

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 12:24:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504419.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_SRR504419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504419_1.fastq.gz SRR504419_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 12:24:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,055,620
Mapped reads	161,048,624 / 99.38%
Unmapped reads	1,006,996 / 0.62%
Mapped paired reads	161,048,624 / 99.38%
Mapped reads, first in pair	80,575,200 / 49.72%
Mapped reads, second in pair	80,473,424 / 49.66%
Mapped reads, both in pair	160,571,734 / 99.08%
Mapped reads, singletons	476,890 / 0.29%
Secondary alignments	0
Supplementary alignments	2,672,256 / 1.65%
Read min/max/mean length	30 / 100 / 99.67
Duplicated reads (estimated)	81,656,836 / 50.39%
Duplication rate	34.05%
Clipped reads	80,845,547 / 49.89%

2.2. ACGT Content

Number/percentage of A's	4,632,841,592 / 29.98%
Number/percentage of C's	3,070,286,615 / 19.87%
Number/percentage of T's	4,657,348,488 / 30.14%
Number/percentage of G's	3,078,371,464 / 19.92%
Number/percentage of N's	12,136,705 / 0.08%

GC Percentage	39.79%
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2.3. Coverage

Mean	4.9927
Standard Deviation	112.9768

2.4. Mapping Quality

Mean Mapping Quality	50.58
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2.5. Insert size

Mean	65,321.08
Standard Deviation	2,352,314.93
P25/Median/P75	132 / 161 / 193

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	84,354,461
Insertions	1,460,486
Mapped reads with at least one insertion	0.9%
Deletions	3,069,655
Mapped reads with at least one deletion	1.88%
Homopolymer indels	47.8%

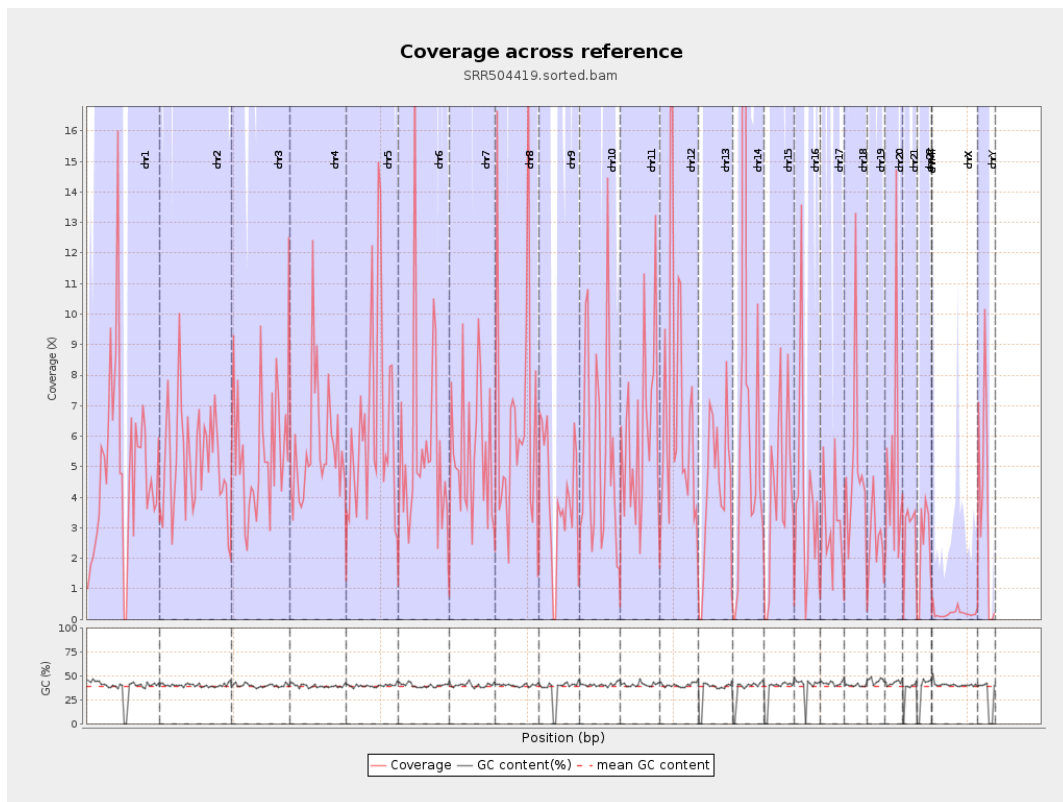
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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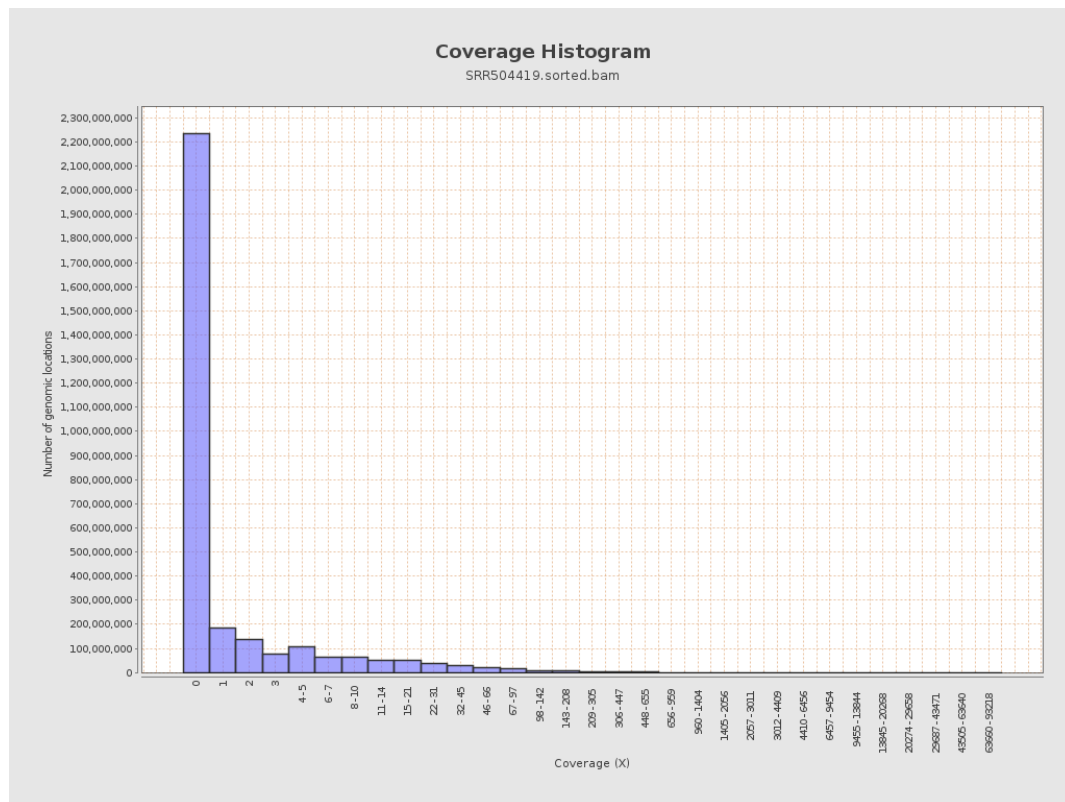
		bases	coverage	deviation
chr1	249250621	1217084526	4.883	49.1108
chr2	243199373	1253861560	5.1557	38.5845
chr3	198022430	1083546312	5.4718	45.3237
chr4	191154276	1073150435	5.6141	37.3634
chr5	180915260	1140800512	6.3057	82.9261
chr6	171115067	954510243	5.5782	71.2134
chr7	159138663	853435990	5.3628	63.2872
chr8	146364022	957460709	6.5416	86.5621
chr9	141213431	544780040	3.8578	28.1073
chr10	135534747	729804679	5.3846	71.913
chr11	135006516	824642620	6.1082	52.7785
chr12	133851895	921967069	6.888	116.1198
chr13	115169878	503000332	4.3675	40.5589
chr14	107349540	1027642988	9.5729	515.698
chr15	102531392	429163644	4.1857	34.1672
chr16	90354753	331794175	3.6721	55.3385
chr17	81195210	236070497	2.9074	24.8966
chr18	78077248	396371752	5.0767	72.785
chr19	59128983	158067999	2.6733	43.9994
chr20	63025520	312523240	4.9587	116.6864
chr21	48129895	138324205	2.874	19.6355
chr22	51304566	117274473	2.2858	33.3674
chrMT	16571	1855	0.1119	0.7593
chrX	155270560	31690443	0.2041	4.2055

chrY	59373566	218975365	3.6881	79.7289
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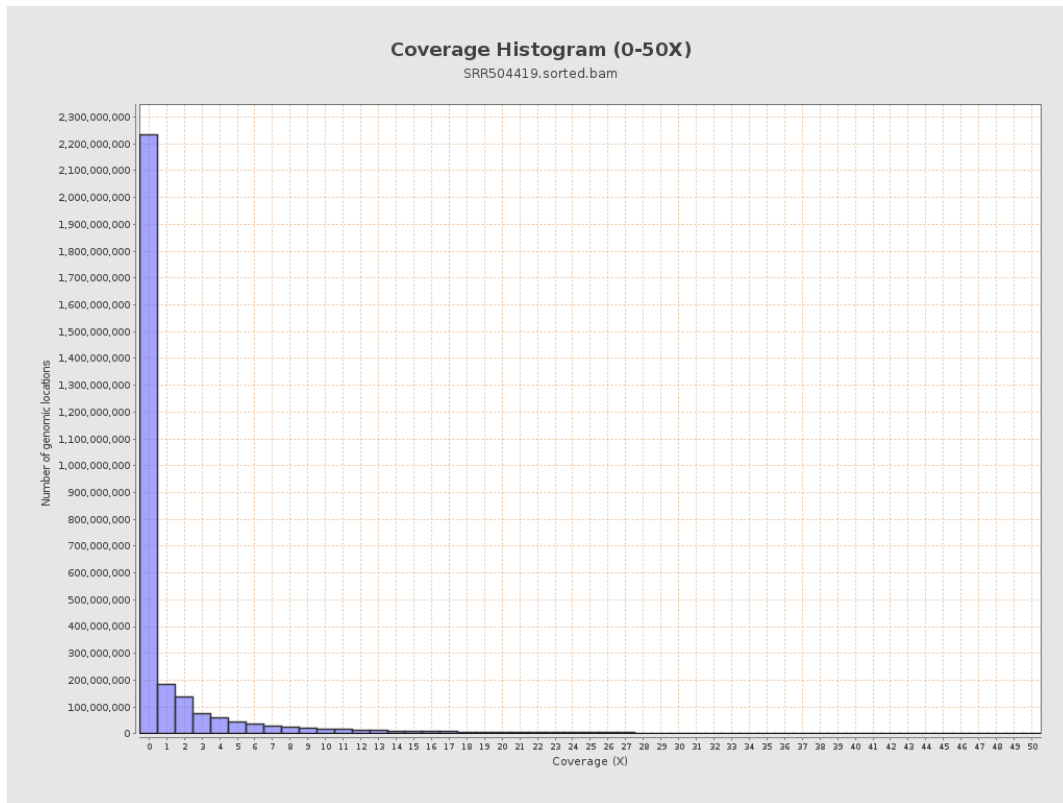
3. Results : Coverage across reference



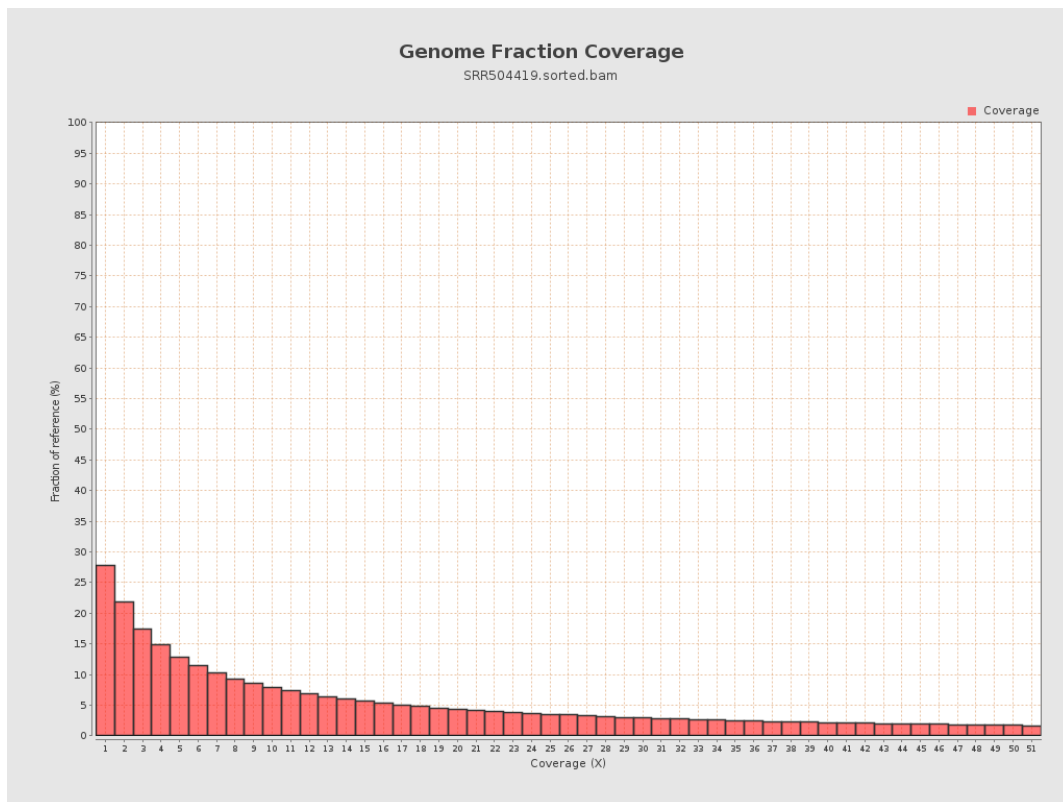
4. Results : Coverage Histogram



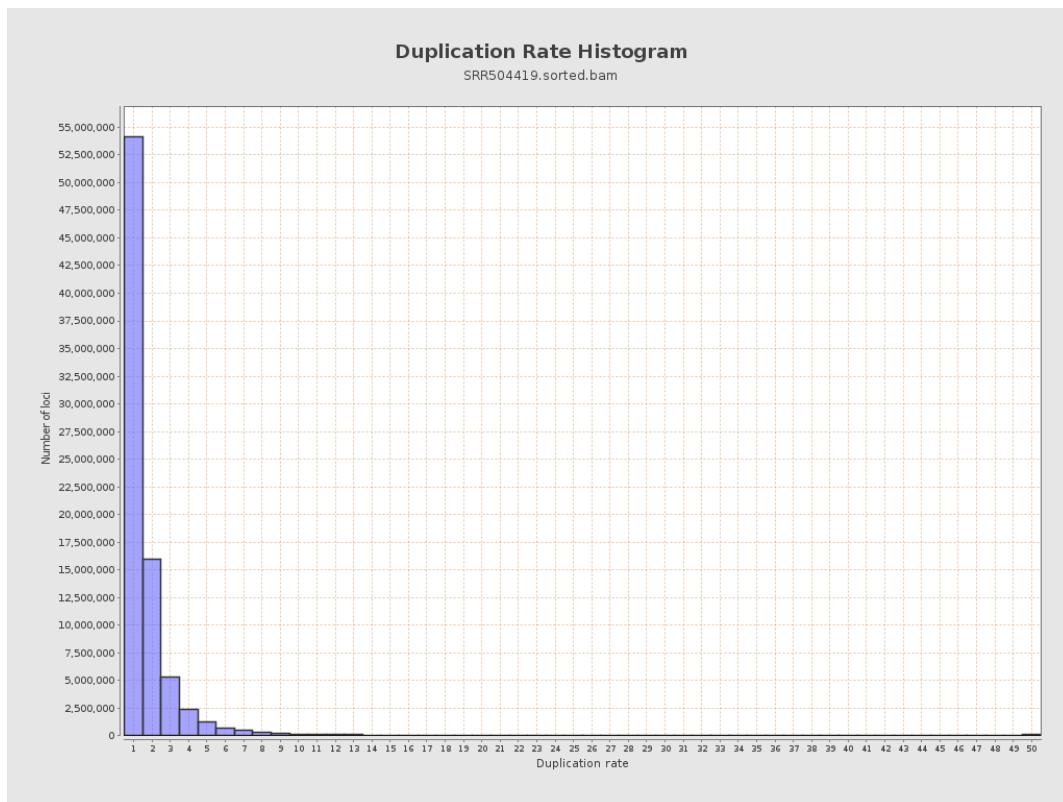
5. Results : Coverage Histogram (0-50X)



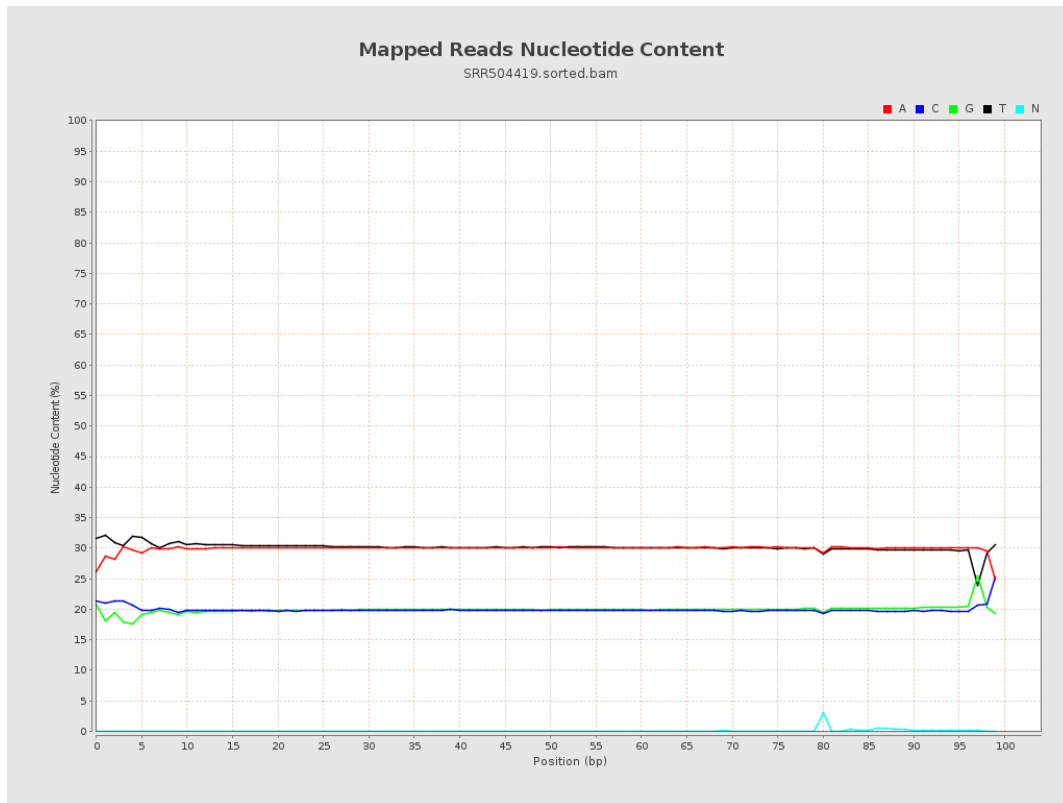
6. Results : Genome Fraction Coverage



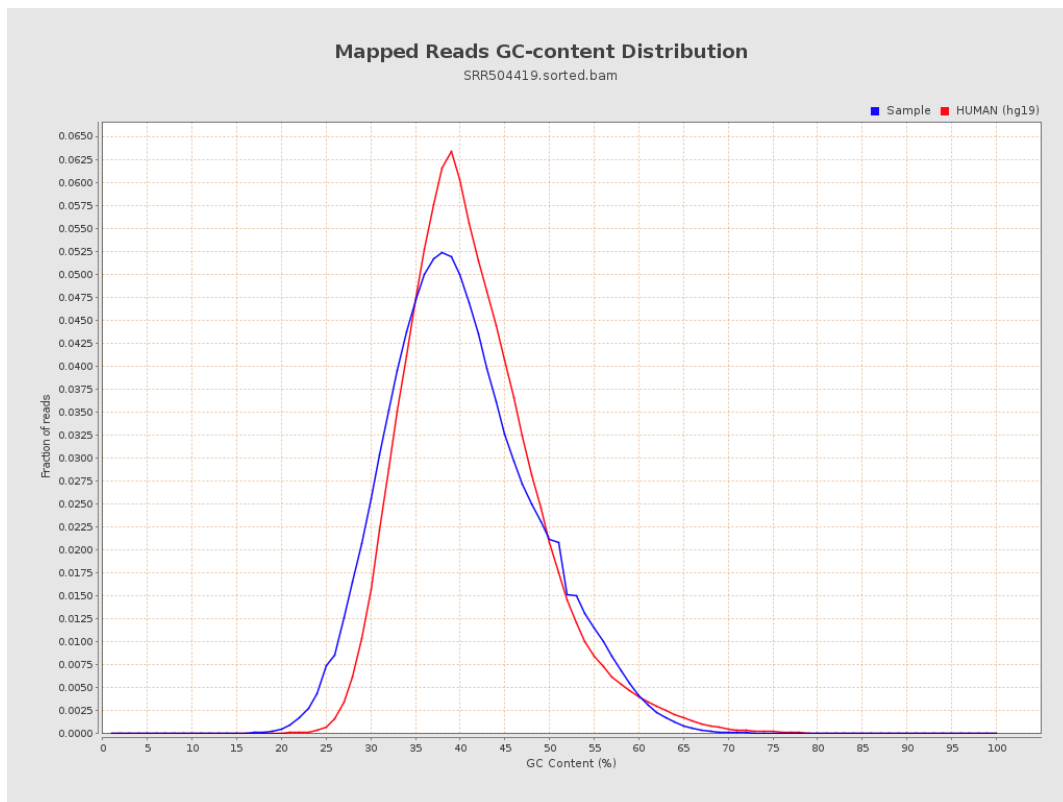
7. Results : Duplication Rate Histogram



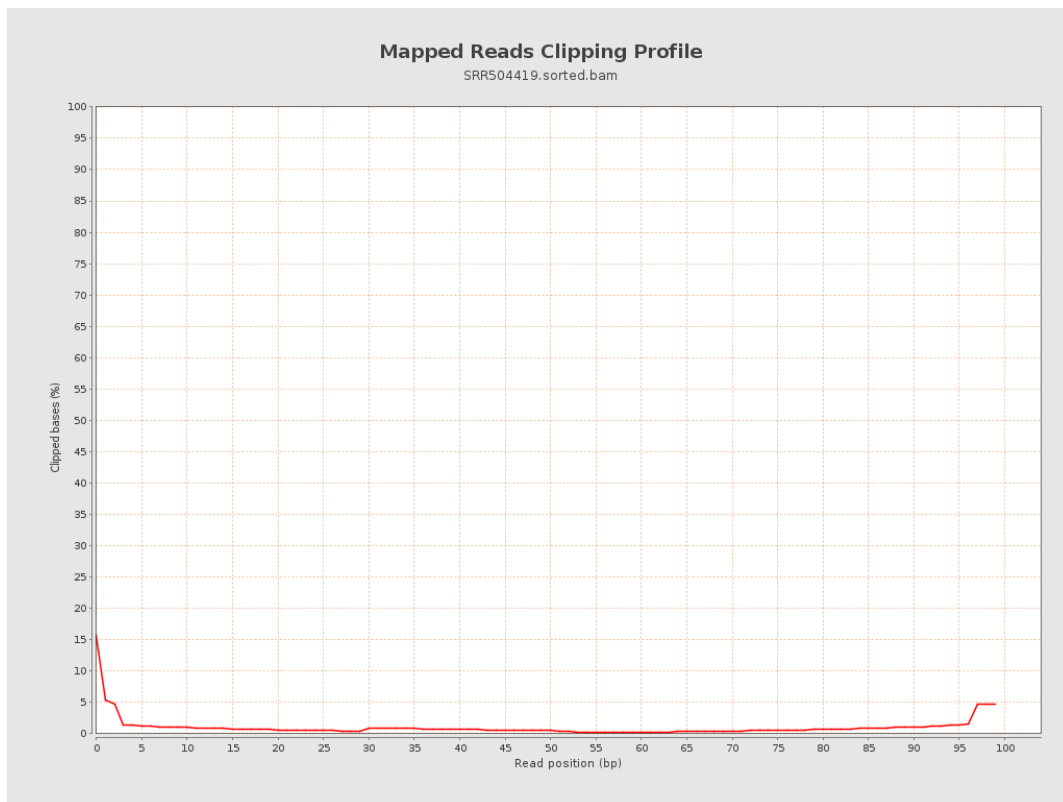
8. Results : Mapped Reads Nucleotide Content



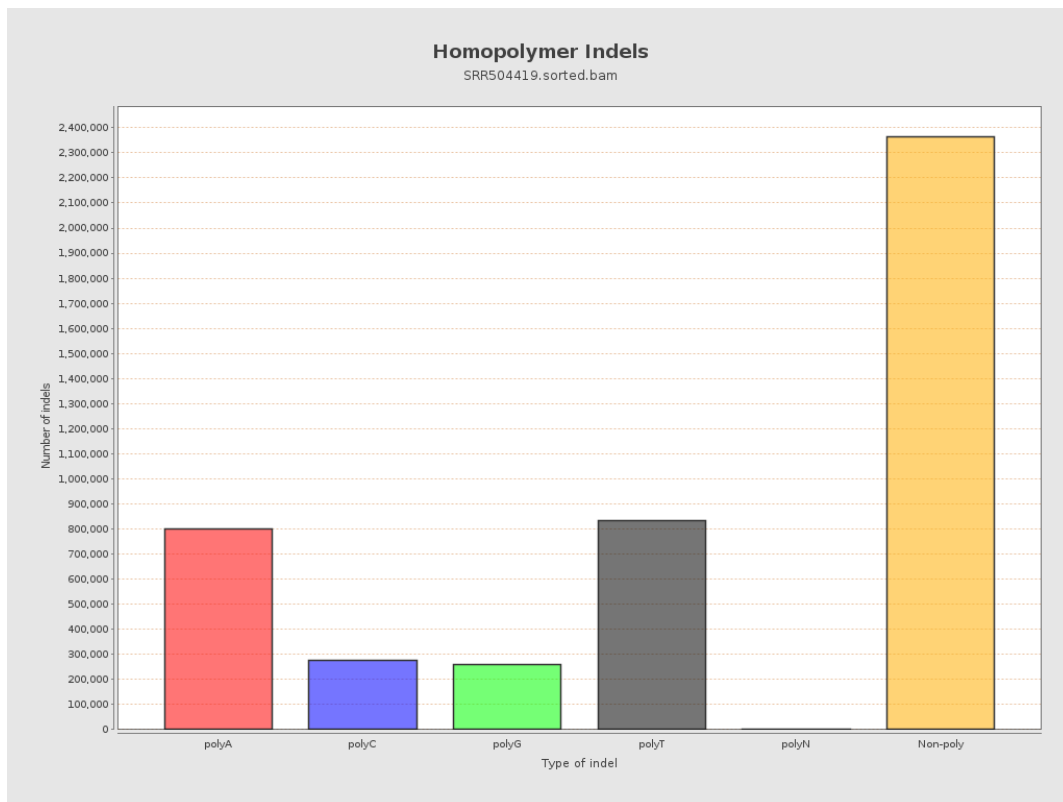
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



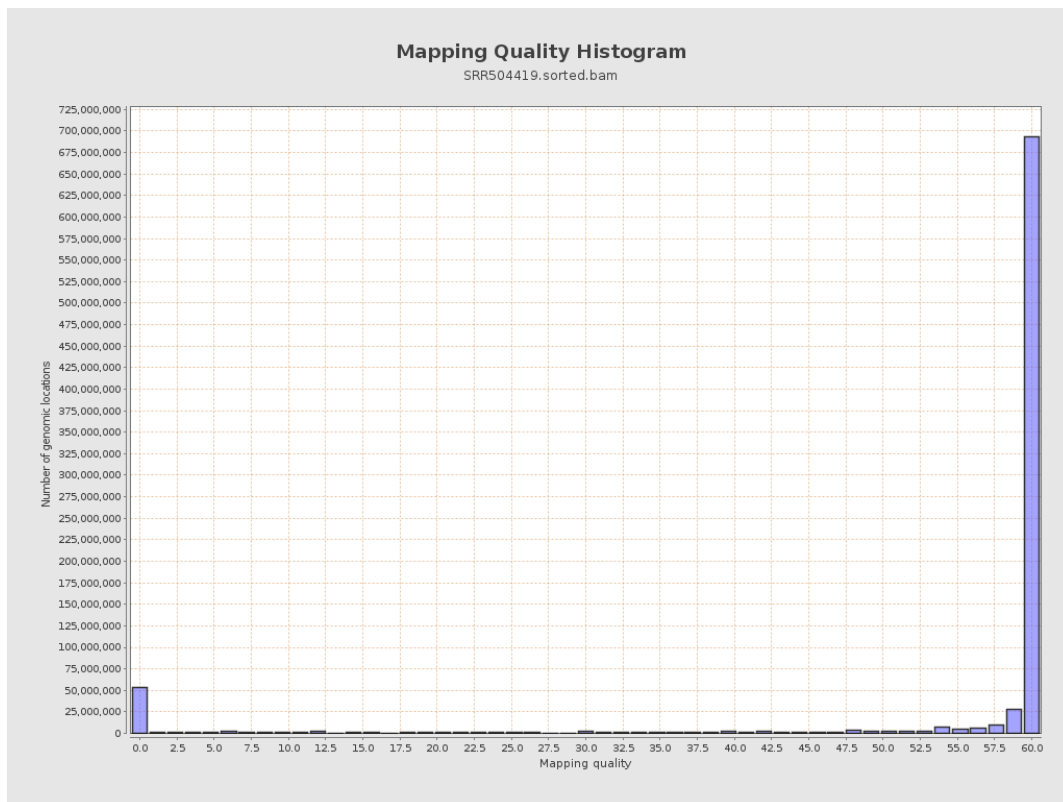
11. Results : Homopolymer Indels



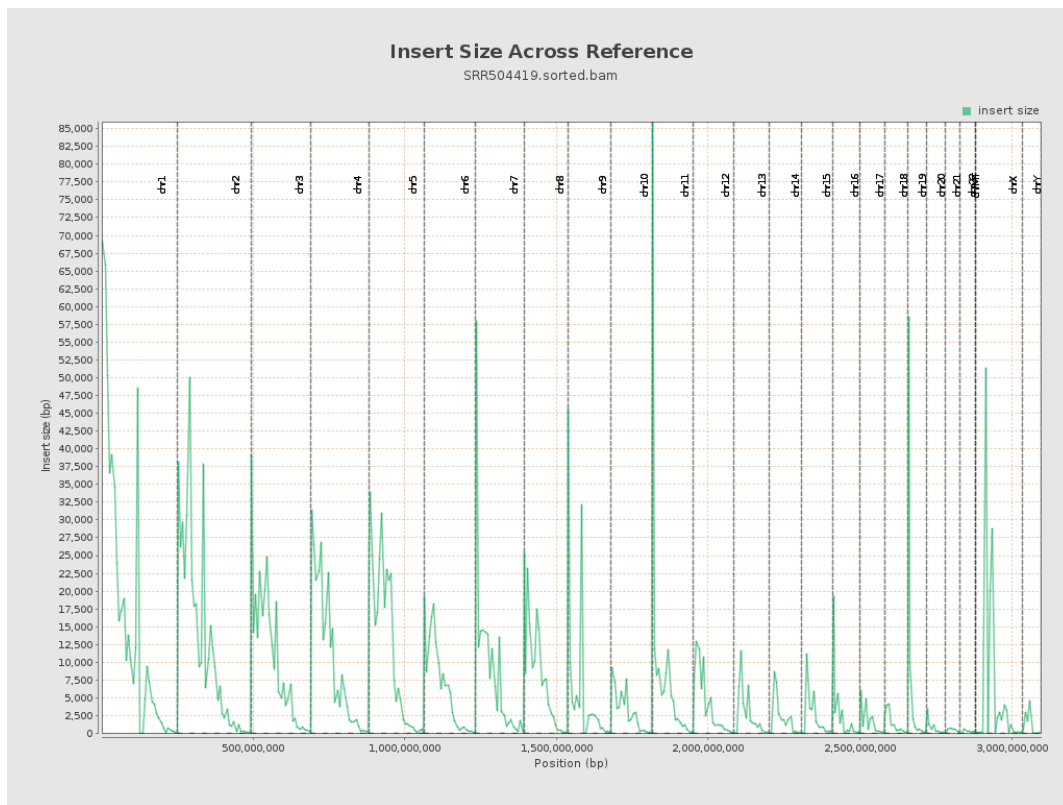
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

