Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:48:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548988.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_SRR1548988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:48:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,141,022
Mapped reads	3,189,115 / 44.66%
Unmapped reads	3,951,907 / 55.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	66,900 / 0.94%
Duplication rate	1.41%
Clipped reads	237,569 / 3.33%

2.2. ACGT Content

Number/percentage of A's	37,334,982 / 29.58%
Number/percentage of C's	25,522,217 / 20.22%
Number/percentage of T's	37,525,212 / 29.73%
Number/percentage of G's	25,831,378 / 20.47%
Number/percentage of N's	6,332 / 0.01%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0408
Standard Deviation	0.3087

2.4. Mapping Quality

Mean Mapping Quality	43.07

2.5. Mismatches and indels

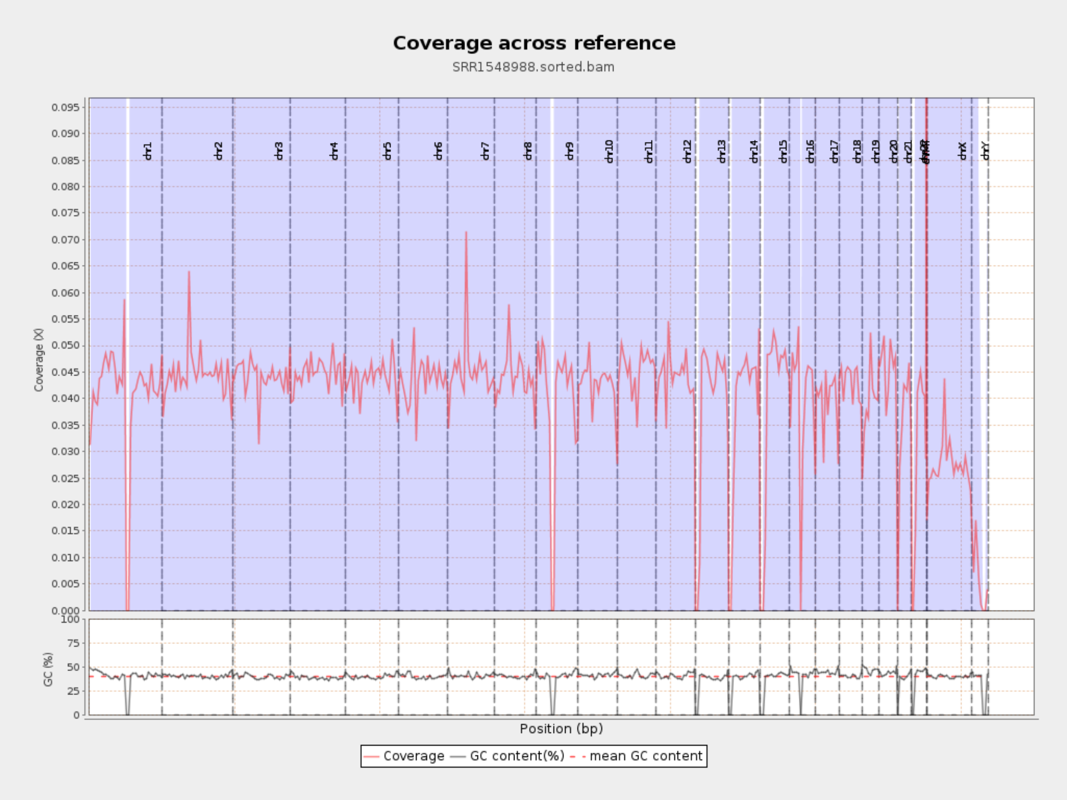
General error rate	0.29%
Mismatches	358,466
Insertions	4,404
Mapped reads with at least one insertion	0.14%
Deletions	11,890
Mapped reads with at least one deletion	0.37%
Homopolymer indels	45.77%

2.6. Chromosome stats

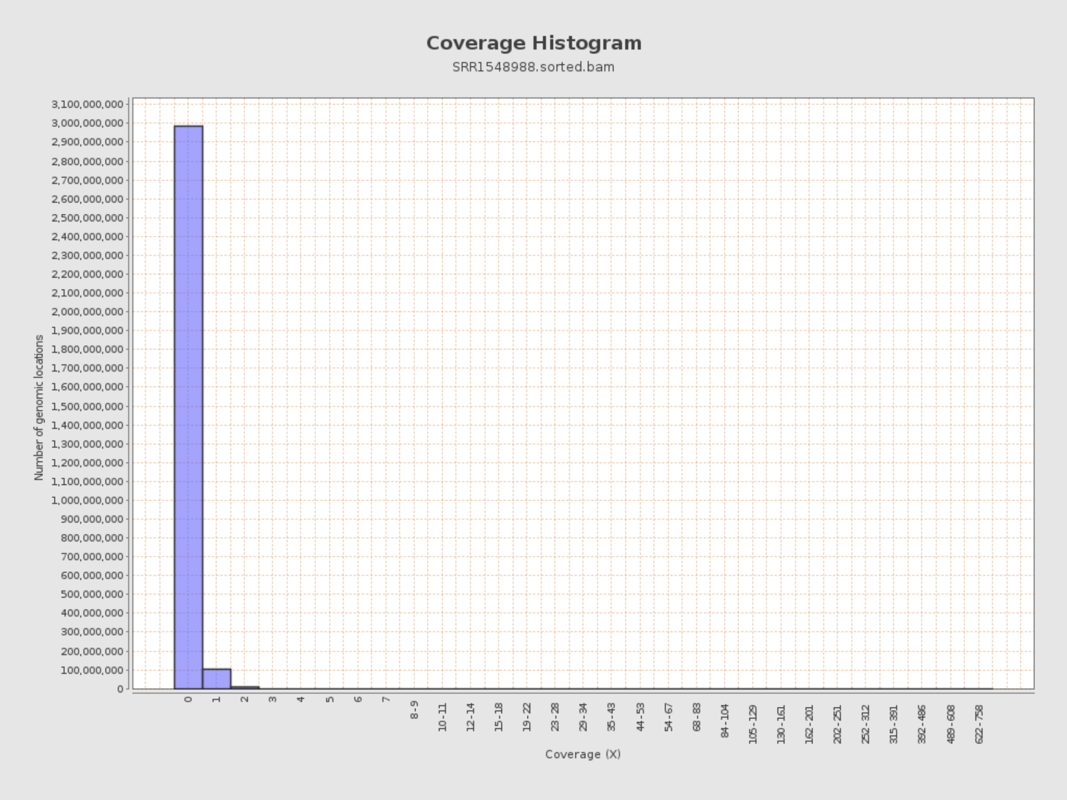
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10124325	0.0406	0.5032
chr2	243199373	10860641	0.0447	0.3009
chr3	198022430	8719676	0.044	0.2301
chr4	191154276	8553782	0.0447	0.2343
chr5	180915260	7953484	0.044	0.2317
chr6	171115067	7451558	0.0435	0.2563
chr7	159138663	7287050	0.0458	0.4601
chr8	146364022	6432009	0.0439	0.4486

chr9	141213431	5556198	0.0393	0.2753
chr10	135534747	5848202	0.0431	0.261
chr11	135006516	6104888	0.0452	0.2902
chr12	133851895	5934433	0.0443	0.2363
chr13	115169878	4350963	0.0378	0.2118
chr14	107349540	3987906	0.0371	0.2306
chr15	102531392	3978147	0.0388	0.2153
chr16	90354753	3576500	0.0396	0.2313
chr17	81195210	3189992	0.0393	0.2304
chr18	78077248	3372118	0.0432	0.4342
chr19	59128983	2349986	0.0397	0.4369
chr20	63025520	2872032	0.0456	0.2381
chr21	48129895	1647949	0.0342	0.2163
chr22	51304566	1468533	0.0286	0.1906
chrMT	16571	5073	0.3061	0.5761
chrX	155270560	4279629	0.0276	0.2082
chrY	59373566	329924	0.0056	0.1046

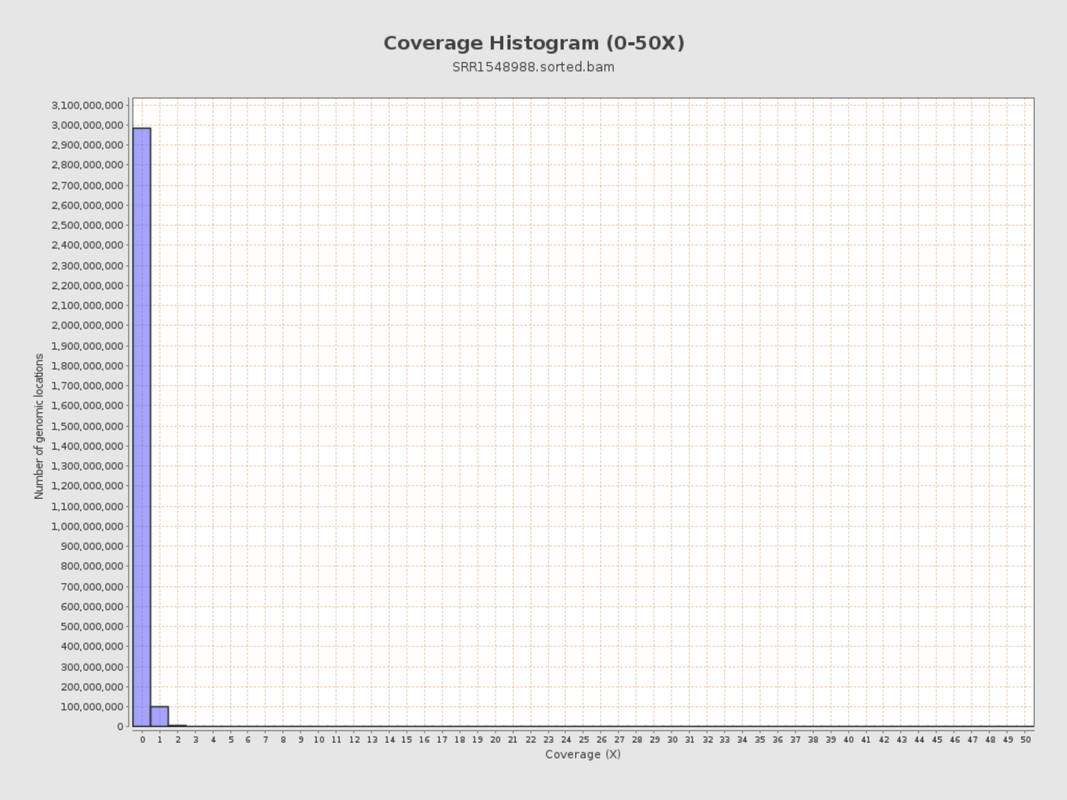
3. Results : Coverage across reference



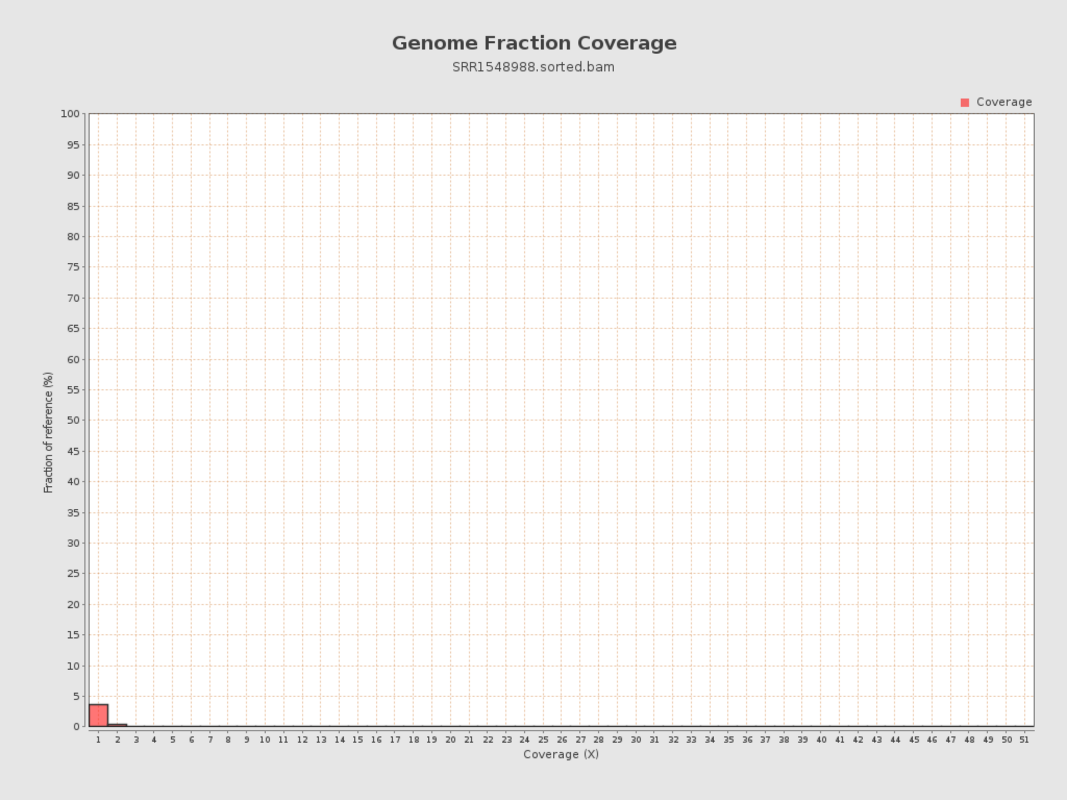
4. Results : Coverage Histogram



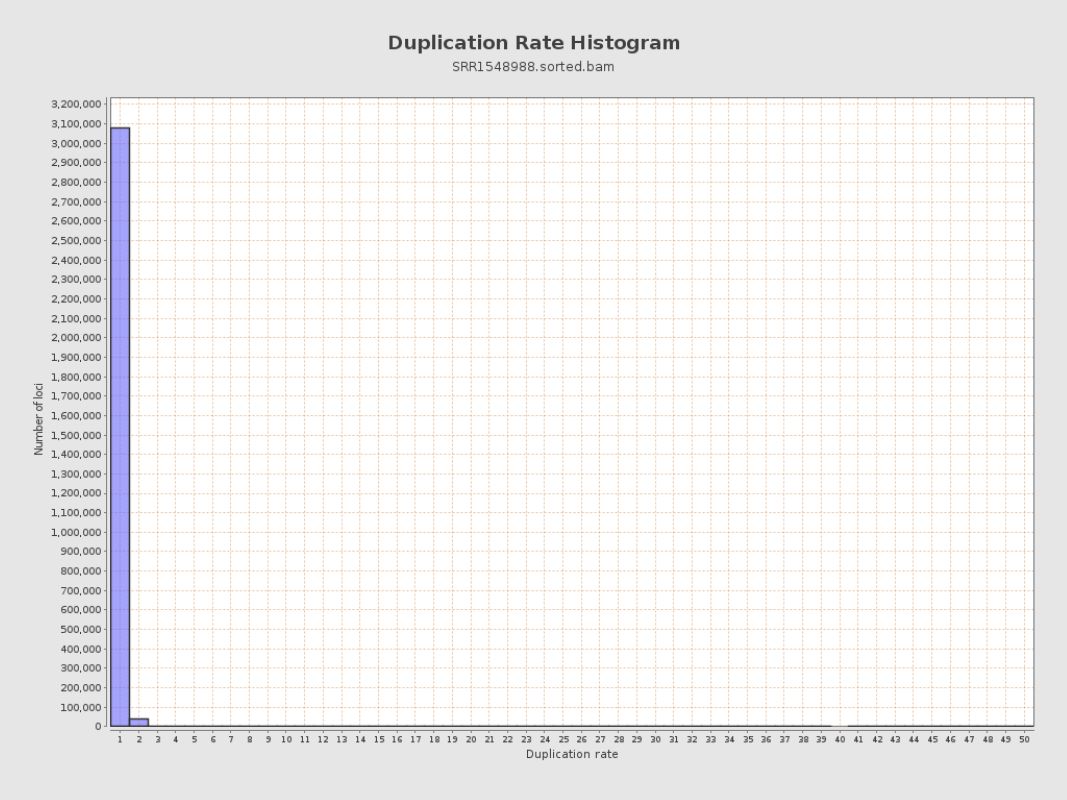
5. Results : Coverage Histogram (0-50X)



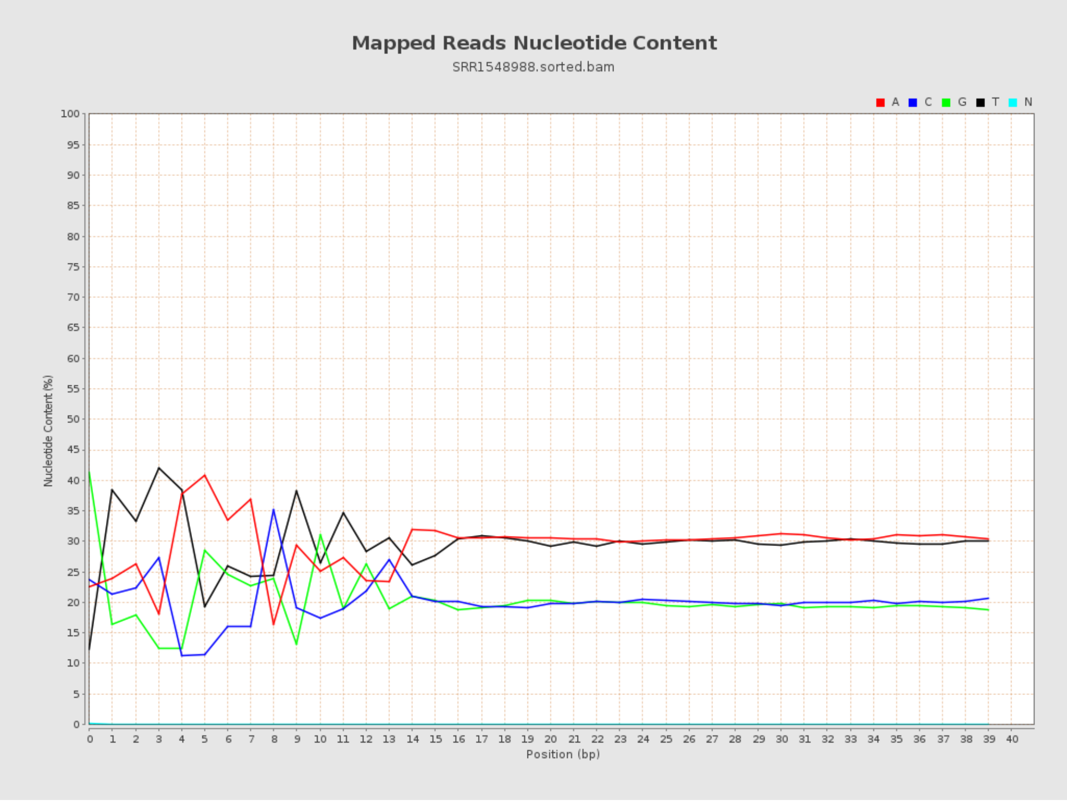
6. Results : Genome Fraction Coverage



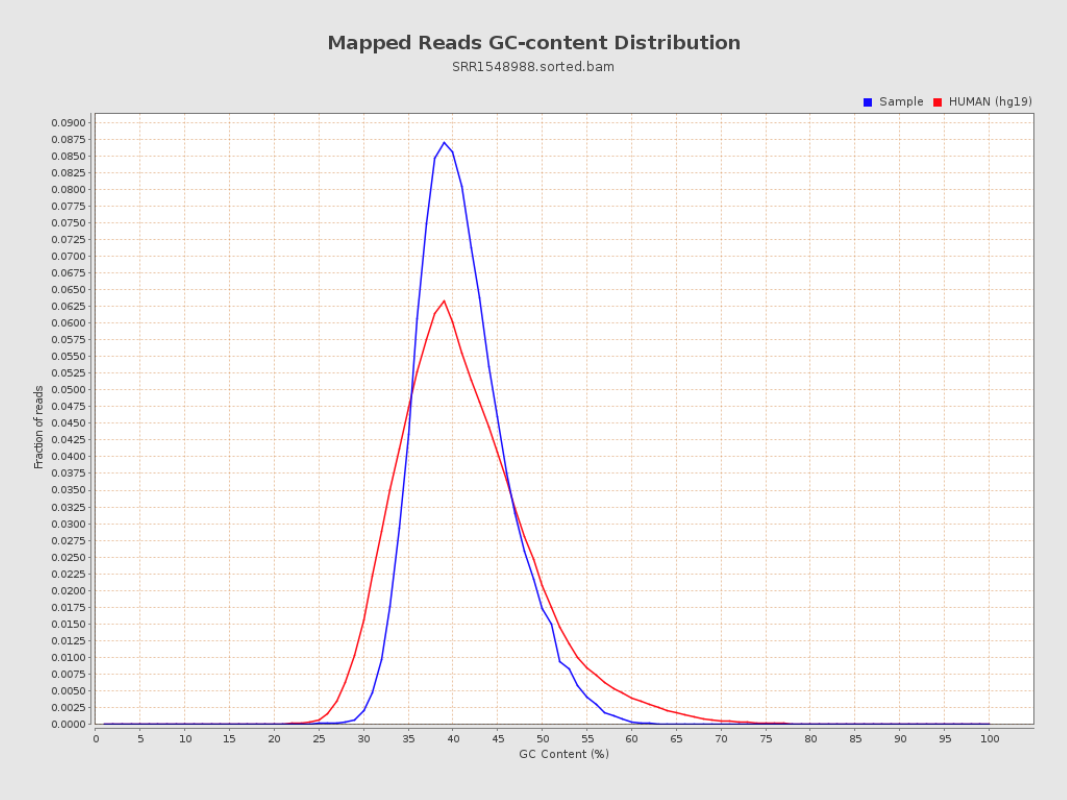
7. Results : Duplication Rate Histogram



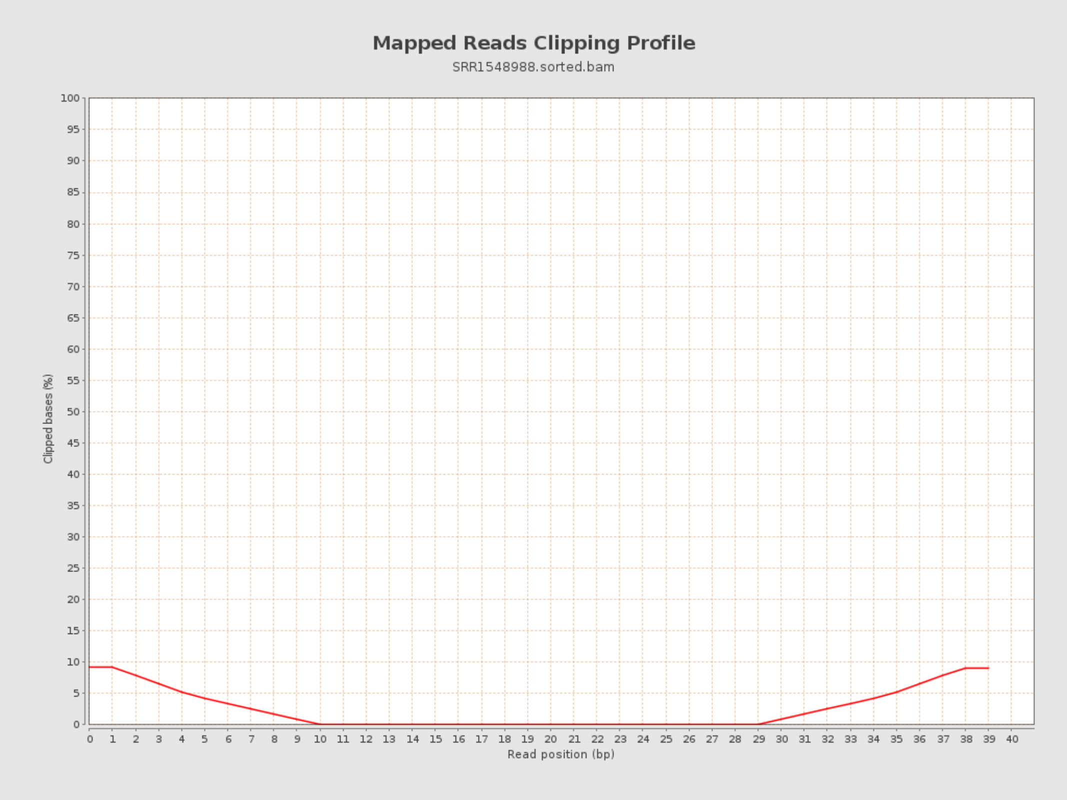
8. Results : Mapped Reads Nucleotide Content



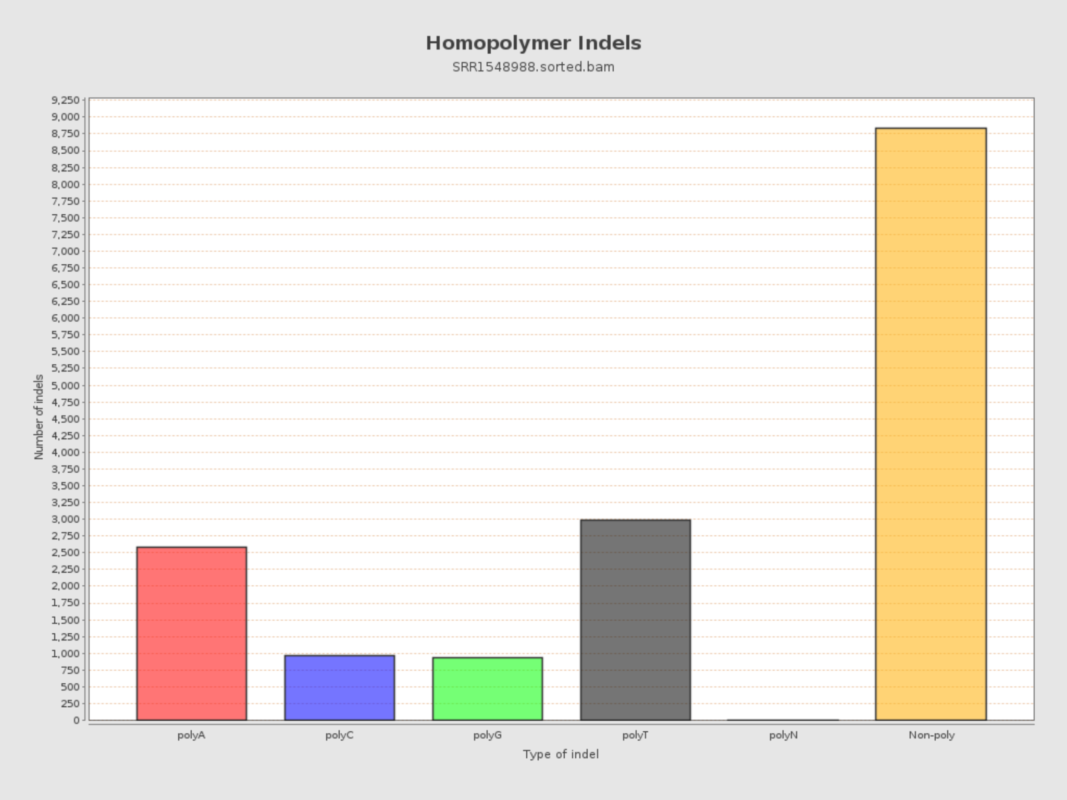
9. Results : Mapped Reads GC-content Distribution



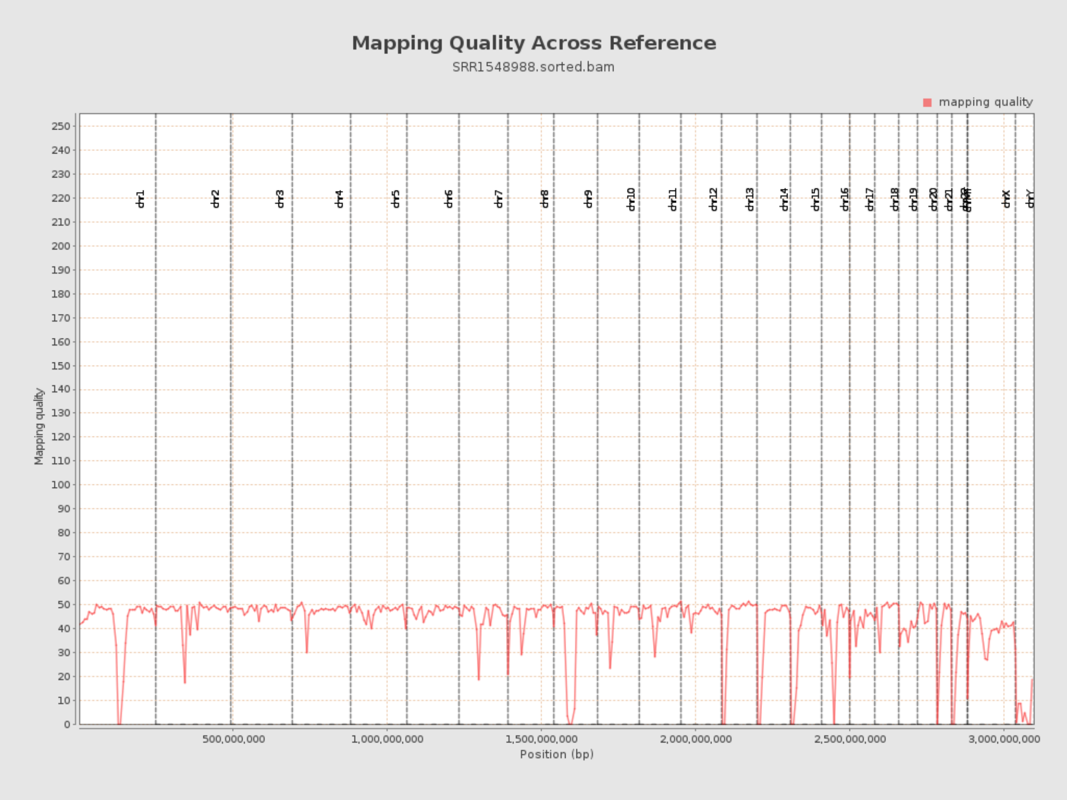
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram