Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:42:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818858.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_SRR1818858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:42:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,356,935
Mapped reads	1,262,952 / 93.07%
Unmapped reads	93,983 / 6.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,245 / 1.57%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	259,857 / 19.15%
Duplication rate	17.7%
Clipped reads	1,273,206 / 93.83%

2.2. ACGT Content

Number/percentage of A's	33,243,094 / 28.48%
Number/percentage of C's	25,953,625 / 22.23%
Number/percentage of T's	33,679,421 / 28.85%
Number/percentage of G's	23,855,932 / 20.44%
Number/percentage of N's	1,560 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.4537

2.4. Mapping Quality

Mean Mapping Quality	49.38

2.5. Mismatches and indels

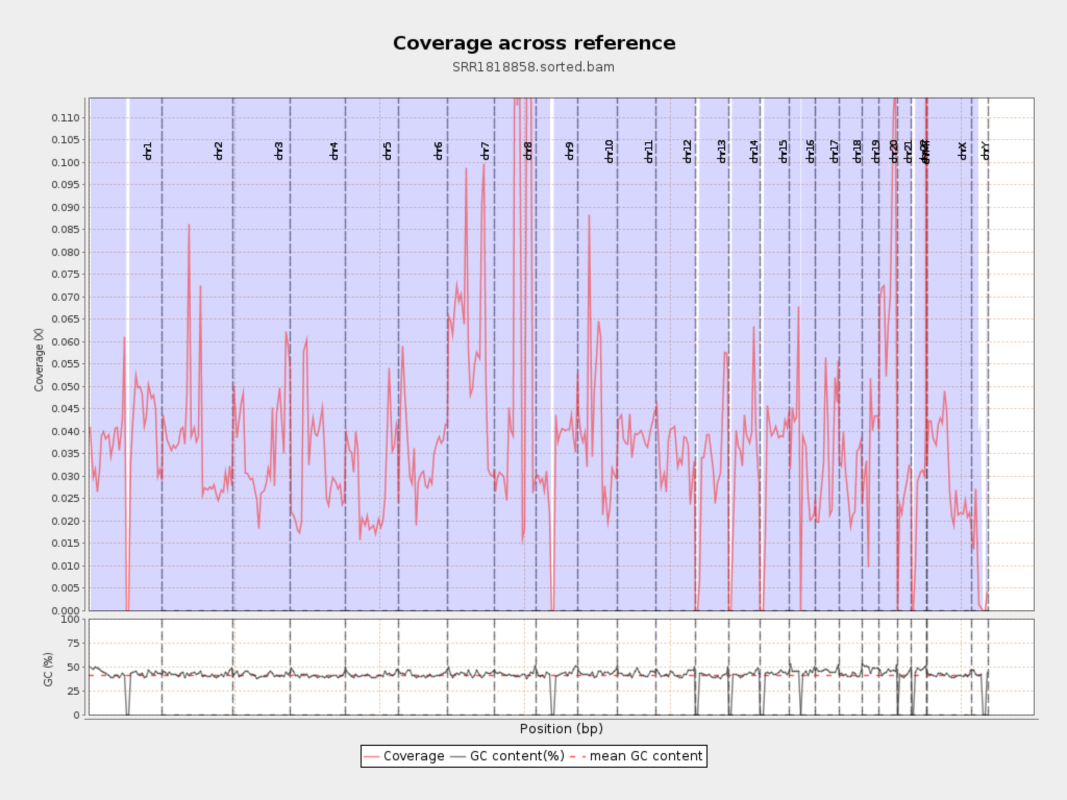
General error rate	0.66%
Mismatches	728,992
Insertions	17,051
Mapped reads with at least one insertion	1.31%
Deletions	39,115
Mapped reads with at least one deletion	3.02%
Homopolymer indels	41.19%

2.6. Chromosome stats

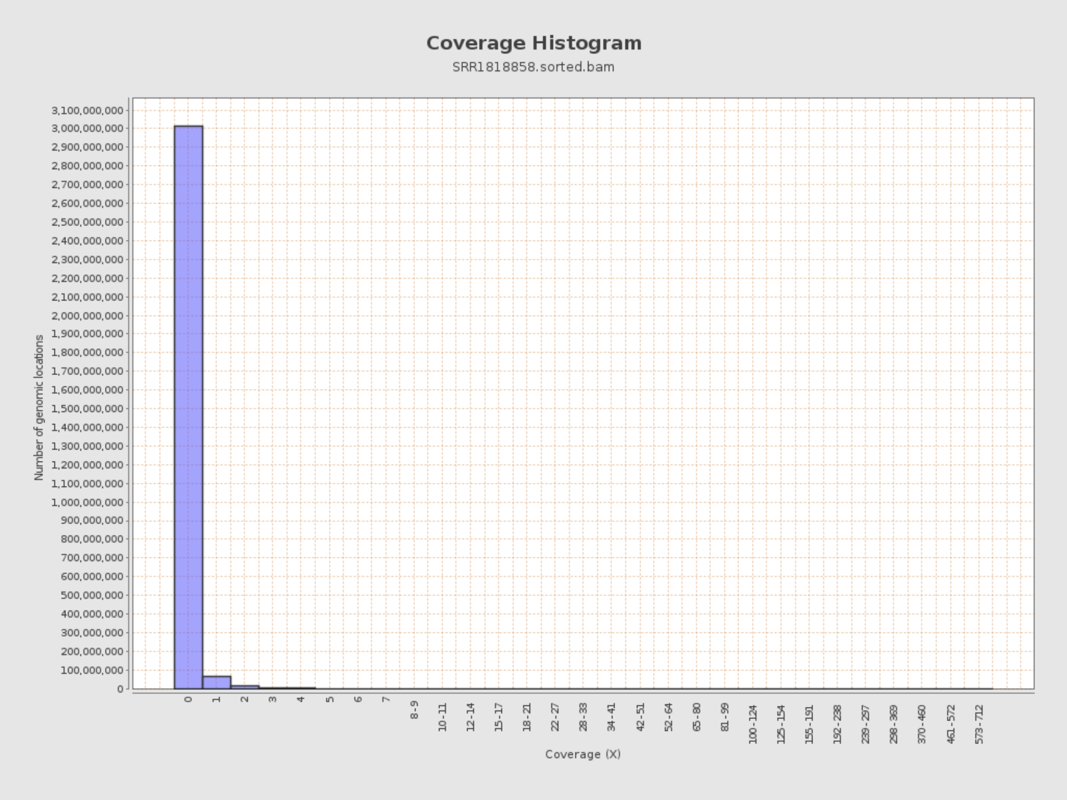
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9489639	0.0381	0.6202
chr2	243199373	8933563	0.0367	0.6994
chr3	198022430	7351357	0.0371	0.251
chr4	191154276	6060150	0.0317	0.3054
chr5	180915260	5199921	0.0287	0.2337
chr6	171115067	5958469	0.0348	0.2616
chr7	159138663	9787281	0.0615	0.8988

chr8	146364022	10441234	0.0713	0.4283
chr9	141213431	4470028	0.0317	0.3874
chr10	135534747	5527541	0.0408	0.5917
chr11	135006516	5351007	0.0396	0.3078
chr12	133851895	4666270	0.0349	0.2435
chr13	115169878	3682685	0.032	0.2291
chr14	107349540	3563535	0.0332	0.2526
chr15	102531392	3400832	0.0332	0.2364
chr16	90354753	2968963	0.0329	0.4991
chr17	81195210	2871070	0.0354	0.2993
chr18	78077248	2346884	0.0301	0.4314
chr19	59128983	2100073	0.0355	0.5248
chr20	63025520	4904840	0.0778	0.391
chr21	48129895	1172865	0.0244	0.2469
chr22	51304566	1093229	0.0213	0.2089
chrMT	16571	106243	6.4114	5.0579
chrX	155270560	4922399	0.0317	0.2654
chrY	59373566	440323	0.0074	0.569

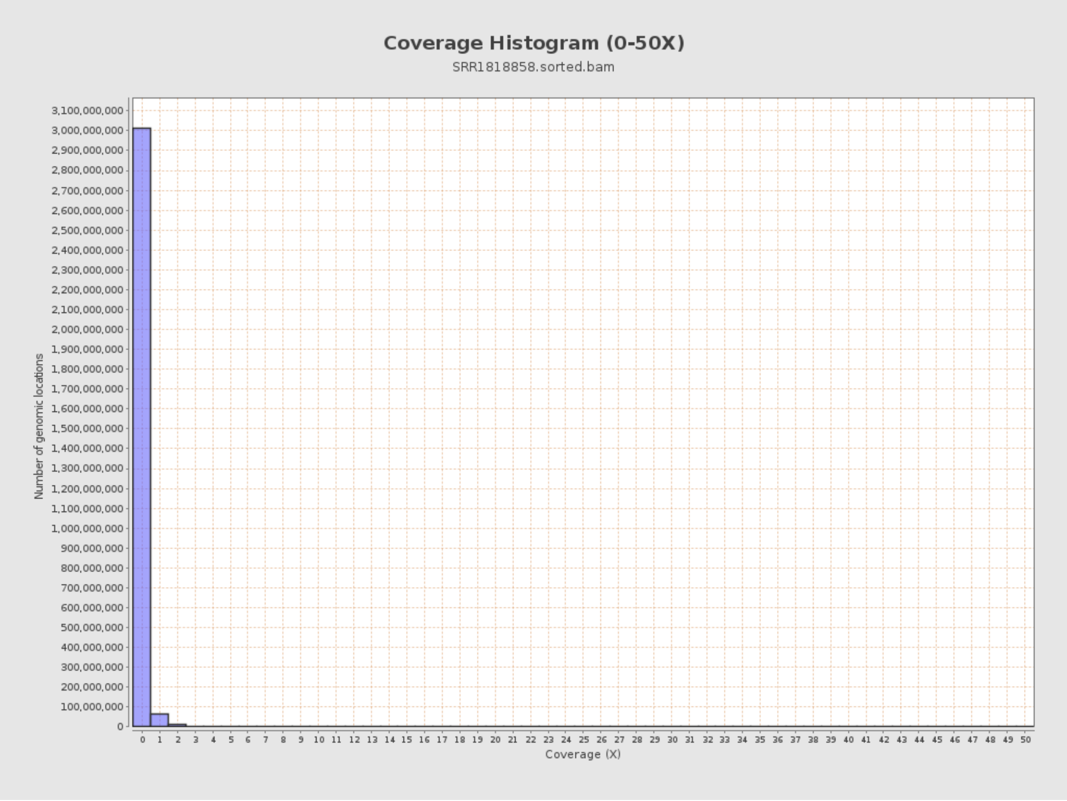
3. Results : Coverage across reference



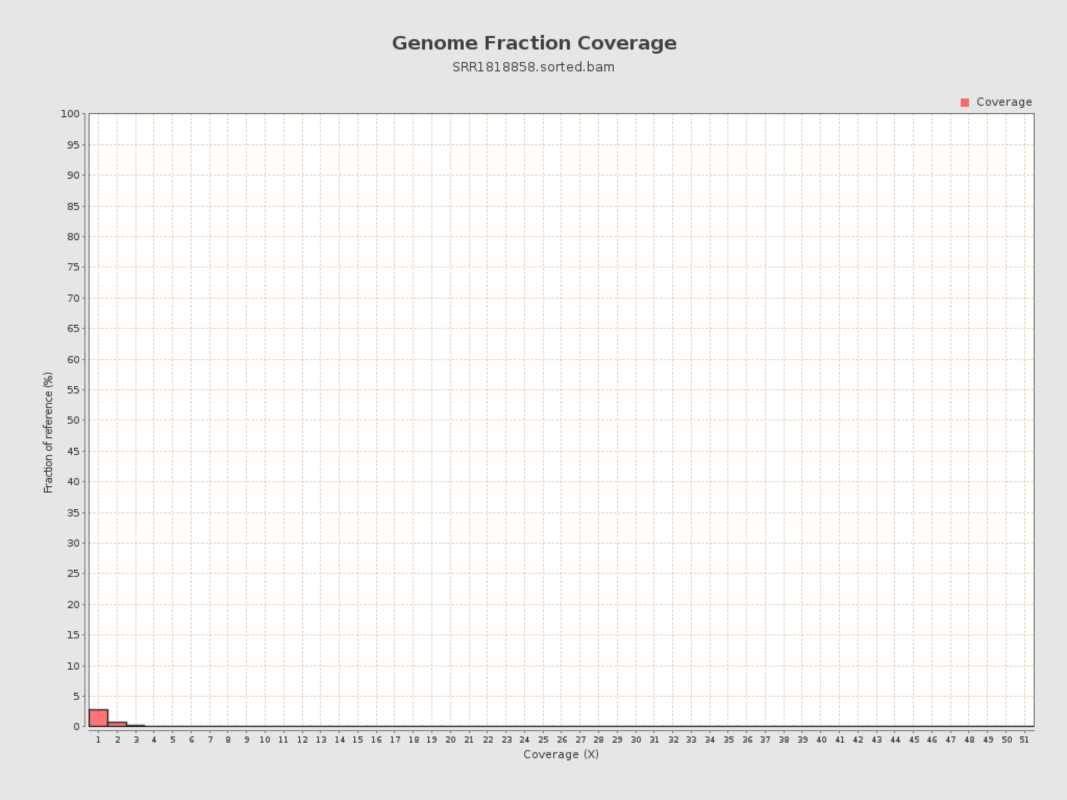
4. Results : Coverage Histogram



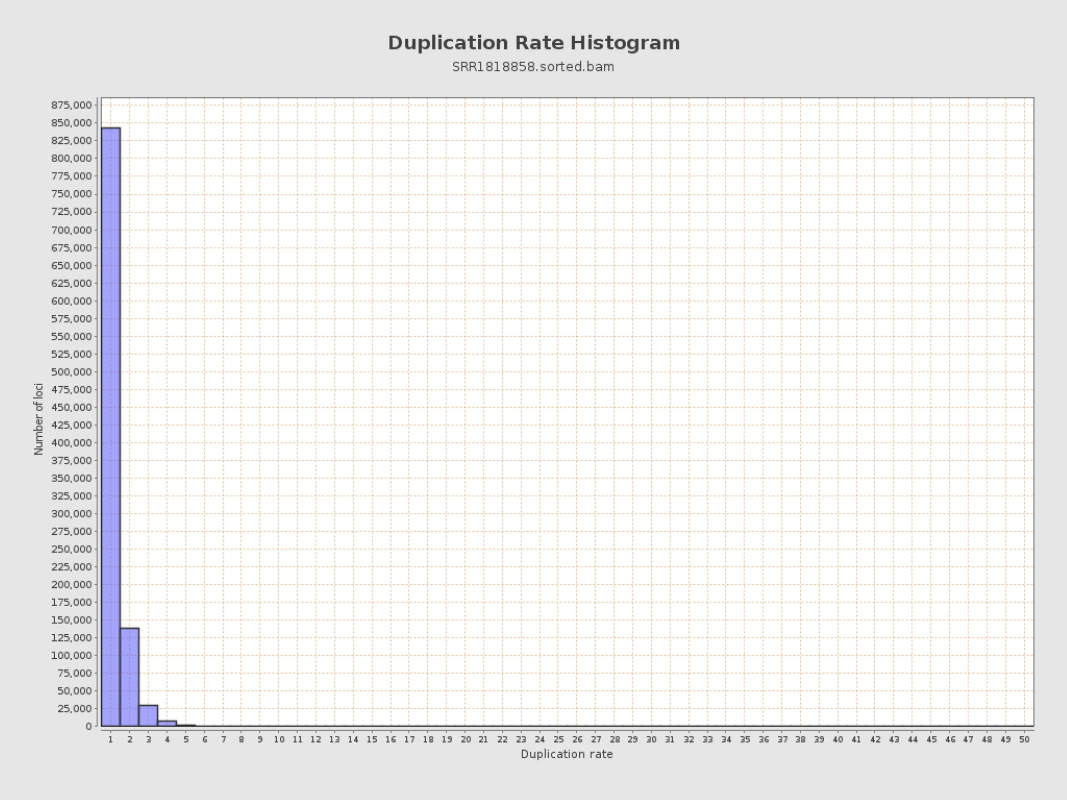
5. Results : Coverage Histogram (0-50X)



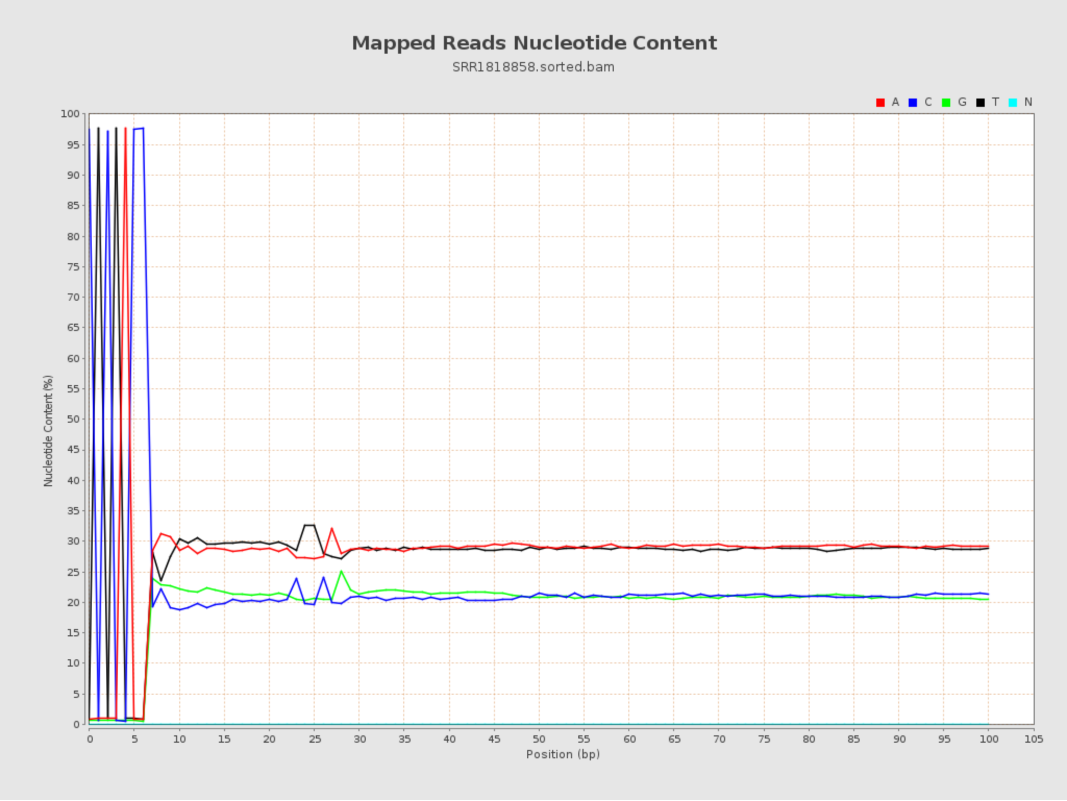
6. Results : Genome Fraction Coverage



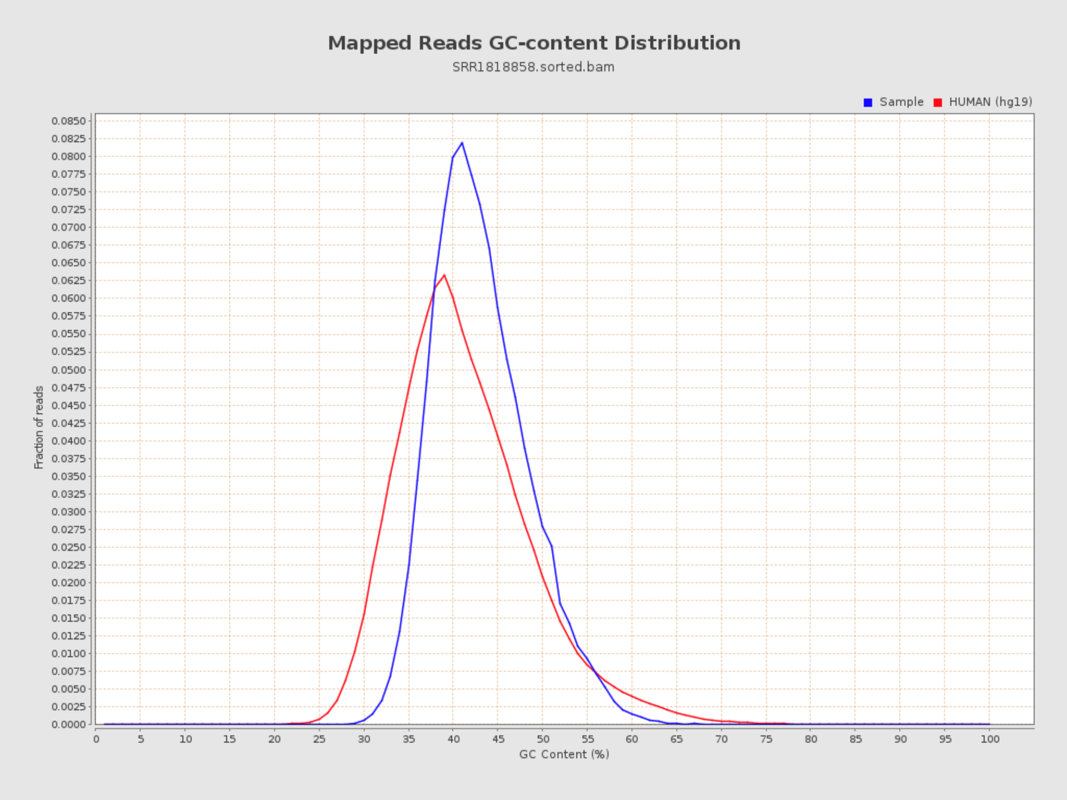
7. Results : Duplication Rate Histogram



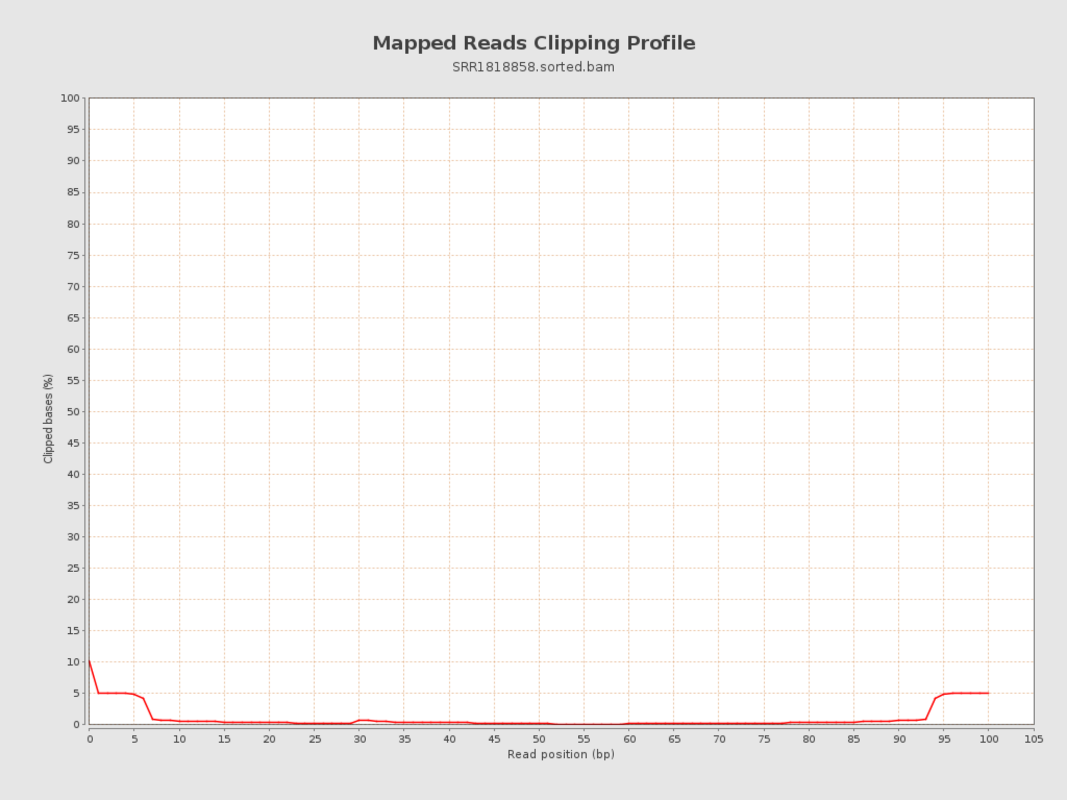
8. Results : Mapped Reads Nucleotide Content



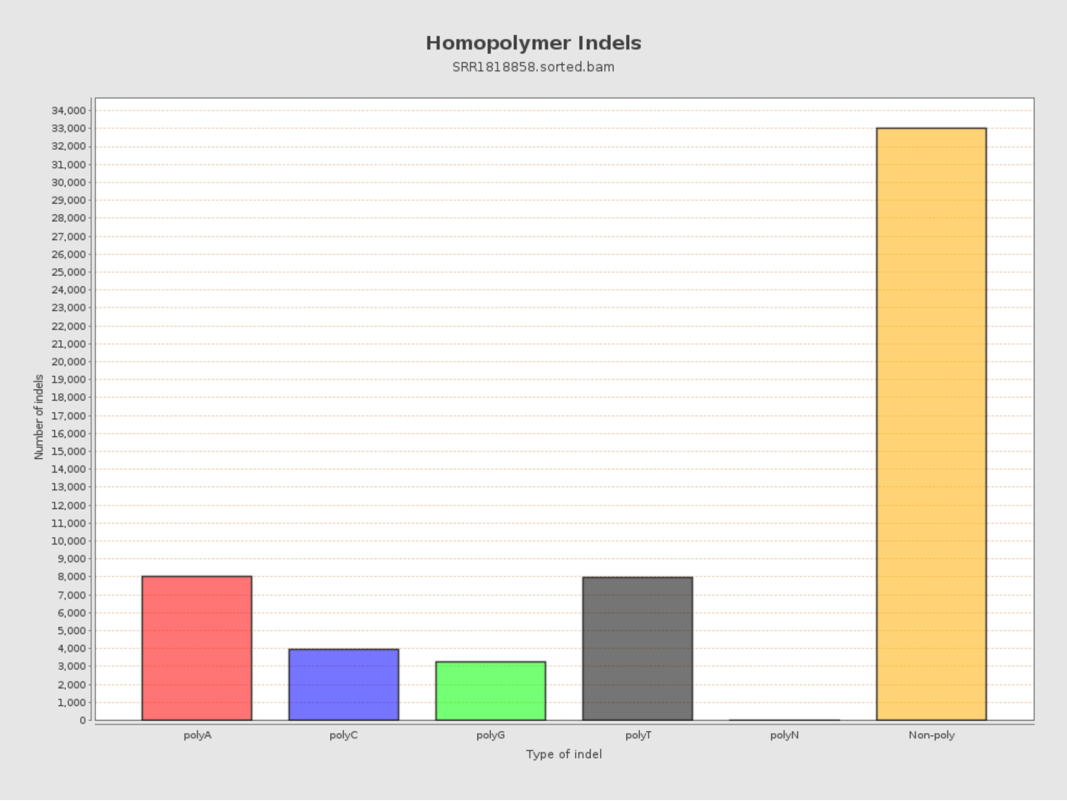
9. Results : Mapped Reads GC-content Distribution



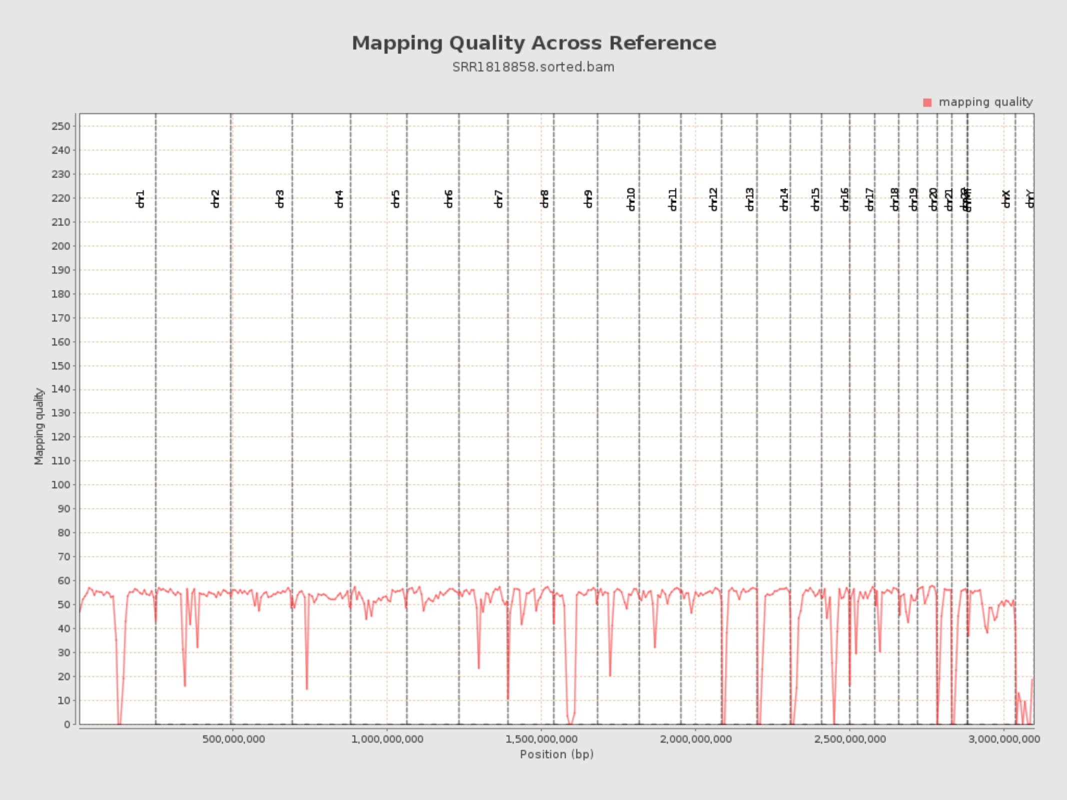
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram