Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:55:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084339.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_SRR3084339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:55:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,298,543
Mapped reads	2,931,297 / 88.87%
Unmapped reads	367,246 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,978 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	101,468 / 3.08%
Duplication rate	2.79%
Clipped reads	1,552,758 / 47.07%

2.2. ACGT Content

Number/percentage of A's	53,225,643 / 27.8%
Number/percentage of C's	36,800,600 / 19.22%
Number/percentage of T's	57,969,408 / 30.28%
Number/percentage of G's	43,203,500 / 22.57%
Number/percentage of N's	242,042 / 0.13%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0619

Standard Deviation	0.3983

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

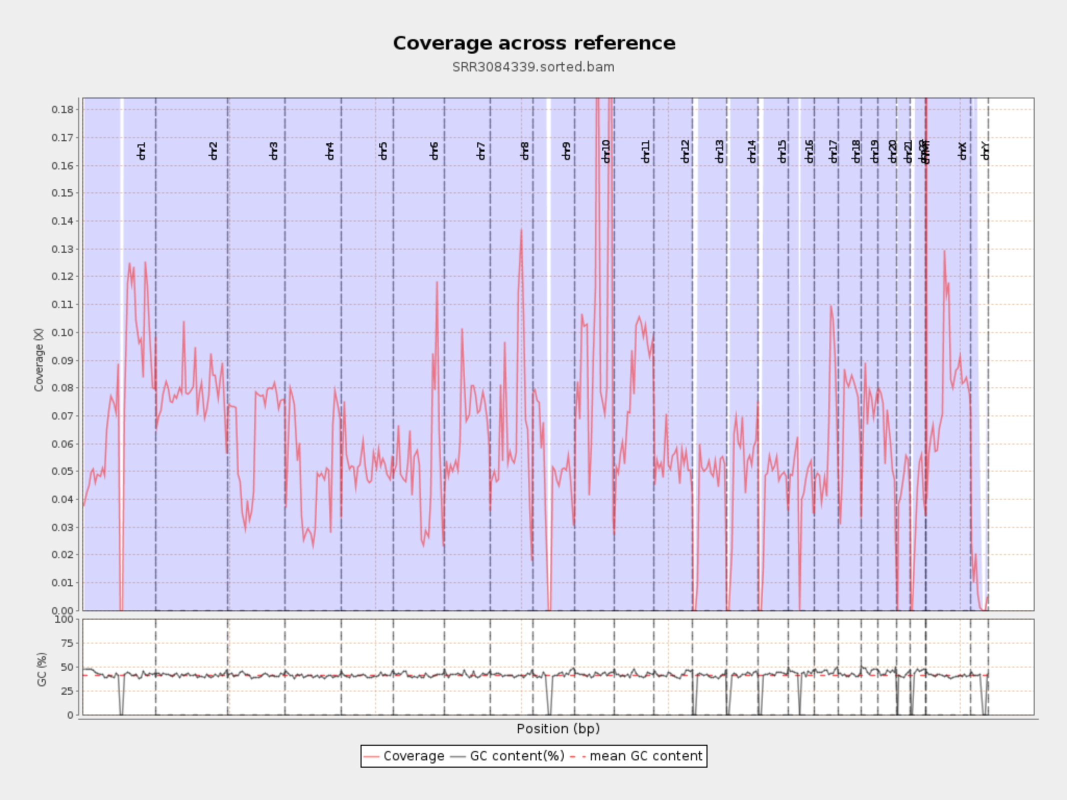
General error rate	1.06%
Mismatches	1,995,792
Insertions	14,858
Mapped reads with at least one insertion	0.5%
Deletions	40,730
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.26%

2.6. Chromosome stats

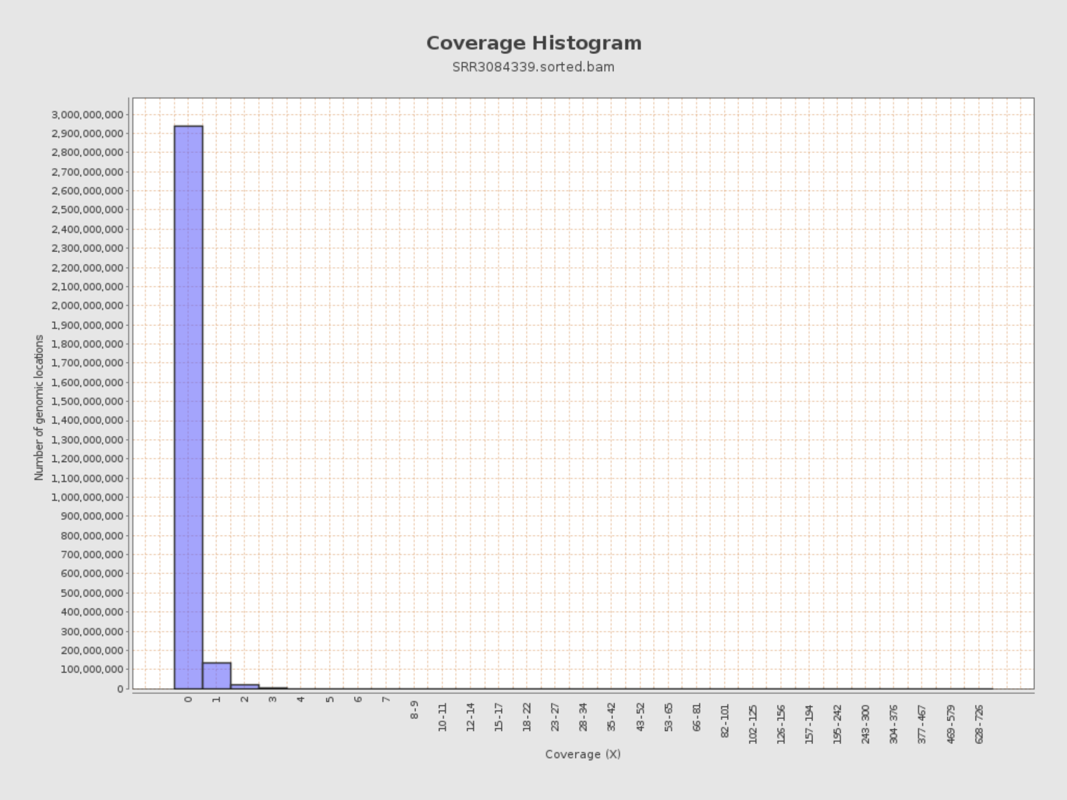
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18405660	0.0738	0.6365
chr2	243199373	19188134	0.0789	0.5008
chr3	198022430	12793424	0.0646	0.2976
chr4	191154276	9568554	0.0501	0.272
chr5	180915260	9548180	0.0528	0.2655
chr6	171115067	8992376	0.0526	0.2992
chr7	159138663	10666815	0.067	0.5665

chr8	146364022	9613736	0.0657	0.3686
chr9	141213431	6852420	0.0485	0.3354
chr10	135534747	13962897	0.103	0.5731
chr11	135006516	10820133	0.0801	0.3988
chr12	133851895	7139317	0.0533	0.2669
chr13	115169878	4979589	0.0432	0.2402
chr14	107349540	5242949	0.0488	0.2701
chr15	102531392	4140195	0.0404	0.2495
chr16	90354753	3940972	0.0436	0.269
chr17	81195210	5247849	0.0646	0.3177
chr18	78077248	5521254	0.0707	0.5712
chr19	59128983	4319332	0.073	0.4648
chr20	63025520	3909920	0.062	0.2932
chr21	48129895	2047273	0.0425	0.2492
chr22	51304566	1713597	0.0334	0.2085
chrMT	16571	25389	1.5321	1.6795
chrX	155270560	12416410	0.08	0.3615
chrY	59373566	450204	0.0076	0.1378

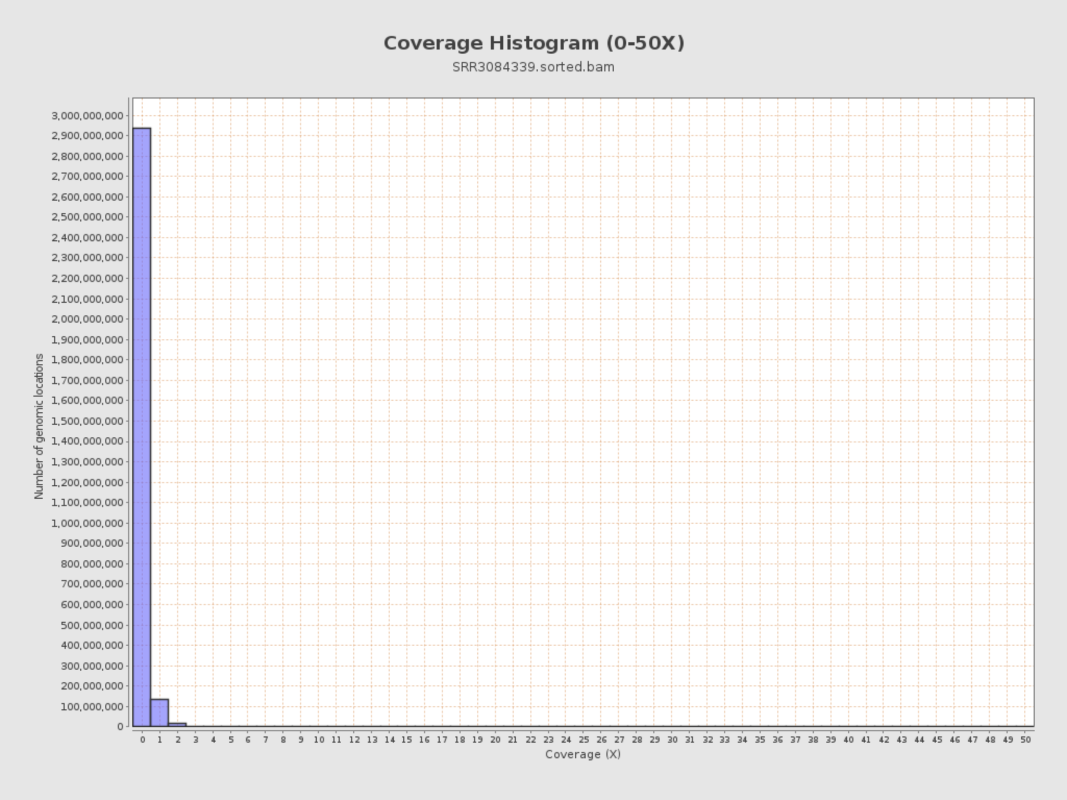
3. Results : Coverage across reference



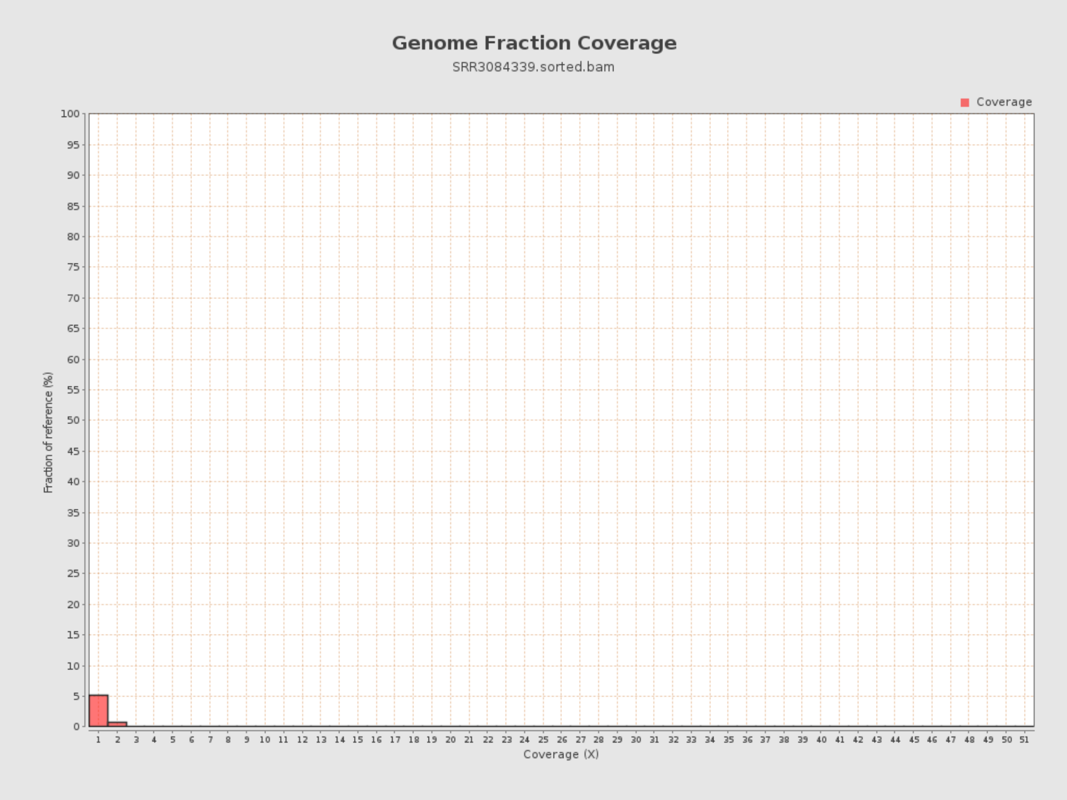
4. Results : Coverage Histogram



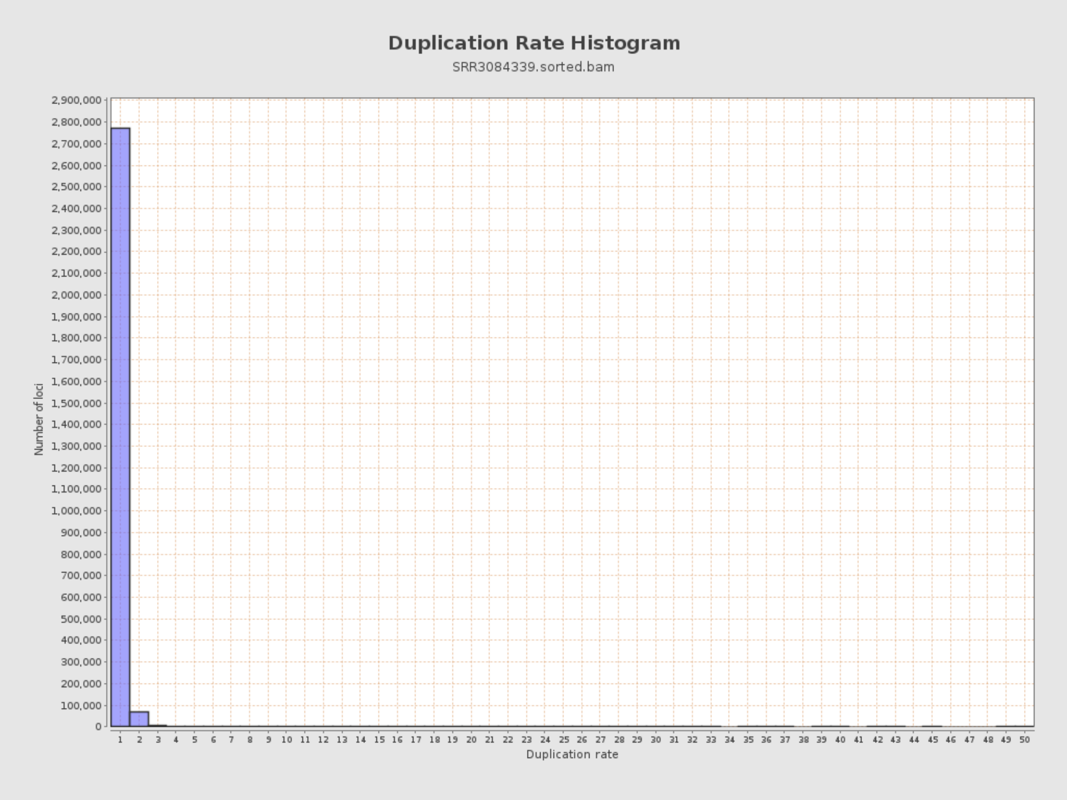
5. Results : Coverage Histogram (0-50X)



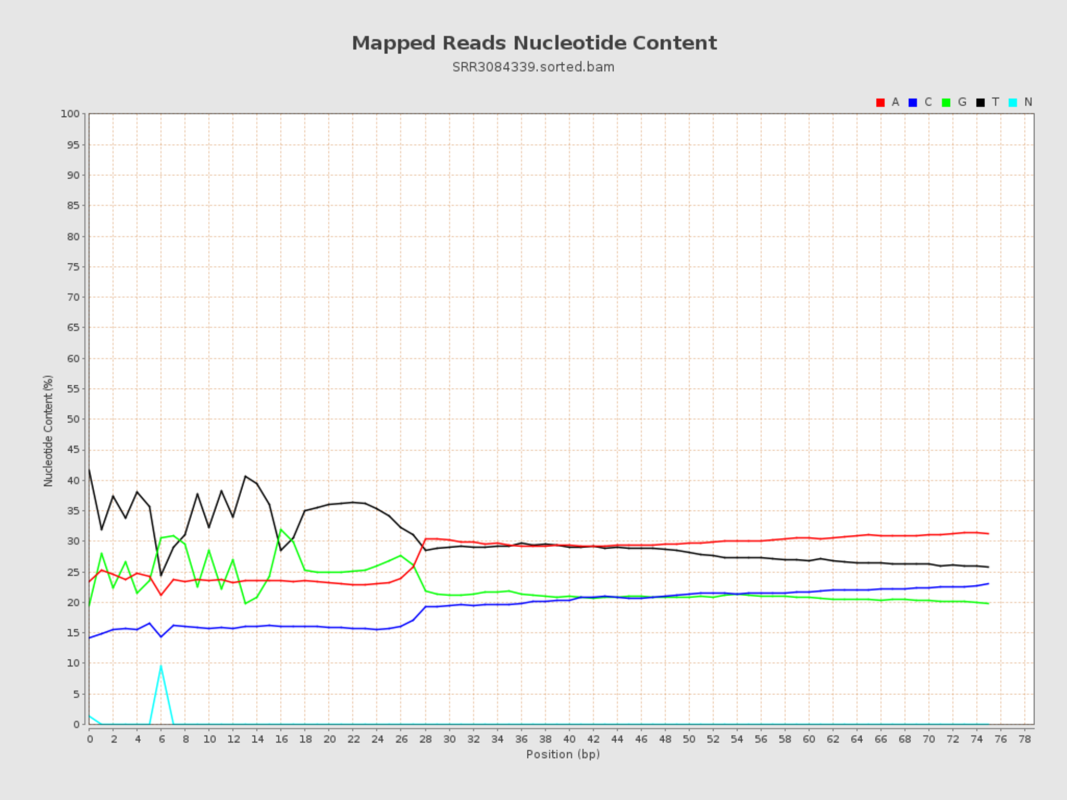
6. Results : Genome Fraction Coverage



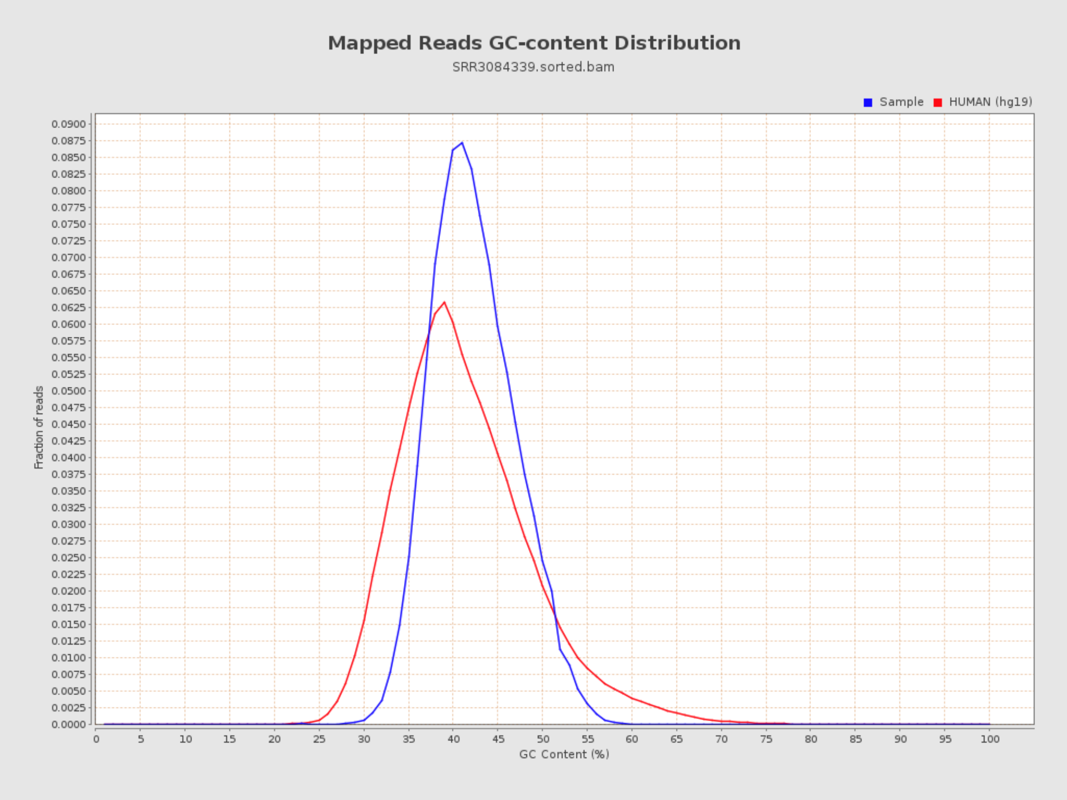
7. Results : Duplication Rate Histogram



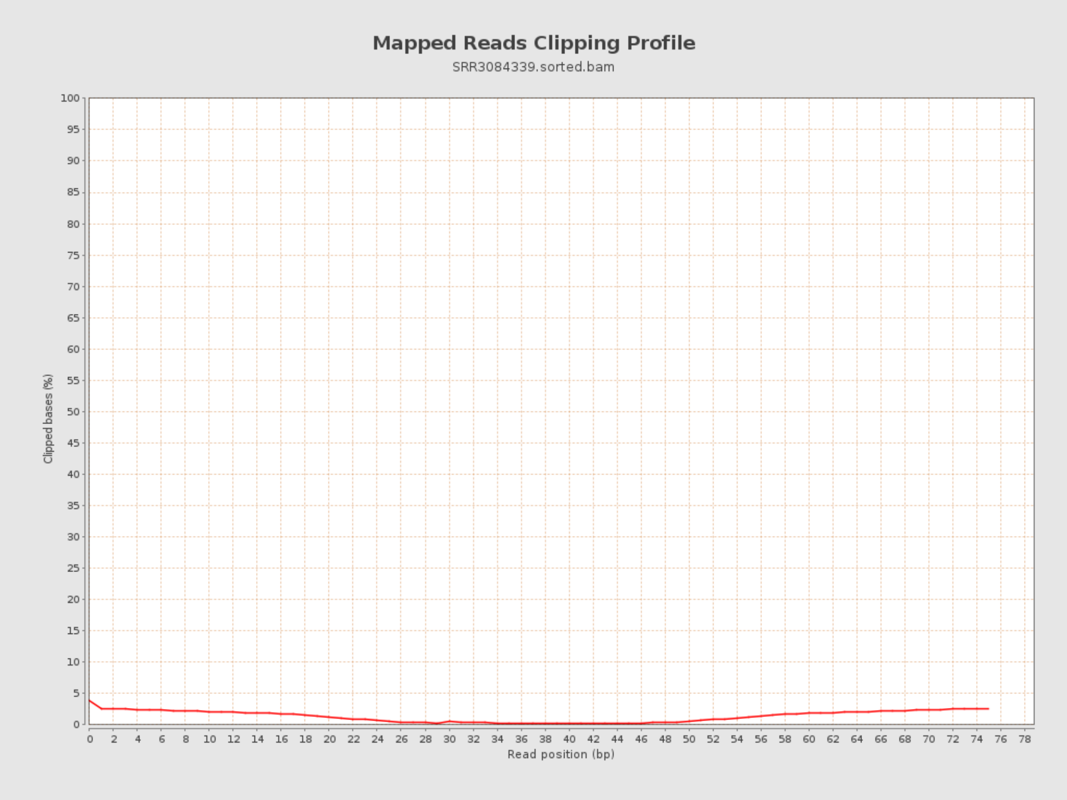
8. Results : Mapped Reads Nucleotide Content



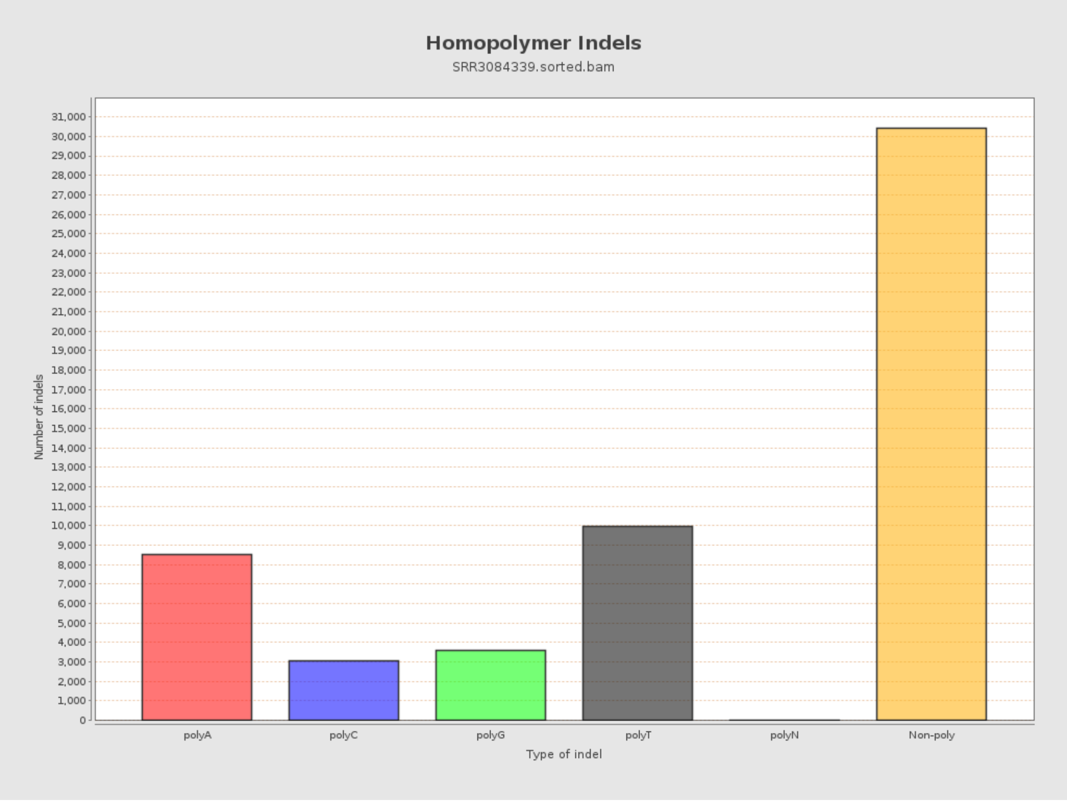
9. Results : Mapped Reads GC-content Distribution



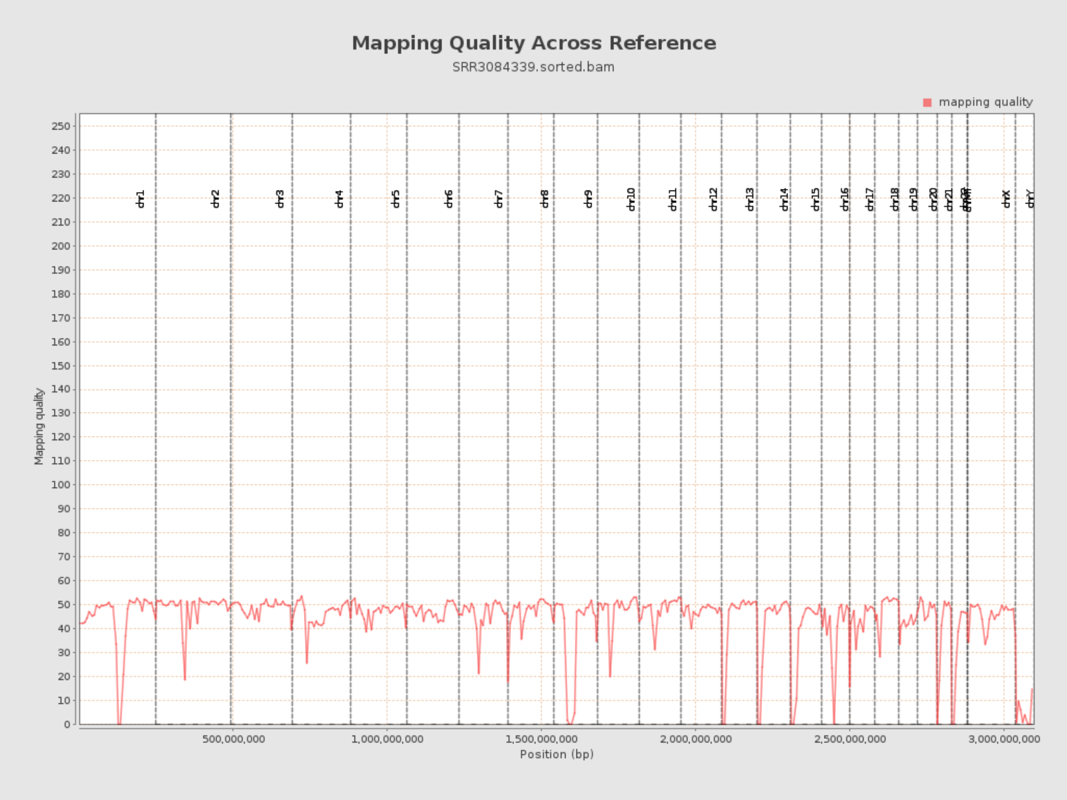
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram