Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818760.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_SRR1818760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:53:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,238,227
Mapped reads	1,204,135 / 97.25%
Unmapped reads	34,092 / 2.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,412 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	523,653 / 42.29%
Duplication rate	37.37%
Clipped reads	1,199,511 / 96.87%

2.2. ACGT Content

Number/percentage of A's	23,212,800 / 28.4%
Number/percentage of C's	16,705,697 / 20.44%
Number/percentage of T's	24,186,288 / 29.6%
Number/percentage of G's	17,614,336 / 21.55%
Number/percentage of N's	4,583 / 0.01%
GC Percentage	42%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.3647

2.4. Mapping Quality

Mean Mapping Quality	47.88

2.5. Mismatches and indels

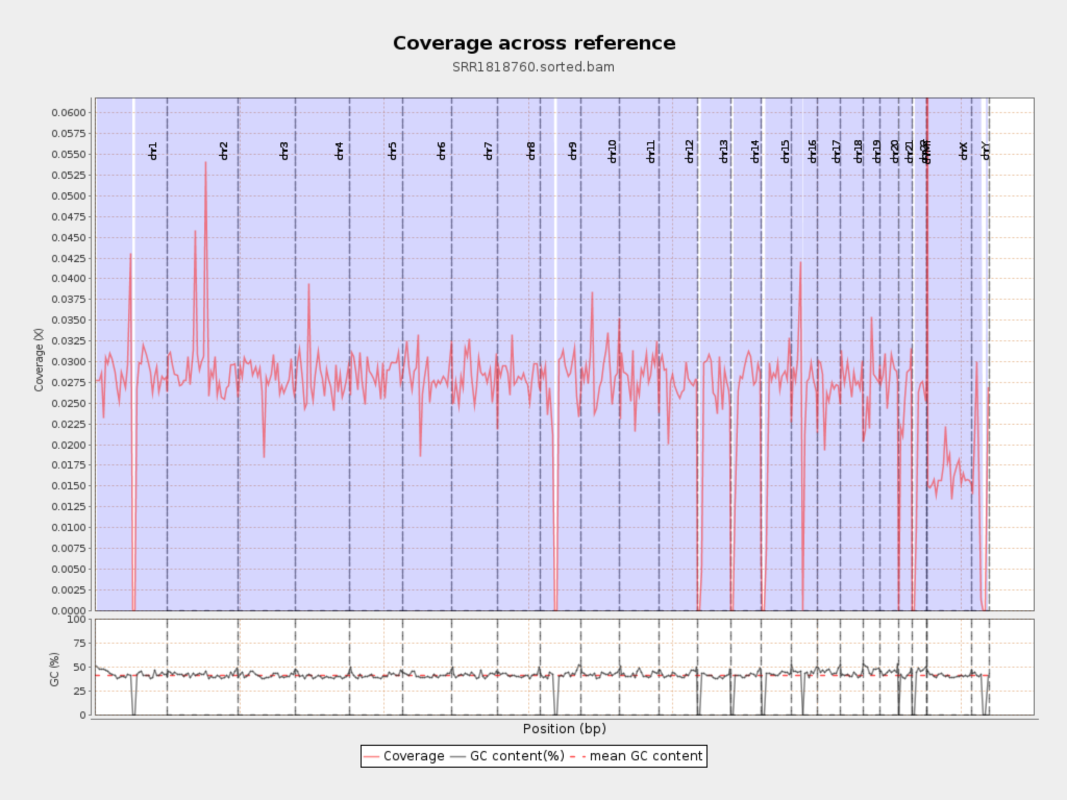
General error rate	0.54%
Mismatches	422,487
Insertions	10,254
Mapped reads with at least one insertion	0.84%
Deletions	21,148
Mapped reads with at least one deletion	1.74%
Homopolymer indels	39.63%

2.6. Chromosome stats

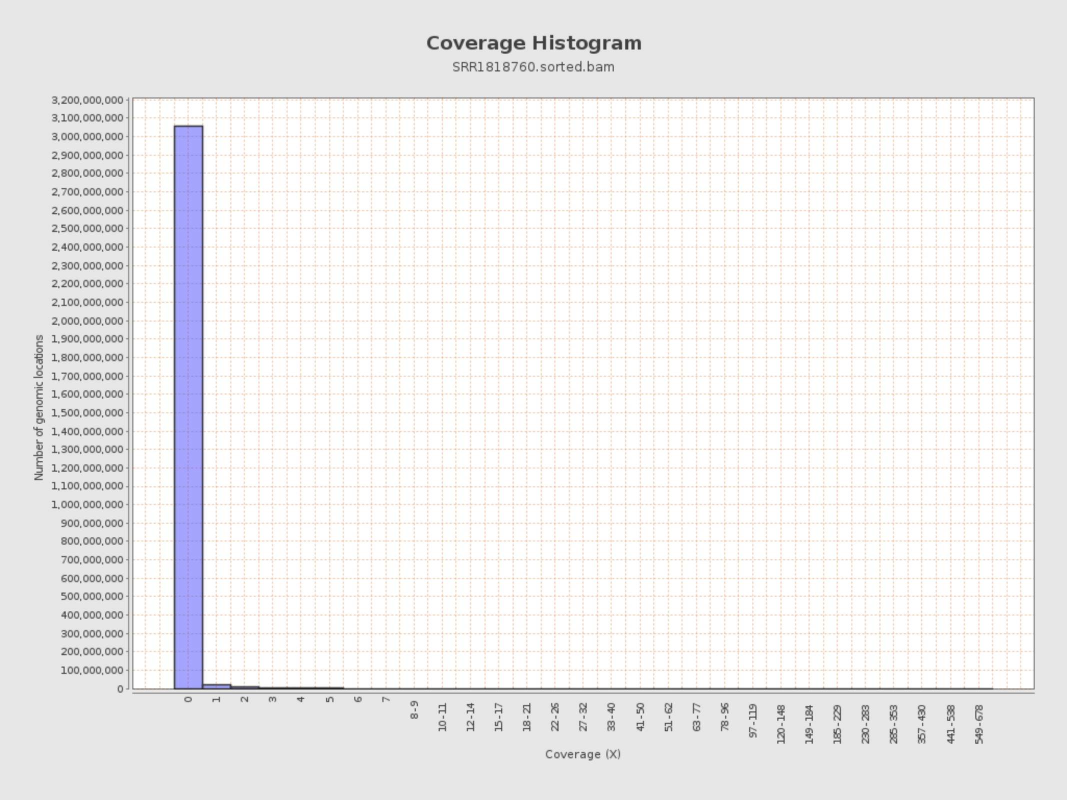
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6764454	0.0271	0.4709
chr2	243199373	7274922	0.0299	0.5565
chr3	198022430	5551950	0.028	0.2942
chr4	191154276	5366052	0.0281	0.3248
chr5	180915260	5194161	0.0287	0.3111
chr6	171115067	4814973	0.0281	0.3156
chr7	159138663	4471309	0.0281	0.3419

chr8	146364022	4147369	0.0283	0.3259
chr9	141213431	3517765	0.0249	0.31
chr10	135534747	3948220	0.0291	0.3817
chr11	135006516	3838715	0.0284	0.3294
chr12	133851895	3677328	0.0275	0.3083
chr13	115169878	2677584	0.0232	0.2667
chr14	107349540	2568212	0.0239	0.2922
chr15	102531392	2377365	0.0232	0.2716
chr16	90354753	2366758	0.0262	0.4227
chr17	81195210	2164716	0.0267	0.3011
chr18	78077248	2199133	0.0282	0.379
chr19	59128983	1583153	0.0268	0.4319
chr20	63025520	1792772	0.0284	0.3175
chr21	48129895	1135979	0.0236	0.2826
chr22	51304566	960402	0.0187	0.2645
chrMT	16571	11403	0.6881	1.7529
chrX	155270560	2536653	0.0163	0.2405
chrY	59373566	817004	0.0138	0.5937

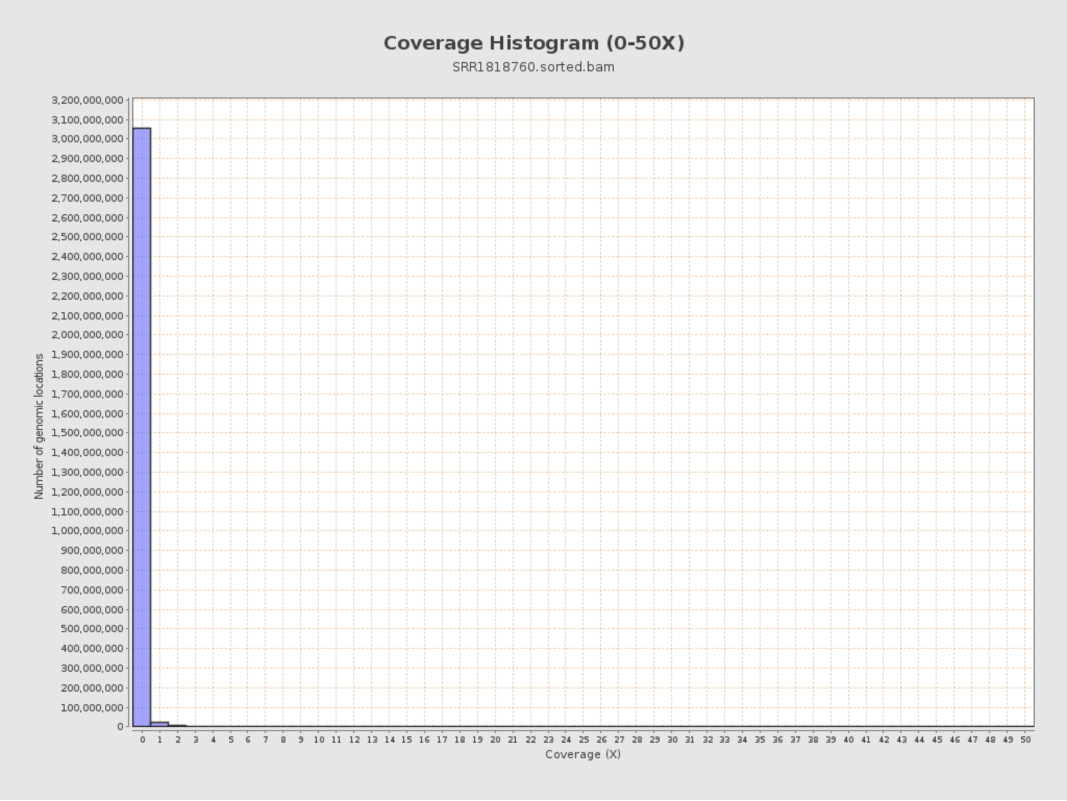
3. Results : Coverage across reference



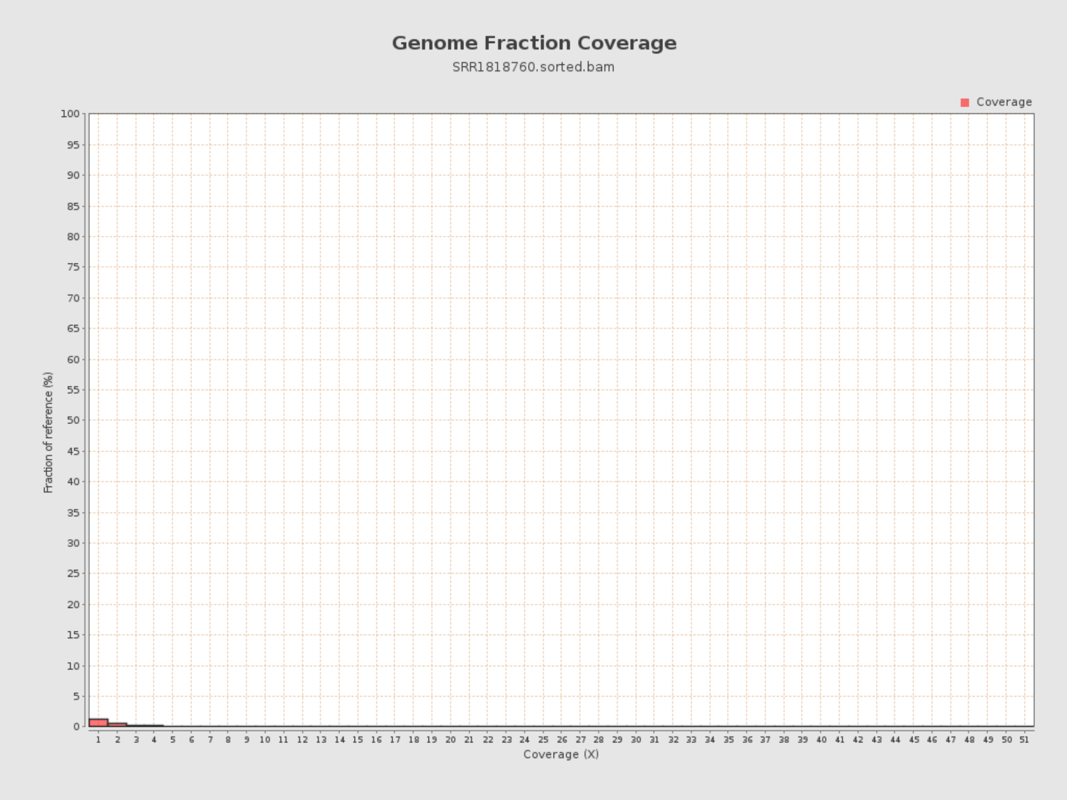
4. Results : Coverage Histogram



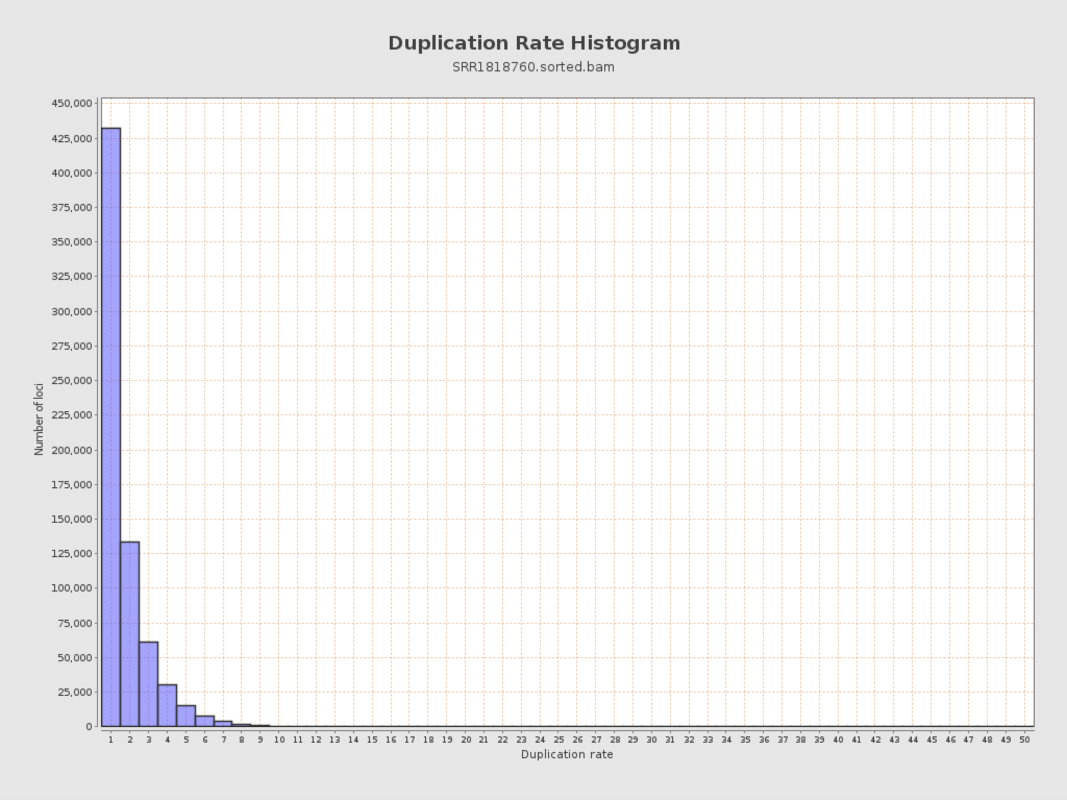
5. Results : Coverage Histogram (0-50X)



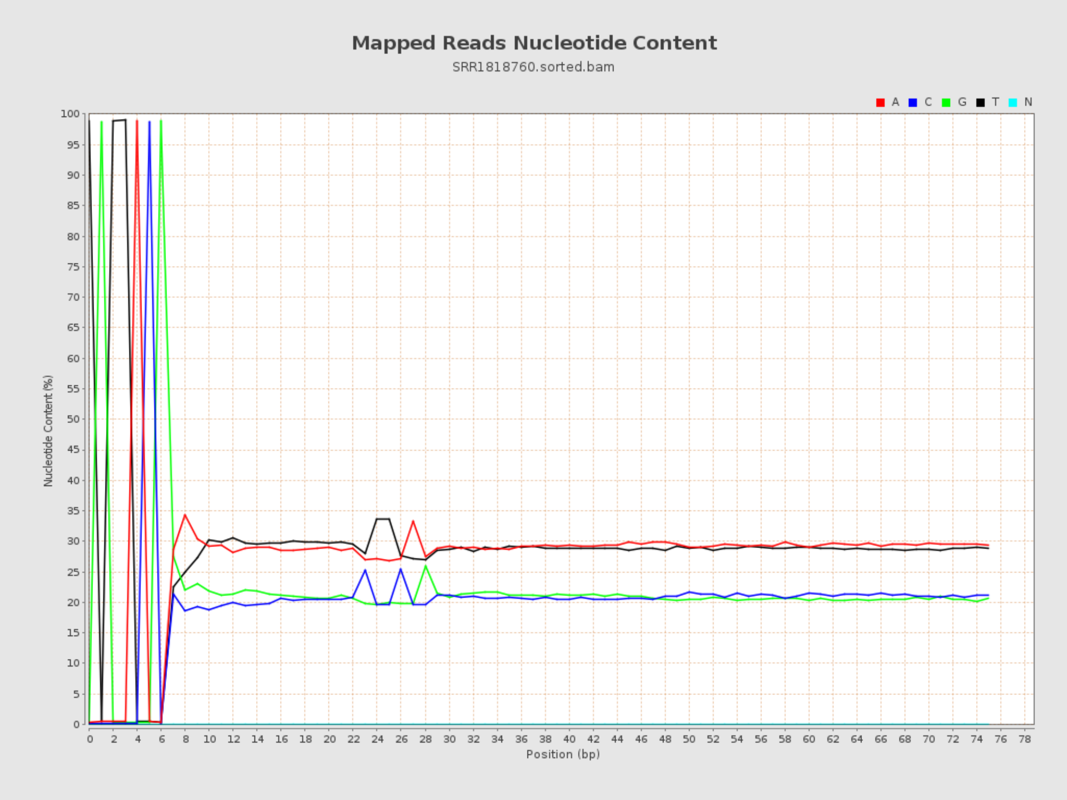
6. Results : Genome Fraction Coverage



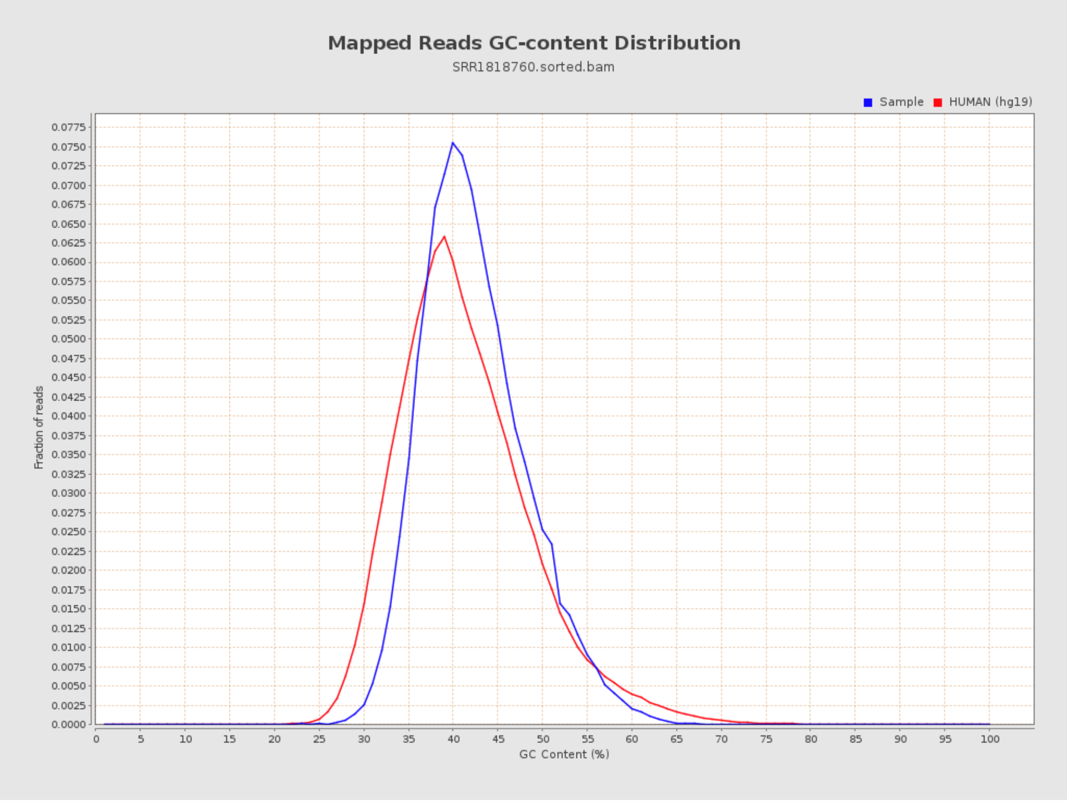
7. Results : Duplication Rate Histogram



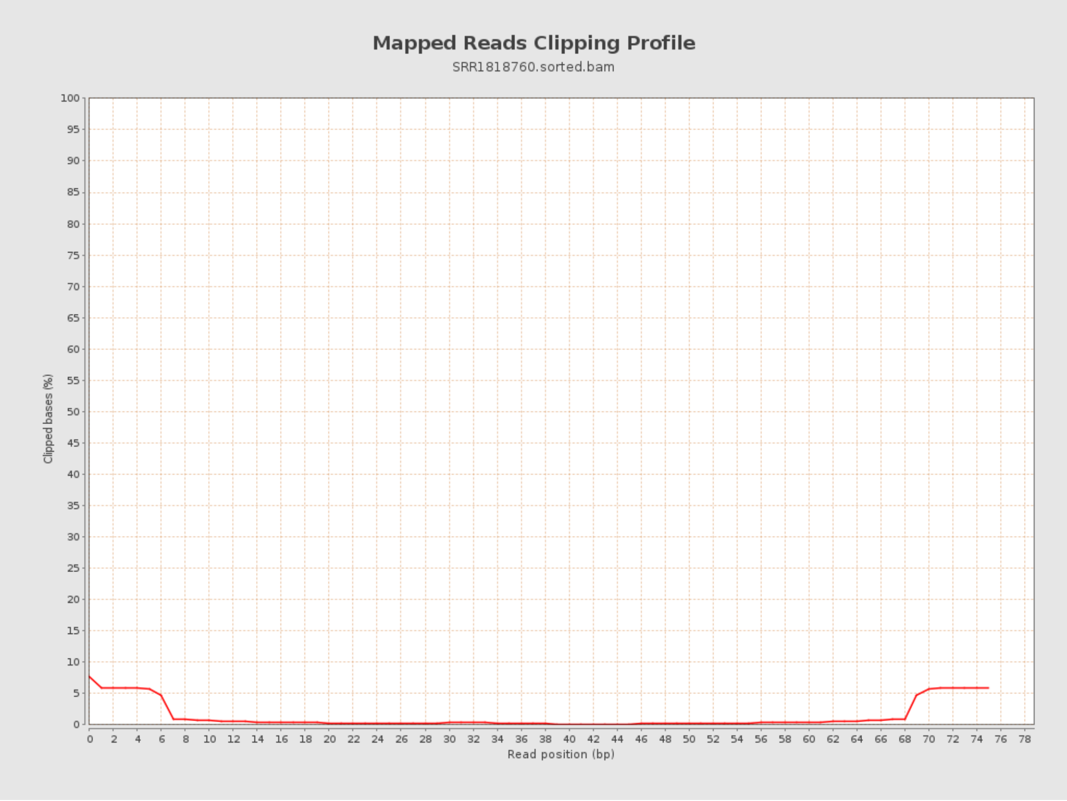
8. Results : Mapped Reads Nucleotide Content



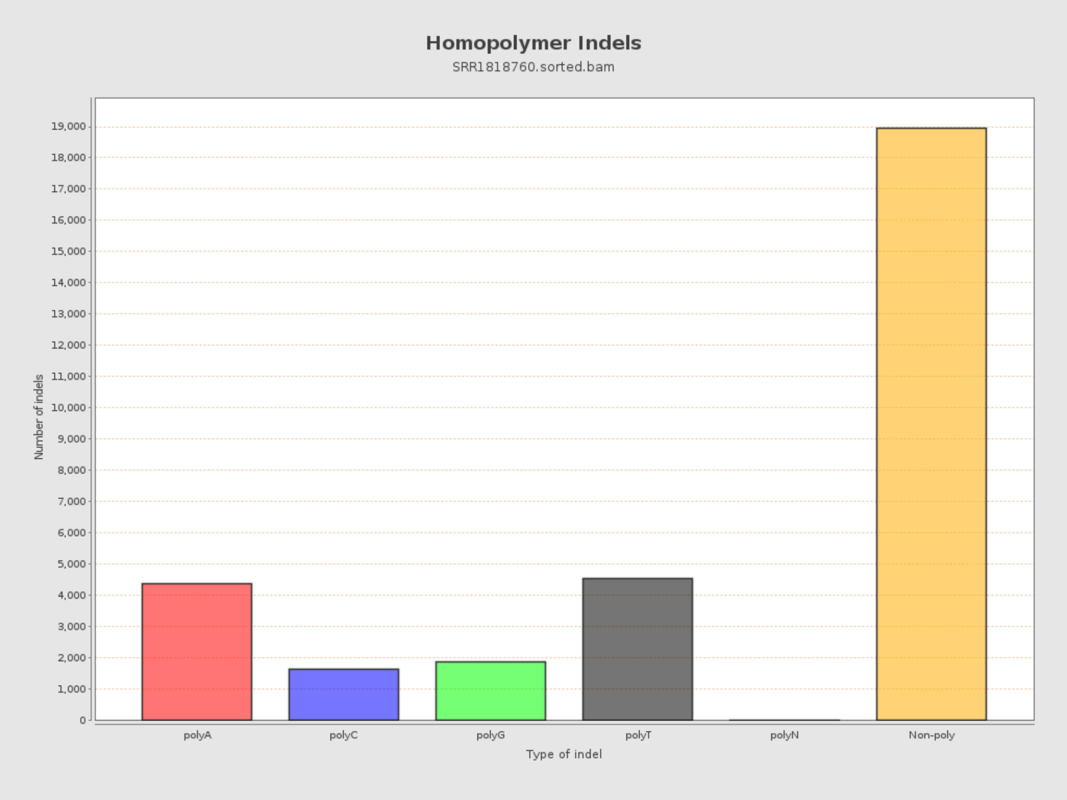
9. Results : Mapped Reads GC-content Distribution



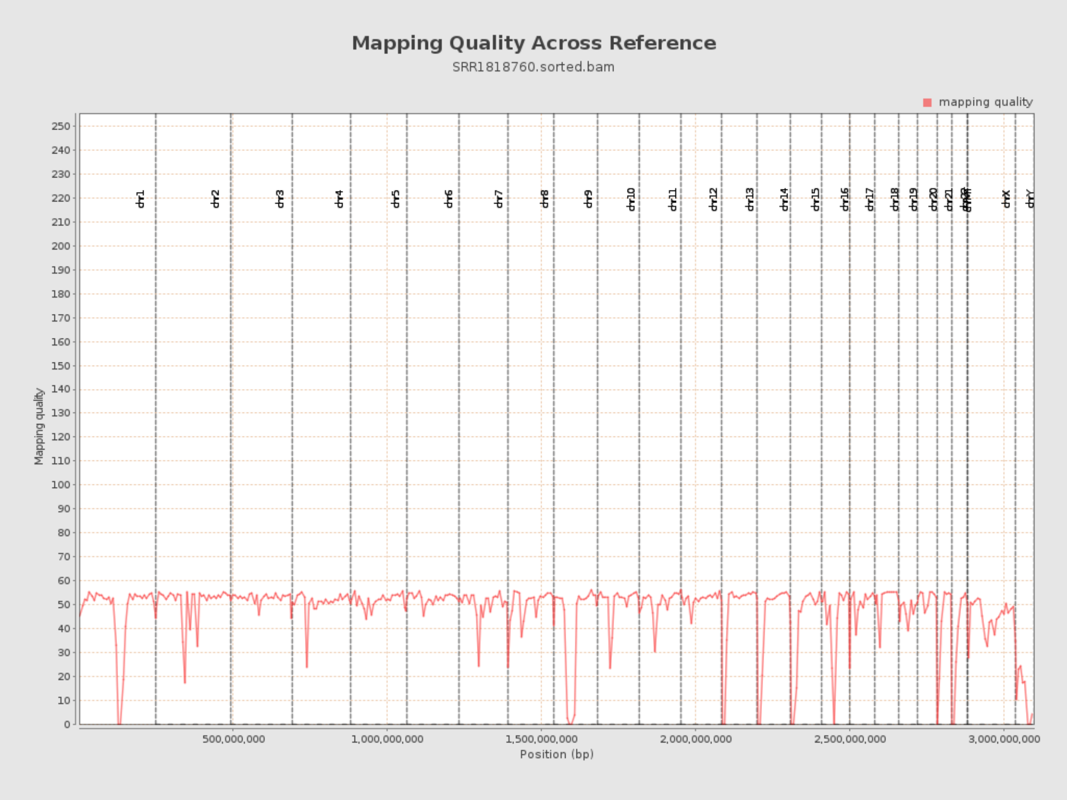
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram