

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/25 04:55:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504673.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_SRR504673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504673_1.fastq.gz SRR504673_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jun 25 04:55:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	91,791,990
Mapped reads	91,363,235 / 99.53%
Unmapped reads	428,755 / 0.47%
Mapped paired reads	91,363,235 / 99.53%
Mapped reads, first in pair	45,730,850 / 49.82%
Mapped reads, second in pair	45,632,385 / 49.71%
Mapped reads, both in pair	91,222,086 / 99.38%
Mapped reads, singletons	141,149 / 0.15%
Secondary alignments	0
Supplementary alignments	1,372,855 / 1.5%
Read min/max/mean length	30 / 121 / 111.65
Duplicated reads (estimated)	42,277,244 / 46.06%
Duplication rate	27.98%
Clipped reads	35,213,751 / 38.36%

2.2. ACGT Content

Number/percentage of A's	2,694,367,069 / 29.77%
Number/percentage of C's	1,775,781,029 / 19.62%
Number/percentage of T's	2,733,453,100 / 30.21%
Number/percentage of G's	1,773,670,130 / 19.6%
Number/percentage of N's	71,965,989 / 0.8%

GC Percentage	39.22%
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2.3. Coverage

Mean	2.9239
Standard Deviation	369.8762

2.4. Mapping Quality

Mean Mapping Quality	53.28
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2.5. Insert size

Mean	29,956.76
Standard Deviation	1,619,527.75
P25/Median/P75	94 / 146 / 221

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	93,351,463
Insertions	965,329
Mapped reads with at least one insertion	1.04%
Deletions	1,208,692
Mapped reads with at least one deletion	1.3%
Homopolymer indels	50.95%

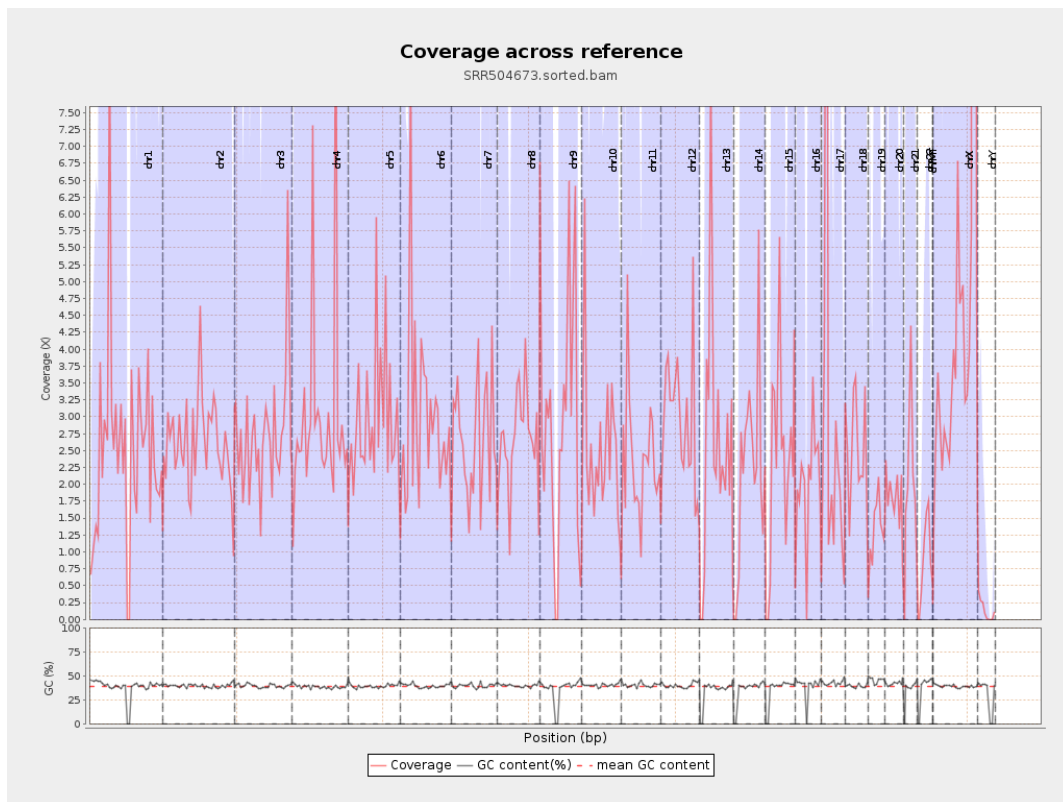
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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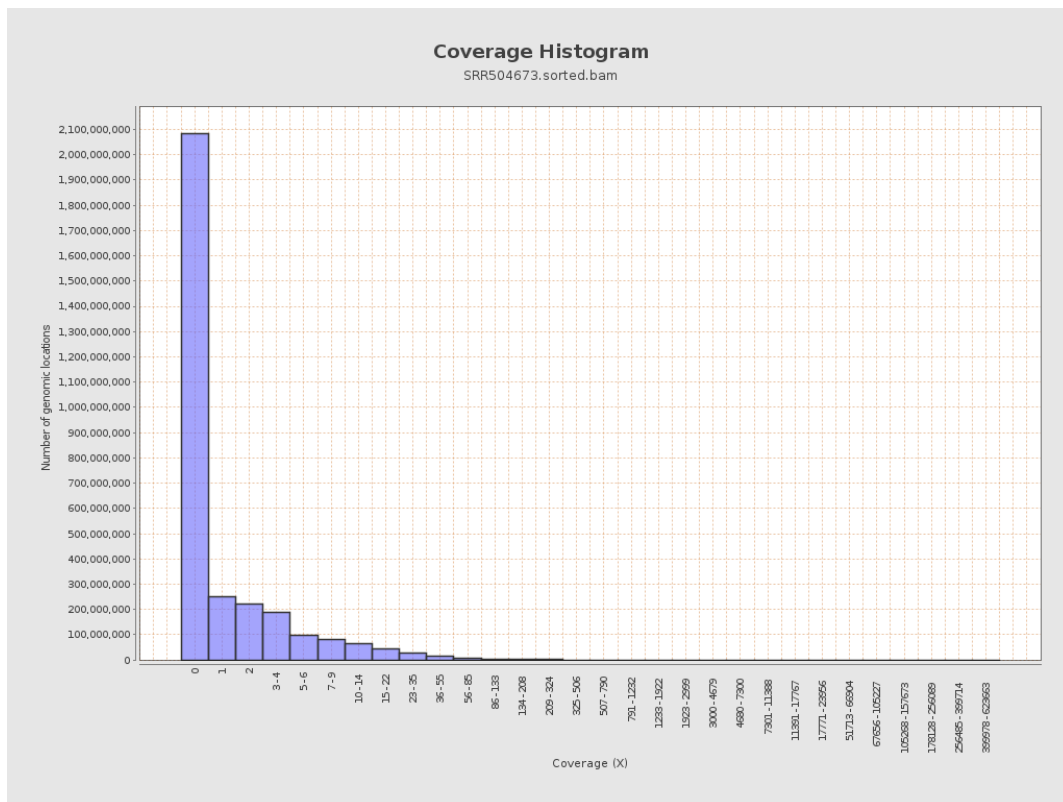
		bases	coverage	deviation
chr1	249250621	623269347	2.5006	36.9794
chr2	243199373	633358947	2.6043	14.979
chr3	198022430	539926439	2.7266	26.4745
chr4	191154276	579562608	3.0319	49.8702
chr5	180915260	528048379	2.9188	17.7415
chr6	171115067	502786528	2.9383	30.1738
chr7	159138663	421584625	2.6492	14.854
chr8	146364022	388885134	2.657	9.6232
chr9	141213431	396289986	2.8063	35.2812
chr10	135534747	342922586	2.5301	39.9093
chr11	135006516	320138605	2.3713	14.0481
chr12	133851895	396420102	2.9616	32.3457
chr13	115169878	294571140	2.5577	46.2741
chr14	107349540	238862798	2.2251	15.1095
chr15	102531392	234029783	2.2825	16.851
chr16	90354753	178544567	1.976	9.8504
chr17	81195210	260502829	3.2084	139.0409
chr18	78077248	194607495	2.4925	12.5789
chr19	59128983	80238924	1.357	6.8582
chr20	63025520	114375601	1.8148	7.2046
chr21	48129895	94333372	1.96	11.7663
chr22	51304566	45796318	0.8926	3.4955
chrMT	16571	3769	0.2274	1.3968
chrX	155270560	1634582706	10.5273	1,644.2299

chrY	59373566	7886463	0.1328	1.9196
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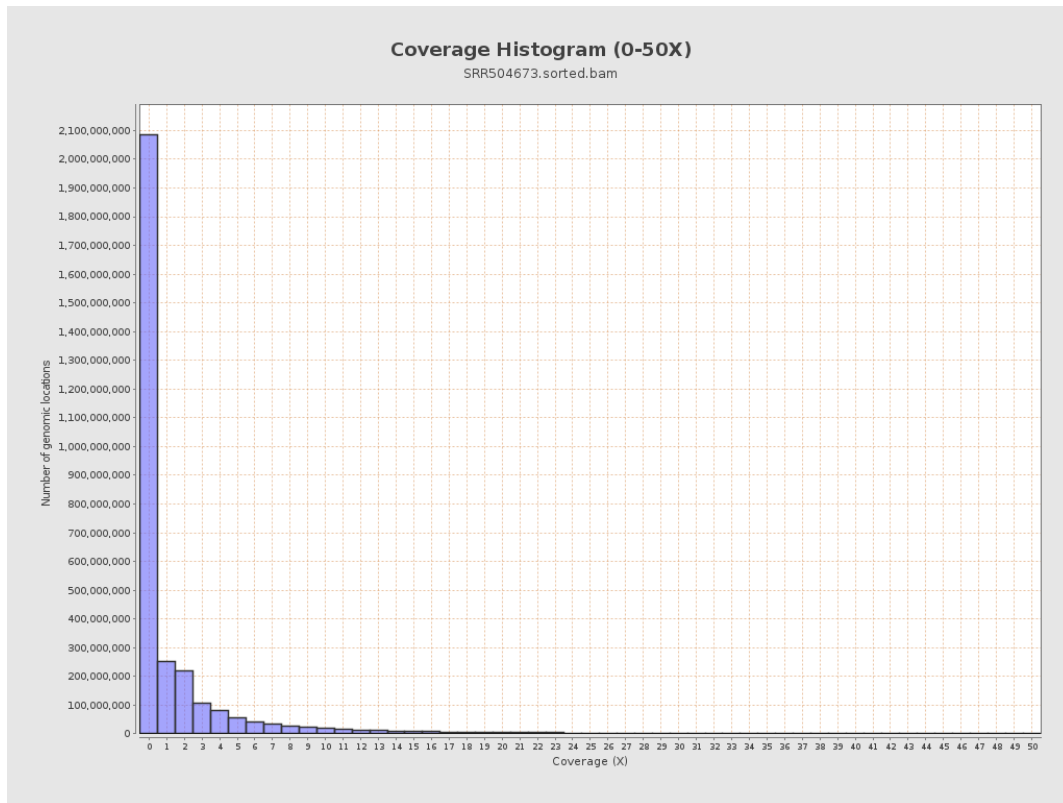
3. Results : Coverage across reference



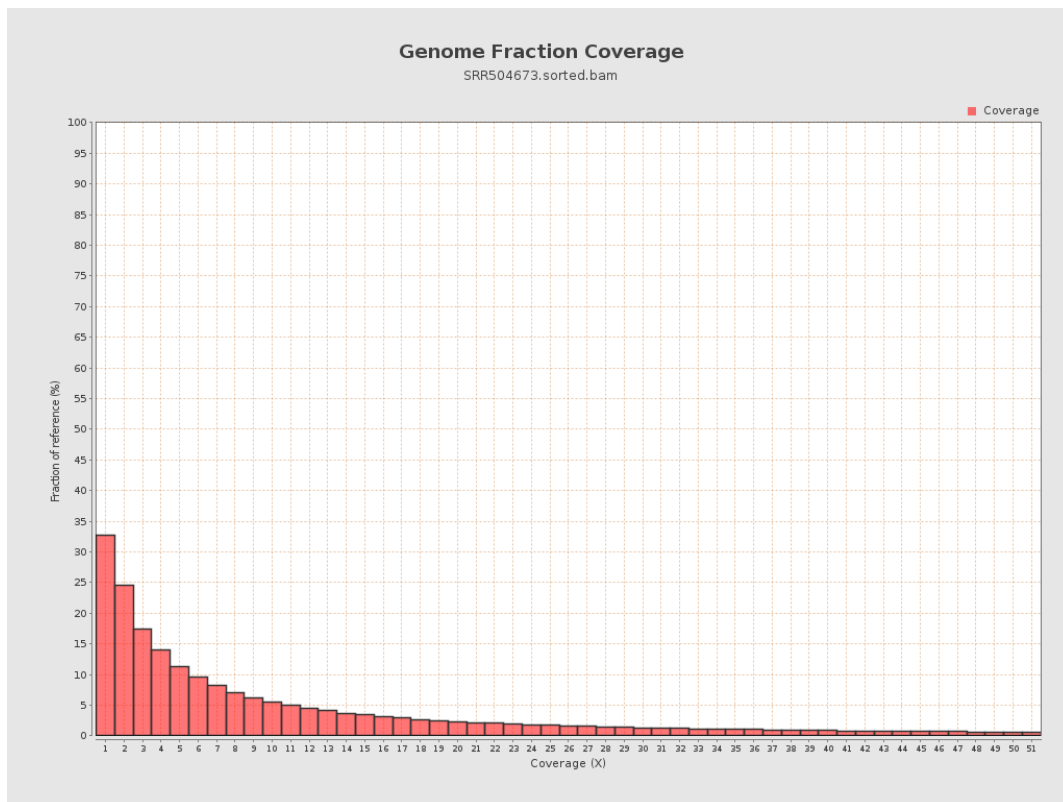
4. Results : Coverage Histogram



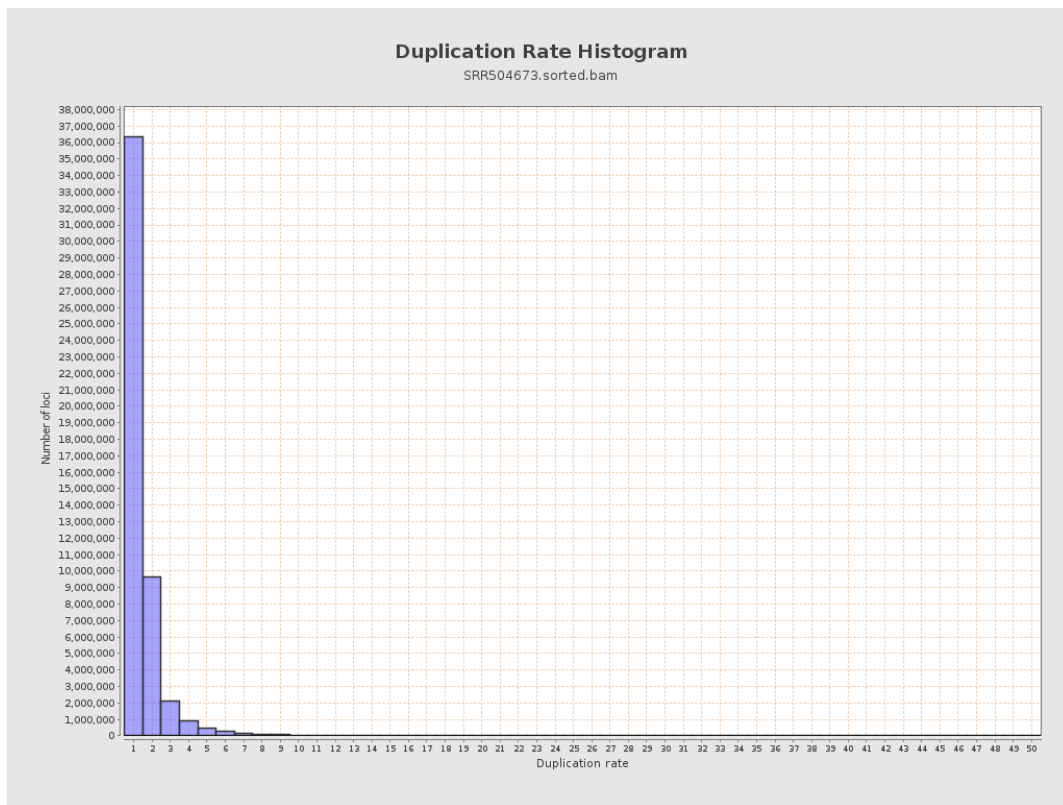
5. Results : Coverage Histogram (0-50X)



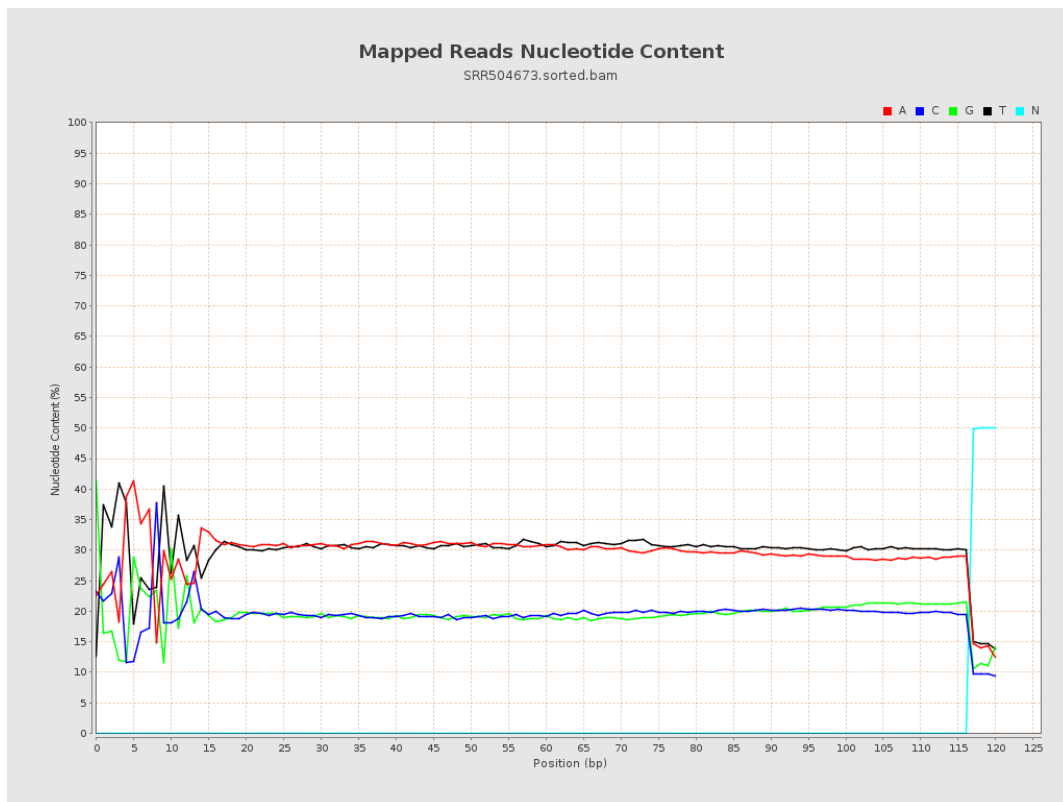
6. Results : Genome Fraction Coverage



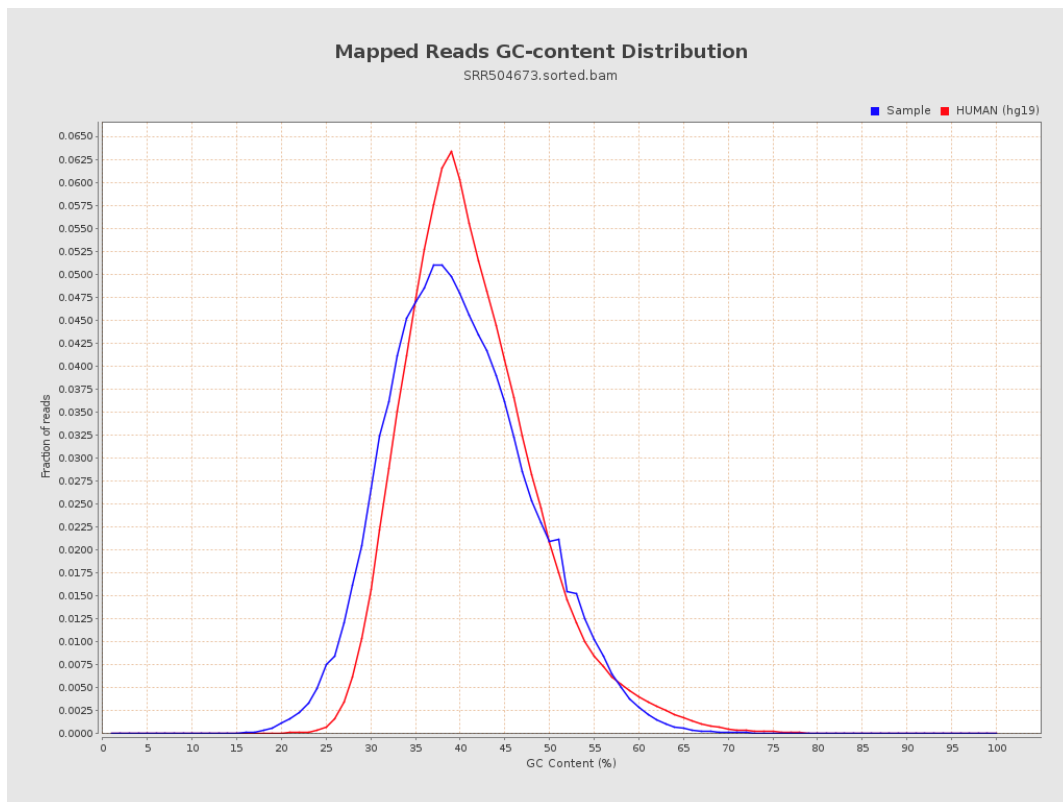
7. Results : Duplication Rate Histogram



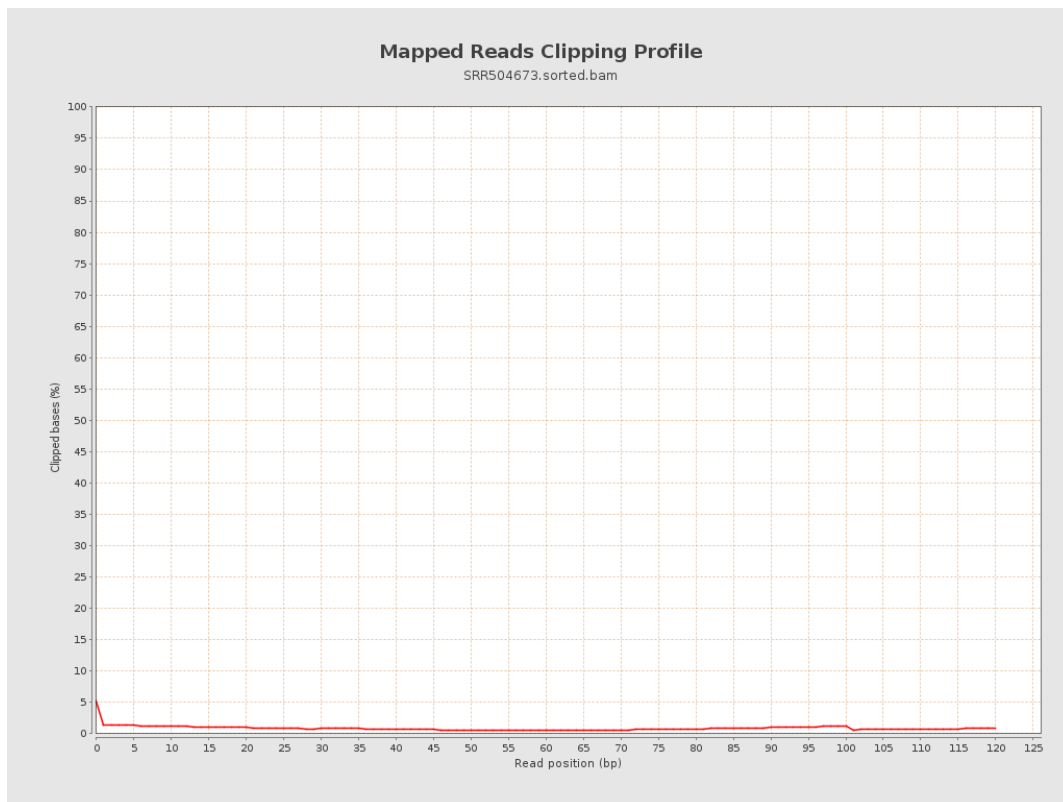
8. Results : Mapped Reads Nucleotide Content



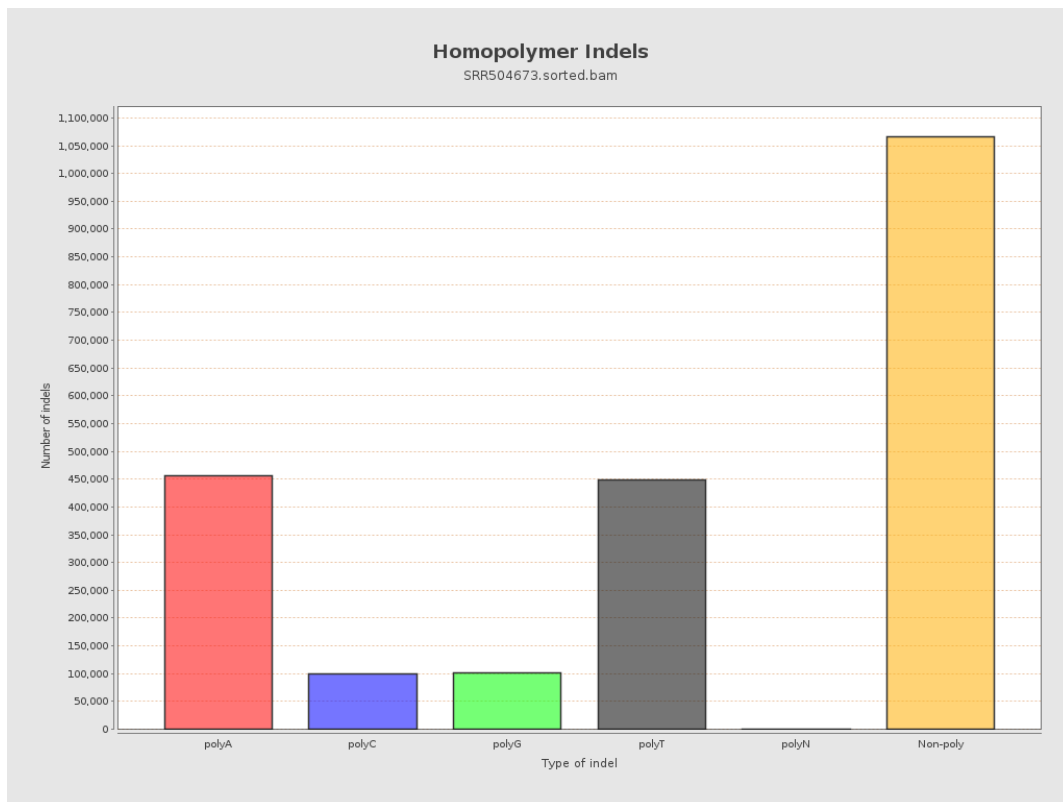
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



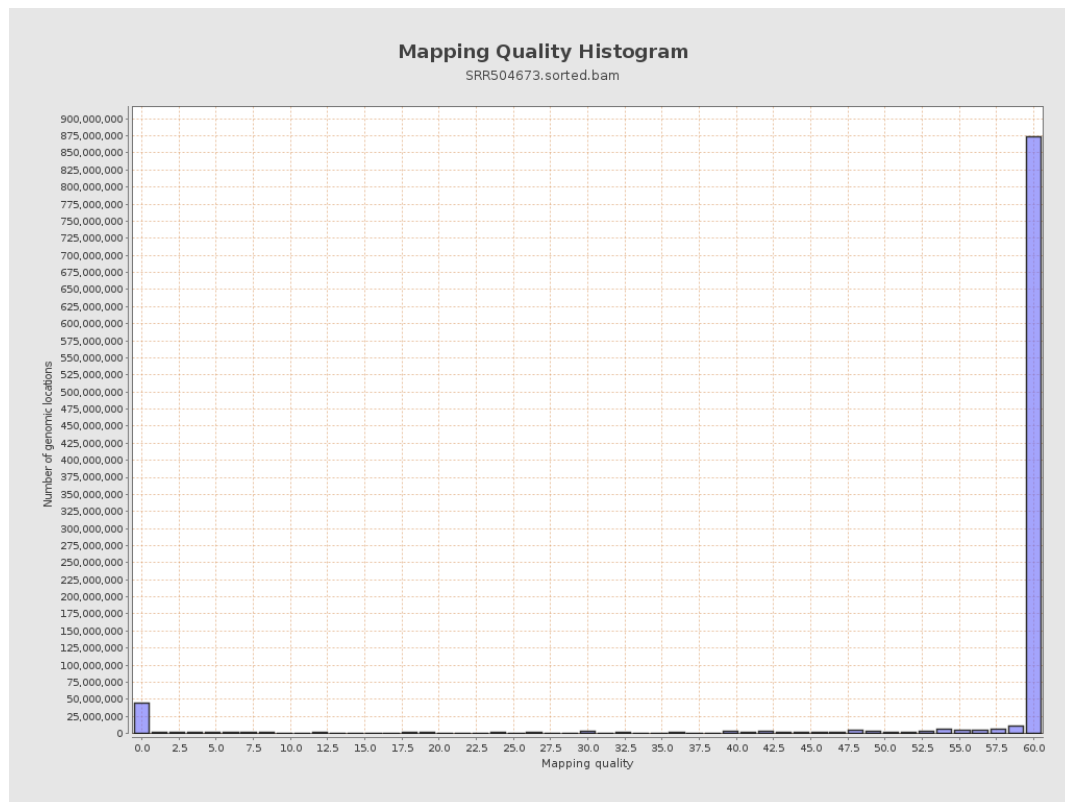
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

