Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:40:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818940.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_SRR1818940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:40:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,117,675
Mapped reads	1,100,612 / 98.47%
Unmapped reads	17,063 / 1.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,013 / 1.25%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	374,768 / 33.53%
Duplication rate	27.79%
Clipped reads	1,105,987 / 98.95%

2.2. ACGT Content

Number/percentage of A's	29,887,675 / 29.32%
Number/percentage of C's	21,465,176 / 21.06%
Number/percentage of T's	28,702,290 / 28.16%
Number/percentage of G's	21,883,181 / 21.47%
Number/percentage of N's	4,073 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.4019

2.4. Mapping Quality

Mean Mapping Quality	49.24

2.5. Mismatches and indels

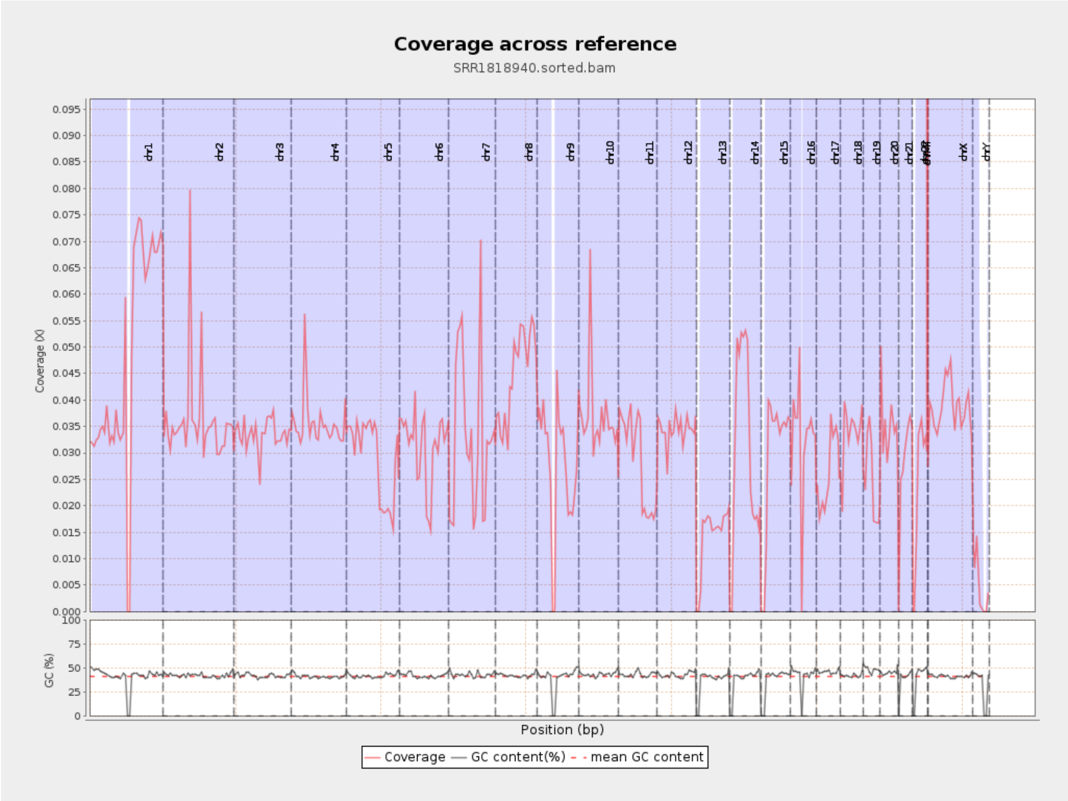
General error rate	0.67%
Mismatches	652,765
Insertions	12,222
Mapped reads with at least one insertion	1.08%
Deletions	31,091
Mapped reads with at least one deletion	2.77%
Homopolymer indels	42.24%

2.6. Chromosome stats

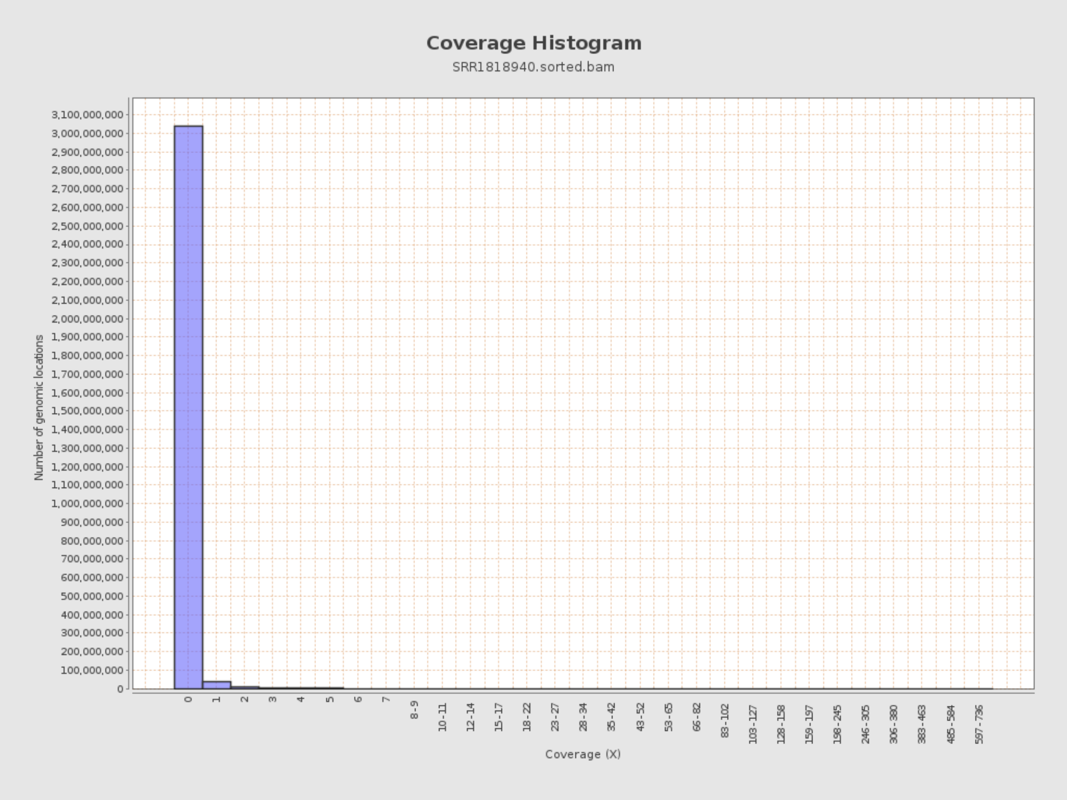
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11837395	0.0475	0.6605
chr2	243199373	8796004	0.0362	0.5186
chr3	198022430	6629748	0.0335	0.2968
chr4	191154276	6779071	0.0355	0.3258
chr5	180915260	5274109	0.0292	0.2809
chr6	171115067	5361250	0.0313	0.3059
chr7	159138663	5229620	0.0329	0.3668

chr8	146364022	6587548	0.045	0.3847
chr9	141213431	3827595	0.0271	0.4689
chr10	135534747	4979732	0.0367	0.4703
chr11	135006516	3840879	0.0284	0.3009
chr12	133851895	4600916	0.0344	0.3082
chr13	115169878	1639090	0.0142	0.1935
chr14	107349540	3309378	0.0308	0.2952
chr15	102531392	3023059	0.0295	0.2801
chr16	90354753	2950040	0.0326	0.3716
chr17	81195210	2144197	0.0264	0.2796
chr18	78077248	2617642	0.0335	0.5908
chr19	59128983	1483721	0.0251	0.5721
chr20	63025520	2200457	0.0349	0.3148
chr21	48129895	1360288	0.0283	0.2924
chr22	51304566	1200882	0.0234	0.2593
chrMT	16571	64040	3.8646	3.8052
chrX	155270560	5980258	0.0385	0.3907
chrY	59373566	280250	0.0047	0.2444

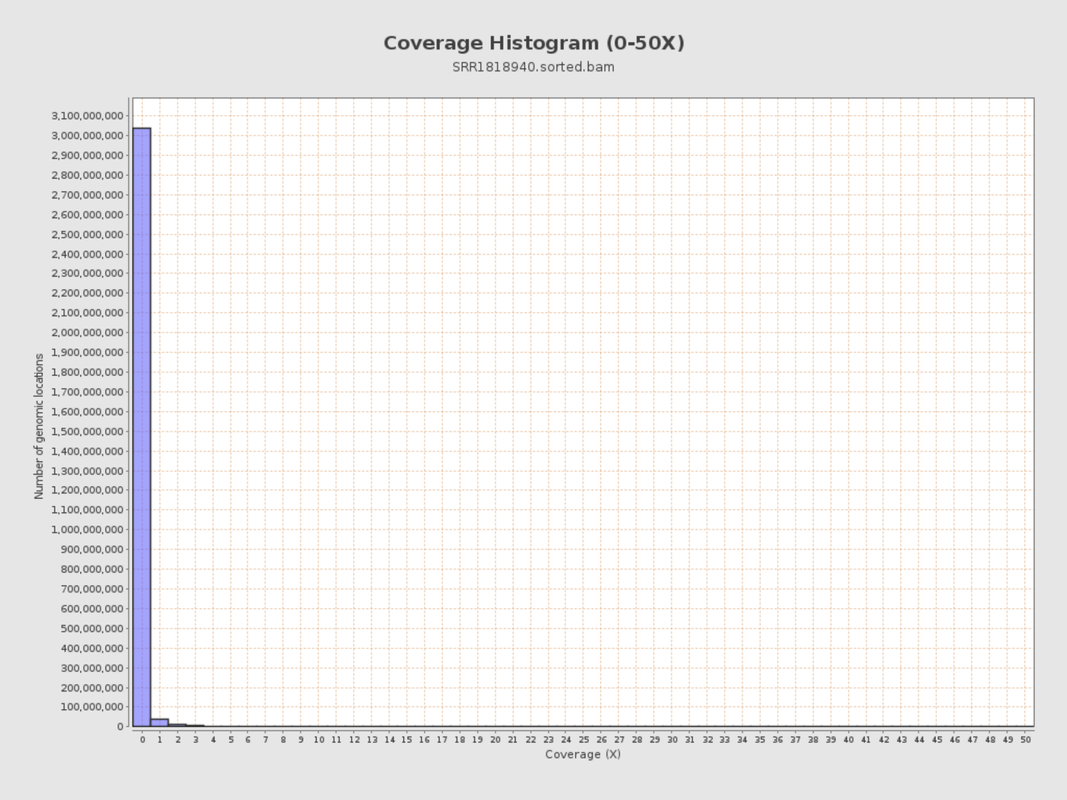
3. Results : Coverage across reference



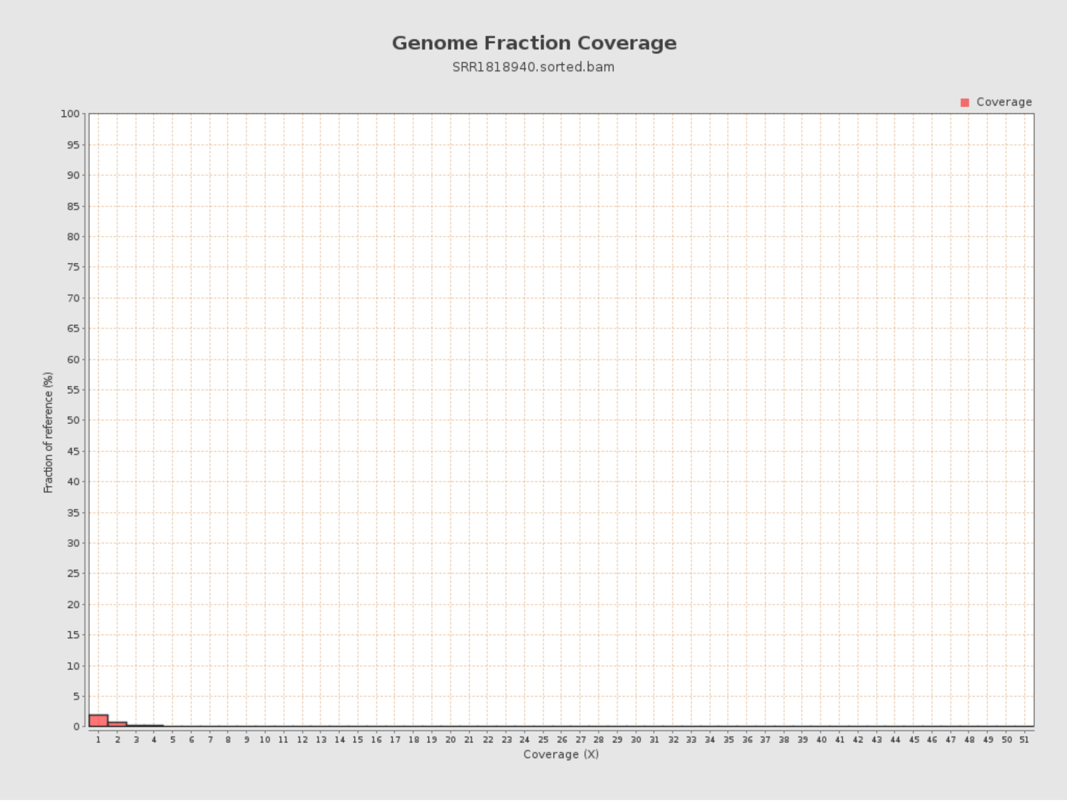
4. Results : Coverage Histogram



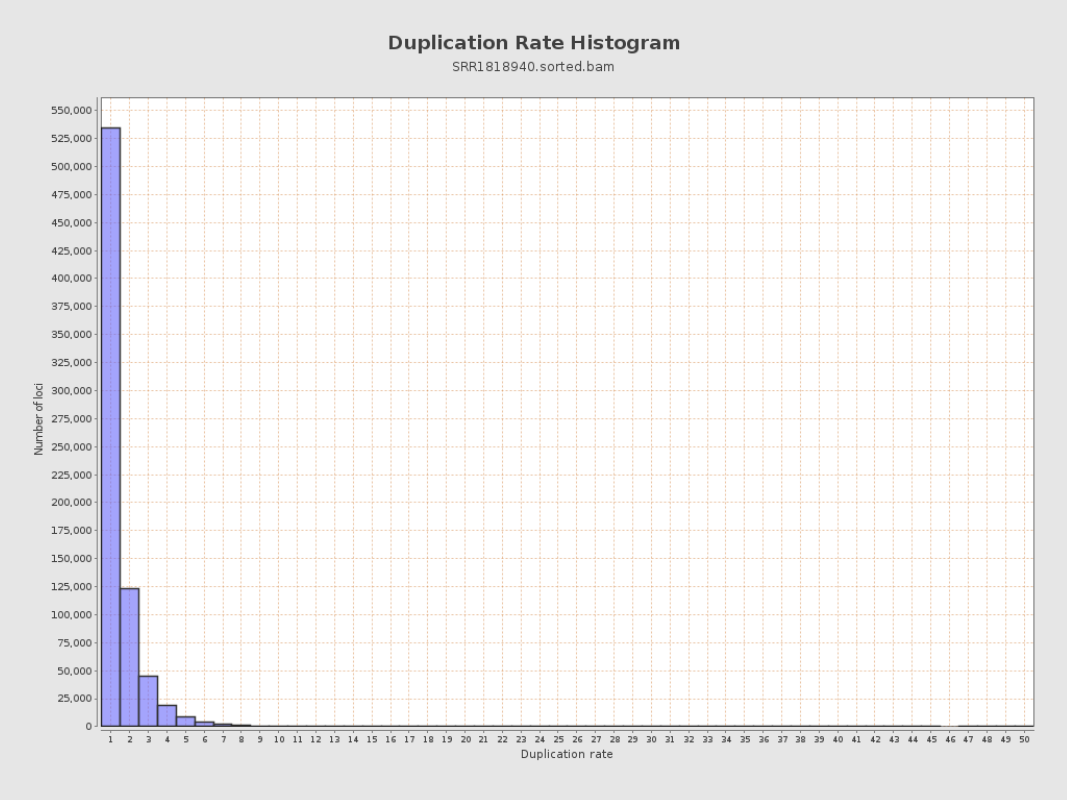
5. Results : Coverage Histogram (0-50X)



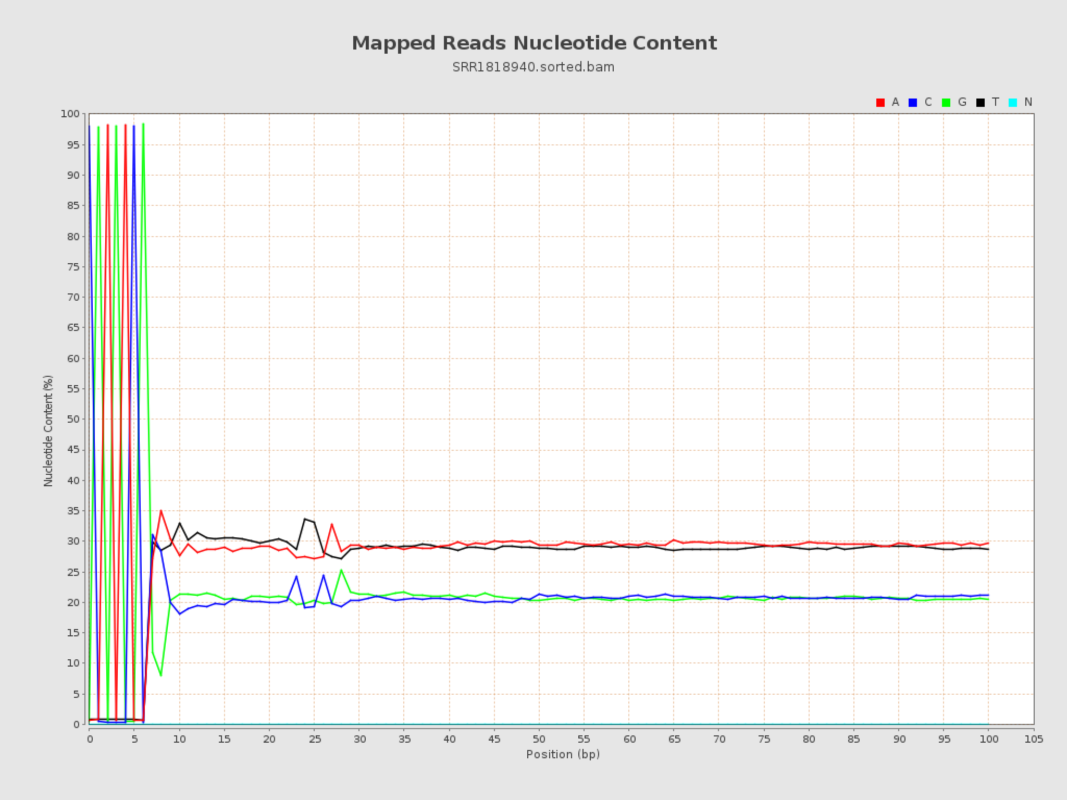
6. Results : Genome Fraction Coverage



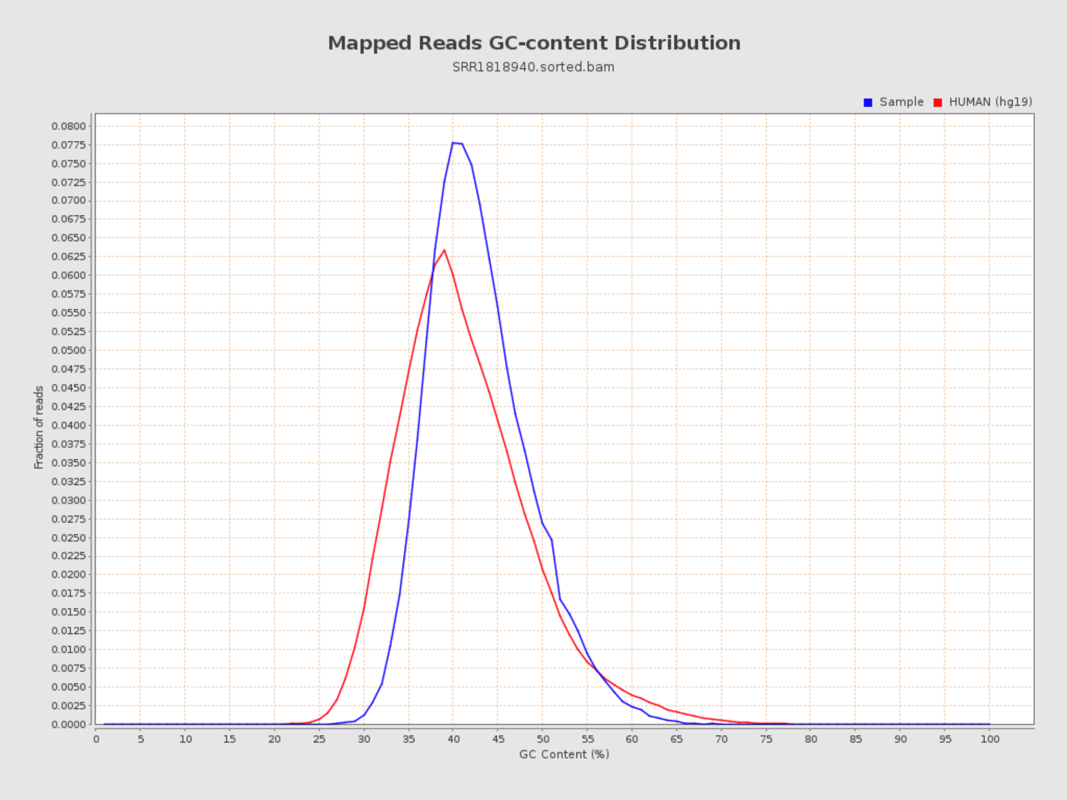
7. Results : Duplication Rate Histogram



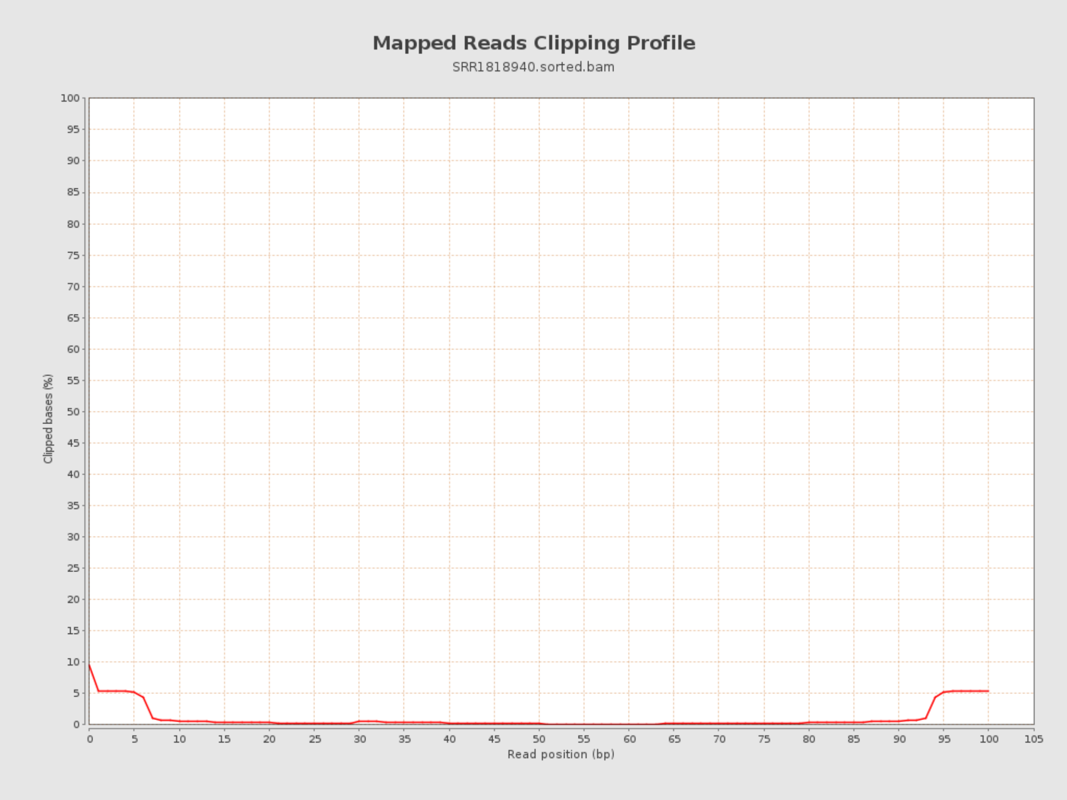
8. Results : Mapped Reads Nucleotide Content



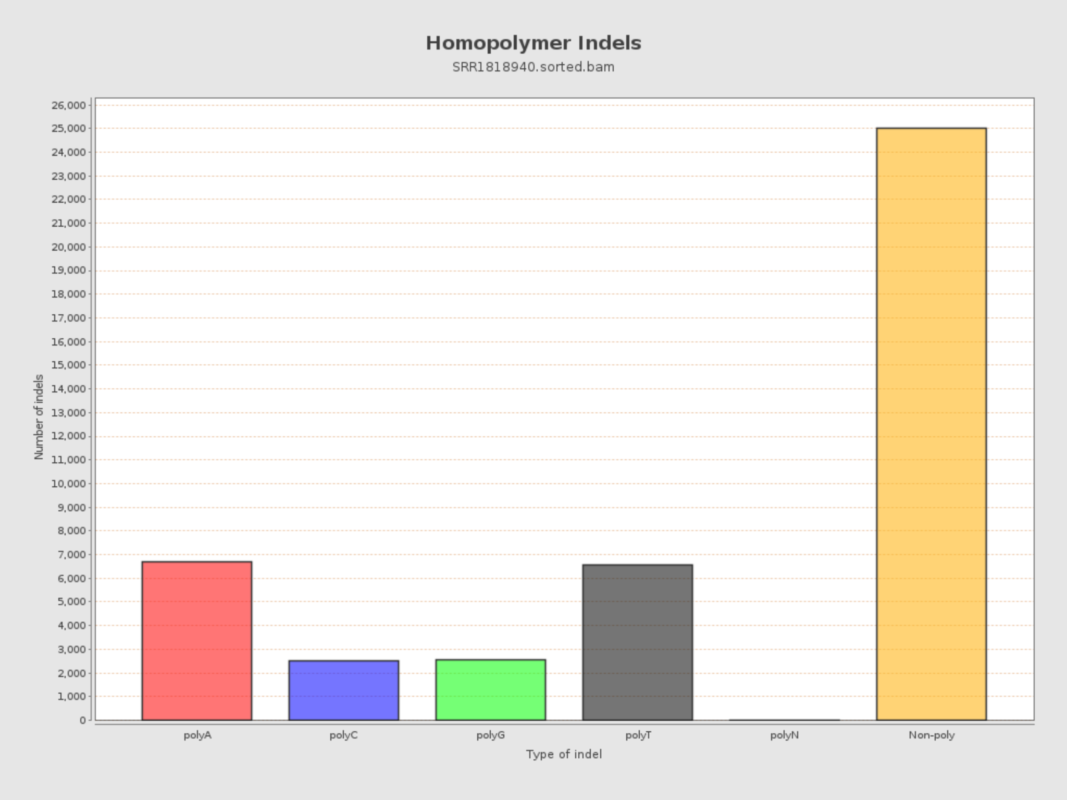
9. Results : Mapped Reads GC-content Distribution



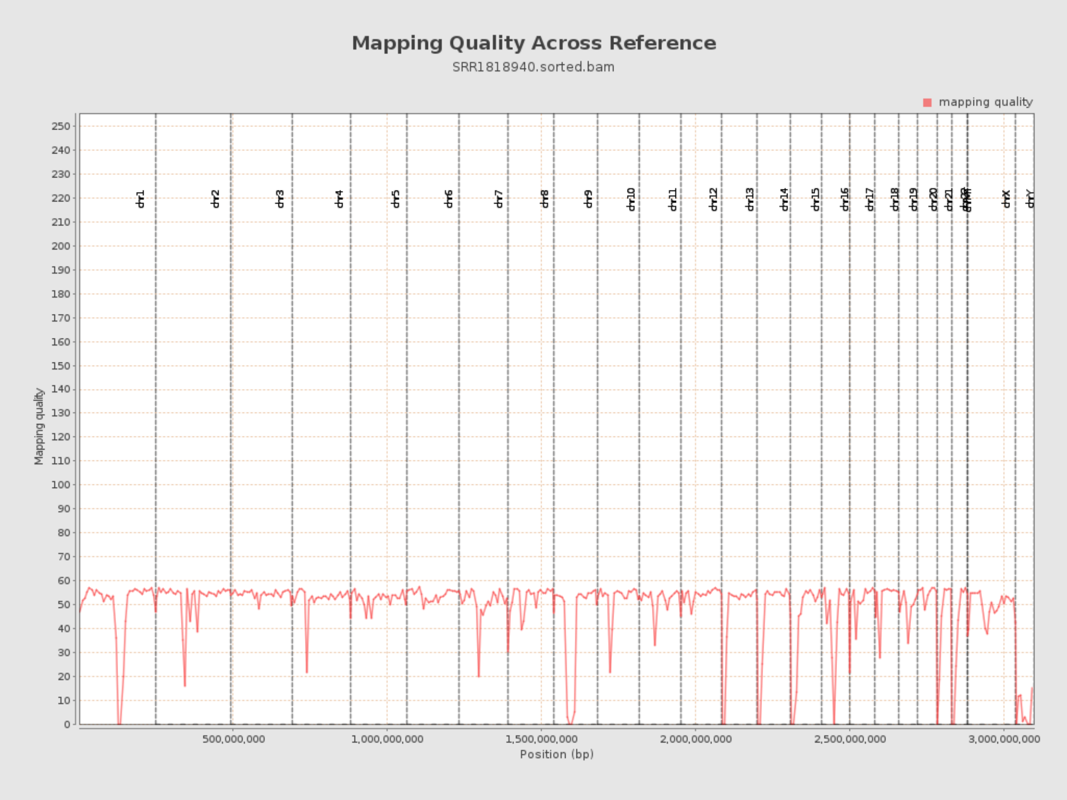
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram