

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 22:44:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630582.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_SRR630582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630582_1.fastq.gz SRR630582_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 22:44:47 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,221,526
Mapped reads	40,274,612 / 97.7%
Unmapped reads	946,914 / 2.3%
Mapped paired reads	40,274,612 / 97.7%
Mapped reads, first in pair	20,232,096 / 49.08%
Mapped reads, second in pair	20,042,516 / 48.62%
Mapped reads, both in pair	39,963,780 / 96.95%
Mapped reads, singletons	310,832 / 0.75%
Secondary alignments	0
Supplementary alignments	89,631 / 0.22%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	4,924,688 / 11.95%
Duplication rate	9.67%
Clipped reads	6,035,217 / 14.64%

2.2. ACGT Content

Number/percentage of A's	1,141,368,351 / 29.26%
Number/percentage of C's	776,413,276 / 19.9%
Number/percentage of T's	1,153,013,821 / 29.56%
Number/percentage of G's	829,852,944 / 21.27%
Number/percentage of N's	579,296 / 0.01%

GC Percentage	41.17%
---------------	--------

2.3. Coverage

Mean	1.2611
Standard Deviation	6.8912

2.4. Mapping Quality

Mean Mapping Quality	52.59
----------------------	-------

2.5. Insert size

Mean	32,808.18
Standard Deviation	1,817,808.12
P25/Median/P75	158 / 202 / 268

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	34,775,792
Insertions	709,427
Mapped reads with at least one insertion	1.73%
Deletions	2,057,830
Mapped reads with at least one deletion	4.97%
Homopolymer indels	54.05%

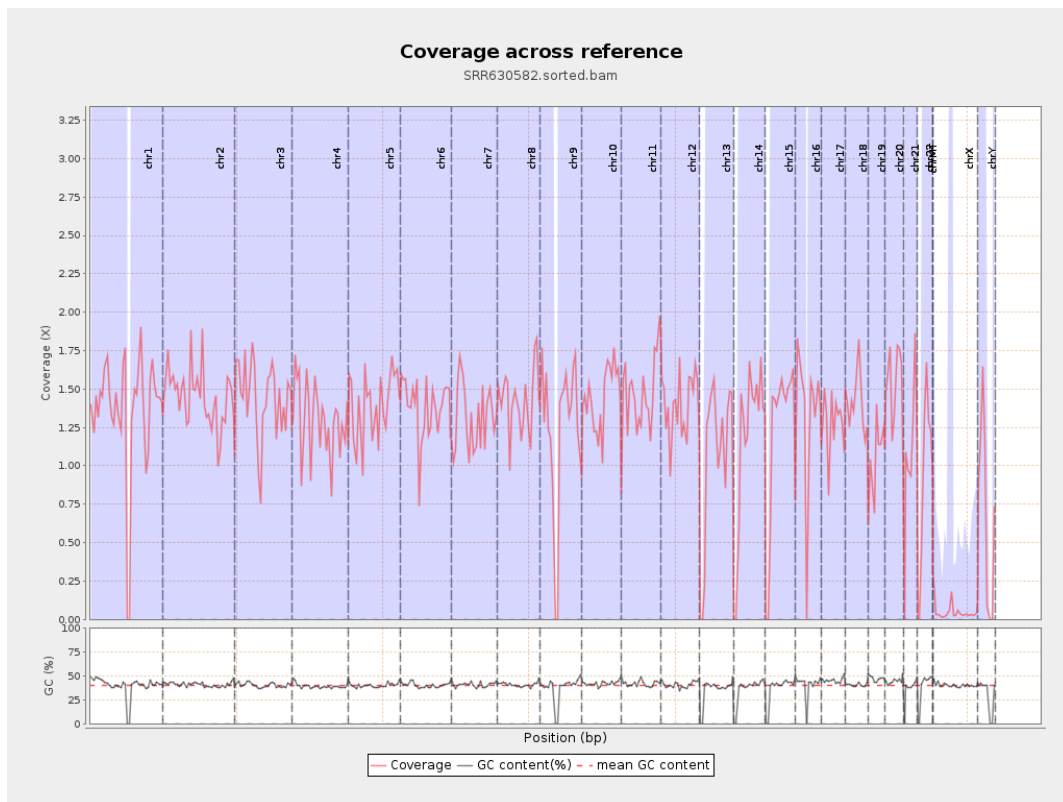
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

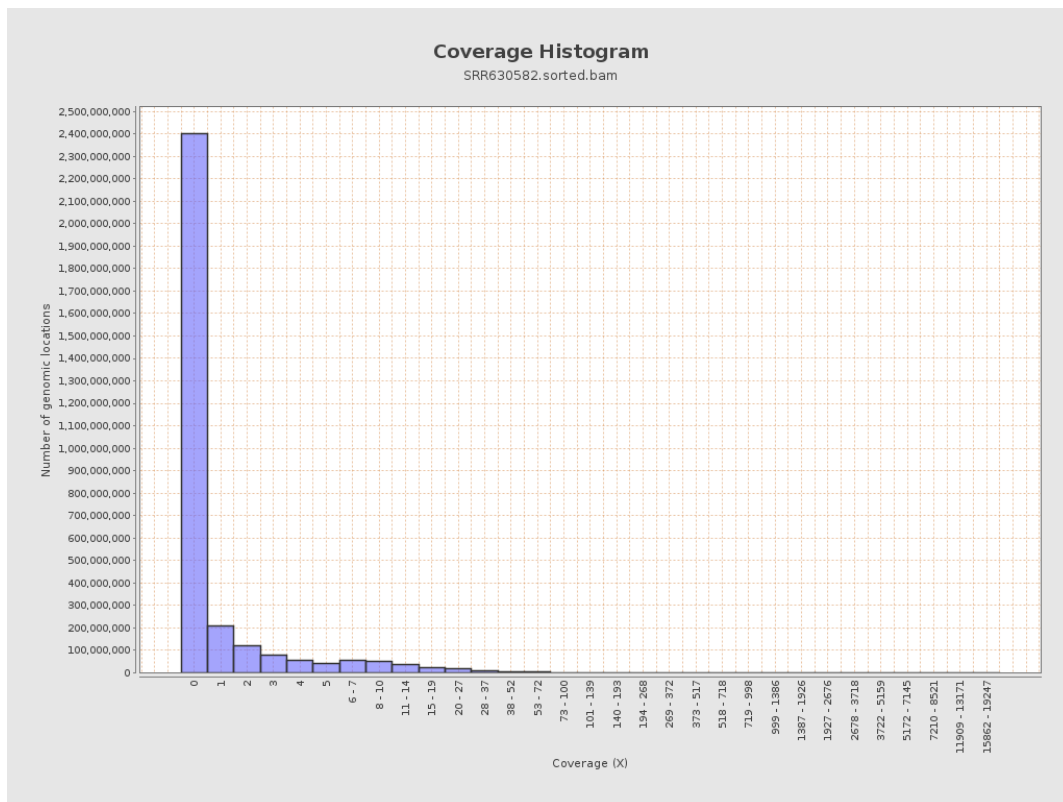
		bases	coverage	deviation
chr1	249250621	339802364	1.3633	8.6601
chr2	243199373	353346139	1.4529	7.7124
chr3	198022430	283603293	1.4322	4.7154
chr4	191154276	248670437	1.3009	5.6769
chr5	180915260	251819526	1.3919	4.6834
chr6	171115067	235903509	1.3786	5.4898
chr7	159138663	207676572	1.305	7.029
chr8	146364022	208365289	1.4236	4.8312
chr9	141213431	174782207	1.2377	8.96
chr10	135534747	195810072	1.4447	5.4764
chr11	135006516	197671669	1.4642	7.802
chr12	133851895	187659254	1.402	15.1768
chr13	115169878	123322124	1.0708	4.1058
chr14	107349540	127036429	1.1834	4.3476
chr15	102531392	123656709	1.206	5.1306
chr16	90354753	119256094	1.3199	6.688
chr17	81195210	104272847	1.2842	5.1054
chr18	78077248	110232946	1.4118	9.1594
chr19	59128983	62361867	1.0547	6.0279
chr20	63025520	98061229	1.5559	5.3404
chr21	48129895	53199579	1.1053	5.4466
chr22	51304566	48085991	0.9373	4.0862
chrMT	16571	5103	0.3079	1.0211
chrX	155270560	7458221	0.048	2.1592

chrY	59373566	41983816	0.7071	5.4931
------	----------	----------	--------	--------

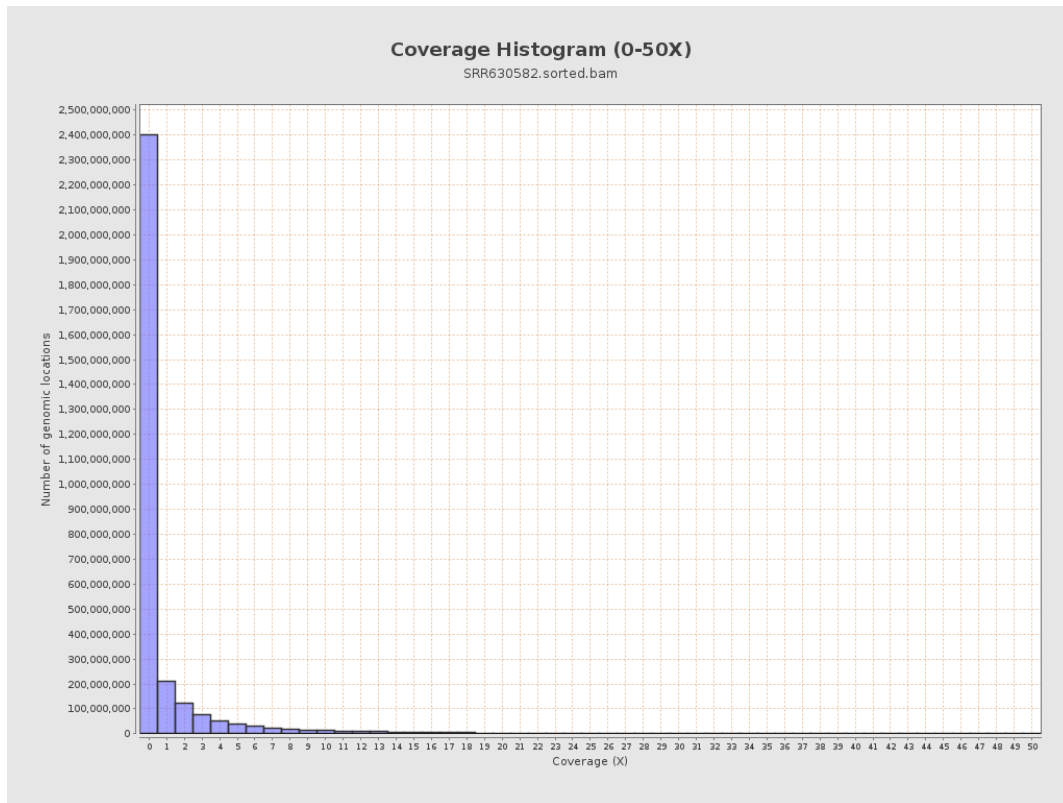
3. Results : Coverage across reference



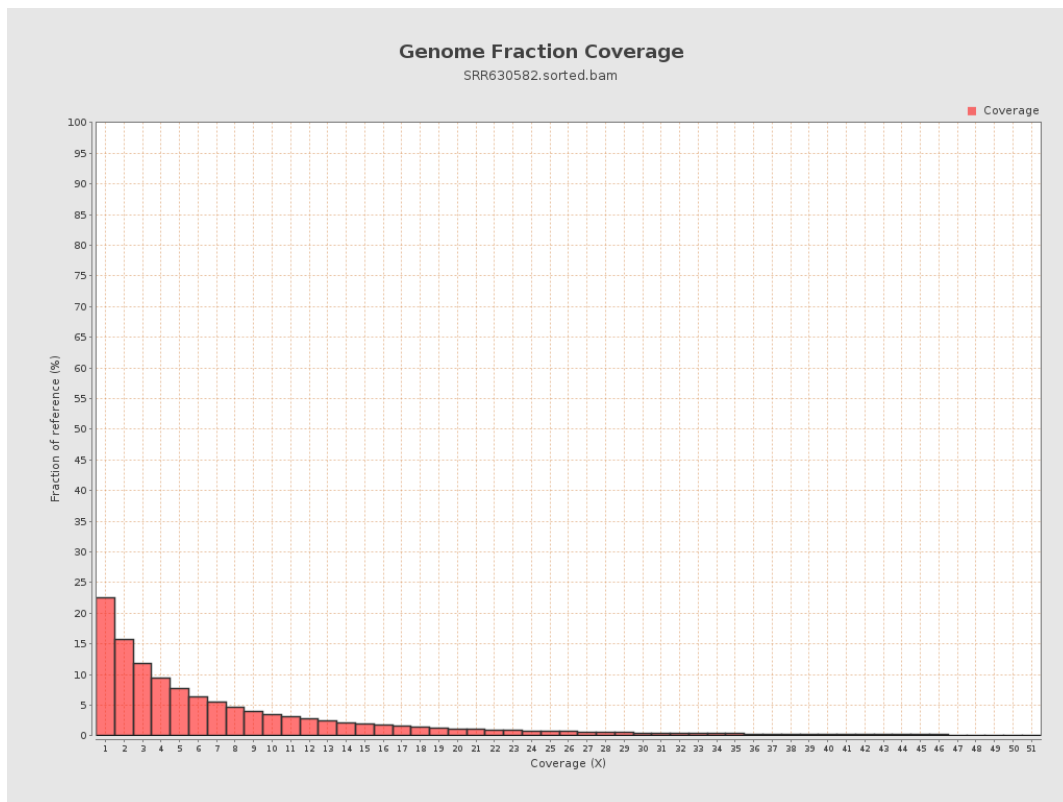
4. Results : Coverage Histogram



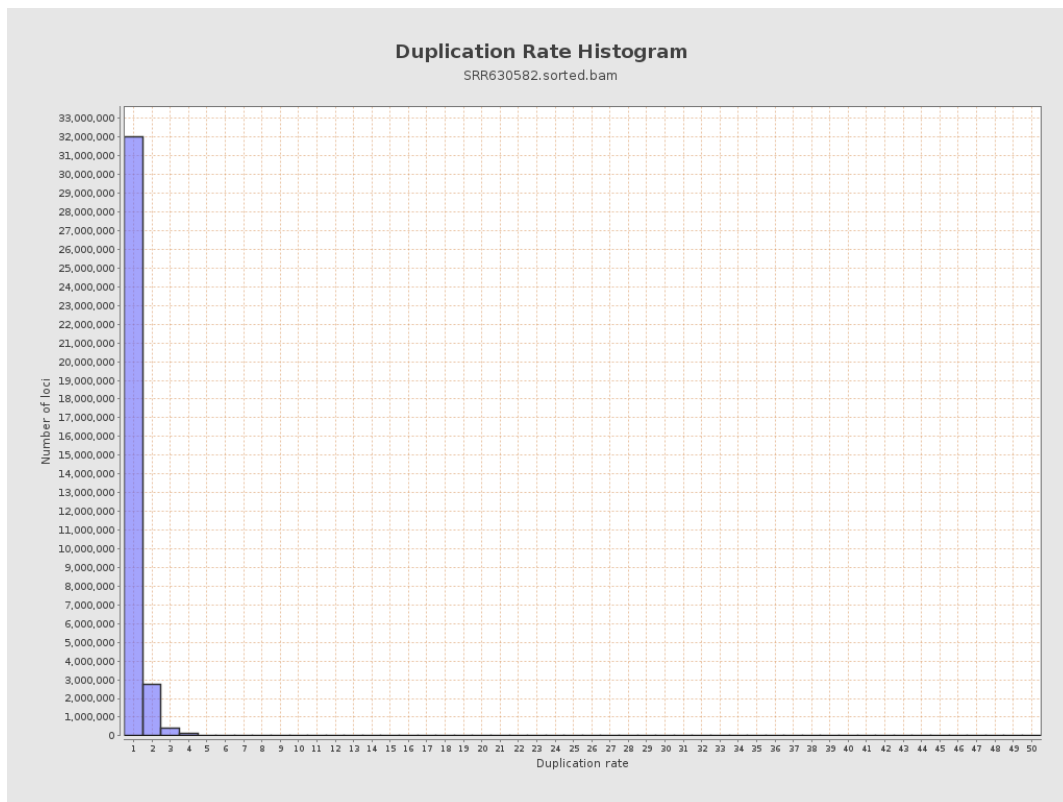
5. Results : Coverage Histogram (0-50X)



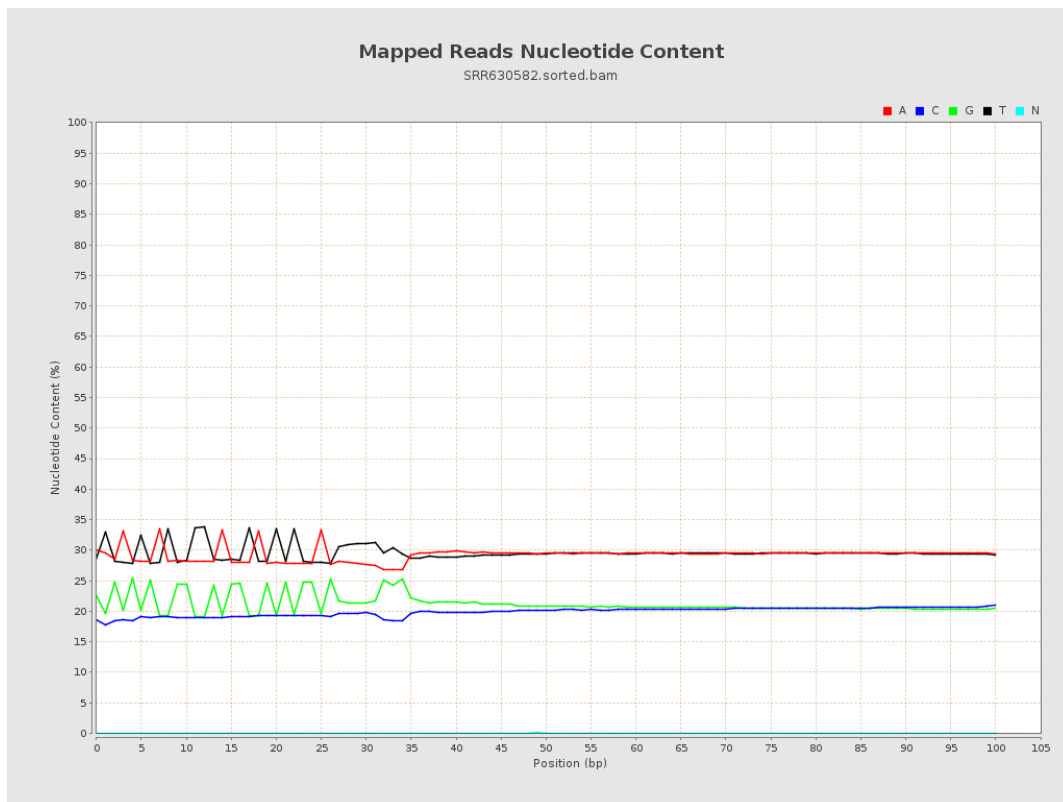
6. Results : Genome Fraction Coverage



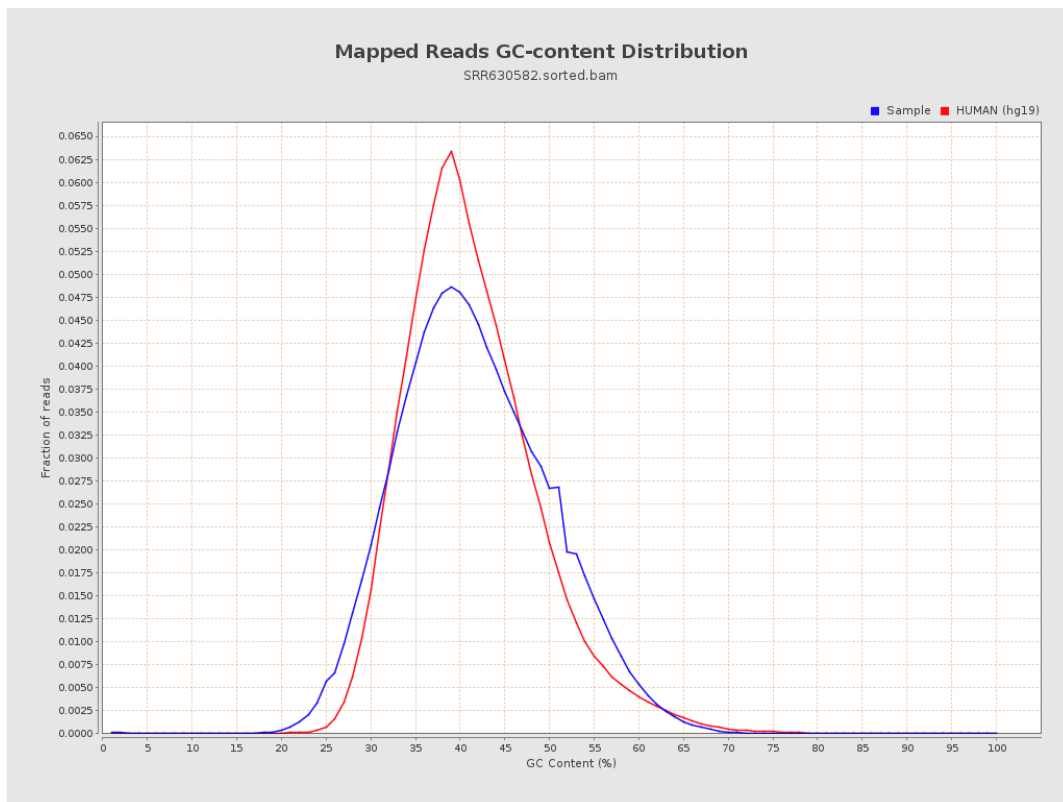
7. Results : Duplication Rate Histogram



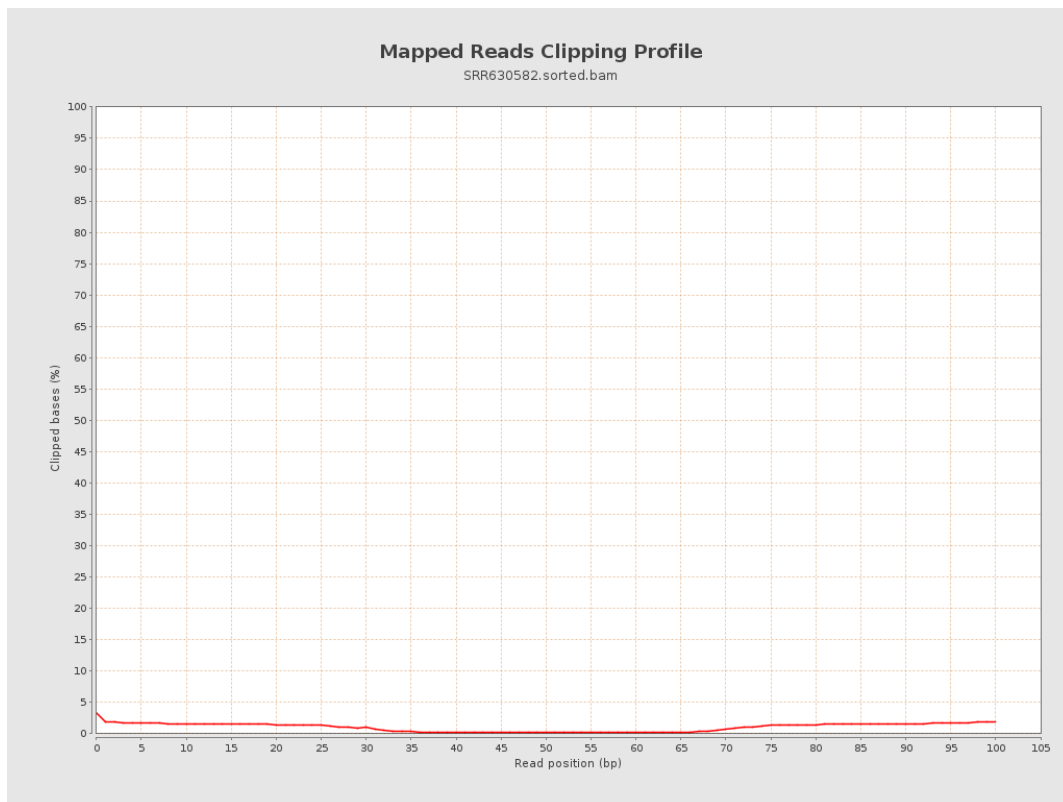
8. Results : Mapped Reads Nucleotide Content



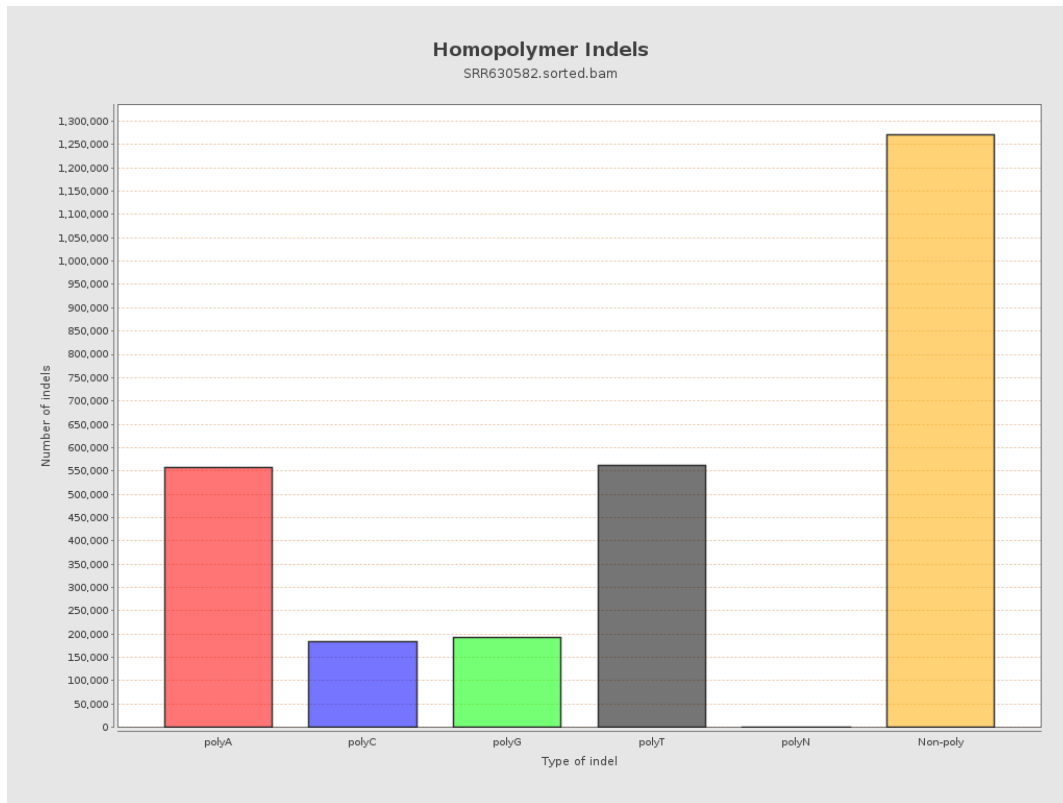
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



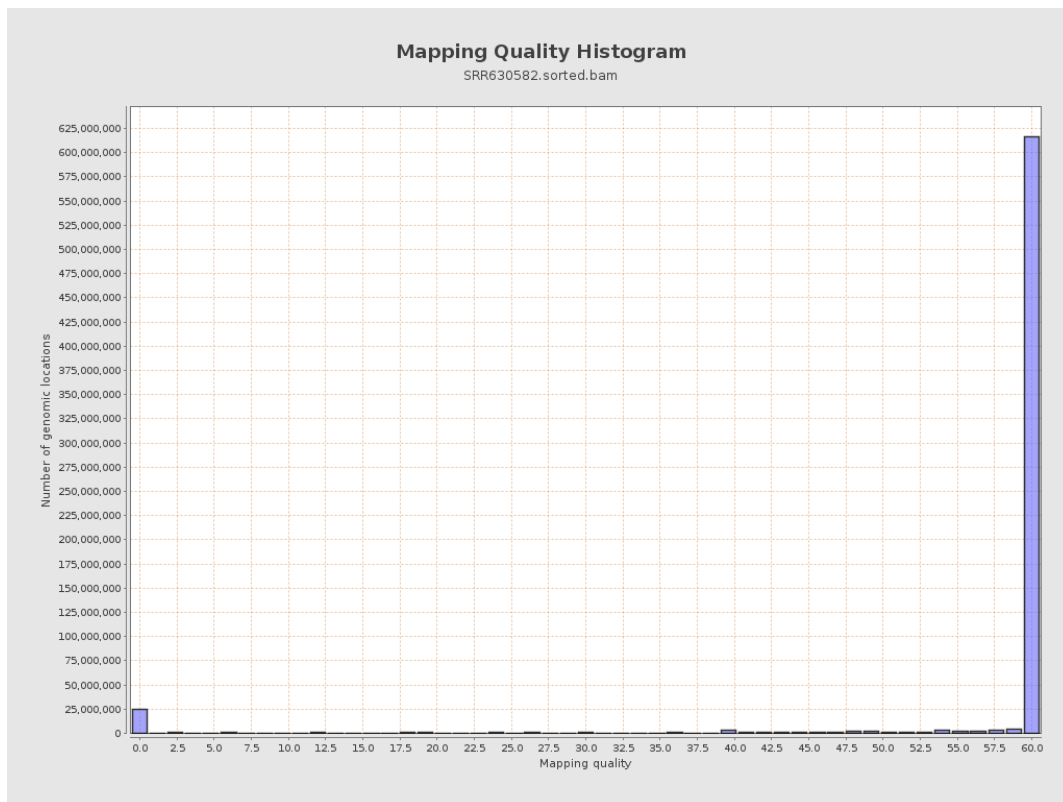
11. Results : Homopolymer Indels



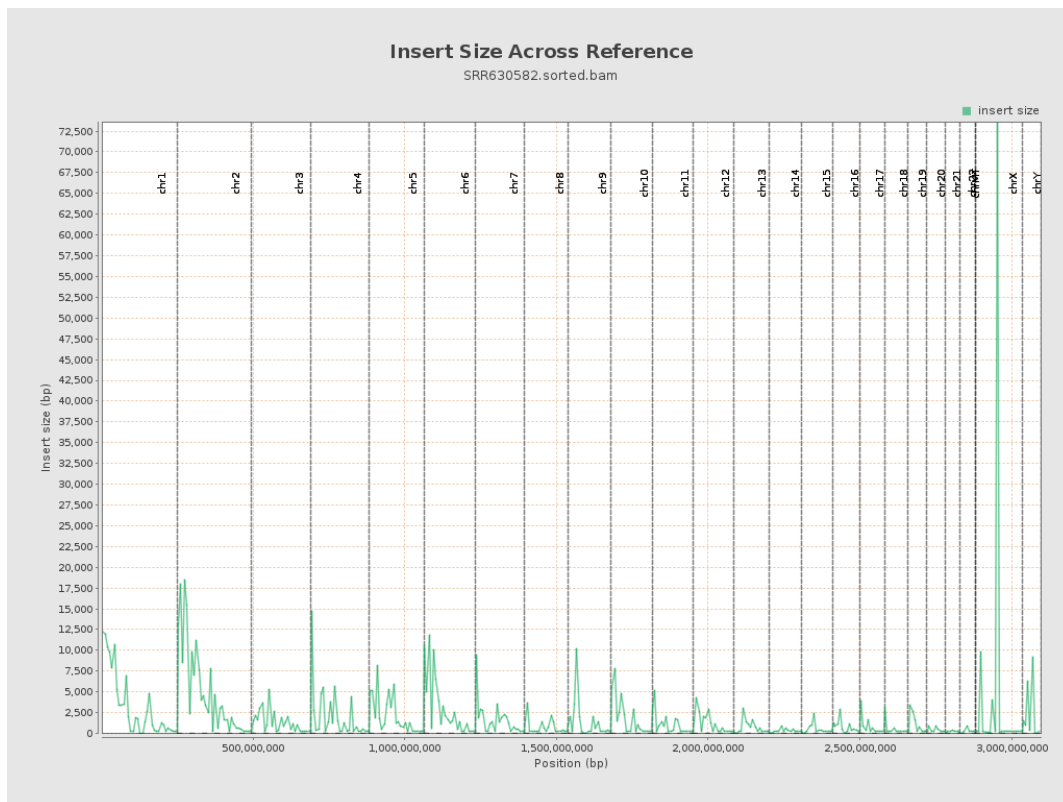
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

