Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:11:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818811.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_SRR1818811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:11:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,269,773
Mapped reads	1,234,691 / 97.24%
Unmapped reads	35,082 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,146 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	439,376 / 34.6%
Duplication rate	31.57%
Clipped reads	1,228,121 / 96.72%

2.2. ACGT Content

Number/percentage of A's	23,137,167 / 27.6%
Number/percentage of C's	17,534,885 / 20.92%
Number/percentage of T's	24,487,526 / 29.21%
Number/percentage of G's	18,658,080 / 22.26%
Number/percentage of N's	4,985 / 0.01%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.3306

2.4. Mapping Quality

Mean Mapping Quality	47.66

2.5. Mismatches and indels

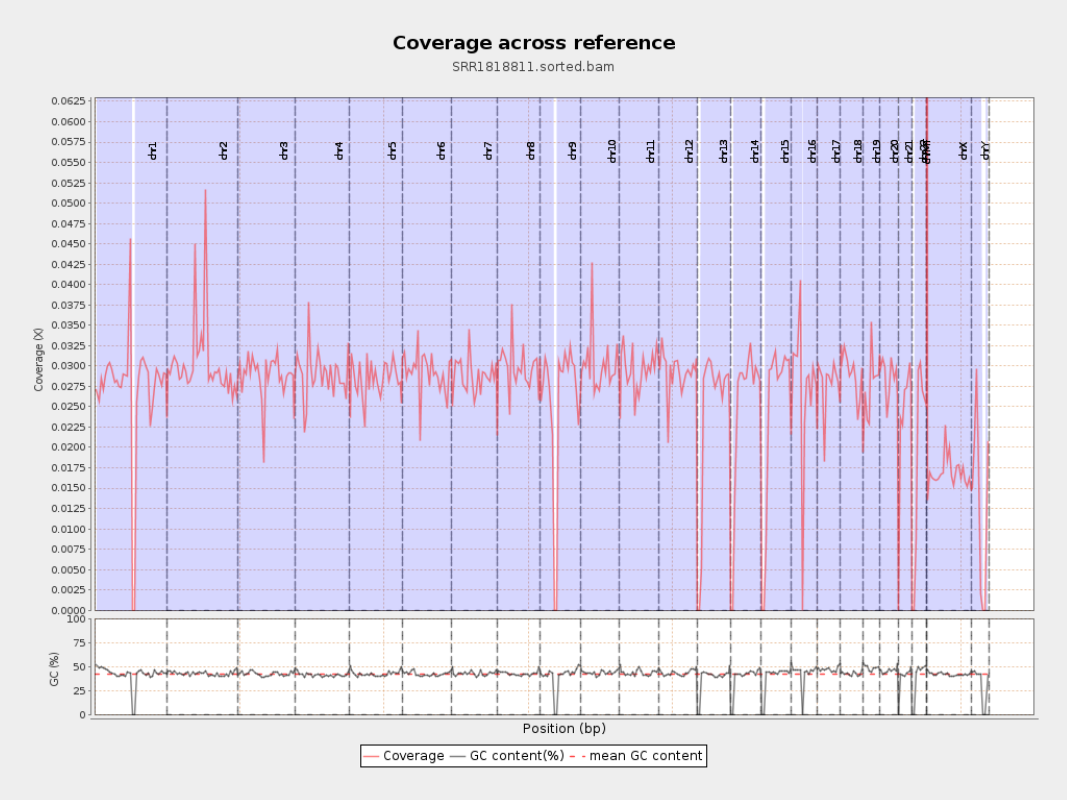
General error rate	0.53%
Mismatches	426,420
Insertions	10,588
Mapped reads with at least one insertion	0.85%
Deletions	21,142
Mapped reads with at least one deletion	1.7%
Homopolymer indels	40.4%

2.6. Chromosome stats

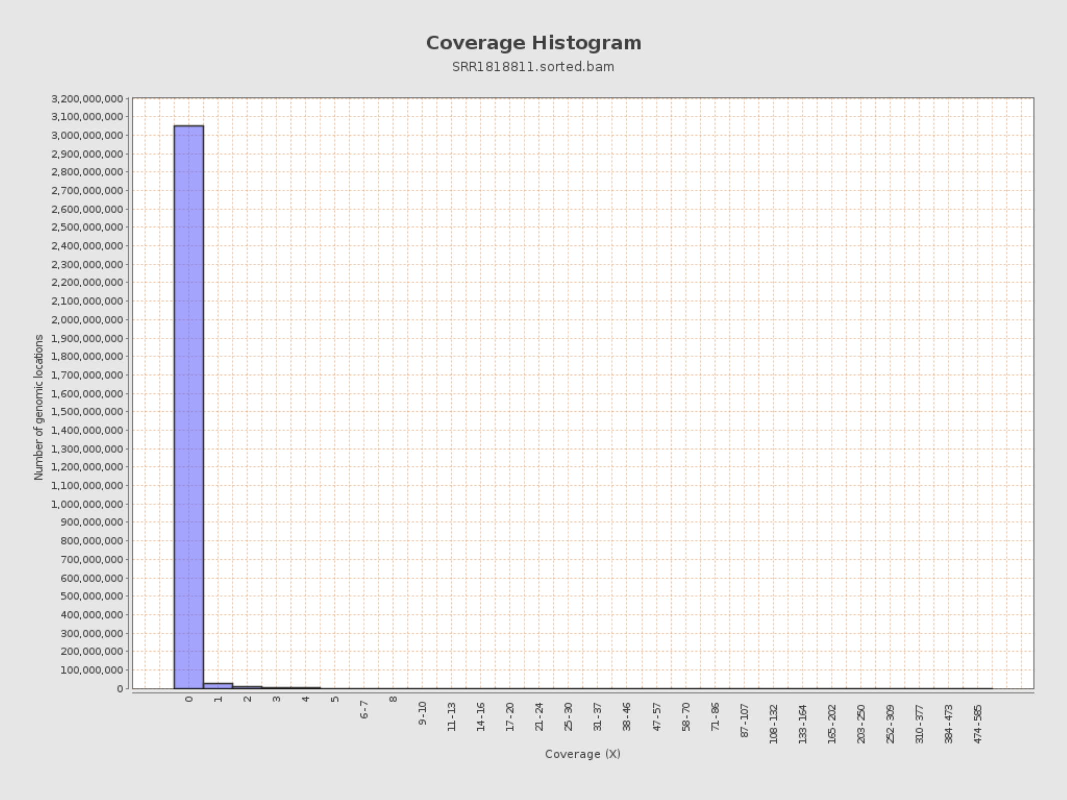
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6736015	0.027	0.4821
chr2	243199373	7397532	0.0304	0.4494
chr3	198022430	5708724	0.0288	0.2703
chr4	191154276	5540420	0.029	0.2903
chr5	180915260	5171228	0.0286	0.2766
chr6	171115067	4994683	0.0292	0.2958
chr7	159138663	4578166	0.0288	0.3171

chr8	146364022	4355789	0.0298	0.3173
chr9	141213431	3586649	0.0254	0.2897
chr10	135534747	4093706	0.0302	0.3562
chr11	135006516	3984720	0.0295	0.3074
chr12	133851895	3898158	0.0291	0.2863
chr13	115169878	2763947	0.024	0.2452
chr14	107349540	2620668	0.0244	0.2648
chr15	102531392	2468975	0.0241	0.25
chr16	90354753	2417206	0.0268	0.3346
chr17	81195210	2260643	0.0278	0.279
chr18	78077248	2266137	0.029	0.3941
chr19	59128983	1628727	0.0275	0.4023
chr20	63025520	1800940	0.0286	0.2802
chr21	48129895	1150585	0.0239	0.2617
chr22	51304566	988550	0.0193	0.2371
chrMT	16571	32269	1.9473	2.616
chrX	155270560	2629497	0.0169	0.2237
chrY	59373566	782324	0.0132	0.4145

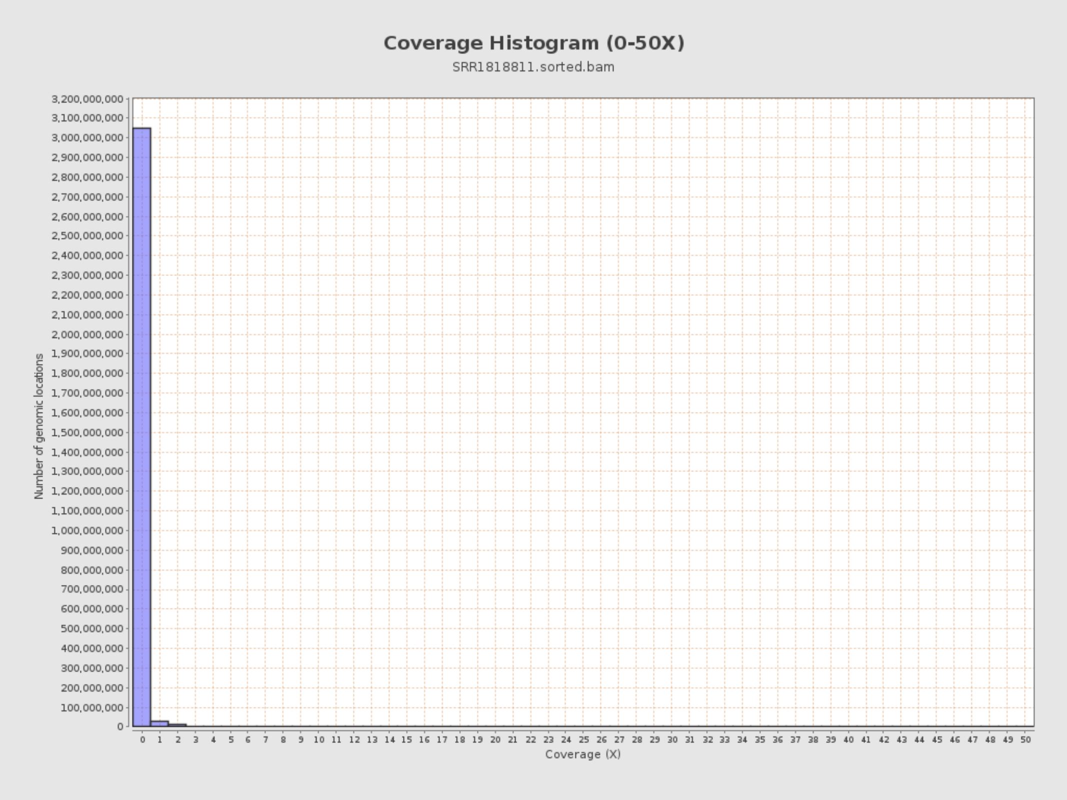
3. Results : Coverage across reference



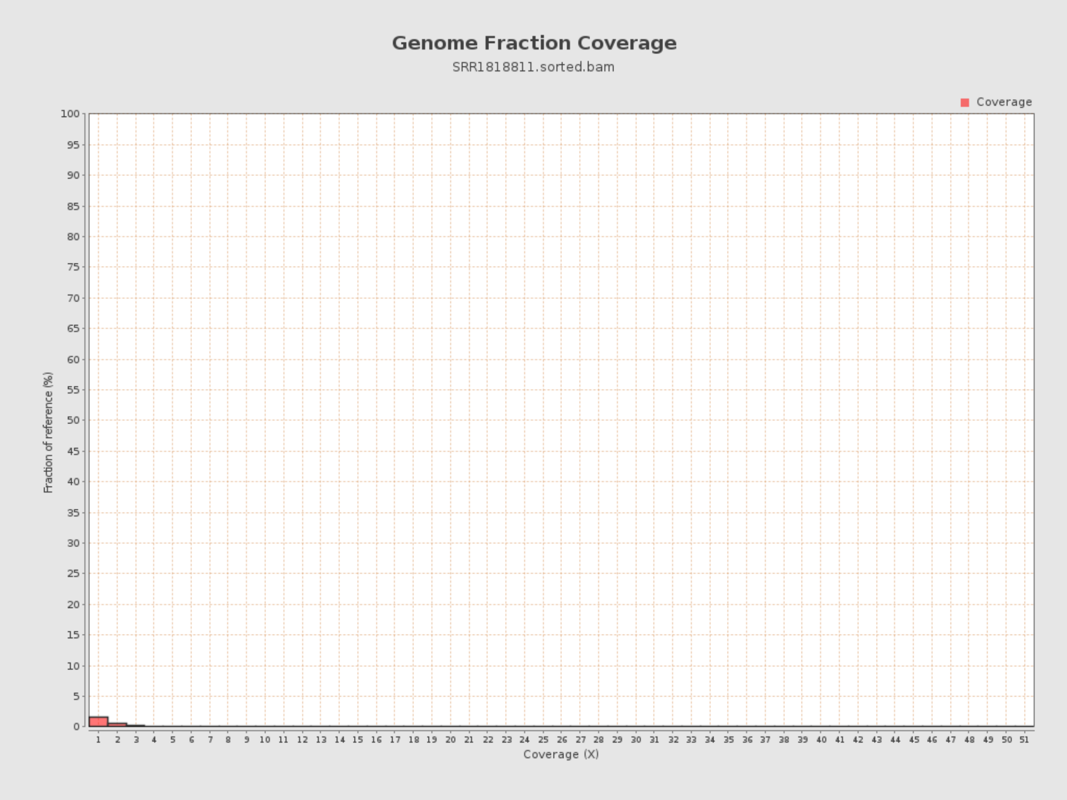
4. Results : Coverage Histogram



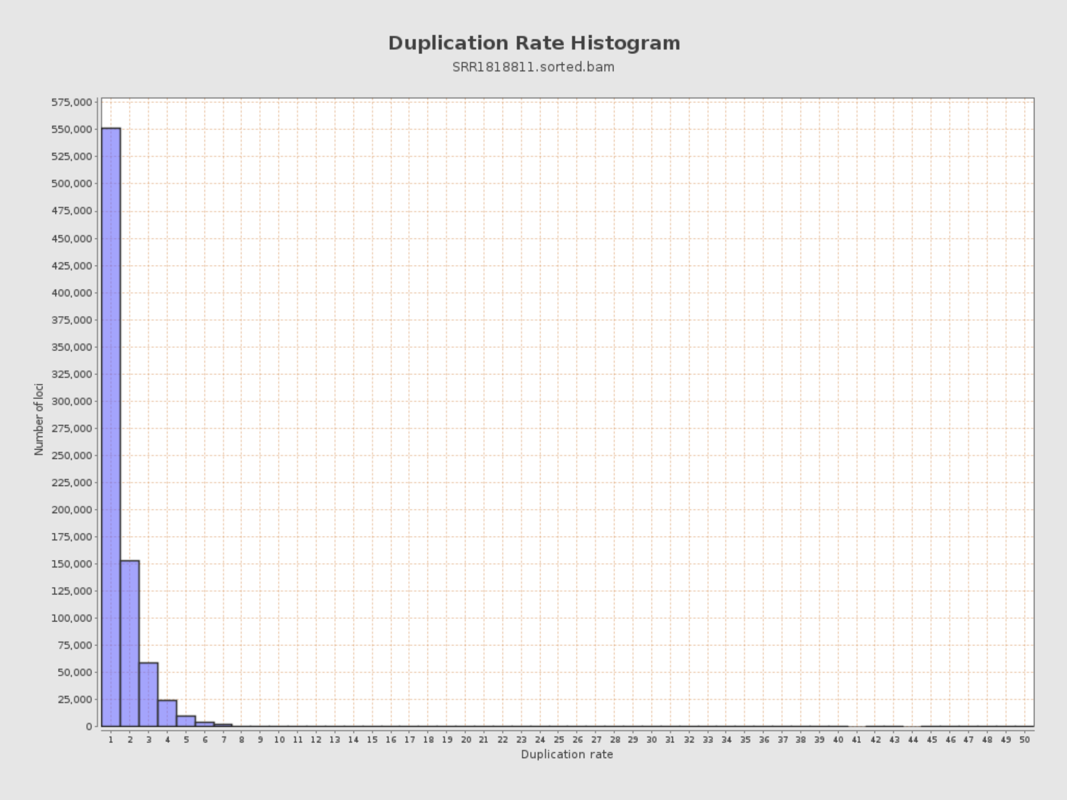
5. Results : Coverage Histogram (0-50X)



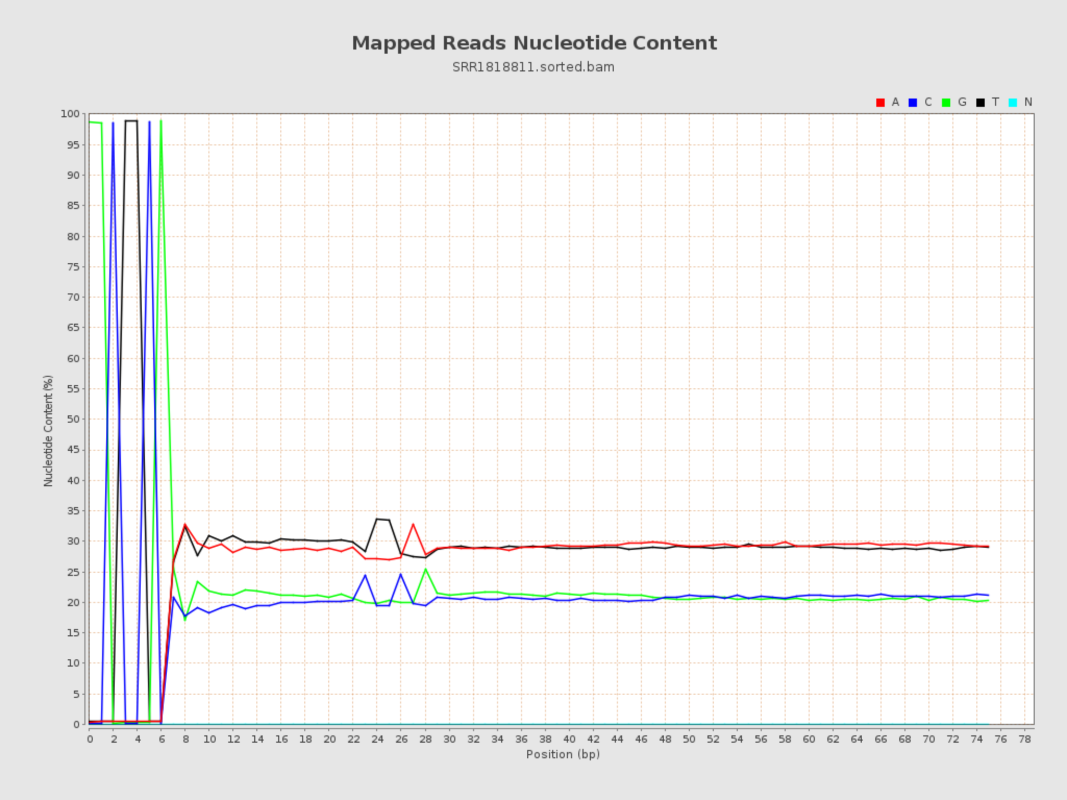
6. Results : Genome Fraction Coverage



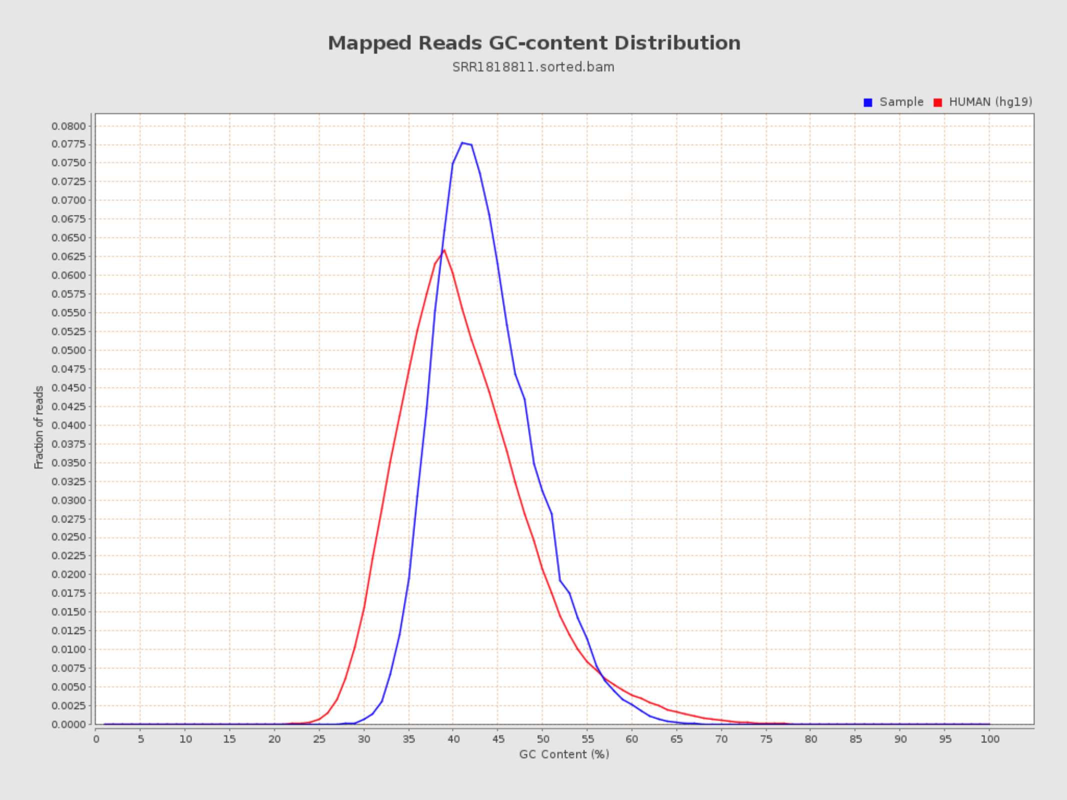
7. Results : Duplication Rate Histogram



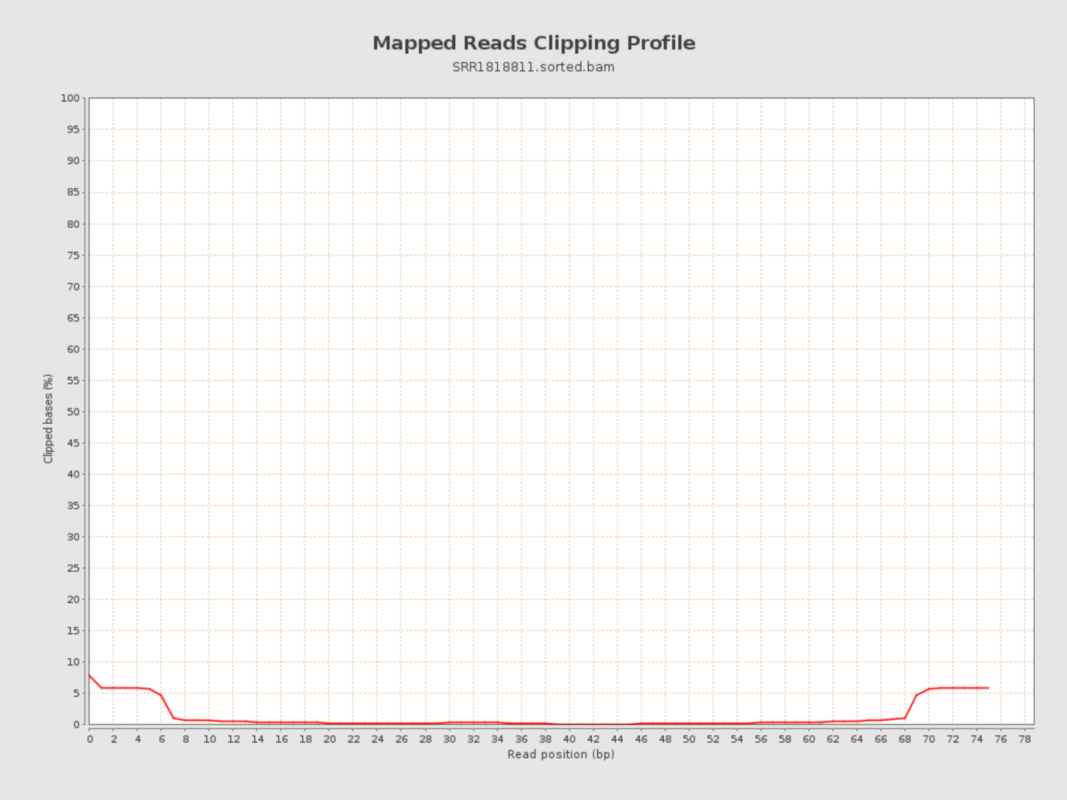
8. Results : Mapped Reads Nucleotide Content



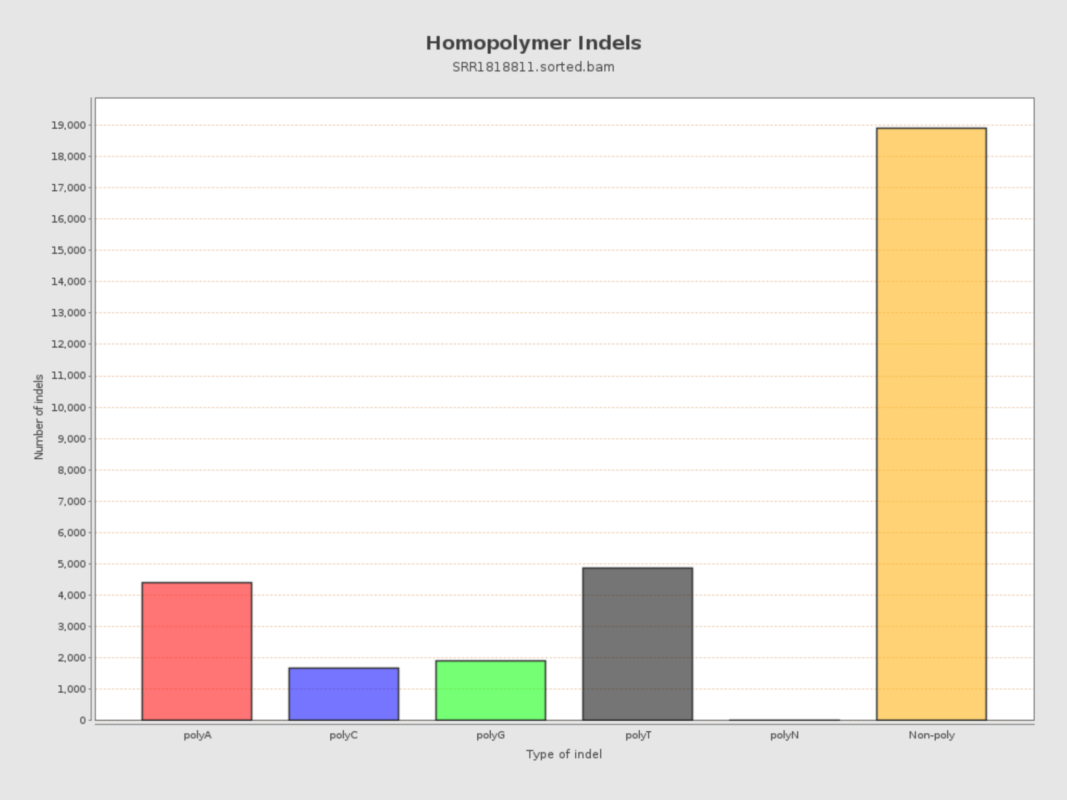
9. Results : Mapped Reads GC-content Distribution



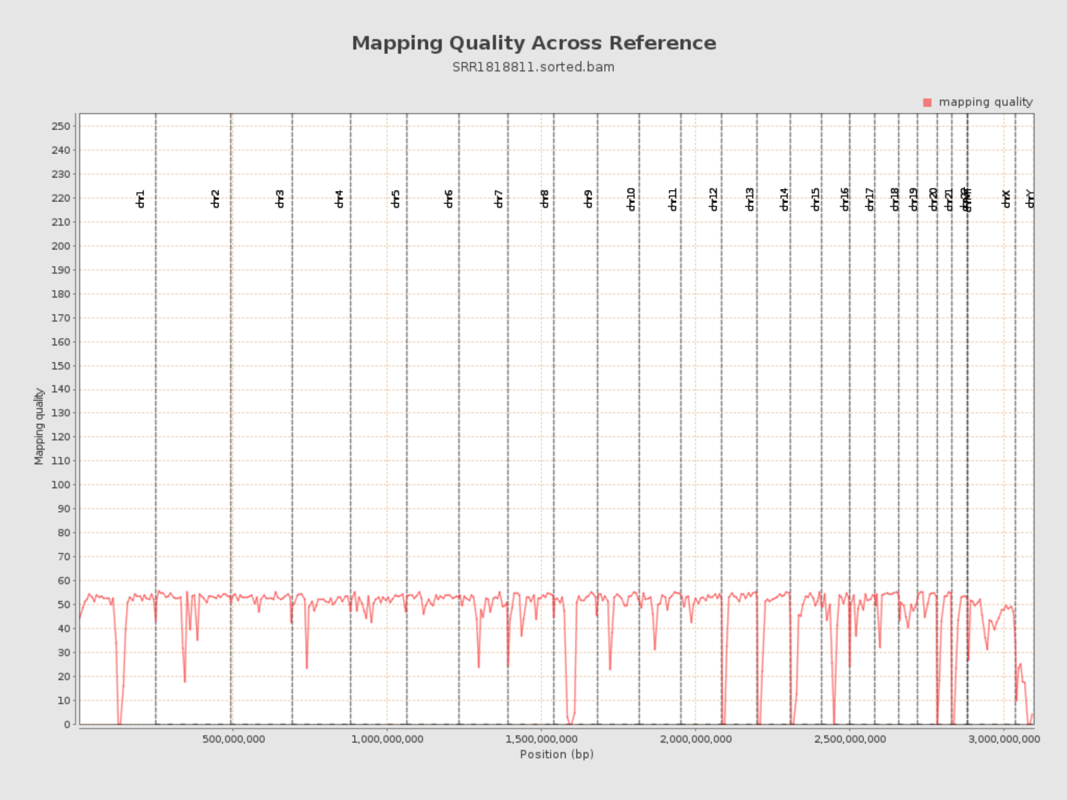
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram