

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 03:46:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504664.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_SRR504664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504664_1.fastq.gz SRR504664_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 03:46:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	217,581,292
Mapped reads	216,714,616 / 99.6%
Unmapped reads	866,676 / 0.4%
Mapped paired reads	216,714,616 / 99.6%
Mapped reads, first in pair	108,503,001 / 49.87%
Mapped reads, second in pair	108,211,615 / 49.73%
Mapped reads, both in pair	216,332,246 / 99.43%
Mapped reads, singletons	382,370 / 0.18%
Secondary alignments	0
Supplementary alignments	2,932,065 / 1.35%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	134,869,804 / 61.99%
Duplication rate	35.13%
Clipped reads	69,305,774 / 31.85%

2.2. ACGT Content

Number/percentage of A's	6,076,612,648 / 30.08%
Number/percentage of C's	3,999,504,634 / 19.8%
Number/percentage of T's	6,145,727,342 / 30.43%
Number/percentage of G's	3,960,365,811 / 19.61%
Number/percentage of N's	16,696,052 / 0.08%

GC Percentage	39.41%
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2.3. Coverage

Mean	6.5265
Standard Deviation	831.1217

2.4. Mapping Quality

Mean Mapping Quality	51.33
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2.5. Insert size

Mean	37,306.69
Standard Deviation	1,808,533.37
P25/Median/P75	96 / 146 / 216

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	106,119,598
Insertions	2,259,361
Mapped reads with at least one insertion	1.03%
Deletions	2,835,111
Mapped reads with at least one deletion	1.29%
Homopolymer indels	50.2%

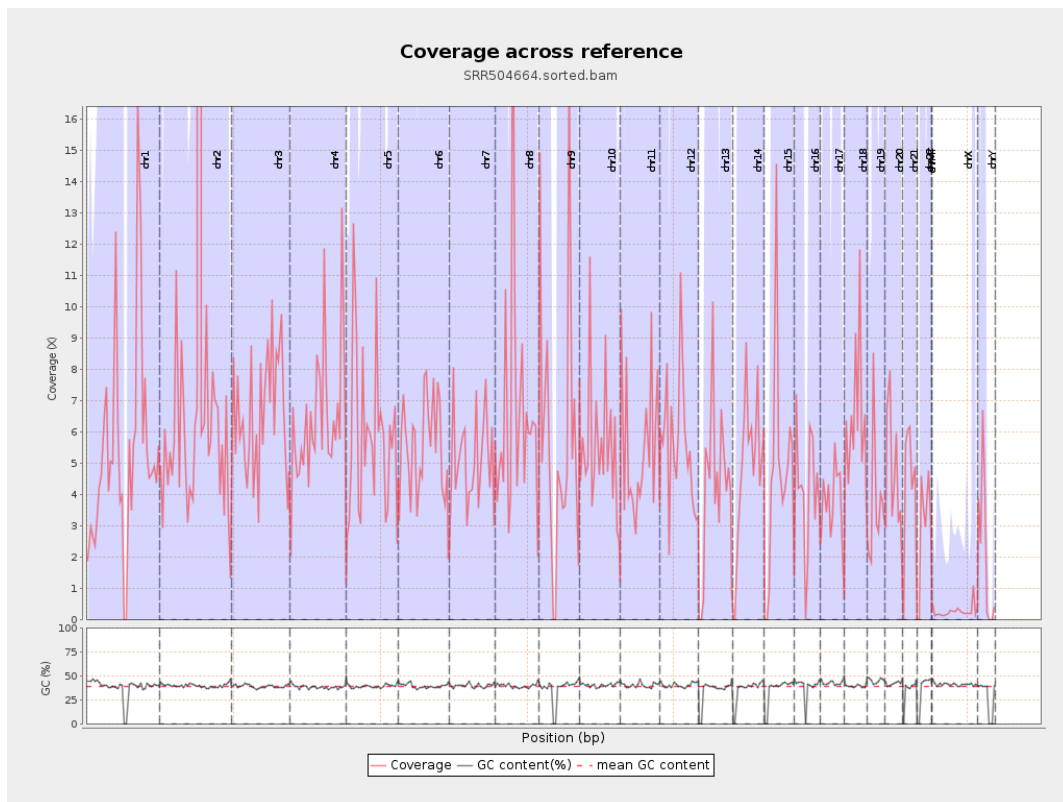
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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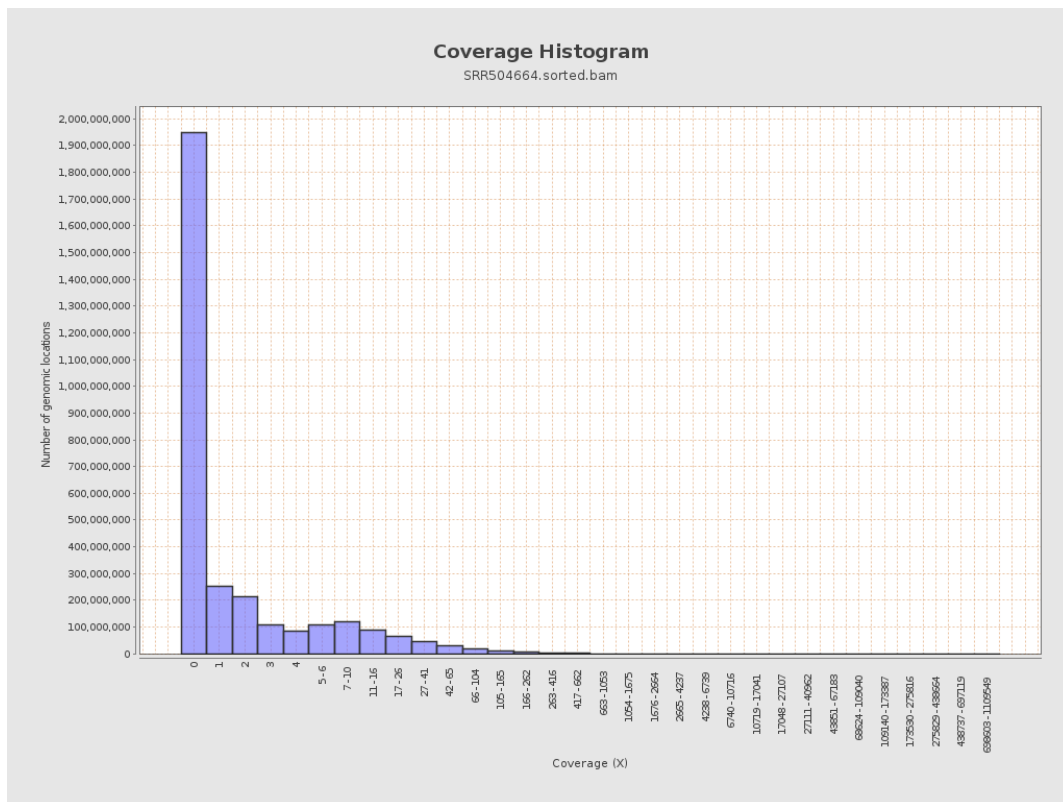
		bases	coverage	deviation
chr1	249250621	1318322200	5.2891	57.7257
chr2	243199373	5898905818	24.2554	2,961.9819
chr3	198022430	1299118138	6.5605	37.3143
chr4	191154276	1220604552	6.3854	43.0027
chr5	180915260	1029924576	5.6929	36.7215
chr6	171115067	957304511	5.5945	28.1667
chr7	159138663	812584978	5.1061	27.7688
chr8	146364022	959222728	6.5537	62.2425
chr9	141213431	782973877	5.5446	62.6796
chr10	135534747	747166810	5.5127	33.4194
chr11	135006516	734842450	5.443	33.2714
chr12	133851895	758203840	5.6645	27.7457
chr13	115169878	483824285	4.201	21.7243
chr14	107349540	524838967	4.8891	28.9794
chr15	102531392	467782537	4.5623	72.0573
chr16	90354753	356387357	3.9443	24.7996
chr17	81195210	298676015	3.6785	16.7119
chr18	78077248	511290402	6.5485	36.7309
chr19	59128983	215308389	3.6413	44.258
chr20	63025520	288310264	4.5745	25.3764
chr21	48129895	217998623	4.5294	31.5526
chr22	51304566	150992037	2.9431	28.1609
chrMT	16571	5190	0.3132	1.5651
chrX	155270560	40818564	0.2629	10.6899

chrY	59373566	128694568	2.1675	19.0084
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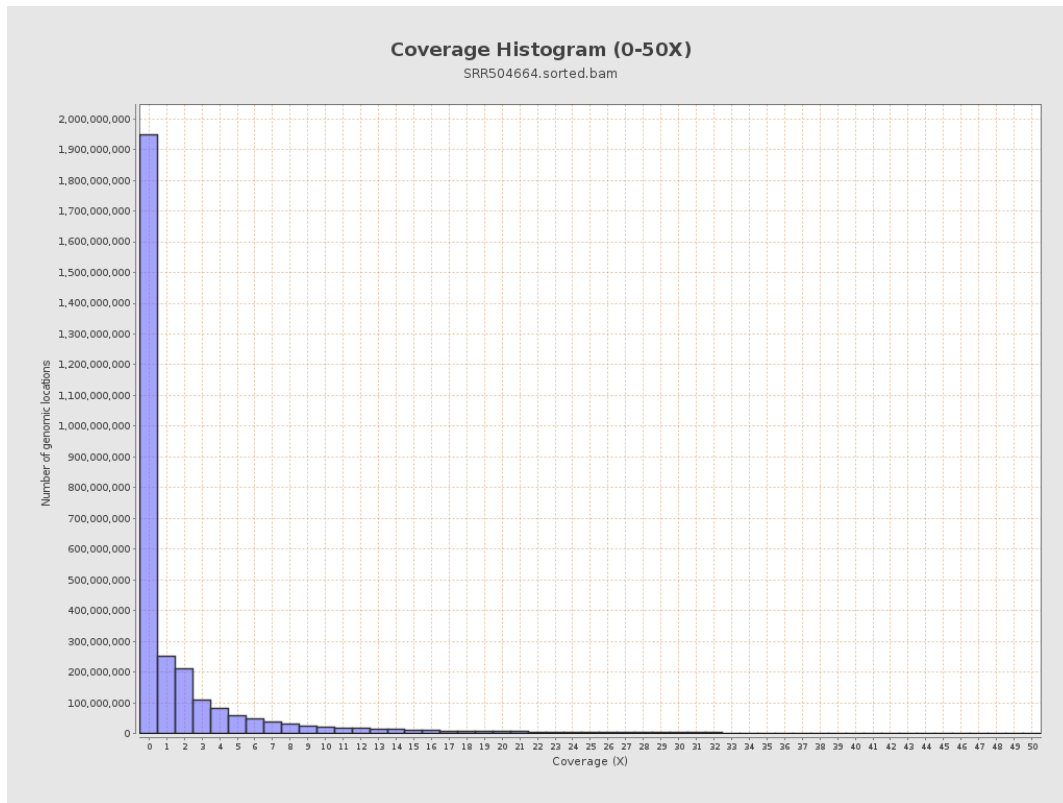
3. Results : Coverage across reference



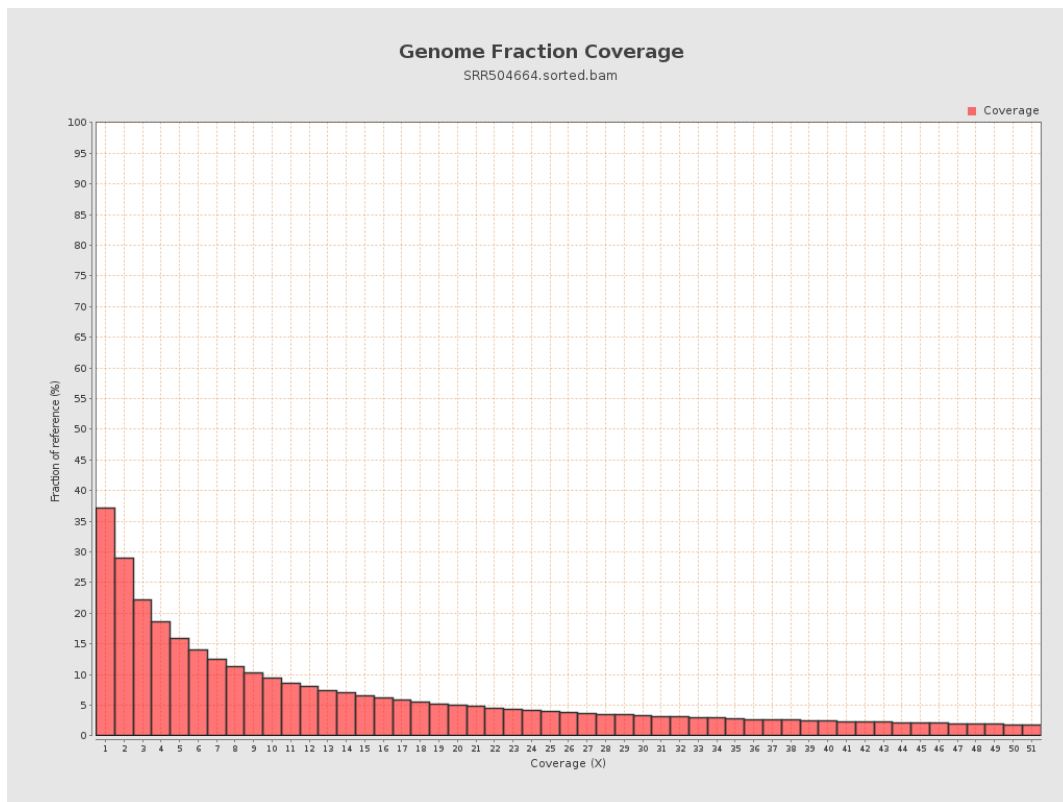
4. Results : Coverage Histogram



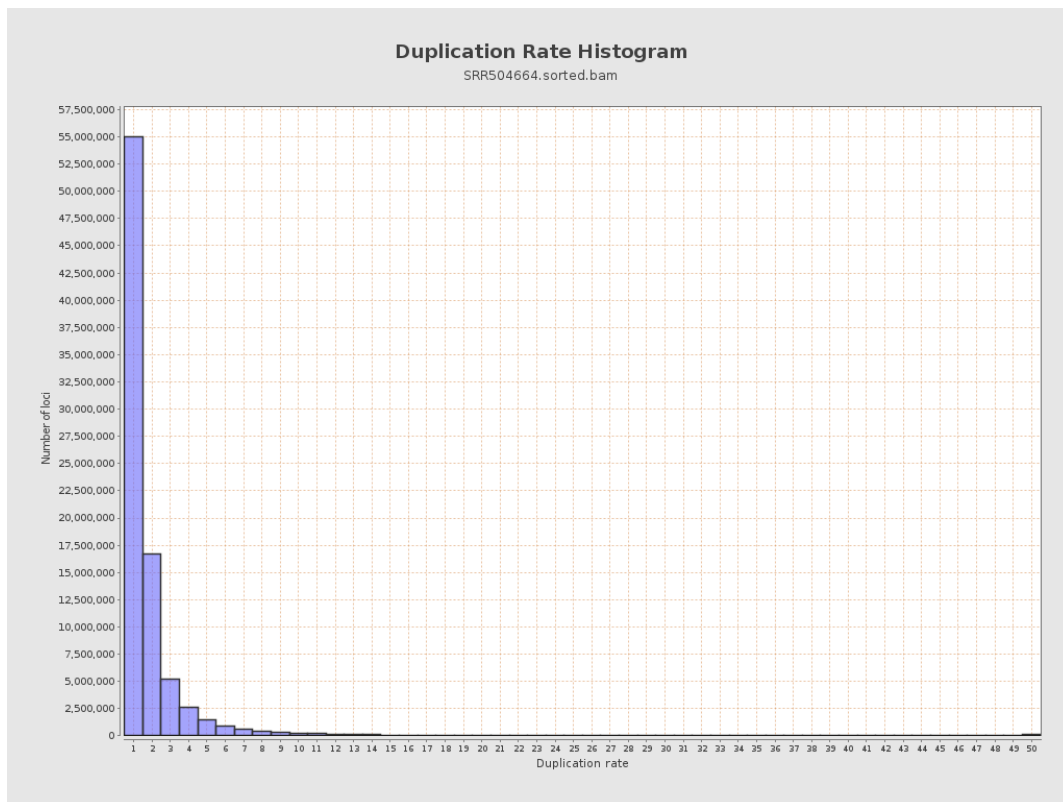
5. Results : Coverage Histogram (0-50X)



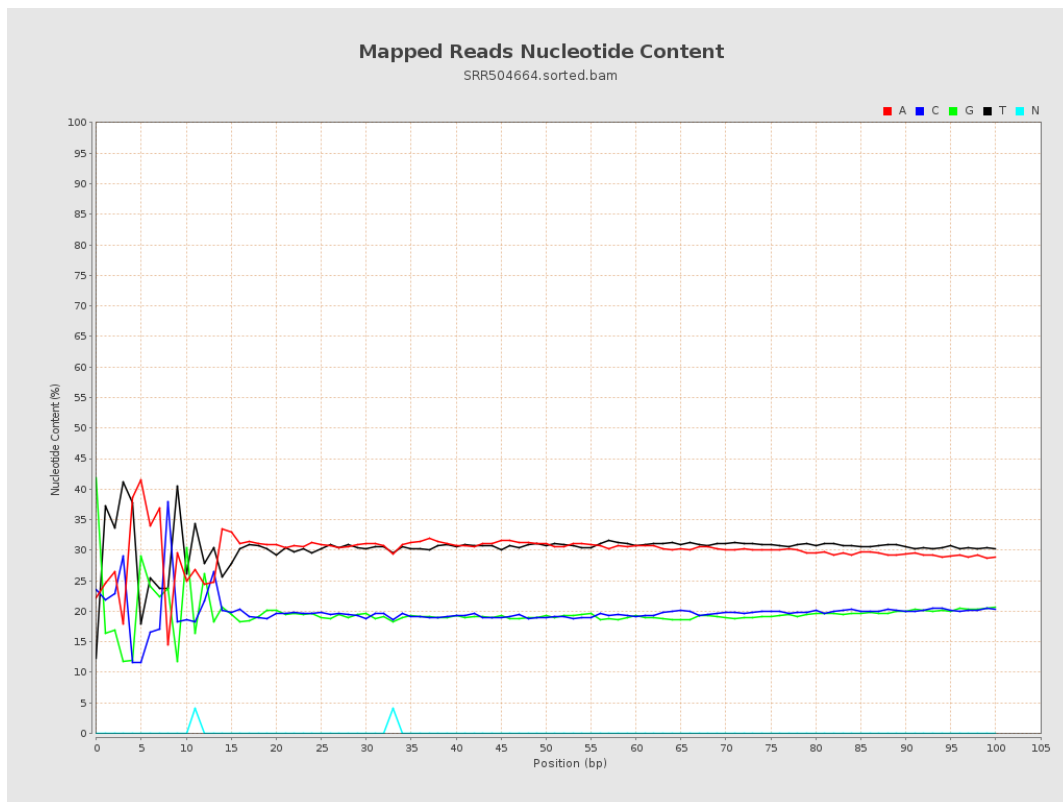
6. Results : Genome Fraction Coverage



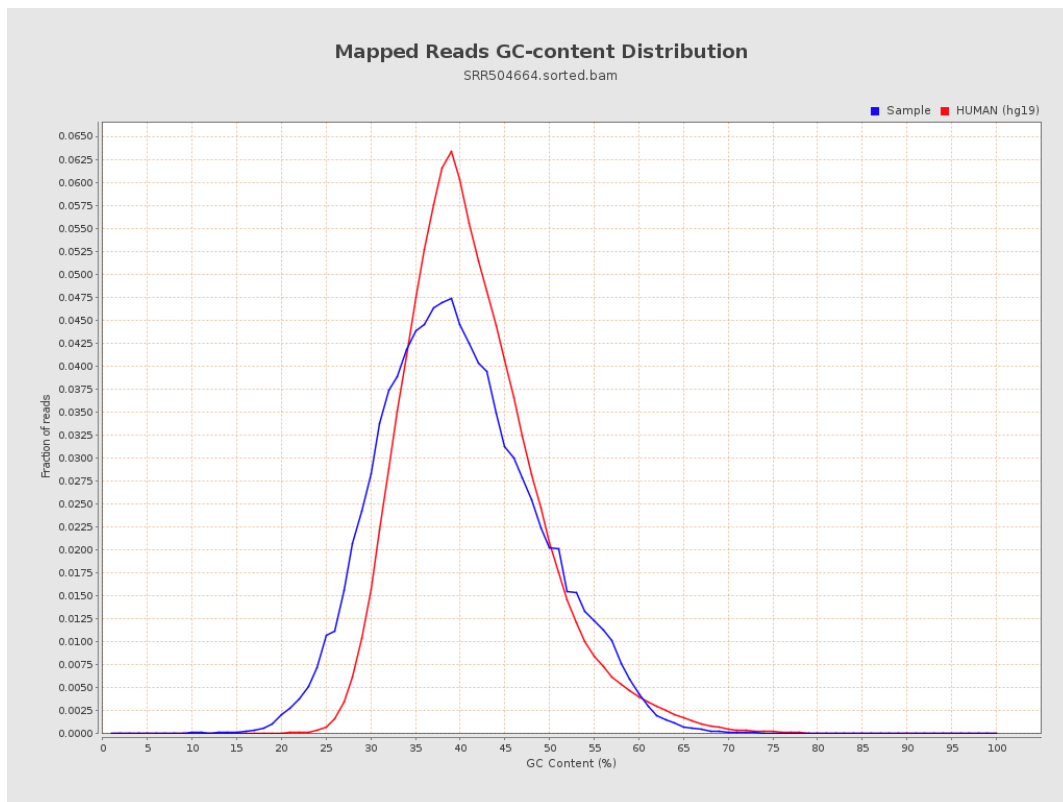
7. Results : Duplication Rate Histogram



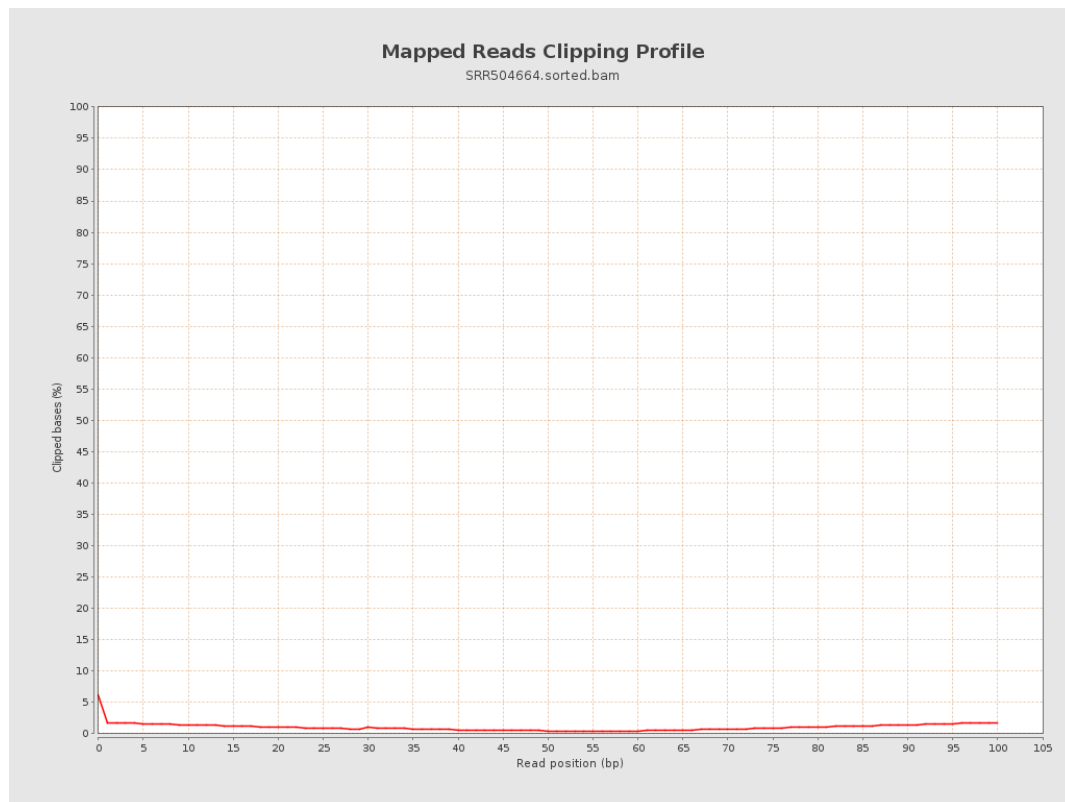
8. Results : Mapped Reads Nucleotide Content



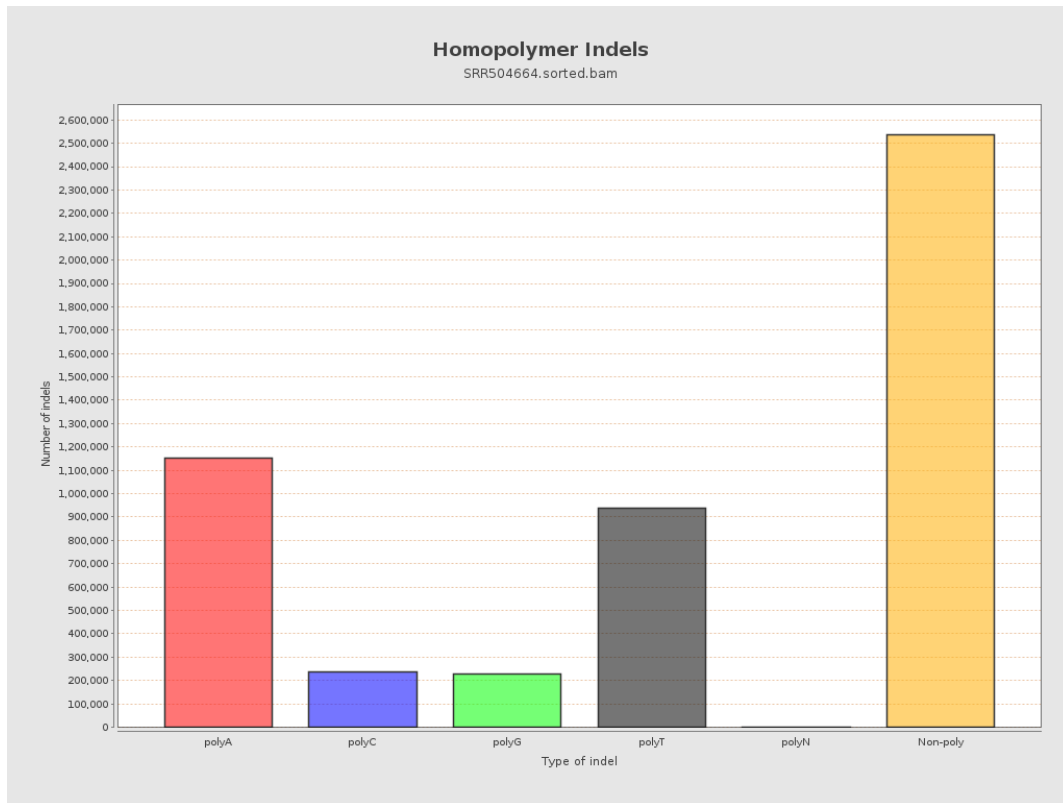
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



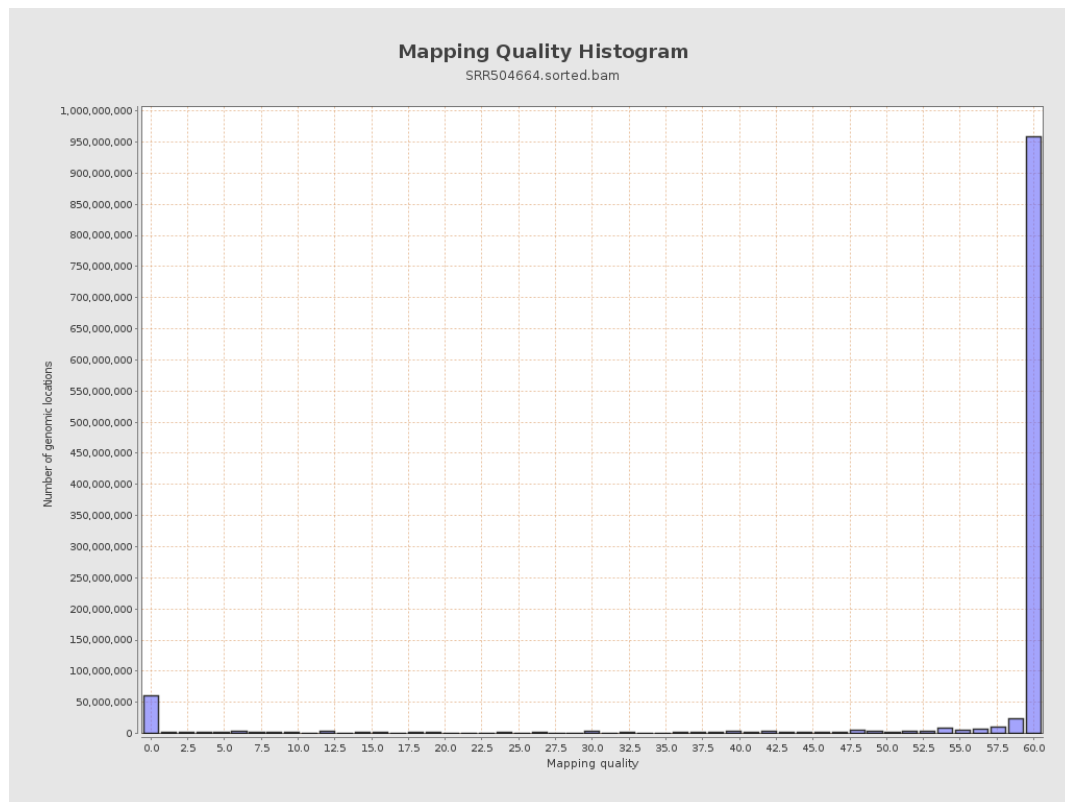
11. Results : Homopolymer Indels



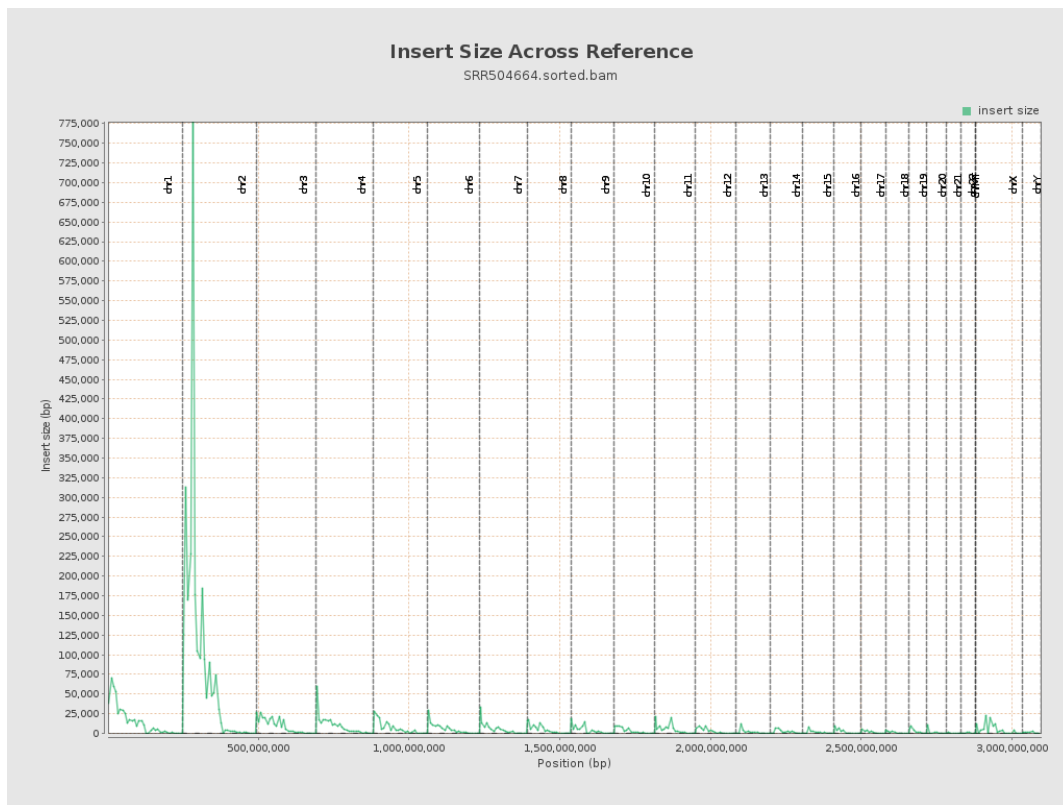
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

