

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 00:33:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504671.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_SRR504671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504671_1.fastq.gz SRR504671_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 00:33:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	214,985,014
Mapped reads	213,906,381 / 99.5%
Unmapped reads	1,078,633 / 0.5%
Mapped paired reads	213,906,381 / 99.5%
Mapped reads, first in pair	107,090,062 / 49.81%
Mapped reads, second in pair	106,816,319 / 49.69%
Mapped reads, both in pair	213,526,252 / 99.32%
Mapped reads, singletons	380,129 / 0.18%
Secondary alignments	0
Supplementary alignments	2,754,440 / 1.28%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	118,172,268 / 54.97%
Duplication rate	33.57%
Clipped reads	69,731,825 / 32.44%

2.2. ACGT Content

Number/percentage of A's	5,973,042,410 / 30.05%
Number/percentage of C's	3,936,035,827 / 19.8%
Number/percentage of T's	6,054,330,518 / 30.46%
Number/percentage of G's	3,894,489,676 / 19.6%
Number/percentage of N's	16,416,745 / 0.08%

GC Percentage	39.4%
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2.3. Coverage

Mean	6.4216
Standard Deviation	806.64

2.4. Mapping Quality

Mean Mapping Quality	53.15
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2.5. Insert size

Mean	28,346.61
Standard Deviation	1,573,557.69
P25/Median/P75	94 / 143 / 215

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	102,712,131
Insertions	2,189,138
Mapped reads with at least one insertion	1.01%
Deletions	2,680,827
Mapped reads with at least one deletion	1.23%
Homopolymer indels	50.37%

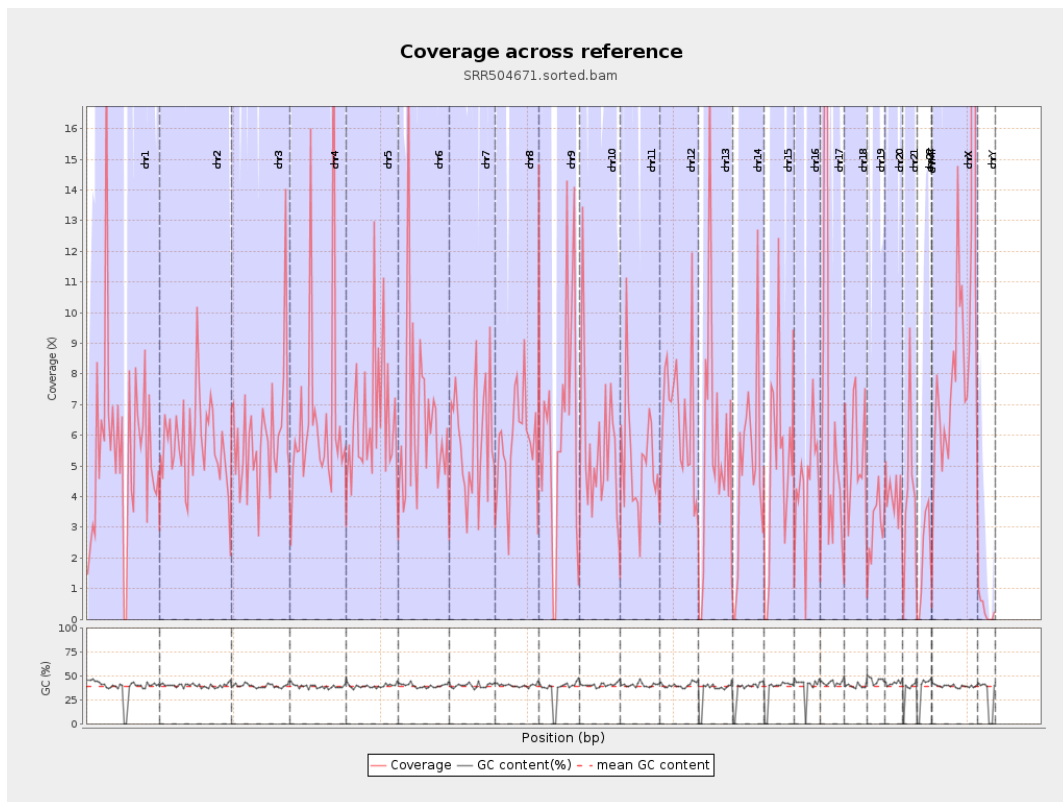
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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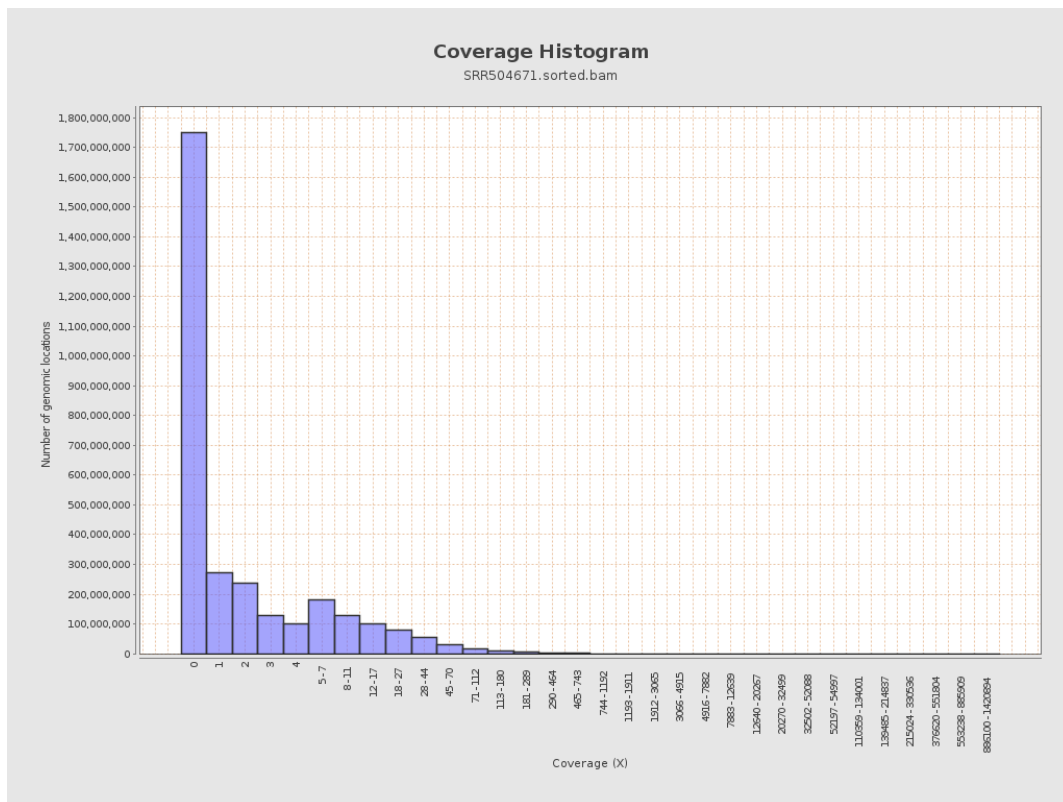
		bases	coverage	deviation
chr1	249250621	1369429340	5.4942	79.5029
chr2	243199373	1396755881	5.7433	33.2505
chr3	198022430	1187188309	5.9952	58.2308
chr4	191154276	1273623529	6.6628	109.4121
chr5	180915260	1159426138	6.4087	38.4819
chr6	171115067	1103417781	6.4484	66.0918
chr7	159138663	925885133	5.8181	32.295
chr8	146364022	854048723	5.8351	20.8126
chr9	141213431	871908948	6.1744	77.3325
chr10	135534747	751676506	5.546	85.2352
chr11	135006516	703373961	5.2099	30.5301
chr12	133851895	871944148	6.5142	71.7438
chr13	115169878	645347154	5.6034	100.803
chr14	107349540	525489580	4.8951	33.1864
chr15	102531392	515329430	5.0261	36.9503
chr16	90354753	393285123	4.3527	21.5332
chr17	81195210	573497187	7.0632	306.433
chr18	78077248	427548251	5.476	27.3626
chr19	59128983	177944480	3.0094	15.0339
chr20	63025520	251647149	3.9928	15.5734
chr21	48129895	207033890	4.3016	25.8271
chr22	51304566	101595839	1.9802	7.459
chrMT	16571	6185	0.3732	2.5929
chrX	155270560	3574176066	23.019	3,585.6624

chrY	59373566	17767872	0.2993	4.0557
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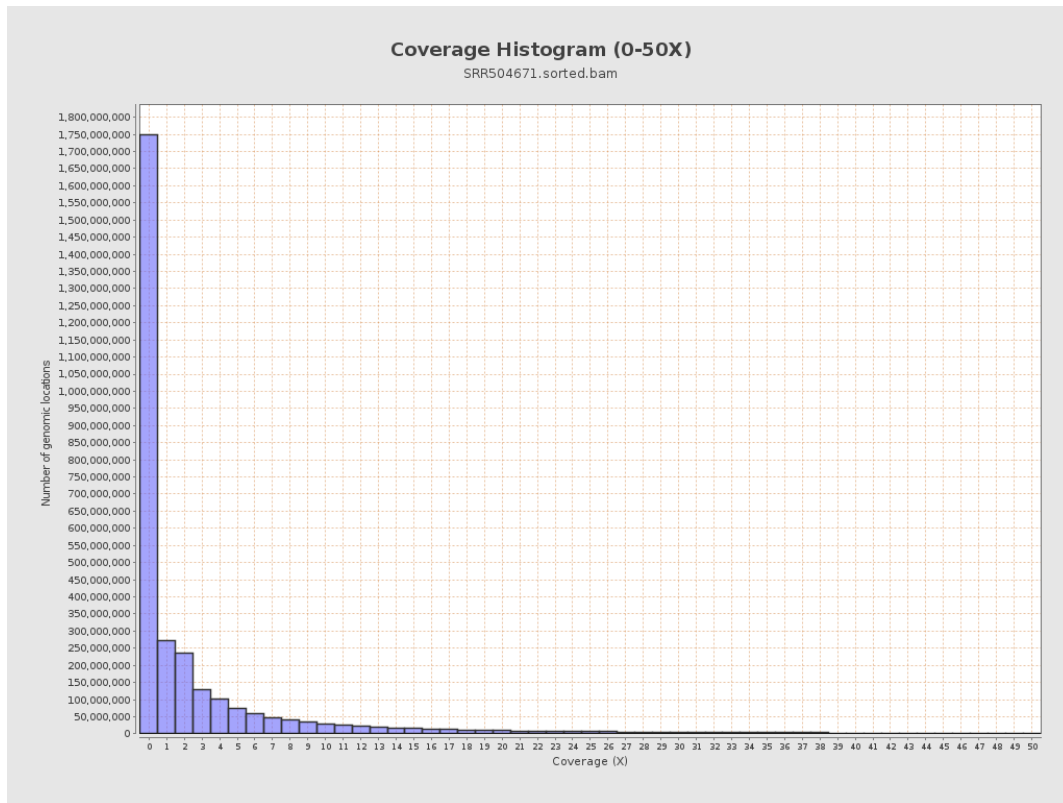
3. Results : Coverage across reference



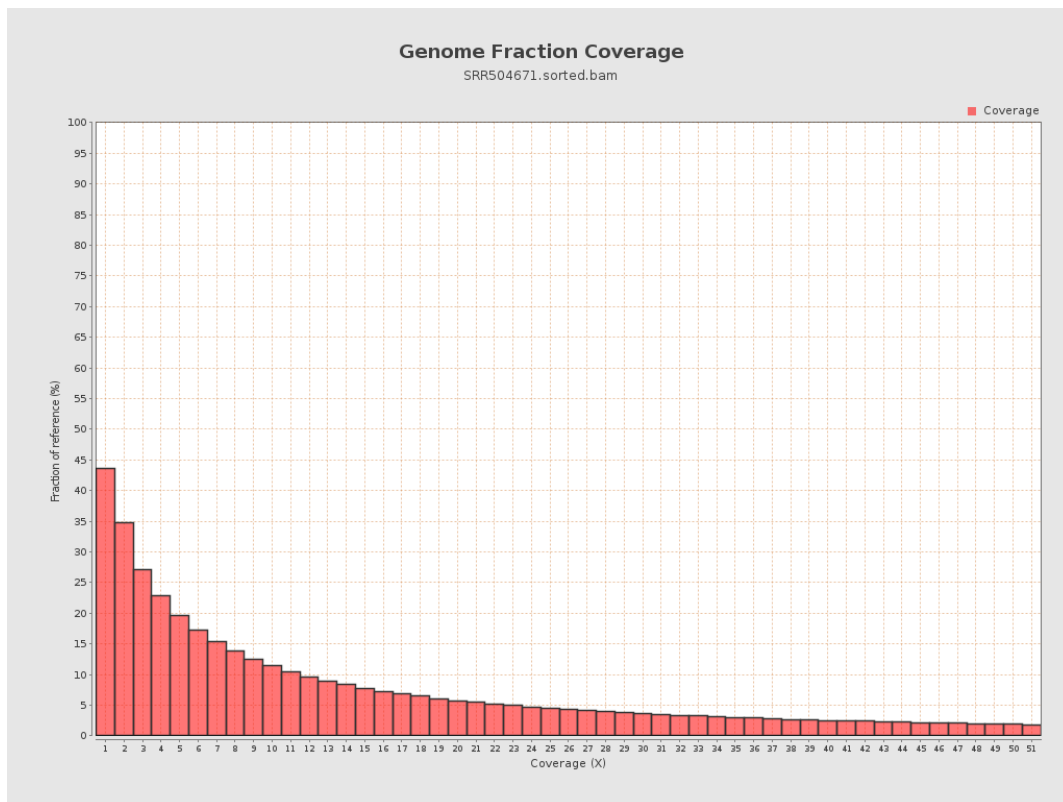
4. Results : Coverage Histogram



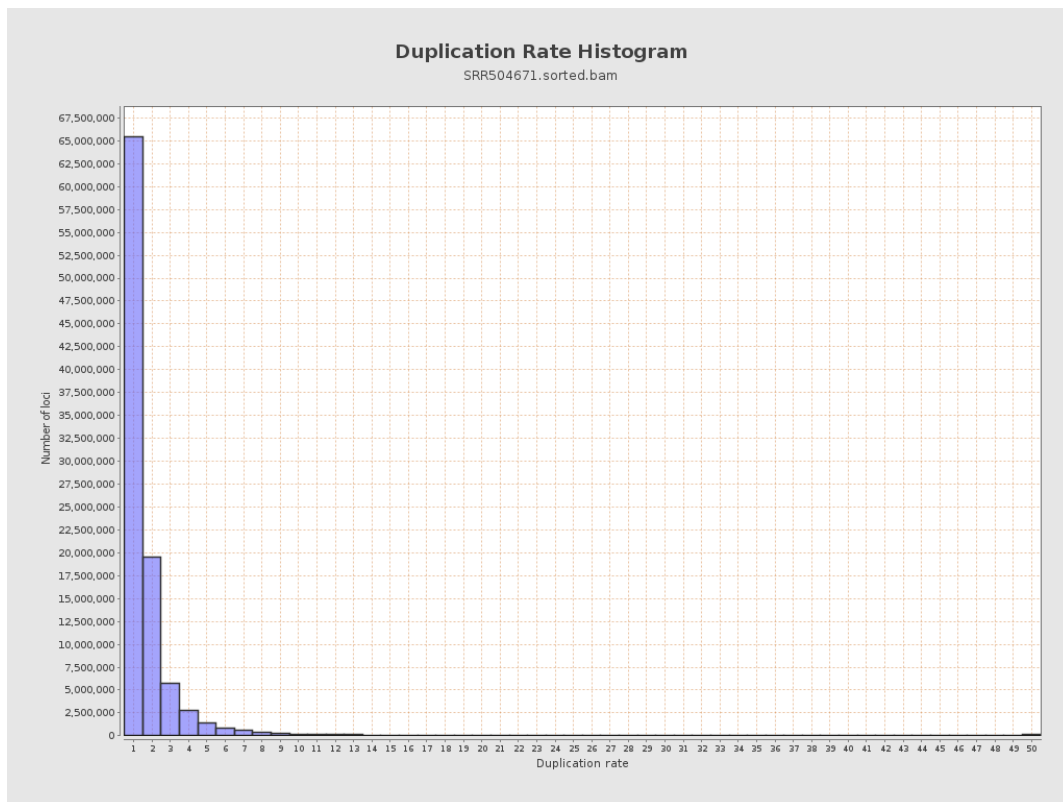
5. Results : Coverage Histogram (0-50X)



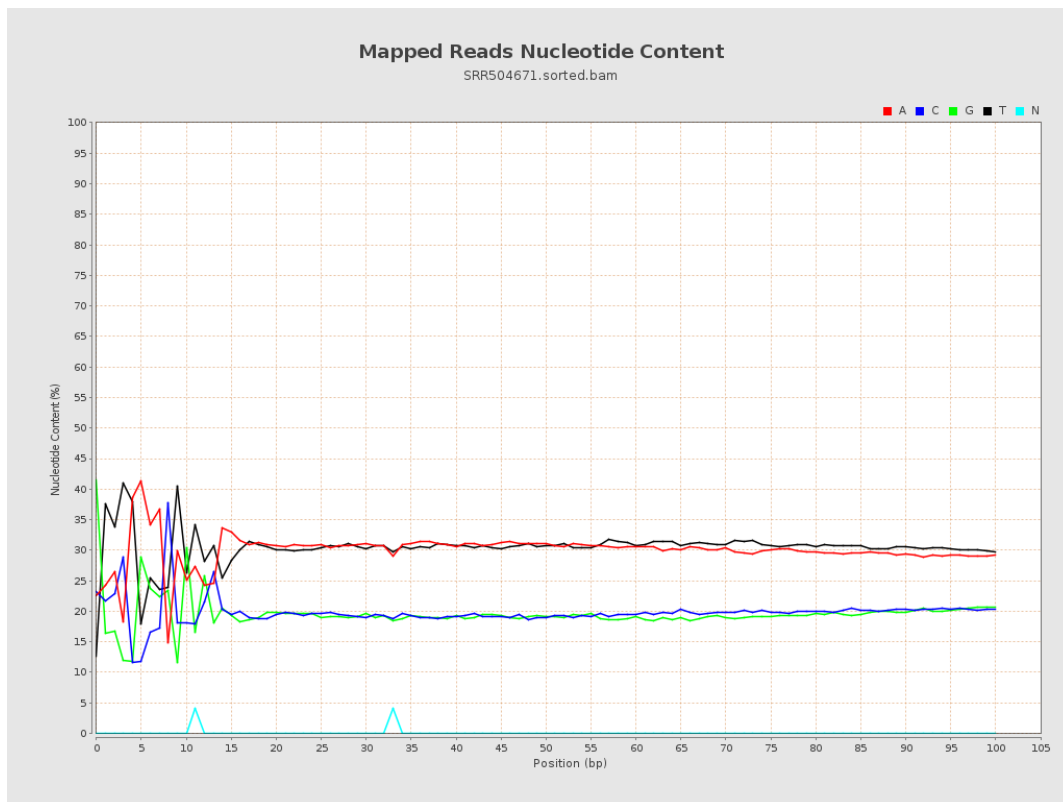
6. Results : Genome Fraction Coverage



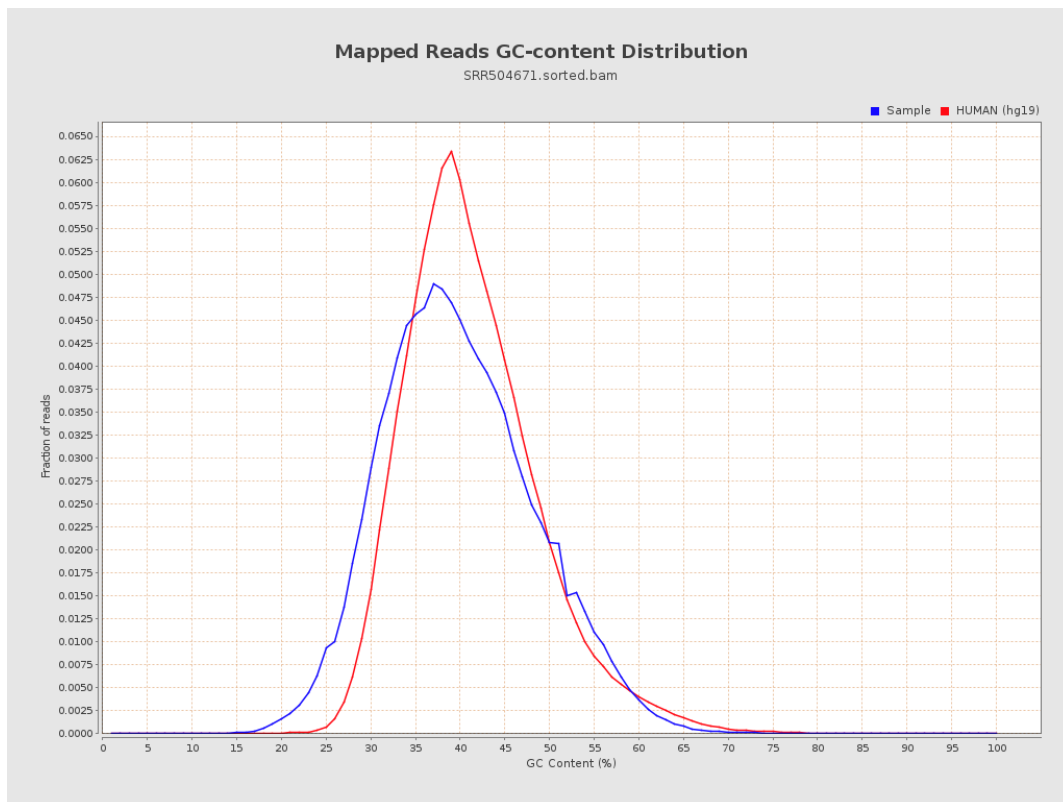
7. Results : Duplication Rate Histogram



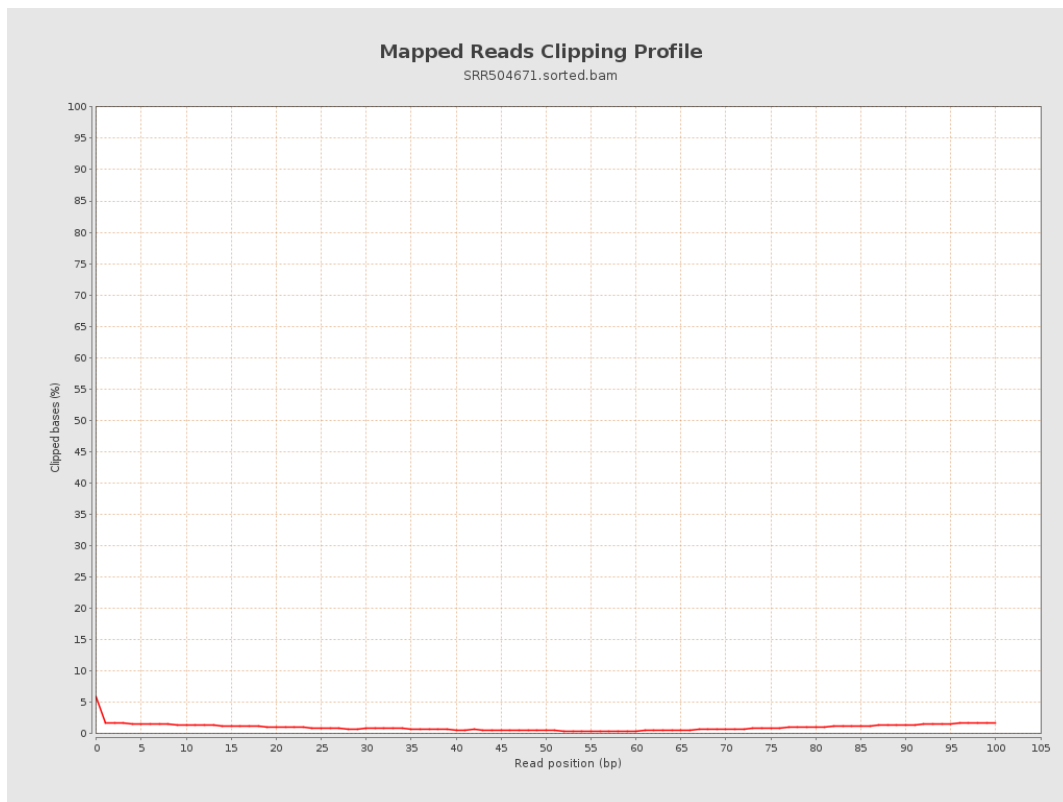
8. Results : Mapped Reads Nucleotide Content



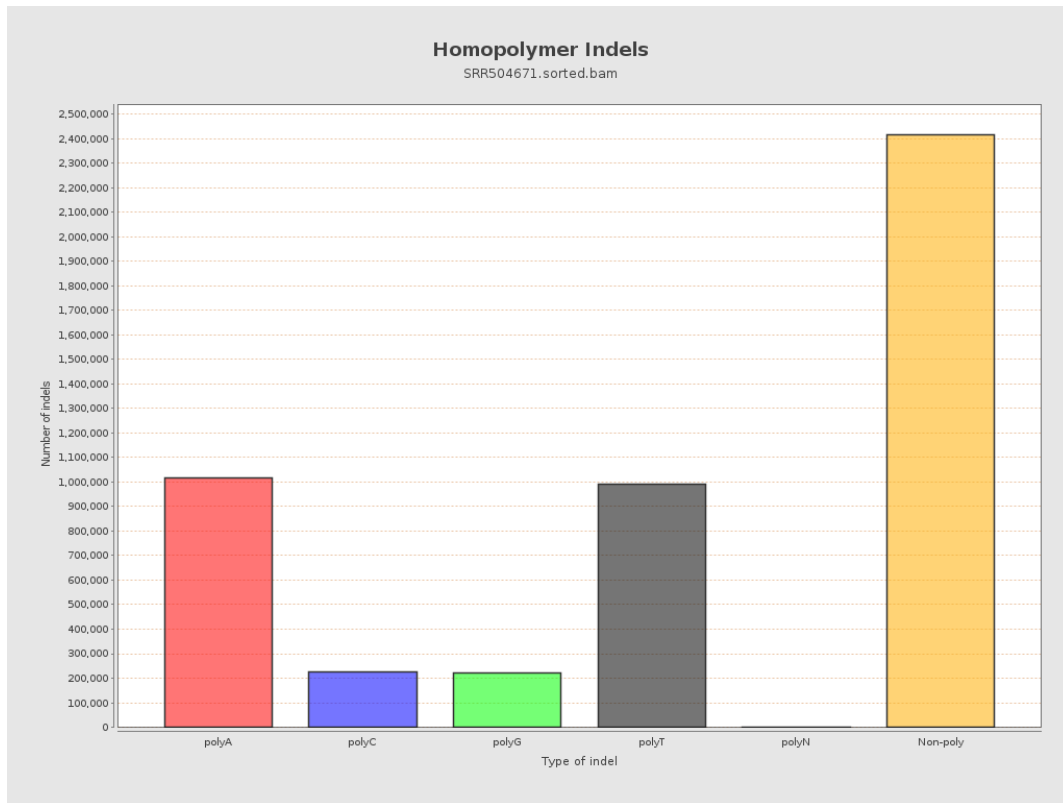
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



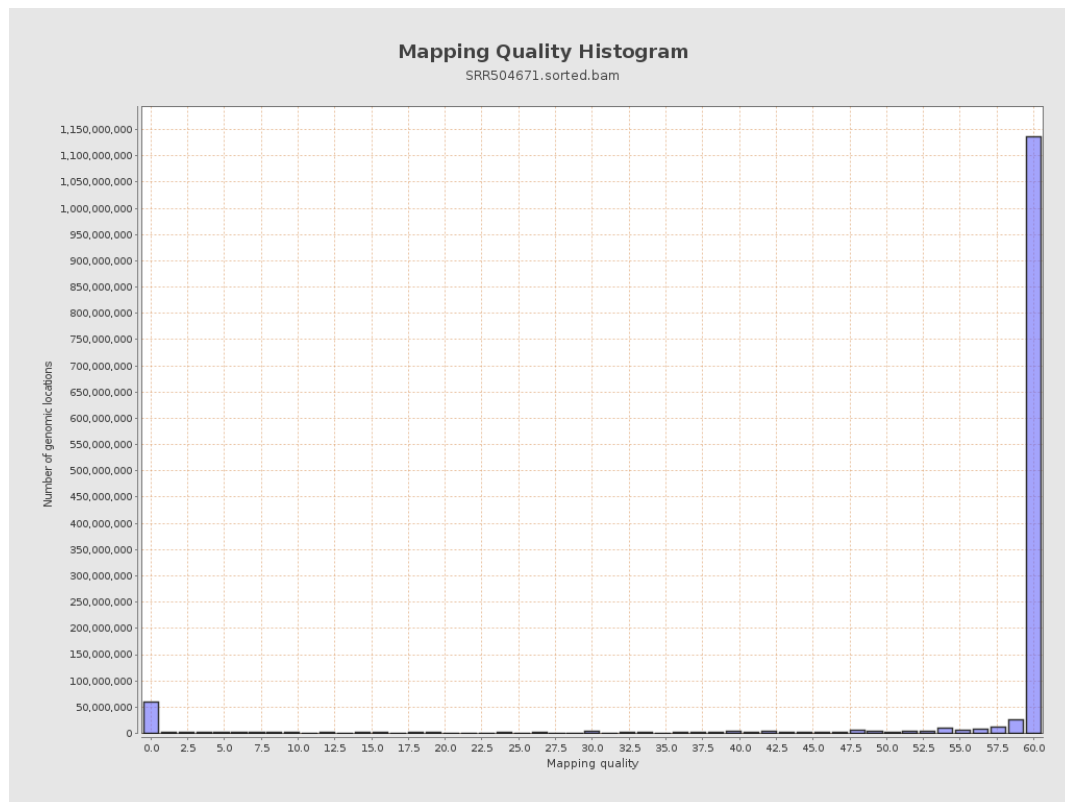
11. Results : Homopolymer Indels



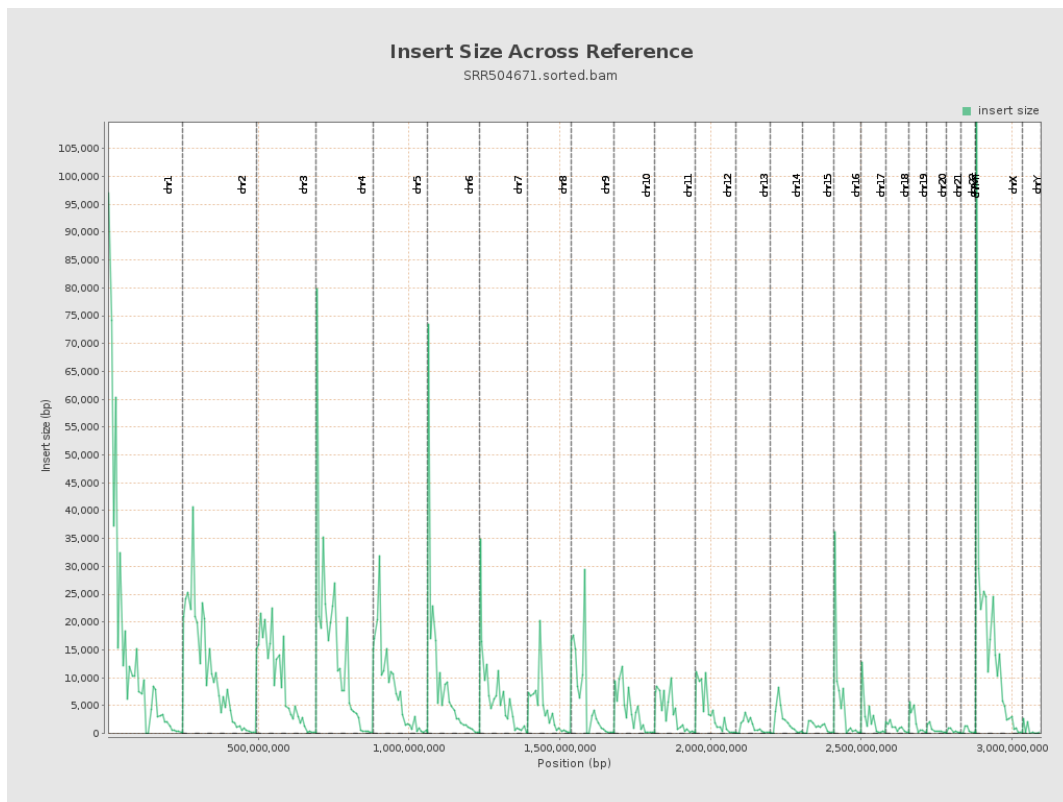
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

