

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 12:33:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472618.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_SRR3472618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472618_1.fastq.gz SRR3472618_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 12:33:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,438,916
Mapped reads	21,256,551 / 99.15%
Unmapped reads	182,365 / 0.85%
Mapped paired reads	21,256,551 / 99.15%
Mapped reads, first in pair	10,667,367 / 49.76%
Mapped reads, second in pair	10,589,184 / 49.39%
Mapped reads, both in pair	21,129,708 / 98.56%
Mapped reads, singletons	126,843 / 0.59%
Secondary alignments	0
Supplementary alignments	102,680 / 0.48%
Read min/max/mean length	30 / 101 / 99.73
Duplicated reads (estimated)	15,218,006 / 70.98%
Duplication rate	51.29%
Clipped reads	1,475,575 / 6.88%

2.2. ACGT Content

Number/percentage of A's	556,525,615 / 26.61%
Number/percentage of C's	492,150,627 / 23.53%
Number/percentage of T's	557,849,407 / 26.68%
Number/percentage of G's	484,340,927 / 23.16%
Number/percentage of N's	383,280 / 0.02%

GC Percentage	46.69%
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2.3. Coverage

Mean	0.6756
Standard Deviation	27.807

2.4. Mapping Quality

Mean Mapping Quality	54.79
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2.5. Insert size

Mean	21,763.23
Standard Deviation	1,495,173.91
P25/Median/P75	159 / 218 / 292

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	12,856,429
Insertions	119,053
Mapped reads with at least one insertion	0.56%
Deletions	117,178
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.3%

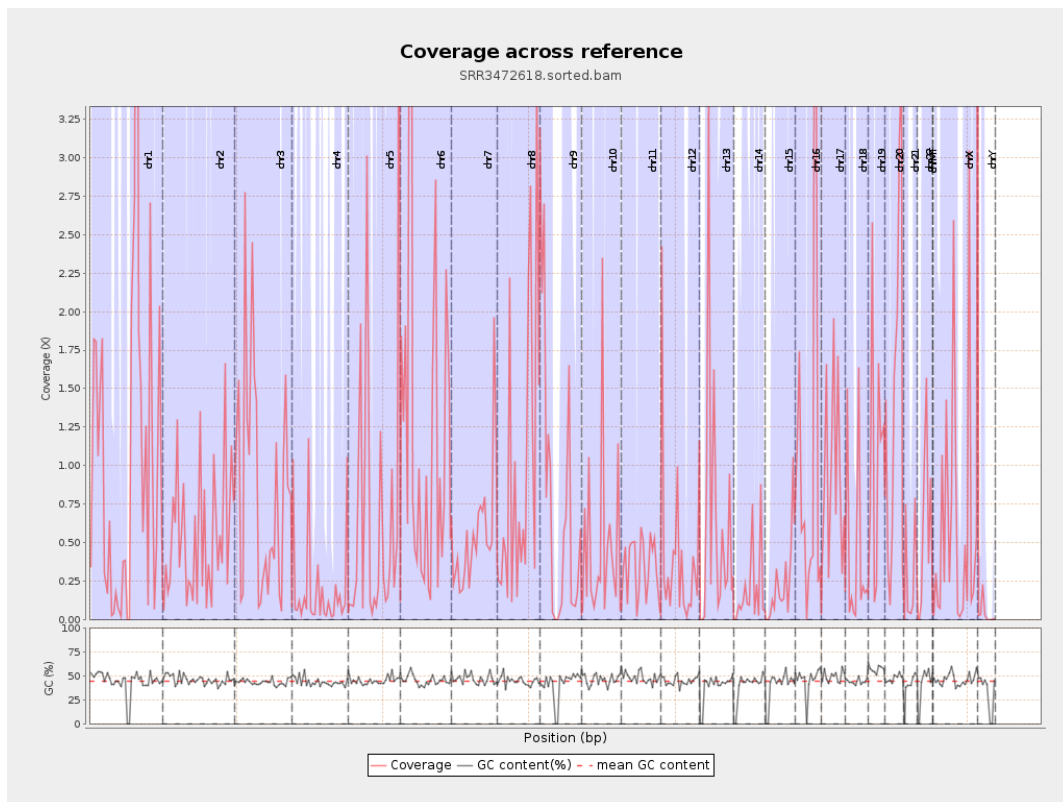
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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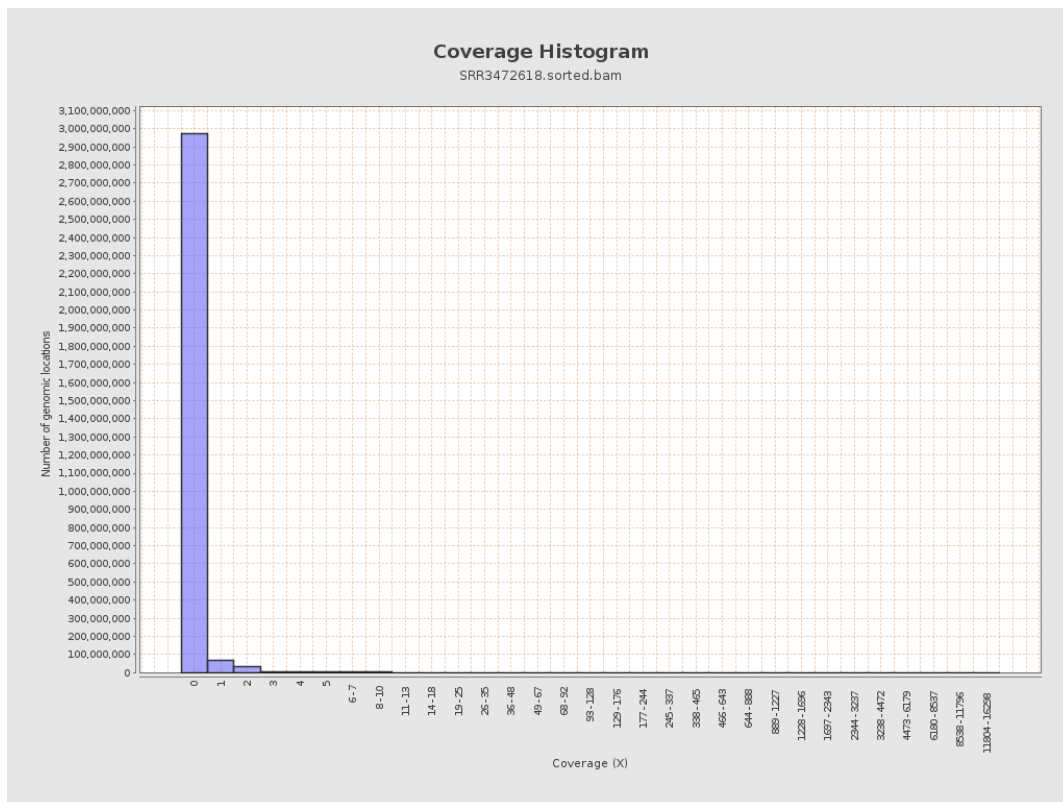
		bases	coverage	deviation
chr1	249250621	269463157	1.0811	35.2192
chr2	243199373	130590989	0.537	19.6516
chr3	198022430	168644229	0.8516	30.1622
chr4	191154276	38746598	0.2027	9.7422
chr5	180915260	135350801	0.7481	45.171
chr6	171115067	213911754	1.2501	42.2586
chr7	159138663	89969353	0.5654	21.7059
chr8	146364022	143938543	0.9834	37.9063
chr9	141213431	95466221	0.676	18.0662
chr10	135534747	65663274	0.4845	24.7542
chr11	135006516	46427205	0.3439	12.819
chr12	133851895	54116922	0.4043	13.6079
chr13	115169878	72681052	0.6311	21.9192
chr14	107349540	20819787	0.1939	7.9866
chr15	102531392	24115091	0.2352	11.6757
chr16	90354753	94342590	1.0441	36.2922
chr17	81195210	78859526	0.9712	23.8473
chr18	78077248	31933355	0.409	24.8284
chr19	59128983	61617536	1.0421	26.2875
chr20	63025520	96386409	1.5293	52.2814
chr21	48129895	14468845	0.3006	17.5387
chr22	51304566	31148998	0.6071	19.5797
chrMT	16571	4000	0.2414	0.5832
chrX	155270560	110450475	0.7113	27.5515

chrY	59373566	2423557	0.0408	3.8778
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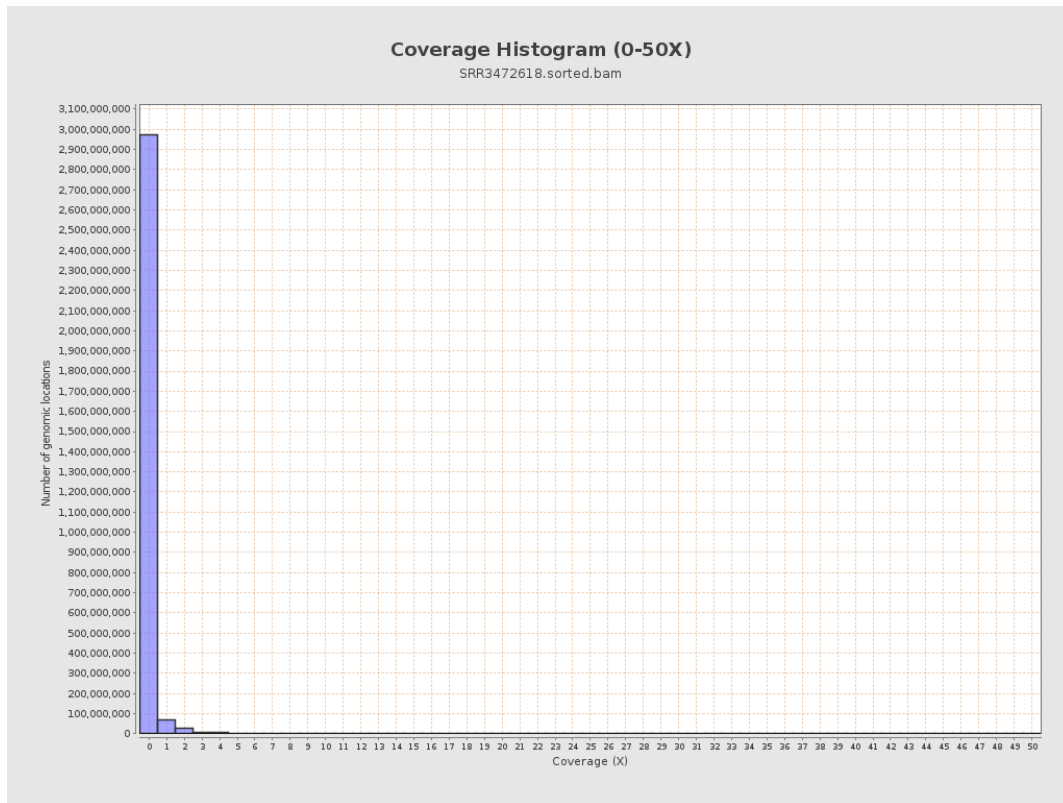
3. Results : Coverage across reference



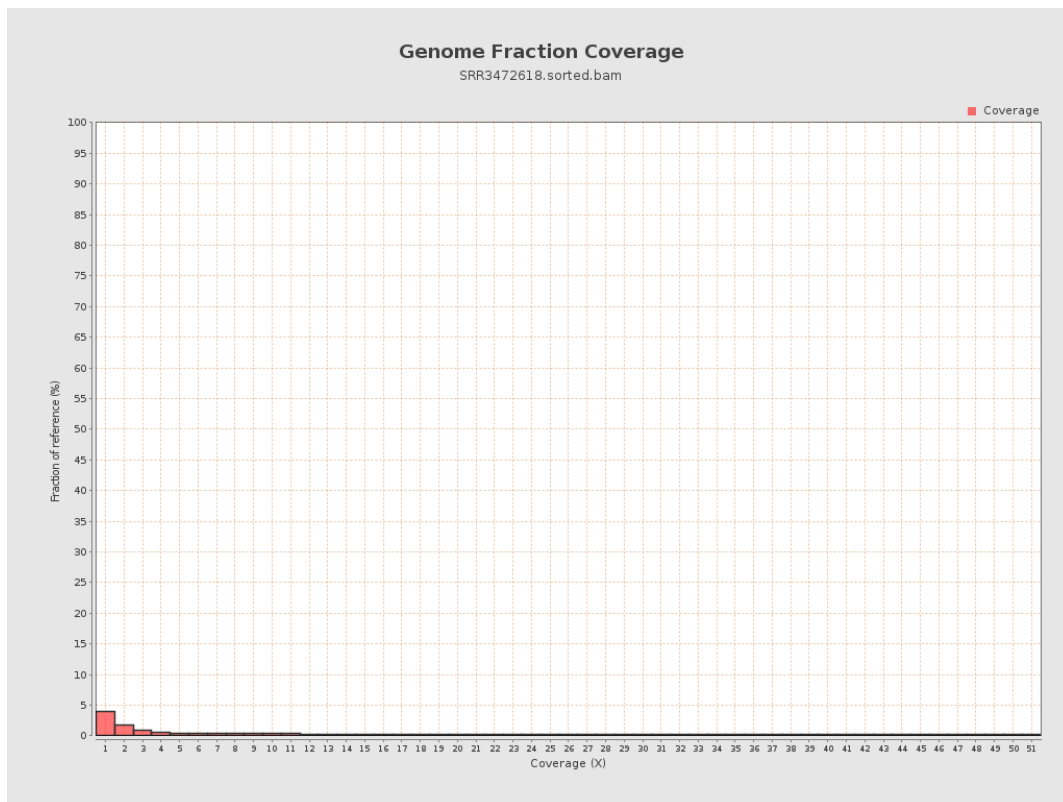
4. Results : Coverage Histogram



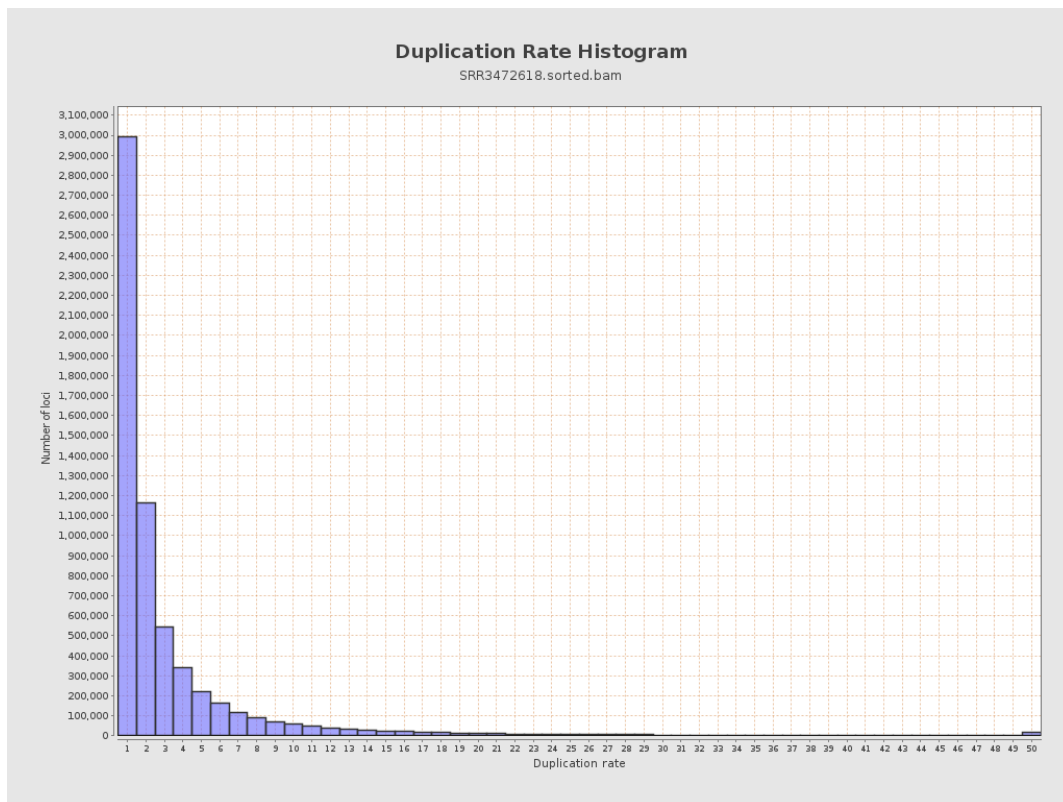
5. Results : Coverage Histogram (0-50X)



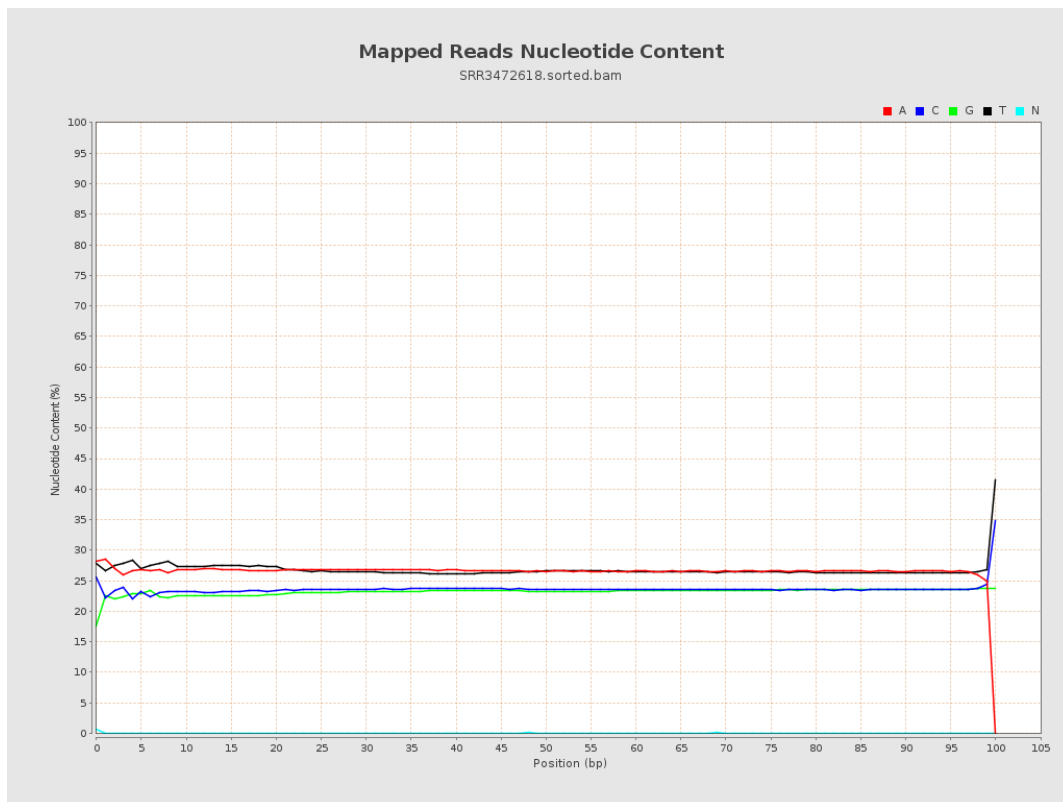
6. Results : Genome Fraction Coverage



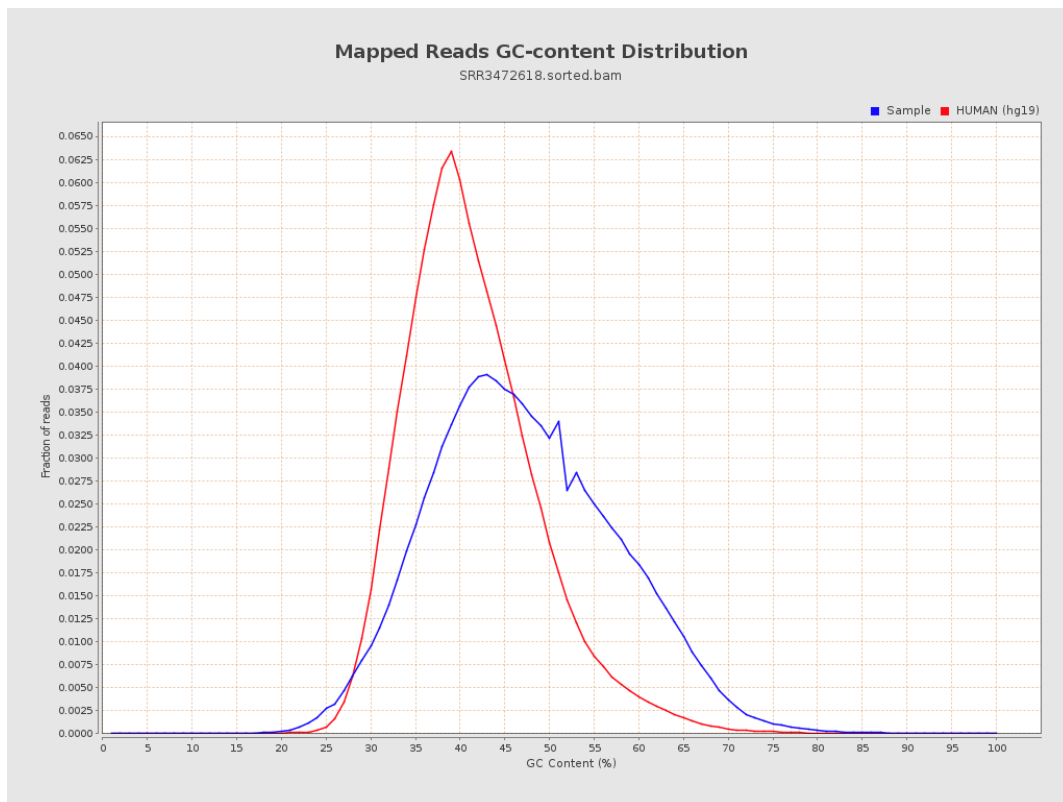
7. Results : Duplication Rate Histogram



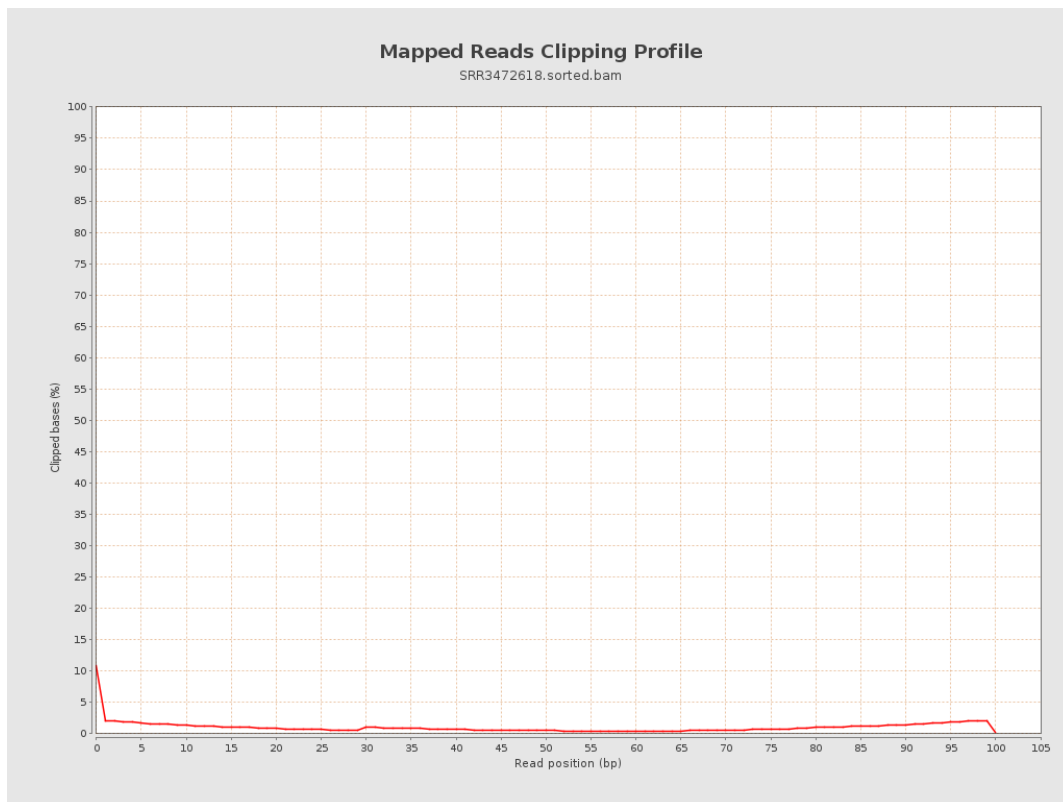
8. Results : Mapped Reads Nucleotide Content



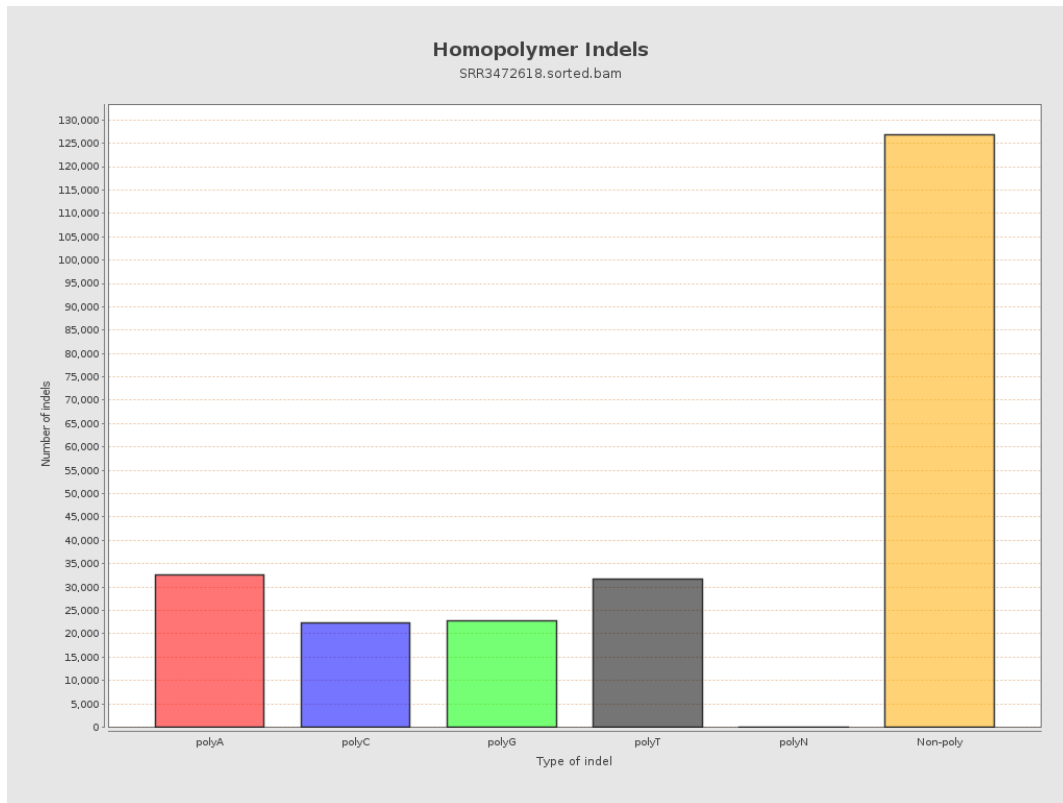
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



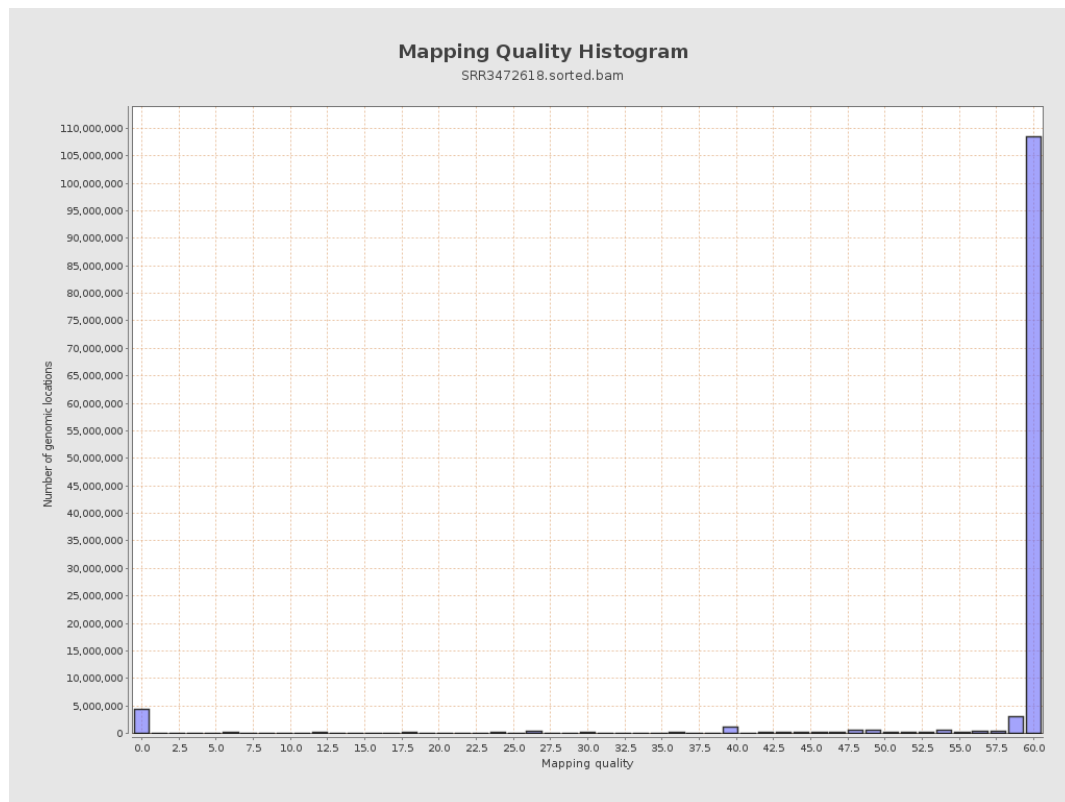
11. Results : Homopolymer Indels



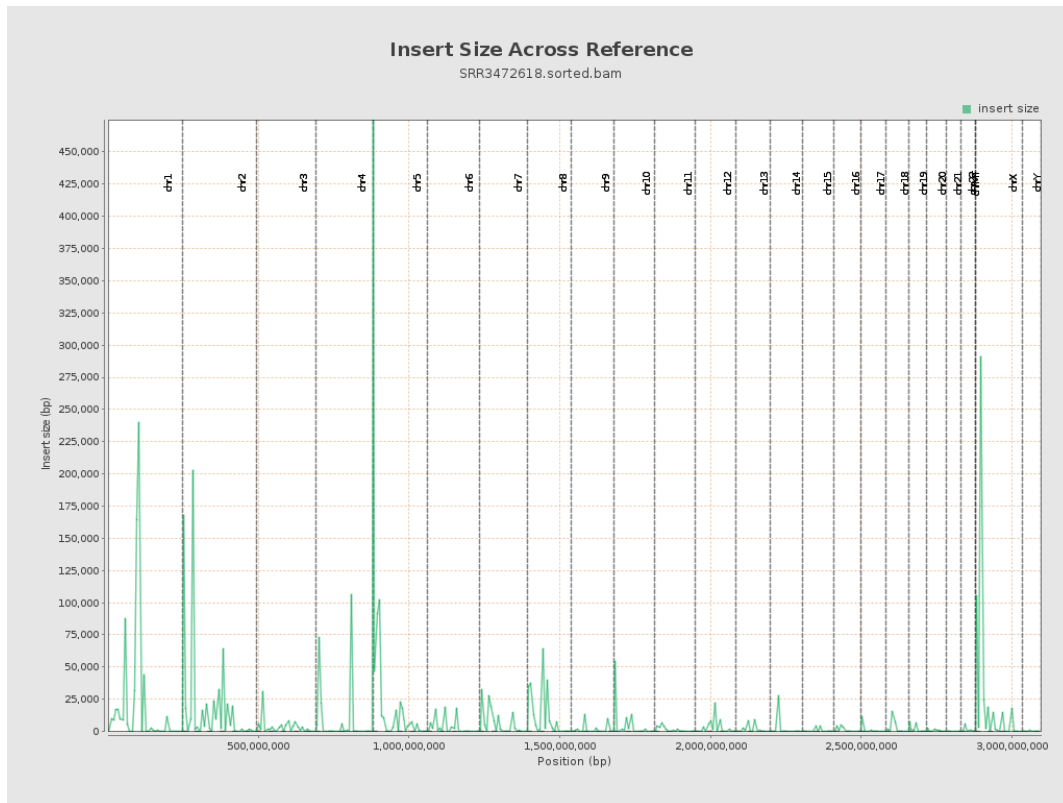
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

