Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:14:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525033.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_SRR10525033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,205,317
Mapped reads	2,013,377 / 91.3%
Unmapped reads	191,940 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,730 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	70,325 / 3.19%
Duplication rate	2.58%
Clipped reads	2,015,750 / 91.4%

2.2. ACGT Content

Number/percentage of A's	30,375,443 / 26.16%
Number/percentage of C's	21,185,788 / 18.24%
Number/percentage of T's	35,858,260 / 30.88%
Number/percentage of G's	28,712,439 / 24.72%
Number/percentage of N's	3,414 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3124

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

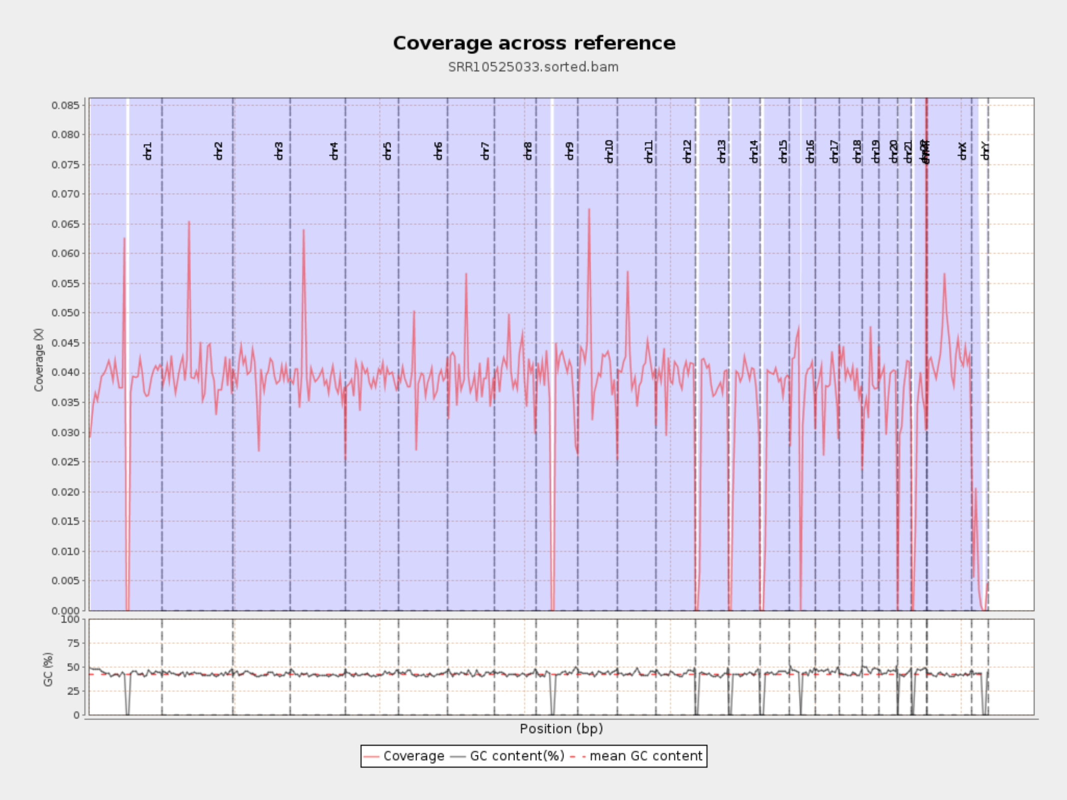
General error rate	0.49%
Mismatches	561,599
Insertions	7,096
Mapped reads with at least one insertion	0.35%
Deletions	18,307
Mapped reads with at least one deletion	0.9%
Homopolymer indels	41.74%

2.6. Chromosome stats

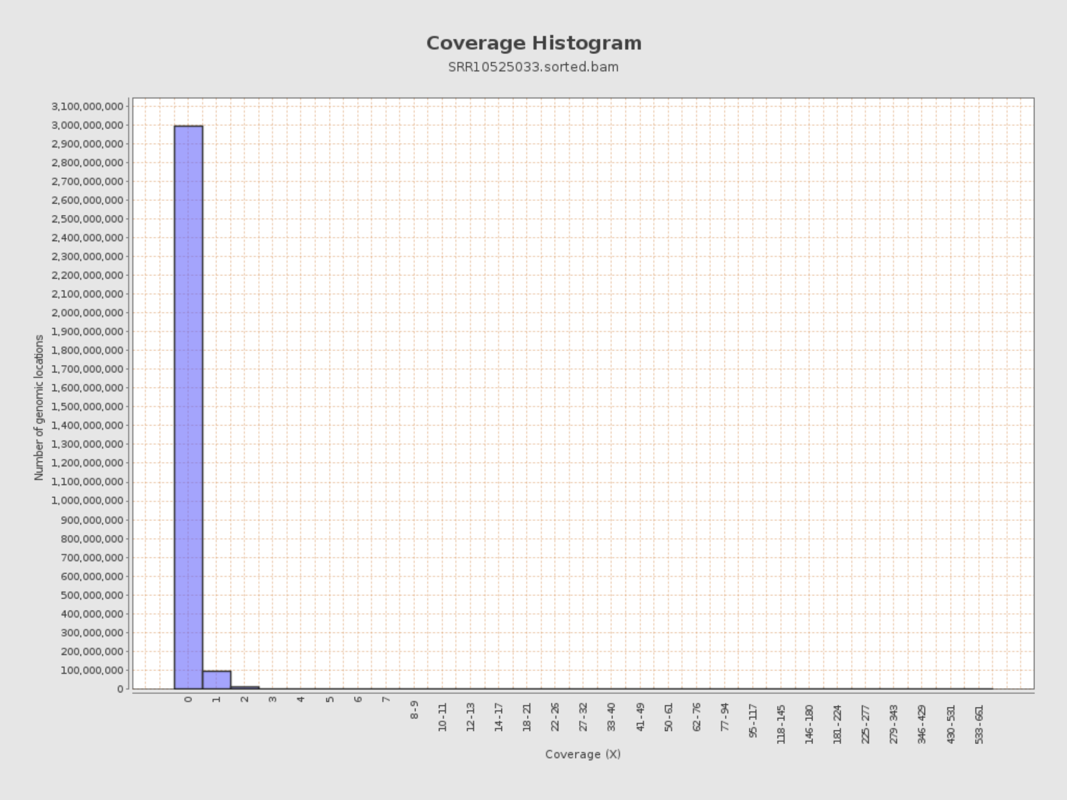
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9209441	0.0369	0.5575
chr2	243199373	9853420	0.0405	0.3372
chr3	198022430	7874458	0.0398	0.2203
chr4	191154276	7554857	0.0395	0.2461
chr5	180915260	7044226	0.0389	0.2192
chr6	171115067	6648719	0.0389	0.2407
chr7	159138663	6312135	0.0397	0.3419

chr8	146364022	5872858	0.0401	0.3446
chr9	141213431	5011284	0.0355	0.2958
chr10	135534747	5637308	0.0416	0.3191
chr11	135006516	5526118	0.0409	0.3005
chr12	133851895	5281166	0.0395	0.2258
chr13	115169878	3743145	0.0325	0.1977
chr14	107349540	3528901	0.0329	0.2222
chr15	102531392	3241676	0.0316	0.1963
chr16	90354753	3305194	0.0366	0.2297
chr17	81195210	2984817	0.0368	0.227
chr18	78077248	3124081	0.04	0.5452
chr19	59128983	2190591	0.037	0.4174
chr20	63025520	2367307	0.0376	0.2241
chr21	48129895	1562089	0.0325	0.231
chr22	51304566	1279441	0.0249	0.1736
chrMT	16571	4984	0.3008	0.6054
chrX	155270560	6656521	0.0429	0.2675
chrY	59373566	350906	0.0059	0.1505

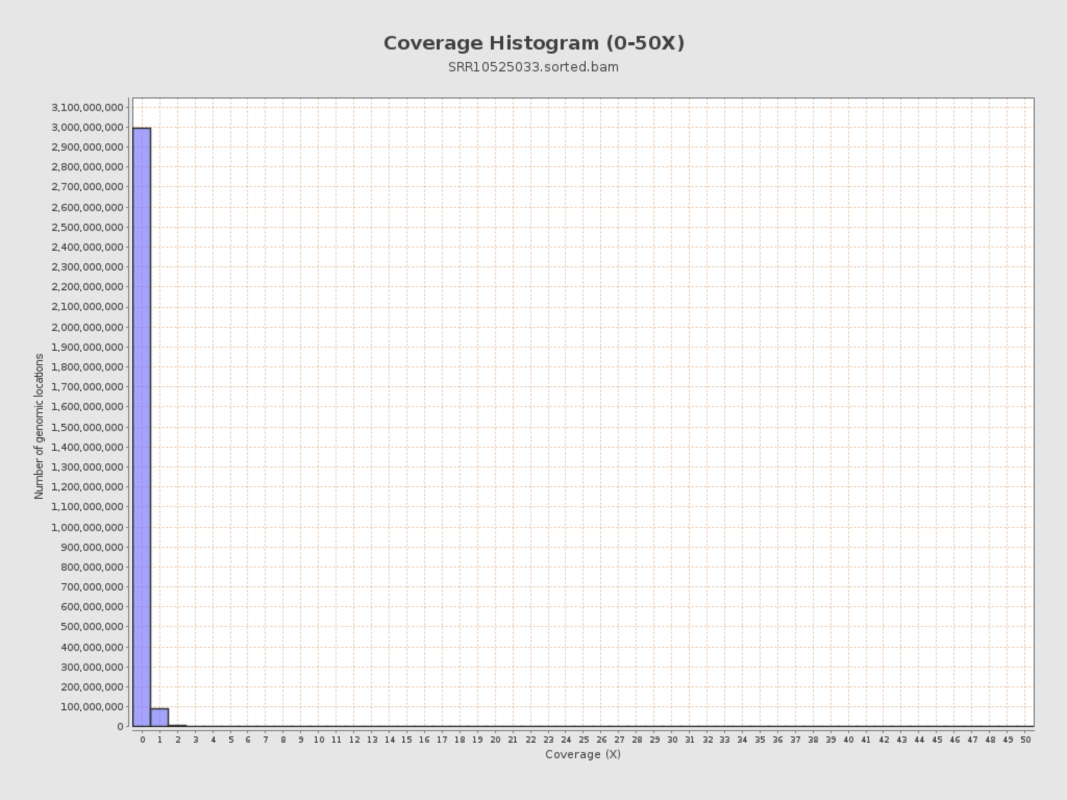
3. Results : Coverage across reference



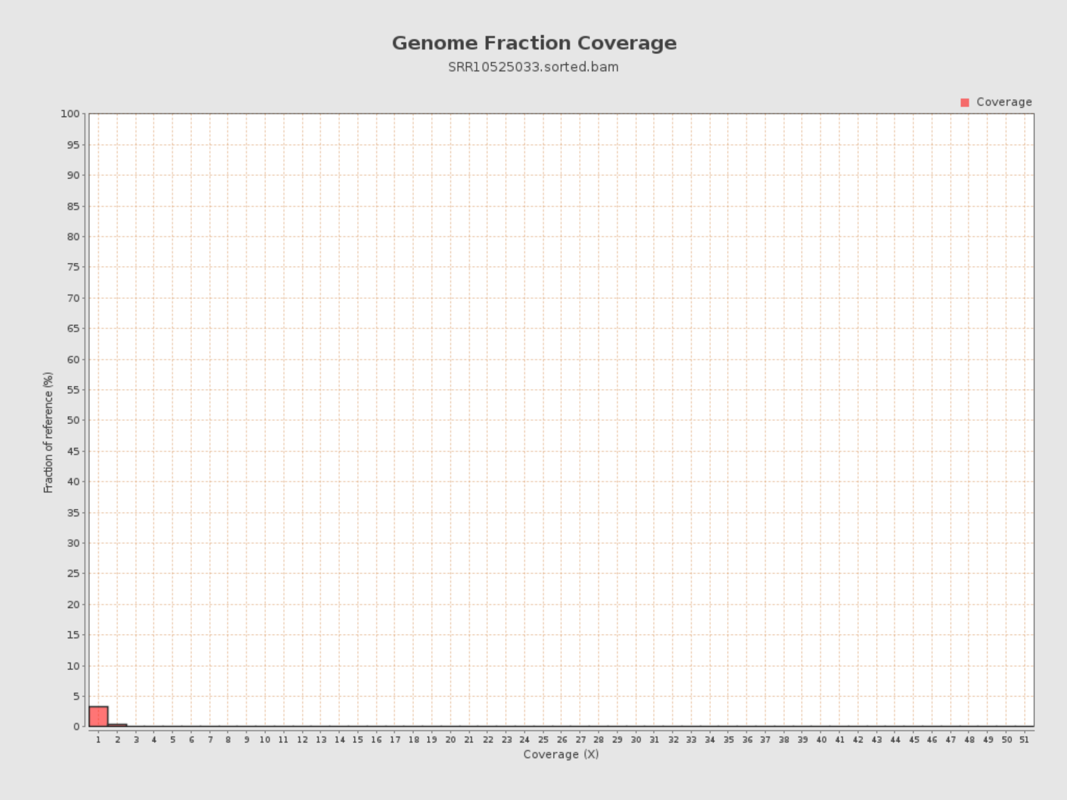
4. Results : Coverage Histogram



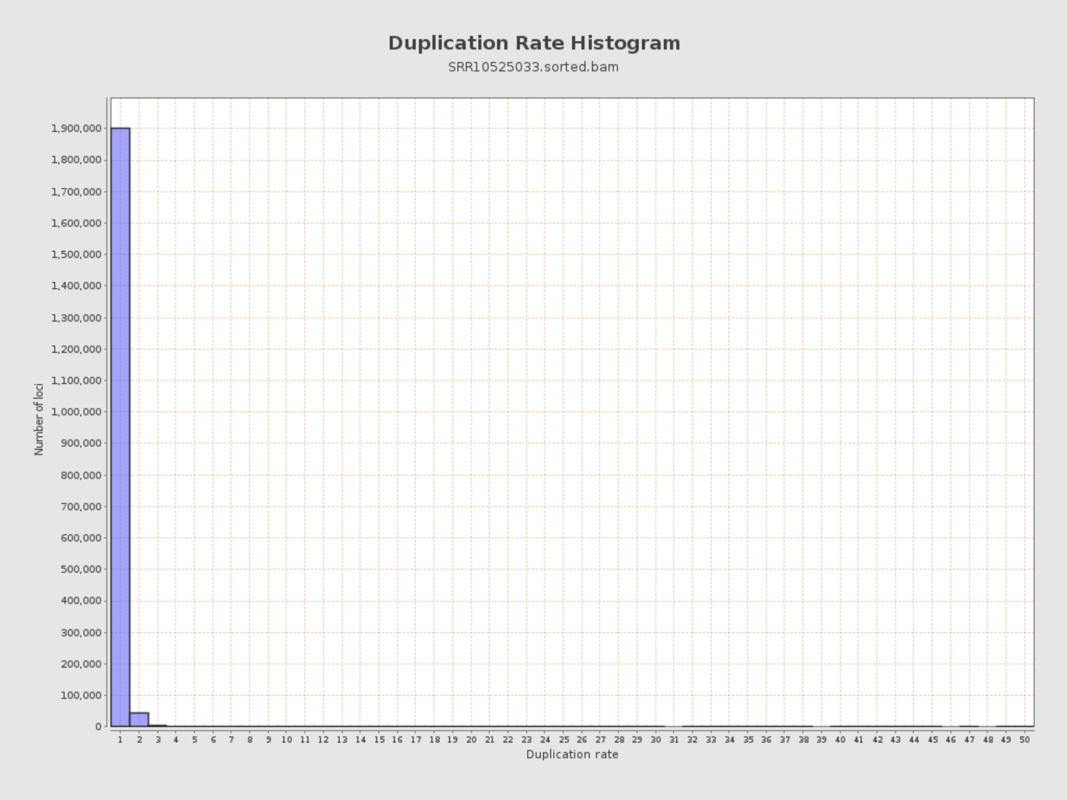
5. Results : Coverage Histogram (0-50X)



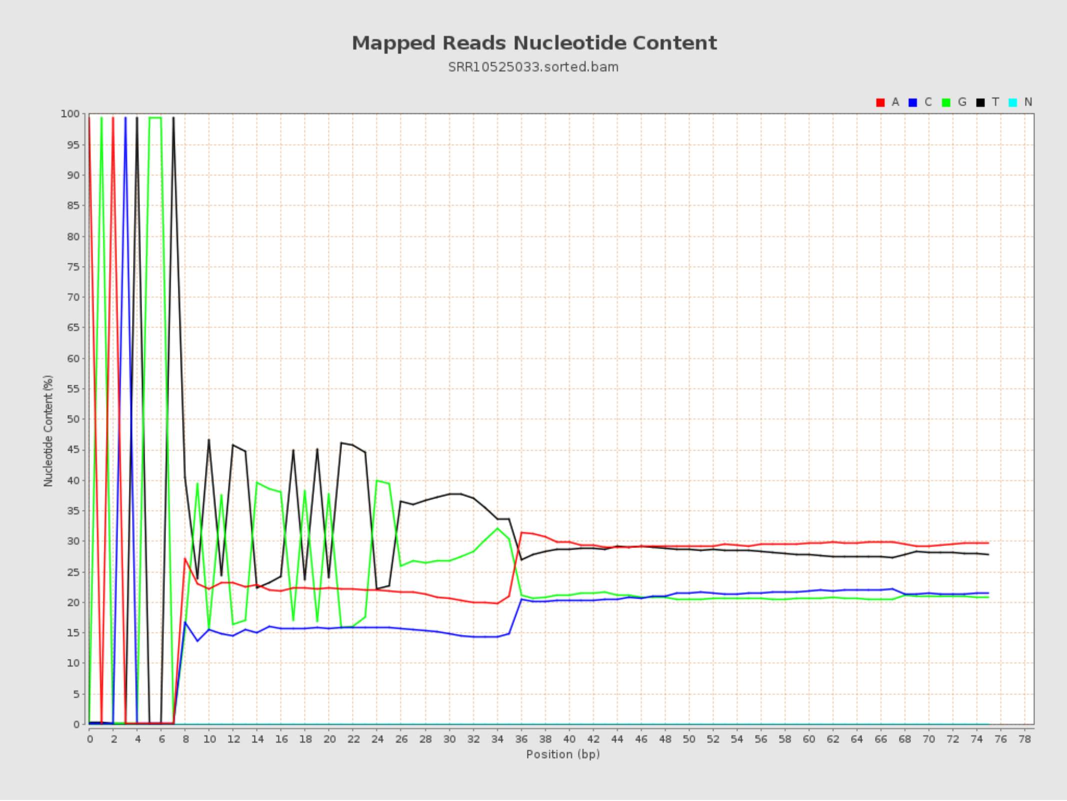
6. Results : Genome Fraction Coverage



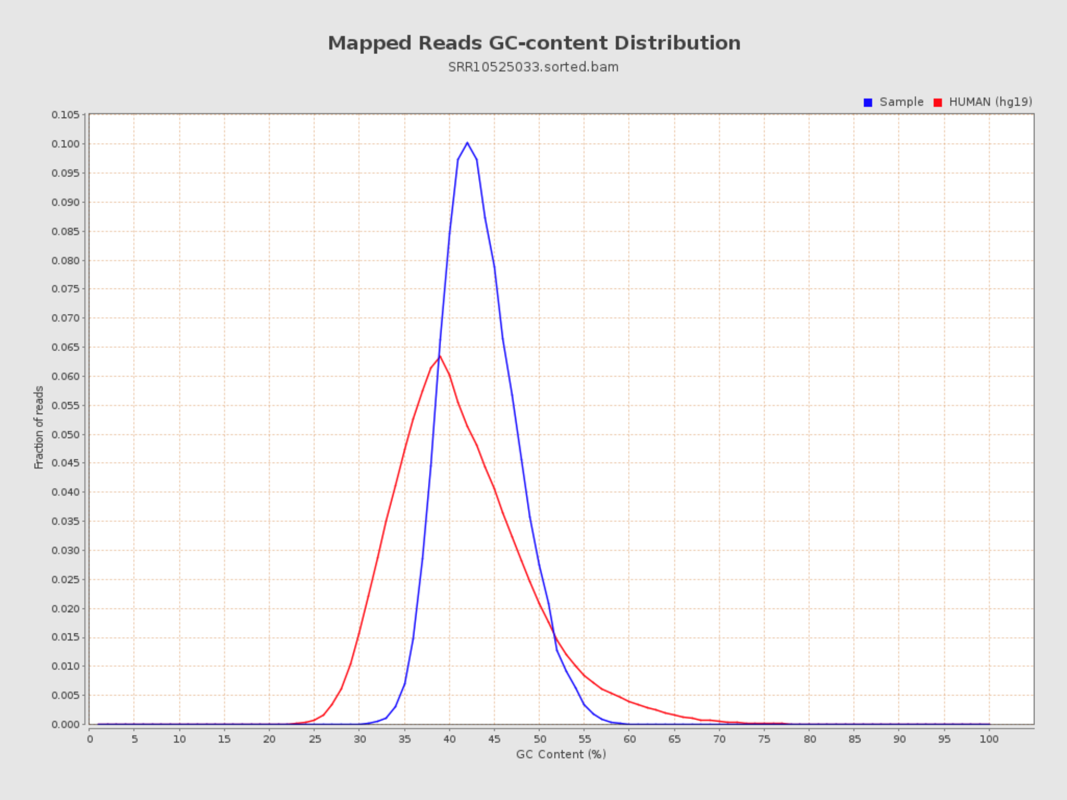
7. Results : Duplication Rate Histogram



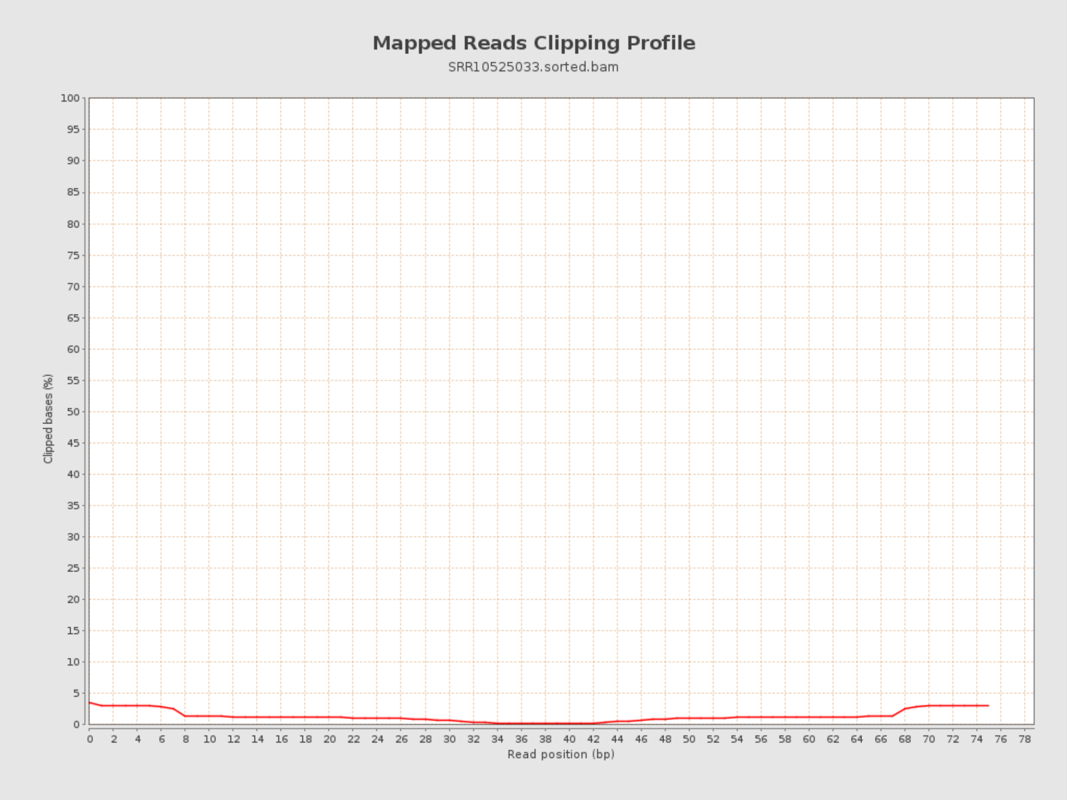
8. Results : Mapped Reads Nucleotide Content



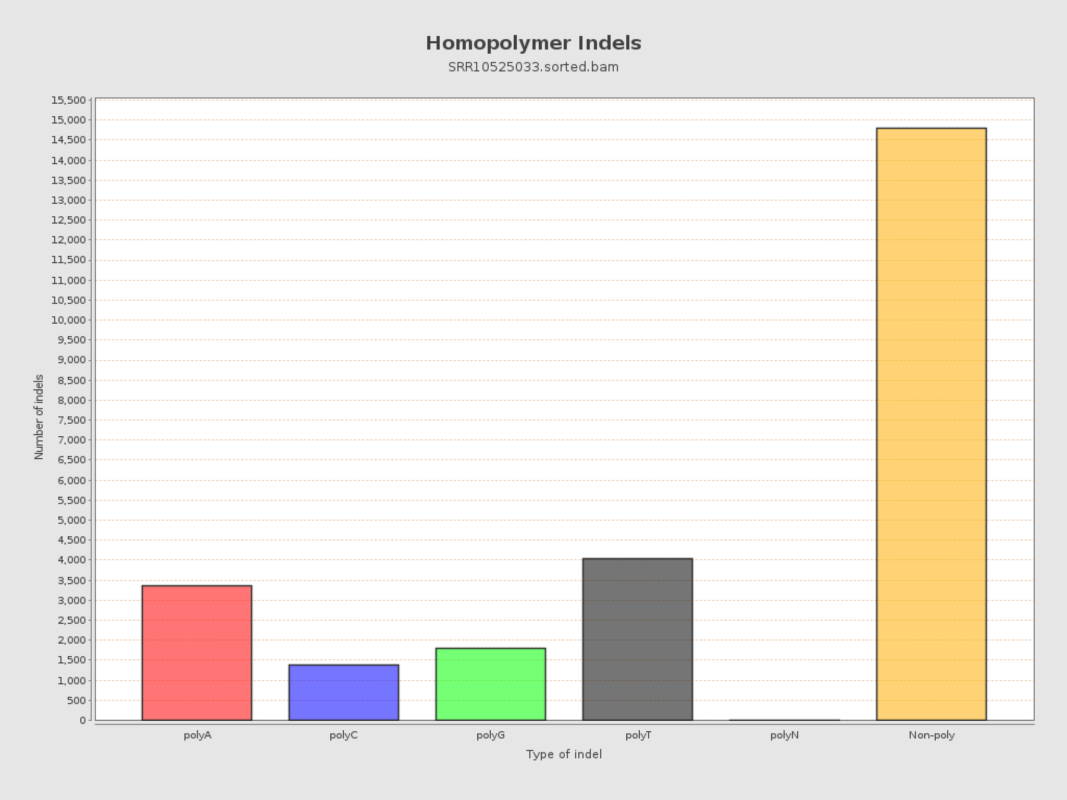
9. Results : Mapped Reads GC-content Distribution



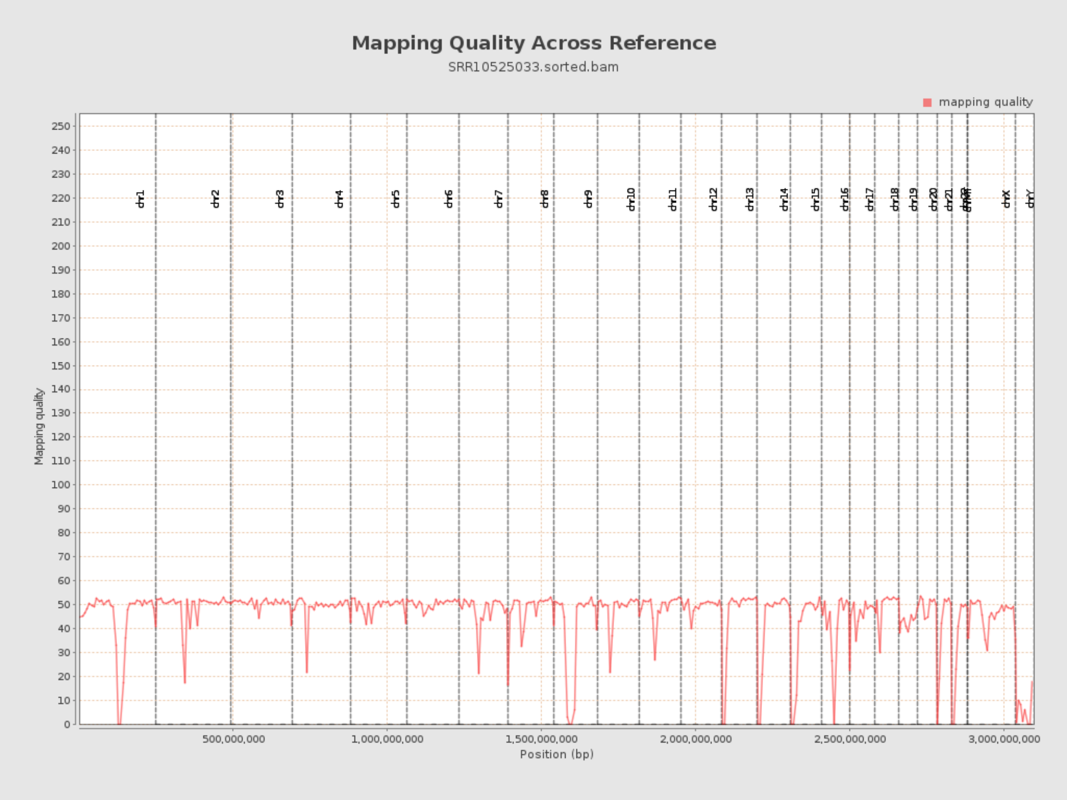
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram