Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:01:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549123.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_SRR1549123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:01:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,815,948
Mapped reads	6,889,973 / 58.31%
Unmapped reads	4,925,975 / 41.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	332,326 / 2.81%
Duplication rate	3.78%
Clipped reads	343,771 / 2.91%

2.2. ACGT Content

Number/percentage of A's	80,650,676 / 29.49%
Number/percentage of C's	55,708,031 / 20.37%
Number/percentage of T's	81,268,455 / 29.71%
Number/percentage of G's	55,862,670 / 20.43%
Number/percentage of N's	11,472 / 0%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0884
Standard Deviation	0.691

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

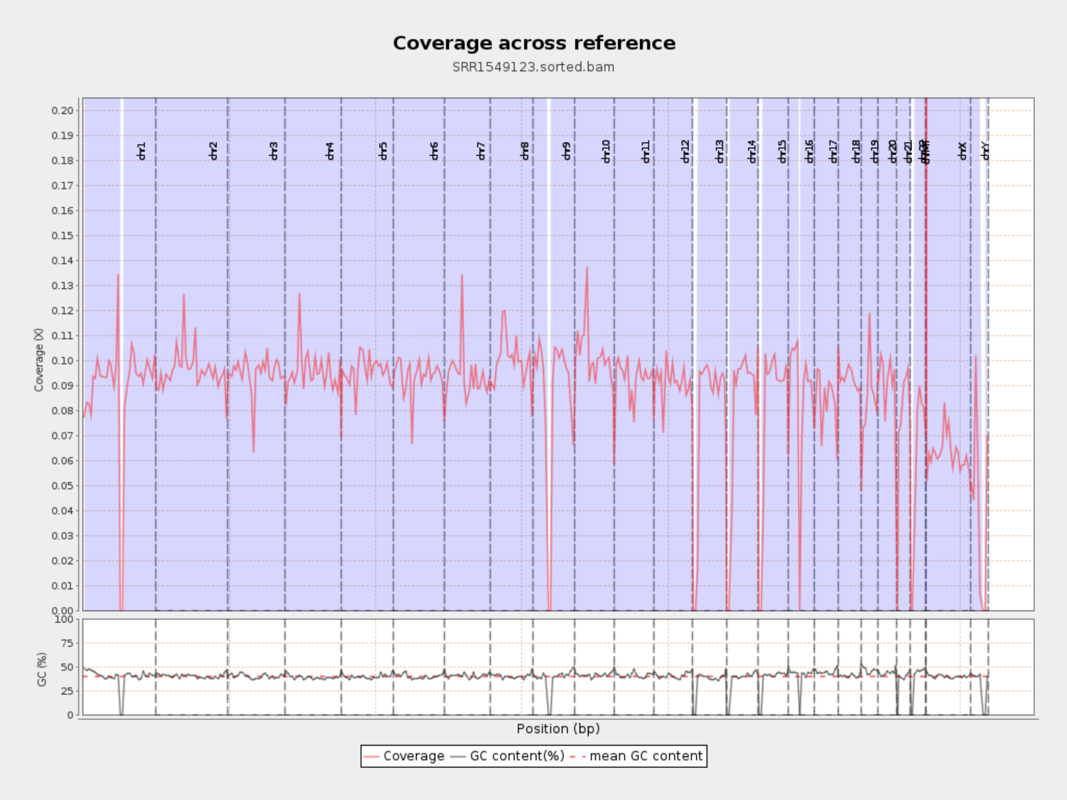
General error rate	0.31%
Mismatches	827,014
Insertions	6,675
Mapped reads with at least one insertion	0.1%
Deletions	20,366
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.13%

2.6. Chromosome stats

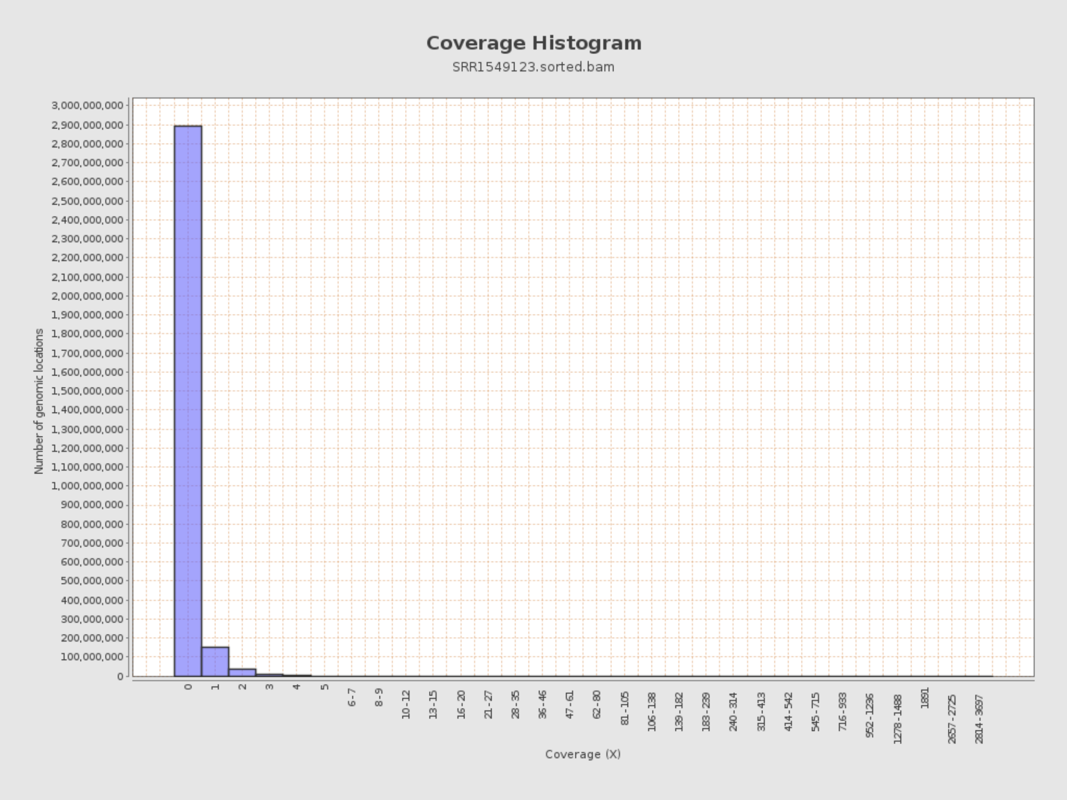
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22186433	0.089	1.1106
chr2	243199373	23450228	0.0964	0.5327
chr3	198022430	18805222	0.095	0.3935
chr4	191154276	18342888	0.096	0.44
chr5	180915260	17310389	0.0957	0.4066
chr6	171115067	16052227	0.0938	0.4049
chr7	159138663	14990153	0.0942	0.7399
chr8	146364022	14656740	0.1001	1.8584

chr9	141213431	12067035	0.0855	0.484
chr10	135534747	13900677	0.1026	0.5904
chr11	135006516	12514965	0.0927	0.4952
chr12	133851895	12256643	0.0916	0.404
chr13	115169878	8931958	0.0776	0.3579
chr14	107349540	8446064	0.0787	0.439
chr15	102531392	8028684	0.0783	0.3537
chr16	90354753	7607650	0.0842	0.3975
chr17	81195210	6872785	0.0846	0.3951
chr18	78077248	7272511	0.0931	0.9334
chr19	59128983	5053243	0.0855	0.8593
chr20	63025520	5789442	0.0919	0.42
chr21	48129895	3684104	0.0765	0.4271
chr22	51304566	2953725	0.0576	0.3149
chrMT	16571	142426	8.5949	10.7269
chrX	155270560	9767318	0.0629	0.3788
chrY	59373566	2443325	0.0412	0.4179

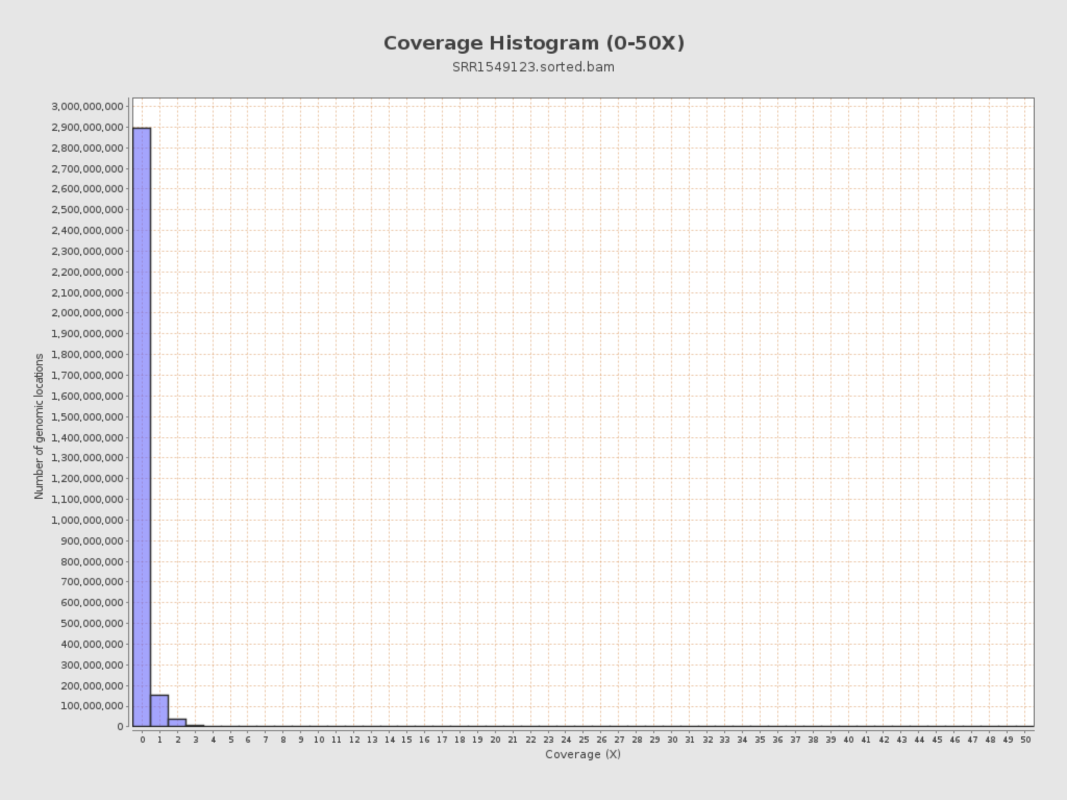
3. Results : Coverage across reference



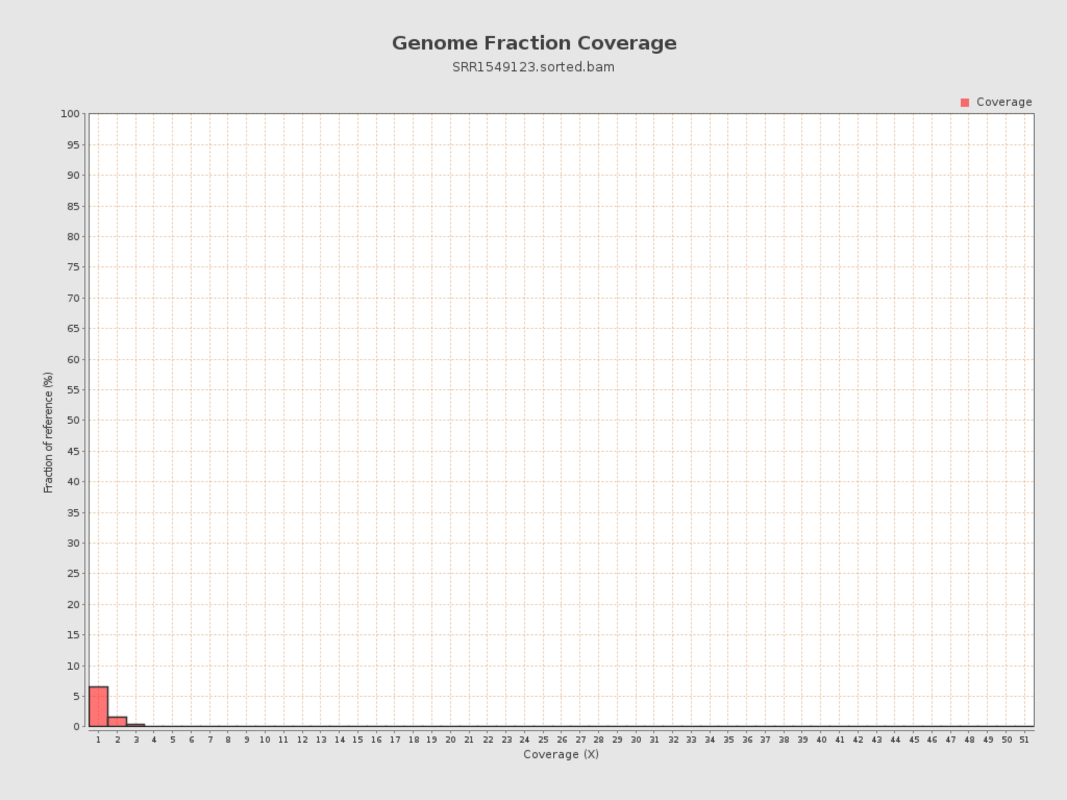
4. Results : Coverage Histogram



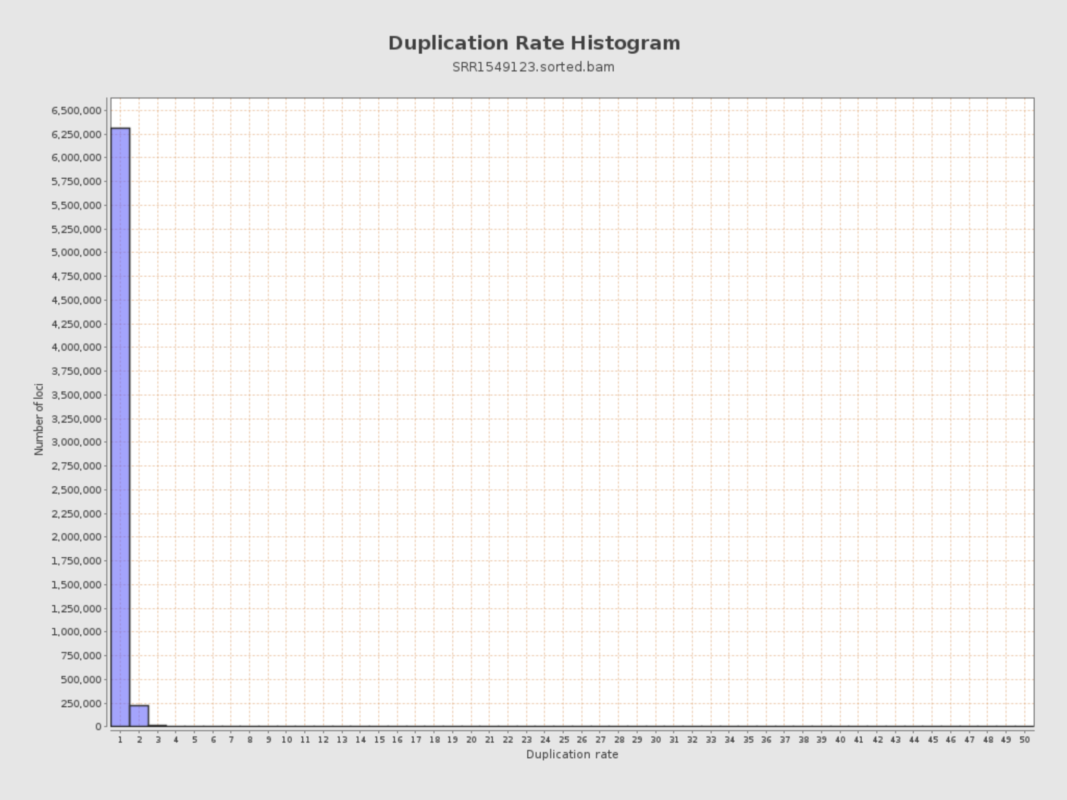
5. Results : Coverage Histogram (0-50X)



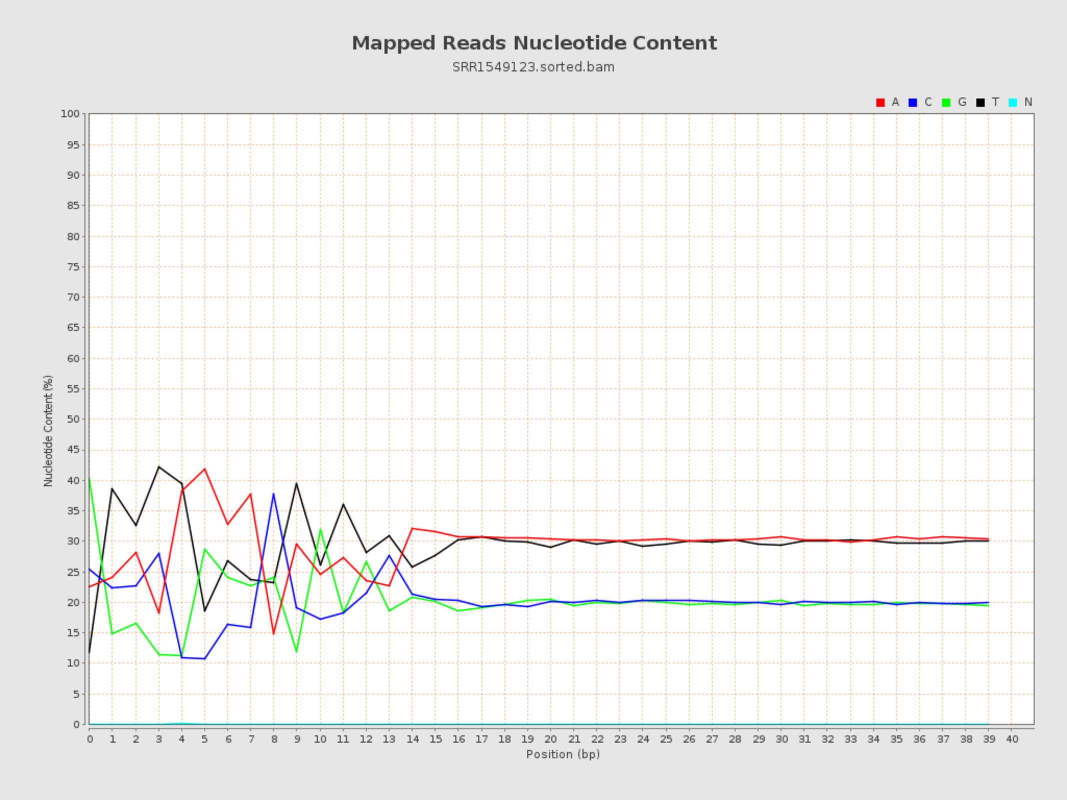
6. Results : Genome Fraction Coverage



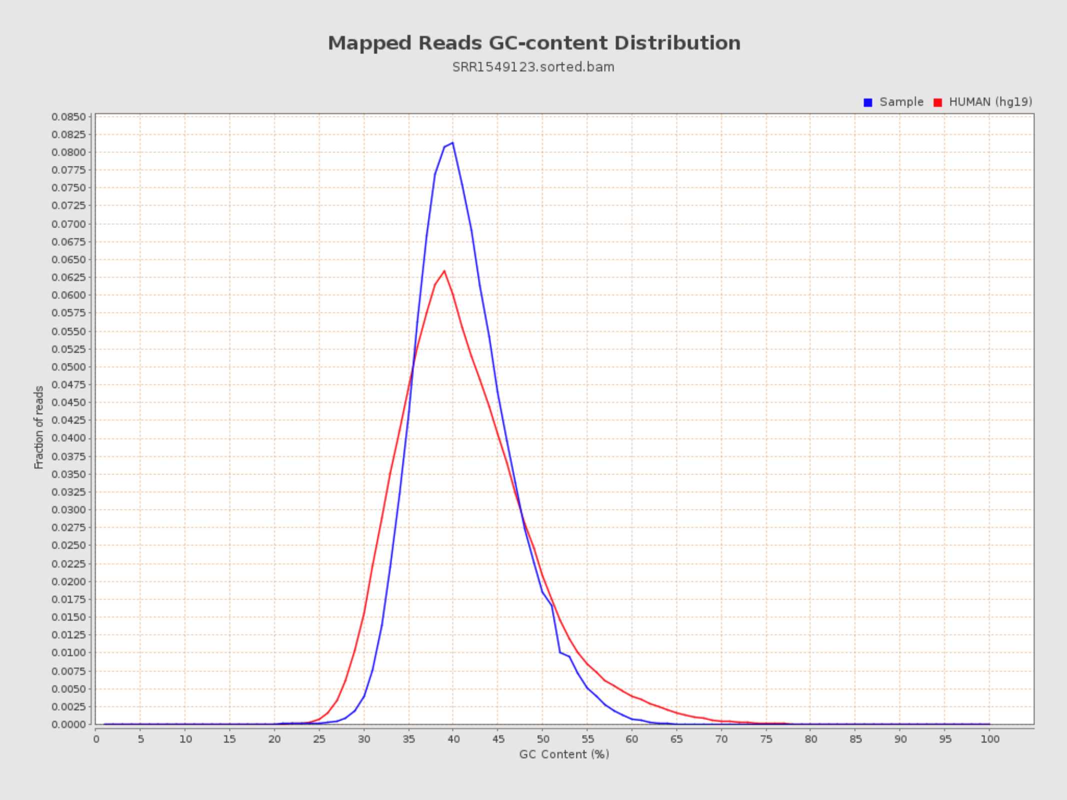
7. Results : Duplication Rate Histogram



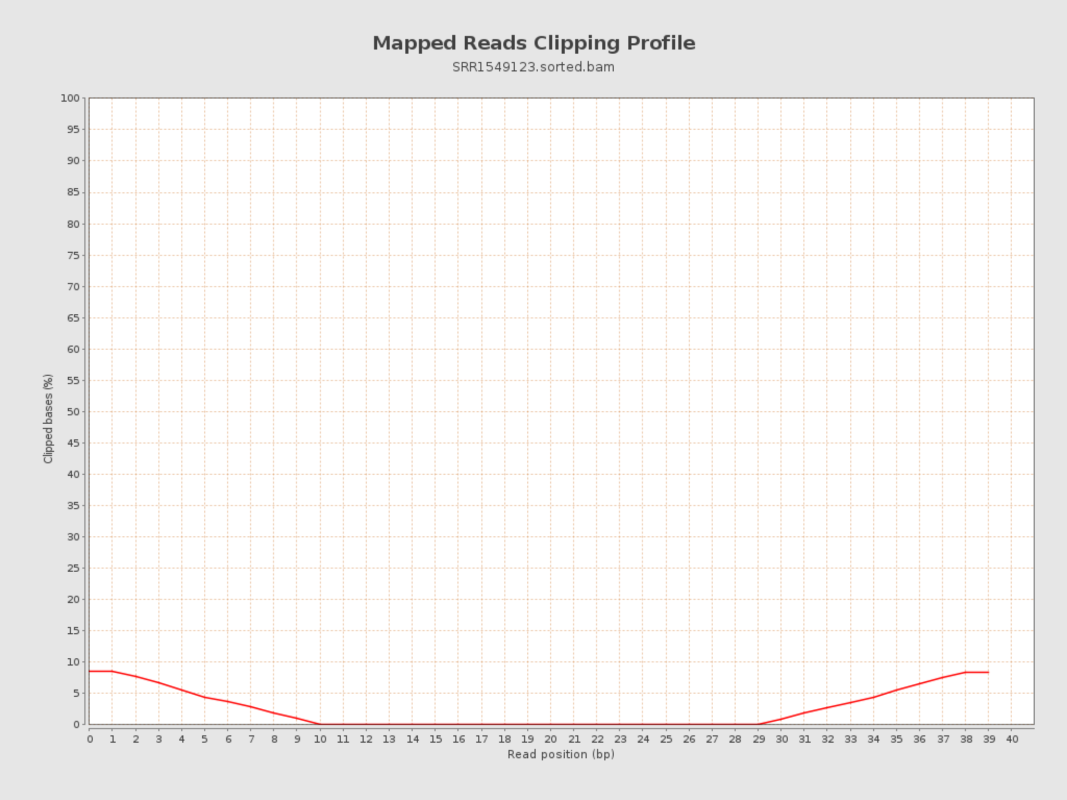
8. Results : Mapped Reads Nucleotide Content



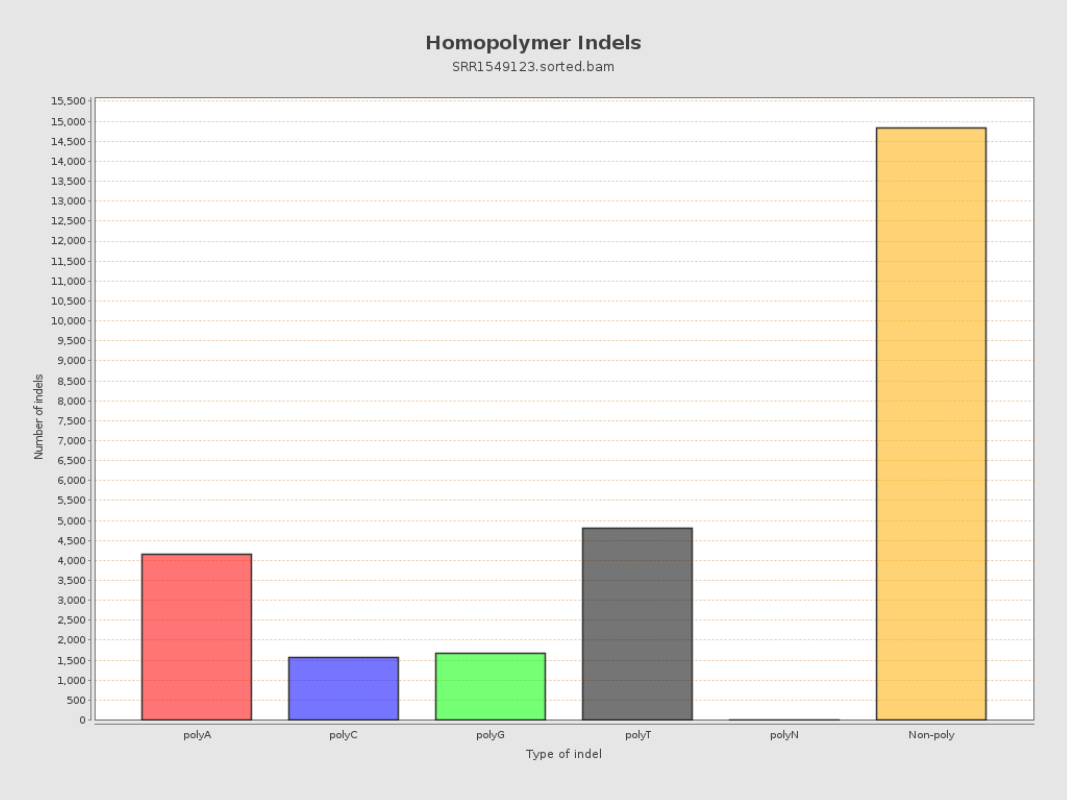
9. Results : Mapped Reads GC-content Distribution



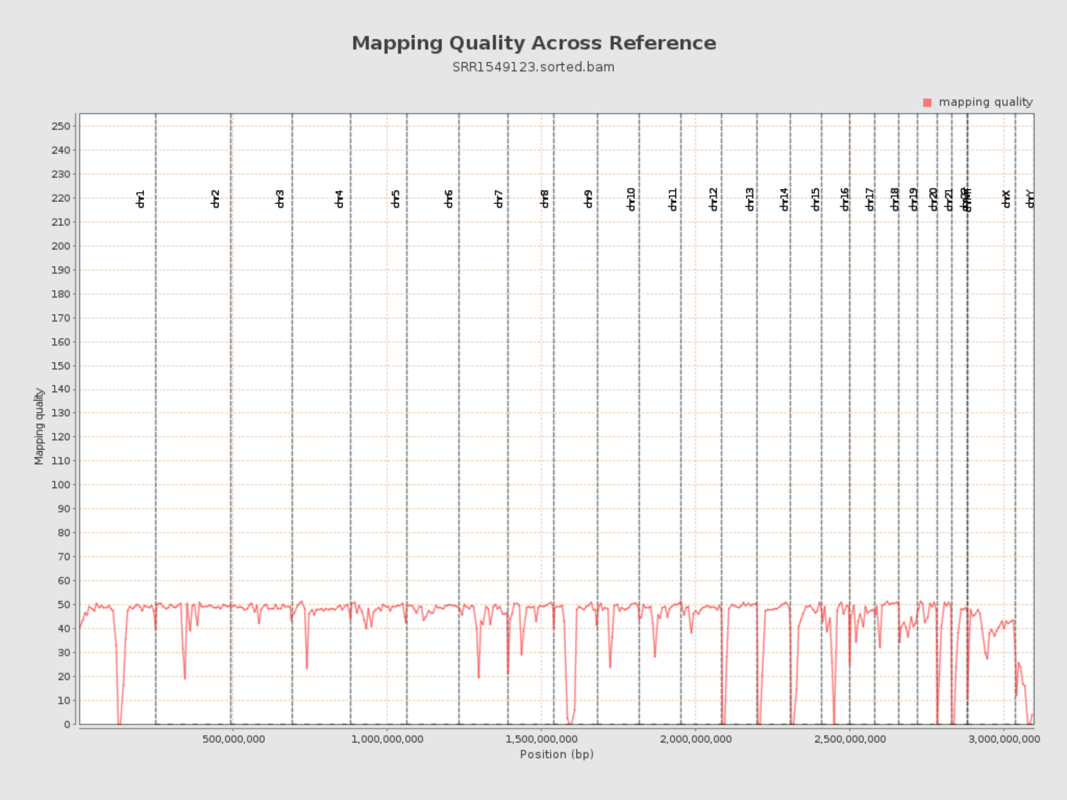
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram