Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818825.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_SRR1818825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:49:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,433,037
Mapped reads	1,397,329 / 97.51%
Unmapped reads	35,708 / 2.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,814 / 0.75%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	545,035 / 38.03%
Duplication rate	33.45%
Clipped reads	1,401,801 / 97.82%

2.2. ACGT Content

Number/percentage of A's	26,065,021 / 27.45%
Number/percentage of C's	20,115,477 / 21.18%
Number/percentage of T's	27,201,207 / 28.64%
Number/percentage of G's	21,575,641 / 22.72%
Number/percentage of N's	5,559 / 0.01%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.3891

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

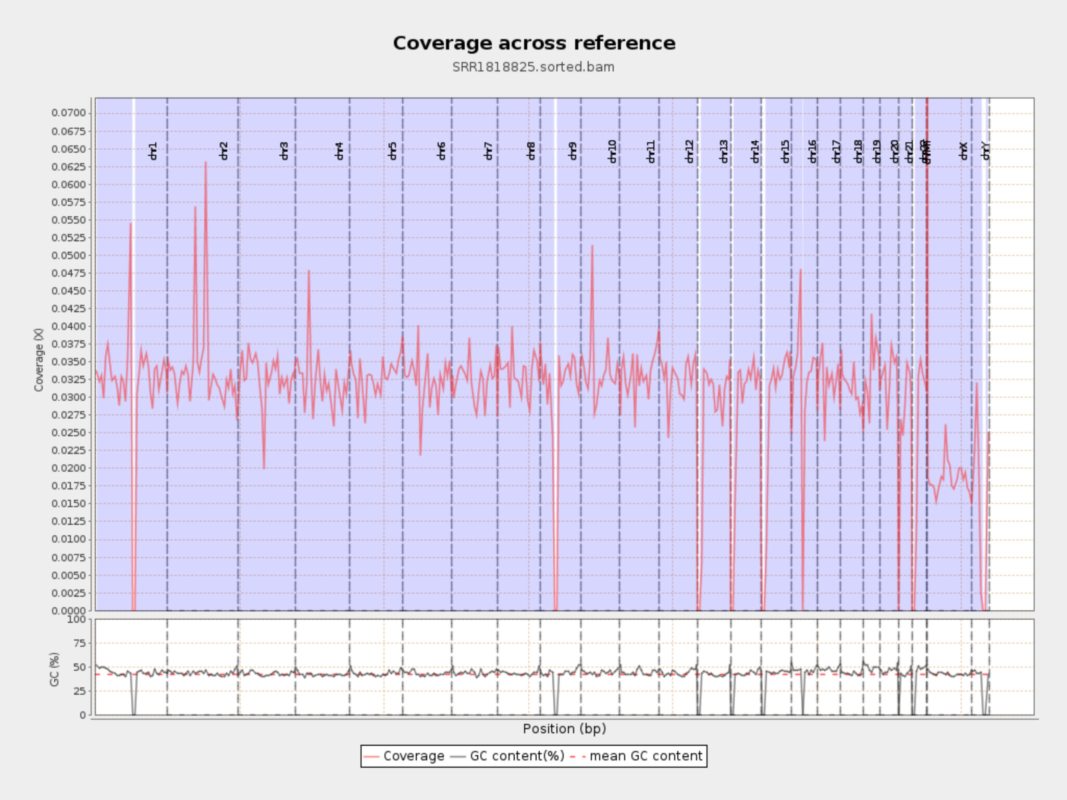
General error rate	0.52%
Mismatches	468,641
Insertions	10,789
Mapped reads with at least one insertion	0.76%
Deletions	23,610
Mapped reads with at least one deletion	1.67%
Homopolymer indels	41.9%

2.6. Chromosome stats

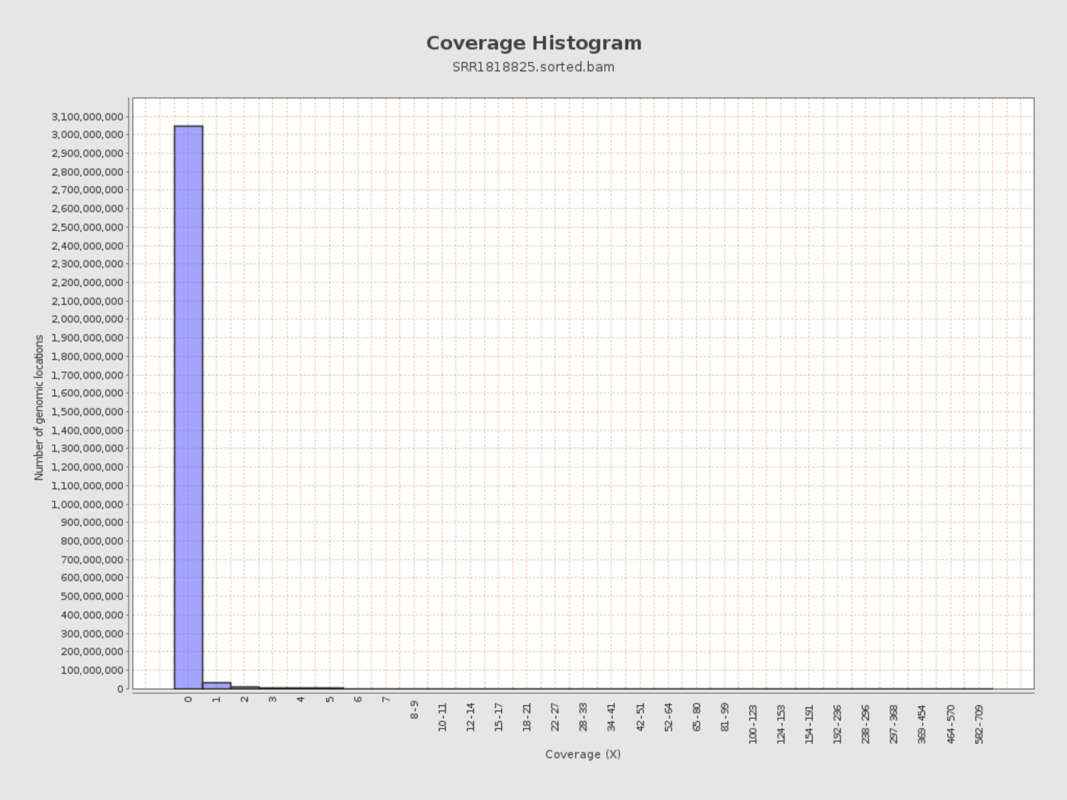
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7892511	0.0317	0.5851
chr2	243199373	8331221	0.0343	0.5722
chr3	198022430	6494244	0.0328	0.3061
chr4	191154276	6168428	0.0323	0.343
chr5	180915260	5942098	0.0328	0.3123
chr6	171115067	5546395	0.0324	0.3245
chr7	159138663	5180906	0.0326	0.3577

chr8	146364022	4892663	0.0334	0.3363
chr9	141213431	4125287	0.0292	0.3392
chr10	135534747	4604207	0.034	0.4069
chr11	135006516	4487981	0.0332	0.3327
chr12	133851895	4378502	0.0327	0.3173
chr13	115169878	3019947	0.0262	0.2679
chr14	107349540	2917916	0.0272	0.3129
chr15	102531392	2767580	0.027	0.2752
chr16	90354753	2840672	0.0314	0.4142
chr17	81195210	2635347	0.0325	0.3226
chr18	78077248	2451270	0.0314	0.4075
chr19	59128983	1991663	0.0337	0.49
chr20	63025520	2077006	0.033	0.3194
chr21	48129895	1296102	0.0269	0.2893
chr22	51304566	1177842	0.023	0.2711
chrMT	16571	5577	0.3366	1.0083
chrX	155270560	2896120	0.0187	0.2552
chrY	59373566	880704	0.0148	0.5943

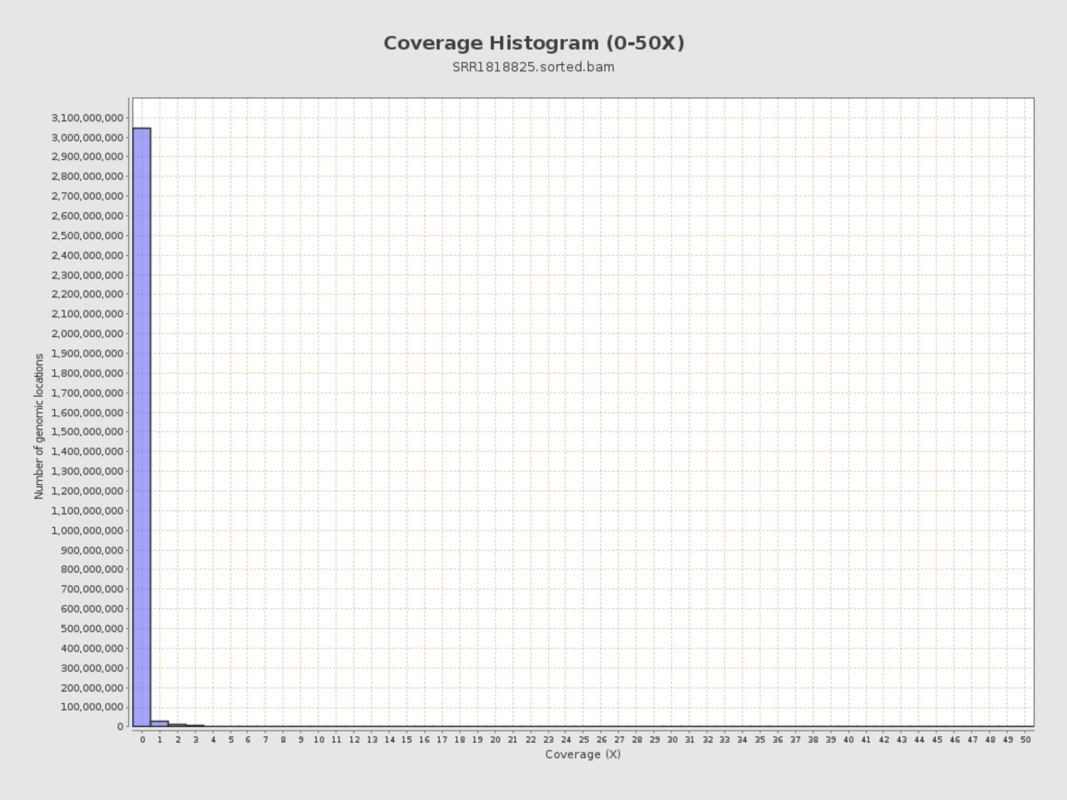
3. Results : Coverage across reference



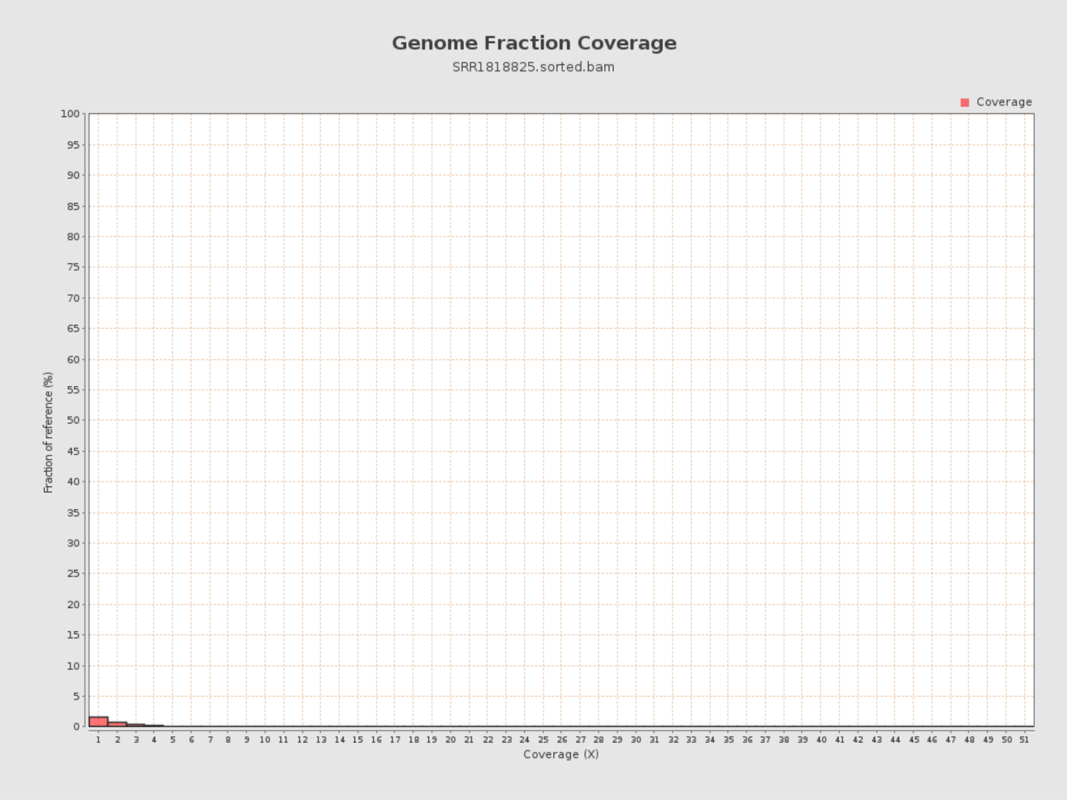
4. Results : Coverage Histogram



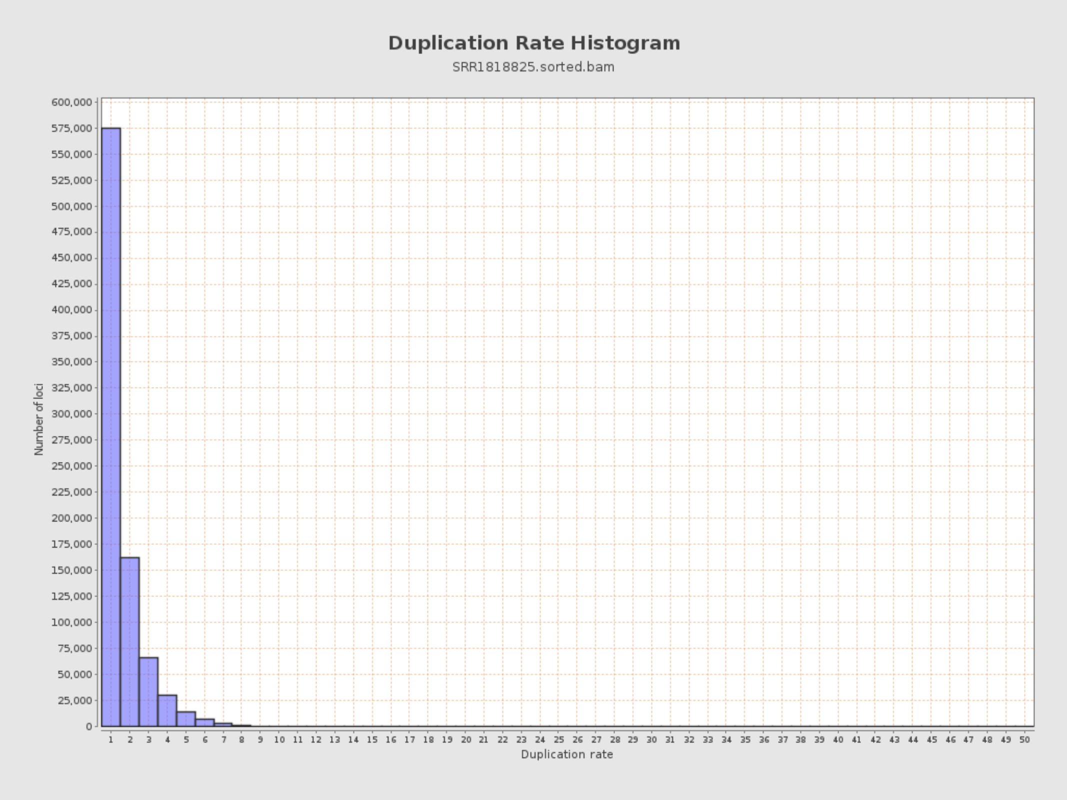
5. Results : Coverage Histogram (0-50X)



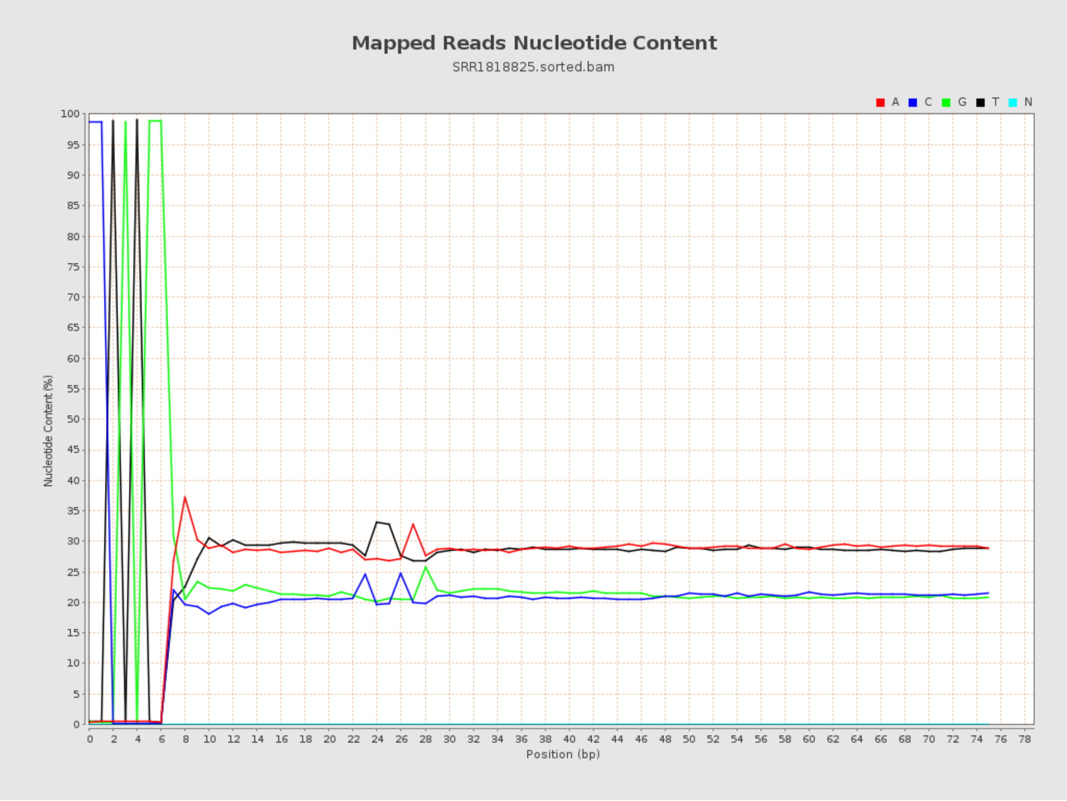
6. Results : Genome Fraction Coverage



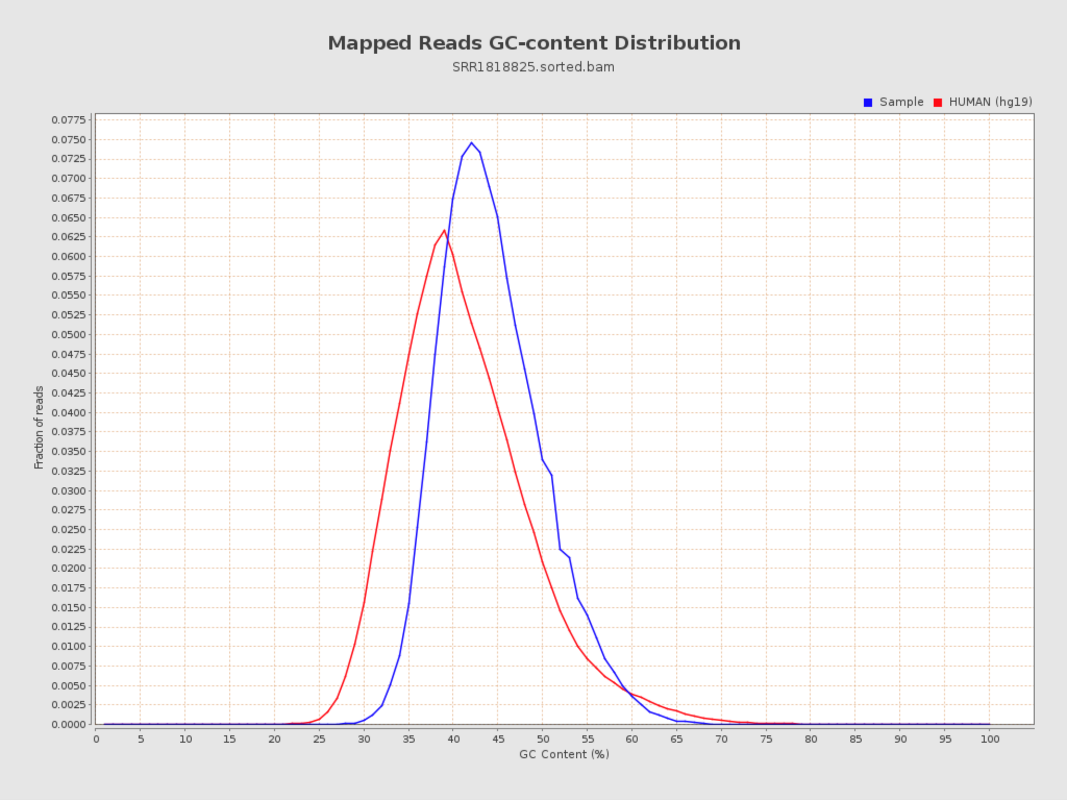
7. Results : Duplication Rate Histogram



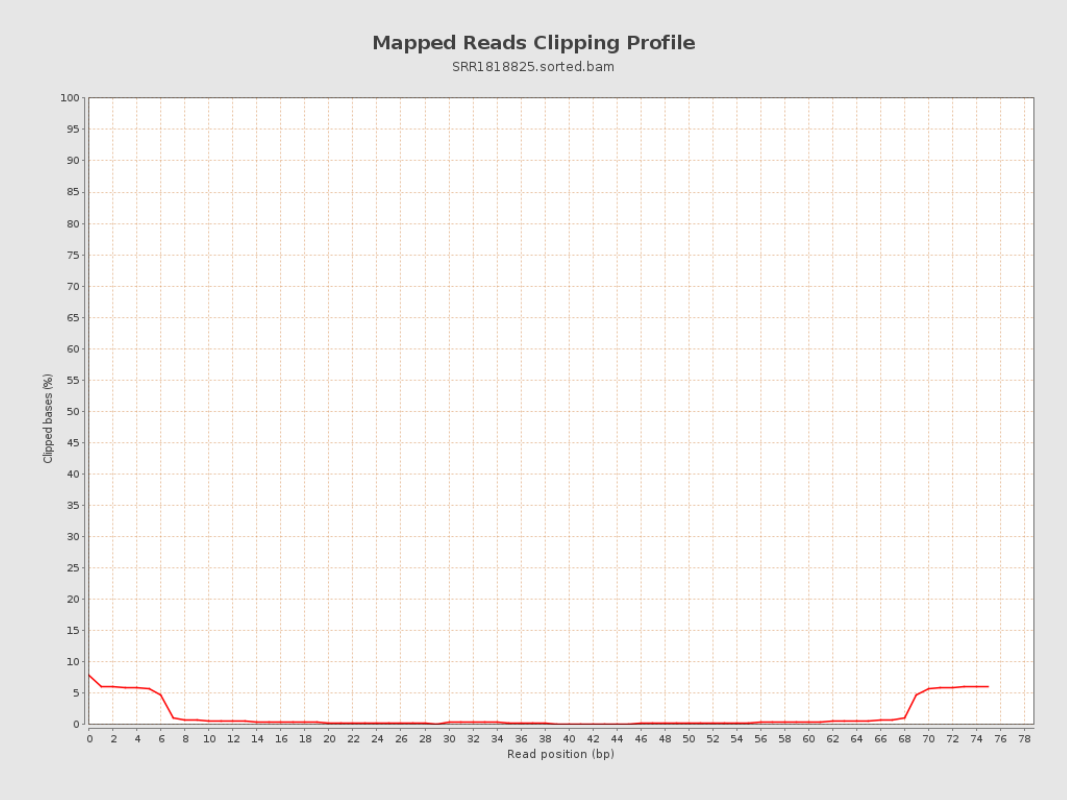
8. Results : Mapped Reads Nucleotide Content



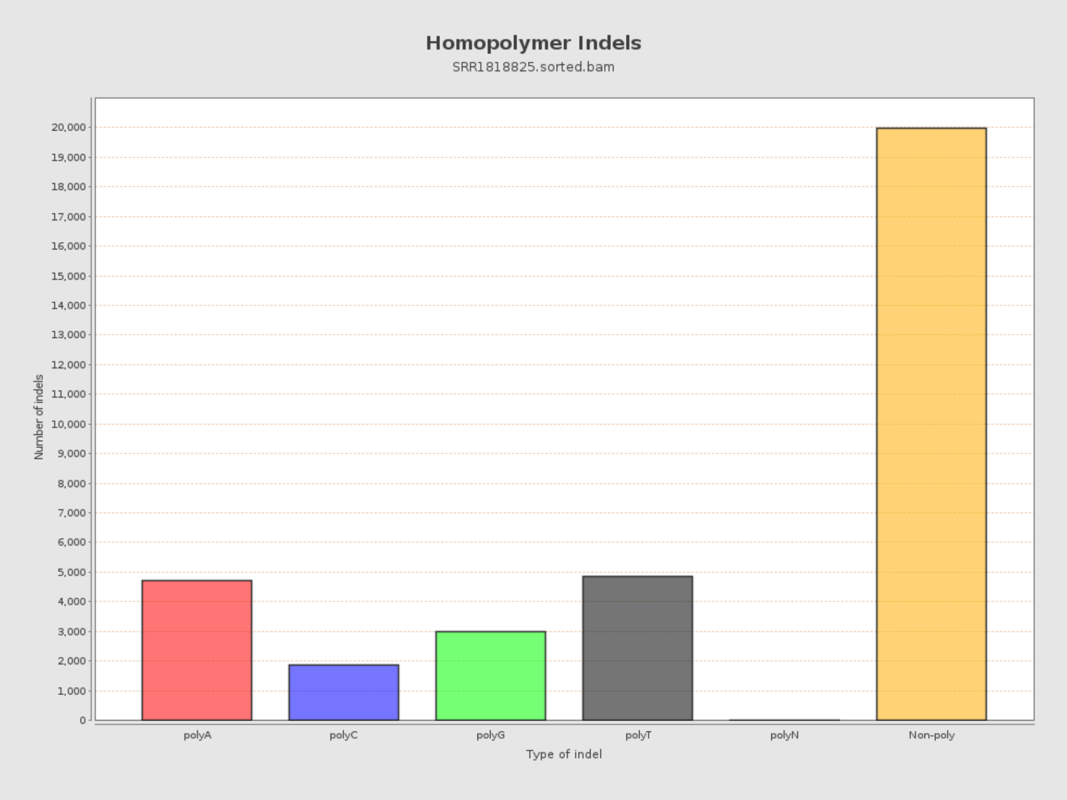
9. Results : Mapped Reads GC-content Distribution



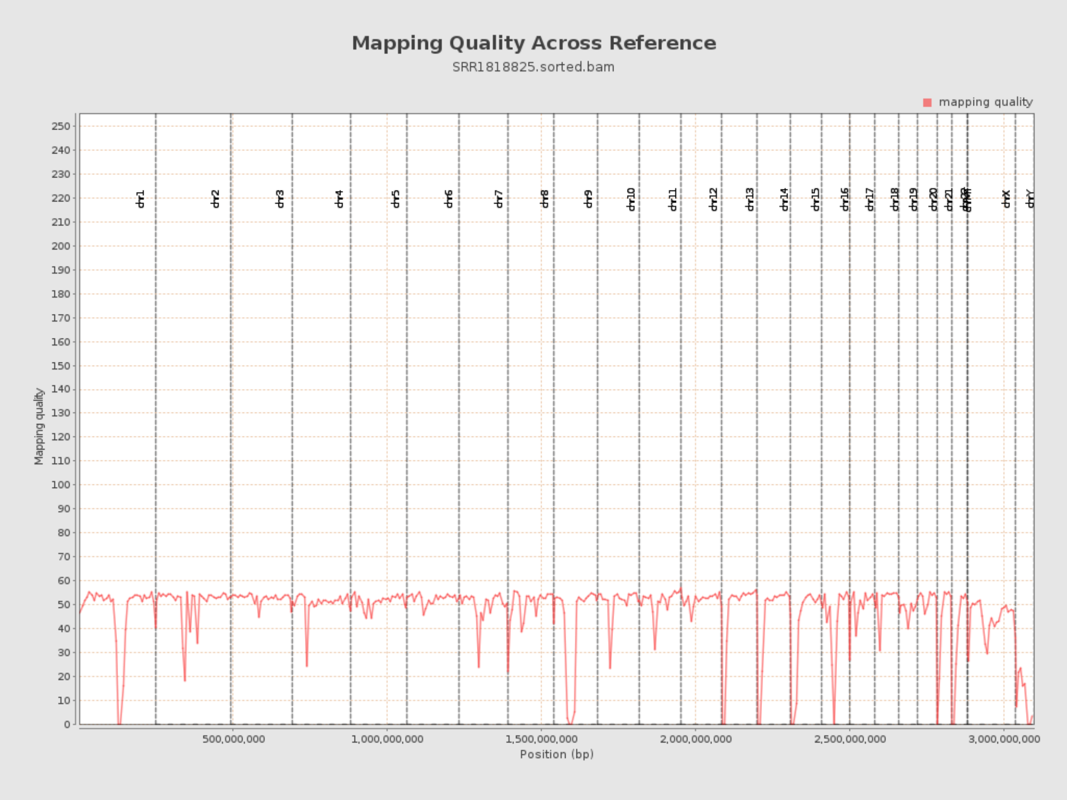
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram