Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 10:14:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089379.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_SRR089379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089379.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 10:14:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,698,848
Mapped reads	26,976,009 / 94%
Unmapped reads	1,722,839 / 6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	132,638 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	6,078,310 / 21.18%
Duplication rate	14.19%
Clipped reads	12,001,831 / 41.82%

2.2. ACGT Content

Number/percentage of A's	468,129,255 / 26.12%
Number/percentage of C's	343,602,662 / 19.18%
Number/percentage of T's	548,404,201 / 30.6%
Number/percentage of G's	431,591,237 / 24.09%
Number/percentage of N's	194,735 / 0.01%
GC Percentage	43.26%

2.3. Coverage

Mean	0.579

Standard Deviation	3.5879

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

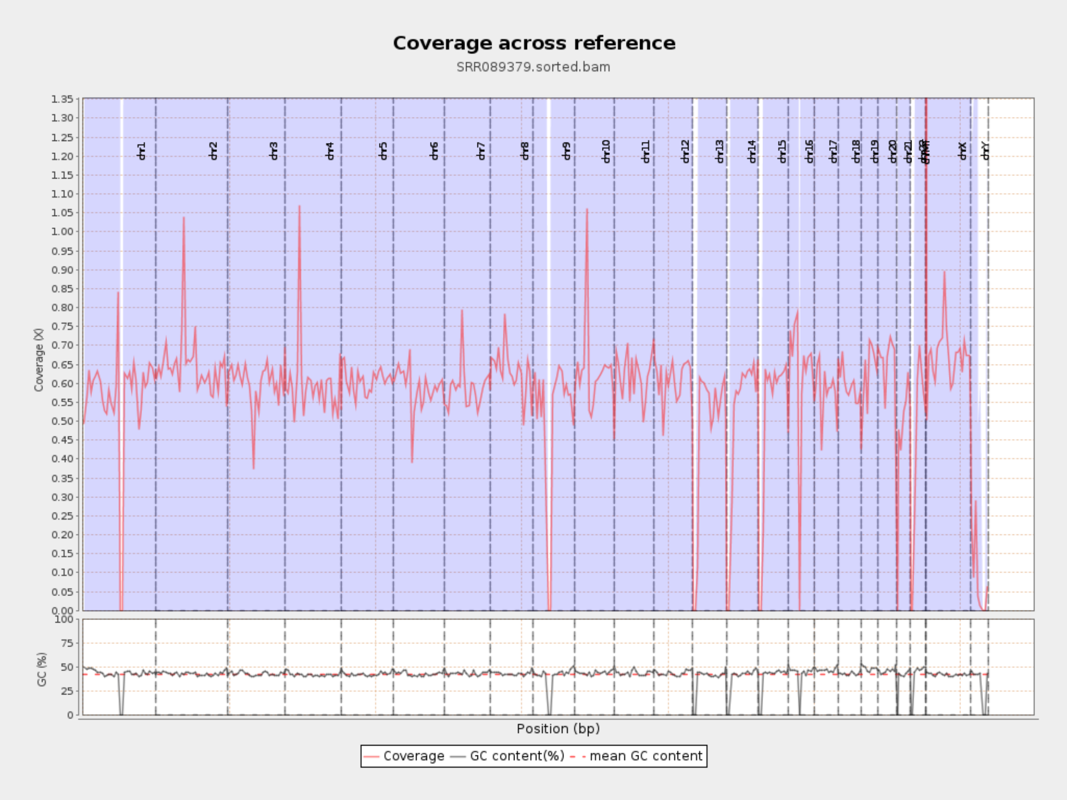
General error rate	0.63%
Mismatches	10,967,978
Insertions	115,625
Mapped reads with at least one insertion	0.42%
Deletions	350,608
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.15%

2.6. Chromosome stats

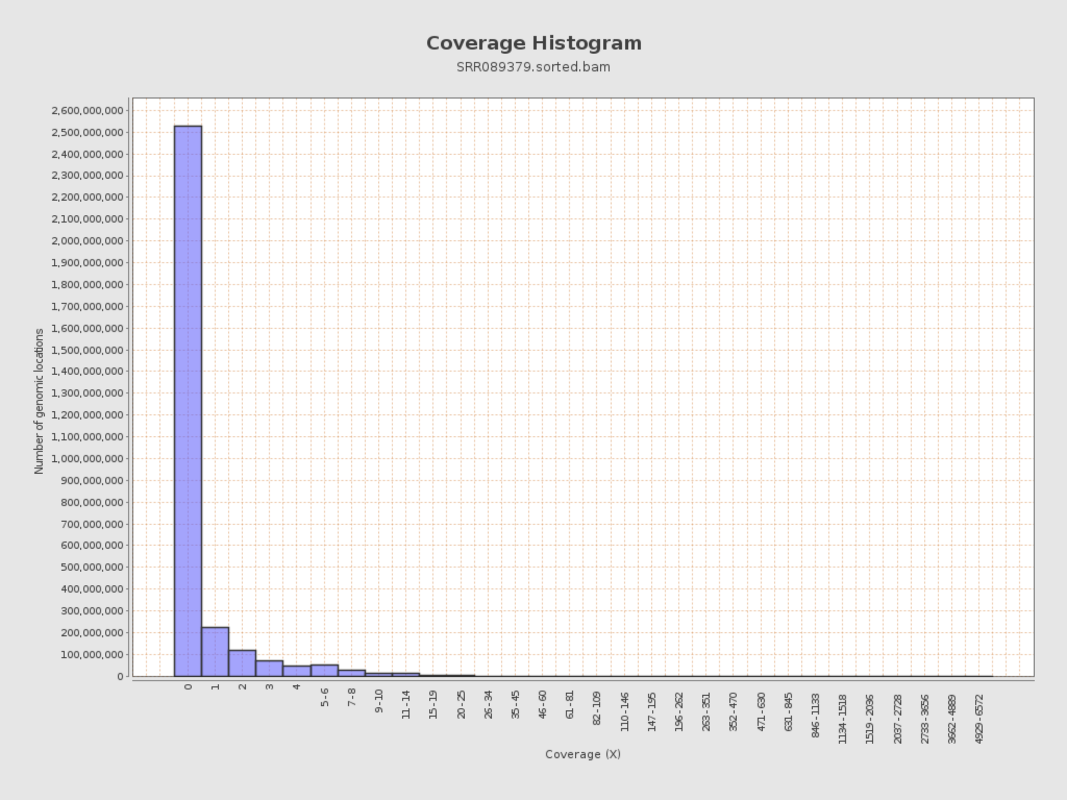
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	139317282	0.5589	6.0367
chr2	243199373	157728268	0.6486	4.415
chr3	198022430	118458766	0.5982	1.9748
chr4	191154276	114977922	0.6015	2.7325
chr5	180915260	109999490	0.608	1.9629
chr6	171115067	100613766	0.588	2.4805
chr7	159138663	93827507	0.5896	4.445

chr8	146364022	92122832	0.6294	3.2355
chr9	141213431	71482457	0.5062	3.5498
chr10	135534747	86098942	0.6353	4.6082
chr11	135006516	83222272	0.6164	4.0825
chr12	133851895	81945405	0.6122	2.0721
chr13	115169878	54775088	0.4756	1.7034
chr14	107349540	54315398	0.506	1.9293
chr15	102531392	51248113	0.4998	1.8905
chr16	90354753	54977623	0.6085	2.5774
chr17	81195210	47362788	0.5833	2.6
chr18	78077248	46584867	0.5967	7.5016
chr19	59128983	37295368	0.6307	4.0156
chr20	63025520	41400083	0.6569	2.3657
chr21	48129895	22852622	0.4748	2.6122
chr22	51304566	22205064	0.4328	1.6683
chrMT	16571	257831	15.5592	22.6375
chrX	155270560	104501145	0.673	2.7817
chrY	59373566	4975299	0.0838	2.0999

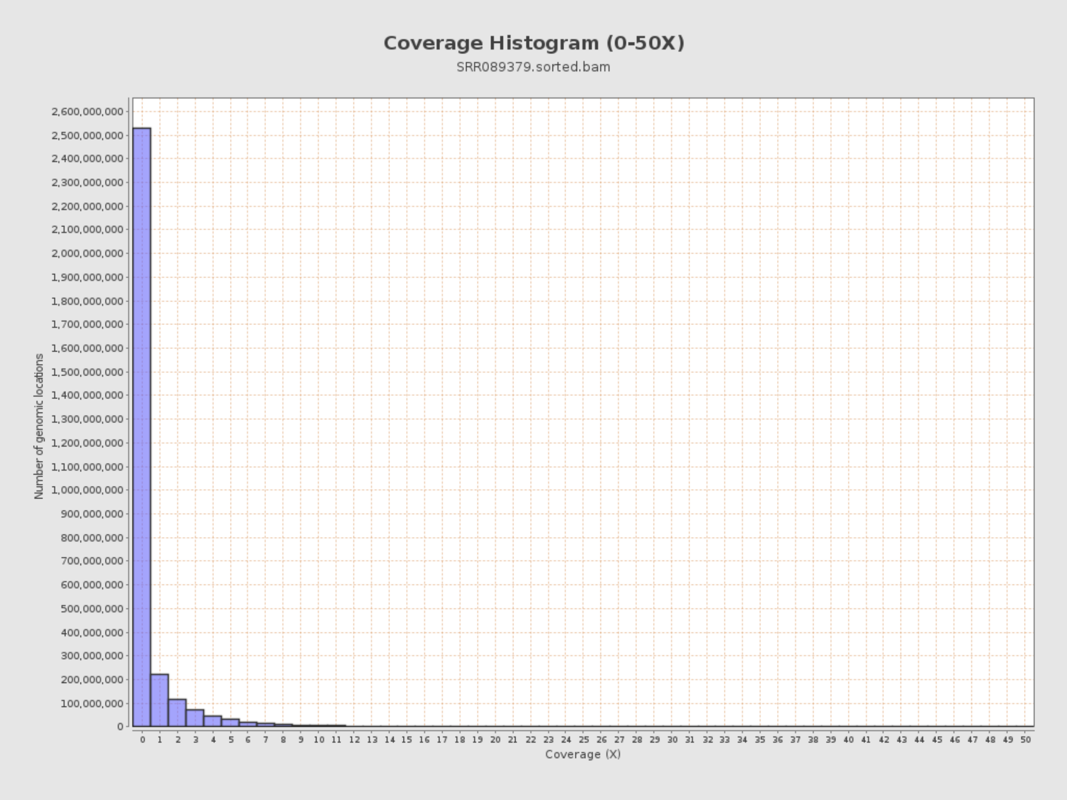
3. Results : Coverage across reference



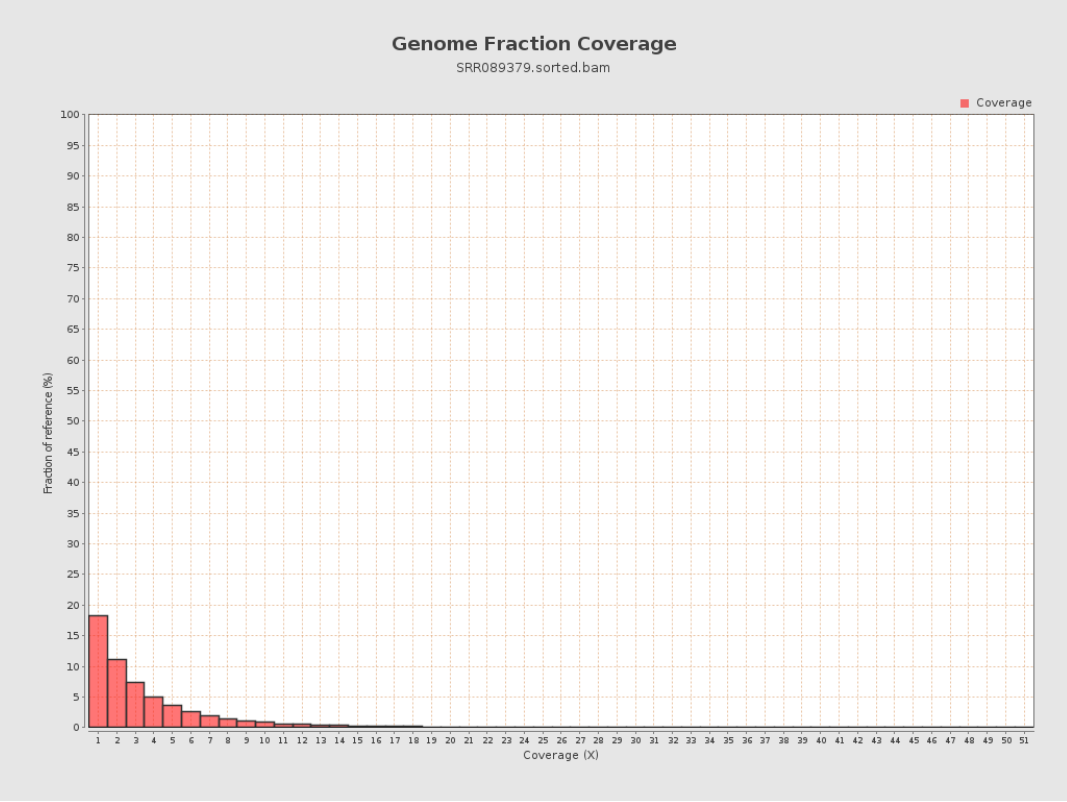
4. Results : Coverage Histogram



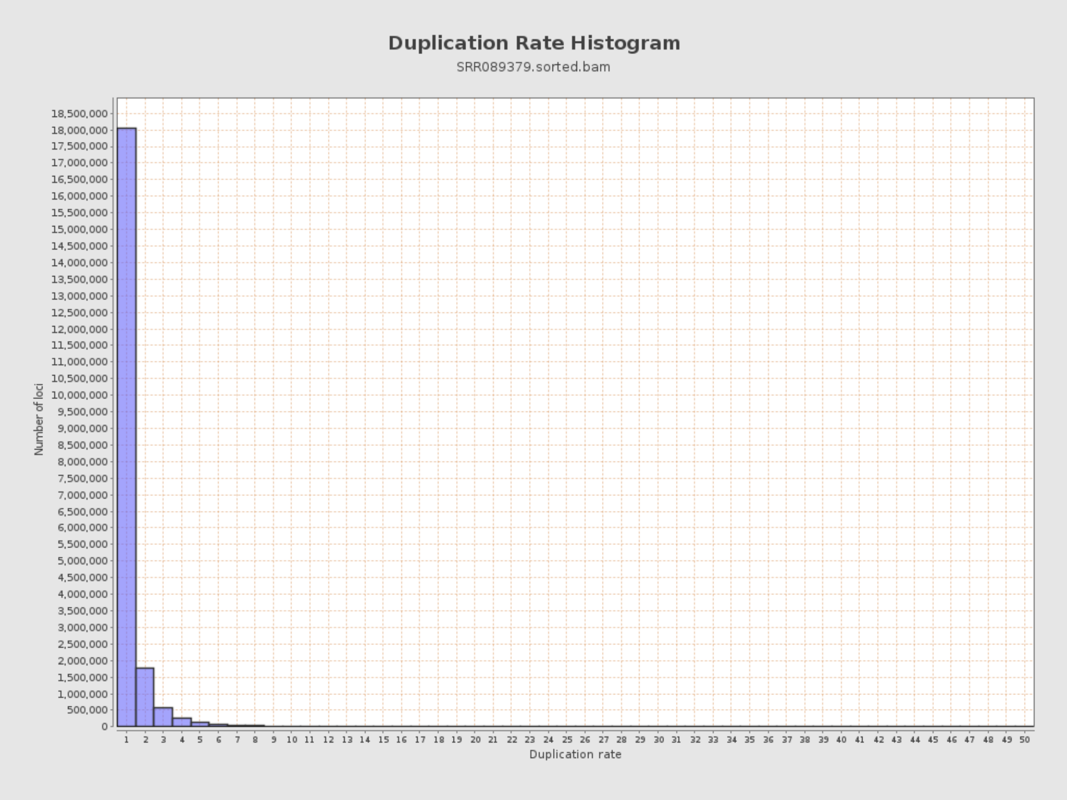
5. Results : Coverage Histogram (0-50X)



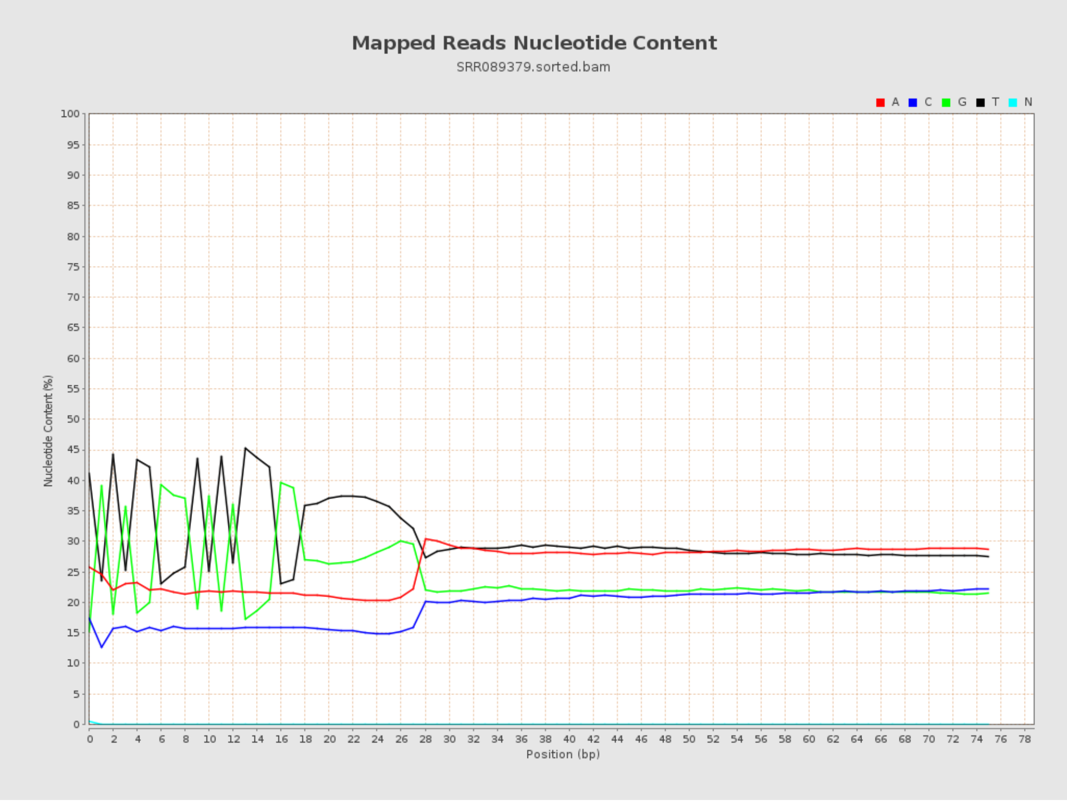
6. Results : Genome Fraction Coverage



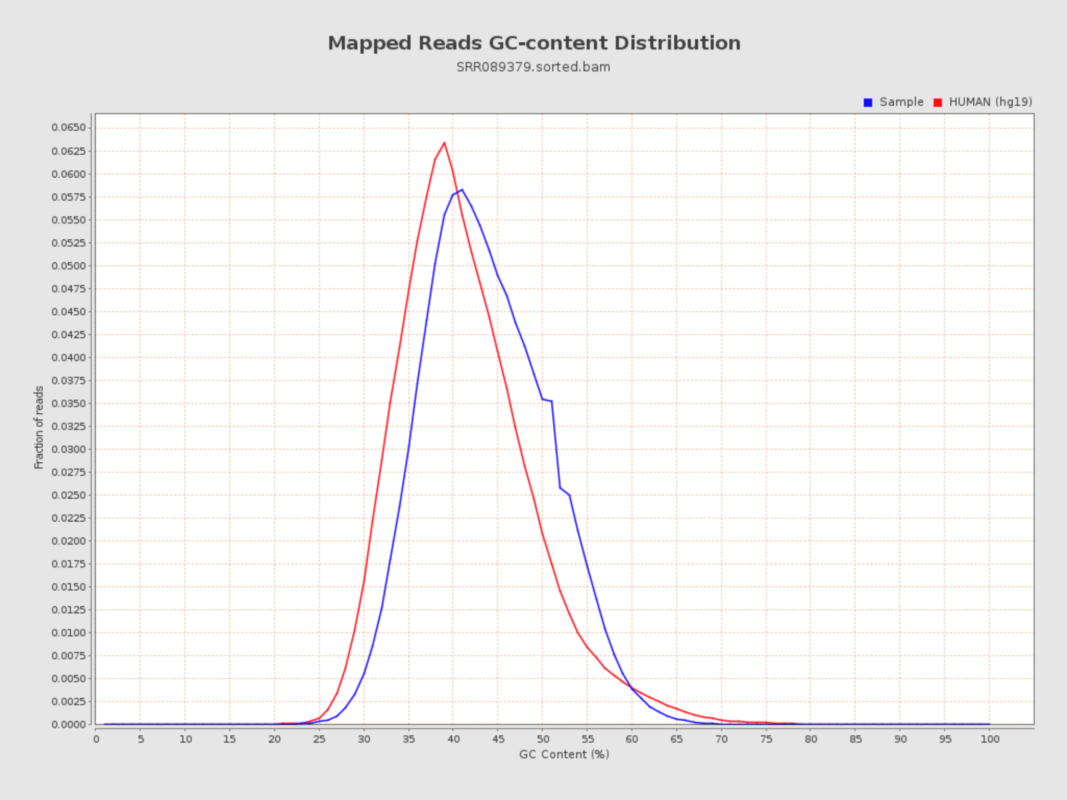
7. Results : Duplication Rate Histogram



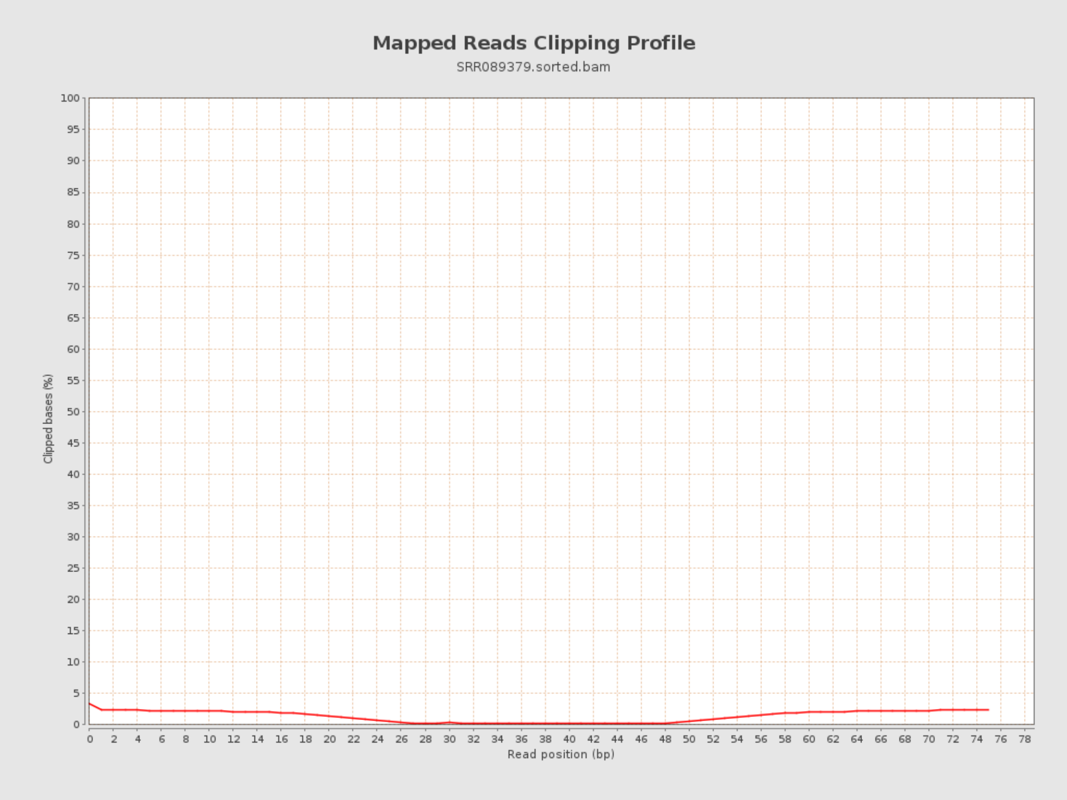
8. Results : Mapped Reads Nucleotide Content



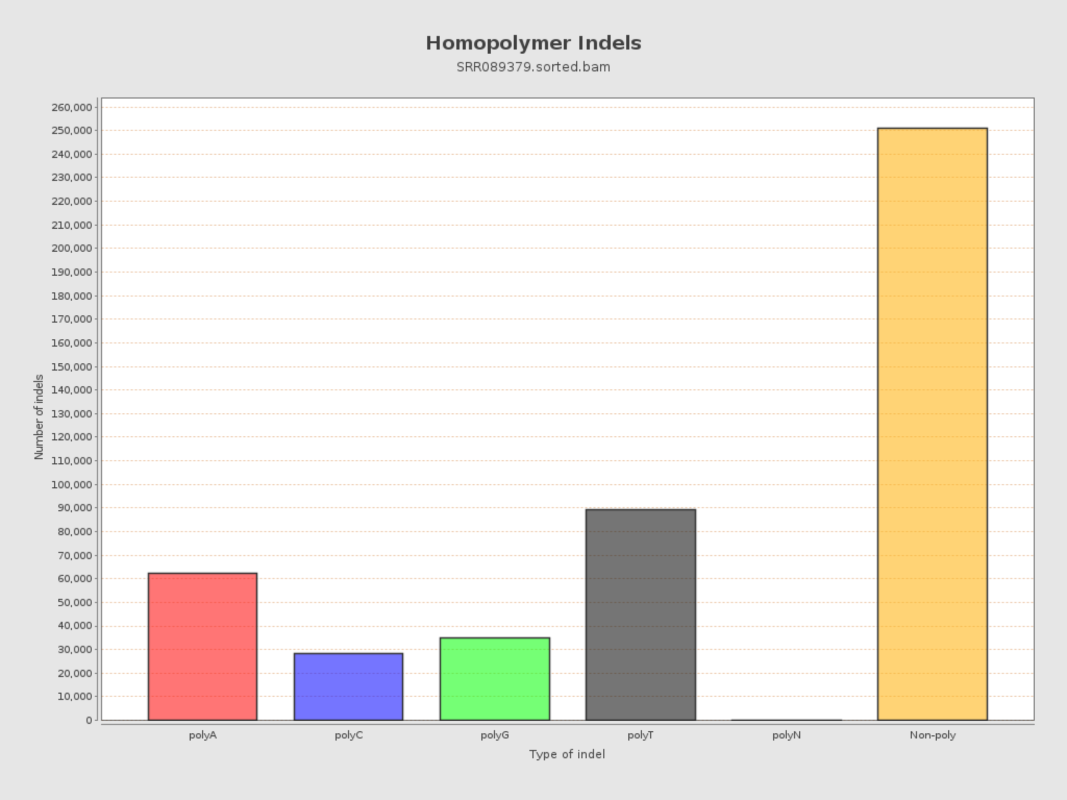
9. Results : Mapped Reads GC-content Distribution



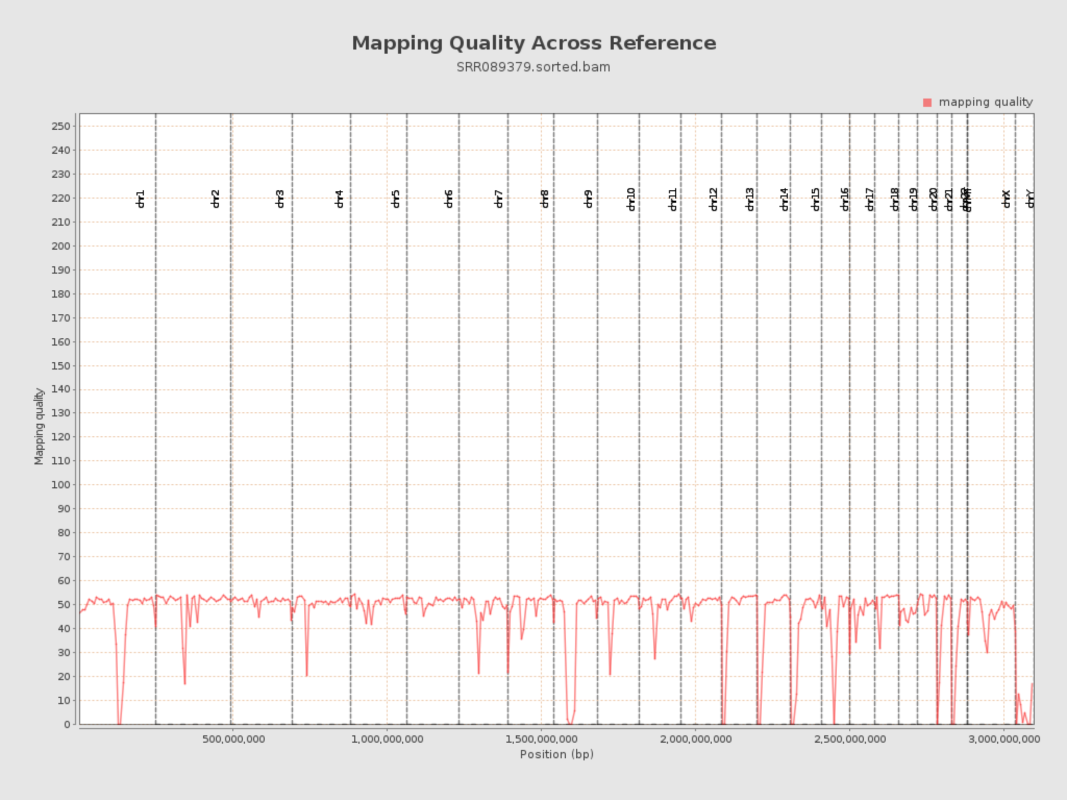
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram