Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:31:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549126.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_SRR1549126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:30:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,975,444
Mapped reads	7,859,224 / 56.24%
Unmapped reads	6,116,220 / 43.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	385,653 / 2.76%
Duplication rate	3.73%
Clipped reads	413,481 / 2.96%

2.2. ACGT Content

Number/percentage of A's	92,252,818 / 29.58%
Number/percentage of C's	62,967,372 / 20.19%
Number/percentage of T's	93,166,083 / 29.87%
Number/percentage of G's	63,490,820 / 20.36%
Number/percentage of N's	12,965 / 0%
GC Percentage	40.55%

2.3. Coverage

Mean	0.1008
Standard Deviation	1.0519

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

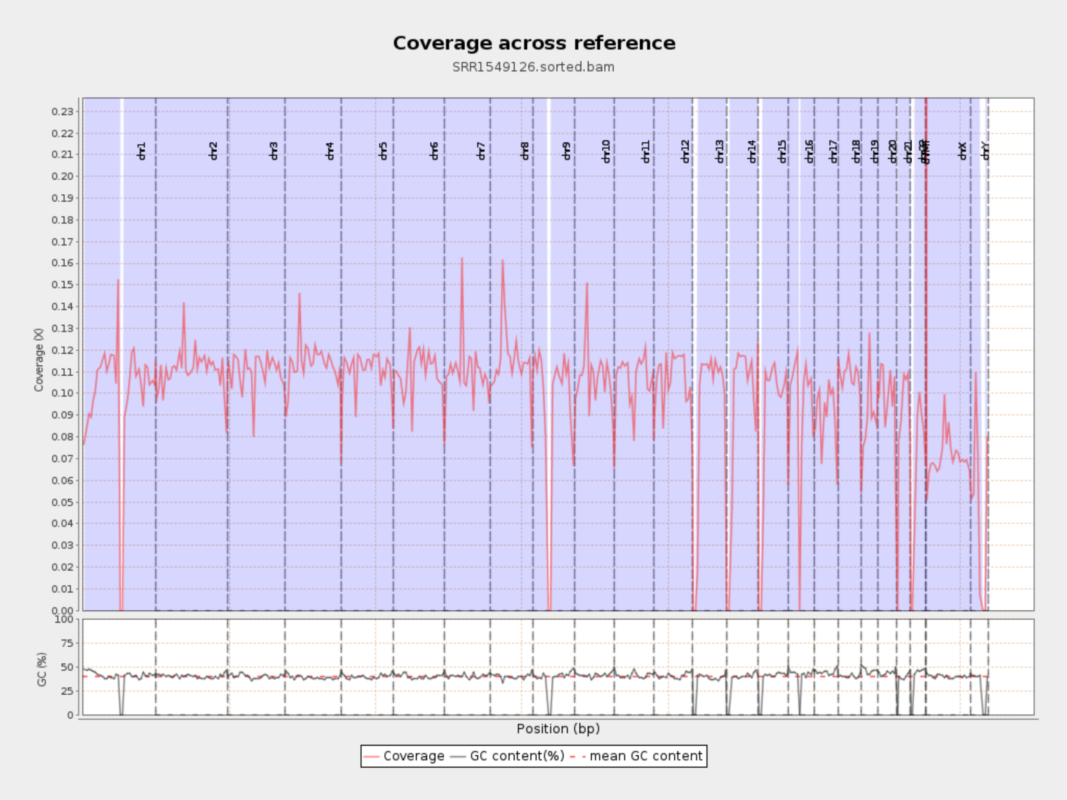
General error rate	0.31%
Mismatches	948,211
Insertions	7,912
Mapped reads with at least one insertion	0.1%
Deletions	22,799
Mapped reads with at least one deletion	0.29%
Homopolymer indels	44.47%

2.6. Chromosome stats

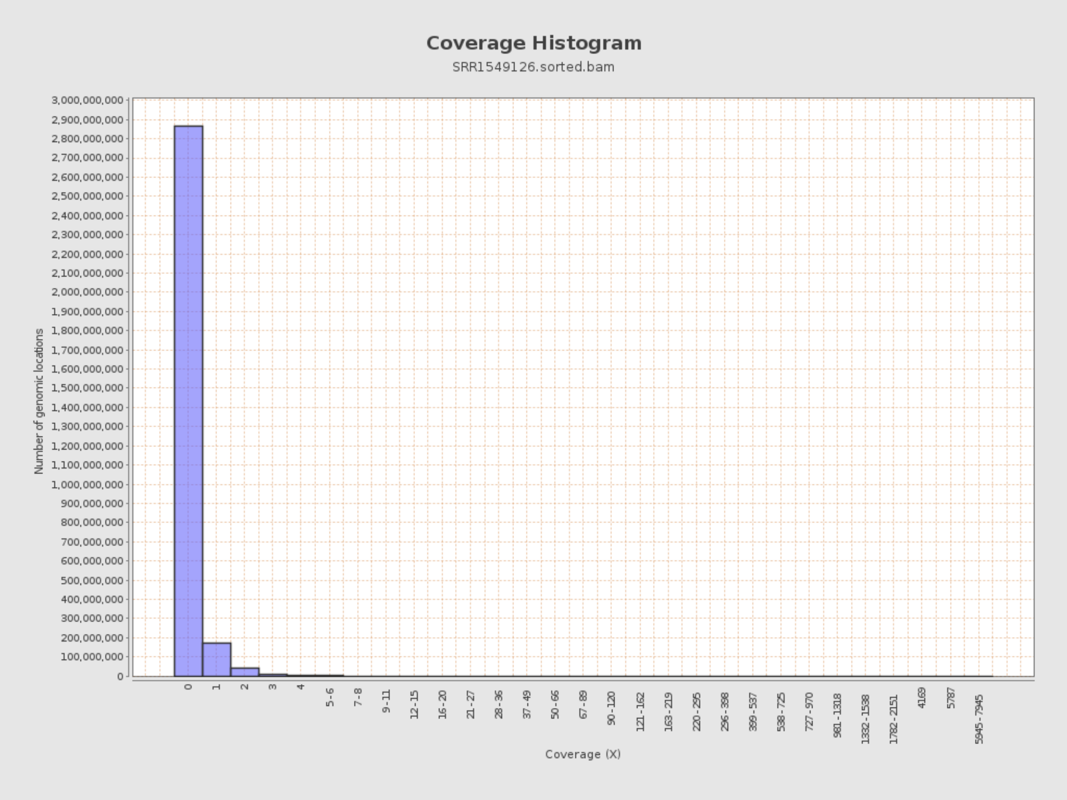
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24964999	0.1002	1.2048
chr2	243199373	27046348	0.1112	0.6091
chr3	198022430	21894406	0.1106	0.4288
chr4	191154276	21850522	0.1143	0.4813
chr5	180915260	20010012	0.1106	0.4349
chr6	171115067	18913449	0.1105	0.4749
chr7	159138663	17545681	0.1103	0.9123
chr8	146364022	16898653	0.1155	3.8919

chr9	141213431	13218590	0.0936	0.563
chr10	135534747	14631072	0.108	0.6271
chr11	135006516	14434727	0.1069	0.5447
chr12	133851895	14382270	0.1074	0.4411
chr13	115169878	10504376	0.0912	0.3873
chr14	107349540	9803422	0.0913	0.4916
chr15	102531392	8860543	0.0864	0.3773
chr16	90354753	8276985	0.0916	0.4332
chr17	81195210	7414474	0.0913	0.4176
chr18	78077248	8490717	0.1087	1.1086
chr19	59128983	5304856	0.0897	0.9492
chr20	63025520	6292233	0.0998	0.4356
chr21	48129895	4174918	0.0867	0.4593
chr22	51304566	3212602	0.0626	0.3427
chrMT	16571	44009	2.6558	3.2738
chrX	155270560	10985437	0.0708	0.413
chrY	59373566	2763319	0.0465	0.4578

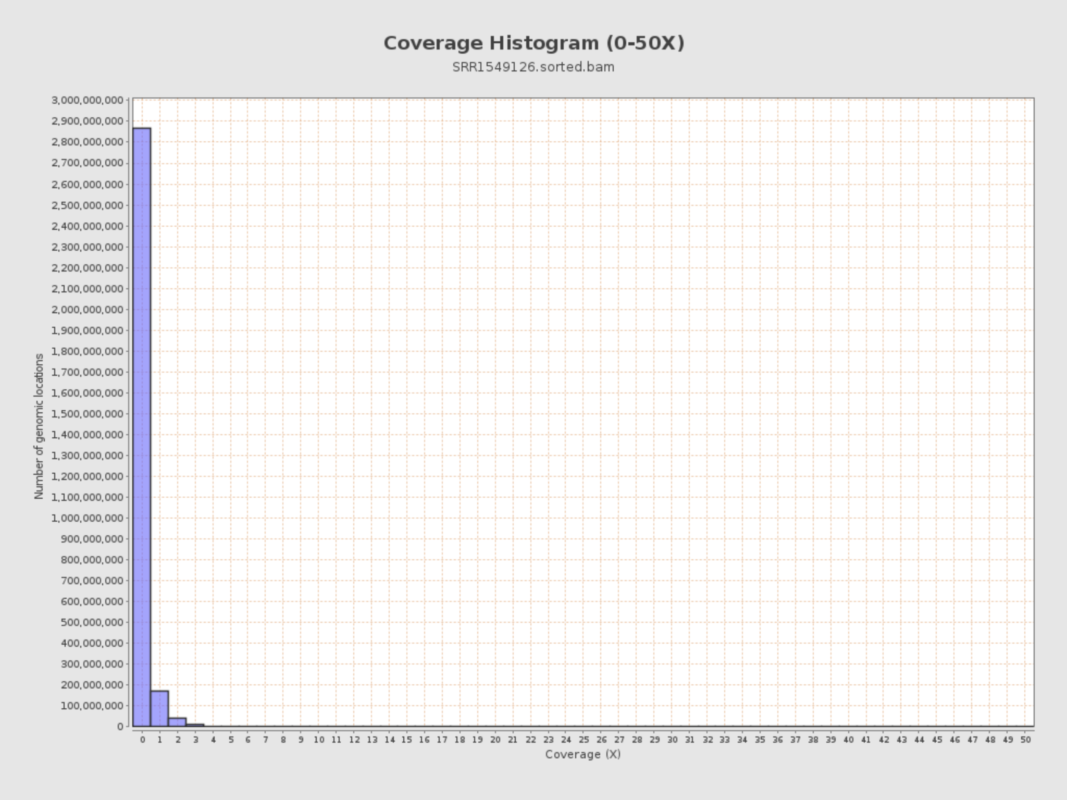
3. Results : Coverage across reference



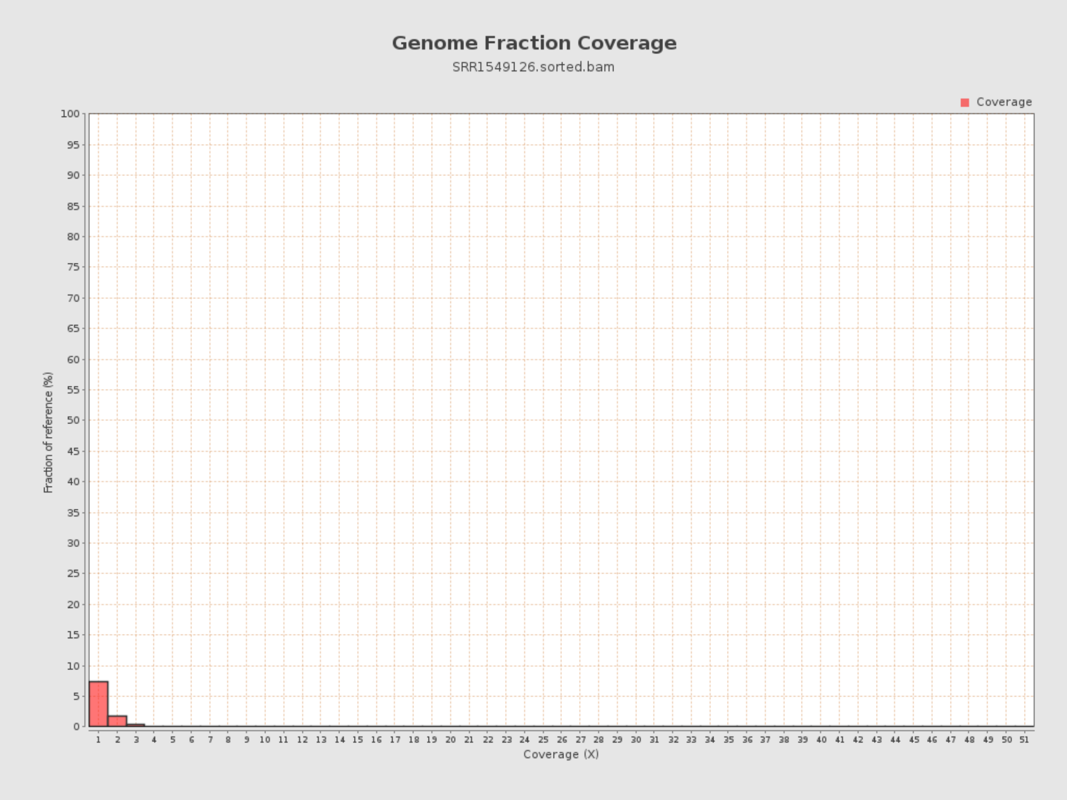
4. Results : Coverage Histogram



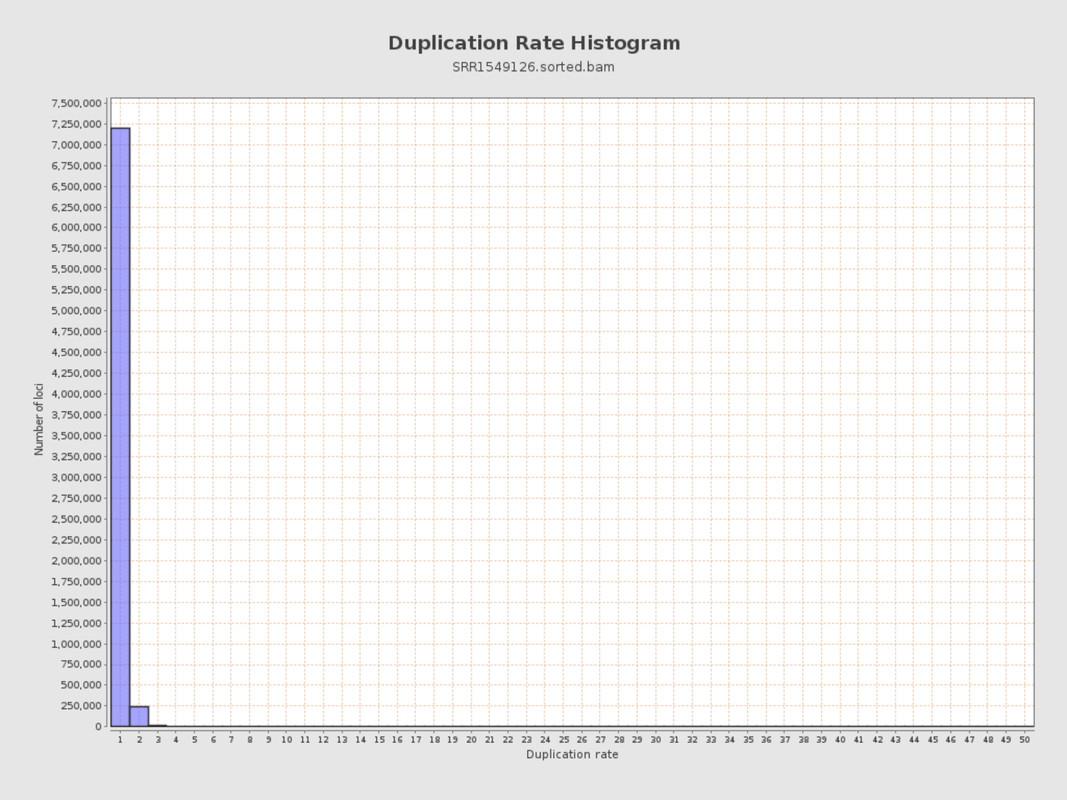
5. Results : Coverage Histogram (0-50X)



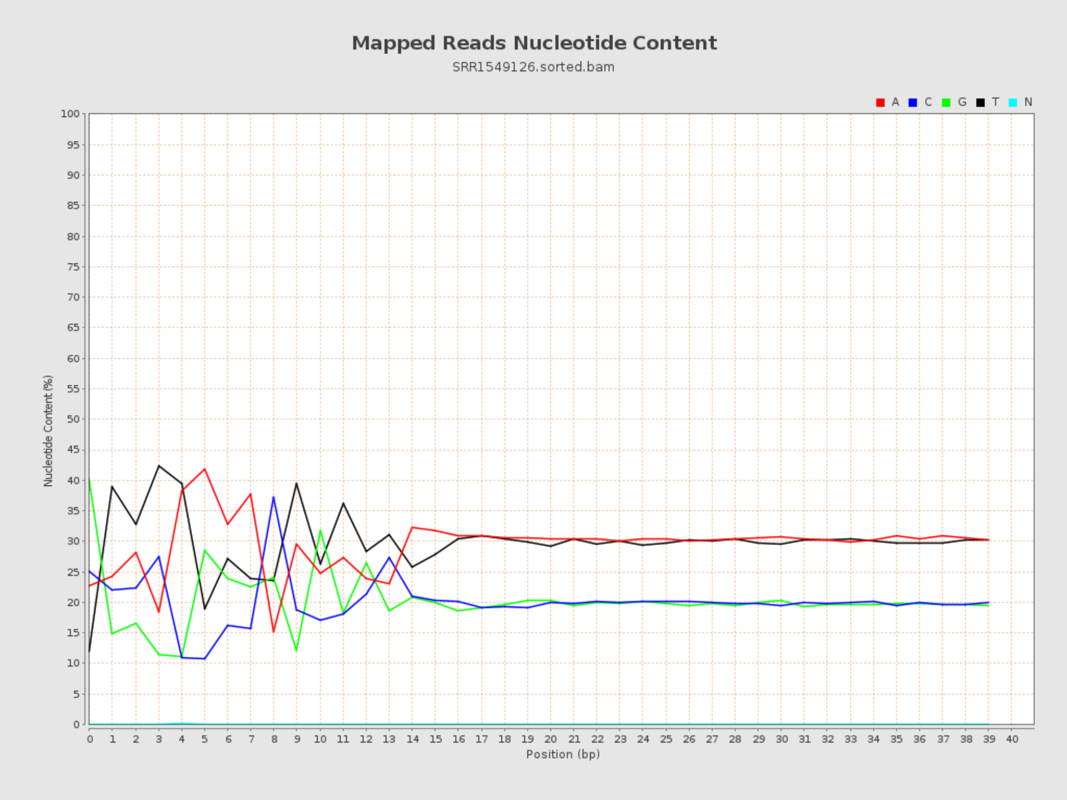
6. Results : Genome Fraction Coverage



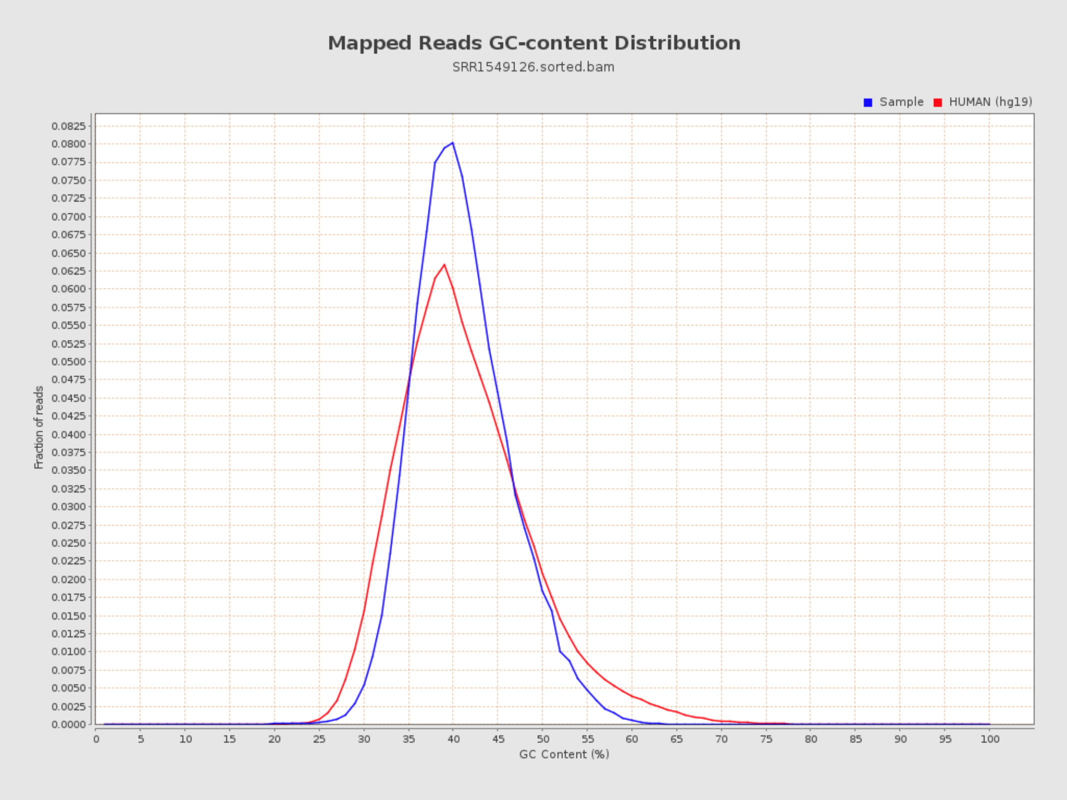
7. Results : Duplication Rate Histogram



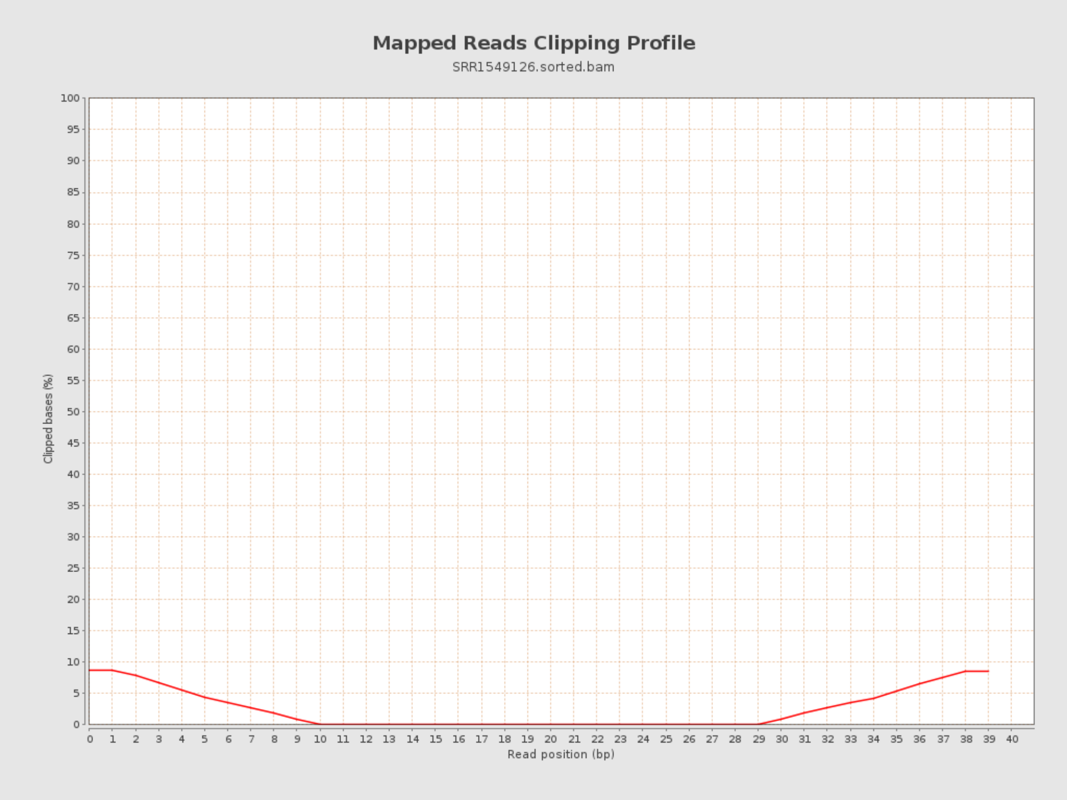
8. Results : Mapped Reads Nucleotide Content



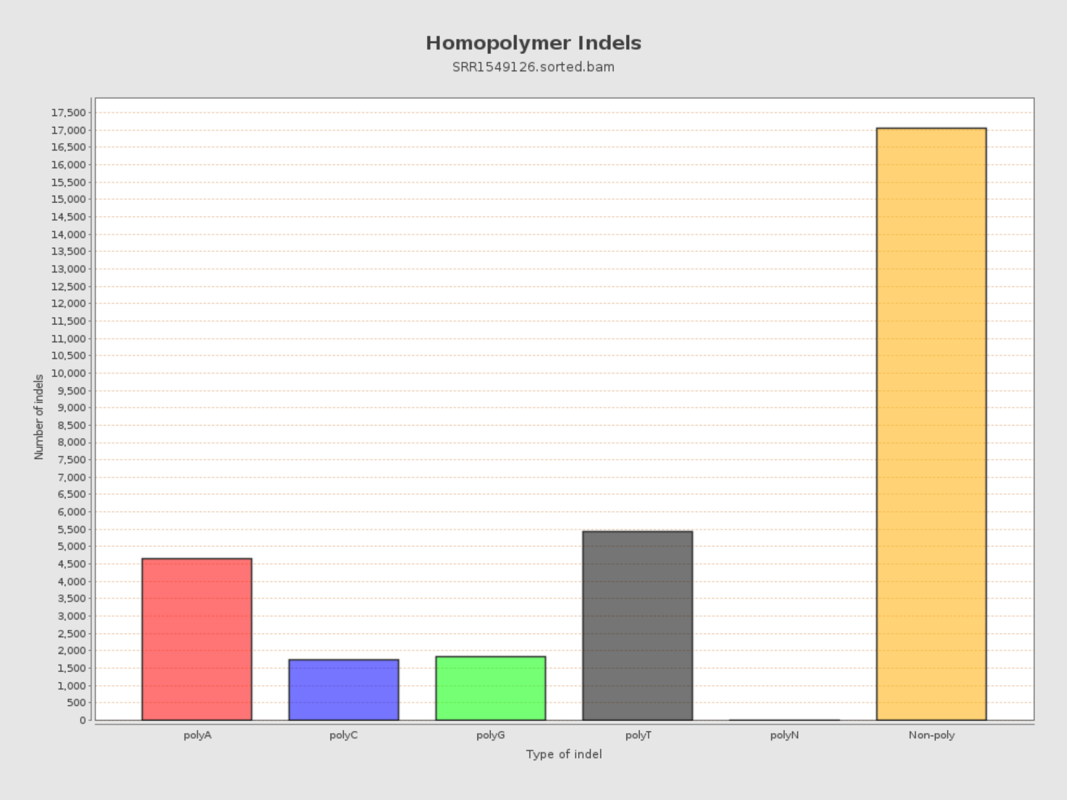
9. Results : Mapped Reads GC-content Distribution



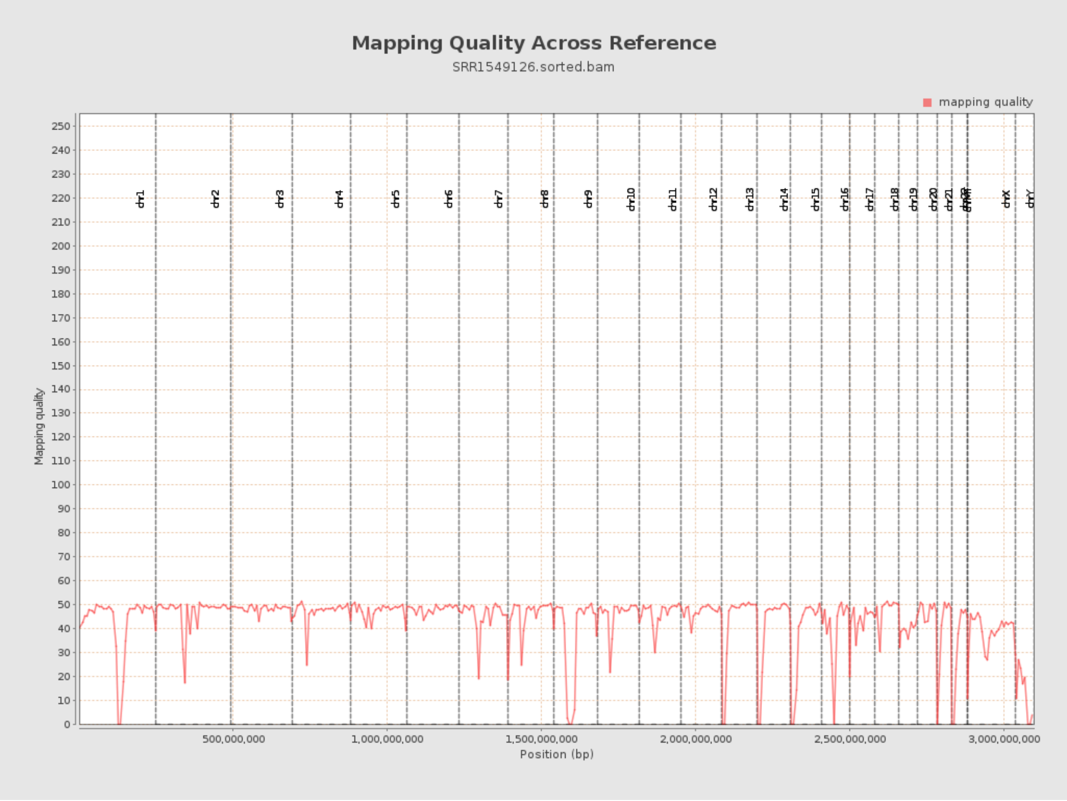
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram