

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 00:49:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779418.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_SRR1779418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779418_1.fastq.gz SRR1779418_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 00:49:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779418.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,622,170
Mapped reads	15,221,618 / 97.44%
Unmapped reads	400,552 / 2.56%
Mapped paired reads	15,221,618 / 97.44%
Mapped reads, first in pair	7,658,711 / 49.02%
Mapped reads, second in pair	7,562,907 / 48.41%
Mapped reads, both in pair	15,095,886 / 96.63%
Mapped reads, singletons	125,732 / 0.8%
Secondary alignments	0
Supplementary alignments	54,822 / 0.35%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	481,702 / 3.08%
Duplication rate	2.78%
Clipped reads	628,601 / 4.02%

2.2. ACGT Content

Number/percentage of A's	367,140,304 / 30.34%
Number/percentage of C's	237,538,648 / 19.63%
Number/percentage of T's	362,373,563 / 29.95%
Number/percentage of G's	242,763,839 / 20.06%
Number/percentage of N's	267,602 / 0.02%

GC Percentage	39.69%
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2.3. Coverage

Mean	0.391
Standard Deviation	1.5331

2.4. Mapping Quality

Mean Mapping Quality	53.46
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2.5. Insert size

Mean	75,885.56
Standard Deviation	2,621,896.6
P25/Median/P75	149 / 191 / 243

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,127,895
Insertions	106,973
Mapped reads with at least one insertion	0.7%
Deletions	123,658
Mapped reads with at least one deletion	0.8%
Homopolymer indels	46.81%

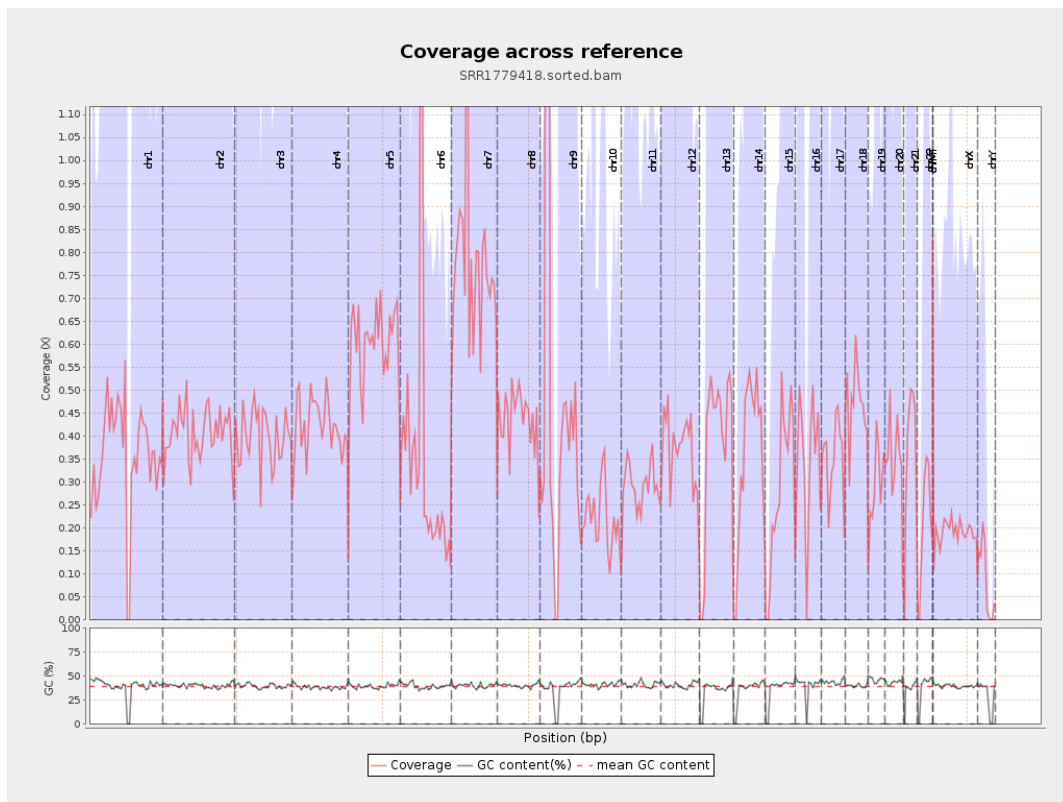
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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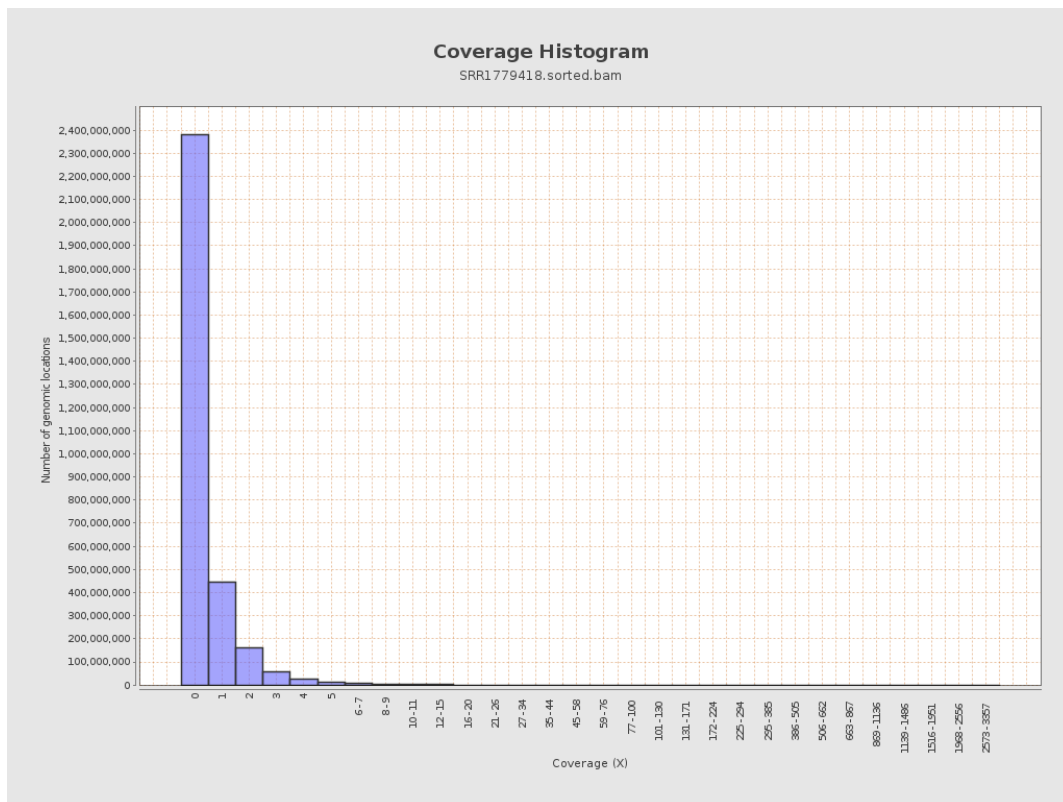
		bases	coverage	deviation
chr1	249250621	88915488	0.3567	3.4956
chr2	243199373	98513819	0.4051	0.963
chr3	198022430	78659445	0.3972	0.8477
chr4	191154276	81064696	0.4241	0.8988
chr5	180915260	107257210	0.5929	1.0551
chr6	171115067	59671230	0.3487	1.2449
chr7	159138663	124049269	0.7795	2.2193
chr8	146364022	63723671	0.4354	0.9413
chr9	141213431	79256648	0.5613	2.037
chr10	135534747	29895590	0.2206	2.0183
chr11	135006516	39265767	0.2908	0.8218
chr12	133851895	49628246	0.3708	0.8451
chr13	115169878	44305743	0.3847	0.8421
chr14	107349540	38765056	0.3611	0.85
chr15	102531392	28875116	0.2816	0.7448
chr16	90354753	30363073	0.336	0.823
chr17	81195210	29206958	0.3597	1.0897
chr18	78077248	36809478	0.4714	1.3615
chr19	59128983	17673513	0.2989	2.0609
chr20	63025520	22173546	0.3518	0.837
chr21	48129895	17007067	0.3534	0.8744
chr22	51304566	10732655	0.2092	0.6457
chrMT	16571	13898	0.8387	0.979
chrX	155270560	29270784	0.1885	0.6304

chrY	59373566	5242062	0.0883	0.4372
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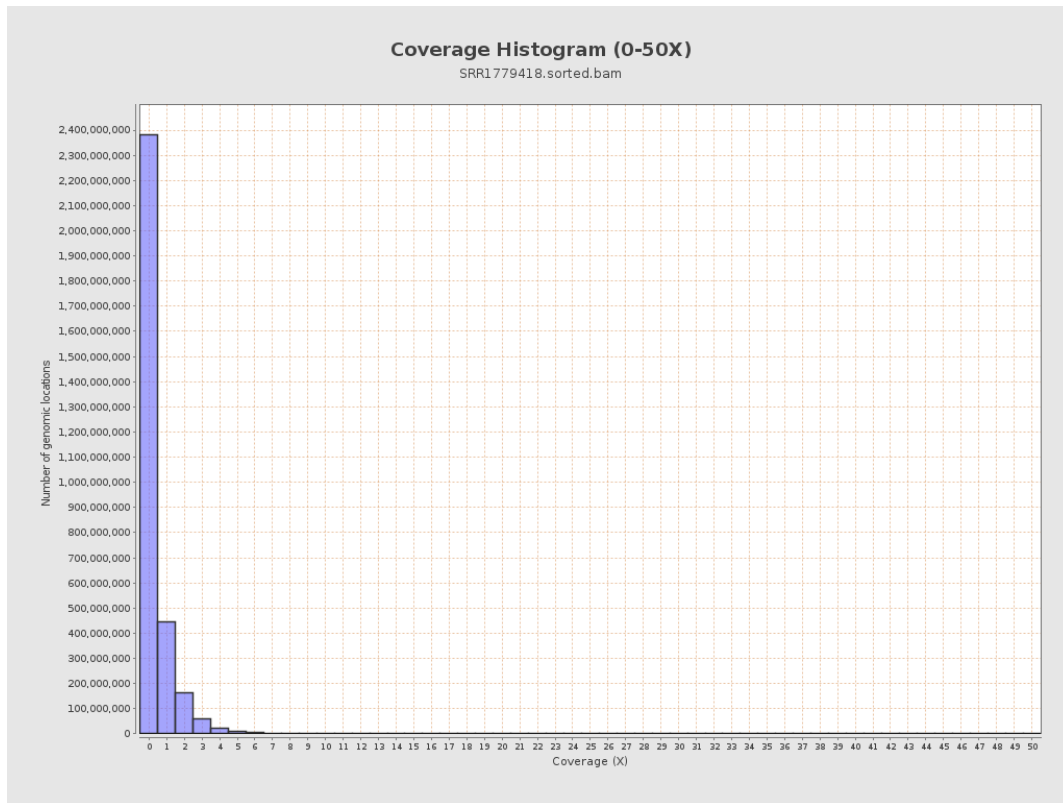
3. Results : Coverage across reference



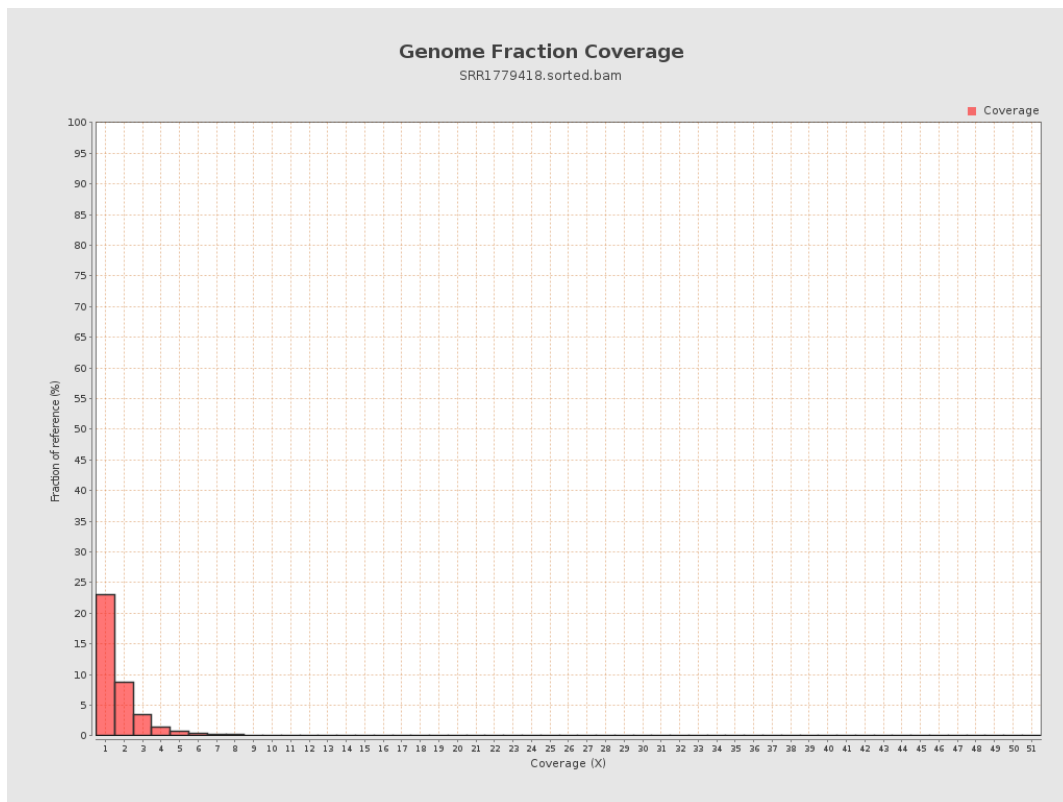
4. Results : Coverage Histogram



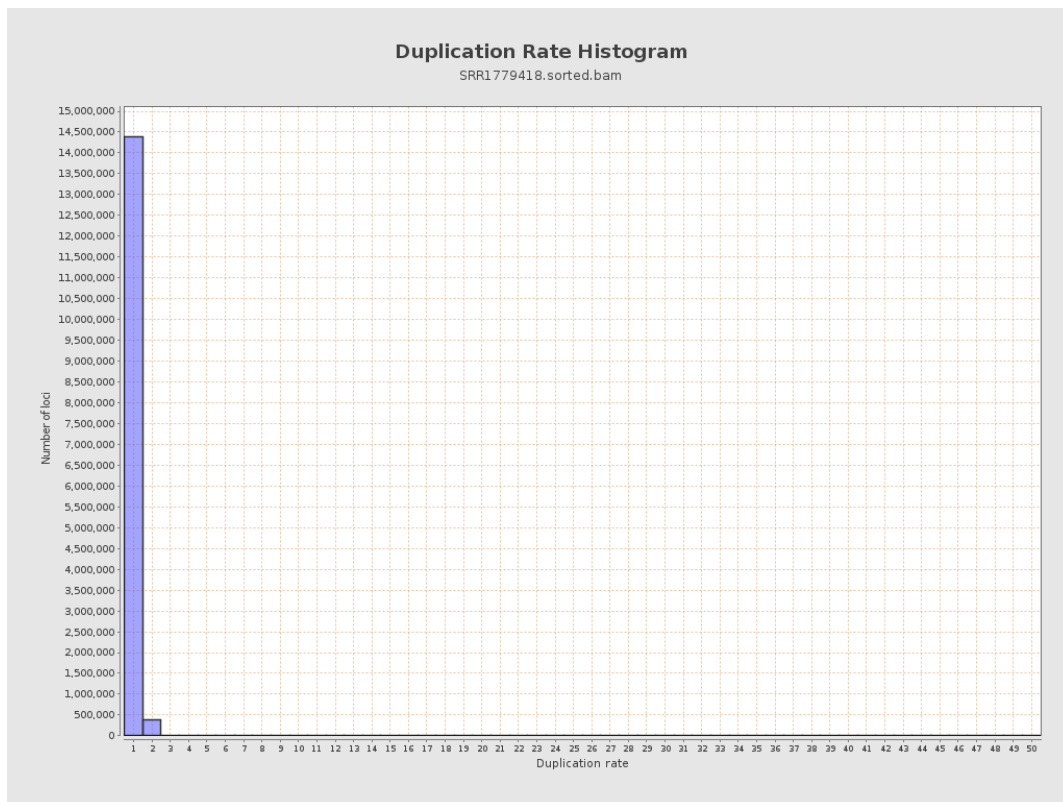
5. Results : Coverage Histogram (0-50X)



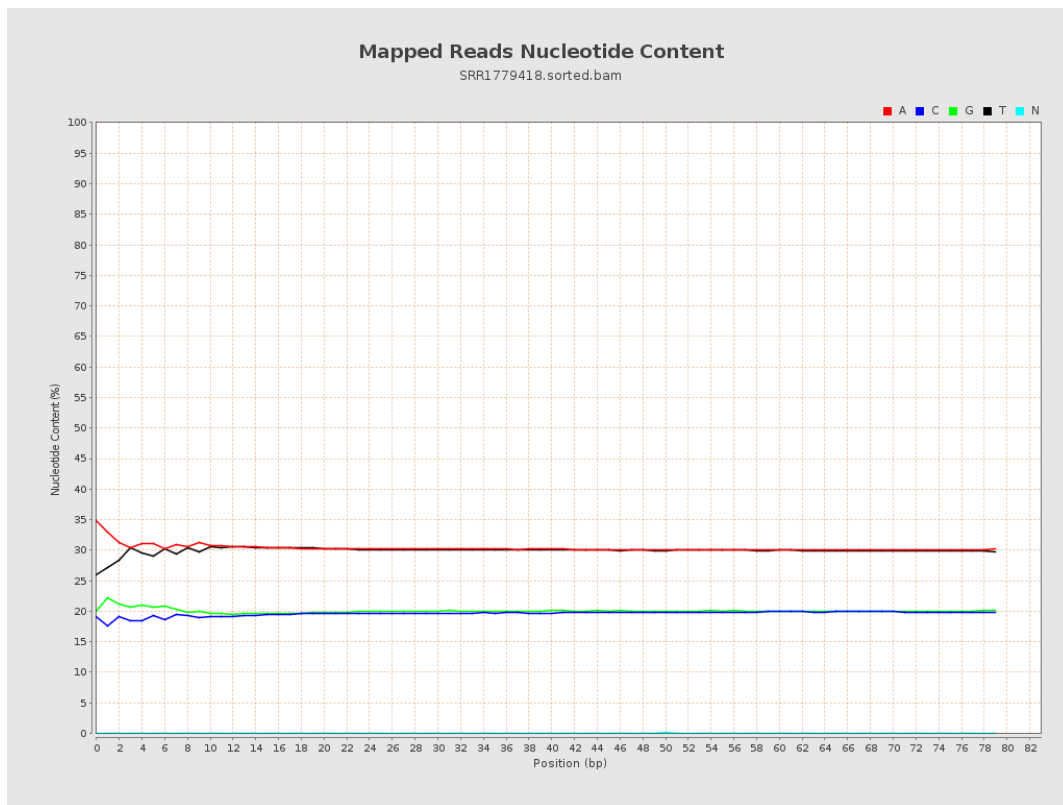
6. Results : Genome Fraction Coverage



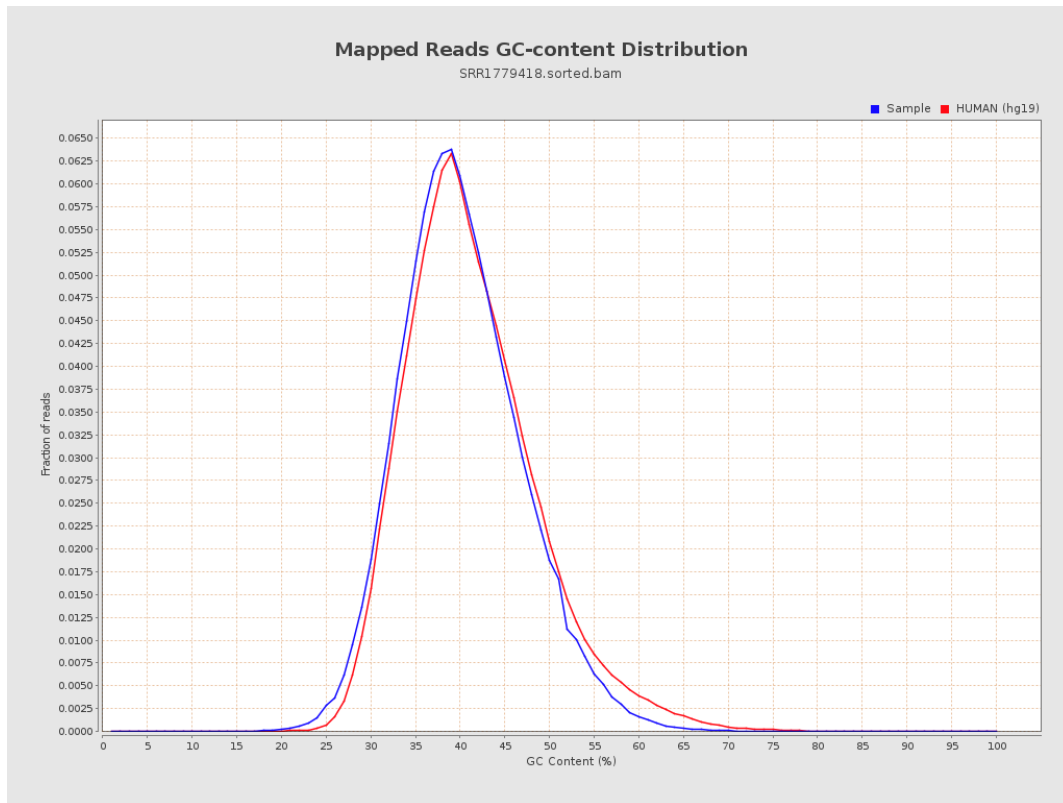
7. Results : Duplication Rate Histogram



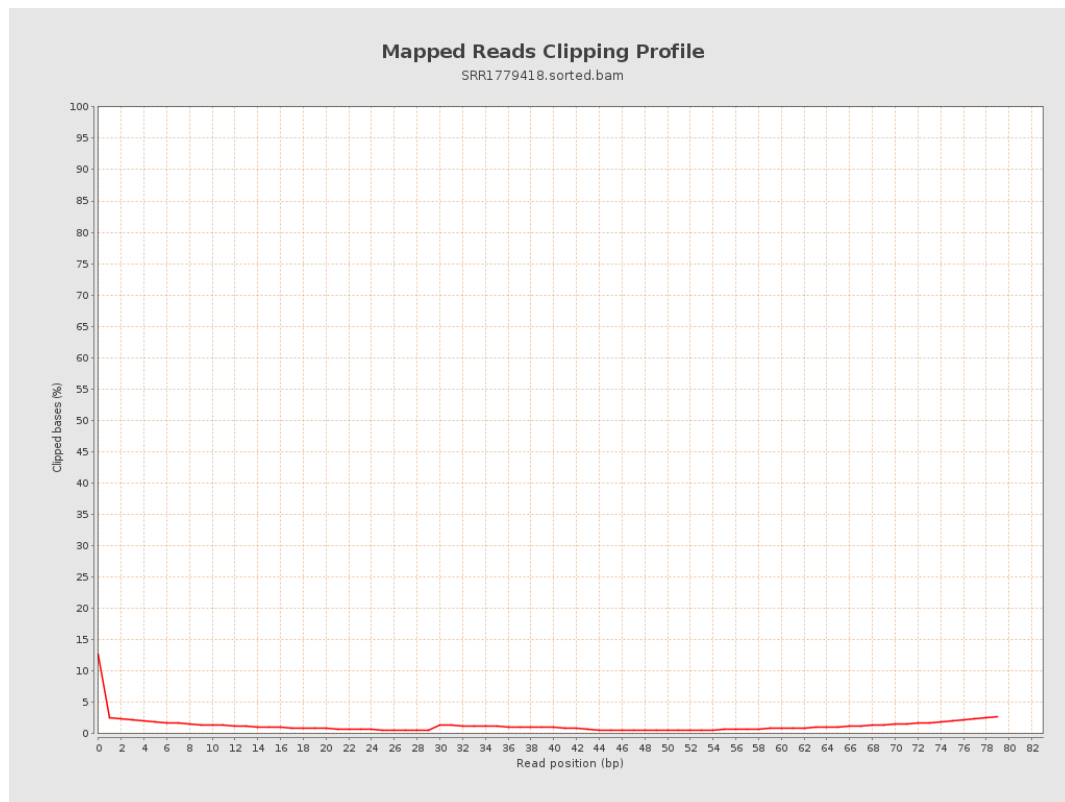
8. Results : Mapped Reads Nucleotide Content



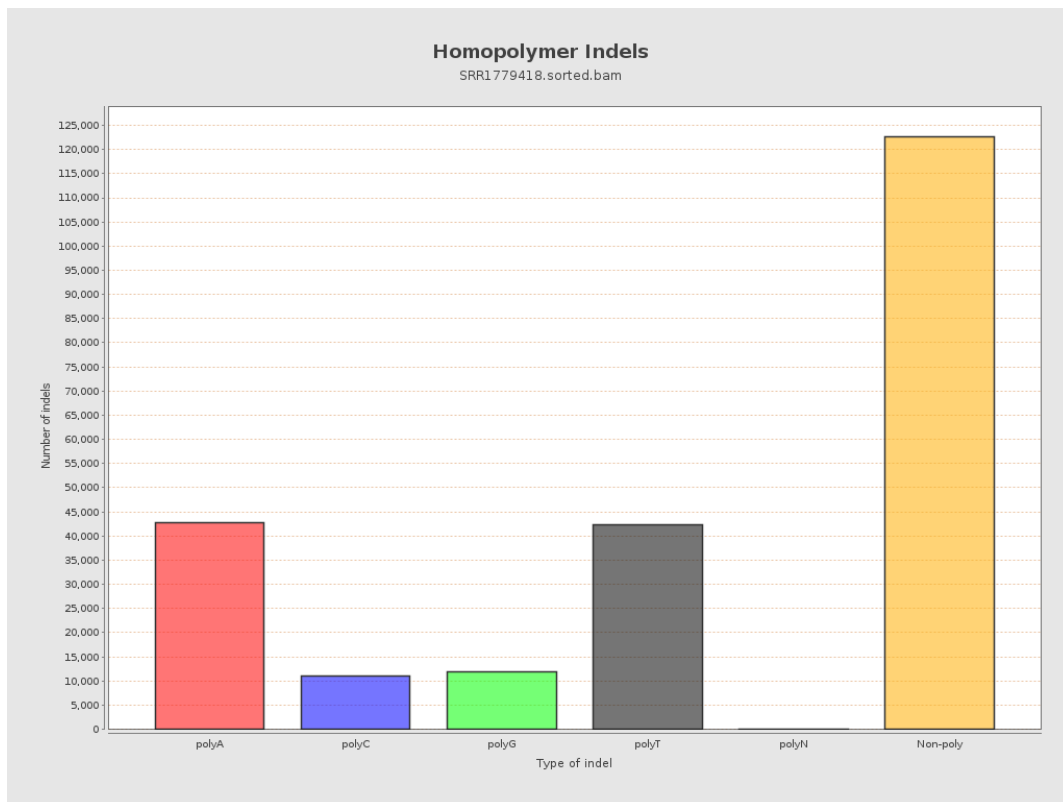
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



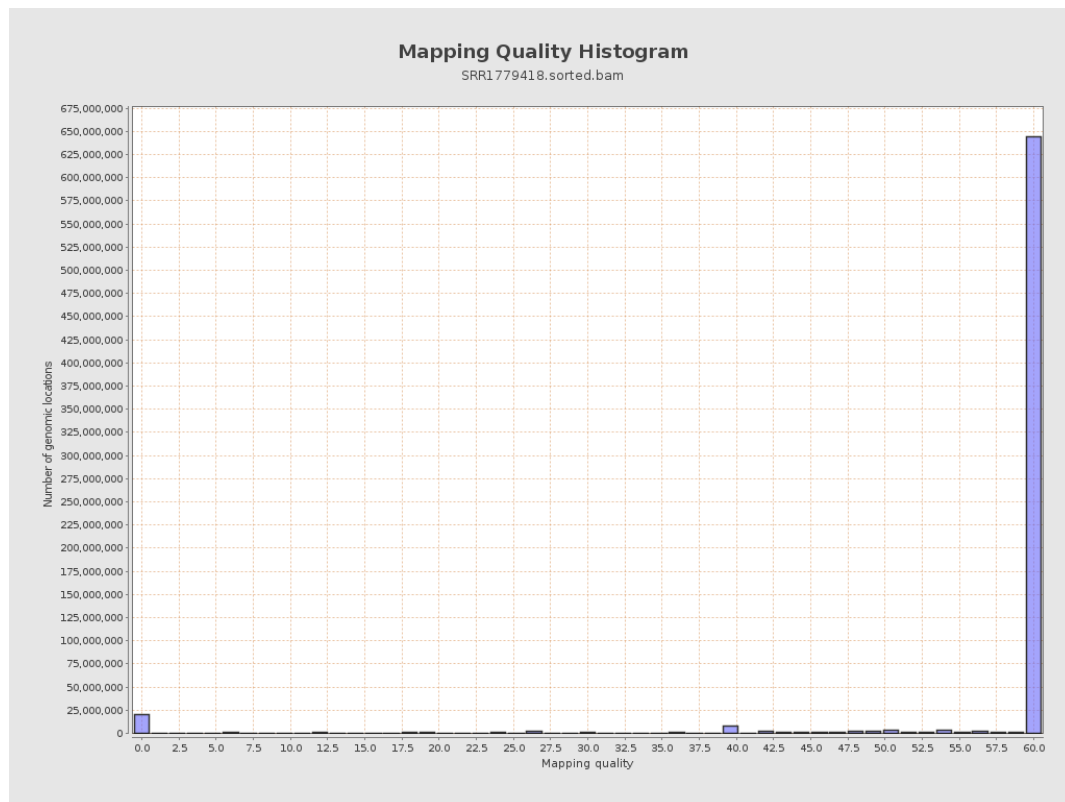
11. Results : Homopolymer Indels



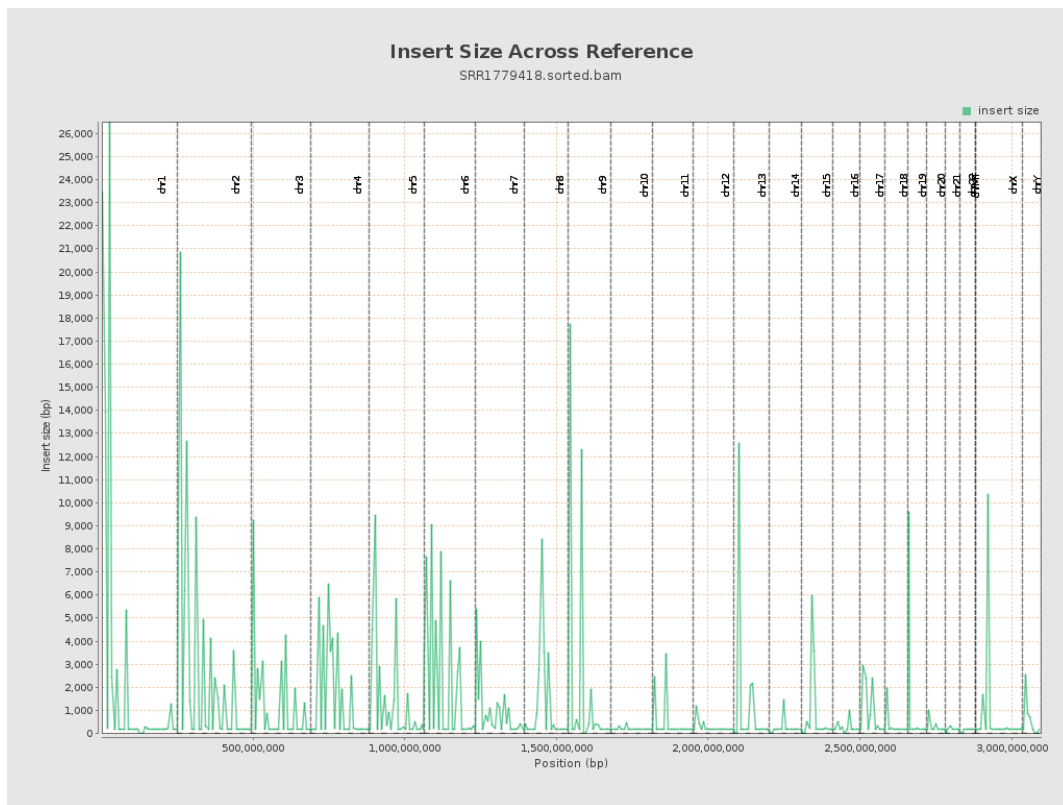
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

