

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 16:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163154.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_SRR1163154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 16:09:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	90,915,068
Mapped reads	88,404,508 / 97.24%
Unmapped reads	2,510,560 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	410,048 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	48,785,664 / 53.66%
Duplication rate	43.37%
Clipped reads	8,790,549 / 9.67%

2.2. ACGT Content

Number/percentage of A's	2,158,246,915 / 24.83%
Number/percentage of C's	2,181,123,600 / 25.09%
Number/percentage of T's	2,164,057,643 / 24.9%
Number/percentage of G's	2,174,575,768 / 25.02%
Number/percentage of N's	14,522,341 / 0.17%
GC Percentage	50.11%

2.3. Coverage

Mean	2.8083

Standard Deviation	34.6438
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2.4. Mapping Quality

Mean Mapping Quality	49.11
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2.5. Mismatches and indels

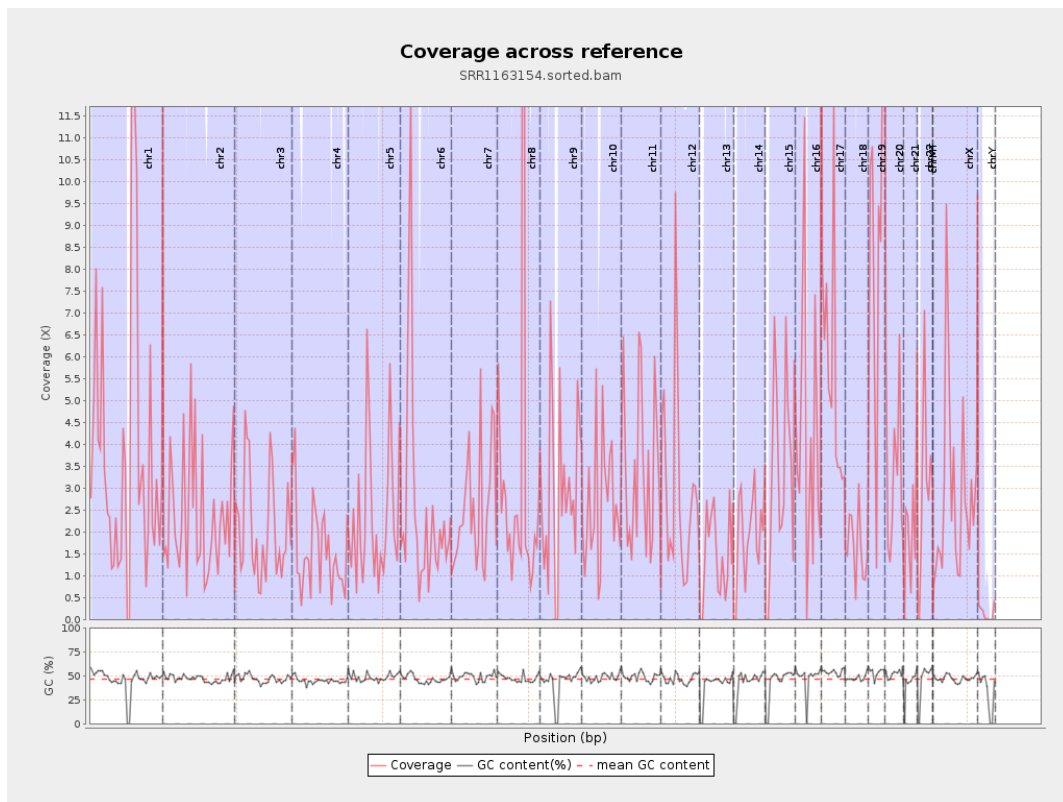
General error rate	0.65%
Mismatches	55,534,514
Insertions	603,147
Mapped reads with at least one insertion	0.67%
Deletions	442,859
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.03%

2.6. Chromosome stats

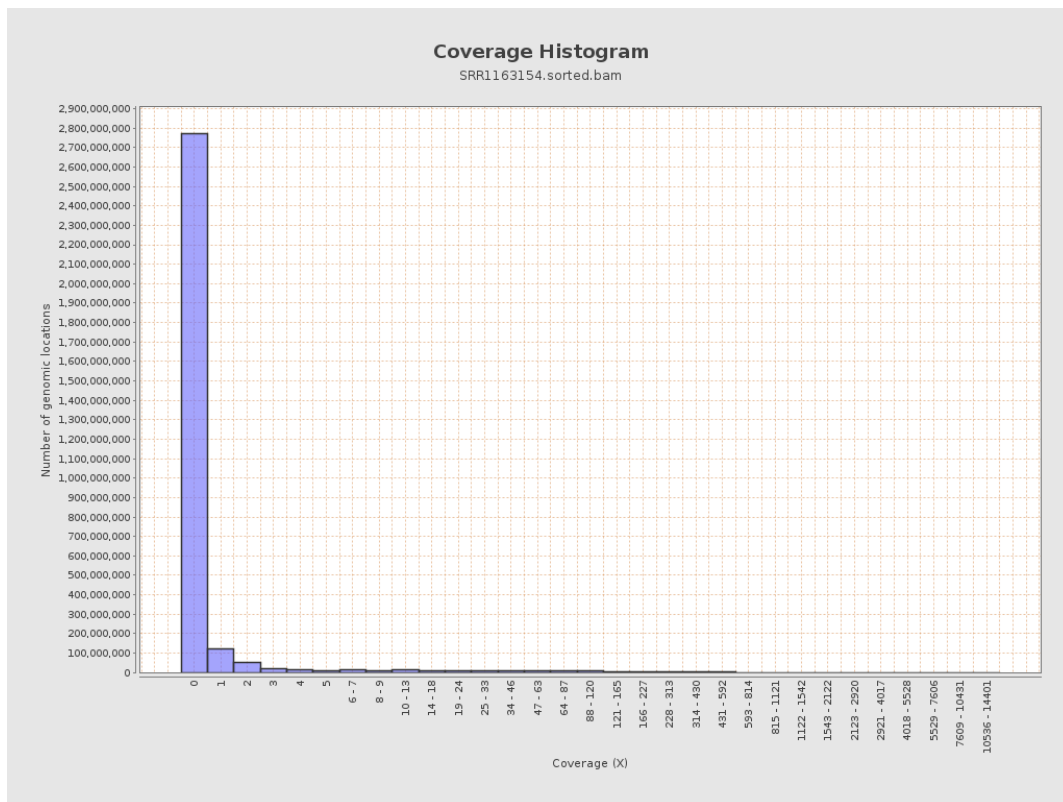
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	939181861	3.768	37.6522
chr2	243199373	571622475	2.3504	26.0061
chr3	198022430	415393306	2.0977	24.0629
chr4	191154276	301406246	1.5768	21.7749
chr5	180915260	432520970	2.3907	33.6524
chr6	171115067	415138683	2.4261	29.2905
chr7	159138663	400861761	2.5189	33.5353

chr8	146364022	484014295	3.3069	73.1455
chr9	141213431	409044364	2.8966	33.5211
chr10	135534747	355343588	2.6218	26.8892
chr11	135006516	464757111	3.4425	30.5301
chr12	133851895	404515062	3.0221	34.0309
chr13	115169878	166710234	1.4475	19.7933
chr14	107349540	199918061	1.8623	20.4018
chr15	102531392	337725211	3.2939	32.5648
chr16	90354753	365675280	4.0471	35.77
chr17	81195210	459556921	5.6599	49.6593
chr18	78077248	128560317	1.6466	19.1199
chr19	59128983	522794773	8.8416	58.7504
chr20	63025520	209240413	3.3199	36.429
chr21	48129895	107456121	2.2326	33.564
chr22	51304566	150696702	2.9373	31.4879
chrMT	16571	914	0.0552	0.2781
chrX	155270560	442559881	2.8502	35.5488
chrY	59373566	8840387	0.1489	8.607

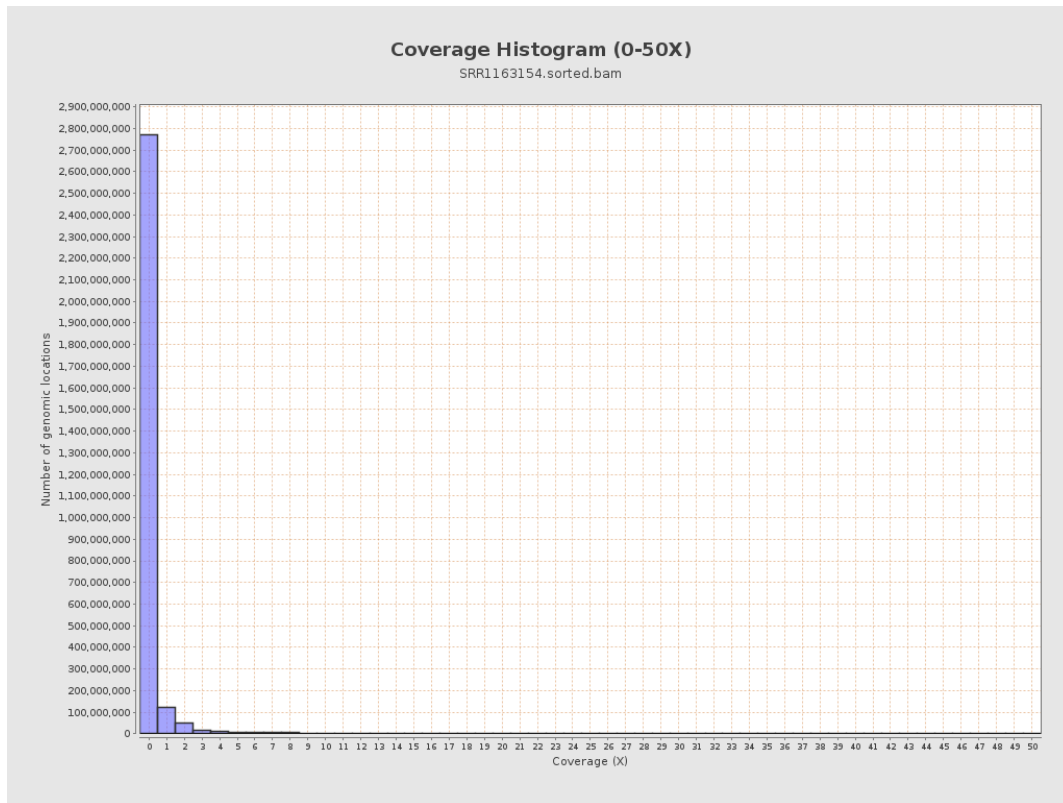
3. Results : Coverage across reference



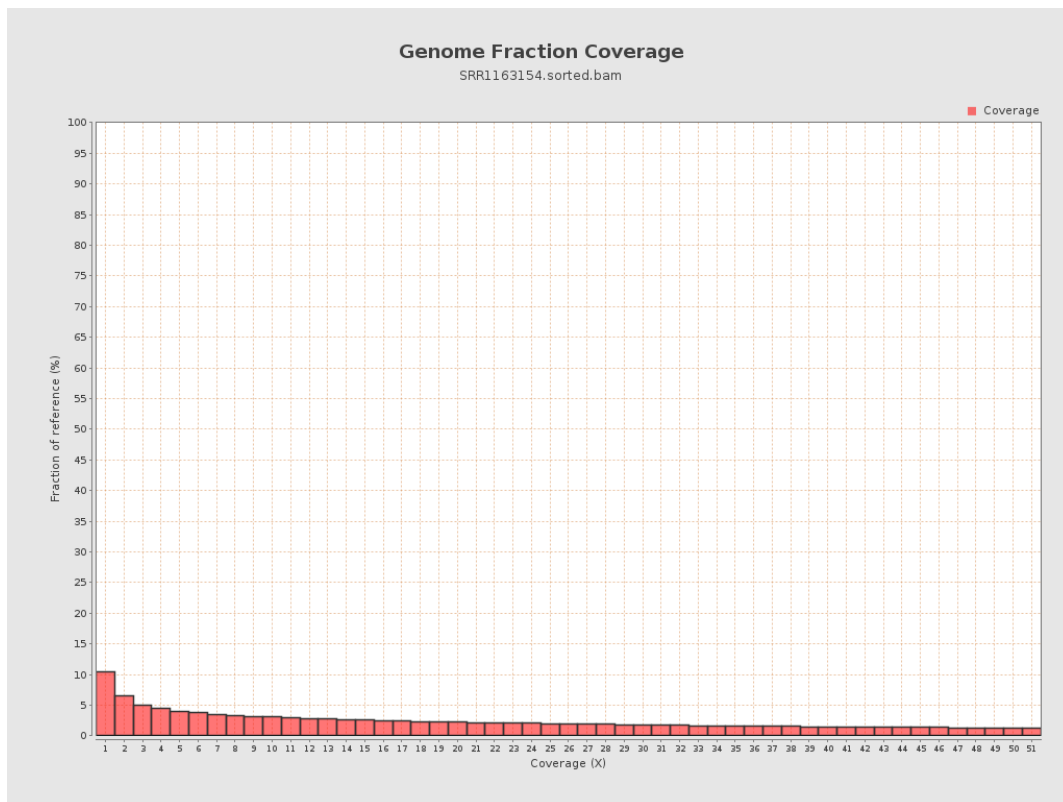
4. Results : Coverage Histogram



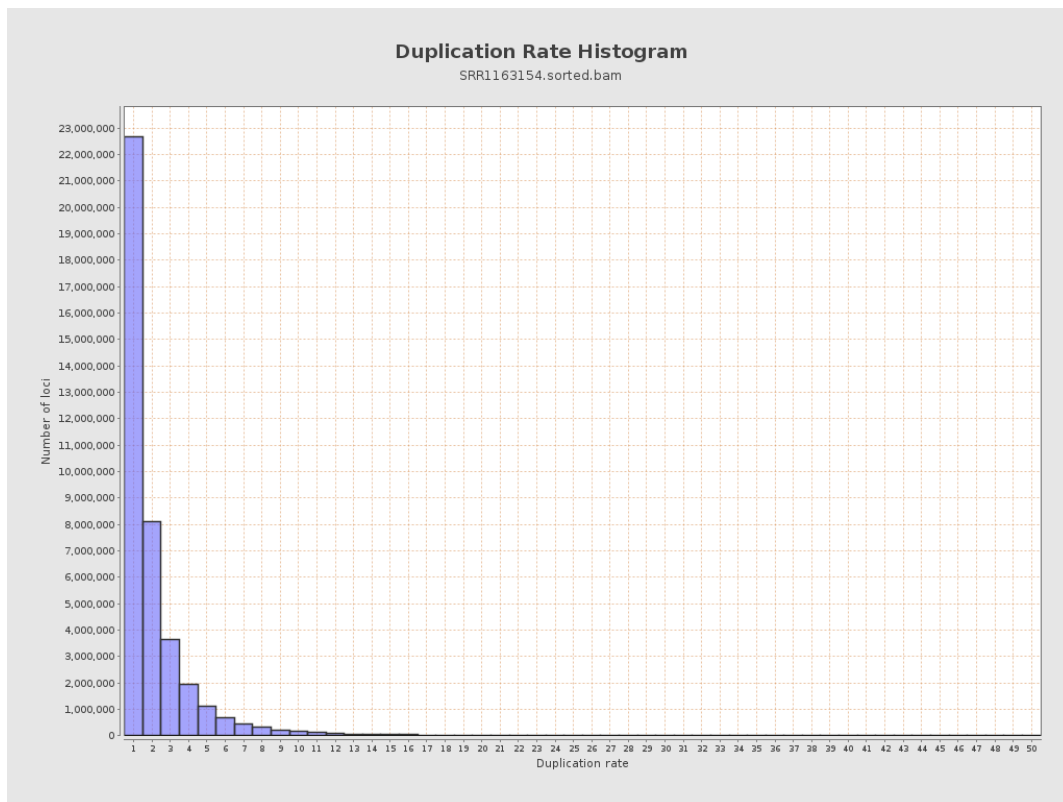
5. Results : Coverage Histogram (0-50X)



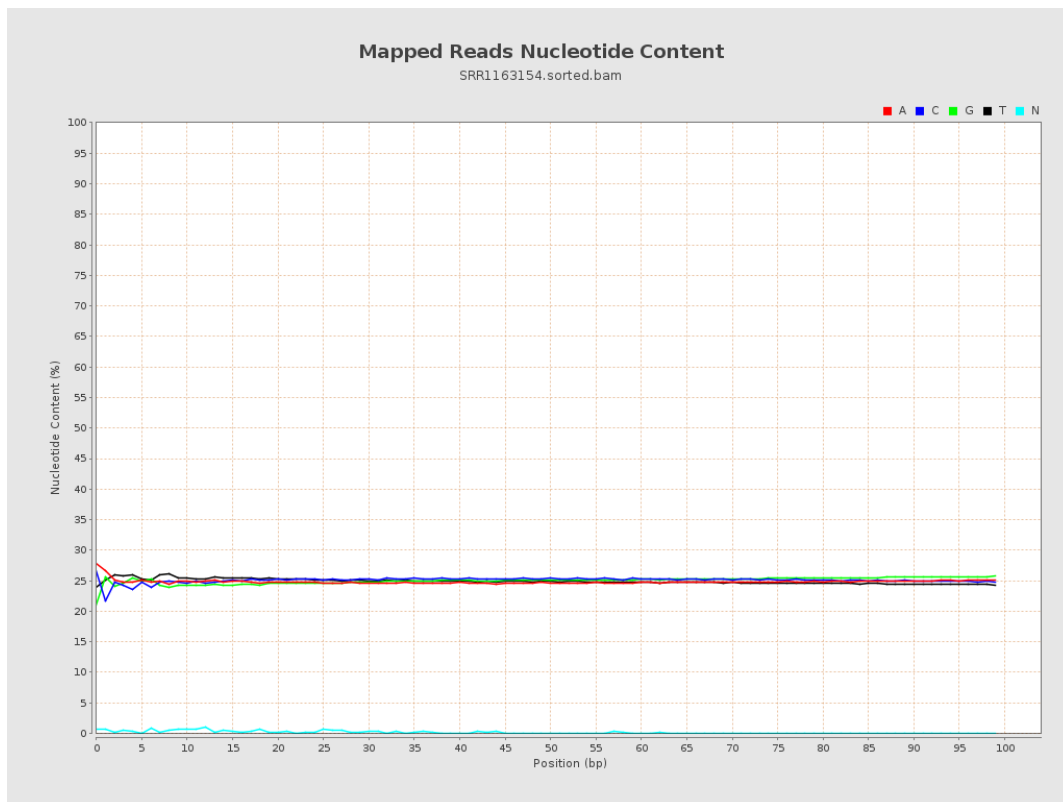
6. Results : Genome Fraction Coverage



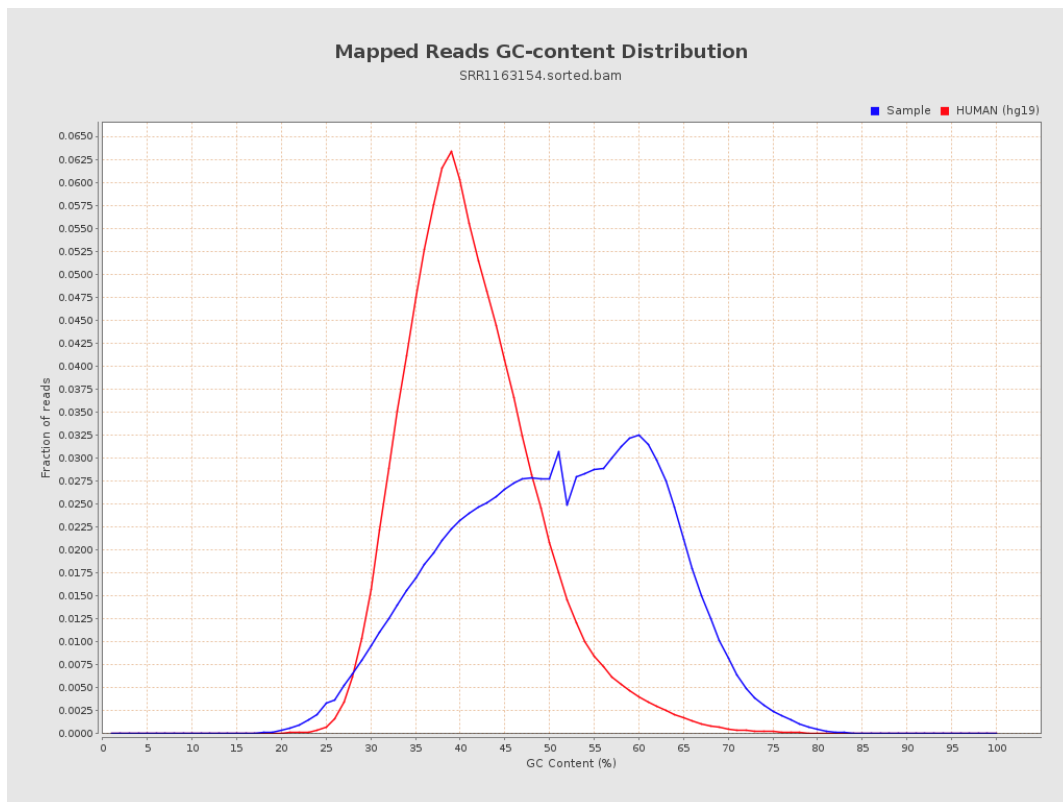
7. Results : Duplication Rate Histogram



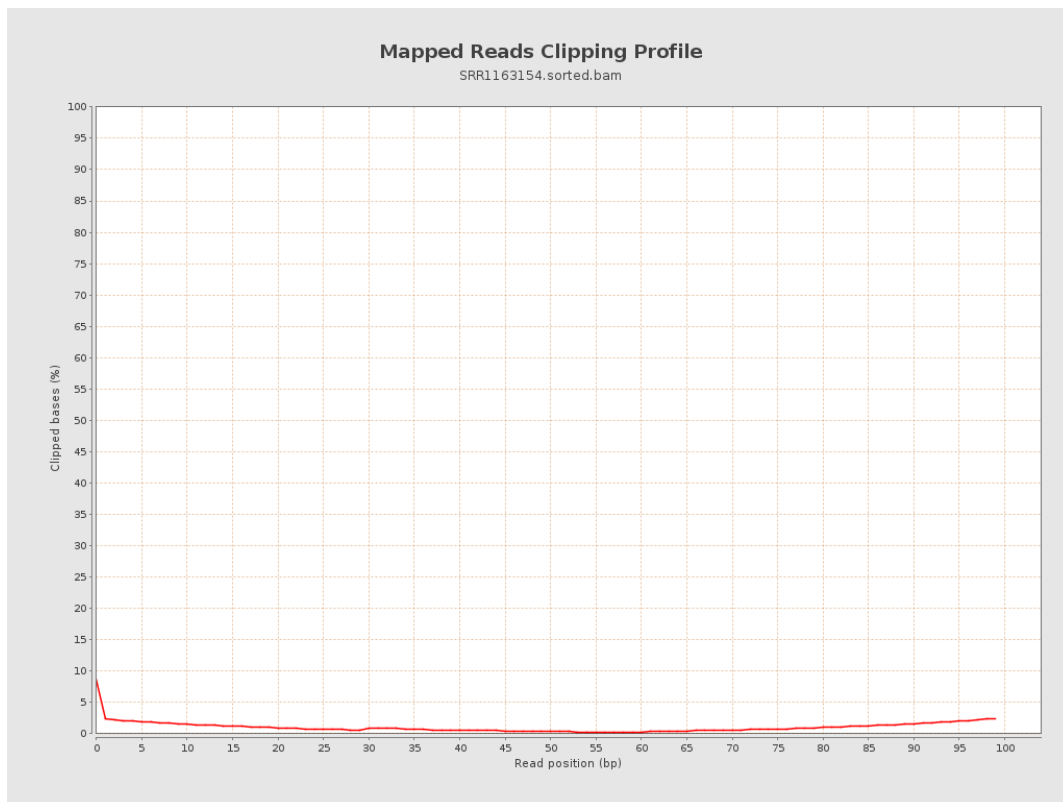
8. Results : Mapped Reads Nucleotide Content



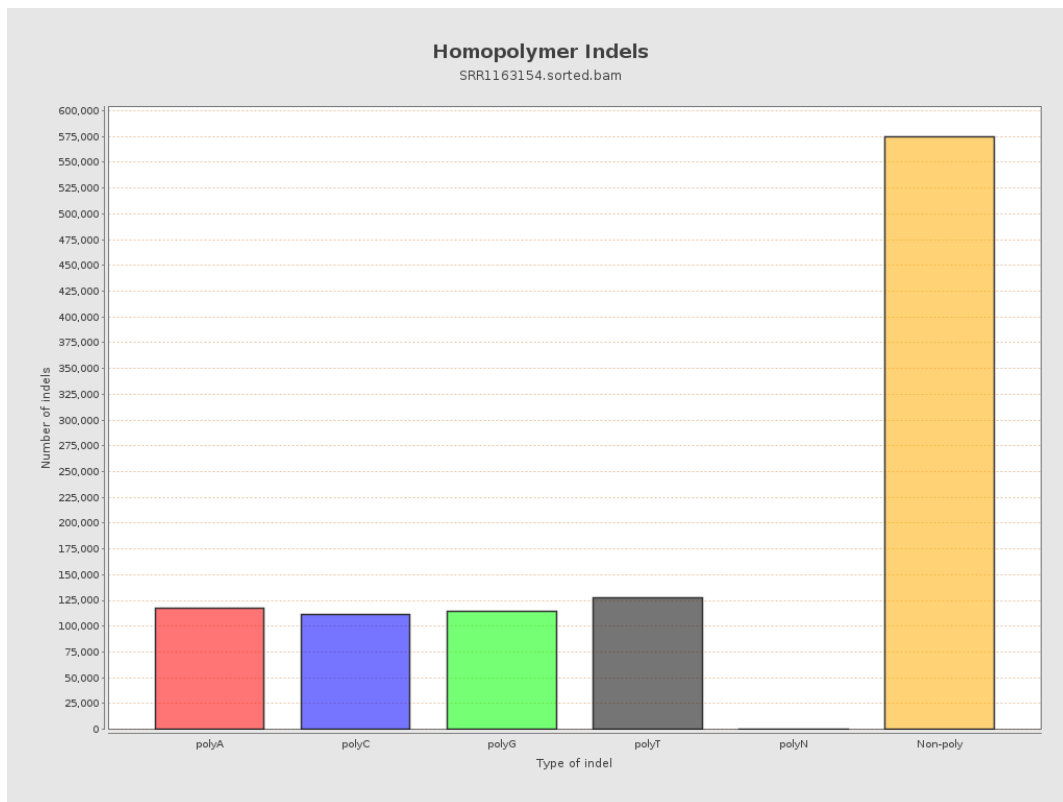
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

