Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:15:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525272.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_SRR10525272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:15:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,581,676
Mapped reads	1,451,234 / 91.75%
Unmapped reads	130,442 / 8.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,009 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	48,237 / 3.05%
Duplication rate	2.37%
Clipped reads	1,456,261 / 92.07%

2.2. ACGT Content

Number/percentage of A's	21,560,651 / 25.78%
Number/percentage of C's	14,284,756 / 17.08%
Number/percentage of T's	26,883,741 / 32.15%
Number/percentage of G's	20,888,371 / 24.98%
Number/percentage of N's	1,682 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2766

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

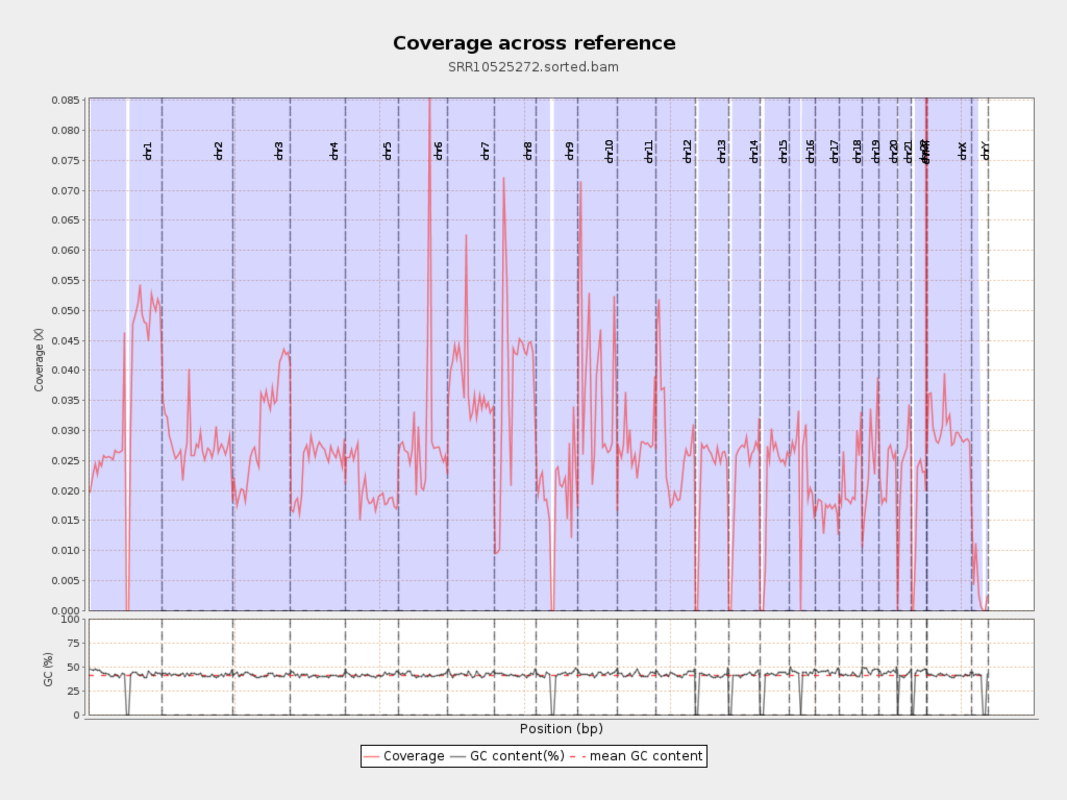
General error rate	0.51%
Mismatches	414,297
Insertions	4,833
Mapped reads with at least one insertion	0.33%
Deletions	17,334
Mapped reads with at least one deletion	1.19%
Homopolymer indels	44.95%

2.6. Chromosome stats

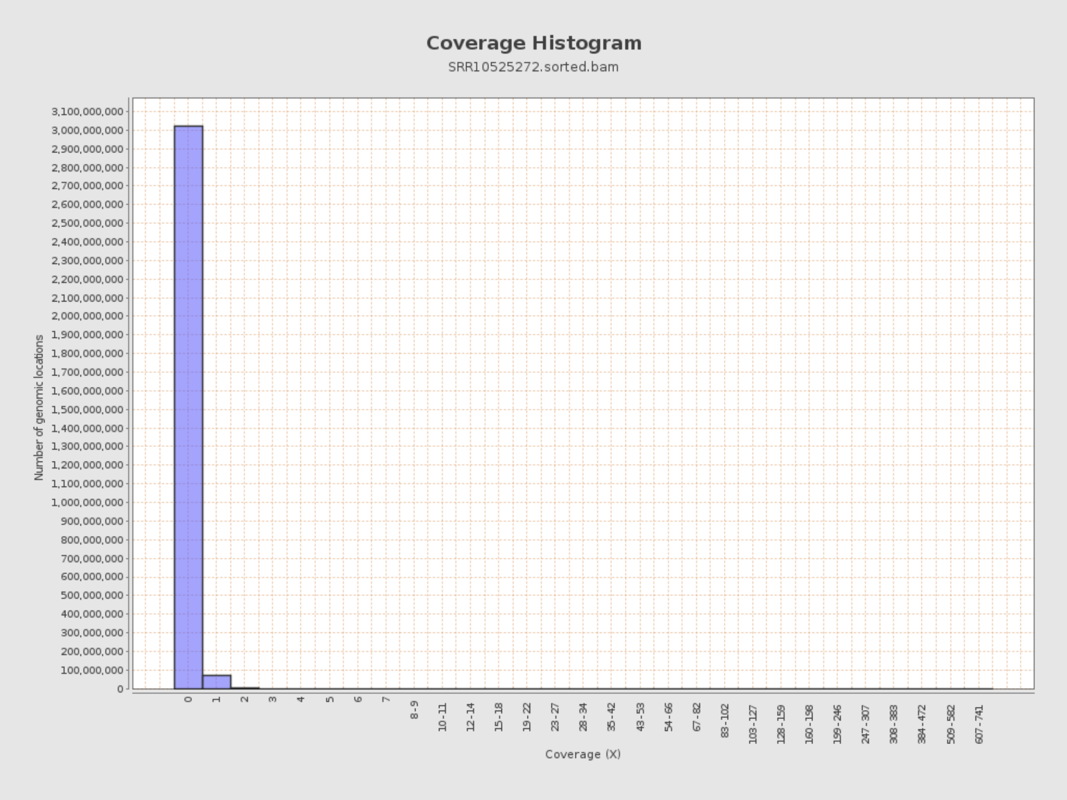
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8572614	0.0344	0.4882
chr2	243199373	6754163	0.0278	0.3498
chr3	198022430	6022775	0.0304	0.1899
chr4	191154276	4681275	0.0245	0.1738
chr5	180915260	3689833	0.0204	0.1549
chr6	171115067	5063291	0.0296	0.2072
chr7	159138663	6044587	0.038	0.5089

chr8	146364022	5482621	0.0375	0.2788
chr9	141213431	2675147	0.0189	0.1884
chr10	135534747	5159952	0.0381	0.2948
chr11	135006516	3751402	0.0278	0.2238
chr12	133851895	3626897	0.0271	0.1789
chr13	115169878	2596568	0.0225	0.1623
chr14	107349540	2405343	0.0224	0.164
chr15	102531392	2168372	0.0211	0.1583
chr16	90354753	2055475	0.0227	0.1759
chr17	81195210	1357709	0.0167	0.1426
chr18	78077248	1717261	0.022	0.3655
chr19	59128983	1472016	0.0249	0.3694
chr20	63025520	1421862	0.0226	0.1637
chr21	48129895	1126060	0.0234	0.1689
chr22	51304566	842504	0.0164	0.1372
chrMT	16571	49266	2.973	2.4098
chrX	155270560	4686344	0.0302	0.2013
chrY	59373566	223564	0.0038	0.0955

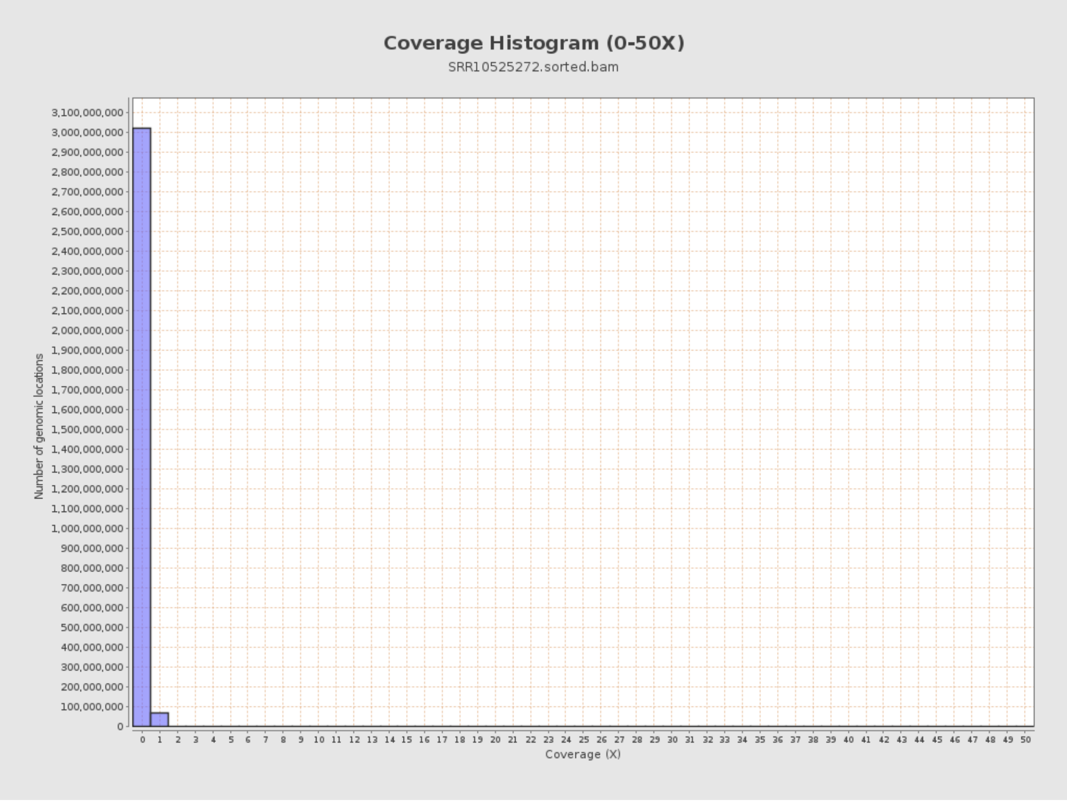
3. Results : Coverage across reference



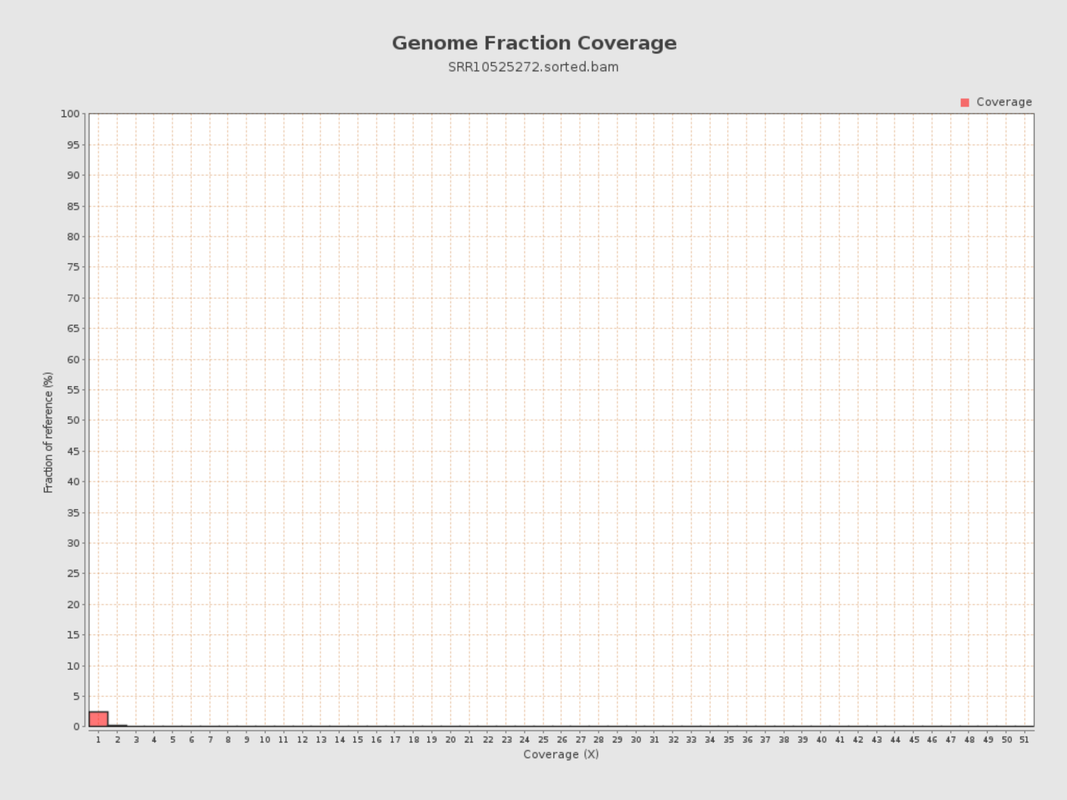
4. Results : Coverage Histogram



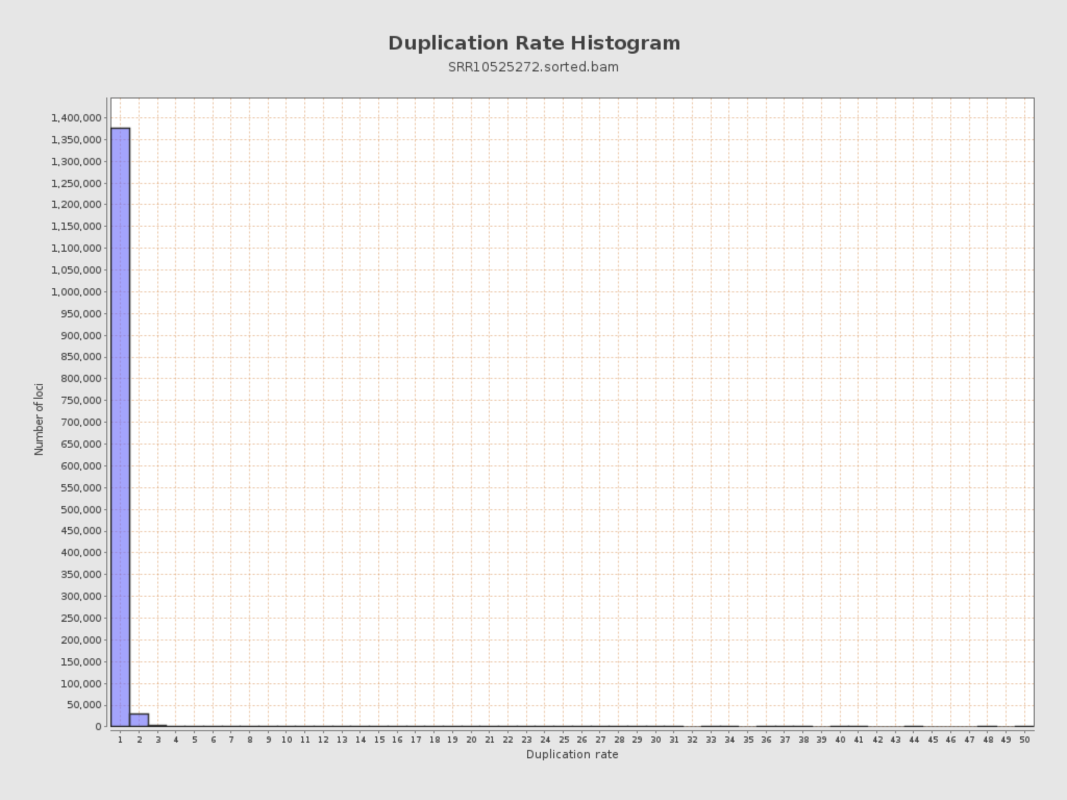
5. Results : Coverage Histogram (0-50X)



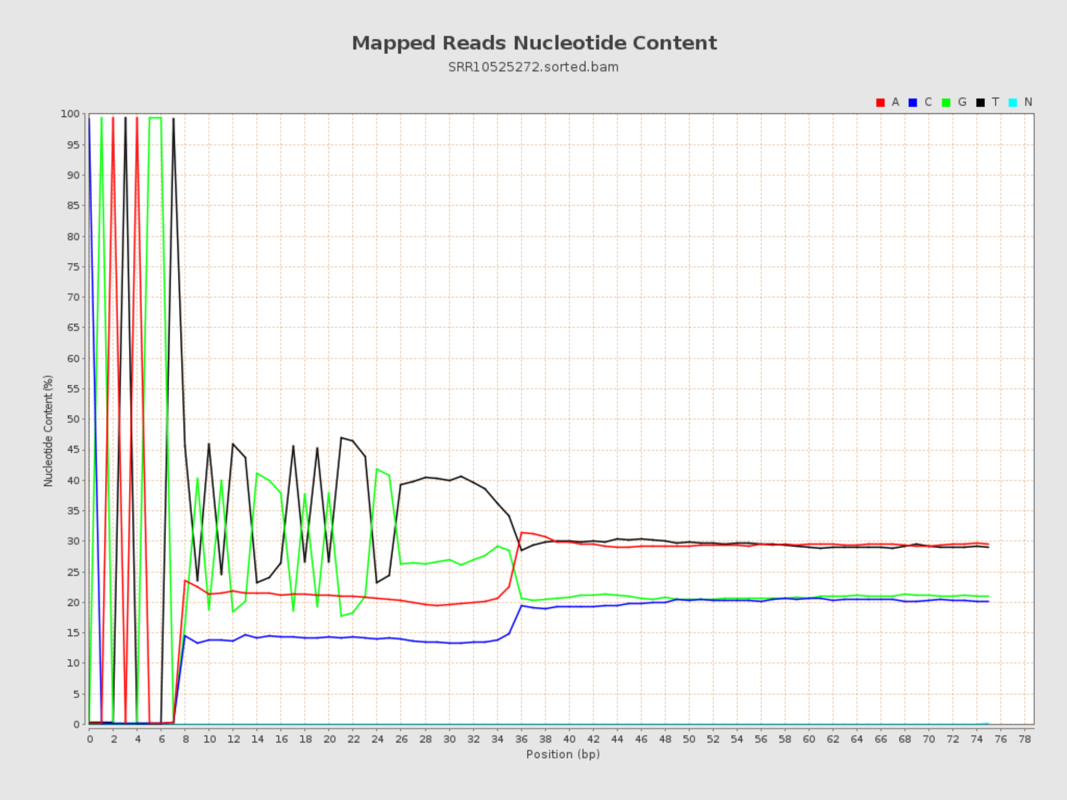
6. Results : Genome Fraction Coverage



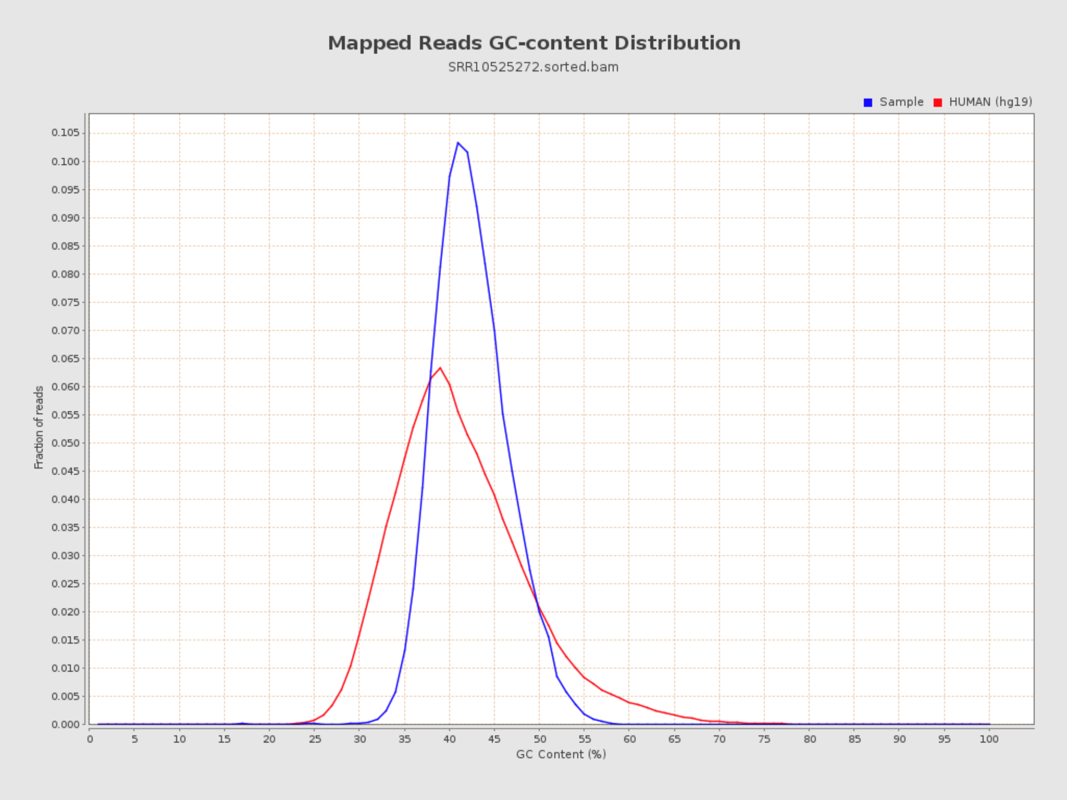
7. Results : Duplication Rate Histogram



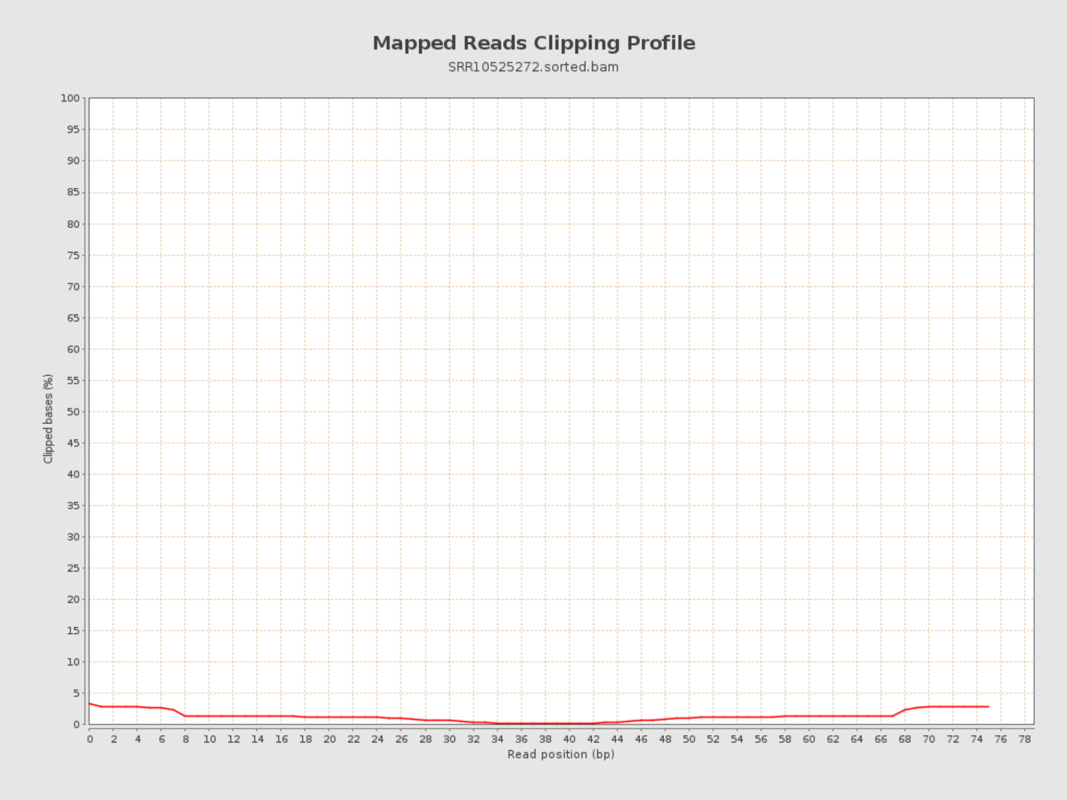
8. Results : Mapped Reads Nucleotide Content



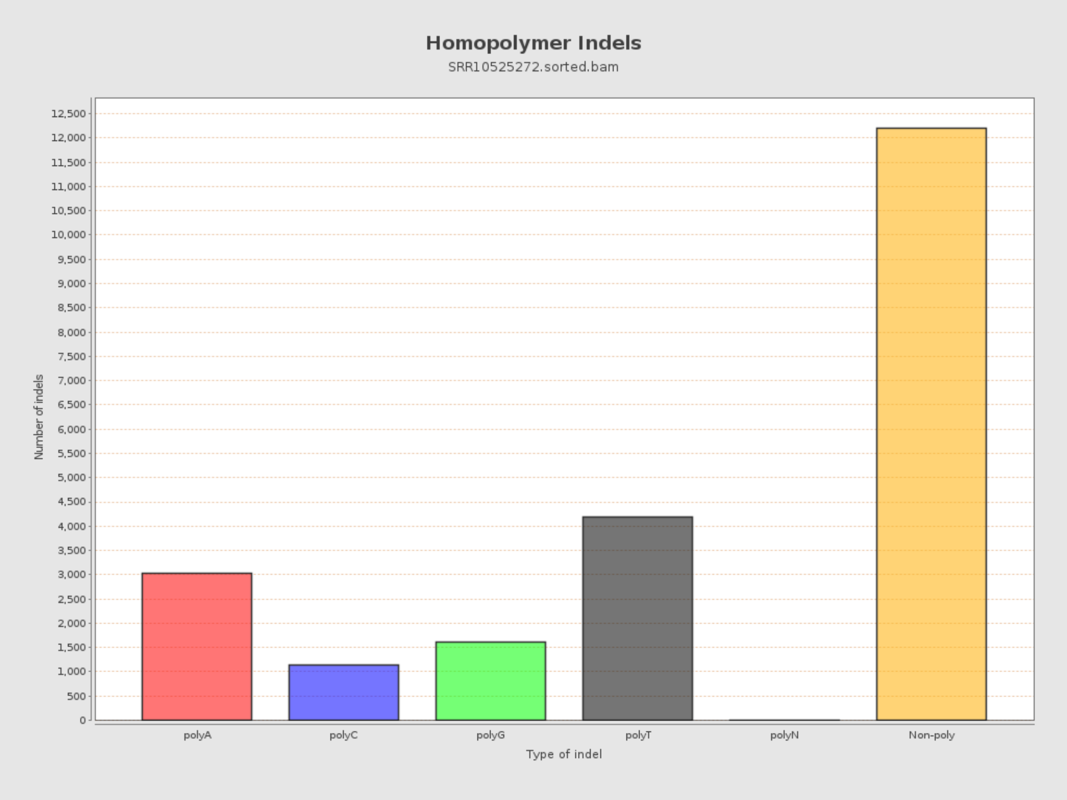
9. Results : Mapped Reads GC-content Distribution



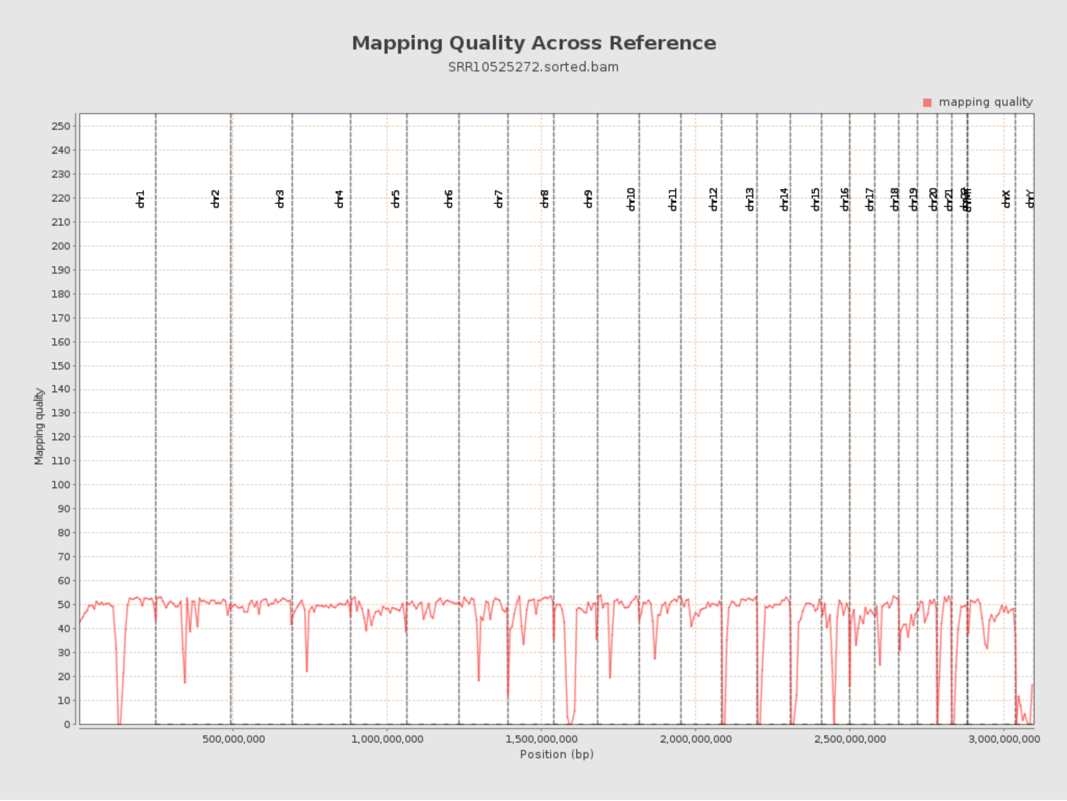
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram