Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:41:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818865.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_SRR1818865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:41:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	562,570
Mapped reads	554,315 / 98.53%
Unmapped reads	8,255 / 1.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,190 / 1.46%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	65,519 / 11.65%
Duplication rate	9.93%
Clipped reads	559,468 / 99.45%

2.2. ACGT Content

Number/percentage of A's	14,807,845 / 28.87%
Number/percentage of C's	11,550,972 / 22.52%
Number/percentage of T's	14,092,646 / 27.48%
Number/percentage of G's	10,830,299 / 21.12%
Number/percentage of N's	882 / 0%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.2257

2.4. Mapping Quality

Mean Mapping Quality	49.17

2.5. Mismatches and indels

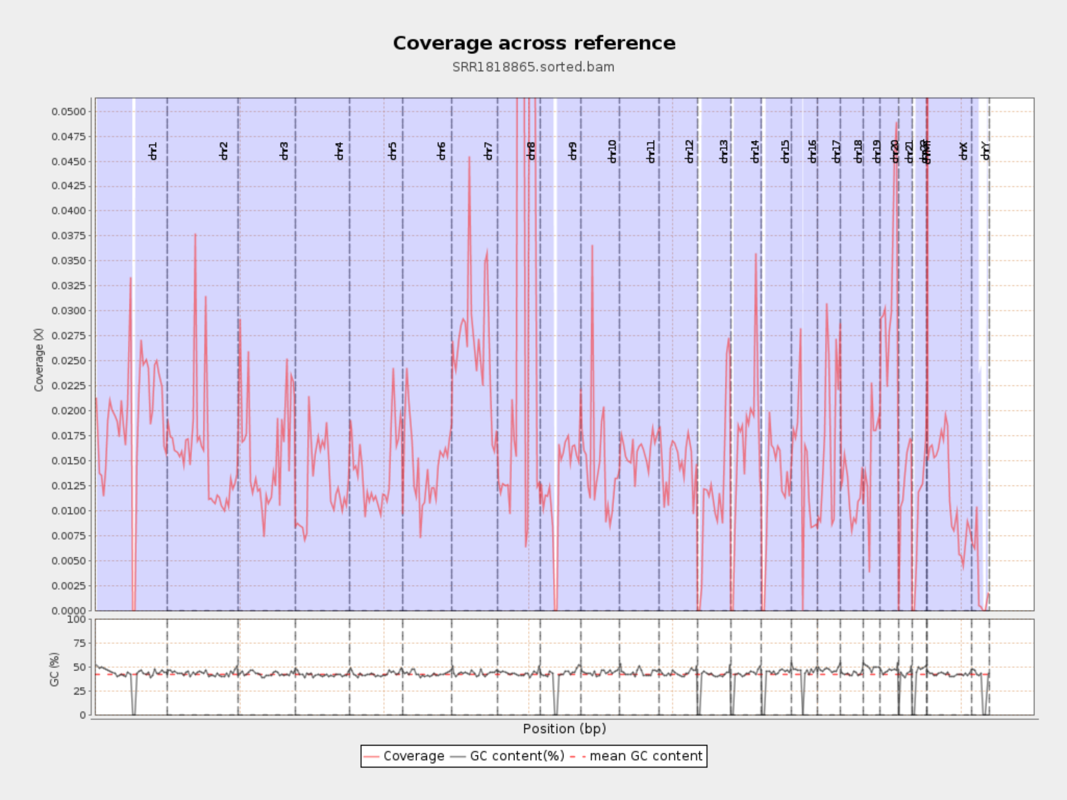
General error rate	0.64%
Mismatches	310,928
Insertions	6,929
Mapped reads with at least one insertion	1.21%
Deletions	16,461
Mapped reads with at least one deletion	2.9%
Homopolymer indels	41.17%

2.6. Chromosome stats

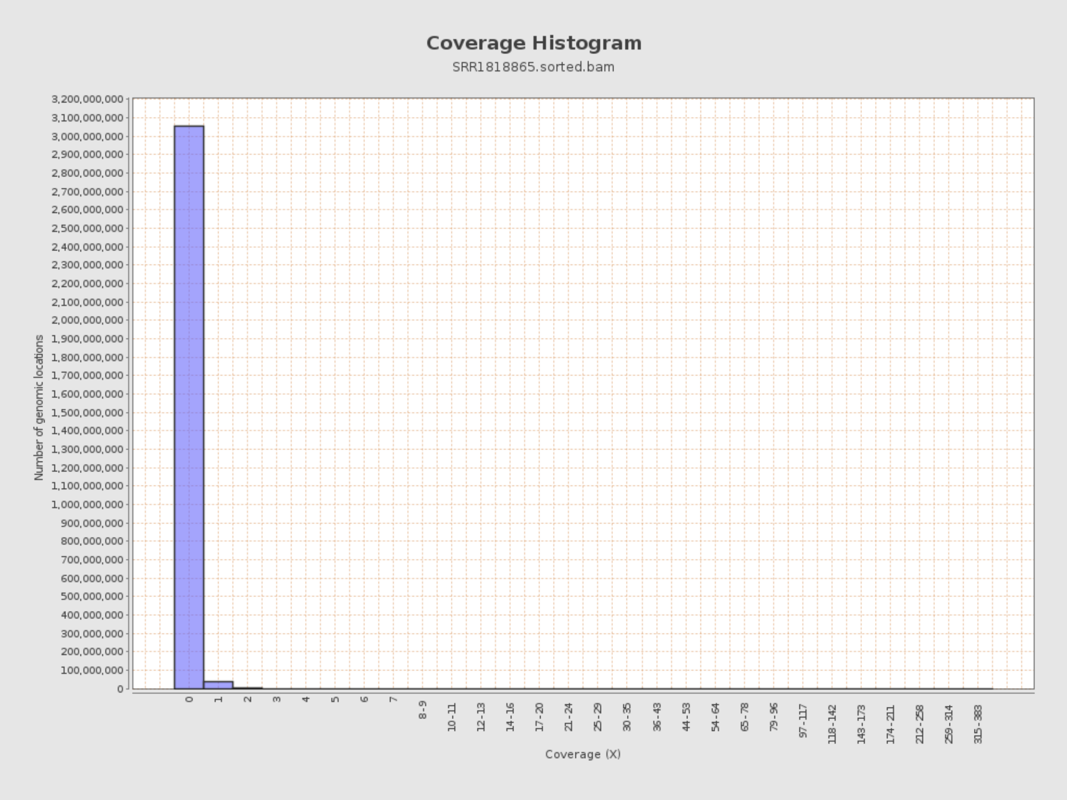
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4718456	0.0189	0.3339
chr2	243199373	3770349	0.0155	0.3168
chr3	198022430	3162528	0.016	0.1456
chr4	191154276	2443111	0.0128	0.1505
chr5	180915260	2536811	0.014	0.139
chr6	171115067	2466452	0.0144	0.1436
chr7	159138663	4248502	0.0267	0.4197

chr8	146364022	5917328	0.0404	0.2673
chr9	141213431	1786939	0.0127	0.1737
chr10	135534747	2004266	0.0148	0.2672
chr11	135006516	2164095	0.016	0.1619
chr12	133851895	1953258	0.0146	0.1391
chr13	115169878	1370014	0.0119	0.1251
chr14	107349540	1758063	0.0164	0.1533
chr15	102531392	1242621	0.0121	0.126
chr16	90354753	1244835	0.0138	0.2133
chr17	81195210	1453956	0.0179	0.176
chr18	78077248	892497	0.0114	0.1947
chr19	59128983	907446	0.0153	0.2839
chr20	63025520	2062573	0.0327	0.2172
chr21	48129895	611099	0.0127	0.1398
chr22	51304566	498012	0.0097	0.1184
chrMT	16571	37445	2.2597	2.1393
chrX	155270560	1879910	0.0121	0.138
chrY	59373566	183762	0.0031	0.233

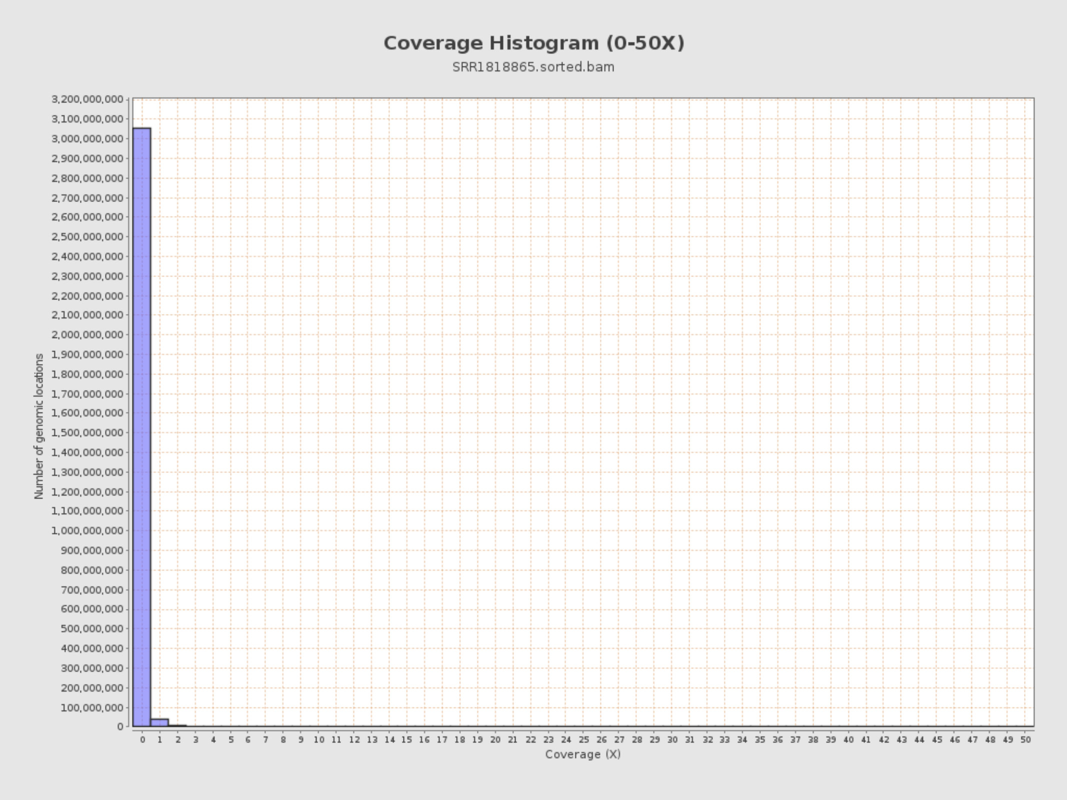
3. Results : Coverage across reference



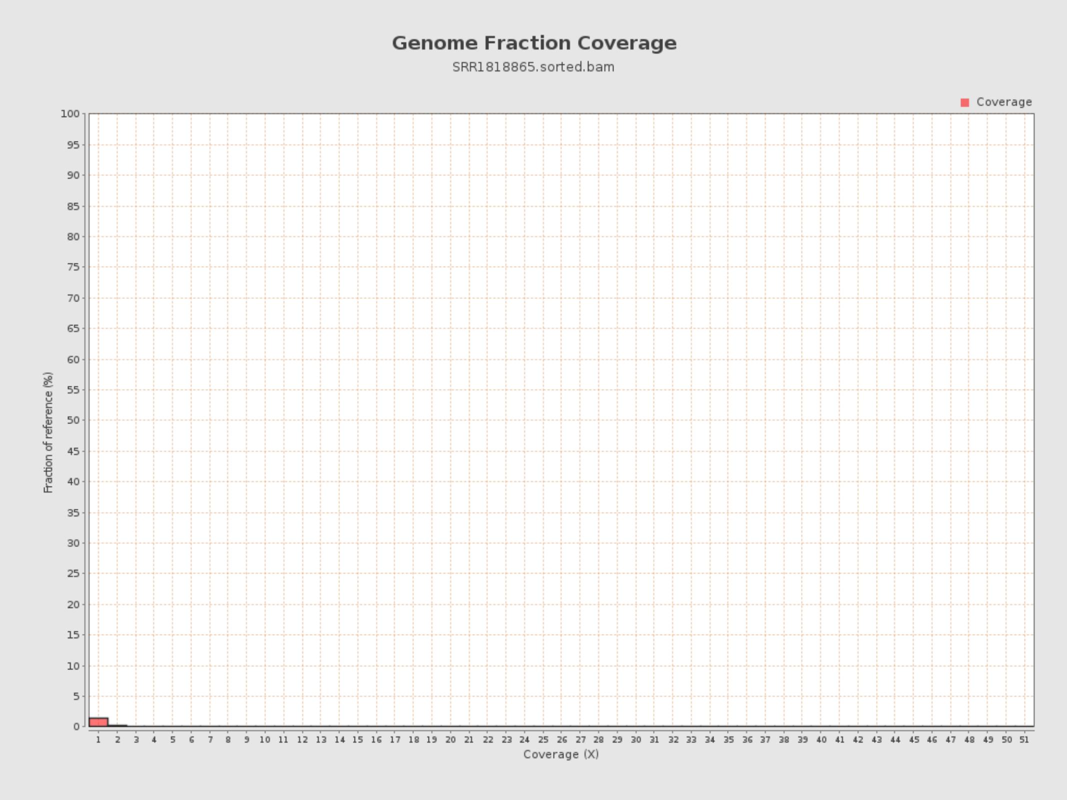
4. Results : Coverage Histogram



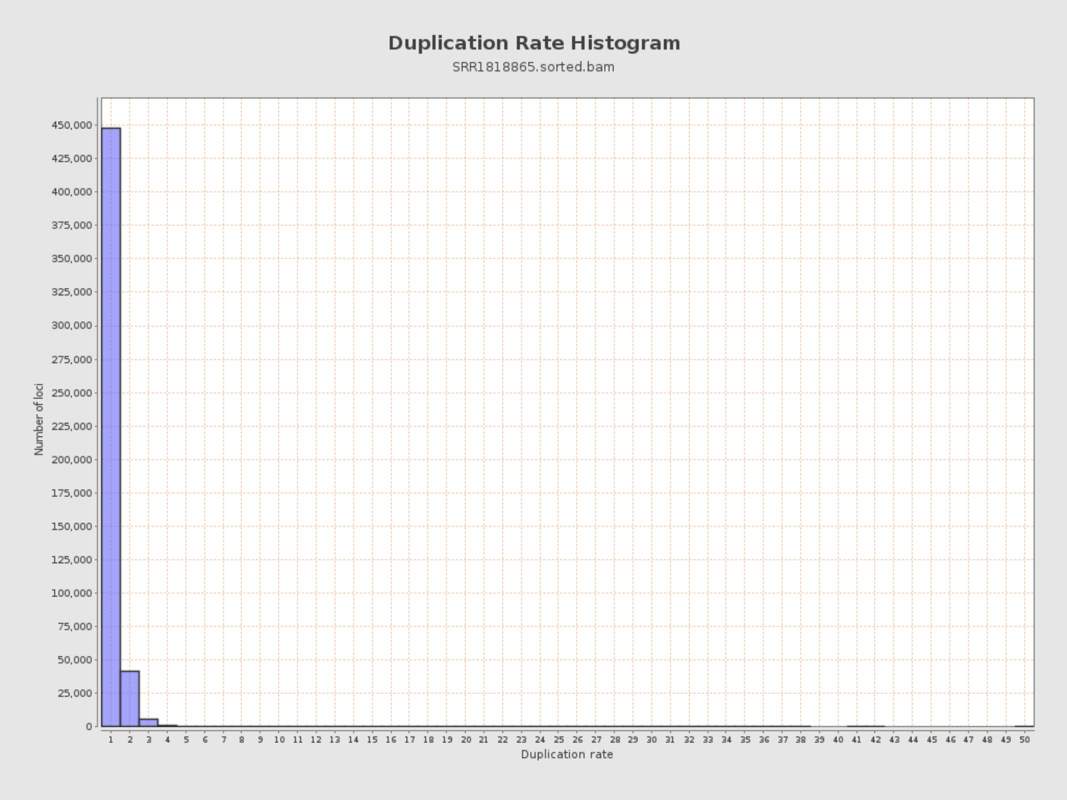
5. Results : Coverage Histogram (0-50X)



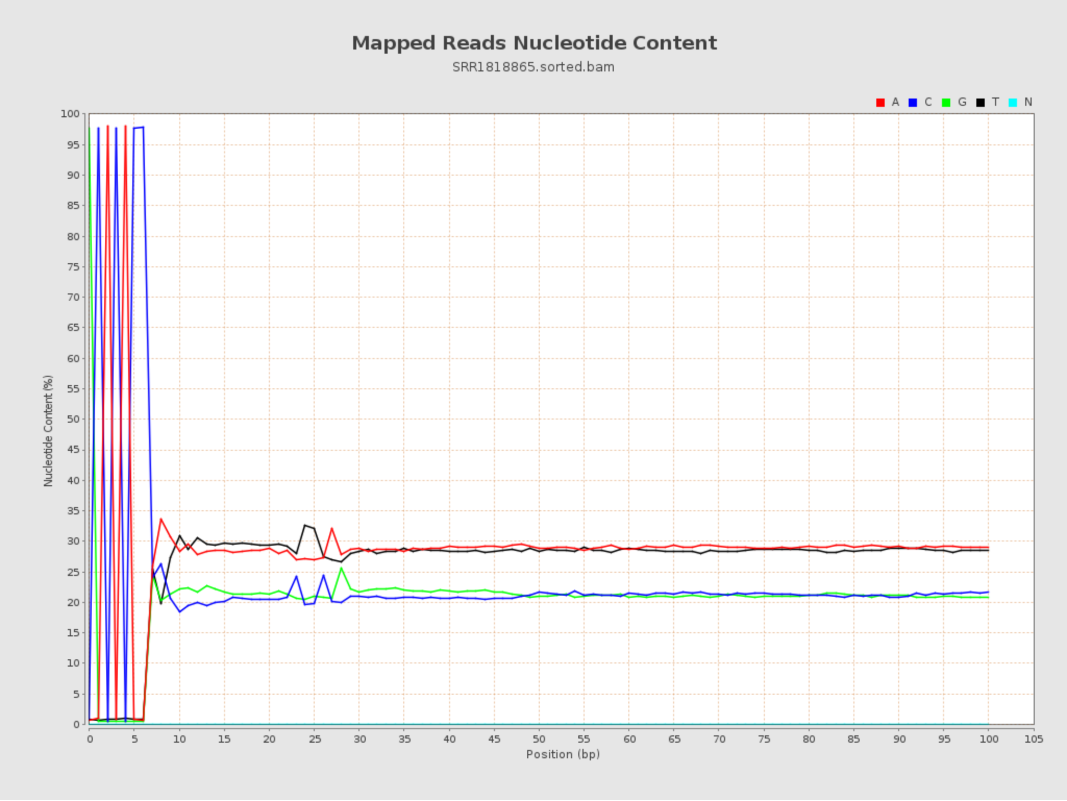
6. Results : Genome Fraction Coverage



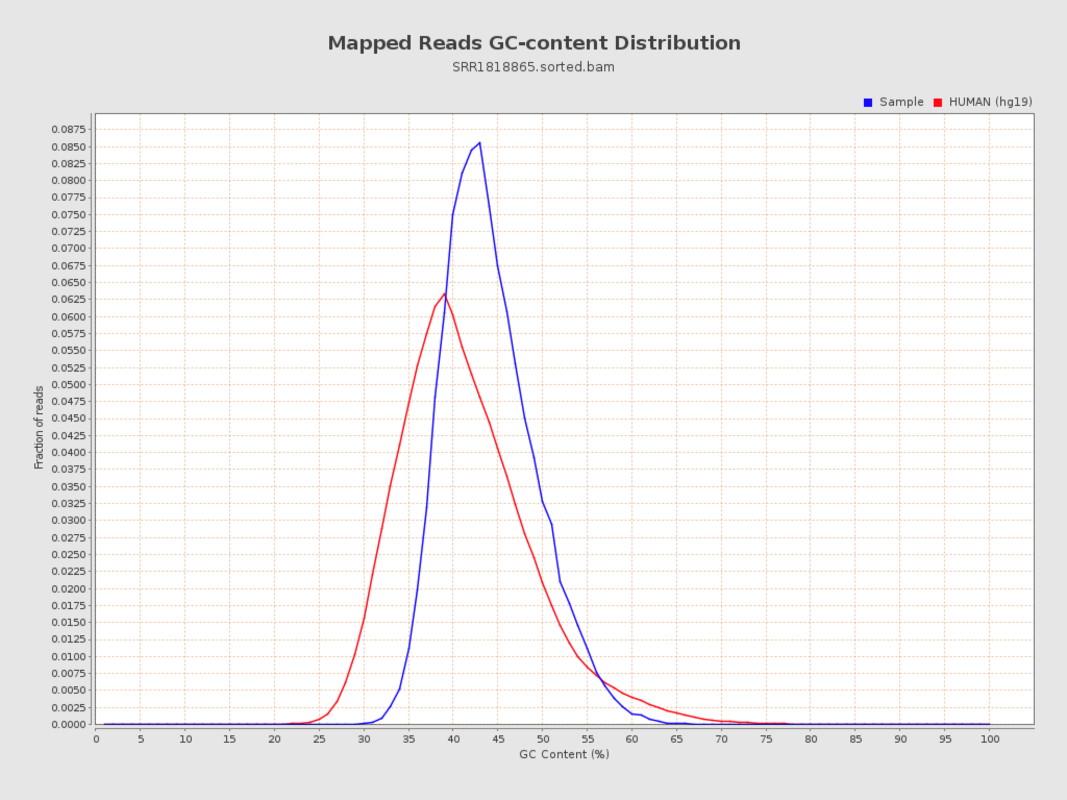
7. Results : Duplication Rate Histogram



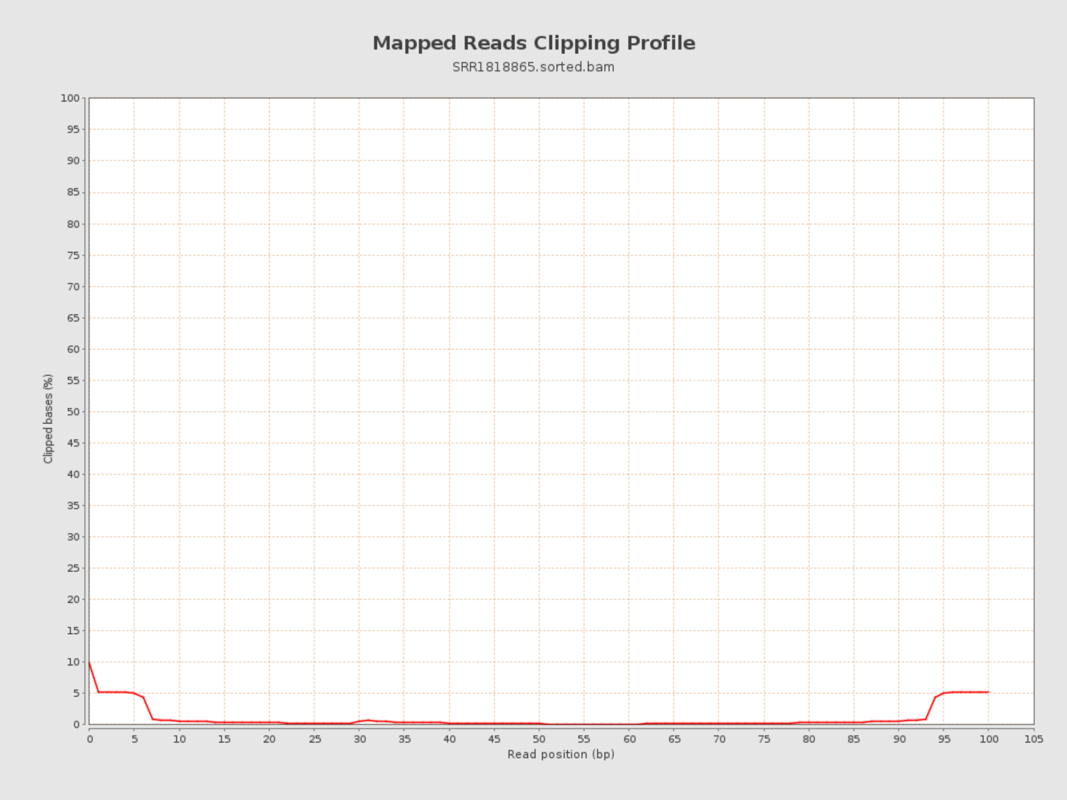
8. Results : Mapped Reads Nucleotide Content



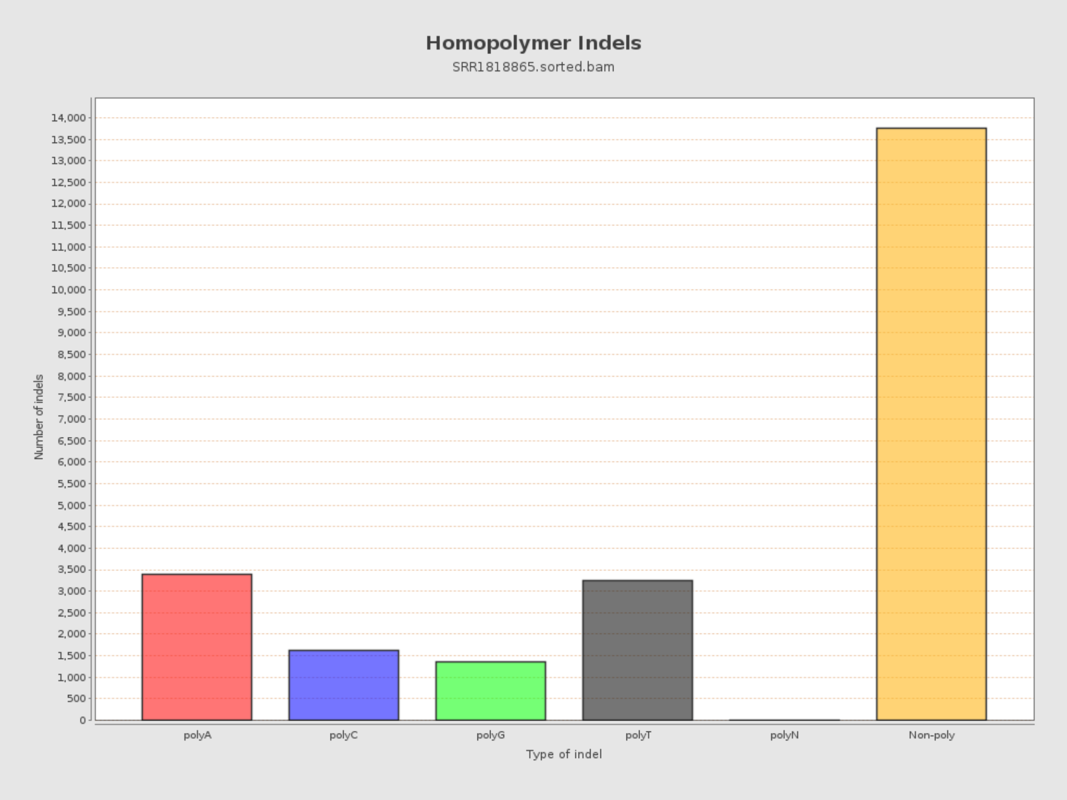
9. Results : Mapped Reads GC-content Distribution



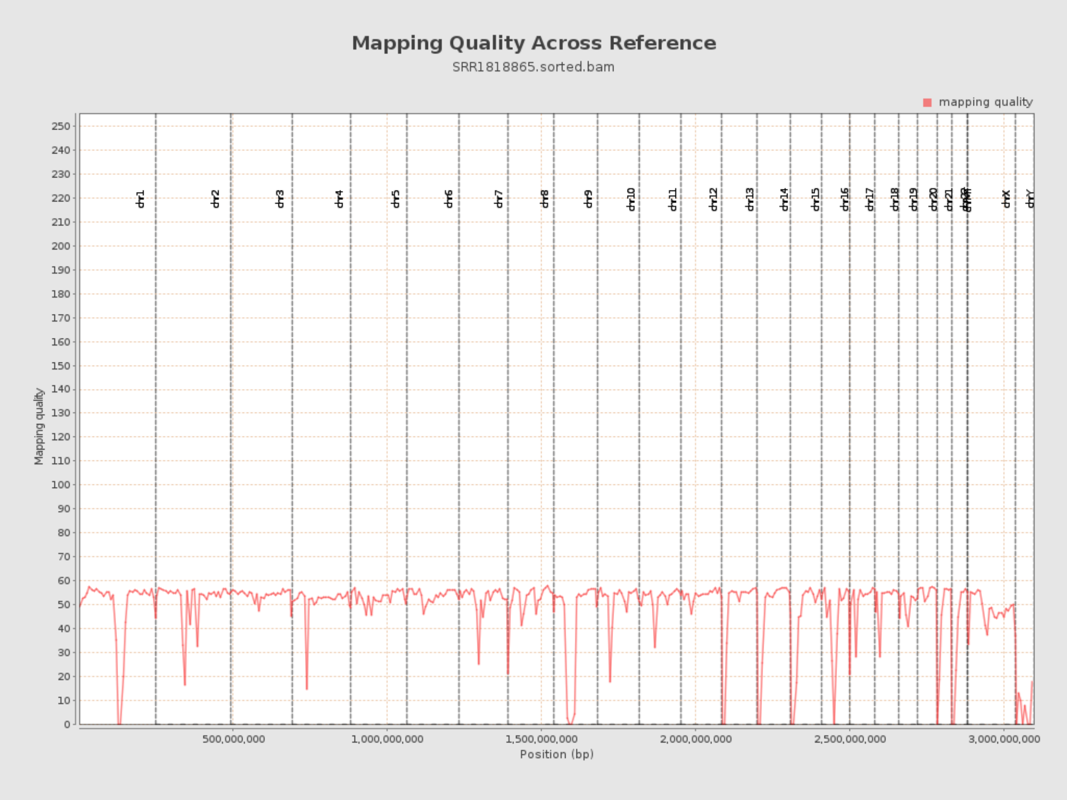
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram