

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 13:55:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354853.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_SRR22354853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354853_1.fastq.gz SRR22354853_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 13:55:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,132,406
Mapped reads	21,165,408 / 95.63%
Unmapped reads	966,998 / 4.37%
Mapped paired reads	21,165,408 / 95.63%
Mapped reads, first in pair	10,638,107 / 48.07%
Mapped reads, second in pair	10,527,301 / 47.57%
Mapped reads, both in pair	21,018,094 / 94.97%
Mapped reads, singletons	147,314 / 0.67%
Secondary alignments	0
Supplementary alignments	189,523 / 0.86%
Read min/max/mean length	30 / 150 / 150.39
Duplicated reads (estimated)	12,975,877 / 58.63%
Duplication rate	60.79%
Clipped reads	3,035,978 / 13.72%

2.2. ACGT Content

Number/percentage of A's	892,893,749 / 29.2%
Number/percentage of C's	628,726,341 / 20.56%
Number/percentage of T's	896,147,436 / 29.31%
Number/percentage of G's	640,177,333 / 20.93%
Number/percentage of N's	21,339 / 0%

GC Percentage	41.5%
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2.3. Coverage

Mean	0.9882
Standard Deviation	14.4923

2.4. Mapping Quality

Mean Mapping Quality	54.32
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2.5. Insert size

Mean	68,360.86
Standard Deviation	2,848,983.12
P25/Median/P75	272 / 404 / 559

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	29,864,257
Insertions	435,917
Mapped reads with at least one insertion	1.94%
Deletions	472,294
Mapped reads with at least one deletion	2.14%
Homopolymer indels	43.23%

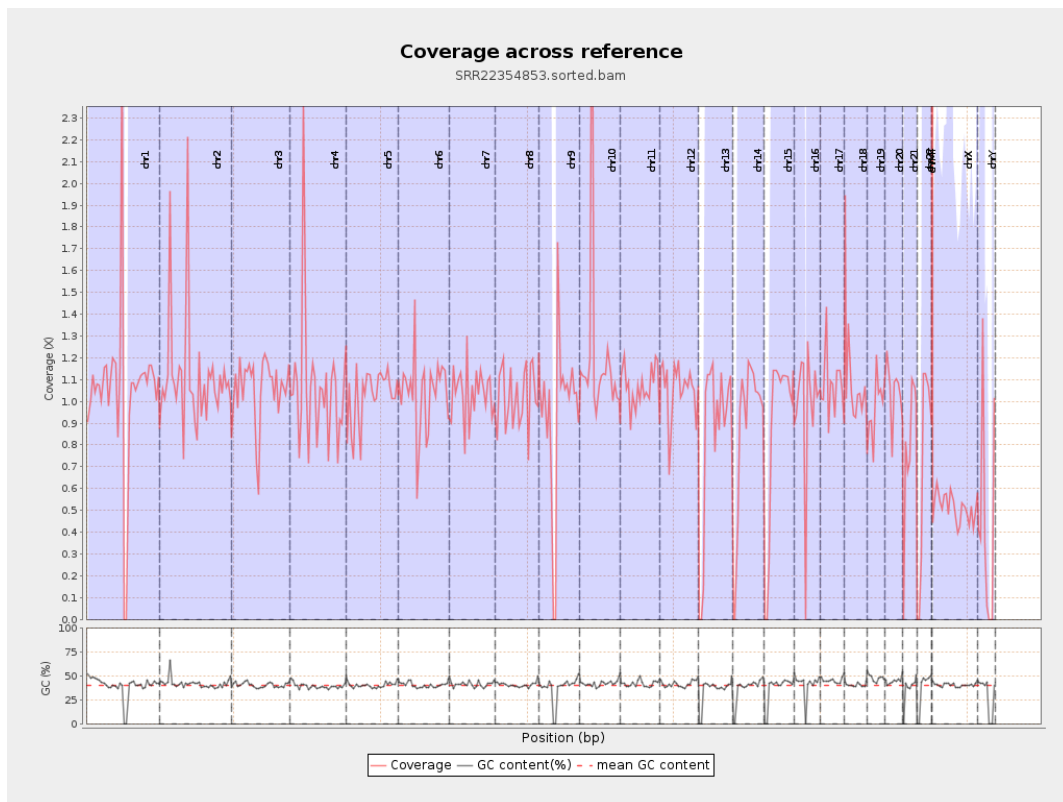
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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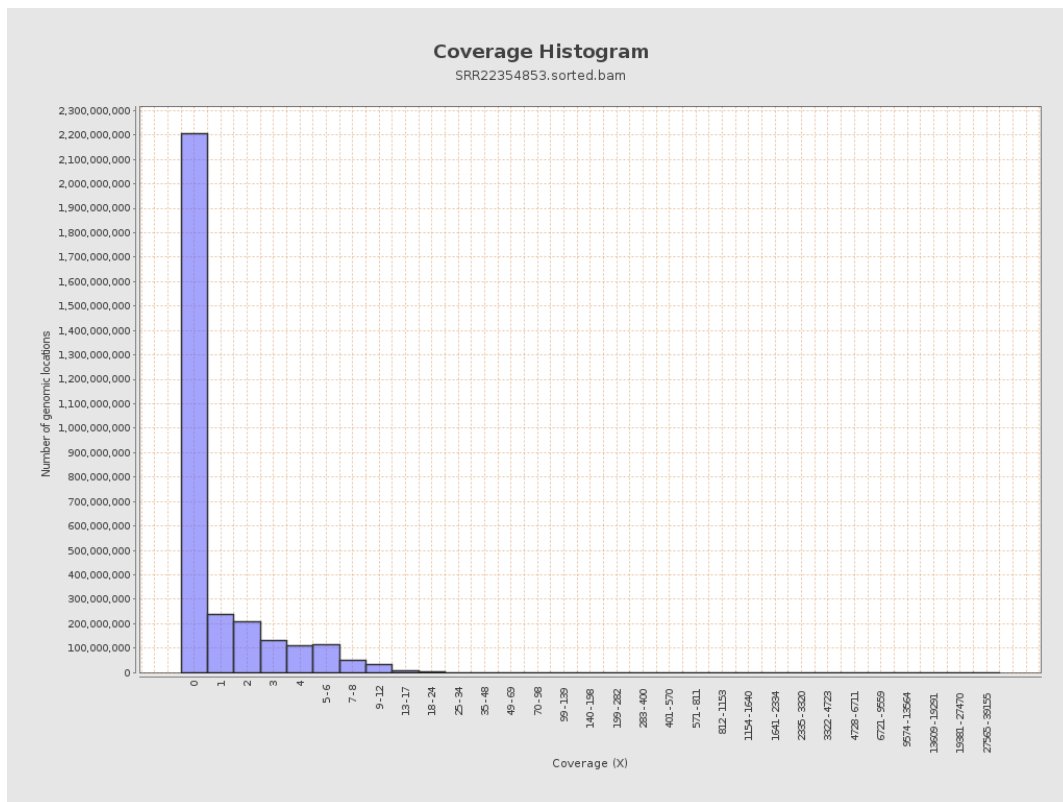
		bases	coverage	deviation
chr1	249250621	263960701	1.059	32.7533
chr2	243199373	272232659	1.1194	26.553
chr3	198022430	209818942	1.0596	2.1637
chr4	191154276	201616688	1.0547	11.5253
chr5	180915260	185230710	1.0239	2.1313
chr6	171115067	178189376	1.0413	4.5395
chr7	159138663	164518331	1.0338	10.7011
chr8	146364022	149741942	1.0231	5.3191
chr9	141213431	131945132	0.9344	19.6804
chr10	135534747	165404408	1.2204	17.5673
chr11	135006516	144238404	1.0684	5.7352
chr12	133851895	140990989	1.0533	2.1392
chr13	115169878	97820252	0.8494	1.9176
chr14	107349540	93149095	0.8677	2.1502
chr15	102531392	88644287	0.8646	1.9432
chr16	90354753	88330402	0.9776	4.1453
chr17	81195210	86472770	1.065	5.3529
chr18	78077248	84117375	1.0774	14.2951
chr19	59128983	57390608	0.9706	17.9976
chr20	63025520	66343670	1.0526	4.1931
chr21	48129895	38804681	0.8062	5.983
chr22	51304566	37127627	0.7237	2.7808
chrMT	16571	7768852	468.8222	94.4231
chrX	155270560	78777456	0.5074	1.9408

chrY	59373566	26636521	0.4486	12.1397
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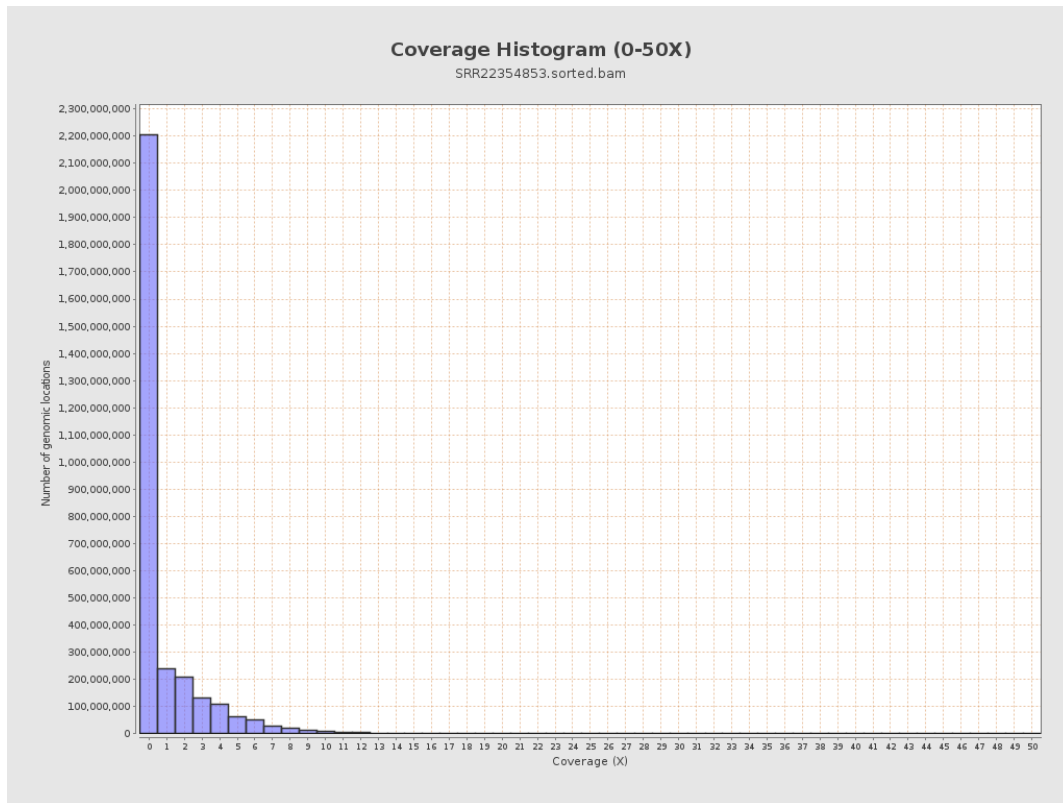
3. Results : Coverage across reference



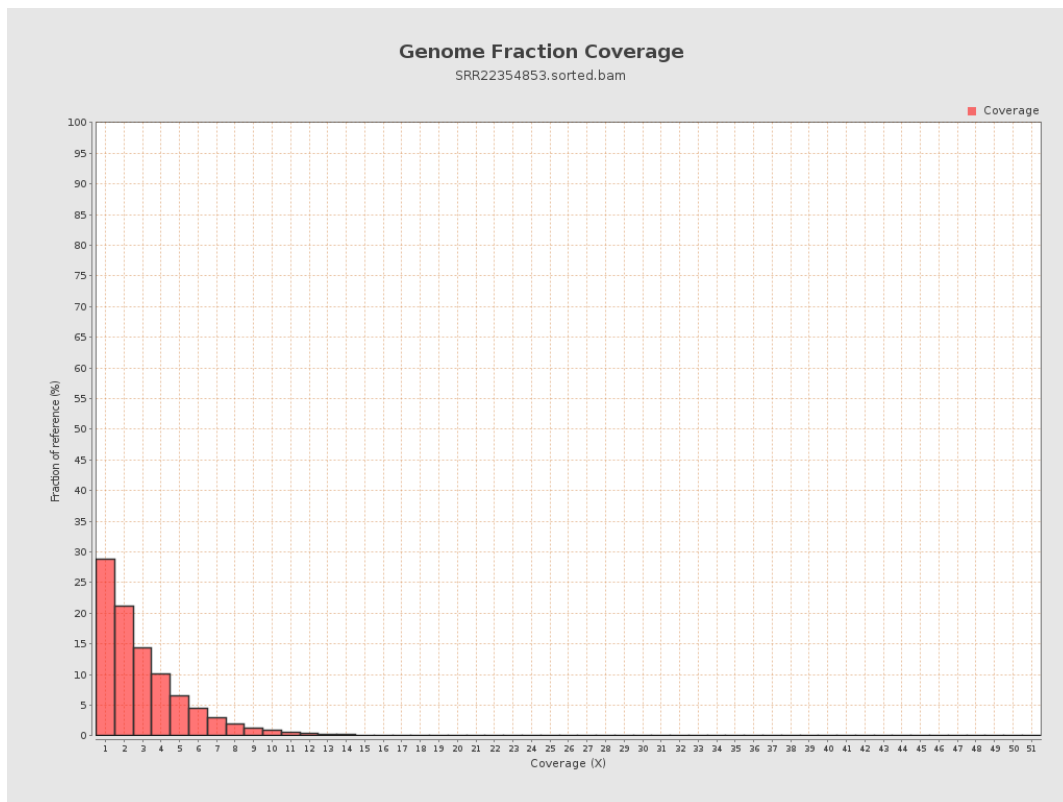
4. Results : Coverage Histogram



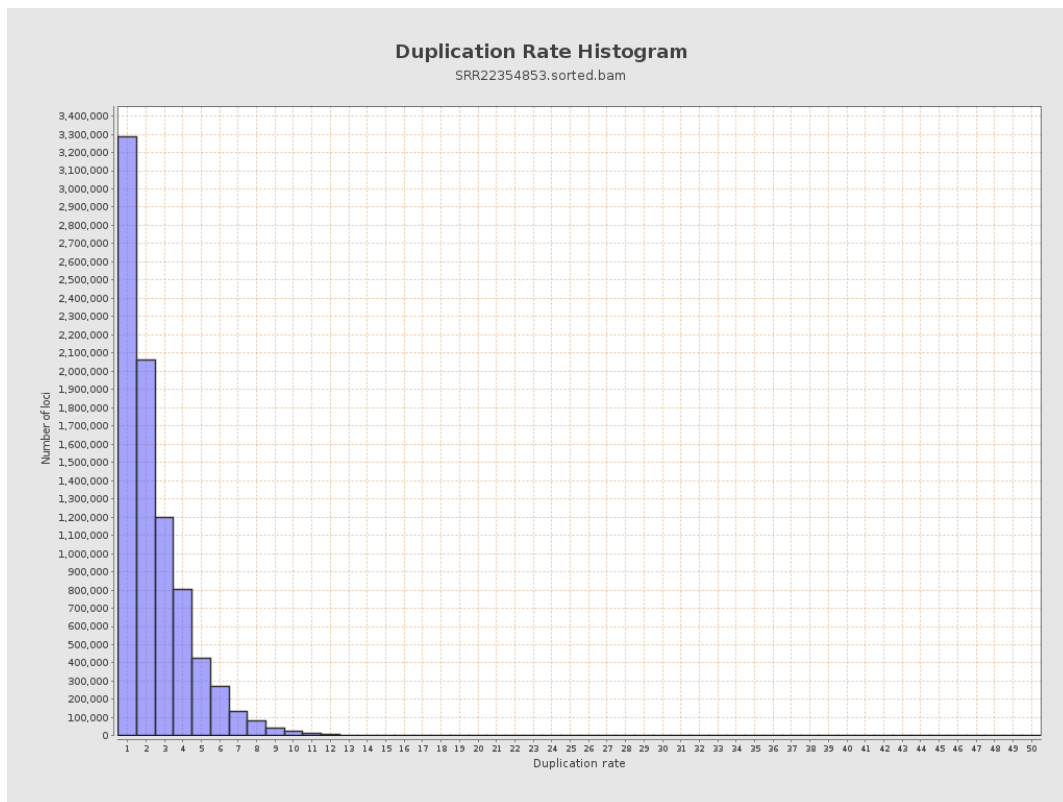
5. Results : Coverage Histogram (0-50X)



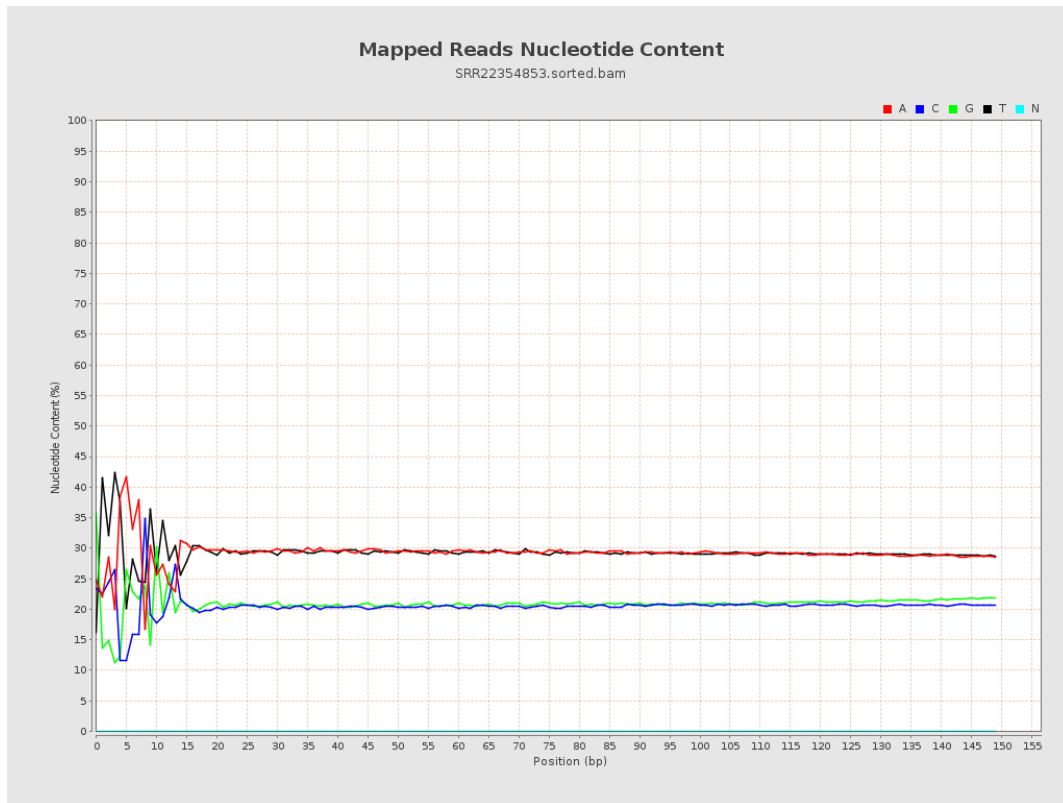
6. Results : Genome Fraction Coverage



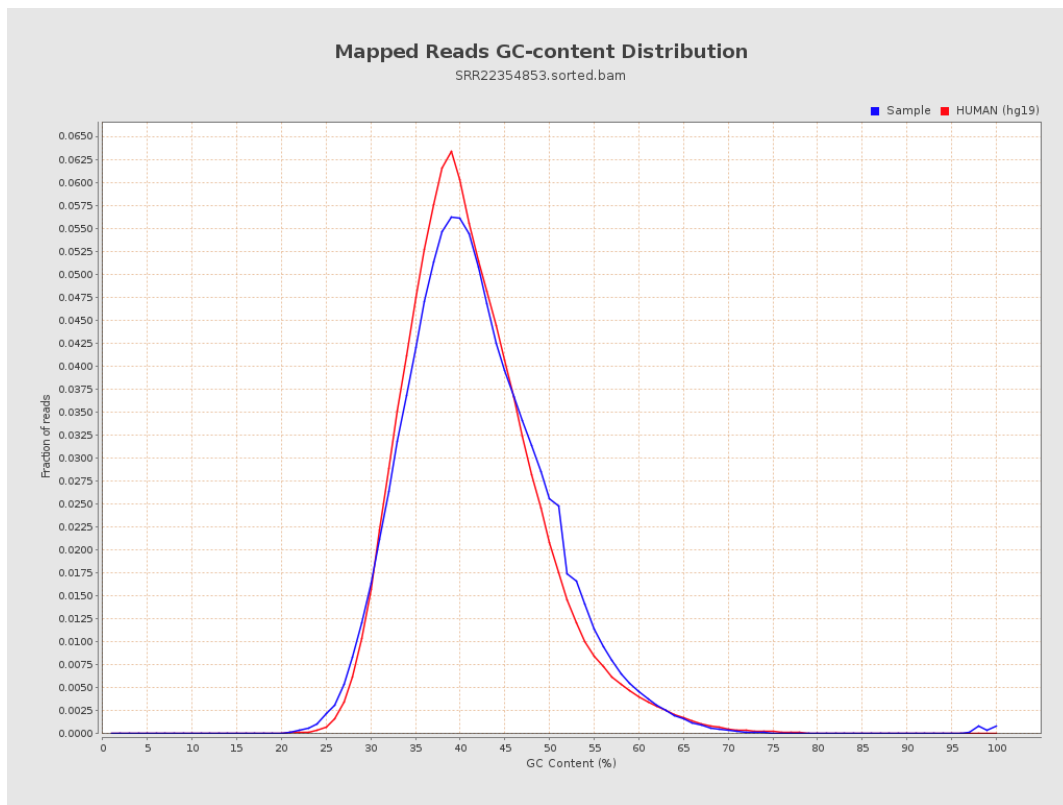
7. Results : Duplication Rate Histogram



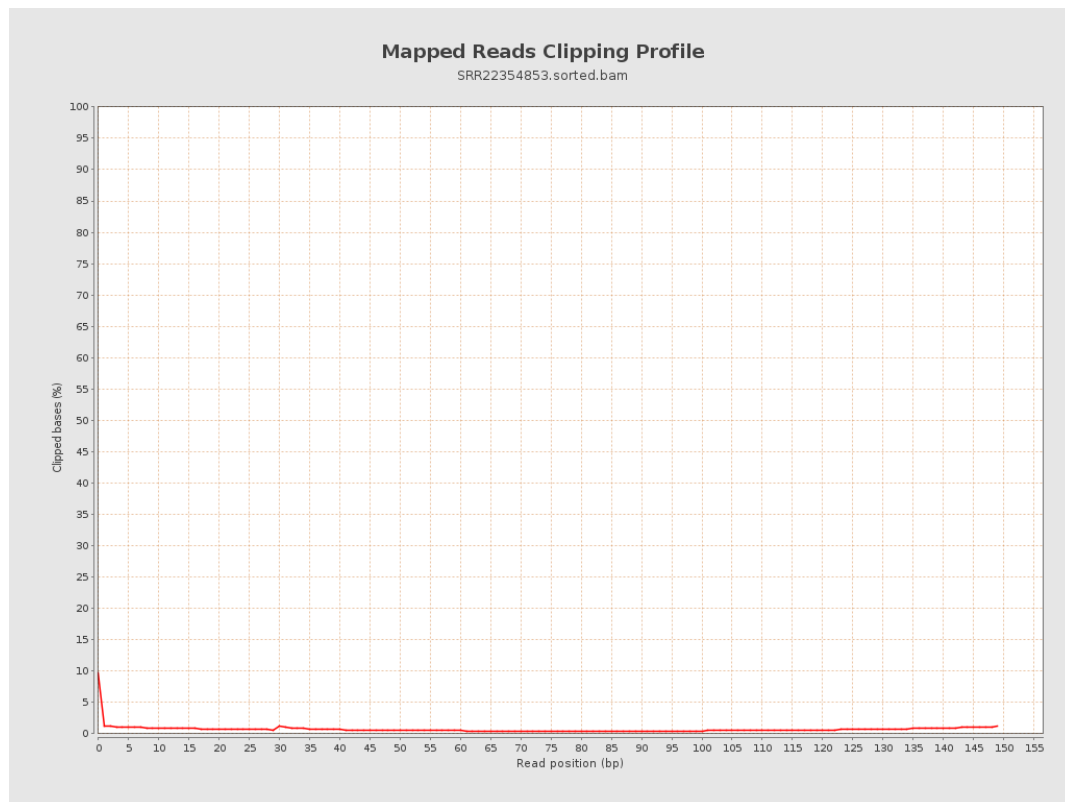
8. Results : Mapped Reads Nucleotide Content



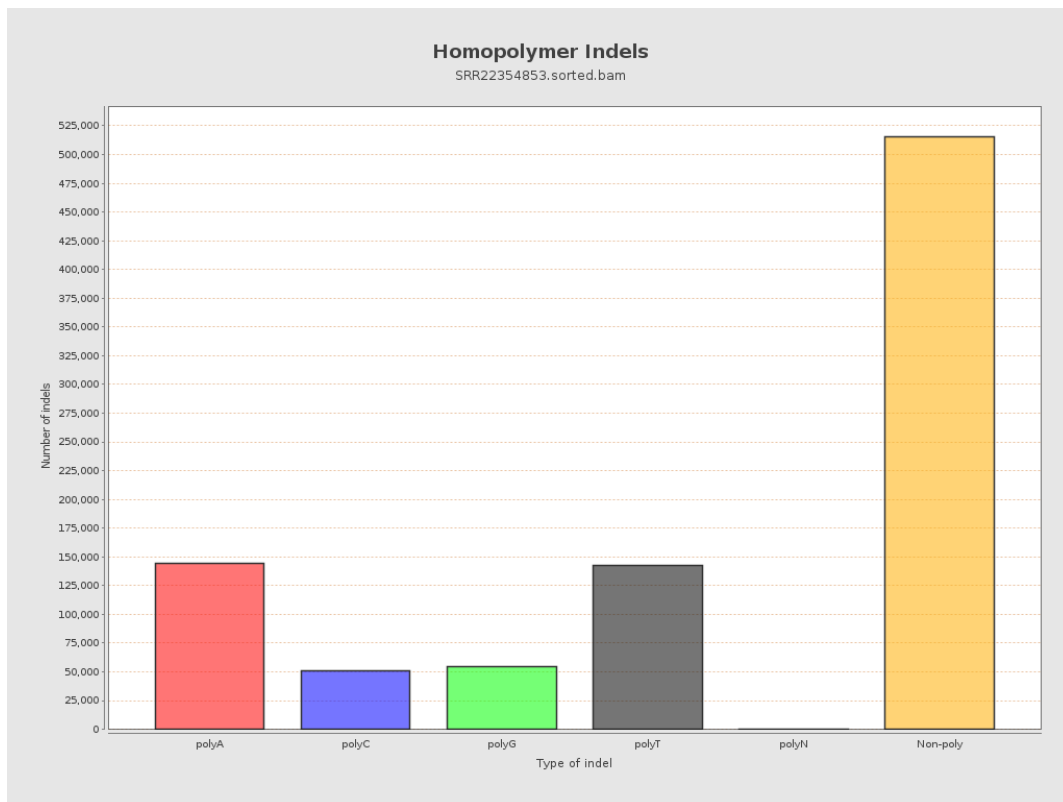
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



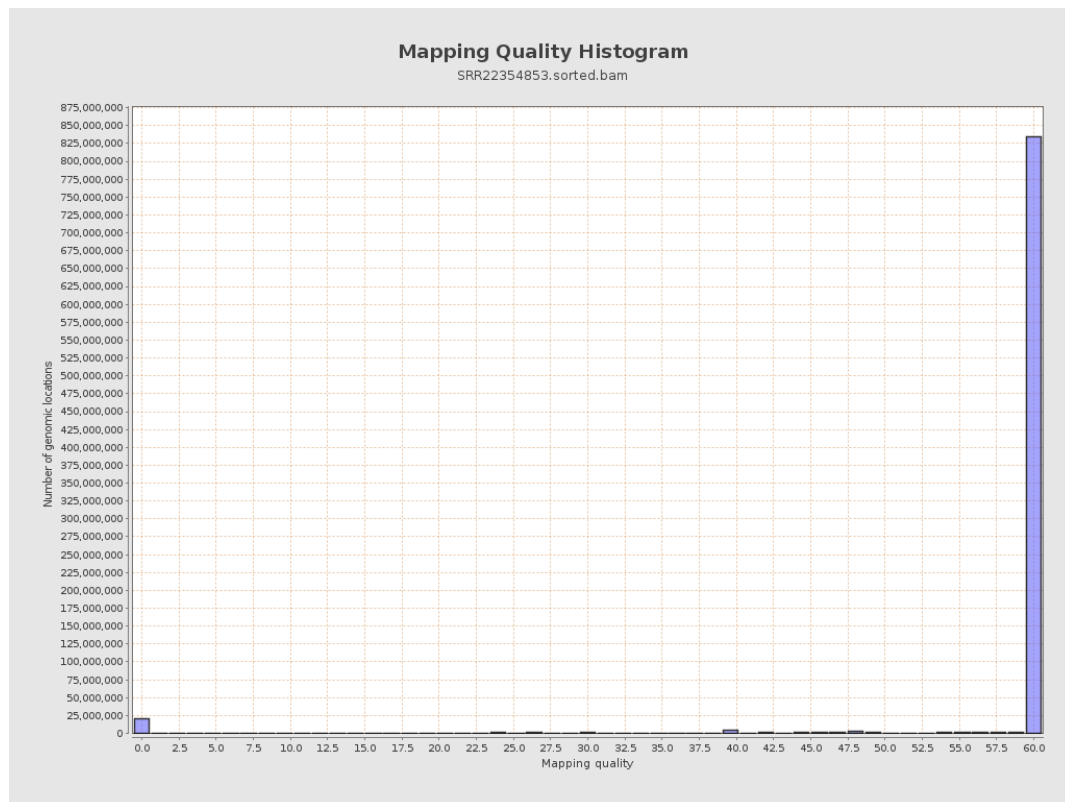
11. Results : Homopolymer Indels



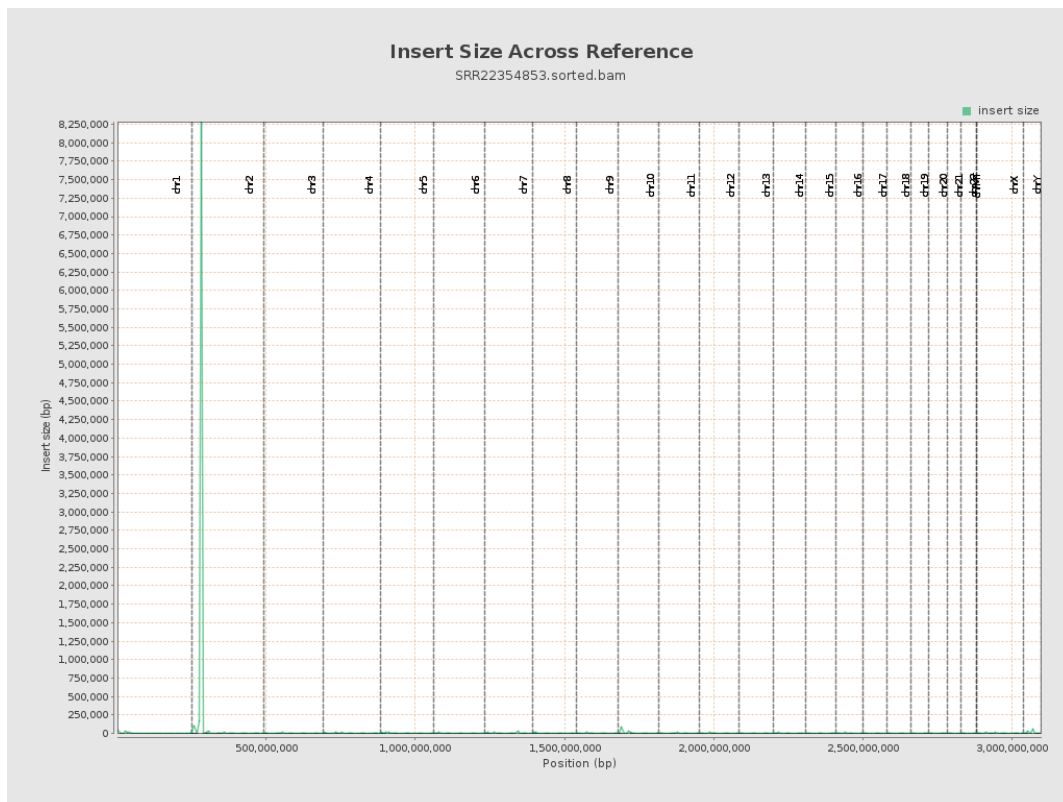
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

