Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:37:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818925.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_SRR1818925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818925.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:37:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	796,637
Mapped reads	784,011 / 98.42%
Unmapped reads	12,626 / 1.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,911 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	202,008 / 25.36%
Duplication rate	23.37%
Clipped reads	789,513 / 99.11%

2.2. ACGT Content

Number/percentage of A's	21,158,715 / 29.14%
Number/percentage of C's	14,759,026 / 20.33%
Number/percentage of T's	20,706,642 / 28.52%
Number/percentage of G's	15,975,638 / 22%
Number/percentage of N's	2,956 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2834

2.4. Mapping Quality

Mean Mapping Quality	49

2.5. Mismatches and indels

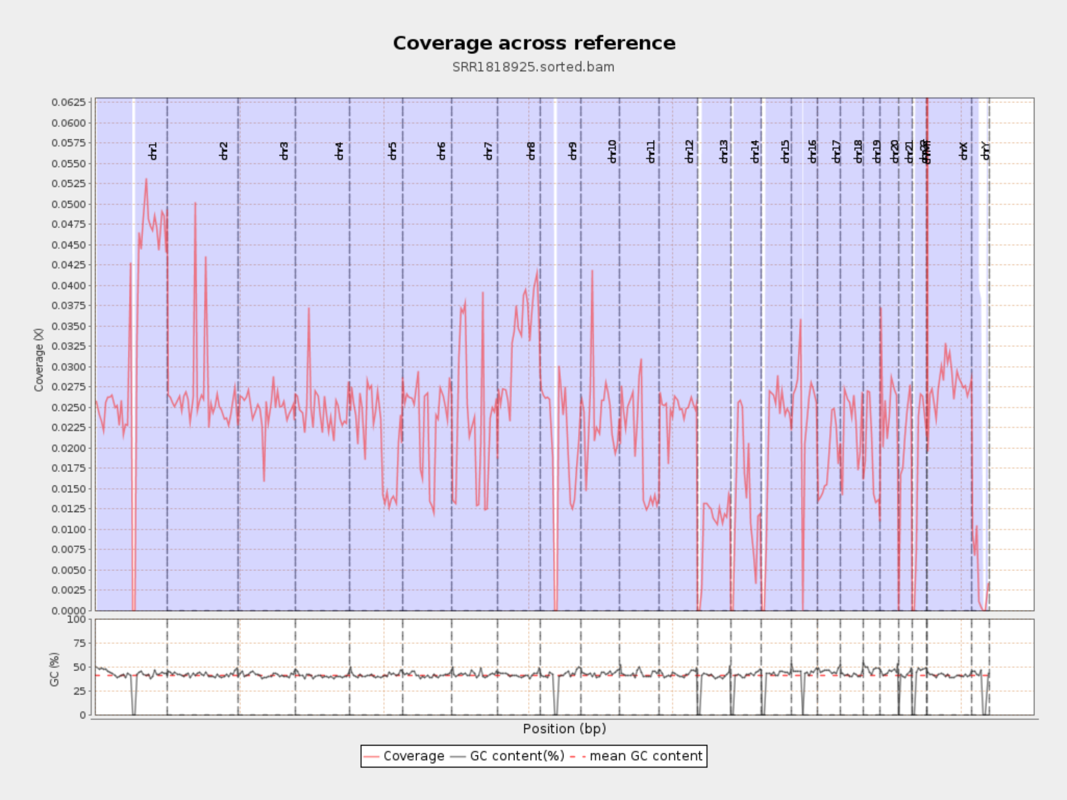
General error rate	0.65%
Mismatches	449,443
Insertions	9,431
Mapped reads with at least one insertion	1.18%
Deletions	22,101
Mapped reads with at least one deletion	2.76%
Homopolymer indels	42.86%

2.6. Chromosome stats

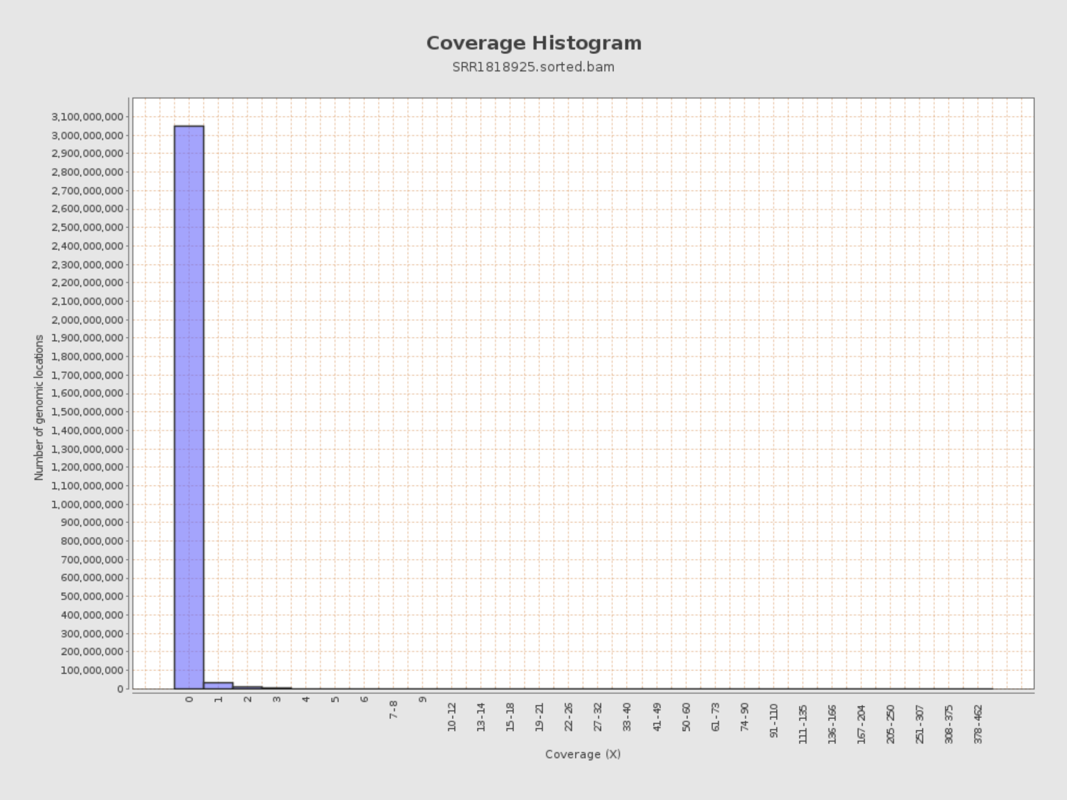
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8270418	0.0332	0.4503
chr2	243199373	6473968	0.0266	0.3823
chr3	198022430	4927118	0.0249	0.2171
chr4	191154276	4755392	0.0249	0.2312
chr5	180915260	3848523	0.0213	0.204
chr6	171115067	4035421	0.0236	0.2218
chr7	159138663	3709722	0.0233	0.2459

chr8	146364022	4861648	0.0332	0.273
chr9	141213431	2812026	0.0199	0.2919
chr10	135534747	3284348	0.0242	0.3135
chr11	135006516	2757013	0.0204	0.2201
chr12	133851895	3316276	0.0248	0.2213
chr13	115169878	1175699	0.0102	0.1395
chr14	107349540	1420758	0.0132	0.1723
chr15	102531392	2136128	0.0208	0.1997
chr16	90354753	2197363	0.0243	0.3049
chr17	81195210	1489873	0.0183	0.1986
chr18	78077248	1759899	0.0225	0.3633
chr19	59128983	1117925	0.0189	0.3779
chr20	63025520	1614351	0.0256	0.2331
chr21	48129895	956268	0.0199	0.2078
chr22	51304566	872016	0.017	0.1871
chrMT	16571	313076	18.893	12.31
chrX	155270560	4317313	0.0278	0.2537
chrY	59373566	220755	0.0037	0.2018

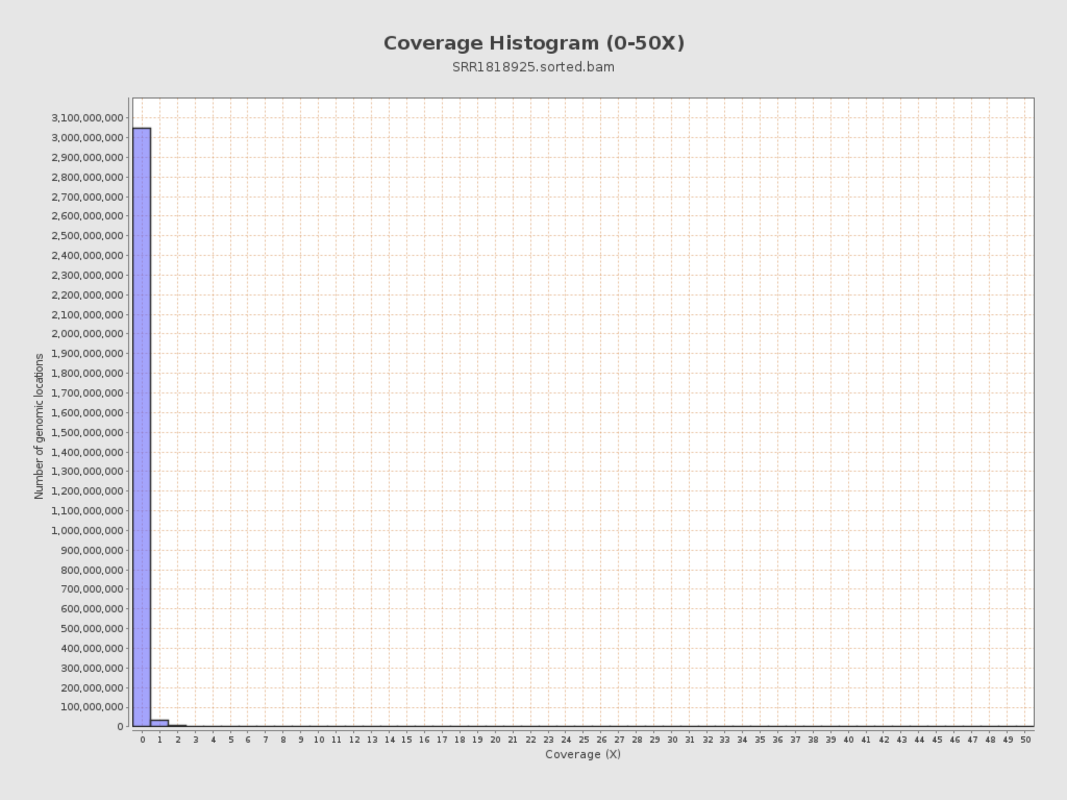
3. Results : Coverage across reference



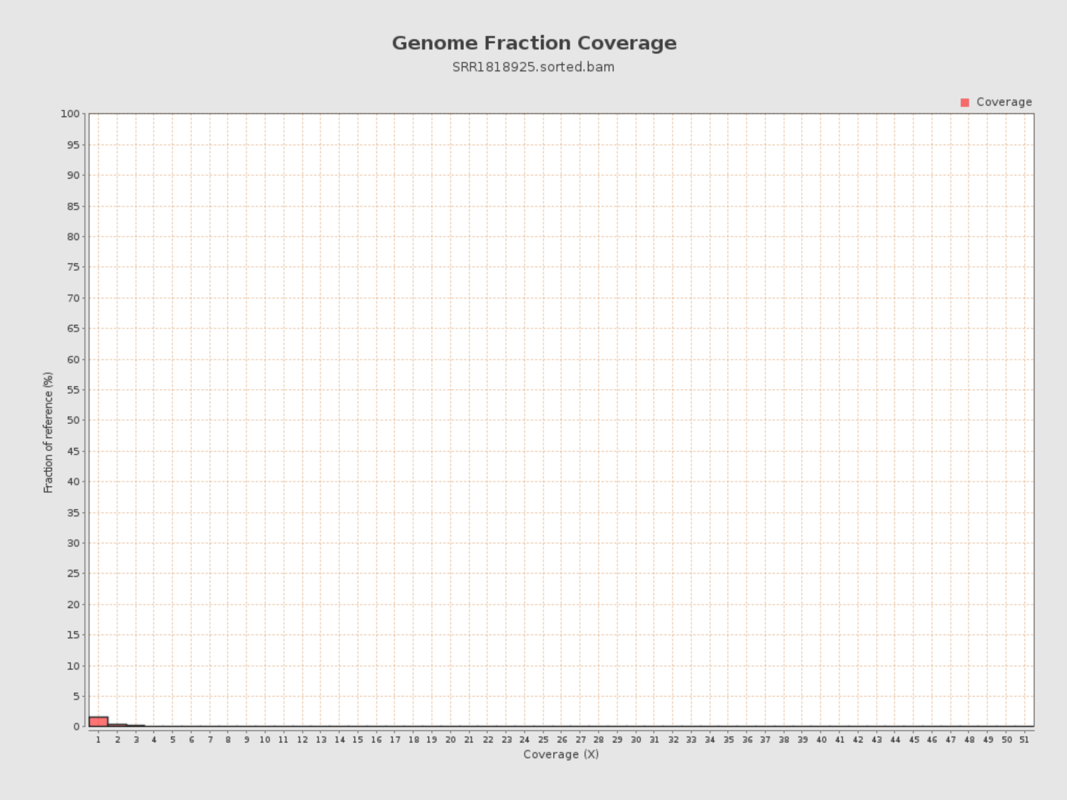
4. Results : Coverage Histogram



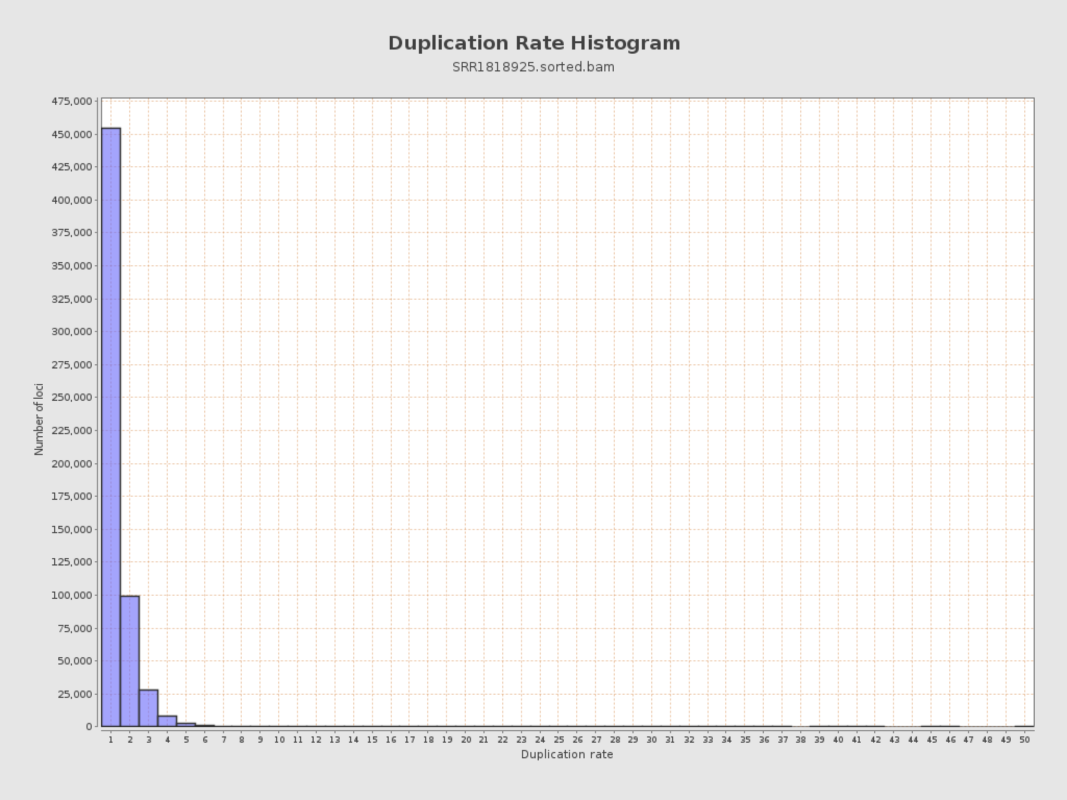
5. Results : Coverage Histogram (0-50X)



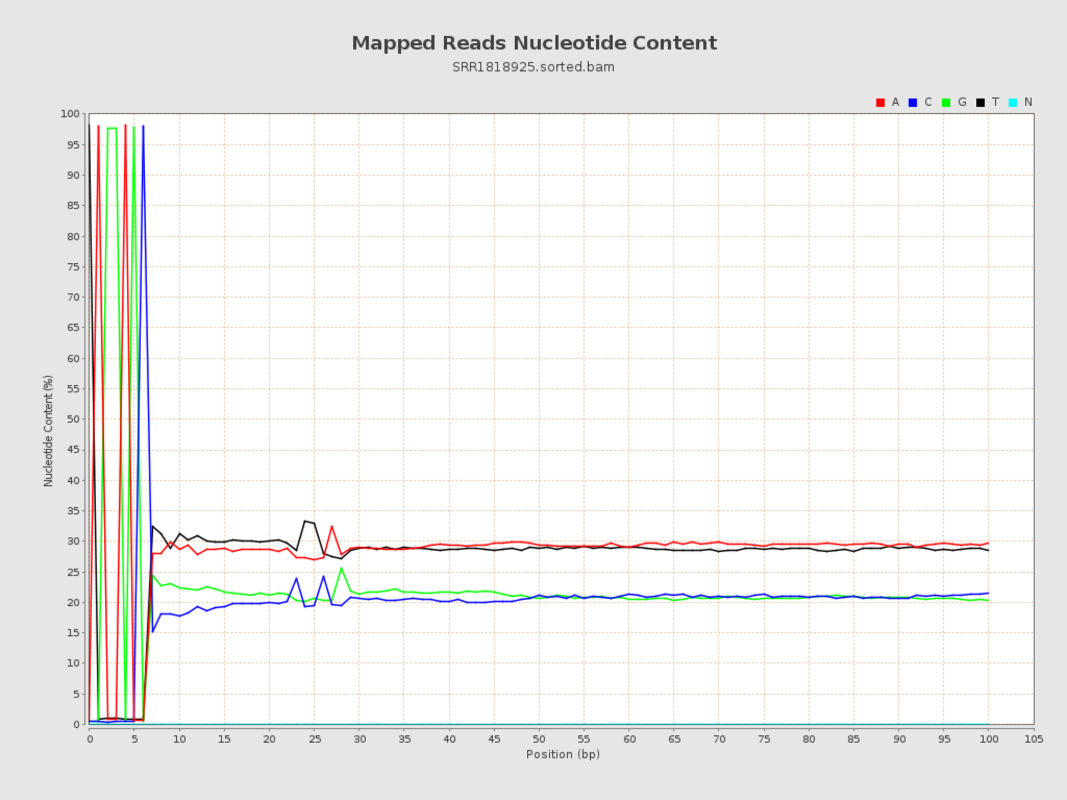
6. Results : Genome Fraction Coverage



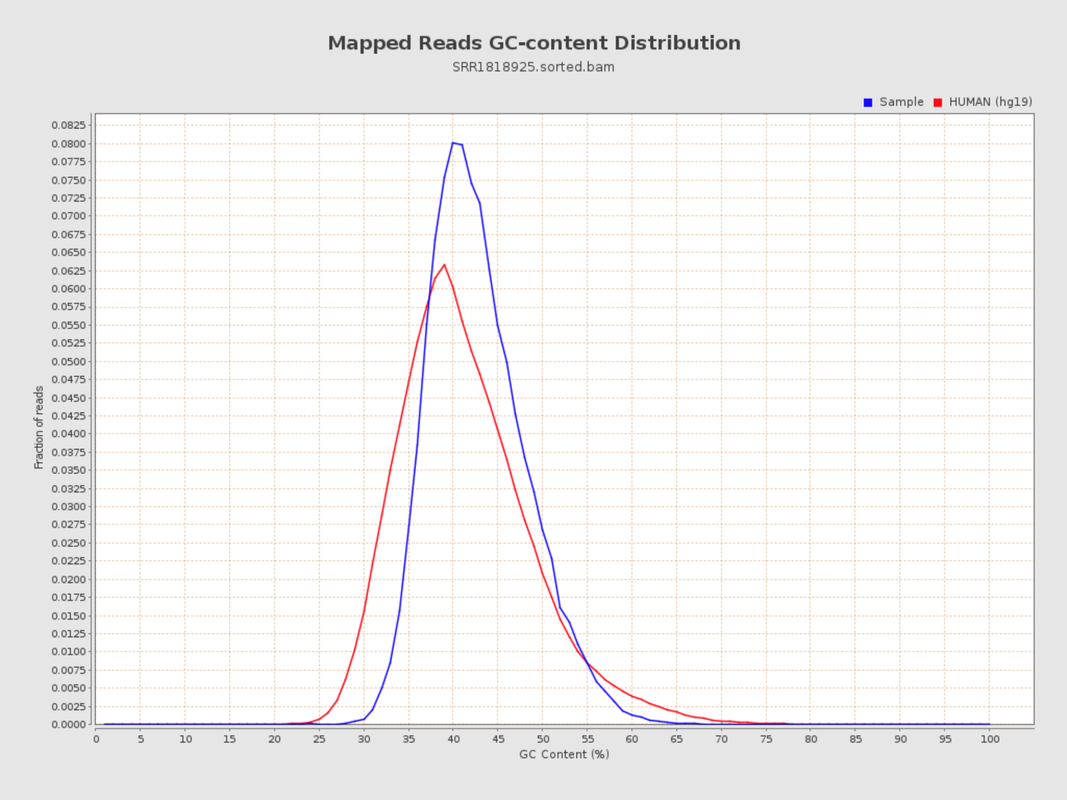
7. Results : Duplication Rate Histogram



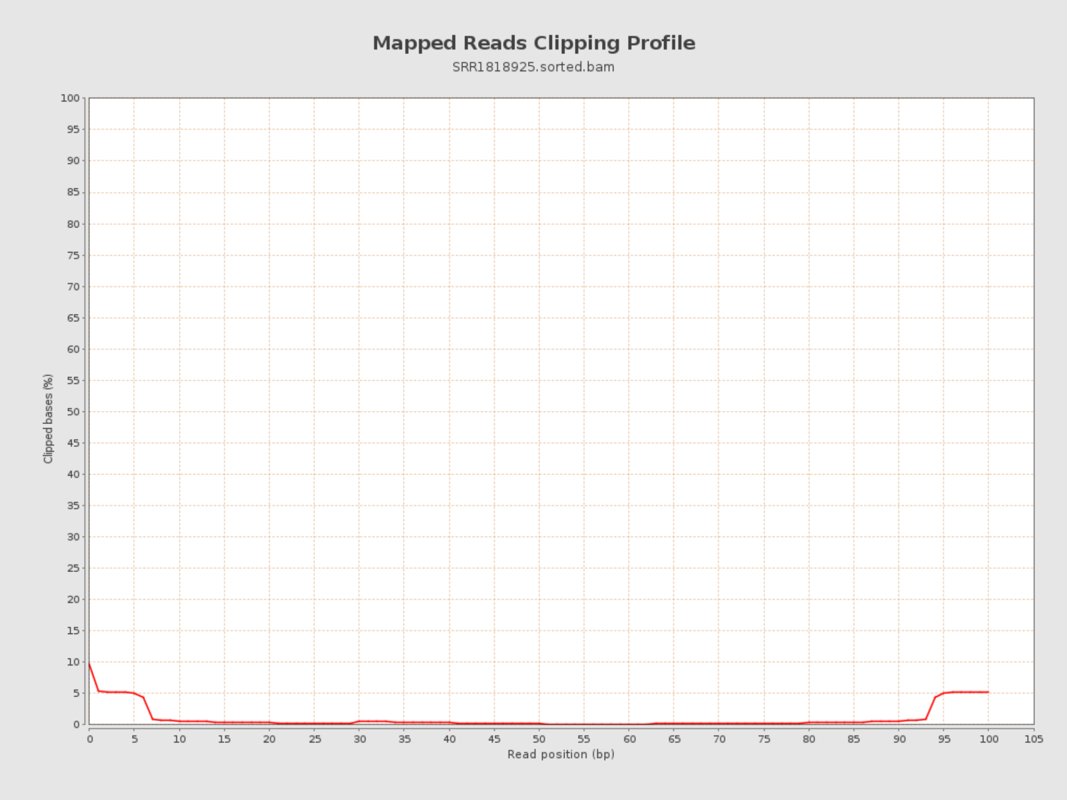
8. Results : Mapped Reads Nucleotide Content



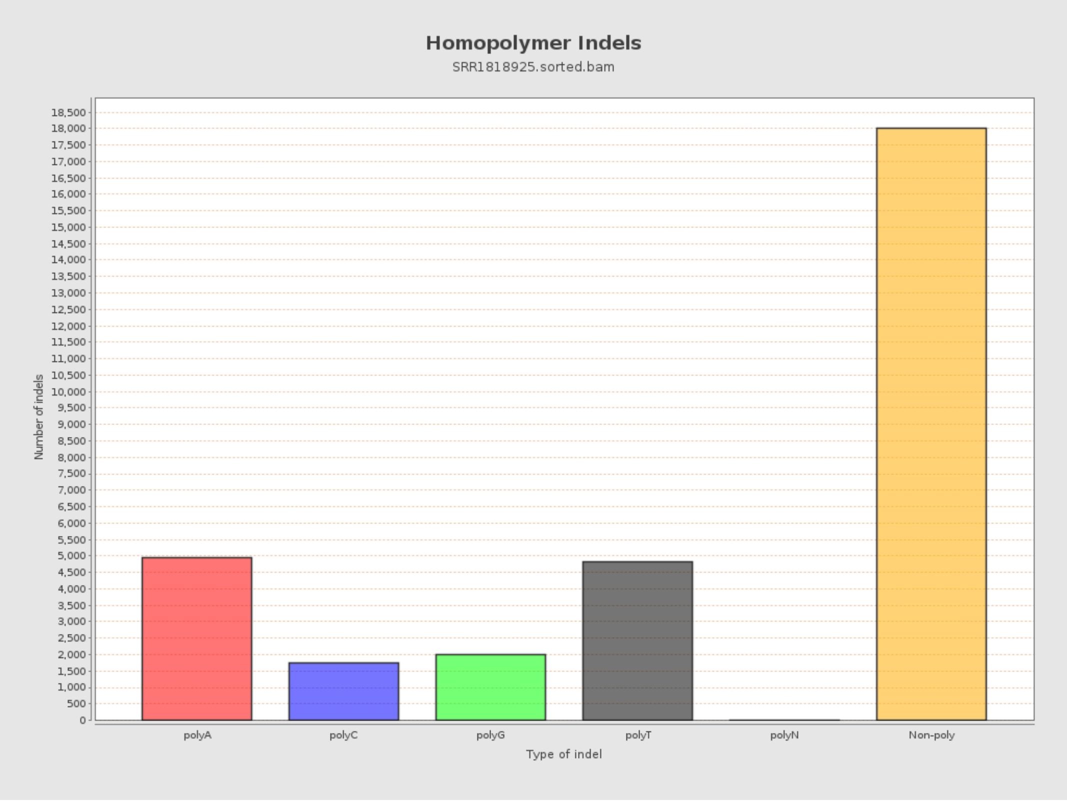
9. Results : Mapped Reads GC-content Distribution



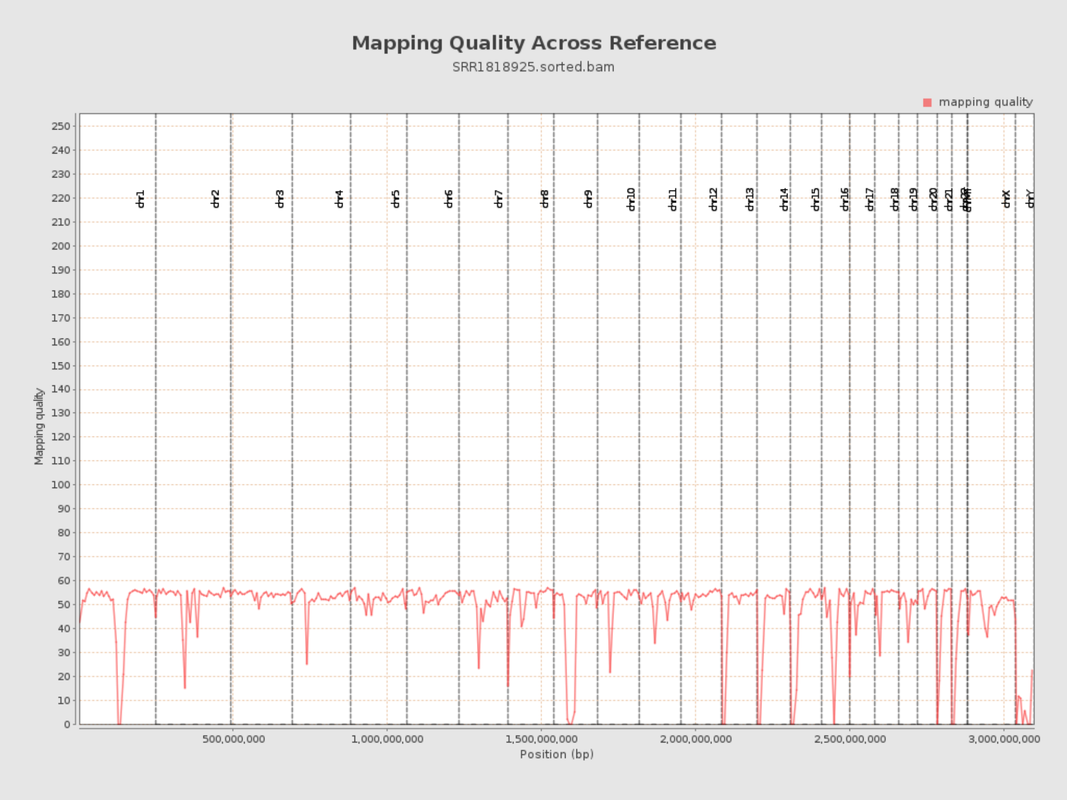
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram