

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 21:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472725.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_SRR3472725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472725_1.fastq.gz SRR3472725_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 21:00:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,454,108
Mapped reads	18,266,258 / 98.98%
Unmapped reads	187,850 / 1.02%
Mapped paired reads	18,266,258 / 98.98%
Mapped reads, first in pair	9,173,015 / 49.71%
Mapped reads, second in pair	9,093,243 / 49.27%
Mapped reads, both in pair	18,146,528 / 98.33%
Mapped reads, singletons	119,730 / 0.65%
Secondary alignments	0
Supplementary alignments	83,923 / 0.45%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	12,358,811 / 66.97%
Duplication rate	44.93%
Clipped reads	1,486,015 / 8.05%

2.2. ACGT Content

Number/percentage of A's	501,321,964 / 27.86%
Number/percentage of C's	401,097,204 / 22.29%
Number/percentage of T's	497,642,320 / 27.65%
Number/percentage of G's	399,125,209 / 22.18%
Number/percentage of N's	346,368 / 0.02%

GC Percentage	44.47%
---------------	--------

2.3. Coverage

Mean	0.5814
Standard Deviation	26.615

2.4. Mapping Quality

Mean Mapping Quality	55.01
----------------------	-------

2.5. Insert size

Mean	27,408.68
Standard Deviation	1,538,043.82
P25/Median/P75	181 / 255 / 347

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	12,005,593
Insertions	118,841
Mapped reads with at least one insertion	0.64%
Deletions	114,885
Mapped reads with at least one deletion	0.62%
Homopolymer indels	45.54%

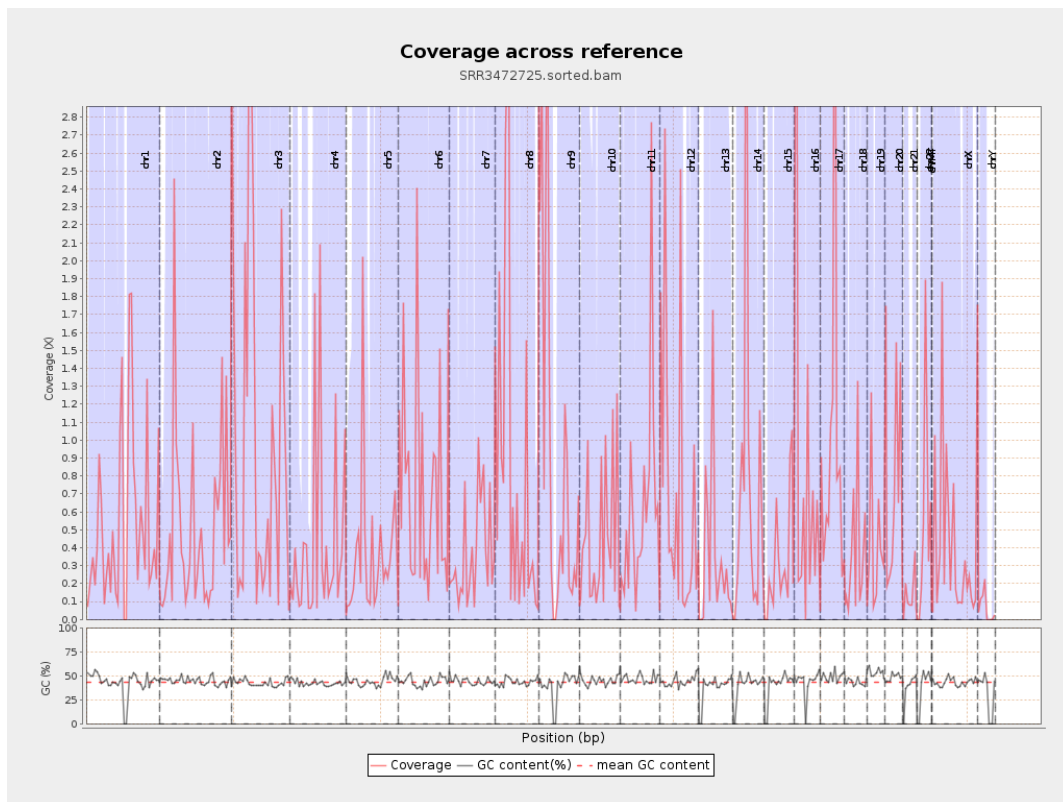
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

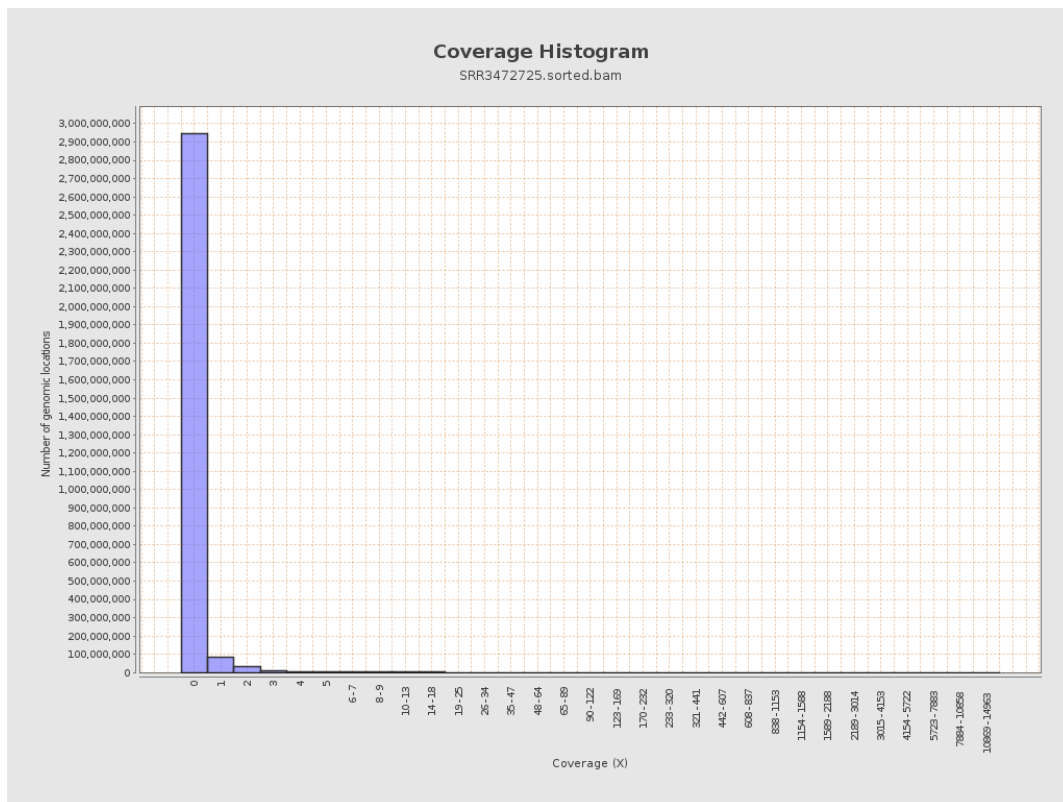
		bases	coverage	deviation
chr1	249250621	133321307	0.5349	22.6161
chr2	243199373	120529125	0.4956	31.3906
chr3	198022430	206476228	1.0427	36.1842
chr4	191154276	80437923	0.4208	22.5955
chr5	180915260	65029851	0.3594	13.0247
chr6	171115067	121915469	0.7125	27.6232
chr7	159138663	57959141	0.3642	12.2873
chr8	146364022	115594734	0.7898	38.8258
chr9	141213431	126656580	0.8969	29.5999
chr10	135534747	63781284	0.4706	24.4753
chr11	135006516	85870727	0.636	28.107
chr12	133851895	98720177	0.7375	30.9729
chr13	115169878	38305527	0.3326	16.8009
chr14	107349540	80719473	0.7519	42.4608
chr15	102531392	33126648	0.3231	15.025
chr16	90354753	78316475	0.8668	29.1175
chr17	81195210	86903912	1.0703	42.3506
chr18	78077248	29508913	0.3779	16.8398
chr19	59128983	25532810	0.4318	14.8473
chr20	63025520	49097583	0.779	29.3551
chr21	48129895	6787788	0.141	7.0554
chr22	51304566	27703287	0.54	21.6216
chrMT	16571	2946	0.1778	0.5063
chrX	155270560	63508042	0.409	14.8764

chrY	59373566	4013561	0.0676	4.3631
------	----------	---------	--------	--------

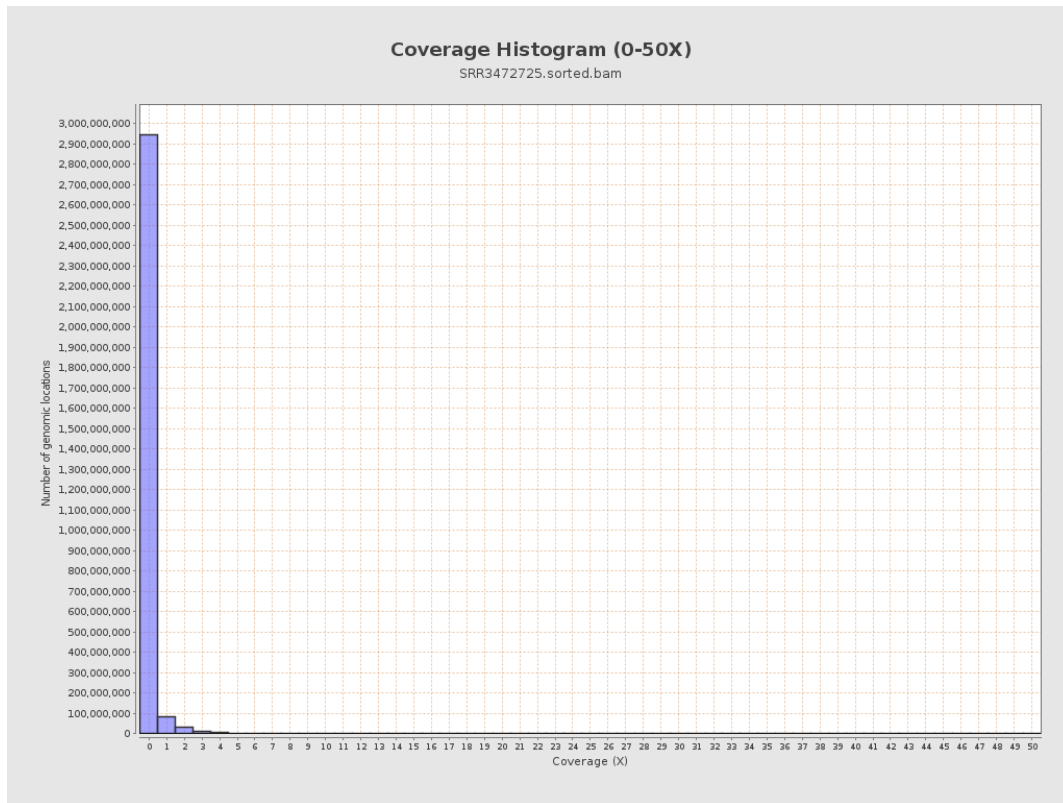
3. Results : Coverage across reference



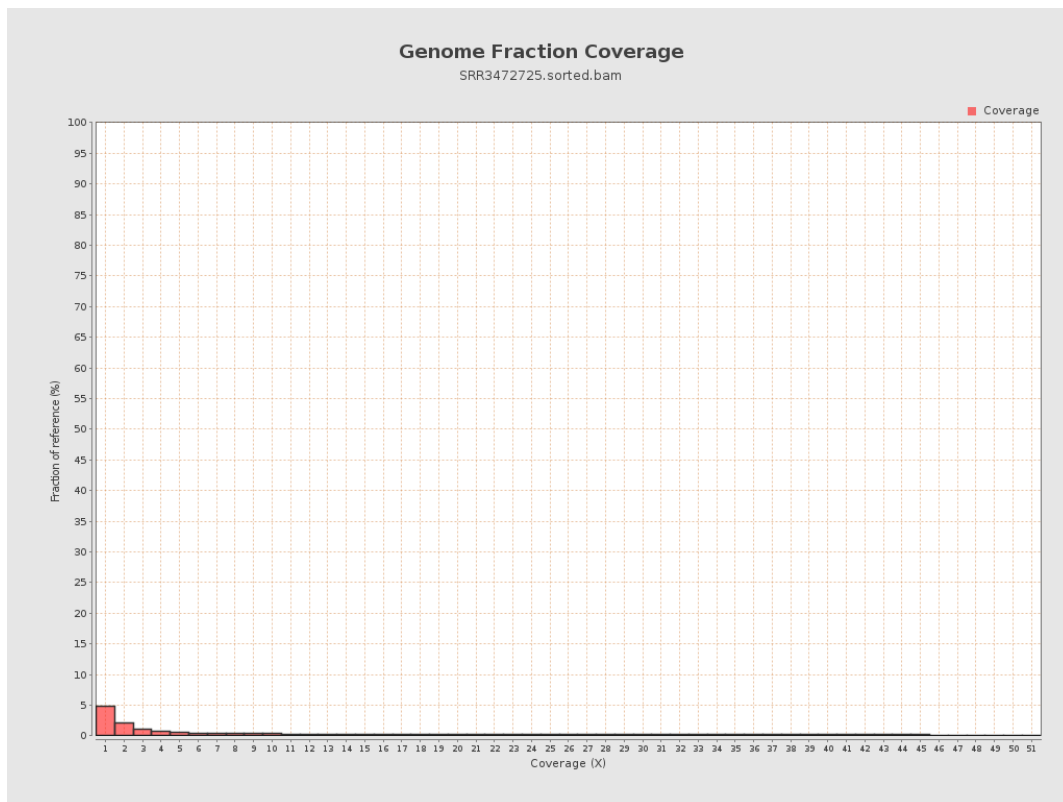
4. Results : Coverage Histogram



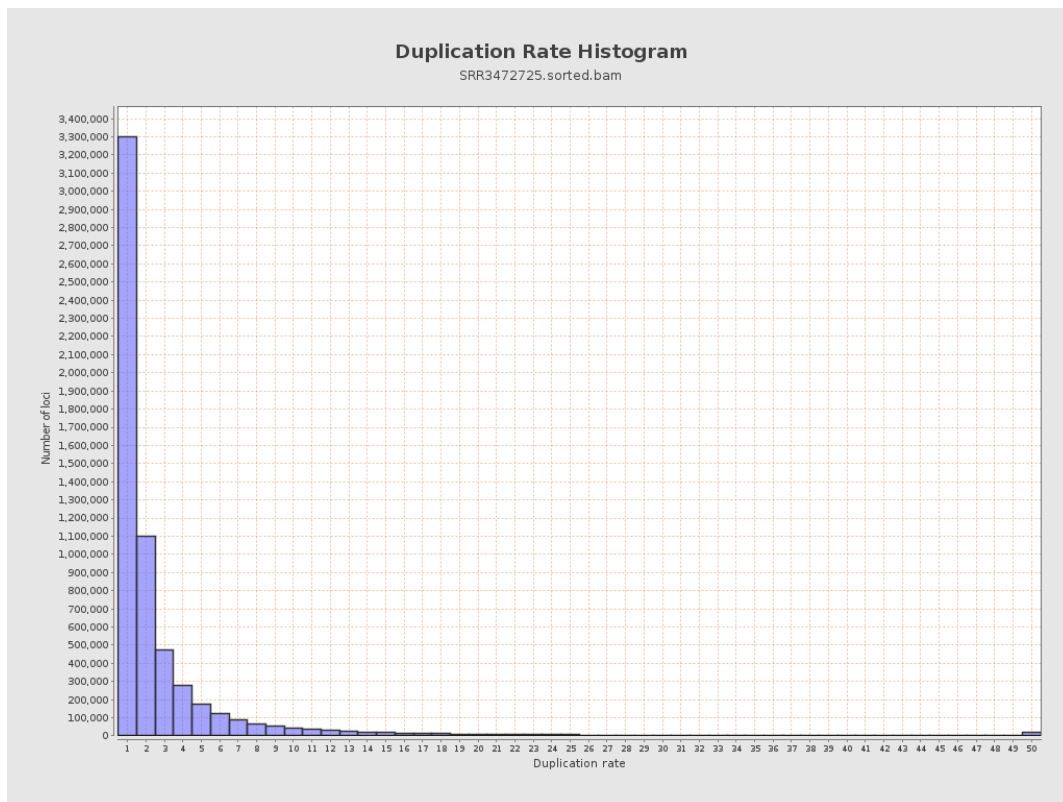
5. Results : Coverage Histogram (0-50X)



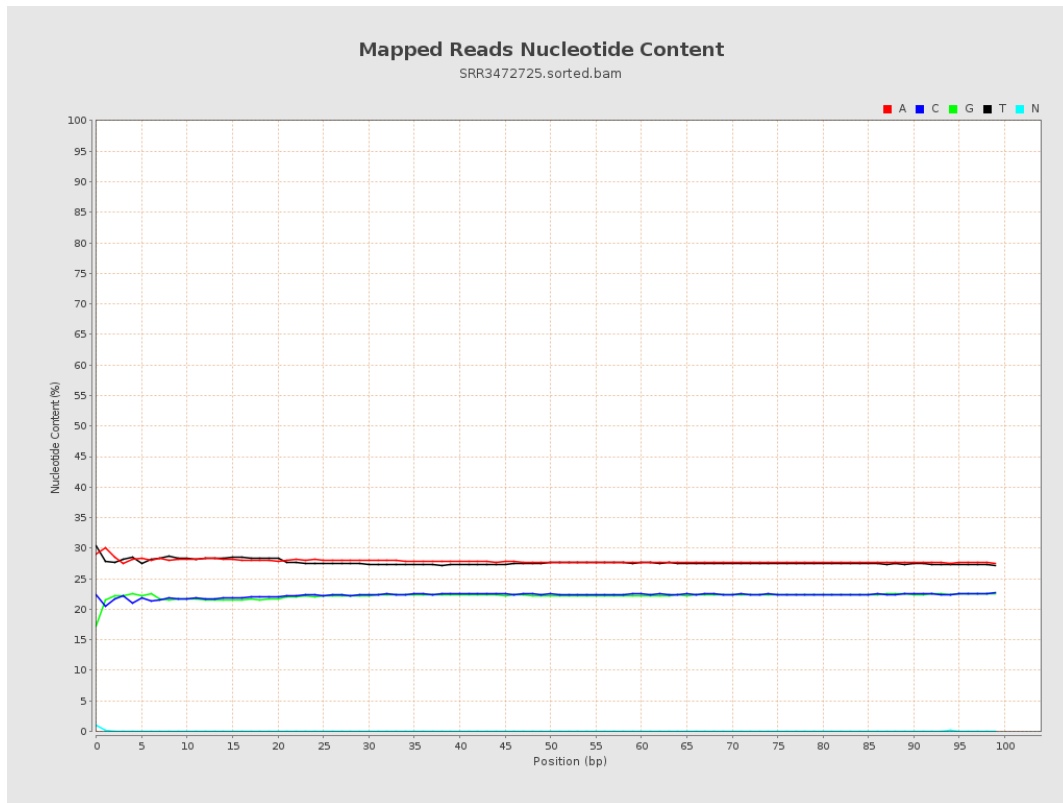
6. Results : Genome Fraction Coverage



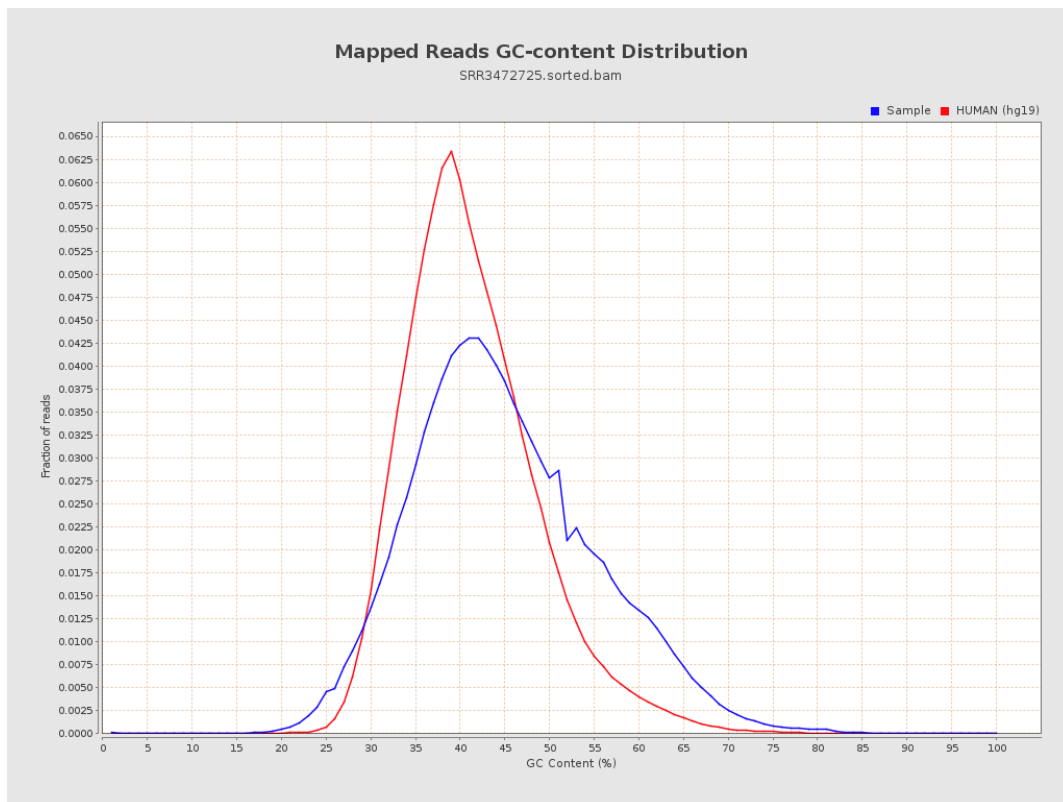
7. Results : Duplication Rate Histogram



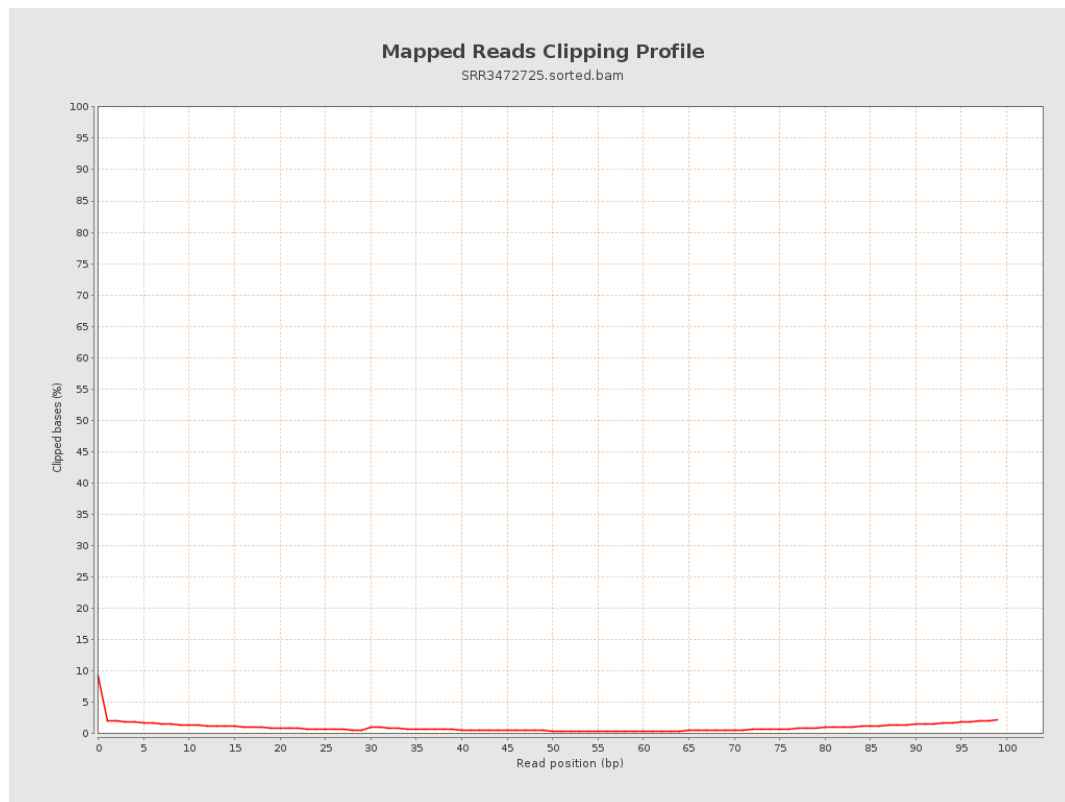
8. Results : Mapped Reads Nucleotide Content



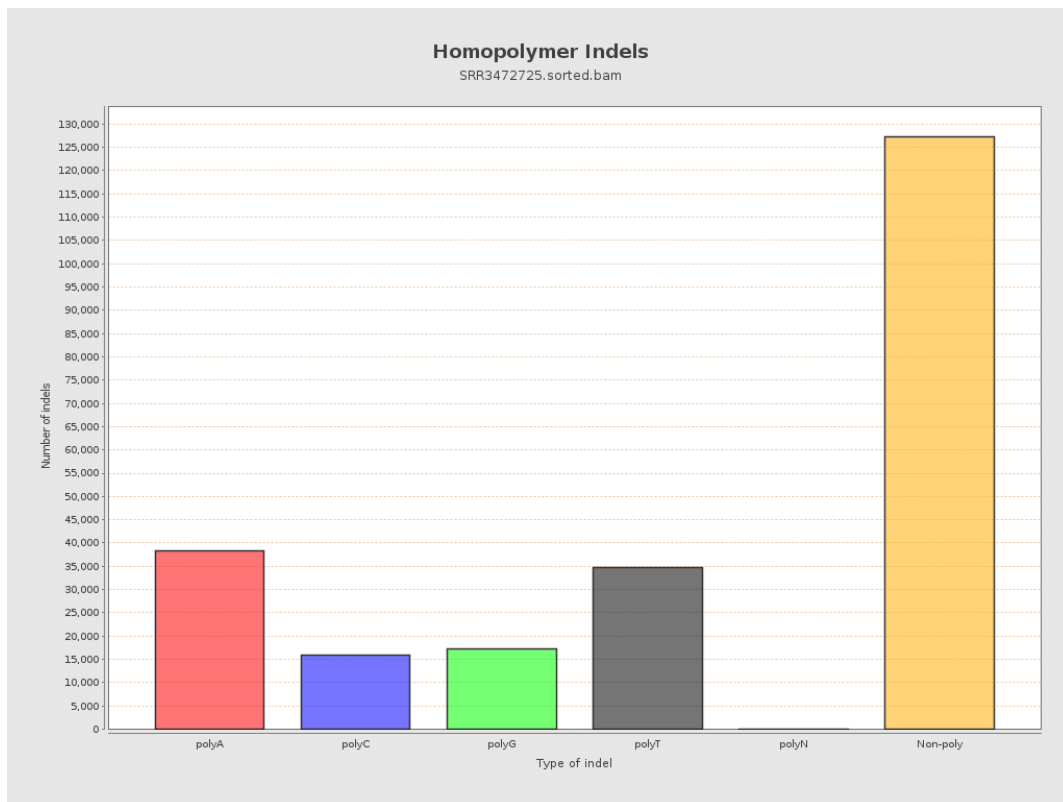
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



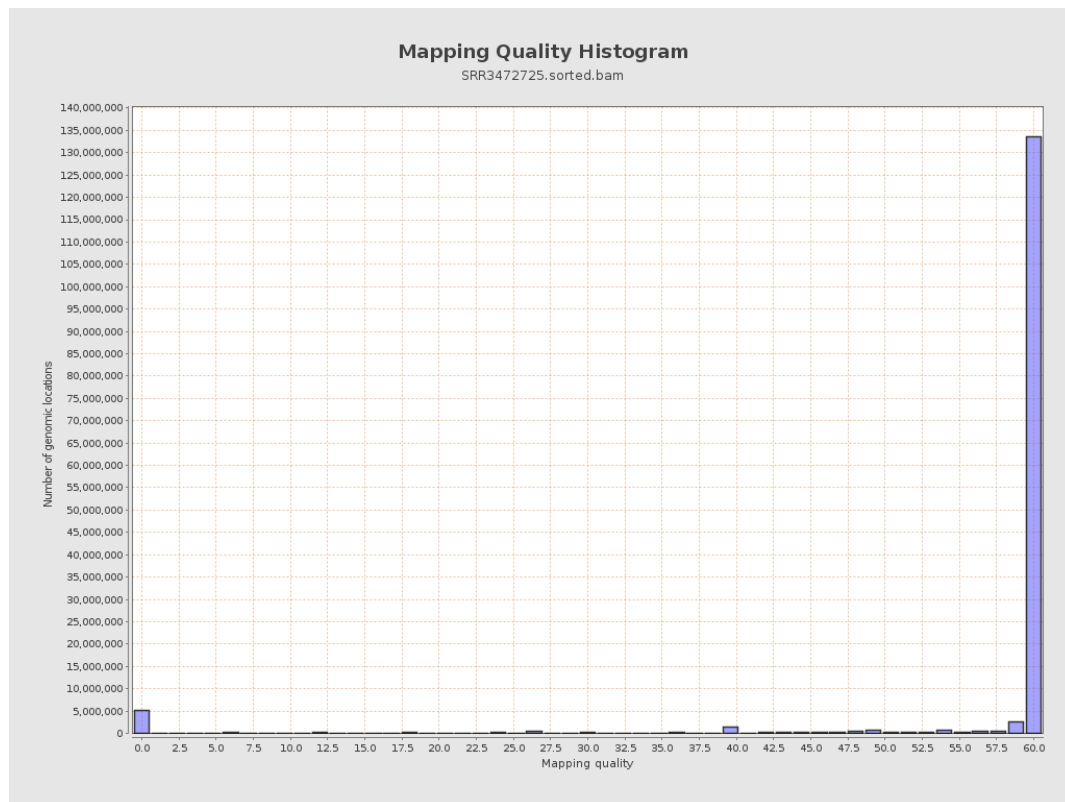
11. Results : Homopolymer Indels



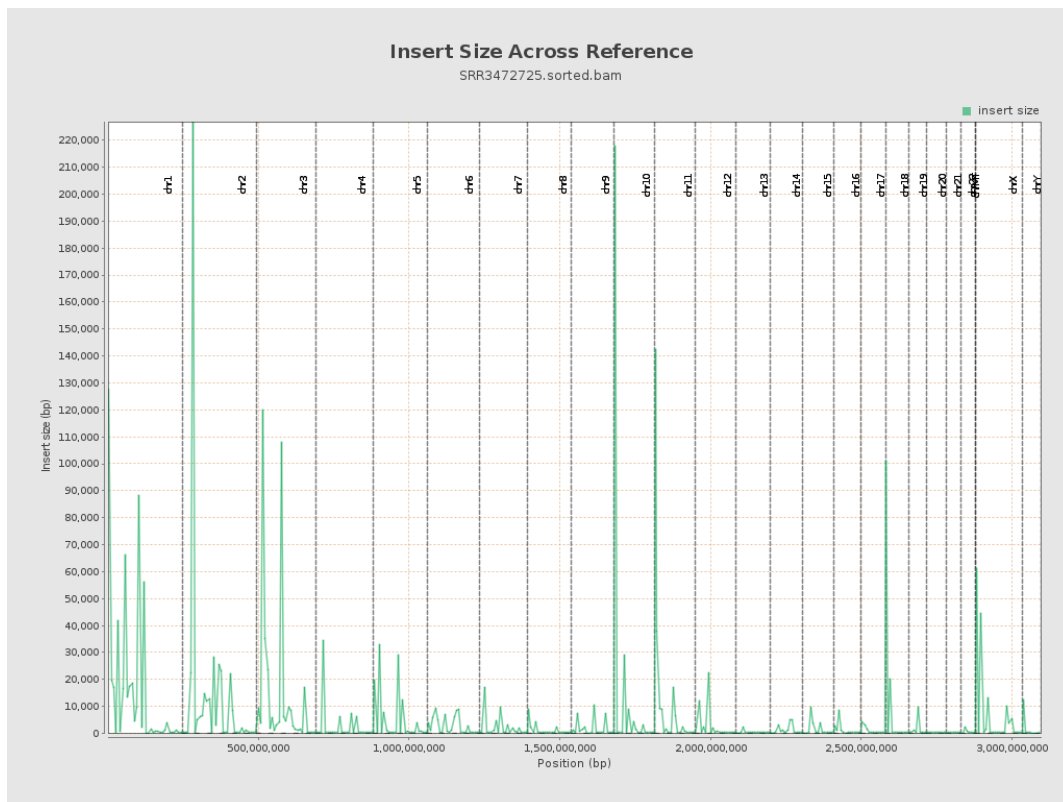
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

