

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/29 23:16:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365375.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_SRR5365375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365375_1.fastq.gz SRR5365375_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 29 23:16:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	659,386,010
Mapped reads	630,780,989 / 95.66%
Unmapped reads	28,605,021 / 4.34%
Mapped paired reads	630,780,989 / 95.66%
Mapped reads, first in pair	315,053,231 / 47.78%
Mapped reads, second in pair	315,727,758 / 47.88%
Mapped reads, both in pair	629,277,342 / 95.43%
Mapped reads, singletons	1,503,647 / 0.23%
Secondary alignments	0
Supplementary alignments	4,360,243 / 0.66%
Read min/max/mean length	30 / 150 / 150.3
Duplicated reads (estimated)	376,487,016 / 57.1%
Duplication rate	39.35%
Clipped reads	481,407,000 / 73.01%

2.2. ACGT Content

Number/percentage of A's	21,888,552,623 / 29.68%
Number/percentage of C's	14,988,240,469 / 20.32%
Number/percentage of T's	21,230,398,218 / 28.78%
Number/percentage of G's	15,646,326,079 / 21.21%
Number/percentage of N's	3,901,691 / 0.01%

GC Percentage	41.53%
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2.3. Coverage

Mean	23.8345
Standard Deviation	324.2984

2.4. Mapping Quality

Mean Mapping Quality	53.9
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2.5. Insert size

Mean	61,166.3
Standard Deviation	2,403,566
P25/Median/P75	100 / 135 / 186

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	350,517,526
Insertions	23,917,806
Mapped reads with at least one insertion	3.68%
Deletions	12,038,088
Mapped reads with at least one deletion	1.85%
Homopolymer indels	49.82%

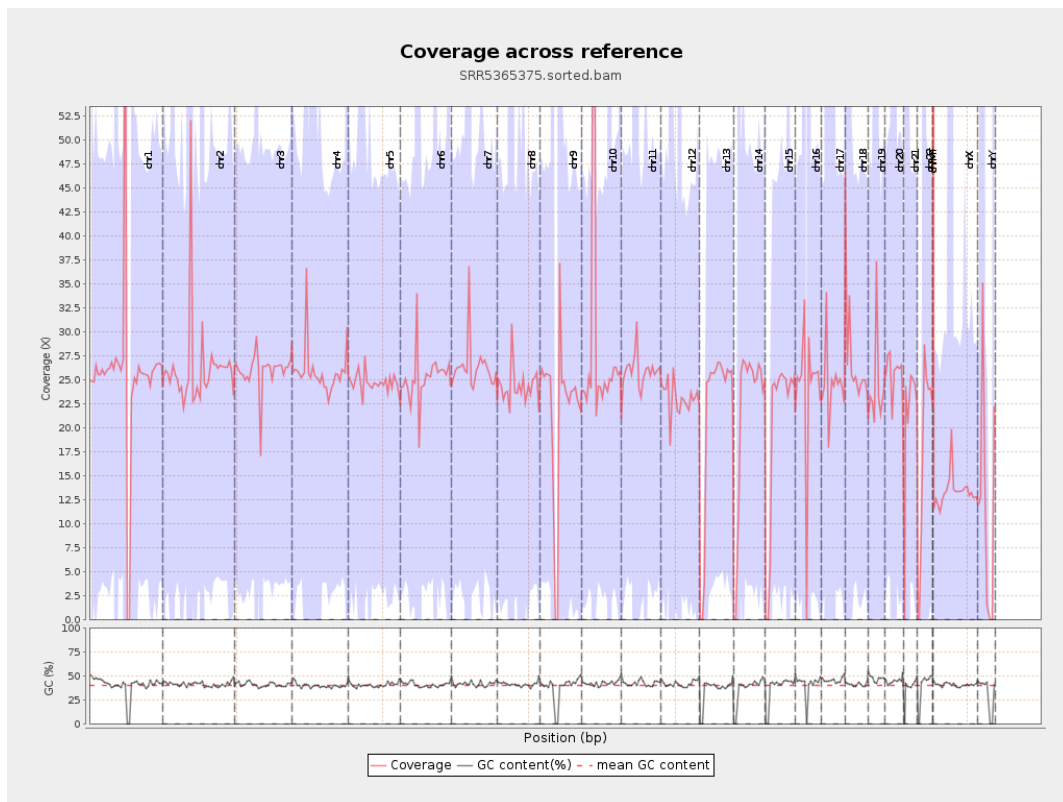
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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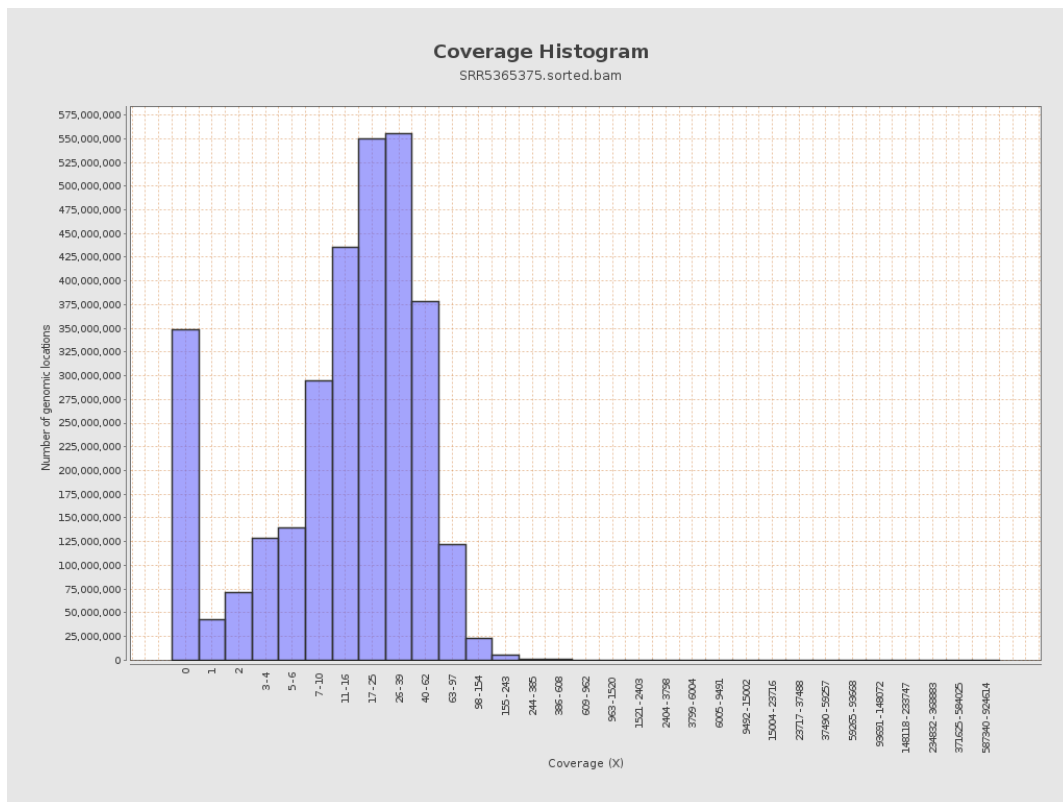
		bases	coverage	deviation
chr1	249250621	6378797771	25.5919	919.579
chr2	243199373	6364238223	26.1688	190.4467
chr3	198022430	5136031842	25.9366	47.3145
chr4	191154276	4943454556	25.8611	107.5421
chr5	180915260	4456842295	24.635	30.846
chr6	171115067	4320361658	25.2483	117.8642
chr7	159138663	4184832651	26.2968	230.5543
chr8	146364022	3550365094	24.2571	91.0403
chr9	141213431	3105577353	21.9921	294.9102
chr10	135534747	3815473038	28.1513	559.1329
chr11	135006516	3493759530	25.8785	188.2895
chr12	133851895	3088732221	23.0757	36.7747
chr13	115169878	2468729175	21.4355	22.1213
chr14	107349540	2322756316	21.6373	31.4376
chr15	102531392	2030781575	19.8064	24.0009
chr16	90354753	2151223408	23.8086	87.7612
chr17	81195210	2004951837	24.693	147.649
chr18	78077248	2089493510	26.7619	341.2074
chr19	59128983	1446921409	24.4706	486.8948
chr20	63025520	1620186477	25.7068	47.9879
chr21	48129895	1035600436	21.5168	99.1125
chr22	51304566	905171699	17.6431	83.6095
chrMT	16571	71155188	4,293.9586	893.8563
chrX	155270560	2071605941	13.3419	74.6009

chrY	59373566	727130236	12.2467	242.4902
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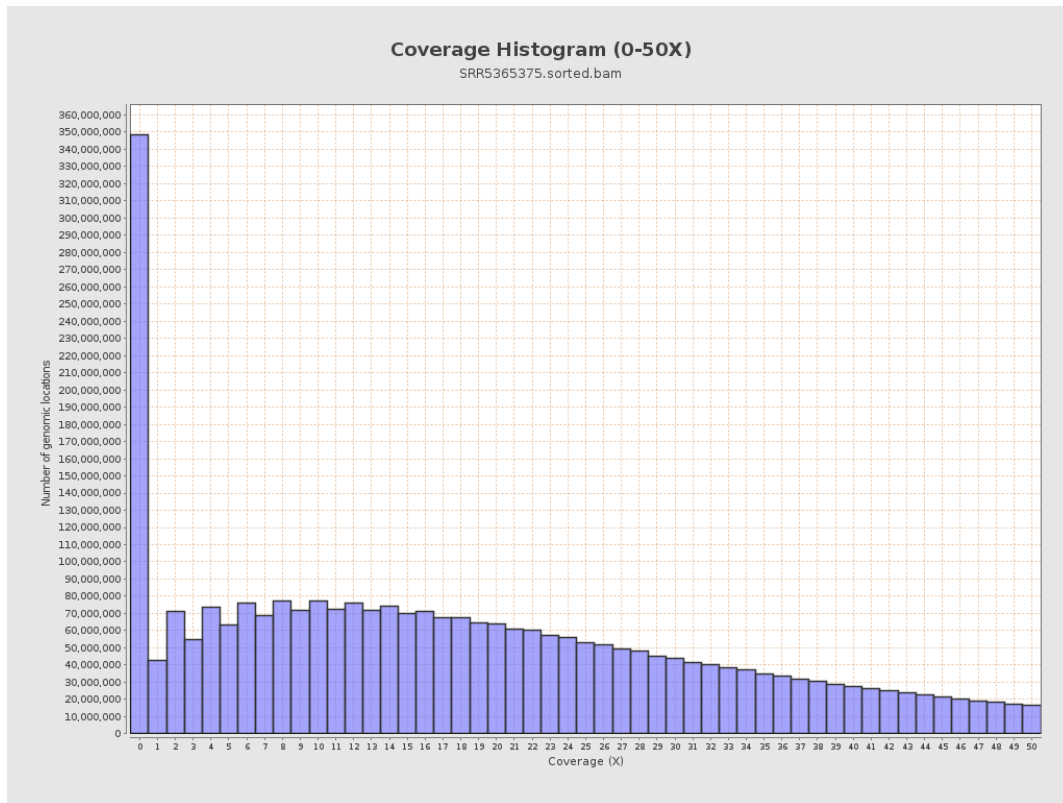
3. Results : Coverage across reference



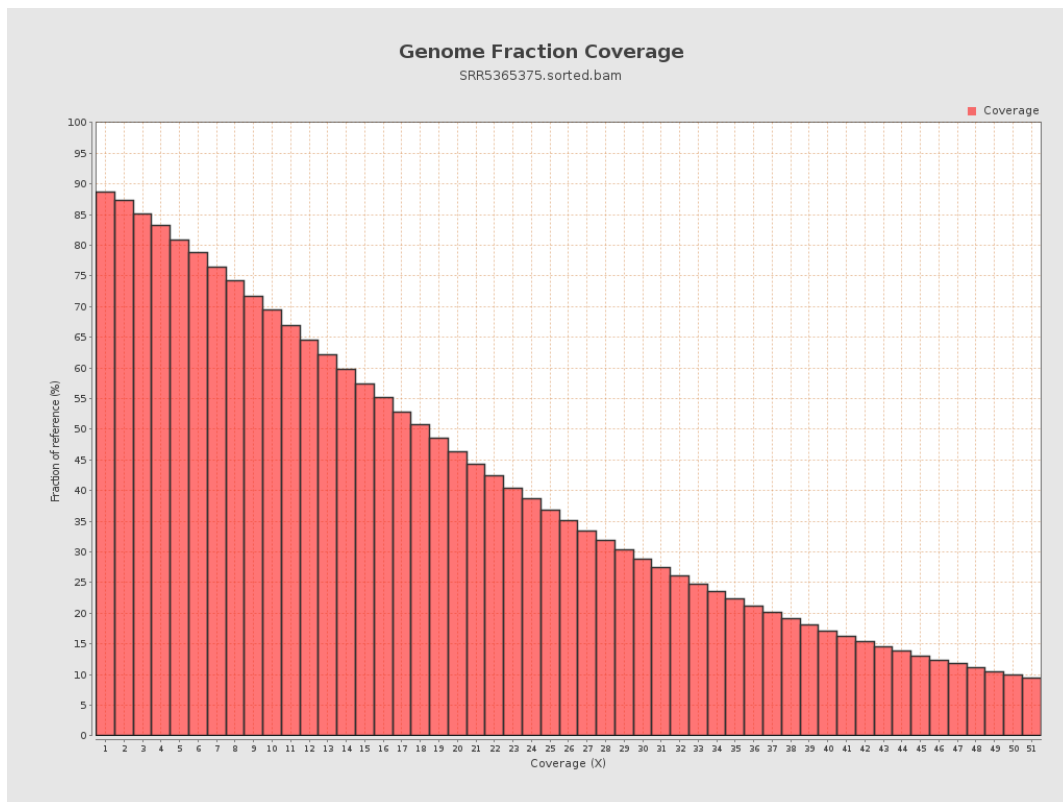
4. Results : Coverage Histogram



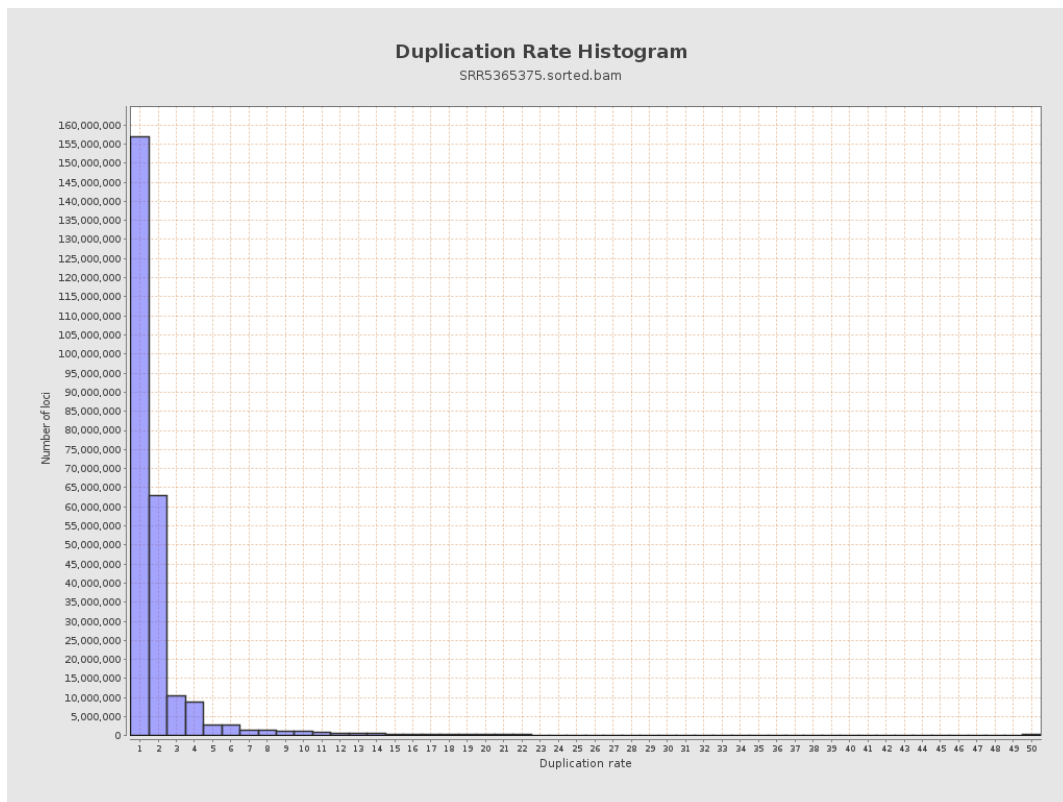
5. Results : Coverage Histogram (0-50X)



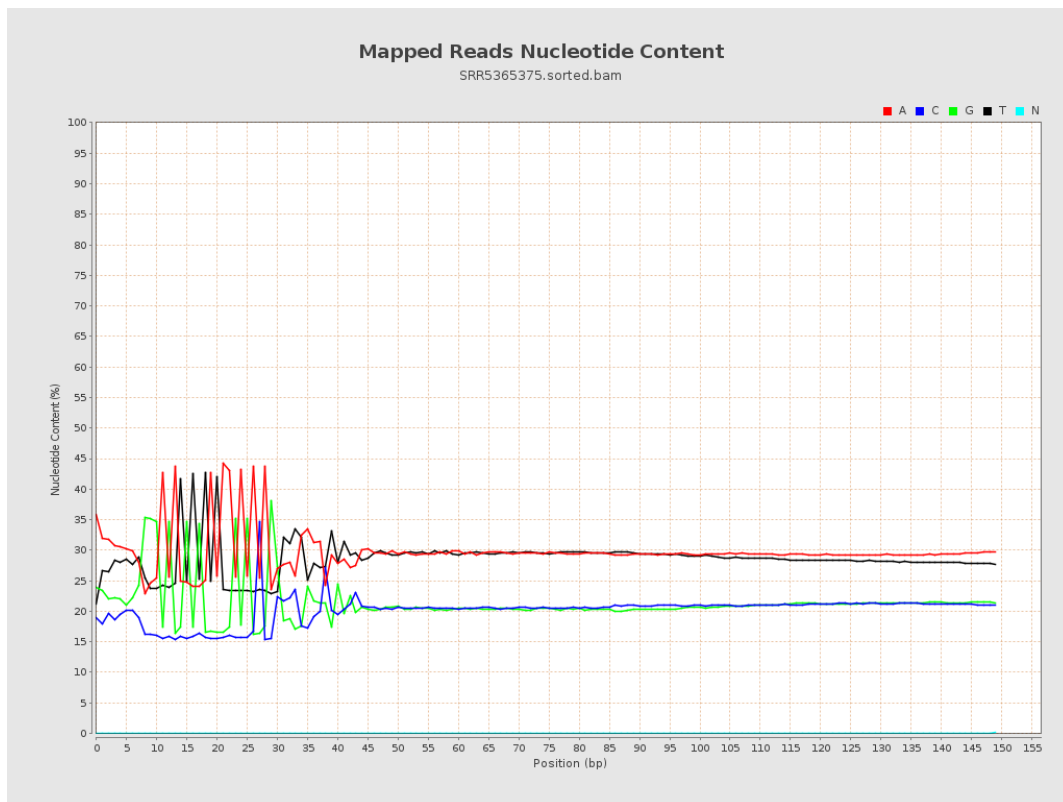
6. Results : Genome Fraction Coverage



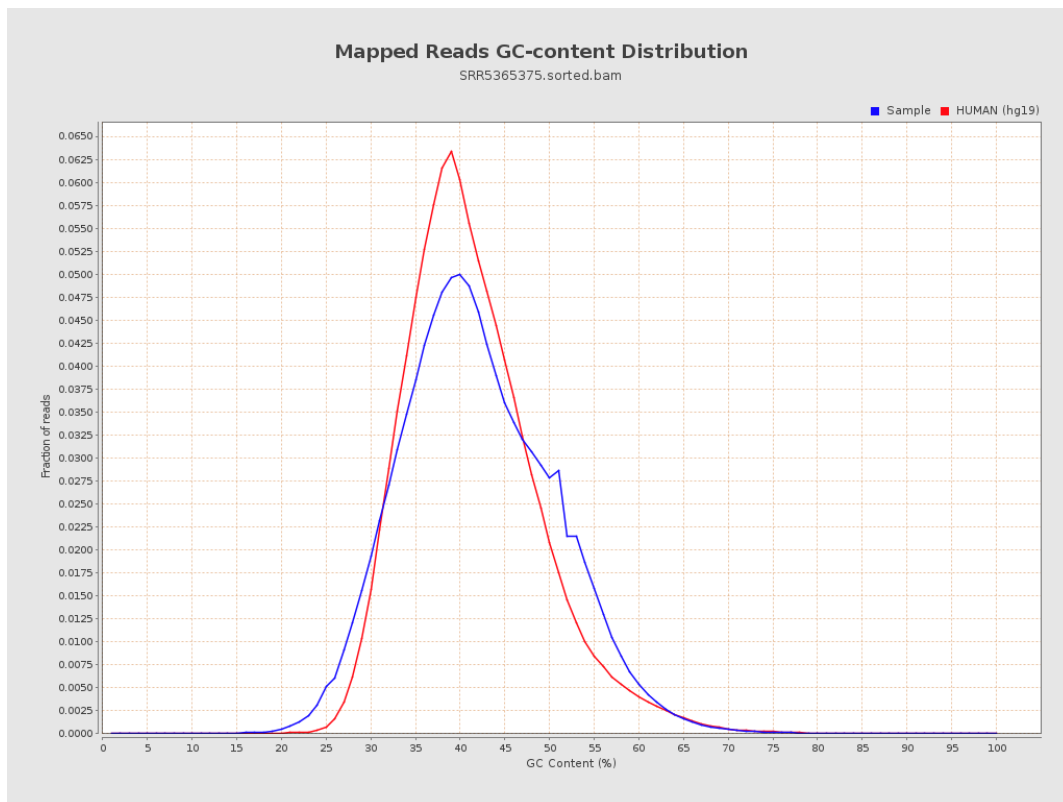
7. Results : Duplication Rate Histogram



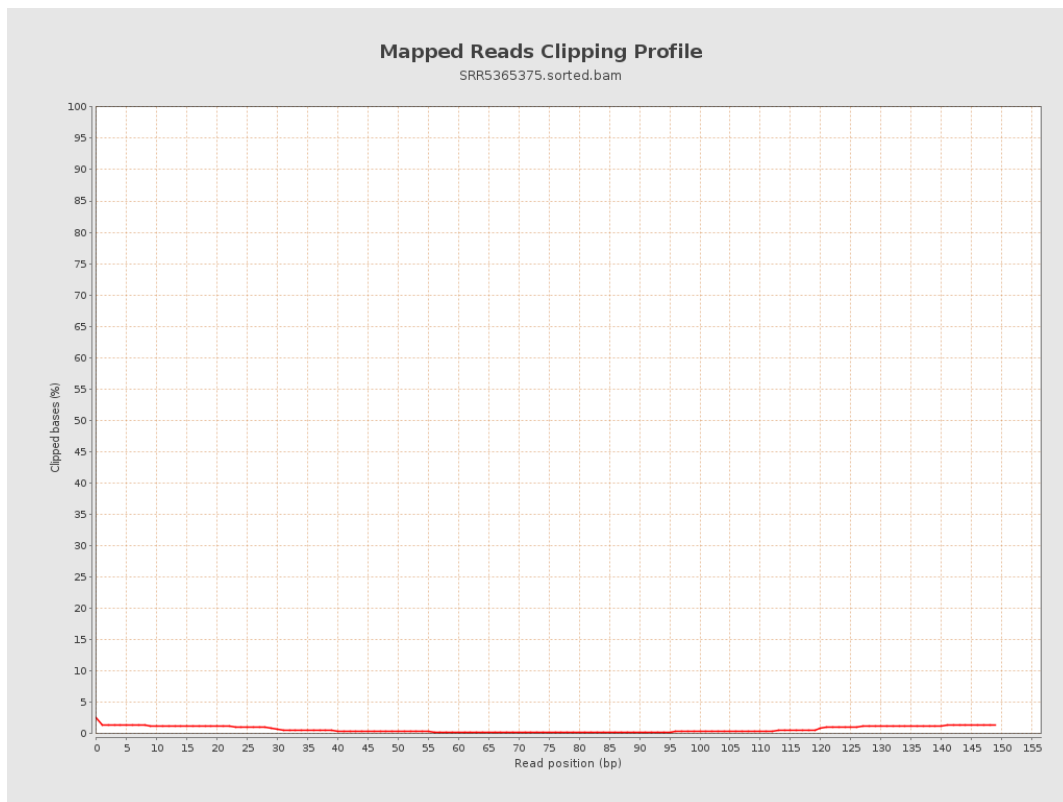
8. Results : Mapped Reads Nucleotide Content



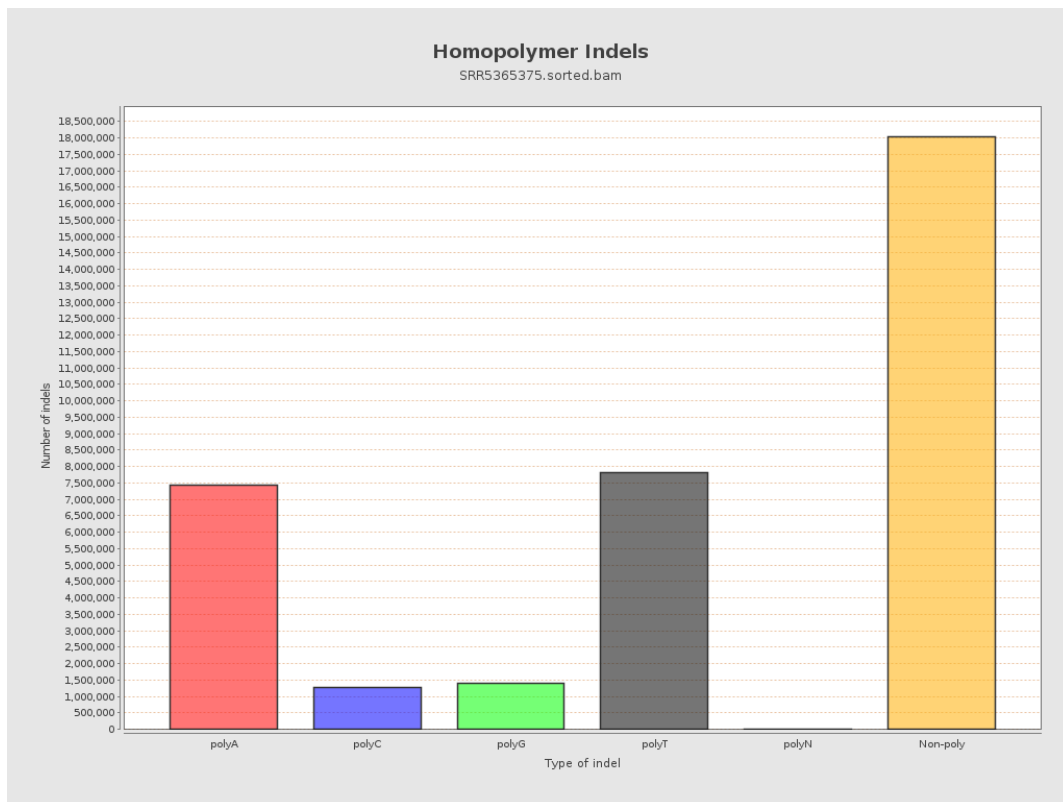
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



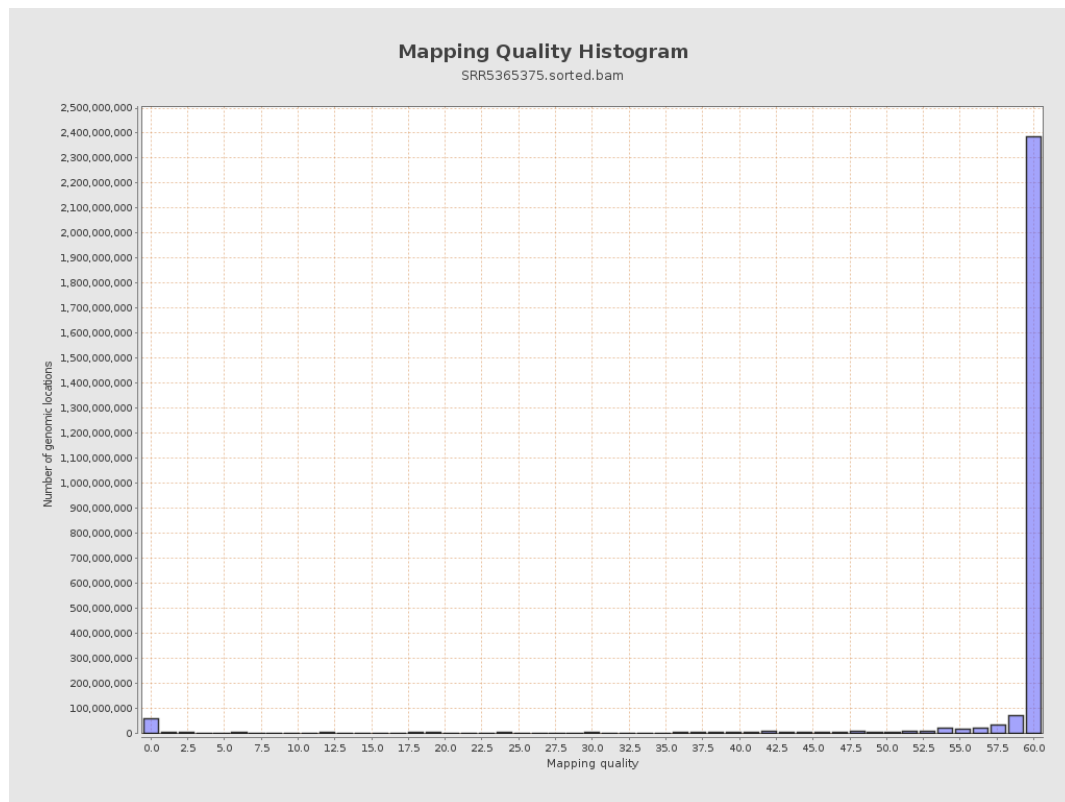
11. Results : Homopolymer Indels



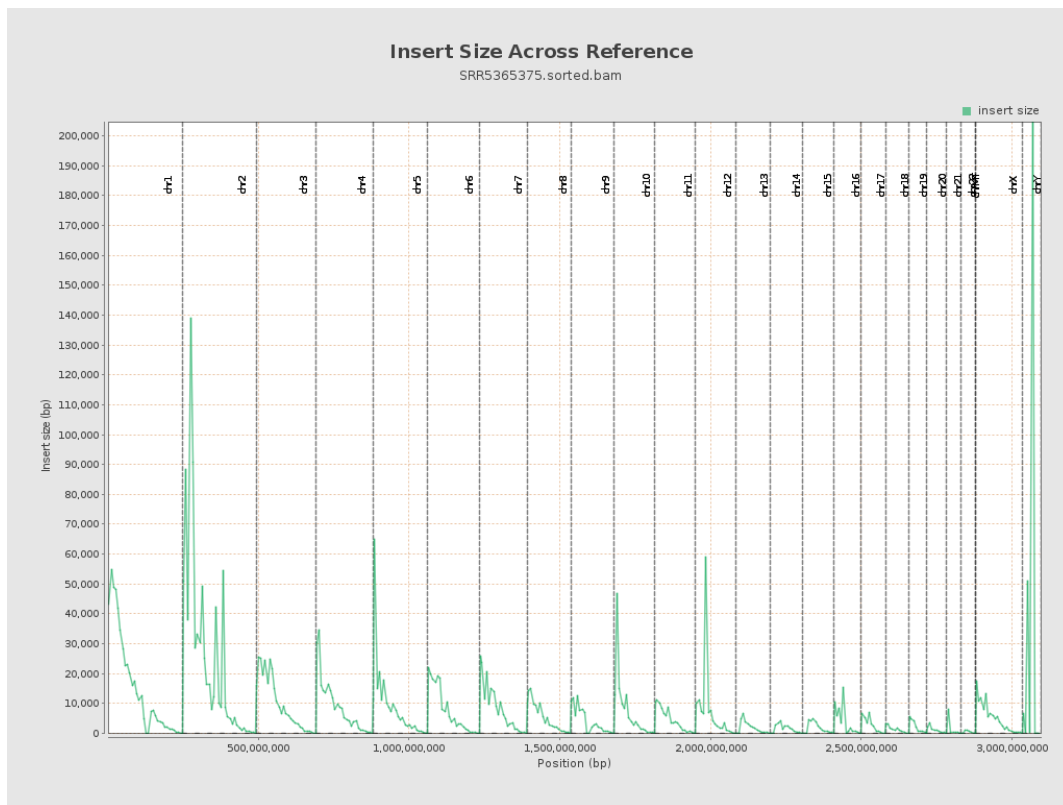
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

