

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 06:22:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504666.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_SRR504666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504666_1.fastq.gz SRR504666_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 06:22:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	89,173,462
Mapped reads	88,782,516 / 99.56%
Unmapped reads	390,946 / 0.44%
Mapped paired reads	88,782,516 / 99.56%
Mapped reads, first in pair	44,480,764 / 49.88%
Mapped reads, second in pair	44,301,752 / 49.68%
Mapped reads, both in pair	88,566,880 / 99.32%
Mapped reads, singletons	215,636 / 0.24%
Secondary alignments	0
Supplementary alignments	1,138,772 / 1.28%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	46,505,880 / 52.15%
Duplication rate	27.19%
Clipped reads	27,910,014 / 31.3%

2.2. ACGT Content

Number/percentage of A's	2,496,646,180 / 30.22%
Number/percentage of C's	1,632,301,881 / 19.75%
Number/percentage of T's	2,518,046,398 / 30.47%
Number/percentage of G's	1,611,123,823 / 19.5%
Number/percentage of N's	4,687,774 / 0.06%

GC Percentage	39.25%
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2.3. Coverage

Mean	2.6713
Standard Deviation	339.4808

2.4. Mapping Quality

Mean Mapping Quality	51.18
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2.5. Insert size

Mean	38,638.98
Standard Deviation	1,842,593.6
P25/Median/P75	98 / 150 / 222

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	83,117,687
Insertions	2,641,979
Mapped reads with at least one insertion	2.91%
Deletions	2,825,340
Mapped reads with at least one deletion	3.1%
Homopolymer indels	37.98%

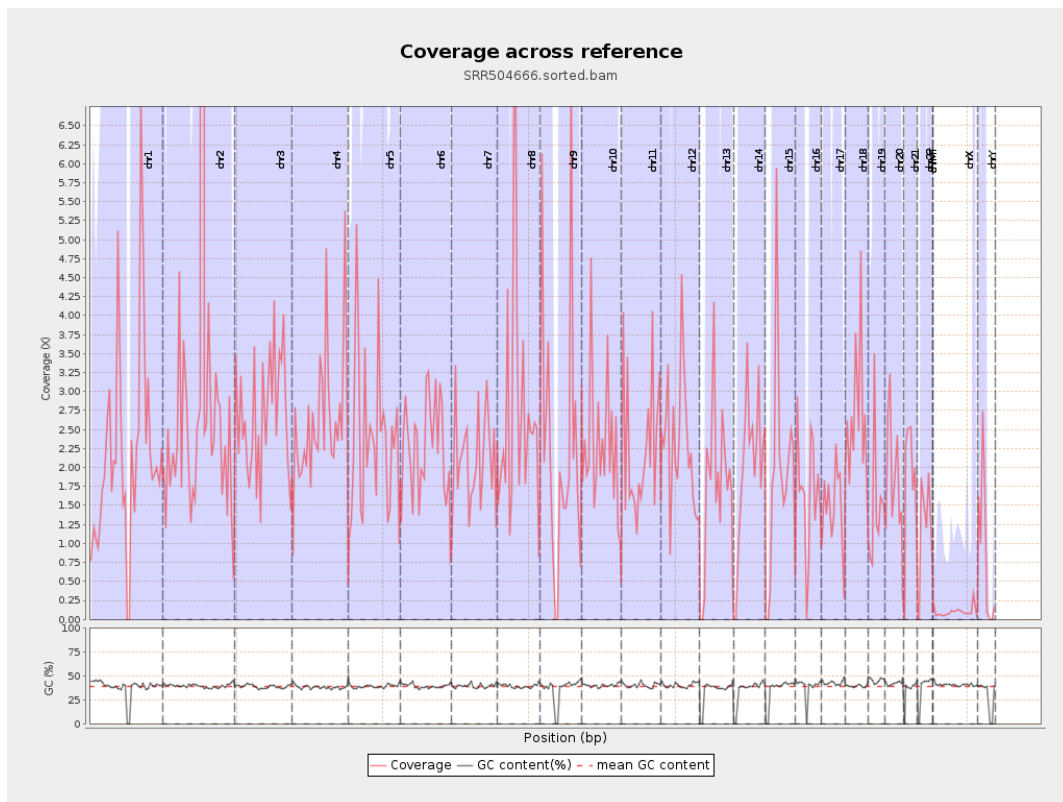
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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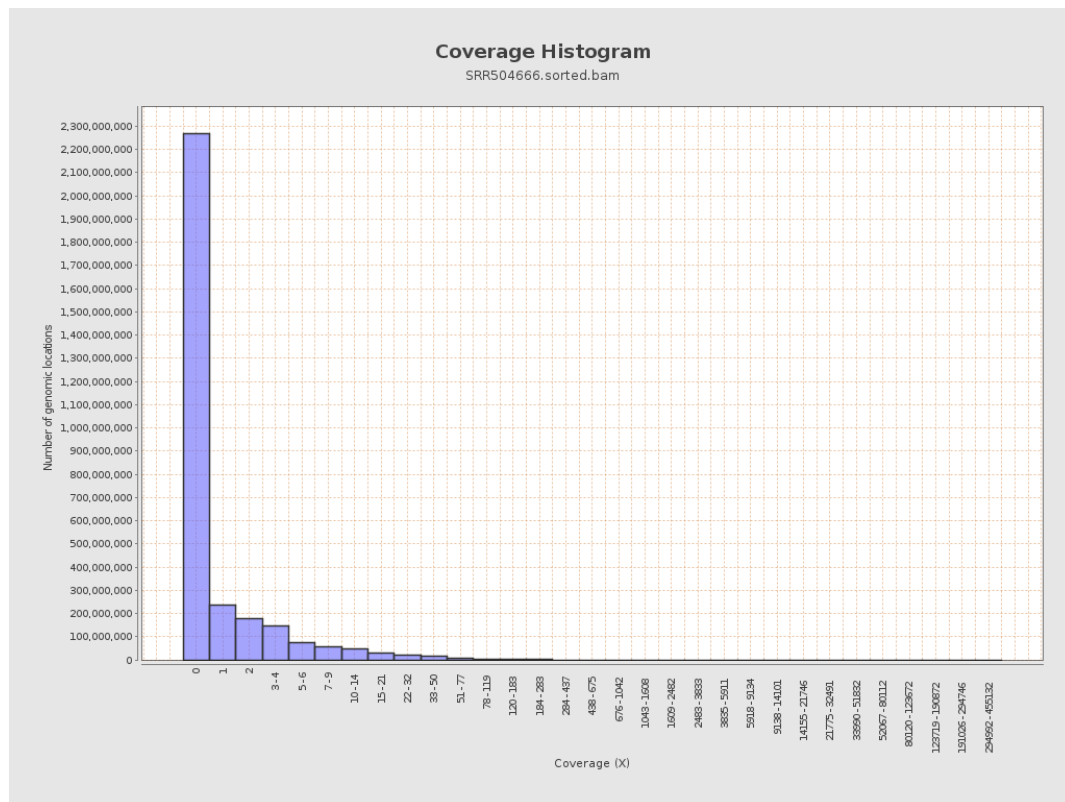
		bases	coverage	deviation
chr1	249250621	539506320	2.1645	23.7583
chr2	243199373	2413298801	9.9231	1,209.8366
chr3	198022430	533382611	2.6935	15.4074
chr4	191154276	500197788	2.6167	17.7118
chr5	180915260	422321268	2.3344	15.172
chr6	171115067	392263865	2.2924	11.634
chr7	159138663	332615556	2.0901	11.4303
chr8	146364022	393872556	2.691	25.7036
chr9	141213431	320327288	2.2684	25.7469
chr10	135534747	305732153	2.2557	13.8044
chr11	135006516	300858062	2.2285	13.6373
chr12	133851895	310477111	2.3196	11.4532
chr13	115169878	198847566	1.7266	9.0165
chr14	107349540	215046439	2.0032	11.9717
chr15	102531392	190720041	1.8601	29.3902
chr16	90354753	145357593	1.6087	10.2263
chr17	81195210	121458358	1.4959	6.9009
chr18	78077248	209745216	2.6864	15.1076
chr19	59128983	87364782	1.4775	18.3138
chr20	63025520	117322191	1.8615	10.3798
chr21	48129895	89305609	1.8555	12.8601
chr22	51304566	61314818	1.1951	11.4664
chrMT	16571	1529	0.0923	0.445
chrX	155270560	15452146	0.0995	3.3057

chrY	59373566	52859325	0.8903	7.8506
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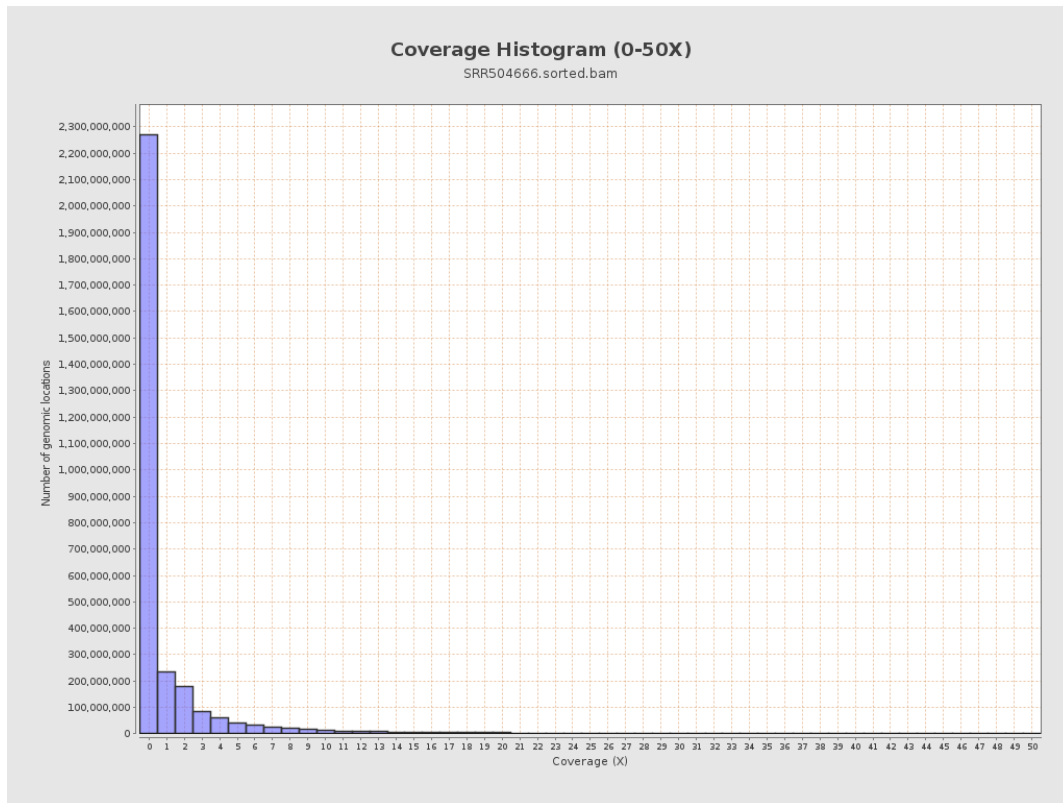
3. Results : Coverage across reference



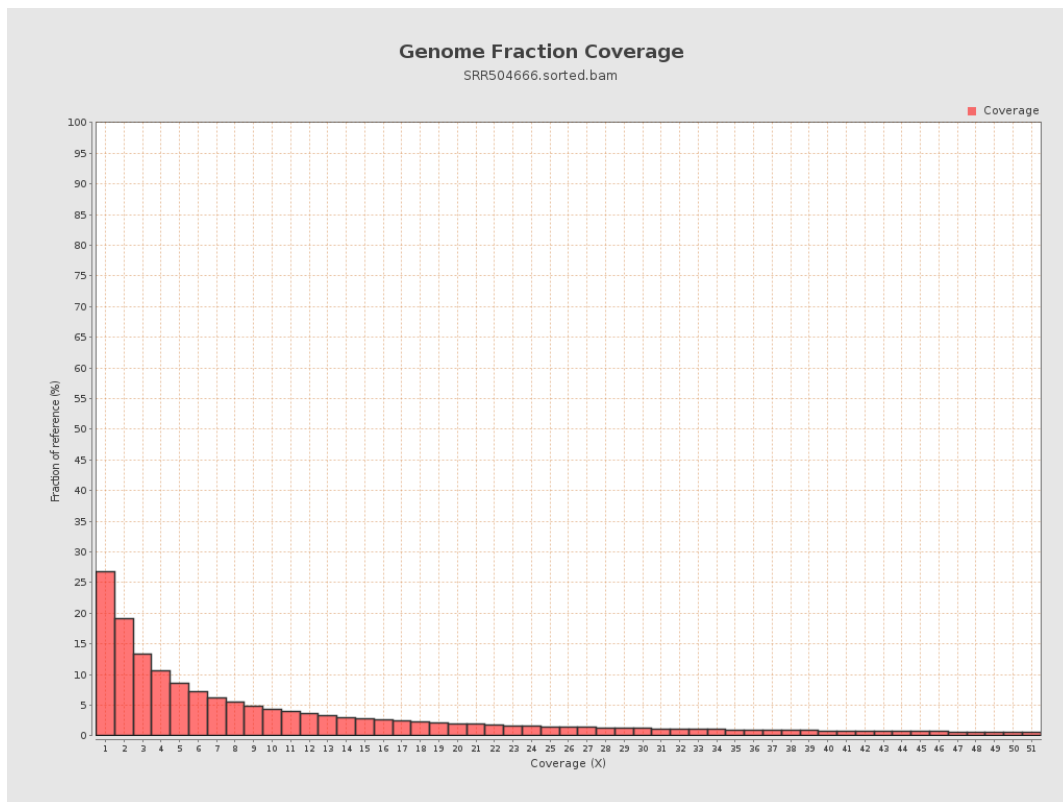
4. Results : Coverage Histogram



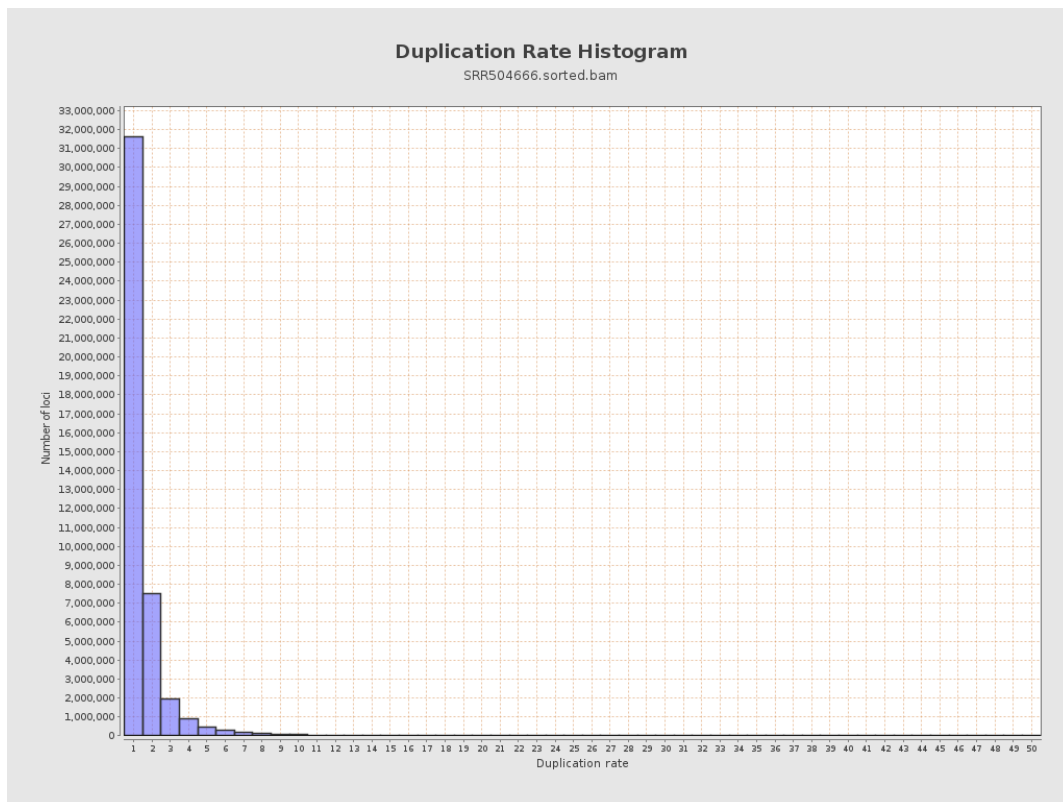
5. Results : Coverage Histogram (0-50X)



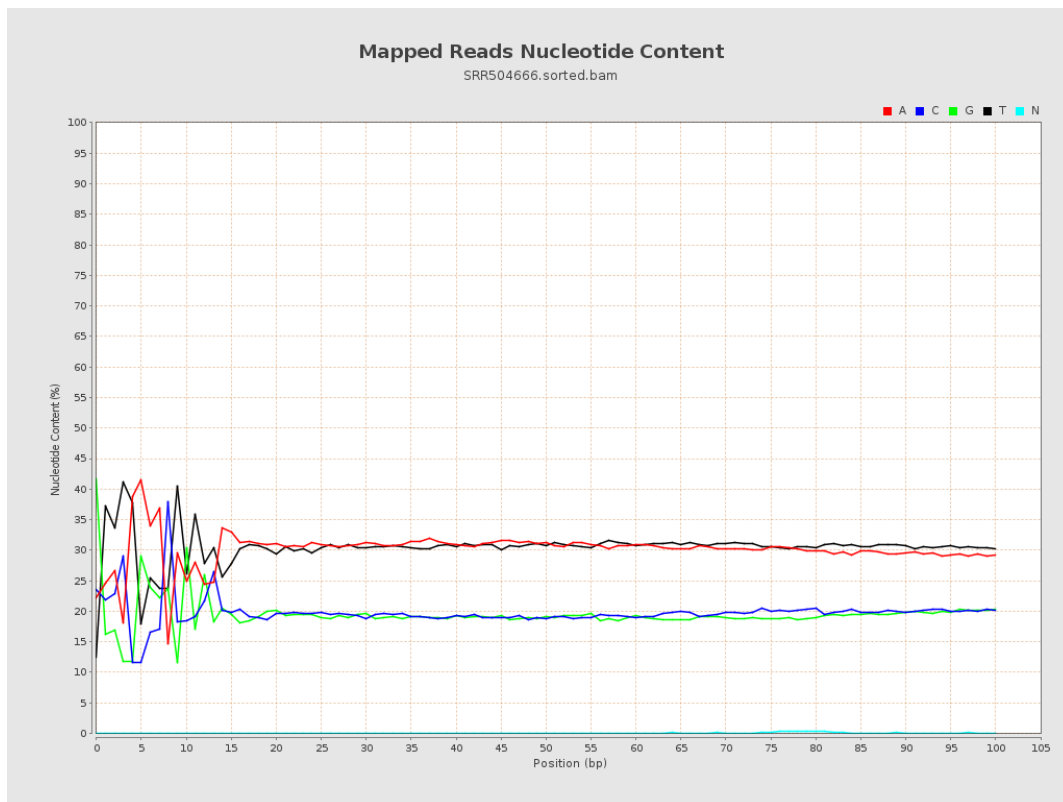
6. Results : Genome Fraction Coverage



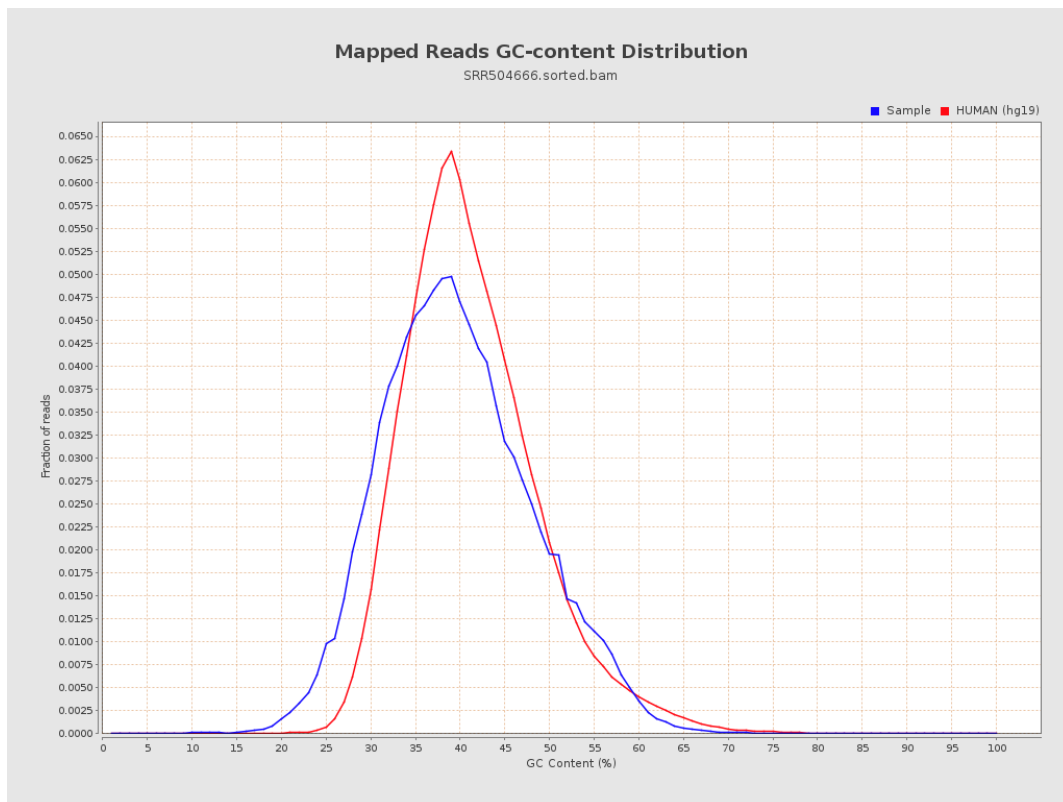
7. Results : Duplication Rate Histogram



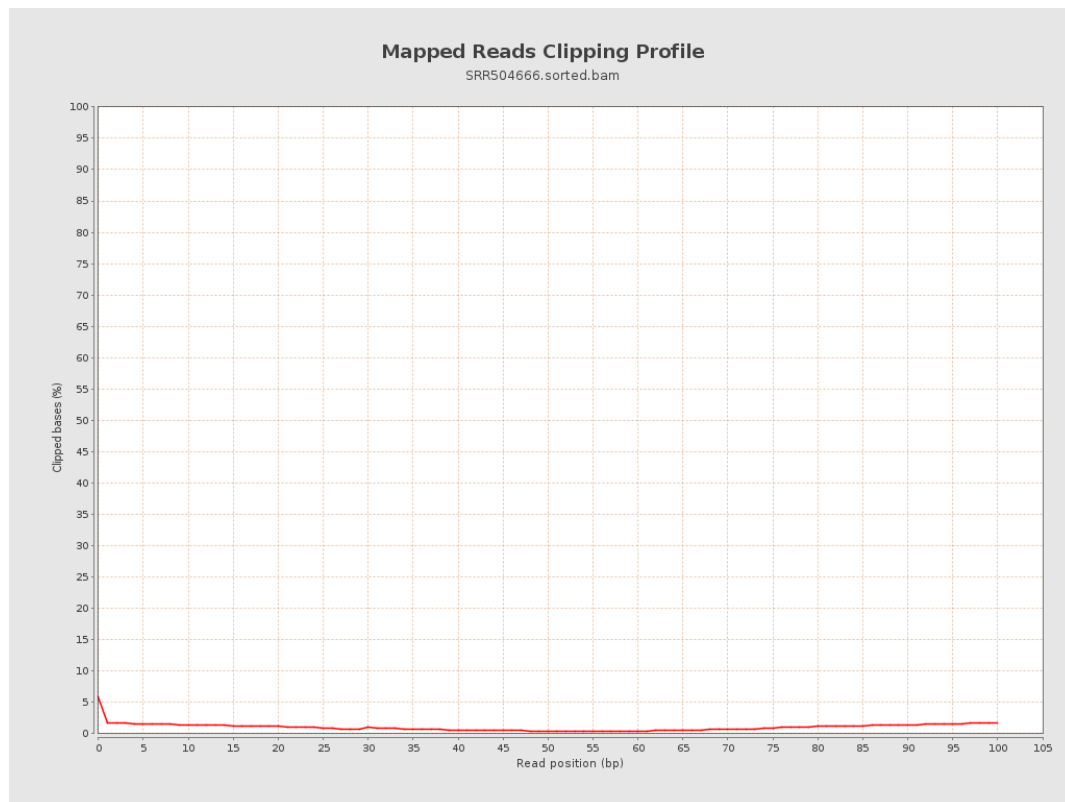
8. Results : Mapped Reads Nucleotide Content



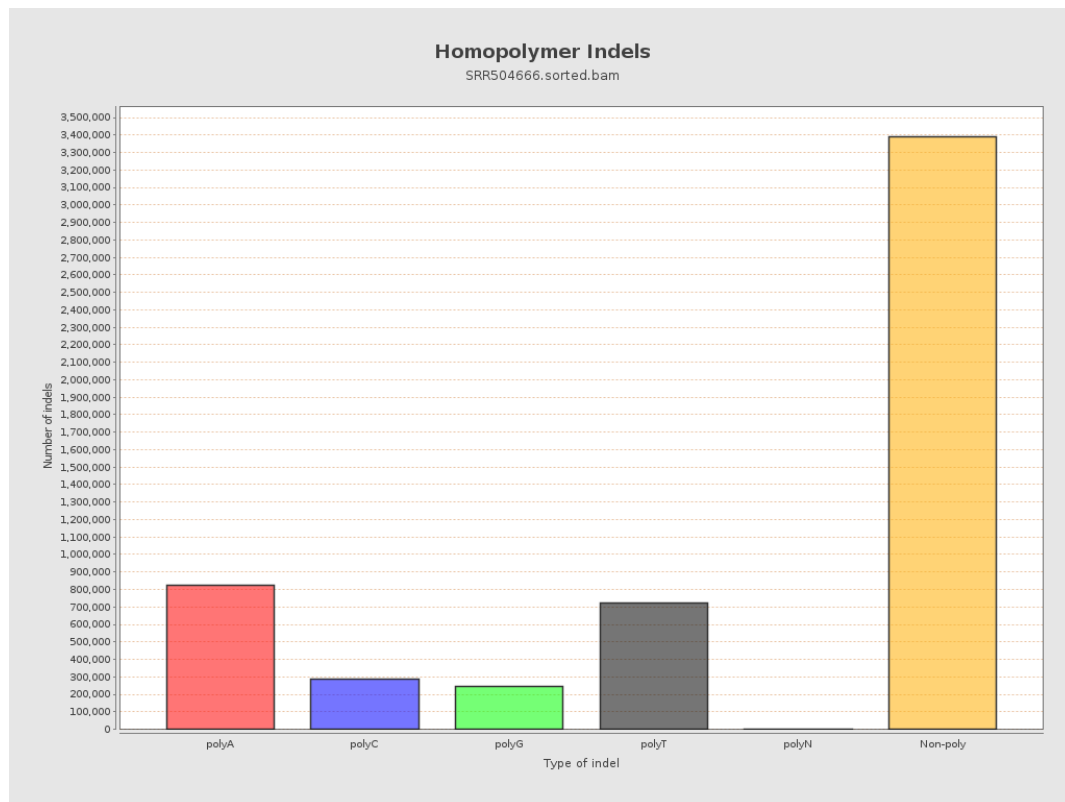
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



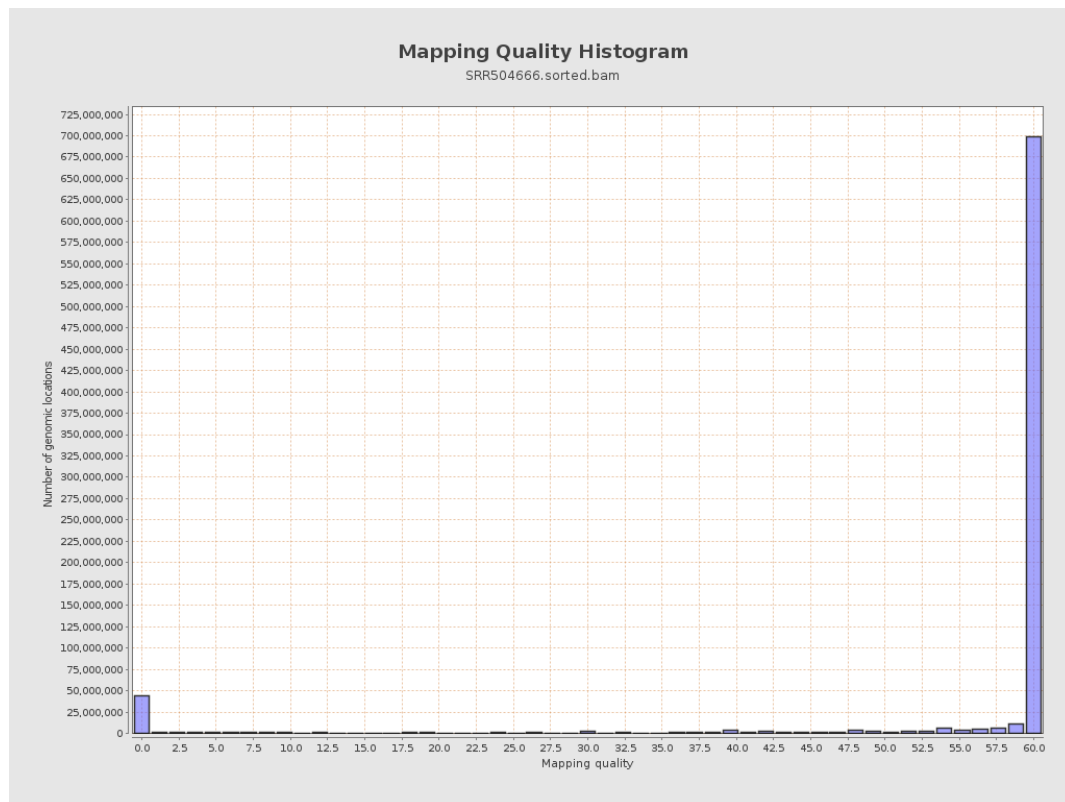
11. Results : Homopolymer Indels



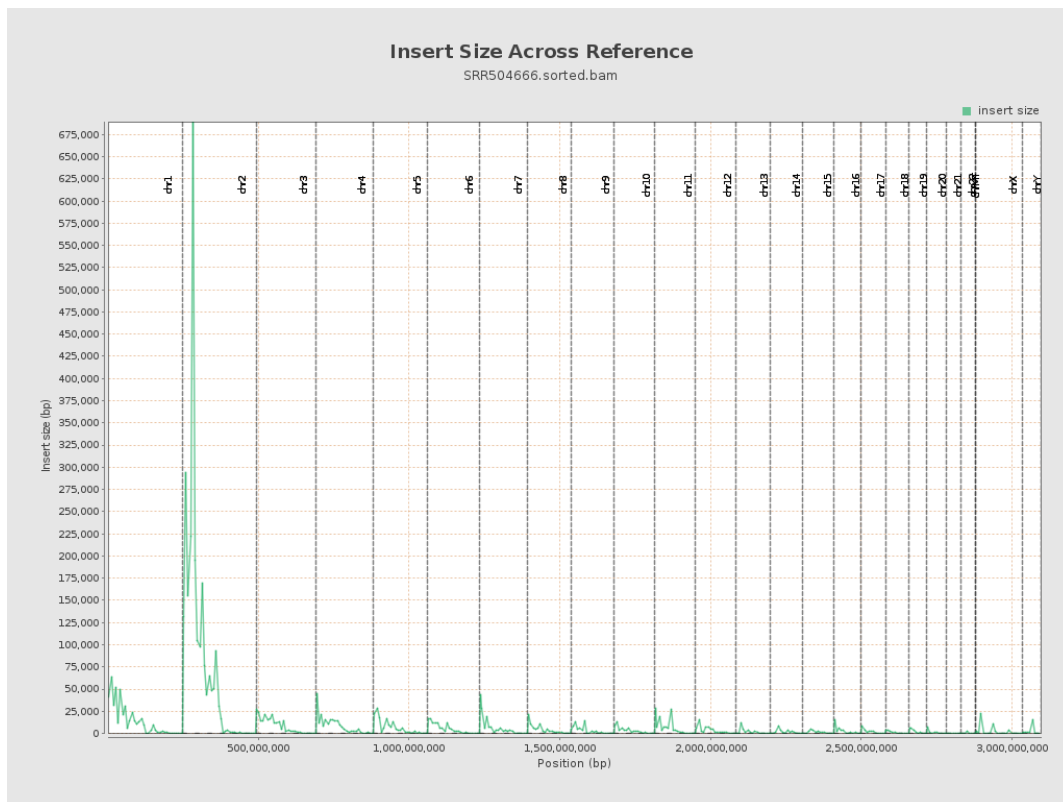
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

