

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 21:01:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104284.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_SRR26104284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104284_1.fastq.gz SRR26104284_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 20:43:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	178,813,988
Mapped reads	175,282,347 / 98.02%
Unmapped reads	3,531,641 / 1.98%
Mapped paired reads	175,282,347 / 98.02%
Mapped reads, first in pair	88,346,542 / 49.41%
Mapped reads, second in pair	86,935,805 / 48.62%
Mapped reads, both in pair	173,540,884 / 97.05%
Mapped reads, singletons	1,741,463 / 0.97%
Secondary alignments	0
Supplementary alignments	176,858 / 0.1%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	74,791,370 / 41.83%
Duplication rate	33.2%
Clipped reads	33,726,392 / 18.86%

2.2. ACGT Content

Number/percentage of A's	4,739,552,612 / 31.28%
Number/percentage of C's	2,835,907,246 / 18.72%
Number/percentage of T's	4,784,342,965 / 31.58%
Number/percentage of G's	2,782,198,897 / 18.36%
Number/percentage of N's	7,968,063 / 0.05%

GC Percentage	37.08%
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2.3. Coverage

Mean	4.8952
Standard Deviation	75.9756

2.4. Mapping Quality

Mean Mapping Quality	53.28
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2.5. Insert size

Mean	11,545.21
Standard Deviation	1,042,147.4
P25/Median/P75	107 / 173 / 271

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	95,457,260
Insertions	1,455,282
Mapped reads with at least one insertion	0.82%
Deletions	1,741,442
Mapped reads with at least one deletion	0.98%
Homopolymer indels	44.46%

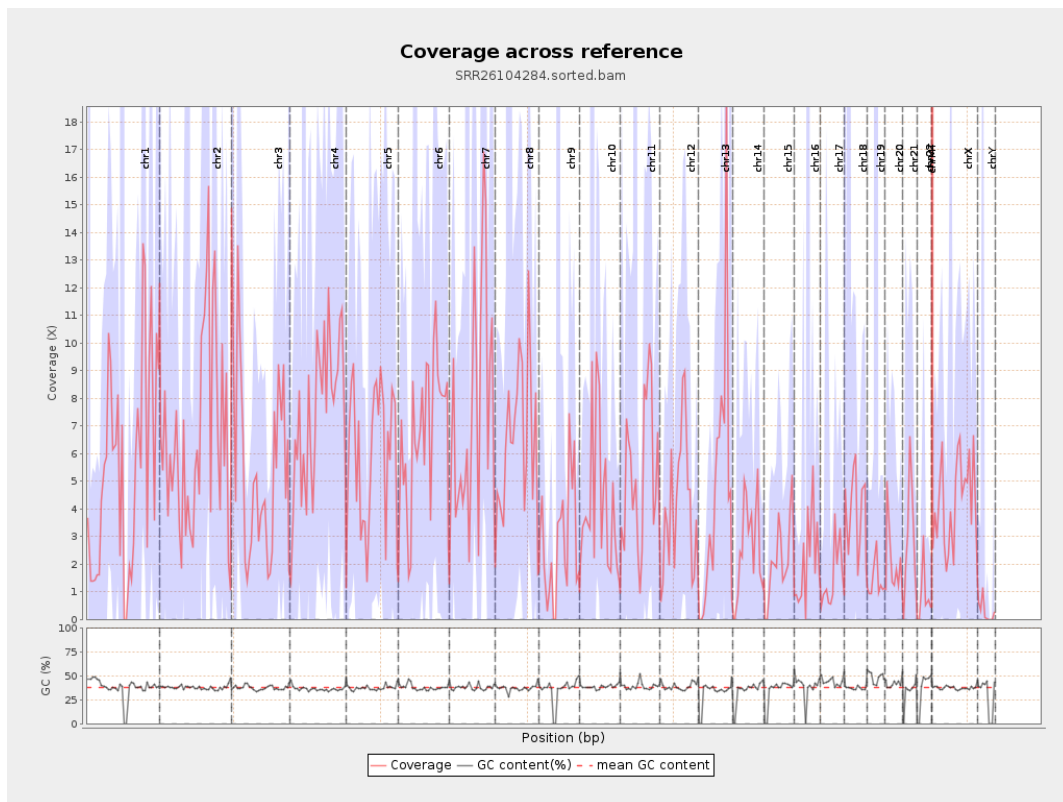
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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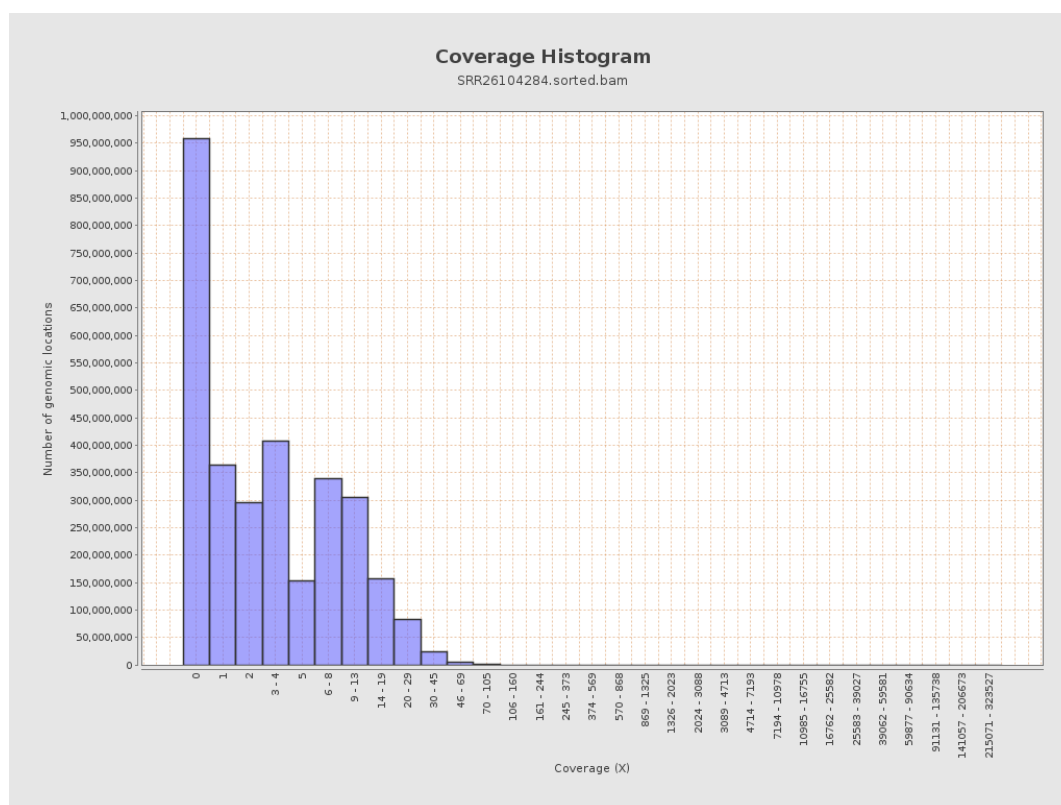
		bases	coverage	deviation
chr1	249250621	1375031619	5.5167	86.4139
chr2	243199373	1585204731	6.5181	16.9344
chr3	198022430	1073476287	5.421	7.4449
chr4	191154276	1419503980	7.426	13.9433
chr5	180915260	1066758536	5.8965	8.4
chr6	171115067	1176610164	6.8761	13.59
chr7	159138663	1181571511	7.4248	48.0871
chr8	146364022	959199376	6.5535	204.2097
chr9	141213431	383716948	2.7173	22.1495
chr10	135534747	565716587	4.174	45.0403
chr11	135006516	707417701	5.2399	14.9897
chr12	133851895	537066894	4.0124	5.8098
chr13	115169878	538403580	4.6749	11.9371
chr14	107349540	280322676	2.6113	5.1896
chr15	102531392	227163614	2.2156	3.9572
chr16	90354753	189160775	2.0935	17.1238
chr17	81195210	122667067	1.5108	6.948
chr18	78077248	306038460	3.9197	24.641
chr19	59128983	81559567	1.3794	51.1422
chr20	63025520	128833854	2.0442	4.9571
chr21	48129895	145390612	3.0208	7.095
chr22	51304566	45745942	0.8917	3.8478
chrMT	16571	372669779	22,489.2752	4,514.4991
chrX	155270560	667338177	4.2979	7.0221

chrY	59373566	17319431	0.2917	9.866
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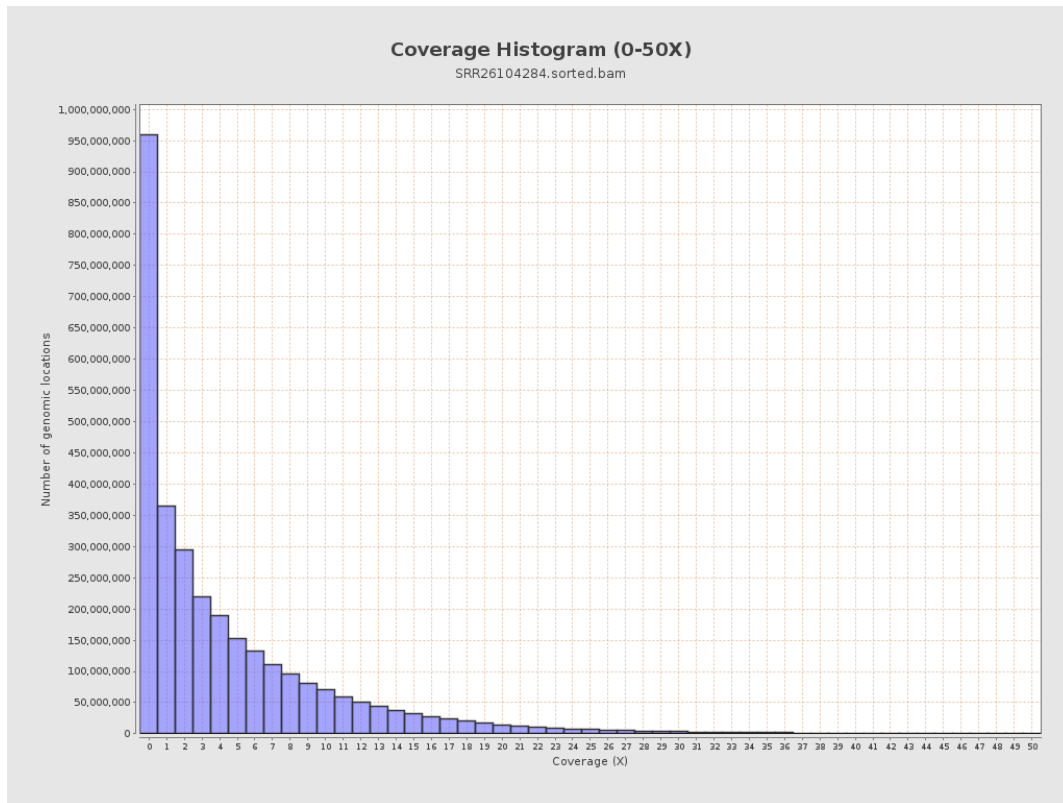
3. Results : Coverage across reference



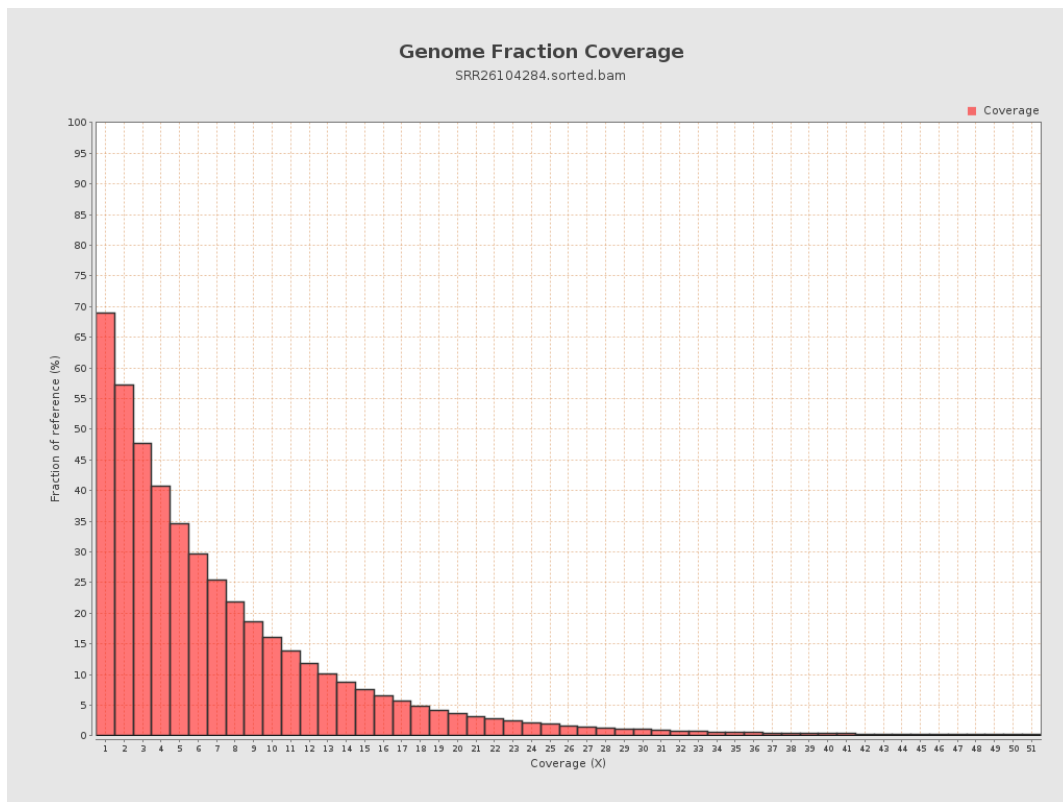
4. Results : Coverage Histogram



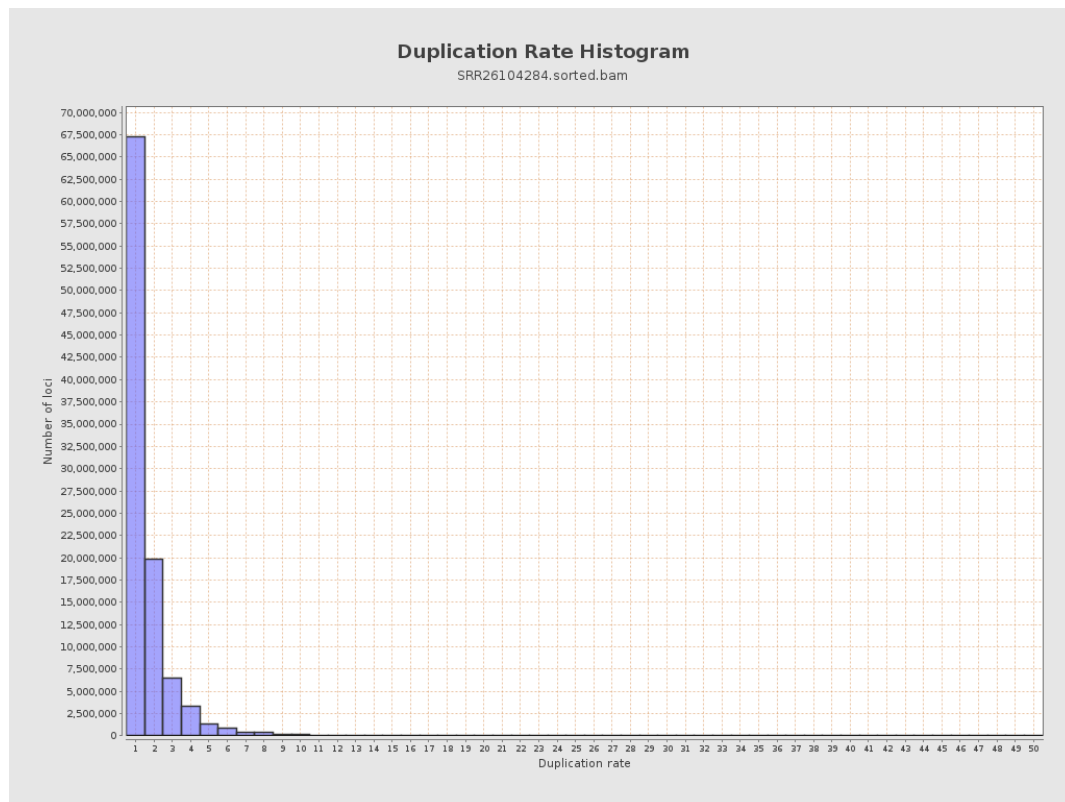
5. Results : Coverage Histogram (0-50X)



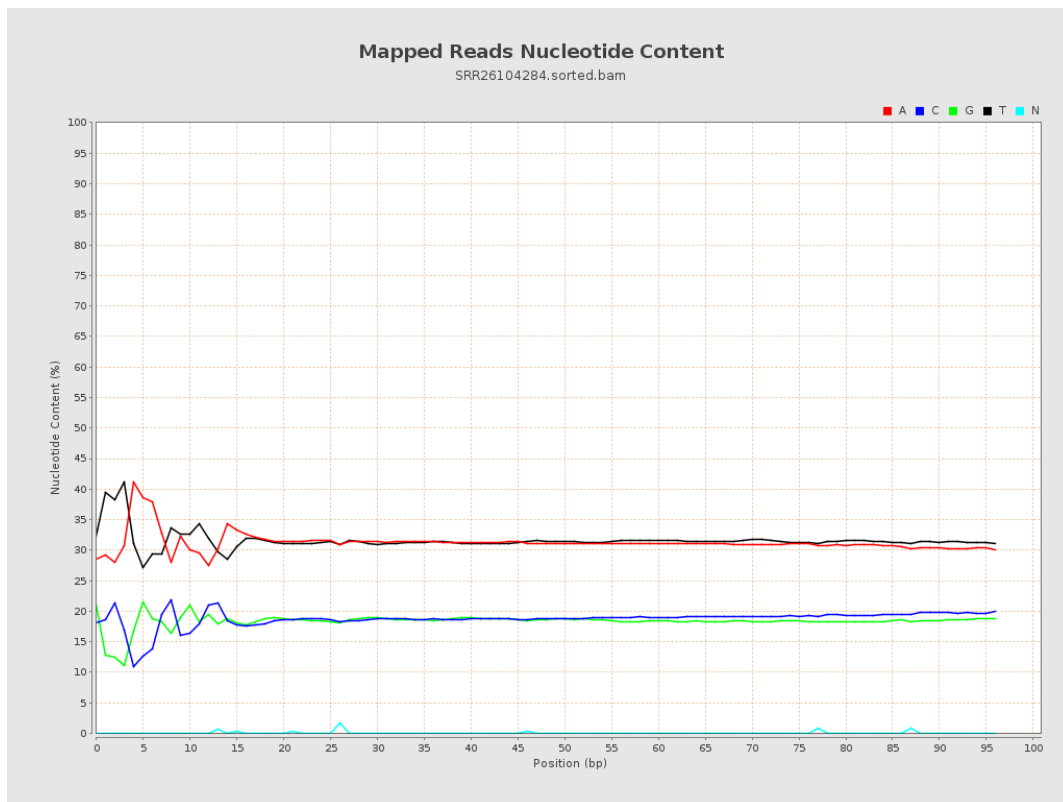
6. Results : Genome Fraction Coverage



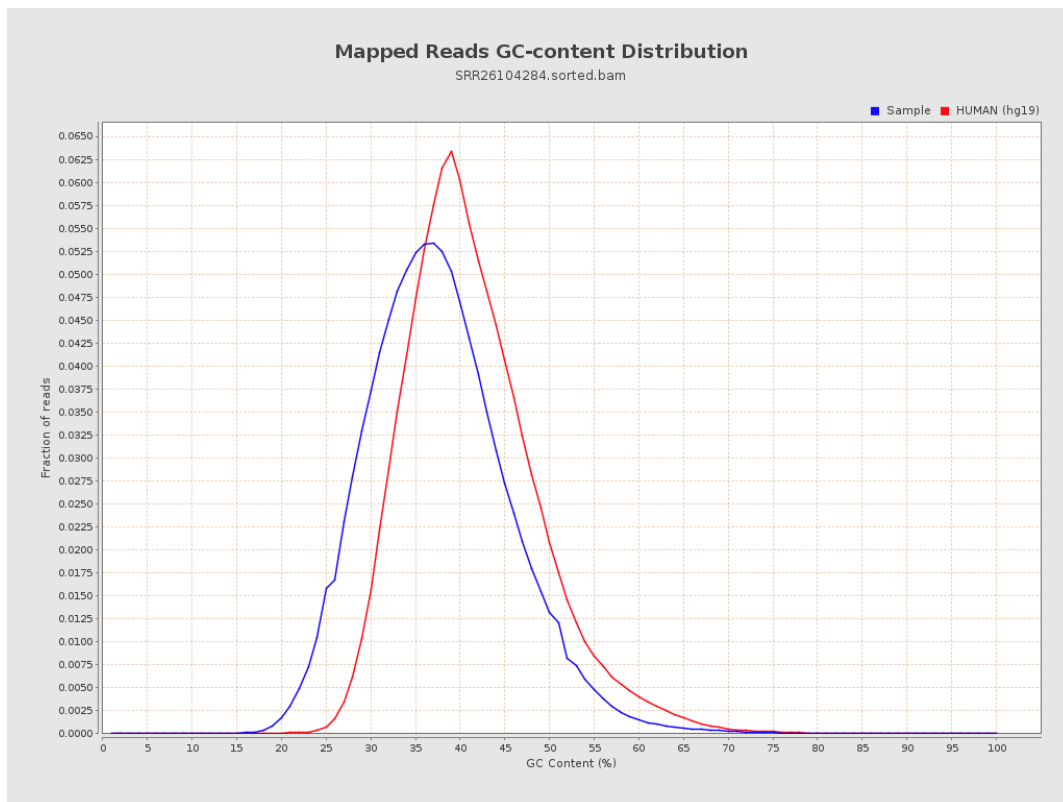
7. Results : Duplication Rate Histogram



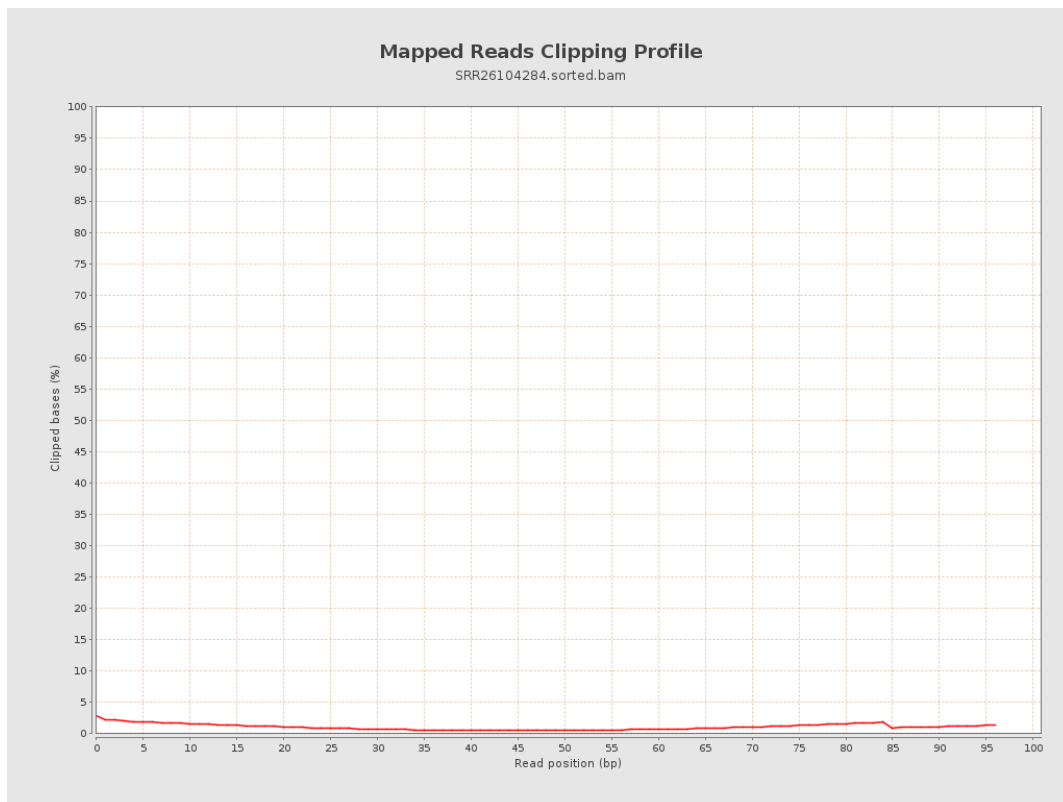
8. Results : Mapped Reads Nucleotide Content



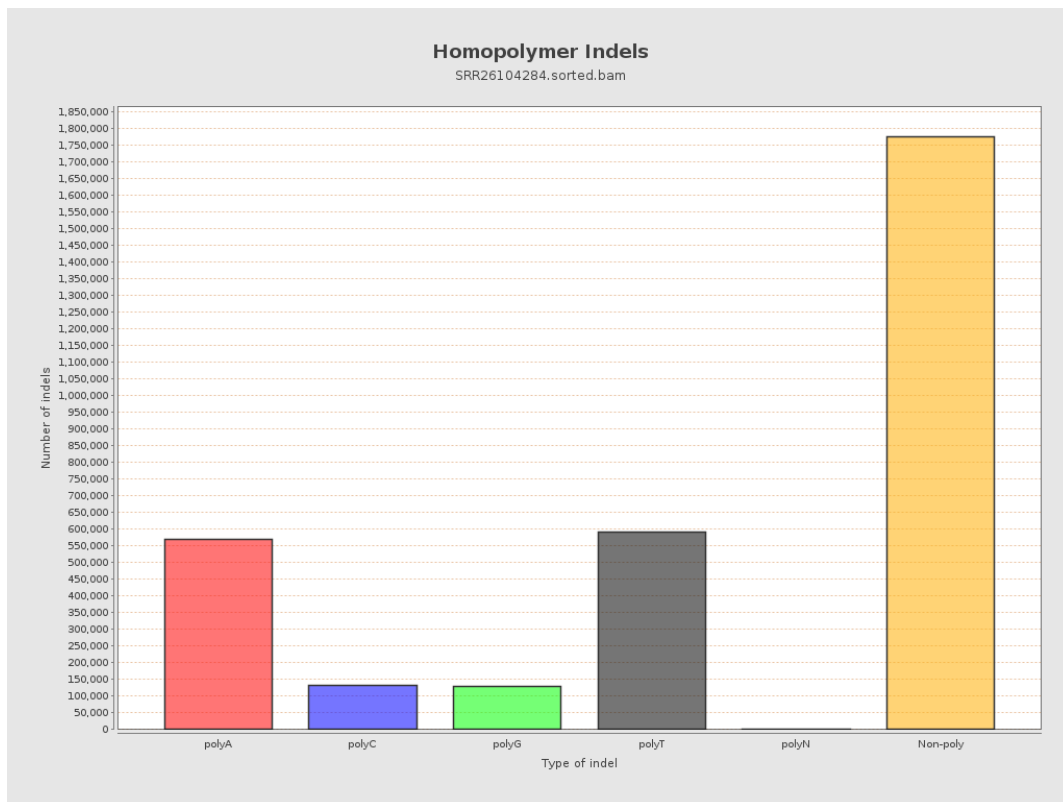
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



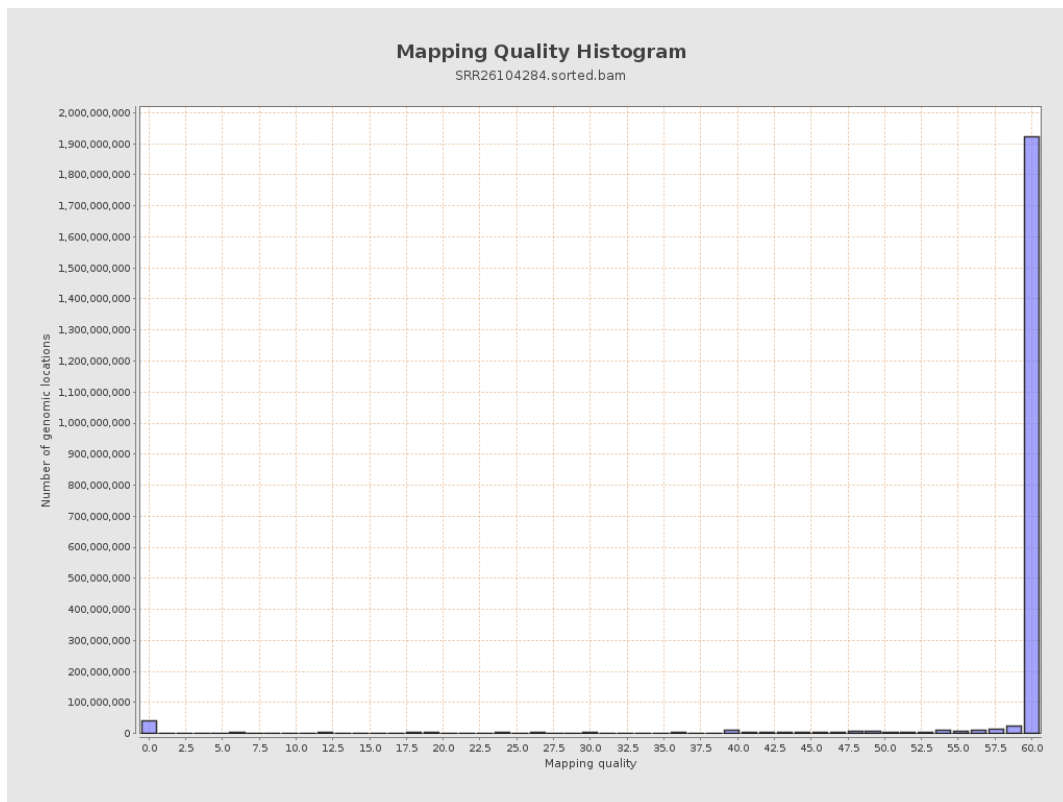
11. Results : Homopolymer Indels



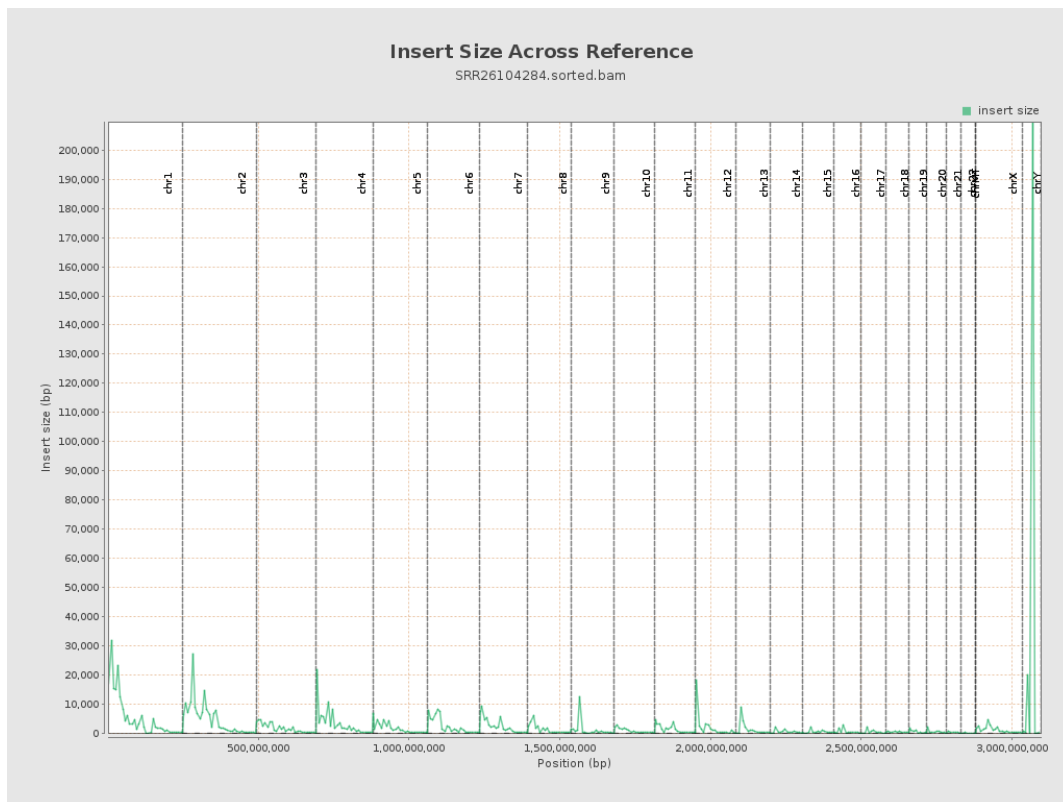
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

