Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:39:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525162.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_SRR10525162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:39:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,324,110
Mapped reads	2,145,545 / 92.32%
Unmapped reads	178,565 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,243 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	89,650 / 3.86%
Duplication rate	3.1%
Clipped reads	2,148,144 / 92.43%

2.2. ACGT Content

Number/percentage of A's	30,732,405 / 24.54%
Number/percentage of C's	24,456,954 / 19.53%
Number/percentage of T's	39,170,748 / 31.28%
Number/percentage of G's	30,872,158 / 24.65%
Number/percentage of N's	2,884 / 0%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.3421

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

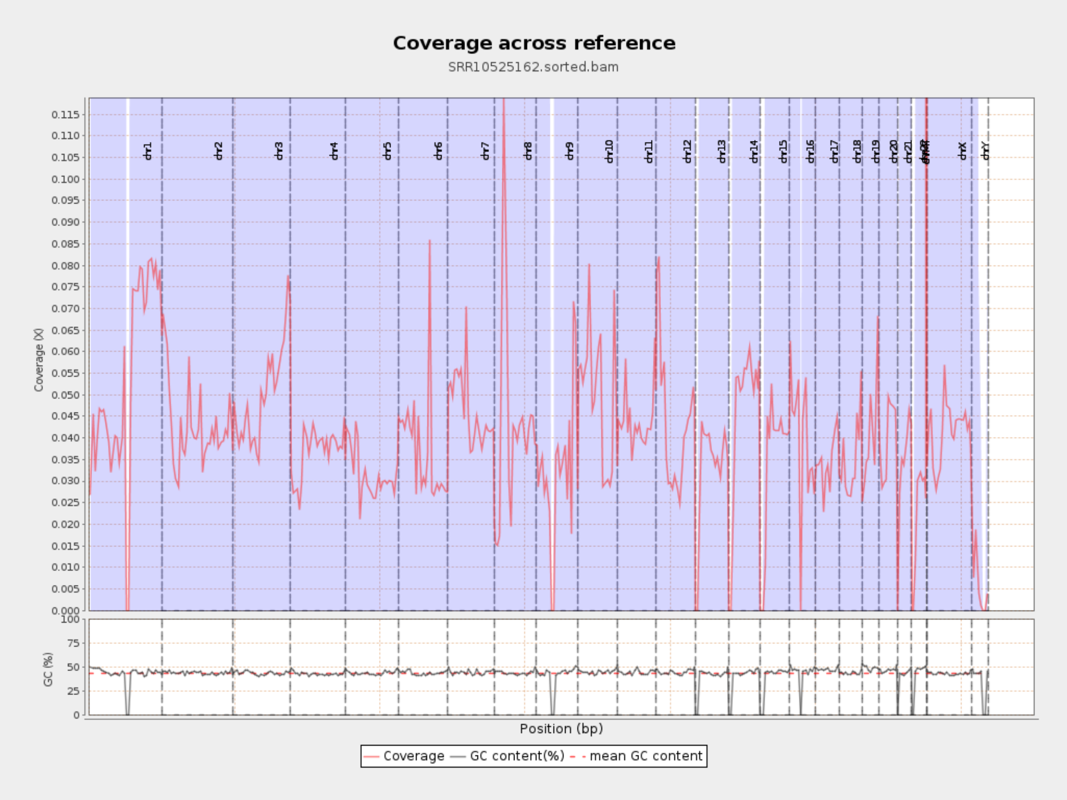
General error rate	0.51%
Mismatches	628,984
Insertions	8,129
Mapped reads with at least one insertion	0.38%
Deletions	24,503
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.63%

2.6. Chromosome stats

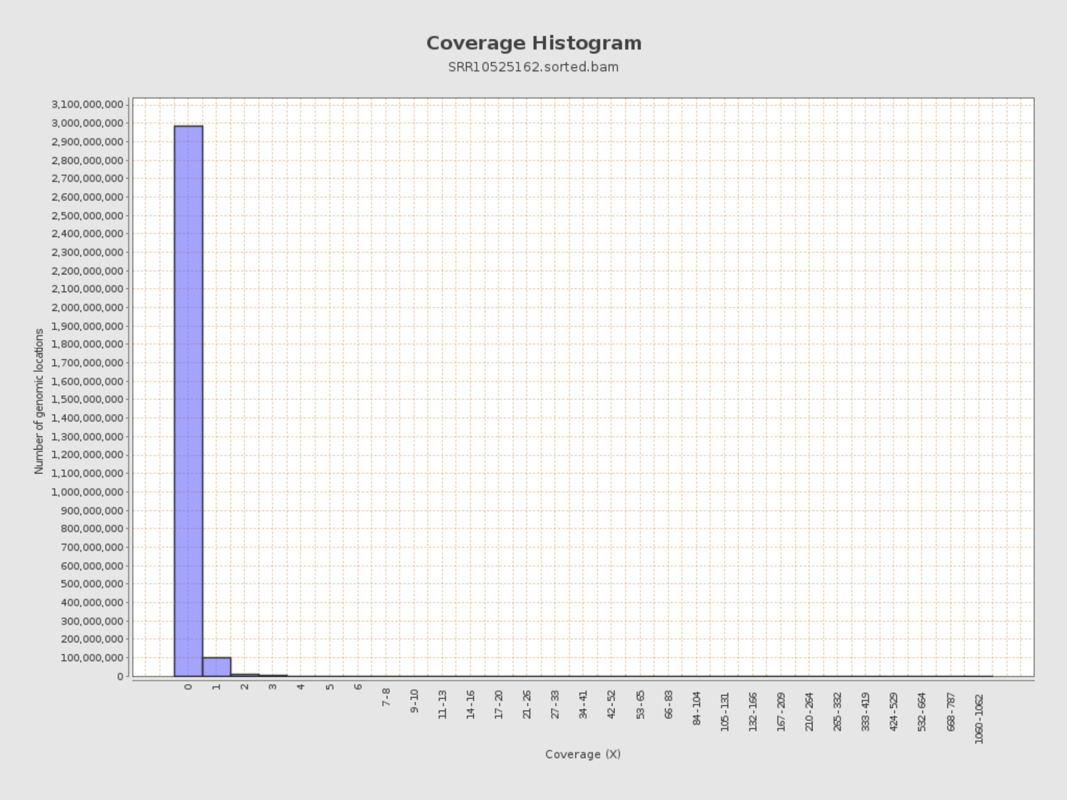
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13235176	0.0531	0.5682
chr2	243199373	10479356	0.0431	0.4937
chr3	198022430	9843940	0.0497	0.2505
chr4	191154276	7026902	0.0368	0.2259
chr5	180915260	5697082	0.0315	0.198
chr6	171115067	6432157	0.0376	0.2521
chr7	159138663	7433367	0.0467	0.5318

chr8	146364022	6278283	0.0429	0.3127
chr9	141213431	4568130	0.0323	0.2617
chr10	135534747	6837323	0.0504	0.3722
chr11	135006516	5929657	0.0439	0.2966
chr12	133851895	5760383	0.043	0.2342
chr13	115169878	3782202	0.0328	0.2047
chr14	107349540	4839214	0.0451	0.2448
chr15	102531392	3528183	0.0344	0.2078
chr16	90354753	3505679	0.0388	0.2473
chr17	81195210	2812332	0.0346	0.2192
chr18	78077248	2692732	0.0345	0.505
chr19	59128983	2437832	0.0412	0.4257
chr20	63025520	2493744	0.0396	0.2251
chr21	48129895	1629807	0.0339	0.2204
chr22	51304566	1091342	0.0213	0.1603
chrMT	16571	126345	7.6245	4.7819
chrX	155270560	6454308	0.0416	0.2496
chrY	59373566	358817	0.006	0.161

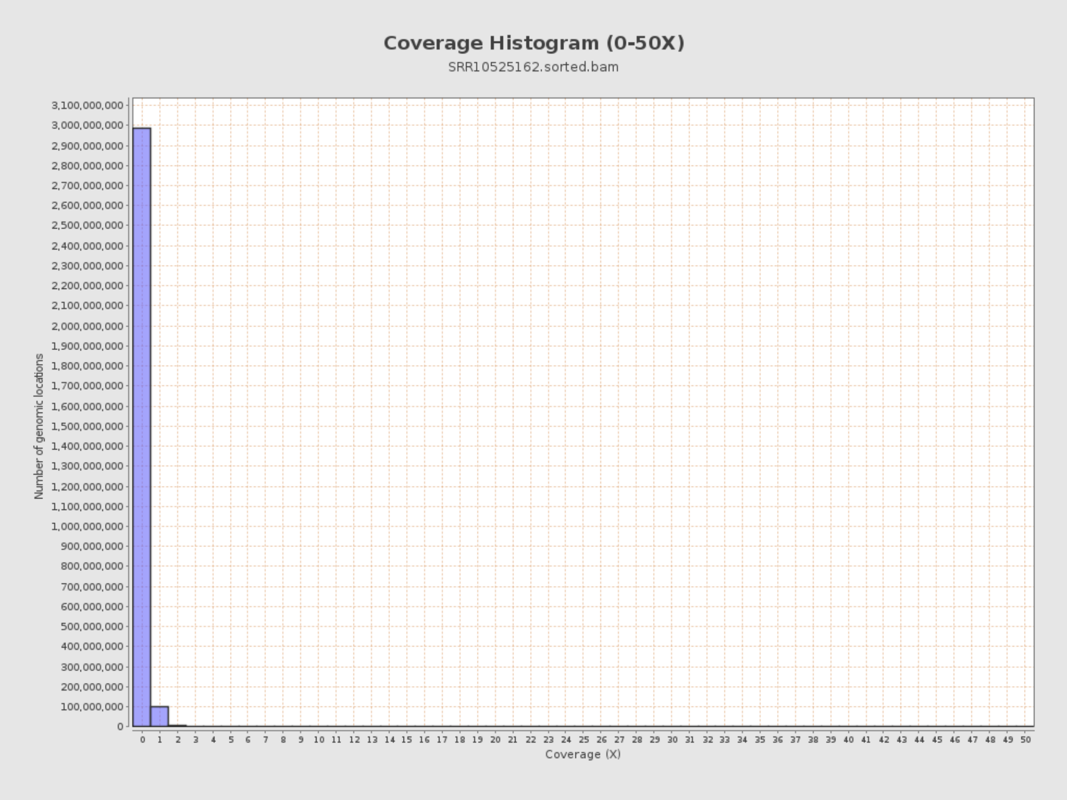
3. Results : Coverage across reference



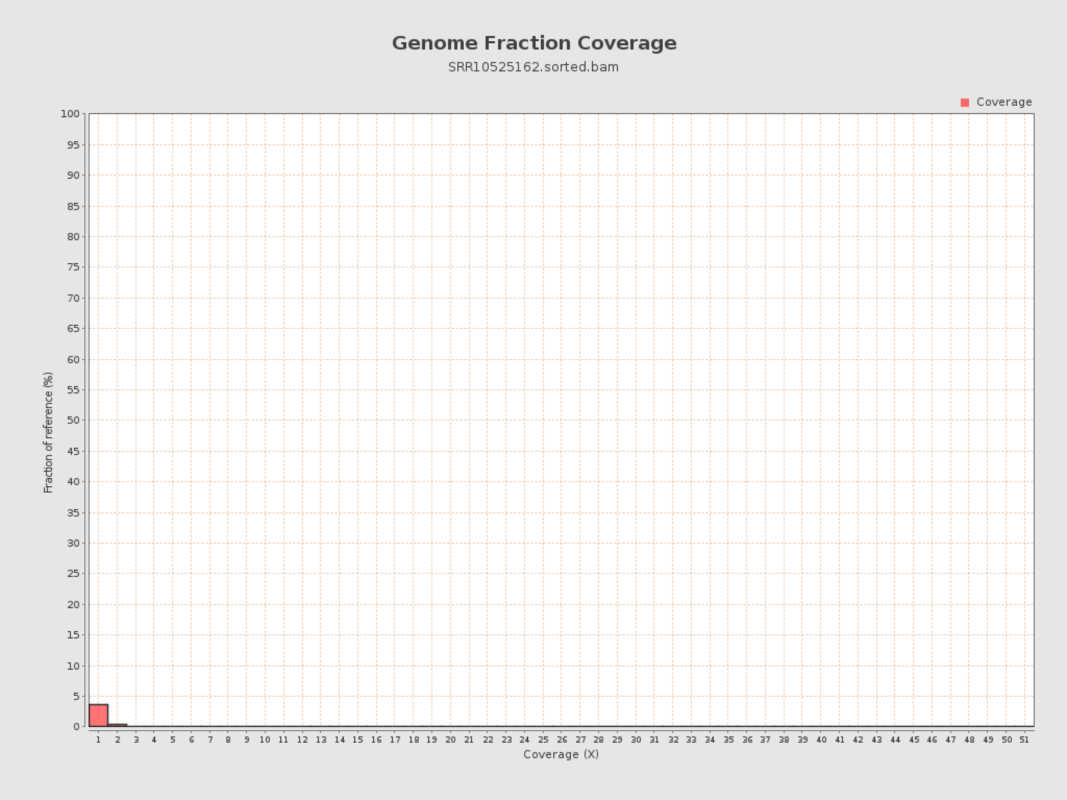
4. Results : Coverage Histogram



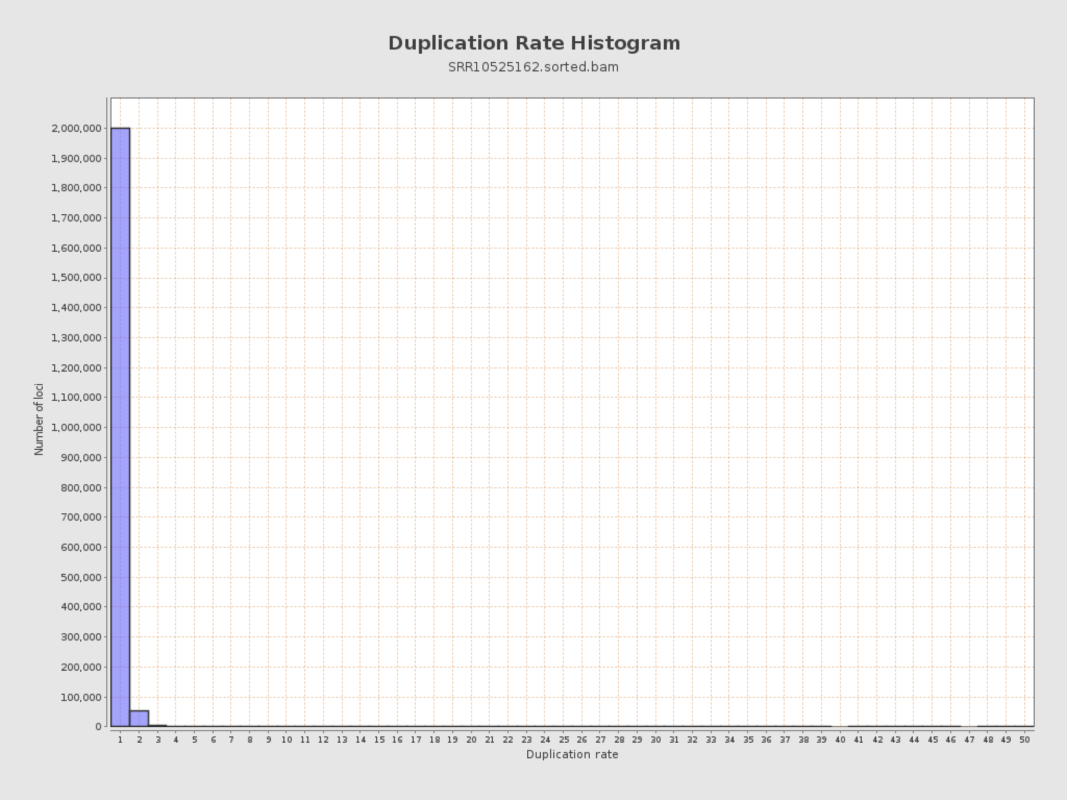
5. Results : Coverage Histogram (0-50X)



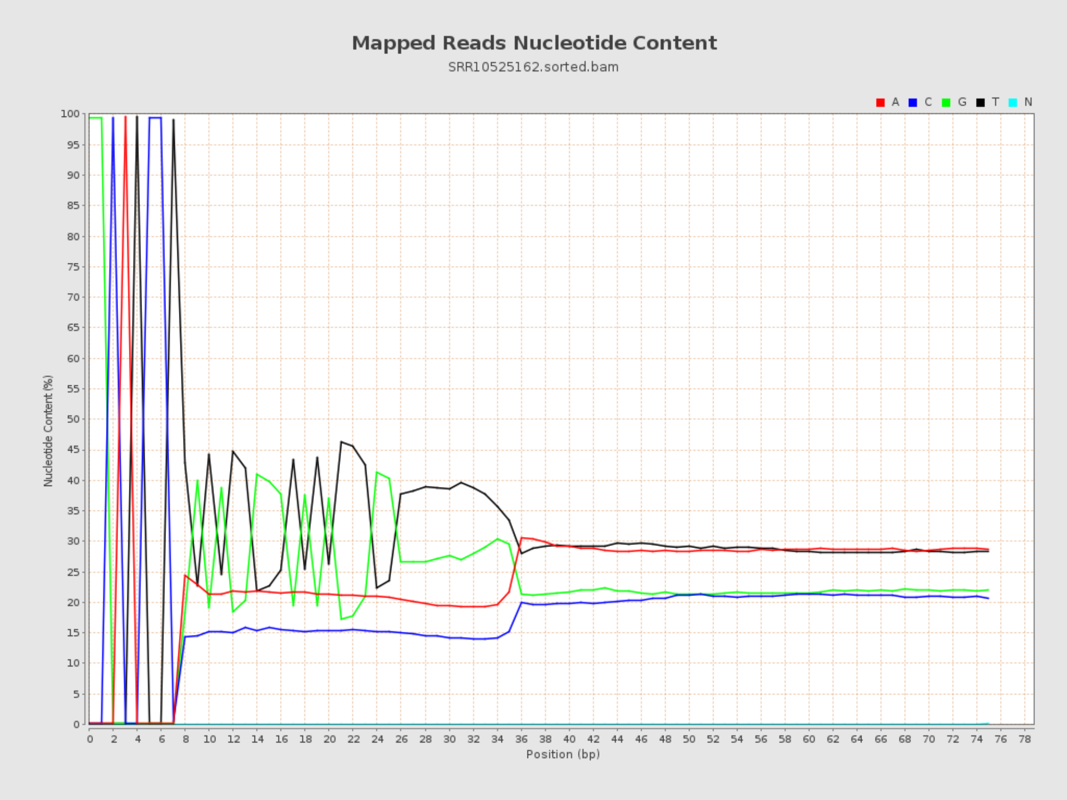
6. Results : Genome Fraction Coverage



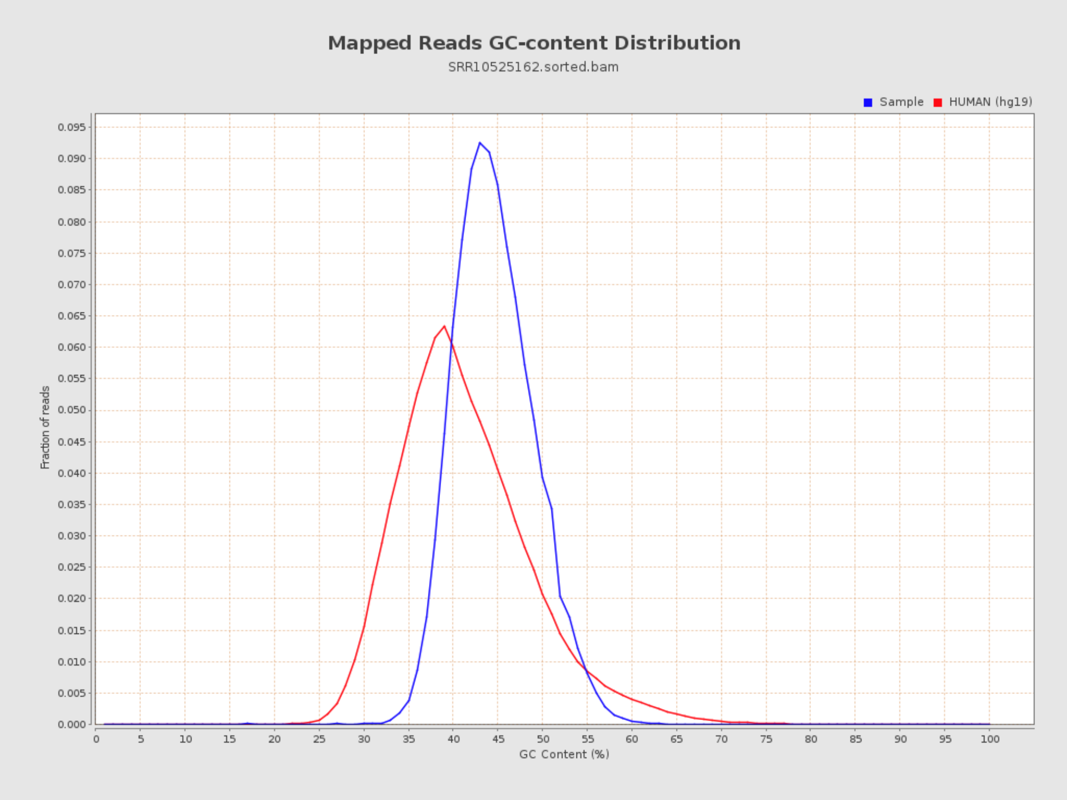
7. Results : Duplication Rate Histogram



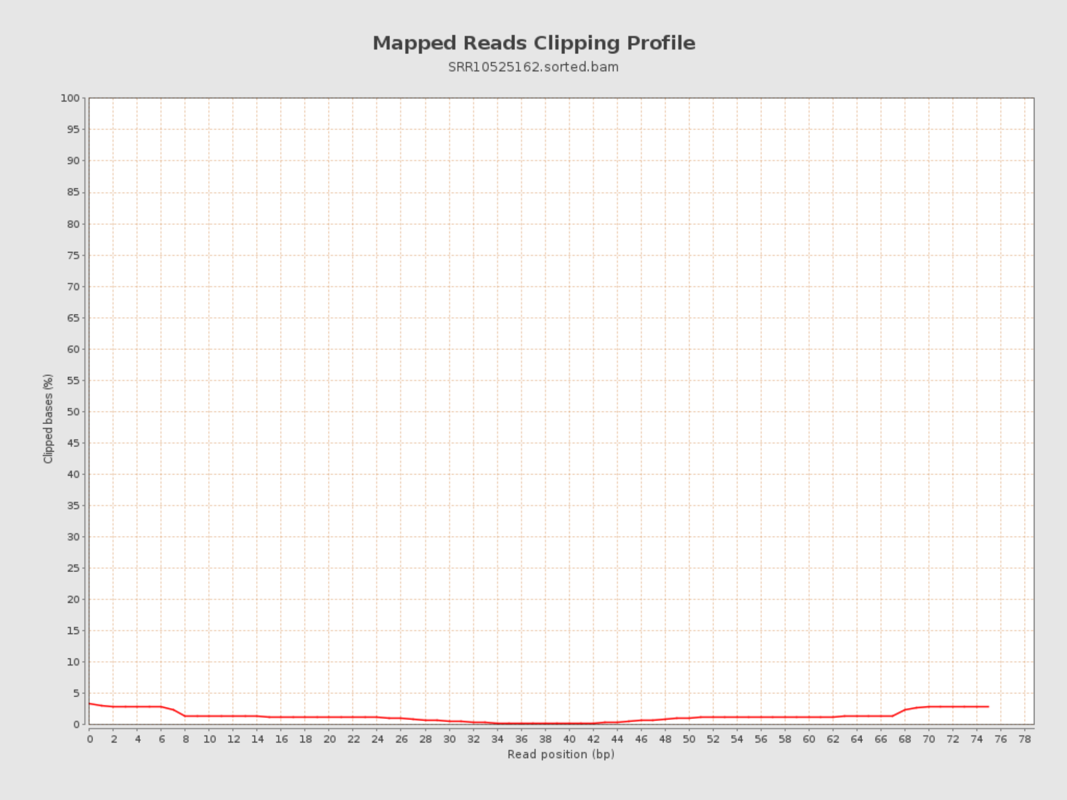
8. Results : Mapped Reads Nucleotide Content



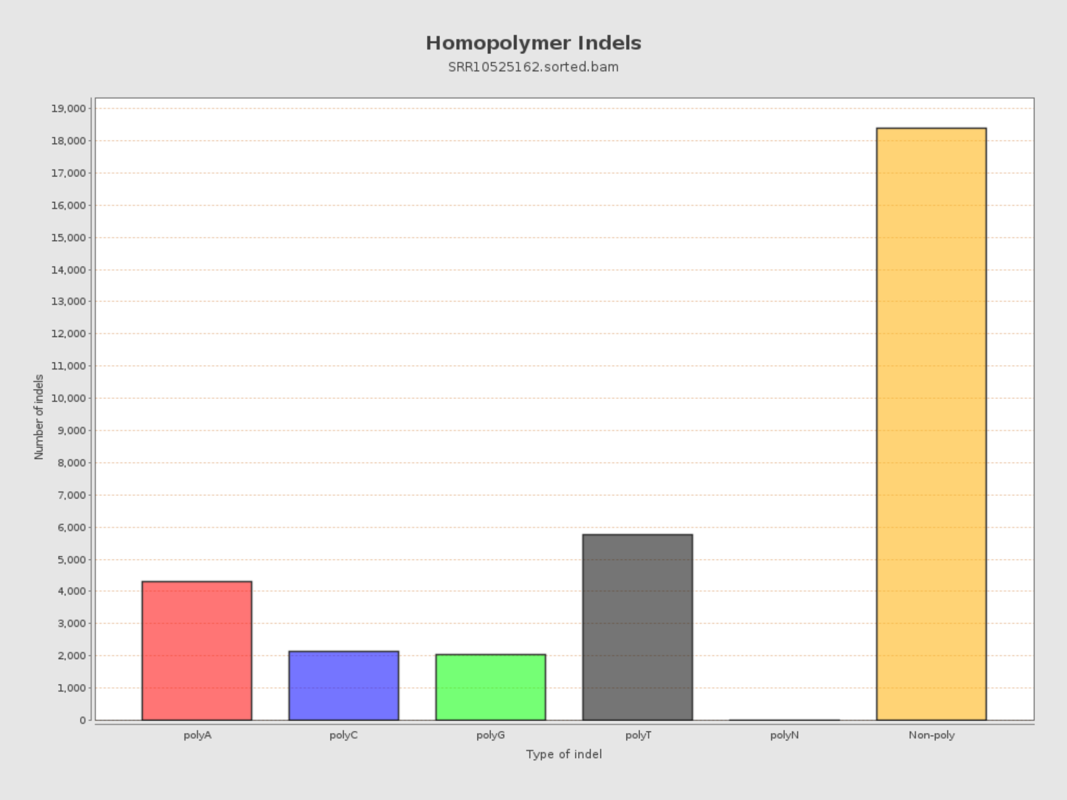
9. Results : Mapped Reads GC-content Distribution



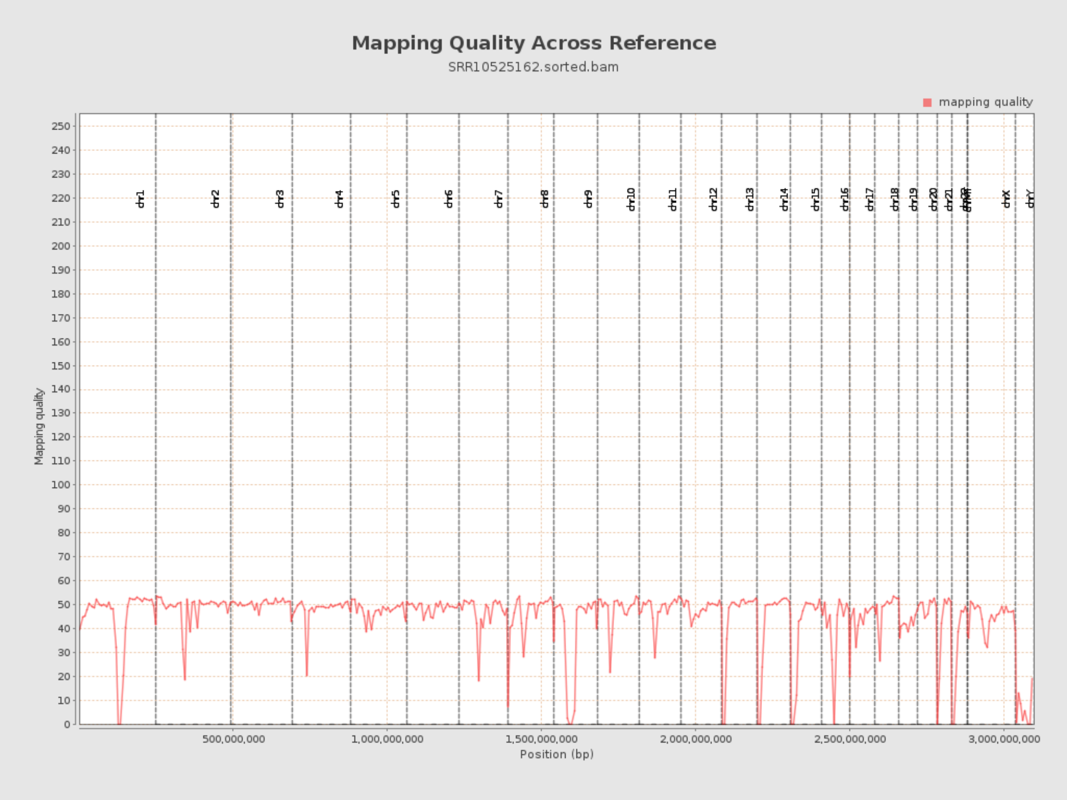
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram