

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 11:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618618.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_SRR618618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618618_1.fastq.gz SRR618618_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 11:17:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,968,190
Mapped reads	31,140,571 / 97.41%
Unmapped reads	827,619 / 2.59%
Mapped paired reads	31,140,571 / 97.41%
Mapped reads, first in pair	15,684,130 / 49.06%
Mapped reads, second in pair	15,456,441 / 48.35%
Mapped reads, both in pair	30,748,410 / 96.18%
Mapped reads, singletons	392,161 / 1.23%
Secondary alignments	0
Supplementary alignments	62,709 / 0.2%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	7,477,345 / 23.39%
Duplication rate	20.91%
Clipped reads	6,341,114 / 19.84%

2.2. ACGT Content

Number/percentage of A's	813,207,291 / 27.62%
Number/percentage of C's	628,770,947 / 21.36%
Number/percentage of T's	823,205,050 / 27.96%
Number/percentage of G's	678,441,286 / 23.05%
Number/percentage of N's	234,926 / 0.01%

GC Percentage	44.4%
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2.3. Coverage

Mean	0.9516
Standard Deviation	3.7607

2.4. Mapping Quality

Mean Mapping Quality	53.95
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2.5. Insert size

Mean	39,658.26
Standard Deviation	1,974,485.04
P25/Median/P75	165 / 194 / 232

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	33,306,865
Insertions	511,695
Mapped reads with at least one insertion	1.62%
Deletions	1,506,045
Mapped reads with at least one deletion	4.71%
Homopolymer indels	53.57%

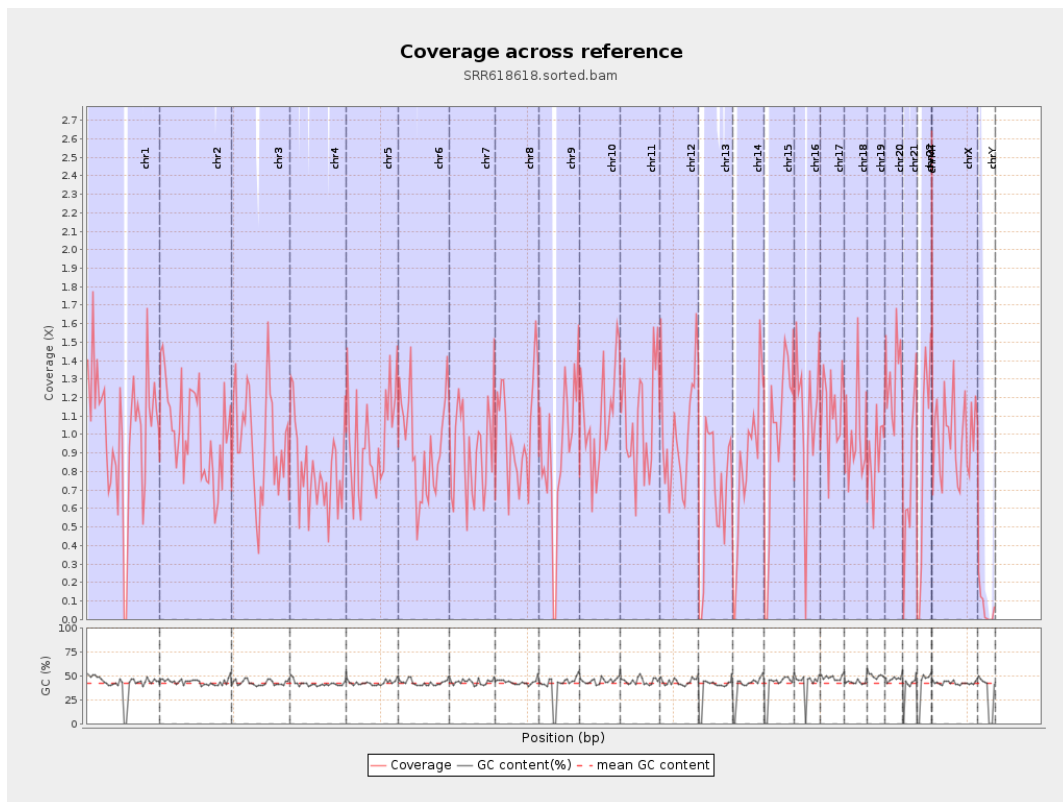
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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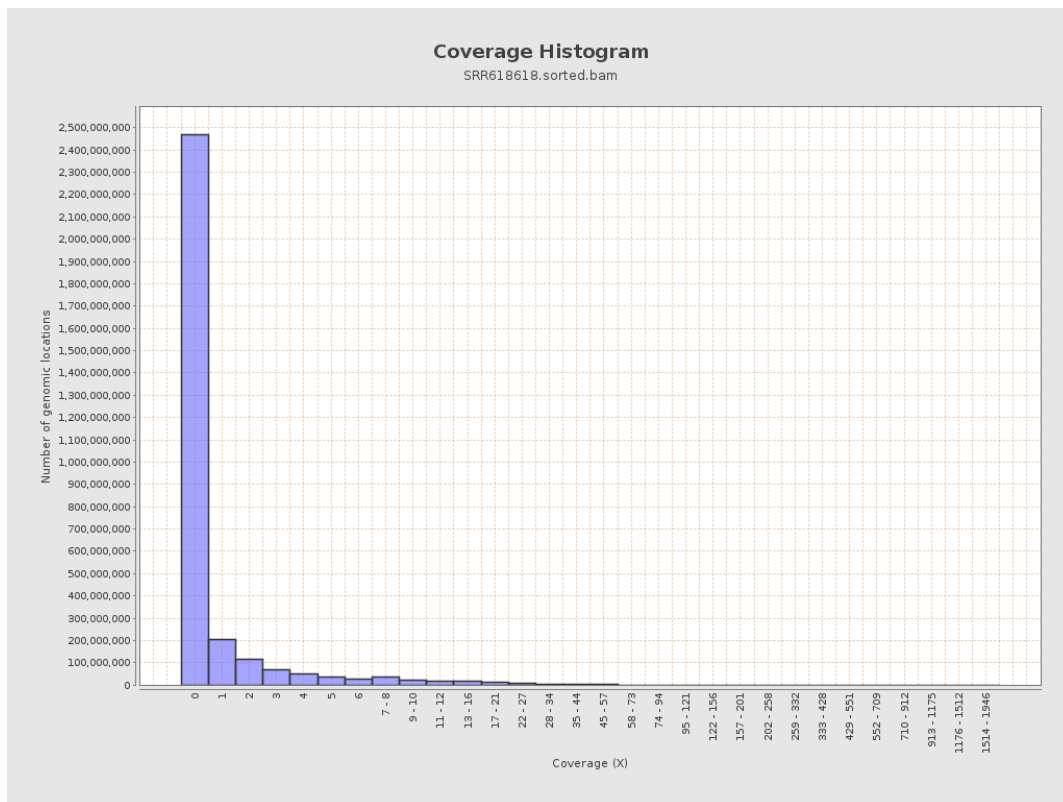
		bases	coverage	deviation
chr1	249250621	253431444	1.0168	4.4129
chr2	243199373	247639643	1.0183	3.8967
chr3	198022430	189969037	0.9593	3.3769
chr4	191154276	153530904	0.8032	3.1755
chr5	180915260	174861735	0.9665	3.4619
chr6	171115067	160613028	0.9386	3.5625
chr7	159138663	145830468	0.9164	3.4402
chr8	146364022	149842288	1.0238	3.6242
chr9	141213431	129023719	0.9137	4.1538
chr10	135534747	148849261	1.0982	3.8713
chr11	135006516	146091347	1.0821	4.1642
chr12	133851895	134282328	1.0032	3.6445
chr13	115169878	77523896	0.6731	2.7083
chr14	107349540	89790757	0.8364	3.3315
chr15	102531392	100695645	0.9821	3.7531
chr16	90354753	97398390	1.078	4.7746
chr17	81195210	92075217	1.134	4.2019
chr18	78077248	78260983	1.0024	4.0898
chr19	59128983	52528085	0.8884	3.9458
chr20	63025520	82812649	1.314	4.5232
chr21	48129895	38171573	0.7931	4.615
chr22	51304566	46726434	0.9108	3.8289
chrMT	16571	43807	2.6436	6.591
chrX	155270560	152121240	0.9797	3.4487

chrY	59373566	3765890	0.0634	1.4134
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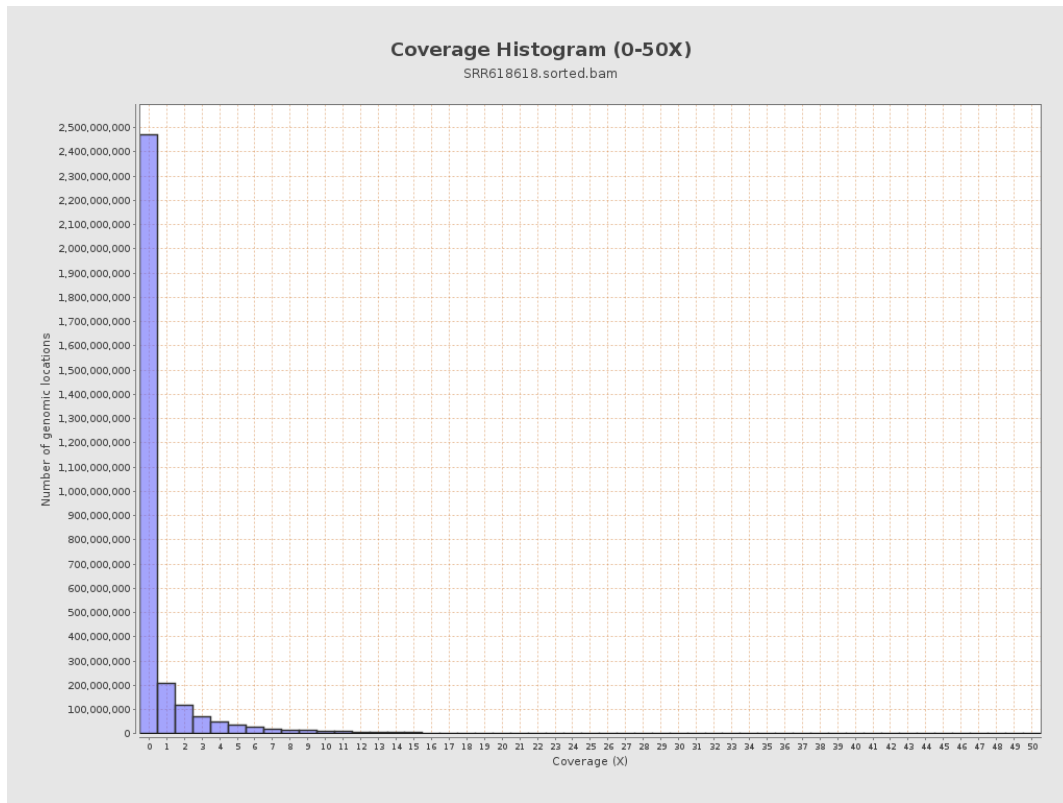
3. Results : Coverage across reference



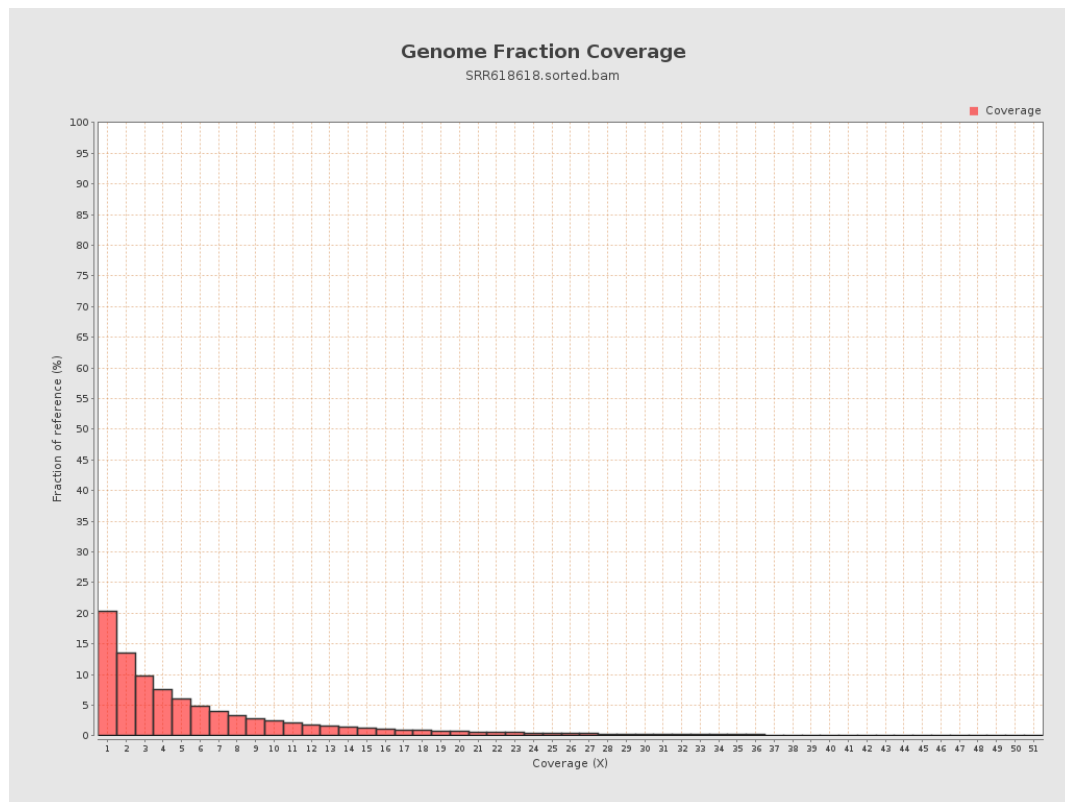
4. Results : Coverage Histogram



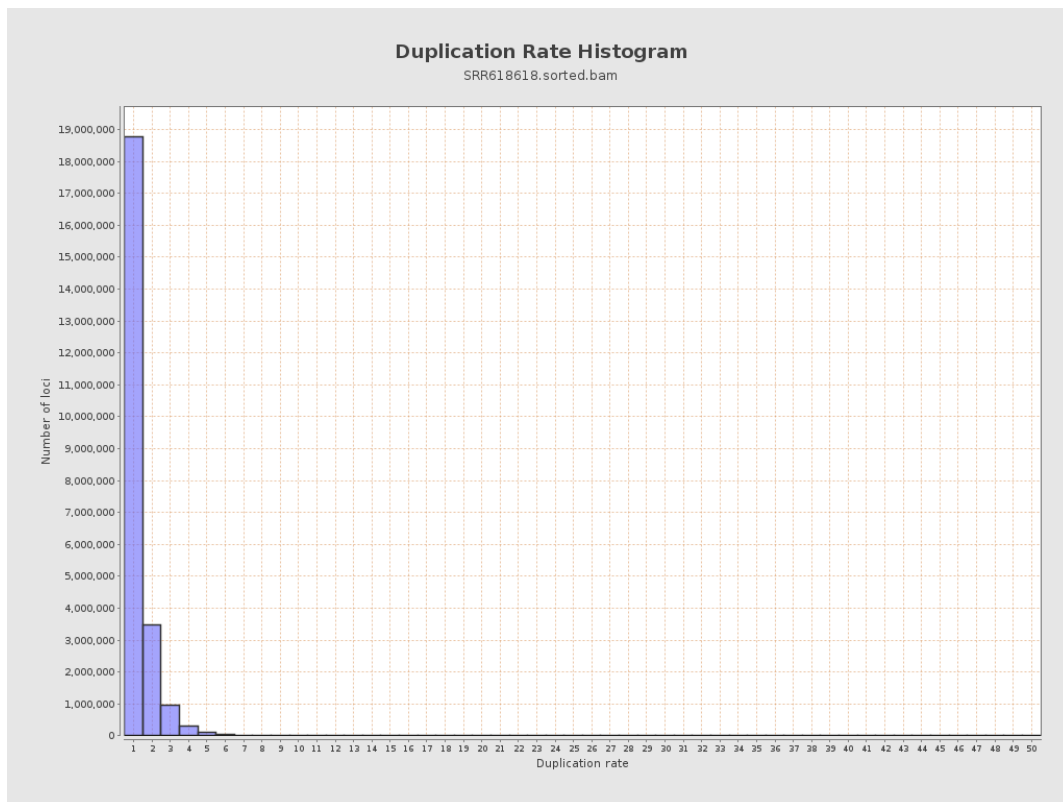
5. Results : Coverage Histogram (0-50X)



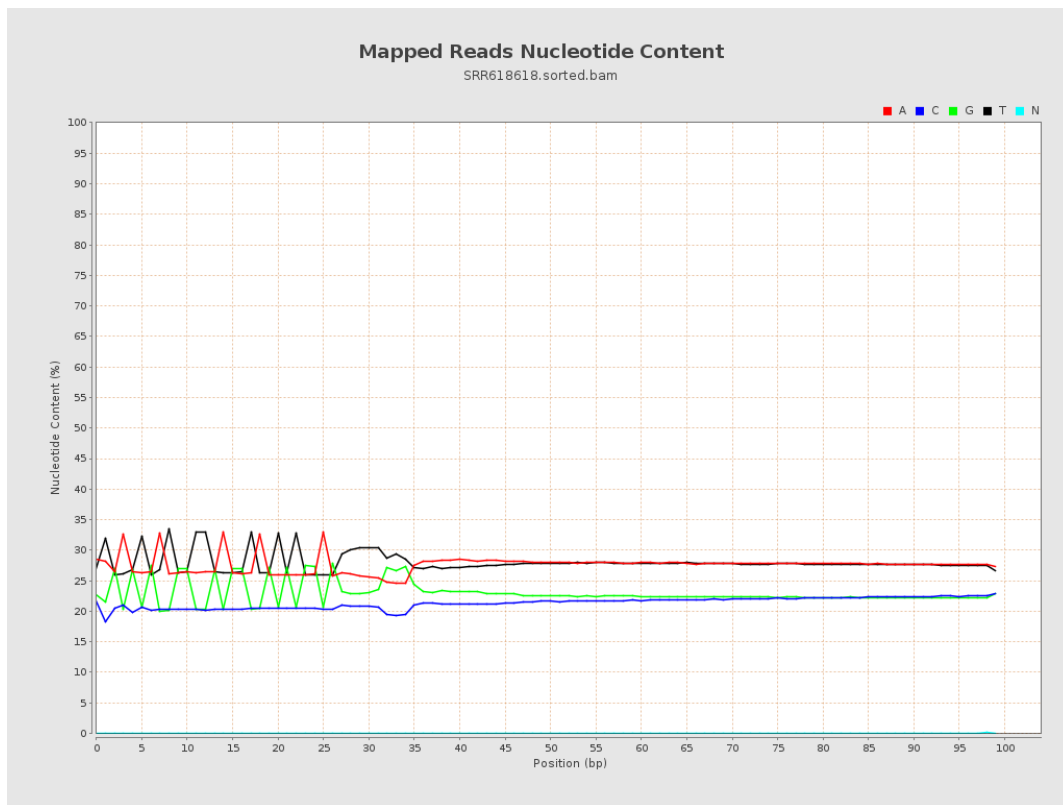
6. Results : Genome Fraction Coverage



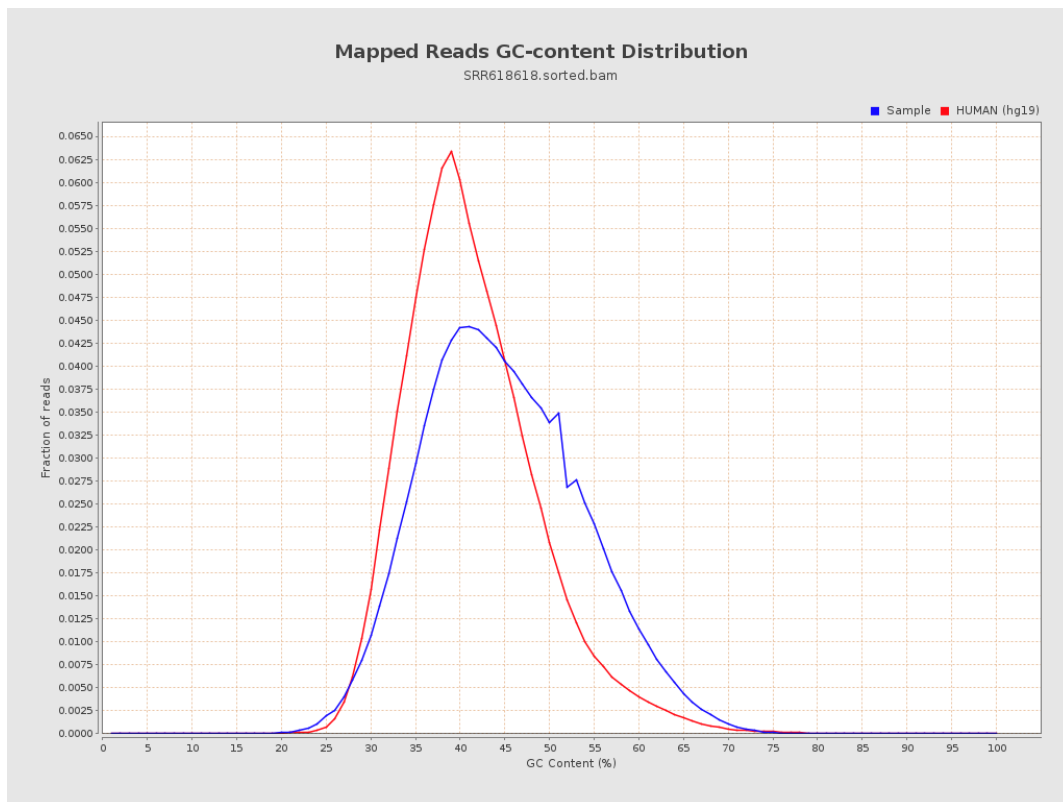
7. Results : Duplication Rate Histogram



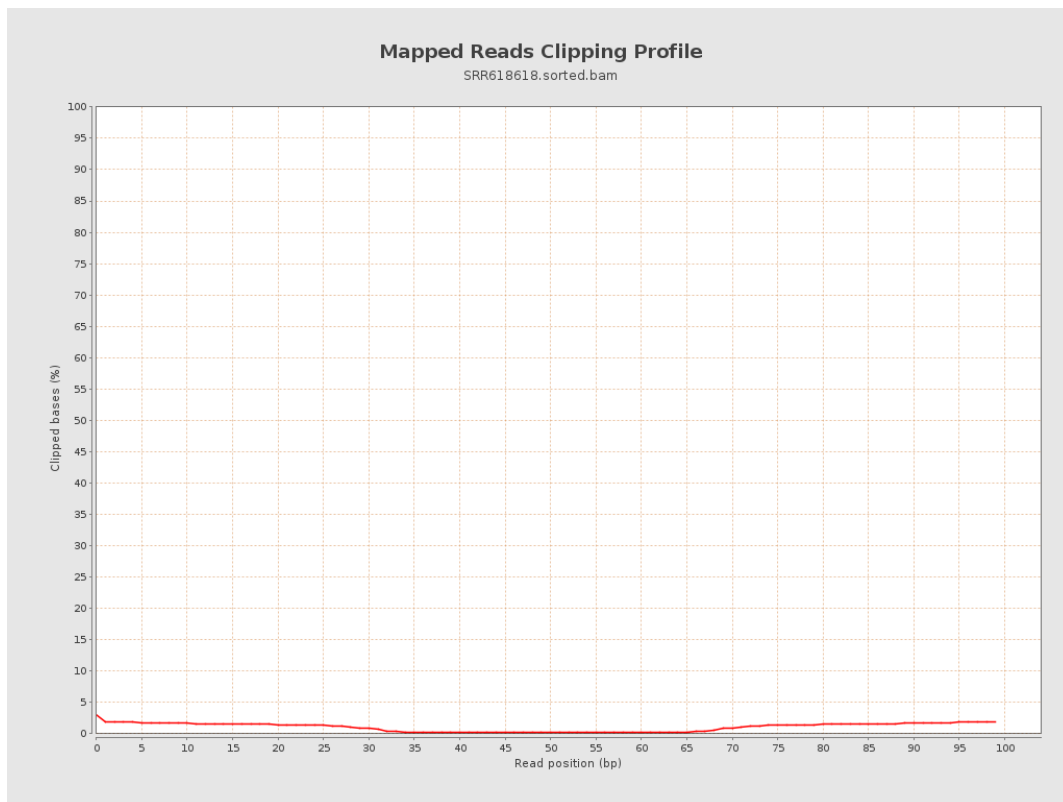
8. Results : Mapped Reads Nucleotide Content



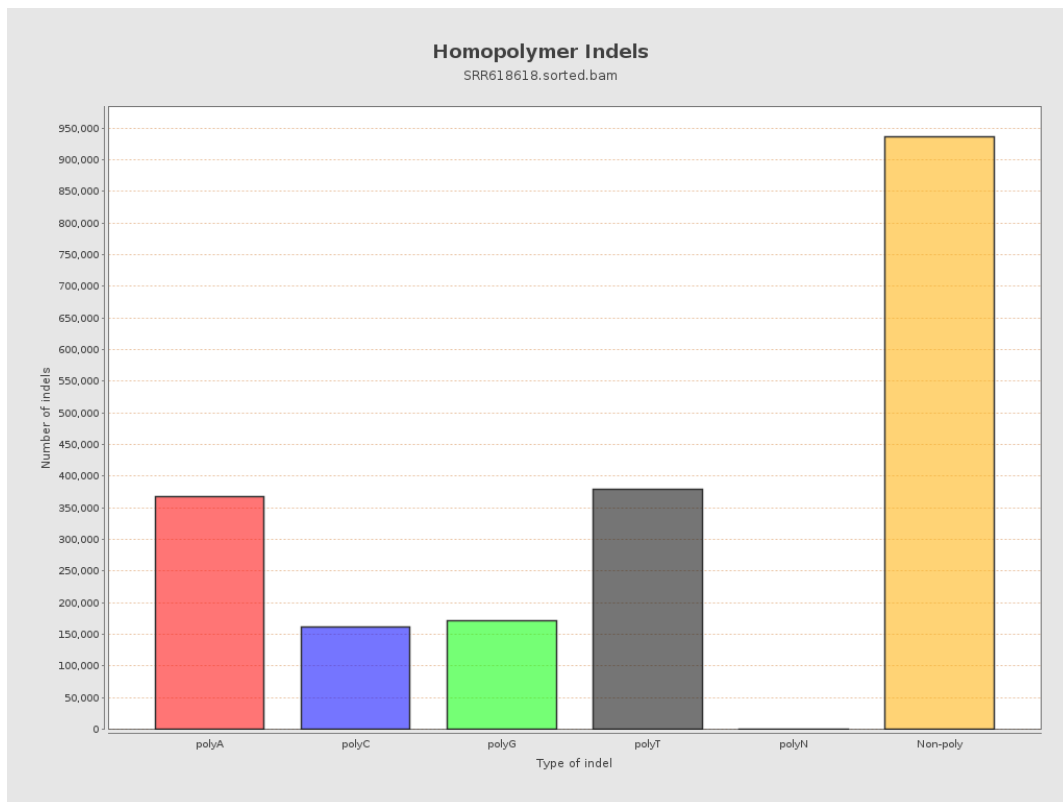
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



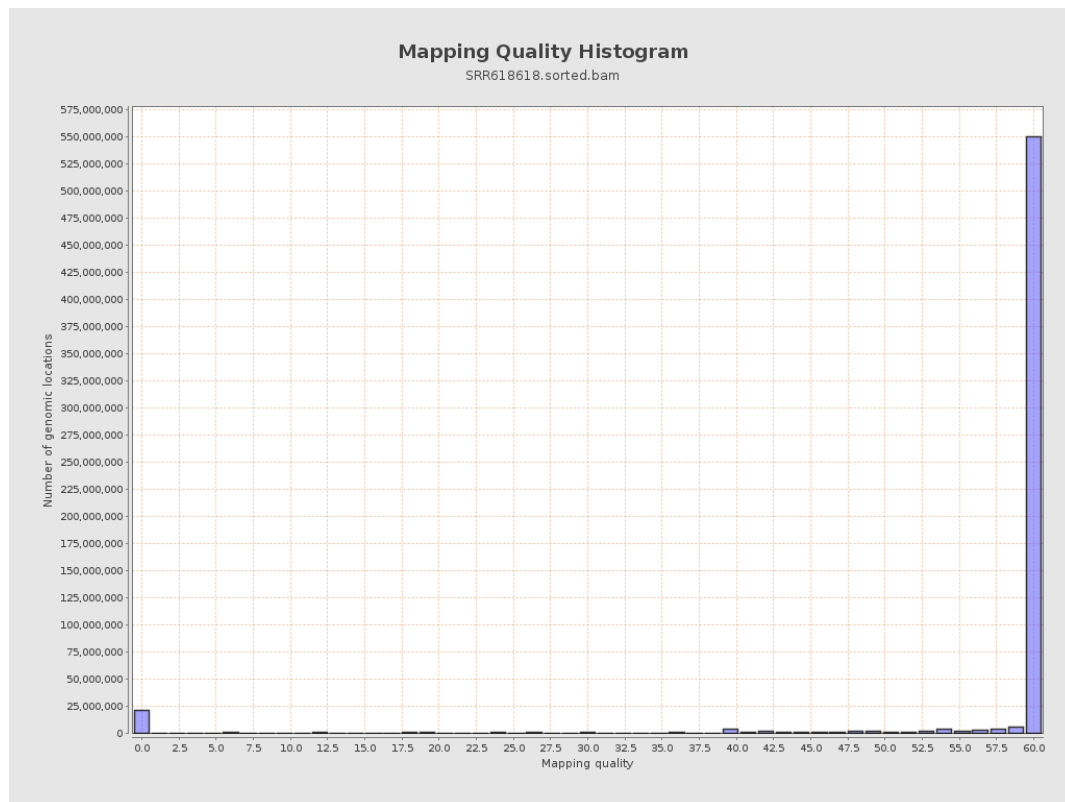
11. Results : Homopolymer Indels



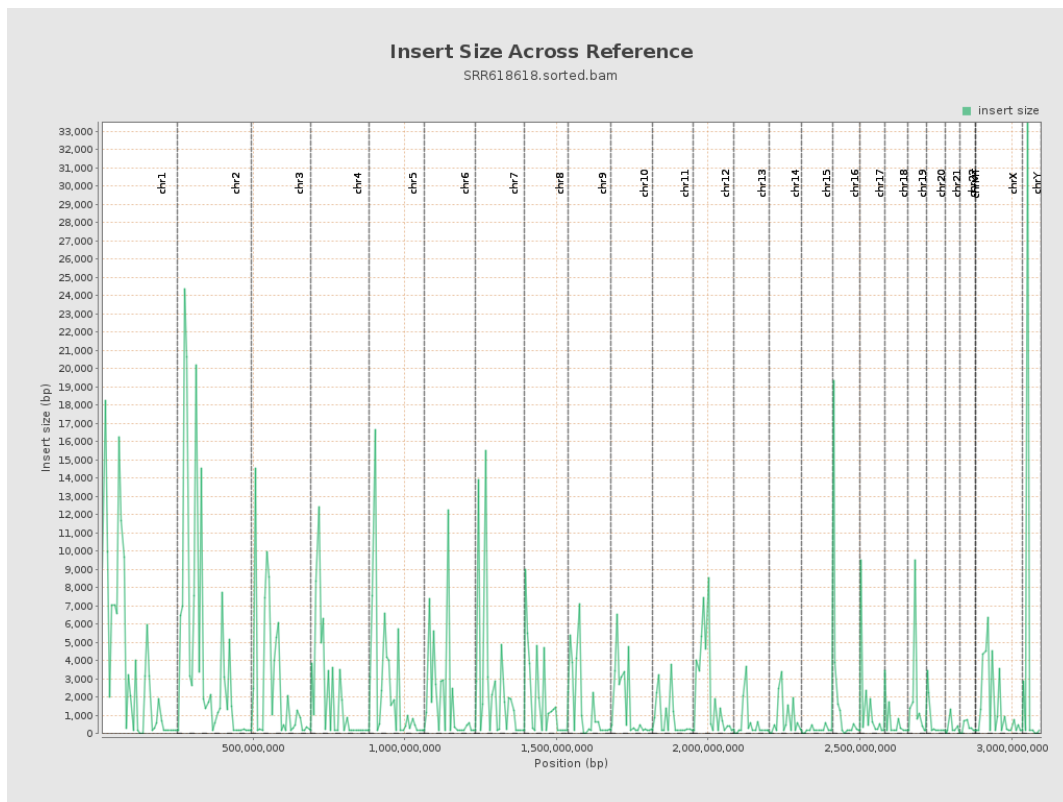
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

