

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/07 03:11:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362017.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_SRR16362017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362017_1.fastq.gz SRR16362017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Feb 07 03:11:53 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,565,782,248
Mapped reads	1,541,168,499 / 98.43%
Unmapped reads	24,613,749 / 1.57%
Mapped paired reads	1,541,168,499 / 98.43%
Mapped reads, first in pair	773,089,795 / 49.37%
Mapped reads, second in pair	768,078,704 / 49.05%
Mapped reads, both in pair	1,530,316,416 / 97.73%
Mapped reads, singletons	10,852,083 / 0.69%
Secondary alignments	0
Supplementary alignments	67,511,084 / 4.31%
Read min/max/mean length	30 / 150 / 152.16
Duplicated reads (estimated)	698,145,813 / 44.59%
Duplication rate	40.82%
Clipped reads	982,436,667 / 62.74%

2.2. ACGT Content

Number/percentage of A's	62,001,820,167 / 28.79%
Number/percentage of C's	45,257,288,082 / 21.01%
Number/percentage of T's	61,403,282,921 / 28.51%
Number/percentage of G's	46,702,787,600 / 21.68%
Number/percentage of N's	4,031,065 / 0%

GC Percentage	42.7%
---------------	-------

2.3. Coverage

Mean	69.6285
Standard Deviation	945.7837

2.4. Mapping Quality

Mean Mapping Quality	53.83
----------------------	-------

2.5. Insert size

Mean	170,702.89
Standard Deviation	4,047,151.62
P25/Median/P75	204 / 279 / 407

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	1,670,588,867
Insertions	37,841,345
Mapped reads with at least one insertion	2.34%
Deletions	98,859,424
Mapped reads with at least one deletion	6.16%
Homopolymer indels	44.99%

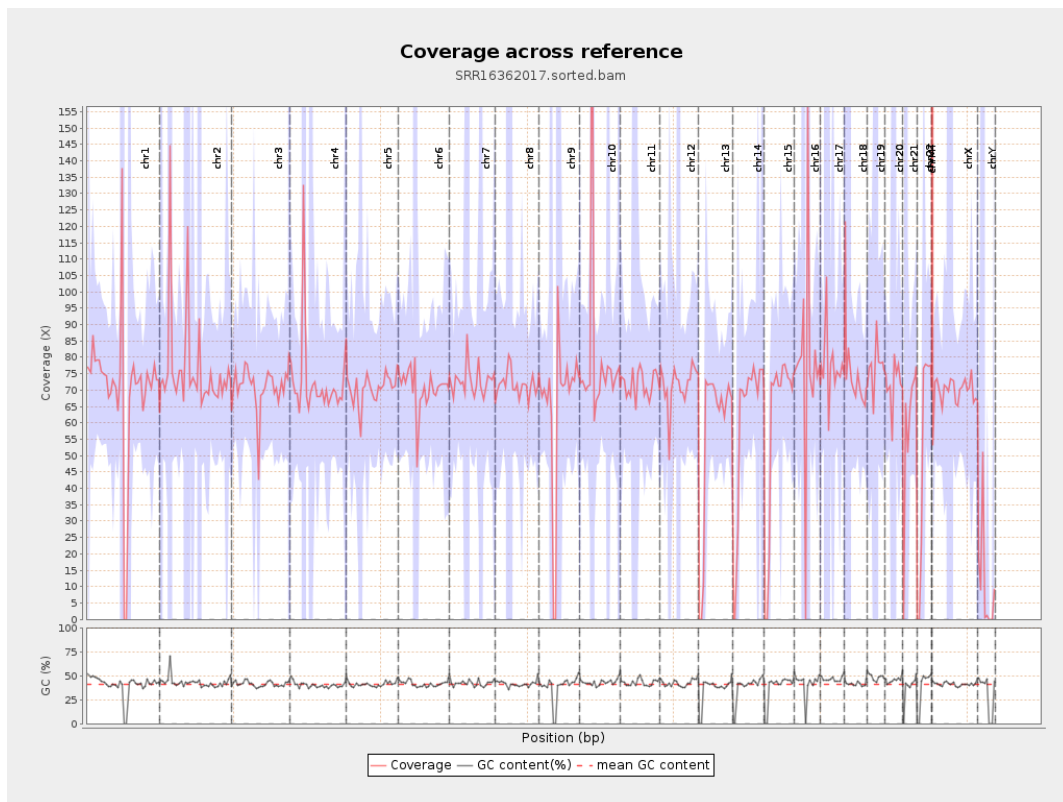
2.7. Chromosome stats

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

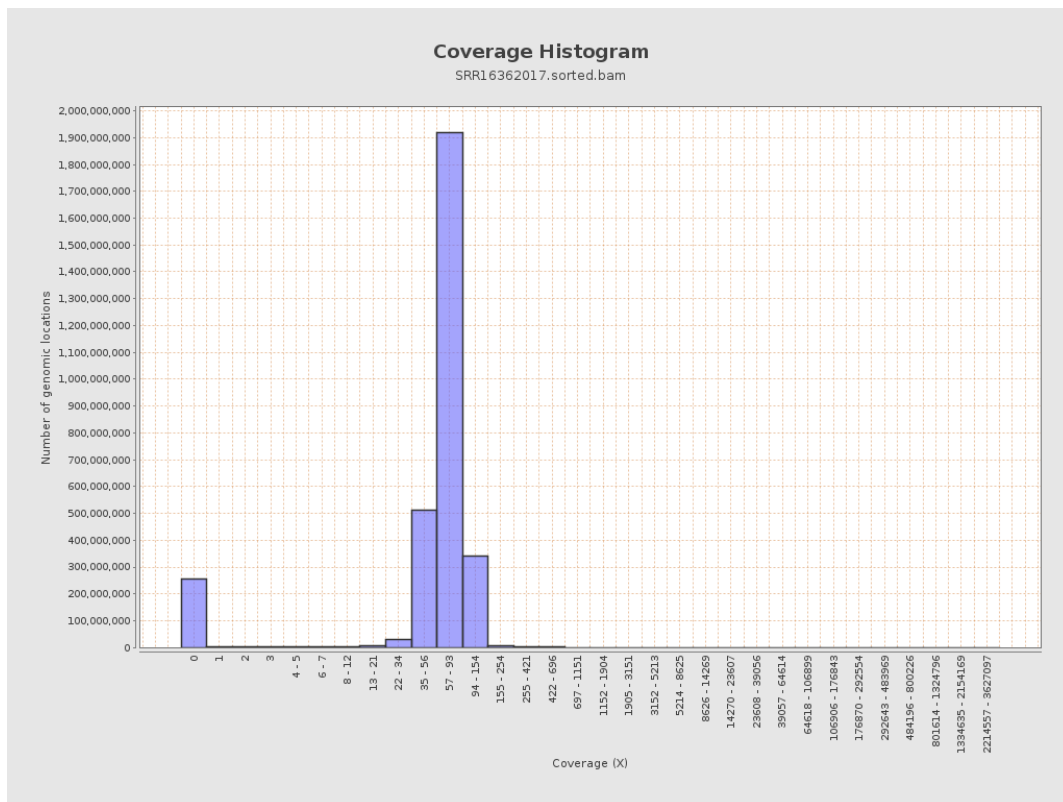
		bases	coverage	deviation
chr1	249250621	17675768841	70.9156	1,482.6555
chr2	243199373	18629354995	76.6012	2,517.5487
chr3	198022430	14022462001	70.8125	54.7419
chr4	191154276	13754497462	71.955	603.9985
chr5	180915260	12764445983	70.5548	46.5789
chr6	171115067	12076545514	70.5756	153.1659
chr7	159138663	11604981858	72.9237	456.638
chr8	146364022	10502816180	71.7582	793.8217
chr9	141213431	9244005300	65.4612	764.759
chr10	135534747	10824962554	79.8685	1,130.0028
chr11	135006516	9711378213	71.9327	300.3888
chr12	133851895	9565860889	71.466	99.0566
chr13	115169878	6610339106	57.3964	36.4726
chr14	107349540	6442024629	60.0098	65.3835
chr15	102531392	6046593432	58.9731	41.485
chr16	90354753	7107080039	78.6575	615.9389
chr17	81195210	6255874077	77.0473	374.4783
chr18	78077248	5769132948	73.8901	744.9868
chr19	59128983	4576062438	77.3912	887.0735
chr20	63025520	4525754075	71.8083	178.4246
chr21	48129895	2902822975	60.3123	276.1647
chr22	51304566	2715716446	52.9332	58.1178
chrMT	16571	782016983	47,191.9005	6,650.0269
chrX	155270560	10789382388	69.4876	147.5477

chrY	59373566	648774212	10.927	676.0338
------	----------	-----------	--------	----------

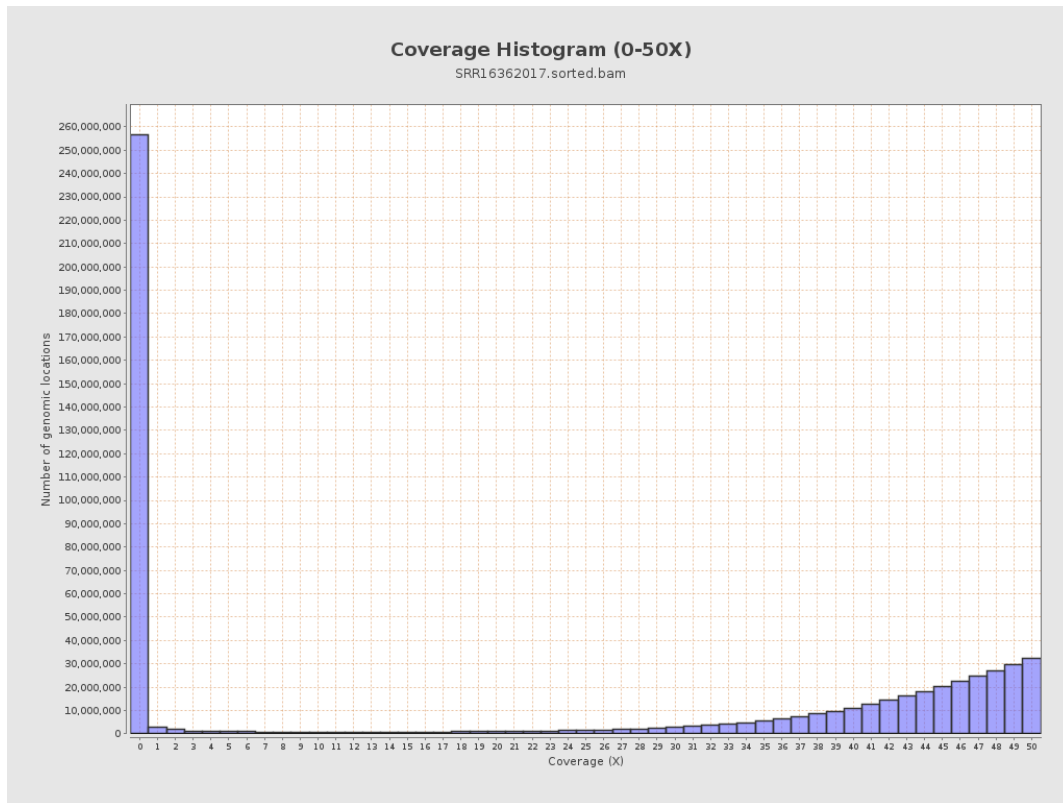
3. Results : Coverage across reference



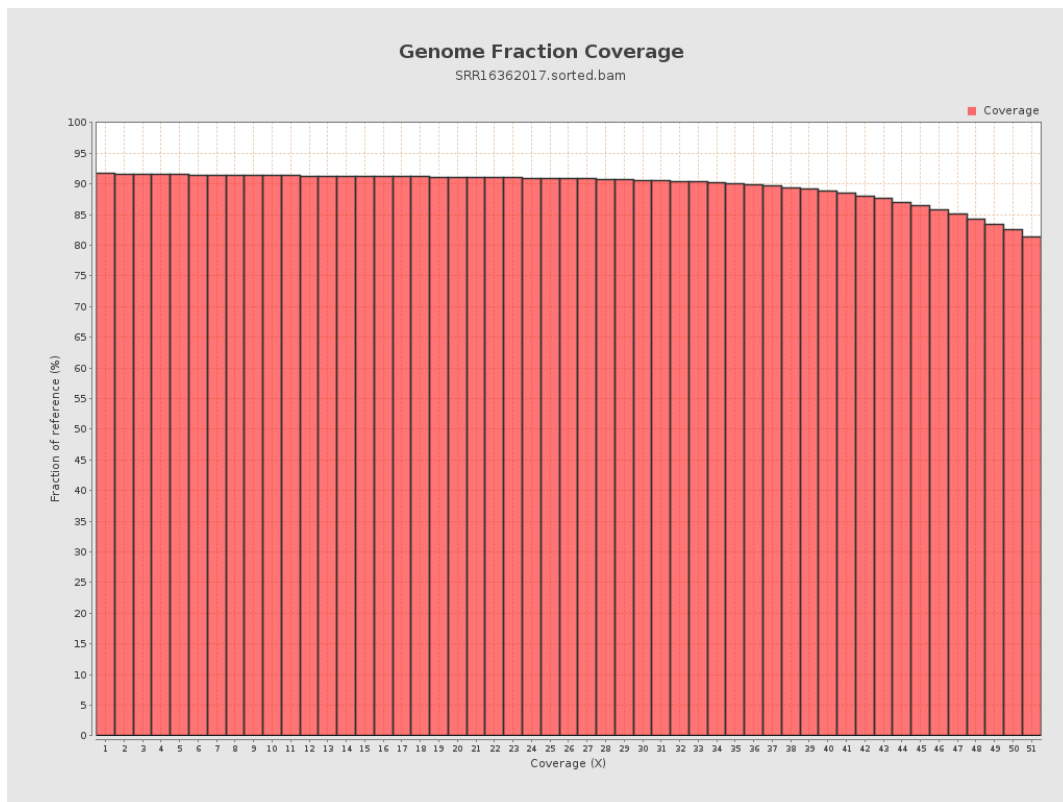
4. Results : Coverage Histogram



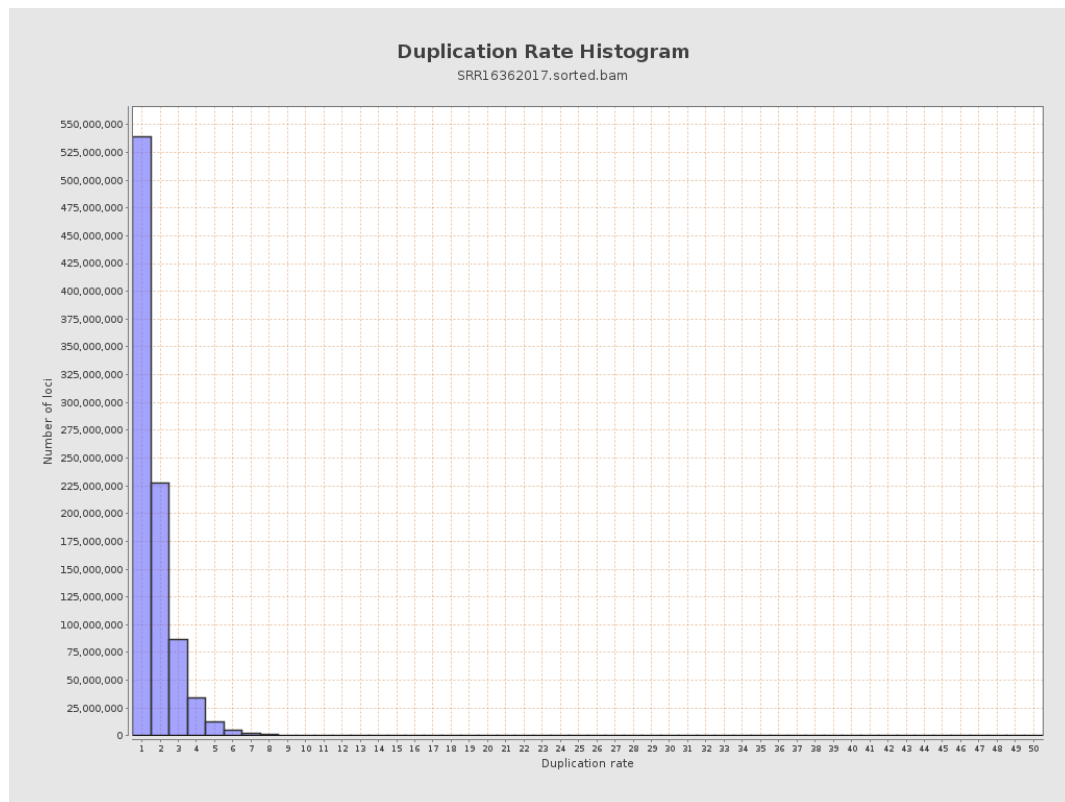
5. Results : Coverage Histogram (0-50X)



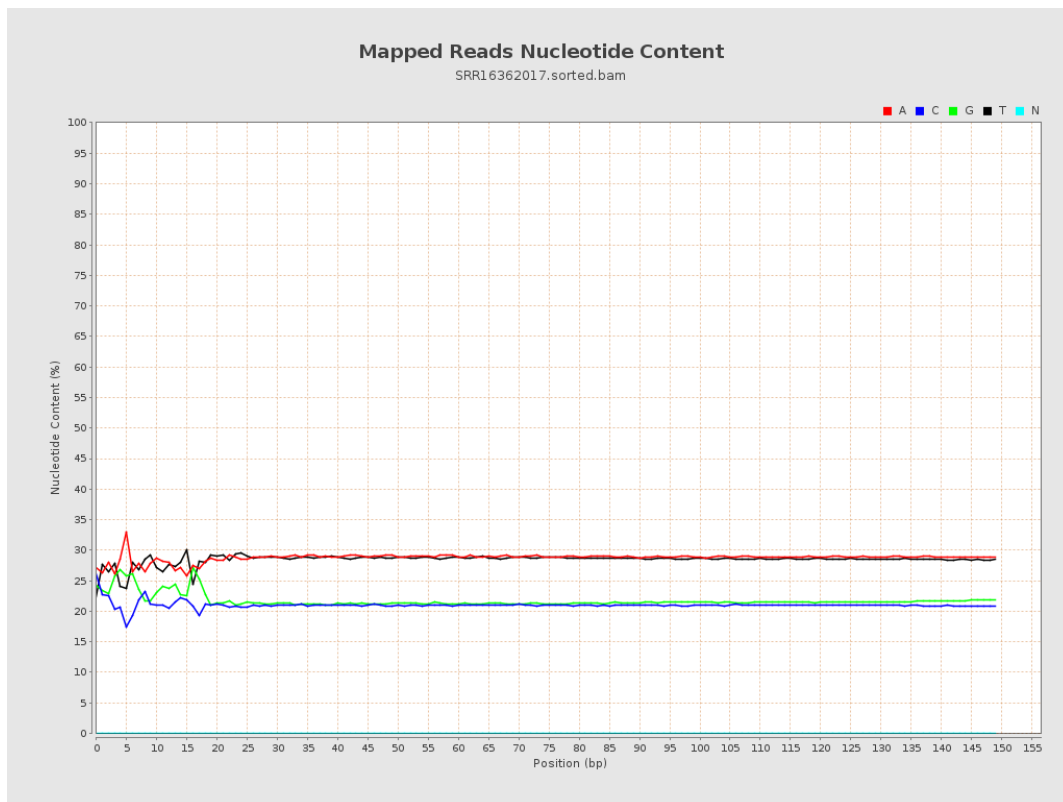
6. Results : Genome Fraction Coverage



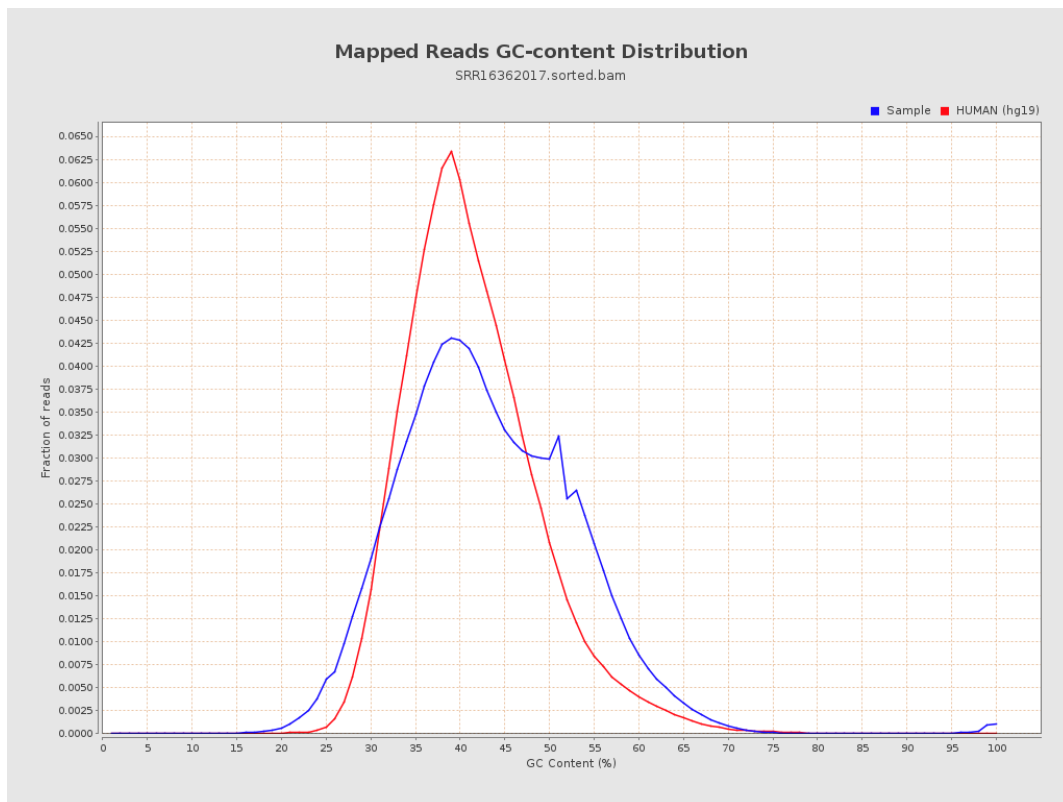
7. Results : Duplication Rate Histogram



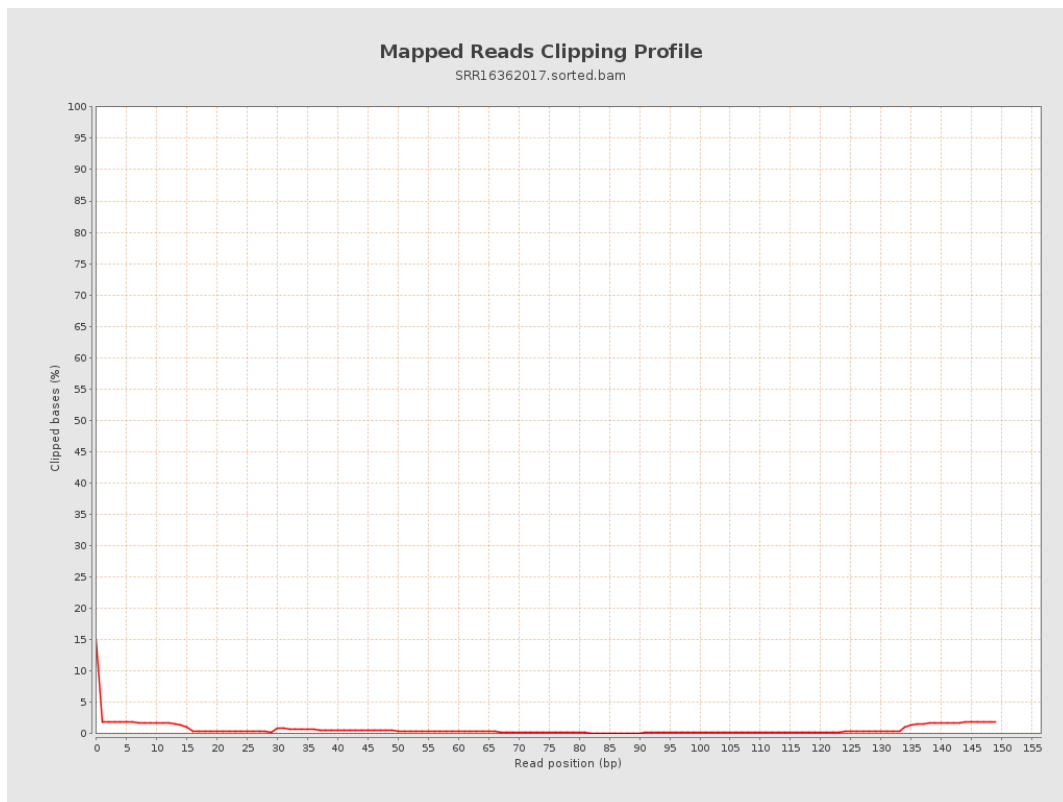
8. Results : Mapped Reads Nucleotide Content



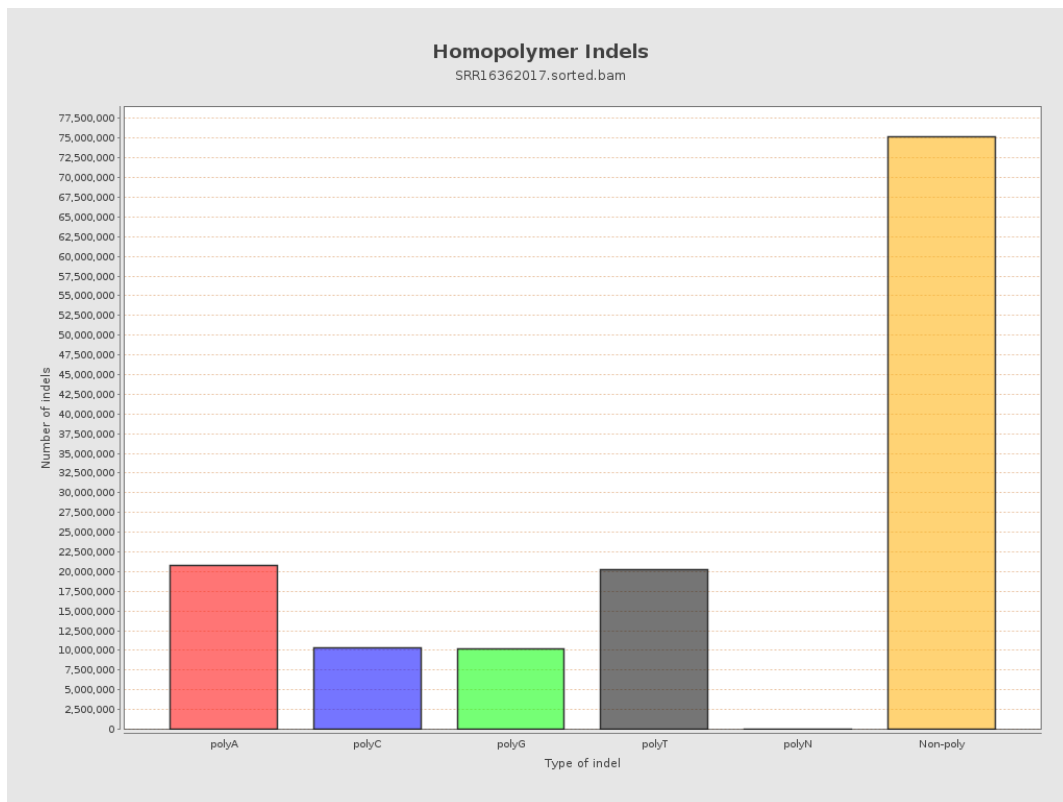
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



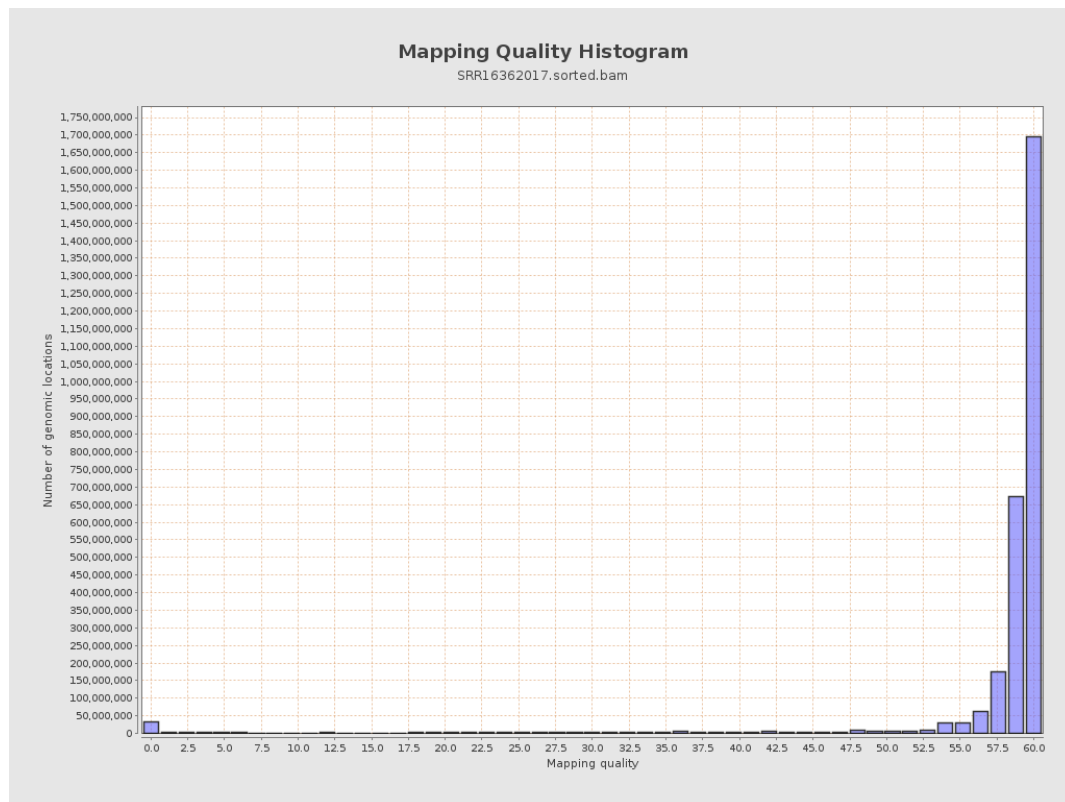
11. Results : Homopolymer Indels



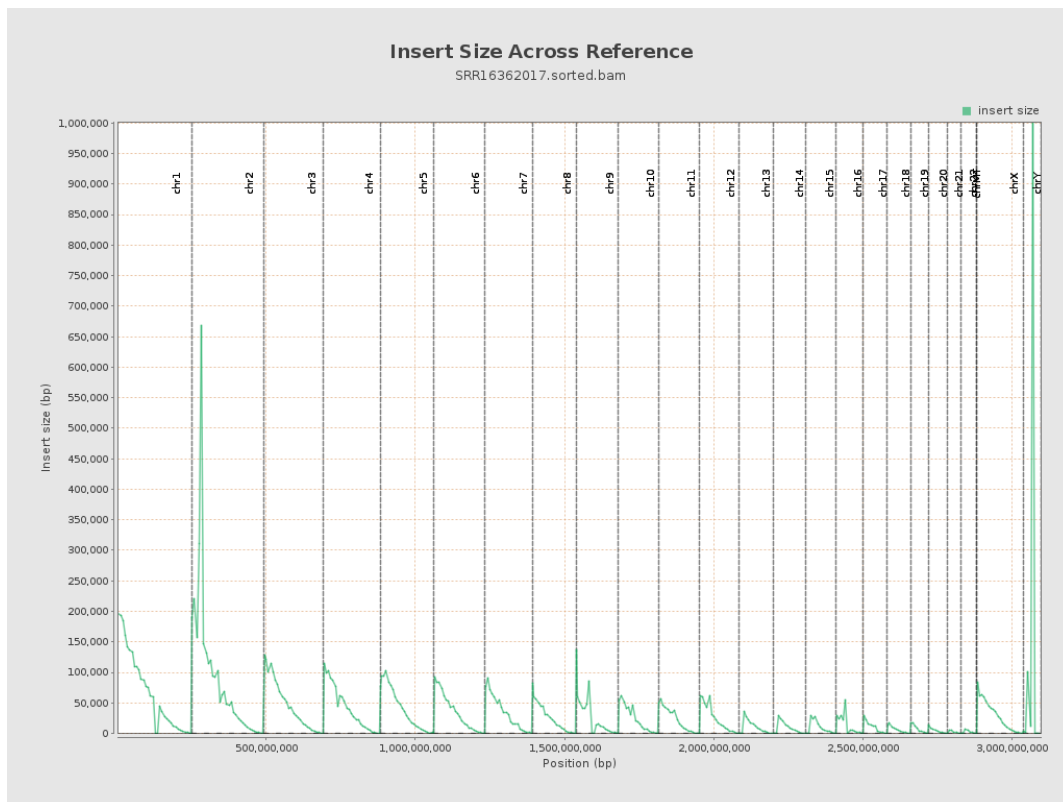
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

