Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:01:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083775.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_SRR3083775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:01:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,218,144
Mapped reads	1,188,119 / 53.56%
Unmapped reads	1,030,025 / 46.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,503 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	34,566 / 1.56%
Duplication rate	2.46%
Clipped reads	617,175 / 27.82%

2.2. ACGT Content

Number/percentage of A's	21,516,540 / 28.24%
Number/percentage of C's	14,127,211 / 18.54%
Number/percentage of T's	23,413,143 / 30.73%
Number/percentage of G's	17,137,409 / 22.49%
Number/percentage of N's	844 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2024

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

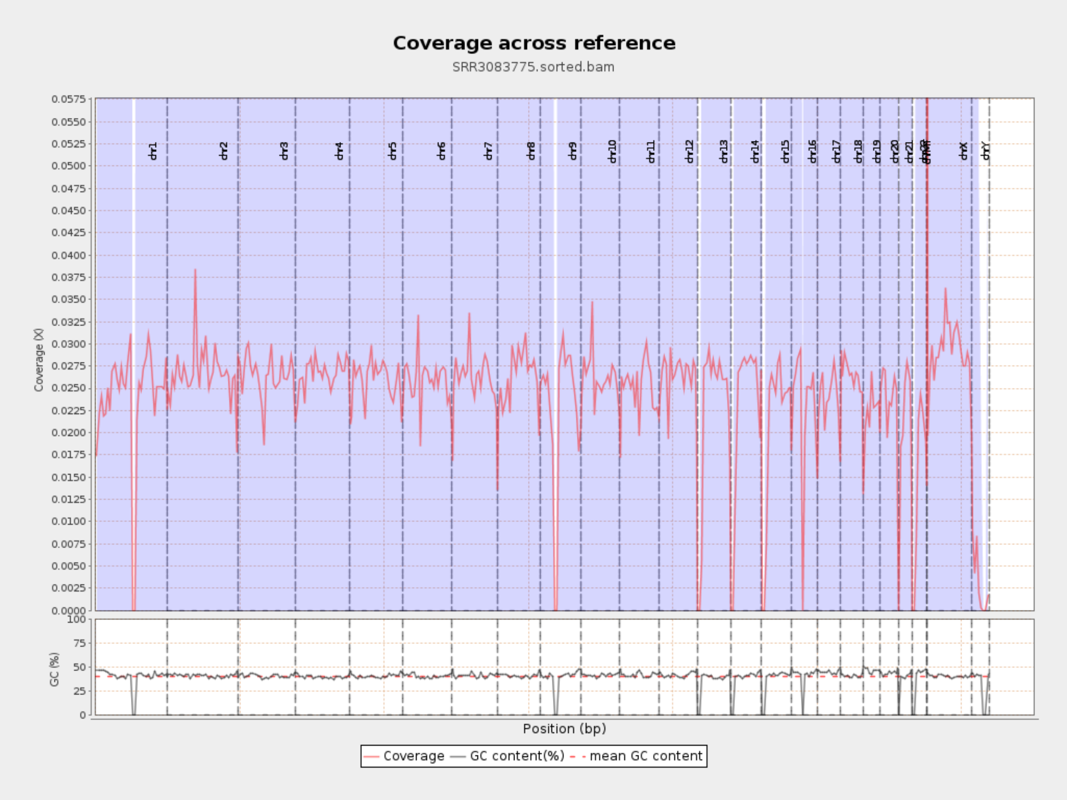
General error rate	0.85%
Mismatches	640,110
Insertions	5,651
Mapped reads with at least one insertion	0.47%
Deletions	16,004
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.19%

2.6. Chromosome stats

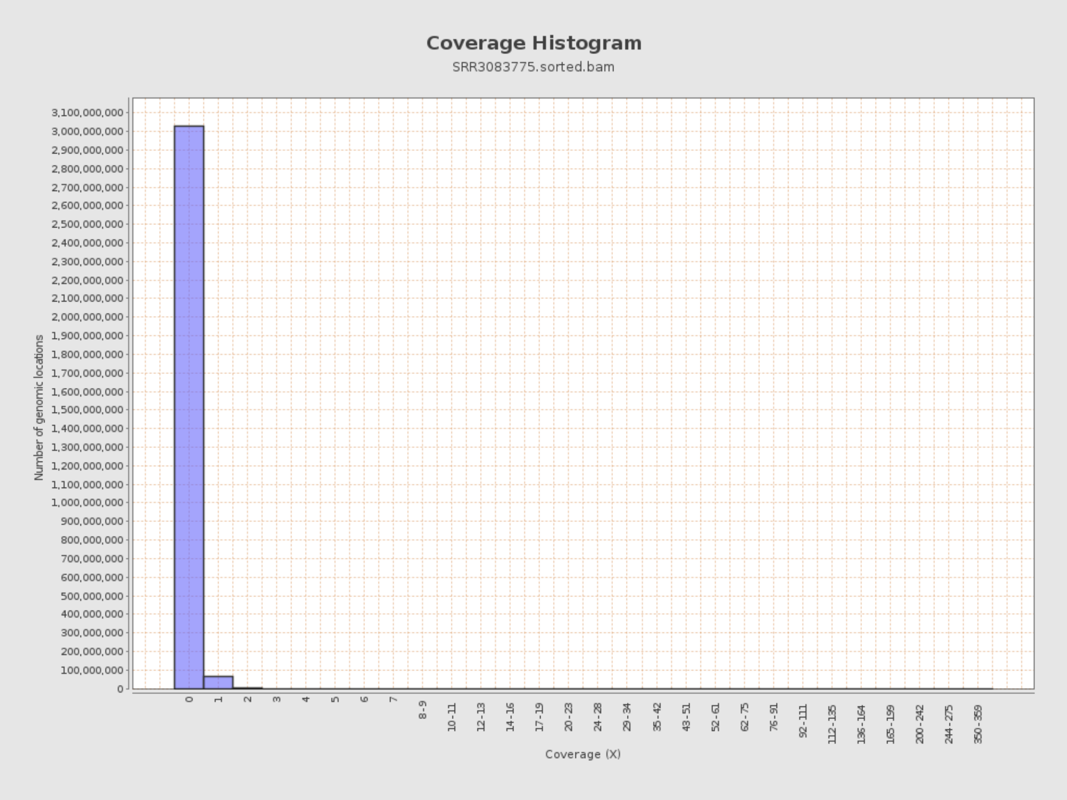
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5939610	0.0238	0.2556
chr2	243199373	6511494	0.0268	0.2595
chr3	198022430	5242365	0.0265	0.1748
chr4	191154276	5082495	0.0266	0.1791
chr5	180915260	4730871	0.0261	0.1745
chr6	171115067	4424818	0.0259	0.1878
chr7	159138663	4177871	0.0263	0.2255

chr8	146364022	3863403	0.0264	0.2139
chr9	141213431	3218143	0.0228	0.1929
chr10	135534747	3567016	0.0263	0.205
chr11	135006516	3406744	0.0252	0.1944
chr12	133851895	3547497	0.0265	0.1769
chr13	115169878	2557881	0.0222	0.1614
chr14	107349540	2396770	0.0223	0.165
chr15	102531392	2110705	0.0206	0.1572
chr16	90354753	2024407	0.0224	0.1708
chr17	81195210	1949433	0.024	0.1799
chr18	78077248	2074582	0.0266	0.3219
chr19	59128983	1322437	0.0224	0.2167
chr20	63025520	1504811	0.0239	0.1715
chr21	48129895	1001122	0.0208	0.1588
chr22	51304566	769517	0.015	0.1314
chrMT	16571	88594	5.3463	3.6681
chrX	155270560	4532809	0.0292	0.1943
chrY	59373566	175117	0.0029	0.0732

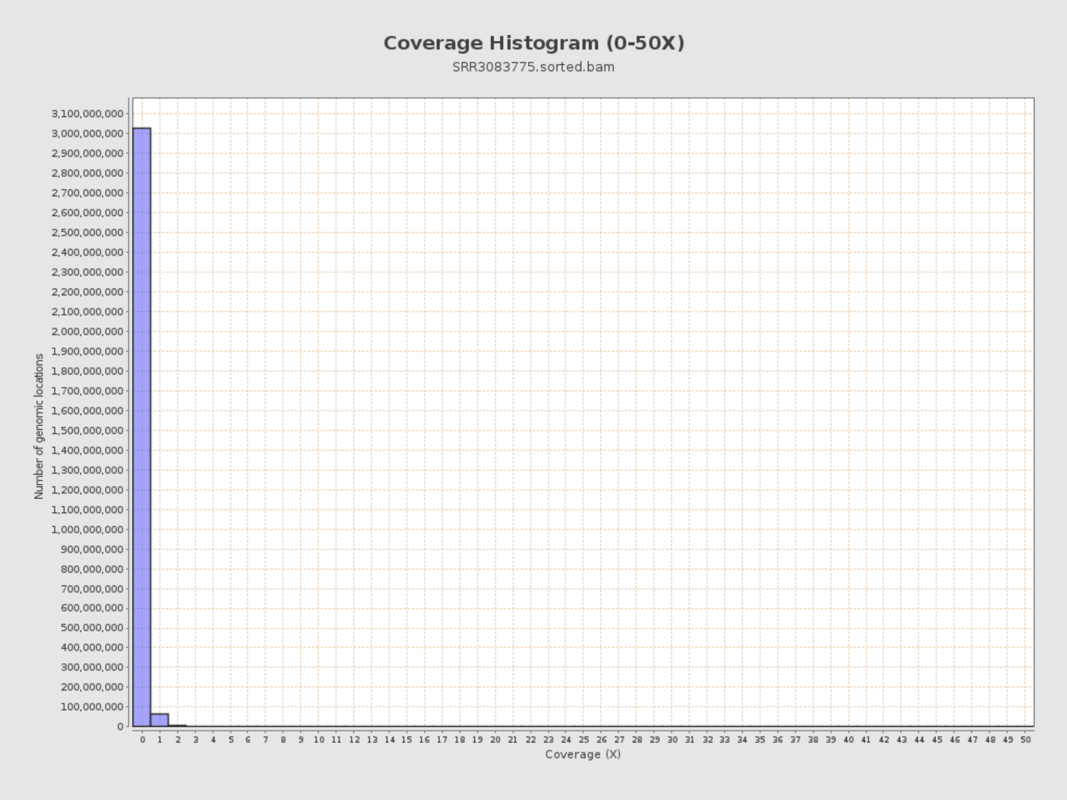
3. Results : Coverage across reference



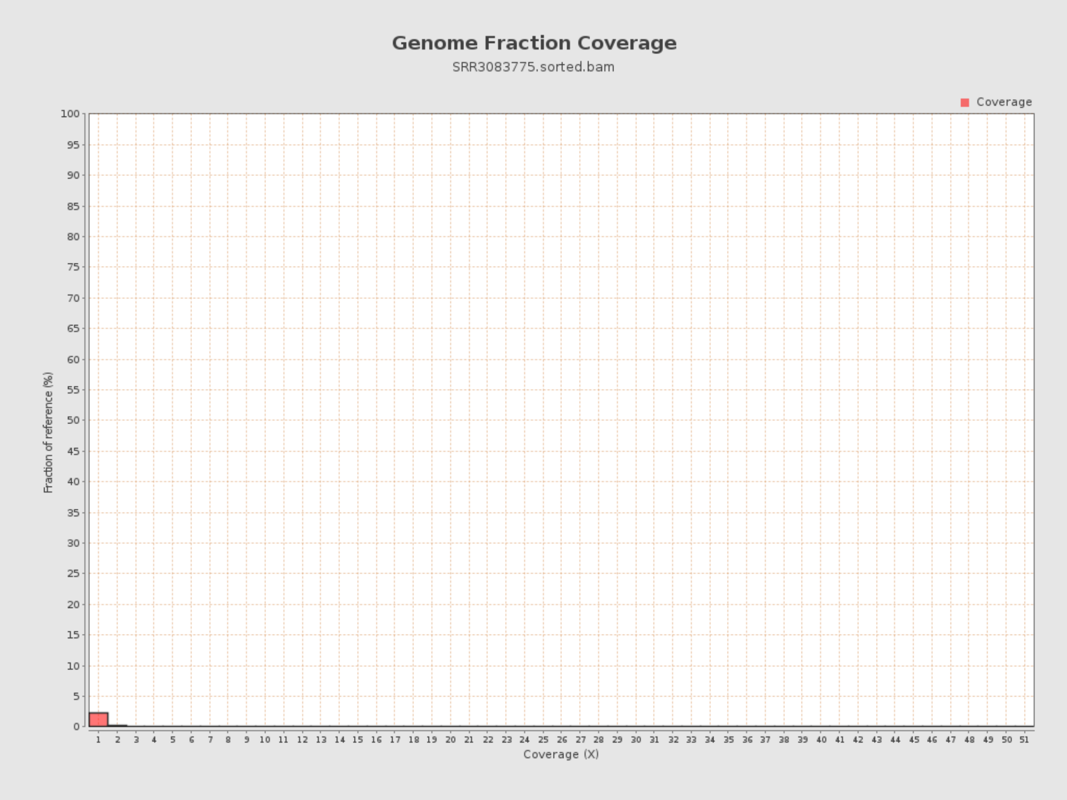
4. Results : Coverage Histogram



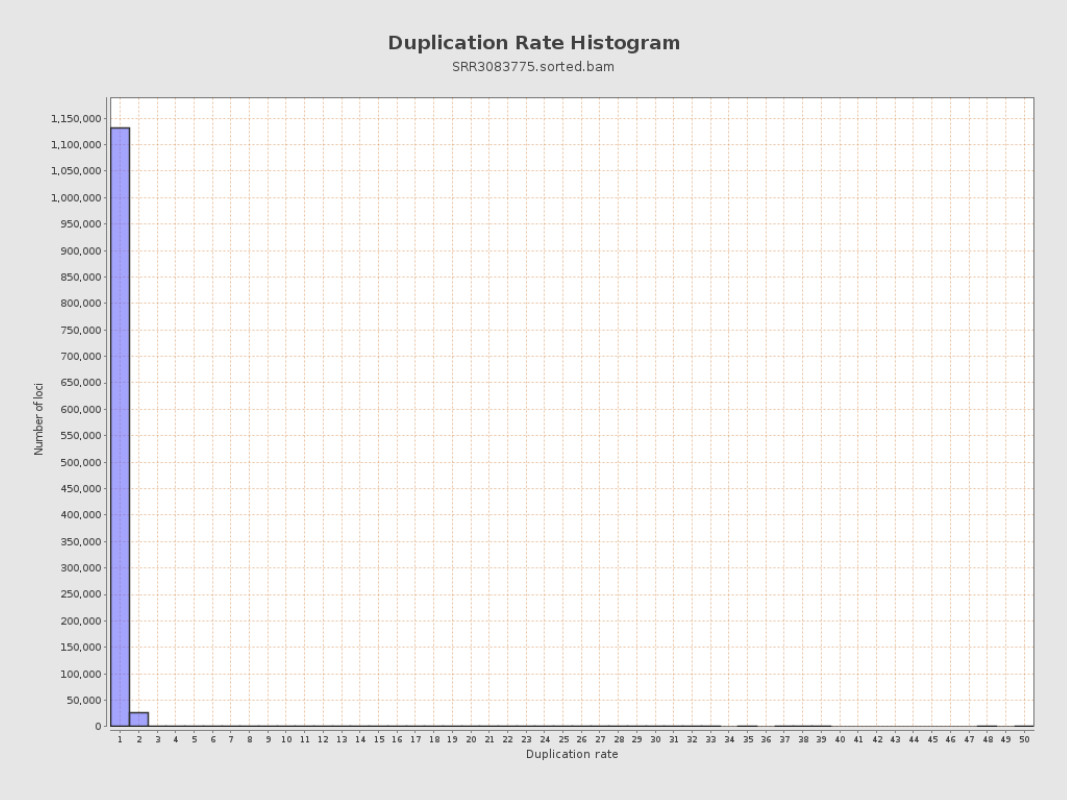
5. Results : Coverage Histogram (0-50X)



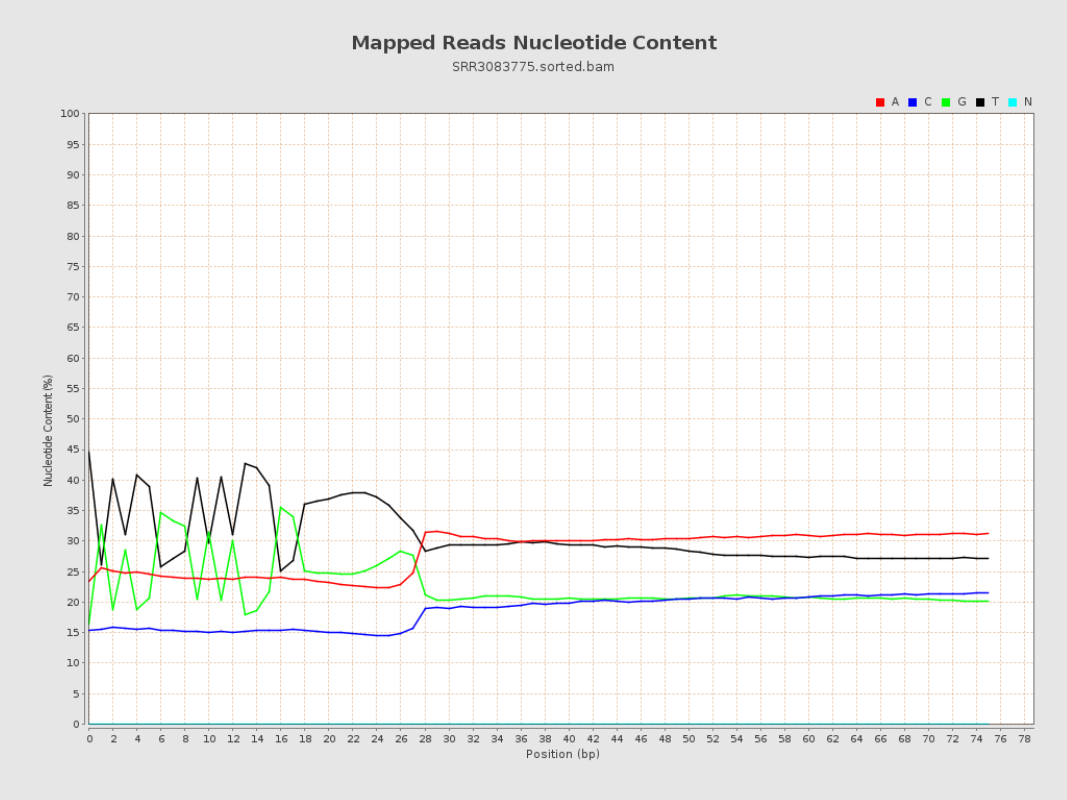
6. Results : Genome Fraction Coverage



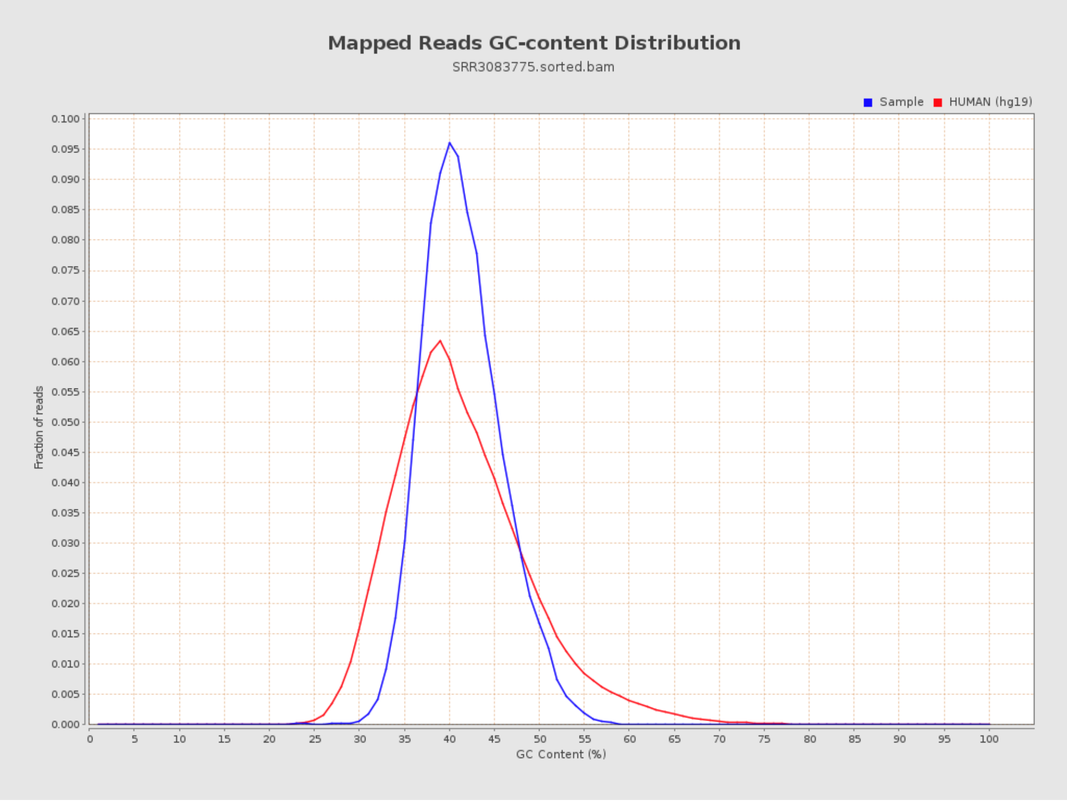
7. Results : Duplication Rate Histogram



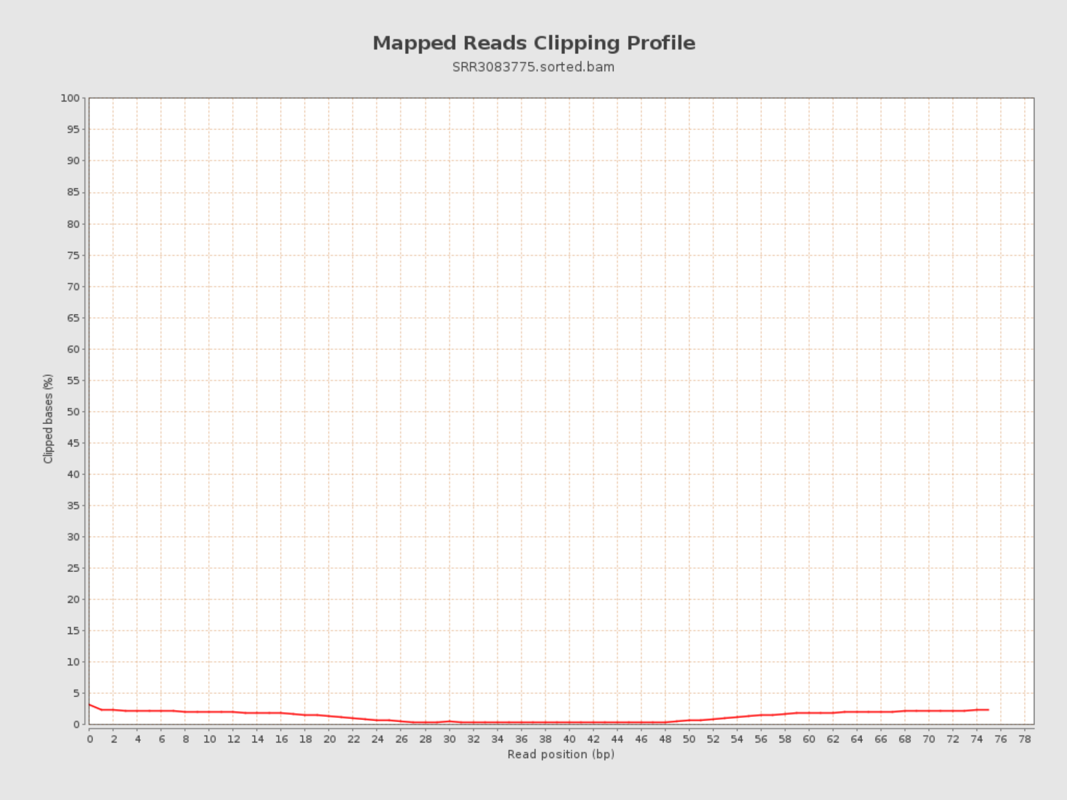
8. Results : Mapped Reads Nucleotide Content



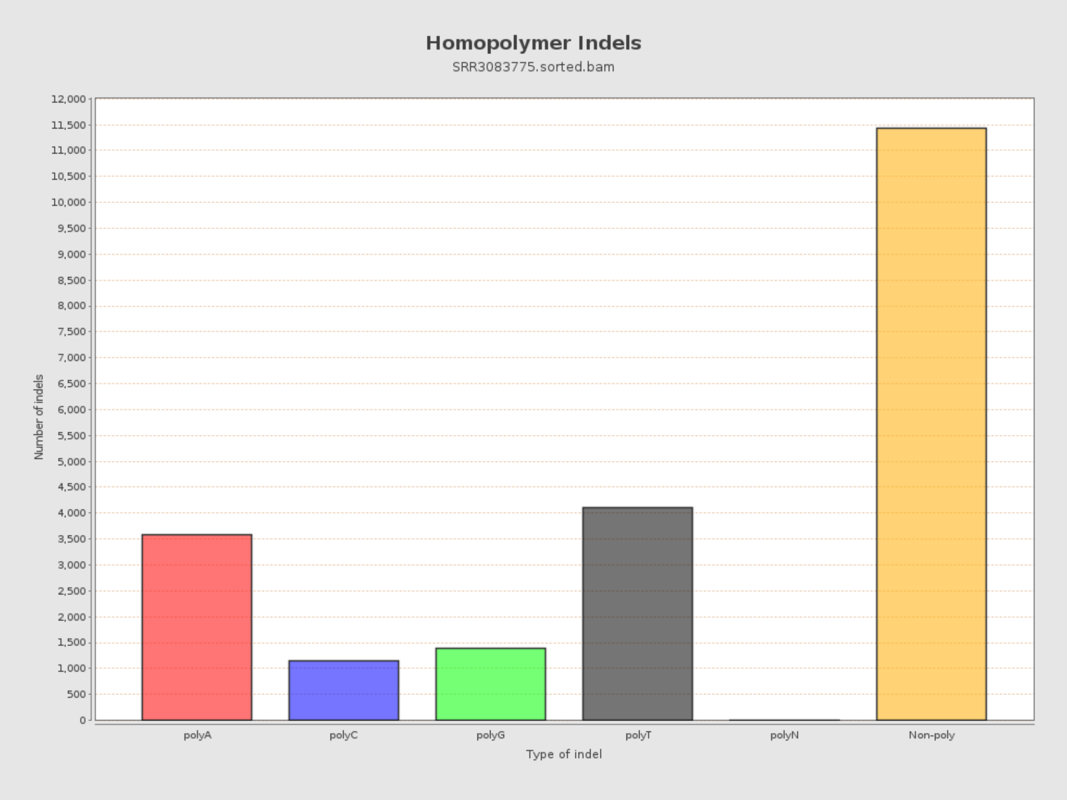
9. Results : Mapped Reads GC-content Distribution



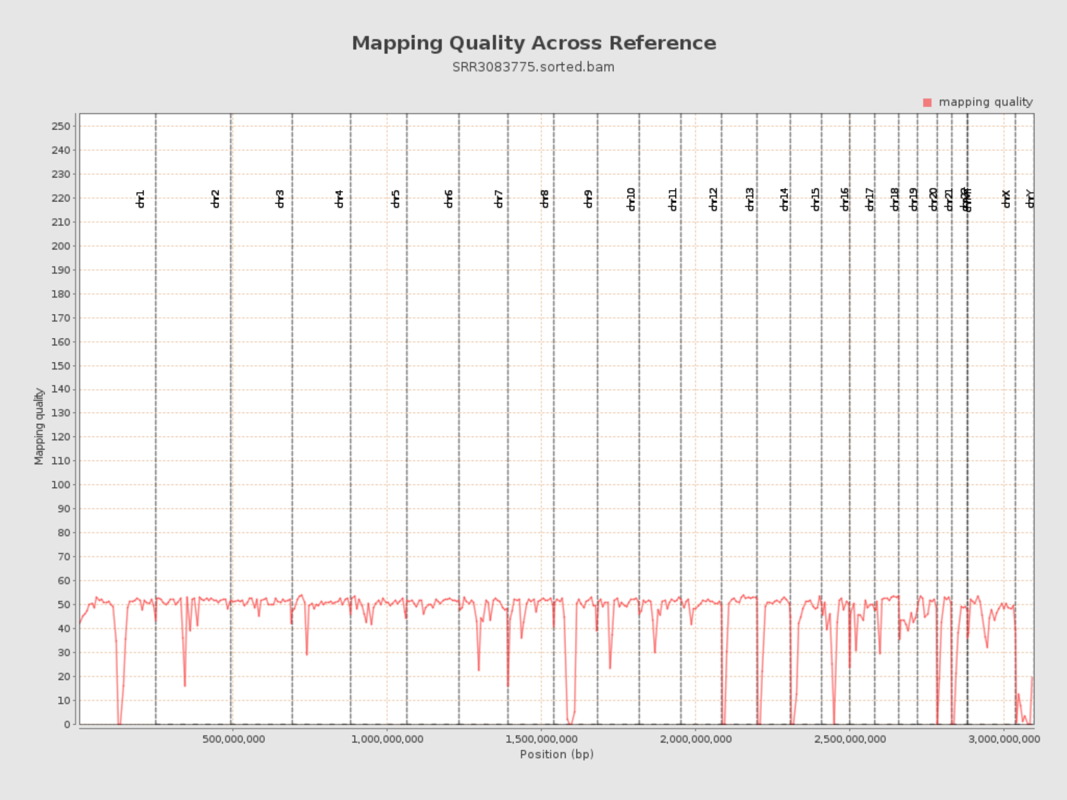
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram