

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 00:41:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504662.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_SRR504662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504662_1.fastq.gz SRR504662_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 00:41:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	99,278,696
Mapped reads	98,499,628 / 99.22%
Unmapped reads	779,068 / 0.78%
Mapped paired reads	98,499,628 / 99.22%
Mapped reads, first in pair	49,467,961 / 49.83%
Mapped reads, second in pair	49,031,667 / 49.39%
Mapped reads, both in pair	98,031,450 / 98.74%
Mapped reads, singletons	468,178 / 0.47%
Secondary alignments	0
Supplementary alignments	1,176,251 / 1.18%
Read min/max/mean length	30 / 111 / 111.5
Duplicated reads (estimated)	47,098,614 / 47.44%
Duplication rate	22.52%
Clipped reads	71,956,513 / 72.48%

2.2. ACGT Content

Number/percentage of A's	2,705,593,029 / 29.24%
Number/percentage of C's	1,857,095,956 / 20.07%
Number/percentage of T's	2,753,556,744 / 29.76%
Number/percentage of G's	1,860,021,087 / 20.1%
Number/percentage of N's	77,084,286 / 0.83%

GC Percentage	40.17%
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2.3. Coverage

Mean	2.9898
Standard Deviation	436.5112

2.4. Mapping Quality

Mean Mapping Quality	53.09
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2.5. Insert size

Mean	24,295.73
Standard Deviation	1,487,080.35
P25/Median/P75	83 / 133 / 205

2.6. Mismatches and indels

General error rate	1%
Mismatches	90,899,920
Insertions	901,898
Mapped reads with at least one insertion	0.91%
Deletions	1,164,312
Mapped reads with at least one deletion	1.16%
Homopolymer indels	50.8%

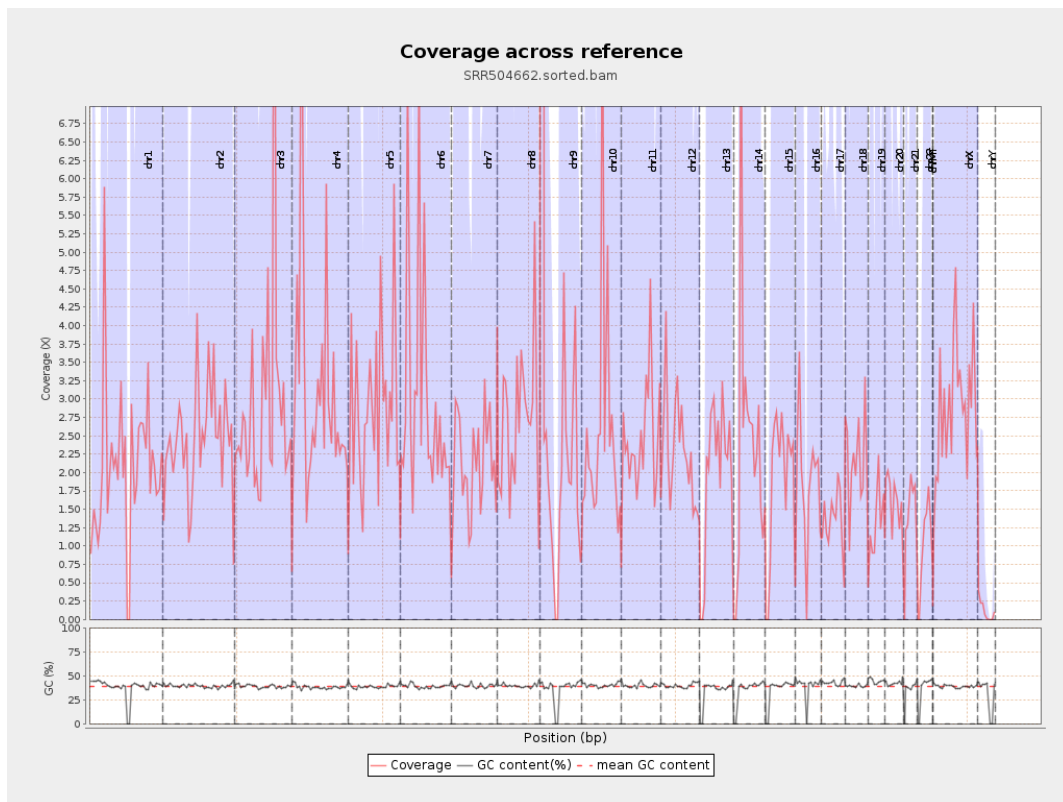
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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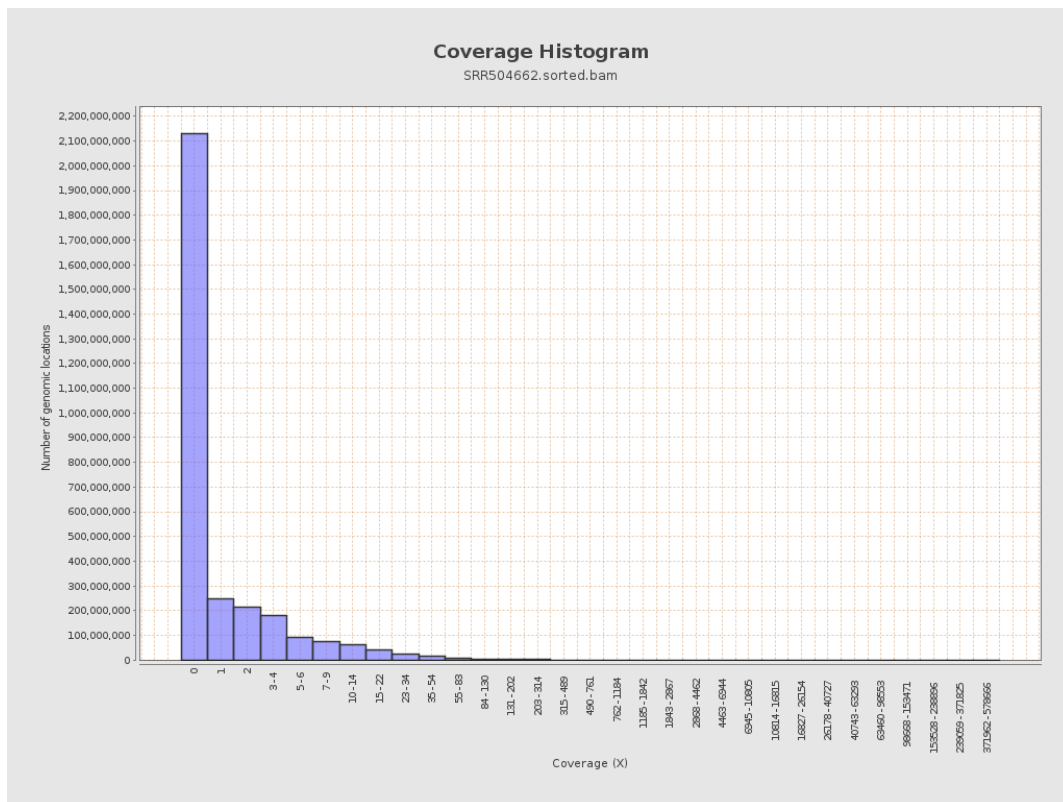
		bases	coverage	deviation
chr1	249250621	511006095	2.0502	15.0612
chr2	243199373	600605875	2.4696	11.257
chr3	198022430	581579789	2.9369	54.2189
chr4	191154276	592332311	3.0987	30.8171
chr5	180915260	513136742	2.8363	19.6023
chr6	171115067	511602041	2.9898	29.1786
chr7	159138663	333146181	2.0934	8.9395
chr8	146364022	402566351	2.7504	19.9182
chr9	141213431	2327569846	16.4826	2,040.9514
chr10	135534747	353767532	2.6102	40.5459
chr11	135006516	334305771	2.4762	13.9863
chr12	133851895	308906287	2.3078	10.9885
chr13	115169878	229097976	1.9892	8.4906
chr14	107349540	261657933	2.4374	32.9271
chr15	102531392	193817071	1.8903	9.2776
chr16	90354753	165369429	1.8302	16.3914
chr17	81195210	111316614	1.371	6.1413
chr18	78077248	167432433	2.1444	9.2834
chr19	59128983	78986747	1.3358	7.7159
chr20	63025520	101505182	1.6105	6.7274
chr21	48129895	66288239	1.3773	6.2256
chr22	51304566	52369737	1.0208	5.3749
chrMT	16571	2896	0.1748	0.6313
chrX	155270560	450183963	2.8994	13.8938

chrY	59373566	6961721	0.1173	1.378
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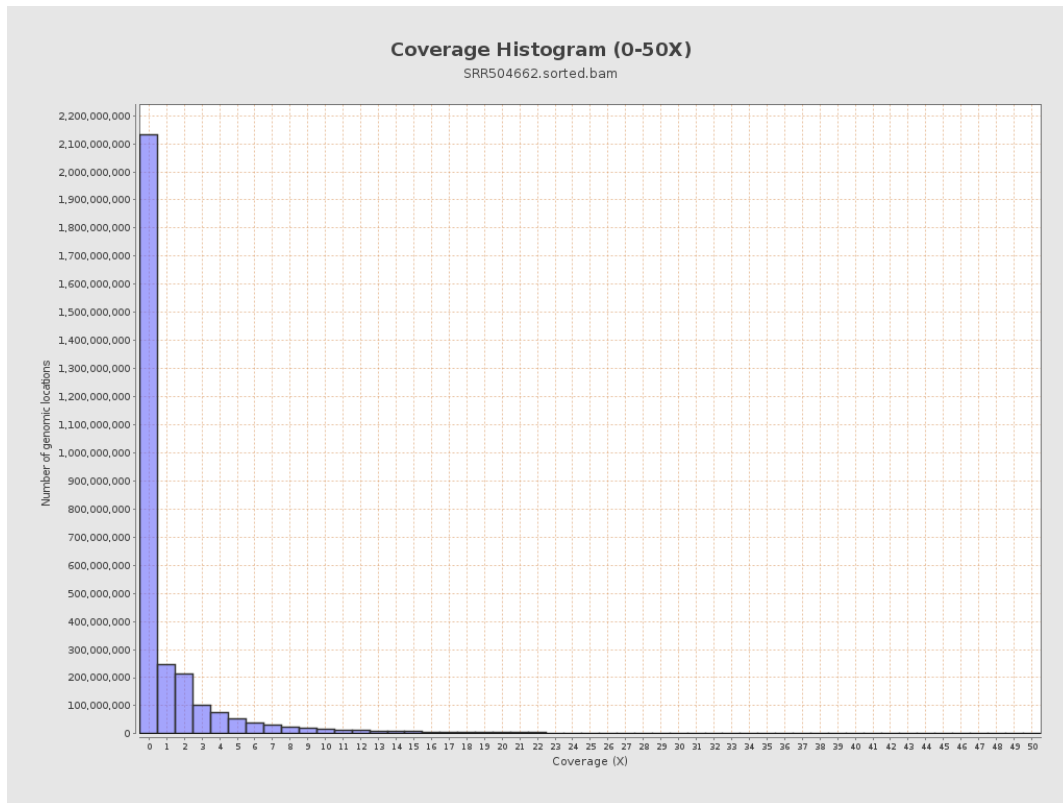
3. Results : Coverage across reference



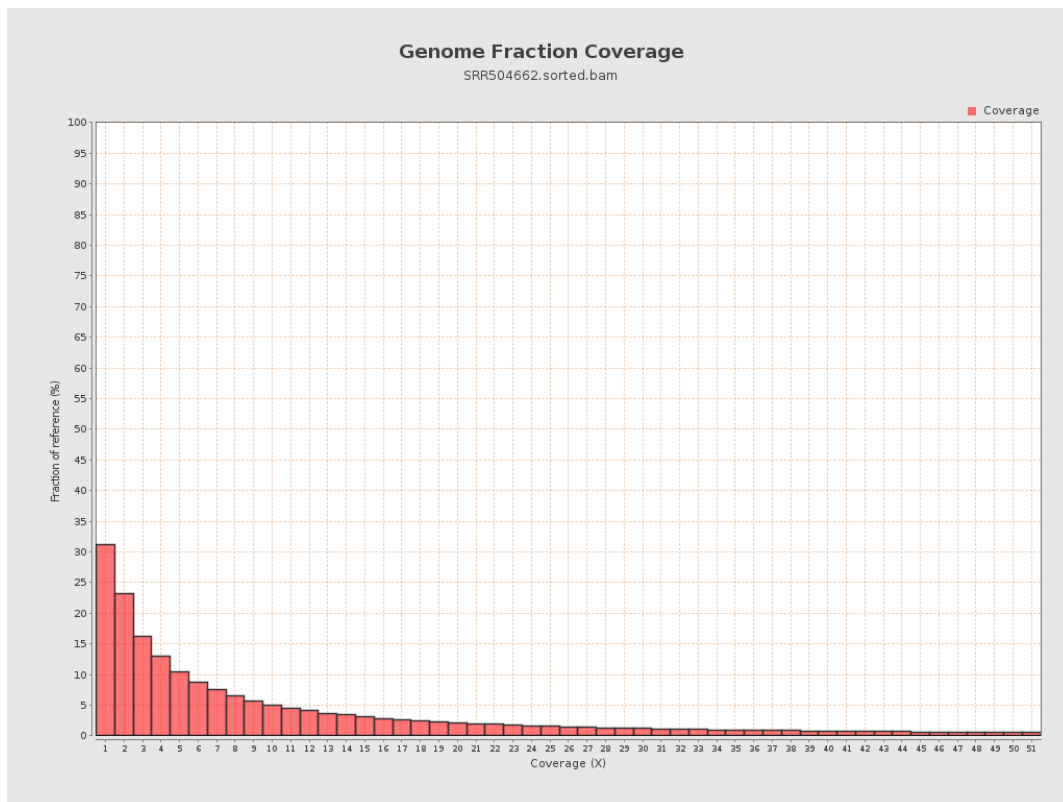
4. Results : Coverage Histogram



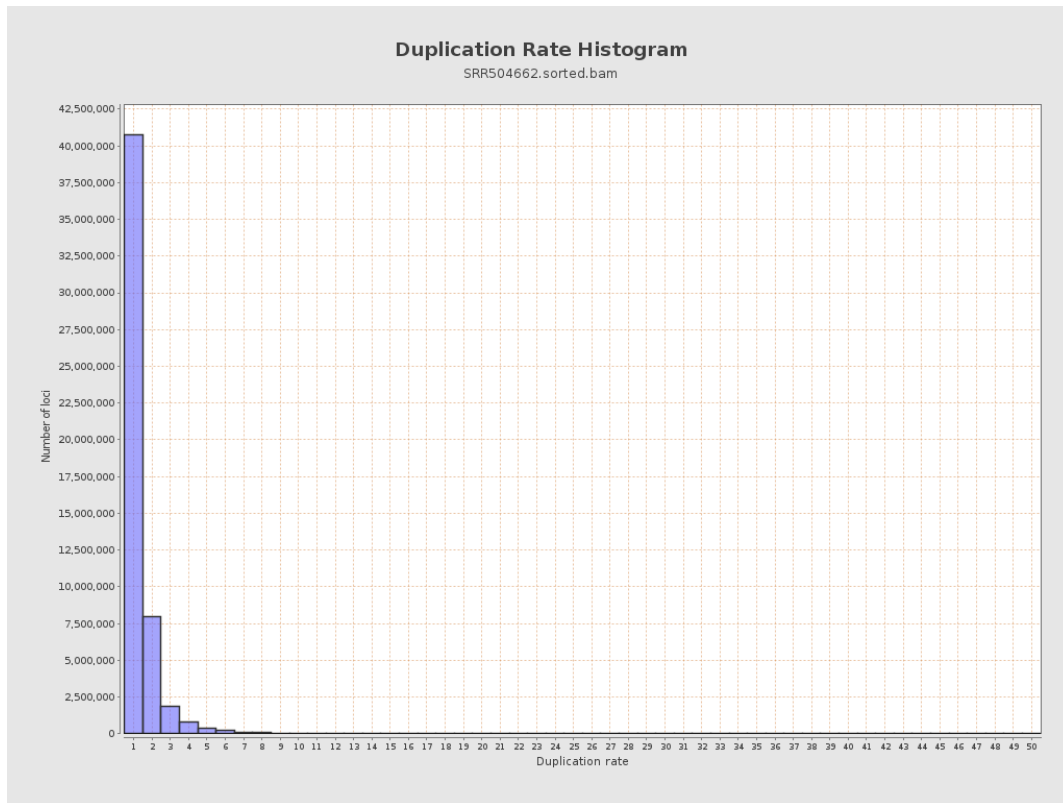
5. Results : Coverage Histogram (0-50X)



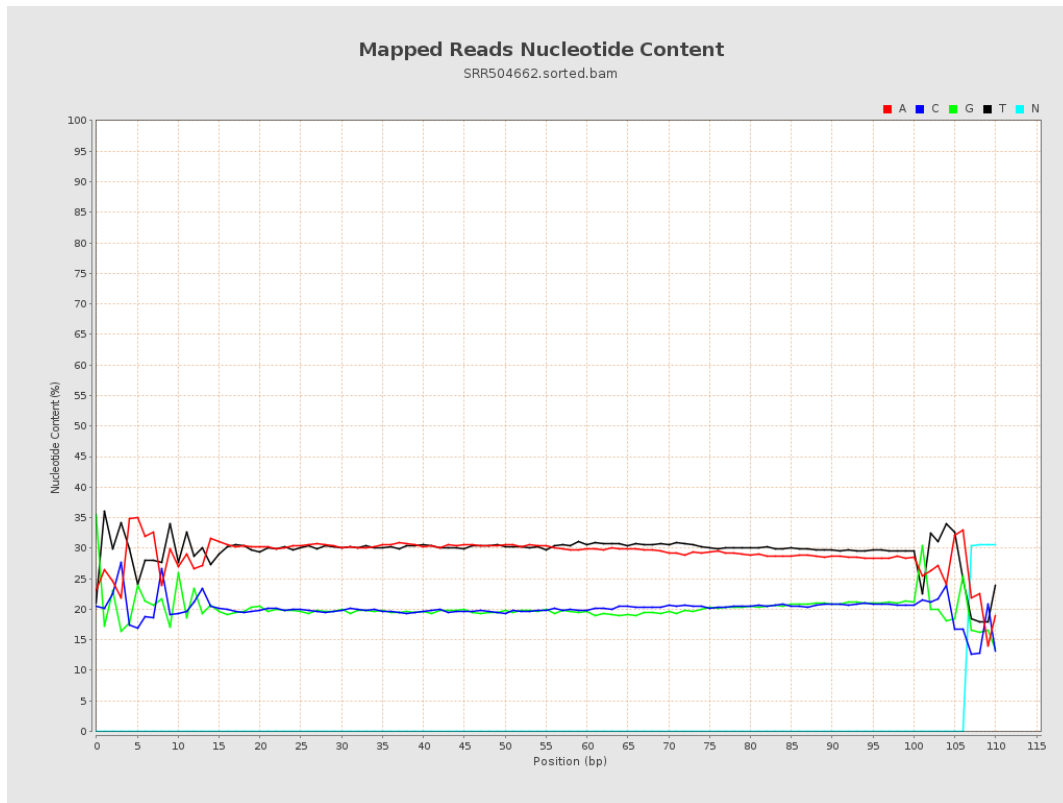
6. Results : Genome Fraction Coverage



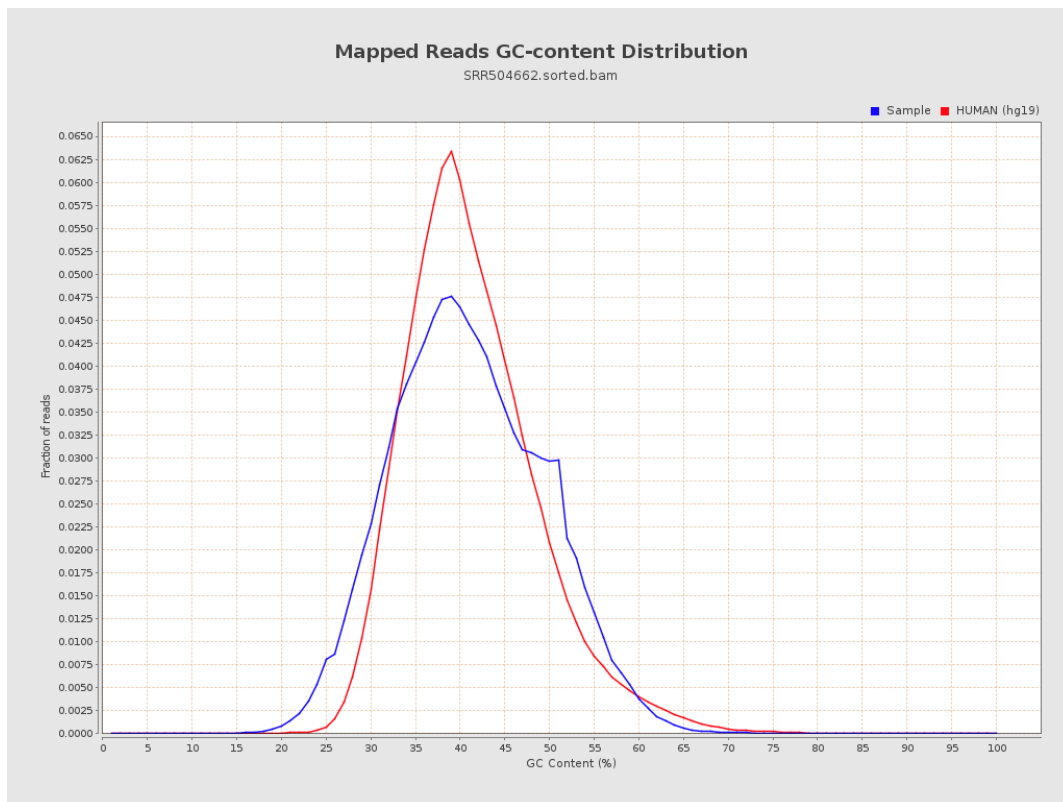
7. Results : Duplication Rate Histogram



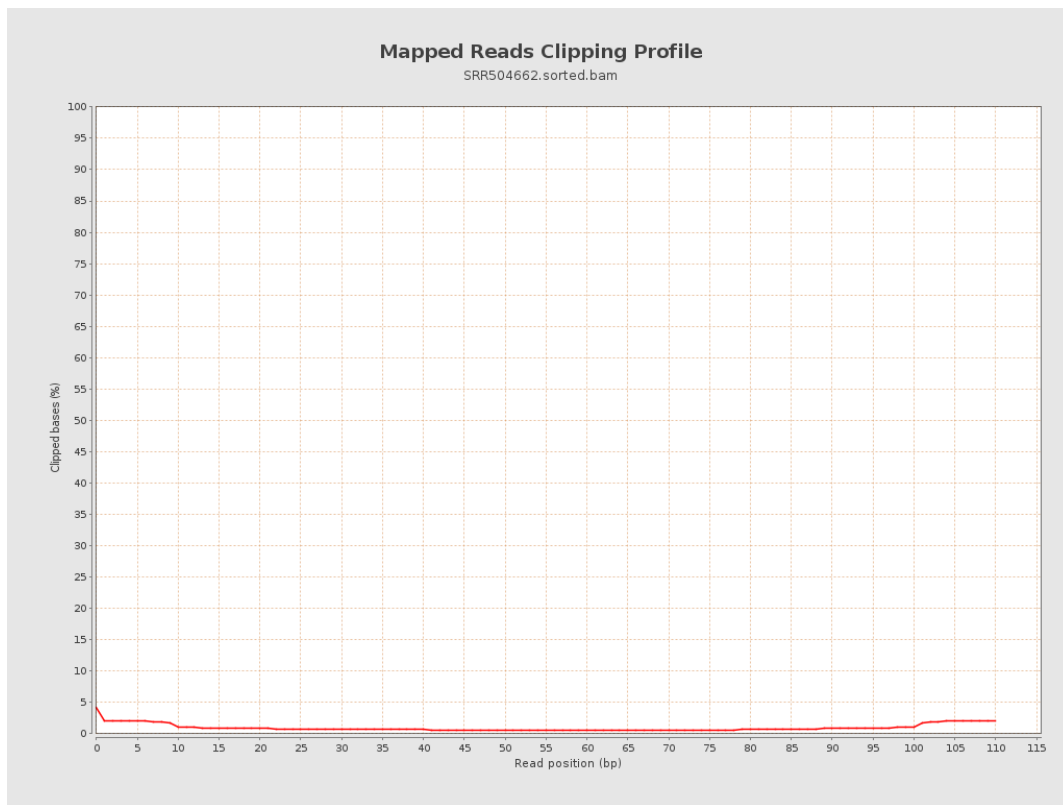
8. Results : Mapped Reads Nucleotide Content



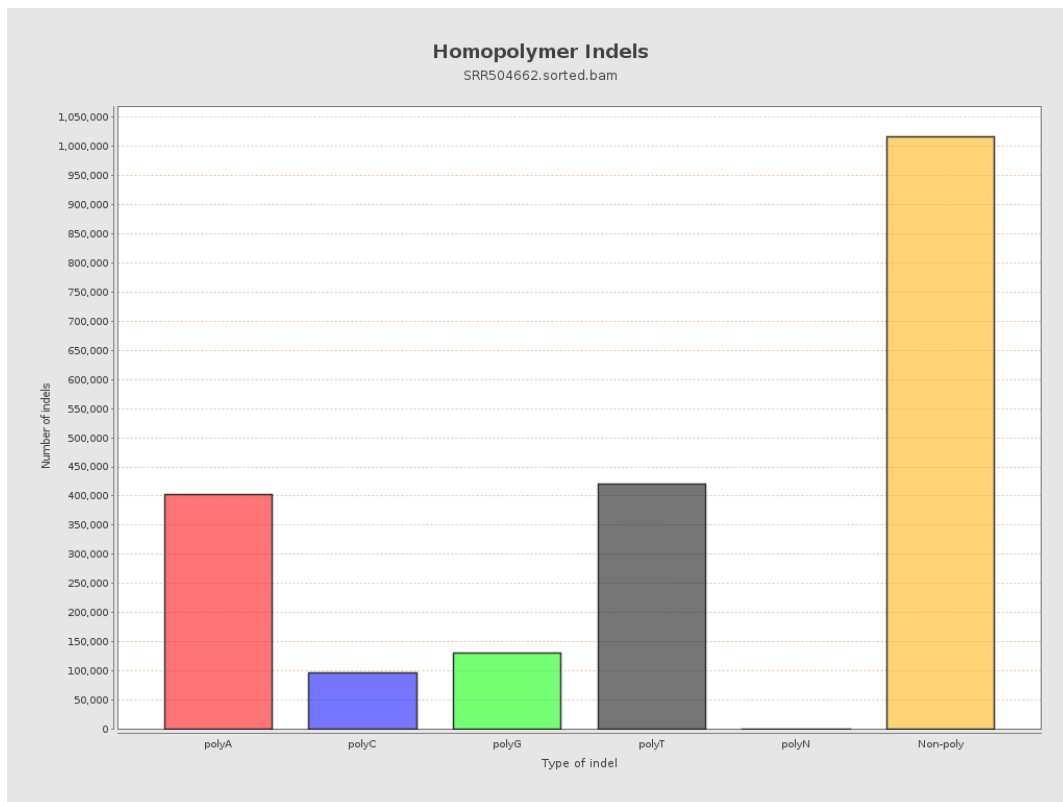
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



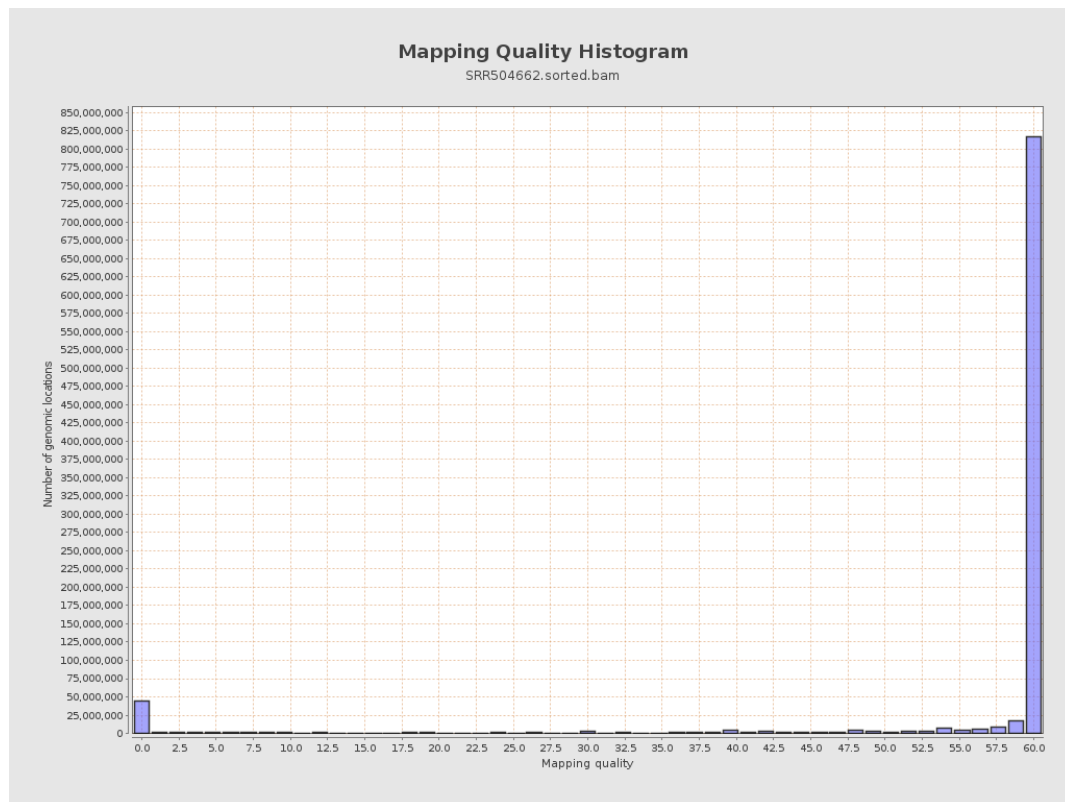
11. Results : Homopolymer Indels



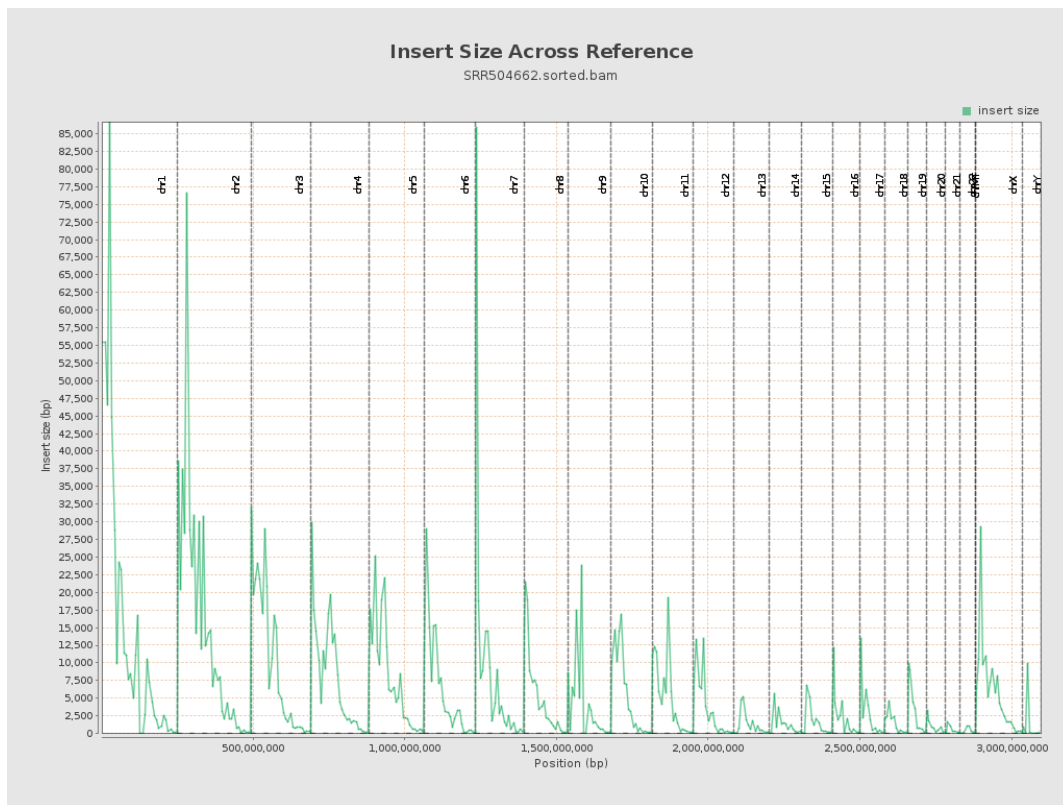
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

