

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 20:39:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777307.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_SRR1777307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777307_1.fastq.gz SRR1777307_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 20:39:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	361,068,554
Mapped reads	341,076,545 / 94.46%
Unmapped reads	19,992,009 / 5.54%
Mapped paired reads	341,076,545 / 94.46%
Mapped reads, first in pair	171,534,661 / 47.51%
Mapped reads, second in pair	169,541,884 / 46.96%
Mapped reads, both in pair	335,454,002 / 92.91%
Mapped reads, singletons	5,622,543 / 1.56%
Secondary alignments	0
Supplementary alignments	10,671,708 / 2.96%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	149,756,008 / 41.48%
Duplication rate	22.76%
Clipped reads	103,040,760 / 28.54%

2.2. ACGT Content

Number/percentage of A's	9,359,101,404 / 28.87%
Number/percentage of C's	6,894,107,575 / 21.26%
Number/percentage of T's	9,156,958,530 / 28.24%
Number/percentage of G's	7,008,532,191 / 21.62%
Number/percentage of N's	1,283,456 / 0%

GC Percentage	42.88%
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2.3. Coverage

Mean	10.4838
Standard Deviation	381.2508

2.4. Mapping Quality

Mean Mapping Quality	52.47
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2.5. Insert size

Mean	146,278.76
Standard Deviation	3,742,194.09
P25/Median/P75	113 / 163 / 238

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	297,524,650
Insertions	11,788,842
Mapped reads with at least one insertion	3.17%
Deletions	10,749,768
Mapped reads with at least one deletion	2.84%
Homopolymer indels	28.89%

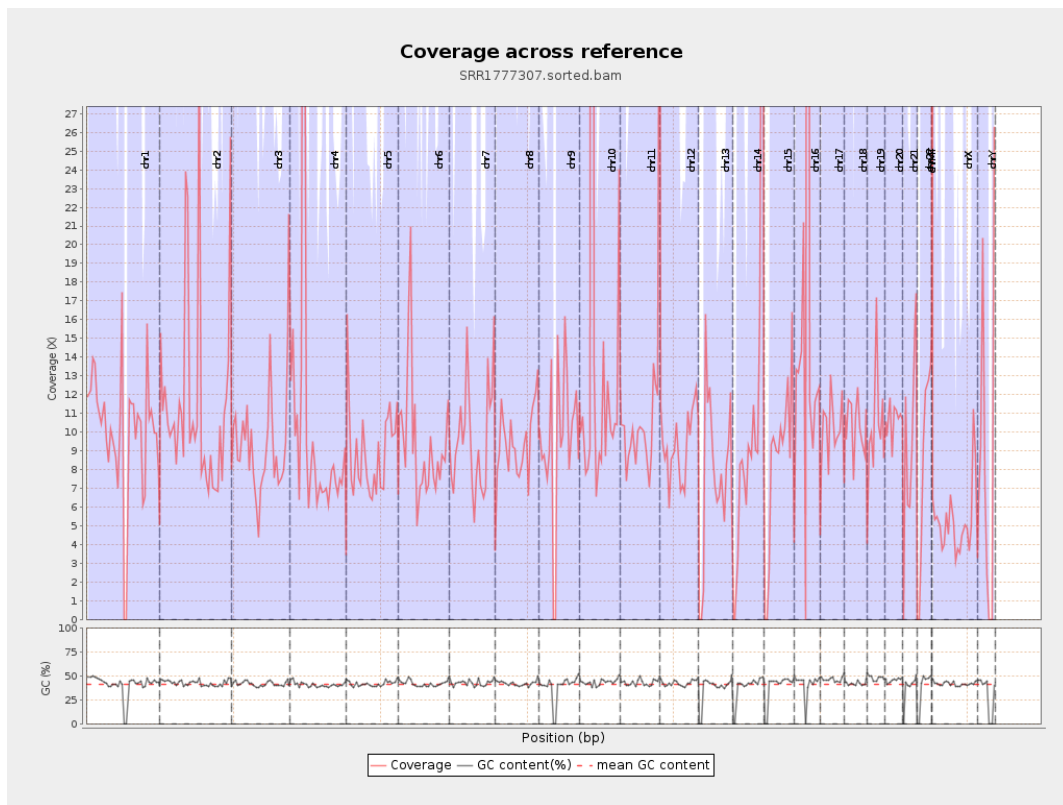
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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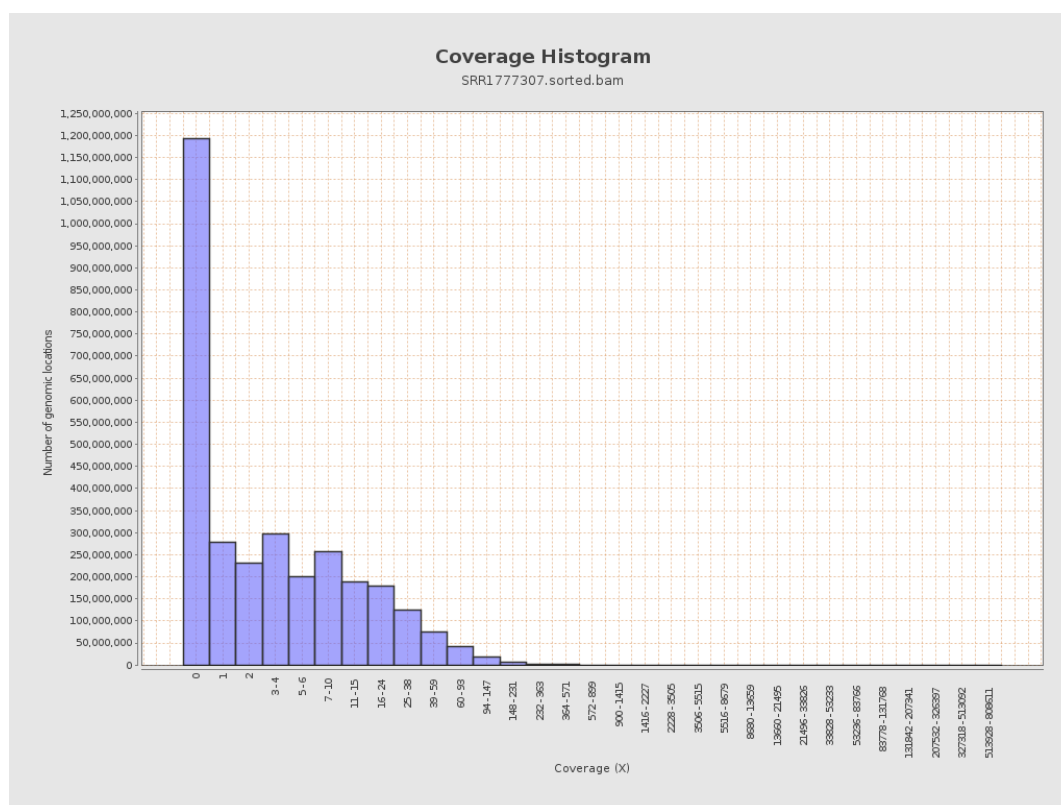
		bases	coverage	deviation
chr1	249250621	2498563007	10.0243	173.4874
chr2	243199373	2820389587	11.597	297.6168
chr3	198022430	1828357576	9.2331	178.3514
chr4	191154276	1960691645	10.2571	284.6623
chr5	180915260	1631374679	9.0173	78.9411
chr6	171115067	1622616775	9.4826	182.7597
chr7	159138663	1546559737	9.7183	95.485
chr8	146364022	1401223453	9.5736	59.9491
chr9	141213431	1349466594	9.5562	162.0757
chr10	135534747	2657159918	19.605	1,467.029
chr11	135006516	1366700777	10.1232	73.3911
chr12	133851895	1246533911	9.3128	40.2241
chr13	115169878	887172979	7.7032	132.622
chr14	107349540	1190639407	11.0912	478.1815
chr15	102531392	860042009	8.3881	125.7827
chr16	90354753	1776311775	19.6593	563.9108
chr17	81195210	824987021	10.1605	61.2654
chr18	78077248	805408502	10.3155	130.7261
chr19	59128983	620936592	10.5014	125.6811
chr20	63025520	669651321	10.6251	85.4969
chr21	48129895	465097830	9.6634	172.9225
chr22	51304566	434816993	8.4752	78.8867
chrMT	16571	637353010	38,461.9522	6,148.6614
chrX	155270560	812578051	5.2333	111.4601

chrY	59373566	540145244	9.0974	295.1747
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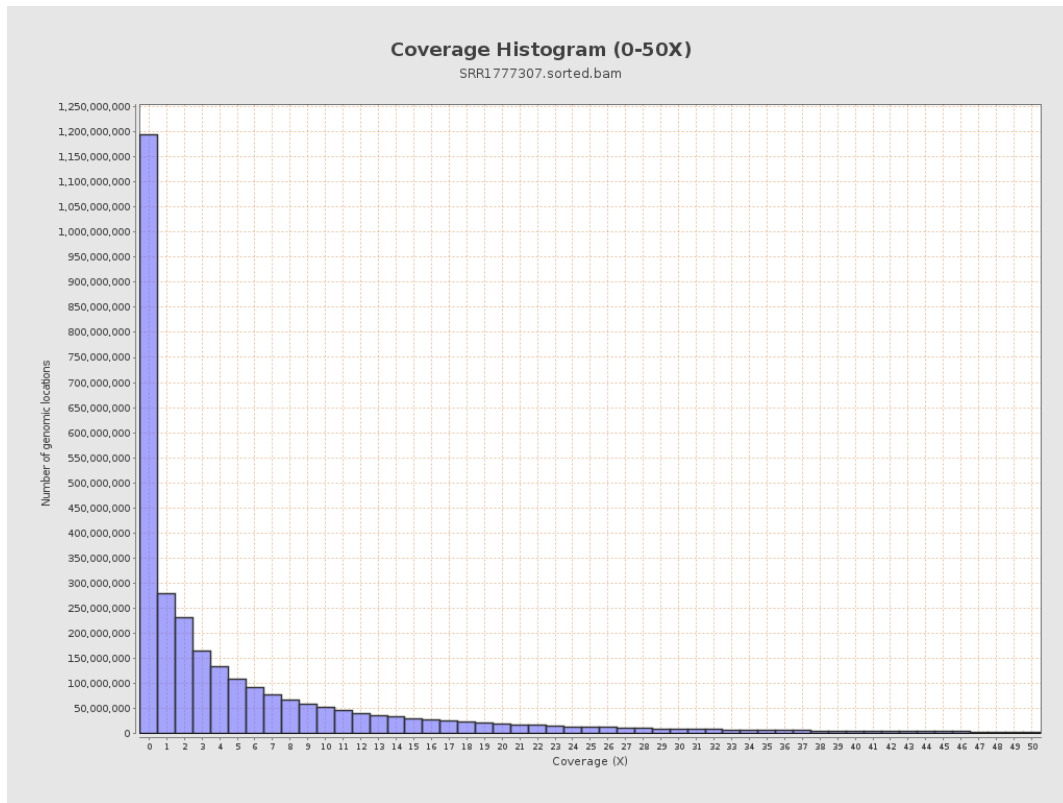
3. Results : Coverage across reference



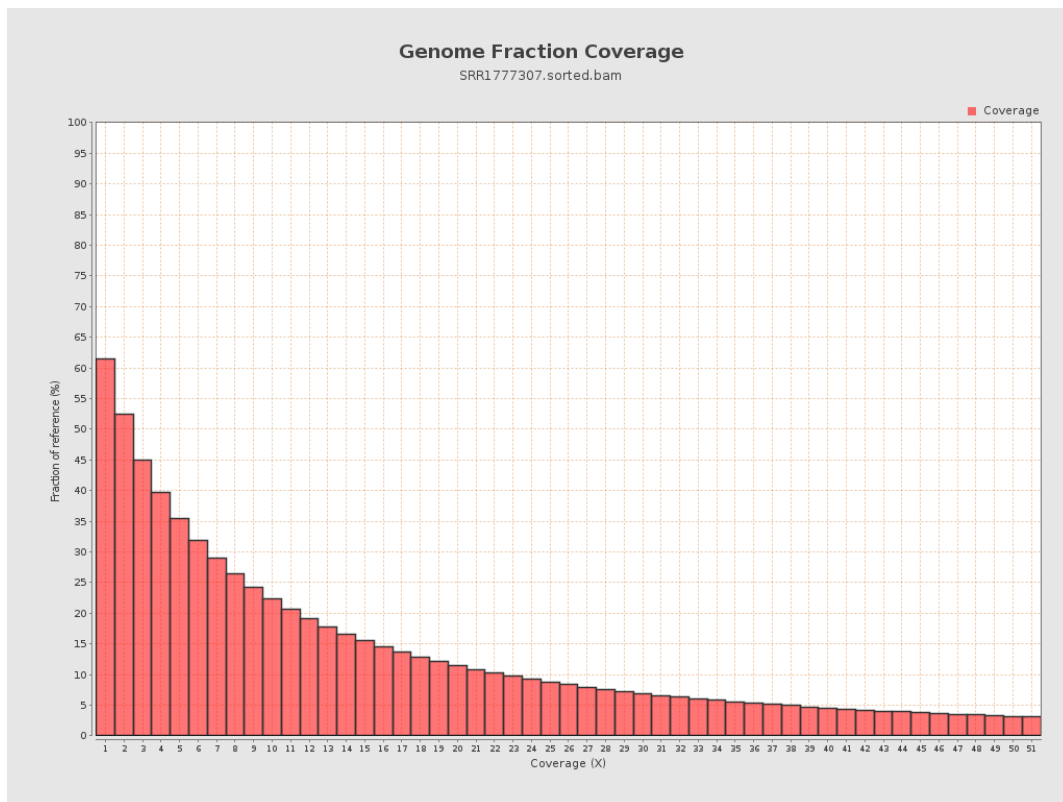
4. Results : Coverage Histogram



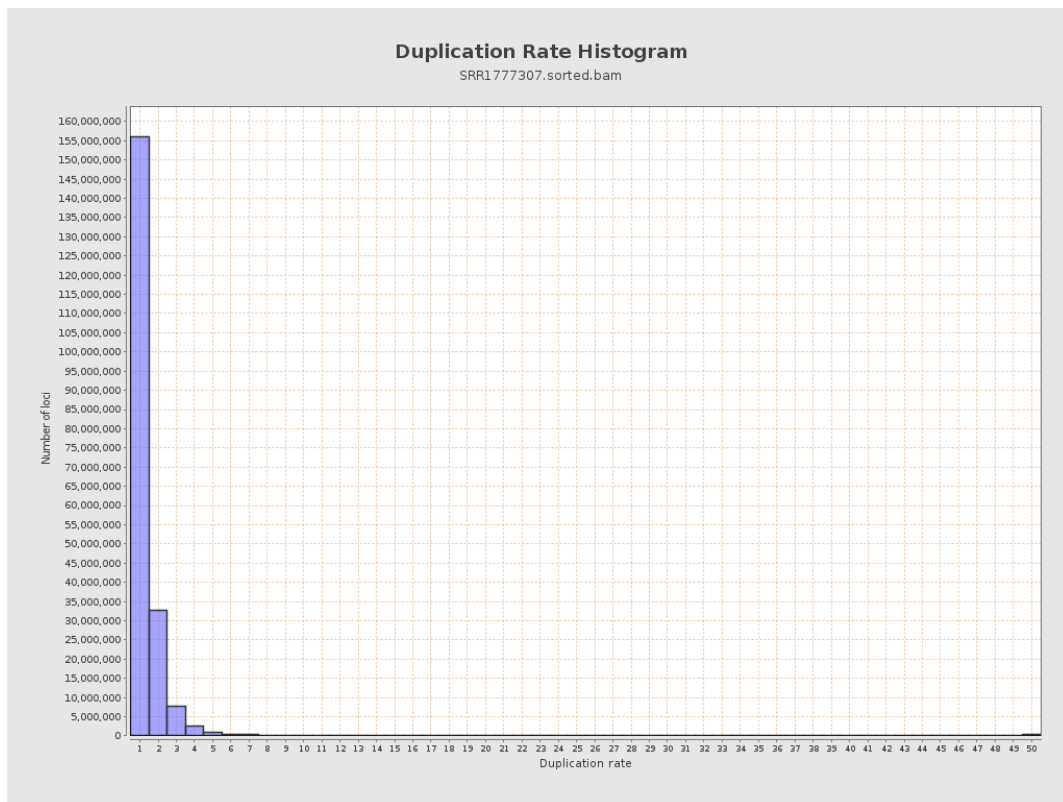
5. Results : Coverage Histogram (0-50X)



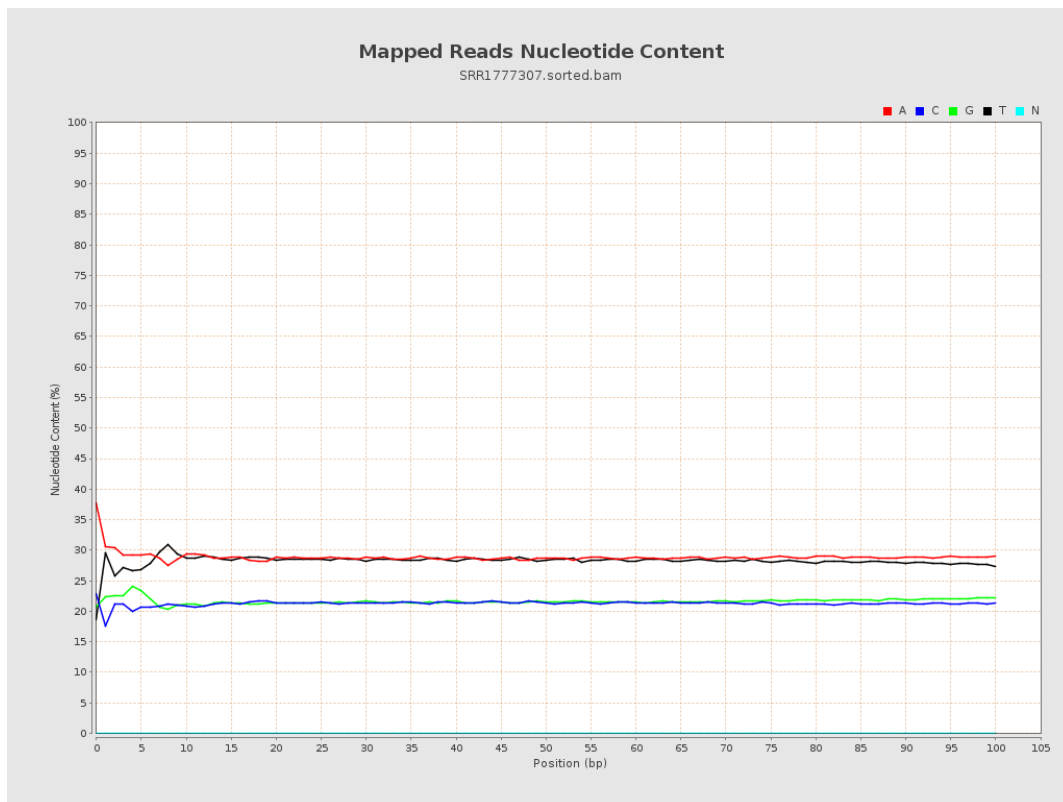
6. Results : Genome Fraction Coverage



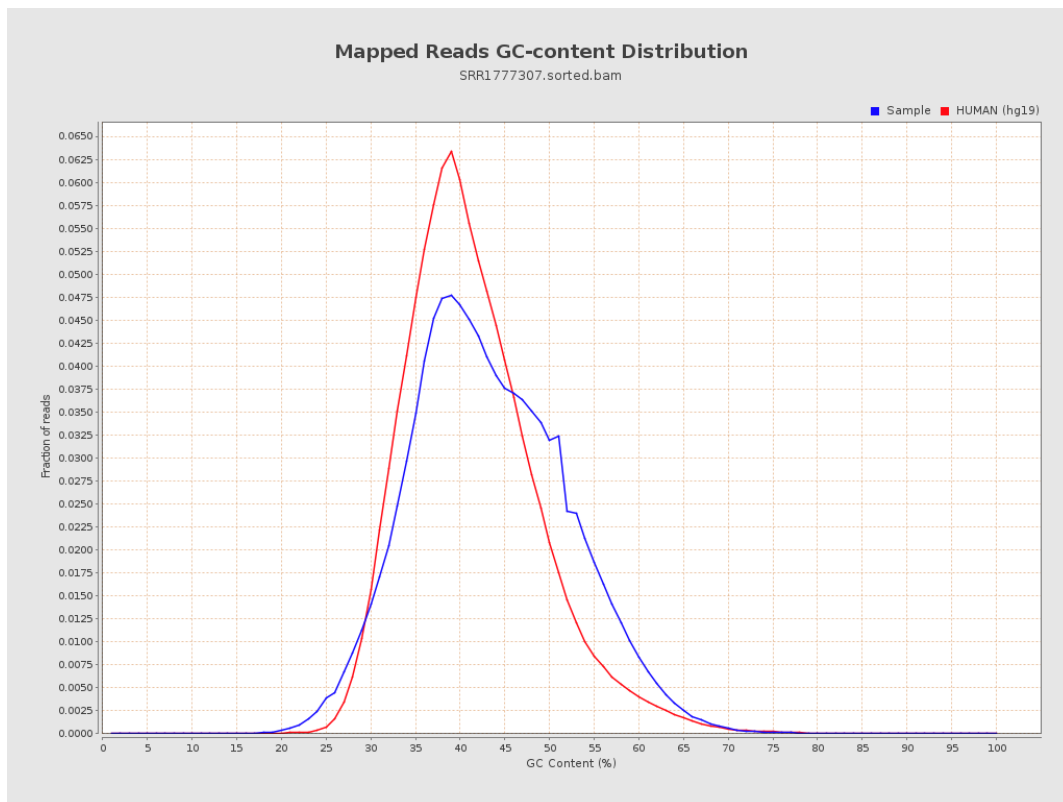
7. Results : Duplication Rate Histogram



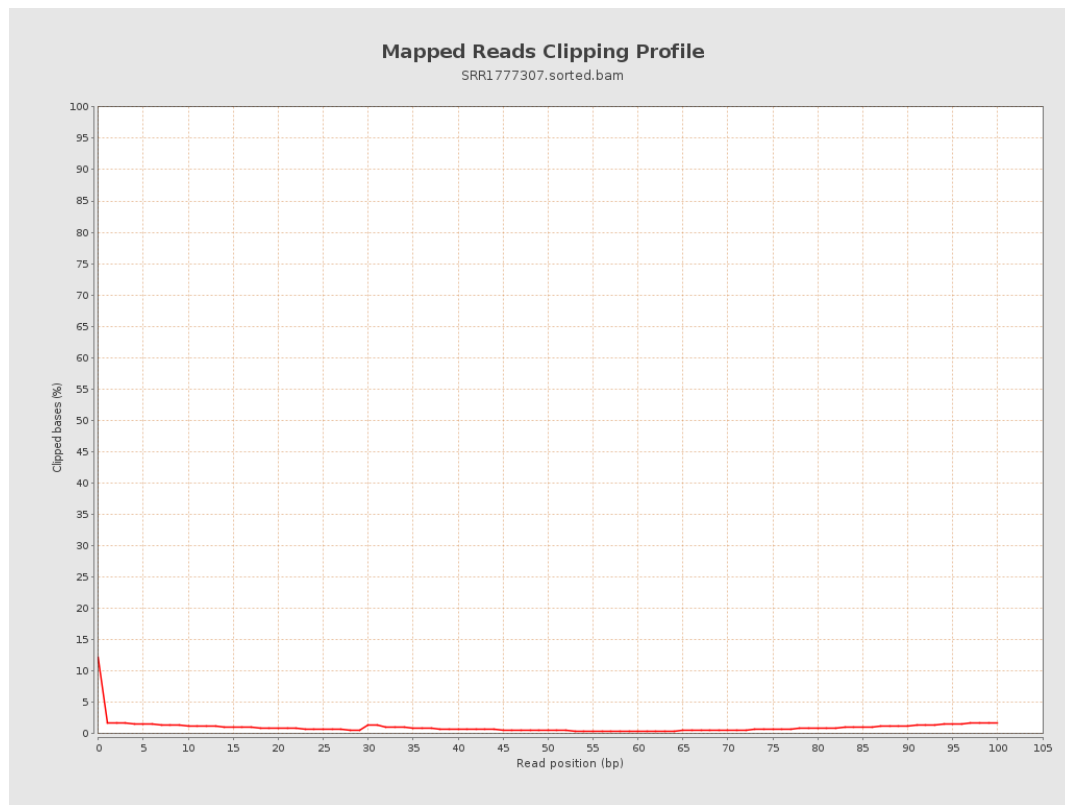
8. Results : Mapped Reads Nucleotide Content



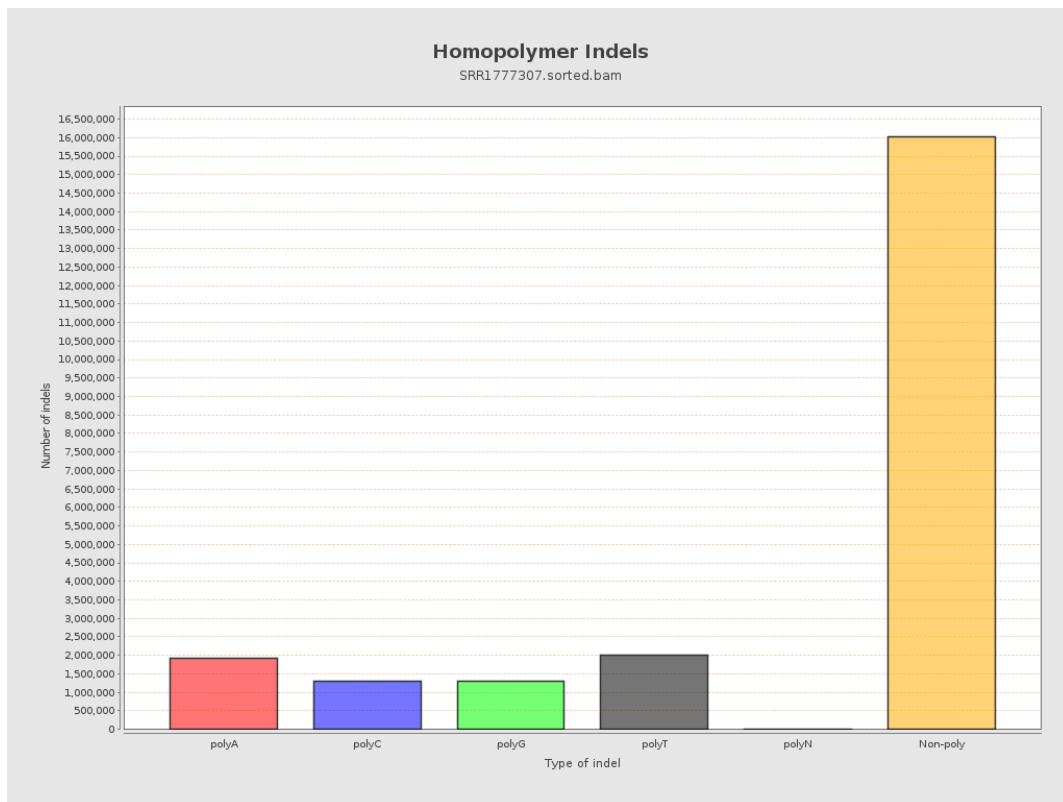
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



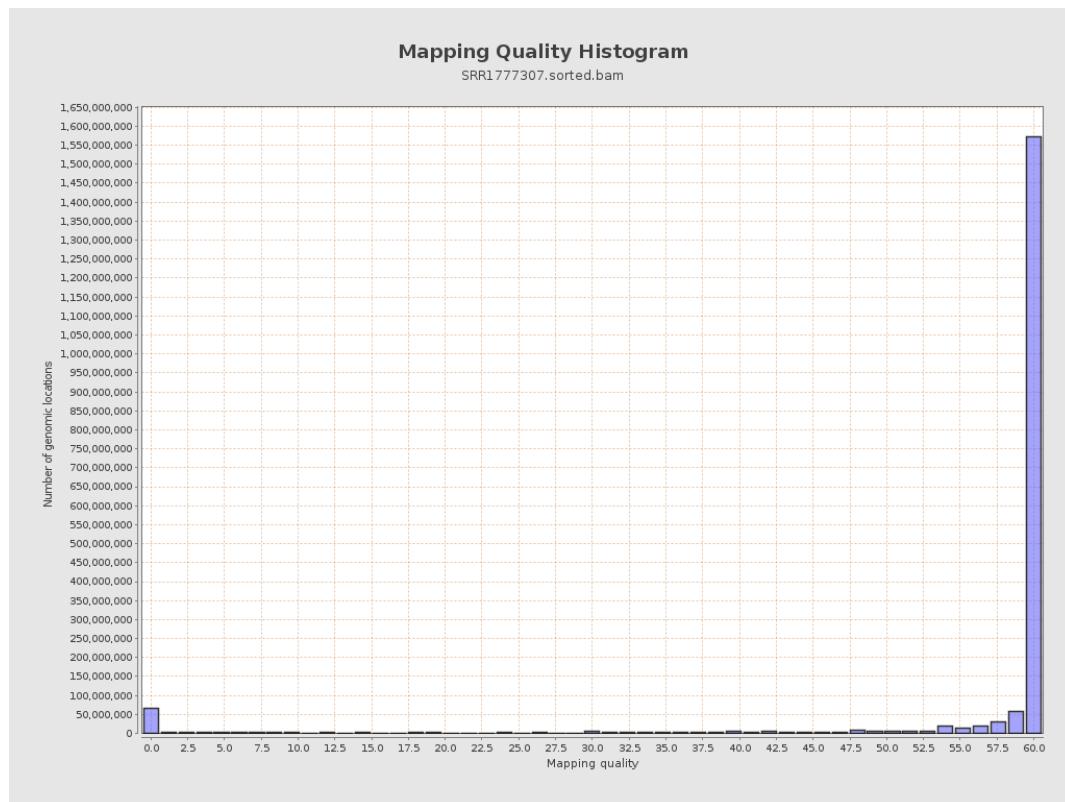
11. Results : Homopolymer Indels



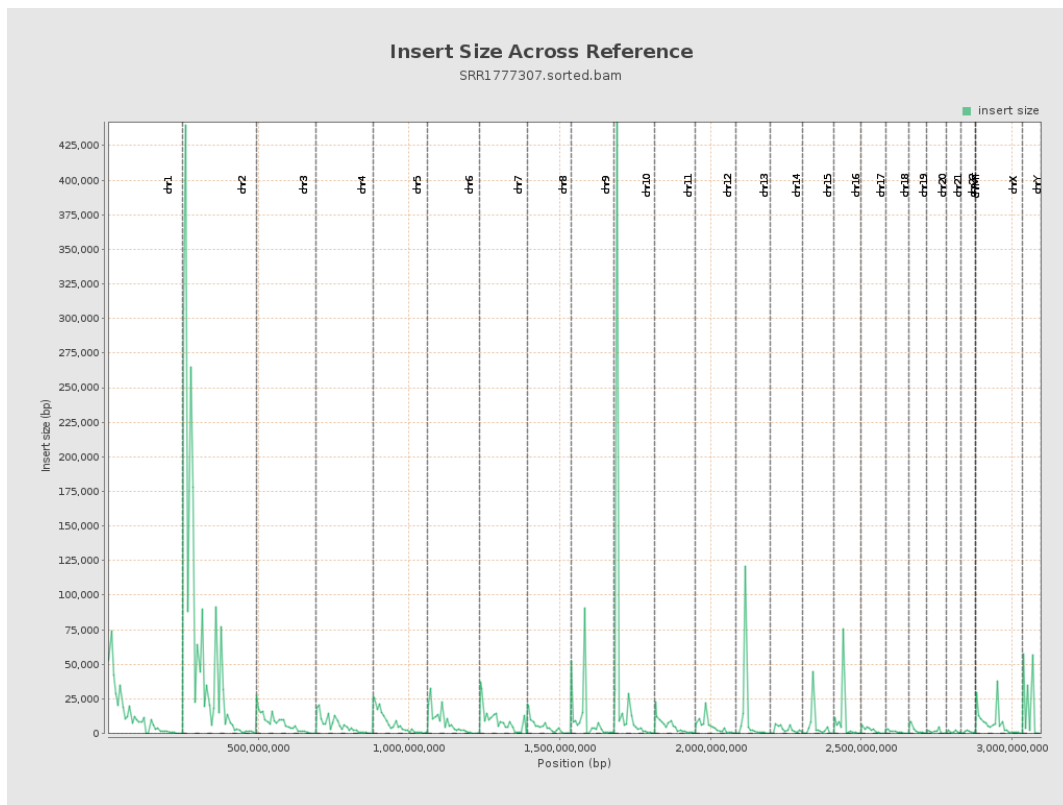
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

