Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:47:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525003.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_SRR10525003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525003.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:47:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,539,448
Mapped reads	1,418,966 / 92.17%
Unmapped reads	120,482 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,170 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	45,193 / 2.94%
Duplication rate	2.22%
Clipped reads	1,421,639 / 92.35%

2.2. ACGT Content

Number/percentage of A's	19,925,572 / 24.25%
Number/percentage of C's	15,296,939 / 18.62%
Number/percentage of T's	26,470,239 / 32.21%
Number/percentage of G's	20,476,802 / 24.92%
Number/percentage of N's	699 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0266

Standard Deviation	0.257

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

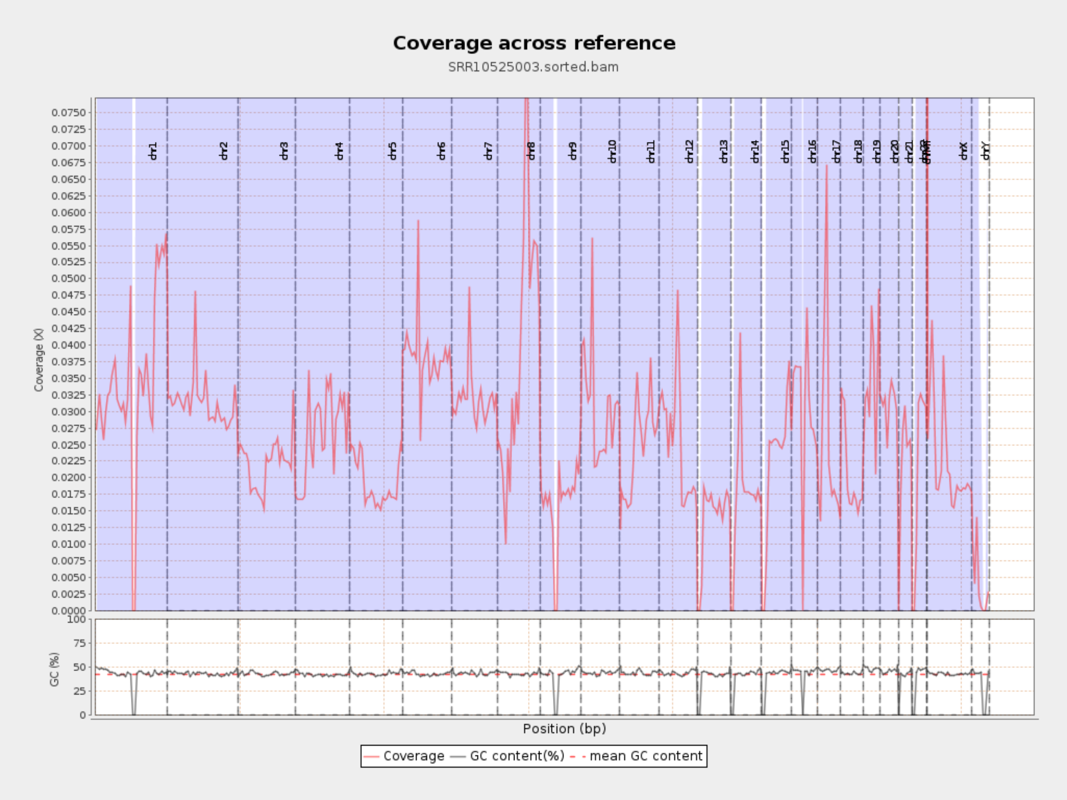
General error rate	0.5%
Mismatches	405,352
Insertions	4,535
Mapped reads with at least one insertion	0.32%
Deletions	15,842
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.95%

2.6. Chromosome stats

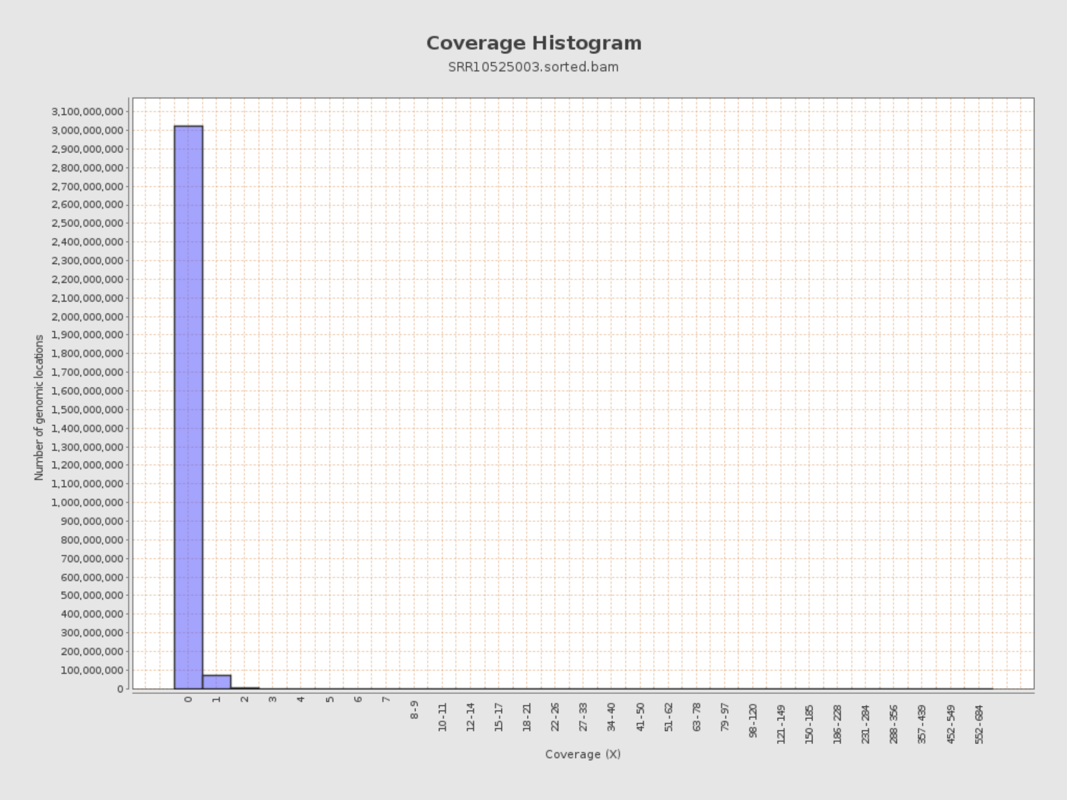
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8567203	0.0344	0.488
chr2	243199373	7631585	0.0314	0.294
chr3	198022430	4401764	0.0222	0.163
chr4	191154276	5128960	0.0268	0.1903
chr5	180915260	3489847	0.0193	0.1525
chr6	171115067	6562312	0.0384	0.3081
chr7	159138663	5105952	0.0321	0.3287

chr8	146364022	5822566	0.0398	0.2583
chr9	141213431	2272212	0.0161	0.1897
chr10	135534747	4195232	0.031	0.2508
chr11	135006516	3372800	0.025	0.2323
chr12	133851895	3397949	0.0254	0.1739
chr13	115169878	1575976	0.0137	0.1267
chr14	107349540	1862032	0.0173	0.1444
chr15	102531392	2274924	0.0222	0.1702
chr16	90354753	2734849	0.0303	0.1953
chr17	81195210	2123072	0.0261	0.2213
chr18	78077248	1594698	0.0204	0.3103
chr19	59128983	2065675	0.0349	0.3071
chr20	63025520	1928471	0.0306	0.1896
chr21	48129895	1092711	0.0227	0.173
chr22	51304566	1108660	0.0216	0.1565
chrMT	16571	70214	4.2372	3.1197
chrX	155270560	3578588	0.023	0.1899
chrY	59373566	238494	0.004	0.1117

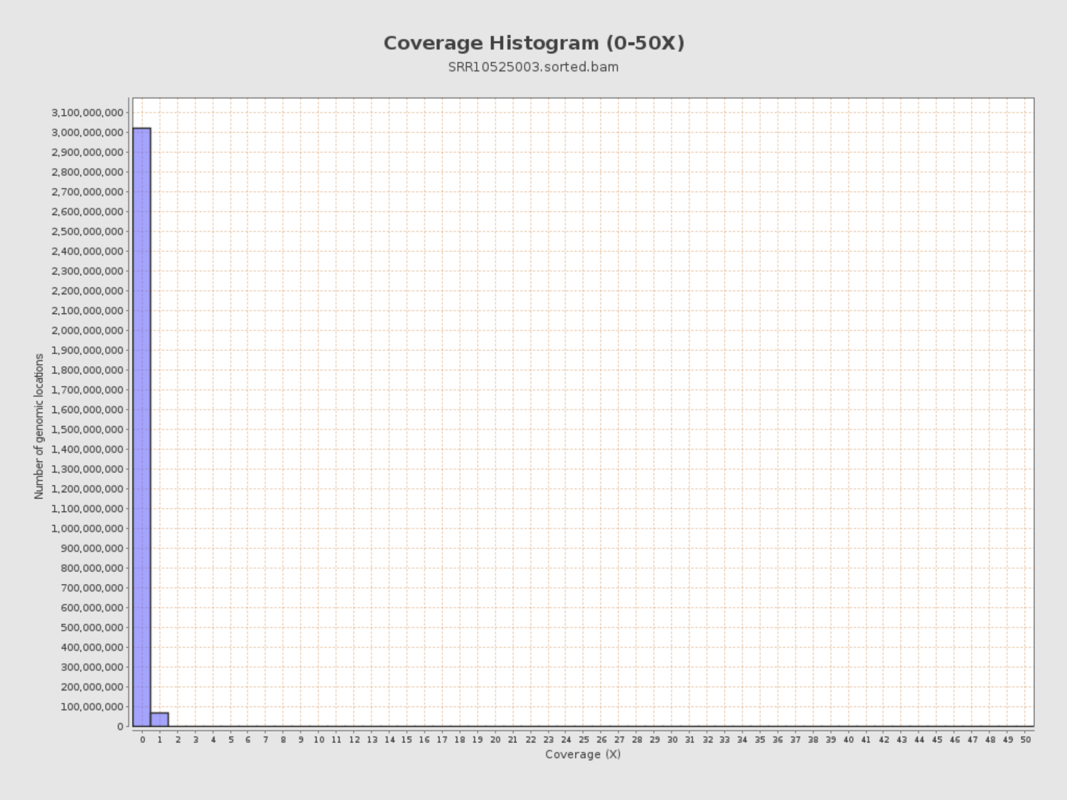
3. Results : Coverage across reference



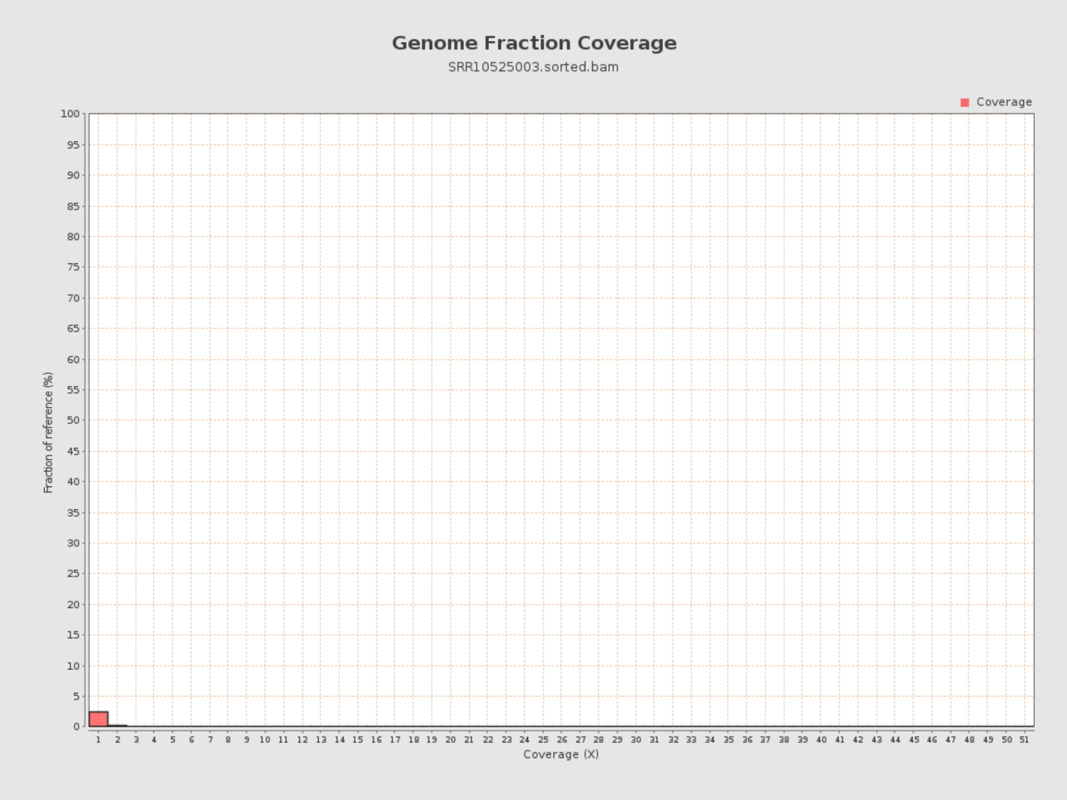
4. Results : Coverage Histogram



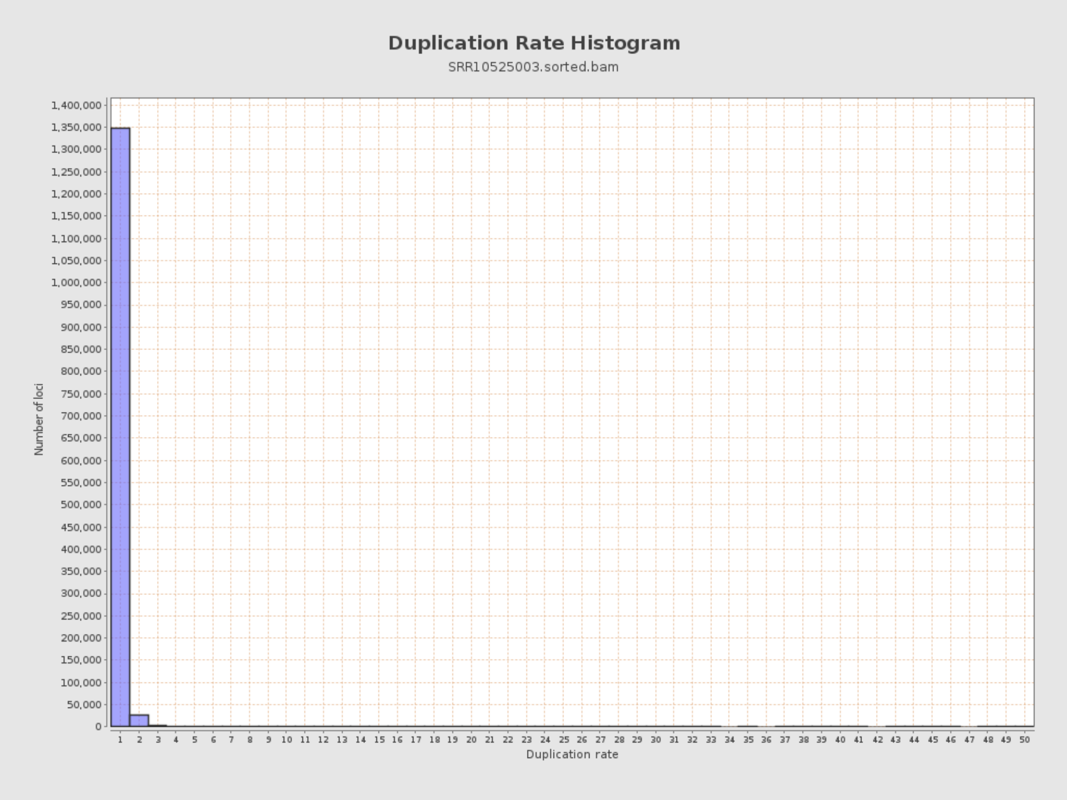
5. Results : Coverage Histogram (0-50X)



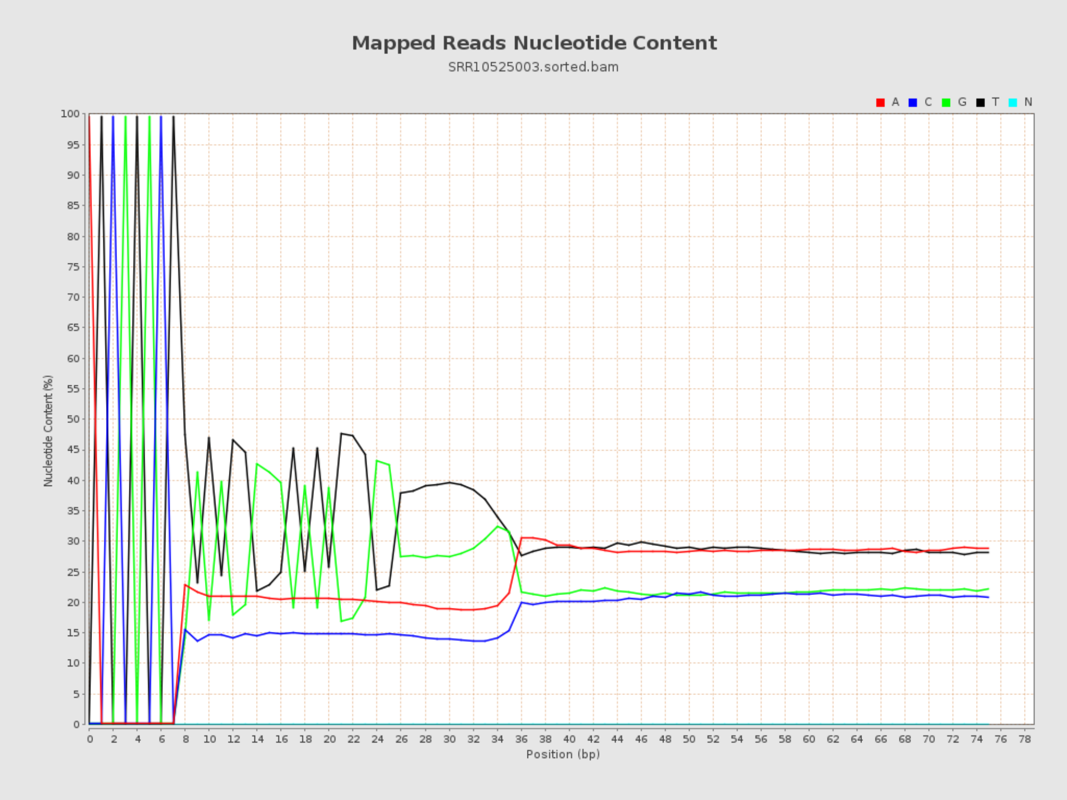
6. Results : Genome Fraction Coverage



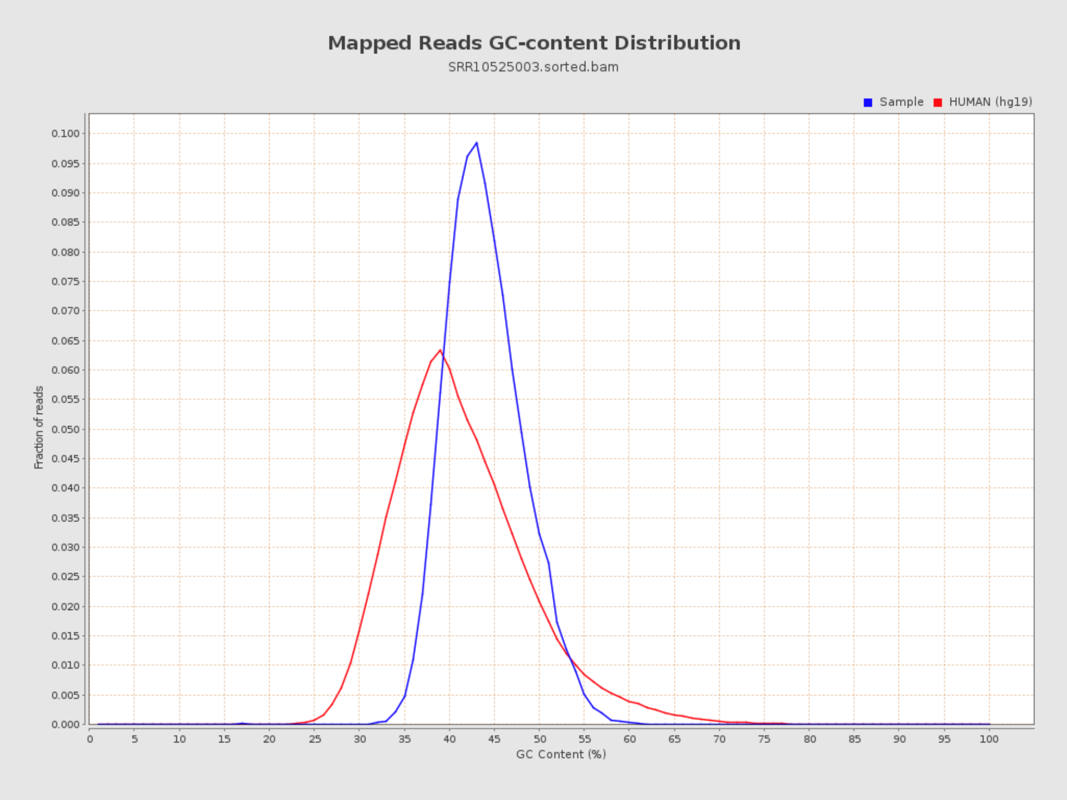
7. Results : Duplication Rate Histogram



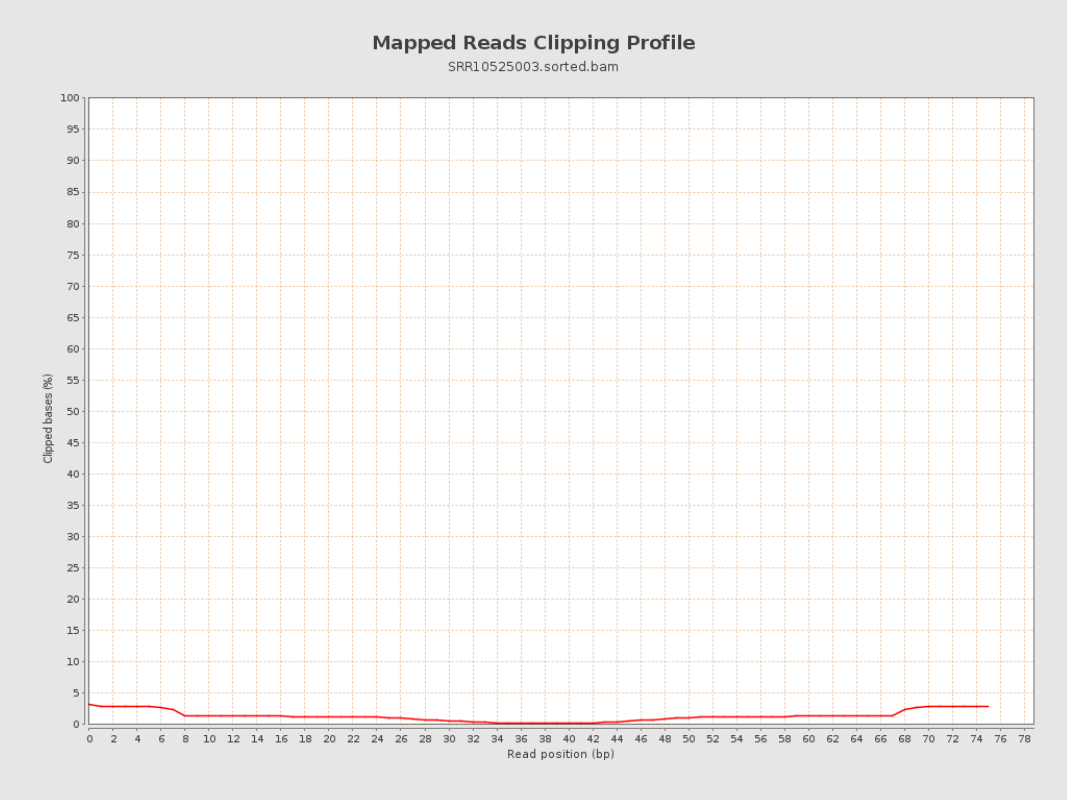
8. Results : Mapped Reads Nucleotide Content



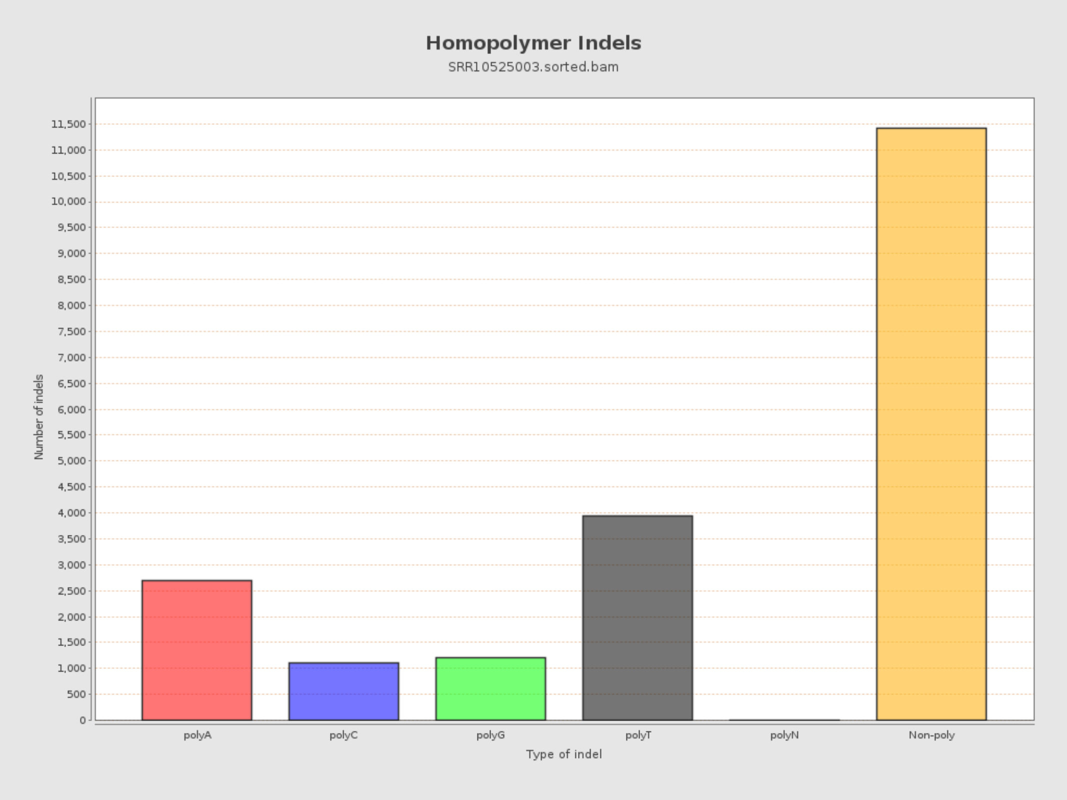
9. Results : Mapped Reads GC-content Distribution



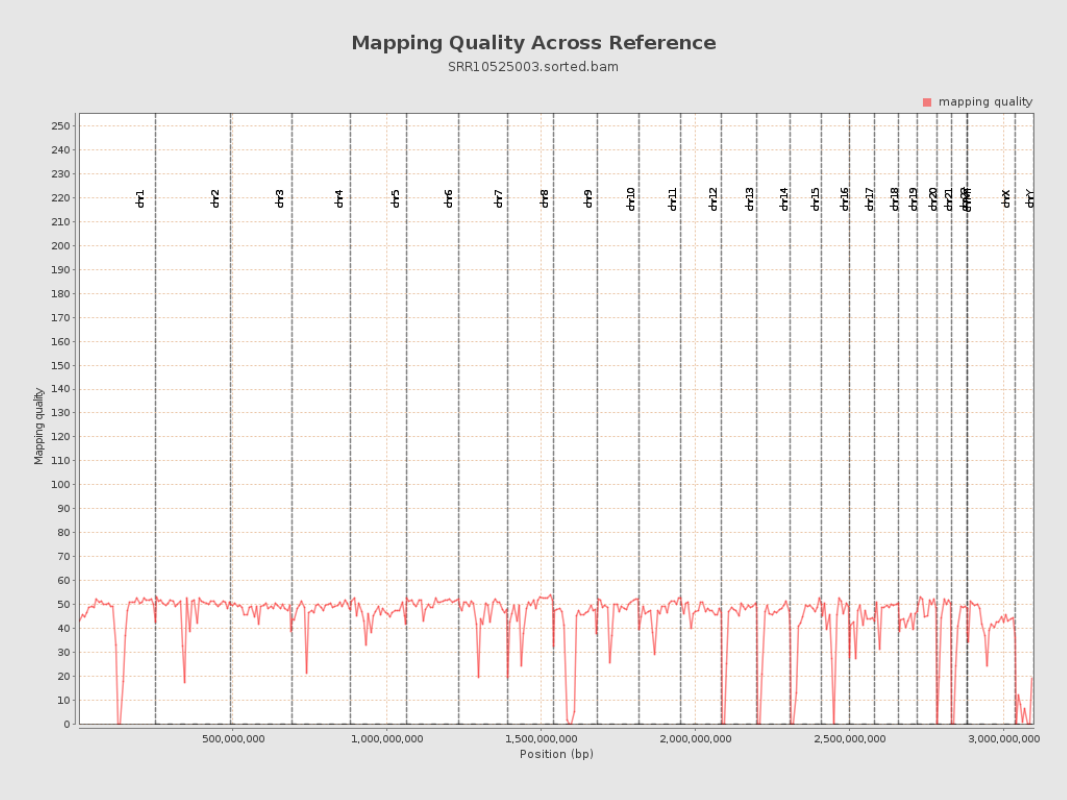
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram