Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 15:16:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867857.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_SRR9867857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 15:16:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,118,527
Mapped reads	2,871,312 / 92.07%
Unmapped reads	247,215 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,716 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	193,084 / 6.19%
Duplication rate	5.02%
Clipped reads	2,873,990 / 92.16%

2.2. ACGT Content

Number/percentage of A's	43,817,774 / 25.87%
Number/percentage of C's	28,902,169 / 17.06%
Number/percentage of T's	54,264,498 / 32.04%
Number/percentage of G's	42,370,057 / 25.01%
Number/percentage of N's	24,401 / 0.01%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0547

Standard Deviation	0.4869

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

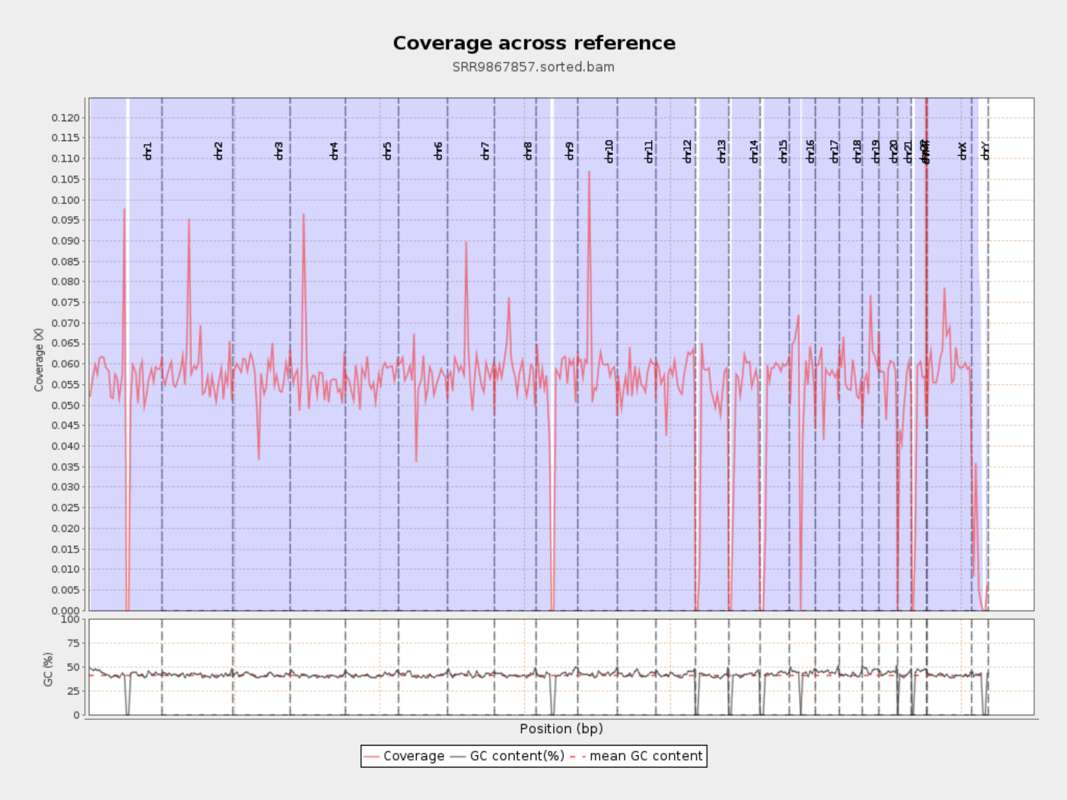
General error rate	0.52%
Mismatches	852,560
Insertions	12,803
Mapped reads with at least one insertion	0.44%
Deletions	32,673
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.71%

2.6. Chromosome stats

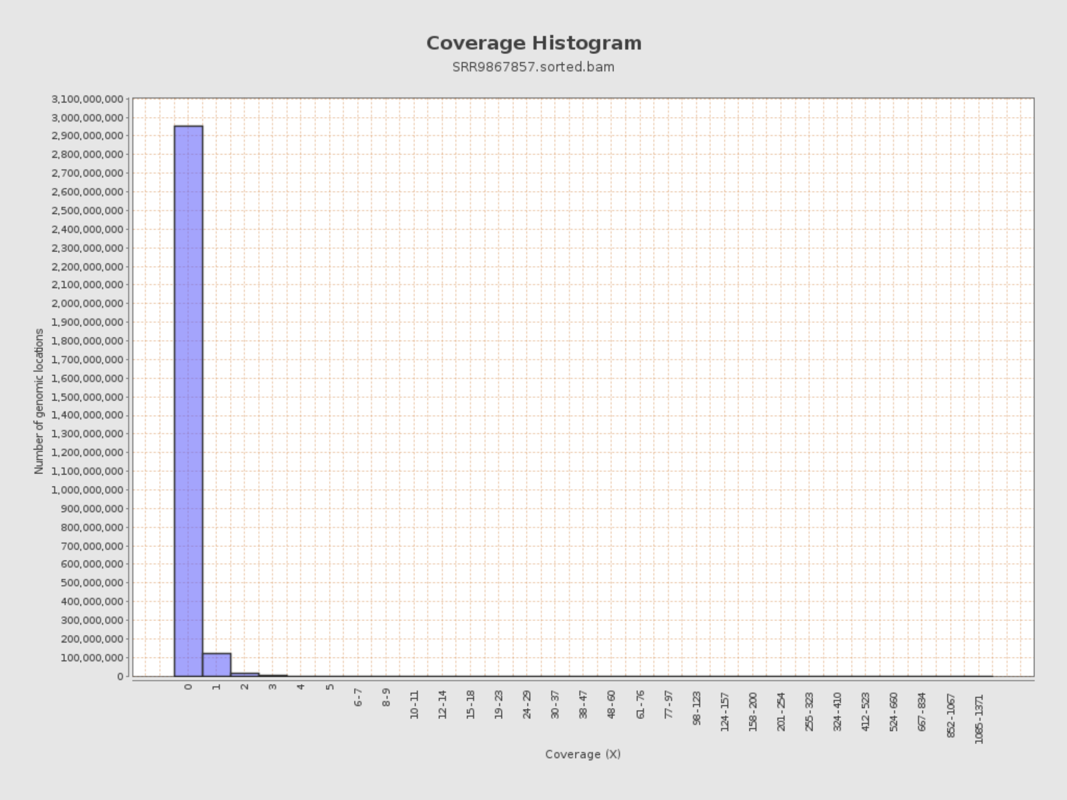
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13576226	0.0545	0.9309
chr2	243199373	14225230	0.0585	0.6807
chr3	198022430	11299086	0.0571	0.2774
chr4	191154276	10924236	0.0571	0.3421
chr5	180915260	10232594	0.0566	0.2816
chr6	171115067	9684288	0.0566	0.3335
chr7	159138663	9411922	0.0591	0.5783

chr8	146364022	8587918	0.0587	0.5518
chr9	141213431	7164500	0.0507	0.3991
chr10	135534747	8281270	0.0611	0.4908
chr11	135006516	7591936	0.0562	0.4087
chr12	133851895	7678070	0.0574	0.283
chr13	115169878	5343910	0.0464	0.2521
chr14	107349540	5081759	0.0473	0.2693
chr15	102531392	4889295	0.0477	0.2584
chr16	90354753	4963453	0.0549	0.3069
chr17	81195210	4624622	0.057	0.3108
chr18	78077248	4450503	0.057	0.7561
chr19	59128983	3579084	0.0605	0.6851
chr20	63025520	3577121	0.0568	0.2872
chr21	48129895	2219859	0.0461	0.3176
chr22	51304566	2043996	0.0398	0.2322
chrMT	16571	51660	3.1175	2.577
chrX	155270560	9390872	0.0605	0.3316
chrY	59373566	557216	0.0094	0.342

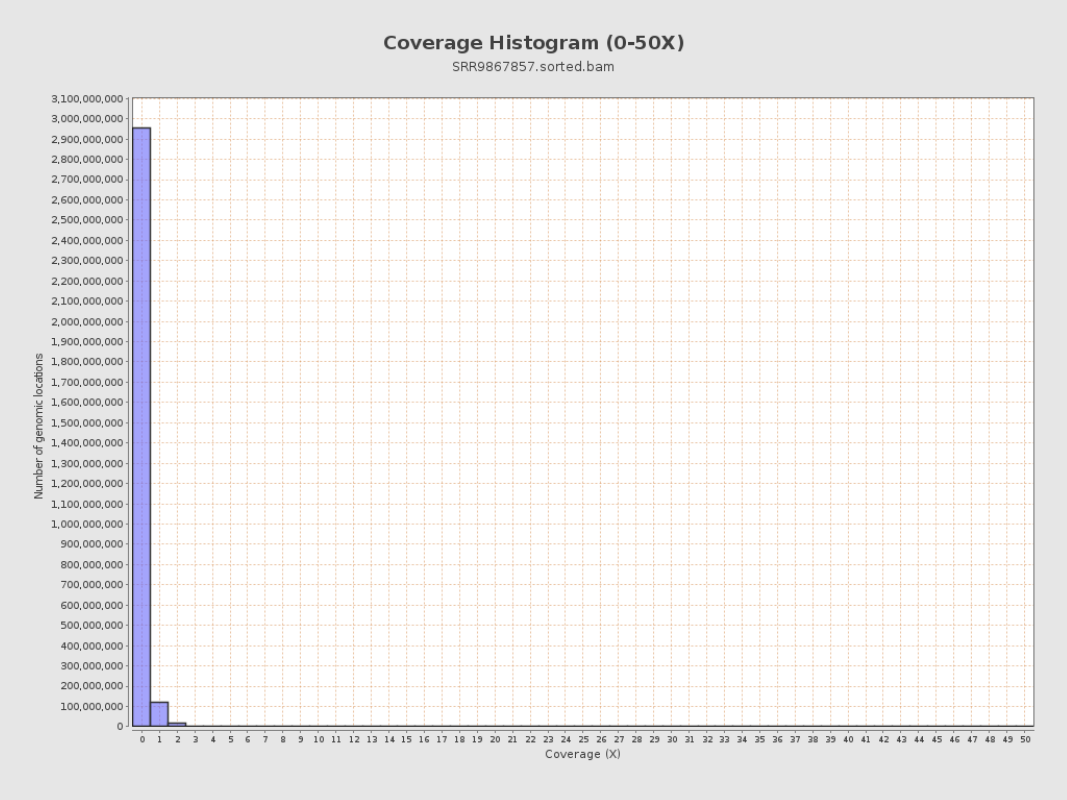
3. Results : Coverage across reference



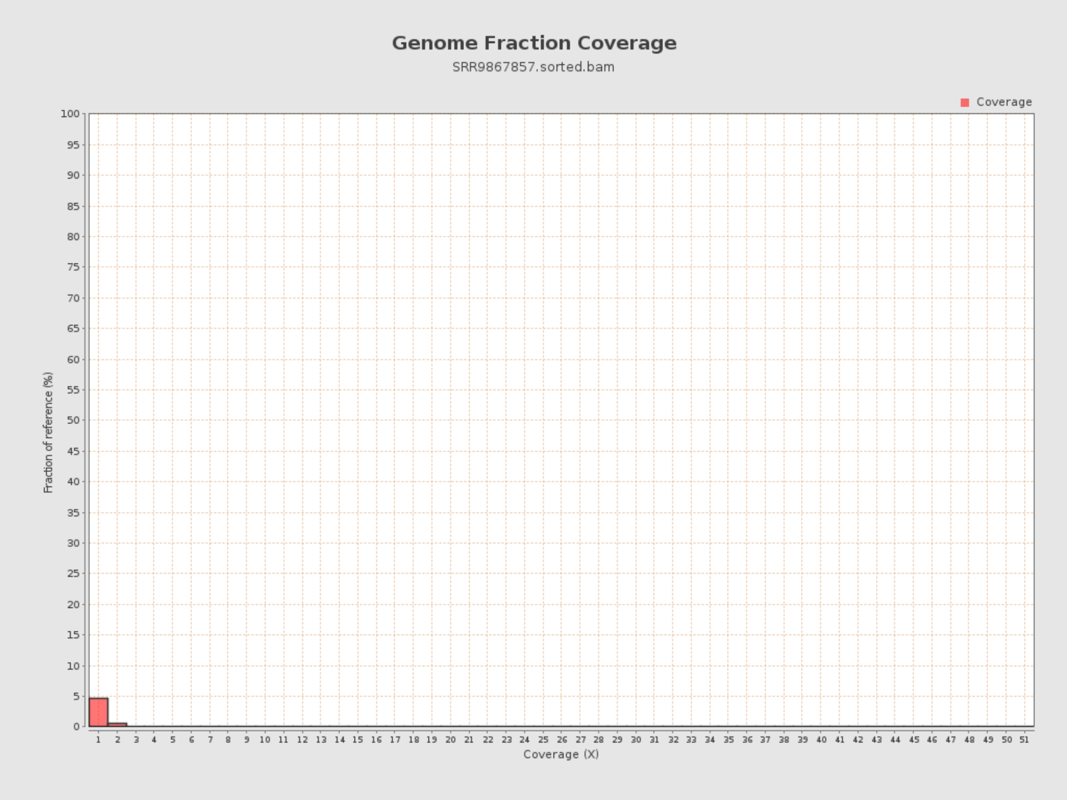
4. Results : Coverage Histogram



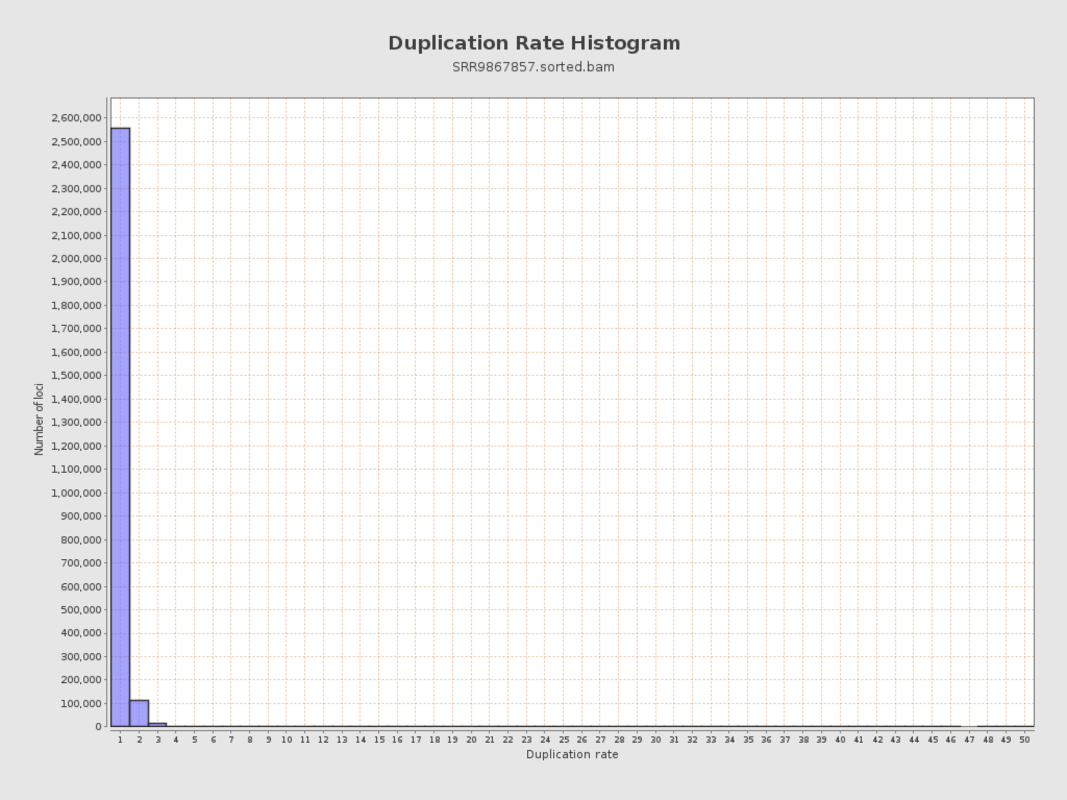
5. Results : Coverage Histogram (0-50X)



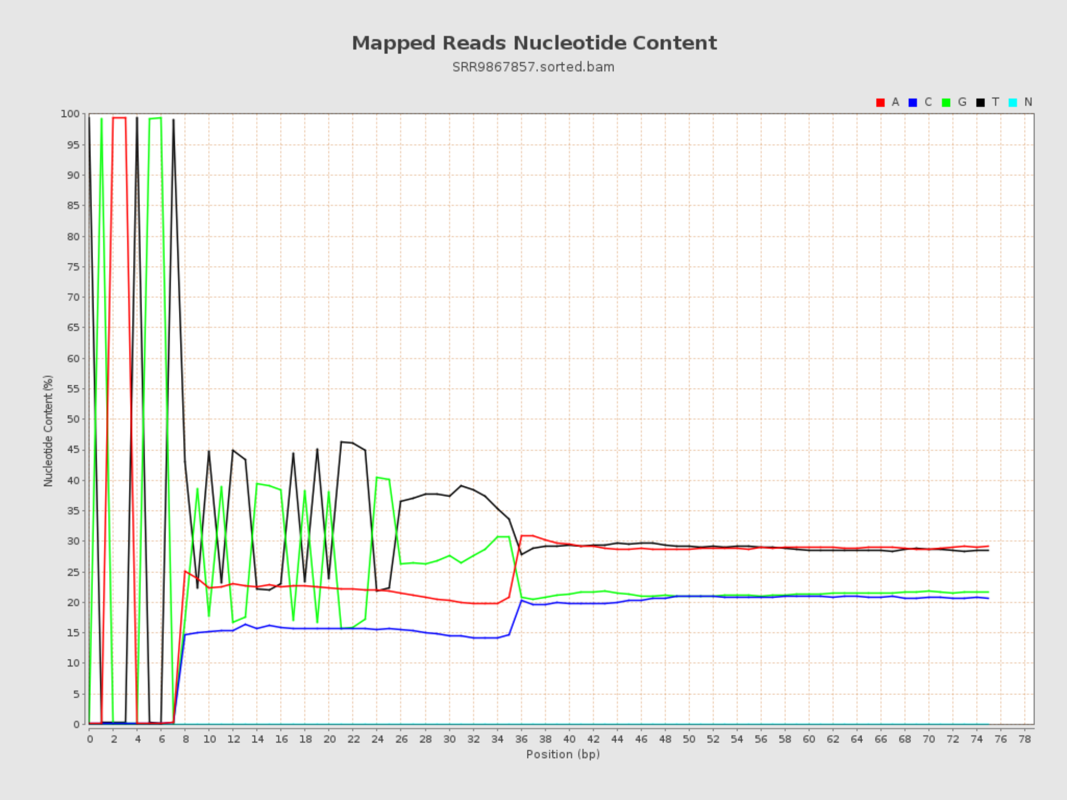
6. Results : Genome Fraction Coverage



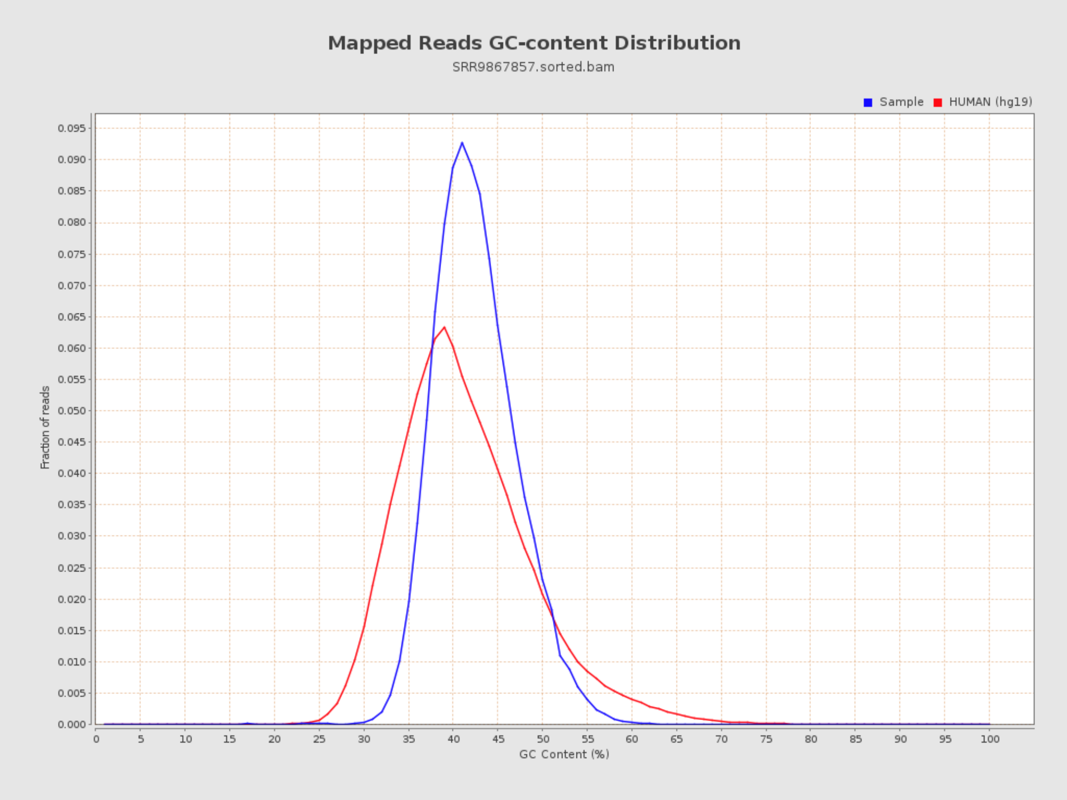
7. Results : Duplication Rate Histogram



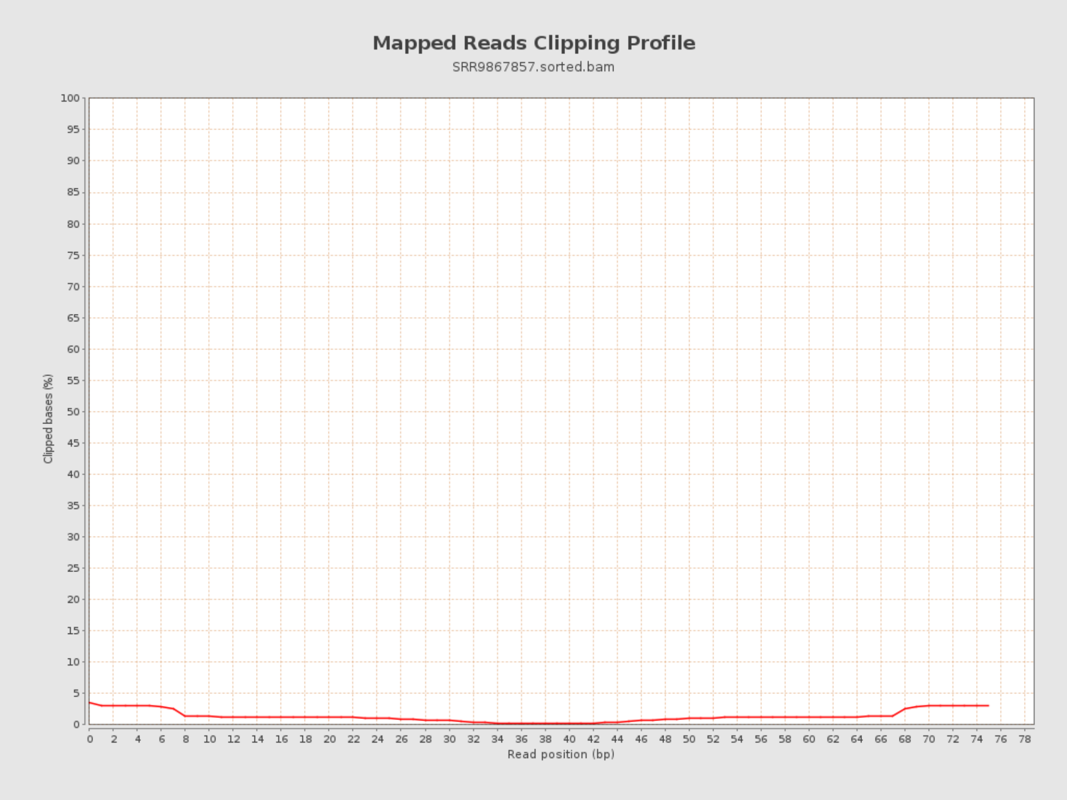
8. Results : Mapped Reads Nucleotide Content



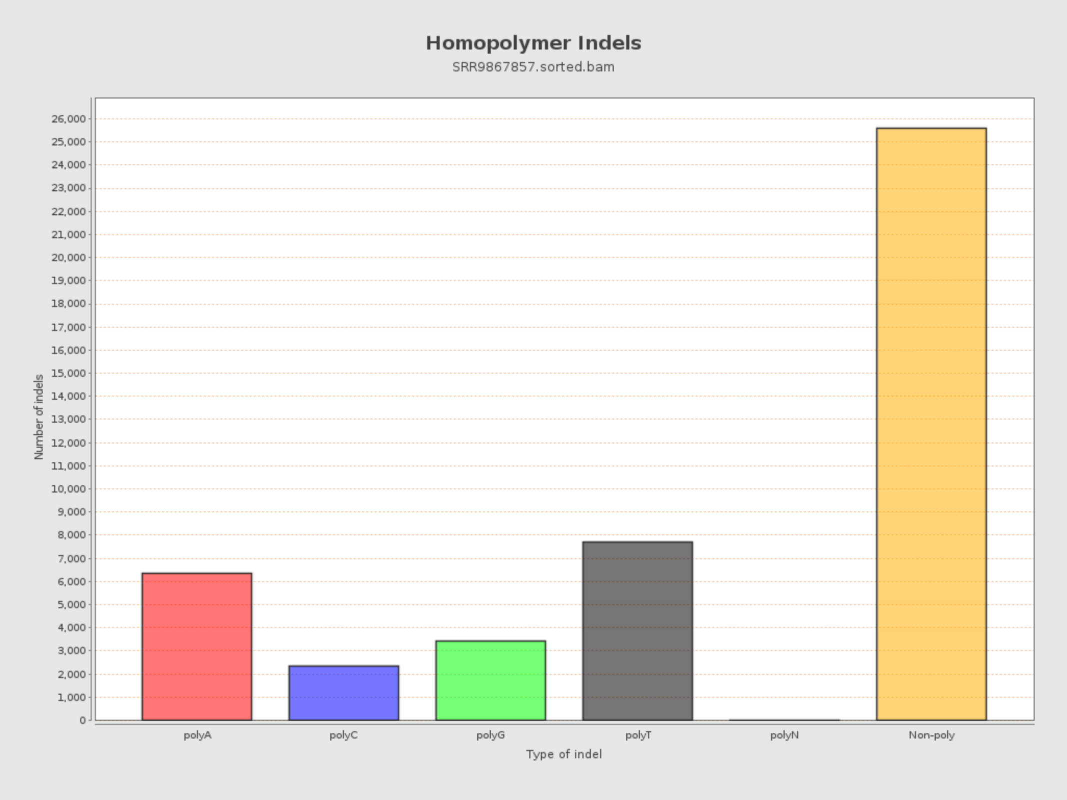
9. Results : Mapped Reads GC-content Distribution



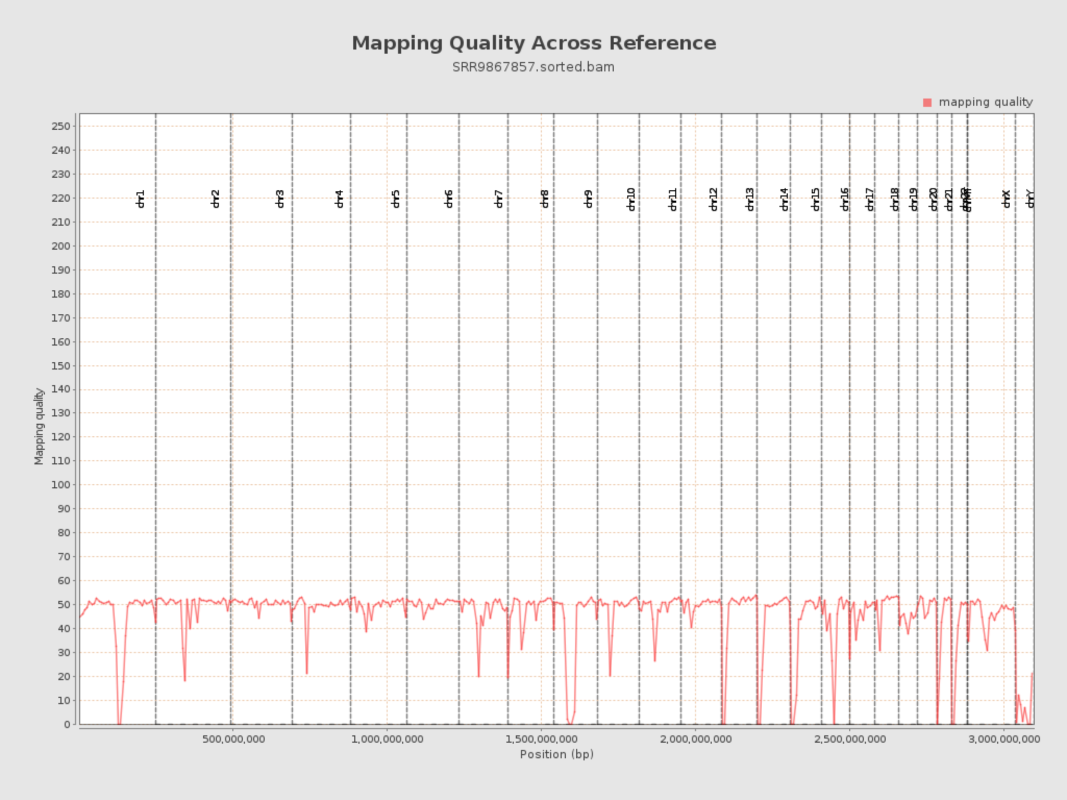
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram