Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:31:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818848.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_SRR1818848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:30:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,541,904
Mapped reads	1,522,117 / 98.72%
Unmapped reads	19,787 / 1.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,094 / 1.69%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	325,513 / 21.11%
Duplication rate	18.22%
Clipped reads	1,532,578 / 99.4%

2.2. ACGT Content

Number/percentage of A's	40,721,515 / 28.94%
Number/percentage of C's	29,852,591 / 21.21%
Number/percentage of T's	38,823,202 / 27.59%
Number/percentage of G's	31,331,925 / 22.26%
Number/percentage of N's	1,915 / 0%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0455

Standard Deviation	0.5677

2.4. Mapping Quality

Mean Mapping Quality	48.79

2.5. Mismatches and indels

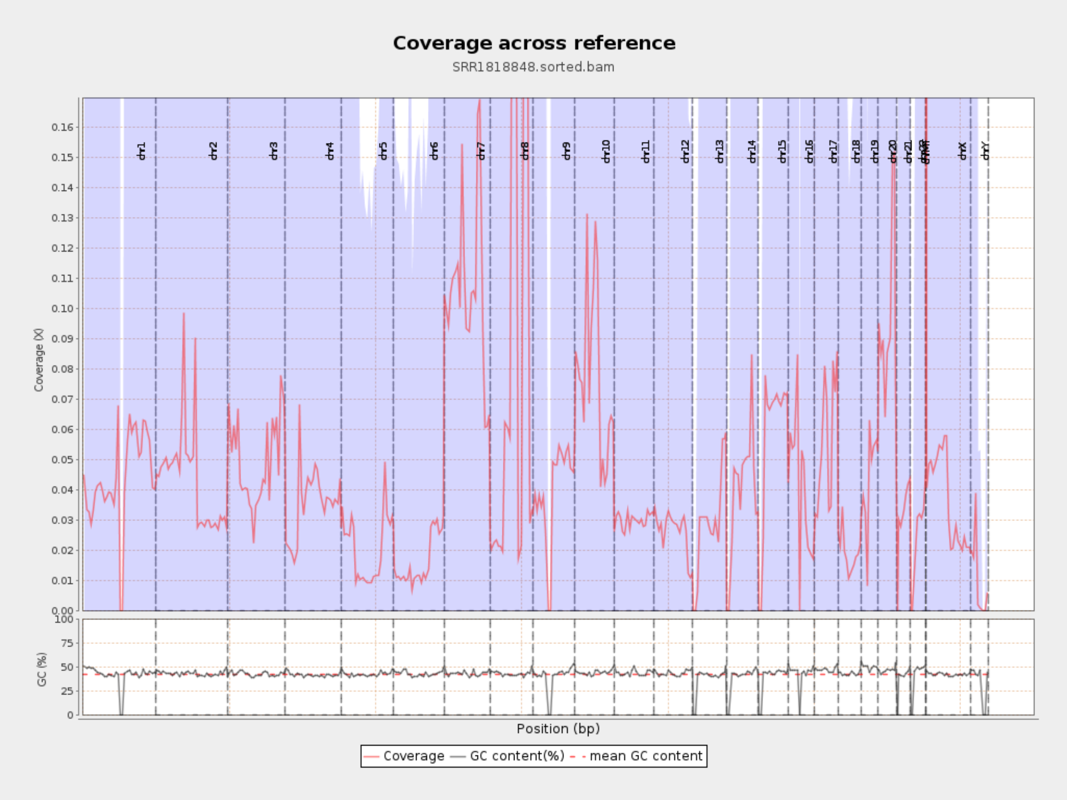
General error rate	0.65%
Mismatches	860,818
Insertions	23,405
Mapped reads with at least one insertion	1.49%
Deletions	47,478
Mapped reads with at least one deletion	3.04%
Homopolymer indels	38.64%

2.6. Chromosome stats

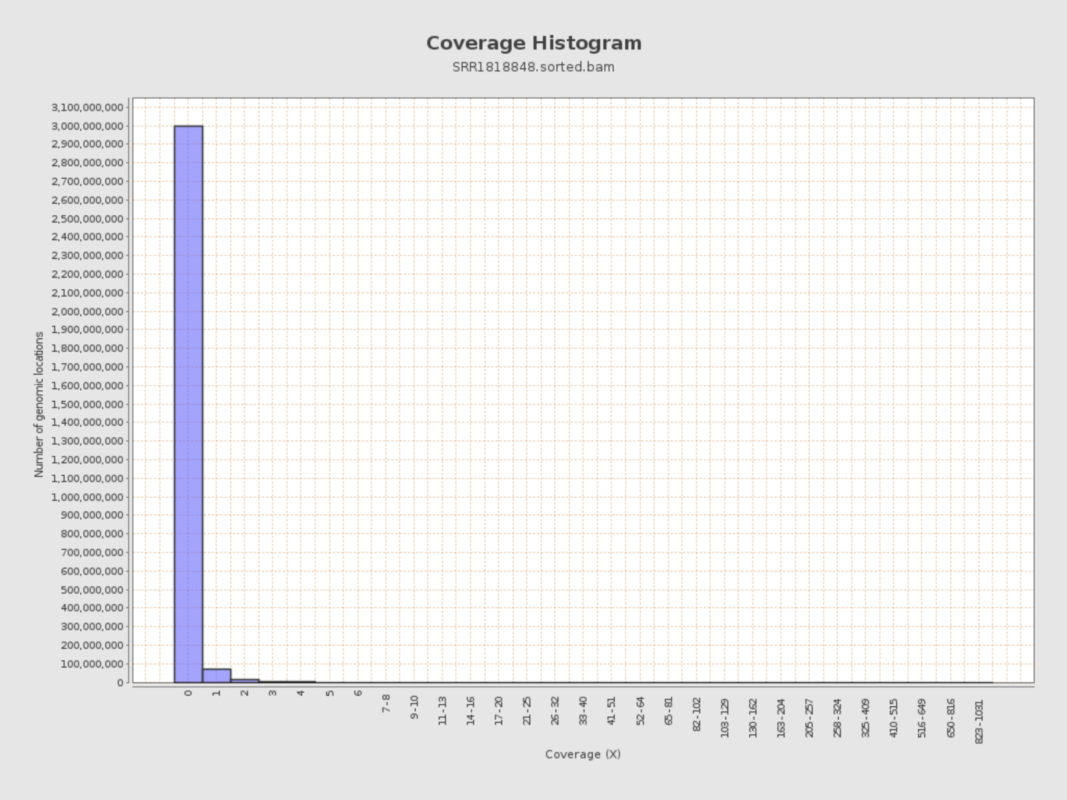
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10909653	0.0438	0.6886
chr2	243199373	10596763	0.0436	0.8852
chr3	198022430	9746697	0.0492	0.2916
chr4	191154276	6830189	0.0357	0.3459
chr5	180915260	3742514	0.0207	0.2168
chr6	171115067	2753143	0.0161	0.1991
chr7	159138663	16842998	0.1058	1.3007

chr8	146364022	14529360	0.0993	0.5173
chr9	141213431	5575406	0.0395	0.424
chr10	135534747	10523147	0.0776	0.7827
chr11	135006516	4032629	0.0299	0.2732
chr12	133851895	3546745	0.0265	0.215
chr13	115169878	3319084	0.0288	0.2231
chr14	107349540	4346661	0.0405	0.2878
chr15	102531392	5833485	0.0569	0.3148
chr16	90354753	3617126	0.04	0.639
chr17	81195210	4451755	0.0548	0.3802
chr18	78077248	1487933	0.0191	0.4345
chr19	59128983	2535388	0.0429	0.6956
chr20	63025520	6294676	0.0999	0.4519
chr21	48129895	1542744	0.0321	0.298
chr22	51304566	1173682	0.0229	0.2213
chrMT	16571	324833	19.6025	12.8688
chrX	155270560	5662759	0.0365	0.2894
chrY	59373566	605491	0.0102	0.8235

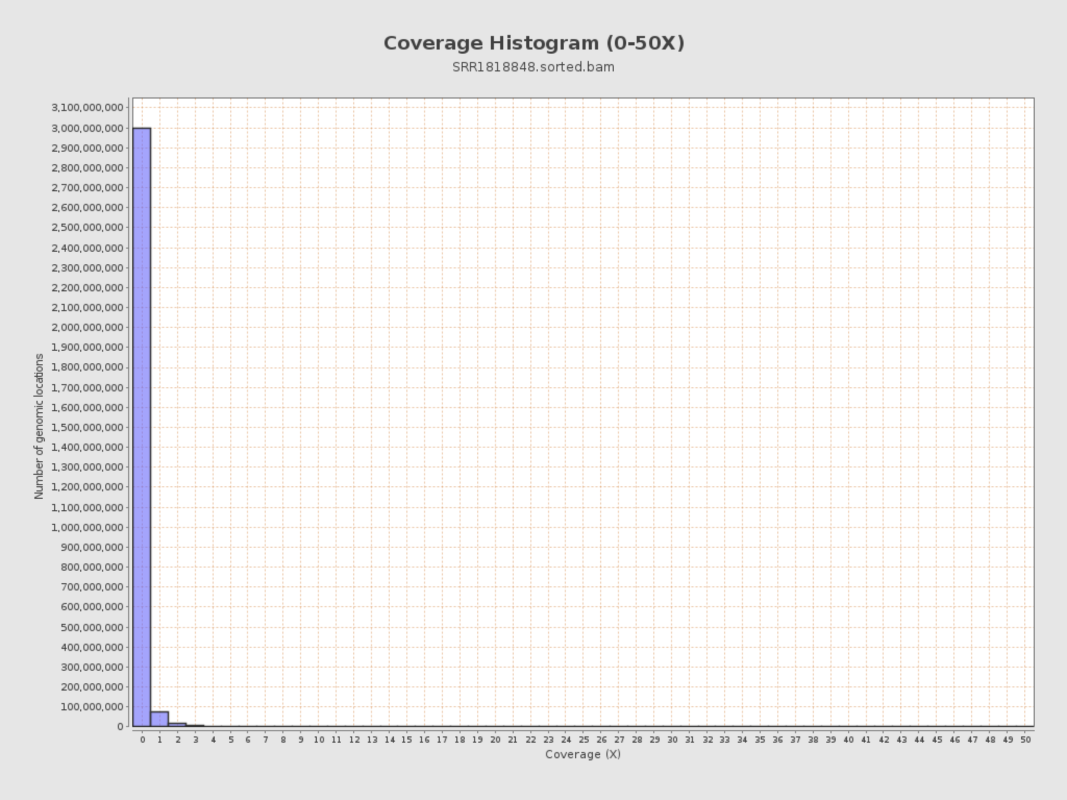
3. Results : Coverage across reference



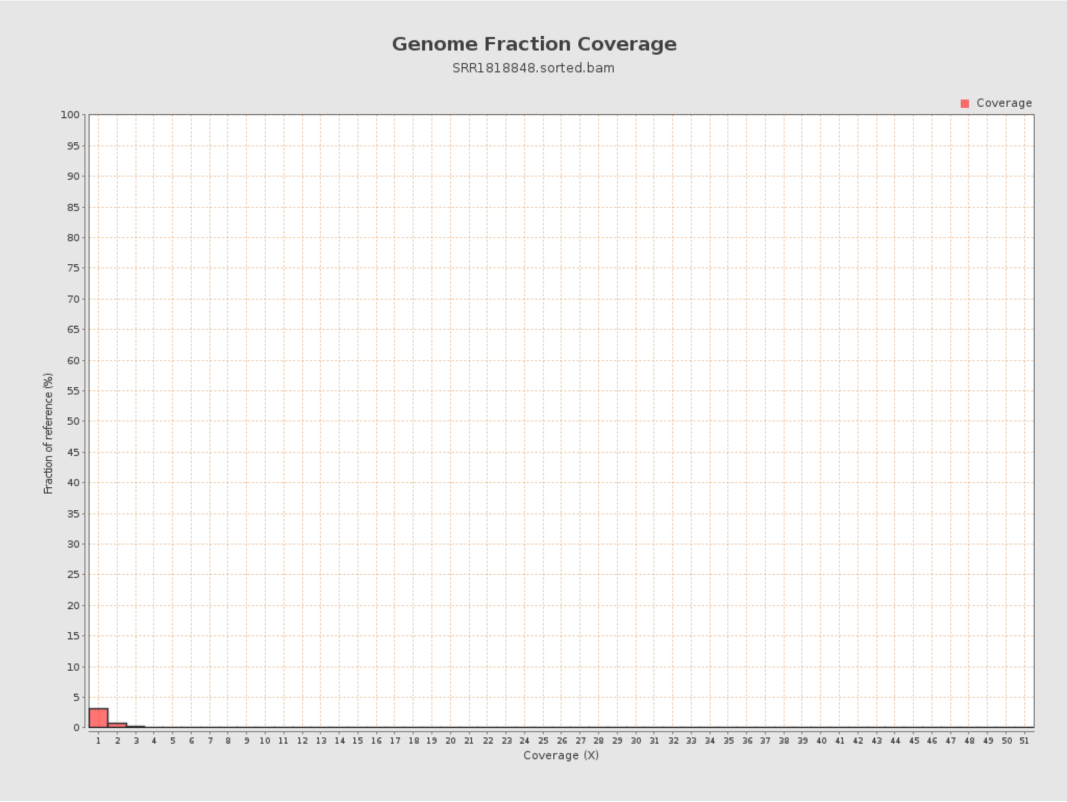
4. Results : Coverage Histogram



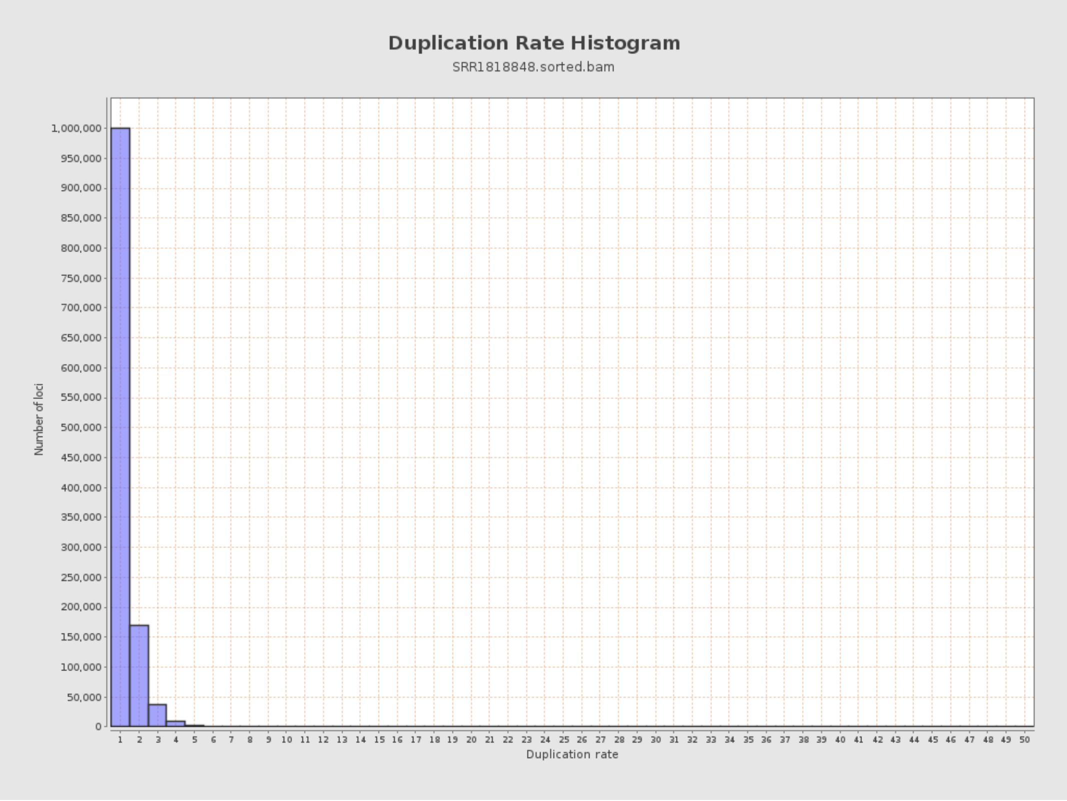
5. Results : Coverage Histogram (0-50X)



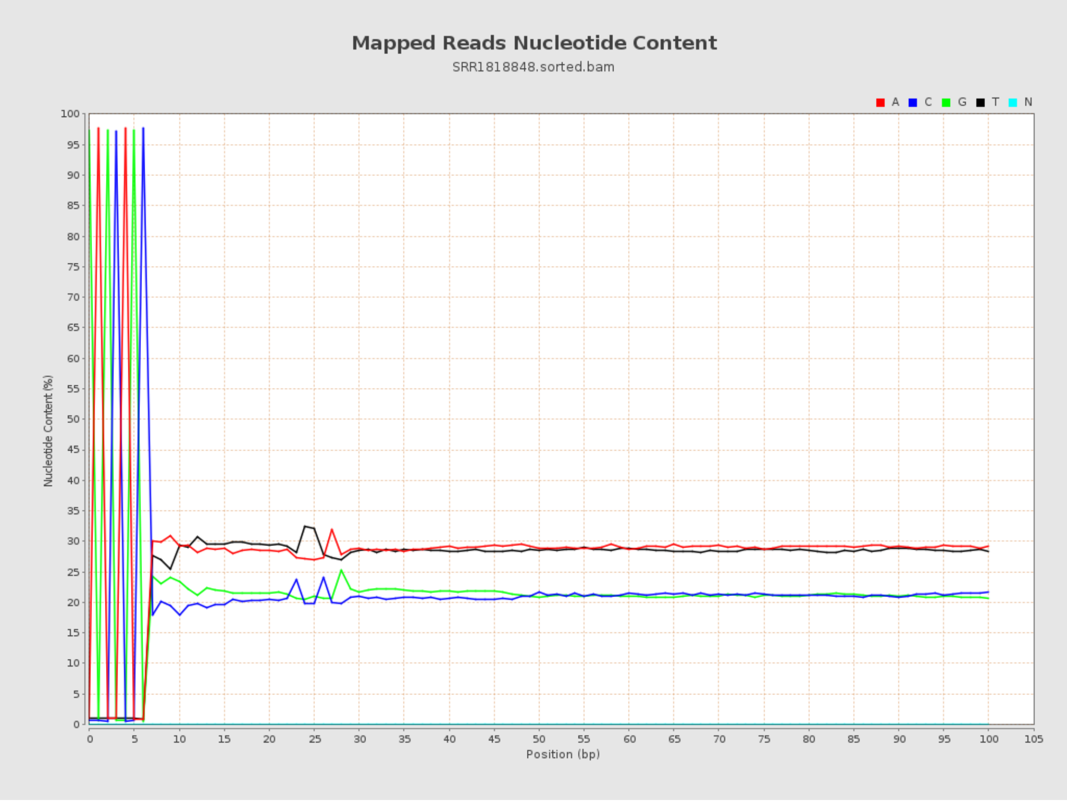
6. Results : Genome Fraction Coverage



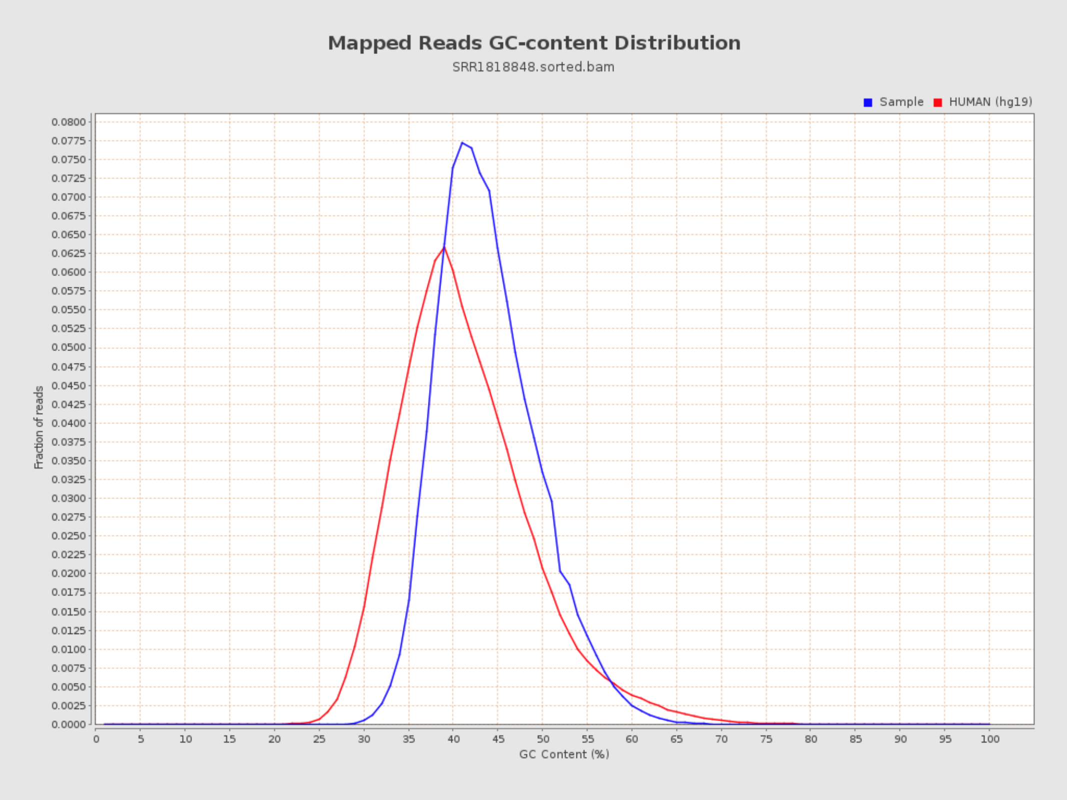
7. Results : Duplication Rate Histogram



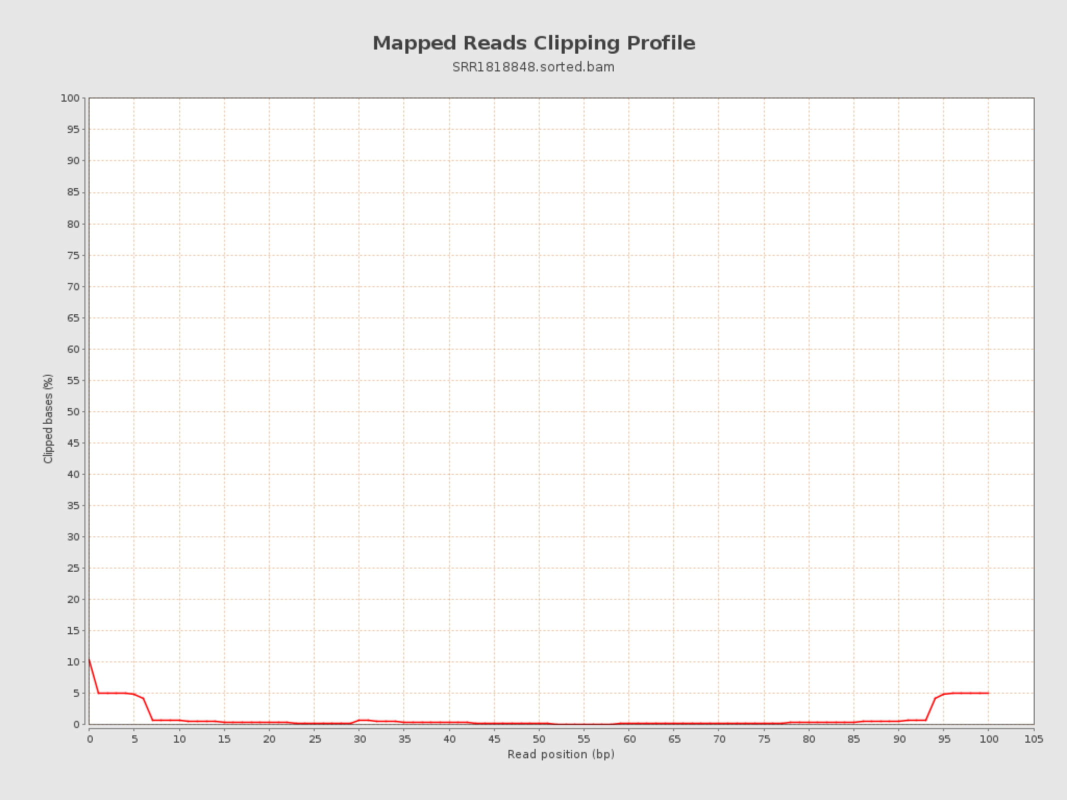
8. Results : Mapped Reads Nucleotide Content



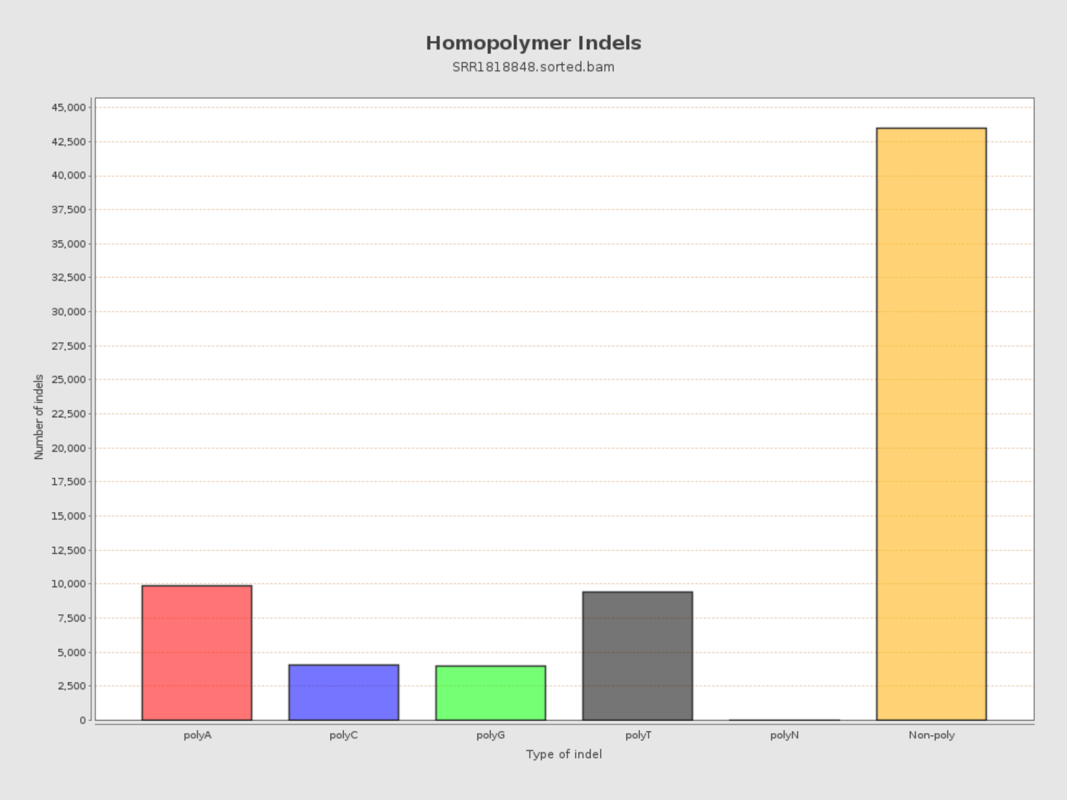
9. Results : Mapped Reads GC-content Distribution



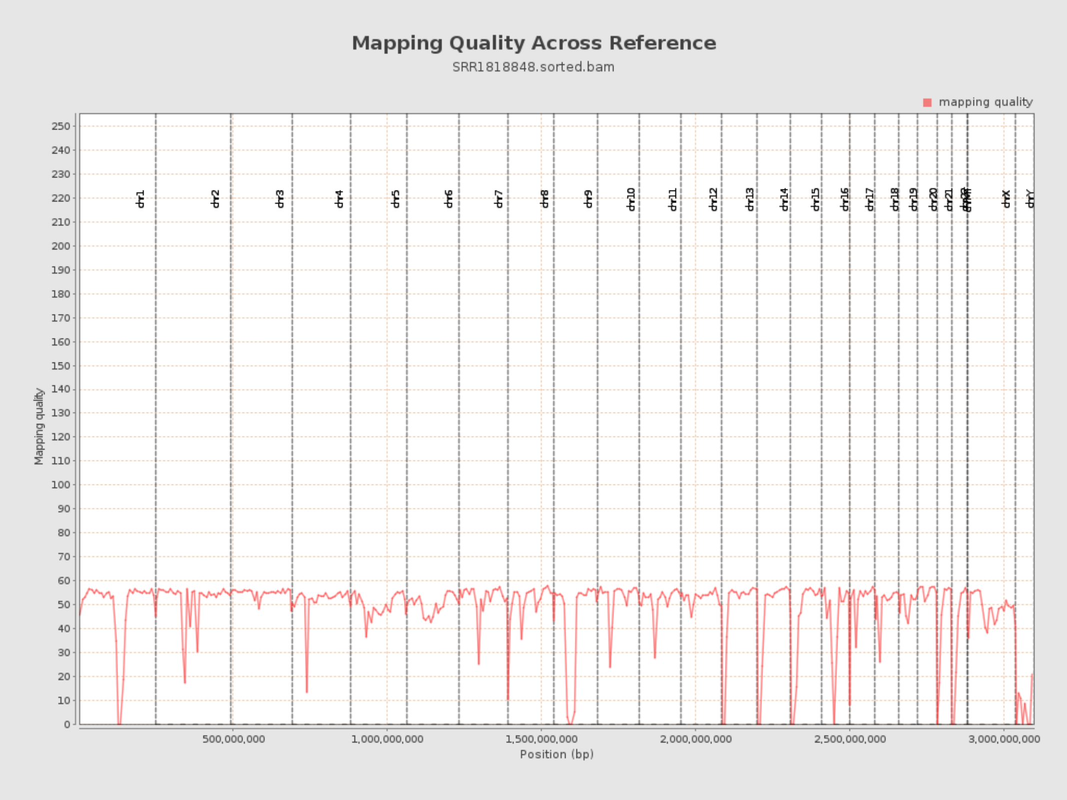
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram