Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:43:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548959.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_SRR1548959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:43:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,258,775
Mapped reads	5,415,130 / 86.52%
Unmapped reads	843,645 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	219,480 / 3.51%
Duplication rate	3.08%
Clipped reads	317,946 / 5.08%

2.2. ACGT Content

Number/percentage of A's	61,551,727 / 28.66%
Number/percentage of C's	45,618,414 / 21.24%
Number/percentage of T's	61,981,255 / 28.86%
Number/percentage of G's	45,605,043 / 21.24%
Number/percentage of N's	299 / 0%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0694
Standard Deviation	0.8149

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

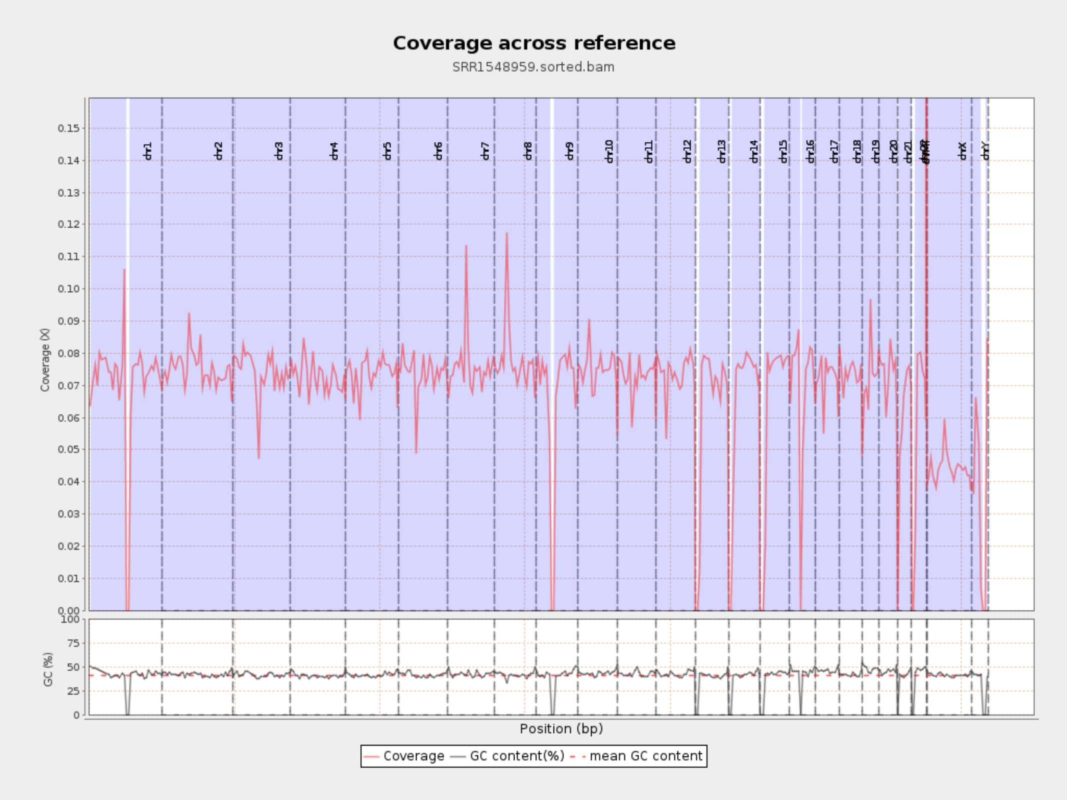
General error rate	0.23%
Mismatches	481,383
Insertions	5,597
Mapped reads with at least one insertion	0.1%
Deletions	15,963
Mapped reads with at least one deletion	0.29%
Homopolymer indels	43.32%

2.6. Chromosome stats

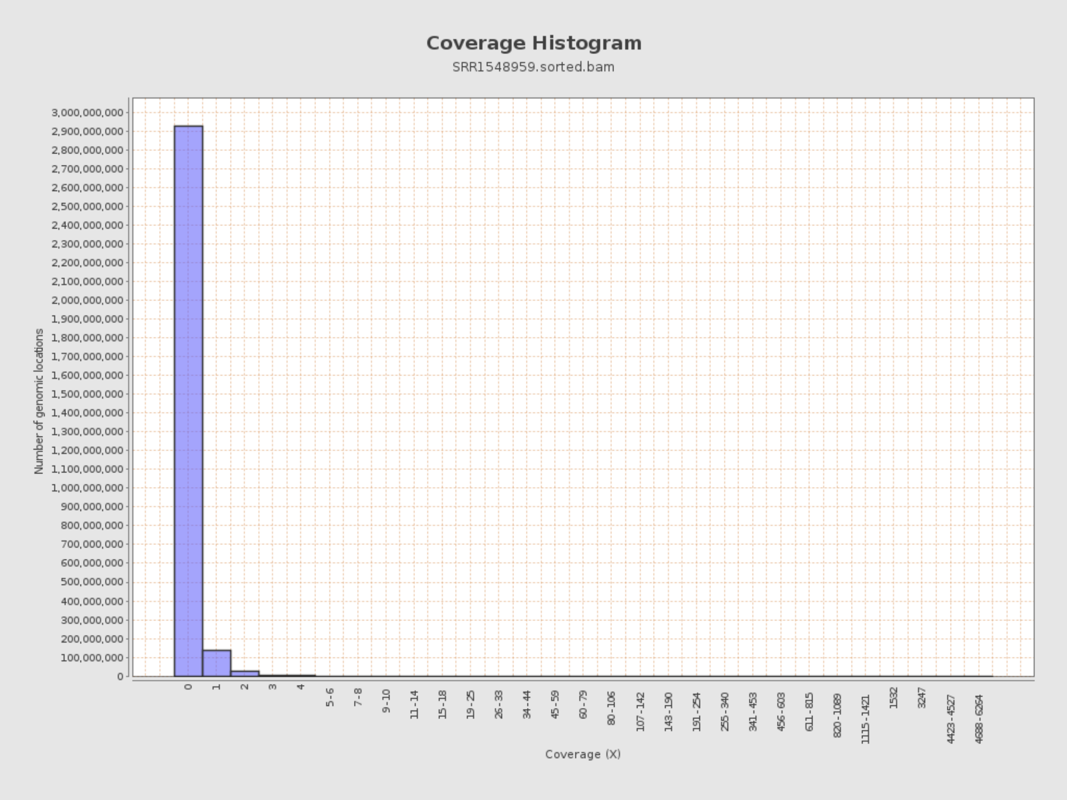
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17537164	0.0704	0.9812
chr2	243199373	18307948	0.0753	0.4224
chr3	198022430	14650859	0.074	0.3308
chr4	191154276	13859285	0.0725	0.3429
chr5	180915260	13369528	0.0739	0.3344
chr6	171115067	12656336	0.074	0.3463
chr7	159138663	12124740	0.0762	0.6724
chr8	146364022	11399636	0.0779	3.0562

chr9	141213431	9228533	0.0654	0.3928
chr10	135534747	10248720	0.0756	0.4218
chr11	135006516	9862943	0.0731	0.4153
chr12	133851895	9894426	0.0739	0.3402
chr13	115169878	7067424	0.0614	0.2993
chr14	107349540	6819537	0.0635	0.3344
chr15	102531392	6405758	0.0625	0.3029
chr16	90354753	6233894	0.069	0.3354
chr17	81195210	5847144	0.072	0.335
chr18	78077248	5769232	0.0739	0.6551
chr19	59128983	4308590	0.0729	0.7609
chr20	63025520	4673974	0.0742	0.343
chr21	48129895	2829265	0.0588	0.3468
chr22	51304566	2673747	0.0521	0.3519
chrMT	16571	12147	0.733	1.1848
chrX	155270560	6892880	0.0444	0.3018
chrY	59373566	2104491	0.0354	0.4268

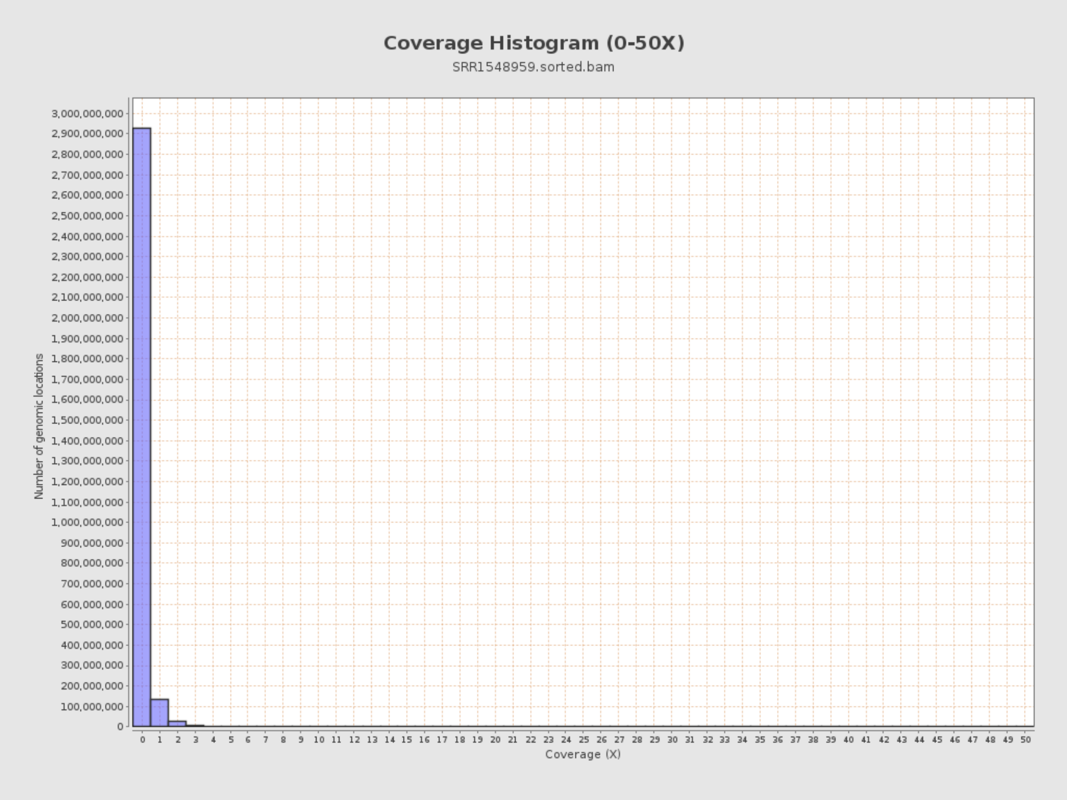
3. Results : Coverage across reference



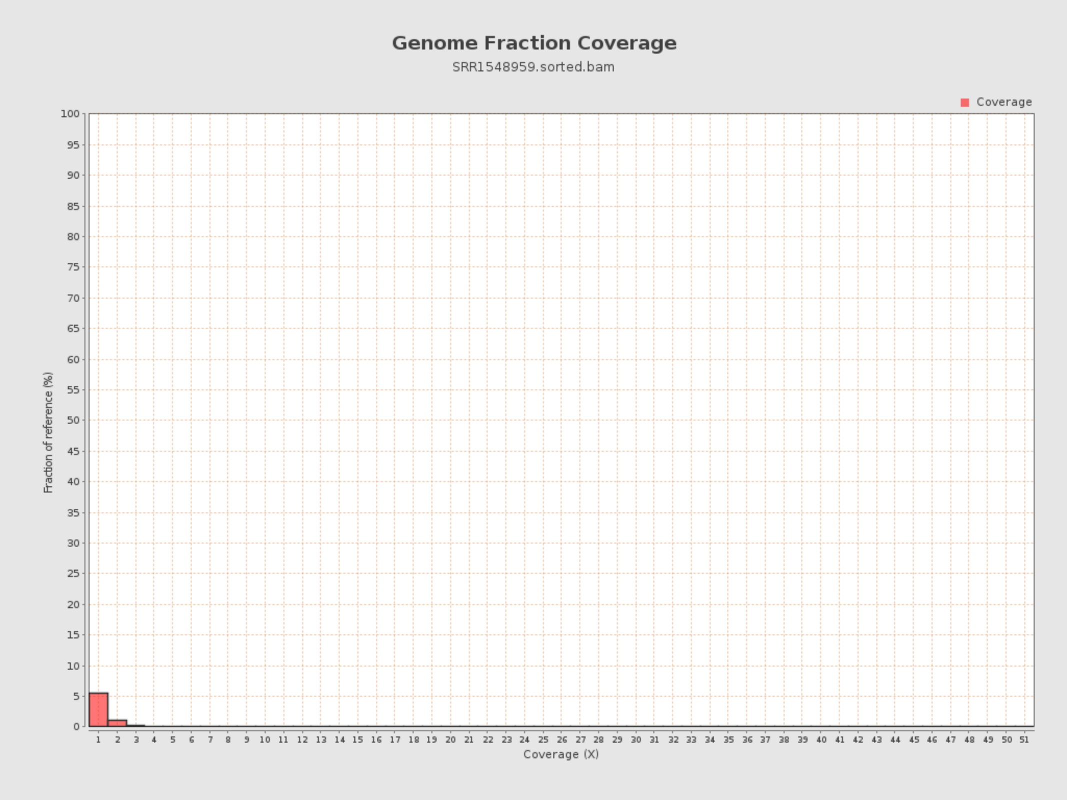
4. Results : Coverage Histogram



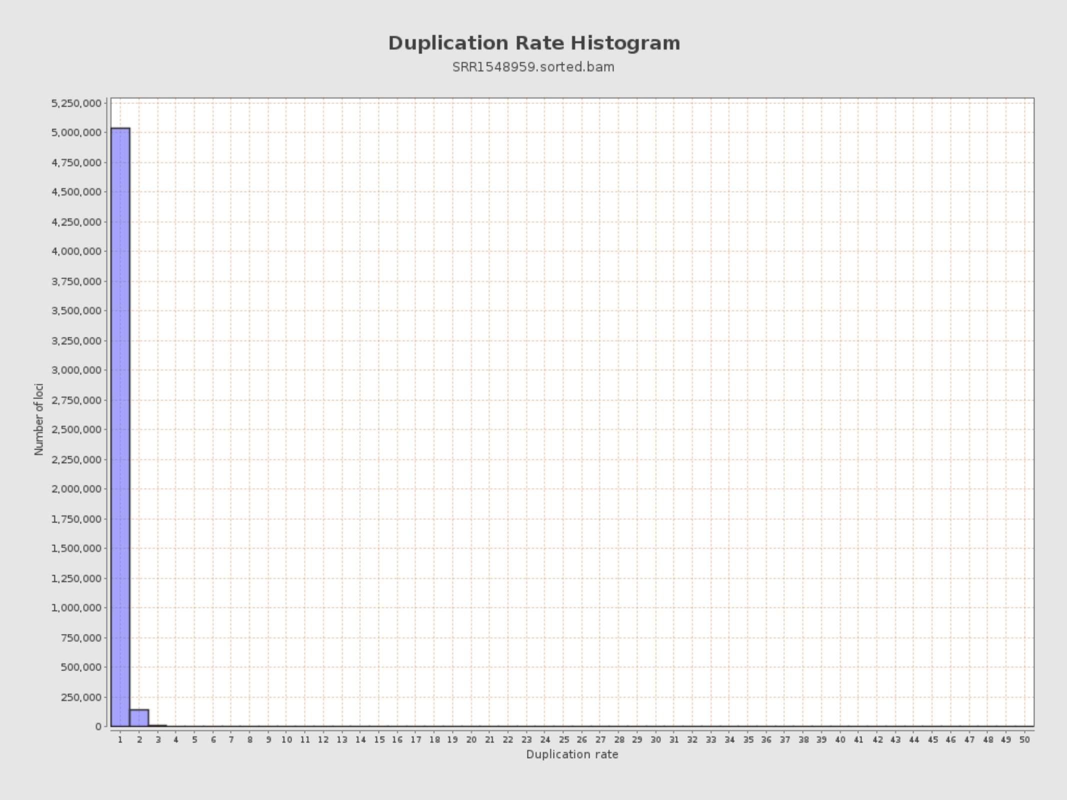
5. Results : Coverage Histogram (0-50X)



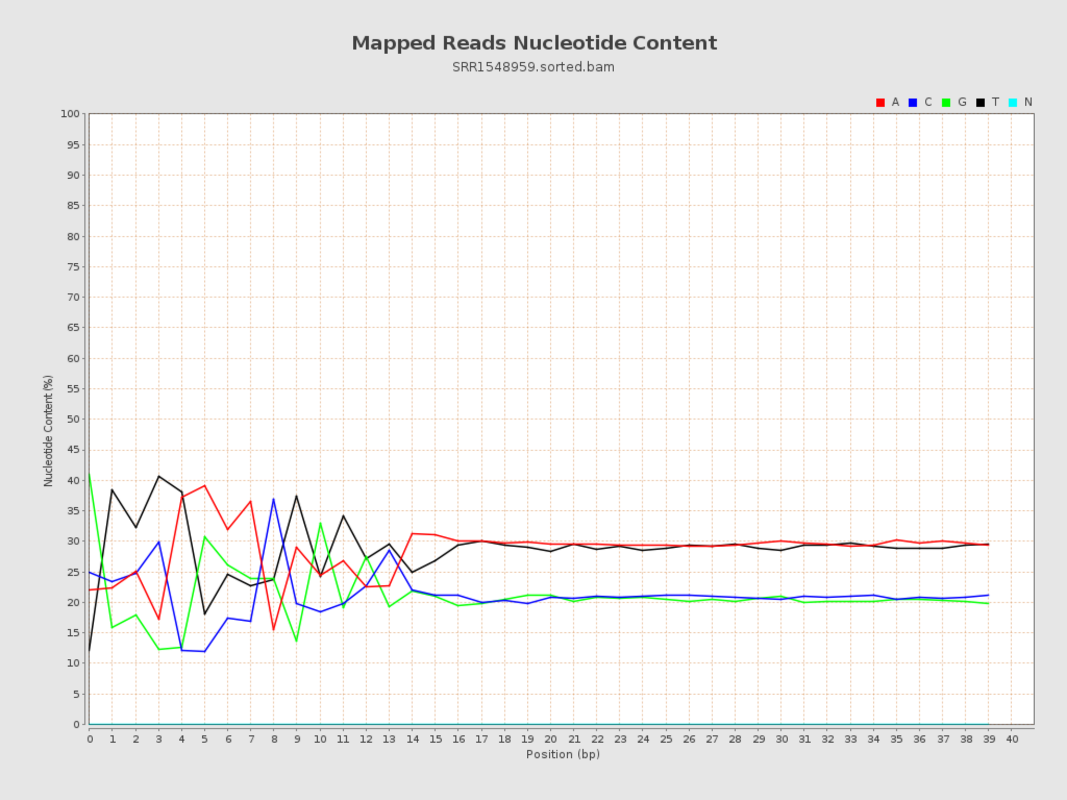
6. Results : Genome Fraction Coverage



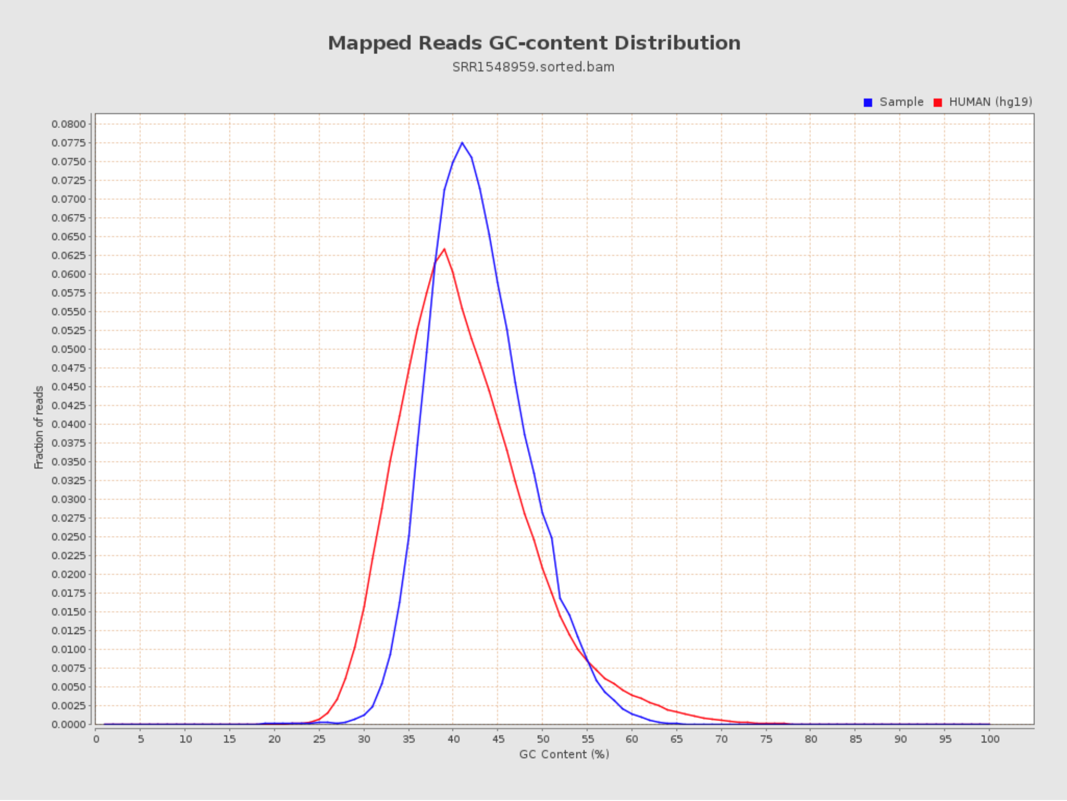
7. Results : Duplication Rate Histogram



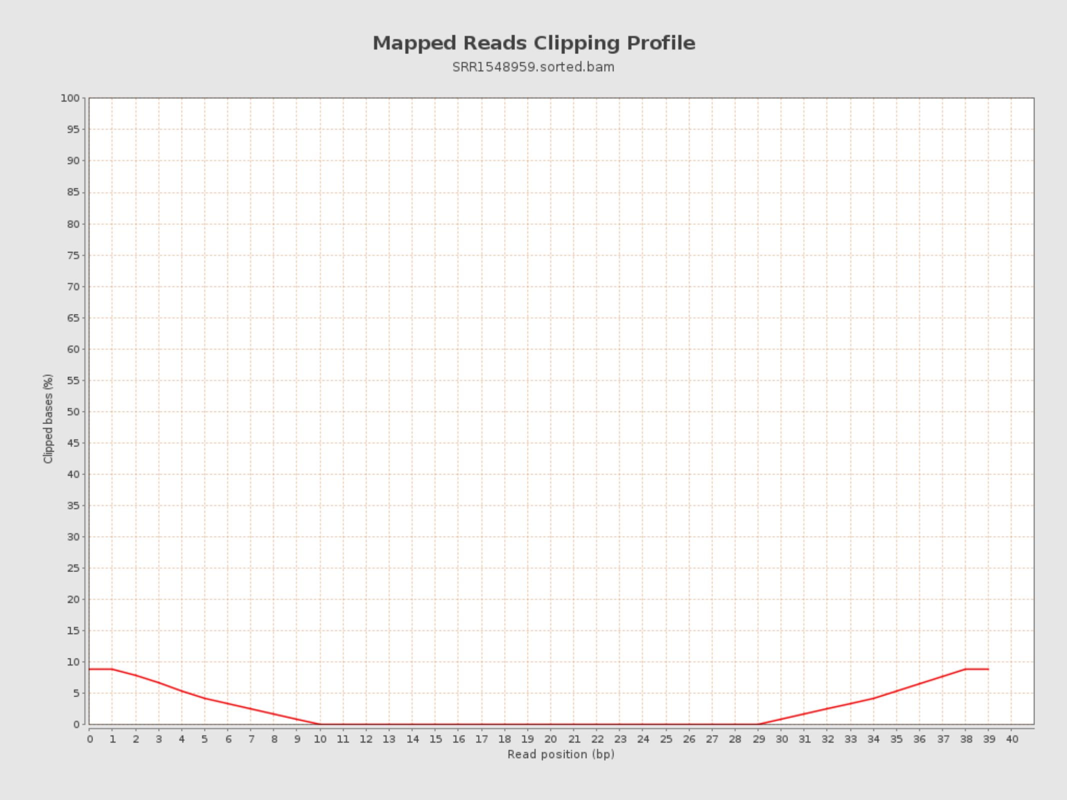
8. Results : Mapped Reads Nucleotide Content



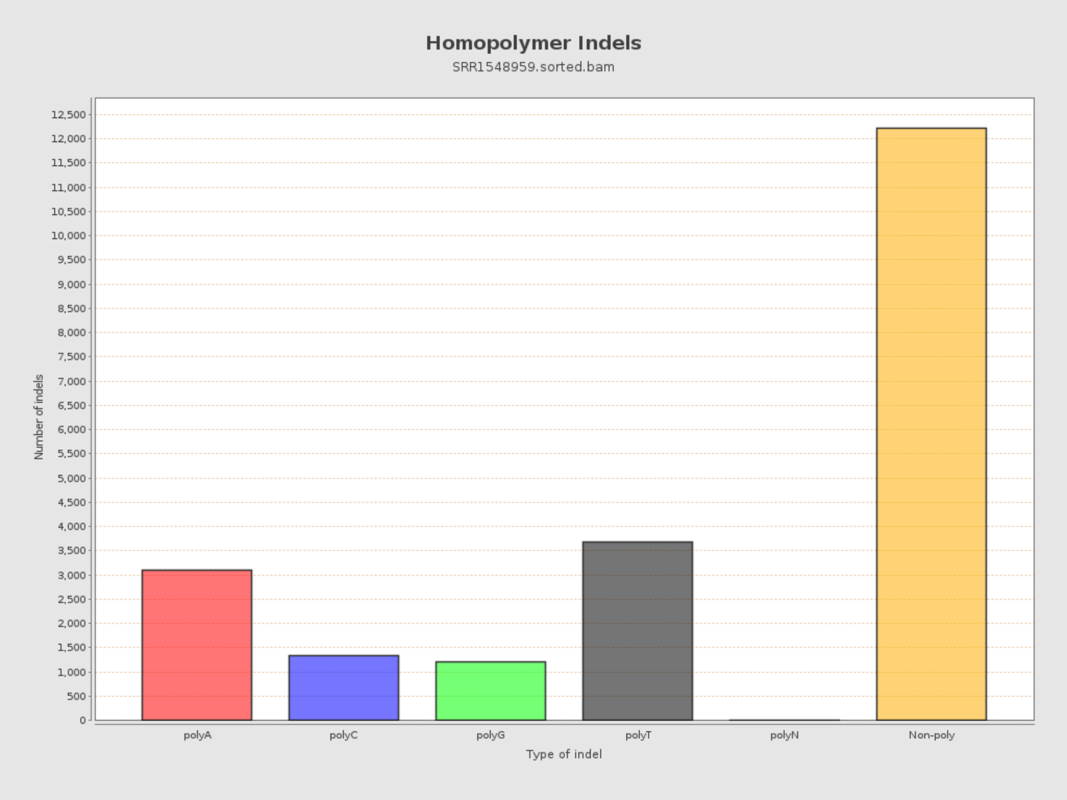
9. Results : Mapped Reads GC-content Distribution



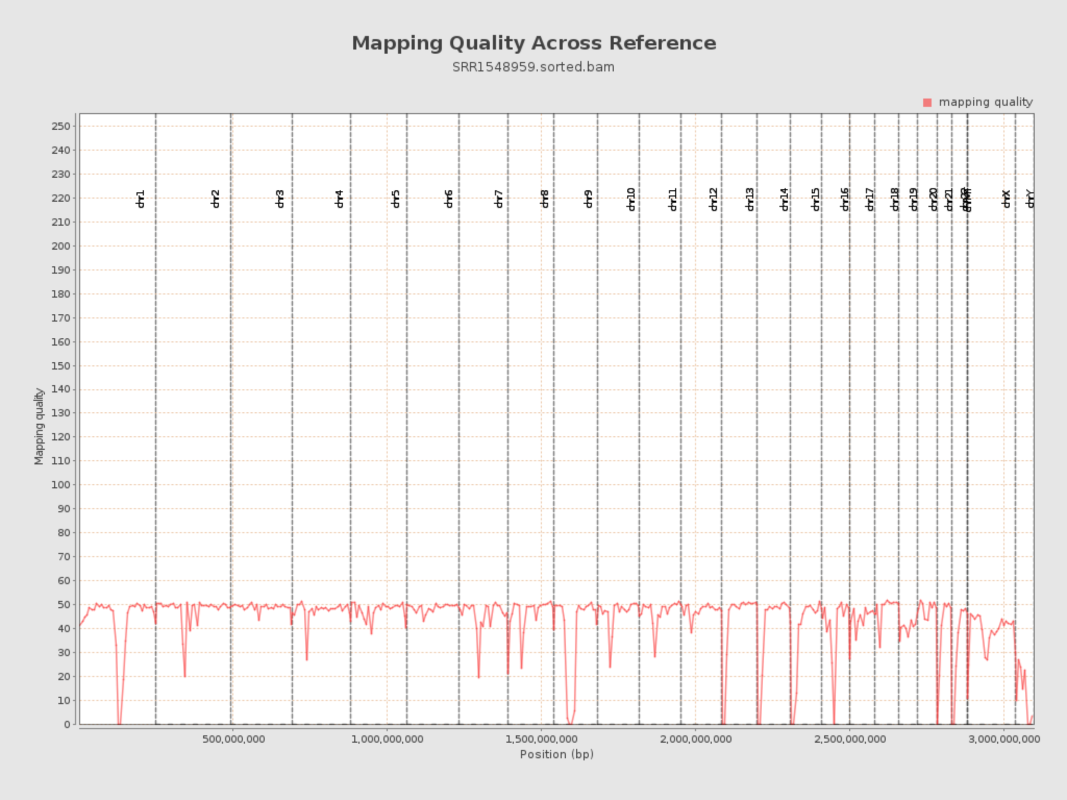
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram