Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:08:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818832.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_SRR1818832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:08:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,620,218
Mapped reads	2,582,958 / 98.58%
Unmapped reads	37,260 / 1.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,190 / 1.5%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	706,684 / 26.97%
Duplication rate	23.18%
Clipped reads	2,601,775 / 99.3%

2.2. ACGT Content

Number/percentage of A's	69,158,209 / 28.89%
Number/percentage of C's	50,208,163 / 20.97%
Number/percentage of T's	66,086,728 / 27.61%
Number/percentage of G's	53,942,354 / 22.53%
Number/percentage of N's	3,660 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.8963

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

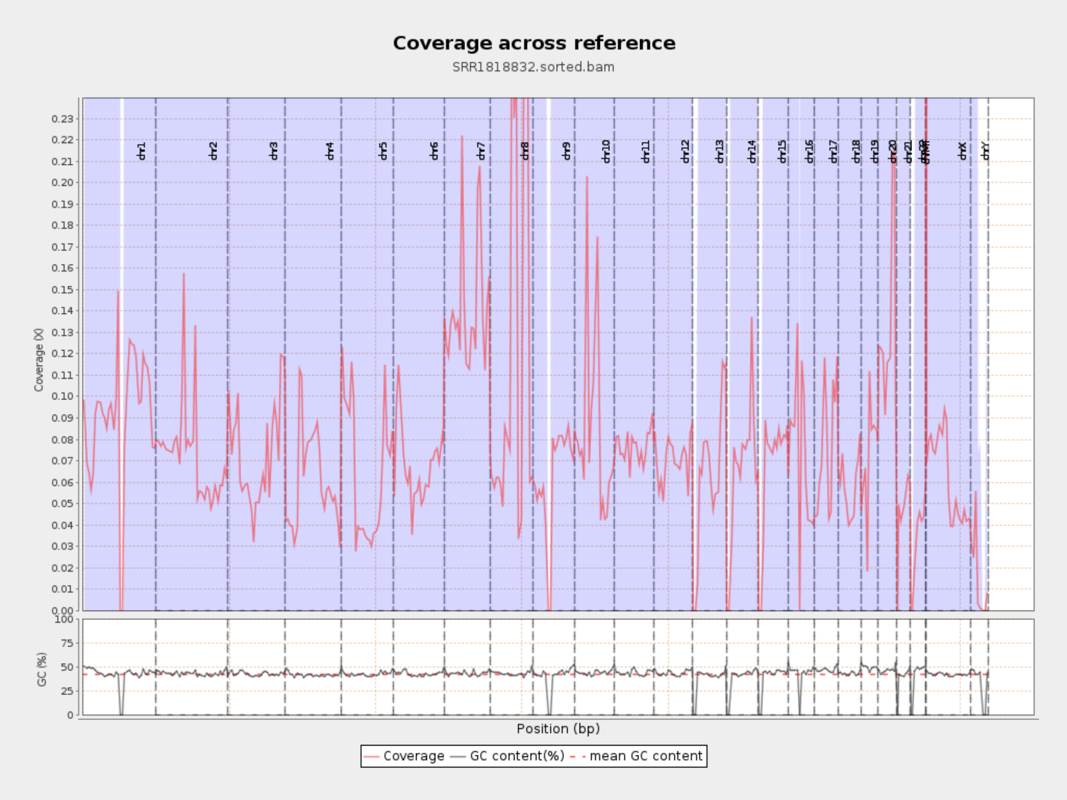
General error rate	0.63%
Mismatches	1,421,589
Insertions	33,854
Mapped reads with at least one insertion	1.27%
Deletions	75,957
Mapped reads with at least one deletion	2.87%
Homopolymer indels	40.51%

2.6. Chromosome stats

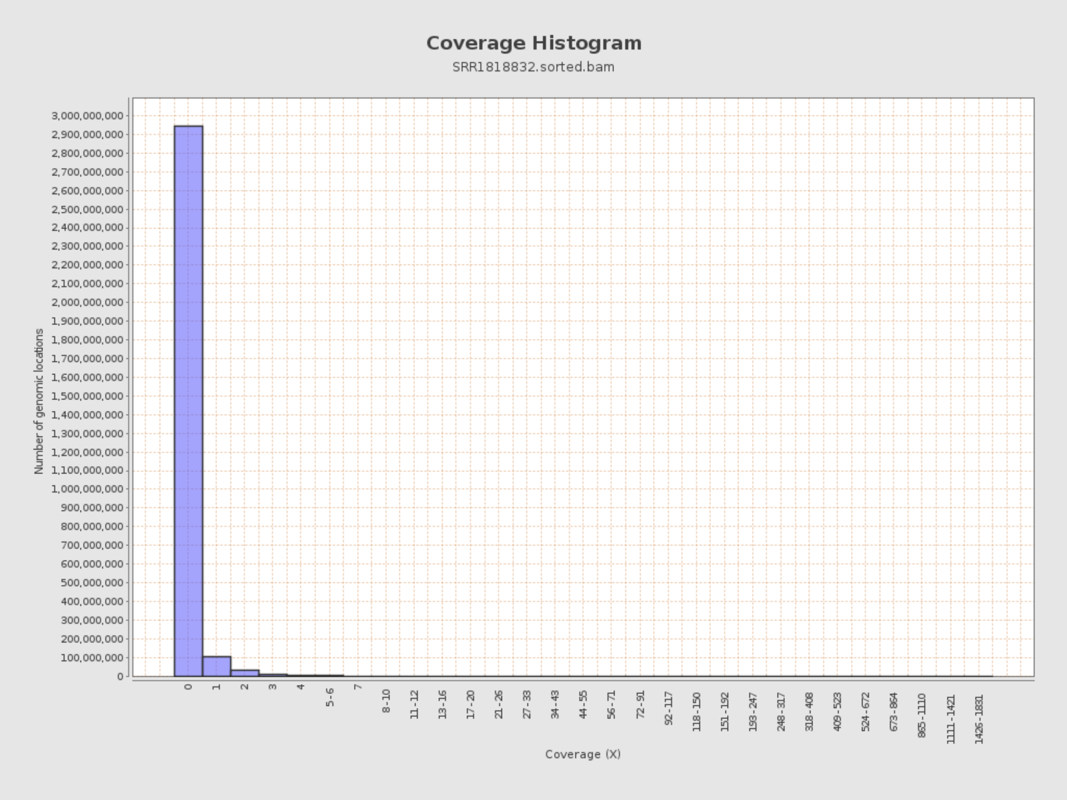
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22685252	0.091	1.4098
chr2	243199373	17702327	0.0728	1.227
chr3	198022430	14466700	0.0731	0.3944
chr4	191154276	11745157	0.0614	0.5115
chr5	180915260	11814779	0.0653	0.3967
chr6	171115067	11656284	0.0681	0.4209
chr7	159138663	22569342	0.1418	2.0047

chr8	146364022	21318902	0.1457	0.7215
chr9	141213431	8711584	0.0617	0.6694
chr10	135534747	11552071	0.0852	1.2675
chr11	135006516	10342209	0.0766	0.4971
chr12	133851895	9408073	0.0703	0.3929
chr13	115169878	7257004	0.063	0.3633
chr14	107349540	7095482	0.0661	0.412
chr15	102531392	6665793	0.065	0.3708
chr16	90354753	6507491	0.072	0.8856
chr17	81195210	6026963	0.0742	0.574
chr18	78077248	4514408	0.0578	0.8083
chr19	59128983	4246433	0.0718	1.323
chr20	63025520	8721007	0.1384	0.5997
chr21	48129895	2295570	0.0477	0.3913
chr22	51304566	1602726	0.0312	0.3183
chrMT	16571	98501	5.9442	4.9425
chrX	155270560	9660644	0.0622	0.4289
chrY	59373566	885813	0.0149	1.074

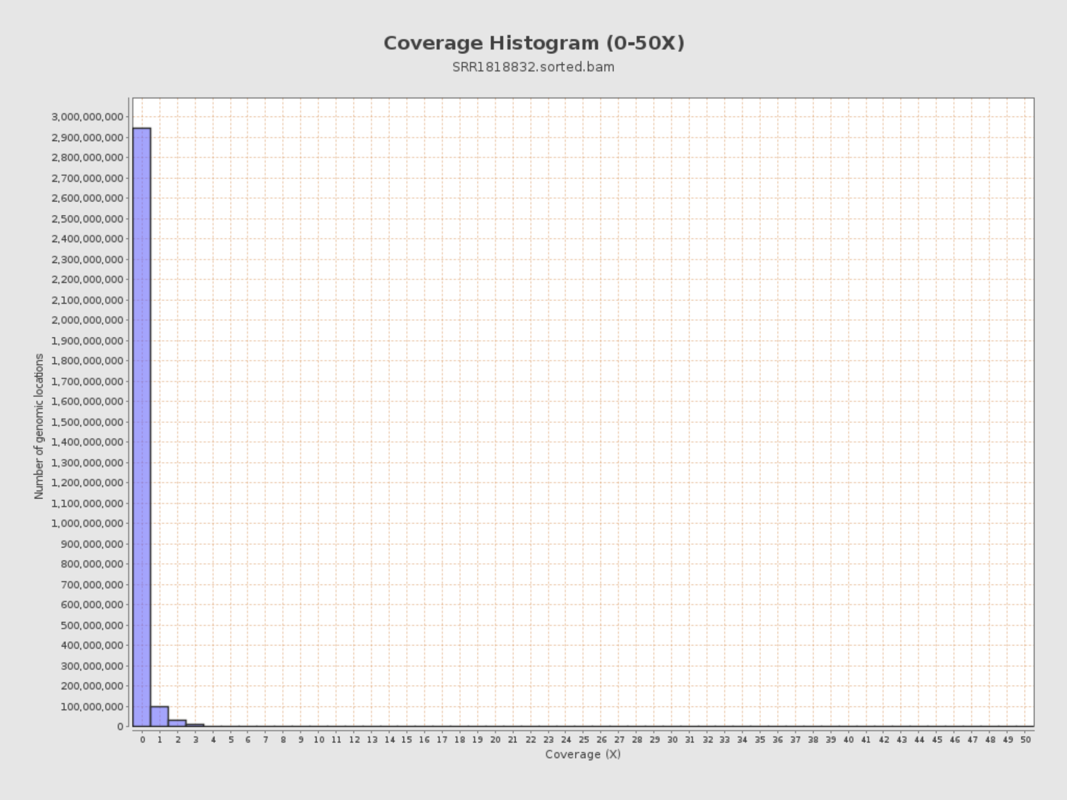
3. Results : Coverage across reference



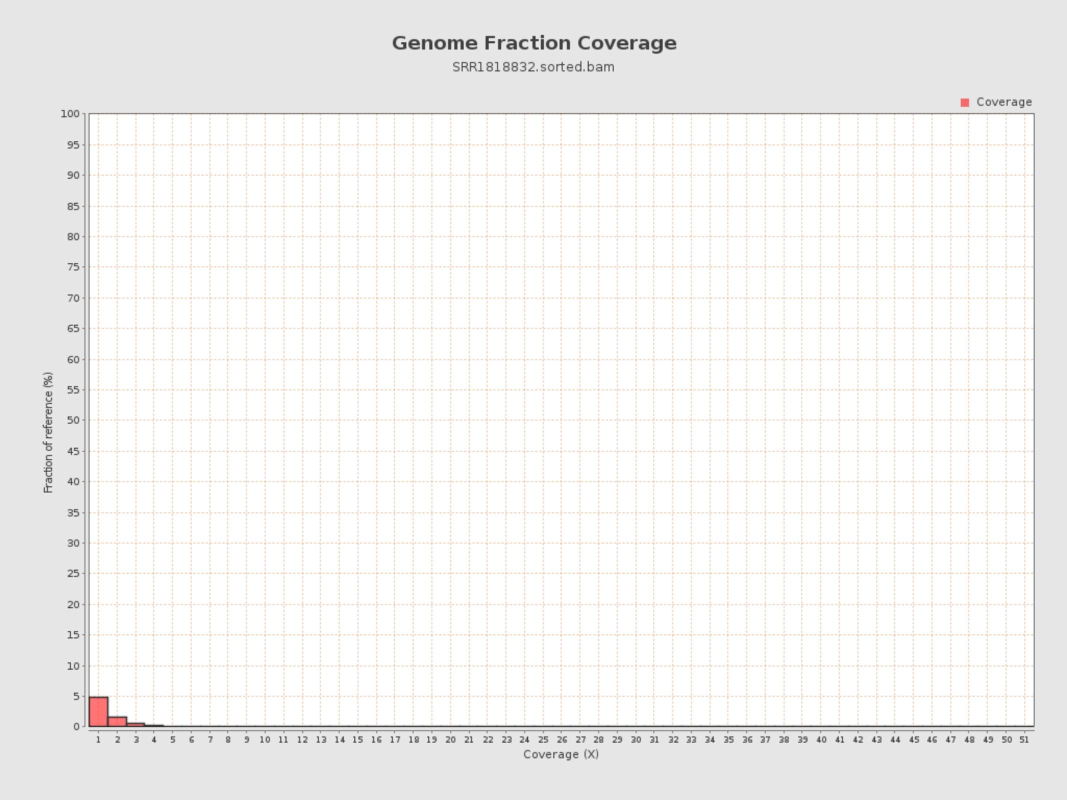
4. Results : Coverage Histogram



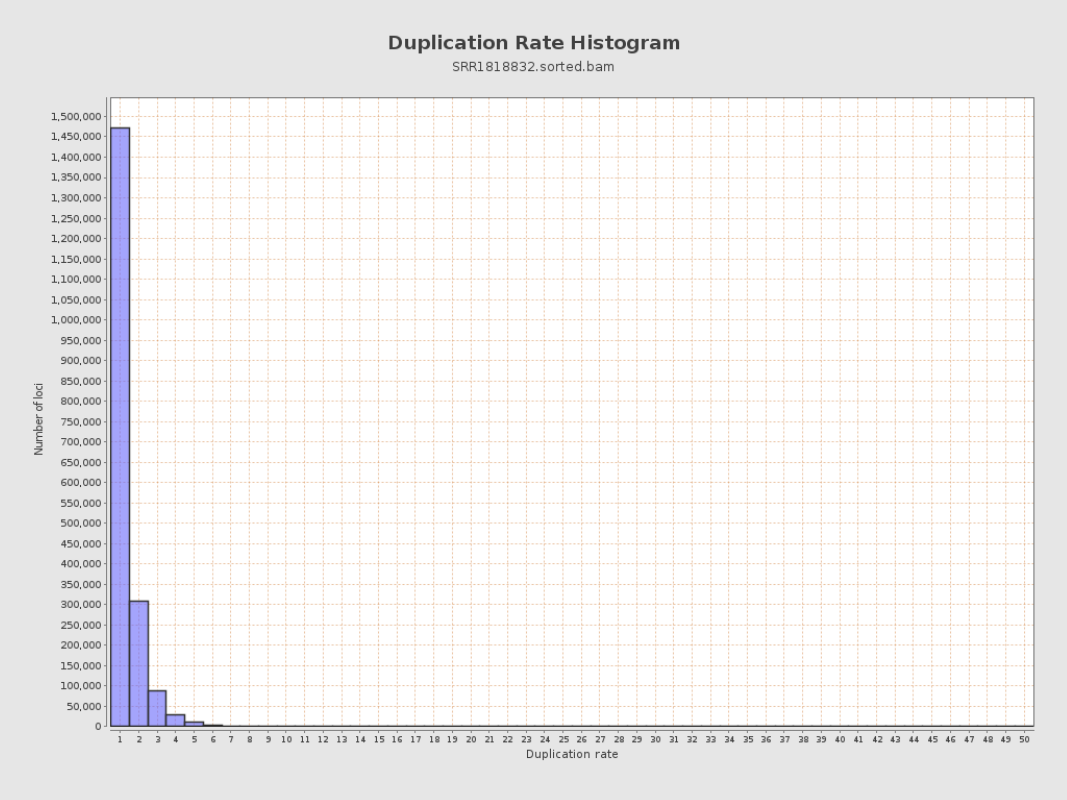
5. Results : Coverage Histogram (0-50X)



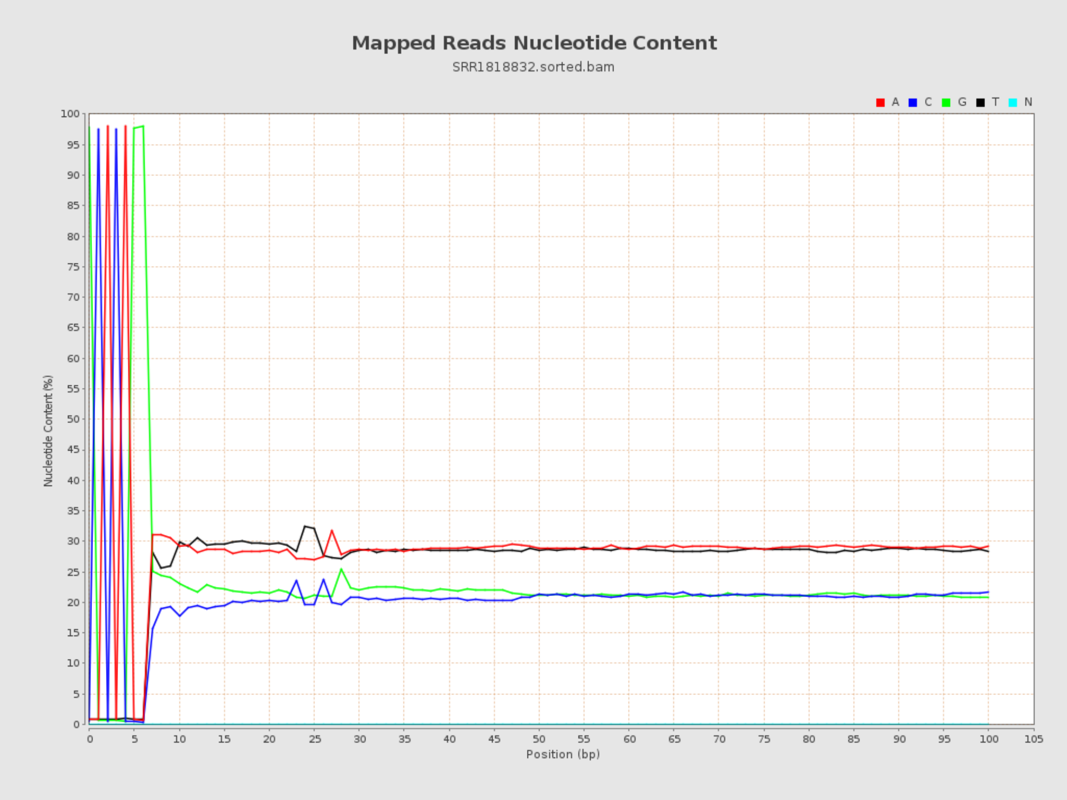
6. Results : Genome Fraction Coverage



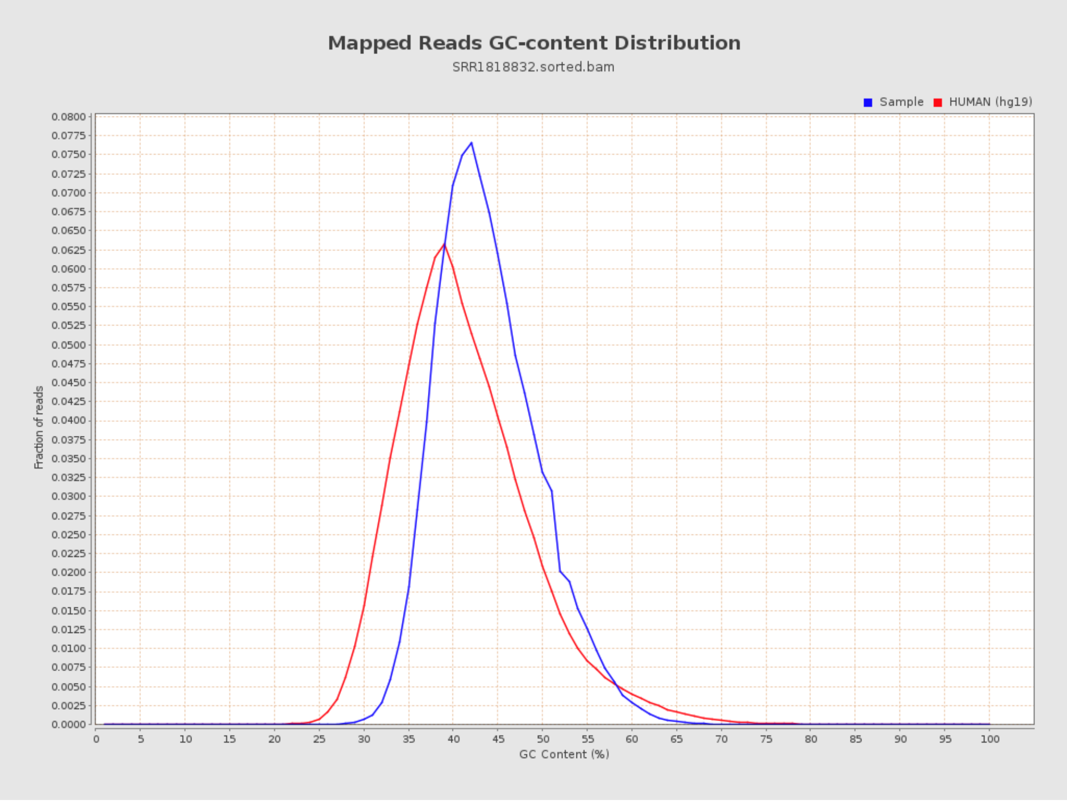
7. Results : Duplication Rate Histogram



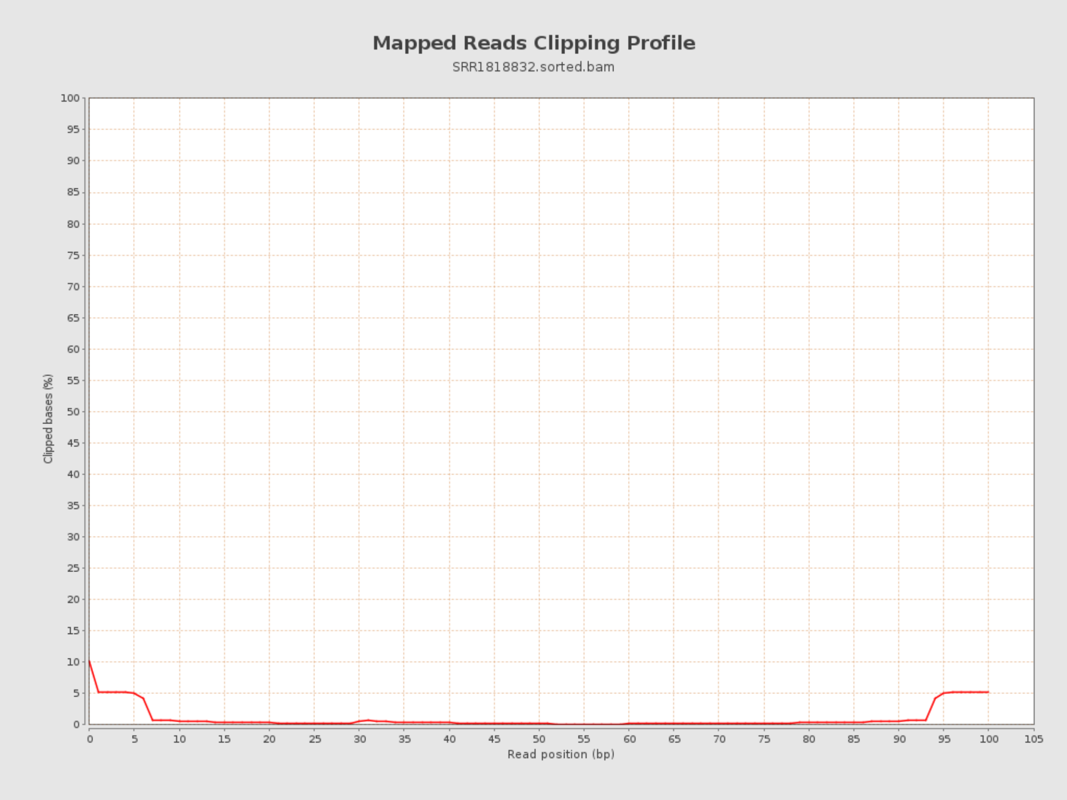
8. Results : Mapped Reads Nucleotide Content



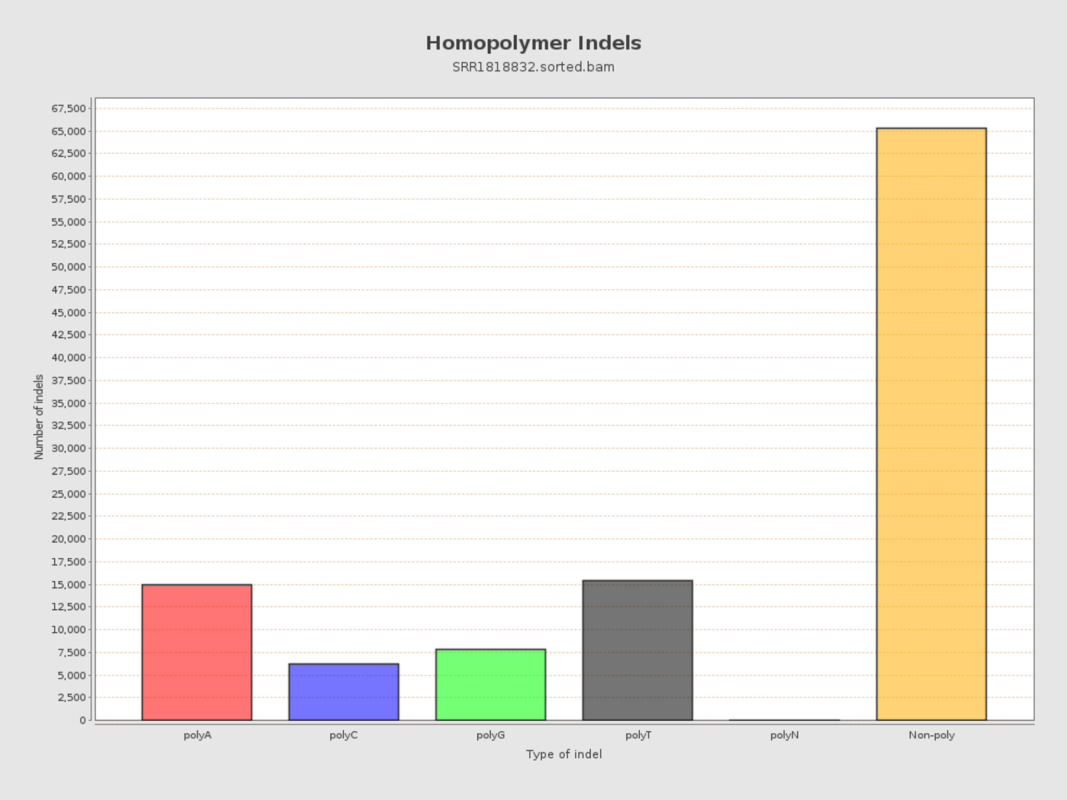
9. Results : Mapped Reads GC-content Distribution



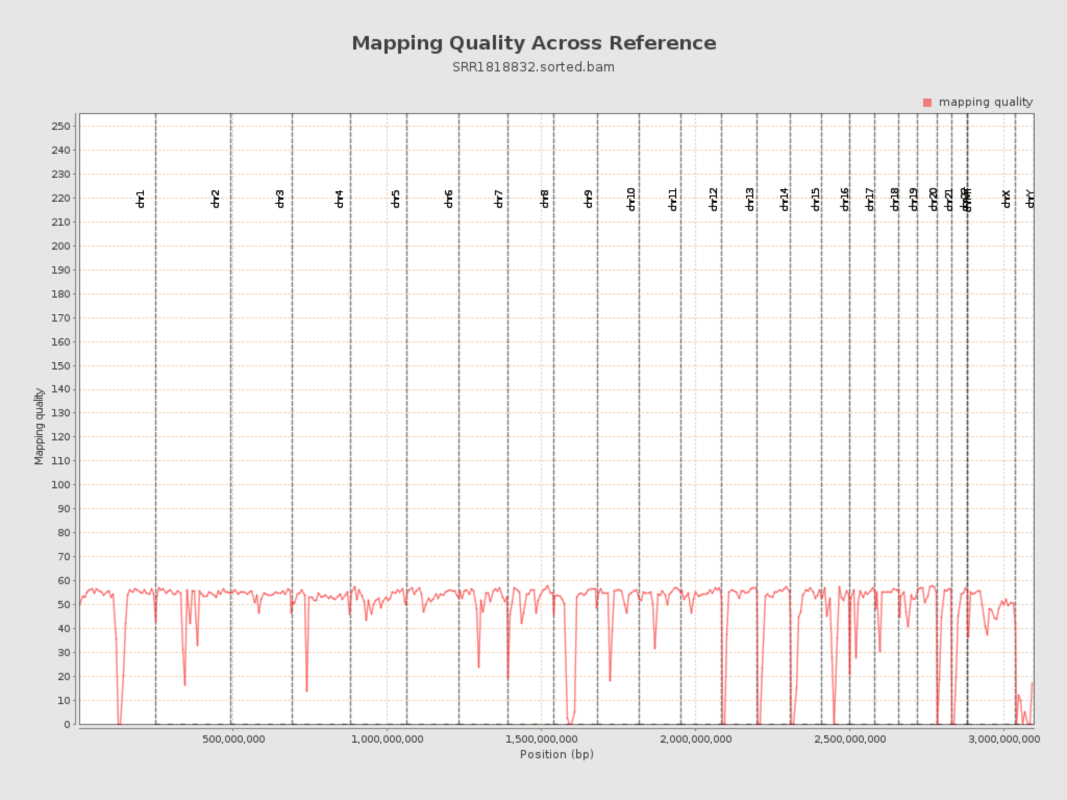
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram