

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 08:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504667.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_SRR504667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504667_1.fastq.gz SRR504667_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 08:04:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	89,546,796
Mapped reads	88,953,975 / 99.34%
Unmapped reads	592,821 / 0.66%
Mapped paired reads	88,953,975 / 99.34%
Mapped reads, first in pair	44,657,225 / 49.87%
Mapped reads, second in pair	44,296,750 / 49.47%
Mapped reads, both in pair	88,558,468 / 98.9%
Mapped reads, singletons	395,507 / 0.44%
Secondary alignments	0
Supplementary alignments	1,290,061 / 1.44%
Read min/max/mean length	30 / 111 / 111.61
Duplicated reads (estimated)	43,740,024 / 48.85%
Duplication rate	23.89%
Clipped reads	64,486,261 / 72.01%

2.2. ACGT Content

Number/percentage of A's	2,517,464,158 / 29.9%
Number/percentage of C's	1,643,462,168 / 19.52%
Number/percentage of T's	2,544,698,645 / 30.22%
Number/percentage of G's	1,643,730,930 / 19.52%
Number/percentage of N's	70,305,606 / 0.84%

GC Percentage	39.04%
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2.3. Coverage

Mean	2.7205
Standard Deviation	345.9458

2.4. Mapping Quality

Mean Mapping Quality	51.13
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2.5. Insert size

Mean	43,668.19
Standard Deviation	1,956,813.49
P25/Median/P75	87 / 139 / 211

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	86,330,276
Insertions	915,522
Mapped reads with at least one insertion	1.02%
Deletions	1,151,028
Mapped reads with at least one deletion	1.27%
Homopolymer indels	50.43%

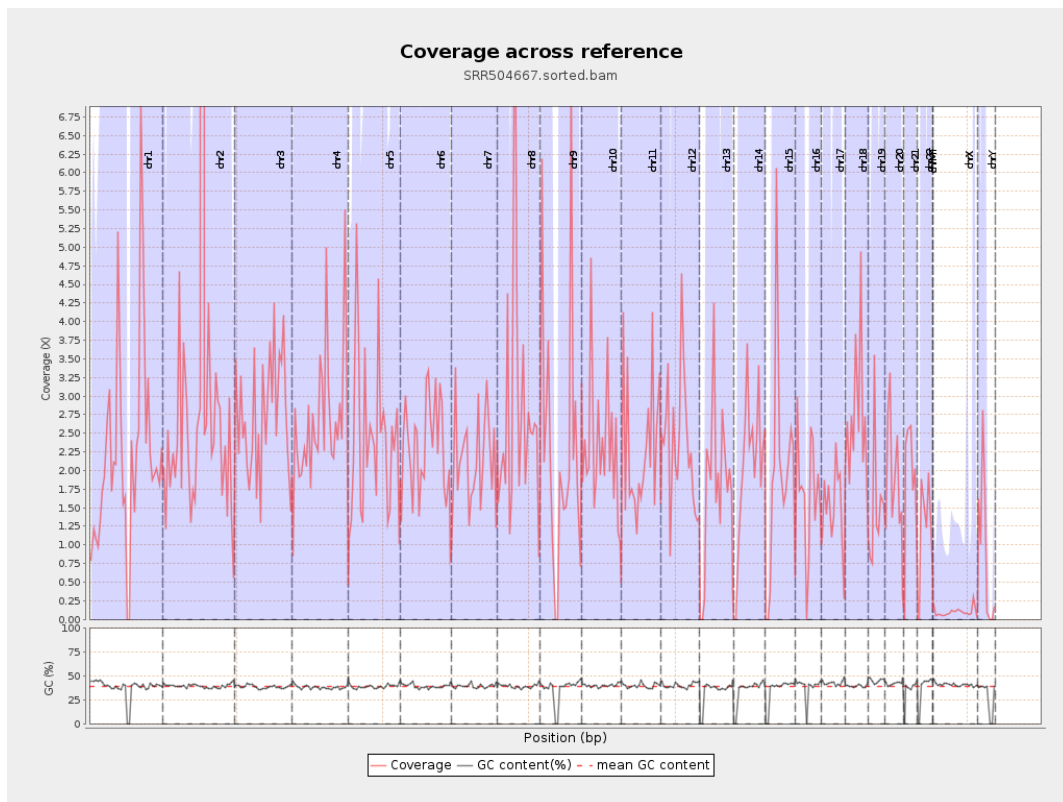
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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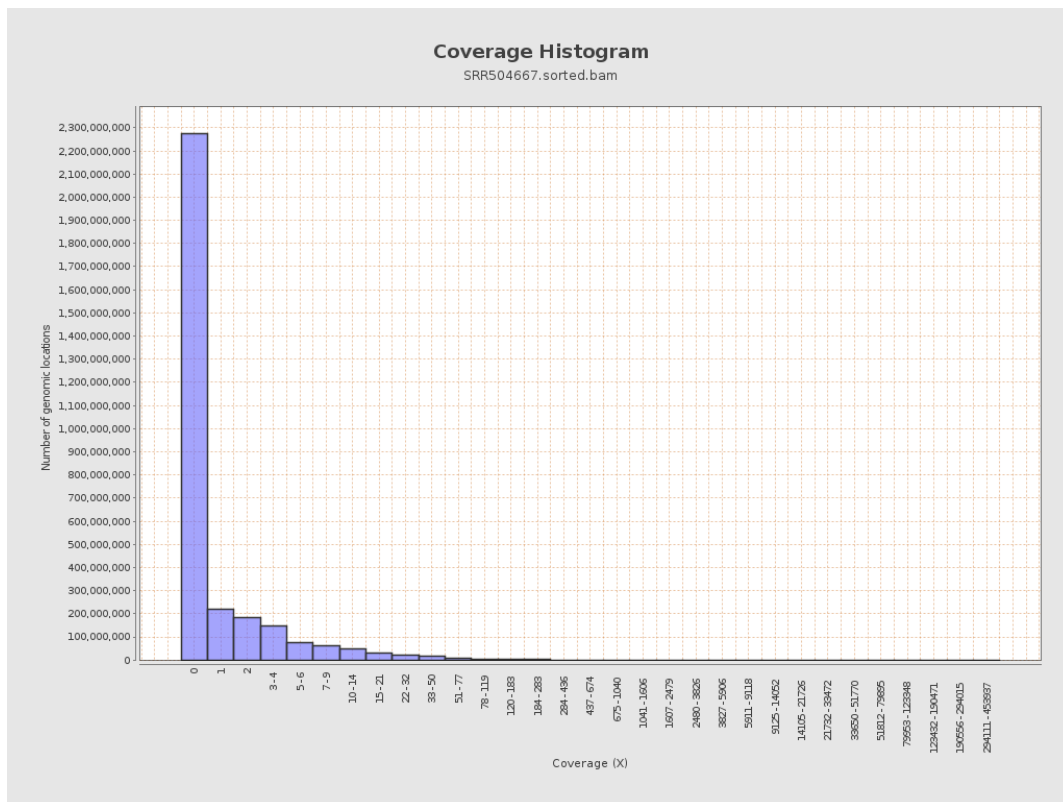
		bases	coverage	deviation
chr1	249250621	549279605	2.2037	24.2701
chr2	243199373	2455873460	10.0982	1,232.8533
chr3	198022430	543006966	2.7421	17.6988
chr4	191154276	510324224	2.6697	18.0327
chr5	180915260	430658413	2.3804	15.4637
chr6	171115067	399541465	2.3349	11.8775
chr7	159138663	338676310	2.1282	12.0698
chr8	146364022	401058955	2.7401	26.2292
chr9	141213431	325944141	2.3082	25.9905
chr10	135534747	311906863	2.3013	14.094
chr11	135006516	306736042	2.272	13.931
chr12	133851895	316668690	2.3658	11.717
chr13	115169878	201968199	1.7537	9.1824
chr14	107349540	218261115	2.0332	11.7841
chr15	102531392	194617371	1.8981	30.0676
chr16	90354753	148251766	1.6408	10.4532
chr17	81195210	124063913	1.528	7.1088
chr18	78077248	213443647	2.7337	15.526
chr19	59128983	89152631	1.5078	18.7365
chr20	63025520	119933225	1.9029	10.6872
chr21	48129895	90935230	1.8894	12.8881
chr22	51304566	62352699	1.2153	11.6342
chrMT	16571	2547	0.1537	0.7574
chrX	155270560	15385822	0.0991	2.915

chrY	59373566	53734924	0.905	7.9473
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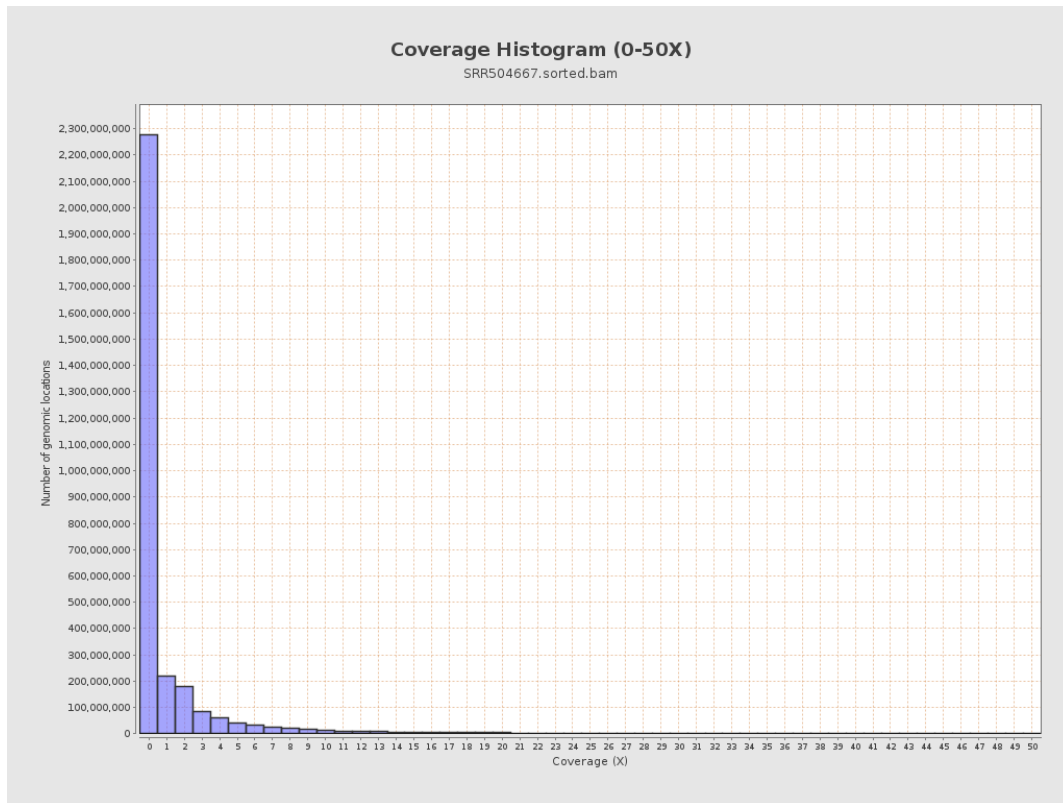
3. Results : Coverage across reference



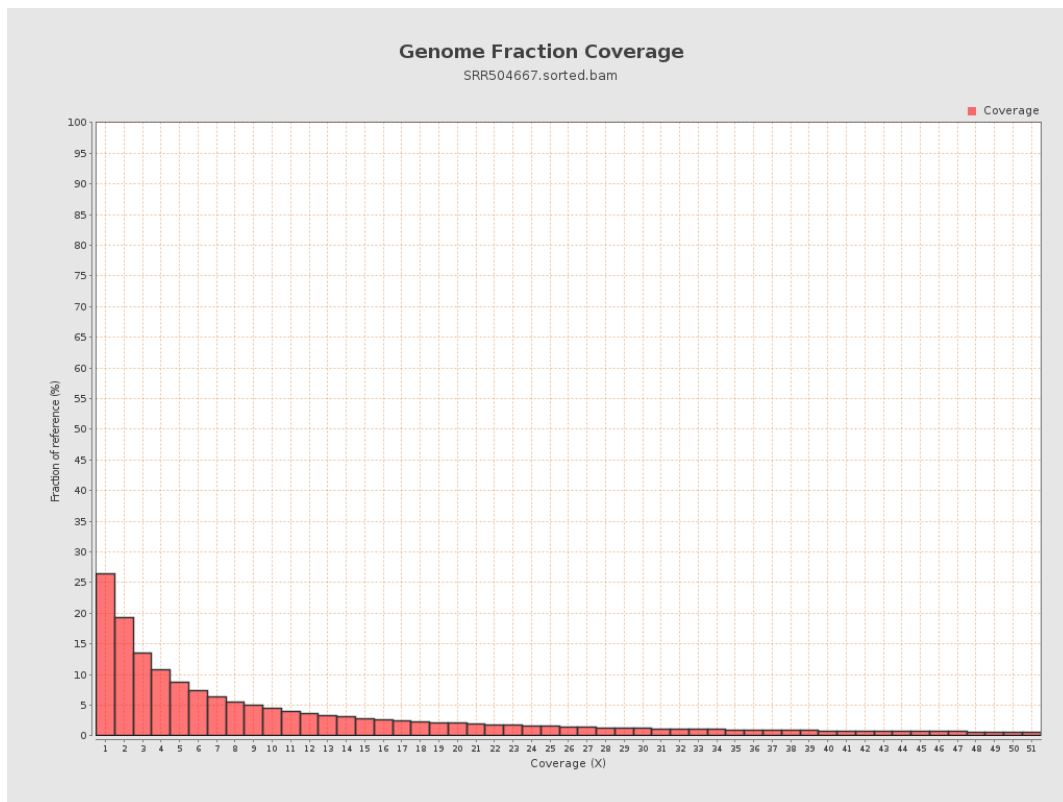
4. Results : Coverage Histogram



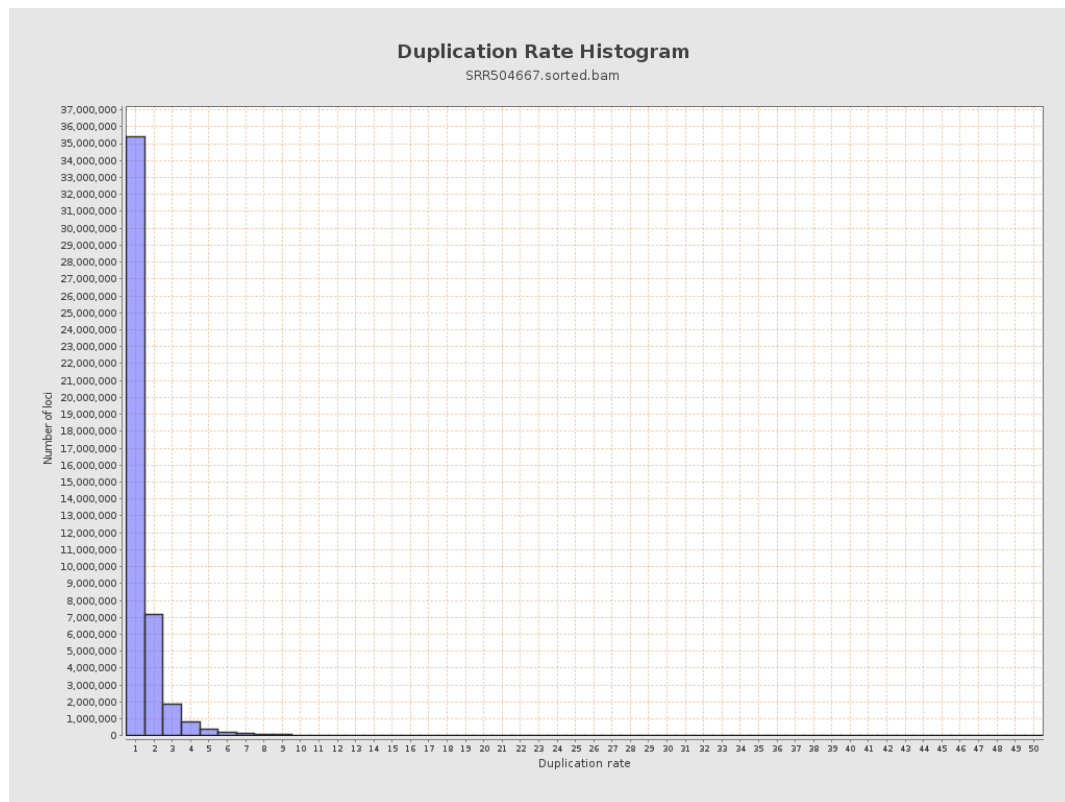
5. Results : Coverage Histogram (0-50X)



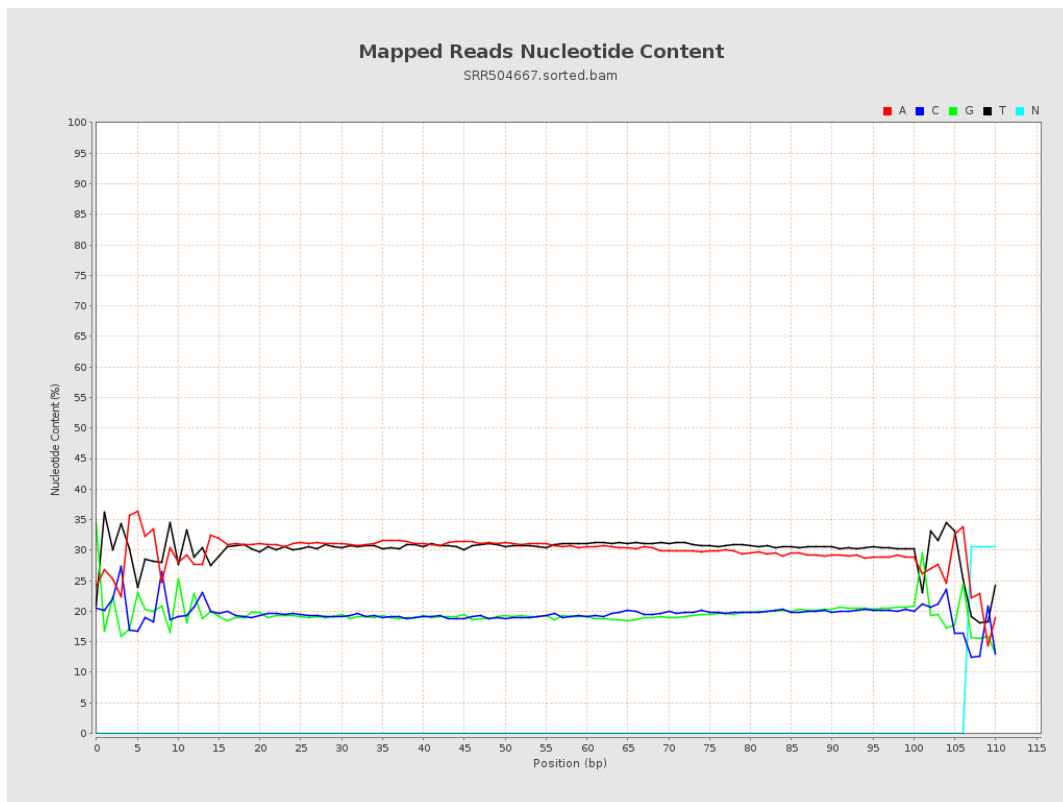
6. Results : Genome Fraction Coverage



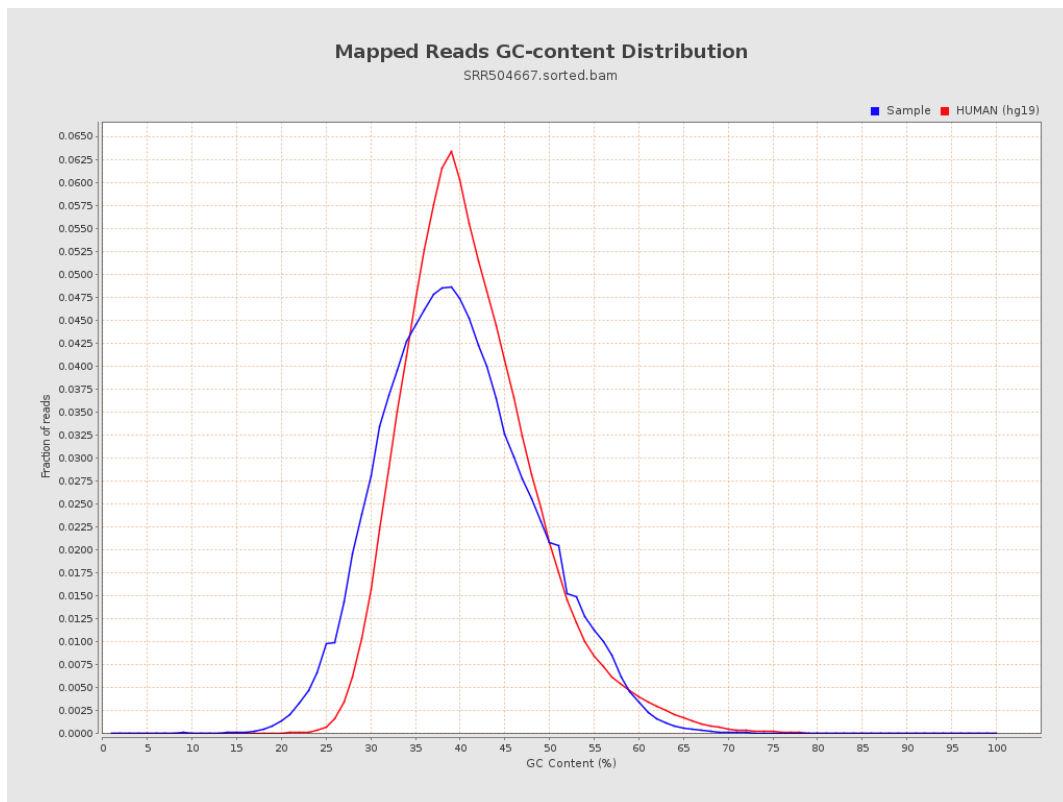
7. Results : Duplication Rate Histogram



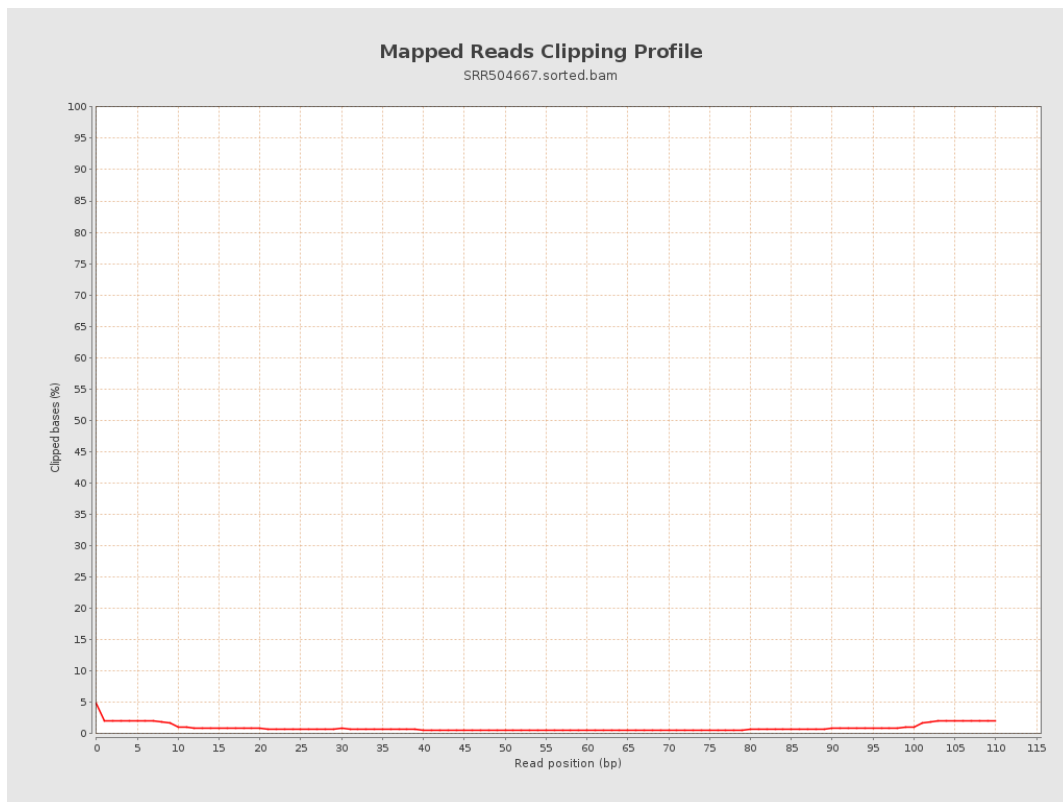
8. Results : Mapped Reads Nucleotide Content



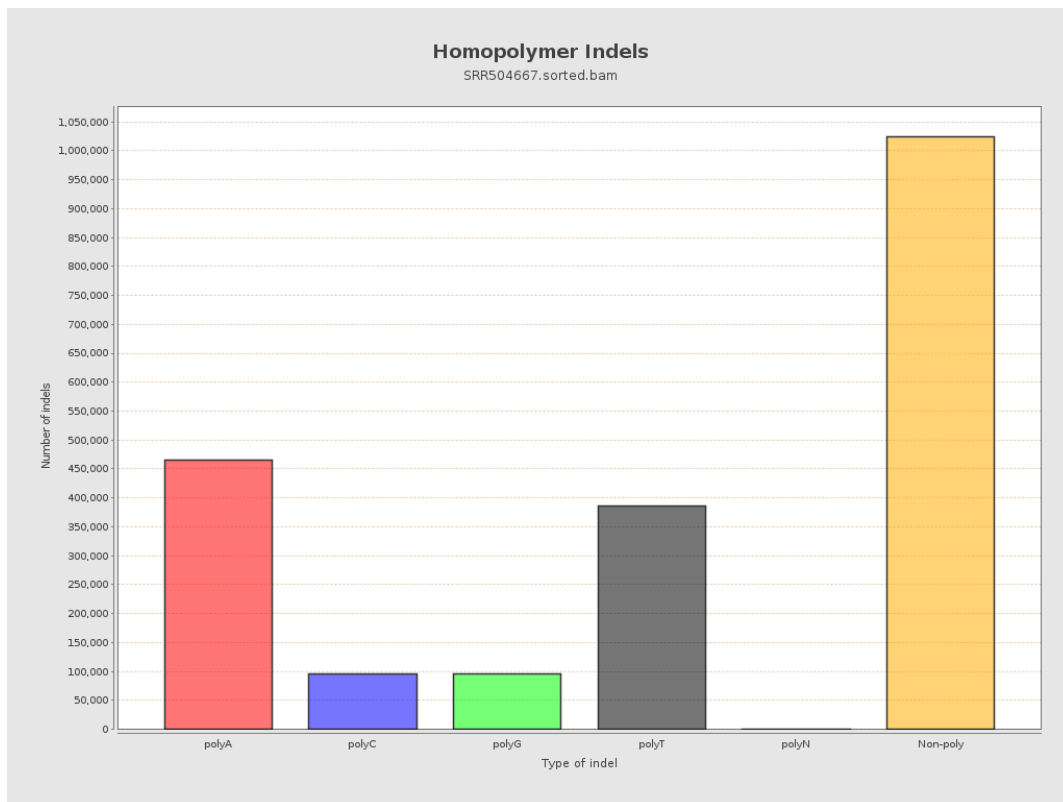
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



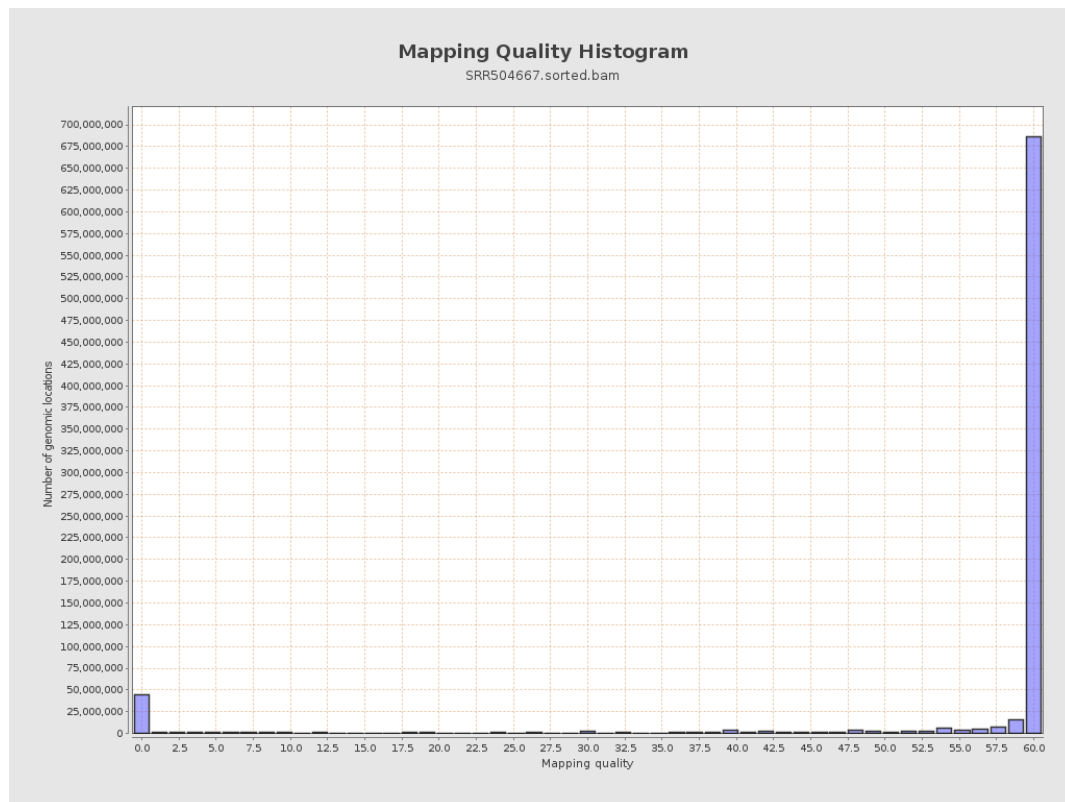
11. Results : Homopolymer Indels



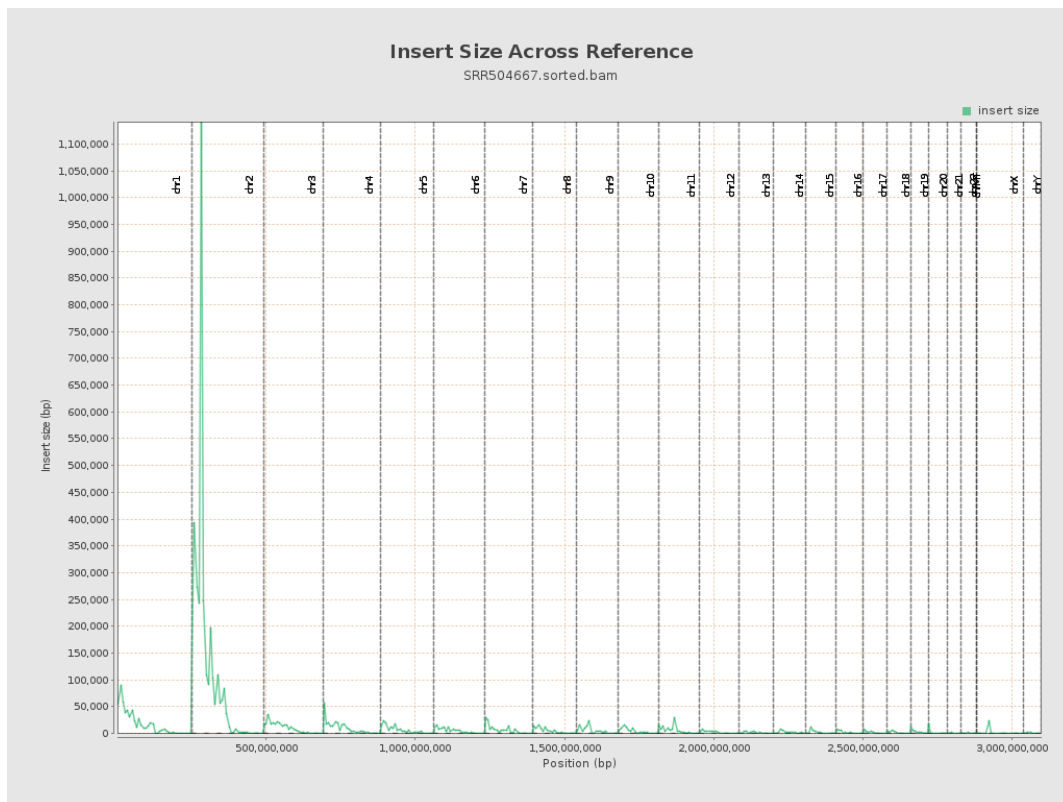
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

