Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:11:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818957.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_SRR1818957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:11:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,508,129
Mapped reads	2,355,860 / 93.93%
Unmapped reads	152,269 / 6.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,814 / 0.95%
Read min/max/mean length	30 / 101 / 101.37
Duplicated reads (estimated)	375,249 / 14.96%
Duplication rate	13.31%
Clipped reads	2,367,174 / 94.38%

2.2. ACGT Content

Number/percentage of A's	63,850,472 / 29.21%
Number/percentage of C's	44,974,942 / 20.58%
Number/percentage of T's	63,534,680 / 29.07%
Number/percentage of G's	46,213,120 / 21.14%
Number/percentage of N's	10,215 / 0%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0706

Standard Deviation	0.7054

2.4. Mapping Quality

Mean Mapping Quality	49.49

2.5. Mismatches and indels

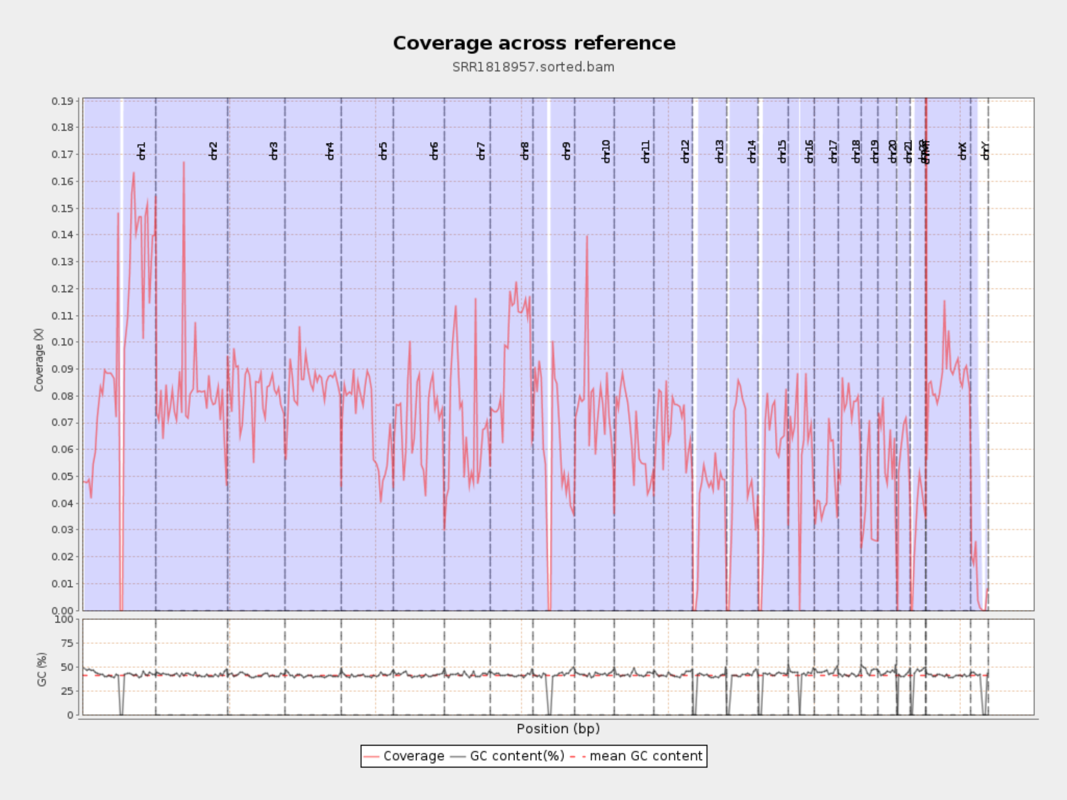
General error rate	0.6%
Mismatches	1,259,264
Insertions	27,205
Mapped reads with at least one insertion	1.13%
Deletions	57,251
Mapped reads with at least one deletion	2.38%
Homopolymer indels	42.95%

2.6. Chromosome stats

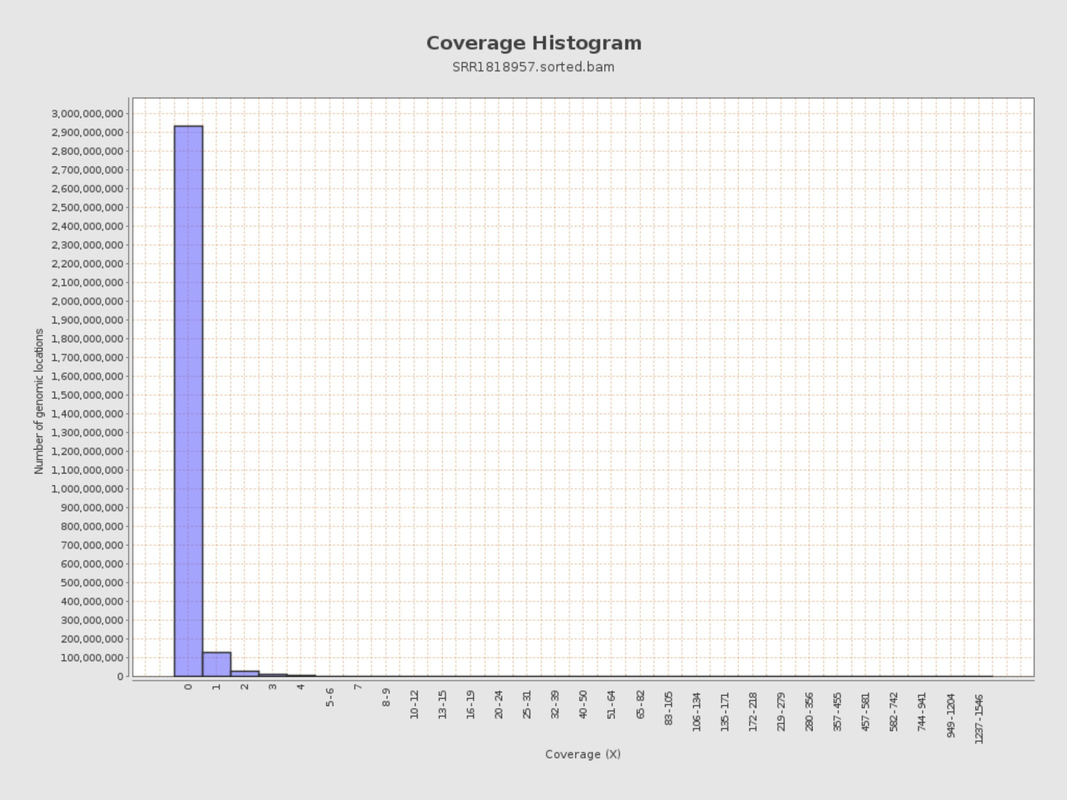
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24047289	0.0965	1.3954
chr2	243199373	19592664	0.0806	0.9416
chr3	198022430	16107740	0.0813	0.3657
chr4	191154276	16289478	0.0852	0.4229
chr5	180915260	12741481	0.0704	0.3649
chr6	171115067	12307672	0.0719	0.4283
chr7	159138663	10789437	0.0678	0.6532

chr8	146364022	14250895	0.0974	0.5197
chr9	141213431	8438780	0.0598	0.8614
chr10	135534747	10484095	0.0774	0.8536
chr11	135006516	8650662	0.0641	0.5054
chr12	133851895	9297829	0.0695	0.3553
chr13	115169878	4639203	0.0403	0.248
chr14	107349540	5569496	0.0519	0.3765
chr15	102531392	5788318	0.0565	0.3026
chr16	90354753	5460203	0.0604	0.5318
chr17	81195210	3787064	0.0466	0.3888
chr18	78077248	5746003	0.0736	1.1495
chr19	59128983	2244792	0.038	1.2377
chr20	63025520	3824721	0.0607	0.3272
chr21	48129895	2622885	0.0545	0.3615
chr22	51304566	1602079	0.0312	0.2368
chrMT	16571	370376	22.3509	17.2346
chrX	155270560	13496550	0.0869	0.5924
chrY	59373566	536828	0.009	0.4711

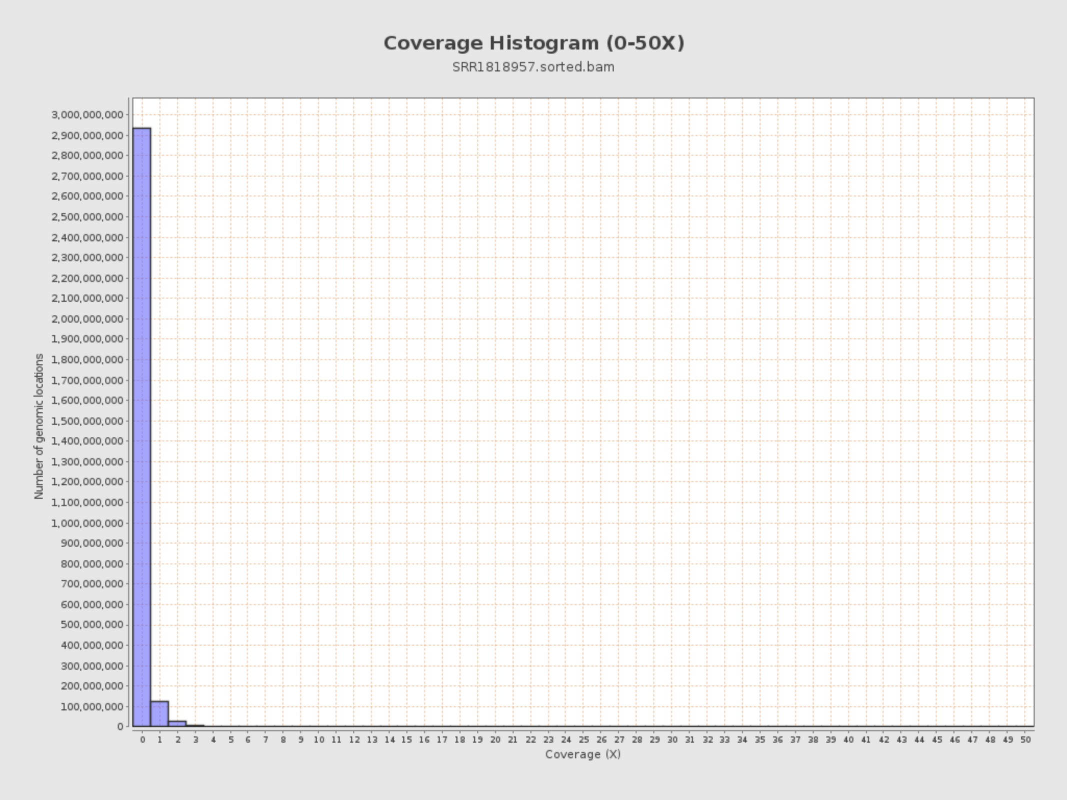
3. Results : Coverage across reference



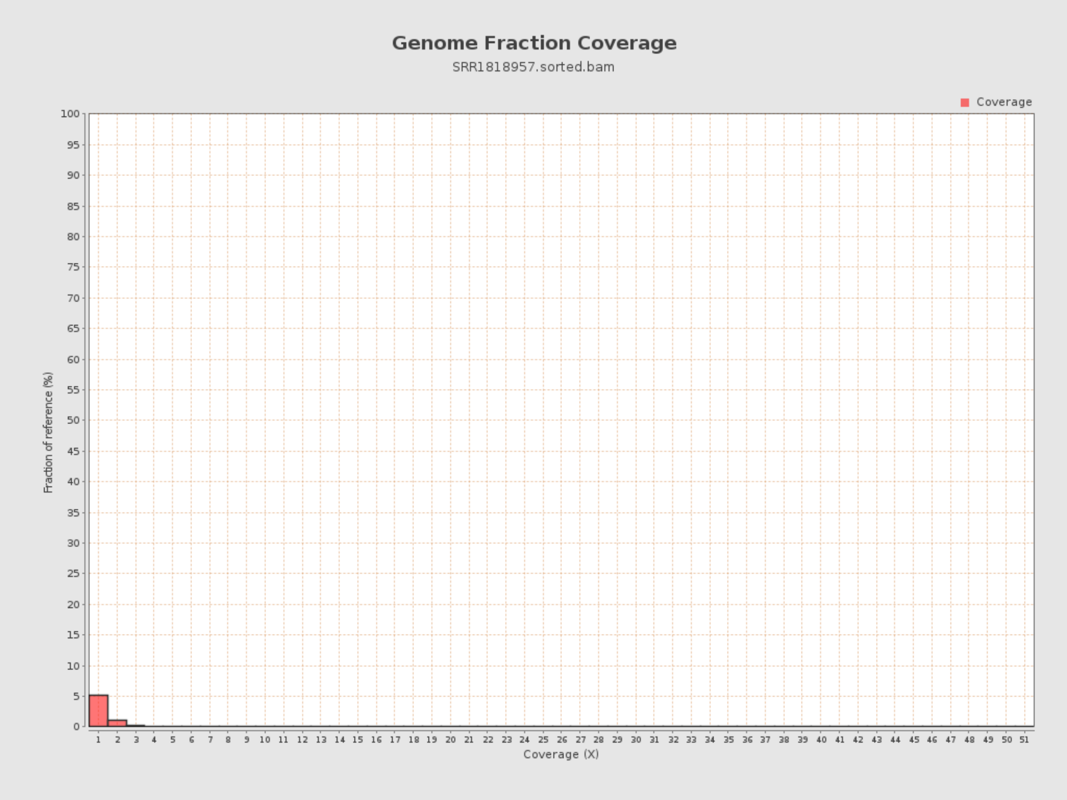
4. Results : Coverage Histogram



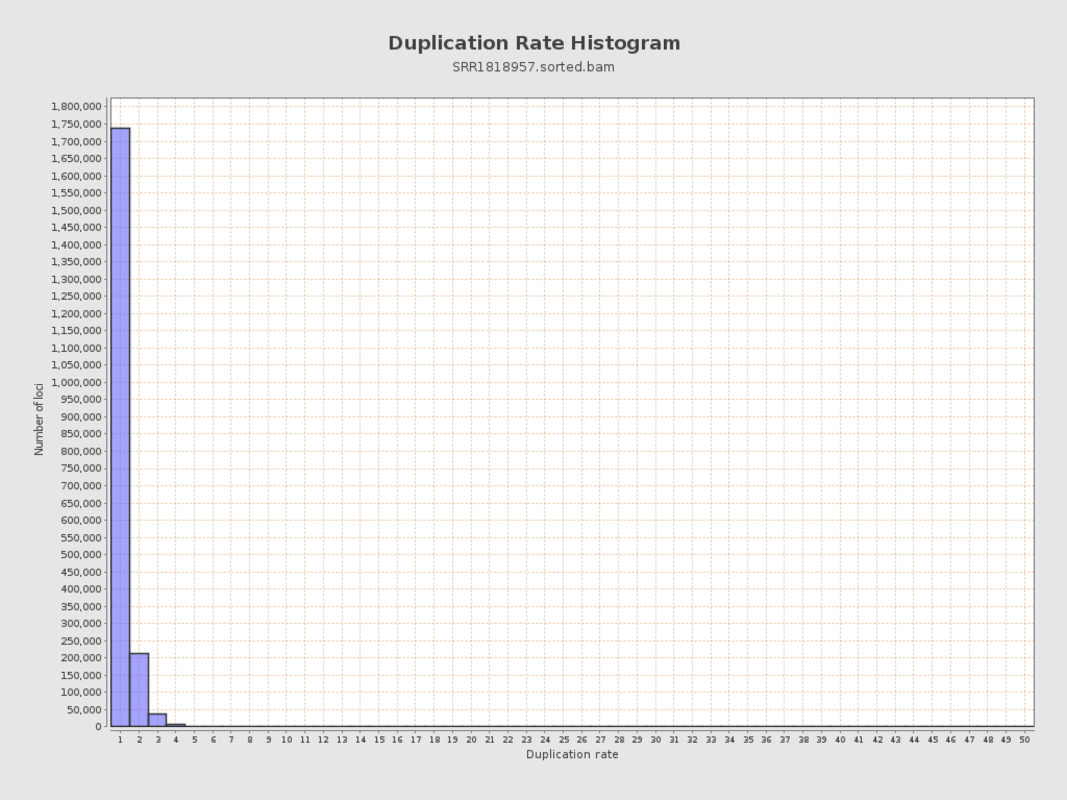
5. Results : Coverage Histogram (0-50X)



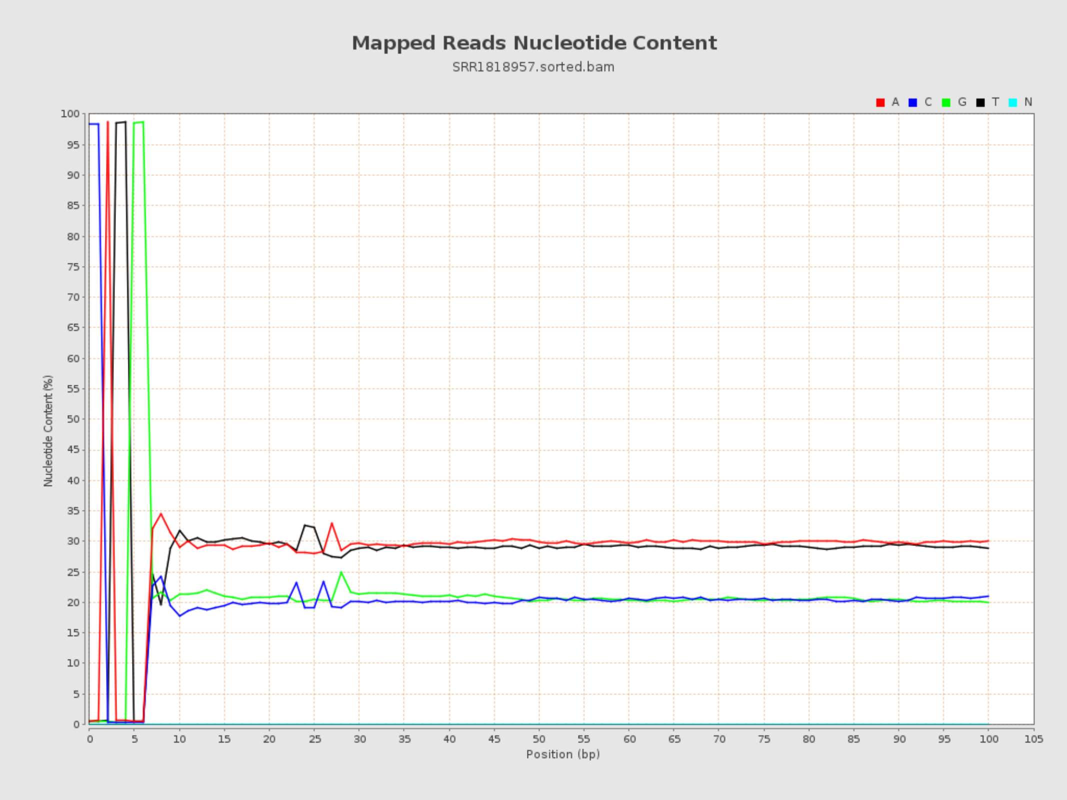
6. Results : Genome Fraction Coverage



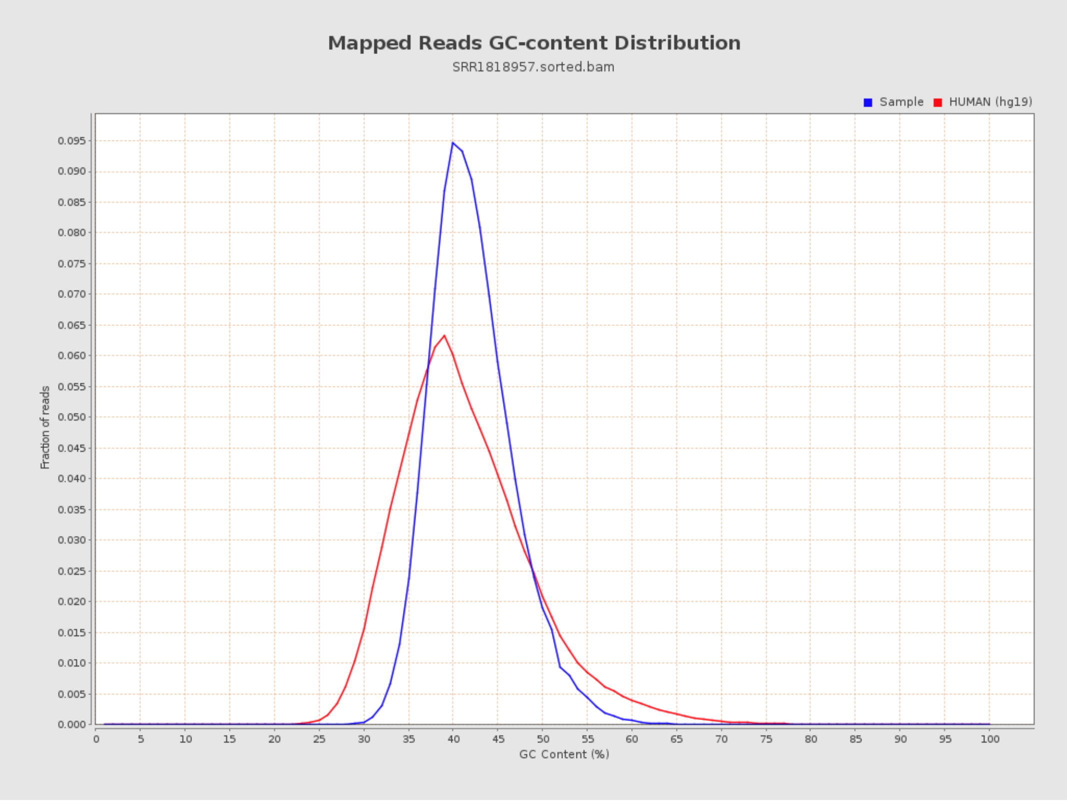
7. Results : Duplication Rate Histogram



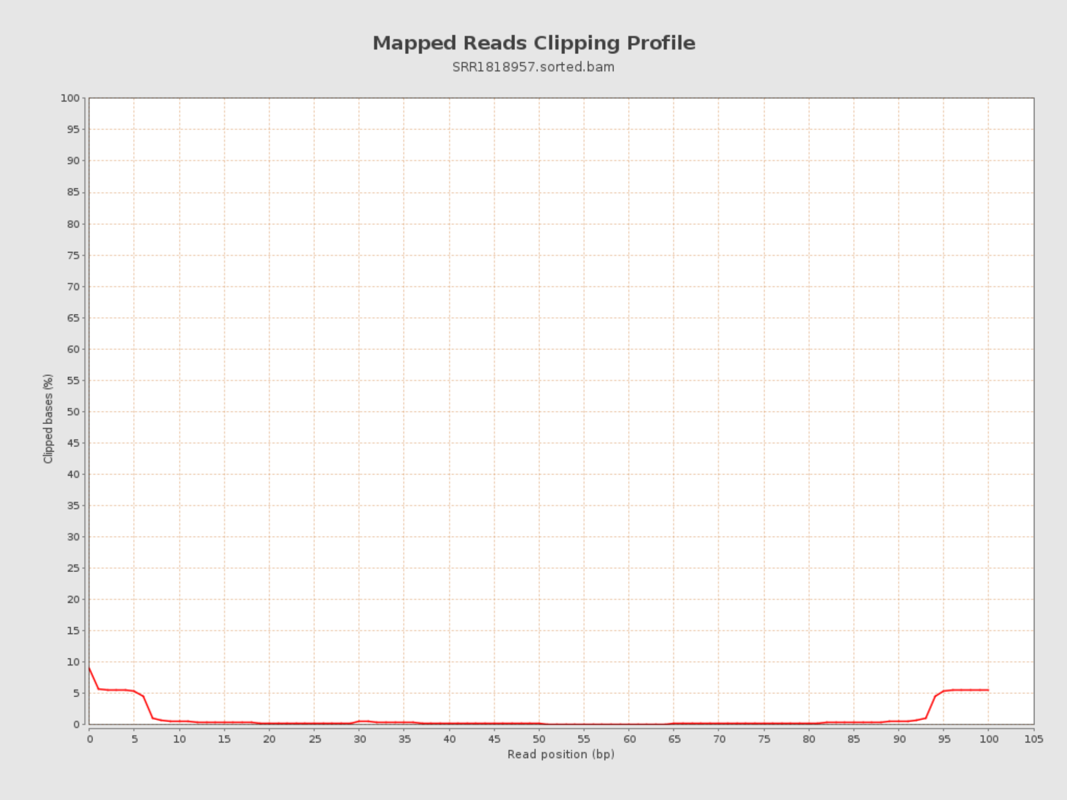
8. Results : Mapped Reads Nucleotide Content



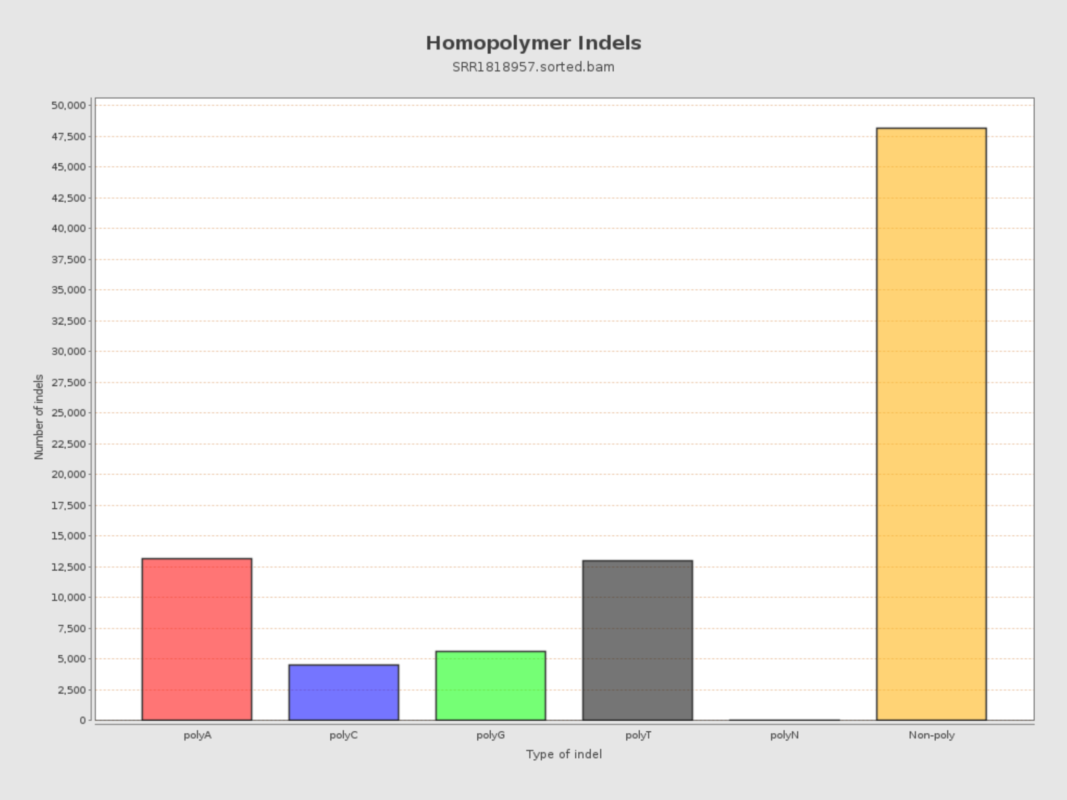
9. Results : Mapped Reads GC-content Distribution



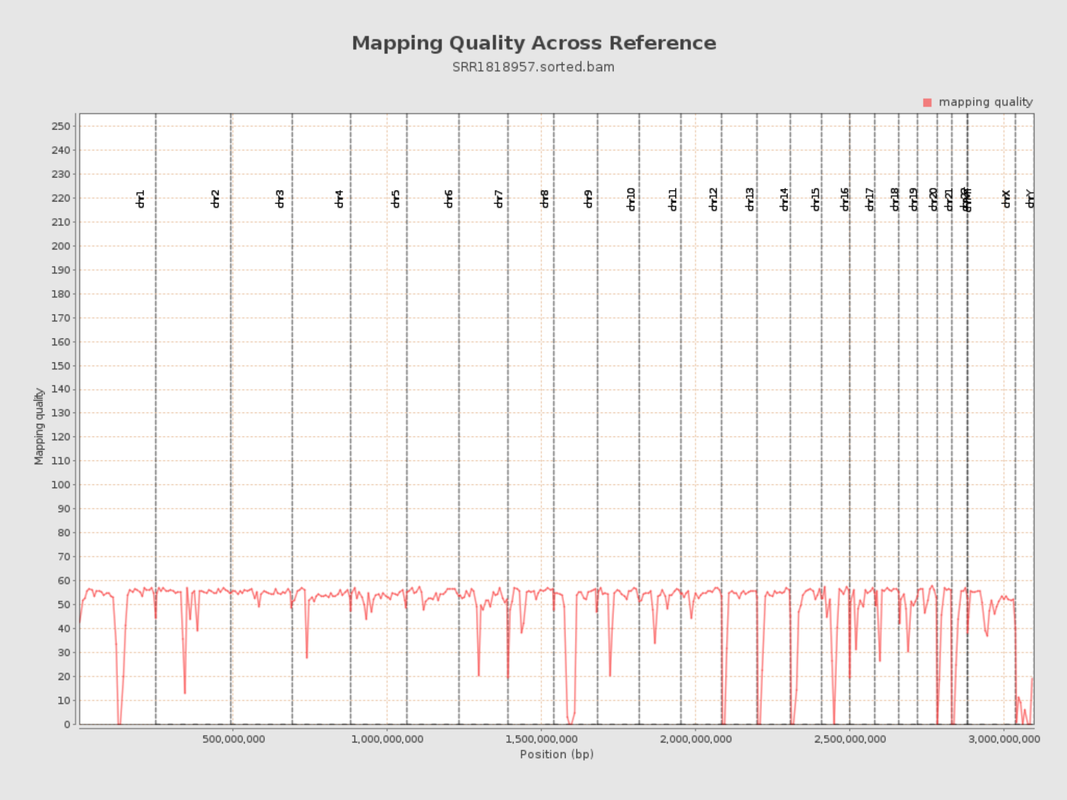
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram