Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:34:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548945.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_SRR1548945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:34:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,542,543
Mapped reads	4,002,582 / 88.11%
Unmapped reads	539,961 / 11.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	147,359 / 3.24%
Duplication rate	2.39%
Clipped reads	318,335 / 7.01%

2.2. ACGT Content

Number/percentage of A's	44,058,037 / 27.83%
Number/percentage of C's	34,622,675 / 21.87%
Number/percentage of T's	45,047,268 / 28.46%
Number/percentage of G's	34,554,855 / 21.83%
Number/percentage of N's	1,313 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0511
Standard Deviation	0.5403

2.4. Mapping Quality

Mean Mapping Quality	37.15

2.5. Mismatches and indels

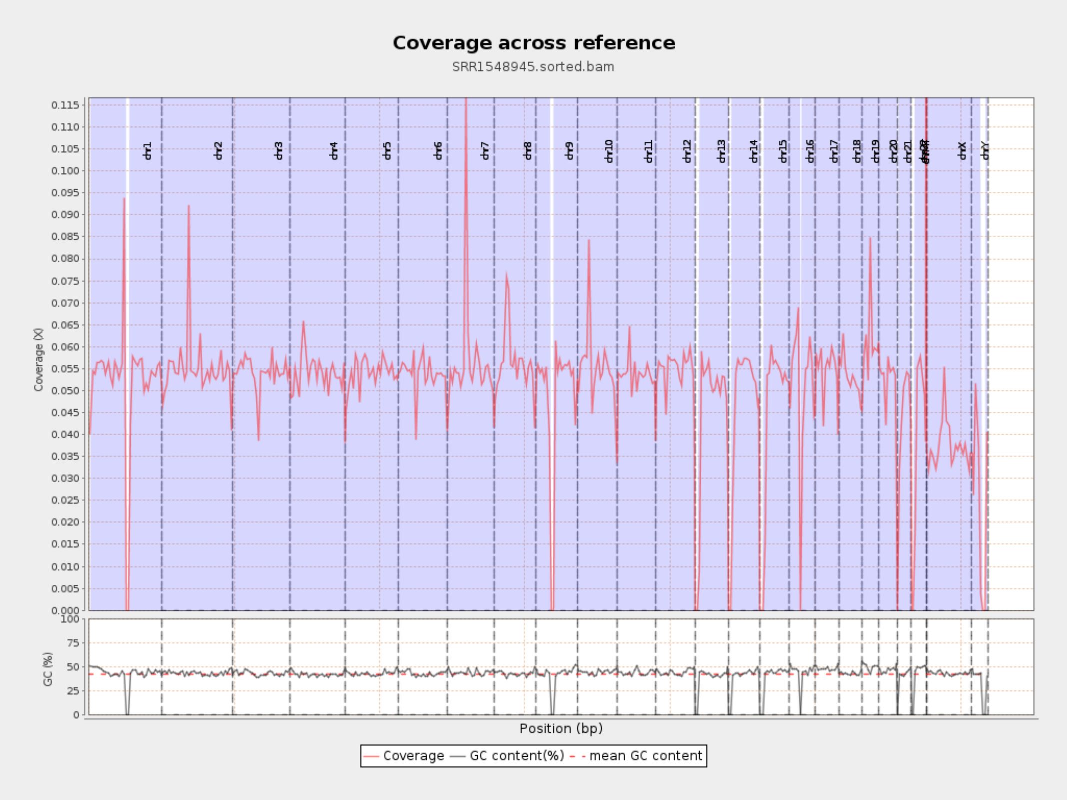
General error rate	0.3%
Mismatches	470,036
Insertions	5,101
Mapped reads with at least one insertion	0.13%
Deletions	12,270
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.7%

2.6. Chromosome stats

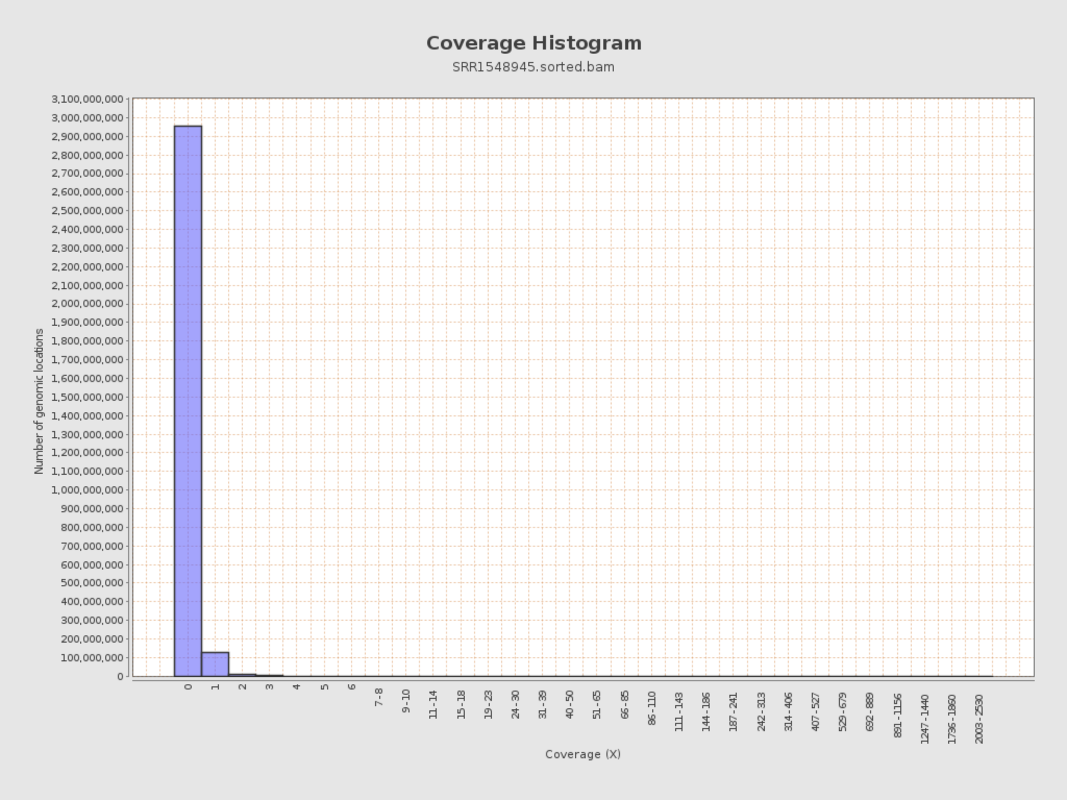
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12900104	0.0518	0.9821
chr2	243199373	13455932	0.0553	0.4355
chr3	198022430	10695191	0.054	0.2556
chr4	191154276	10339183	0.0541	0.2704
chr5	180915260	9797191	0.0542	0.2619
chr6	171115067	9206152	0.0538	0.2731
chr7	159138663	9117402	0.0573	0.7555
chr8	146364022	8216591	0.0561	1.2666

chr9	141213431	6753482	0.0478	0.4357
chr10	135534747	7518834	0.0555	0.4012
chr11	135006516	7208467	0.0534	0.3428
chr12	133851895	7357654	0.055	0.275
chr13	115169878	5042437	0.0438	0.226
chr14	107349540	4898085	0.0456	0.2888
chr15	102531392	4517624	0.0441	0.2322
chr16	90354753	4591660	0.0508	0.288
chr17	81195210	4425375	0.0545	0.266
chr18	78077248	4186059	0.0536	0.8011
chr19	59128983	3627290	0.0613	0.9446
chr20	63025520	3283512	0.0521	0.2624
chr21	48129895	2018161	0.0419	0.2765
chr22	51304566	1884669	0.0367	0.2654
chrMT	16571	8438	0.5092	0.8686
chrX	155270560	5828881	0.0375	0.289
chrY	59373566	1421843	0.0239	0.2461

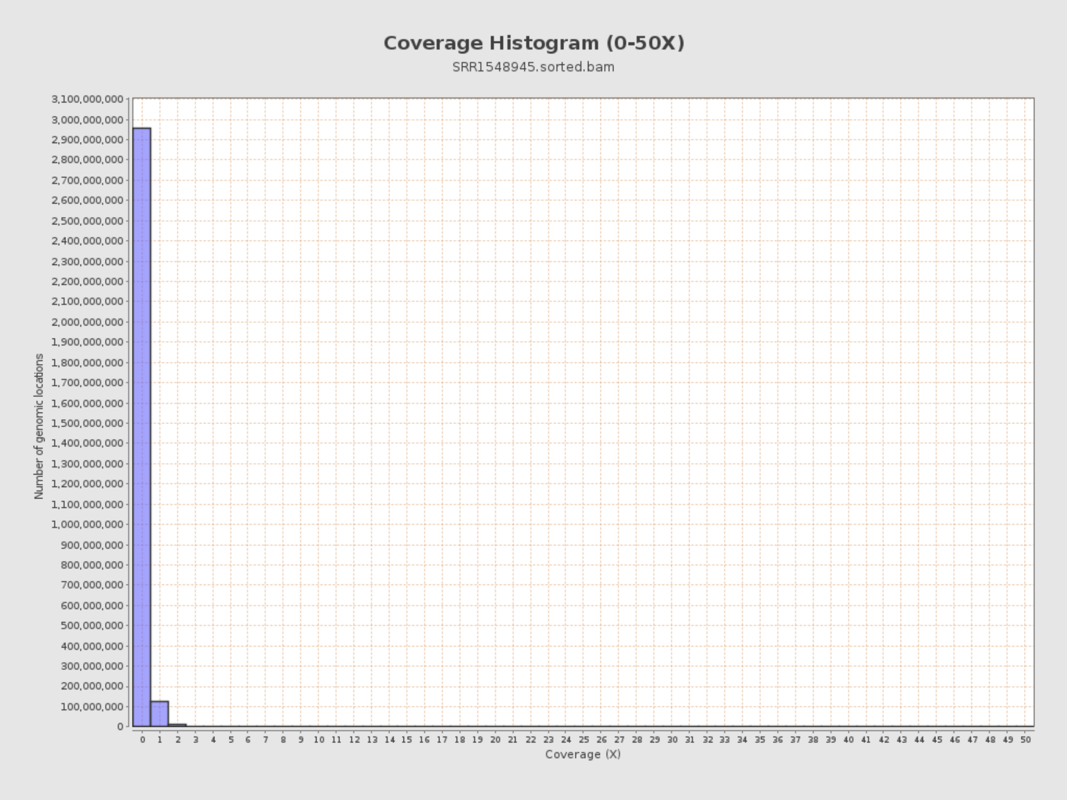
3. Results : Coverage across reference



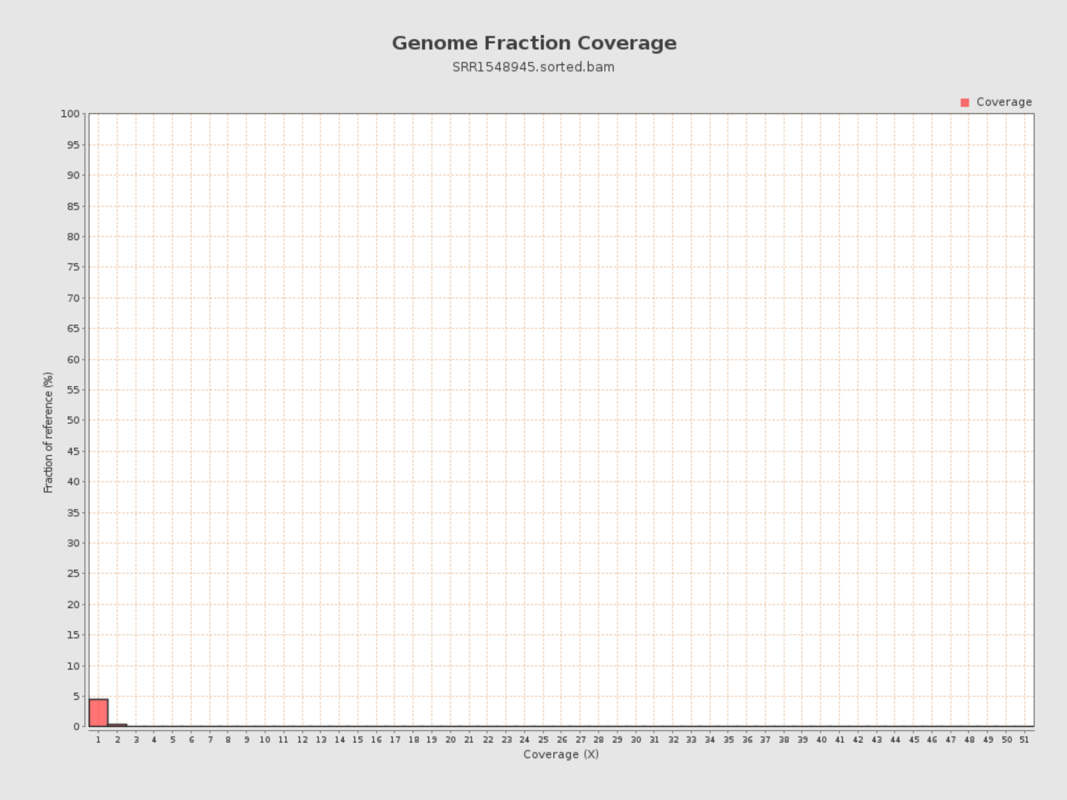
4. Results : Coverage Histogram



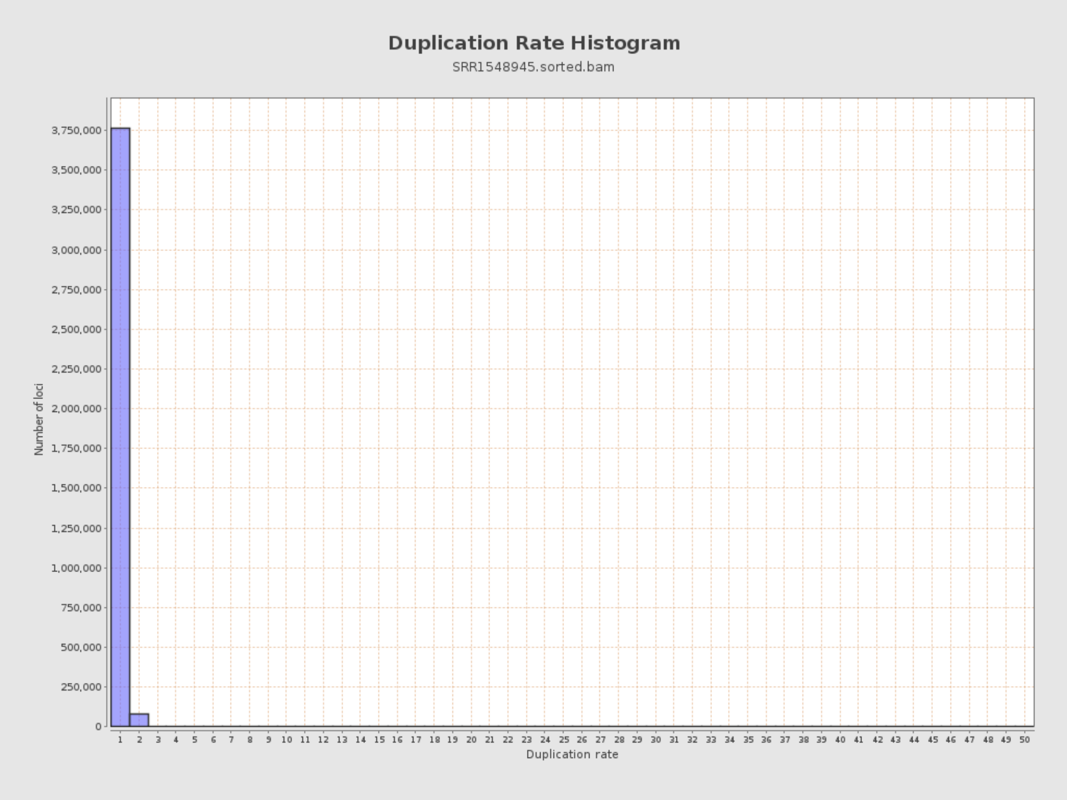
5. Results : Coverage Histogram (0-50X)



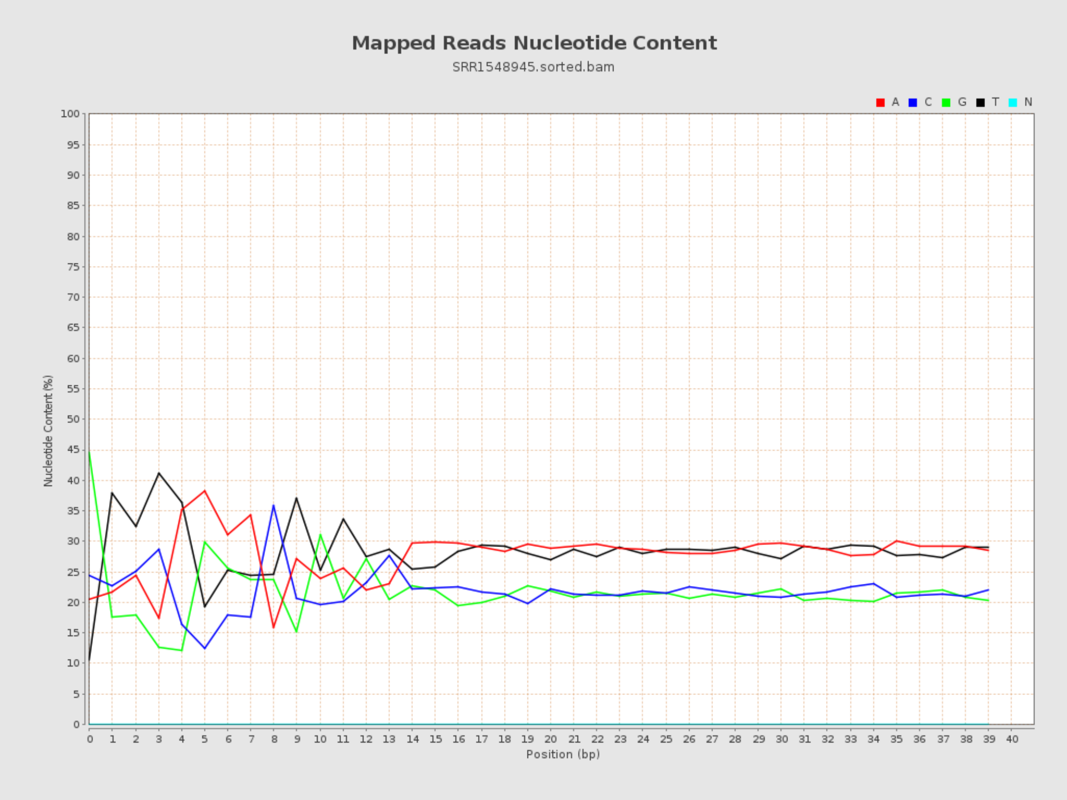
6. Results : Genome Fraction Coverage



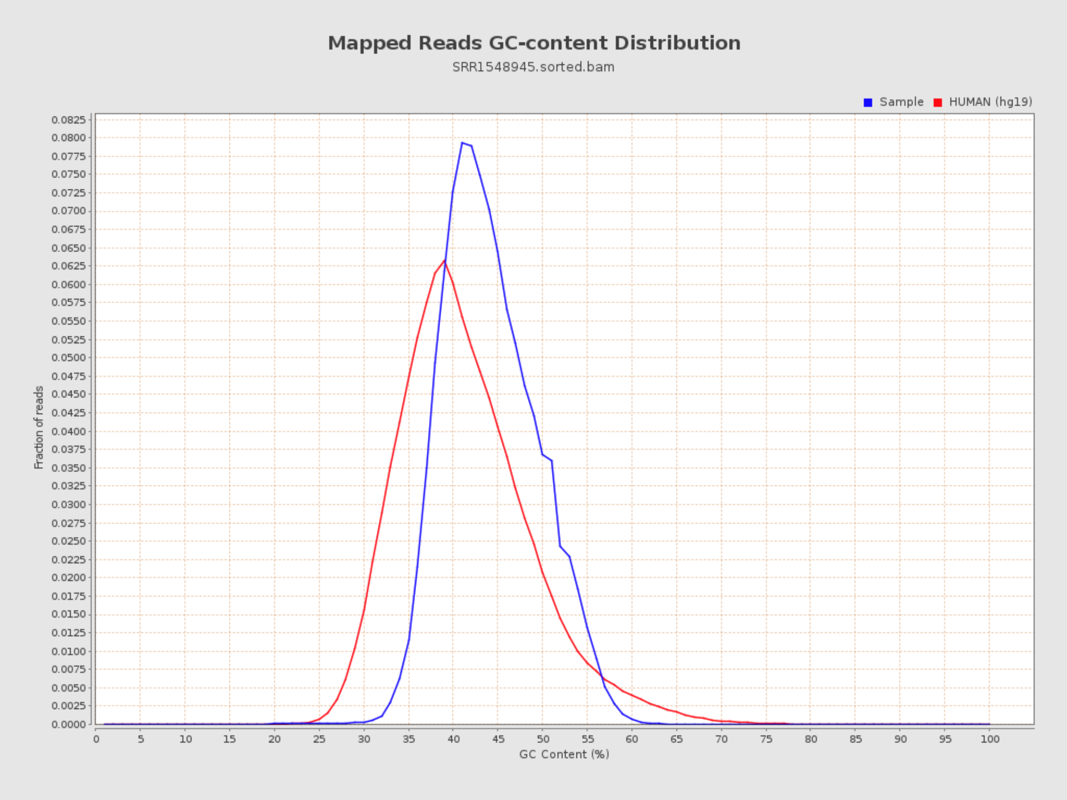
7. Results : Duplication Rate Histogram



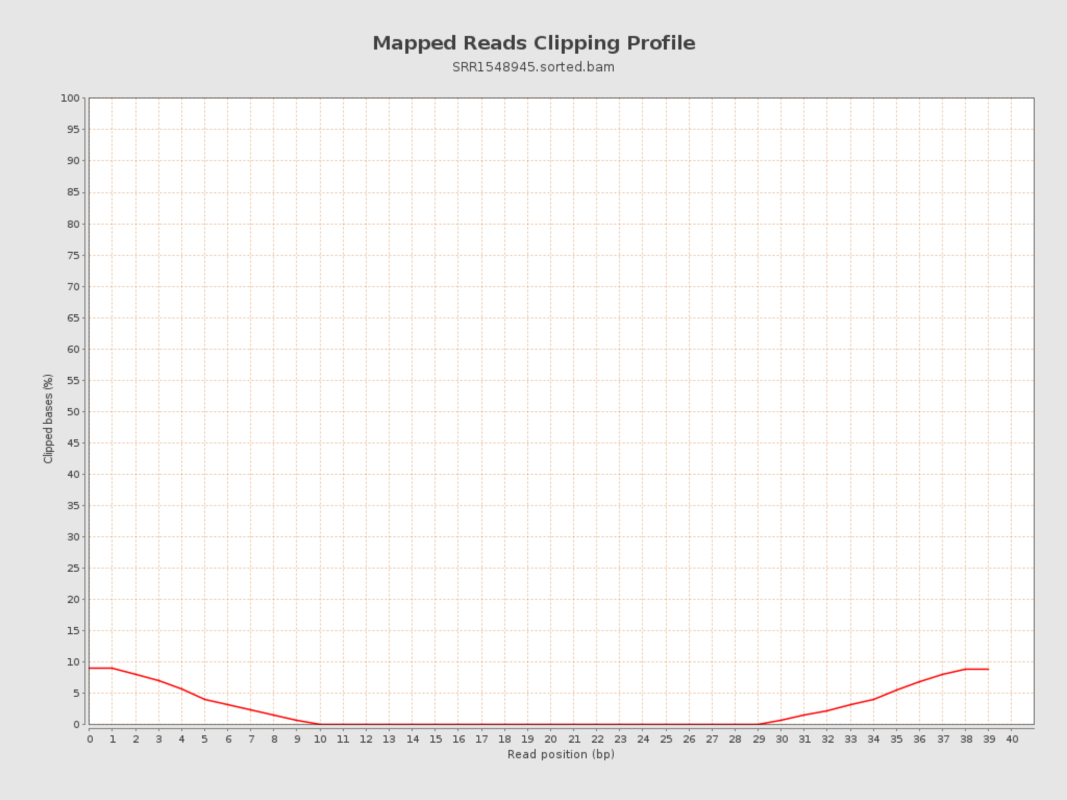
8. Results : Mapped Reads Nucleotide Content



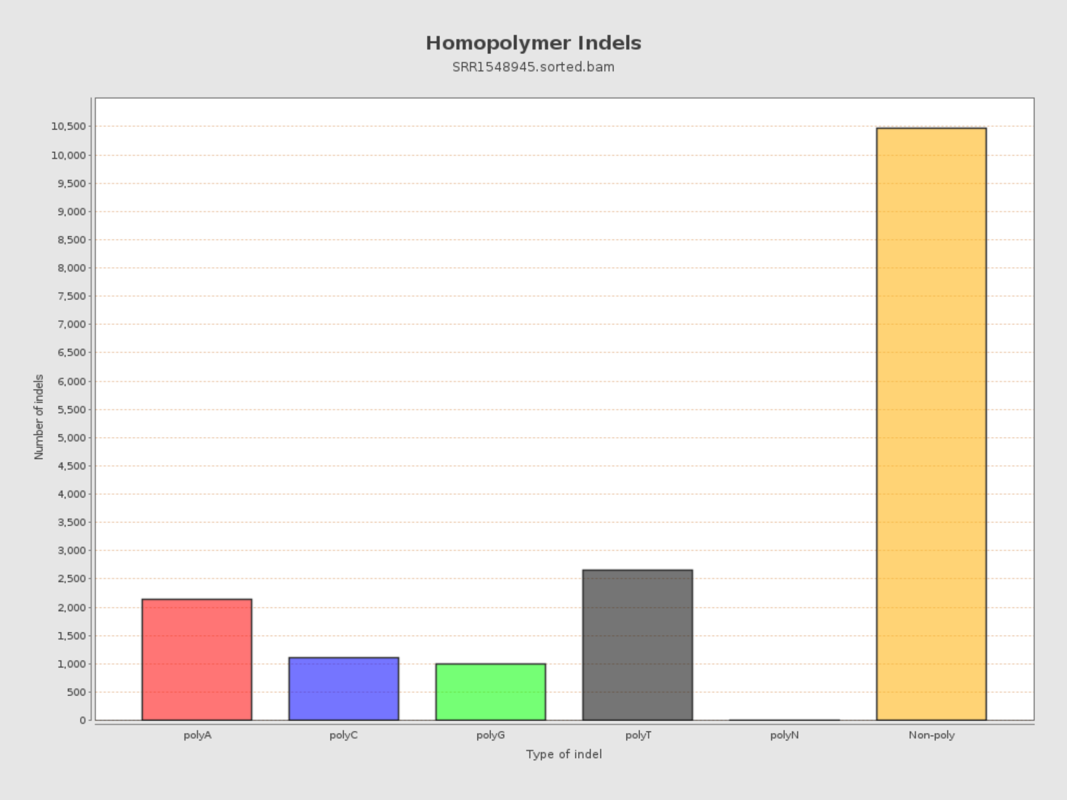
9. Results : Mapped Reads GC-content Distribution



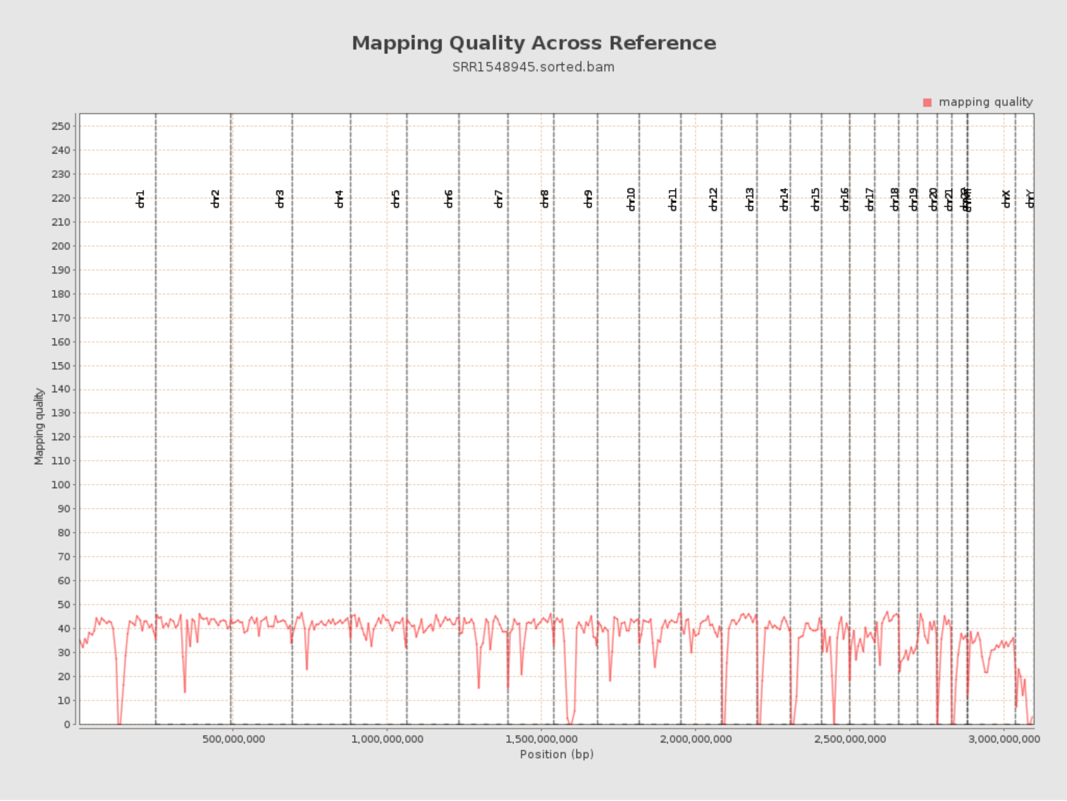
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram