Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:12:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818999.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_SRR1818999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818999.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:12:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	973,888
Mapped reads	949,332 / 97.48%
Unmapped reads	24,556 / 2.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,831 / 1.63%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	232,356 / 23.86%
Duplication rate	21.34%
Clipped reads	952,690 / 97.82%

2.2. ACGT Content

Number/percentage of A's	25,661,777 / 29.3%
Number/percentage of C's	17,888,529 / 20.43%
Number/percentage of T's	24,901,740 / 28.44%
Number/percentage of G's	19,116,513 / 21.83%
Number/percentage of N's	4,340 / 0%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.403

2.4. Mapping Quality

Mean Mapping Quality	49.04

2.5. Mismatches and indels

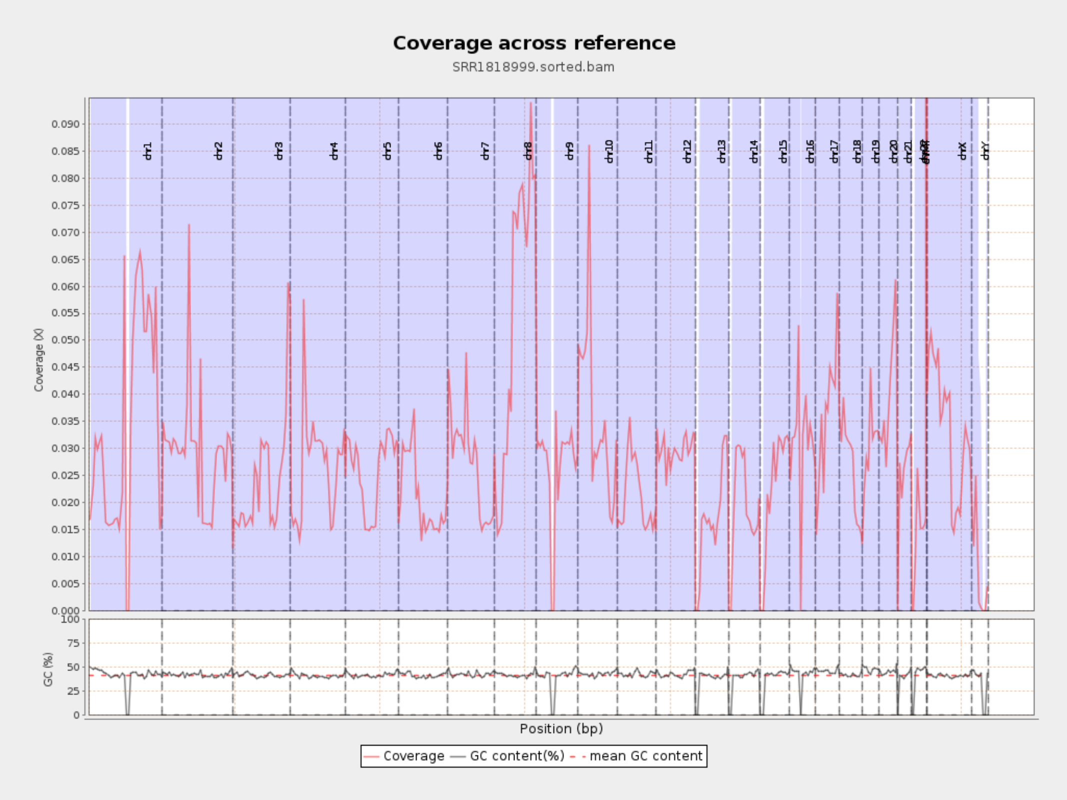
General error rate	0.71%
Mismatches	589,200
Insertions	15,493
Mapped reads with at least one insertion	1.59%
Deletions	29,836
Mapped reads with at least one deletion	3.07%
Homopolymer indels	39.71%

2.6. Chromosome stats

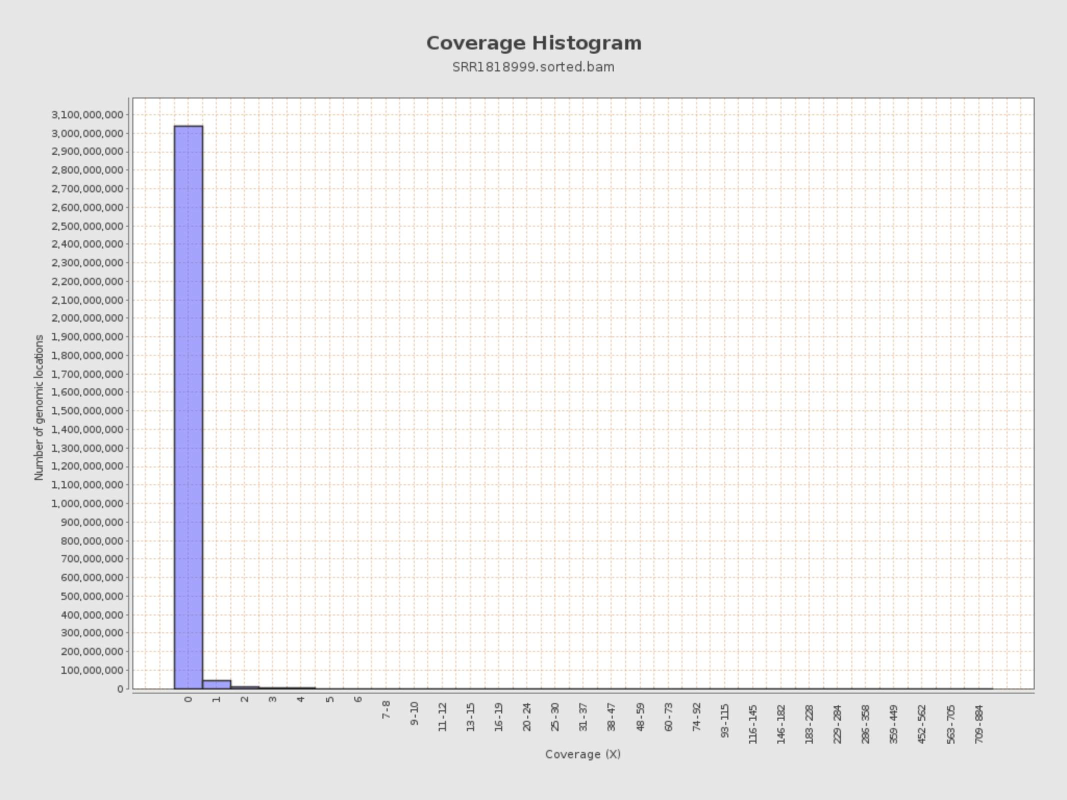
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8554486	0.0343	0.7851
chr2	243199373	7175147	0.0295	0.5506
chr3	198022430	4689598	0.0237	0.2098
chr4	191154276	5069740	0.0265	0.2848
chr5	180915260	4671021	0.0258	0.2263
chr6	171115067	3594274	0.021	0.2296
chr7	159138663	4340823	0.0273	0.4019

chr8	146364022	8027327	0.0548	0.3598
chr9	141213431	3718208	0.0263	0.3289
chr10	135534747	4877750	0.036	0.5689
chr11	135006516	2884056	0.0214	0.2443
chr12	133851895	3961445	0.0296	0.238
chr13	115169878	1953103	0.017	0.1759
chr14	107349540	2006217	0.0187	0.1994
chr15	102531392	2277648	0.0222	0.2014
chr16	90354753	2822498	0.0312	0.4475
chr17	81195210	2984597	0.0368	0.2999
chr18	78077248	2091687	0.0268	0.4137
chr19	59128983	1803093	0.0305	0.6521
chr20	63025520	2555470	0.0405	0.2945
chr21	48129895	1201492	0.025	0.2473
chr22	51304566	669867	0.0131	0.1676
chrMT	16571	17636	1.0643	1.7056
chrX	155270560	5268110	0.0339	0.3117
chrY	59373566	413686	0.007	0.457

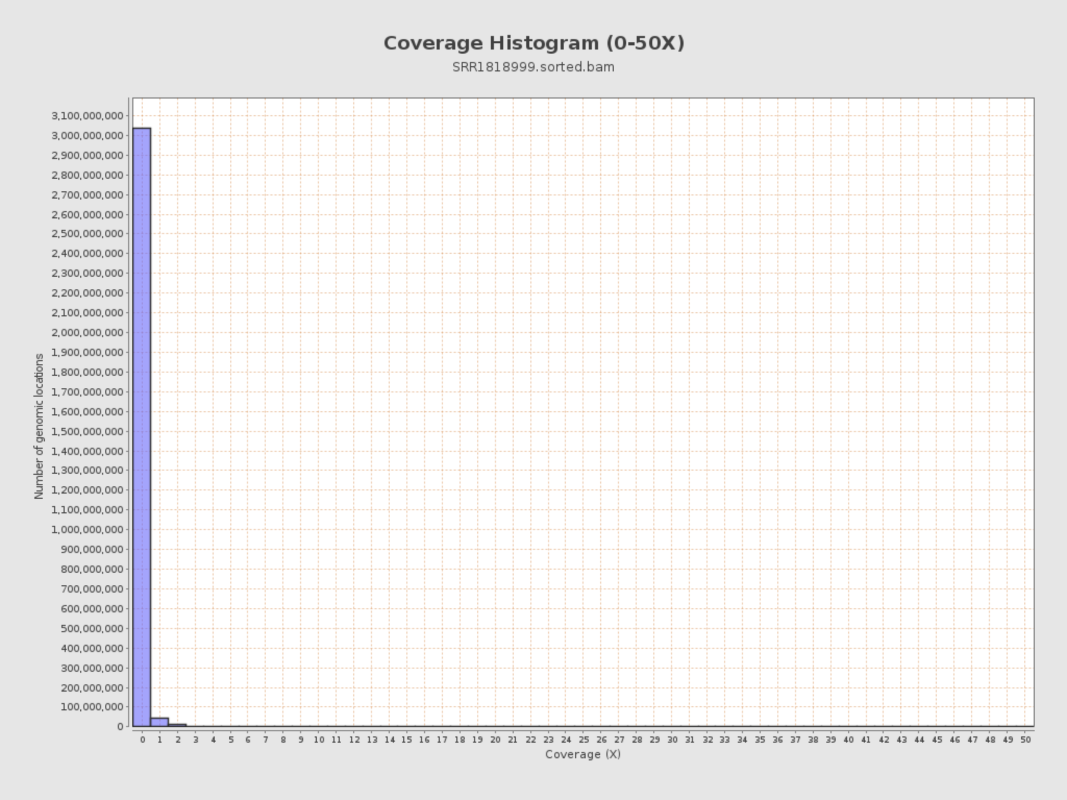
3. Results : Coverage across reference



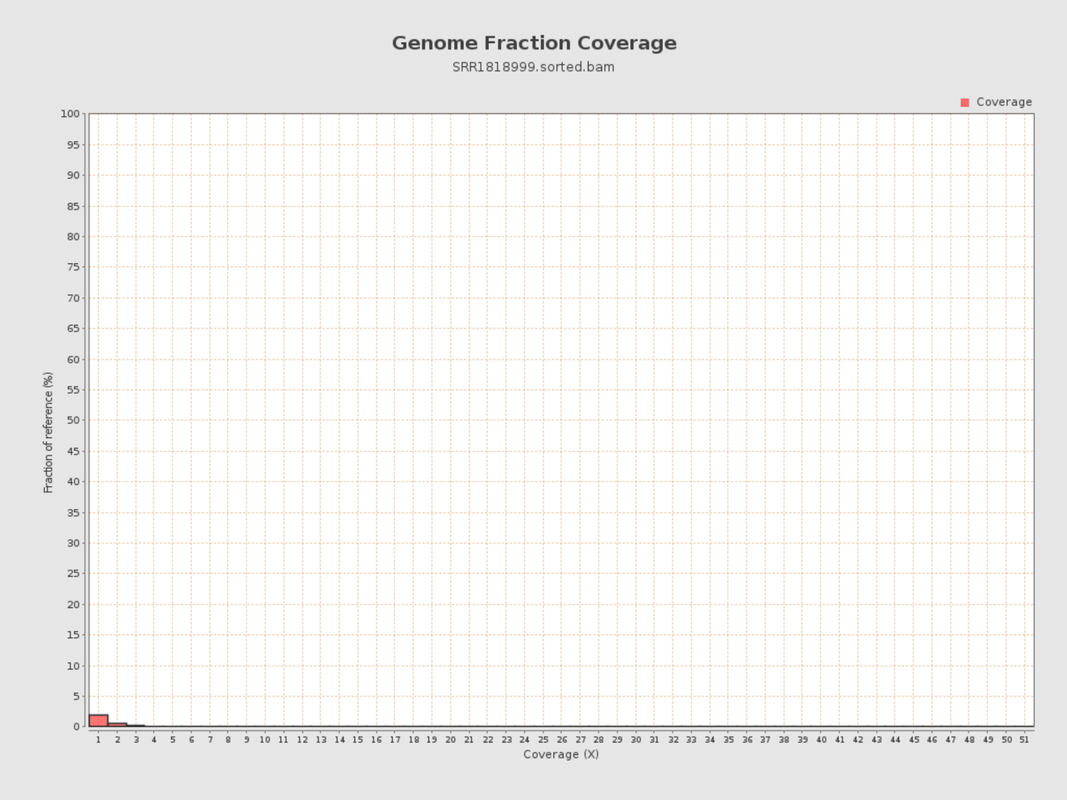
4. Results : Coverage Histogram



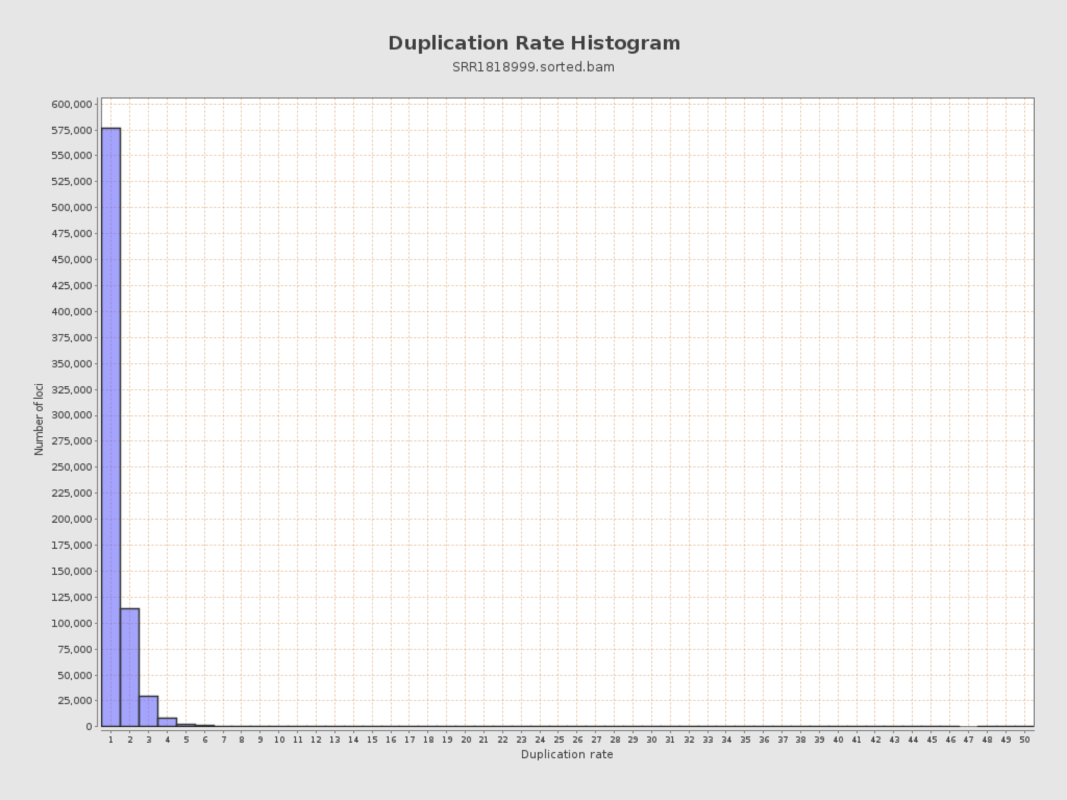
5. Results : Coverage Histogram (0-50X)



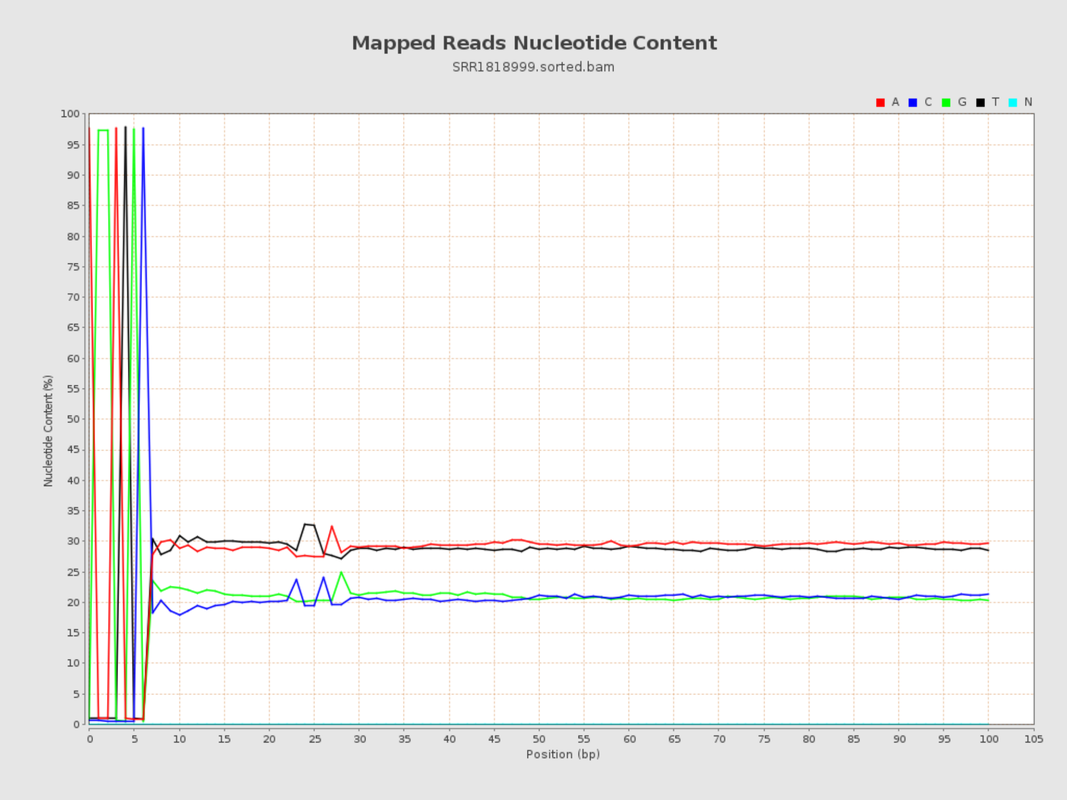
6. Results : Genome Fraction Coverage



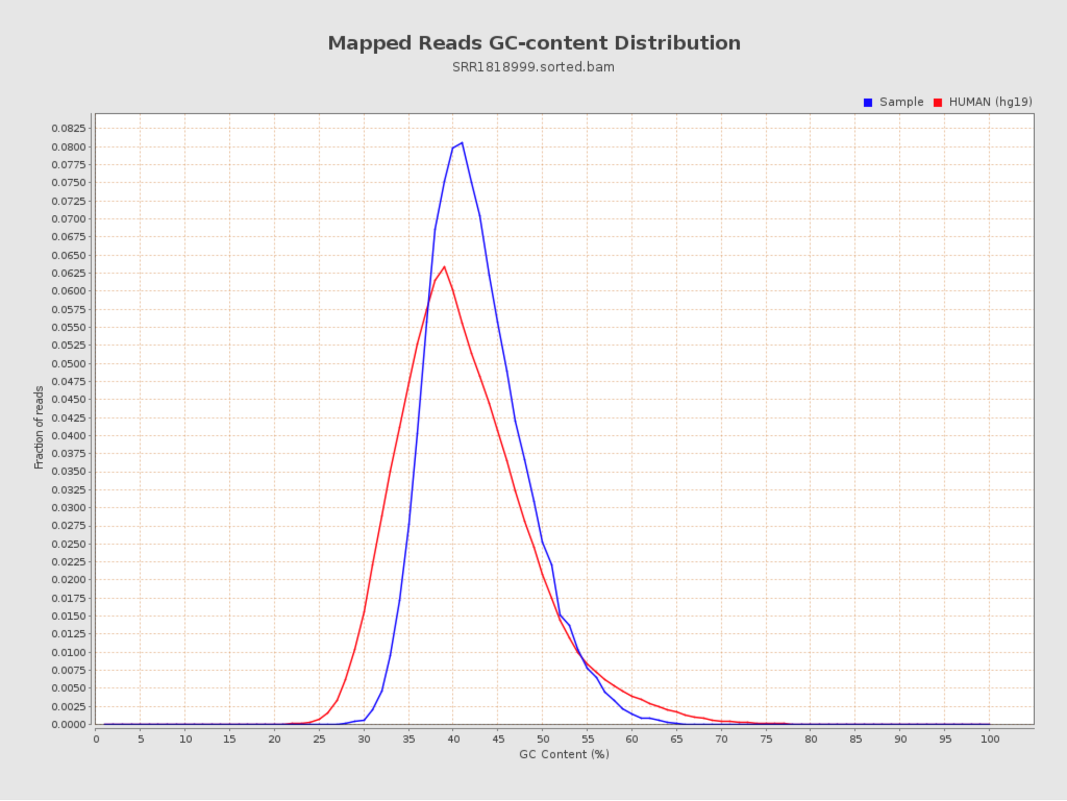
7. Results : Duplication Rate Histogram



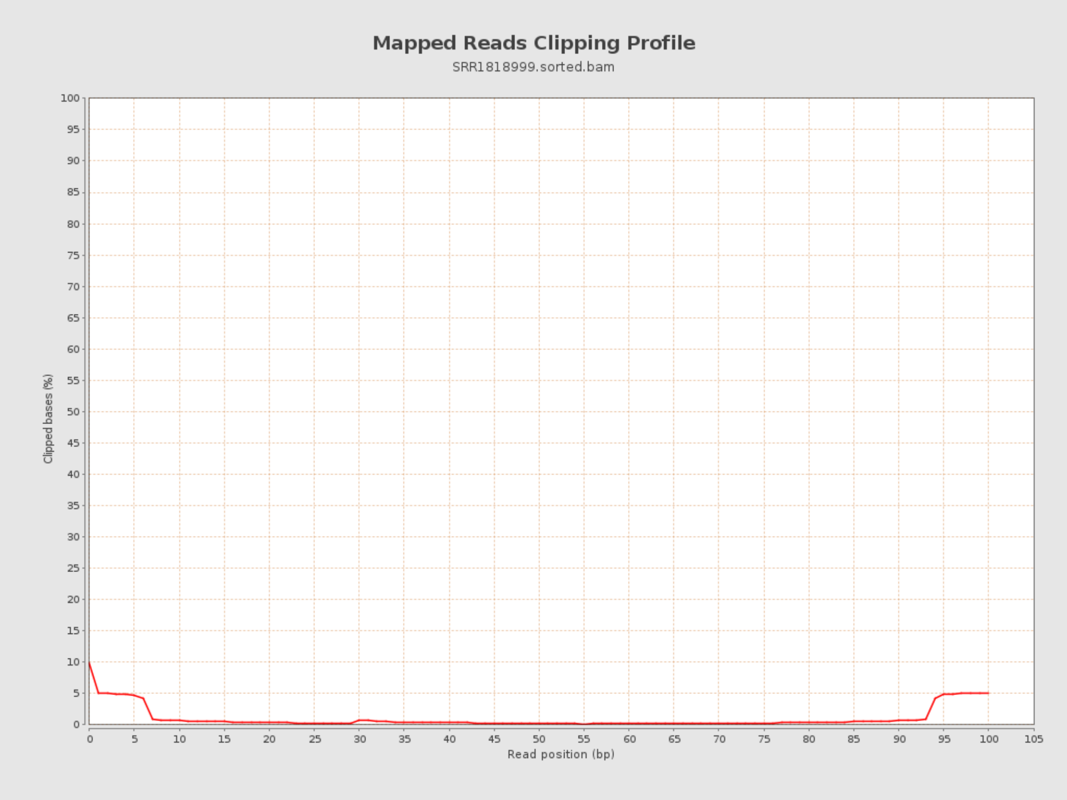
8. Results : Mapped Reads Nucleotide Content



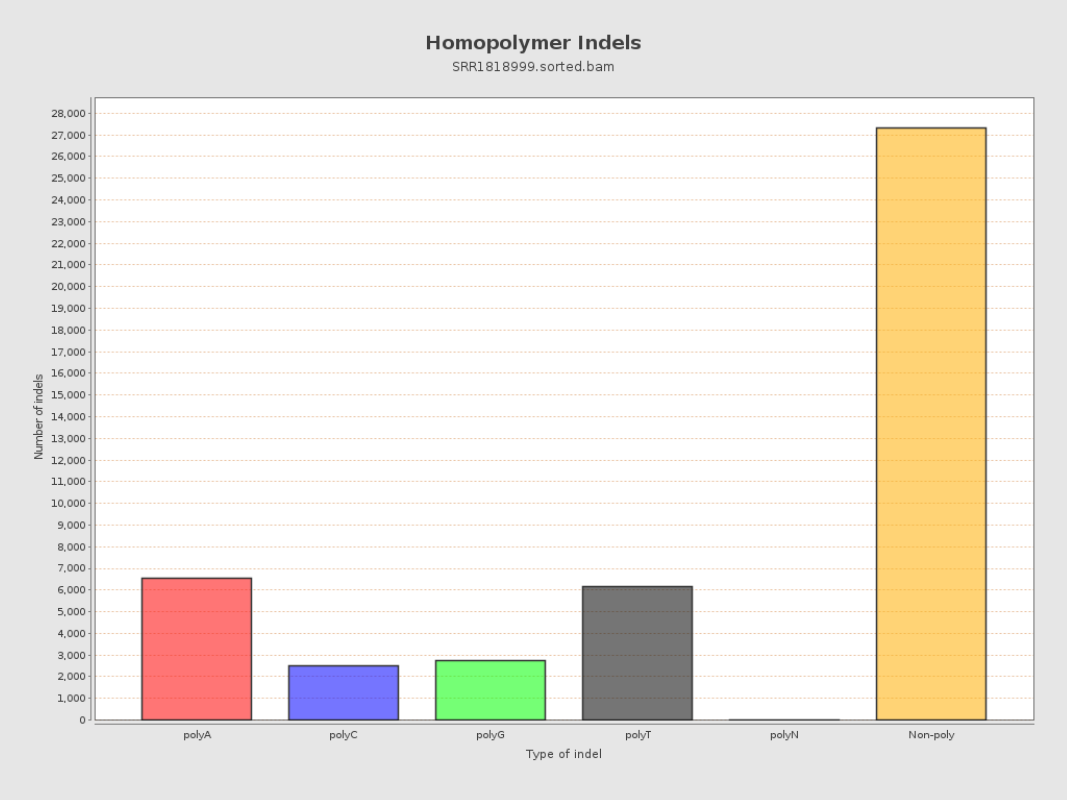
9. Results : Mapped Reads GC-content Distribution



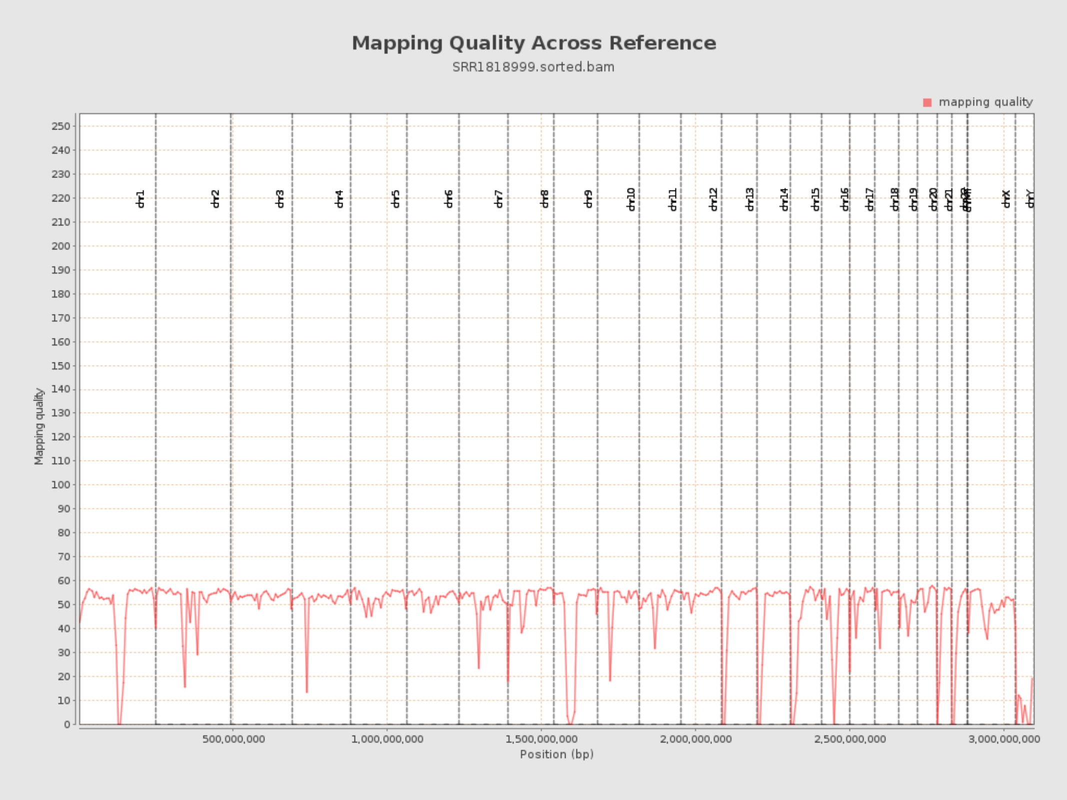
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram