Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:07:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818827.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_SRR1818827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:07:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	749,371
Mapped reads	730,002 / 97.42%
Unmapped reads	19,369 / 2.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,303 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	334,053 / 44.58%
Duplication rate	38.36%
Clipped reads	728,859 / 97.26%

2.2. ACGT Content

Number/percentage of A's	14,382,977 / 29.05%
Number/percentage of C's	10,345,186 / 20.9%
Number/percentage of T's	13,802,113 / 27.88%
Number/percentage of G's	10,975,800 / 22.17%
Number/percentage of N's	3,061 / 0.01%
GC Percentage	43.06%

2.3. Coverage

Mean	0.016

Standard Deviation	0.2736

2.4. Mapping Quality

Mean Mapping Quality	47.91

2.5. Mismatches and indels

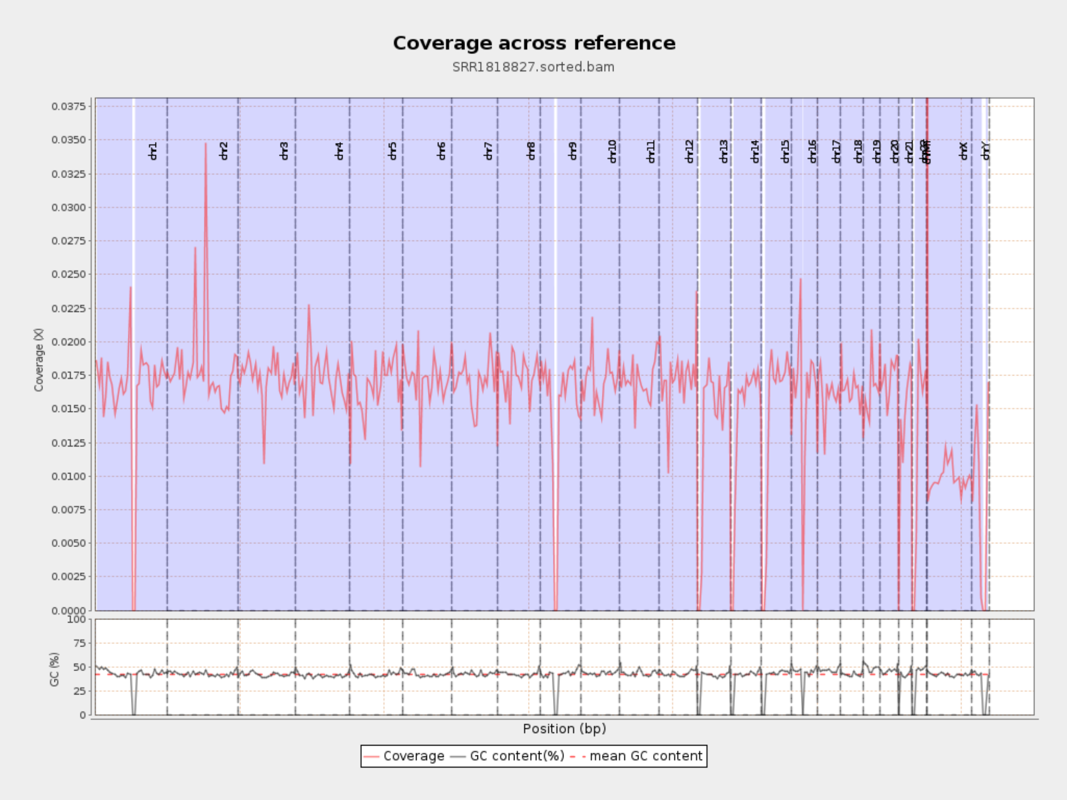
General error rate	0.52%
Mismatches	247,076
Insertions	5,718
Mapped reads with at least one insertion	0.77%
Deletions	13,409
Mapped reads with at least one deletion	1.81%
Homopolymer indels	39.73%

2.6. Chromosome stats

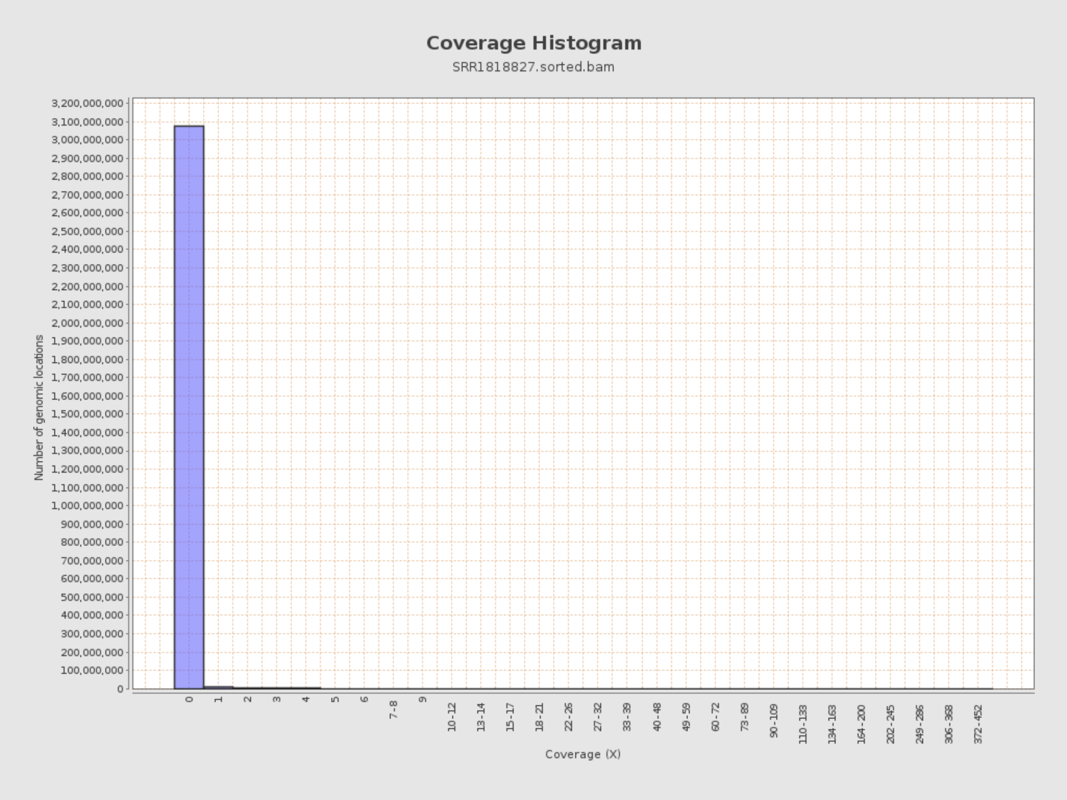
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4048593	0.0162	0.309
chr2	243199373	4376311	0.018	0.4071
chr3	198022430	3427535	0.0173	0.2439
chr4	191154276	3313695	0.0173	0.2581
chr5	180915260	3083927	0.017	0.247
chr6	171115067	2936771	0.0172	0.2507
chr7	159138663	2734309	0.0172	0.2656

chr8	146364022	2565694	0.0175	0.2579
chr9	141213431	2096920	0.0148	0.2372
chr10	135534747	2332205	0.0172	0.2818
chr11	135006516	2309593	0.0171	0.2619
chr12	133851895	2298807	0.0172	0.2529
chr13	115169878	1583058	0.0137	0.2158
chr14	107349540	1507019	0.014	0.2371
chr15	102531392	1463101	0.0143	0.2214
chr16	90354753	1419654	0.0157	0.2925
chr17	81195210	1300601	0.016	0.2428
chr18	78077248	1288785	0.0165	0.2624
chr19	59128983	969791	0.0164	0.2854
chr20	63025520	1094939	0.0174	0.2567
chr21	48129895	665586	0.0138	0.2336
chr22	51304566	633571	0.0123	0.2272
chrMT	16571	60785	3.6682	5.4486
chrX	155270560	1537514	0.0099	0.1848
chrY	59373566	481686	0.0081	0.3952

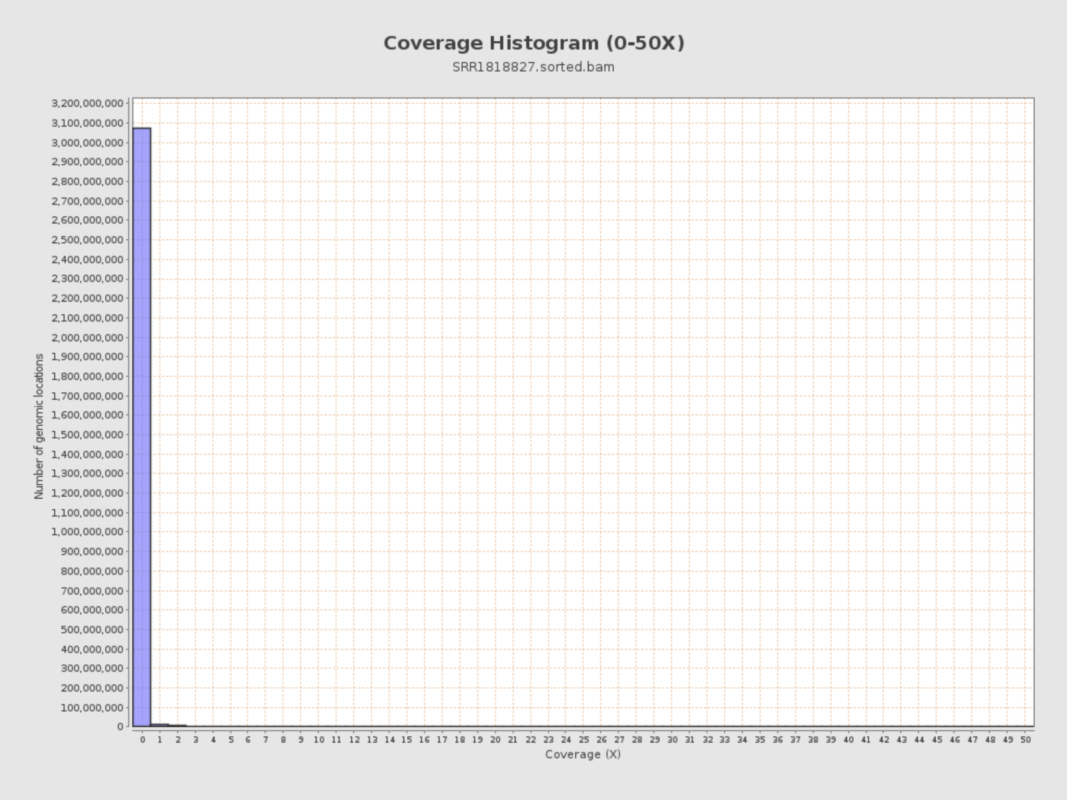
3. Results : Coverage across reference



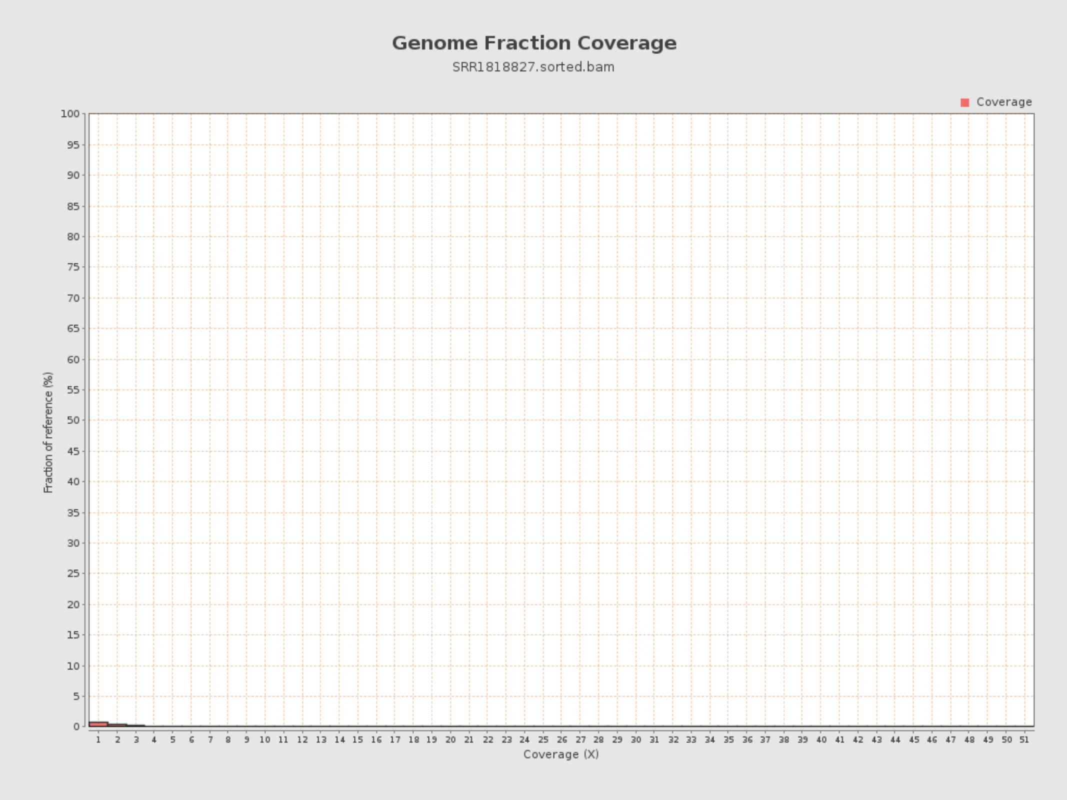
4. Results : Coverage Histogram



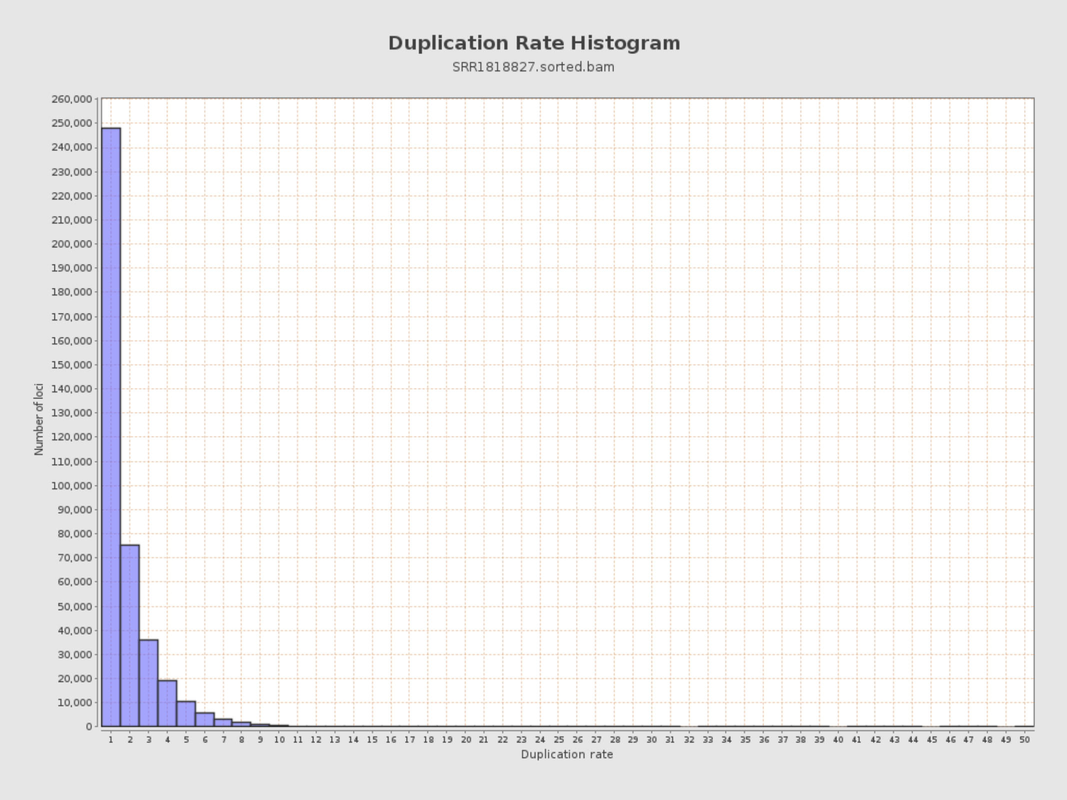
5. Results : Coverage Histogram (0-50X)



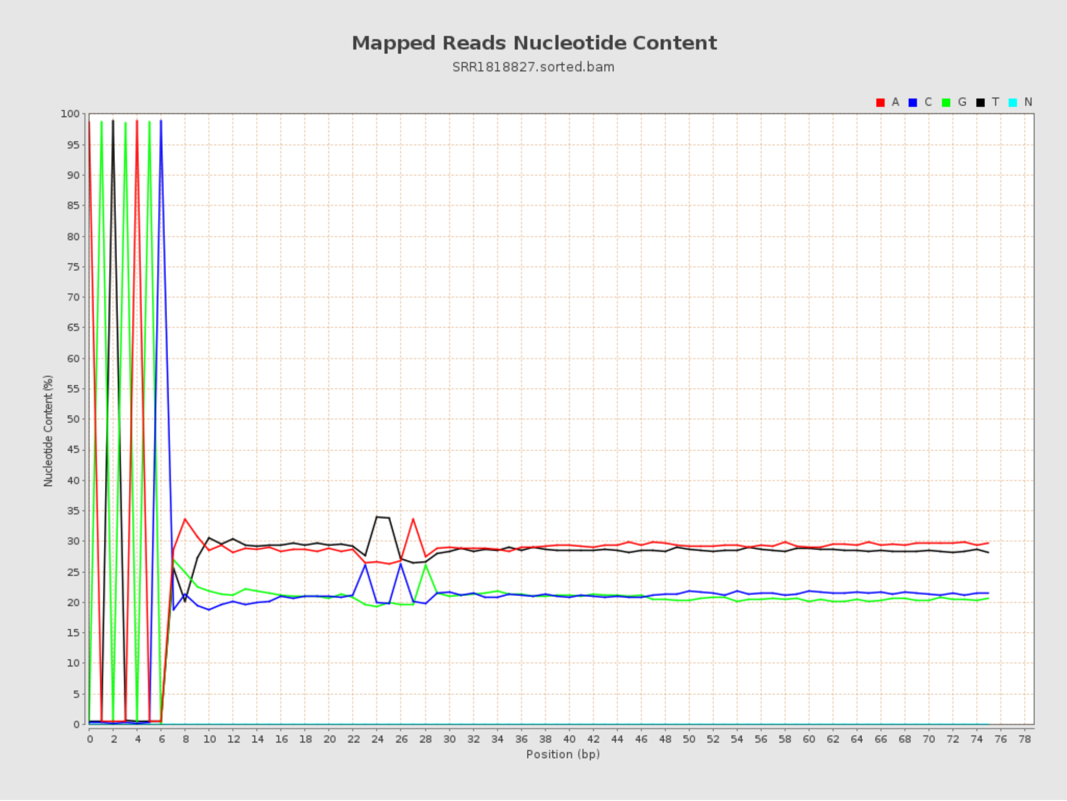
6. Results : Genome Fraction Coverage



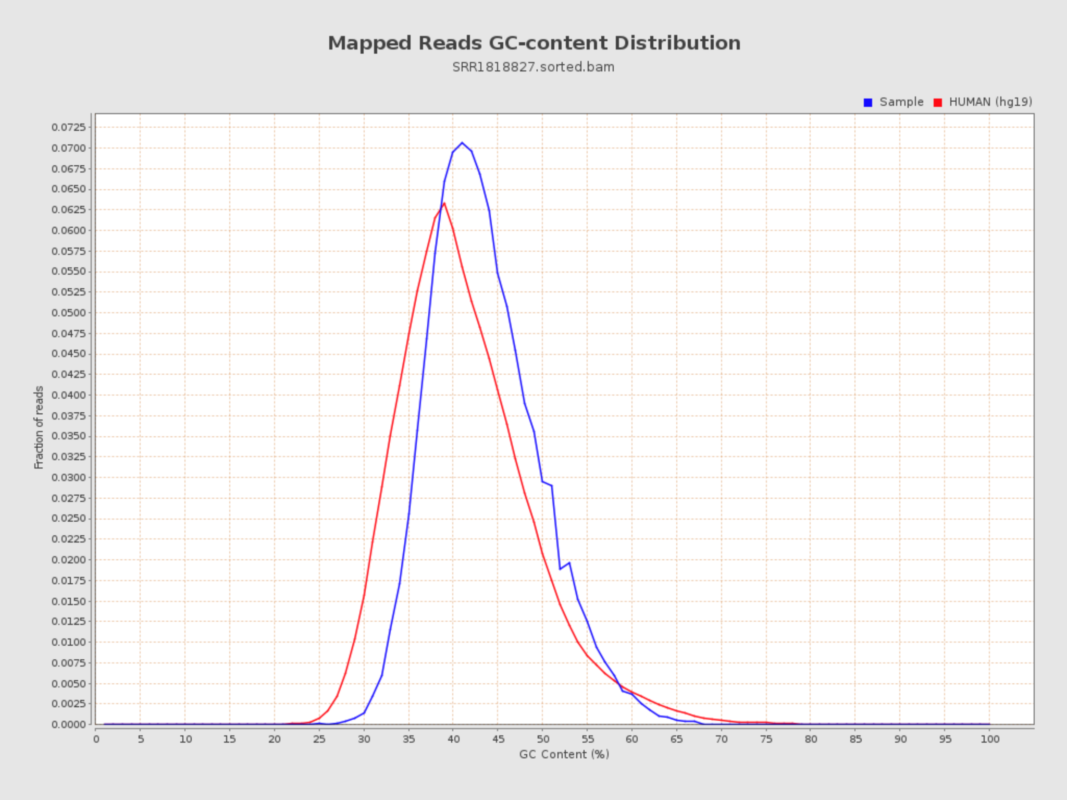
7. Results : Duplication Rate Histogram



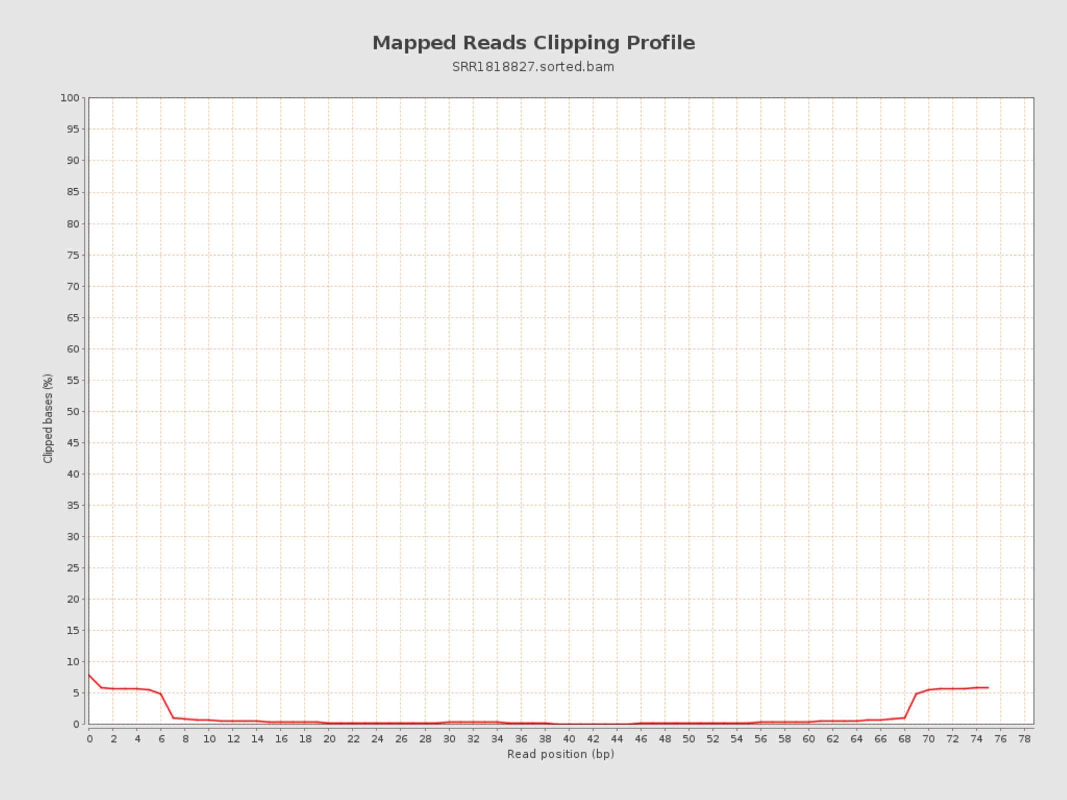
8. Results : Mapped Reads Nucleotide Content



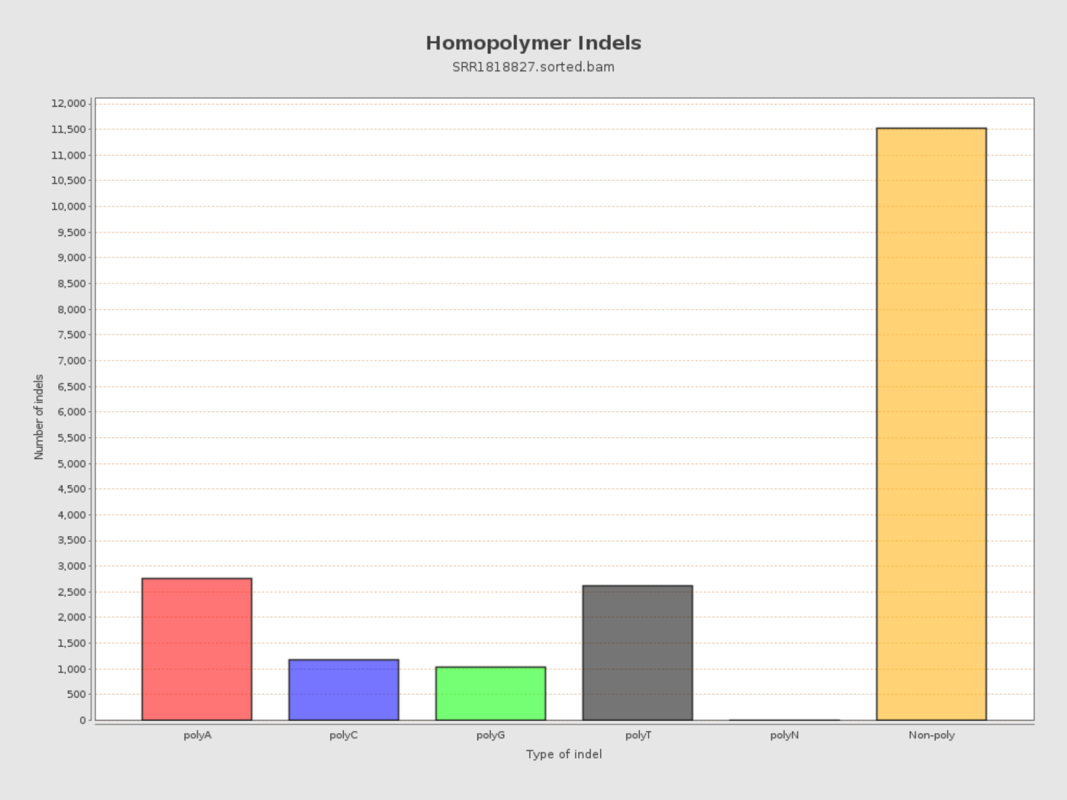
9. Results : Mapped Reads GC-content Distribution



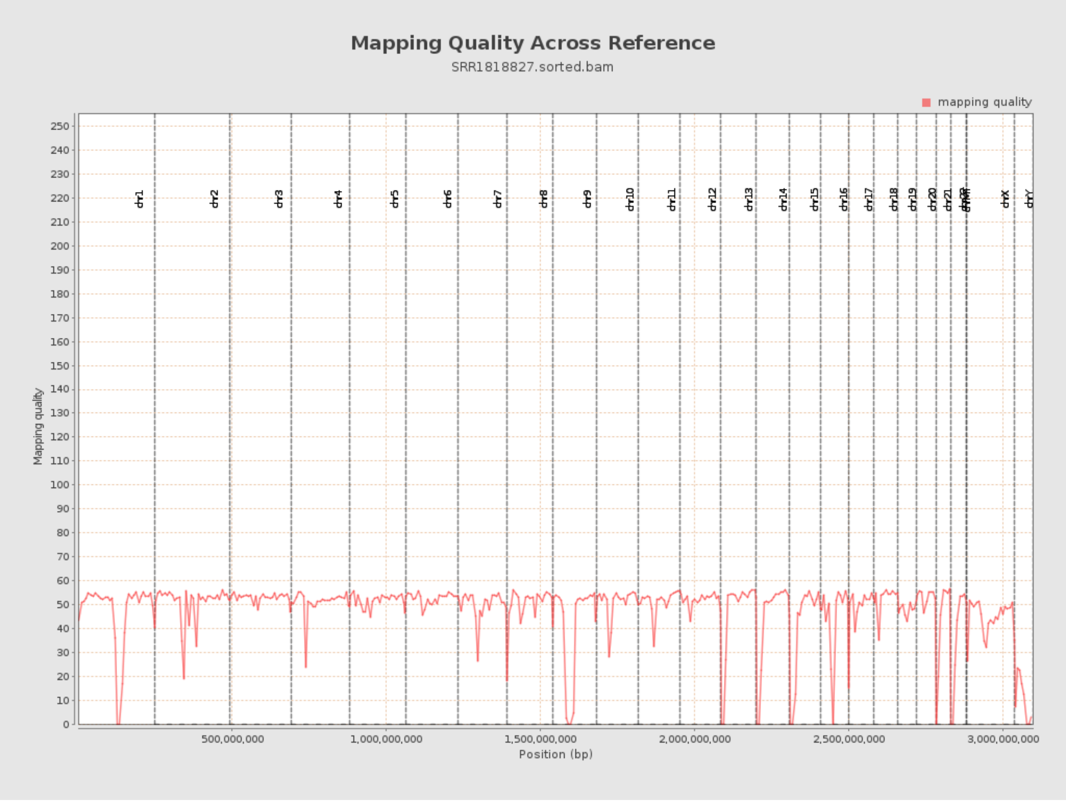
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram