

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:37:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548921.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_SRR1548921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:37:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,386,655
Mapped reads	5,582,903 / 87.42%
Unmapped reads	803,752 / 12.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	158,356 / 2.48%
Duplication rate	1.85%
Clipped reads	413,955 / 6.48%

2.2. ACGT Content

Number/percentage of A's	65,120,694 / 29.47%
Number/percentage of C's	45,351,172 / 20.52%
Number/percentage of T's	65,362,941 / 29.58%
Number/percentage of G's	45,167,251 / 20.44%
Number/percentage of N's	1,971 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0714
Standard Deviation	0.7731

2.4. Mapping Quality

Mean Mapping Quality	41.2
----------------------	------

2.5. Mismatches and indels

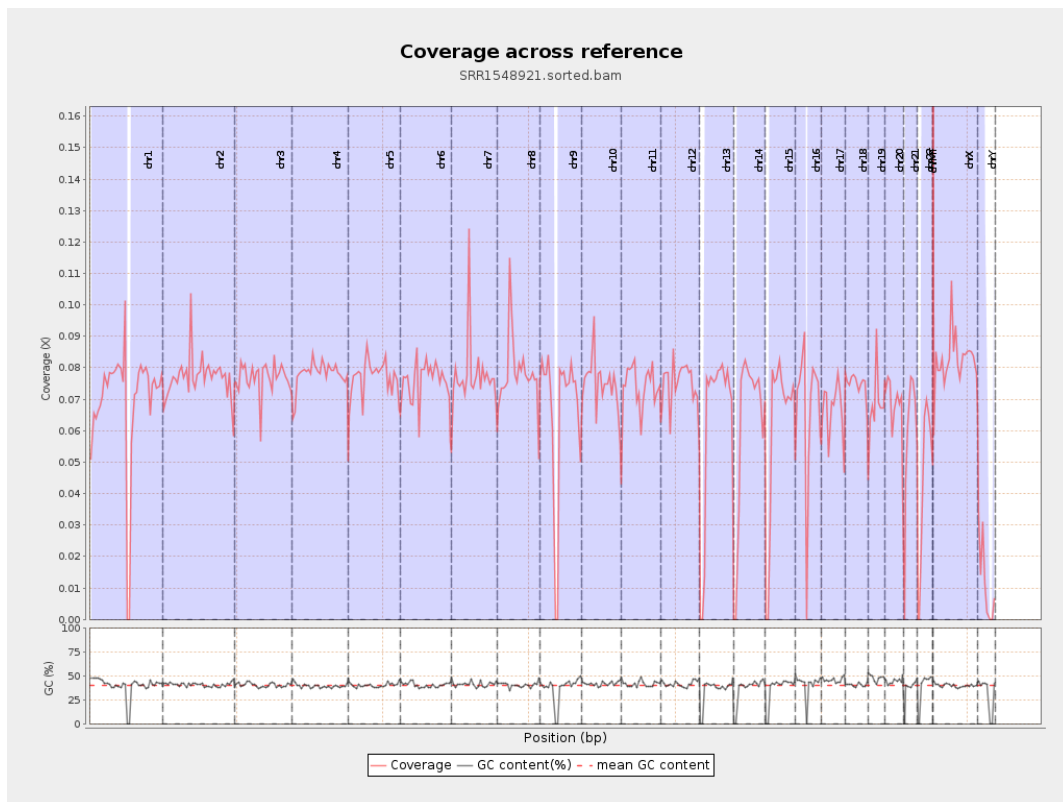
General error rate	0.29%
Mismatches	629,798
Insertions	7,232
Mapped reads with at least one insertion	0.13%
Deletions	18,083
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.44%

2.6. Chromosome stats

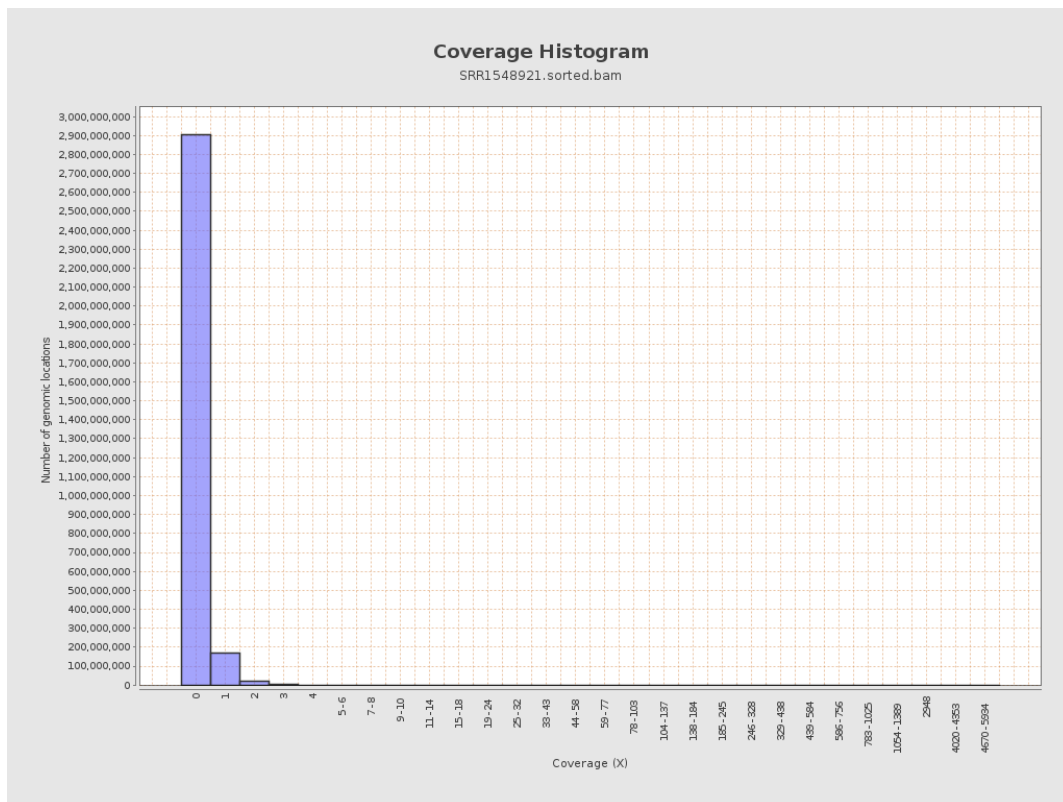
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17358874	0.0696	0.8356
chr2	243199373	18717398	0.077	0.45
chr3	198022430	15218488	0.0769	0.3121
chr4	191154276	14935939	0.0781	0.3228
chr5	180915260	13846346	0.0765	0.3168
chr6	171115067	12998316	0.076	0.3371
chr7	159138663	12338490	0.0775	0.6833
chr8	146364022	11465114	0.0783	2.877

chr9	141213431	9380782	0.0664	0.4406
chr10	135534747	10168314	0.075	0.4142
chr11	135006516	9984016	0.074	0.4634
chr12	133851895	10055300	0.0751	0.3184
chr13	115169878	7297361	0.0634	0.2794
chr14	107349540	6717599	0.0626	0.3291
chr15	102531392	6214599	0.0606	0.275
chr16	90354753	5964789	0.066	0.3172
chr17	81195210	5469221	0.0674	0.3108
chr18	78077248	5862983	0.0751	0.7809
chr19	59128983	4079026	0.069	0.7997
chr20	63025520	4331309	0.0687	0.3042
chr21	48129895	2819693	0.0586	0.3098
chr22	51304566	2288147	0.0446	0.2728
chrMT	16571	6342	0.3827	0.6983
chrX	155270560	12827793	0.0826	0.3962
chrY	59373566	681635	0.0115	0.157

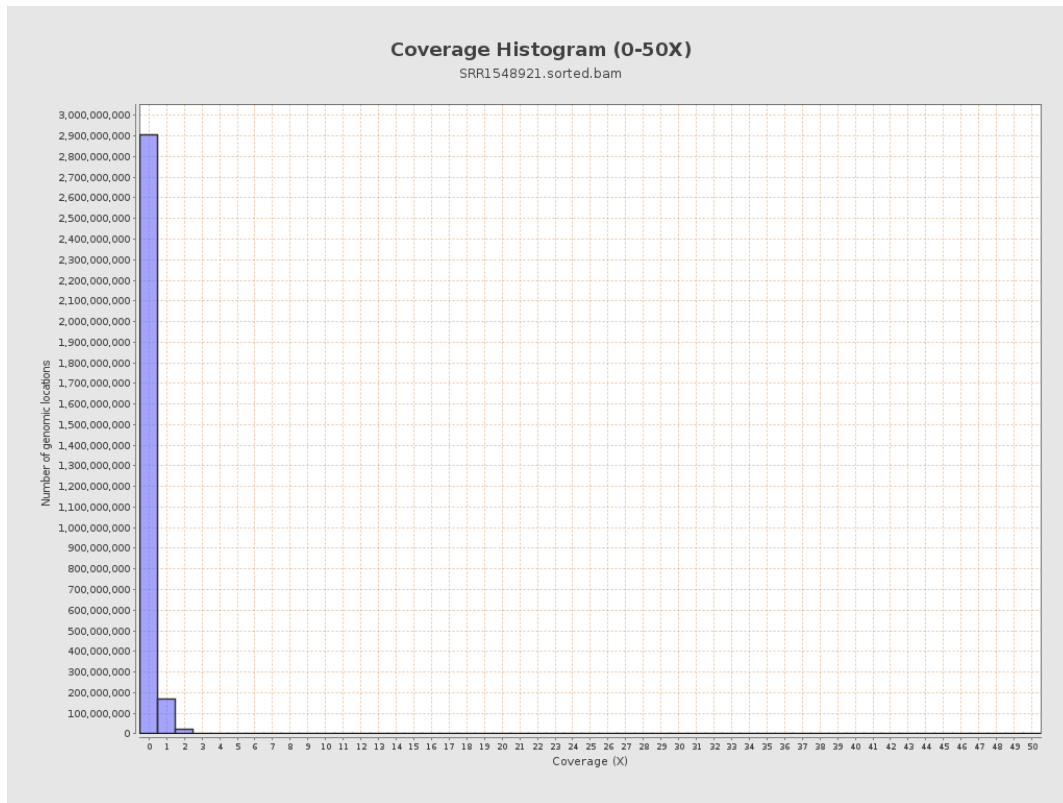
3. Results : Coverage across reference



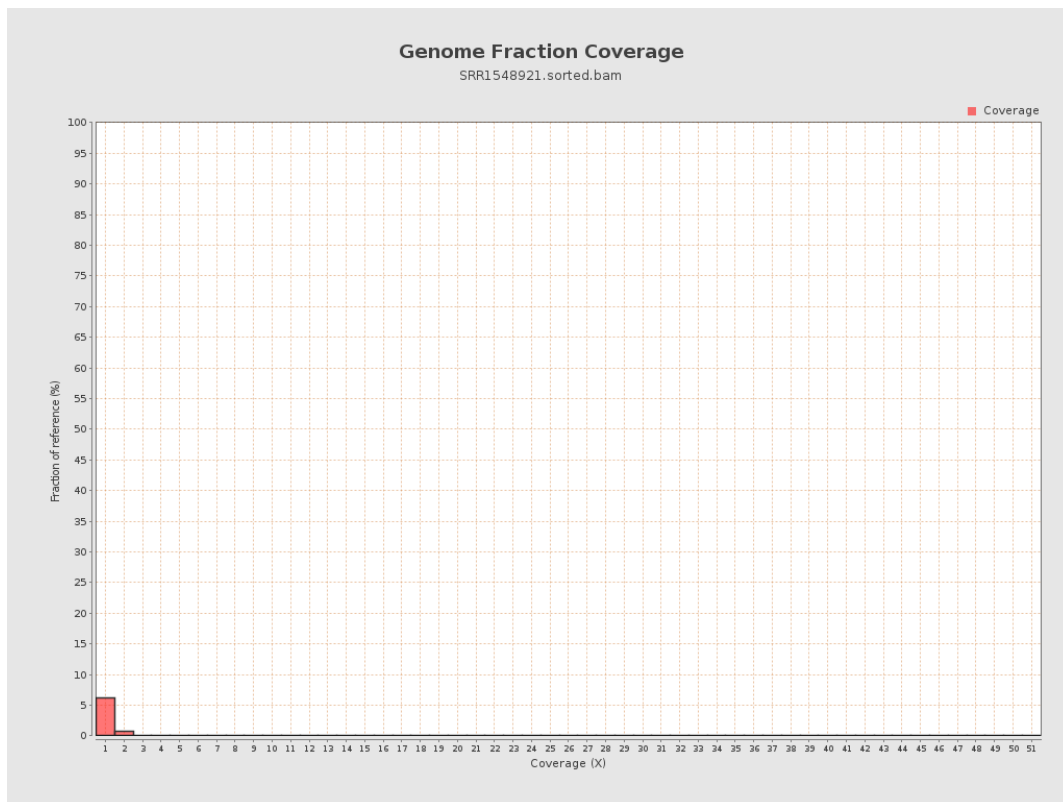
4. Results : Coverage Histogram



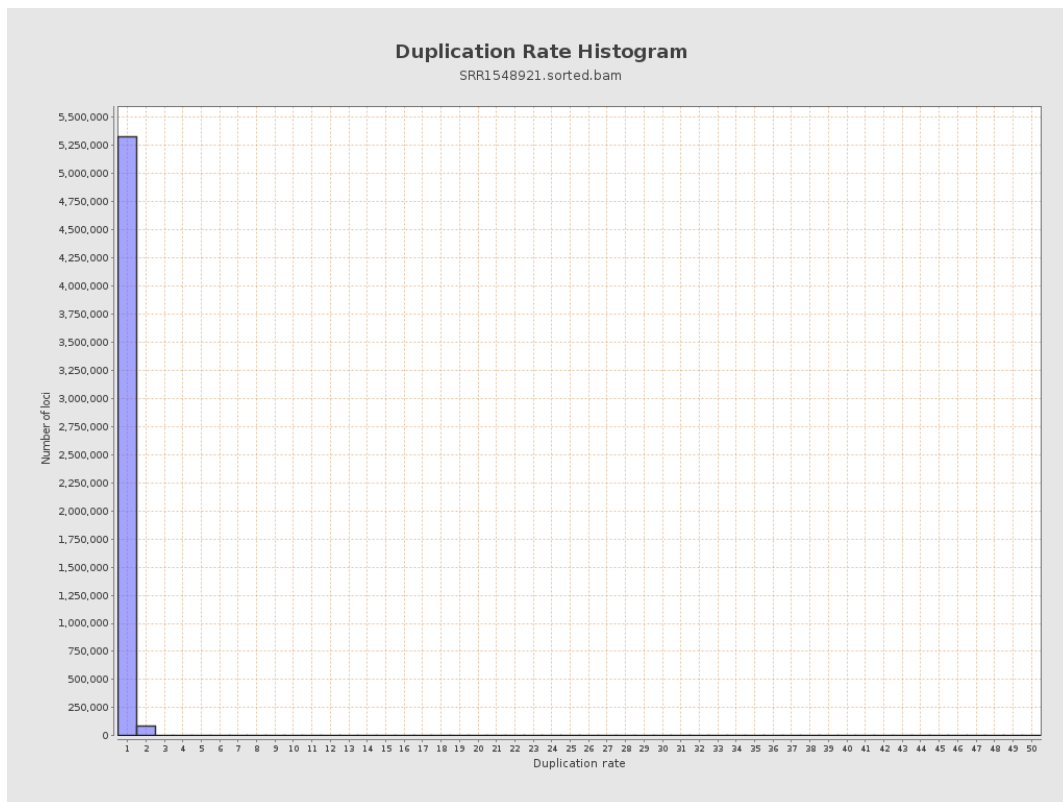
5. Results : Coverage Histogram (0-50X)



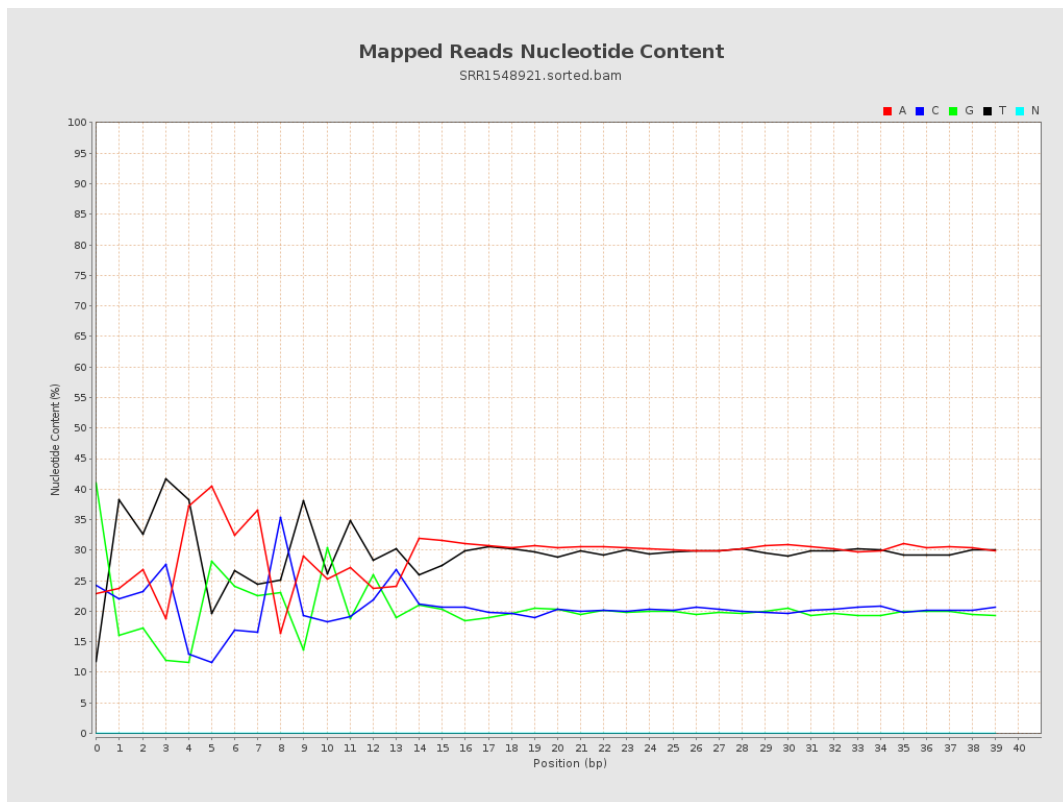
6. Results : Genome Fraction Coverage



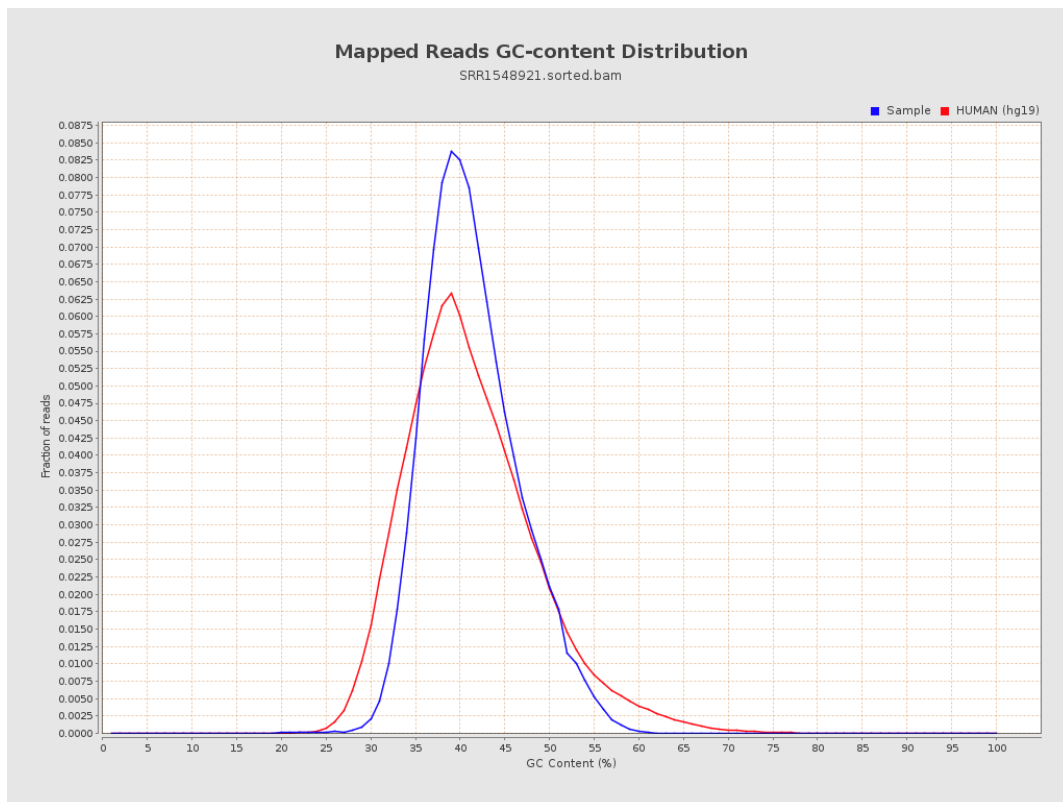
7. Results : Duplication Rate Histogram



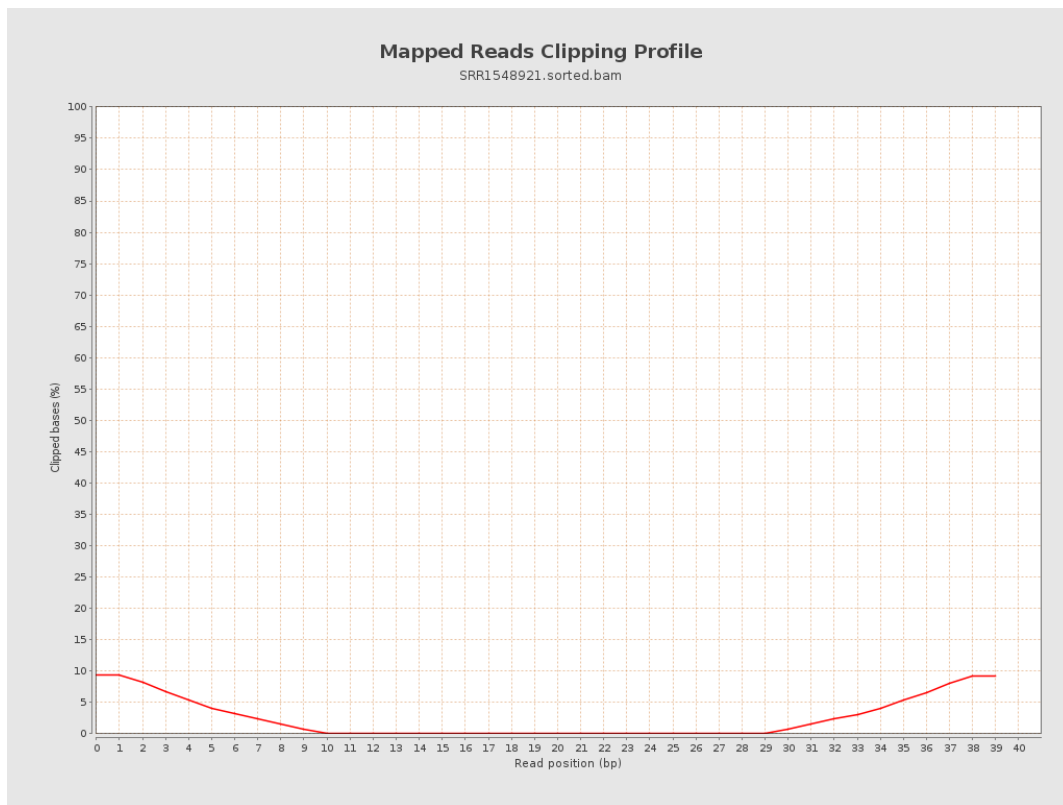
8. Results : Mapped Reads Nucleotide Content



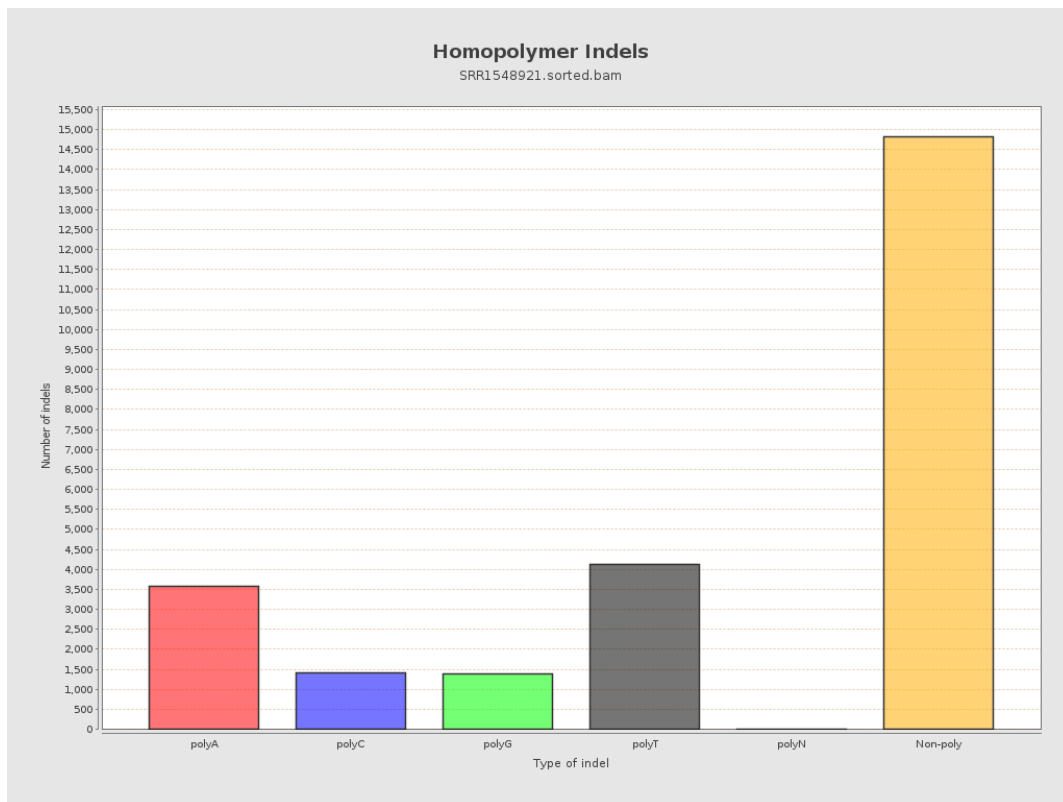
9. Results : Mapped Reads GC-content Distribution



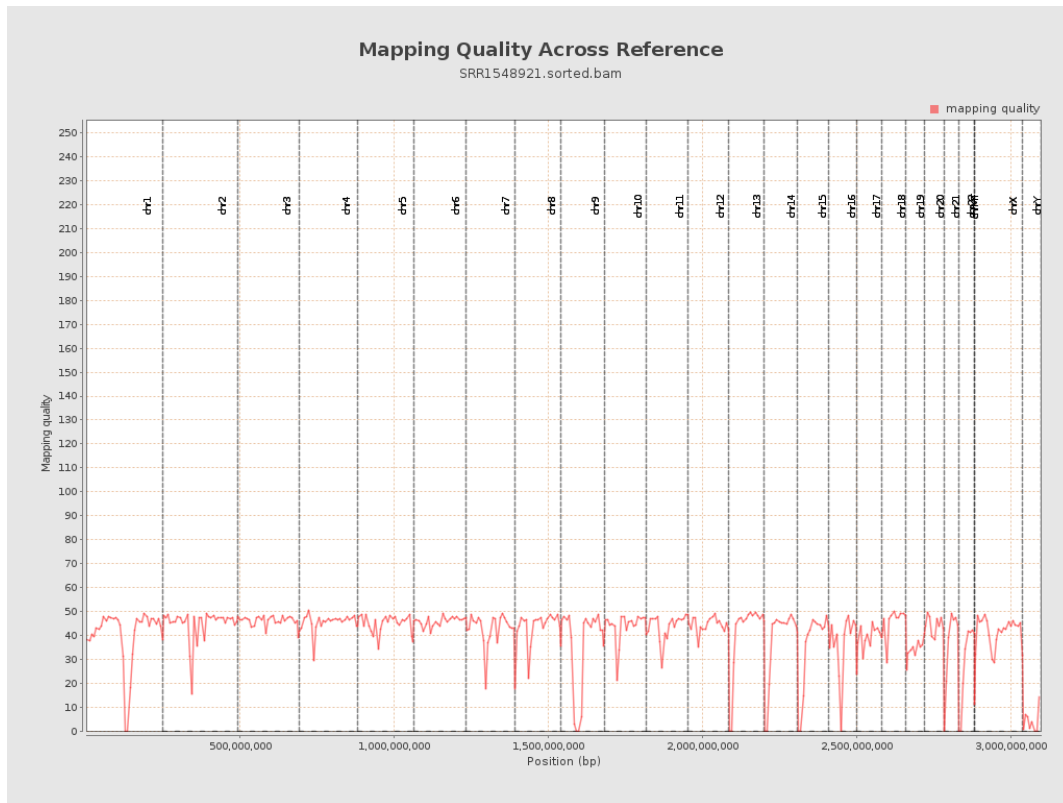
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

