

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/24 13:13:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504668.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_SRR504668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504668_1.fastq.gz SRR504668_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jun 24 13:13:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	123,351,530
Mapped reads	122,775,572 / 99.53%
Unmapped reads	575,958 / 0.47%
Mapped paired reads	122,775,572 / 99.53%
Mapped reads, first in pair	61,471,167 / 49.83%
Mapped reads, second in pair	61,304,405 / 49.7%
Mapped reads, both in pair	122,556,994 / 99.36%
Mapped reads, singletons	218,578 / 0.18%
Secondary alignments	0
Supplementary alignments	1,326,382 / 1.08%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	69,167,891 / 56.07%
Duplication rate	27.45%
Clipped reads	31,363,238 / 25.43%

2.2. ACGT Content

Number/percentage of A's	3,558,436,868 / 30.54%
Number/percentage of C's	2,250,584,433 / 19.31%
Number/percentage of T's	3,596,089,056 / 30.86%
Number/percentage of G's	2,238,169,244 / 19.21%
Number/percentage of N's	9,611,876 / 0.08%

GC Percentage	38.52%
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2.3. Coverage

Mean	3.7653
Standard Deviation	196.9627

2.4. Mapping Quality

Mean Mapping Quality	51.23
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2.5. Insert size

Mean	31,806.02
Standard Deviation	1,745,250.16
P25/Median/P75	107 / 164 / 235

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	61,978,300
Insertions	1,356,998
Mapped reads with at least one insertion	1.1%
Deletions	1,466,833
Mapped reads with at least one deletion	1.18%
Homopolymer indels	52.13%

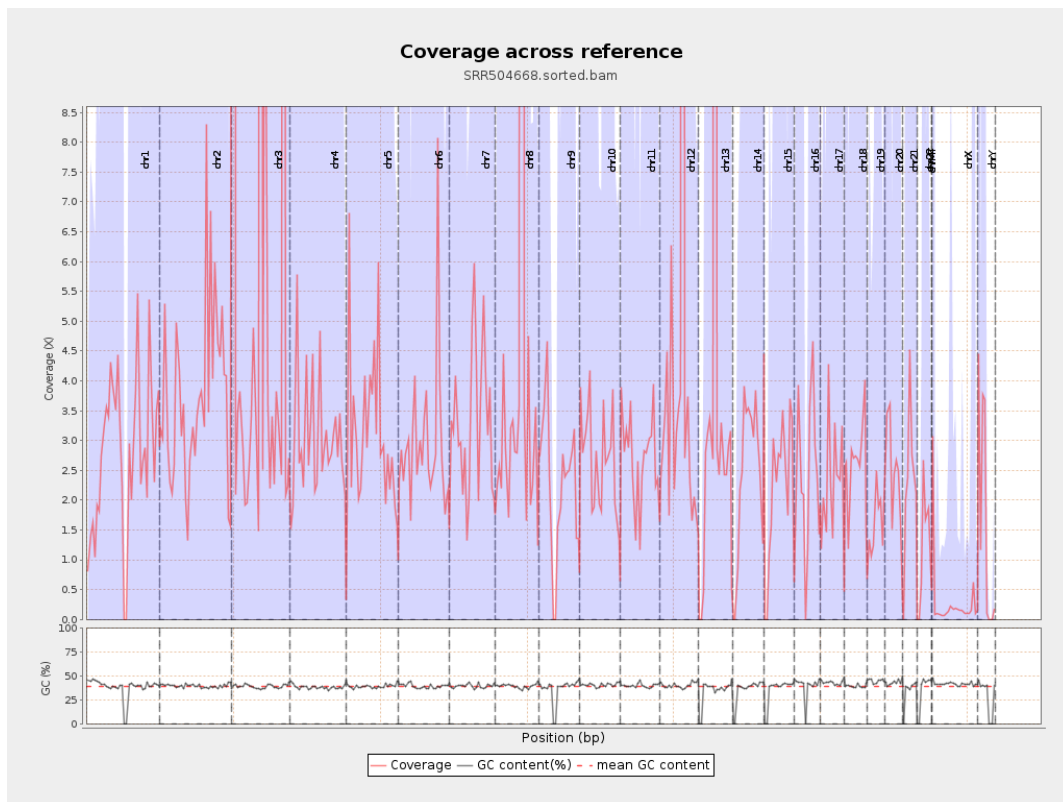
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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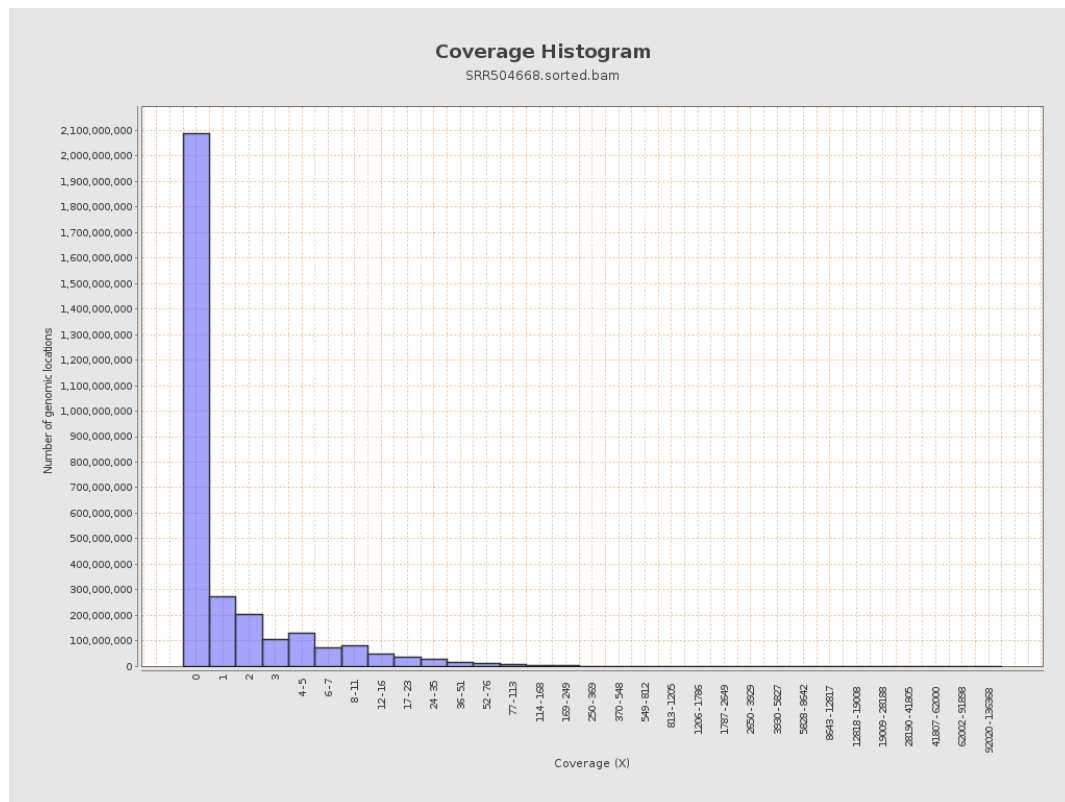
		bases	coverage	deviation
chr1	249250621	695881628	2.7919	14.3268
chr2	243199373	902119726	3.7094	28.7885
chr3	198022430	2241641242	11.3201	583.268
chr4	191154276	582844892	3.0491	15.7734
chr5	180915260	560622772	3.0988	20.1592
chr6	171115067	512223996	2.9934	47.2395
chr7	159138663	520757421	3.2724	15.9272
chr8	146364022	1241370487	8.4814	373.6933
chr9	141213431	314479641	2.227	11.1475
chr10	135534747	366898848	2.707	14.3993
chr11	135006516	363727694	2.6941	13.7308
chr12	133851895	1045589265	7.8115	403.1165
chr13	115169878	655912939	5.6952	286.1685
chr14	107349540	264097756	2.4602	11.5512
chr15	102531392	227253804	2.2164	10.9292
chr16	90354753	208739047	2.3102	13.7736
chr17	81195210	186643725	2.2987	24.9701
chr18	78077248	205992802	2.6383	9.0399
chr19	59128983	93334972	1.5785	8.0007
chr20	63025520	155508192	2.4674	13.6221
chr21	48129895	118496185	2.462	14.2307
chr22	51304566	60268639	1.1747	9.8558
chrMT	16571	9522	0.5746	2.5544
chrX	155270560	39924998	0.2571	17.0481

chrY	59373566	91997217	1.5495	26.0019
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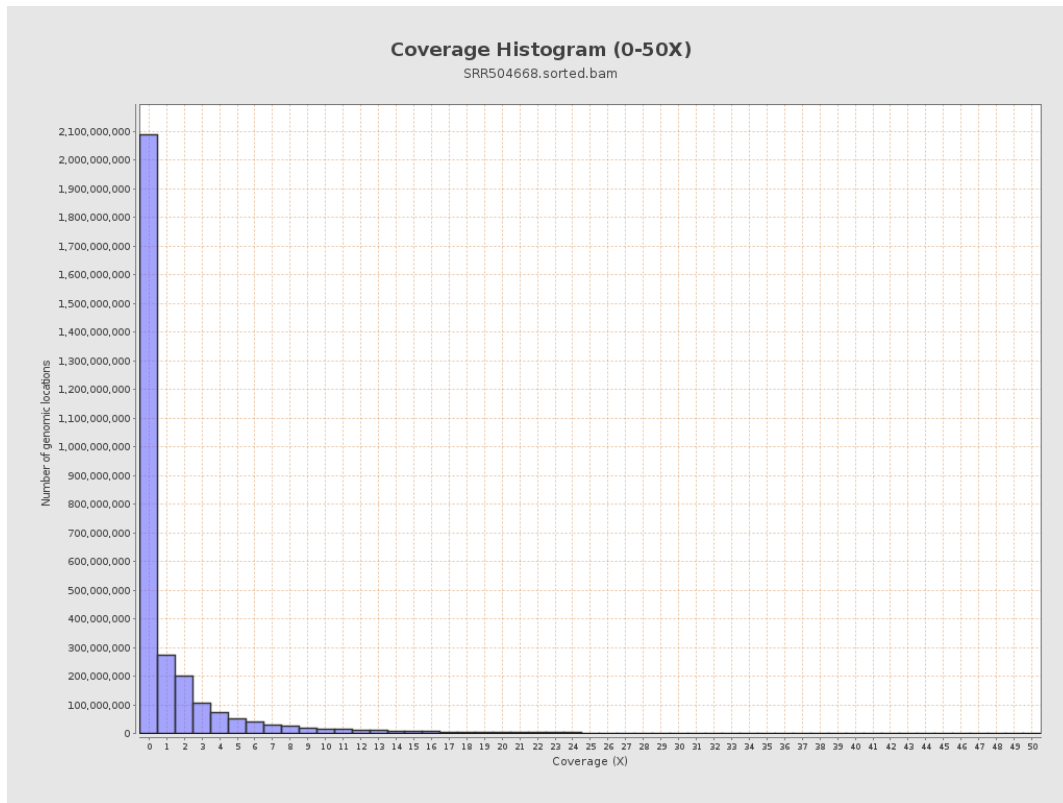
3. Results : Coverage across reference



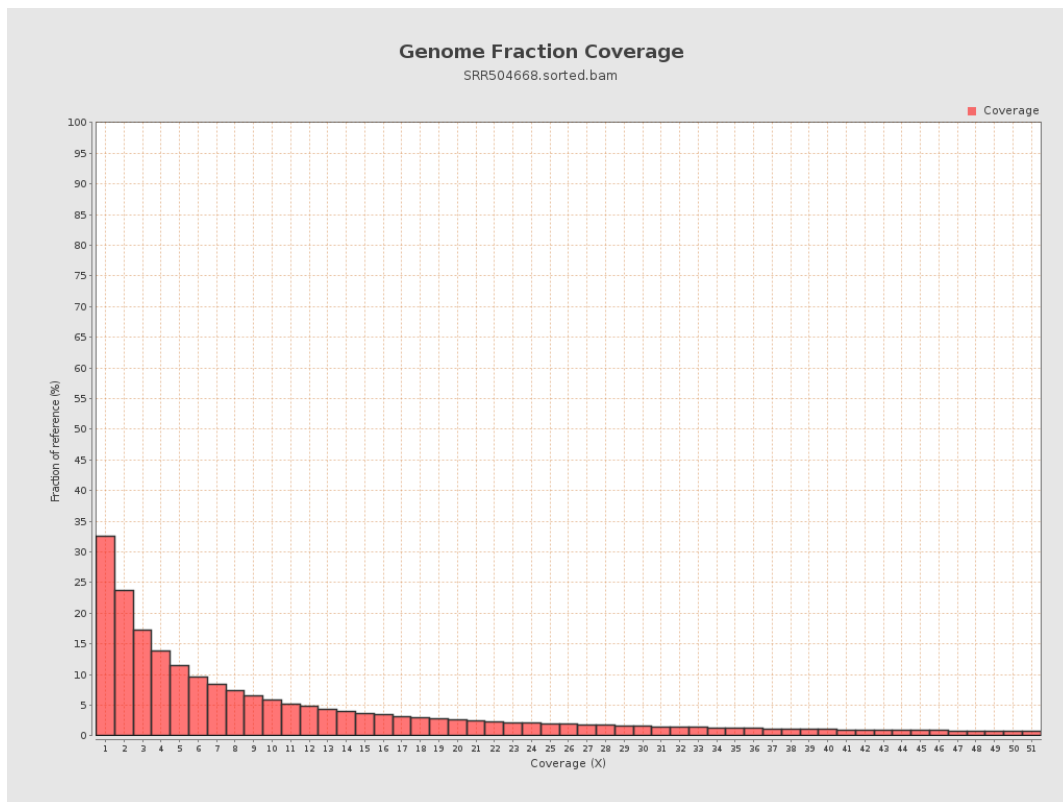
4. Results : Coverage Histogram



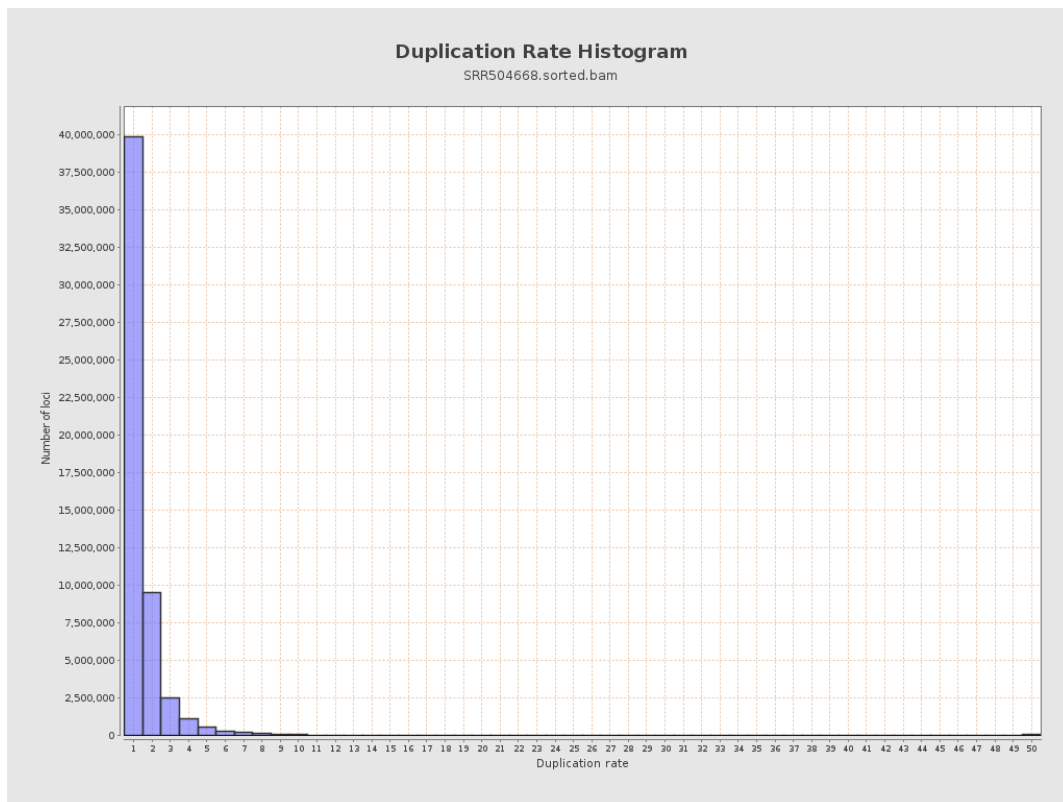
5. Results : Coverage Histogram (0-50X)



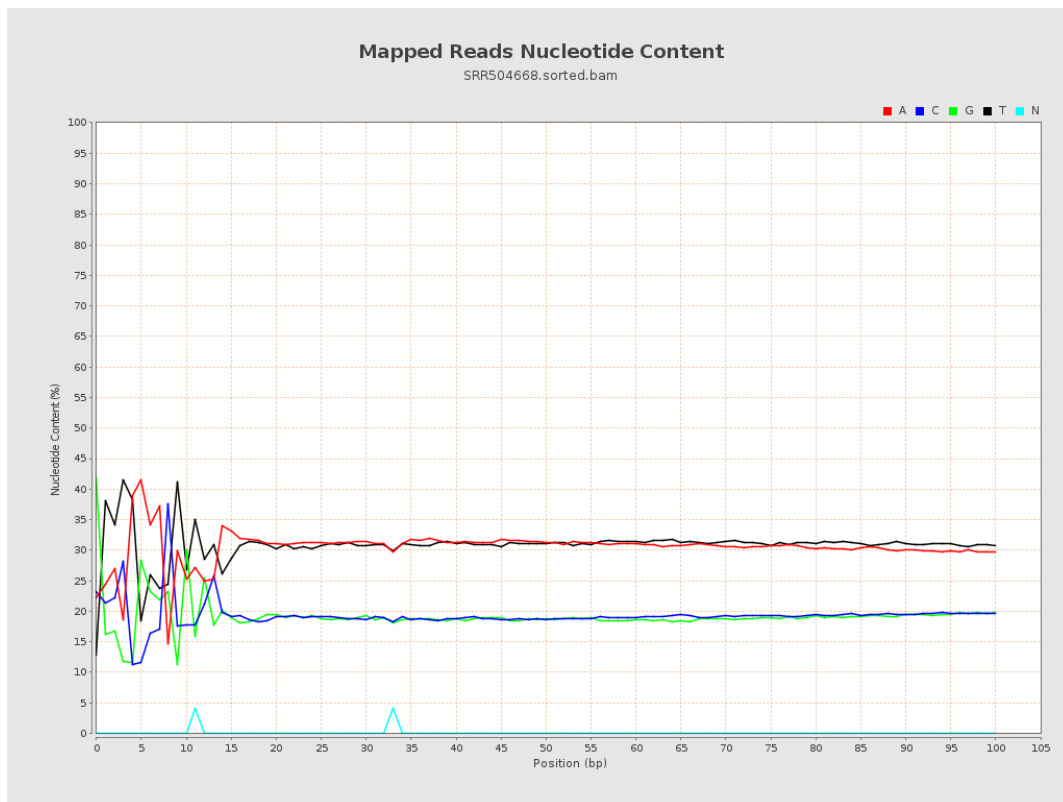
6. Results : Genome Fraction Coverage



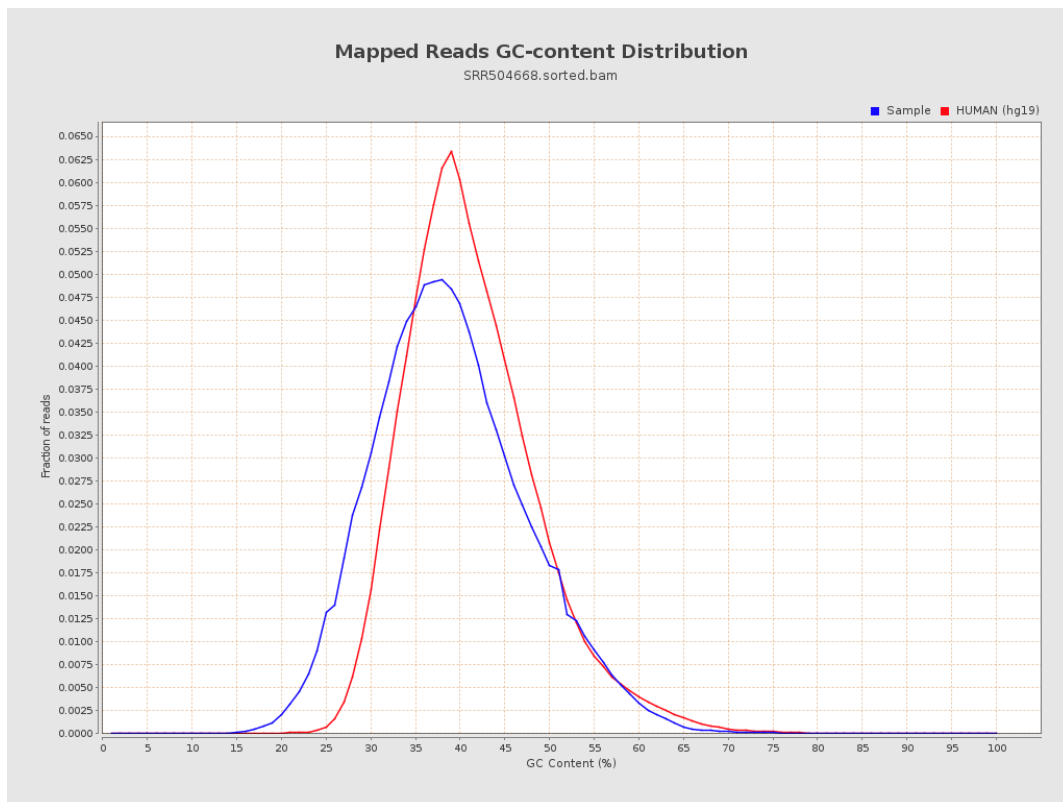
7. Results : Duplication Rate Histogram



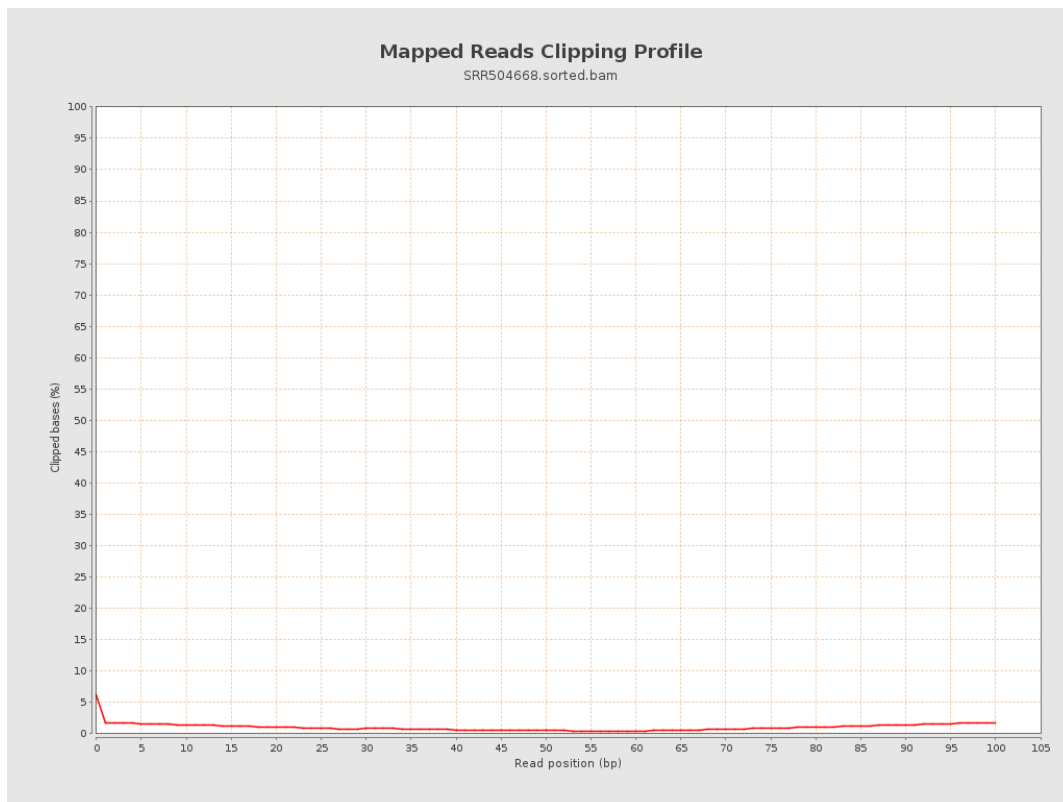
8. Results : Mapped Reads Nucleotide Content



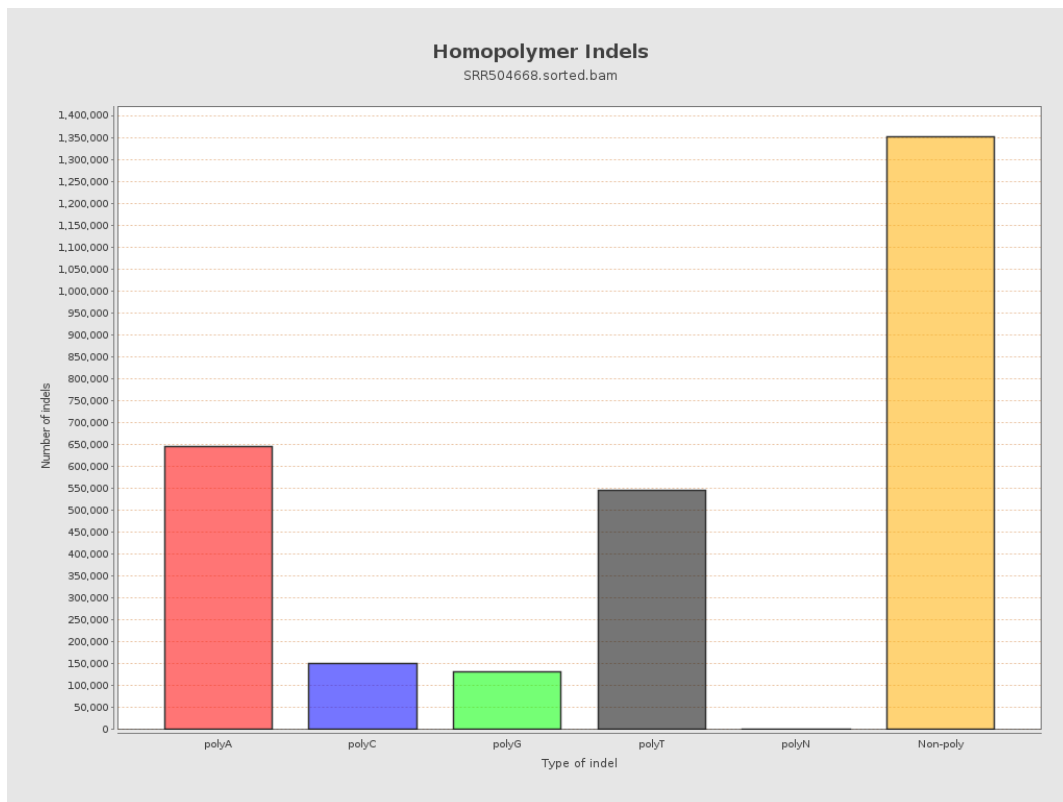
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



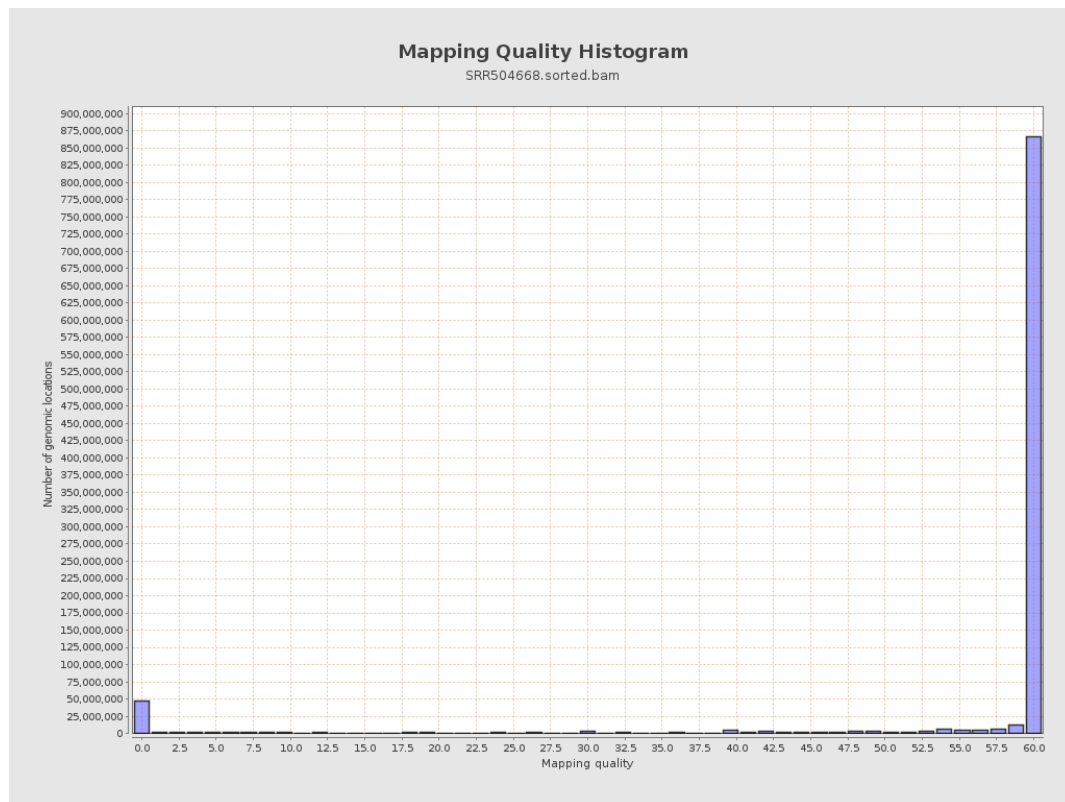
11. Results : Homopolymer Indels



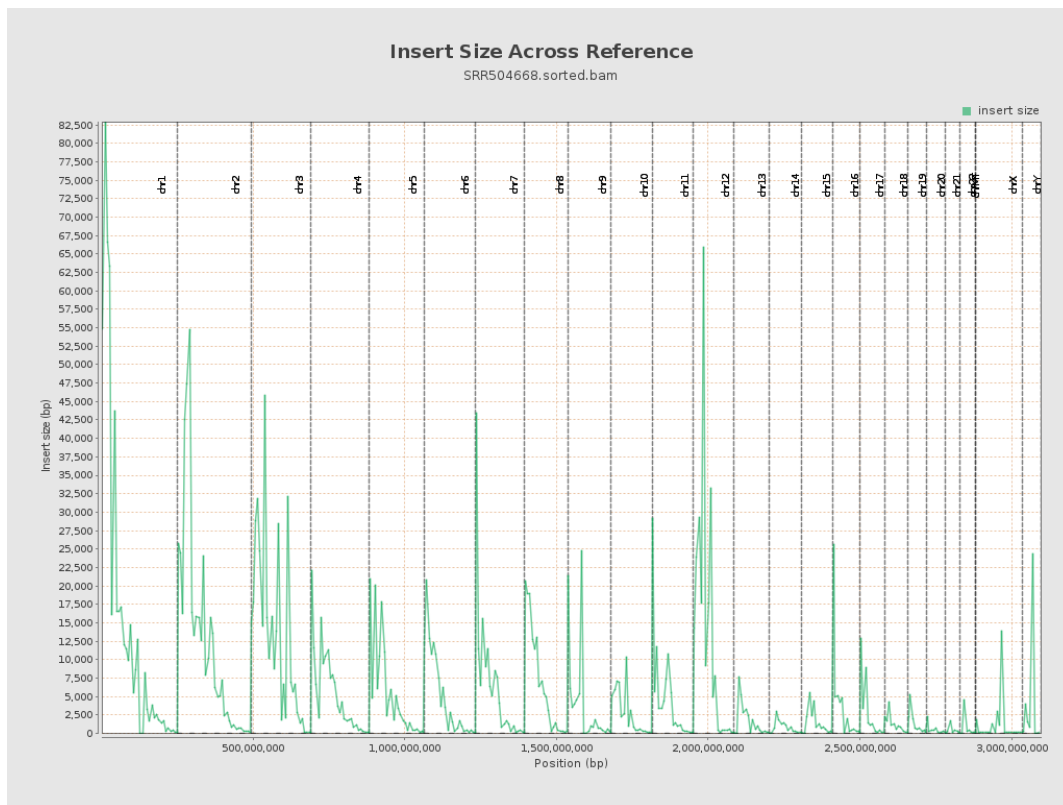
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

