Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:05:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818899.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_SRR1818899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818899.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:05:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,163,123
Mapped reads	1,135,687 / 97.64%
Unmapped reads	27,436 / 2.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,710 / 1.44%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	188,773 / 16.23%
Duplication rate	13.78%
Clipped reads	1,143,512 / 98.31%

2.2. ACGT Content

Number/percentage of A's	30,648,974 / 29.17%
Number/percentage of C's	22,721,845 / 21.63%
Number/percentage of T's	29,581,023 / 28.16%
Number/percentage of G's	22,100,531 / 21.04%
Number/percentage of N's	1,440 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.034

Standard Deviation	0.4575

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

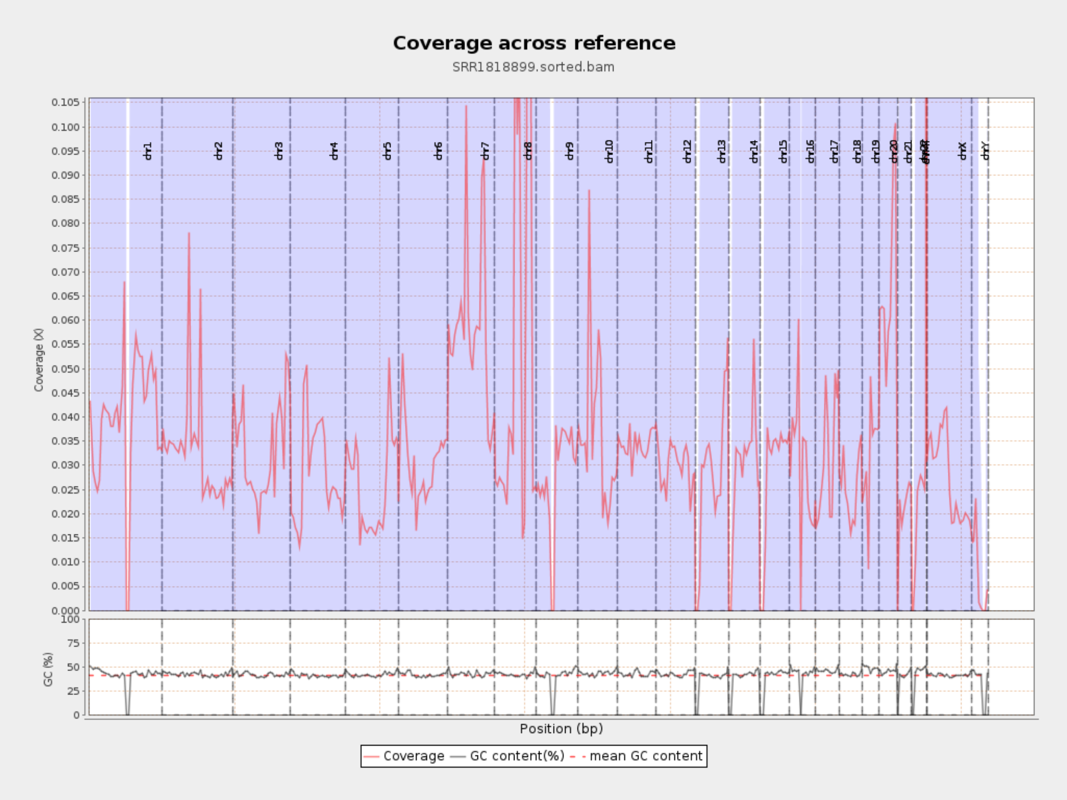
General error rate	0.66%
Mismatches	649,341
Insertions	16,121
Mapped reads with at least one insertion	1.37%
Deletions	35,164
Mapped reads with at least one deletion	3.02%
Homopolymer indels	40.83%

2.6. Chromosome stats

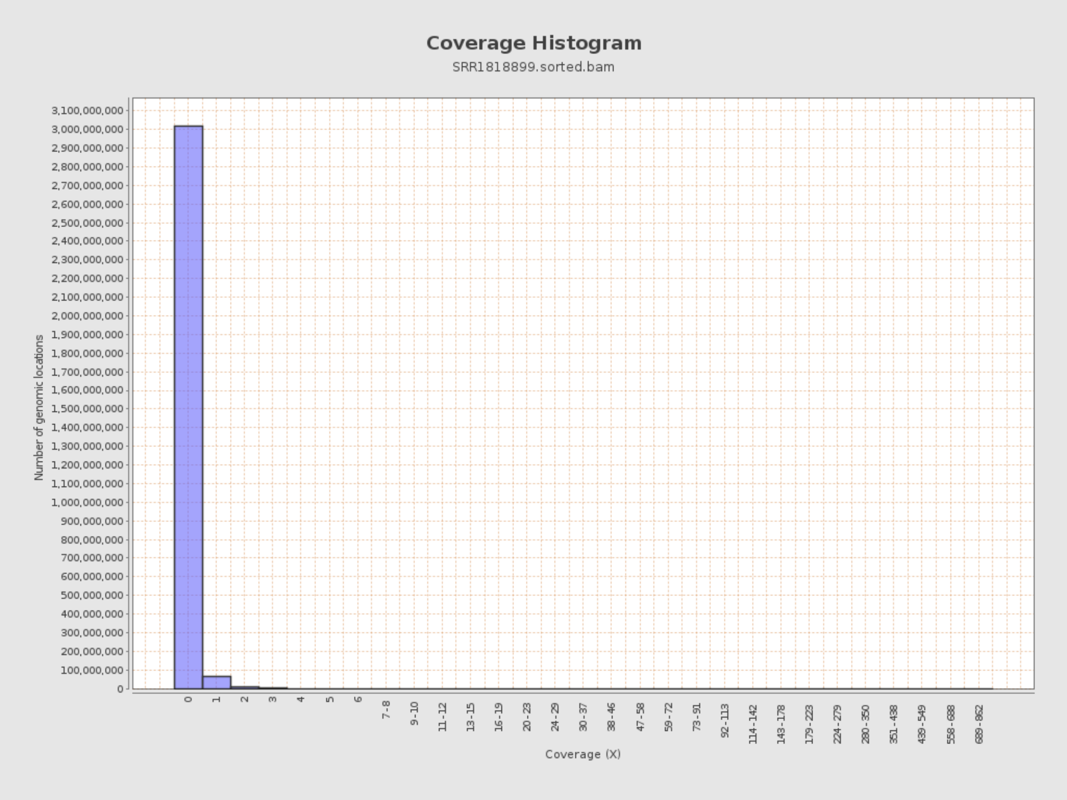
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9919817	0.0398	0.6915
chr2	243199373	7979240	0.0328	0.6708
chr3	198022430	6536672	0.033	0.2245
chr4	191154276	5342479	0.0279	0.2721
chr5	180915260	4663101	0.0258	0.2117
chr6	171115067	5195431	0.0304	0.2378
chr7	159138663	9458042	0.0594	0.9818

chr8	146364022	9099479	0.0622	0.3765
chr9	141213431	3883321	0.0275	0.3489
chr10	135534747	4936547	0.0364	0.5912
chr11	135006516	4624159	0.0343	0.273
chr12	133851895	4034959	0.0301	0.2165
chr13	115169878	3179714	0.0276	0.2021
chr14	107349540	3091512	0.0288	0.2267
chr15	102531392	2908837	0.0284	0.2079
chr16	90354753	2643304	0.0293	0.4933
chr17	81195210	2602164	0.032	0.2726
chr18	78077248	1981549	0.0254	0.3993
chr19	59128983	1864441	0.0315	0.6001
chr20	63025520	4292442	0.0681	0.3433
chr21	48129895	990691	0.0206	0.2148
chr22	51304566	948572	0.0185	0.1877
chrMT	16571	244188	14.7359	8.9239
chrX	155270560	4289477	0.0276	0.2454
chrY	59373566	411836	0.0069	0.5799

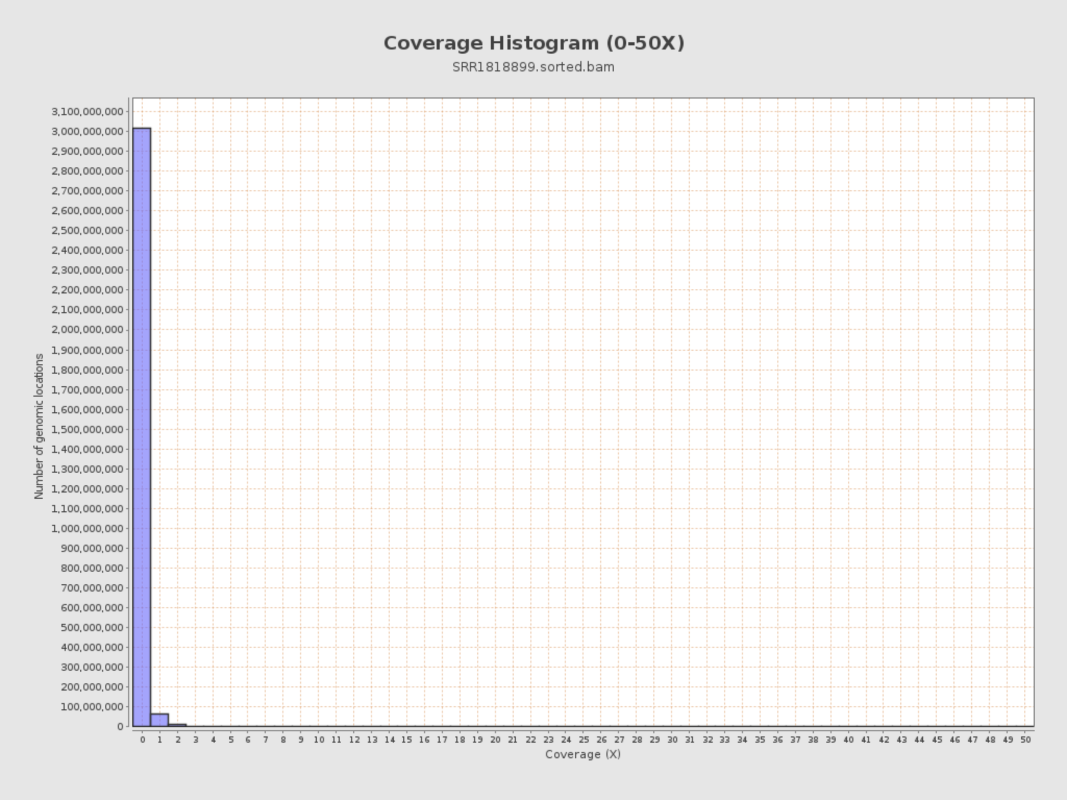
3. Results : Coverage across reference



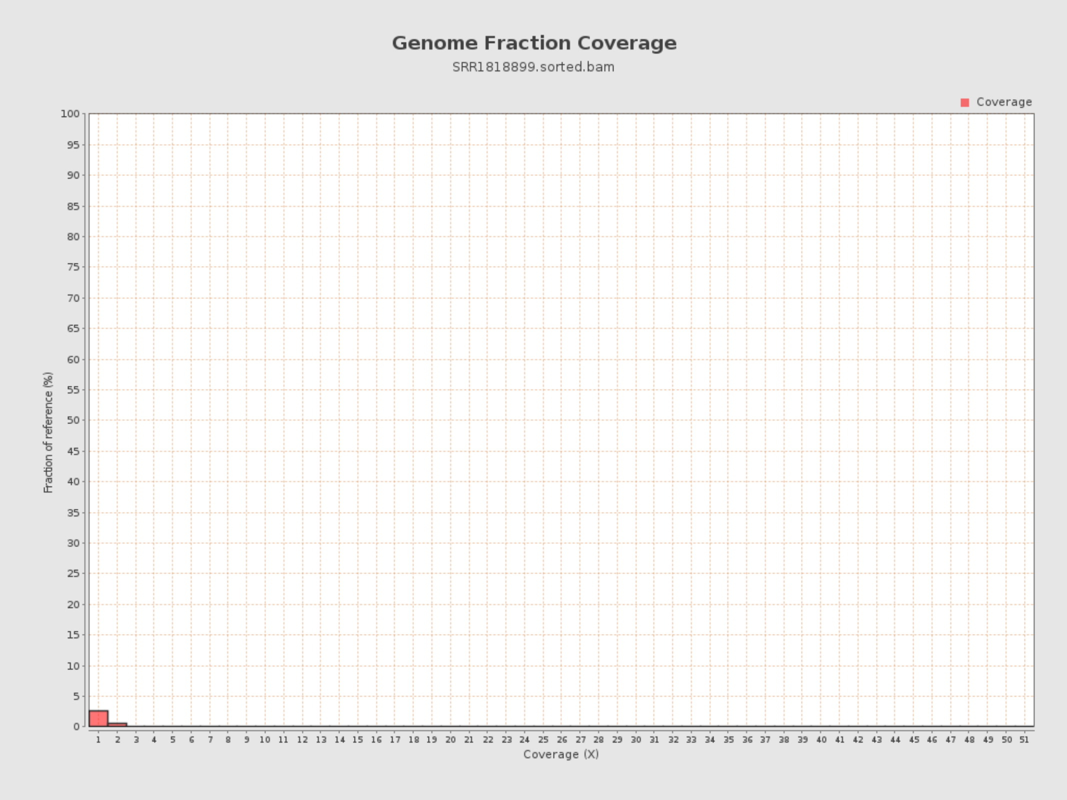
4. Results : Coverage Histogram



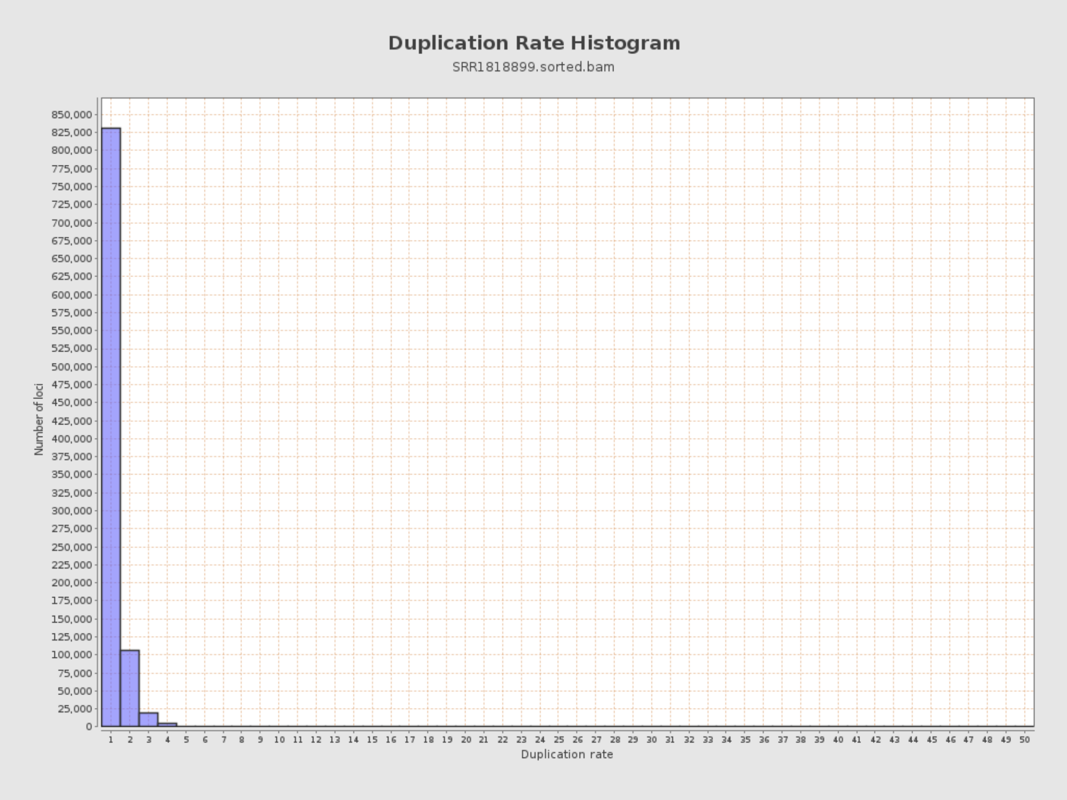
5. Results : Coverage Histogram (0-50X)



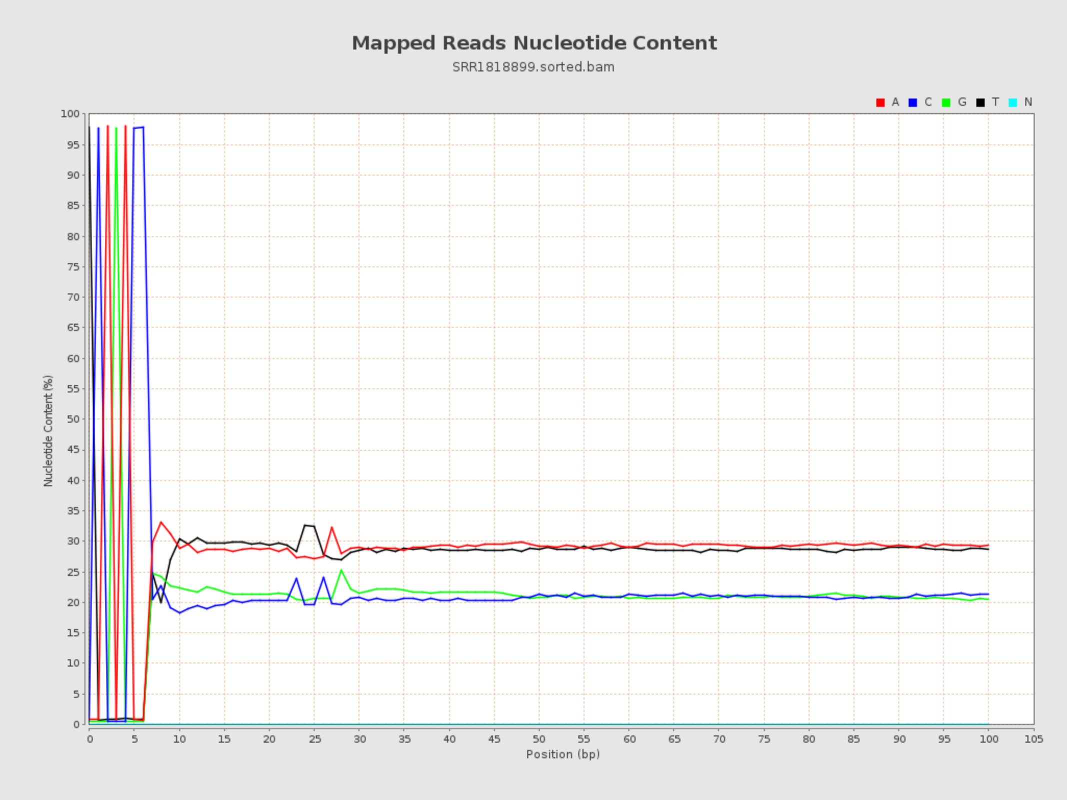
6. Results : Genome Fraction Coverage



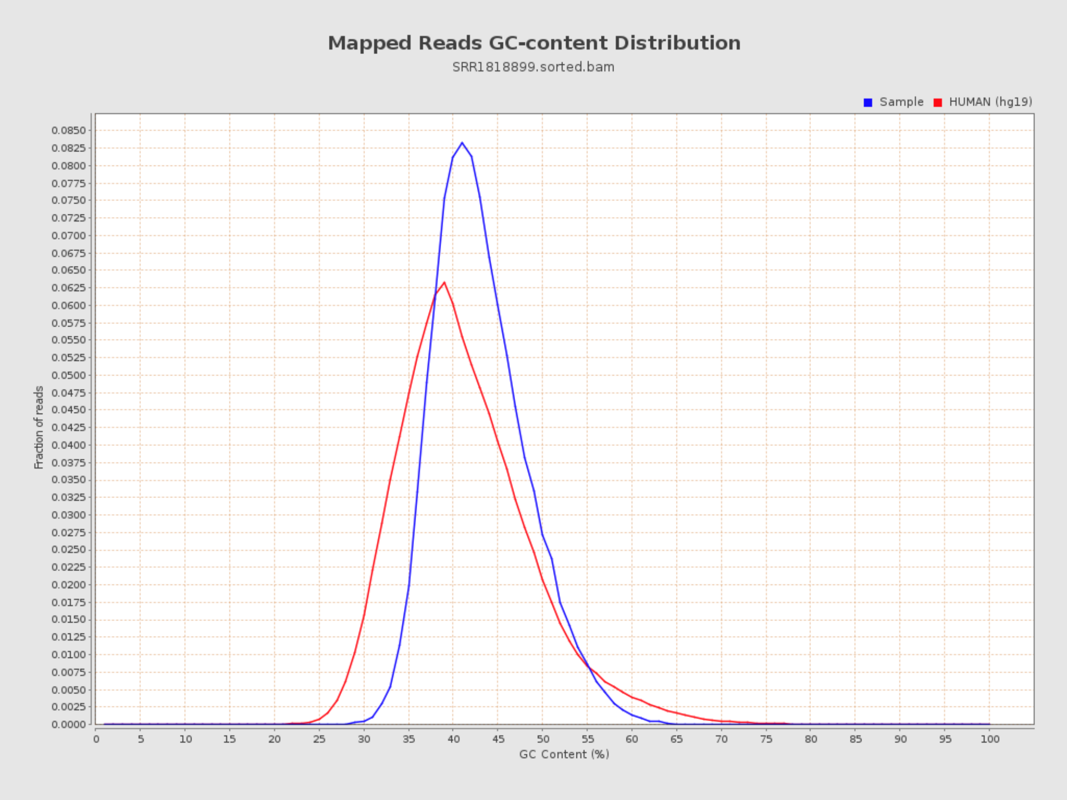
7. Results : Duplication Rate Histogram



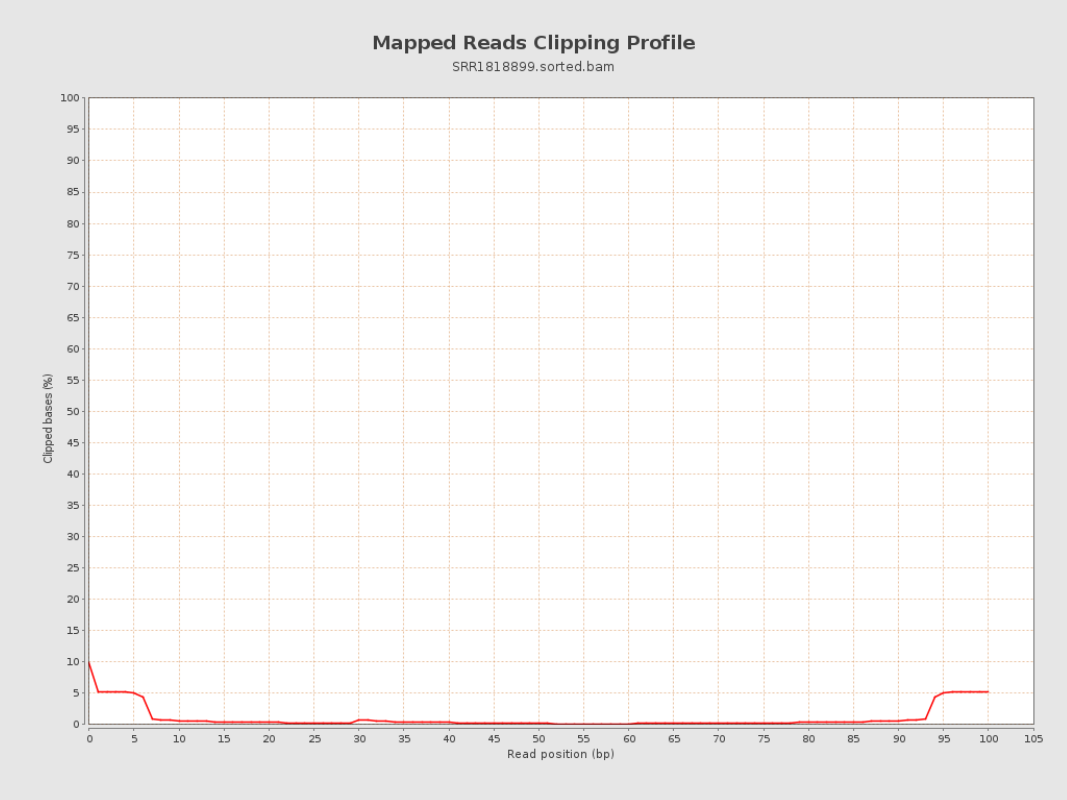
8. Results : Mapped Reads Nucleotide Content



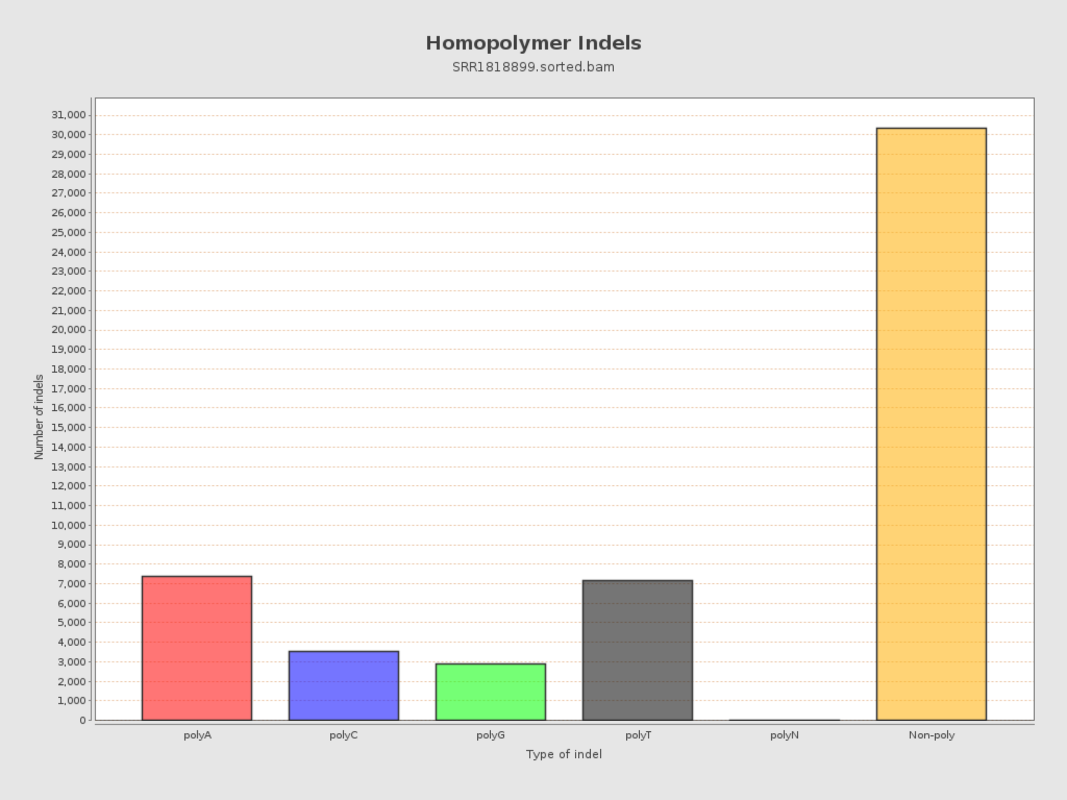
9. Results : Mapped Reads GC-content Distribution



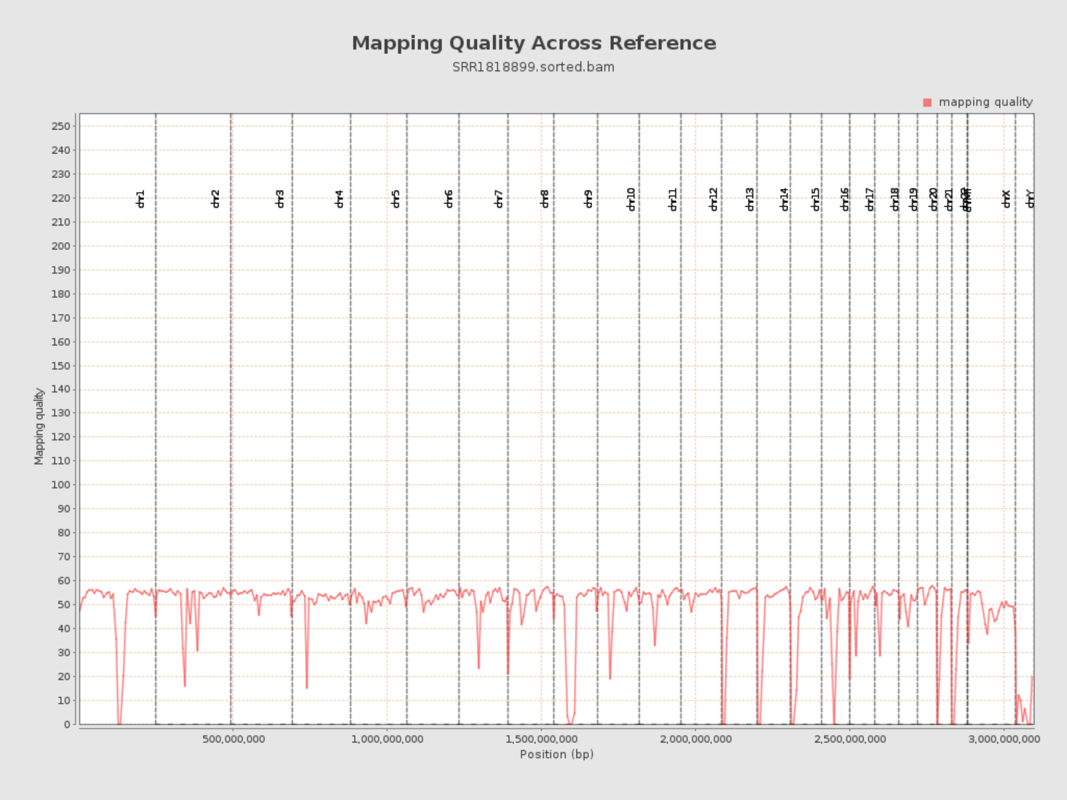
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram