Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:55:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818897.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_SRR1818897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818897.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:55:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,323,022
Mapped reads	1,282,435 / 96.93%
Unmapped reads	40,587 / 3.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,948 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	222,942 / 16.85%
Duplication rate	14.49%
Clipped reads	1,294,470 / 97.84%

2.2. ACGT Content

Number/percentage of A's	34,633,235 / 29.24%
Number/percentage of C's	24,934,623 / 21.05%
Number/percentage of T's	34,200,665 / 28.87%
Number/percentage of G's	24,691,758 / 20.84%
Number/percentage of N's	1,687 / 0%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.4962

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

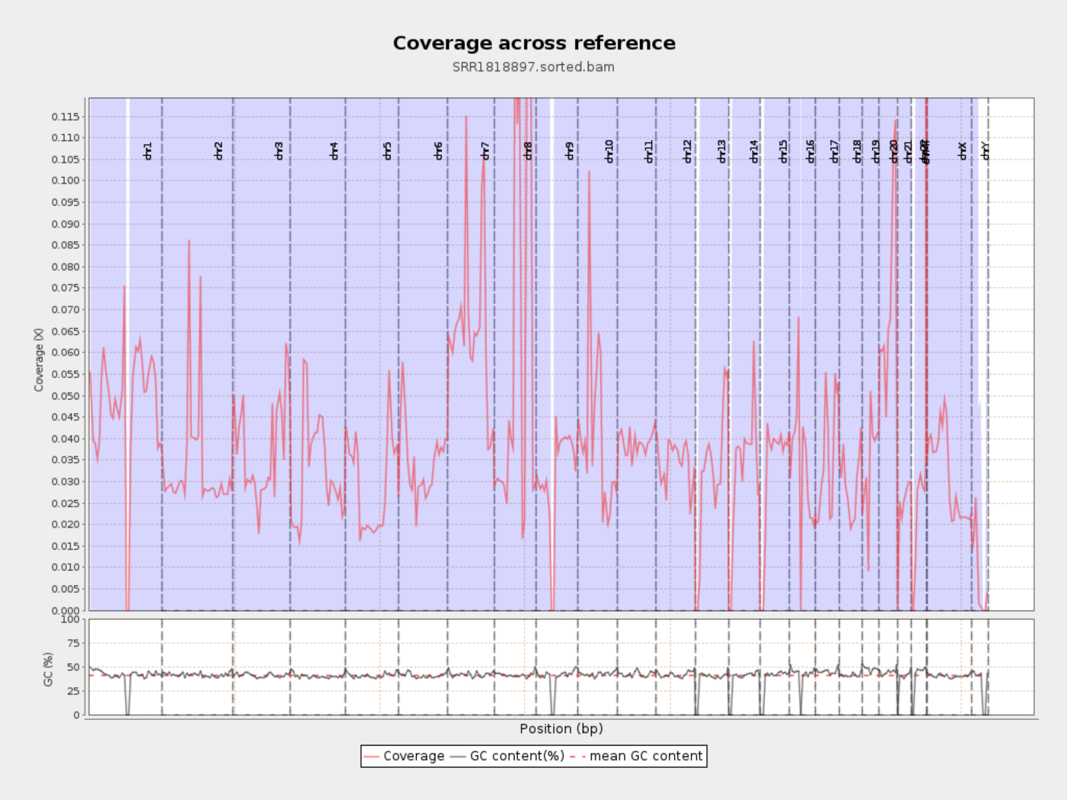
General error rate	0.67%
Mismatches	744,183
Insertions	18,369
Mapped reads with at least one insertion	1.39%
Deletions	41,009
Mapped reads with at least one deletion	3.12%
Homopolymer indels	40.58%

2.6. Chromosome stats

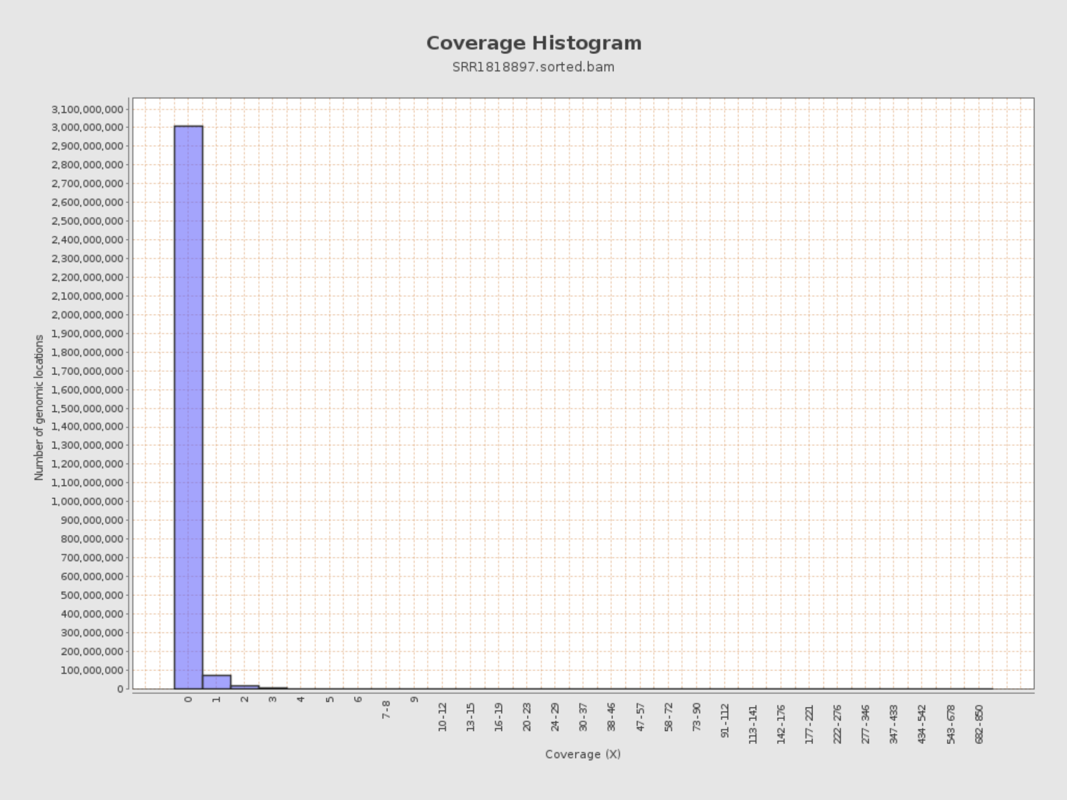
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11898221	0.0477	0.7336
chr2	243199373	8177838	0.0336	0.7454
chr3	198022430	7468385	0.0377	0.2428
chr4	191154276	6115851	0.032	0.2978
chr5	180915260	5293875	0.0293	0.2284
chr6	171115067	5889333	0.0344	0.2571
chr7	159138663	10597019	0.0666	1.05

chr8	146364022	10413640	0.0711	0.4106
chr9	141213431	4399981	0.0312	0.4048
chr10	135534747	5553898	0.041	0.6931
chr11	135006516	5252667	0.0389	0.2946
chr12	133851895	4628577	0.0346	0.2351
chr13	115169878	3624945	0.0315	0.2191
chr14	107349540	3500006	0.0326	0.2457
chr15	102531392	3298424	0.0322	0.2232
chr16	90354753	2973888	0.0329	0.5409
chr17	81195210	2939823	0.0362	0.3047
chr18	78077248	2293587	0.0294	0.4488
chr19	59128983	2009730	0.034	0.6211
chr20	63025520	4558046	0.0723	0.3571
chr21	48129895	1161404	0.0241	0.2294
chr22	51304566	1052924	0.0205	0.2029
chrMT	16571	57749	3.4849	2.9233
chrX	155270560	4924164	0.0317	0.2724
chrY	59373566	457901	0.0077	0.6004

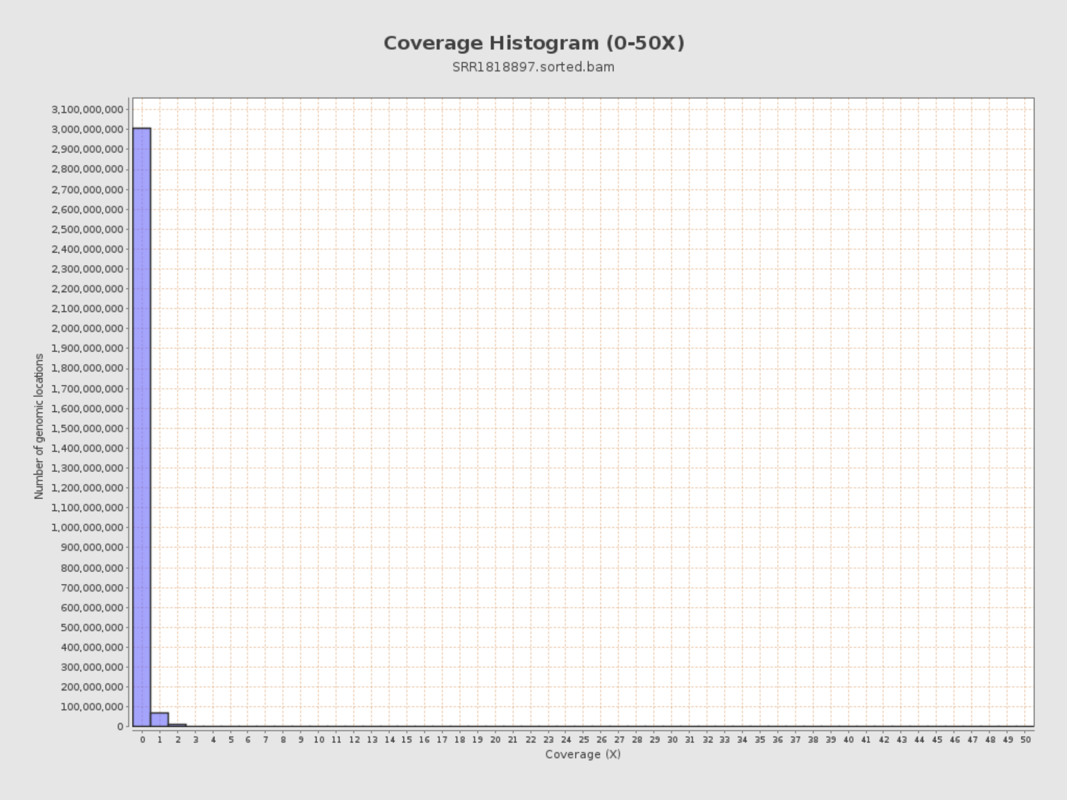
3. Results : Coverage across reference



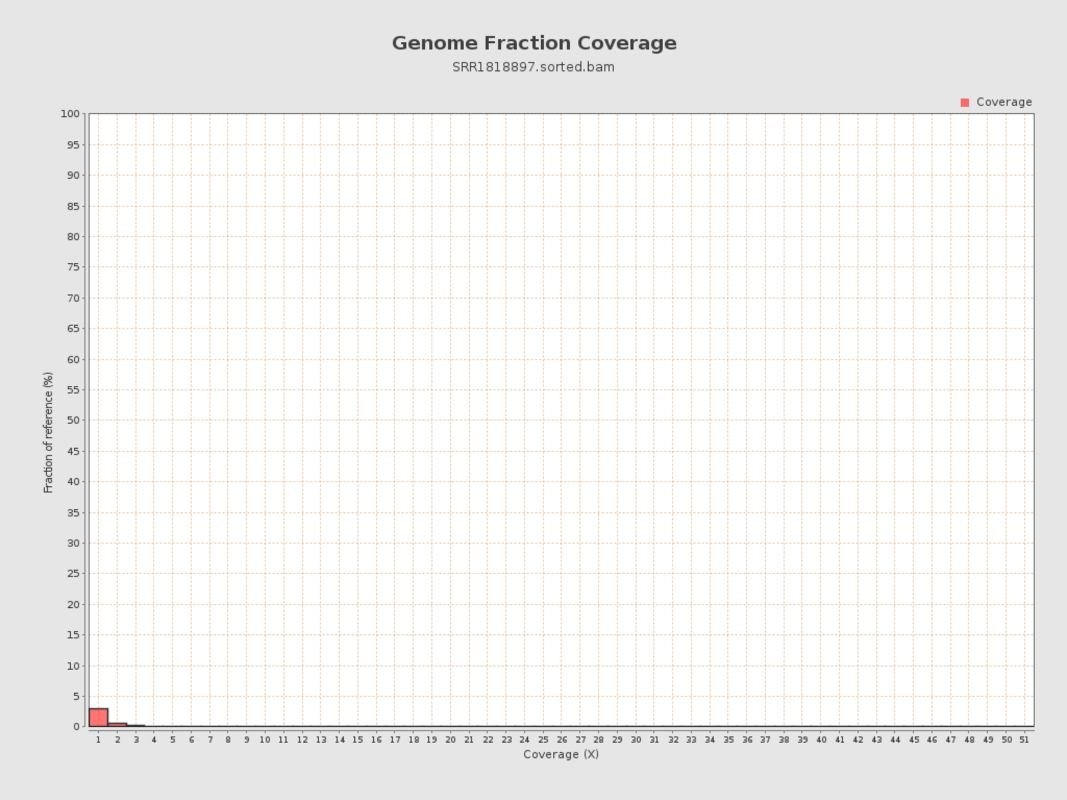
4. Results : Coverage Histogram



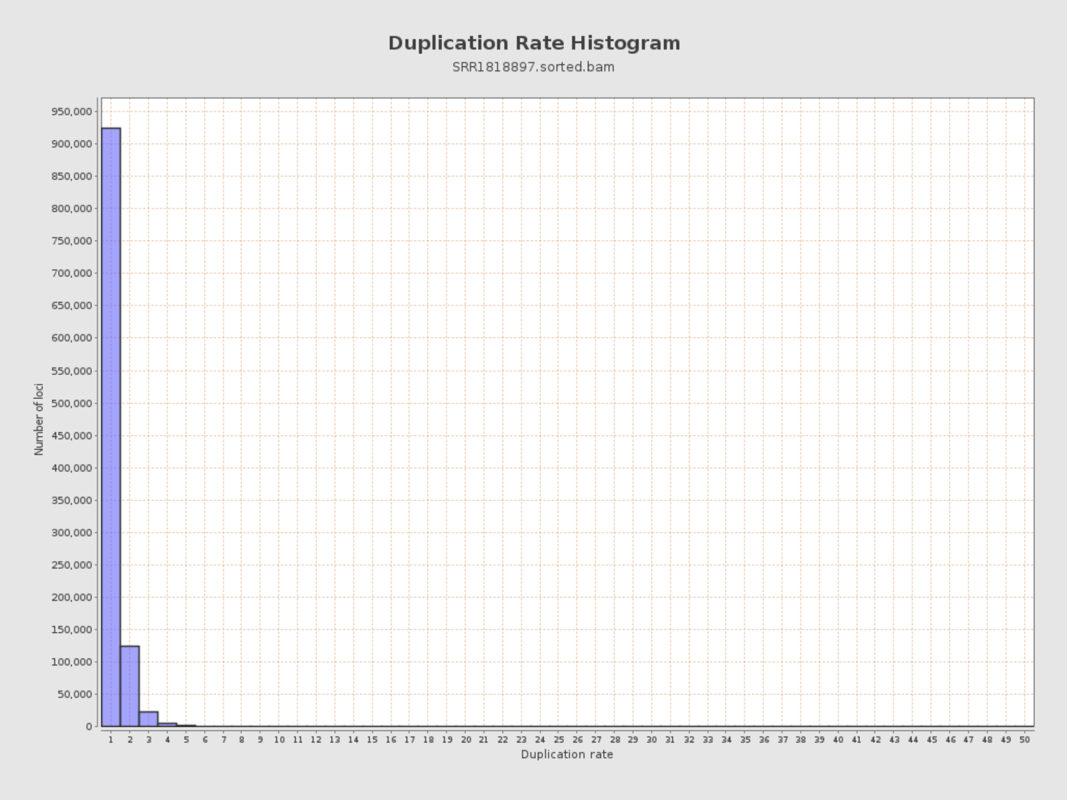
5. Results : Coverage Histogram (0-50X)



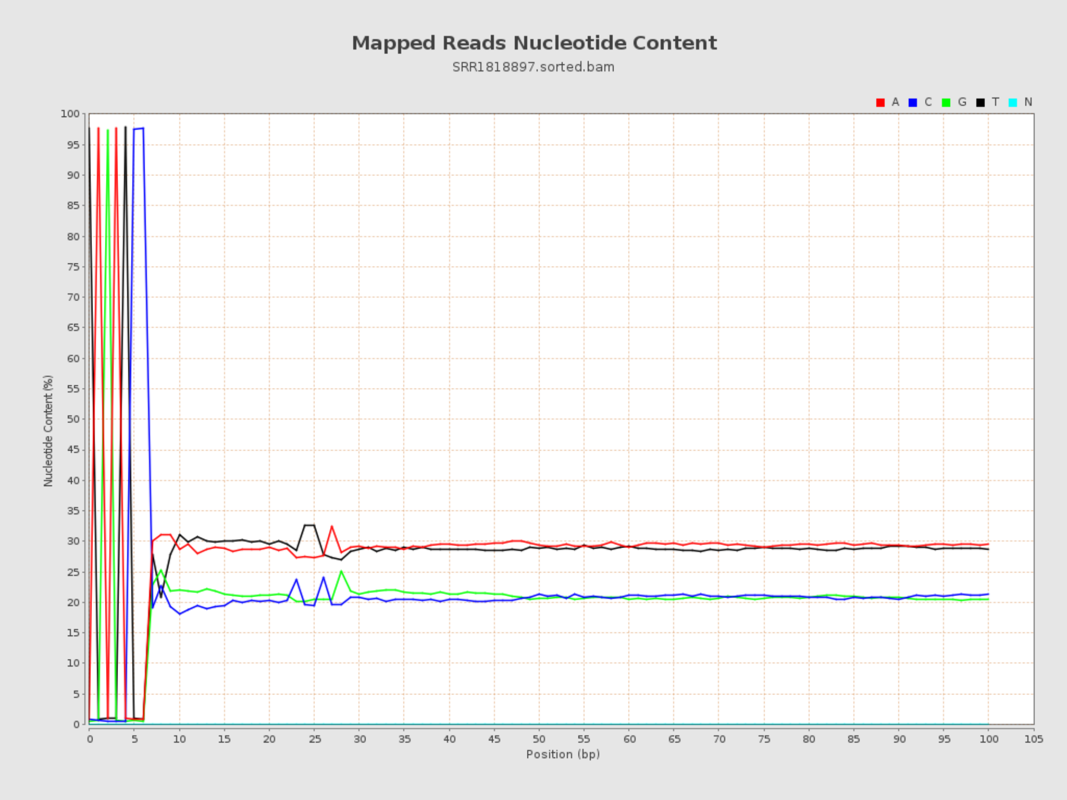
6. Results : Genome Fraction Coverage



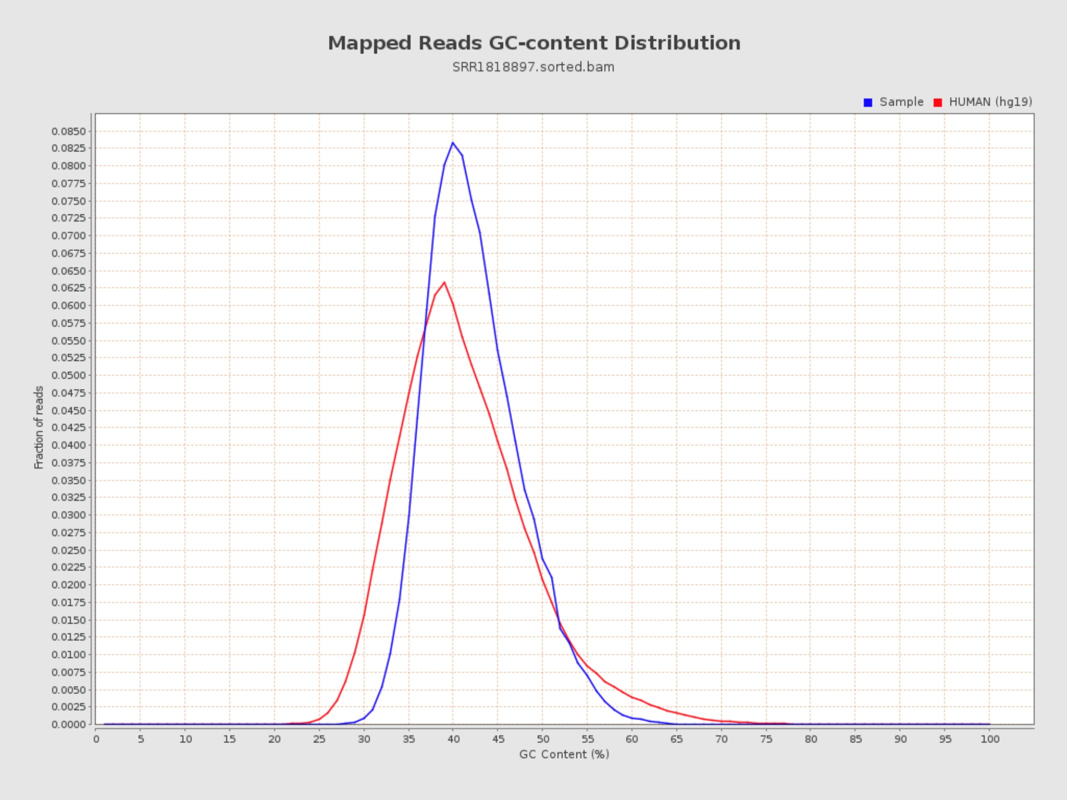
7. Results : Duplication Rate Histogram



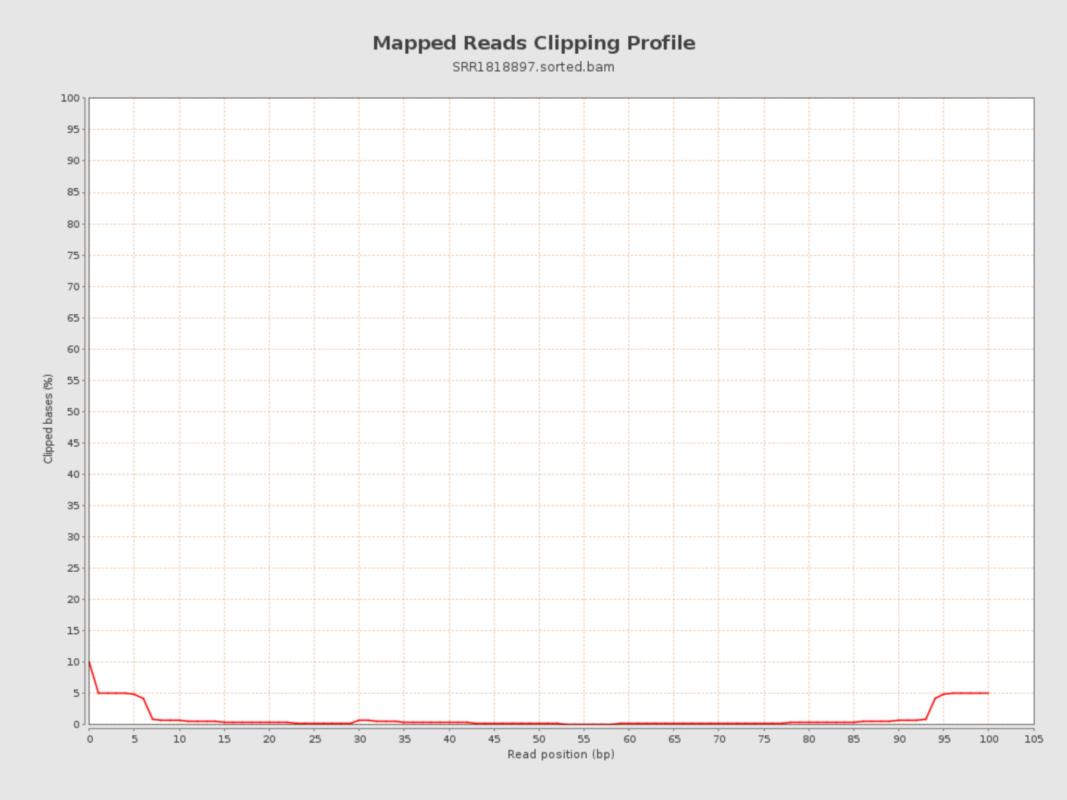
8. Results : Mapped Reads Nucleotide Content



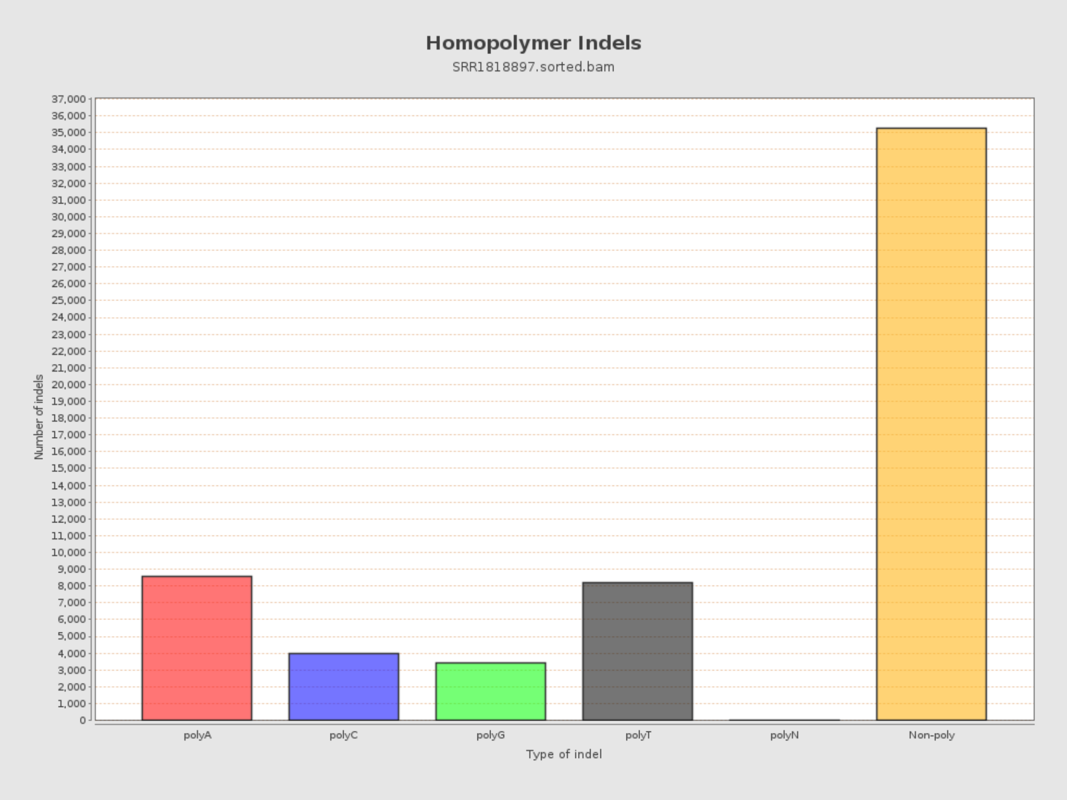
9. Results : Mapped Reads GC-content Distribution



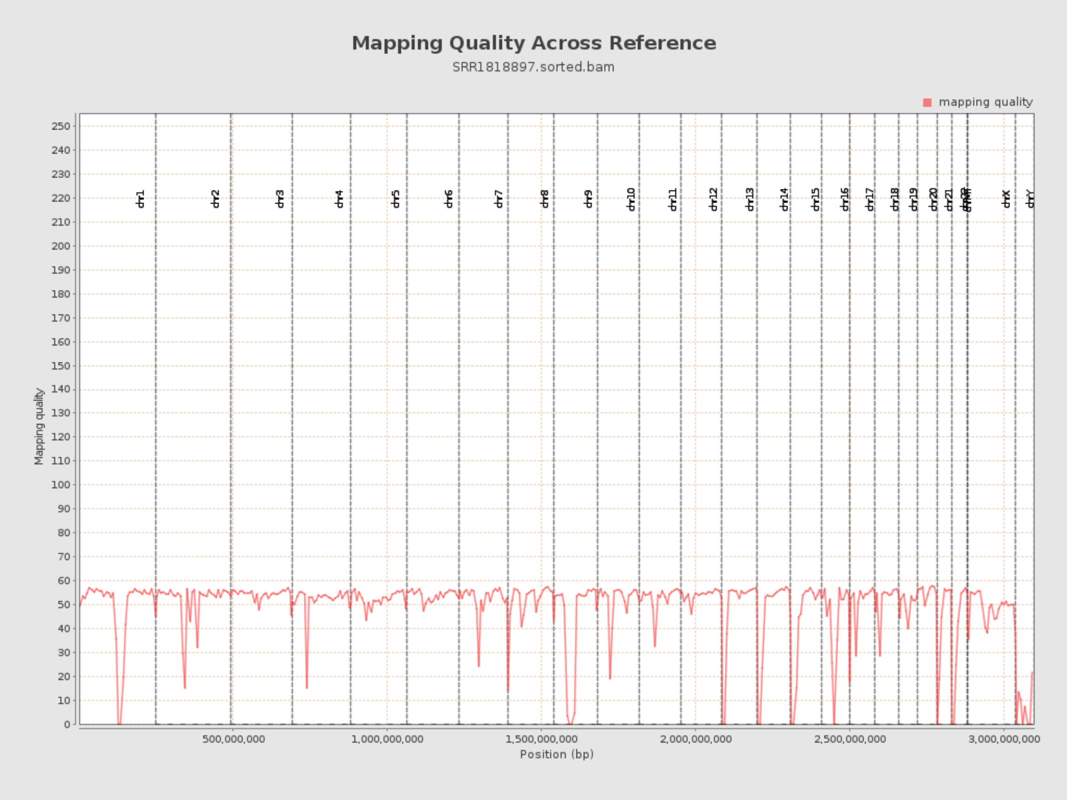
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram