Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:41:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549087.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_SRR1549087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:41:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,261,294
Mapped reads	8,203,783 / 88.58%
Unmapped reads	1,057,511 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	278,096 / 3%
Duplication rate	2.31%
Clipped reads	400,948 / 4.33%

2.2. ACGT Content

Number/percentage of A's	96,382,674 / 29.58%
Number/percentage of C's	66,867,217 / 20.52%
Number/percentage of T's	97,629,485 / 29.97%
Number/percentage of G's	64,837,193 / 19.9%
Number/percentage of N's	79,371 / 0.02%
GC Percentage	40.43%

2.3. Coverage

Mean	0.1053
Standard Deviation	0.7366

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

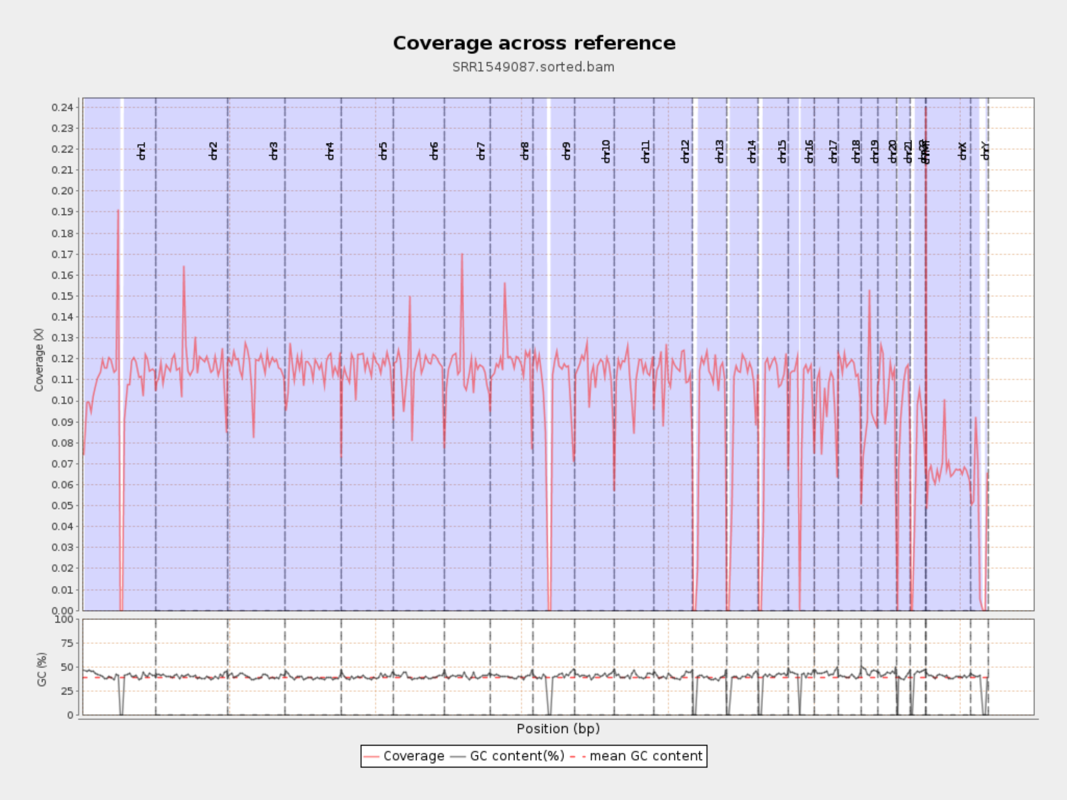
General error rate	0.41%
Mismatches	1,316,695
Insertions	8,077
Mapped reads with at least one insertion	0.1%
Deletions	28,088
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.95%

2.6. Chromosome stats

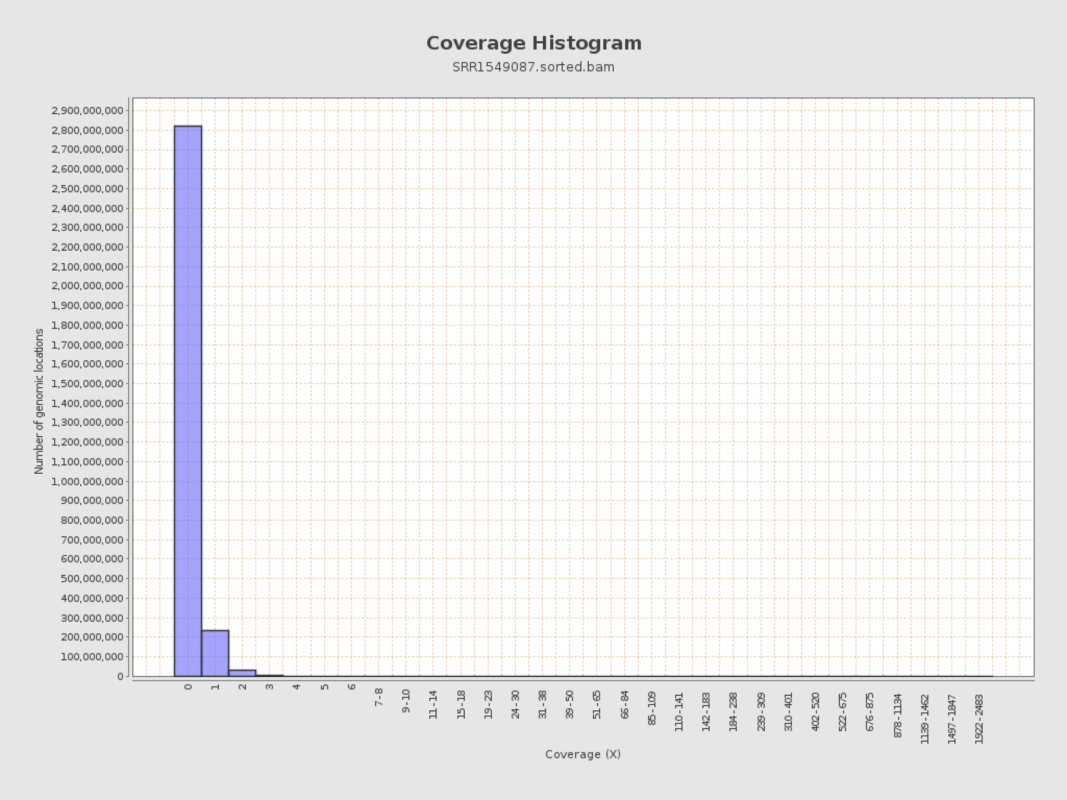
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26391617	0.1059	1.7356
chr2	243199373	28479508	0.1171	0.6414
chr3	198022430	23098953	0.1166	0.4001
chr4	191154276	22110612	0.1157	0.3999
chr5	180915260	20874703	0.1154	0.4049
chr6	171115067	19916648	0.1164	0.5332
chr7	159138663	18299303	0.115	0.8214
chr8	146364022	17310617	0.1183	0.5742

chr9	141213431	13898105	0.0984	0.6078
chr10	135534747	15510076	0.1144	0.5539
chr11	135006516	15166160	0.1123	0.6542
chr12	133851895	15138129	0.1131	0.4129
chr13	115169878	11004150	0.0955	0.3447
chr14	107349540	10107537	0.0942	0.4221
chr15	102531392	9597471	0.0936	0.344
chr16	90354753	8801701	0.0974	0.4312
chr17	81195210	8084018	0.0996	0.4255
chr18	78077248	9069600	0.1162	1.2314
chr19	59128983	5582906	0.0944	1.3267
chr20	63025520	6844514	0.1086	0.3954
chr21	48129895	4292654	0.0892	0.4041
chr22	51304566	3364257	0.0656	0.3353
chrMT	16571	3979	0.2401	0.5331
chrX	155270560	10403766	0.067	0.4218
chrY	59373566	2480464	0.0418	0.3581

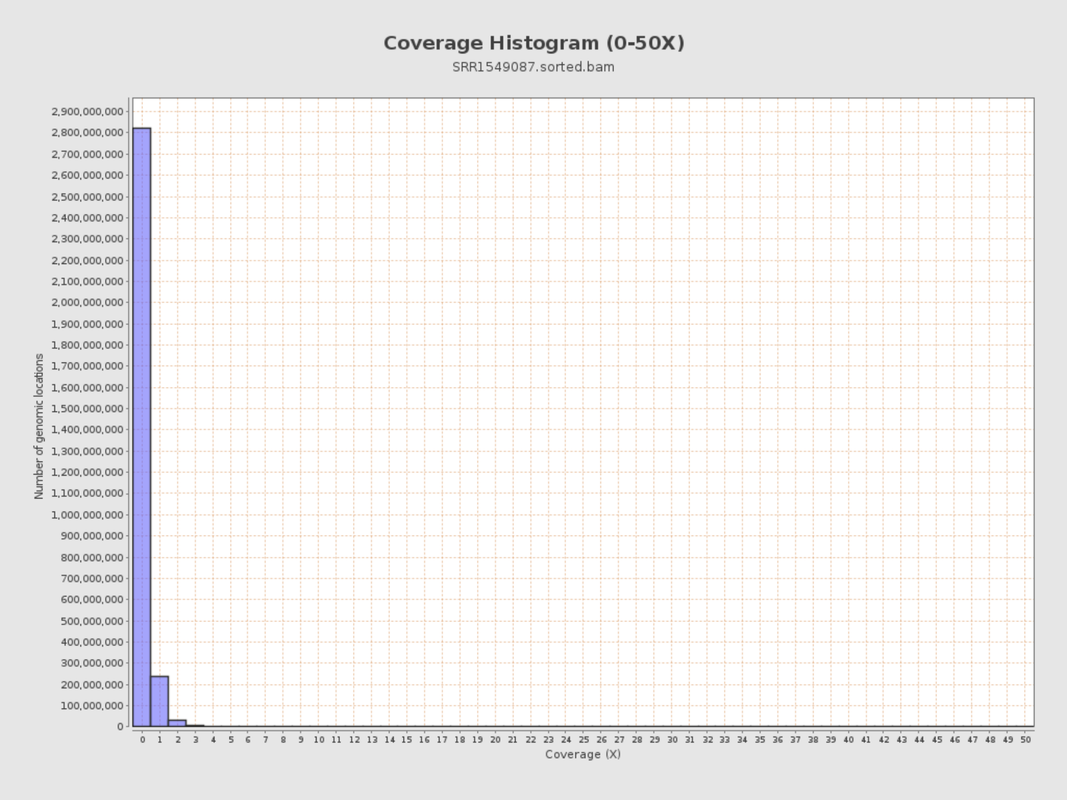
3. Results : Coverage across reference



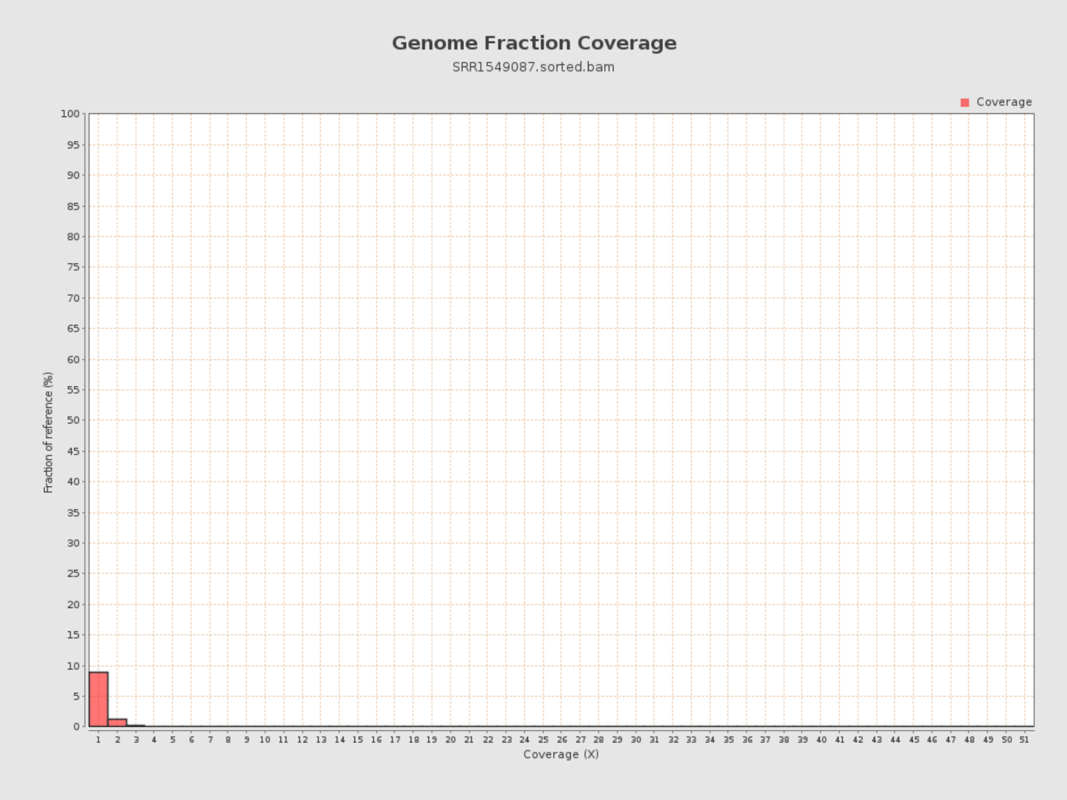
4. Results : Coverage Histogram



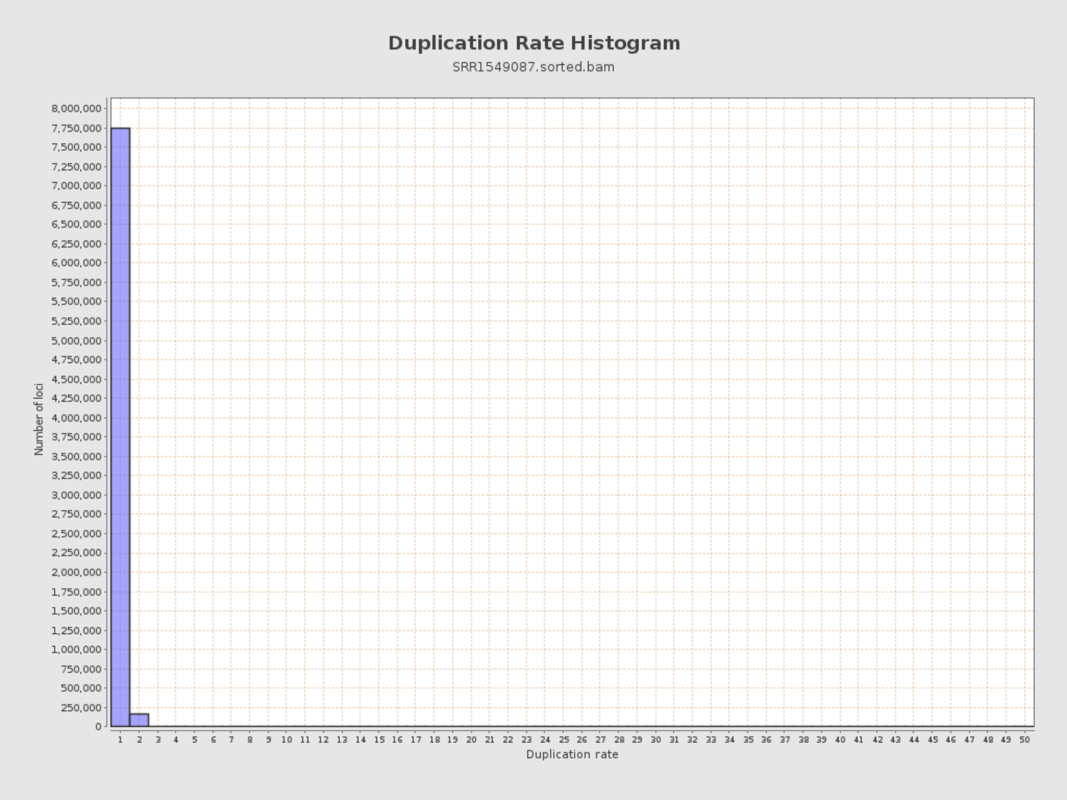
5. Results : Coverage Histogram (0-50X)



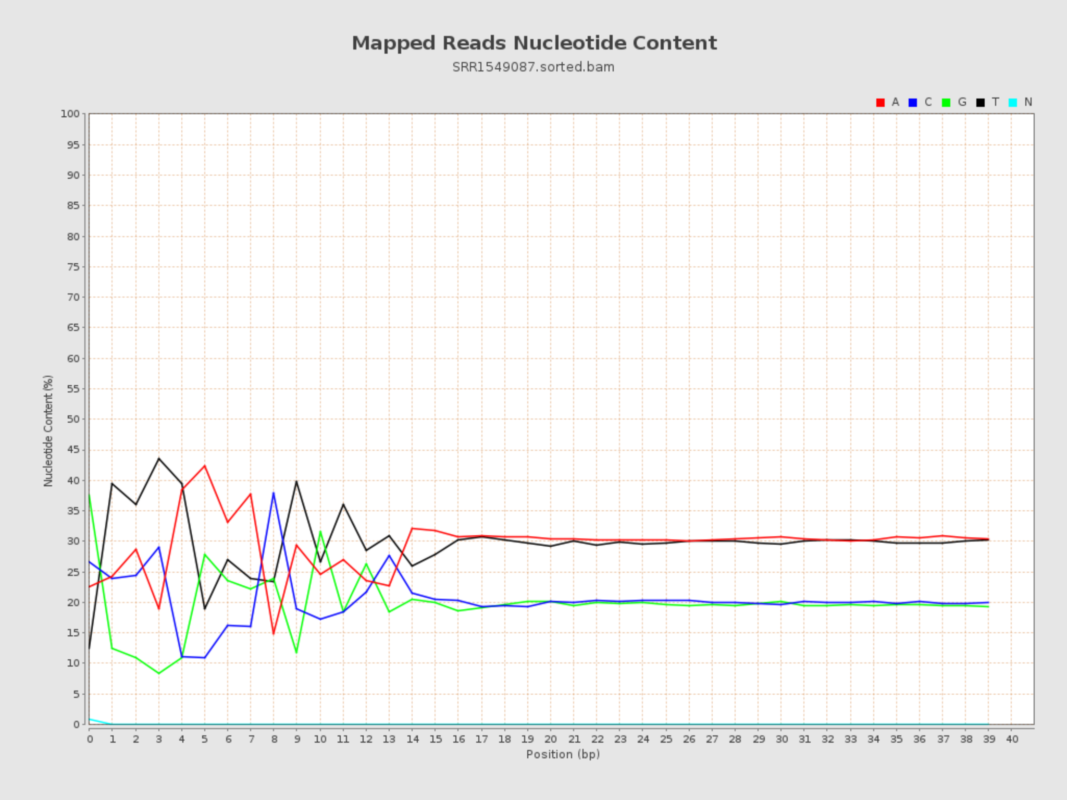
6. Results : Genome Fraction Coverage



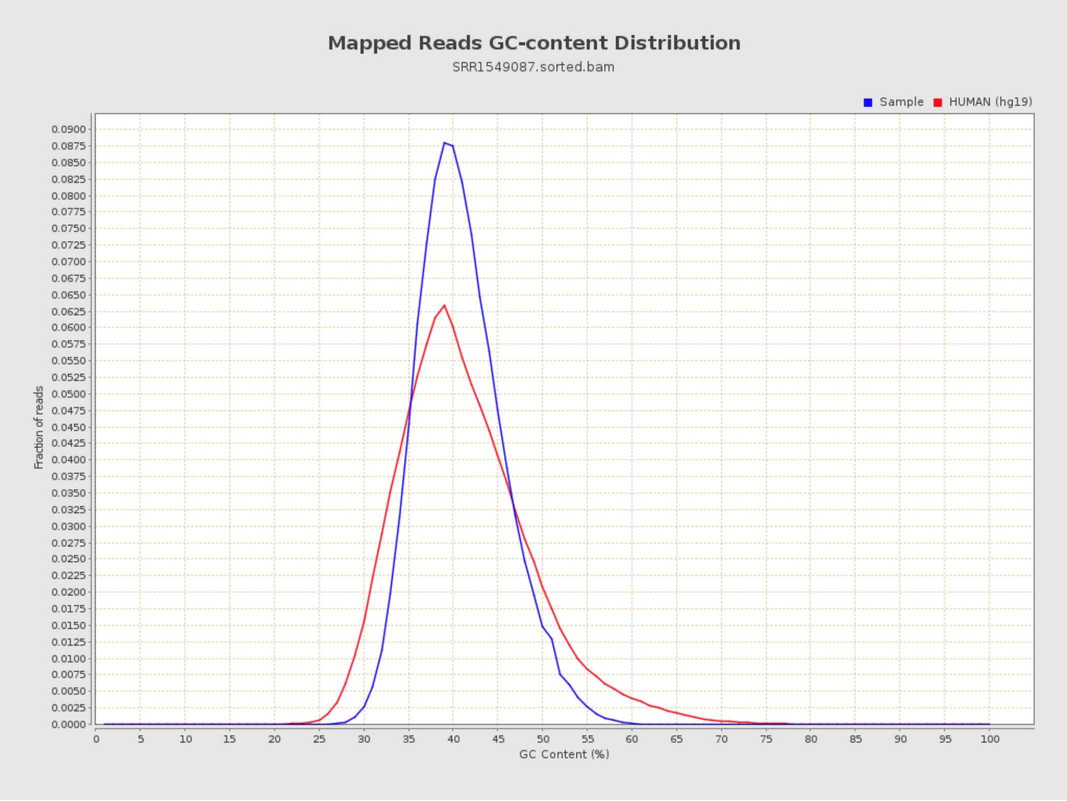
7. Results : Duplication Rate Histogram



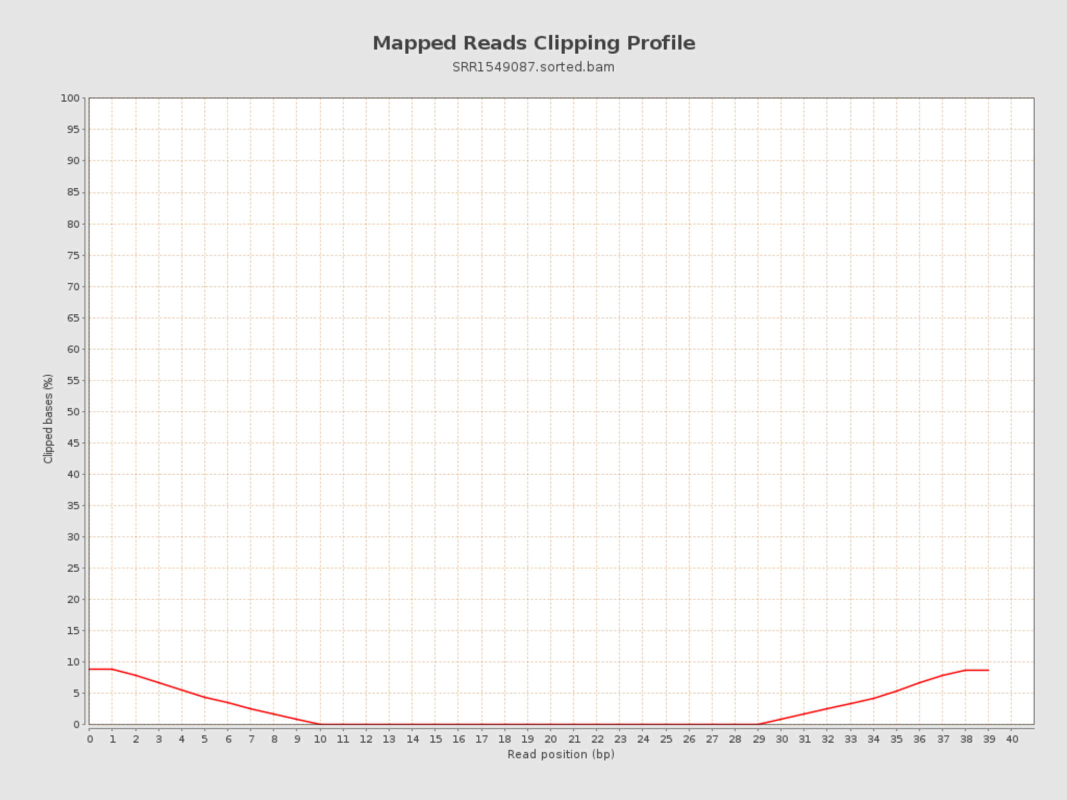
8. Results : Mapped Reads Nucleotide Content



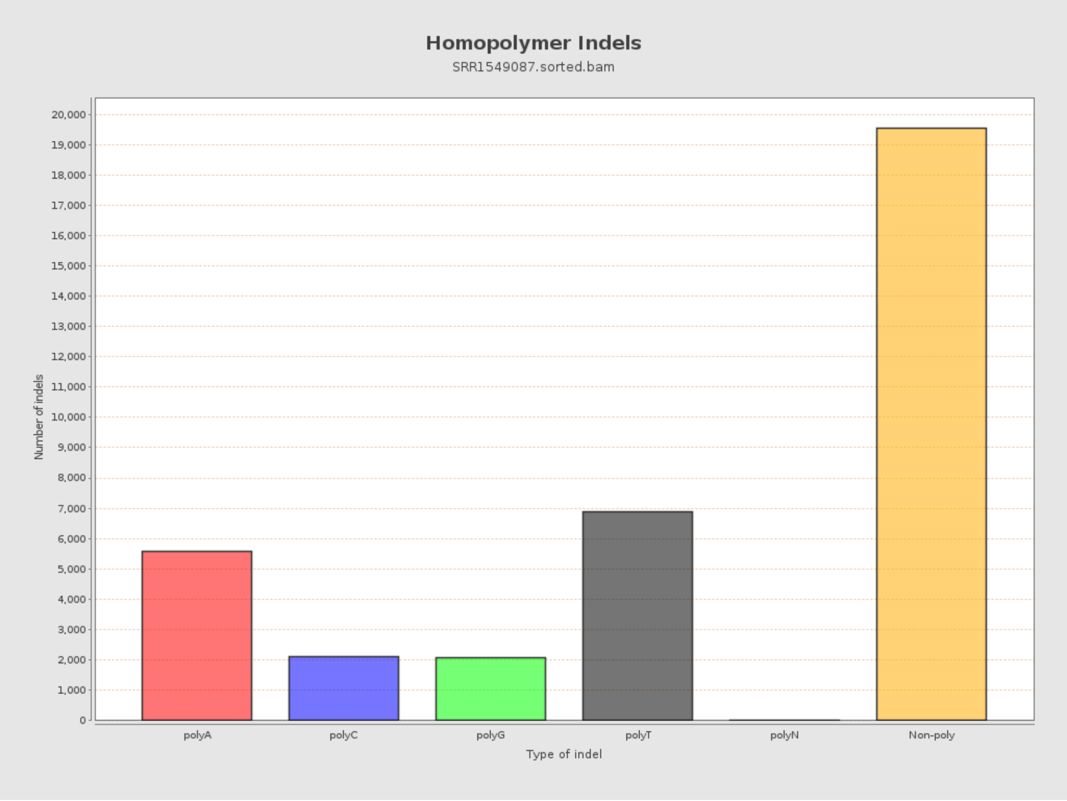
9. Results : Mapped Reads GC-content Distribution



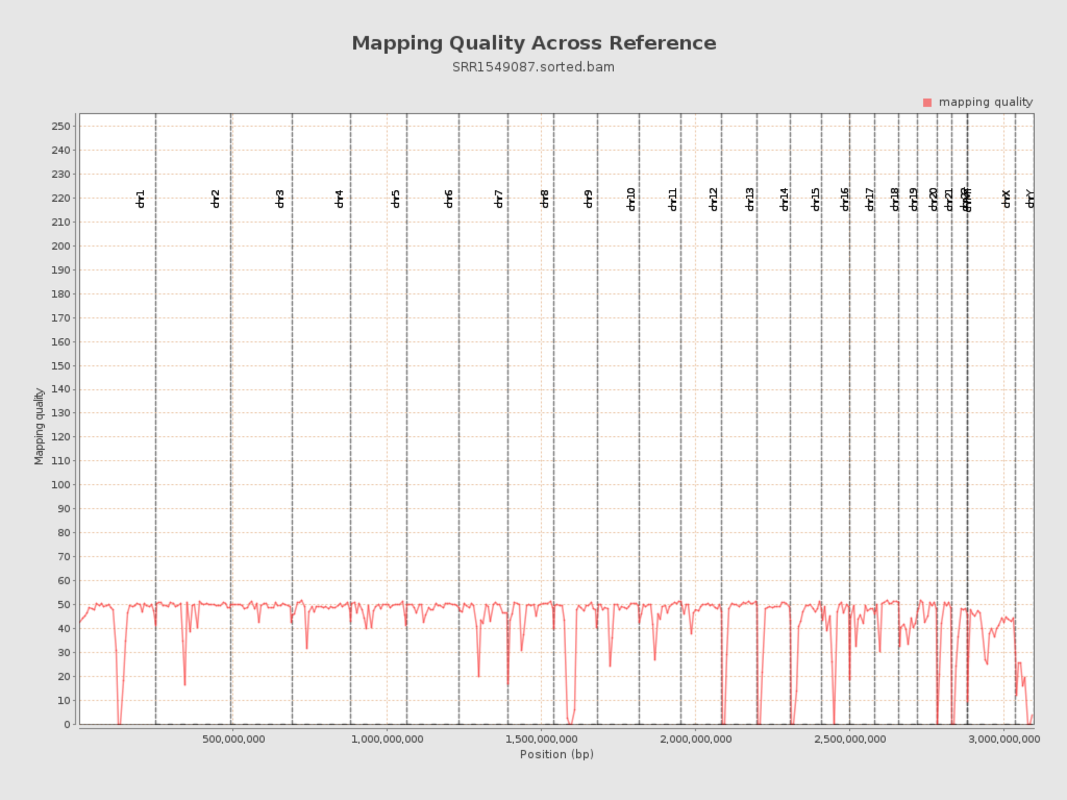
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram