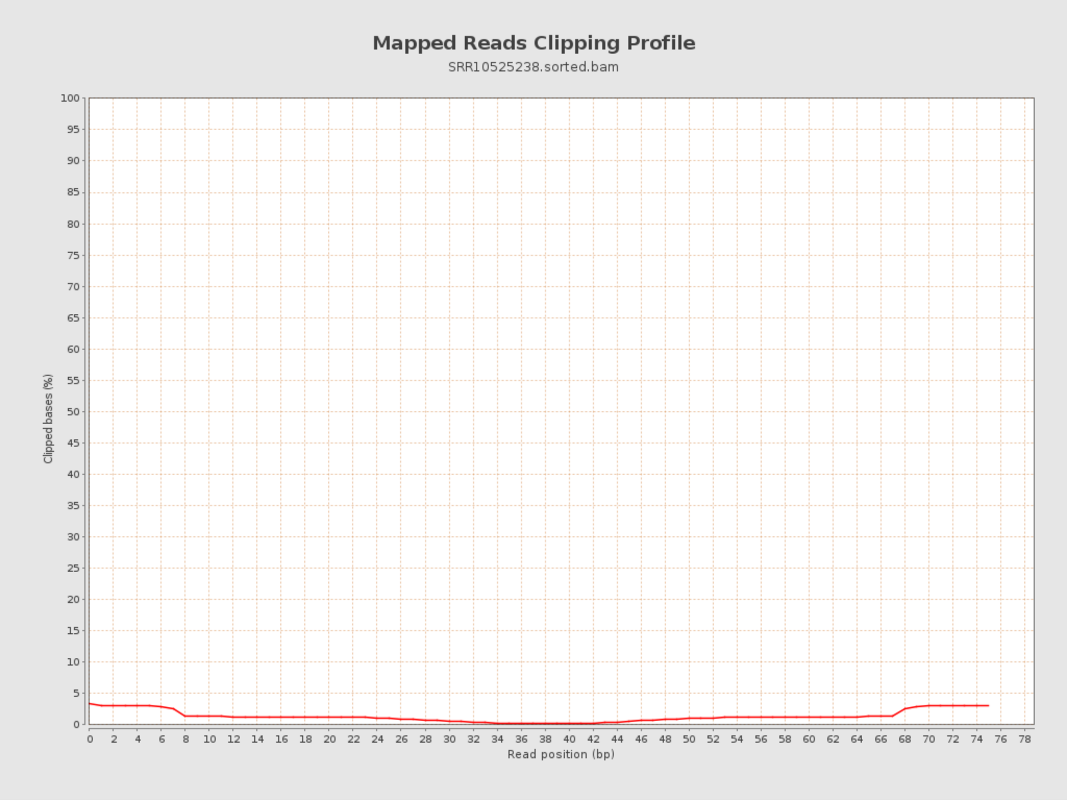
8. Results : Mapped Reads Nucleotide Content



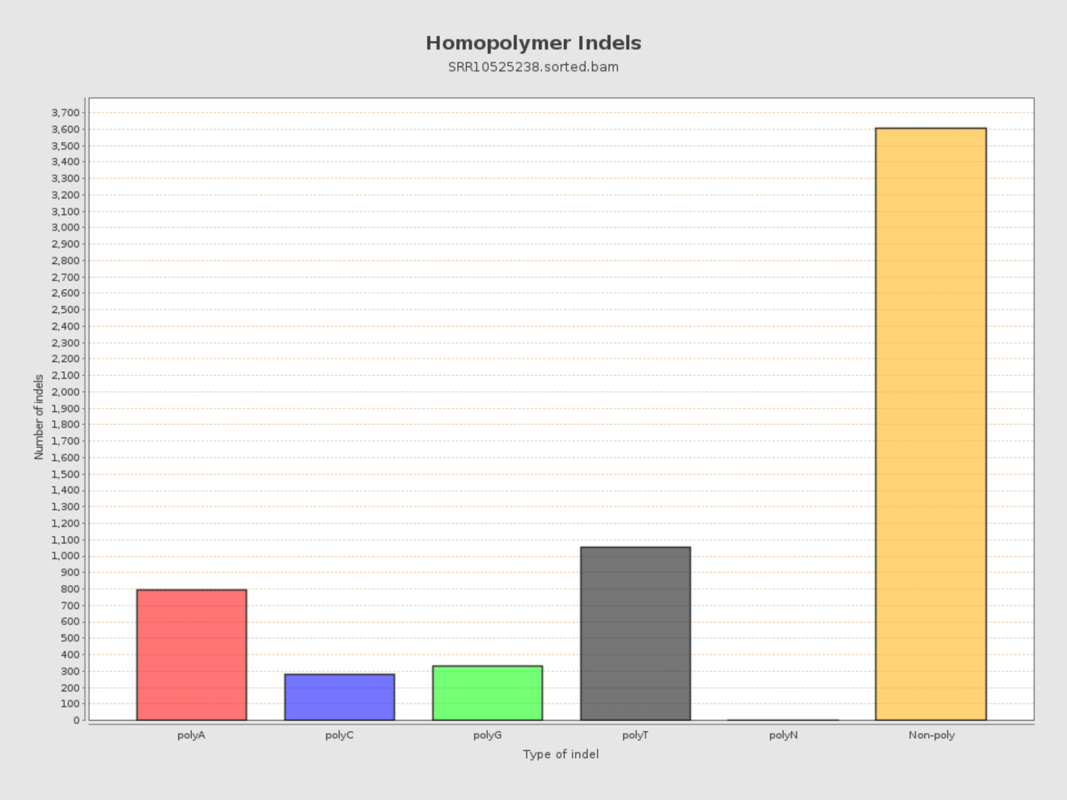
9. Results : Mapped Reads GC-content Distribution



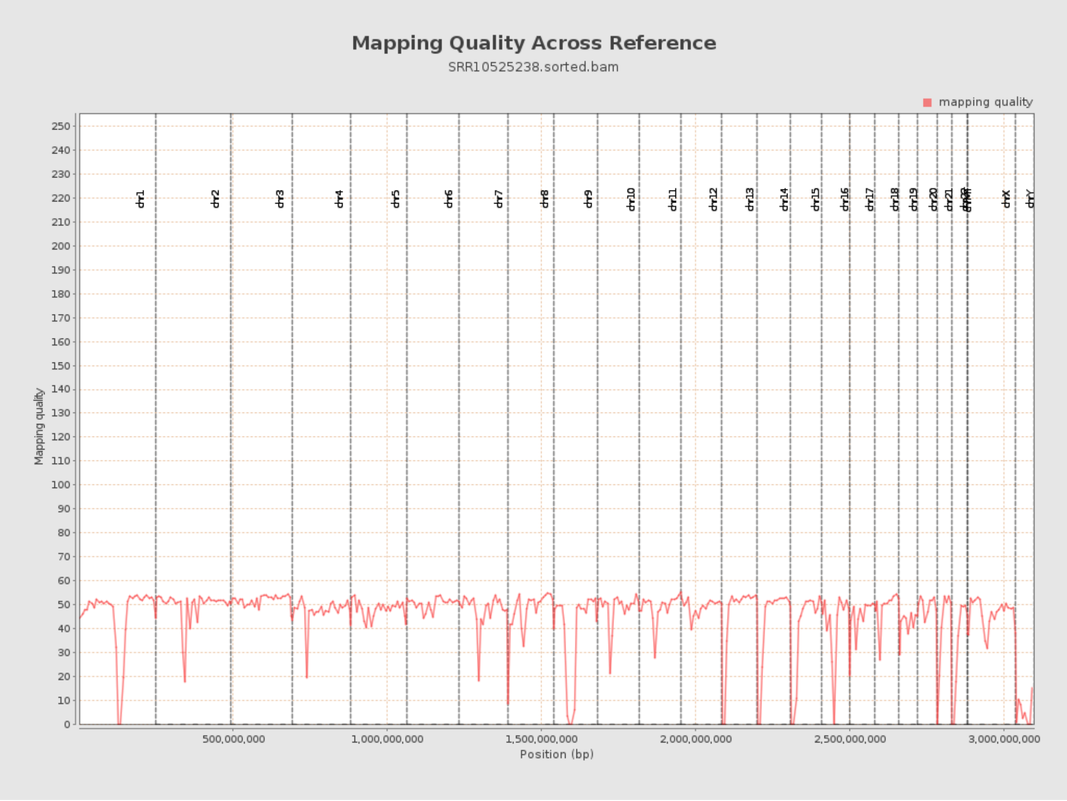
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram