Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:40:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549145.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_SRR1549145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549145.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:40:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,015,465
Mapped reads	10,534,129 / 87.67%
Unmapped reads	1,481,336 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	517,644 / 4.31%
Duplication rate	3.87%
Clipped reads	552,379 / 4.6%

2.2. ACGT Content

Number/percentage of A's	119,400,746 / 28.56%
Number/percentage of C's	88,760,514 / 21.23%
Number/percentage of T's	121,095,885 / 28.97%
Number/percentage of G's	88,727,921 / 21.22%
Number/percentage of N's	84,604 / 0.02%
GC Percentage	42.45%

2.3. Coverage

Mean	0.1351
Standard Deviation	0.7759

2.4. Mapping Quality

Mean Mapping Quality	43.14

2.5. Mismatches and indels

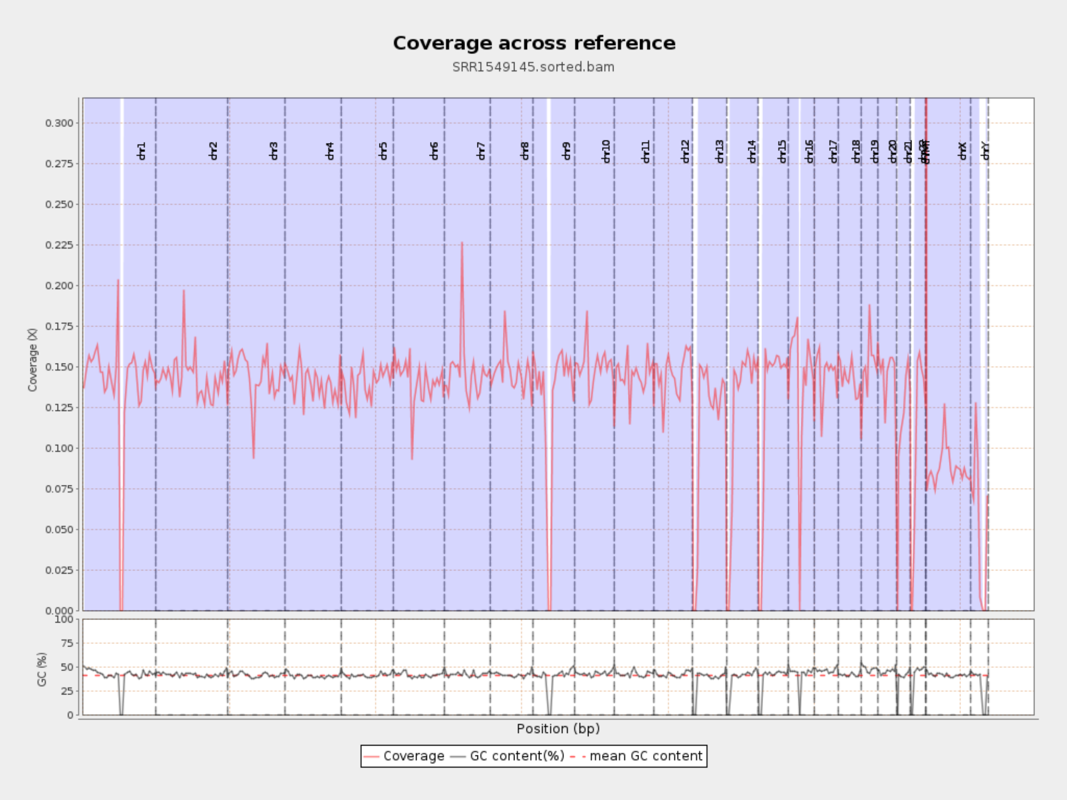
General error rate	0.31%
Mismatches	1,280,909
Insertions	10,522
Mapped reads with at least one insertion	0.1%
Deletions	31,780
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.15%

2.6. Chromosome stats

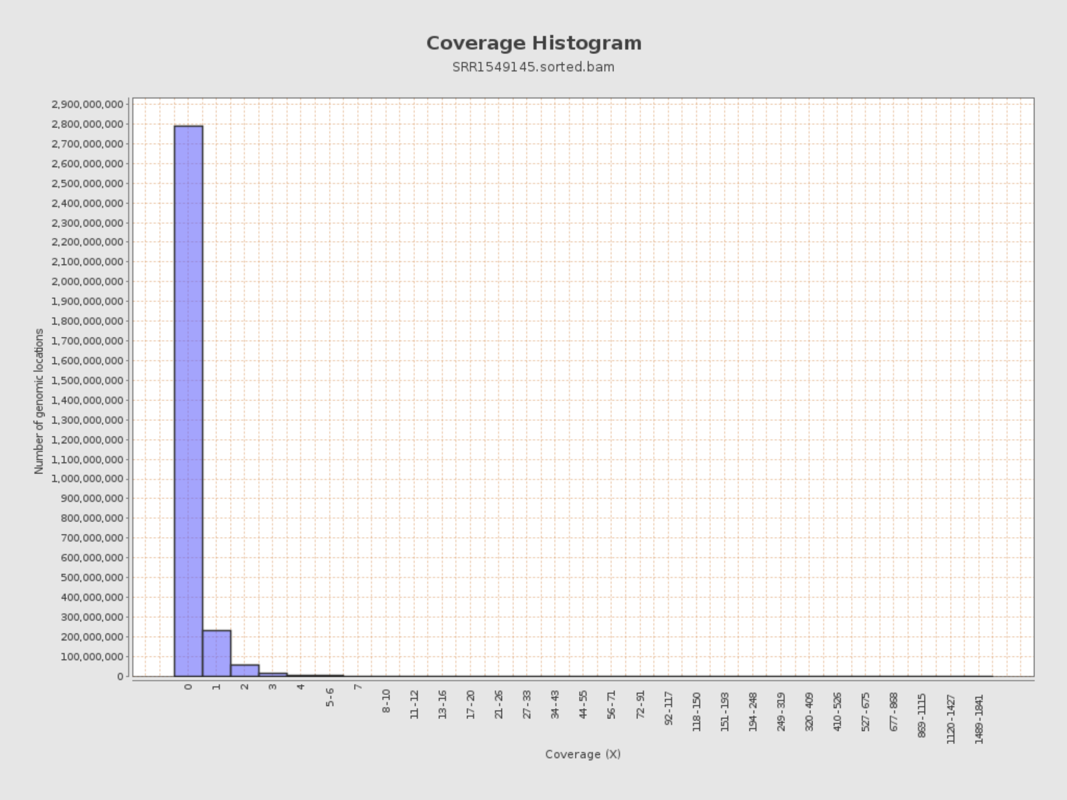
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34735183	0.1394	1.485
chr2	243199373	35014626	0.144	0.7411
chr3	198022430	28577612	0.1443	0.4895
chr4	191154276	26846528	0.1404	0.5122
chr5	180915260	25491527	0.1409	0.4948
chr6	171115067	24125715	0.141	0.5663
chr7	159138663	23486792	0.1476	1.1481
chr8	146364022	21419870	0.1463	0.6955

chr9	141213431	18095612	0.1281	0.7084
chr10	135534747	20347963	0.1501	0.7298
chr11	135006516	19490621	0.1444	0.6556
chr12	133851895	19614435	0.1465	0.5257
chr13	115169878	13180054	0.1144	0.4276
chr14	107349540	13275845	0.1237	0.5974
chr15	102531392	12760680	0.1245	0.4518
chr16	90354753	12567923	0.1391	0.5402
chr17	81195210	11929579	0.1469	0.5405
chr18	78077248	11174013	0.1431	1.3834
chr19	59128983	9001787	0.1522	1.2592
chr20	63025520	9211759	0.1462	0.5271
chr21	48129895	5510022	0.1145	0.5285
chr22	51304566	5294615	0.1032	0.4535
chrMT	16571	59242	3.575	4.8487
chrX	155270560	13663782	0.088	0.4936
chrY	59373566	3233725	0.0545	0.4244

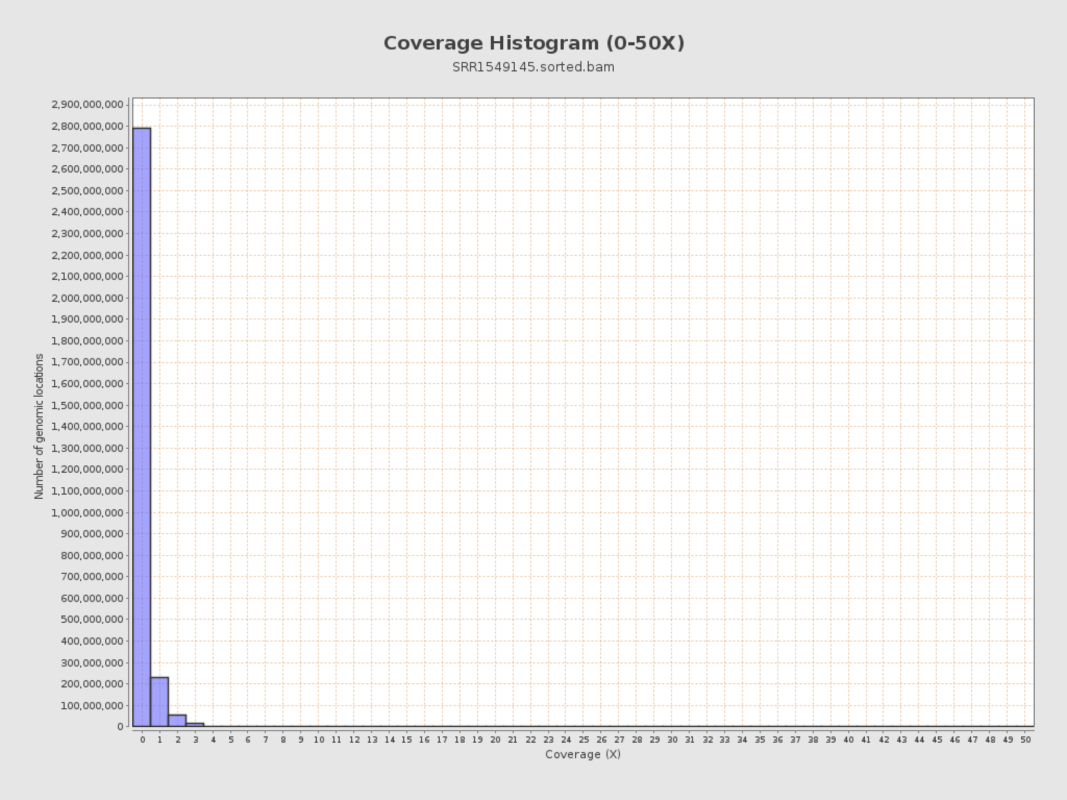
3. Results : Coverage across reference



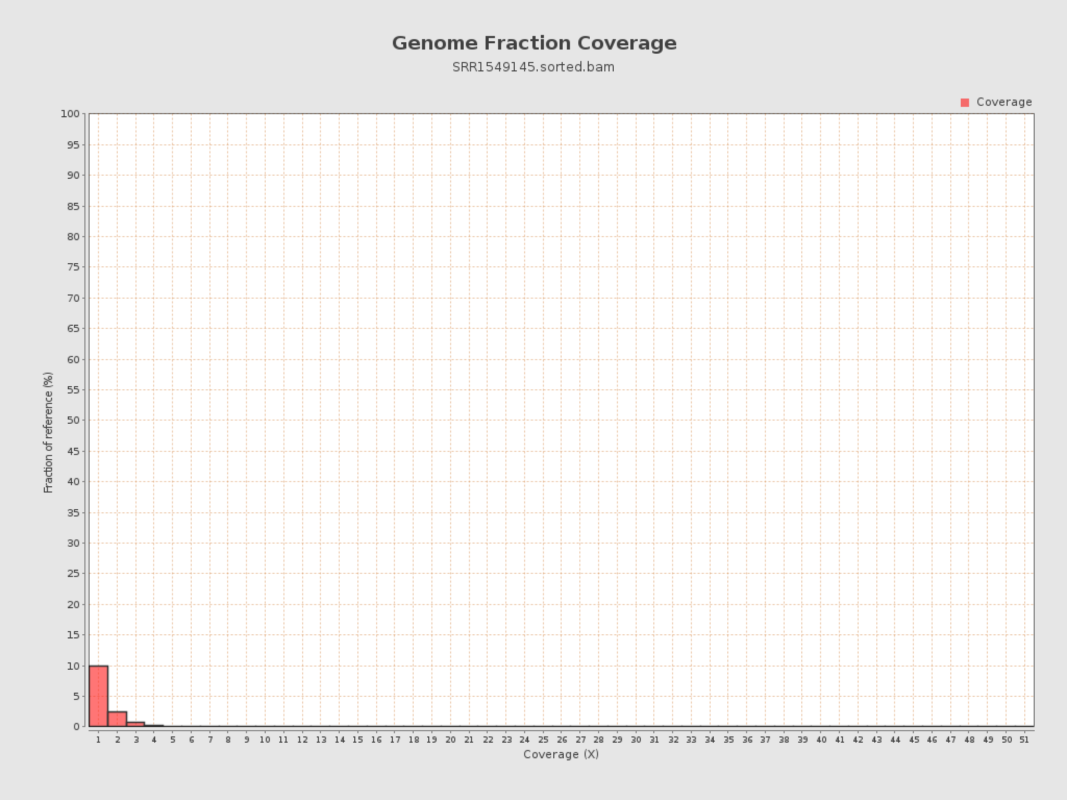
4. Results : Coverage Histogram



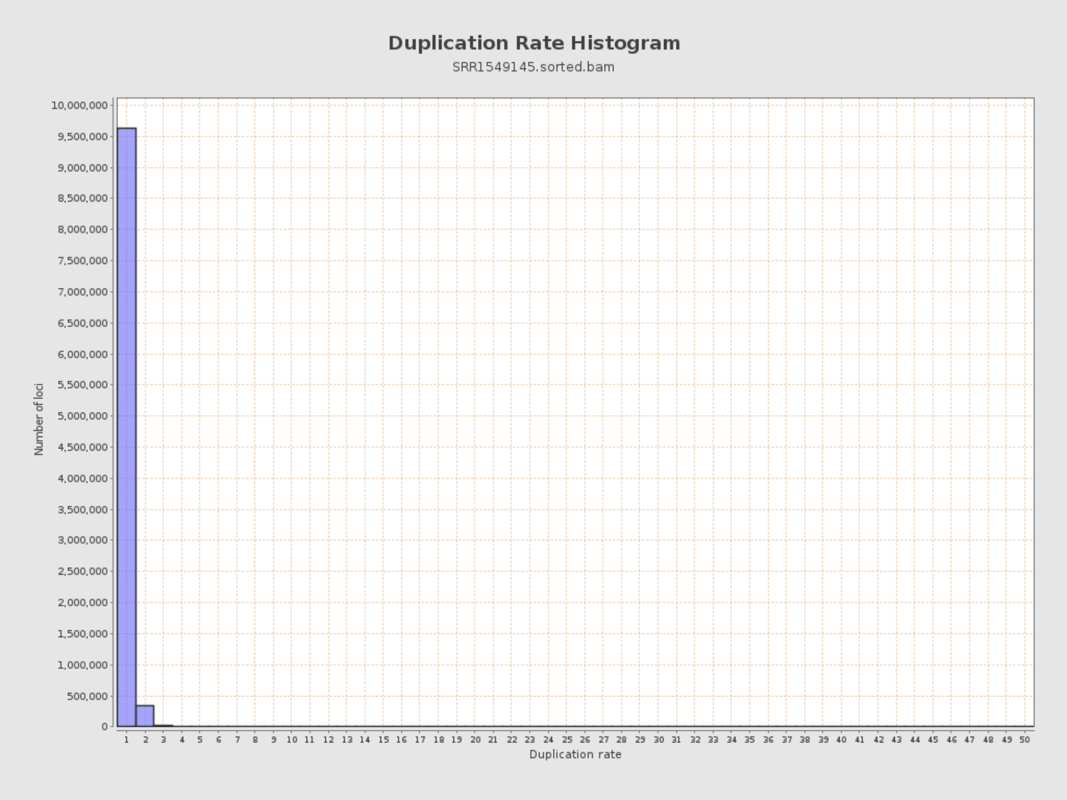
5. Results : Coverage Histogram (0-50X)



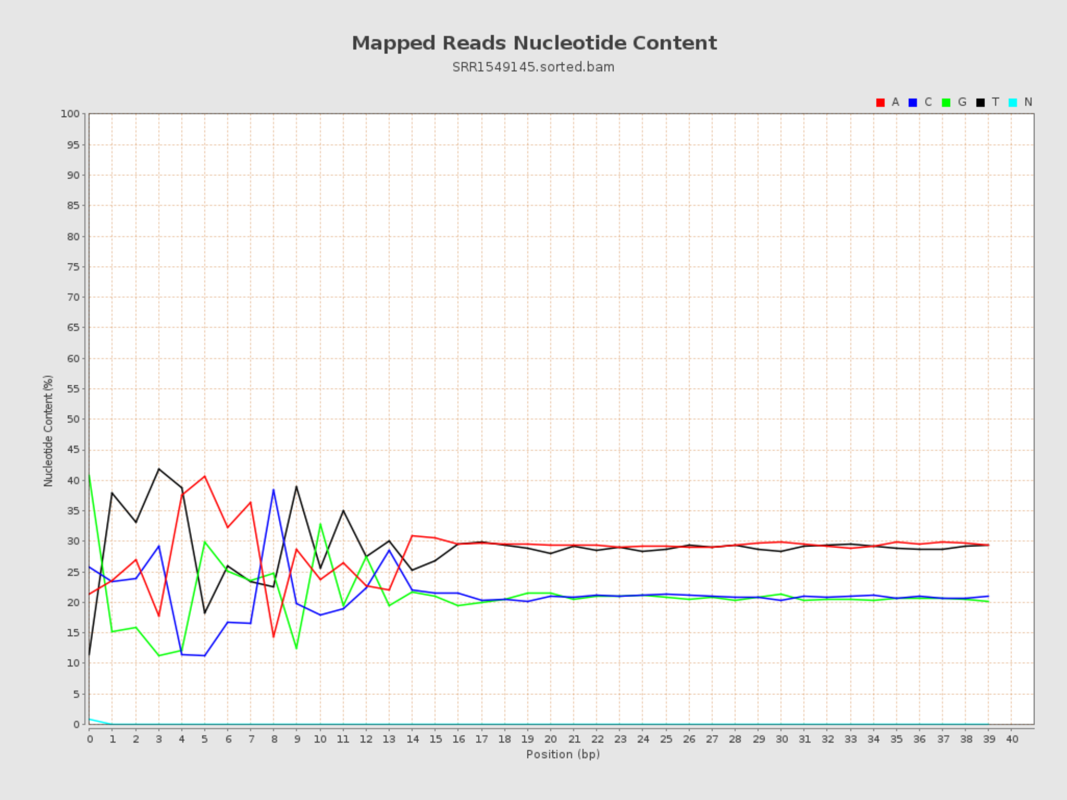
6. Results : Genome Fraction Coverage



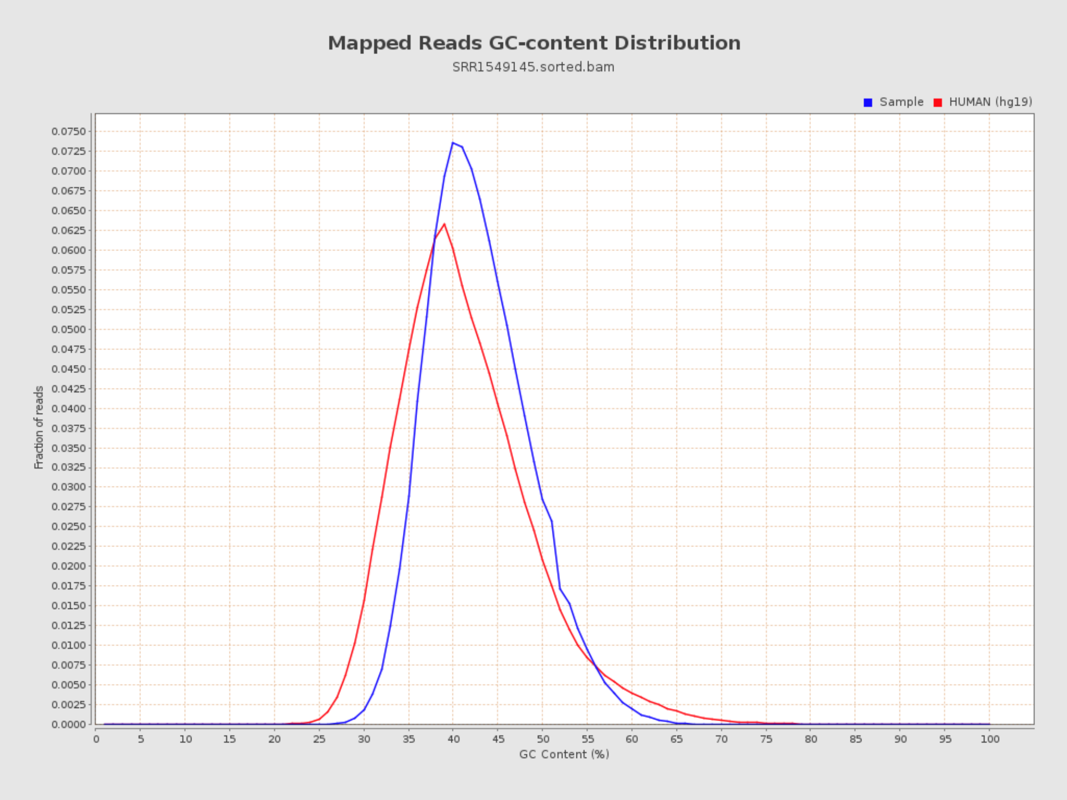
7. Results : Duplication Rate Histogram



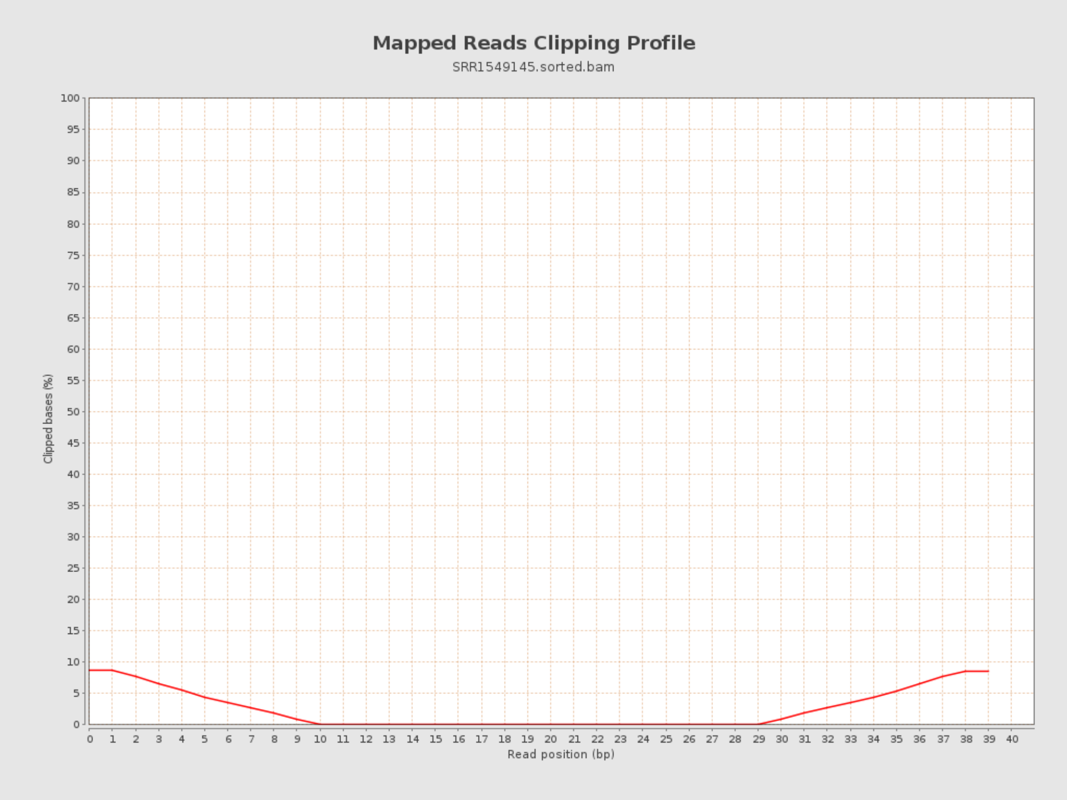
8. Results : Mapped Reads Nucleotide Content



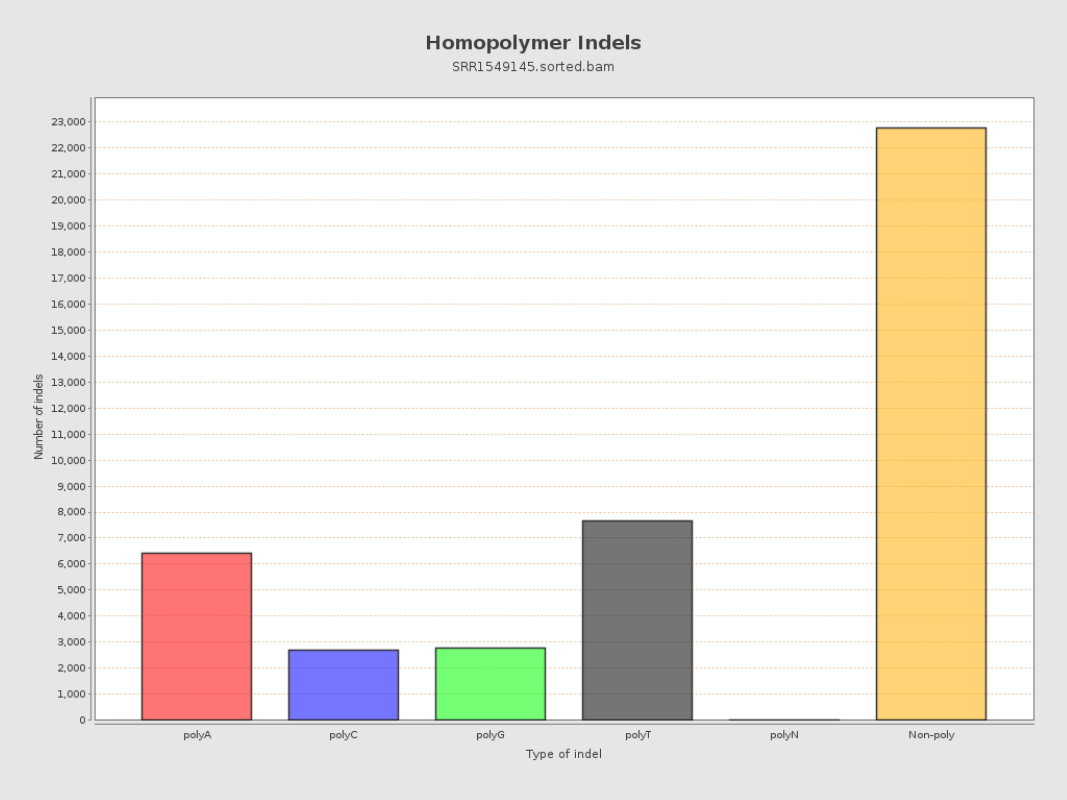
9. Results : Mapped Reads GC-content Distribution



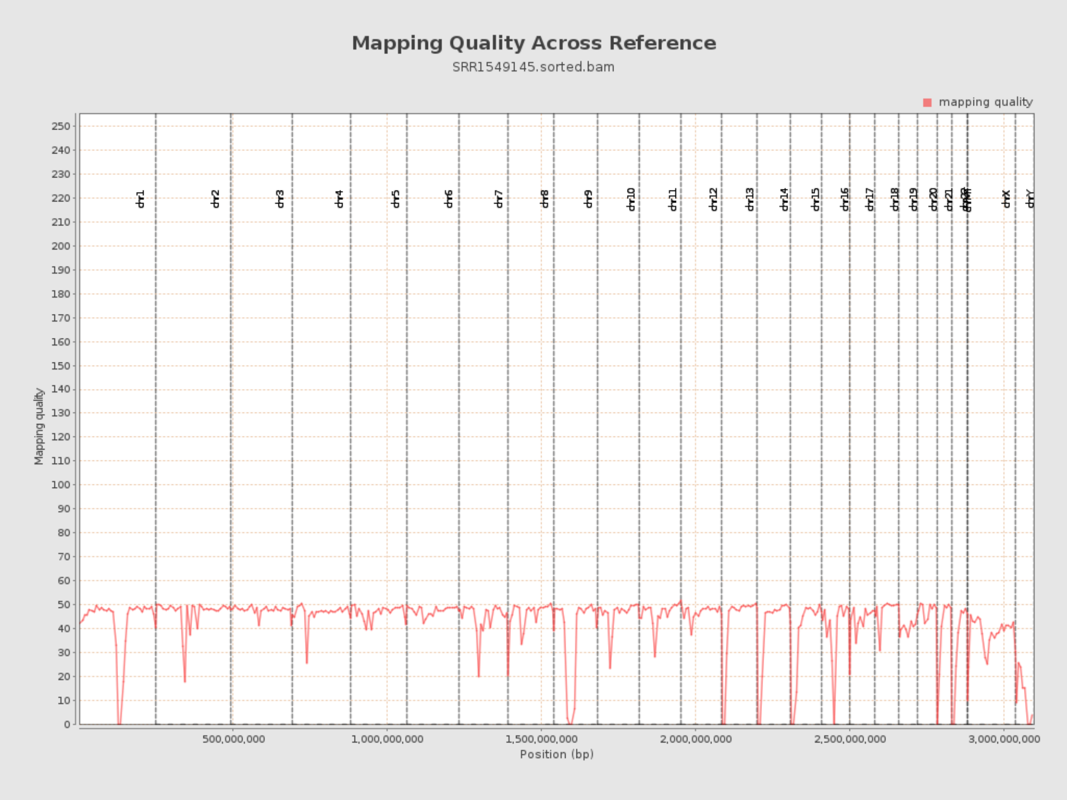
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram