

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:22:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777302.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_SRR1777302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777302_1.fastq.gz SRR1777302_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:22:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,806,594
Mapped reads	1,755,048 / 97.15%
Unmapped reads	51,546 / 2.85%
Mapped paired reads	1,755,048 / 97.15%
Mapped reads, first in pair	879,911 / 48.71%
Mapped reads, second in pair	875,137 / 48.44%
Mapped reads, both in pair	1,745,376 / 96.61%
Mapped reads, singletons	9,672 / 0.54%
Secondary alignments	0
Supplementary alignments	69,329 / 3.84%
Read min/max/mean length	30 / 101 / 102.58
Duplicated reads (estimated)	193,985 / 10.74%
Duplication rate	8.86%
Clipped reads	564,182 / 31.23%

2.2. ACGT Content

Number/percentage of A's	49,546,114 / 29.52%
Number/percentage of C's	34,488,979 / 20.55%
Number/percentage of T's	48,546,738 / 28.92%
Number/percentage of G's	35,276,257 / 21.02%
Number/percentage of N's	2,705 / 0%

GC Percentage	41.56%
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2.3. Coverage

Mean	0.0542
Standard Deviation	0.8882

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	177,868.8
Standard Deviation	4,068,472.33
P25/Median/P75	107 / 155 / 218

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	1,057,663
Insertions	39,043
Mapped reads with at least one insertion	2.16%
Deletions	25,075
Mapped reads with at least one deletion	1.37%
Homopolymer indels	42.25%

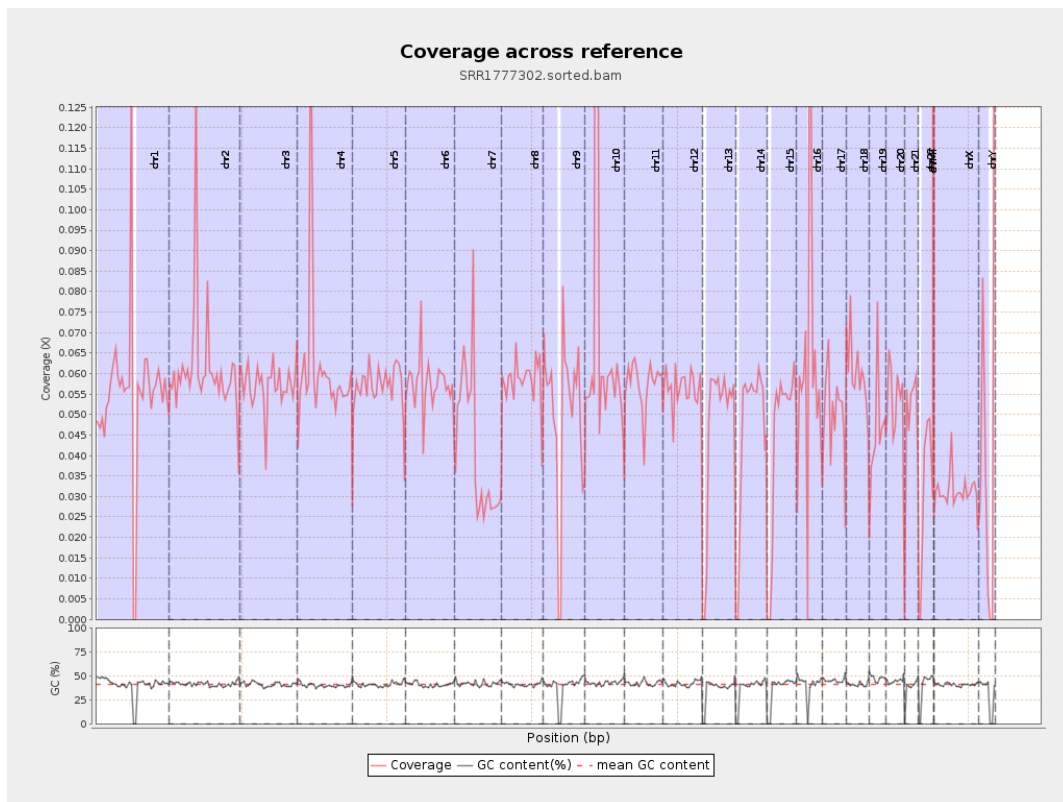
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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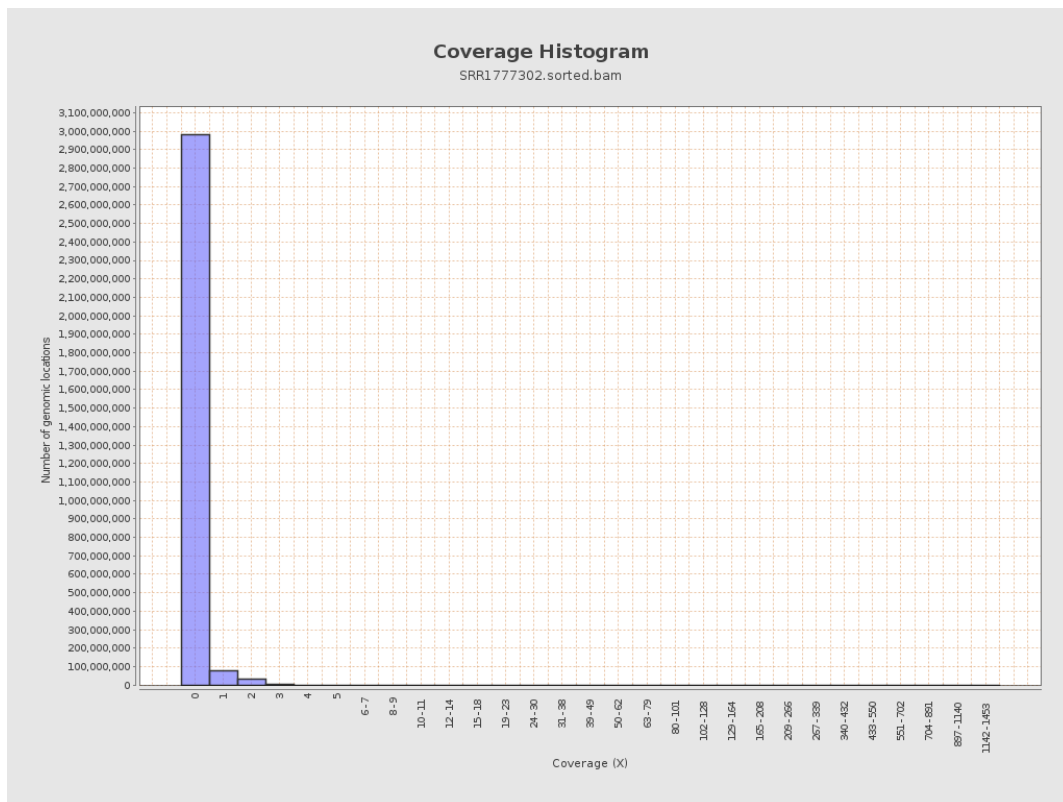
		bases	coverage	deviation
chr1	249250621	13678386	0.0549	1.5257
chr2	243199373	14964929	0.0615	0.6683
chr3	198022430	11308438	0.0571	0.3827
chr4	191154276	11619283	0.0608	0.7374
chr5	180915260	10336430	0.0571	0.3089
chr6	171115067	9795441	0.0572	0.3837
chr7	159138663	6608056	0.0415	0.6457
chr8	146364022	8543180	0.0584	0.4624
chr9	141213431	7090779	0.0502	0.7073
chr10	135534747	9599365	0.0708	2.0926
chr11	135006516	7709534	0.0571	0.3932
chr12	133851895	7528568	0.0562	0.3036
chr13	115169878	5322383	0.0462	0.2748
chr14	107349540	4960460	0.0462	0.2824
chr15	102531392	4540644	0.0443	0.2654
chr16	90354753	5526673	0.0612	0.8751
chr17	81195210	4046670	0.0498	0.463
chr18	78077248	4715277	0.0604	0.8363
chr19	59128983	2744517	0.0464	0.8399
chr20	63025520	3373365	0.0535	0.3326
chr21	48129895	2280896	0.0474	0.3783
chr22	51304566	1568462	0.0306	0.2315
chrMT	16571	2775427	167.487	43.9478
chrX	155270560	4876201	0.0314	0.2585

chrY	59373566	2417529	0.0407	0.9366
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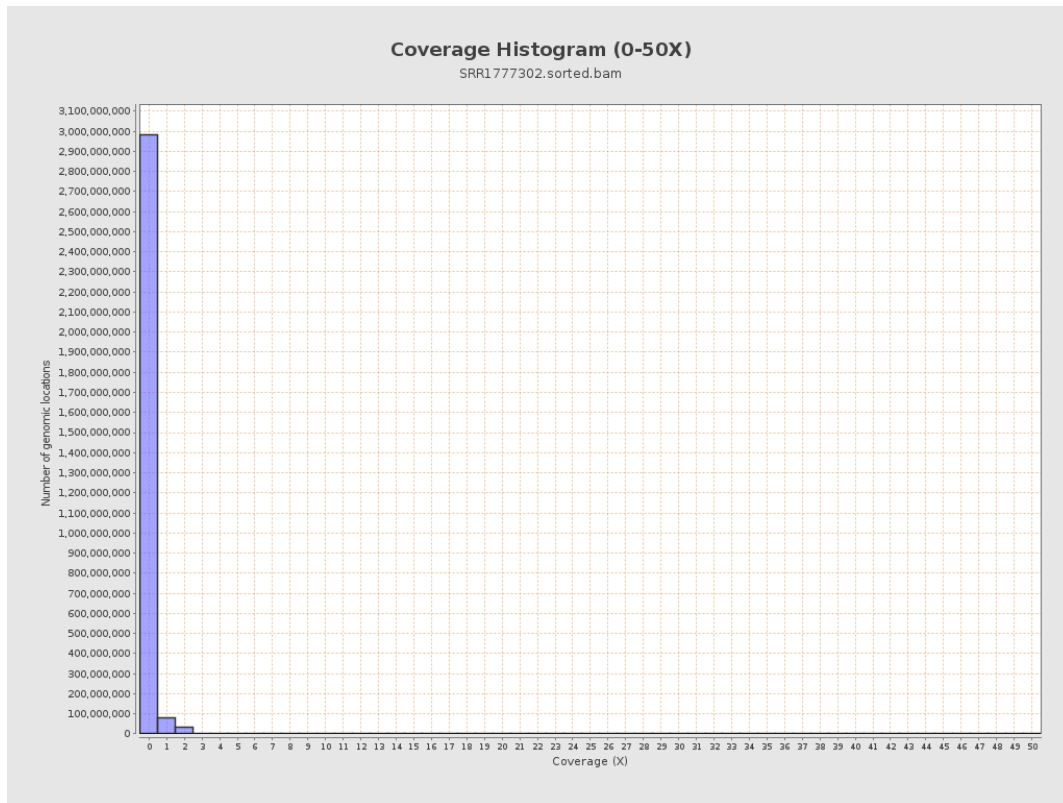
3. Results : Coverage across reference



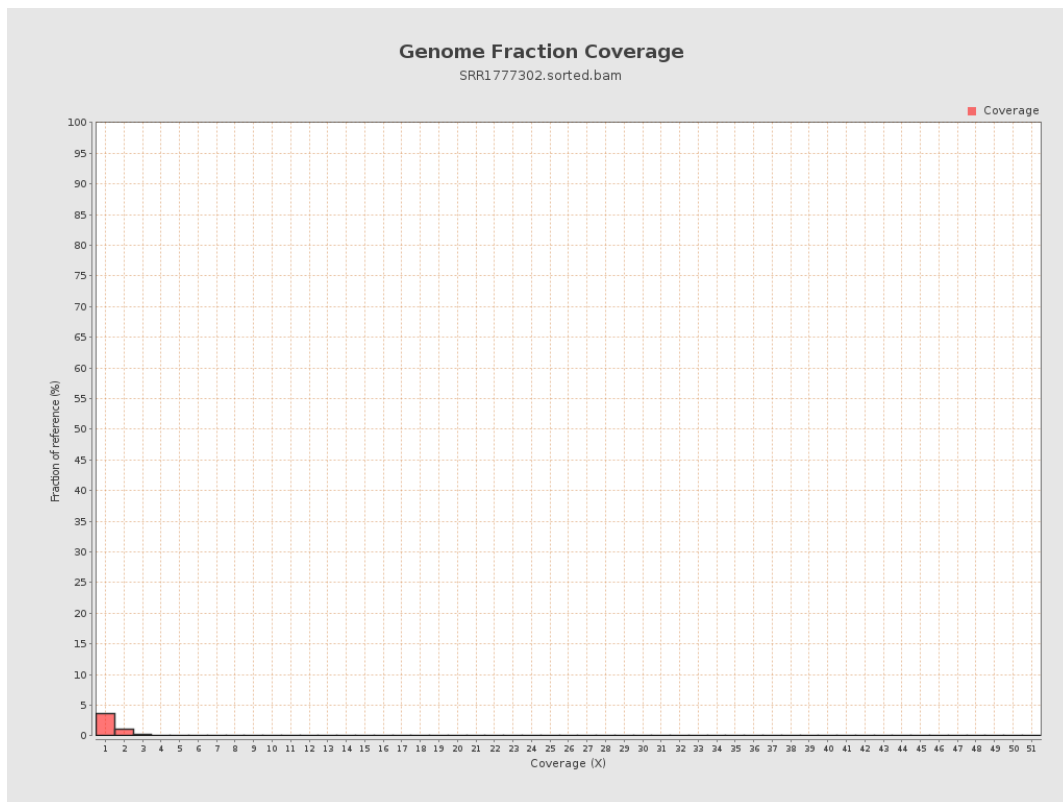
4. Results : Coverage Histogram



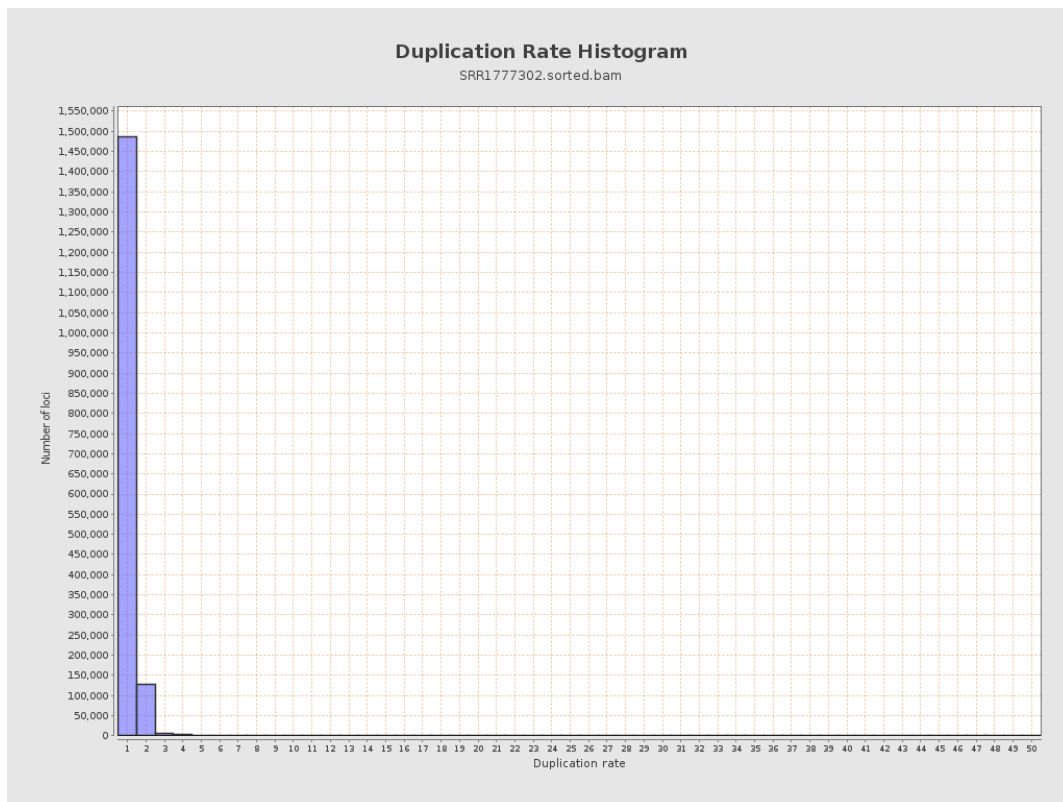
5. Results : Coverage Histogram (0-50X)



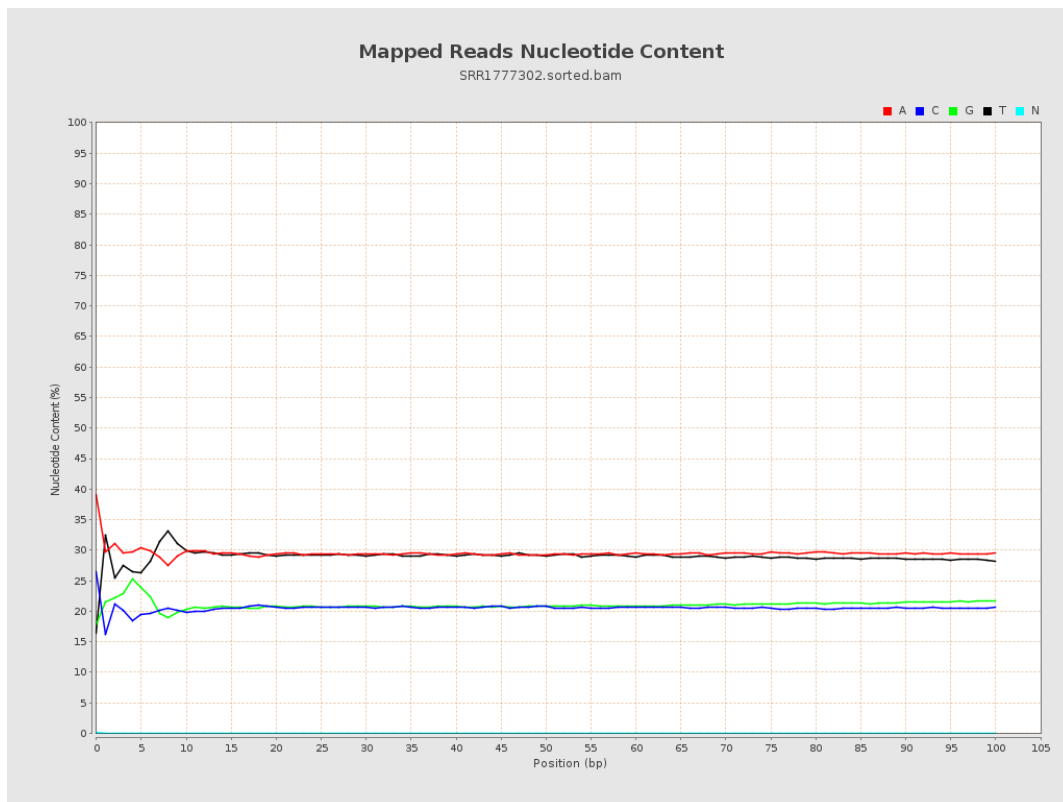
6. Results : Genome Fraction Coverage



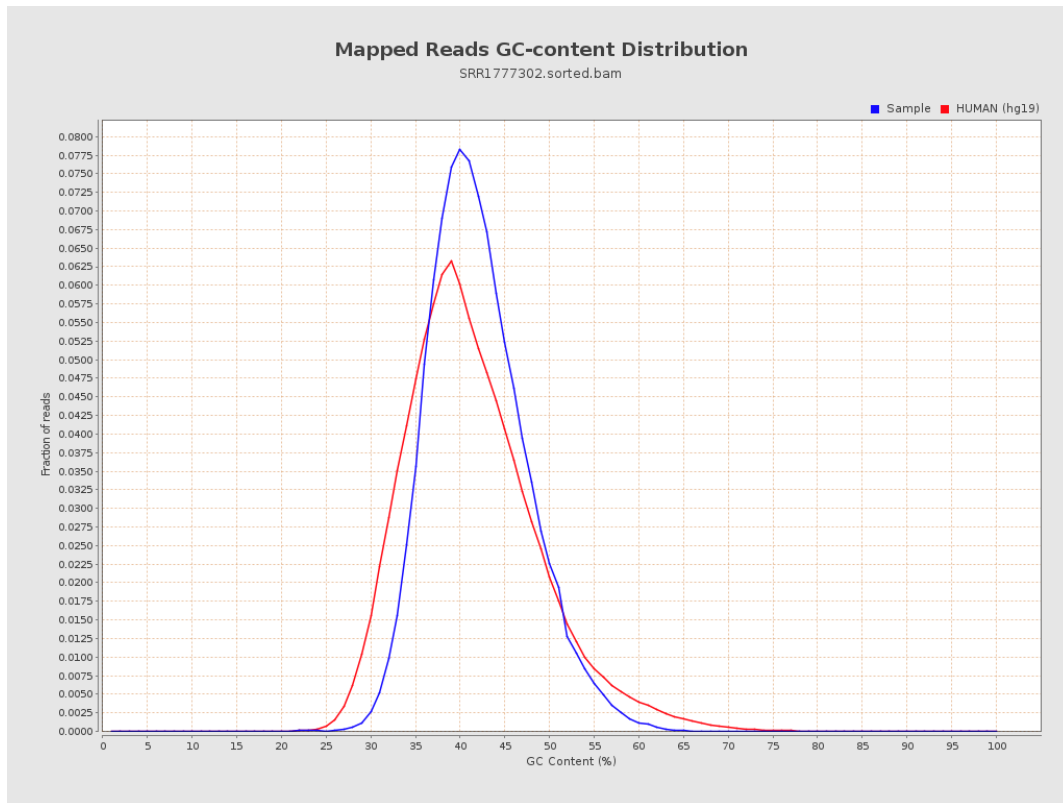
7. Results : Duplication Rate Histogram



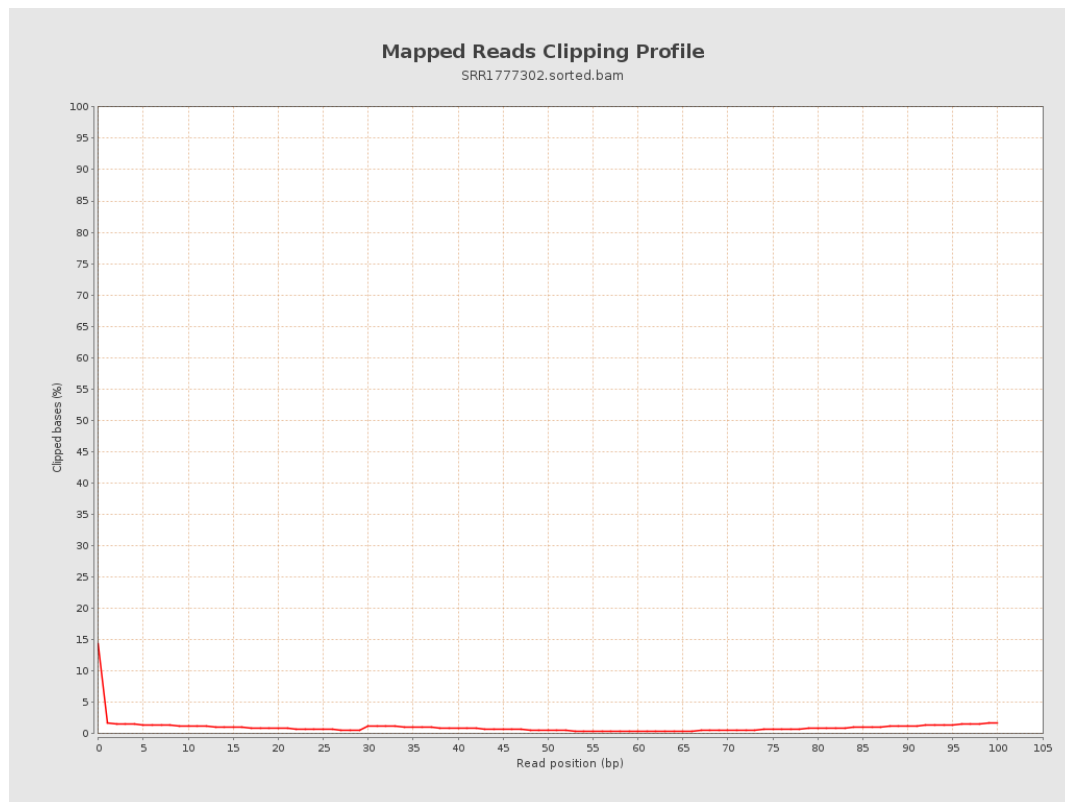
8. Results : Mapped Reads Nucleotide Content



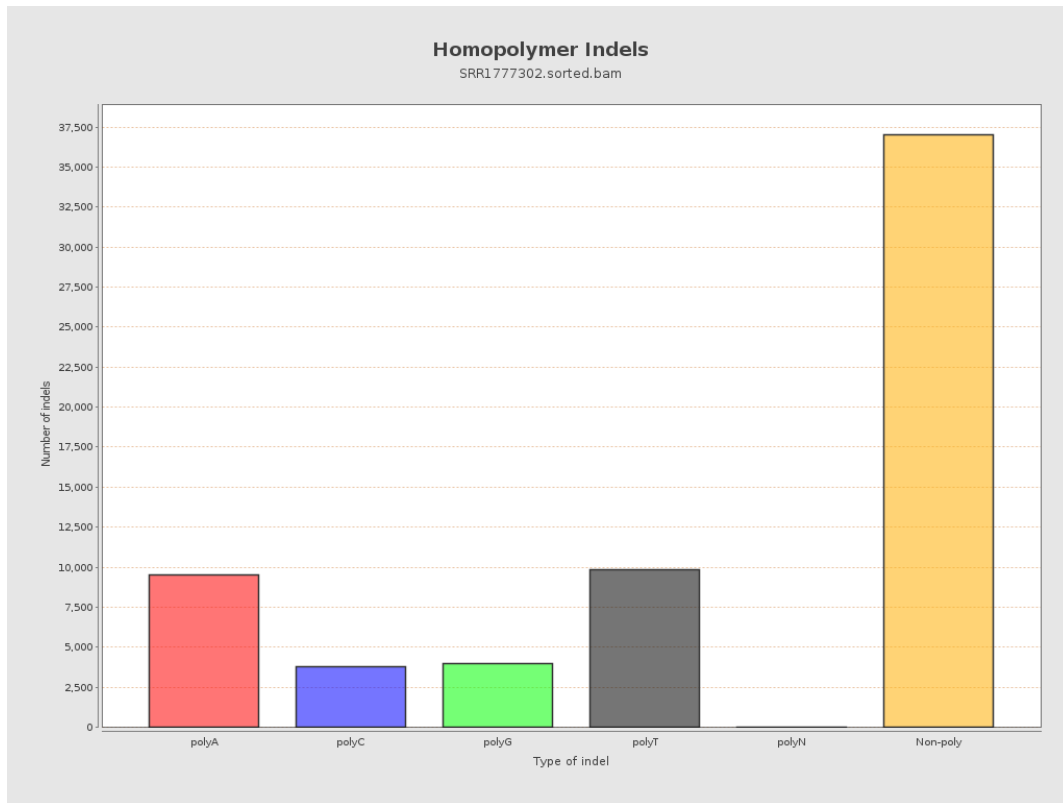
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



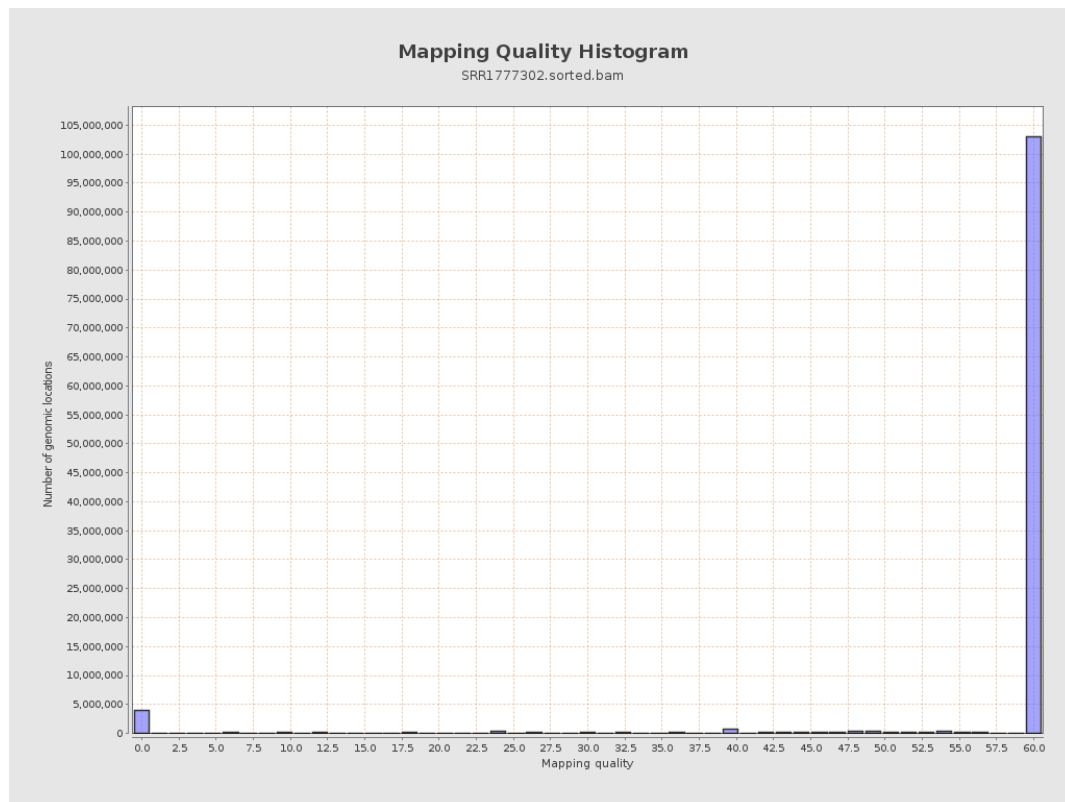
11. Results : Homopolymer Indels



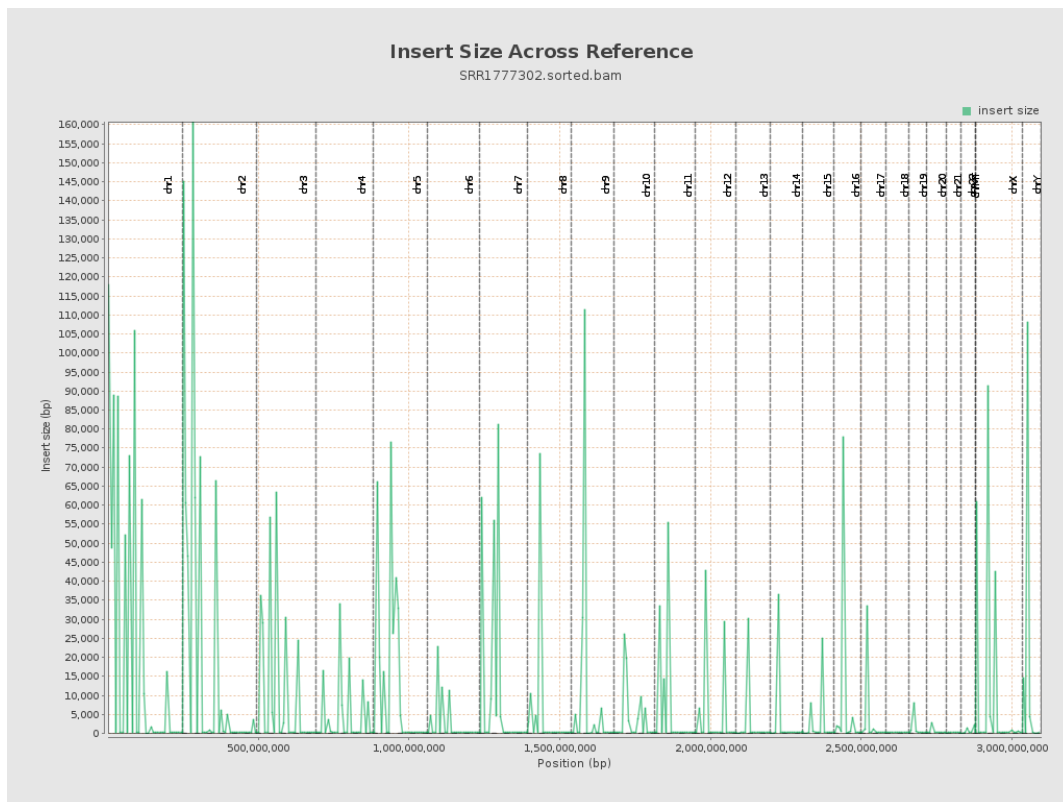
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

