

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 19:08:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432725.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_SRR6432725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432725_1.fastq.gz SRR6432725_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 19:08:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	425,498,240
Mapped reads	425,297,788 / 99.95%
Unmapped reads	200,452 / 0.05%
Mapped paired reads	425,297,788 / 99.95%
Mapped reads, first in pair	212,656,059 / 49.98%
Mapped reads, second in pair	212,641,729 / 49.97%
Mapped reads, both in pair	425,223,044 / 99.94%
Mapped reads, singletons	74,744 / 0.02%
Secondary alignments	0
Supplementary alignments	225,652 / 0.05%
Read min/max/mean length	30 / 150 / 140.3
Duplicated reads (estimated)	209,237,919 / 49.17%
Duplication rate	32.68%
Clipped reads	115,032,759 / 27.03%

2.2. ACGT Content

Number/percentage of A's	15,885,212,055 / 27.18%
Number/percentage of C's	12,763,714,758 / 21.84%
Number/percentage of T's	15,679,588,906 / 26.83%
Number/percentage of G's	14,118,145,307 / 24.16%
Number/percentage of N's	266,488 / 0%

GC Percentage	45.99%
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2.3. Coverage

Mean	18.8991
Standard Deviation	55.2867

2.4. Mapping Quality

Mean Mapping Quality	55.4
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2.5. Insert size

Mean	79,319.55
Standard Deviation	2,872,081.53
P25/Median/P75	285 / 303 / 319

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	599,807,031
Insertions	12,515,642
Mapped reads with at least one insertion	2.86%
Deletions	39,571,798
Mapped reads with at least one deletion	8.86%
Homopolymer indels	51.22%

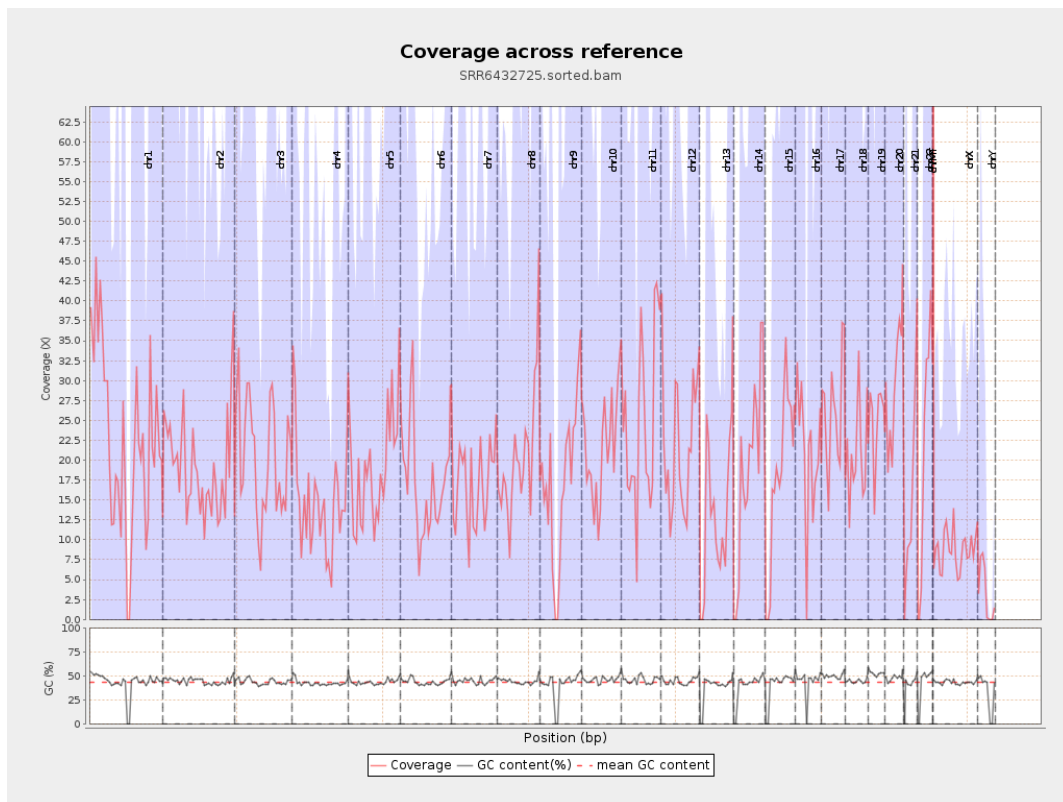
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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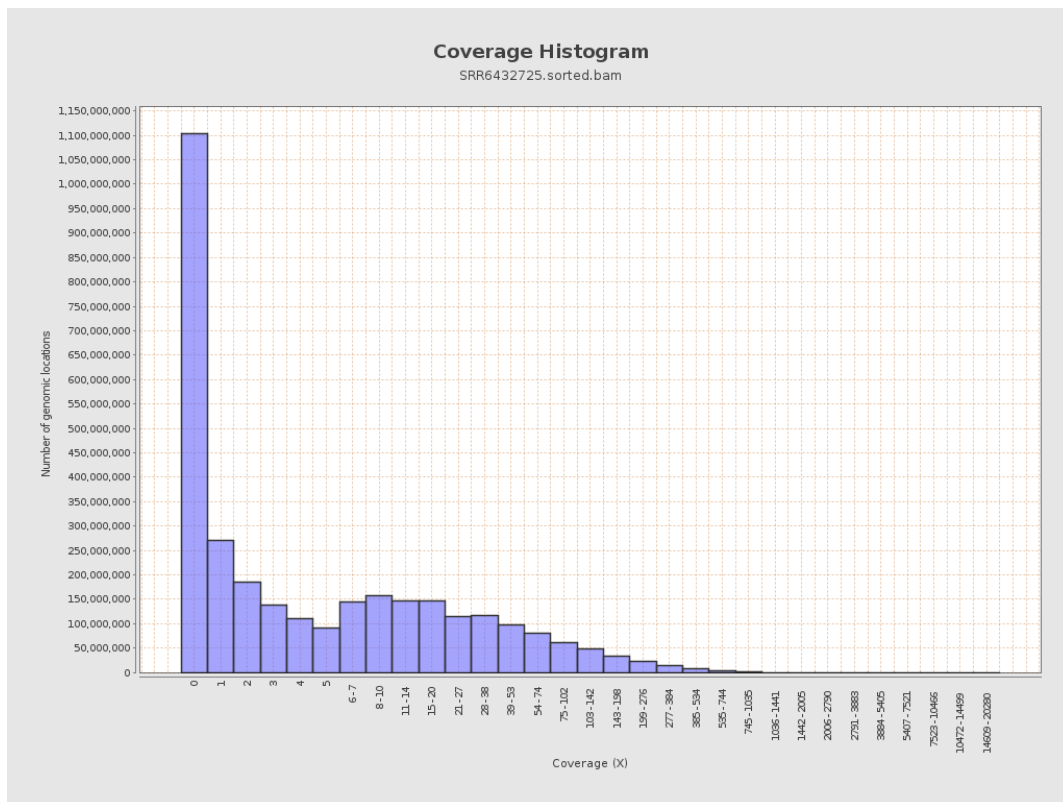
		bases	coverage	deviation
chr1	249250621	5594947078	22.4471	63.8699
chr2	243199373	4669310719	19.1995	59.3945
chr3	198022430	3975271841	20.0749	53.5979
chr4	191154276	2805251068	14.6753	44.8407
chr5	180915260	3476855390	19.2181	53.5489
chr6	171115067	2898542948	16.9391	47.0139
chr7	159138663	2727909300	17.1417	47.399
chr8	146364022	2994409201	20.4586	56.3029
chr9	141213431	2436369797	17.2531	55.9279
chr10	135534747	2891528558	21.3342	56.2138
chr11	135006516	3344253525	24.7711	65.4931
chr12	133851895	2952330359	22.0567	59.0479
chr13	115169878	1499942057	13.0237	42.3735
chr14	107349540	2064125201	19.2281	55.5912
chr15	102531392	1843002888	17.975	52.4038
chr16	90354753	1895744907	20.9811	65.1575
chr17	81195210	2102446147	25.8937	66.5584
chr18	78077248	1587500196	20.3324	57.5807
chr19	59128983	1456320705	24.6296	66.1996
chr20	63025520	1842291374	29.2309	71.2881
chr21	48129895	753240199	15.6502	57.7945
chr22	51304566	1120549955	21.8411	64.2607
chrMT	16571	6979337	421.1778	761.3183
chrX	155270560	1361174576	8.7665	26.3301

chrY	59373566	205495586	3.4611	26.6587
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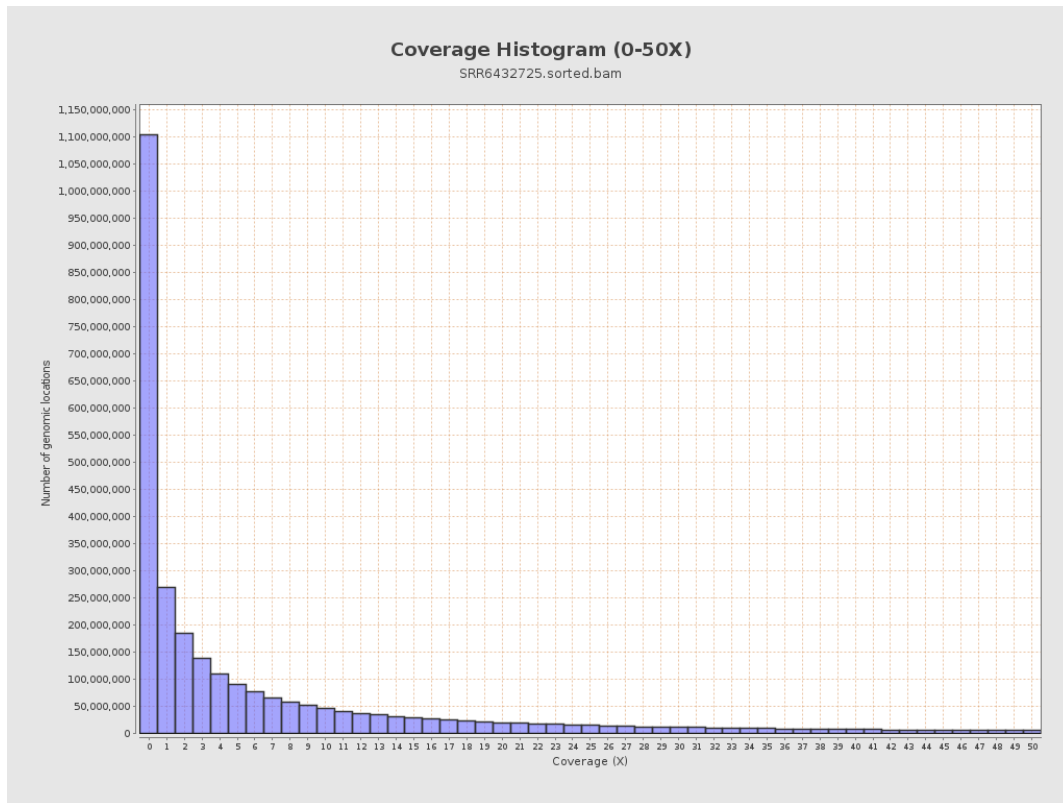
3. Results : Coverage across reference



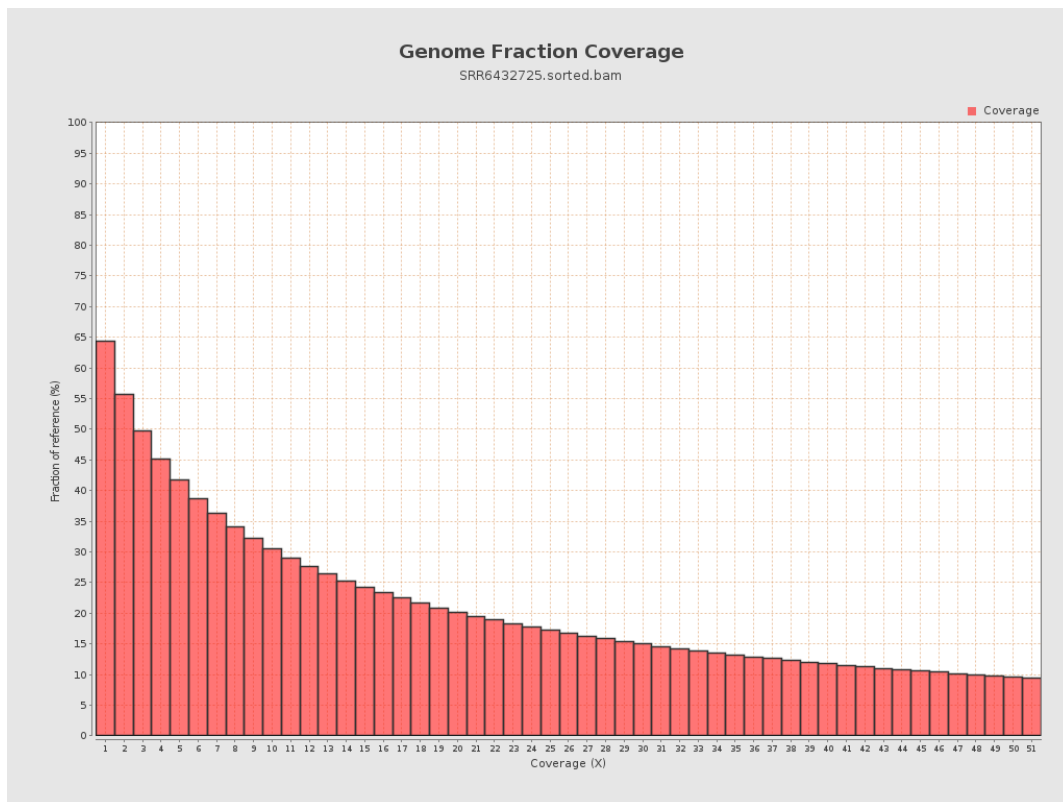
4. Results : Coverage Histogram



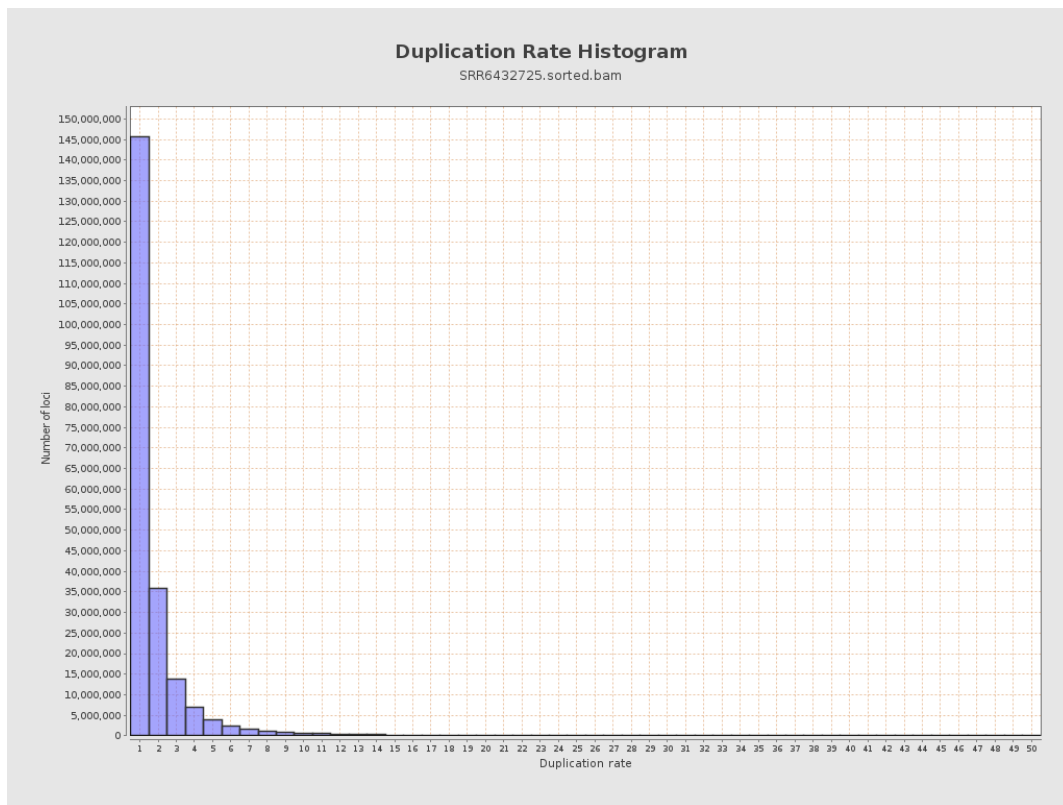
5. Results : Coverage Histogram (0-50X)



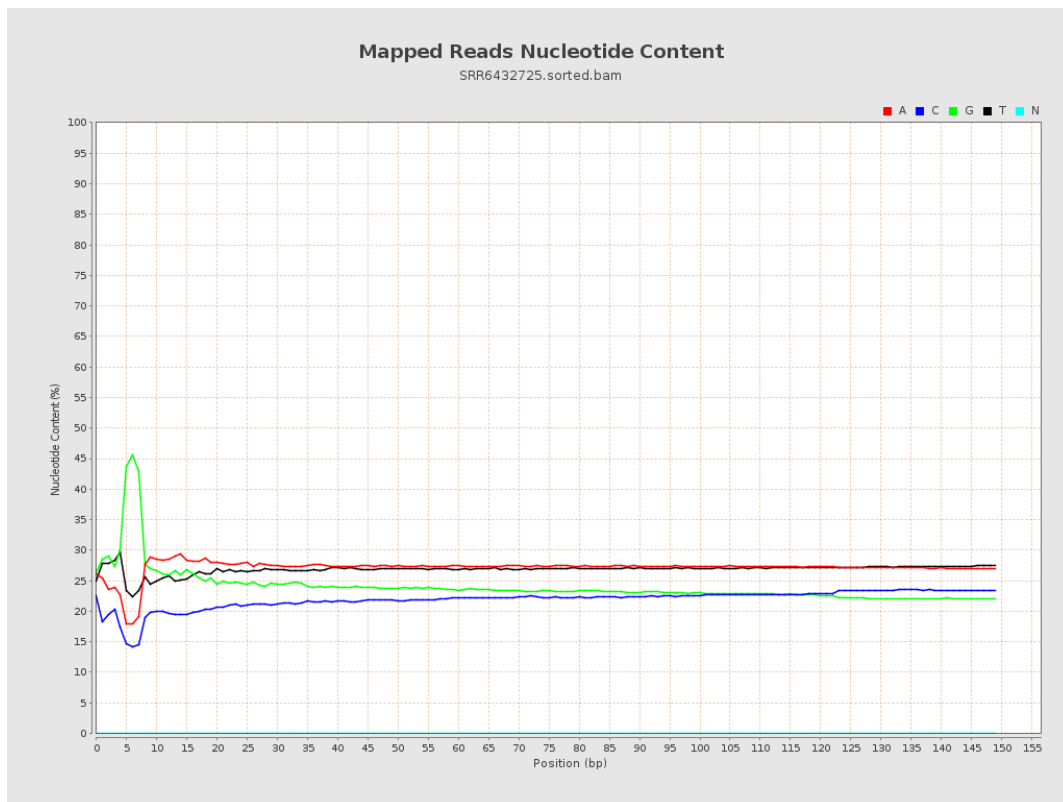
6. Results : Genome Fraction Coverage



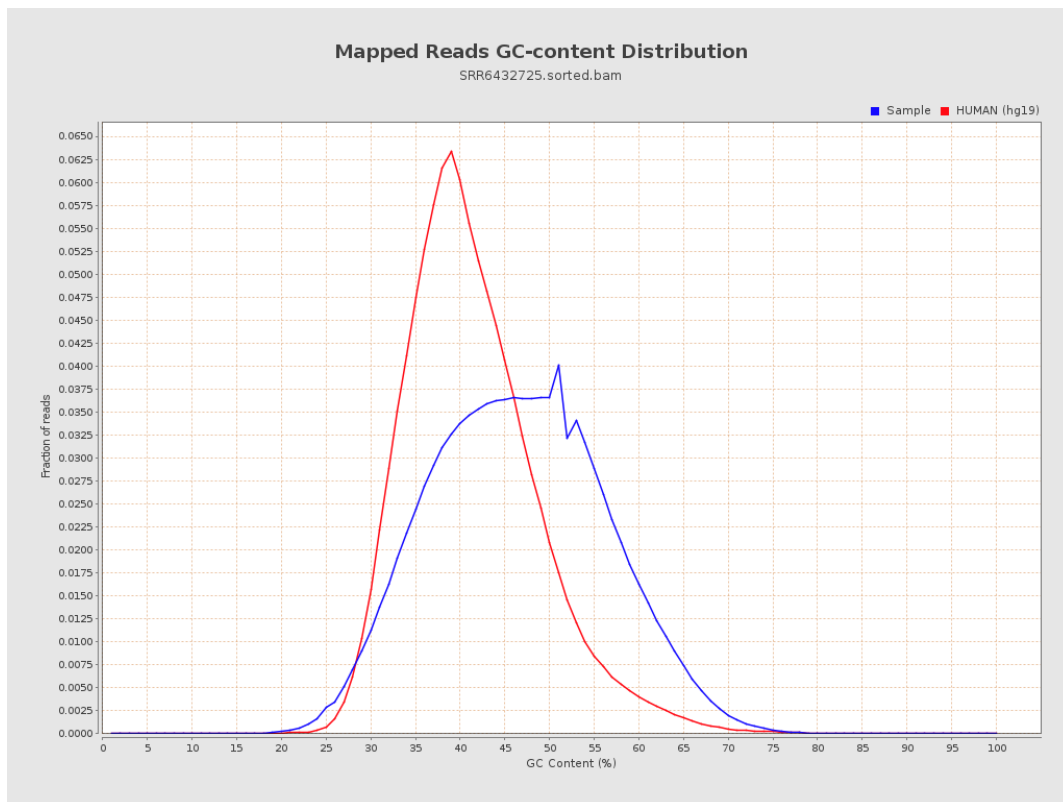
7. Results : Duplication Rate Histogram



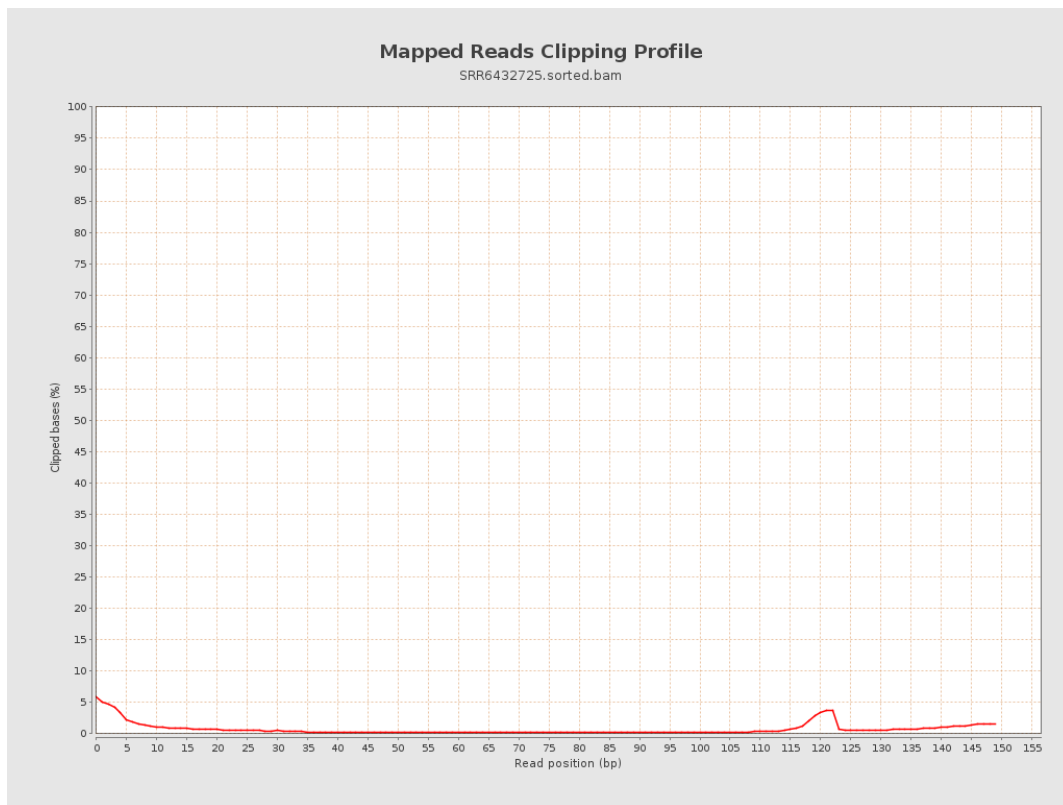
8. Results : Mapped Reads Nucleotide Content



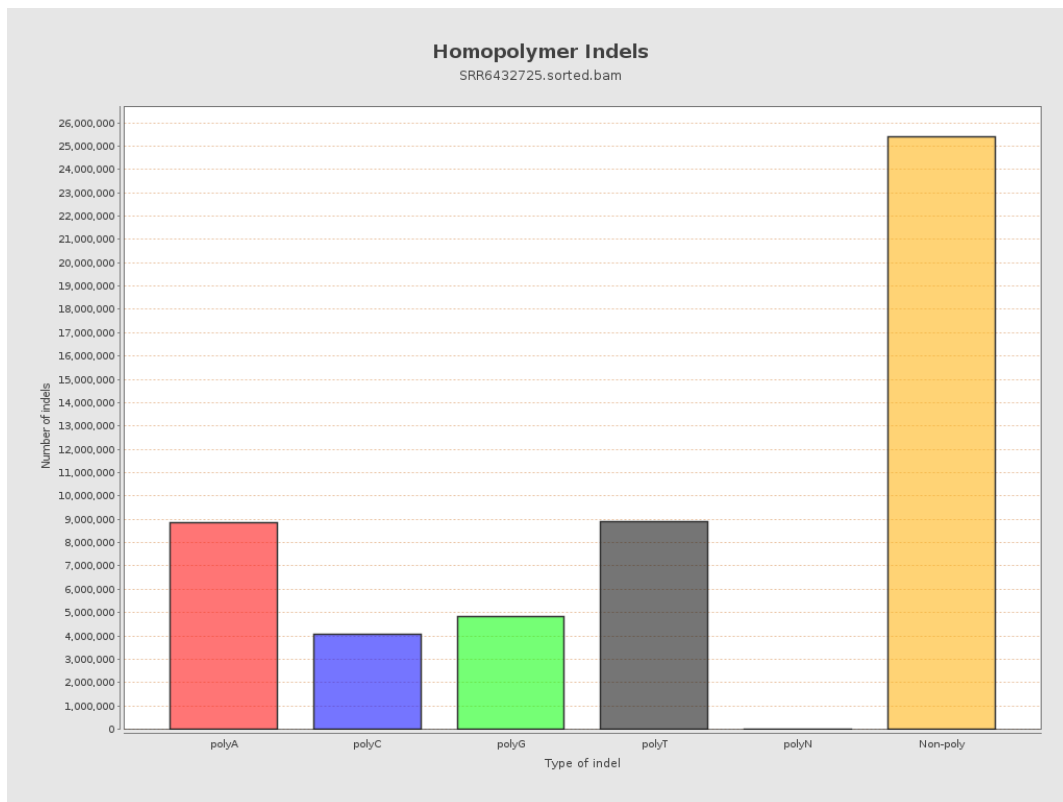
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



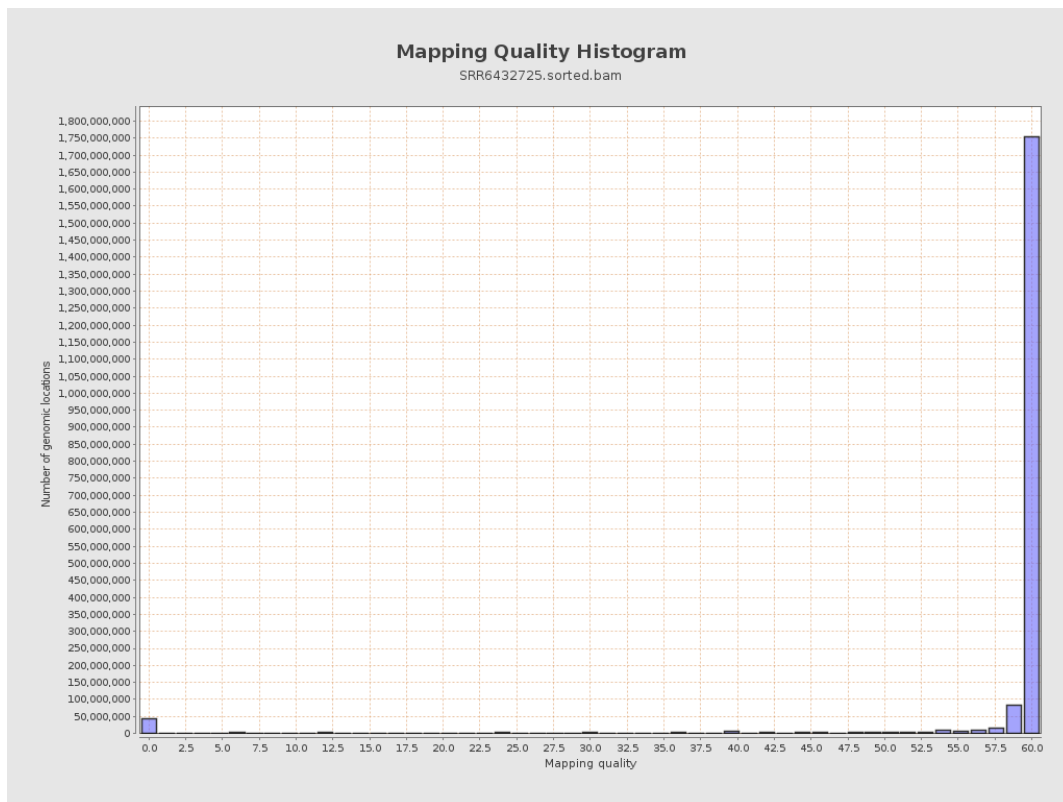
11. Results : Homopolymer Indels



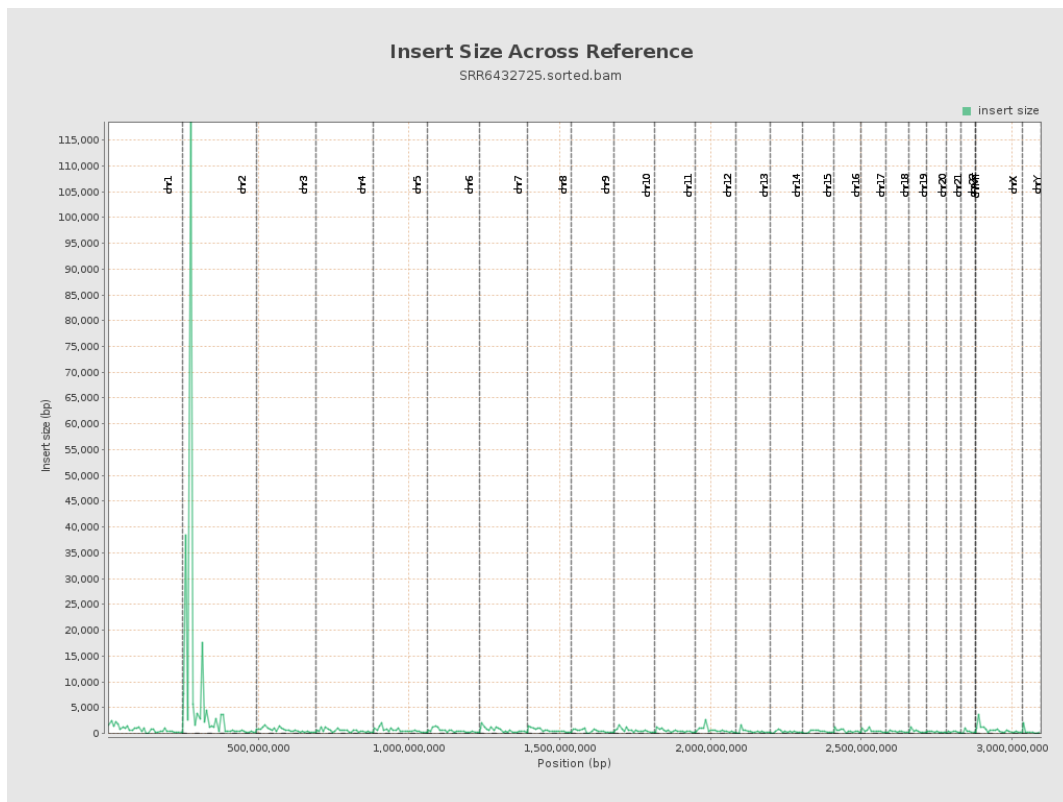
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

