Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:34:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549113.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_SRR1549113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:34:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,847,870
Mapped reads	7,553,416 / 58.79%
Unmapped reads	5,294,454 / 41.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	548,396 / 4.27%
Duplication rate	5.88%
Clipped reads	703,250 / 5.47%

2.2. ACGT Content

Number/percentage of A's	81,783,020 / 27.44%
Number/percentage of C's	67,327,136 / 22.59%
Number/percentage of T's	82,026,689 / 27.52%
Number/percentage of G's	66,909,198 / 22.45%
Number/percentage of N's	11,781 / 0%
GC Percentage	45.04%

2.3. Coverage

Mean	0.0963
Standard Deviation	0.781

2.4. Mapping Quality

Mean Mapping Quality	39.82

2.5. Mismatches and indels

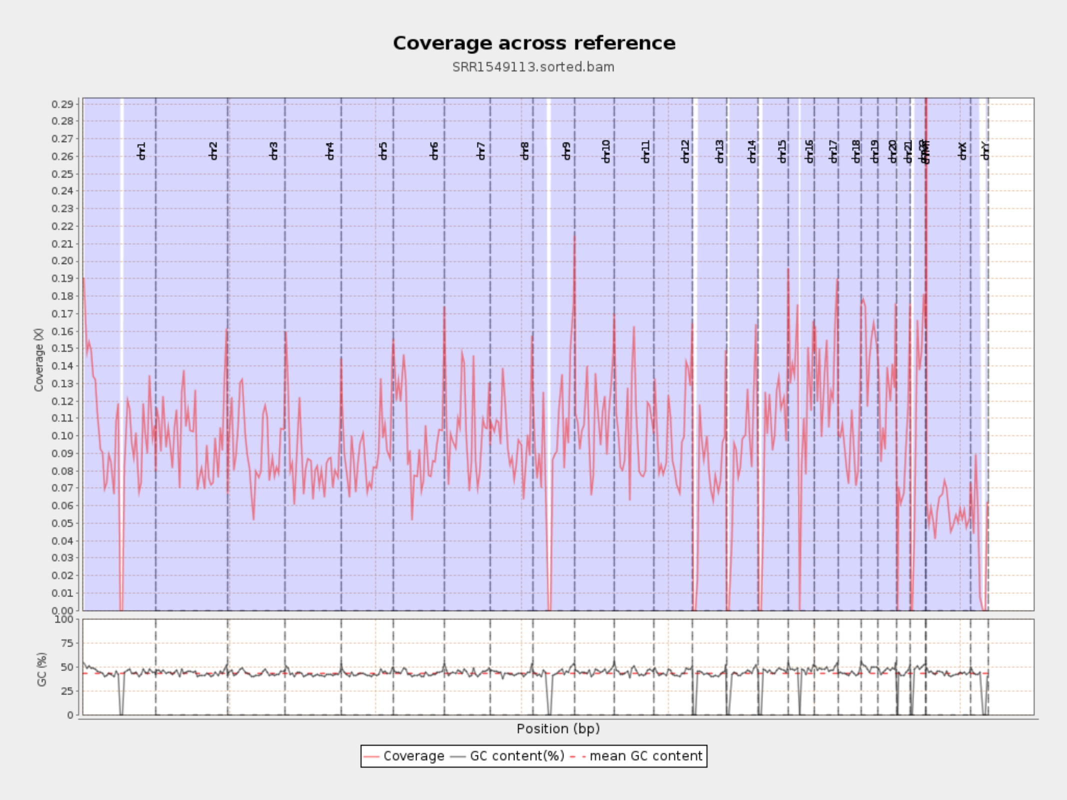
General error rate	0.38%
Mismatches	1,110,475
Insertions	10,546
Mapped reads with at least one insertion	0.14%
Deletions	28,400
Mapped reads with at least one deletion	0.38%
Homopolymer indels	44.17%

2.6. Chromosome stats

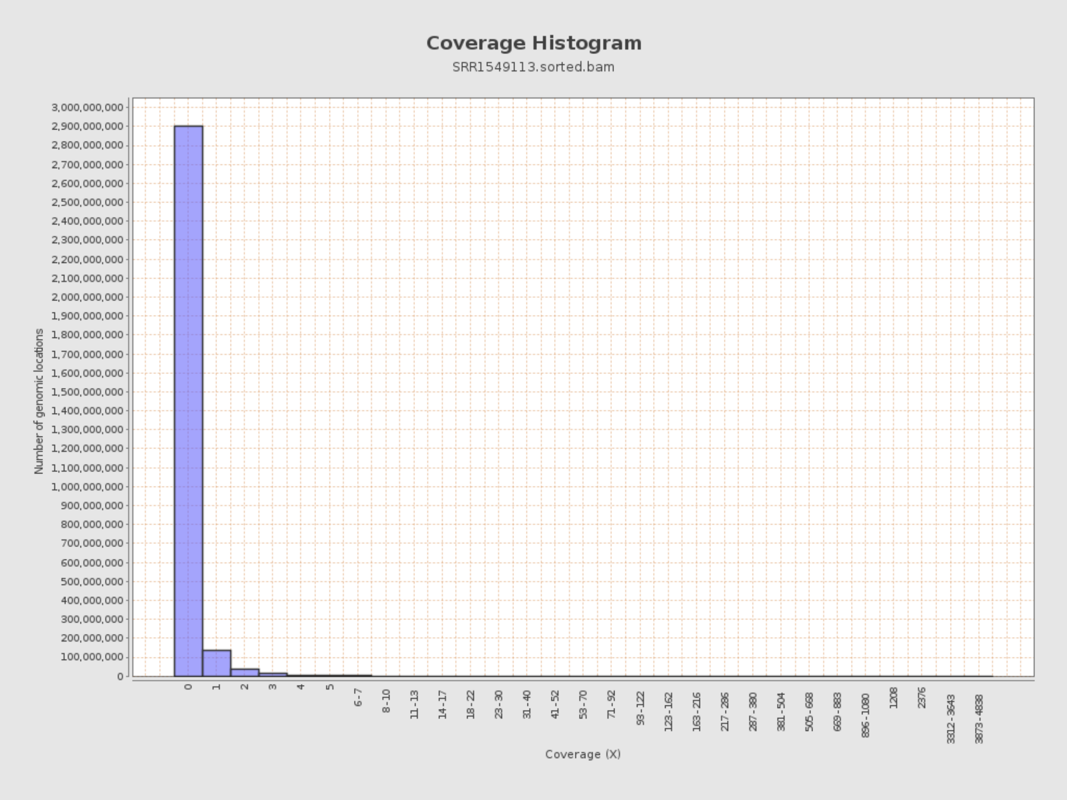
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24946451	0.1001	0.9229
chr2	243199373	24079017	0.099	0.5991
chr3	198022430	18405451	0.0929	0.4512
chr4	191154276	16571270	0.0867	0.484
chr5	180915260	16706653	0.0923	0.4639
chr6	171115067	16678264	0.0975	0.4791
chr7	159138663	16714580	0.105	0.6758
chr8	146364022	14503538	0.0991	2.3826

chr9	141213431	13164522	0.0932	0.5624
chr10	135534747	14684584	0.1083	0.6253
chr11	135006516	13879206	0.1028	0.5294
chr12	133851895	13615323	0.1017	0.4929
chr13	115169878	8398287	0.0729	0.4026
chr14	107349540	9246756	0.0861	0.6223
chr15	102531392	9536907	0.093	0.4495
chr16	90354753	10944030	0.1211	0.5475
chr17	81195210	11101061	0.1367	0.5595
chr18	78077248	7259132	0.093	0.9633
chr19	59128983	9206182	0.1557	1.0023
chr20	63025520	7592618	0.1205	0.5464
chr21	48129895	4028511	0.0837	0.5198
chr22	51304566	5542608	0.108	0.5155
chrMT	16571	206142	12.4399	15.4383
chrX	155270560	8727661	0.0562	0.3993
chrY	59373566	2354455	0.0397	0.4265

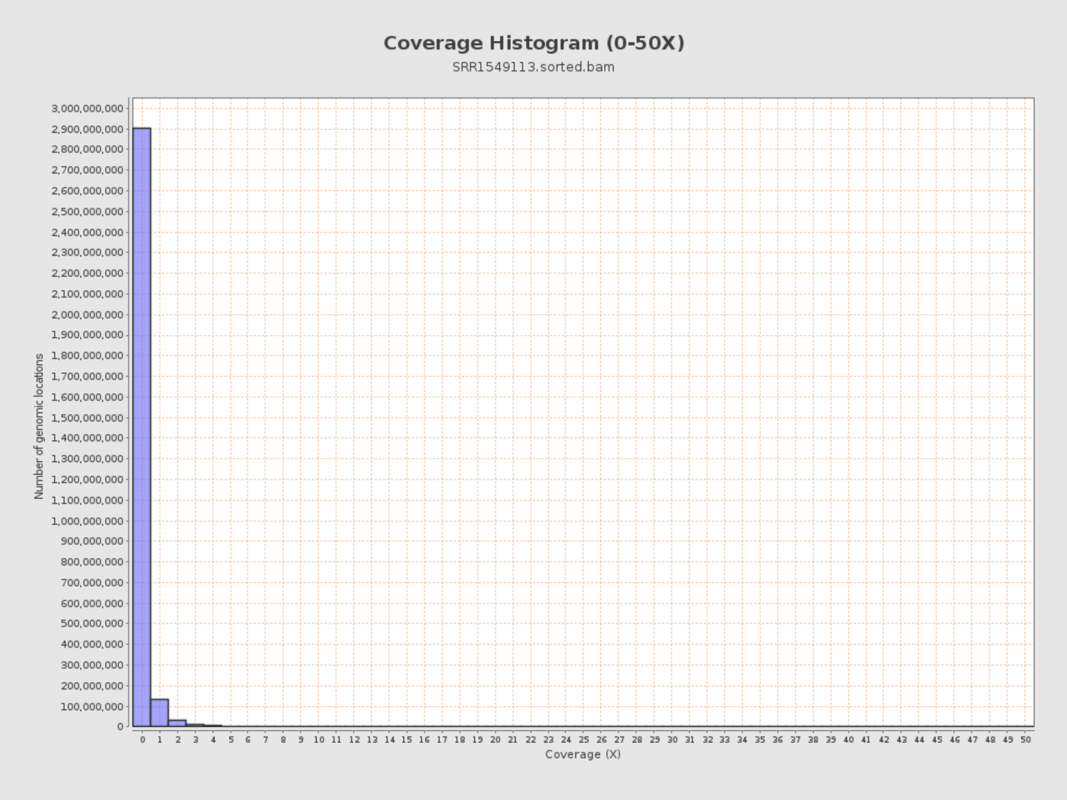
3. Results : Coverage across reference



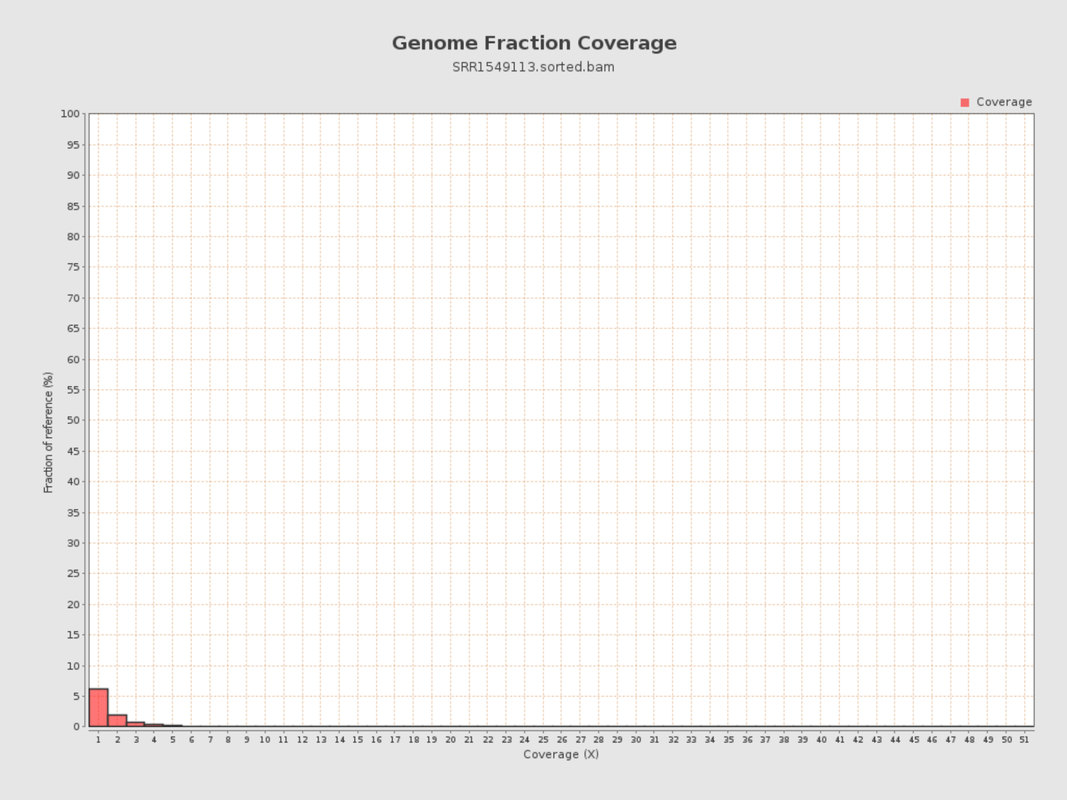
4. Results : Coverage Histogram



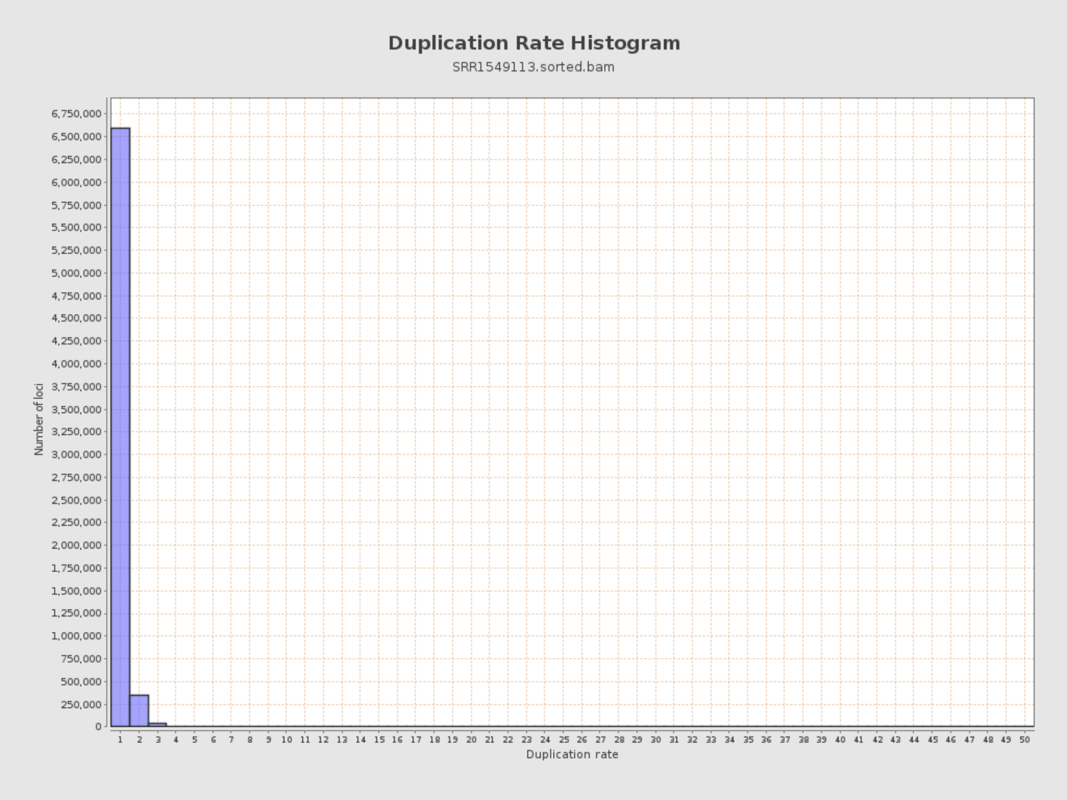
5. Results : Coverage Histogram (0-50X)



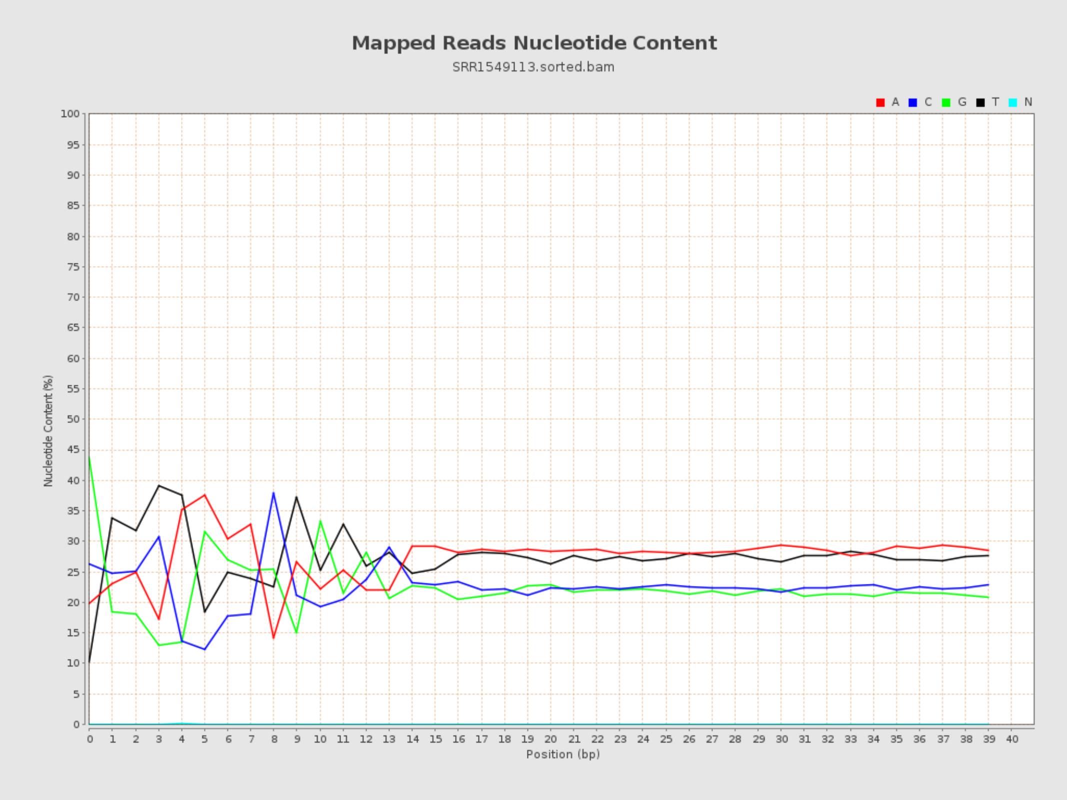
6. Results : Genome Fraction Coverage



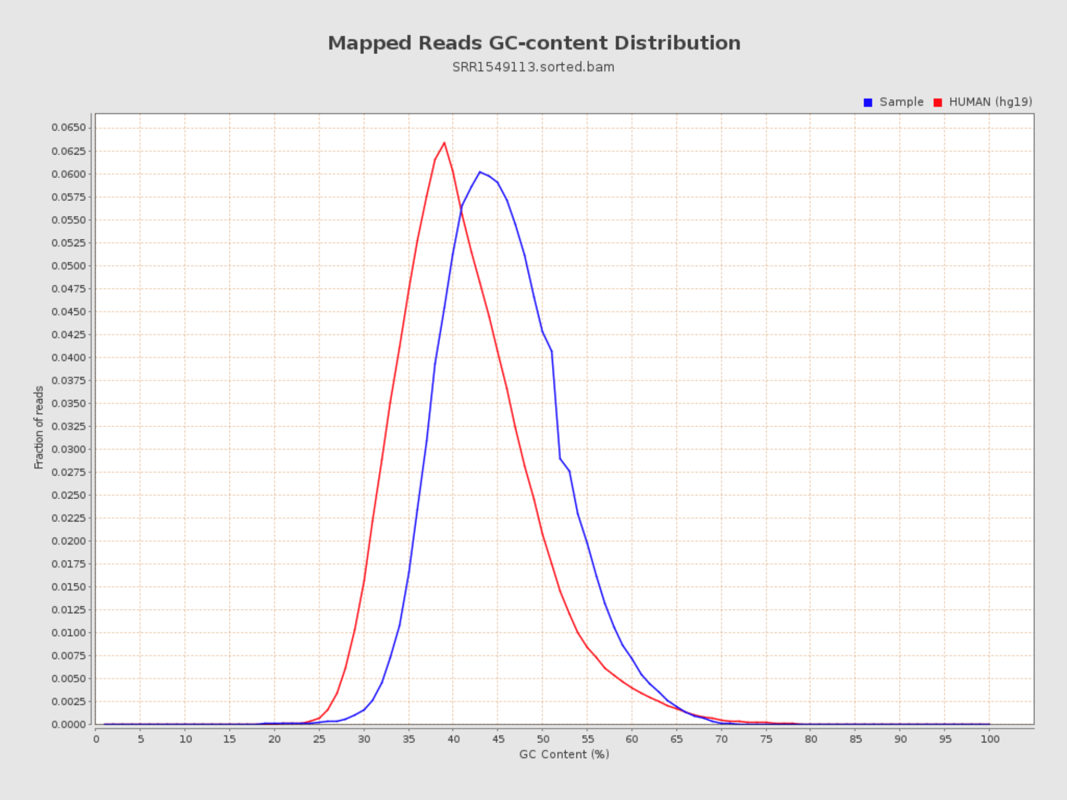
7. Results : Duplication Rate Histogram



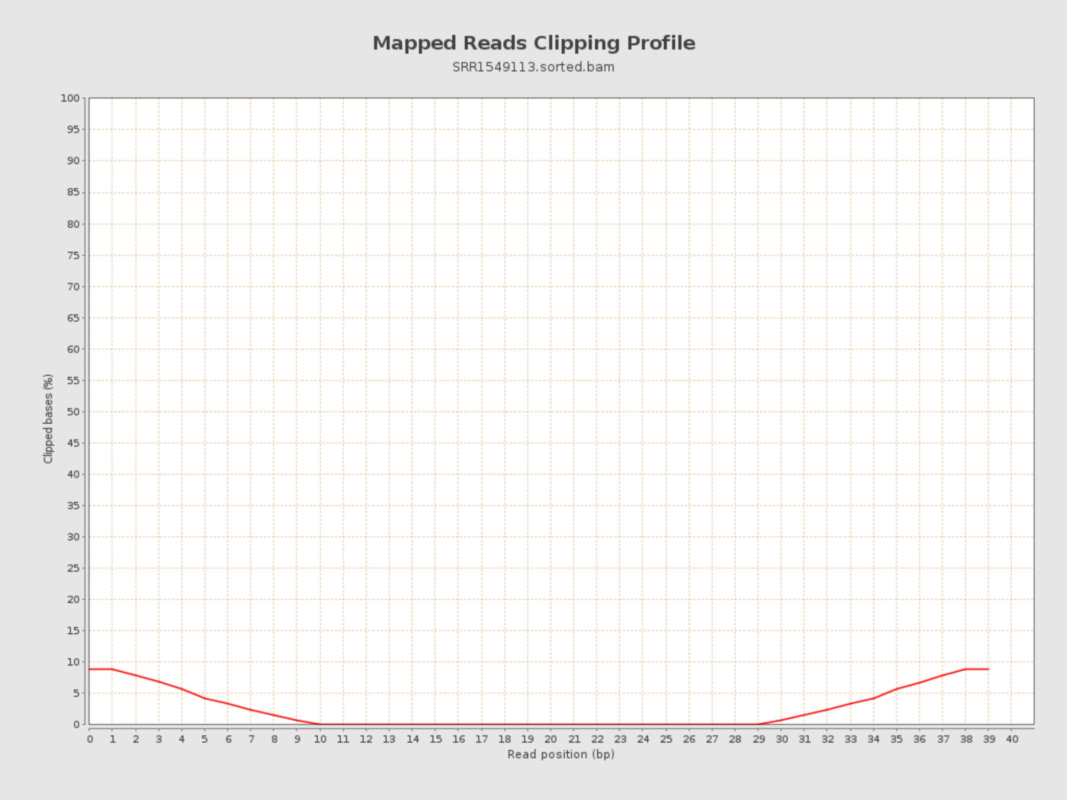
8. Results : Mapped Reads Nucleotide Content



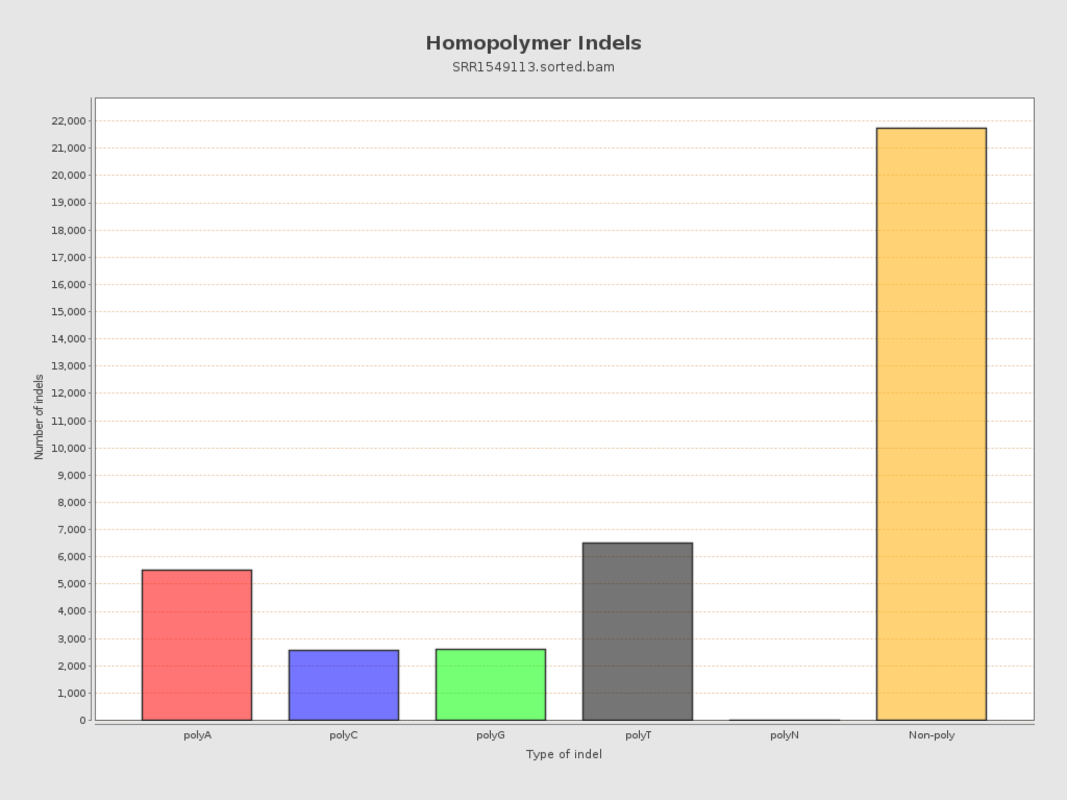
9. Results : Mapped Reads GC-content Distribution



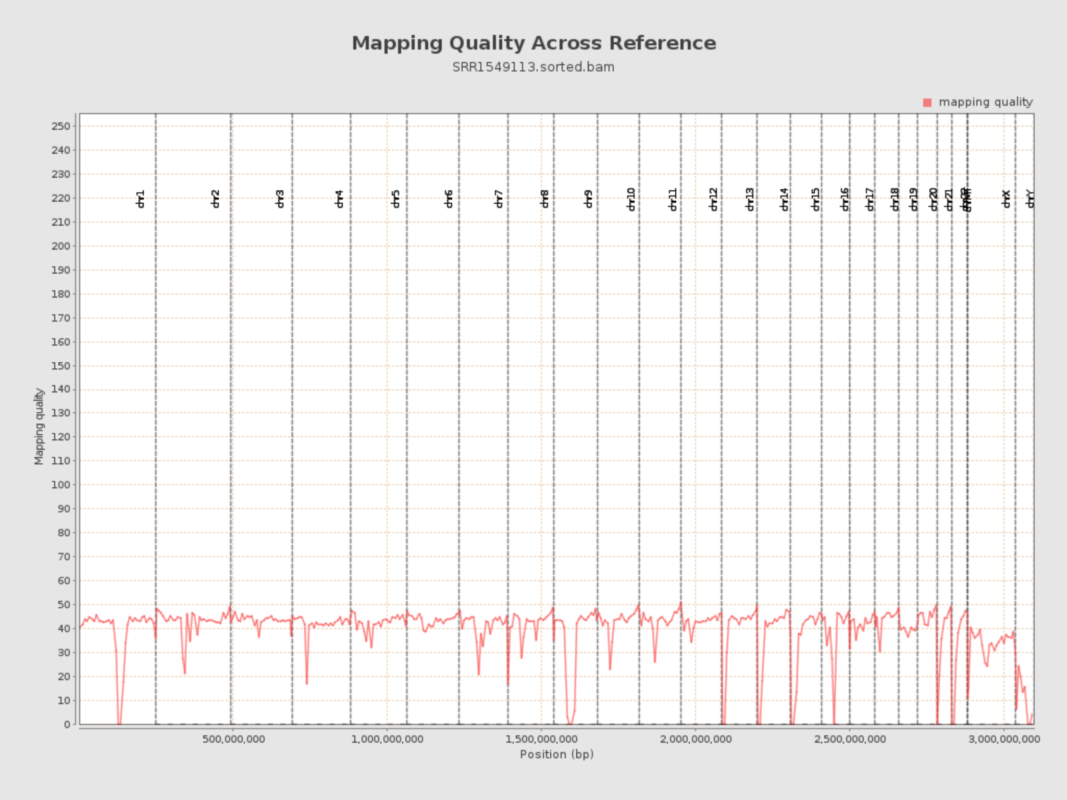
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram