Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:42:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083753.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_SRR3083753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:42:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,696,497
Mapped reads	1,251,226 / 73.75%
Unmapped reads	445,271 / 26.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,569 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	29,452 / 1.74%
Duplication rate	1.68%
Clipped reads	689,589 / 40.65%

2.2. ACGT Content

Number/percentage of A's	23,462,453 / 29.53%
Number/percentage of C's	15,167,713 / 19.09%
Number/percentage of T's	22,630,478 / 28.48%
Number/percentage of G's	18,189,347 / 22.89%
Number/percentage of N's	10,883 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2811

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

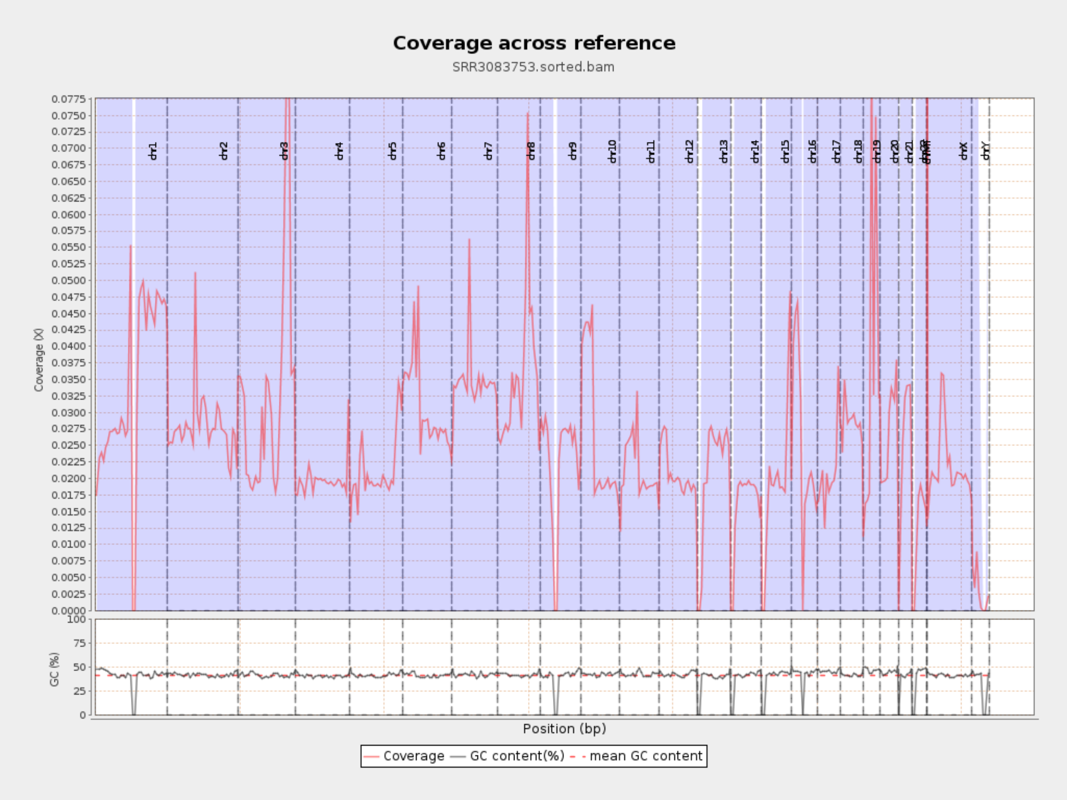
General error rate	0.85%
Mismatches	666,030
Insertions	5,789
Mapped reads with at least one insertion	0.46%
Deletions	13,538
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.43%

2.6. Chromosome stats

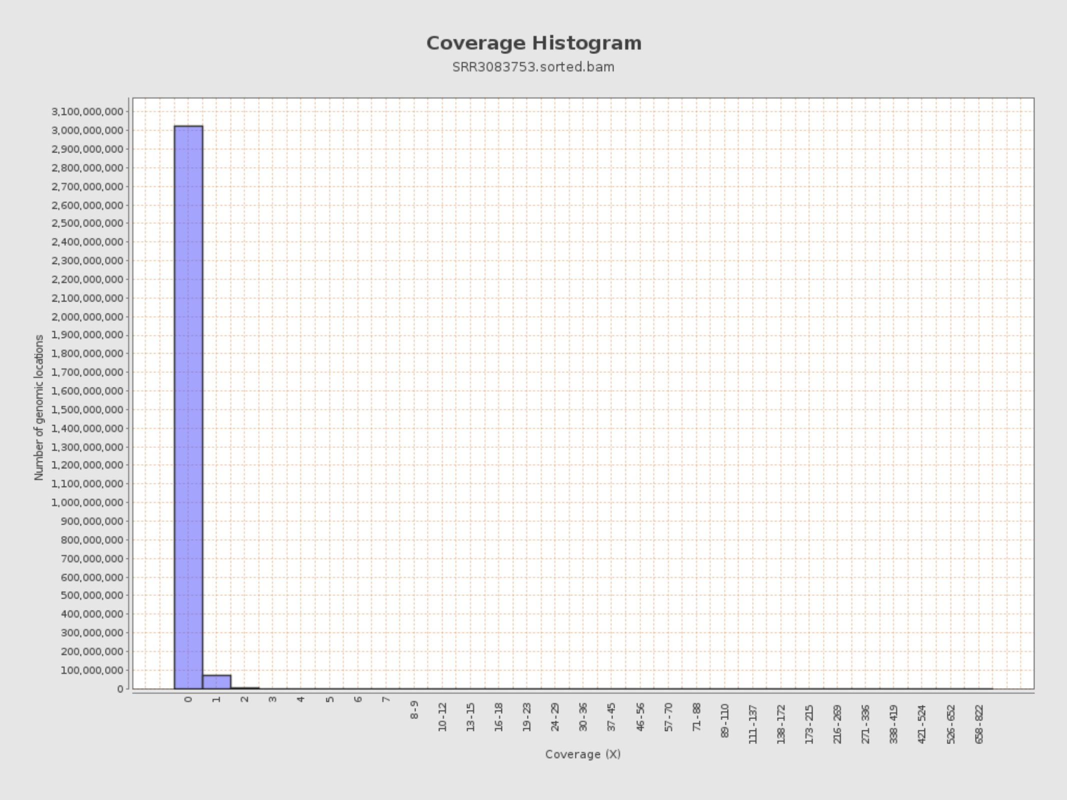
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8401099	0.0337	0.6436
chr2	243199373	6795569	0.0279	0.2448
chr3	198022430	6480899	0.0327	0.1887
chr4	191154276	3776883	0.0198	0.1479
chr5	180915260	3840573	0.0212	0.1516
chr6	171115067	5313188	0.0311	0.2259
chr7	159138663	5562342	0.035	0.4272

chr8	146364022	5249826	0.0359	0.2585
chr9	141213431	3153988	0.0223	0.1957
chr10	135534747	3641359	0.0269	0.2505
chr11	135006516	2897827	0.0215	0.186
chr12	133851895	2786337	0.0208	0.1502
chr13	115169878	2382702	0.0207	0.1479
chr14	107349540	1691228	0.0158	0.1336
chr15	102531392	2012621	0.0196	0.1455
chr16	90354753	2221309	0.0246	0.172
chr17	81195210	1706633	0.021	0.1581
chr18	78077248	2229341	0.0286	0.3656
chr19	59128983	2231082	0.0377	0.4488
chr20	63025520	1676414	0.0266	0.172
chr21	48129895	1215303	0.0253	0.1677
chr22	51304566	630352	0.0123	0.1142
chrMT	16571	7521	0.4539	0.751
chrX	155270560	3409193	0.022	0.1662
chrY	59373566	168984	0.0028	0.0703

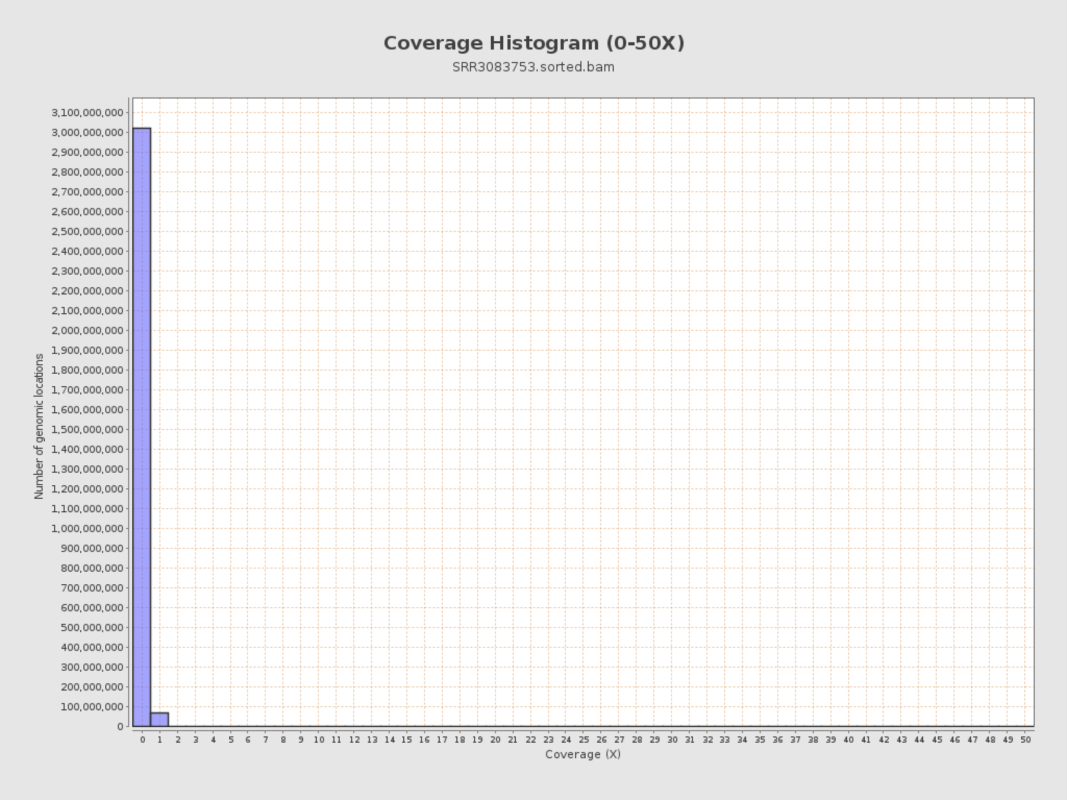
3. Results : Coverage across reference



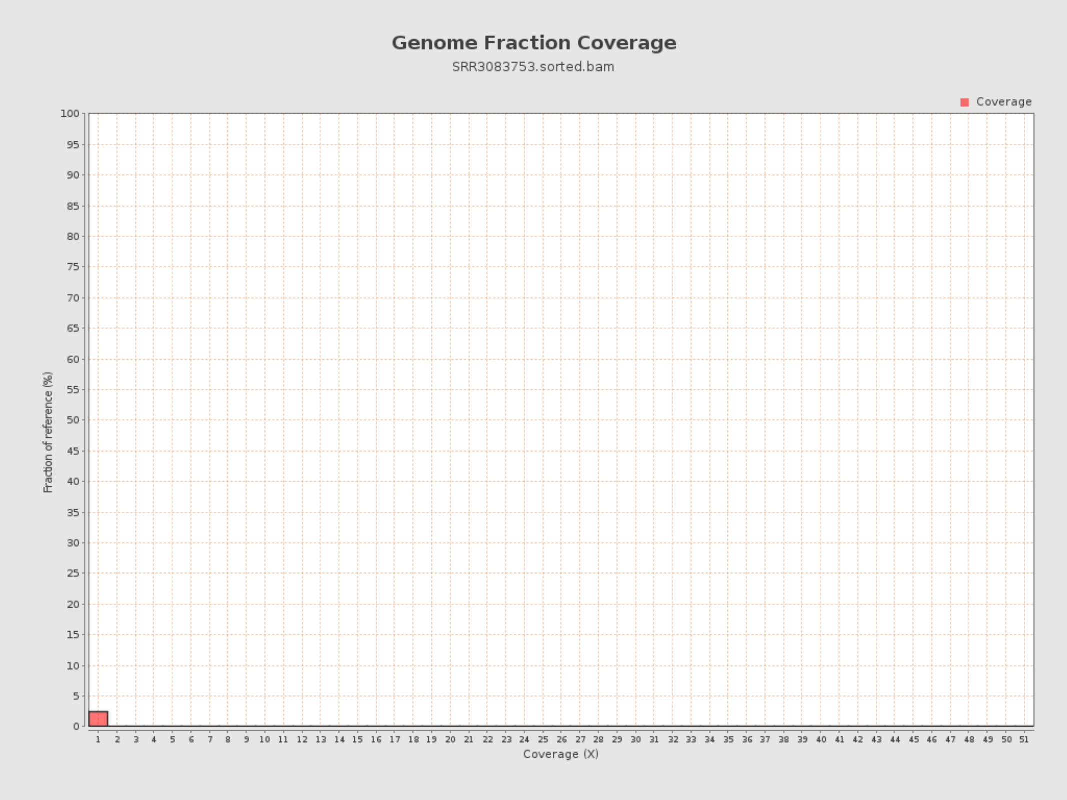
4. Results : Coverage Histogram



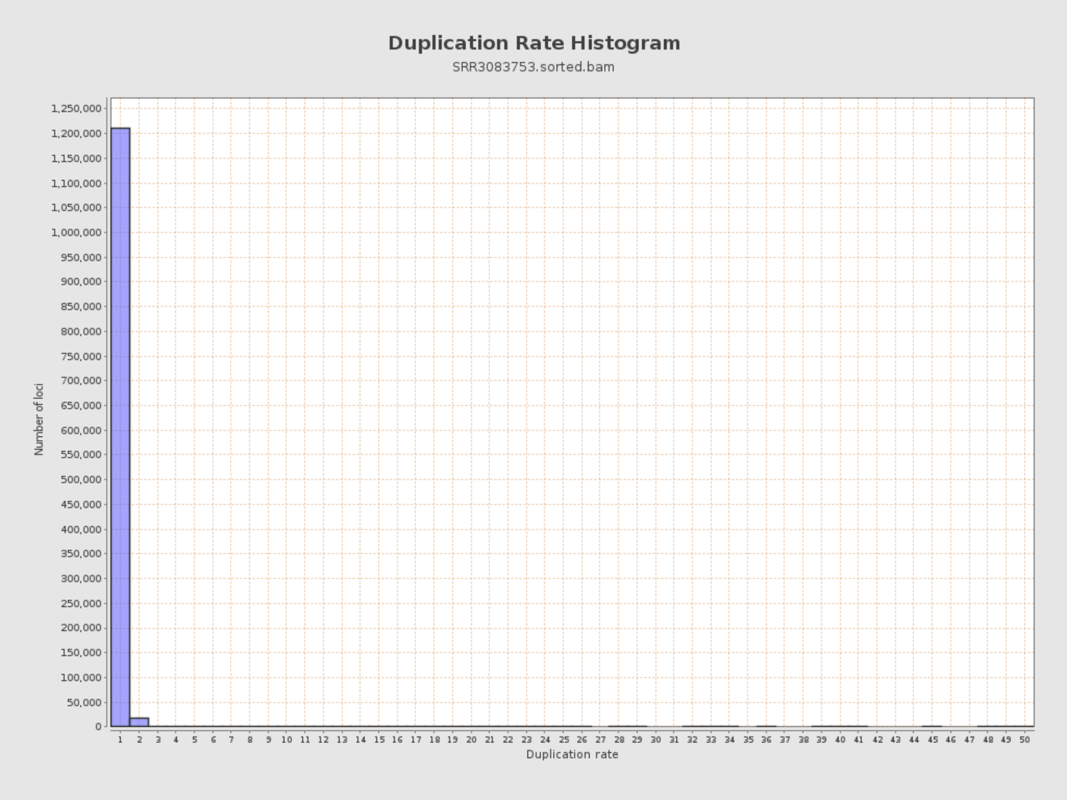
5. Results : Coverage Histogram (0-50X)



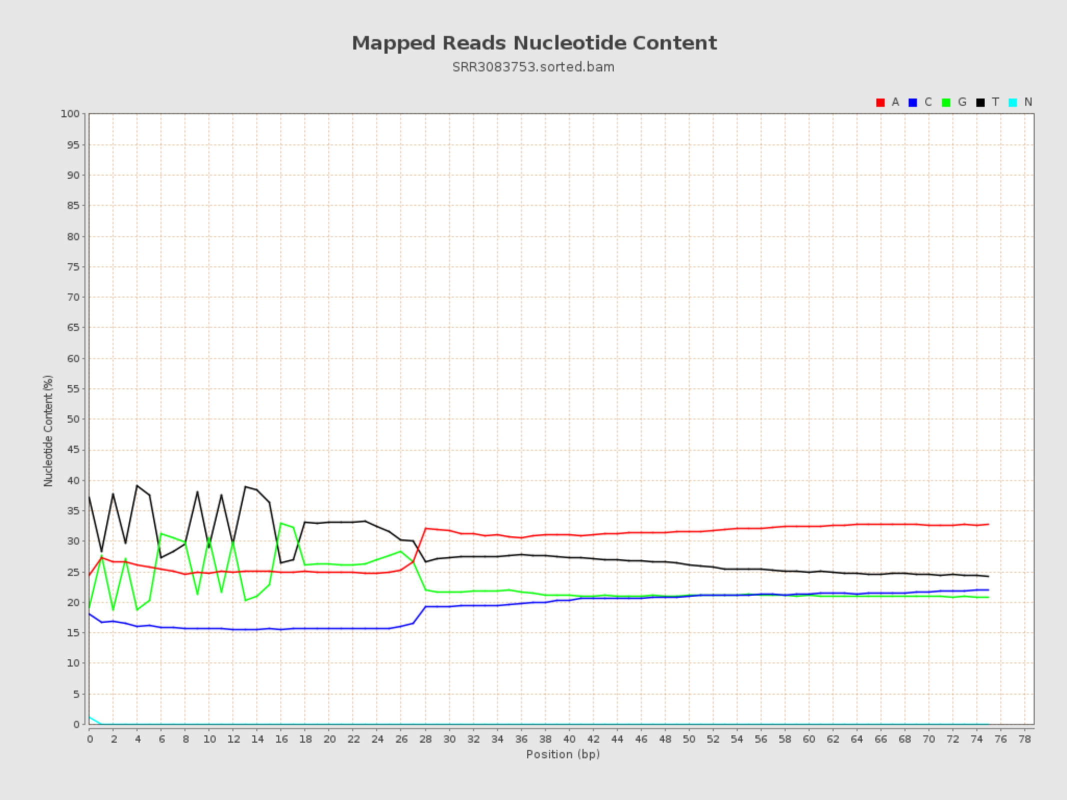
6. Results : Genome Fraction Coverage



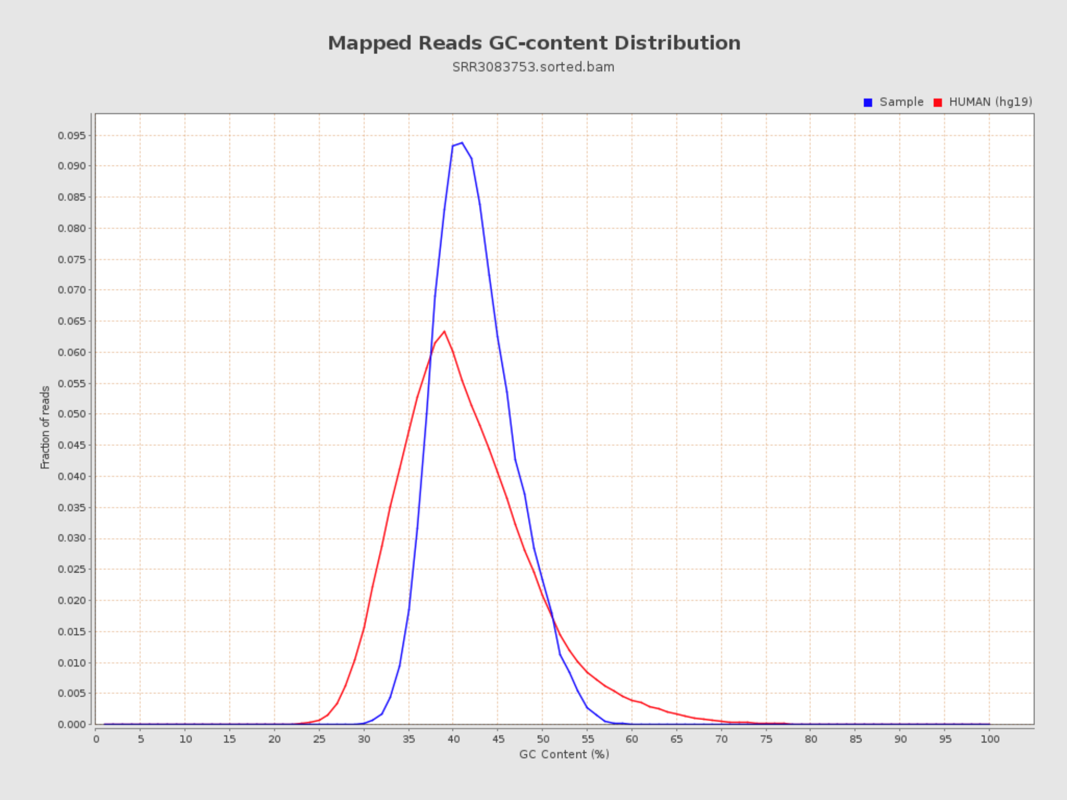
7. Results : Duplication Rate Histogram



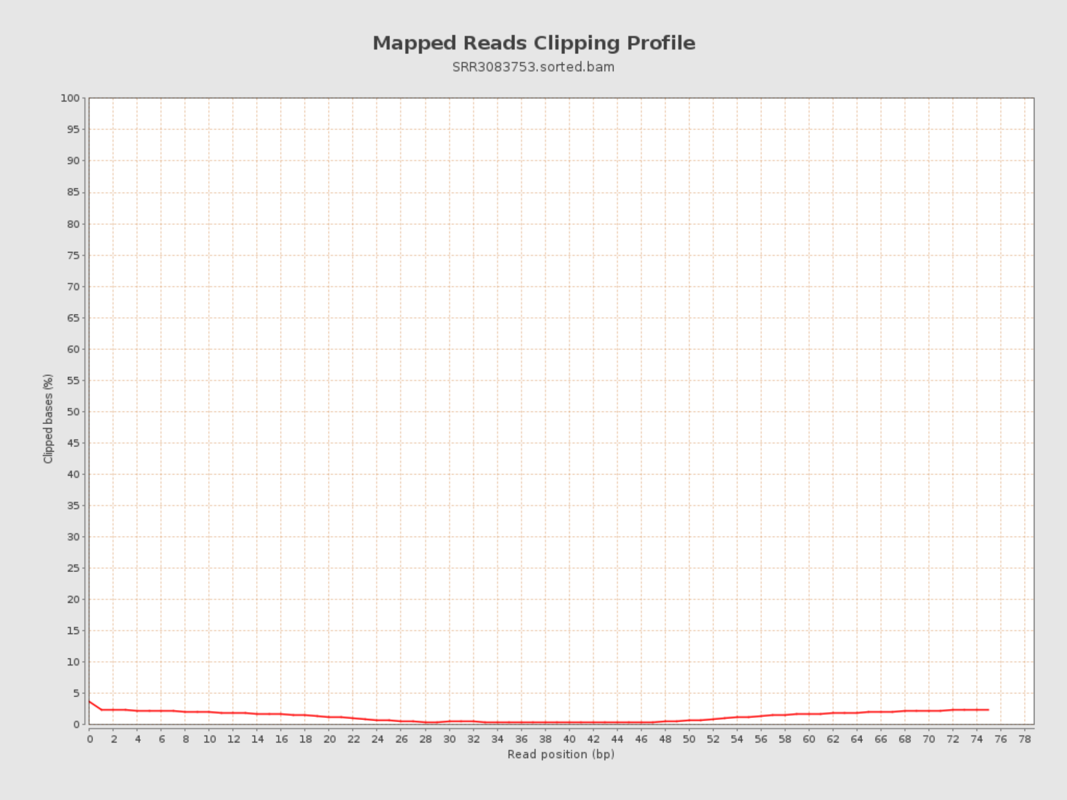
8. Results : Mapped Reads Nucleotide Content



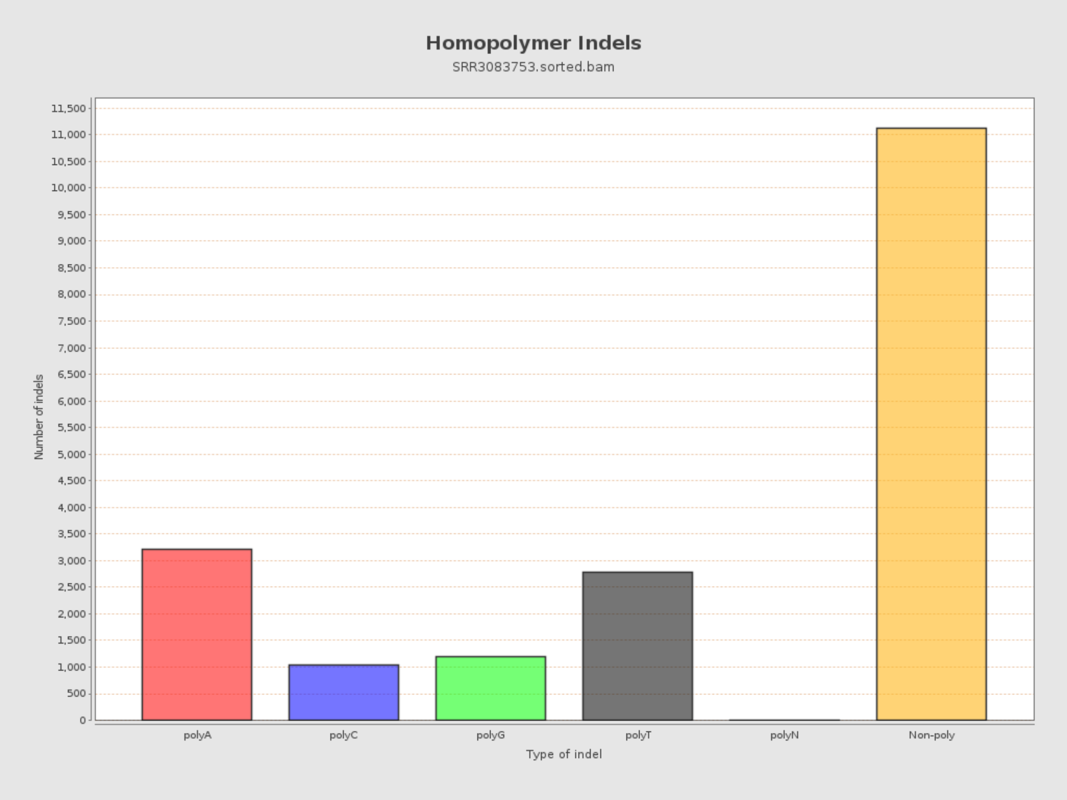
9. Results : Mapped Reads GC-content Distribution



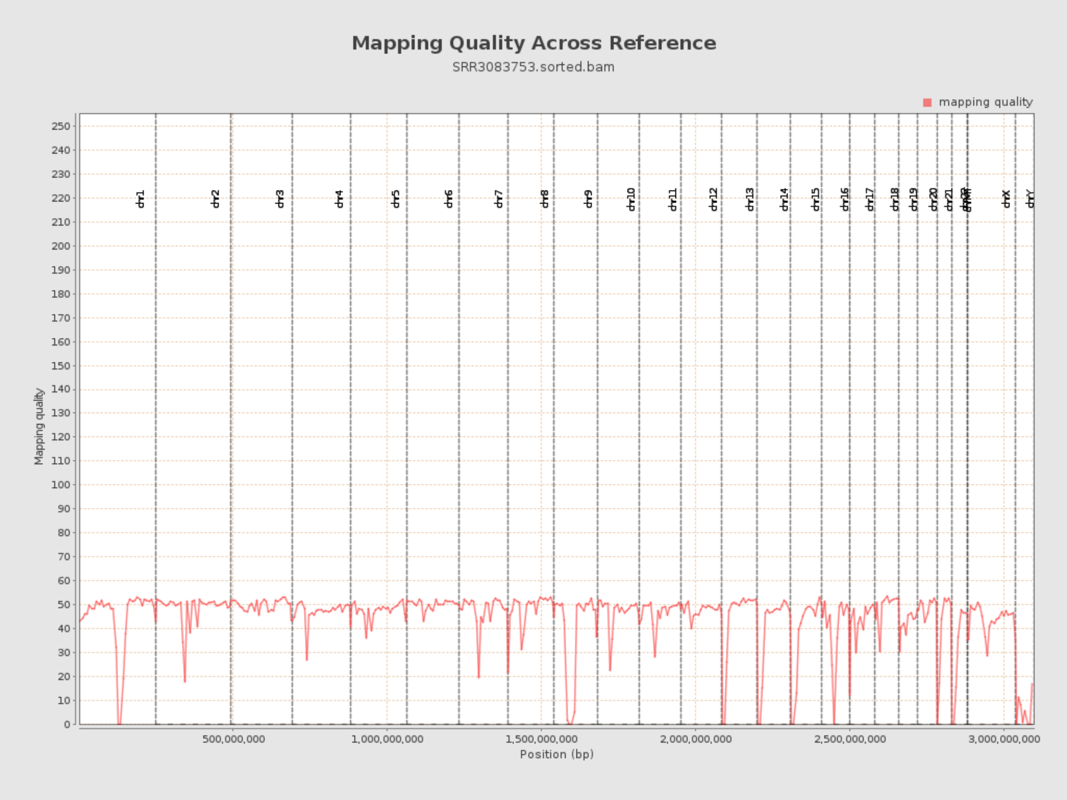
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram