

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 22:54:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504660.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_SRR504660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504660_1.fastq.gz SRR504660_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 22:54:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	96,067,140
Mapped reads	95,571,781 / 99.48%
Unmapped reads	495,359 / 0.52%
Mapped paired reads	95,571,781 / 99.48%
Mapped reads, first in pair	47,884,135 / 49.84%
Mapped reads, second in pair	47,687,646 / 49.64%
Mapped reads, both in pair	95,337,496 / 99.24%
Mapped reads, singletons	234,285 / 0.24%
Secondary alignments	0
Supplementary alignments	1,027,529 / 1.07%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	48,416,666 / 50.4%
Duplication rate	25.84%
Clipped reads	30,671,095 / 31.93%

2.2. ACGT Content

Number/percentage of A's	2,625,397,144 / 29.6%
Number/percentage of C's	1,800,993,314 / 20.31%
Number/percentage of T's	2,661,783,266 / 30.01%
Number/percentage of G's	1,775,636,193 / 20.02%
Number/percentage of N's	4,958,282 / 0.06%

GC Percentage	40.33%
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2.3. Coverage

Mean	2.8672
Standard Deviation	417.8452

2.4. Mapping Quality

Mean Mapping Quality	53.11
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2.5. Insert size

Mean	23,475.63
Standard Deviation	1,446,841.14
P25/Median/P75	95 / 144 / 215

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	86,479,602
Insertions	2,748,606
Mapped reads with at least one insertion	2.81%
Deletions	2,965,258
Mapped reads with at least one deletion	3.02%
Homopolymer indels	37.56%

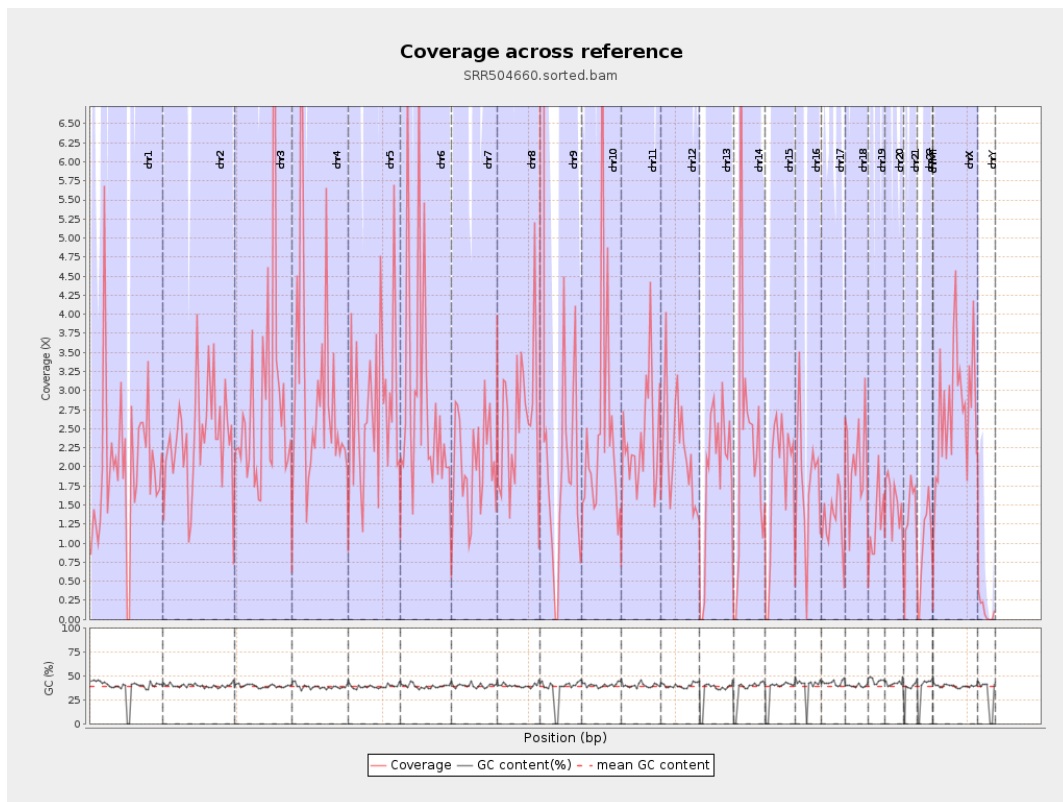
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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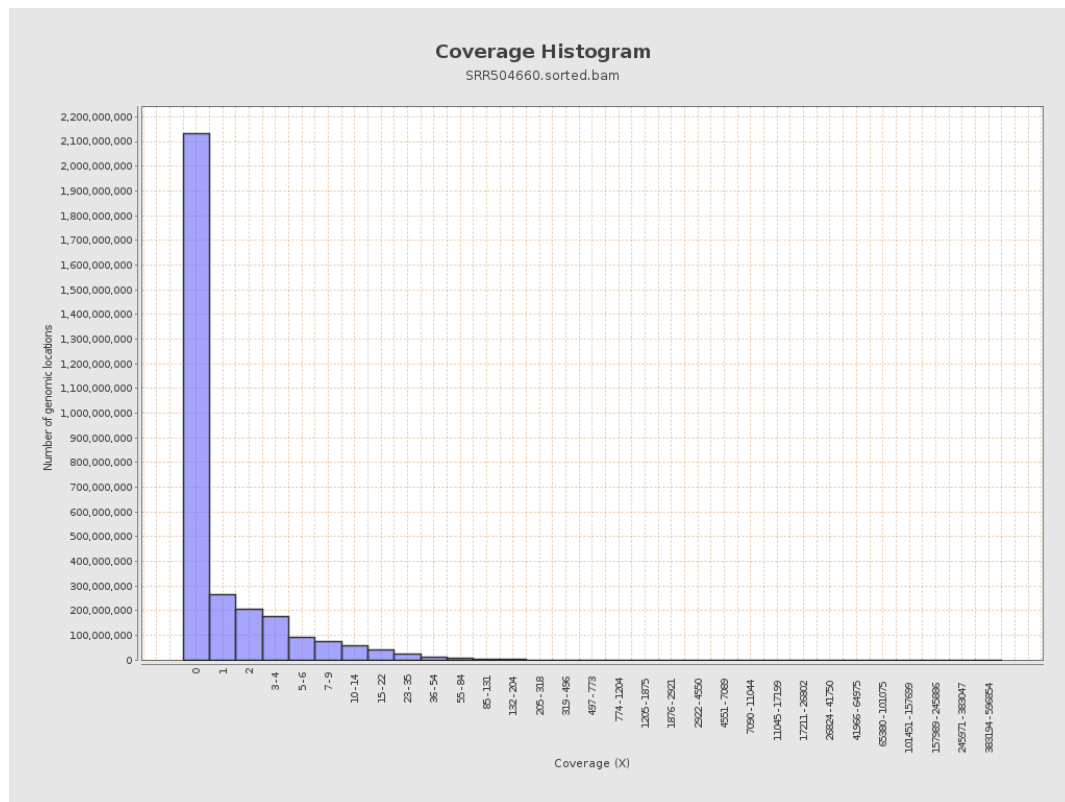
		bases	coverage	deviation
chr1	249250621	490927620	1.9696	14.507
chr2	243199373	577455746	2.3744	10.7843
chr3	198022430	558497747	2.8204	51.8333
chr4	191154276	567212477	2.9673	29.4227
chr5	180915260	492433086	2.7219	18.7423
chr6	171115067	490863431	2.8686	27.8818
chr7	159138663	319551075	2.008	8.5303
chr8	146364022	386151031	2.6383	19.1234
chr9	141213431	2228787583	15.7831	1,953.6753
chr10	135534747	338926305	2.5007	38.9323
chr11	135006516	320436864	2.3735	13.3799
chr12	133851895	297104342	2.2196	10.5188
chr13	115169878	219807477	1.9086	8.1571
chr14	107349540	250967101	2.3378	31.5898
chr15	102531392	186266710	1.8167	8.8873
chr16	90354753	158655446	1.7559	15.7148
chr17	81195210	106590354	1.3128	5.7755
chr18	78077248	160693442	2.0581	8.8721
chr19	59128983	75481838	1.2766	7.2046
chr20	63025520	96910194	1.5376	6.3988
chr21	48129895	63447243	1.3183	5.9113
chr22	51304566	50247365	0.9794	5.0803
chrMT	16571	1968	0.1188	0.5049
chrX	155270560	431931177	2.7818	13.5543

chrY	59373566	6680366	0.1125	1.289
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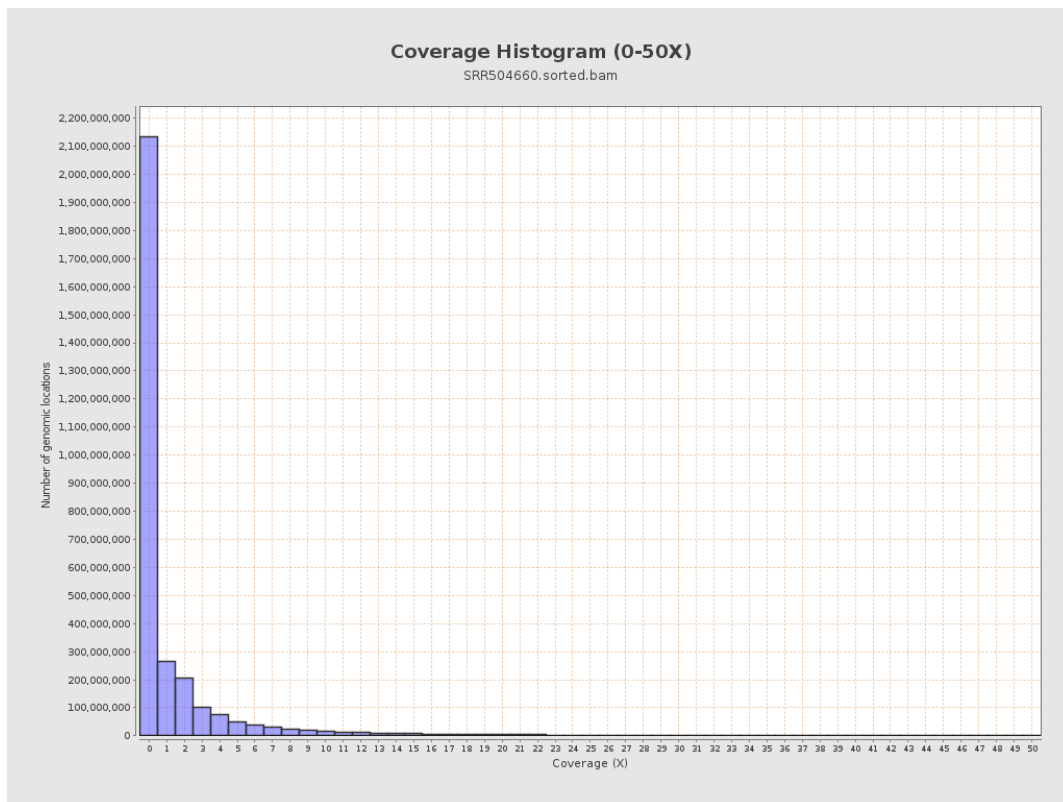
3. Results : Coverage across reference



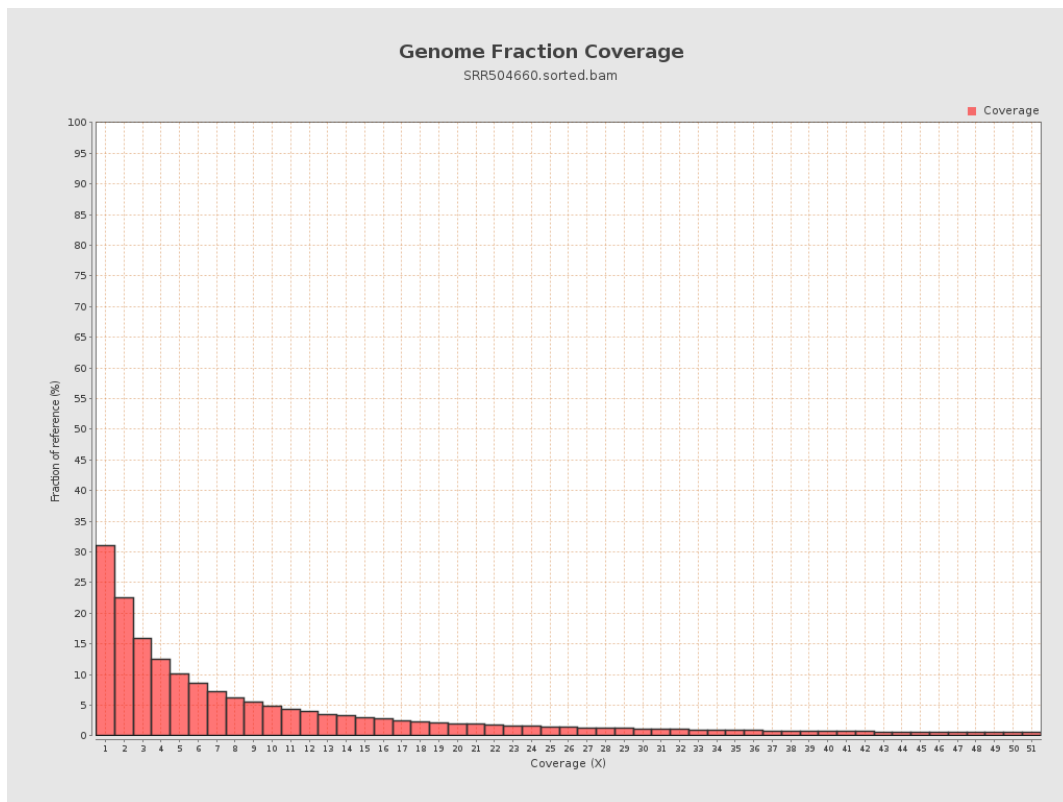
4. Results : Coverage Histogram



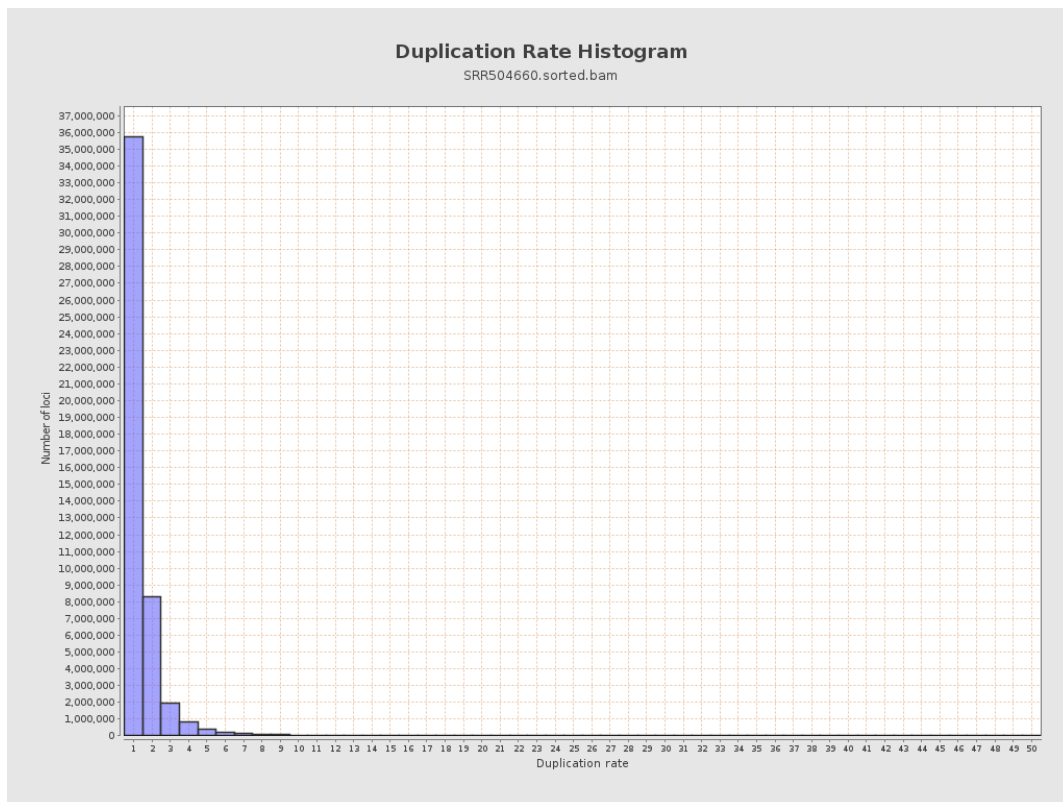
5. Results : Coverage Histogram (0-50X)



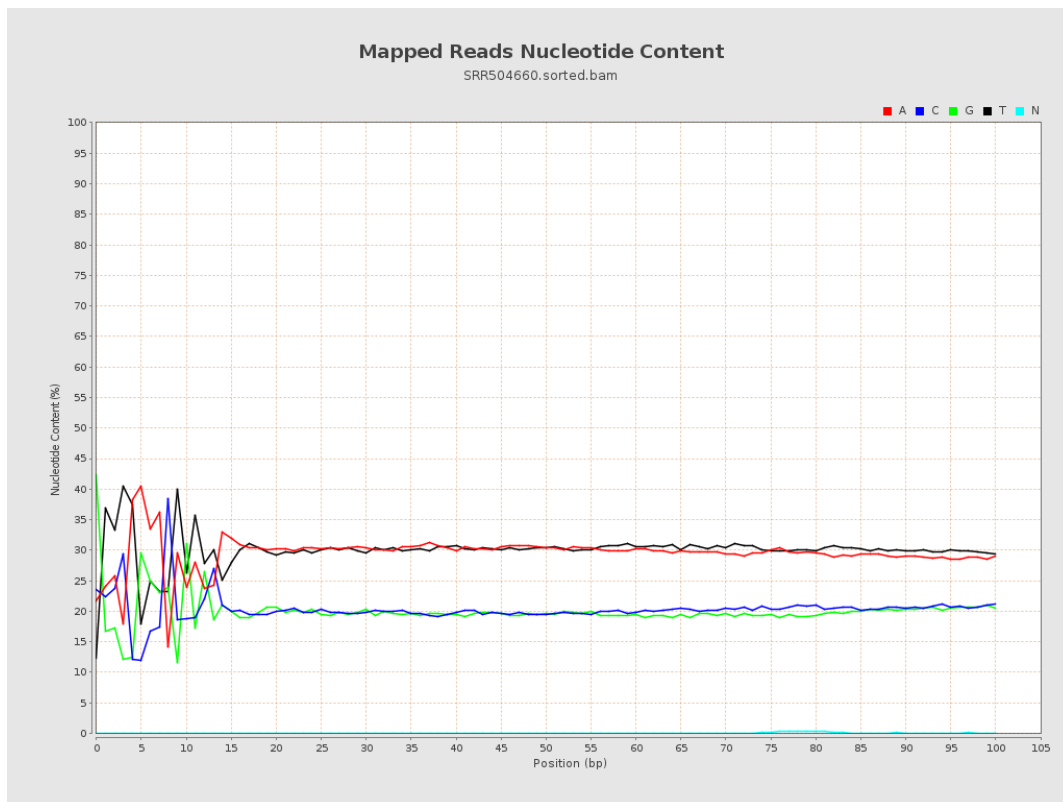
6. Results : Genome Fraction Coverage



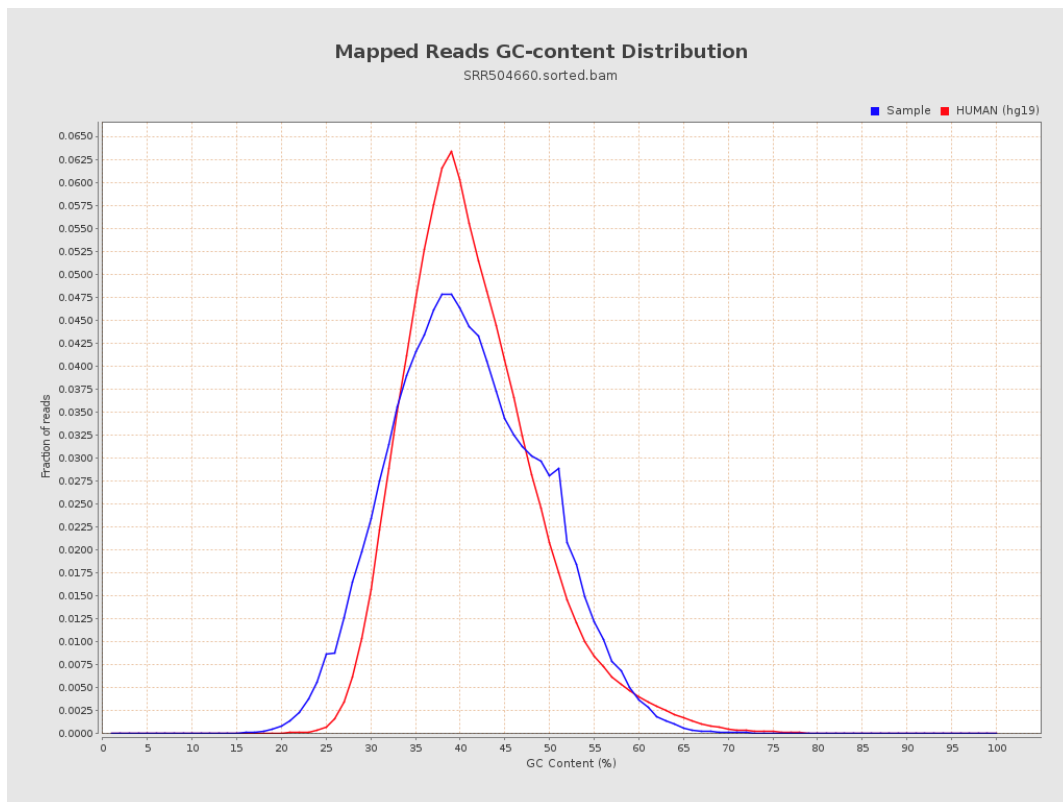
7. Results : Duplication Rate Histogram



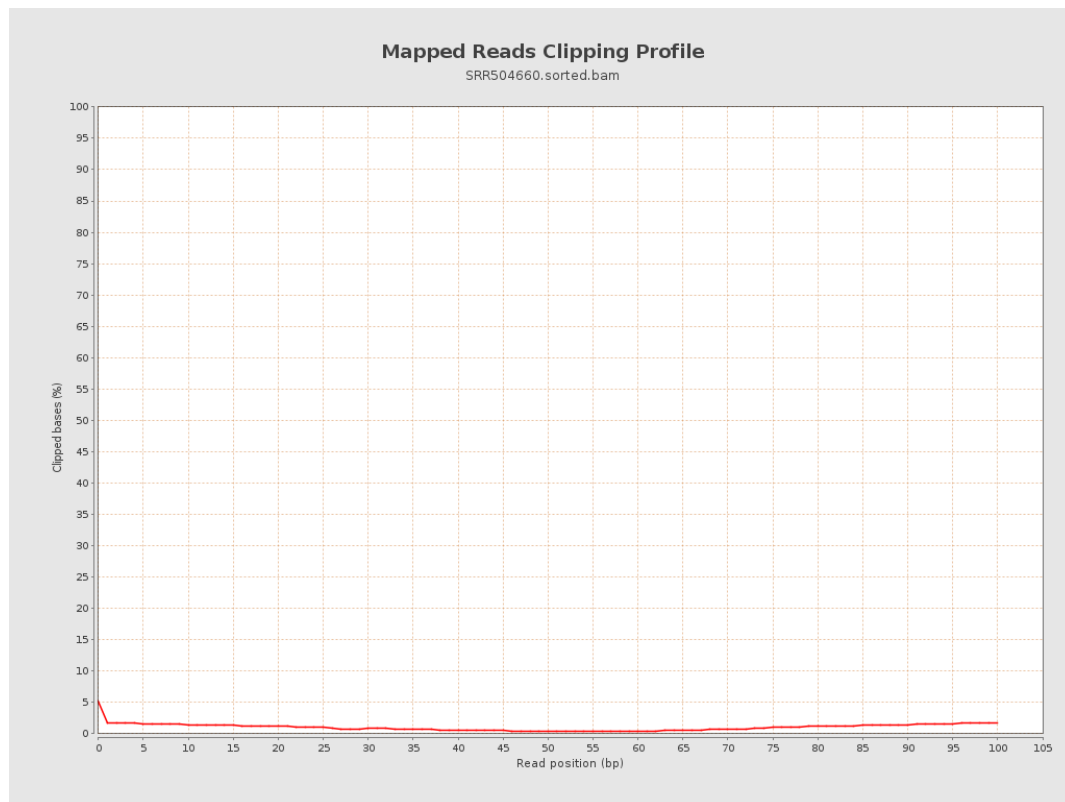
8. Results : Mapped Reads Nucleotide Content



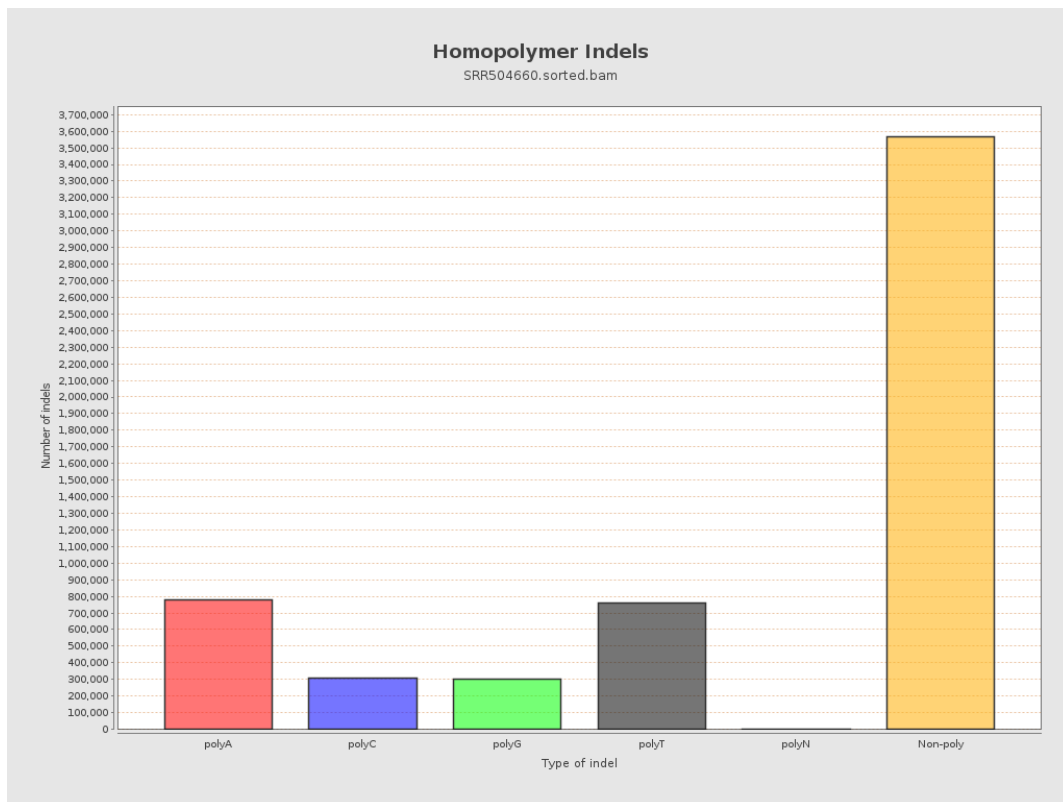
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



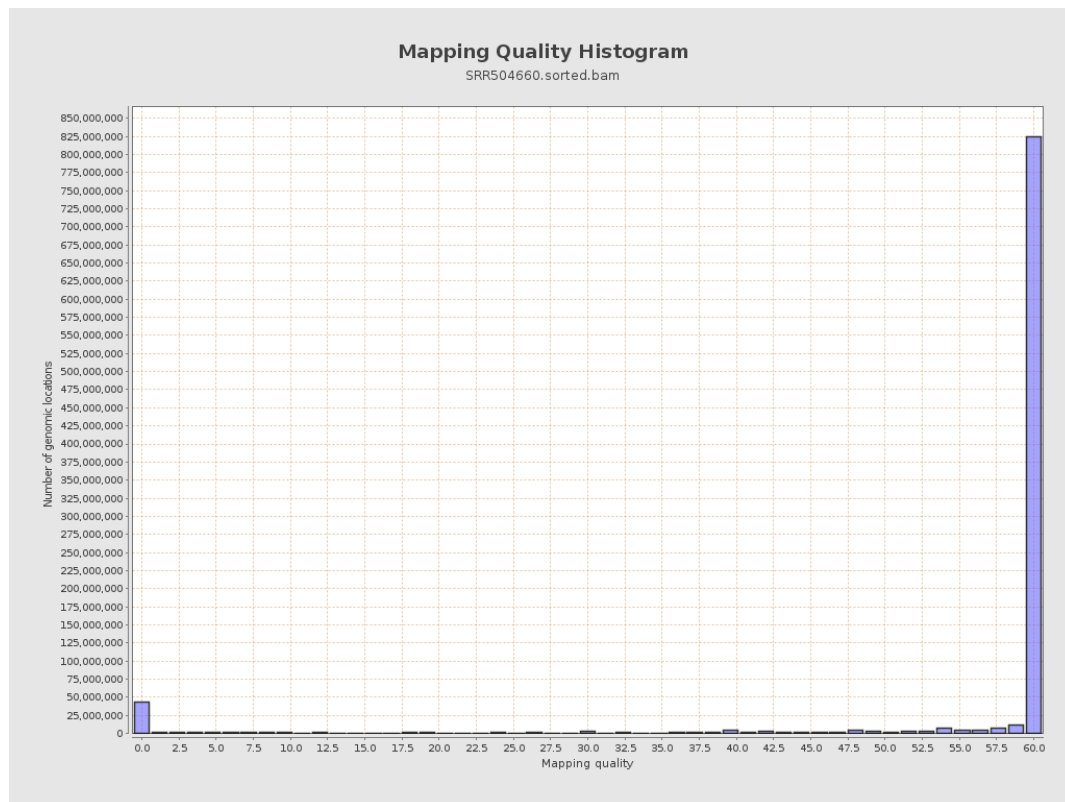
11. Results : Homopolymer Indels



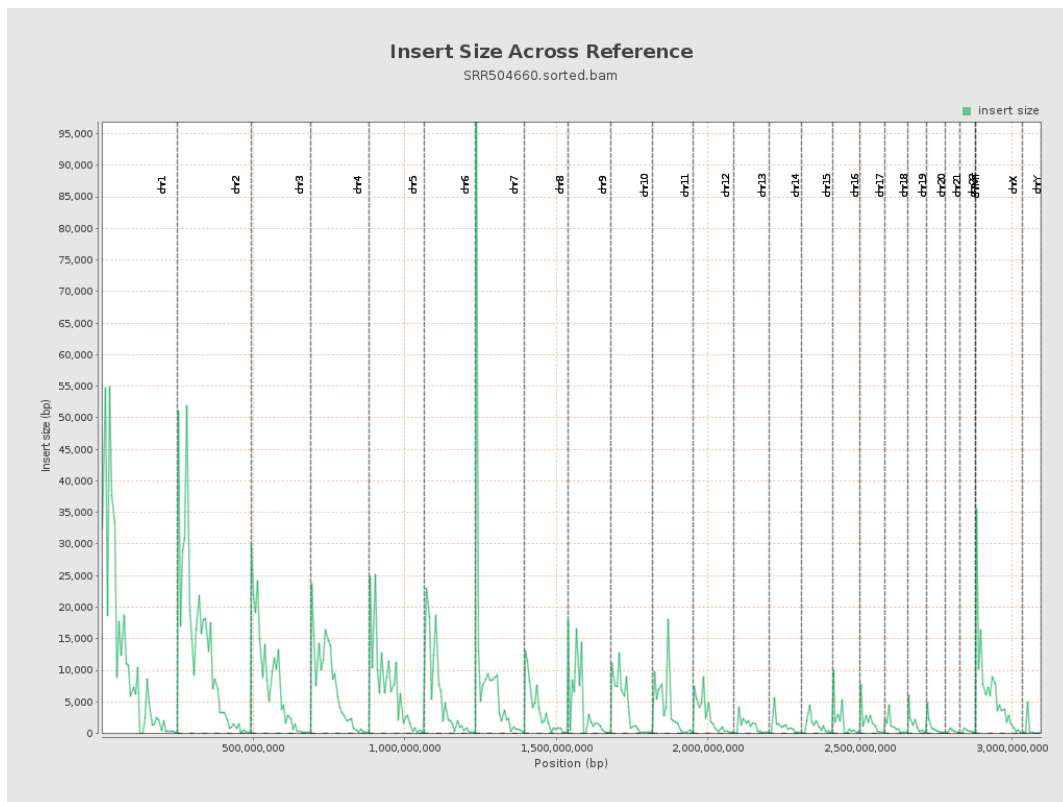
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

