Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:36:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525093.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_SRR10525093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:36:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,026,323
Mapped reads	2,719,838 / 89.87%
Unmapped reads	306,485 / 10.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70,102 / 2.32%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	111,351 / 3.68%
Duplication rate	2.49%
Clipped reads	2,784,092 / 92%

2.2. ACGT Content

Number/percentage of A's	56,557,968 / 27.19%
Number/percentage of C's	39,420,187 / 18.95%
Number/percentage of T's	63,212,366 / 30.39%
Number/percentage of G's	48,794,391 / 23.46%
Number/percentage of N's	7,443 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0672

Standard Deviation	0.6507

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

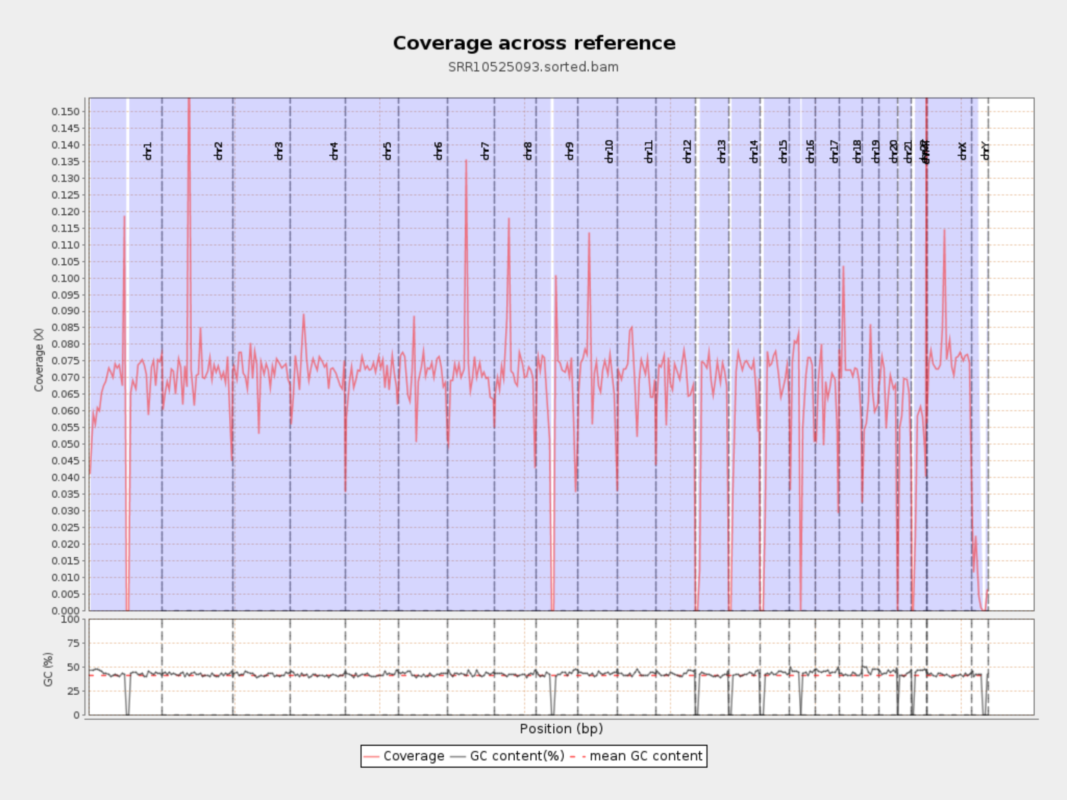
General error rate	0.73%
Mismatches	1,486,740
Insertions	20,402
Mapped reads with at least one insertion	0.74%
Deletions	47,212
Mapped reads with at least one deletion	1.71%
Homopolymer indels	40.56%

2.6. Chromosome stats

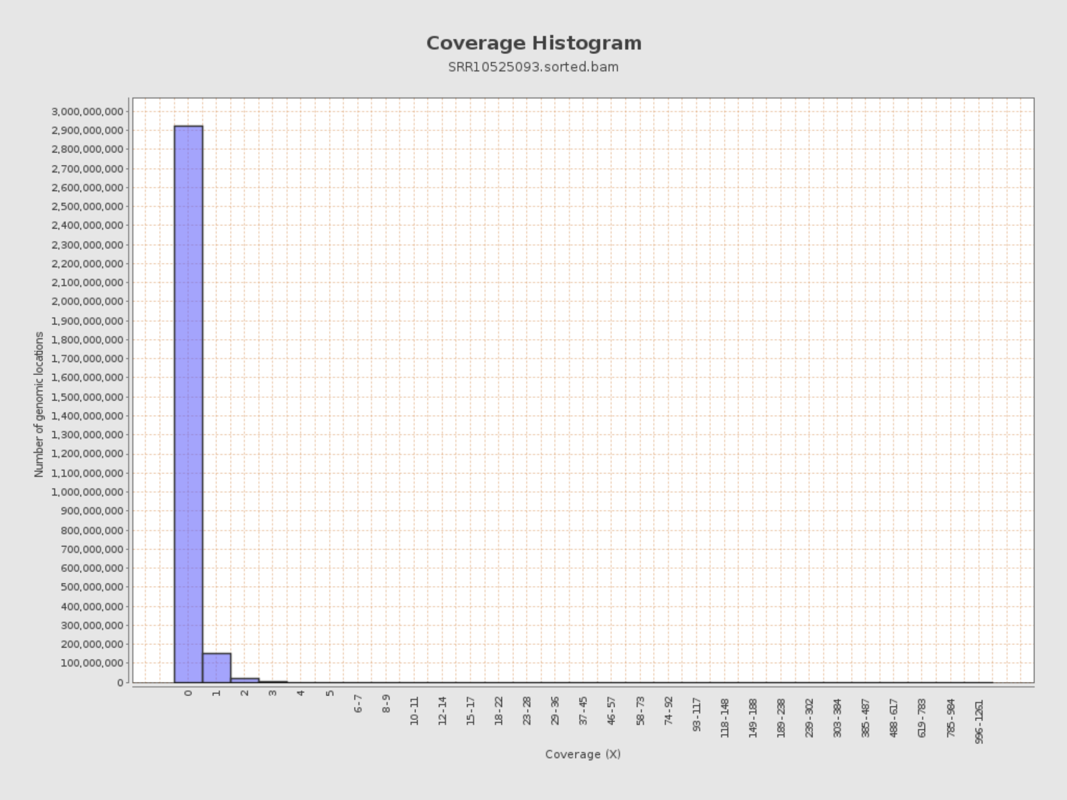
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16345773	0.0656	0.9759
chr2	243199373	17811606	0.0732	1.0076
chr3	198022430	14295401	0.0722	0.3063
chr4	191154276	13807590	0.0722	0.3364
chr5	180915260	12865715	0.0711	0.3242
chr6	171115067	12215740	0.0714	0.3779
chr7	159138663	11639037	0.0731	1.0053

chr8	146364022	10668372	0.0729	0.971
chr9	141213431	8844609	0.0626	0.6791
chr10	135534747	9861894	0.0728	0.5946
chr11	135006516	9507835	0.0704	0.6564
chr12	133851895	9309573	0.0696	0.3121
chr13	115169878	6829022	0.0593	0.2758
chr14	107349540	6455479	0.0601	0.372
chr15	102531392	6025991	0.0588	0.2835
chr16	90354753	5782386	0.064	0.3426
chr17	81195210	5096701	0.0628	0.4156
chr18	78077248	5785370	0.0741	1.2108
chr19	59128983	3694874	0.0625	0.781
chr20	63025520	4152465	0.0659	0.3104
chr21	48129895	2680685	0.0557	0.3086
chr22	51304566	2009799	0.0392	0.2252
chrMT	16571	4841	0.2921	0.6759
chrX	155270560	11911531	0.0767	0.4916
chrY	59373566	470233	0.0079	0.1696

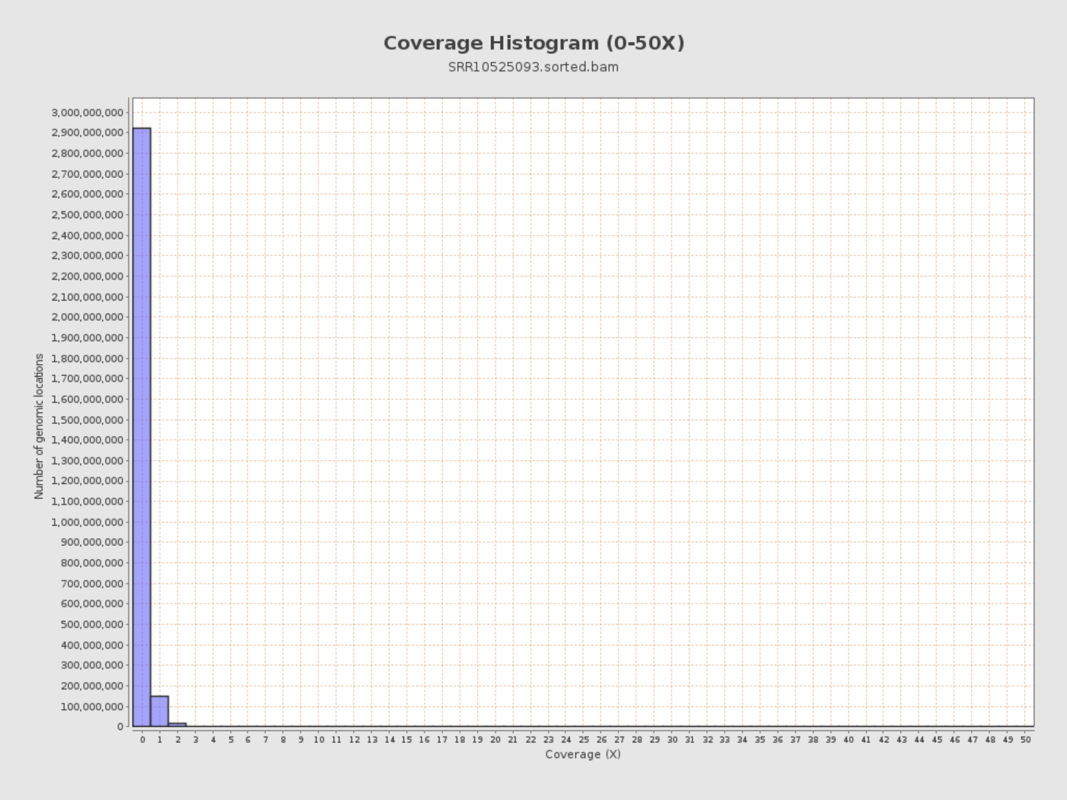
3. Results : Coverage across reference



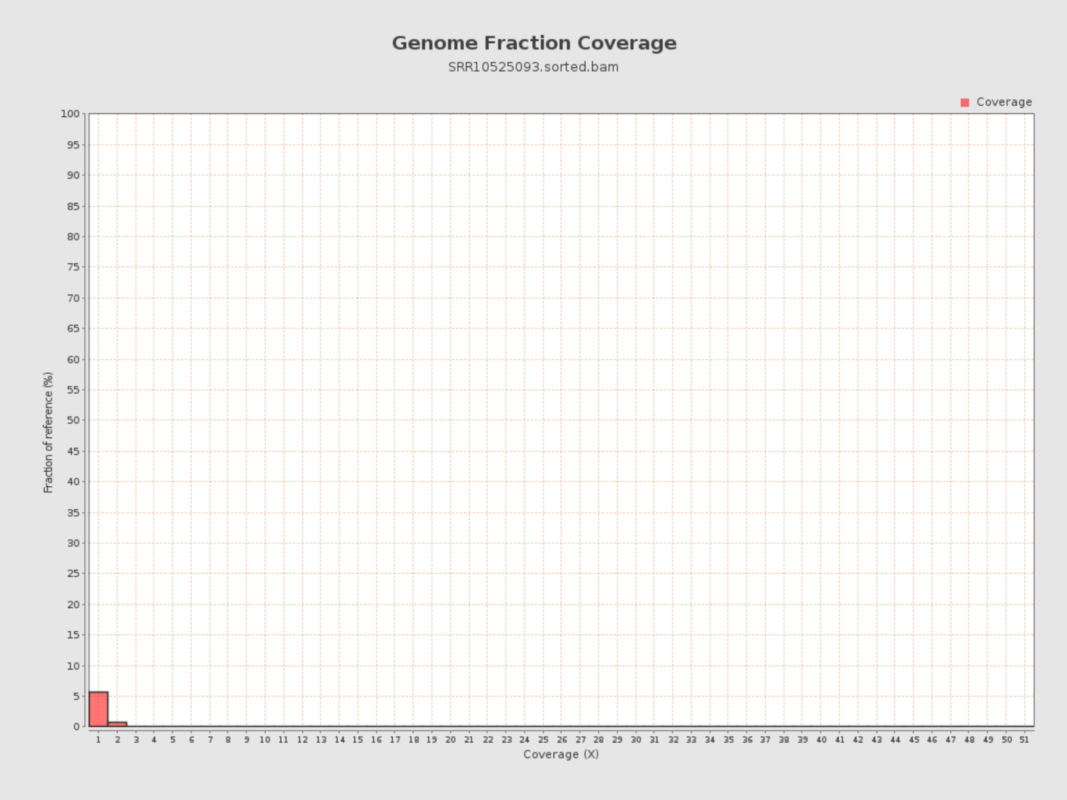
4. Results : Coverage Histogram



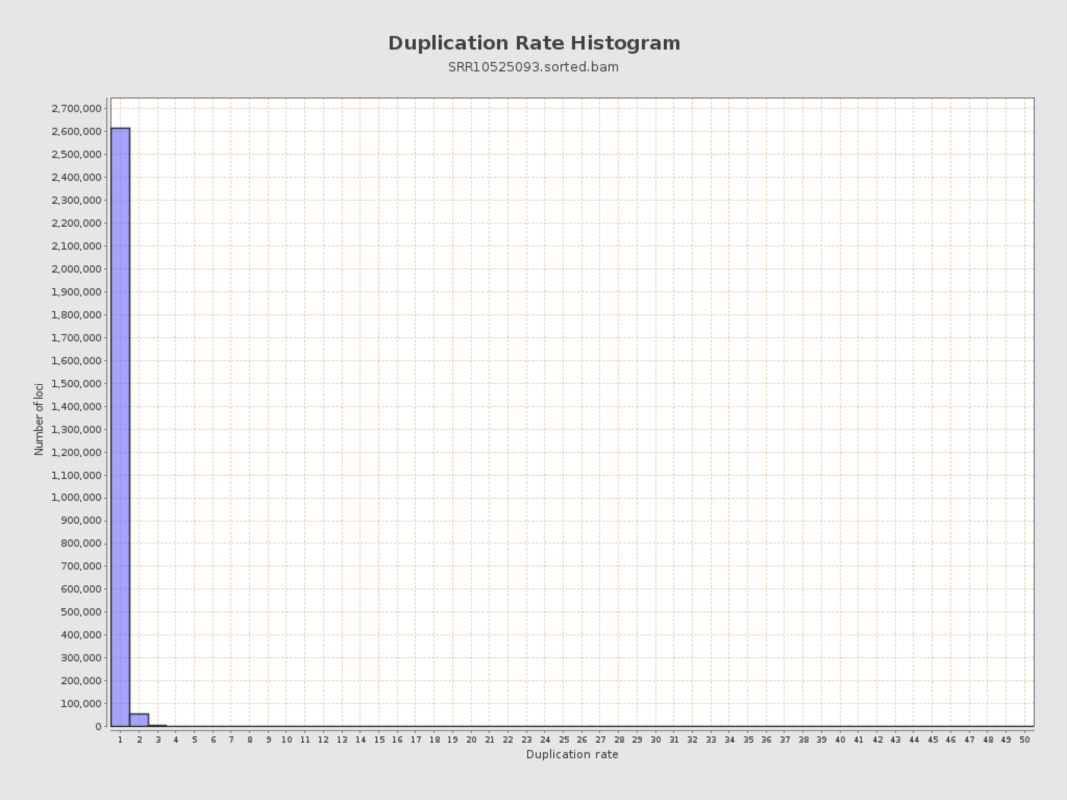
5. Results : Coverage Histogram (0-50X)



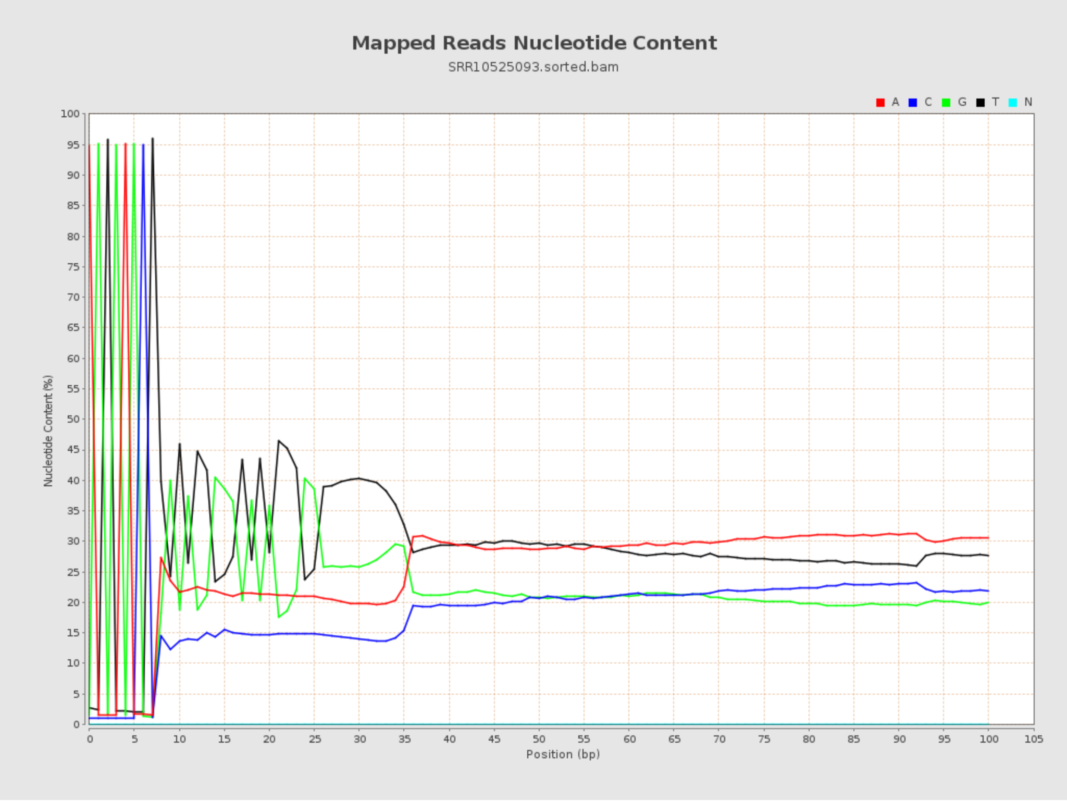
6. Results : Genome Fraction Coverage



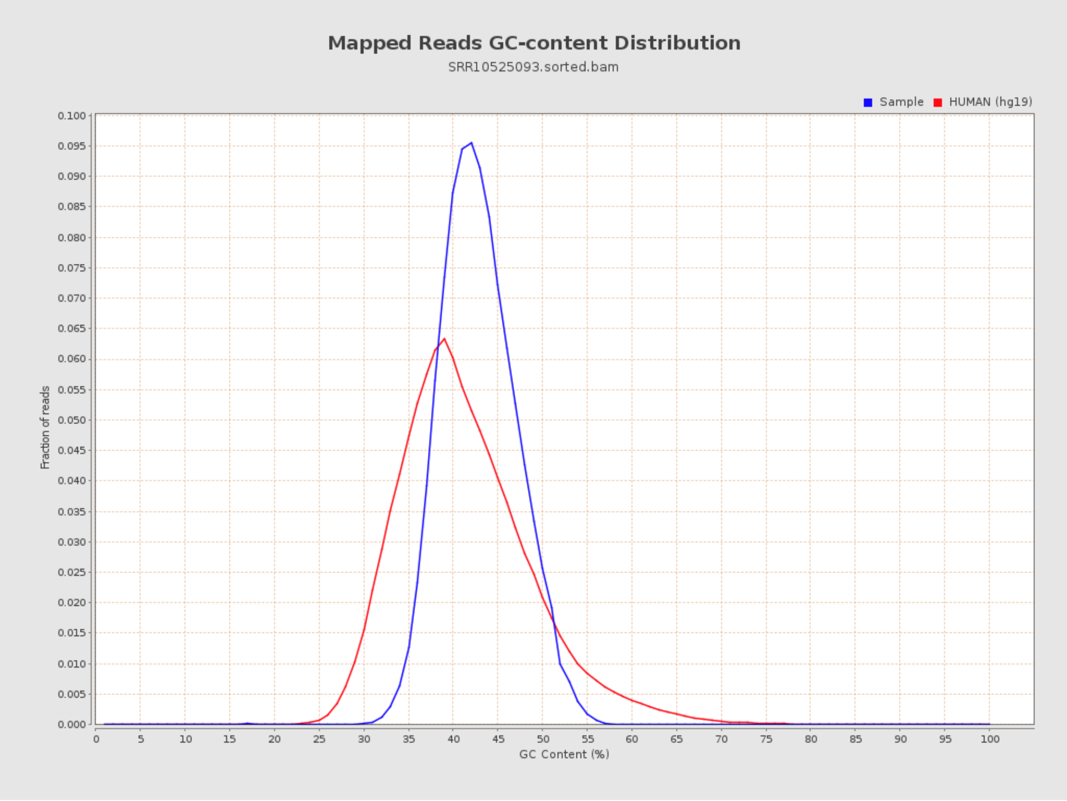
7. Results : Duplication Rate Histogram



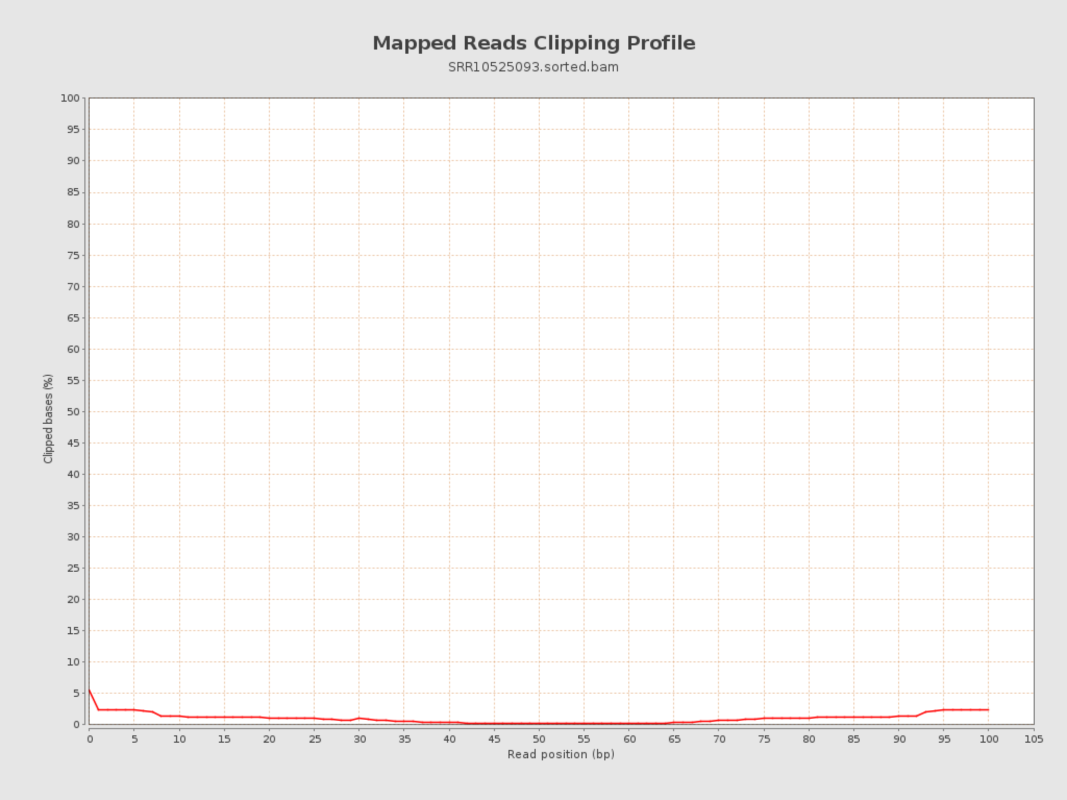
8. Results : Mapped Reads Nucleotide Content



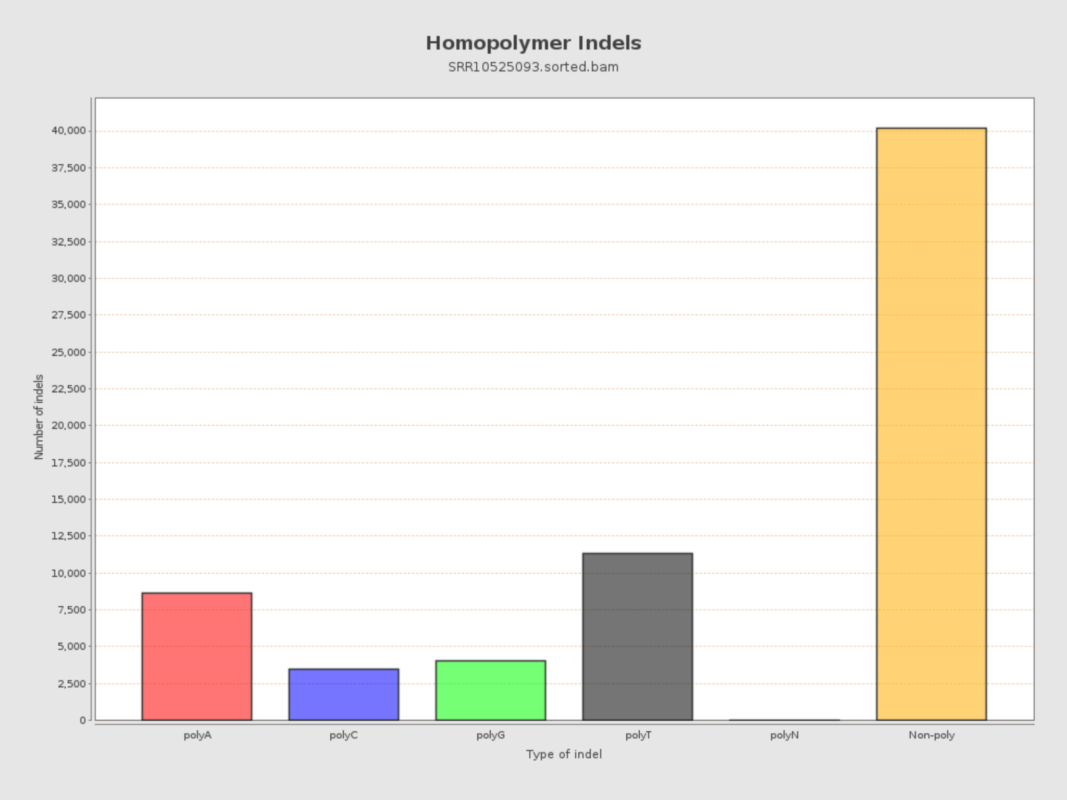
9. Results : Mapped Reads GC-content Distribution



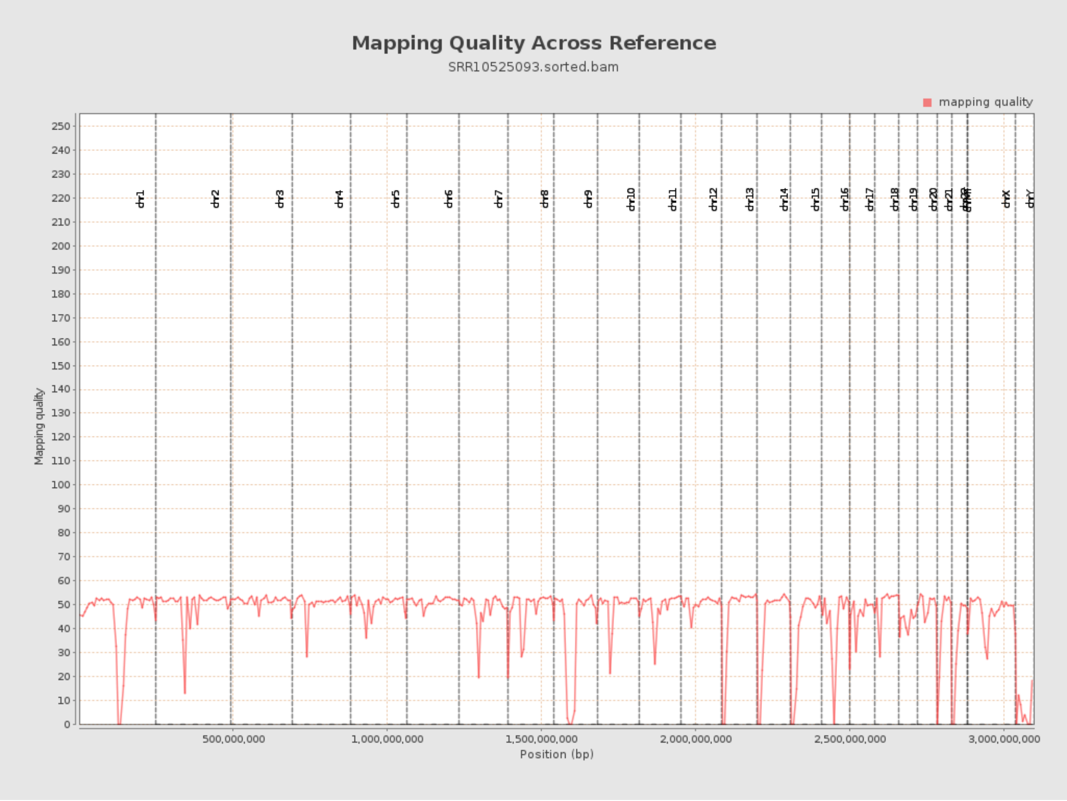
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram