Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:25:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549119.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_SRR1549119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:25:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,114,420
Mapped reads	7,683,498 / 58.59%
Unmapped reads	5,430,922 / 41.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	531,664 / 4.05%
Duplication rate	5.41%
Clipped reads	825,796 / 6.3%

2.2. ACGT Content

Number/percentage of A's	88,241,849 / 29.17%
Number/percentage of C's	62,901,746 / 20.79%
Number/percentage of T's	88,198,369 / 29.16%
Number/percentage of G's	63,152,432 / 20.88%
Number/percentage of N's	11,825 / 0%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0977
Standard Deviation	0.8039

2.4. Mapping Quality

Mean Mapping Quality	39.49

2.5. Mismatches and indels

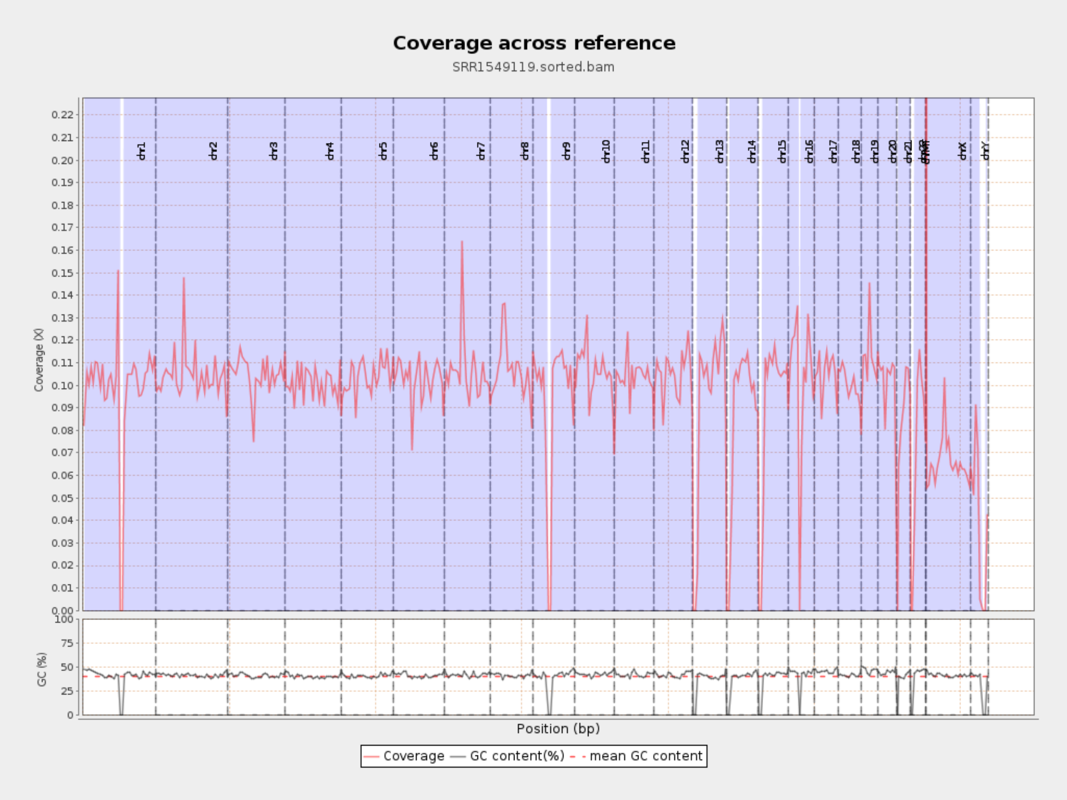
General error rate	0.39%
Mismatches	1,162,264
Insertions	11,467
Mapped reads with at least one insertion	0.15%
Deletions	29,144
Mapped reads with at least one deletion	0.38%
Homopolymer indels	43.45%

2.6. Chromosome stats

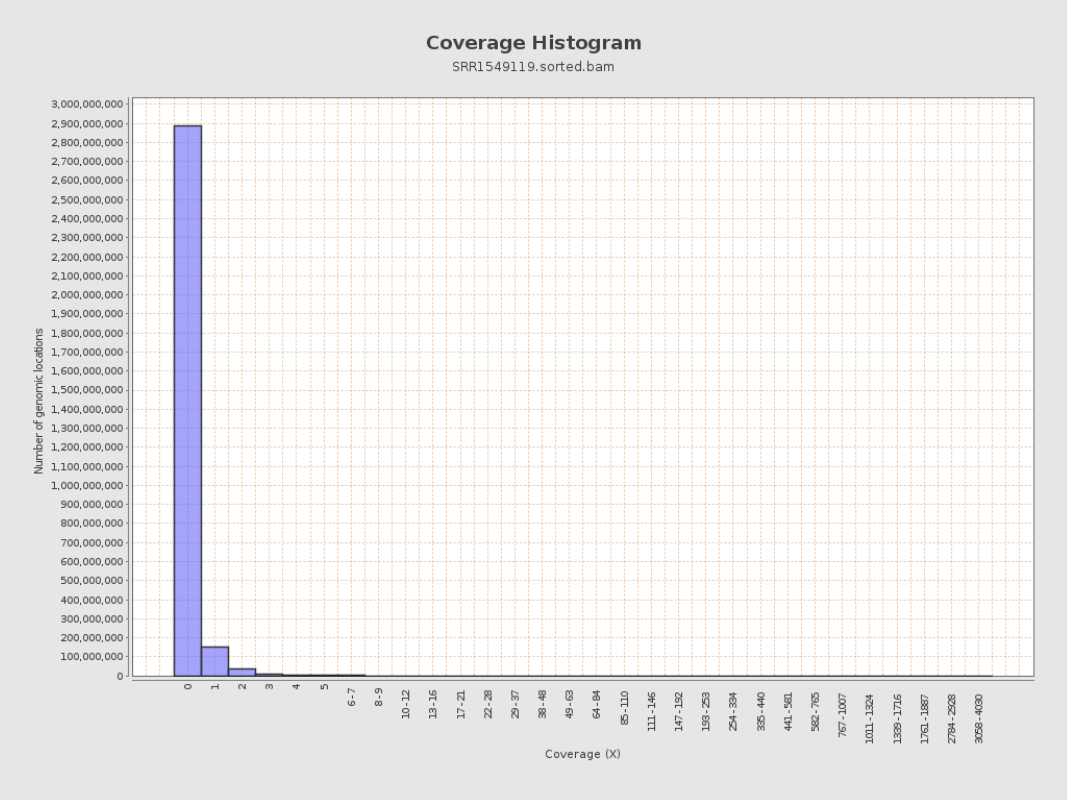
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24320910	0.0976	1.2904
chr2	243199373	25495381	0.1048	0.6241
chr3	198022430	20694887	0.1045	0.4626
chr4	191154276	19289590	0.1009	0.4652
chr5	180915260	18791750	0.1039	0.4722
chr6	171115067	17585049	0.1028	0.494
chr7	159138663	17022436	0.107	0.7995
chr8	146364022	15566655	0.1064	2.0165

chr9	141213431	13141327	0.0931	0.6246
chr10	135534747	14433971	0.1065	0.6214
chr11	135006516	13970988	0.1035	0.5567
chr12	133851895	14160250	0.1058	0.4934
chr13	115169878	10657591	0.0925	0.4365
chr14	107349540	9360101	0.0872	0.797
chr15	102531392	9073100	0.0885	0.4215
chr16	90354753	9043719	0.1001	0.4835
chr17	81195210	8592346	0.1058	0.4845
chr18	78077248	7913343	0.1014	1.2126
chr19	59128983	6641048	0.1123	1.3387
chr20	63025520	6450679	0.1024	0.4789
chr21	48129895	3967581	0.0824	0.4601
chr22	51304566	3650844	0.0712	0.4049
chrMT	16571	152750	9.2179	12.9152
chrX	155270560	10225007	0.0659	0.4615
chrY	59373566	2341255	0.0394	0.3269

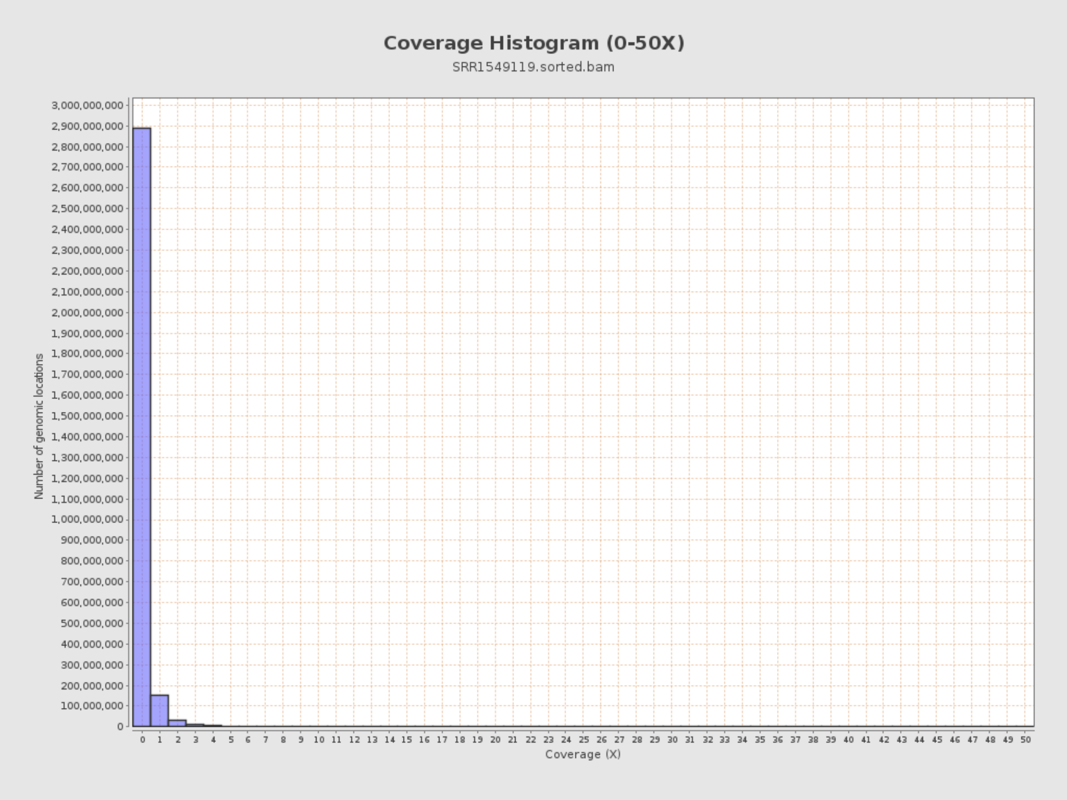
3. Results : Coverage across reference



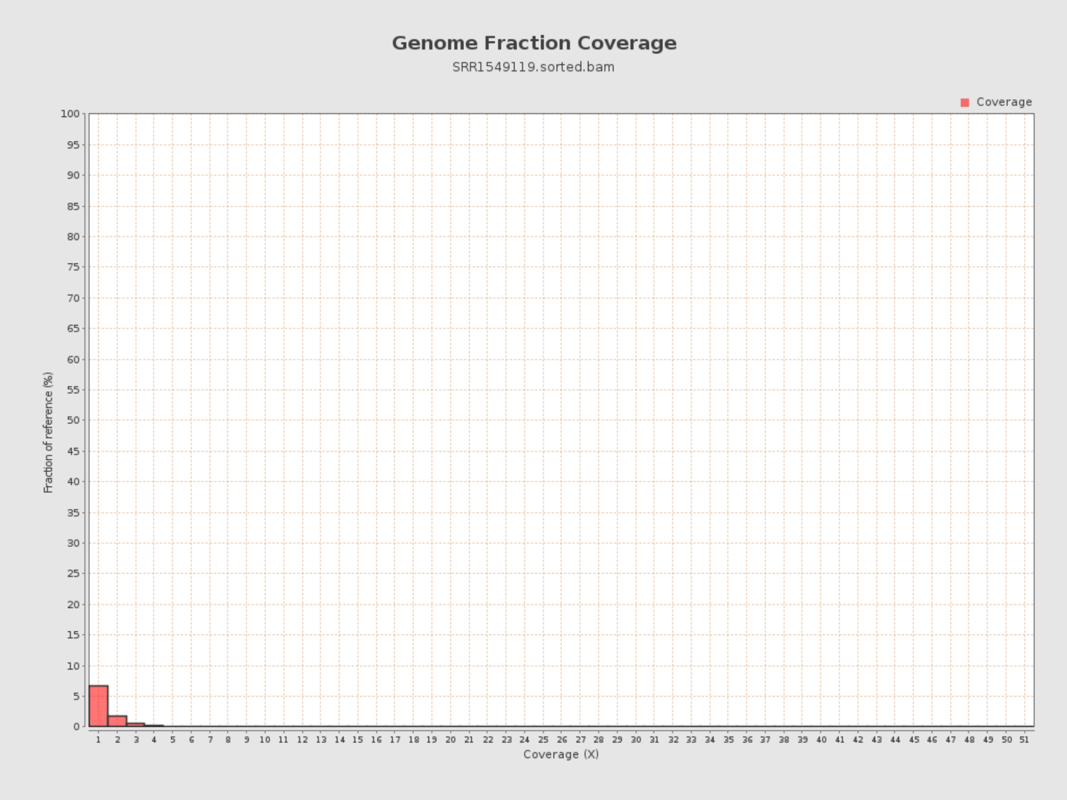
4. Results : Coverage Histogram



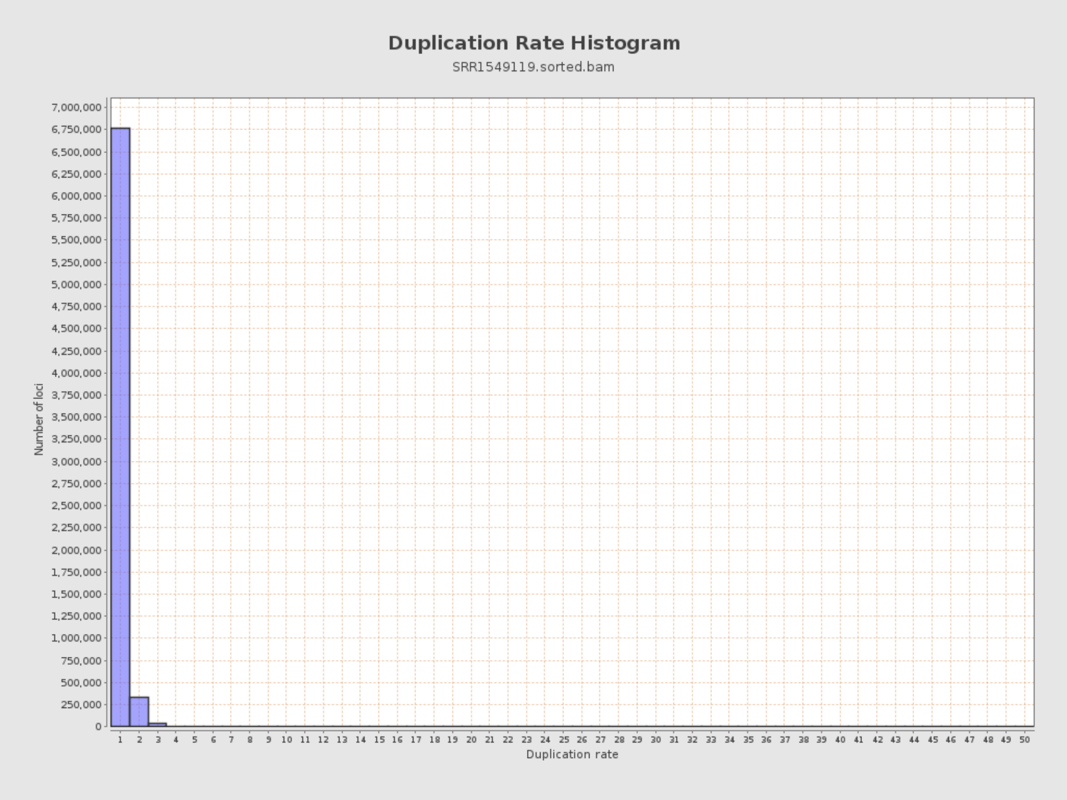
5. Results : Coverage Histogram (0-50X)



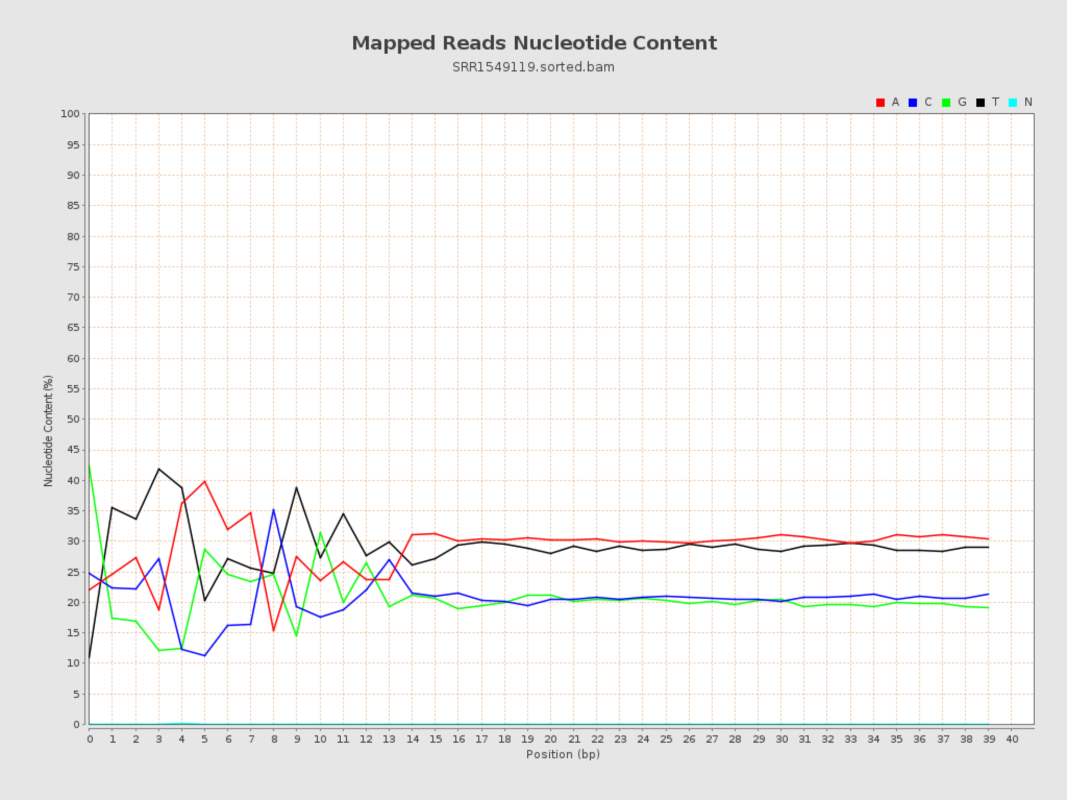
6. Results : Genome Fraction Coverage



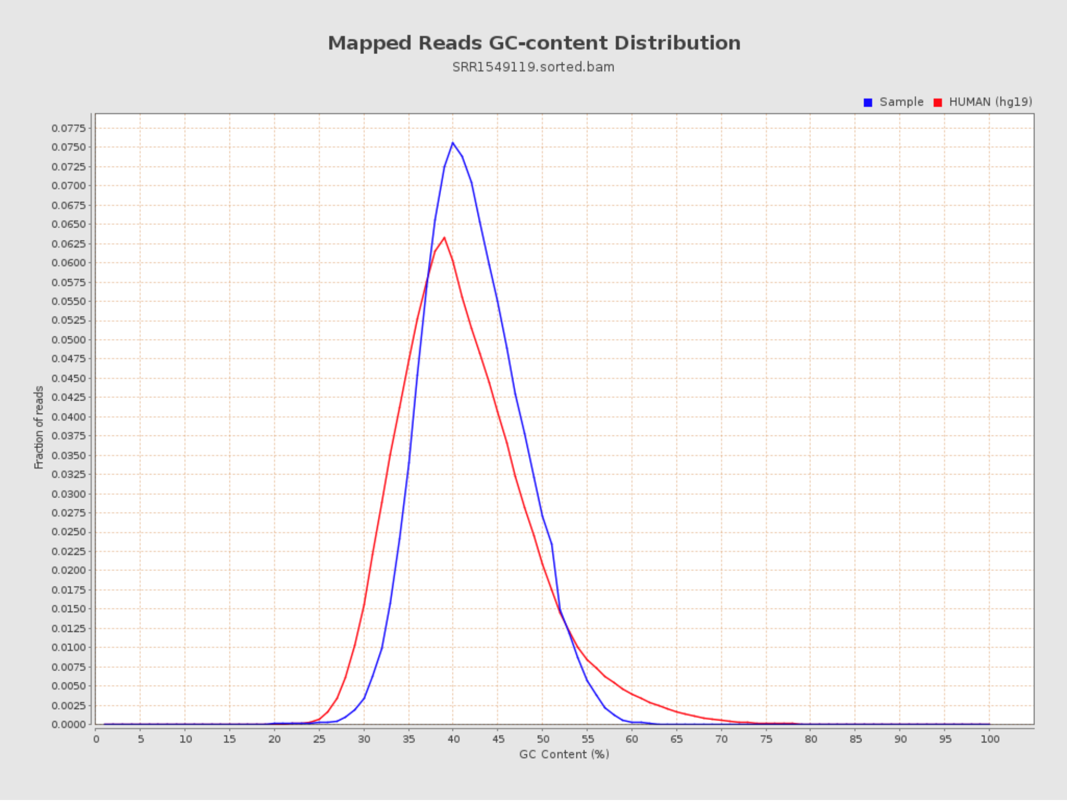
7. Results : Duplication Rate Histogram



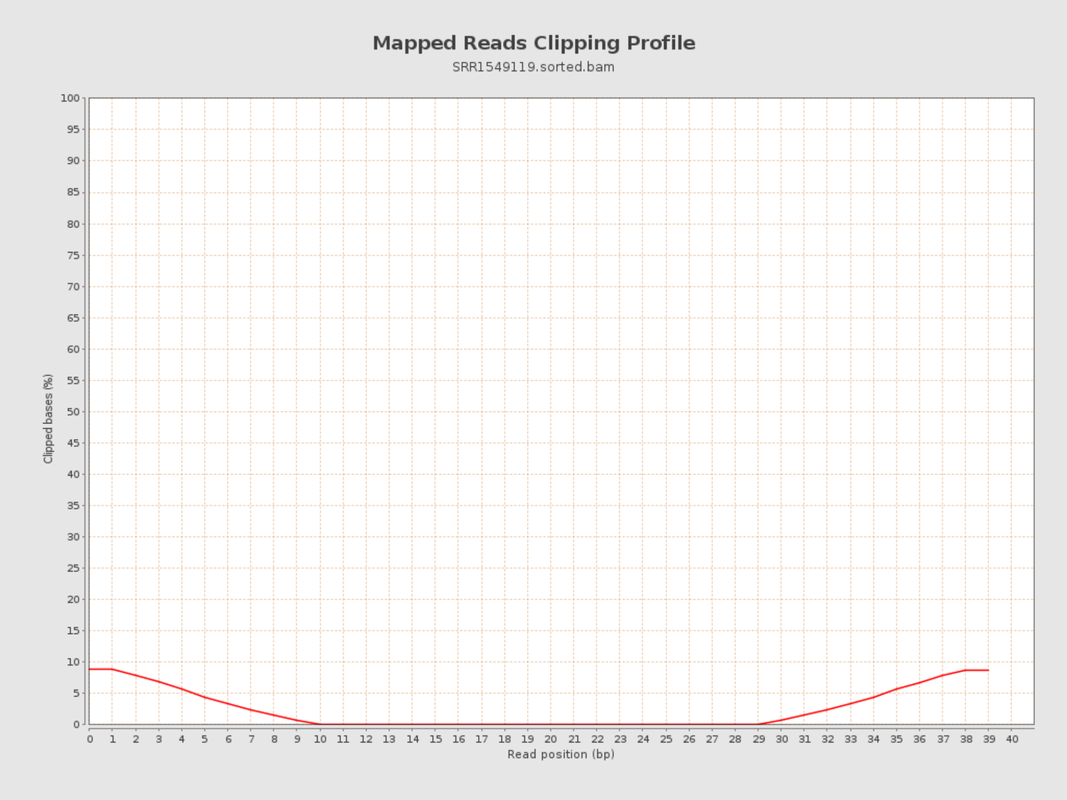
8. Results : Mapped Reads Nucleotide Content



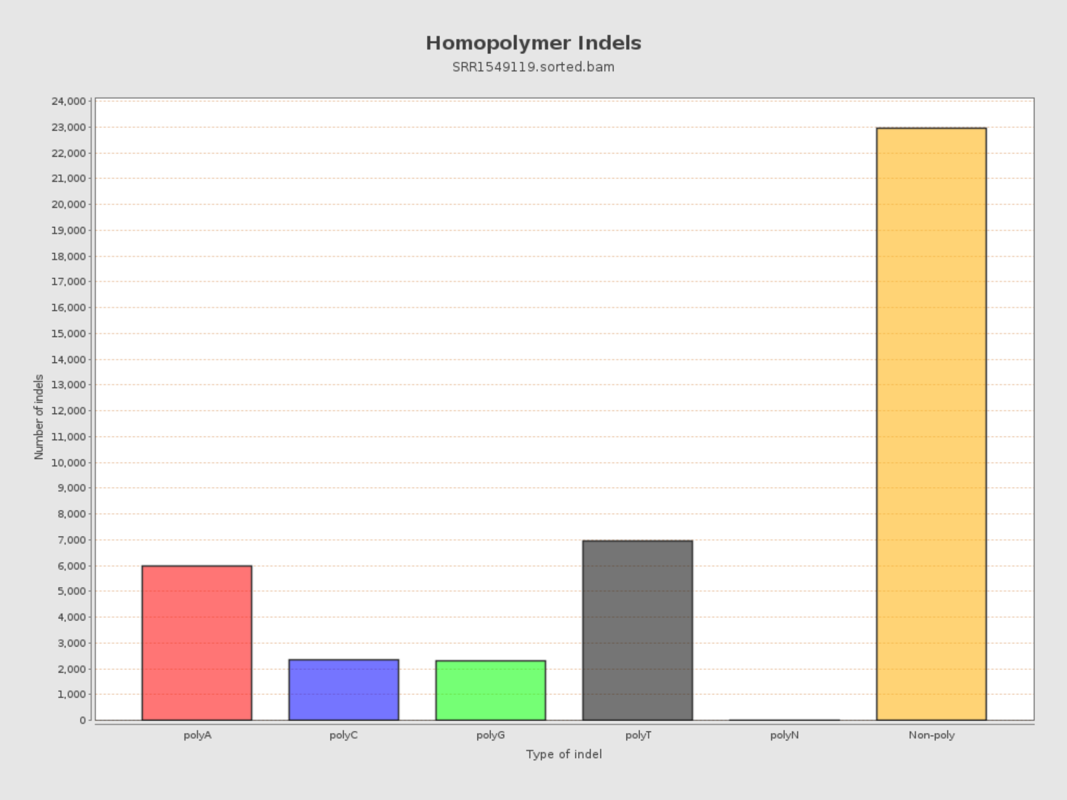
9. Results : Mapped Reads GC-content Distribution



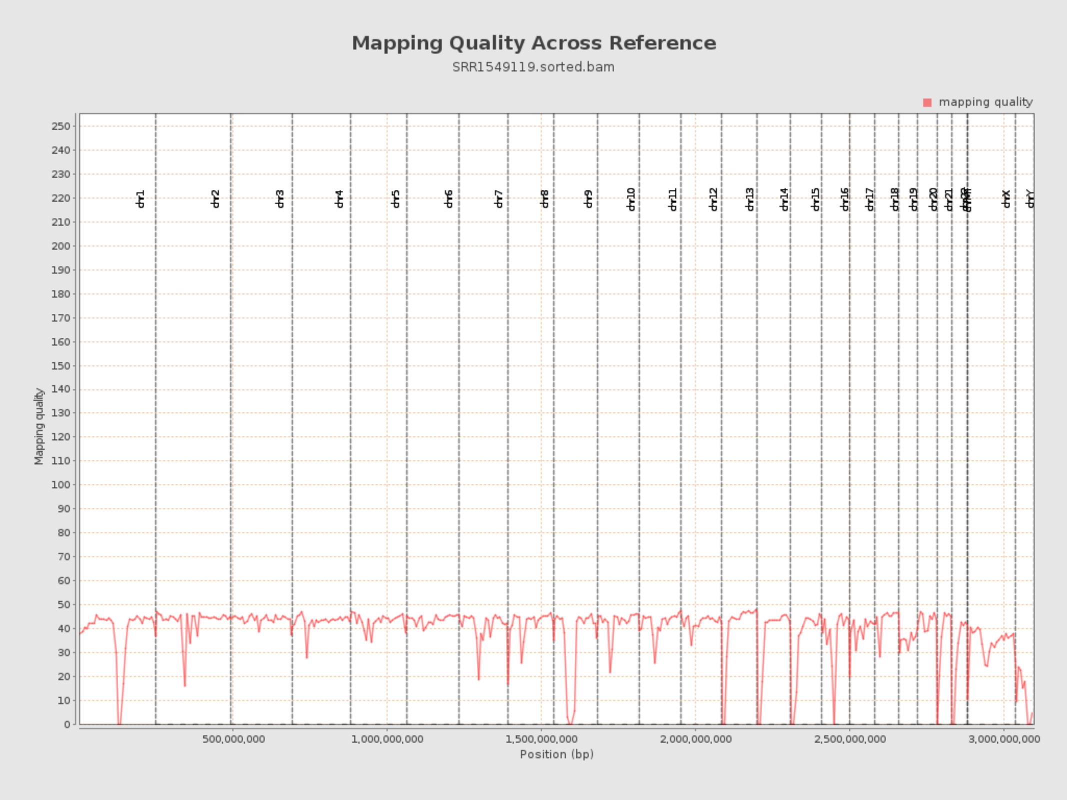
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram