

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 21:22:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504606.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_SRR504606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504606_1.fastq.gz SRR504606_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 21:22:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	422,801,300
Mapped reads	362,970,846 / 85.85%
Unmapped reads	59,830,454 / 14.15%
Mapped paired reads	362,970,846 / 85.85%
Mapped reads, first in pair	181,674,496 / 42.97%
Mapped reads, second in pair	181,296,350 / 42.88%
Mapped reads, both in pair	360,539,246 / 85.27%
Mapped reads, singletons	2,431,600 / 0.58%
Secondary alignments	0
Supplementary alignments	1,971,515 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	88,700,878 / 20.98%
Duplication rate	21.79%
Clipped reads	18,010,888 / 4.26%

2.2. ACGT Content

Number/percentage of A's	9,492,694,526 / 26.35%
Number/percentage of C's	8,414,805,208 / 23.36%
Number/percentage of T's	9,512,206,004 / 26.41%
Number/percentage of G's	8,567,966,391 / 23.79%
Number/percentage of N's	32,702,846 / 0.09%

GC Percentage	47.15%
---------------	--------

2.3. Coverage

Mean	11.6387
Standard Deviation	24.2079

2.4. Mapping Quality

Mean Mapping Quality	53.96
----------------------	-------

2.5. Insert size

Mean	30,862.54
Standard Deviation	1,716,264.46
P25/Median/P75	180 / 213 / 267

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	242,100,821
Insertions	2,720,616
Mapped reads with at least one insertion	0.73%
Deletions	3,718,134
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.27%

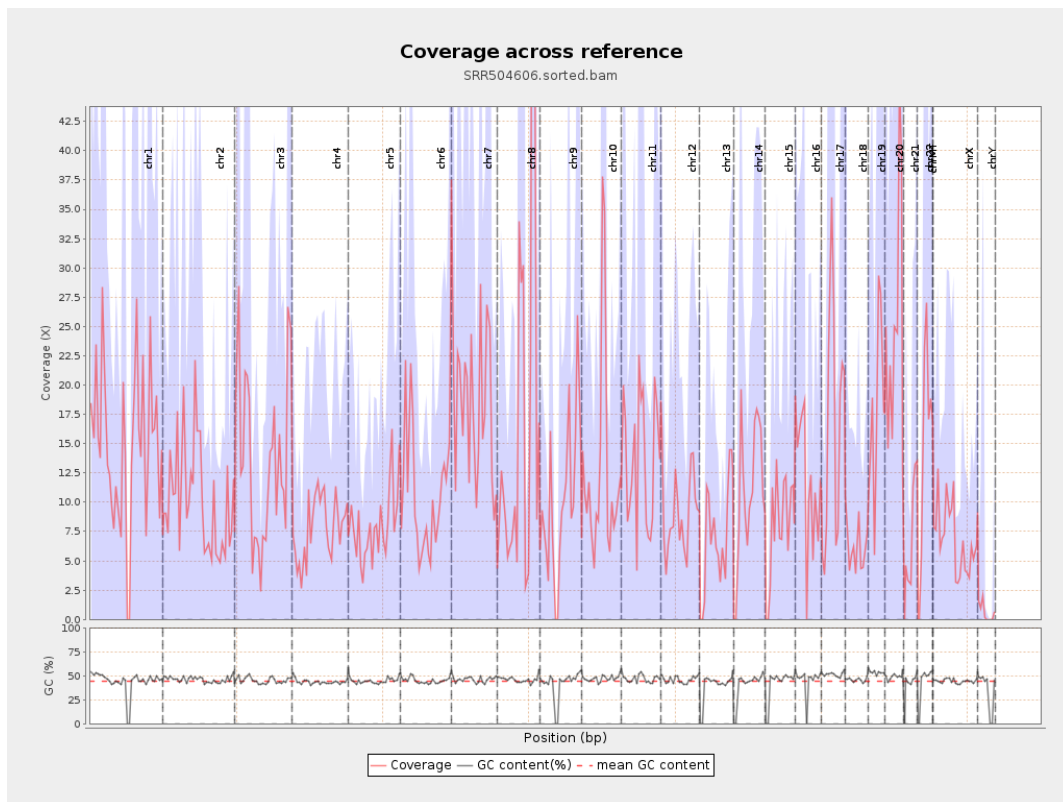
2.7. Chromosome stats

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

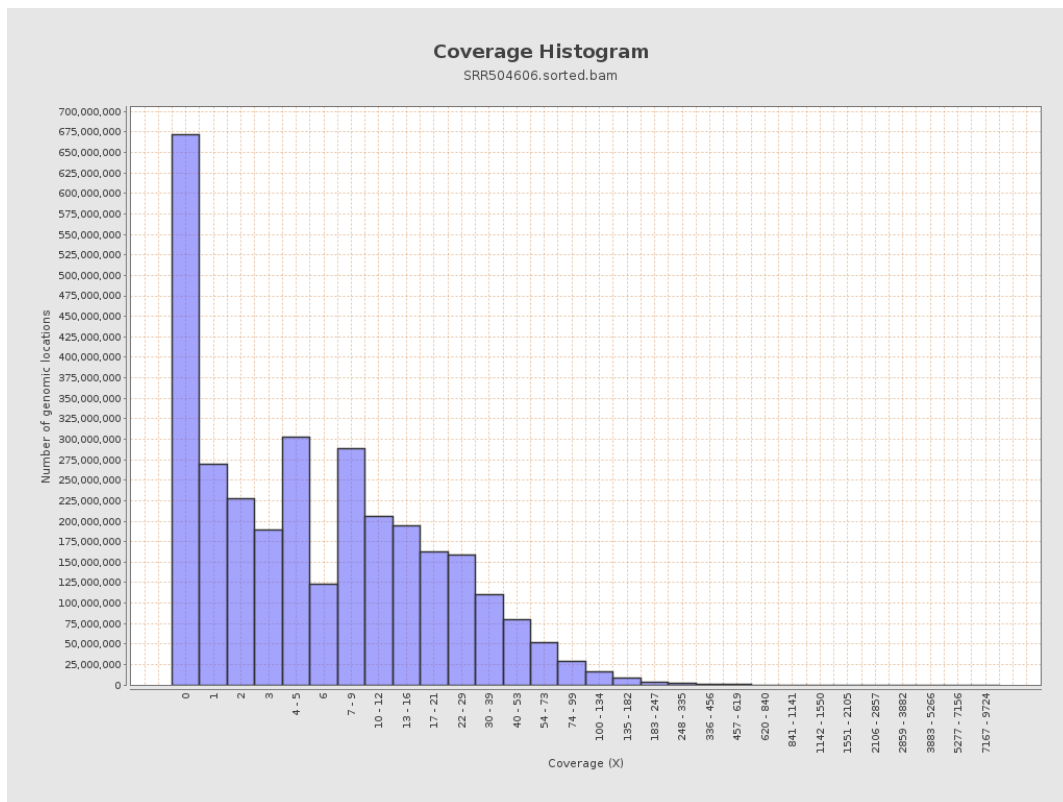
		bases	coverage	deviation
chr1	249250621	3702958602	14.8564	25.1594
chr2	243199373	2471288178	10.1616	18.7516
chr3	198022430	2667040256	13.4684	22.3865
chr4	191154276	1505404696	7.8753	12.5844
chr5	180915260	1464005615	8.0922	13.6676
chr6	171115067	1839926486	10.7526	17.6114
chr7	159138663	2929970727	18.4114	27.5183
chr8	146364022	2746426913	18.7644	46.2945
chr9	141213431	1416145747	10.0284	19.6004
chr10	135534747	1696922128	12.5202	23.7684
chr11	135006516	1837094975	13.6075	23.1396
chr12	133851895	1229076442	9.1824	15.6347
chr13	115169878	818160942	7.1039	13.3852
chr14	107349540	1203174761	11.208	19.5963
chr15	102531392	803576446	7.8374	14.6795
chr16	90354753	1052110381	11.6442	20.0685
chr17	81195210	1309088486	16.1227	49.8384
chr18	78077248	470937178	6.0317	28.0653
chr19	59128983	1064523100	18.0034	31.379
chr20	63025520	1622911635	25.7501	38.5497
chr21	48129895	341555548	7.0965	18.1055
chr22	51304566	742147771	14.4655	26.9922
chrMT	16571	258613	15.6064	12.6842
chrX	155270560	1058838557	6.8193	12.1156

chrY	59373566	36300239	0.6114	14.5558
------	----------	----------	--------	---------

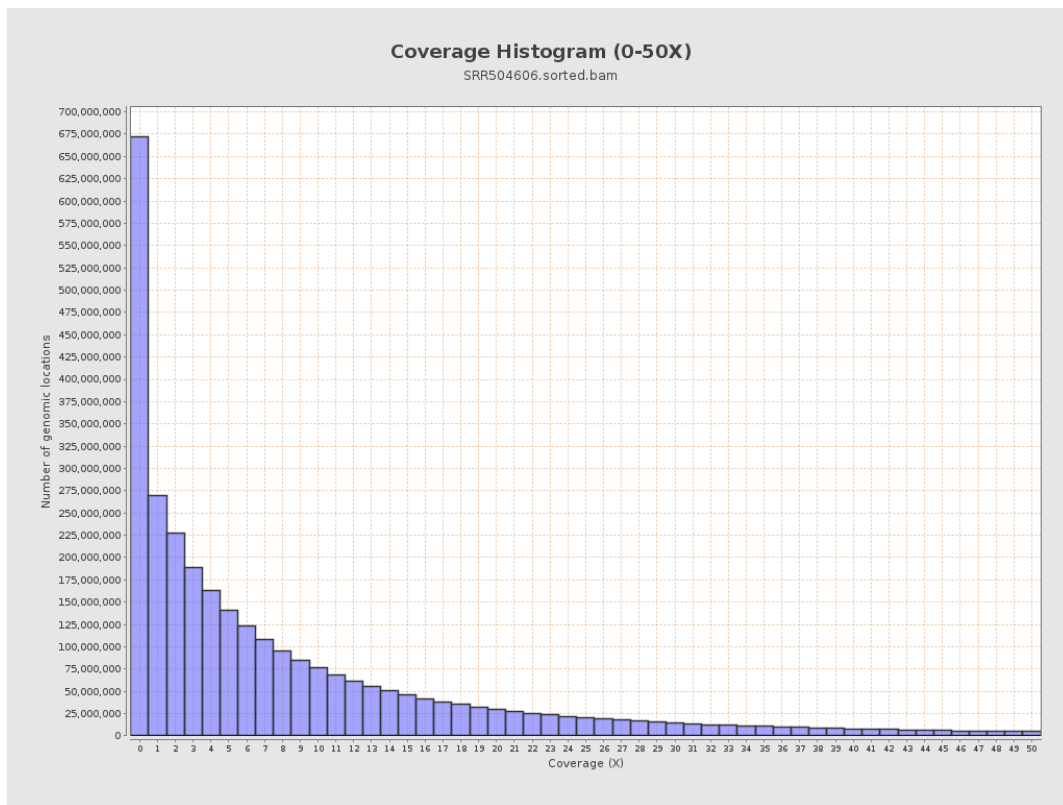
3. Results : Coverage across reference



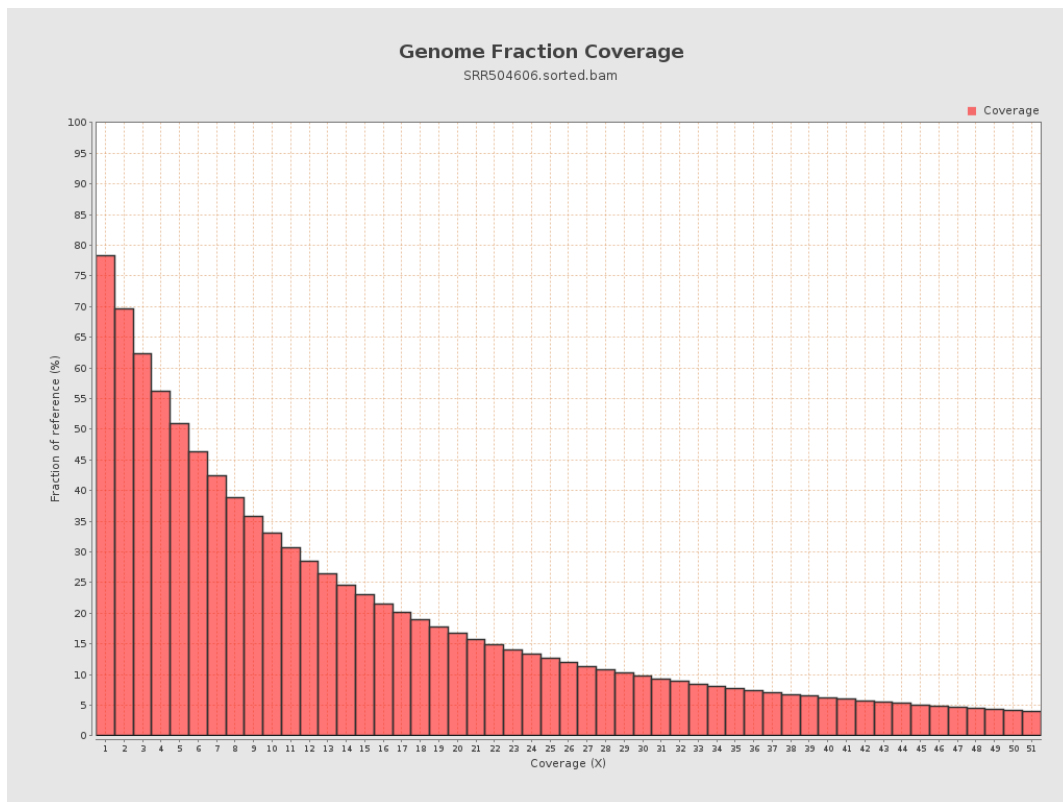
4. Results : Coverage Histogram



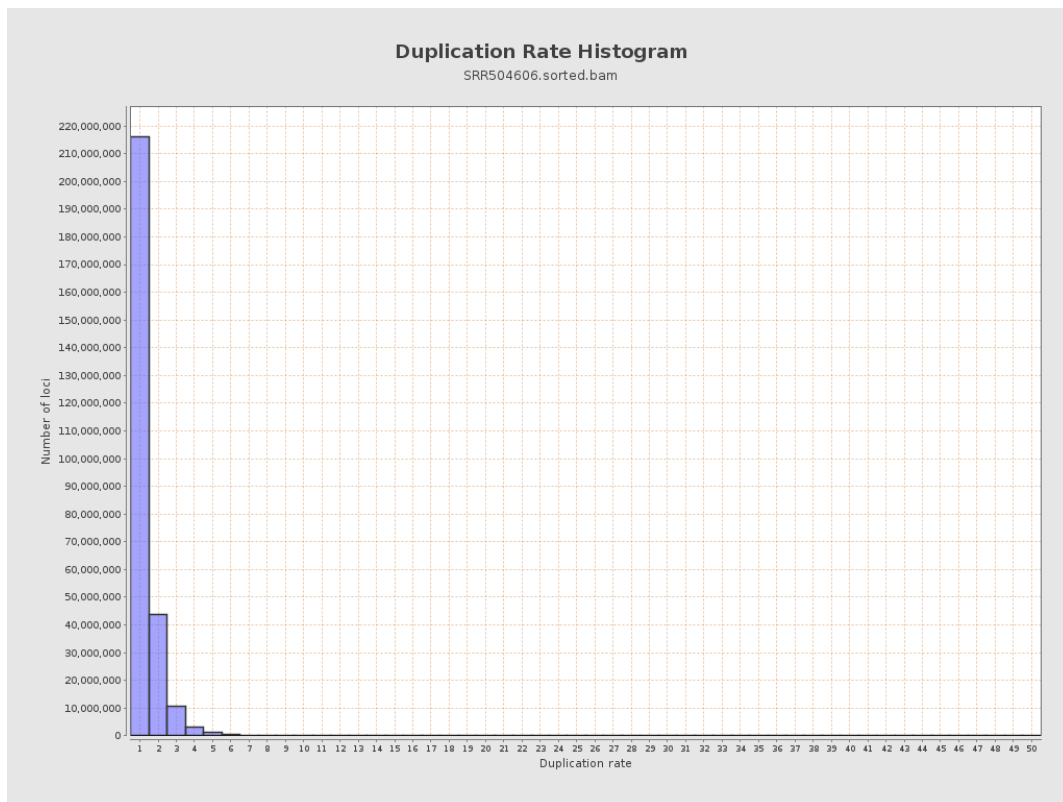
5. Results : Coverage Histogram (0-50X)



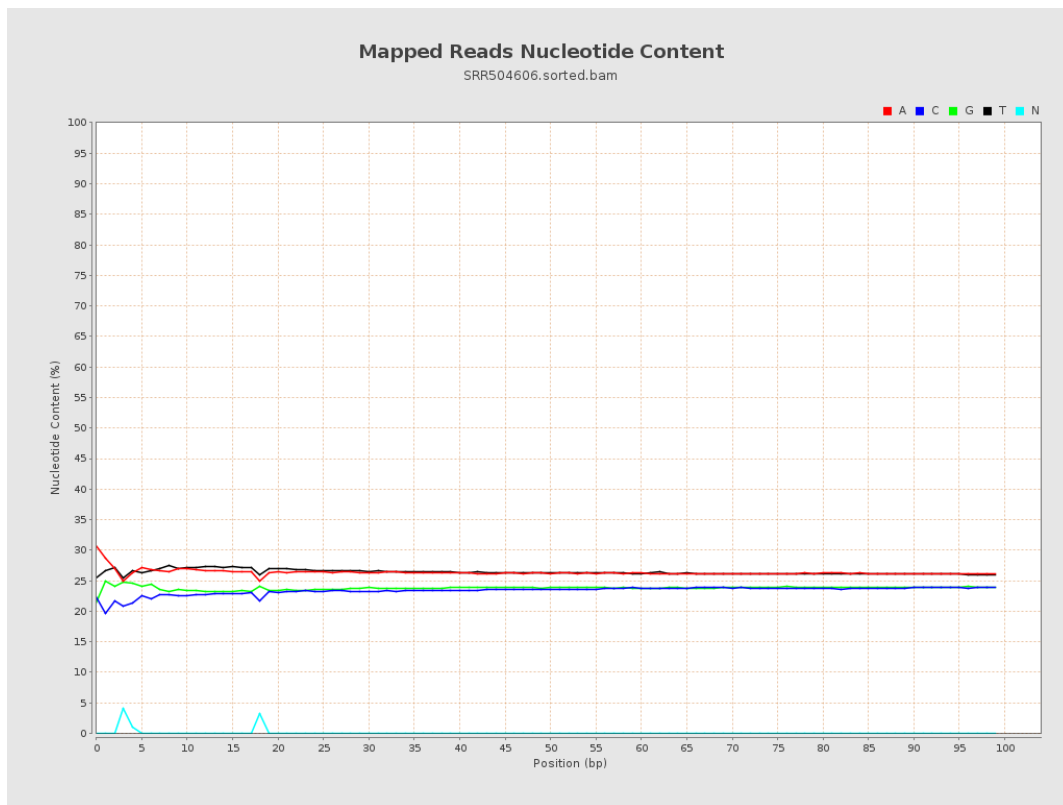
6. Results : Genome Fraction Coverage



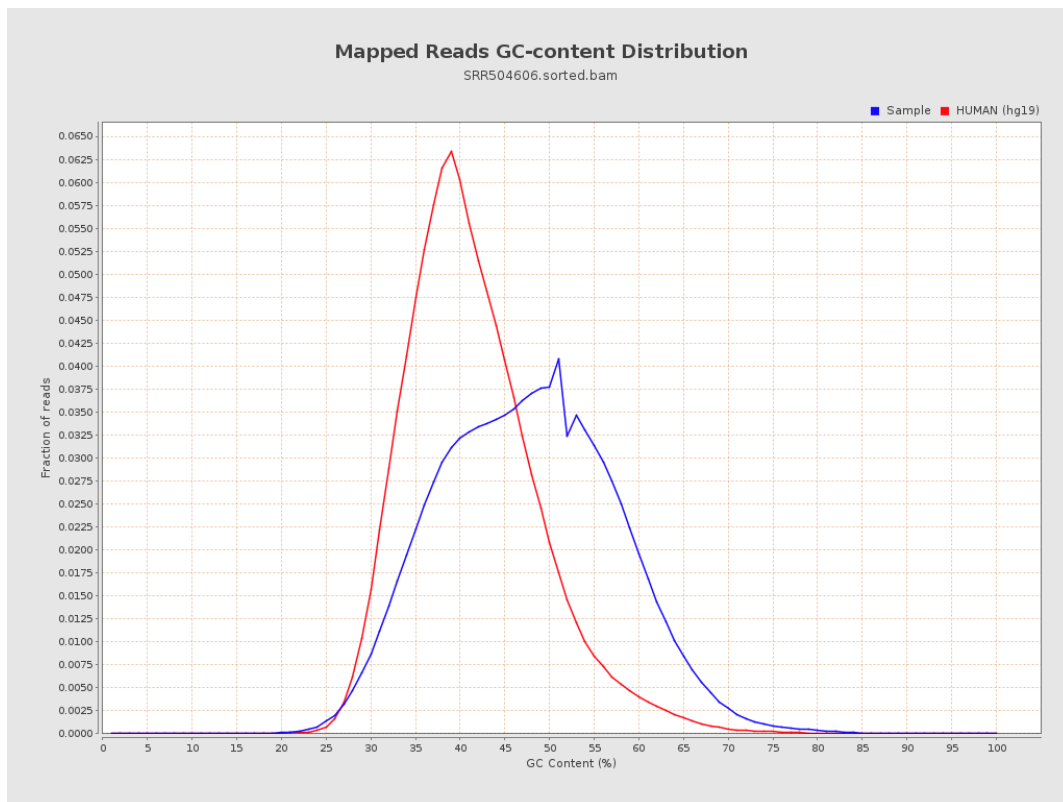
7. Results : Duplication Rate Histogram



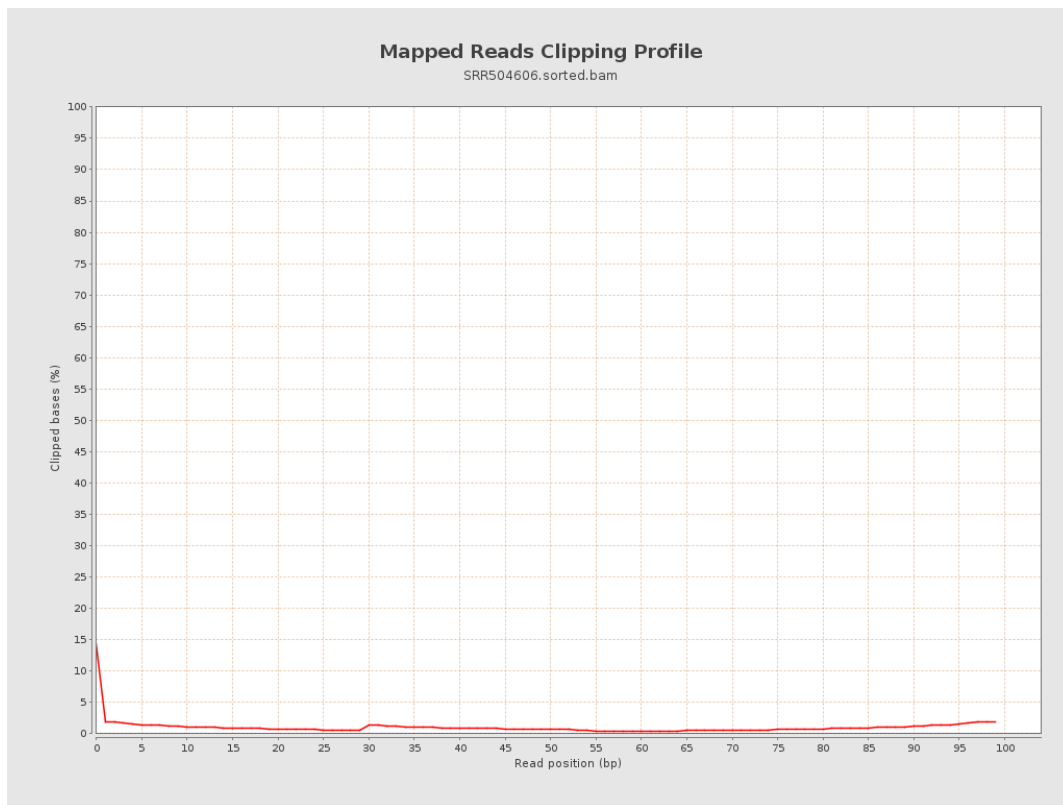
8. Results : Mapped Reads Nucleotide Content



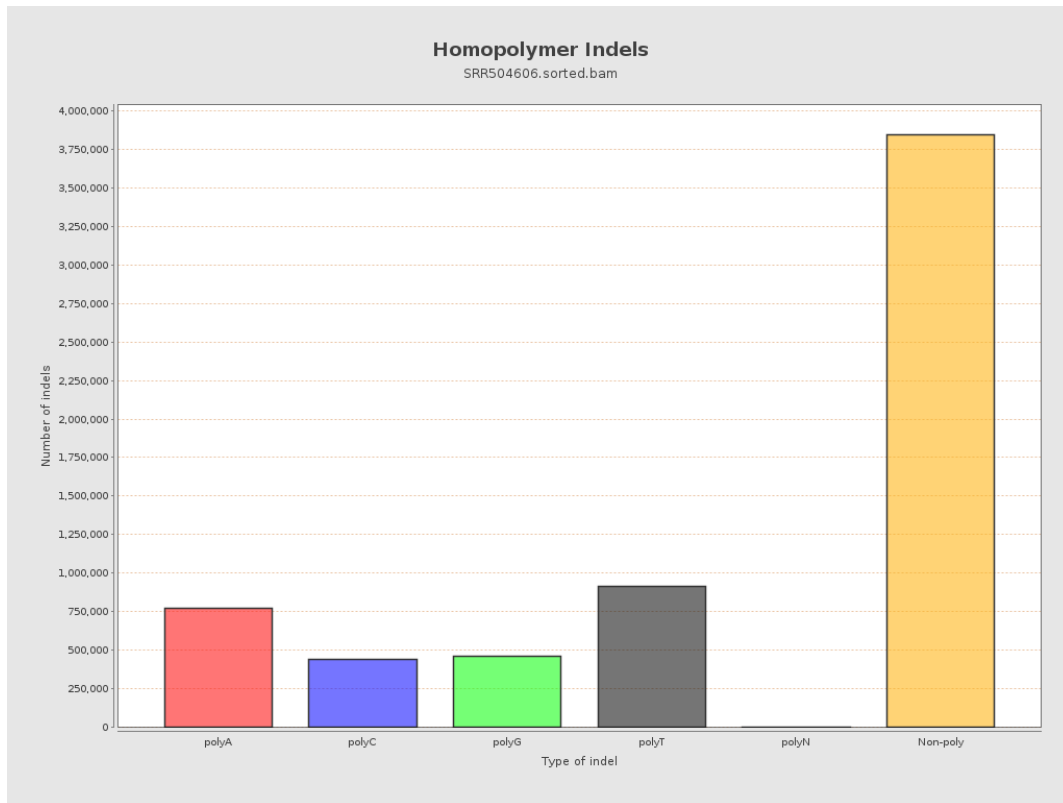
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



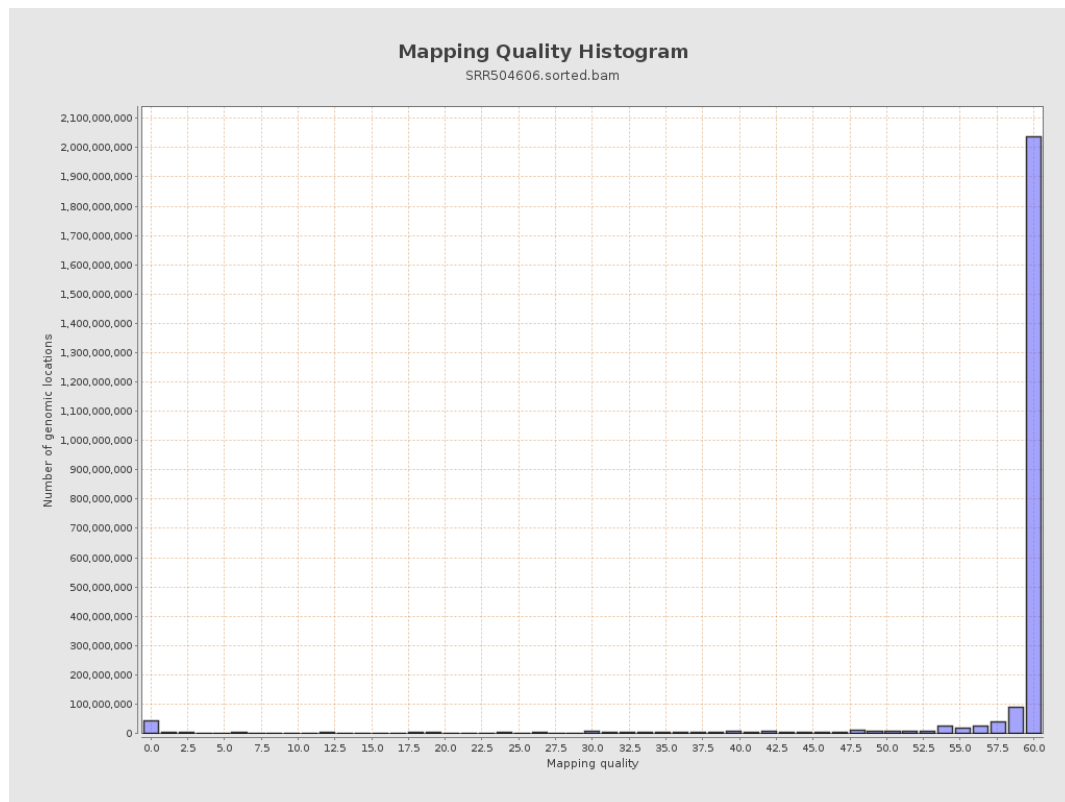
11. Results : Homopolymer Indels



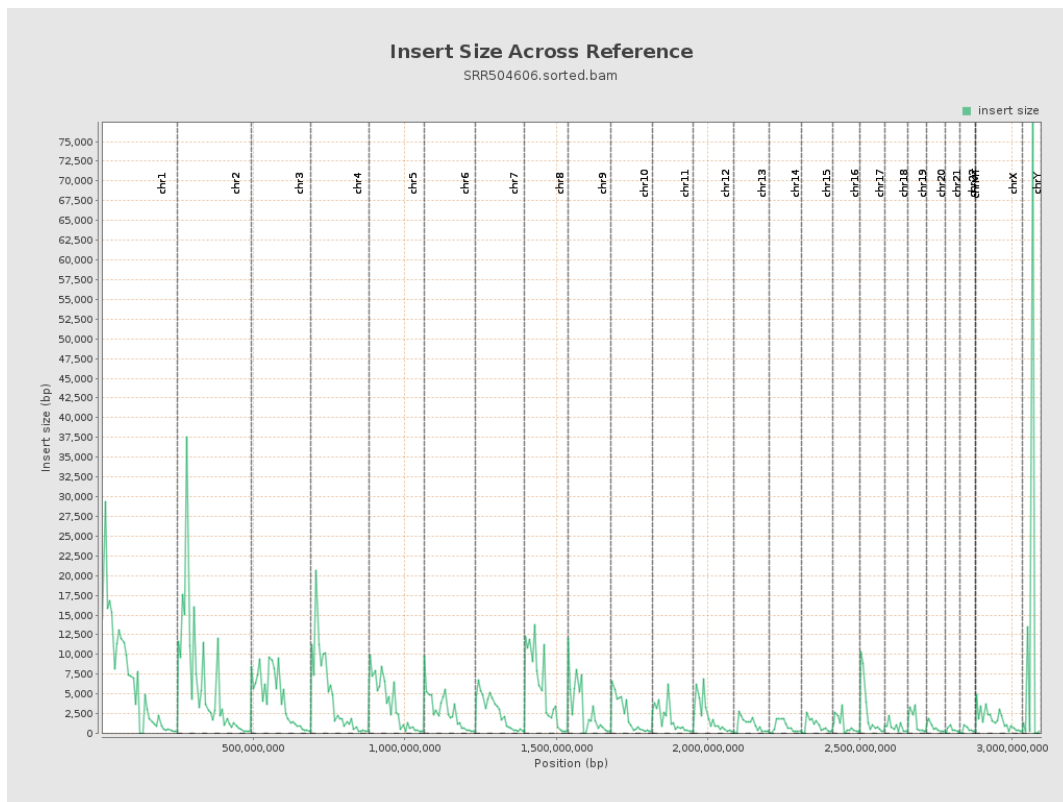
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

