

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 16:48:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777258.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_SRR1777258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777258_1.fastq.gz SRR1777258_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 16:48:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,324,464
Mapped reads	34,196,805 / 99.63%
Unmapped reads	127,659 / 0.37%
Mapped paired reads	34,196,805 / 99.63%
Mapped reads, first in pair	17,098,417 / 49.81%
Mapped reads, second in pair	17,098,388 / 49.81%
Mapped reads, both in pair	34,172,674 / 99.56%
Mapped reads, singletons	24,131 / 0.07%
Secondary alignments	0
Supplementary alignments	870,745 / 2.54%
Read min/max/mean length	30 / 101 / 102.05
Duplicated reads (estimated)	14,863,728 / 43.3%
Duplication rate	35.39%
Clipped reads	3,282,769 / 9.56%

2.2. ACGT Content

Number/percentage of A's	943,379,244 / 27.46%
Number/percentage of C's	775,527,304 / 22.57%
Number/percentage of T's	939,936,713 / 27.36%
Number/percentage of G's	777,015,440 / 22.61%
Number/percentage of N's	144,789 / 0%

GC Percentage	45.18%
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2.3. Coverage

Mean	1.1101
Standard Deviation	12.7431

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	157,534.9
Standard Deviation	3,929,352.06
P25/Median/P75	187 / 236 / 299

2.6. Mismatches and indels

General error rate	0.28%
Mismatches	8,711,601
Insertions	620,798
Mapped reads with at least one insertion	1.79%
Deletions	227,087
Mapped reads with at least one deletion	0.65%
Homopolymer indels	51.63%

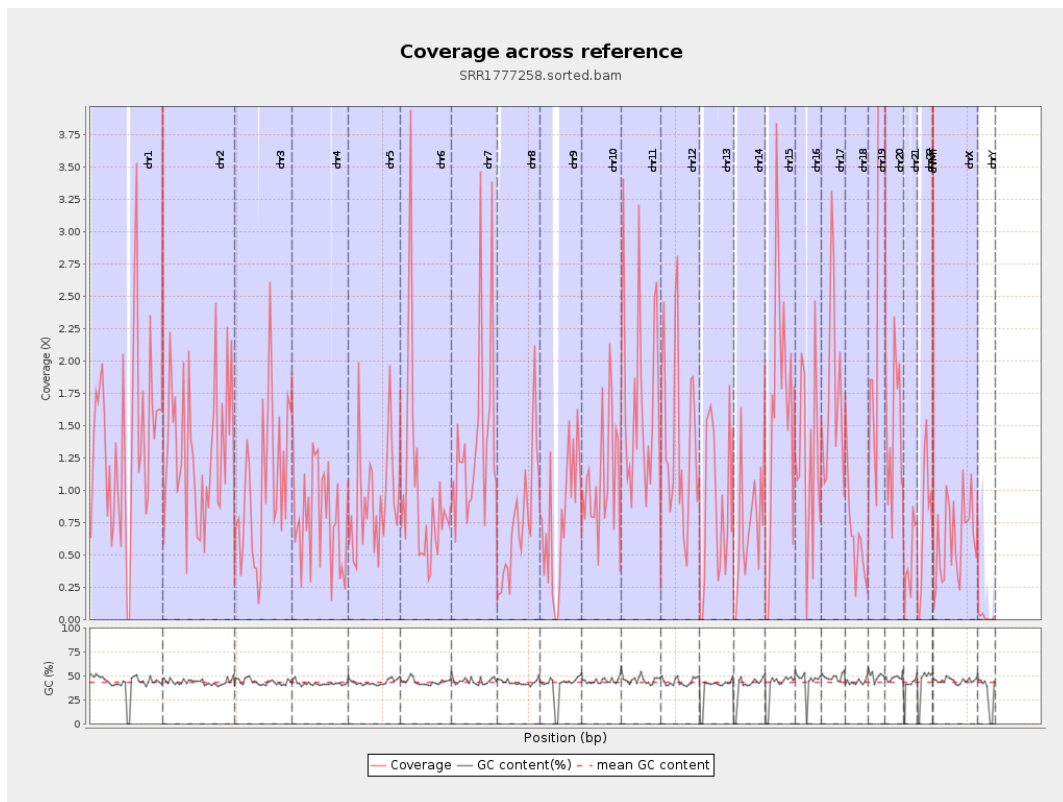
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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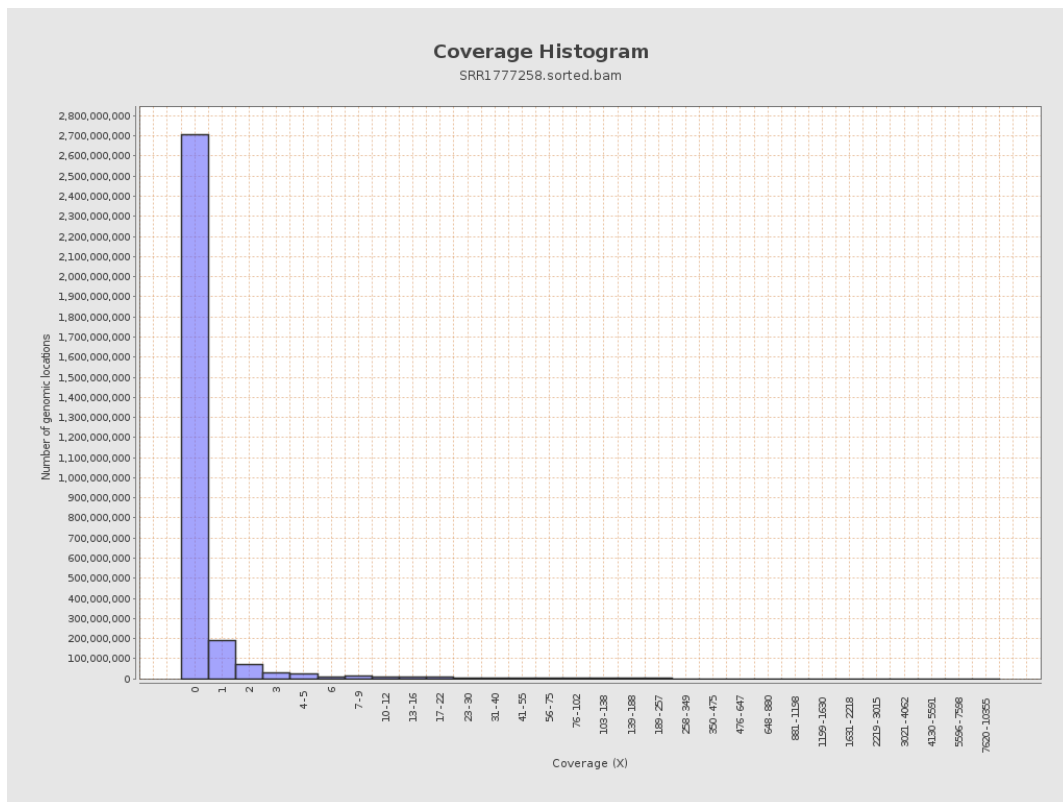
		bases	coverage	deviation
chr1	249250621	347061496	1.3924	14.0707
chr2	243199373	317510291	1.3056	13.5455
chr3	198022430	202294609	1.0216	11.9229
chr4	191154276	150888722	0.7894	10.0357
chr5	180915260	172233316	0.952	10.9768
chr6	171115067	163423700	0.9551	11.6303
chr7	159138663	220061802	1.3828	16.1975
chr8	146364022	113437116	0.775	10.8295
chr9	141213431	107881485	0.764	8.9901
chr10	135534747	149568535	1.1035	12.1484
chr11	135006516	227341669	1.6839	16.8314
chr12	133851895	190159796	1.4207	13.4775
chr13	115169878	100356615	0.8714	10.8631
chr14	107349540	74469741	0.6937	9.0221
chr15	102531392	162539722	1.5853	16.2242
chr16	90354753	107404445	1.1887	13.1149
chr17	81195210	141138974	1.7383	15.4554
chr18	78077248	50815501	0.6508	8.2215
chr19	59128983	185416635	3.1358	25.153
chr20	63025520	92104352	1.4614	14.5113
chr21	48129895	23018366	0.4783	7.2296
chr22	51304566	39535563	0.7706	8.6824
chrMT	16571	866732	52.3041	26.6972
chrX	155270560	95960526	0.618	10.2073

chrY	59373566	1029496	0.0173	0.5755
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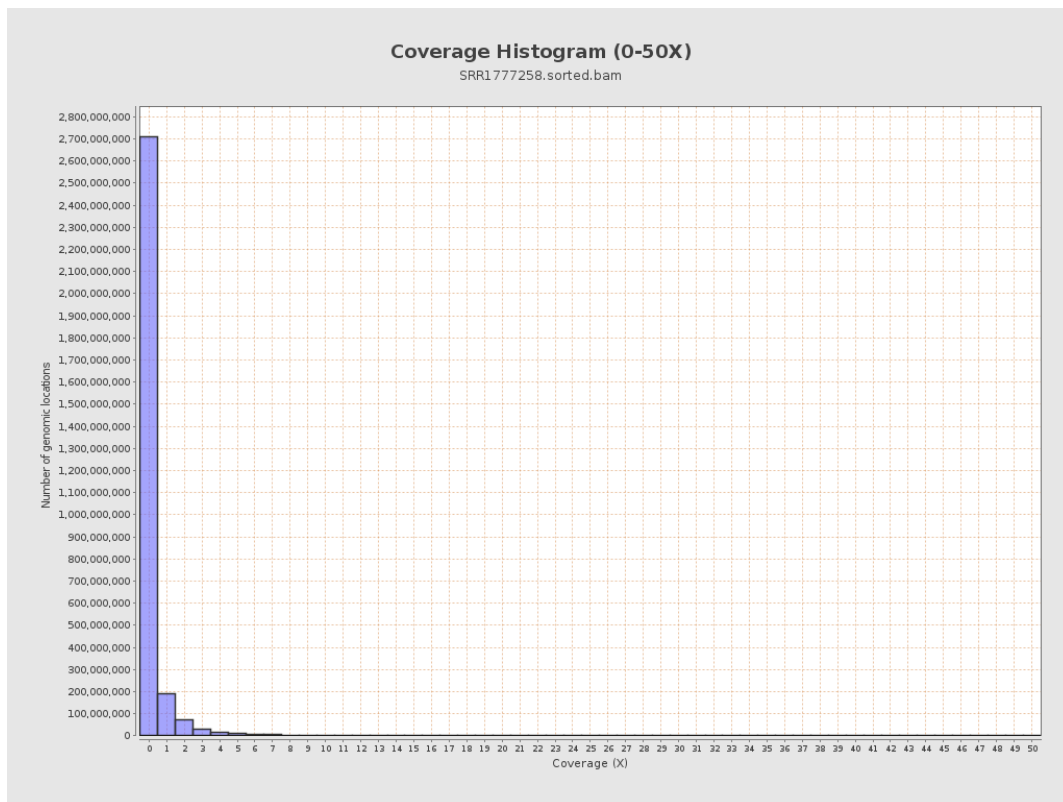
3. Results : Coverage across reference



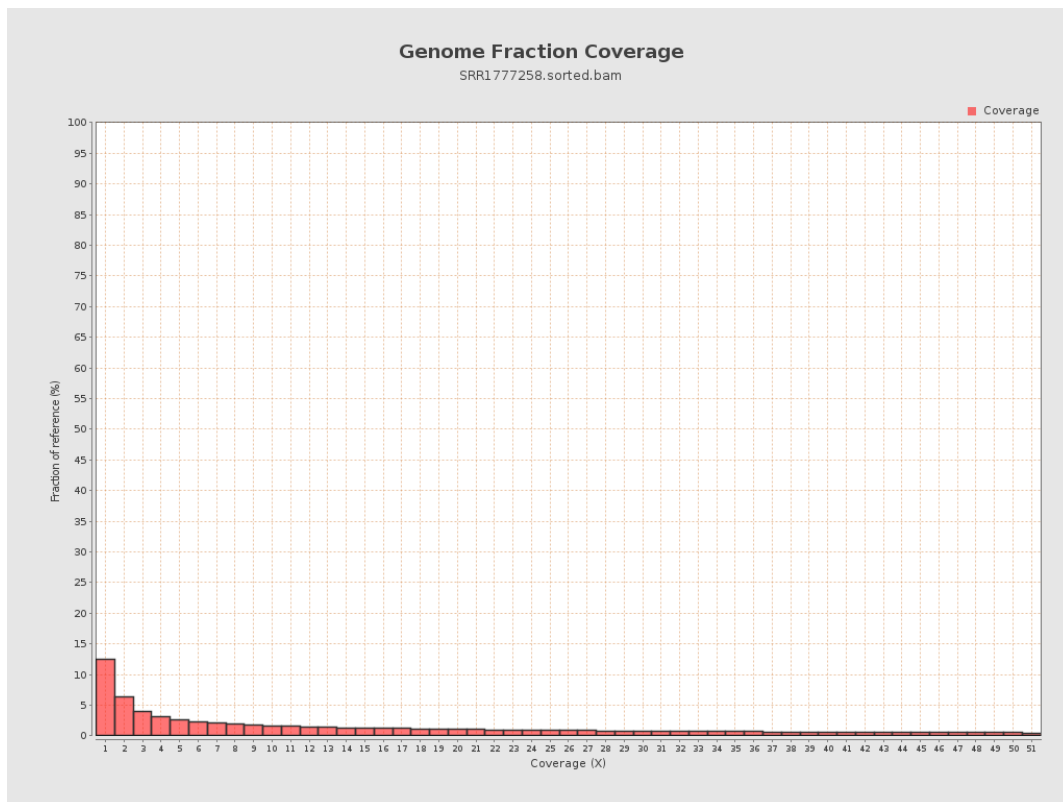
4. Results : Coverage Histogram



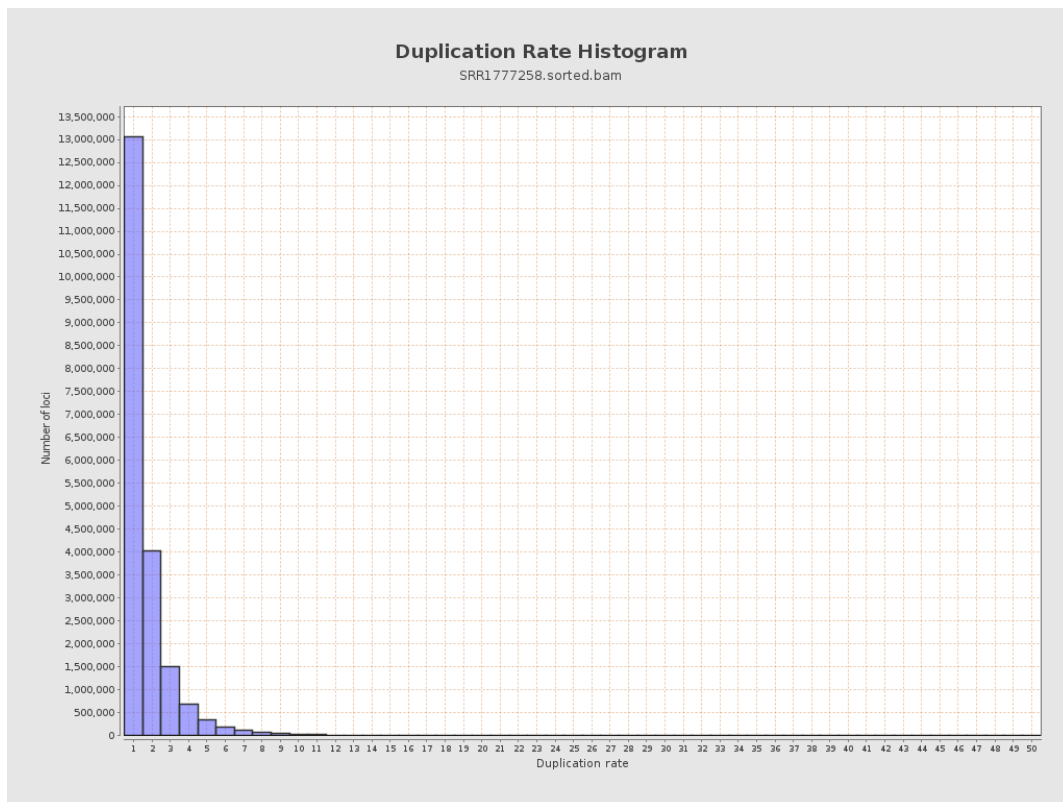
5. Results : Coverage Histogram (0-50X)



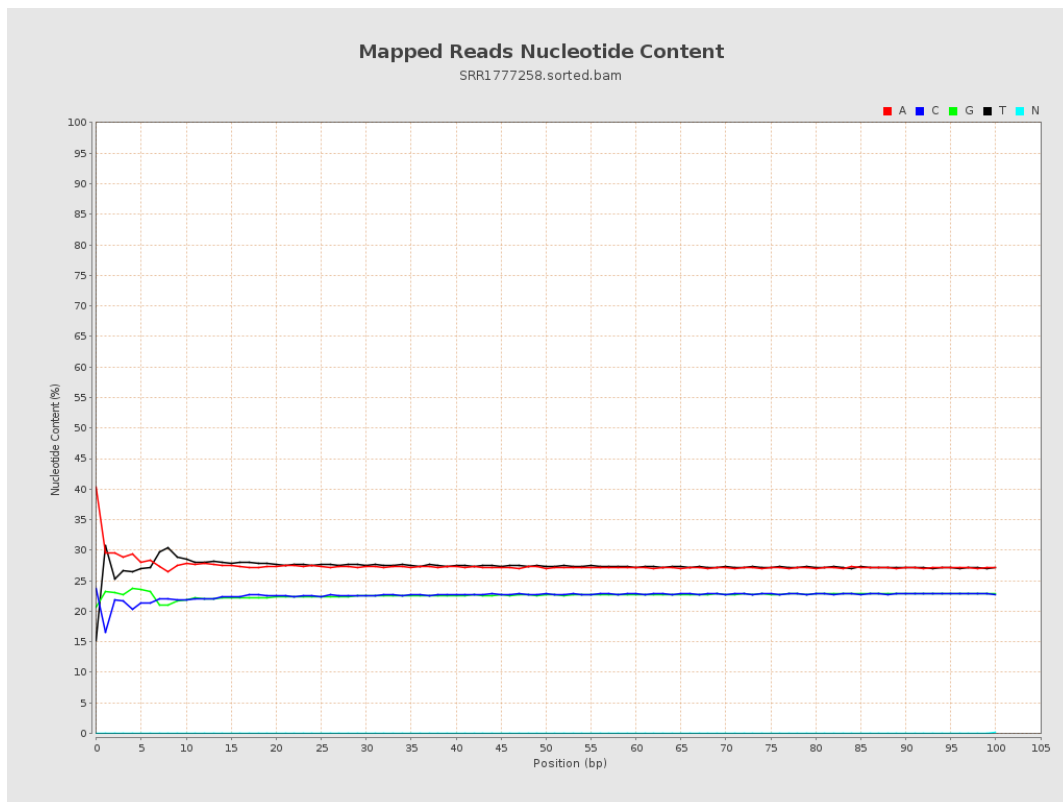
6. Results : Genome Fraction Coverage



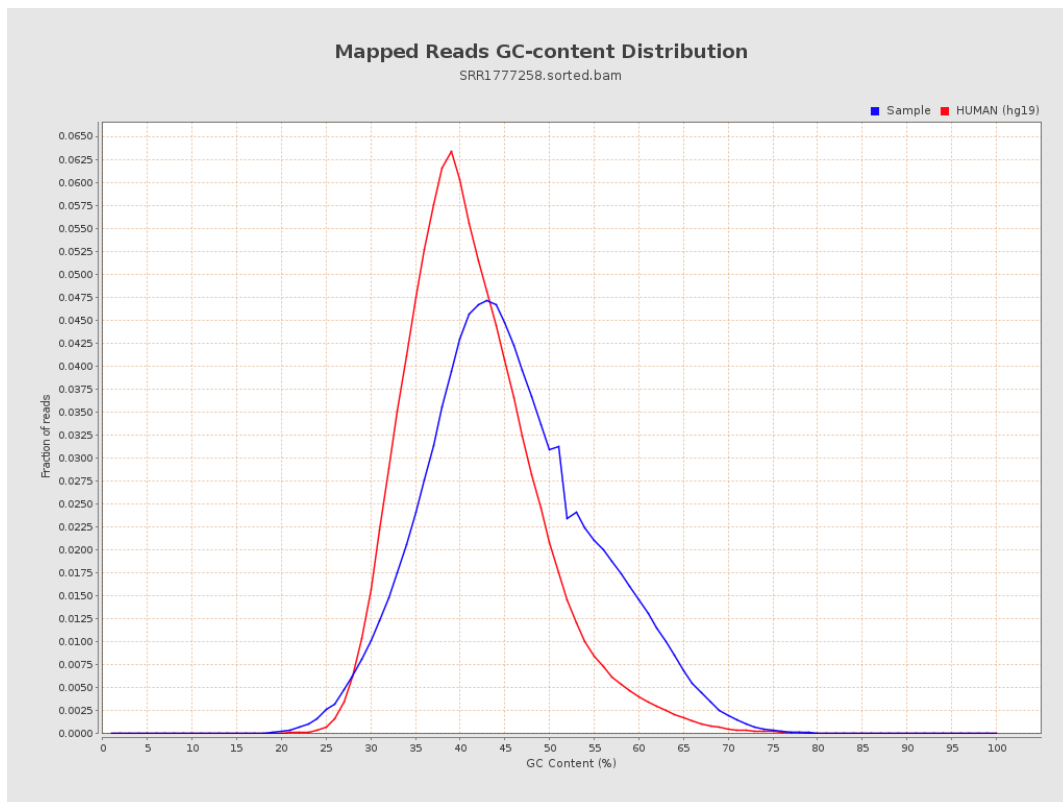
7. Results : Duplication Rate Histogram



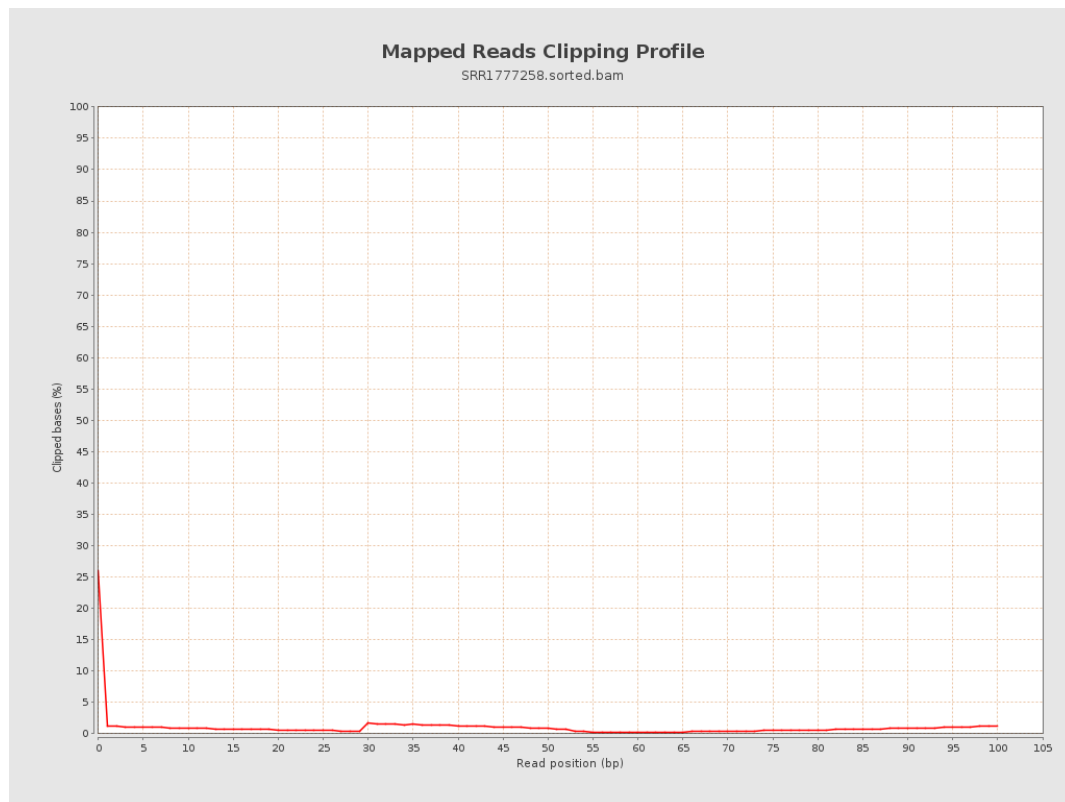
8. Results : Mapped Reads Nucleotide Content



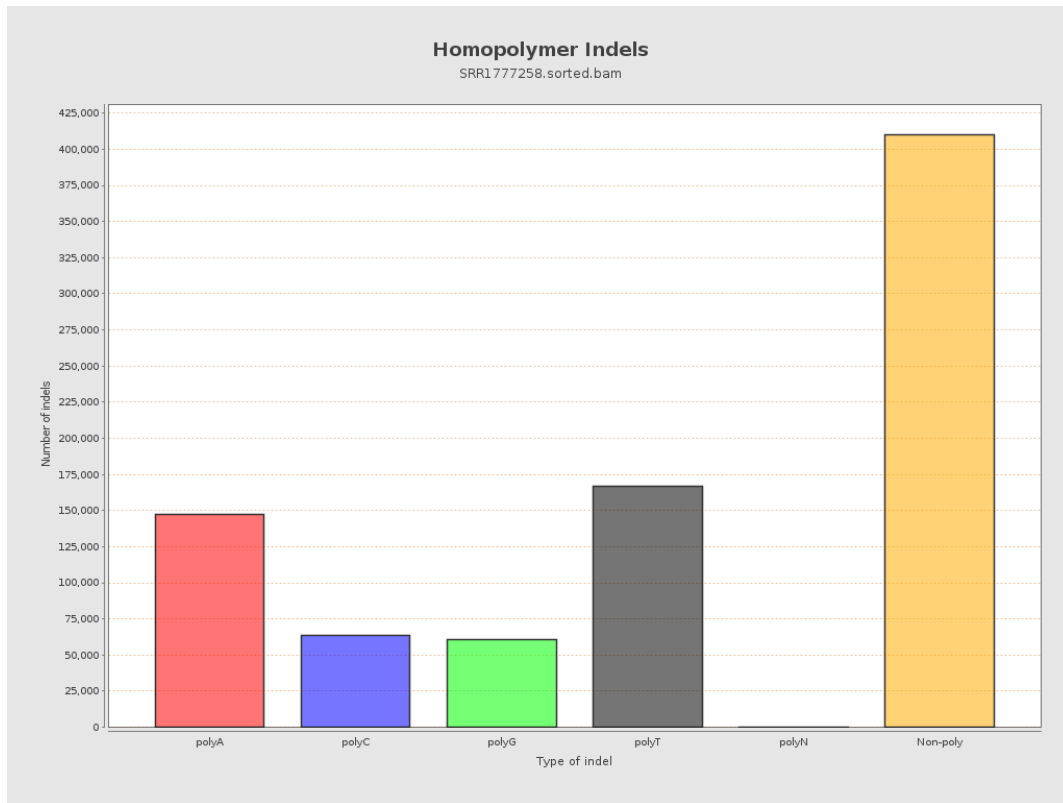
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



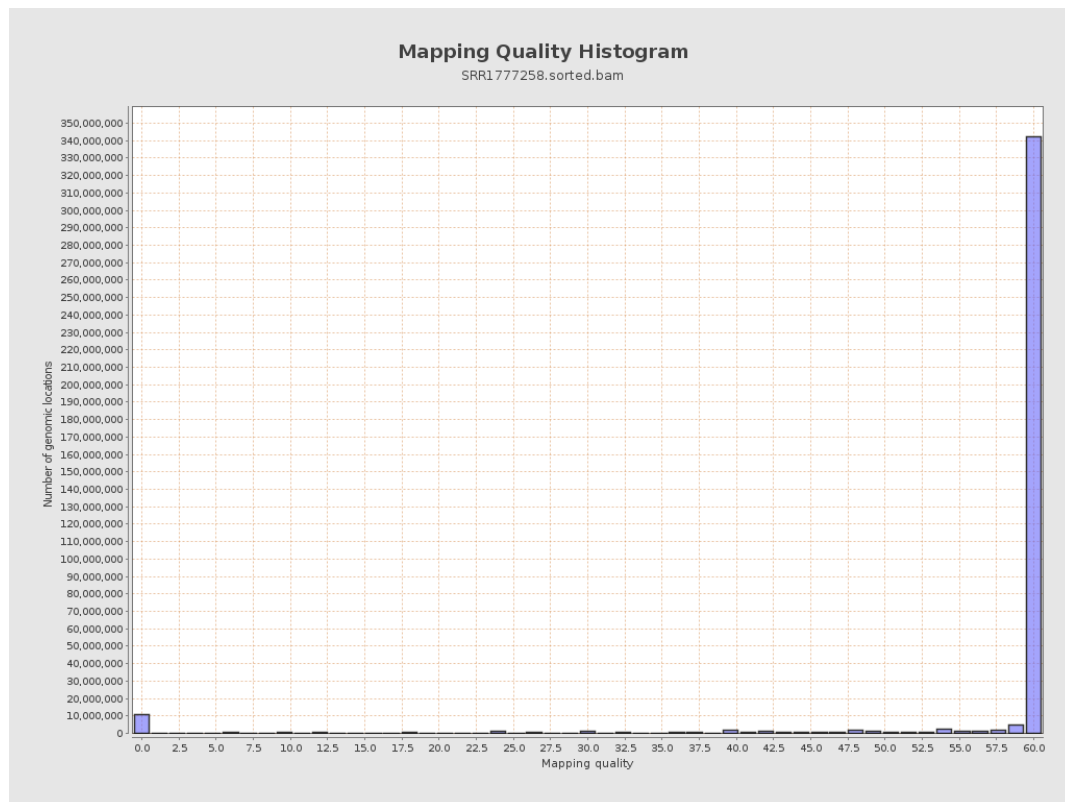
11. Results : Homopolymer Indels



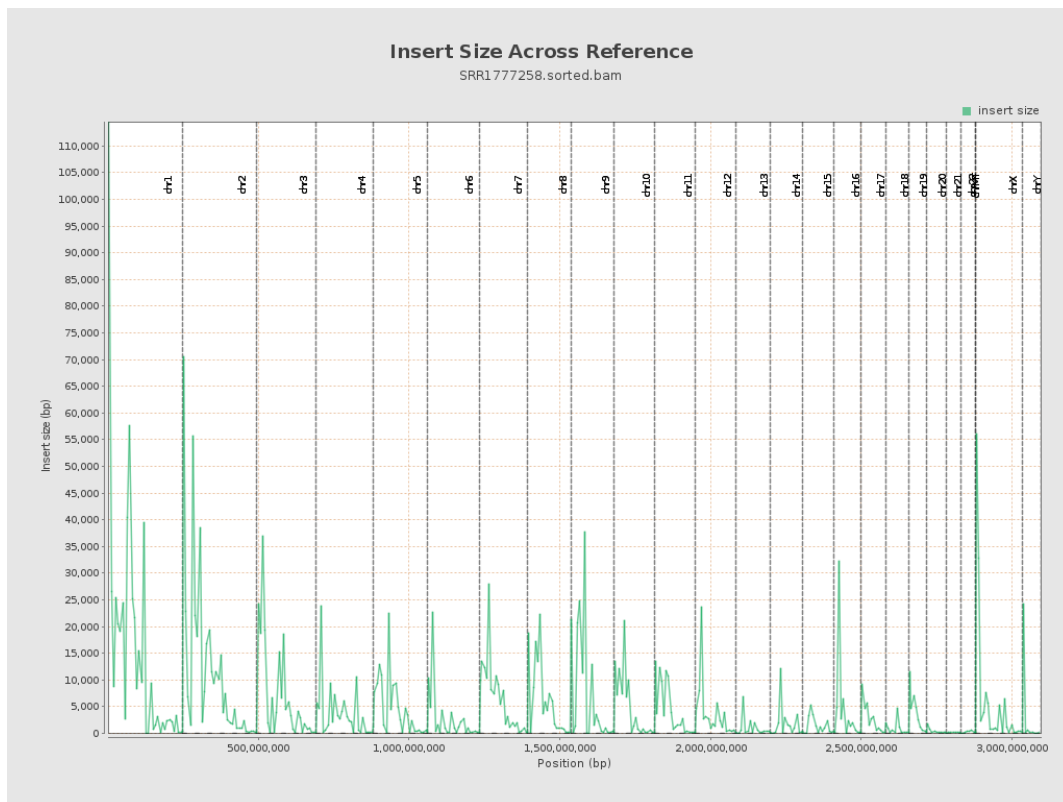
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

