Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818753.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_SRR1818753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:23:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,041,565
Mapped reads	2,969,657 / 97.64%
Unmapped reads	71,908 / 2.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,916 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	1,679,951 / 55.23%
Duplication rate	47.26%
Clipped reads	2,965,079 / 97.49%

2.2. ACGT Content

Number/percentage of A's	58,557,599 / 29.04%
Number/percentage of C's	42,702,866 / 21.18%
Number/percentage of T's	55,309,714 / 27.43%
Number/percentage of G's	45,064,962 / 22.35%
Number/percentage of N's	12,266 / 0.01%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0652

Standard Deviation	0.7947

2.4. Mapping Quality

Mean Mapping Quality	47.74

2.5. Mismatches and indels

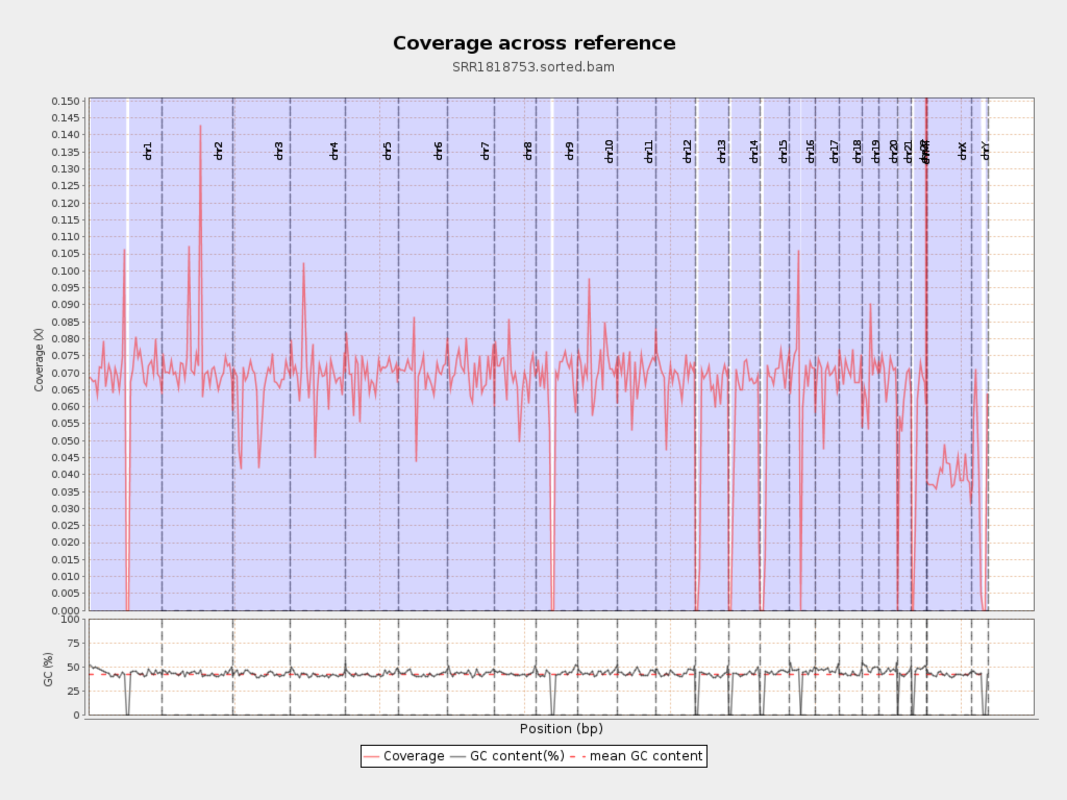
General error rate	0.54%
Mismatches	1,023,656
Insertions	28,816
Mapped reads with at least one insertion	0.96%
Deletions	53,243
Mapped reads with at least one deletion	1.77%
Homopolymer indels	37.44%

2.6. Chromosome stats

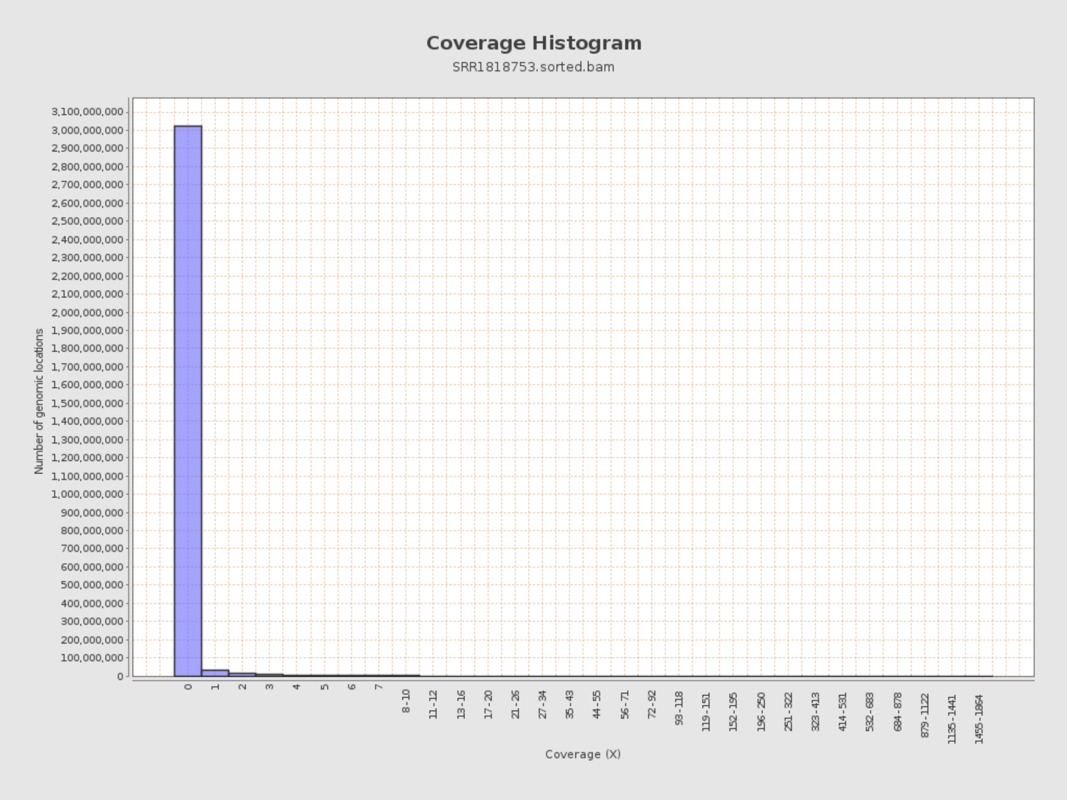
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16801196	0.0674	1.1309
chr2	243199373	17970468	0.0739	1.3047
chr3	198022430	12973896	0.0655	0.5568
chr4	191154276	13357090	0.0699	0.6906
chr5	180915260	12632046	0.0698	0.5943
chr6	171115067	11973324	0.07	0.649
chr7	159138663	11193470	0.0703	0.672

chr8	146364022	10199526	0.0697	0.6593
chr9	141213431	8717319	0.0617	0.644
chr10	135534747	9759423	0.072	0.8152
chr11	135006516	9452846	0.07	0.6553
chr12	133851895	9186827	0.0686	0.6222
chr13	115169878	6527726	0.0567	0.5202
chr14	107349540	6090397	0.0567	0.5842
chr15	102531392	5799385	0.0566	0.5266
chr16	90354753	6084580	0.0673	0.9246
chr17	81195210	5492573	0.0676	0.6083
chr18	78077248	5528953	0.0708	0.8518
chr19	59128983	4062242	0.0687	0.9978
chr20	63025520	4392362	0.0697	0.6197
chr21	48129895	2732553	0.0568	0.544
chr22	51304566	2411501	0.047	0.5453
chrMT	16571	163830	9.8865	10.8513
chrX	155270560	6201774	0.0399	0.494
chrY	59373566	2027890	0.0342	1.452

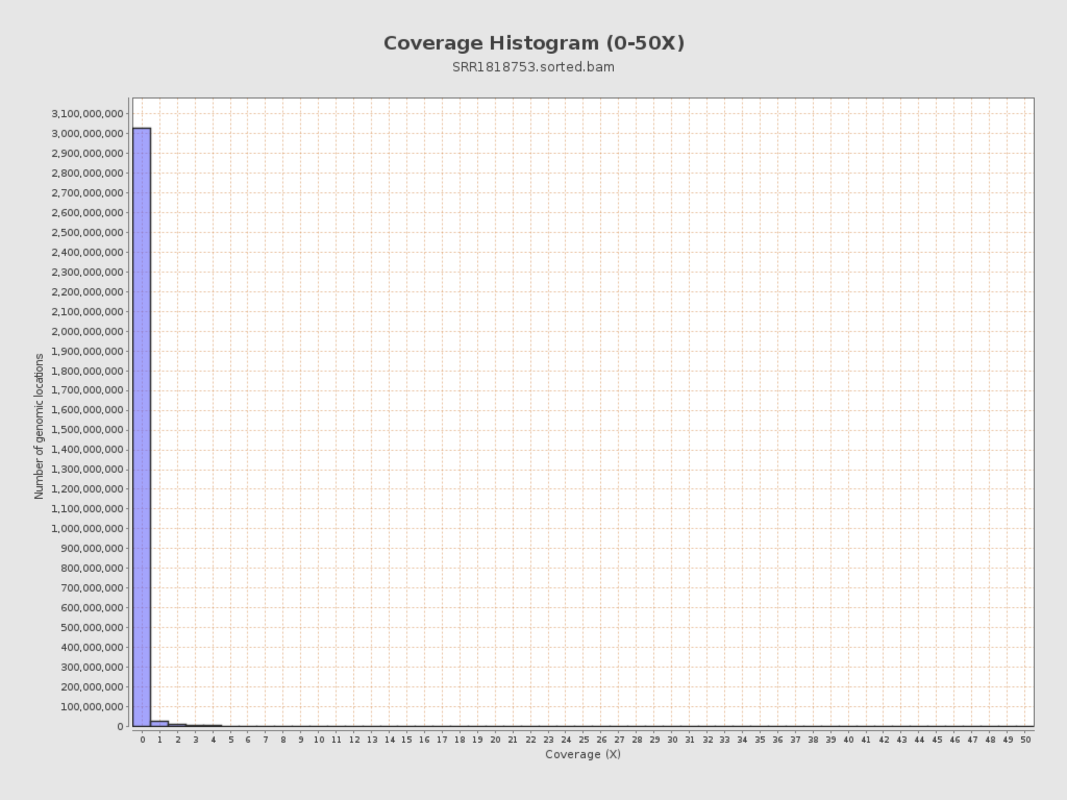
3. Results : Coverage across reference



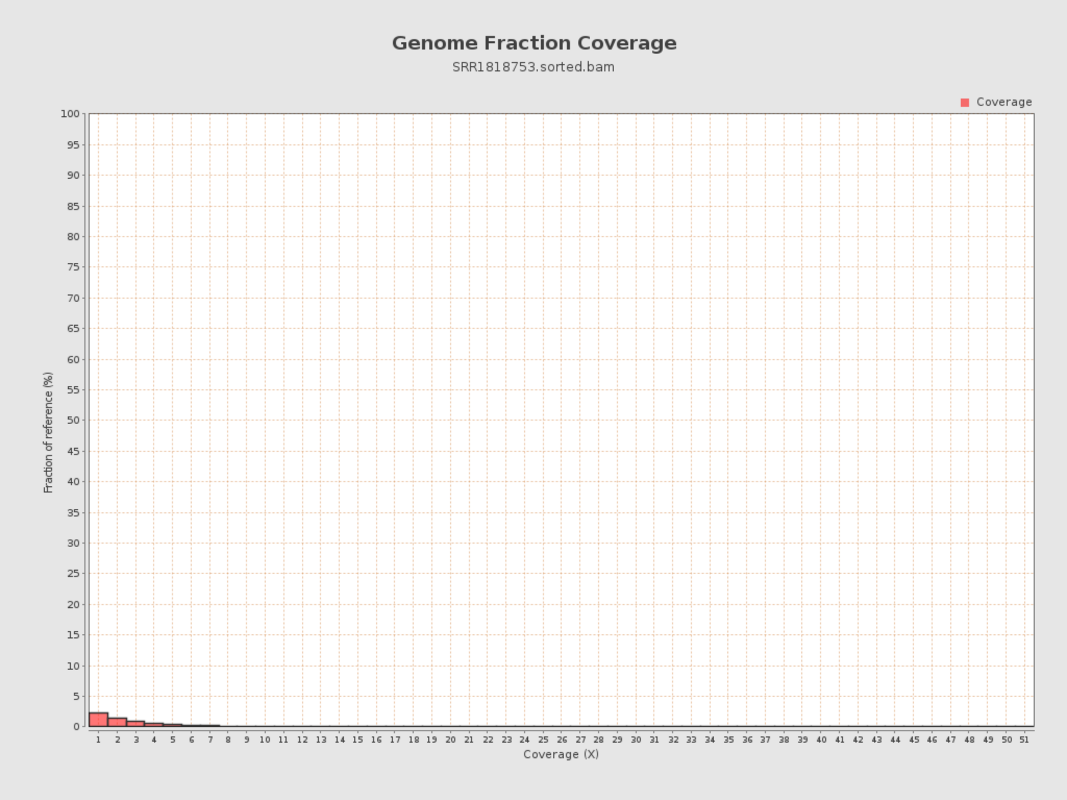
4. Results : Coverage Histogram



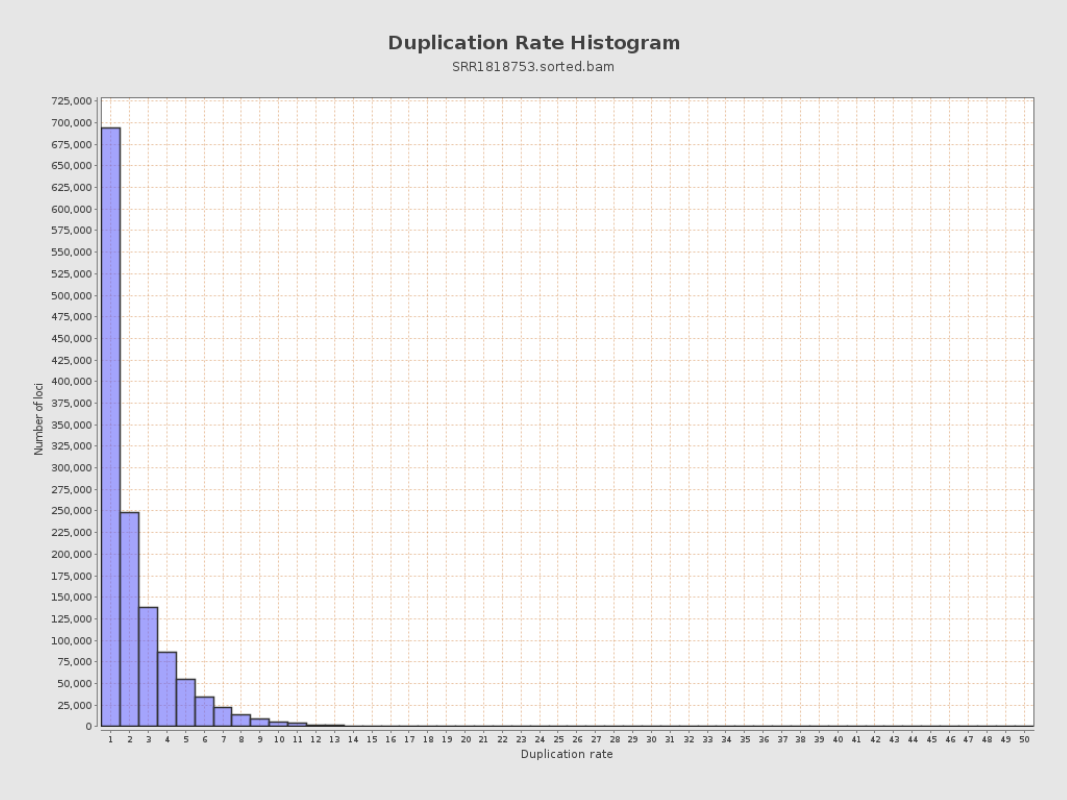
5. Results : Coverage Histogram (0-50X)



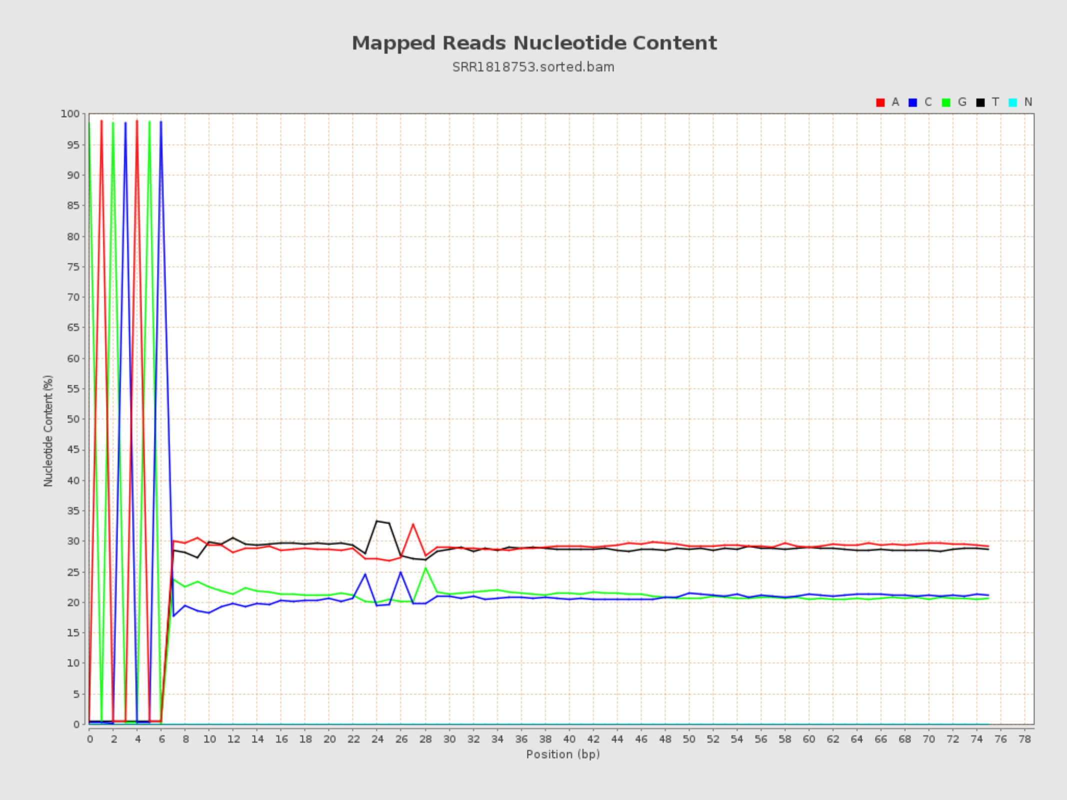
6. Results : Genome Fraction Coverage



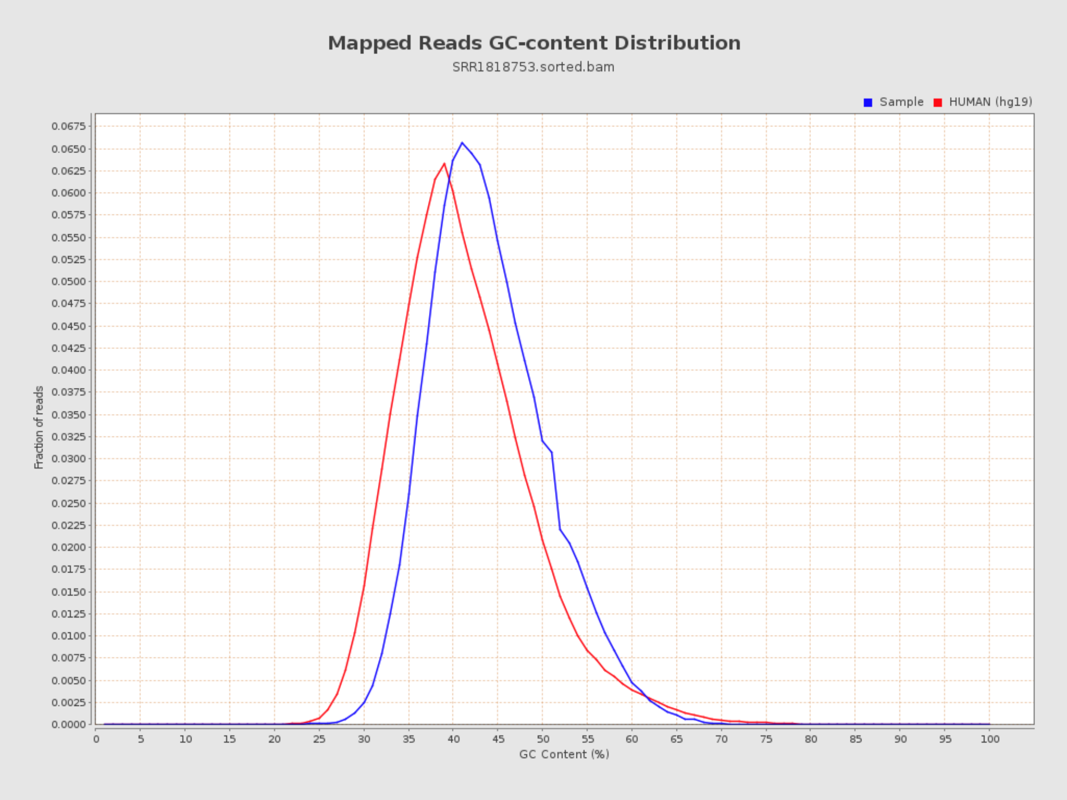
7. Results : Duplication Rate Histogram



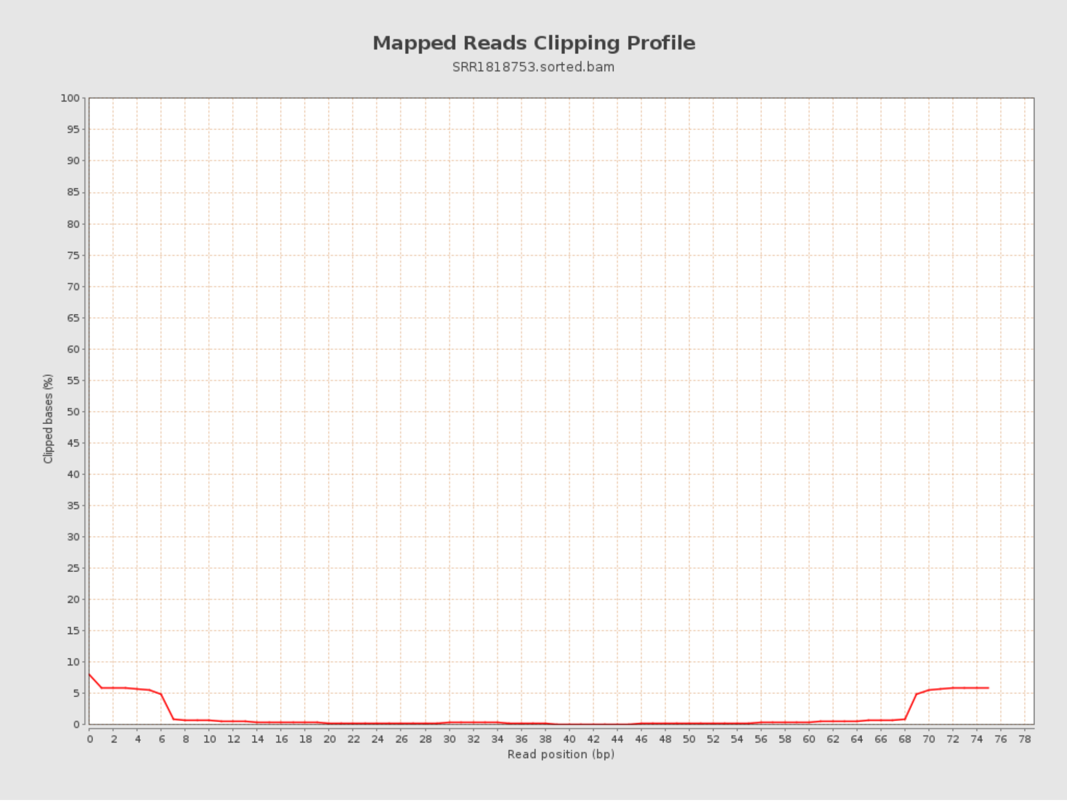
8. Results : Mapped Reads Nucleotide Content



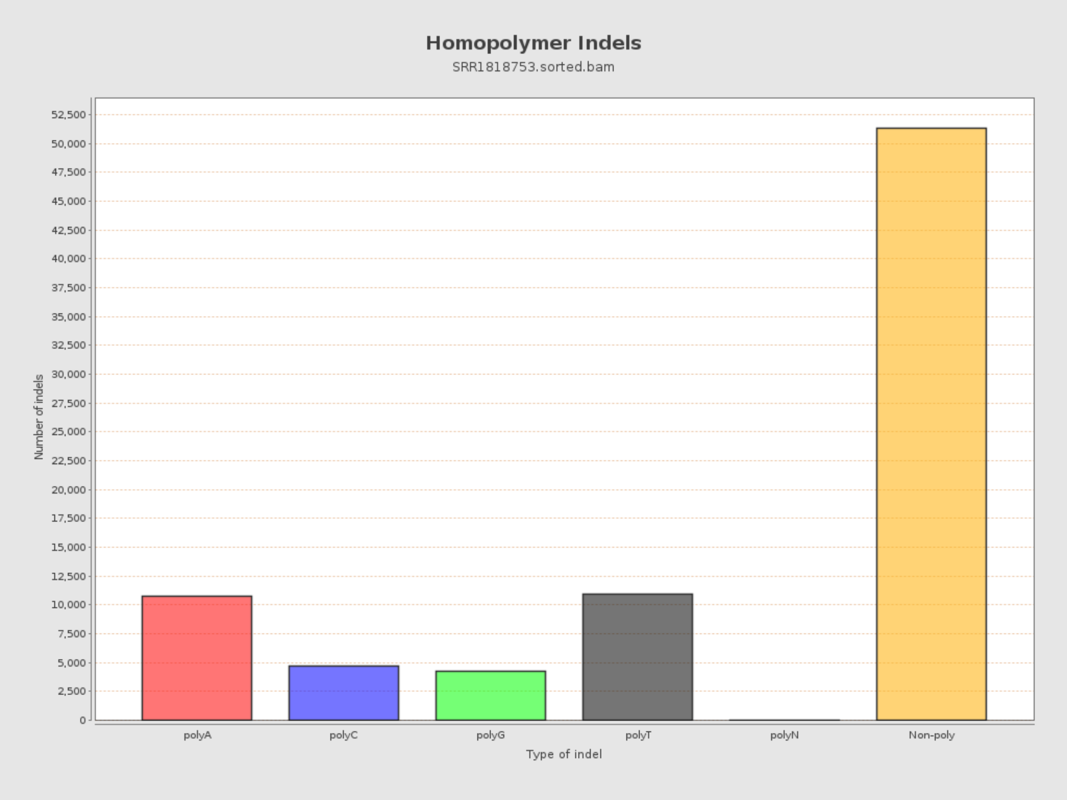
9. Results : Mapped Reads GC-content Distribution



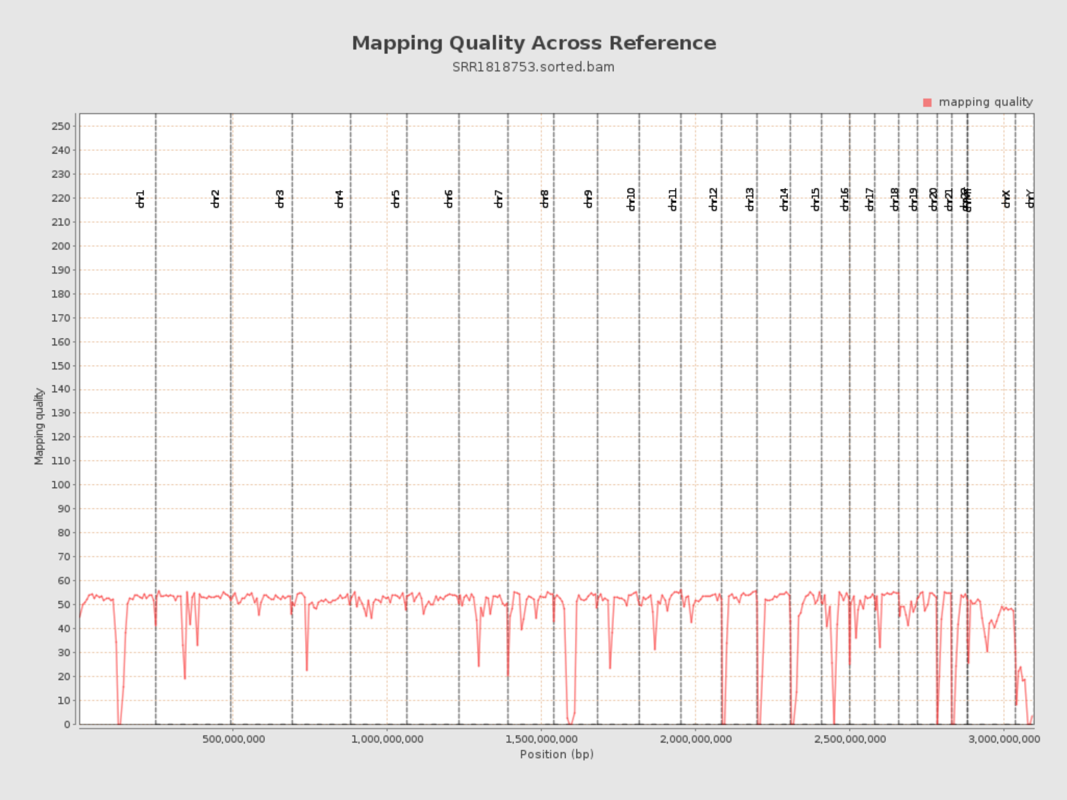
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram