

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173915.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_SRR10173915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173915_1.fastq.gz SRR10173915_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:35:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,866,146
Mapped reads	14,455,113 / 97.24%
Unmapped reads	411,033 / 2.76%
Mapped paired reads	14,455,113 / 97.24%
Mapped reads, first in pair	7,242,817 / 48.72%
Mapped reads, second in pair	7,212,296 / 48.51%
Mapped reads, both in pair	14,186,616 / 95.43%
Mapped reads, singletons	268,497 / 1.81%
Secondary alignments	0
Supplementary alignments	1,395,926 / 9.39%
Read min/max/mean length	30 / 133 / 128.13
Duplicated reads (estimated)	11,416,753 / 76.8%
Duplication rate	65.89%
Clipped reads	5,737,417 / 38.59%

2.2. ACGT Content

Number/percentage of A's	514,331,314 / 30.11%
Number/percentage of C's	334,897,133 / 19.6%
Number/percentage of T's	512,796,378 / 30.02%
Number/percentage of G's	346,201,146 / 20.27%
Number/percentage of N's	20,148 / 0%

GC Percentage	39.87%
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2.3. Coverage

Mean	0.5521
Standard Deviation	7.7234

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	804,241.27
Standard Deviation	8,079,160.74
P25/Median/P75	148 / 206 / 296

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	17,940,821
Insertions	179,600
Mapped reads with at least one insertion	1.2%
Deletions	378,813
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.33%

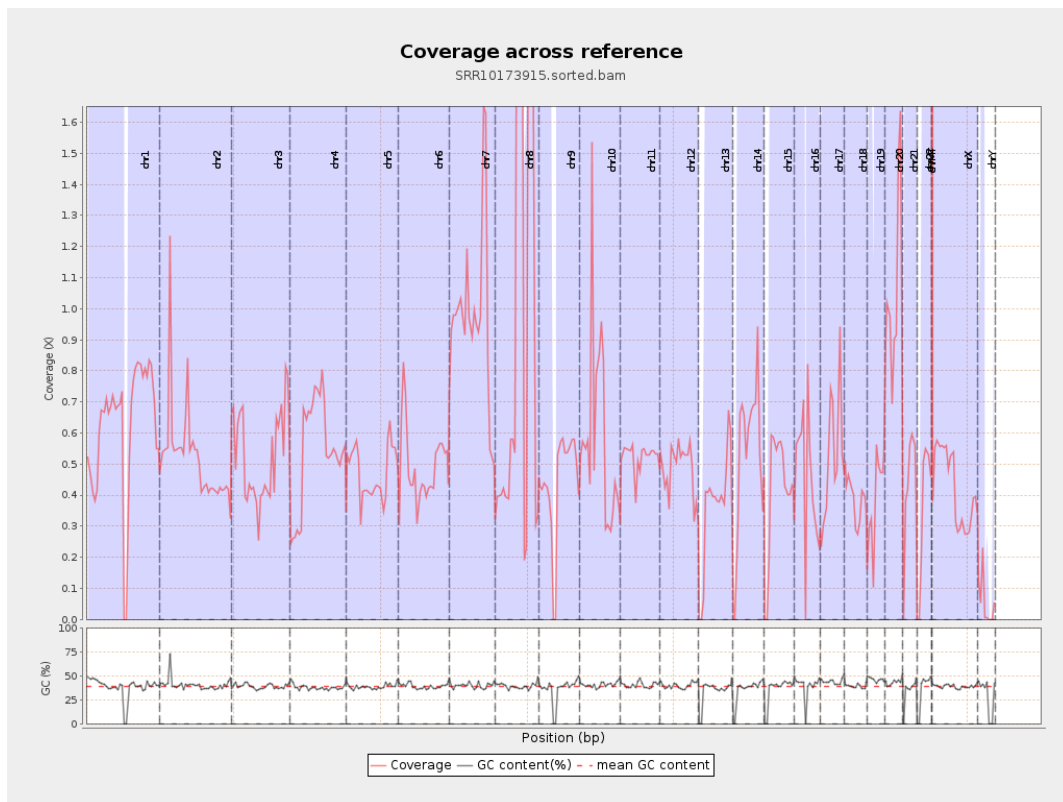
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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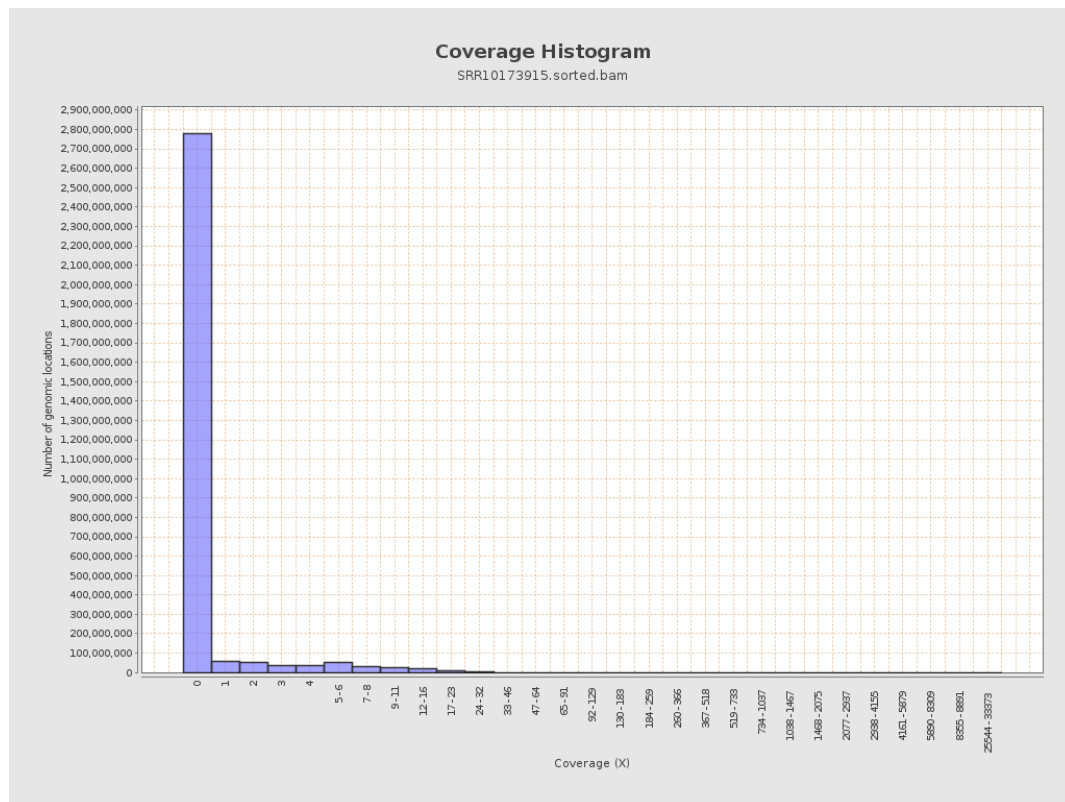
		bases	coverage	deviation
chr1	249250621	155516207	0.6239	3.9737
chr2	243199373	126987305	0.5222	23.343
chr3	198022430	103403375	0.5222	2.1628
chr4	191154276	103477129	0.5413	3.5442
chr5	180915260	85236220	0.4711	2.0141
chr6	171115067	84732873	0.4952	2.3184
chr7	159138663	153496142	0.9645	9.0105
chr8	146364022	164107424	1.1212	5.2437
chr9	141213431	61147293	0.433	3.3287
chr10	135534747	80037402	0.5905	10.3232
chr11	135006516	70347325	0.5211	2.3156
chr12	133851895	64862126	0.4846	2.1209
chr13	115169878	42608977	0.37	1.7905
chr14	107349540	57071855	0.5316	2.2073
chr15	102531392	42141804	0.411	1.9105
chr16	90354753	40493311	0.4482	3.7667
chr17	81195210	42804344	0.5272	2.7671
chr18	78077248	29849203	0.3823	4.8424
chr19	59128983	22690765	0.3838	3.1369
chr20	63025520	66073387	1.0484	3.2562
chr21	48129895	21335562	0.4433	2.4681
chr22	51304566	18383591	0.3583	1.7516
chrMT	16571	3608430	217.7557	149.4495
chrX	155270560	65423912	0.4214	1.9975

chrY	59373566	3363970	0.0567	2.412
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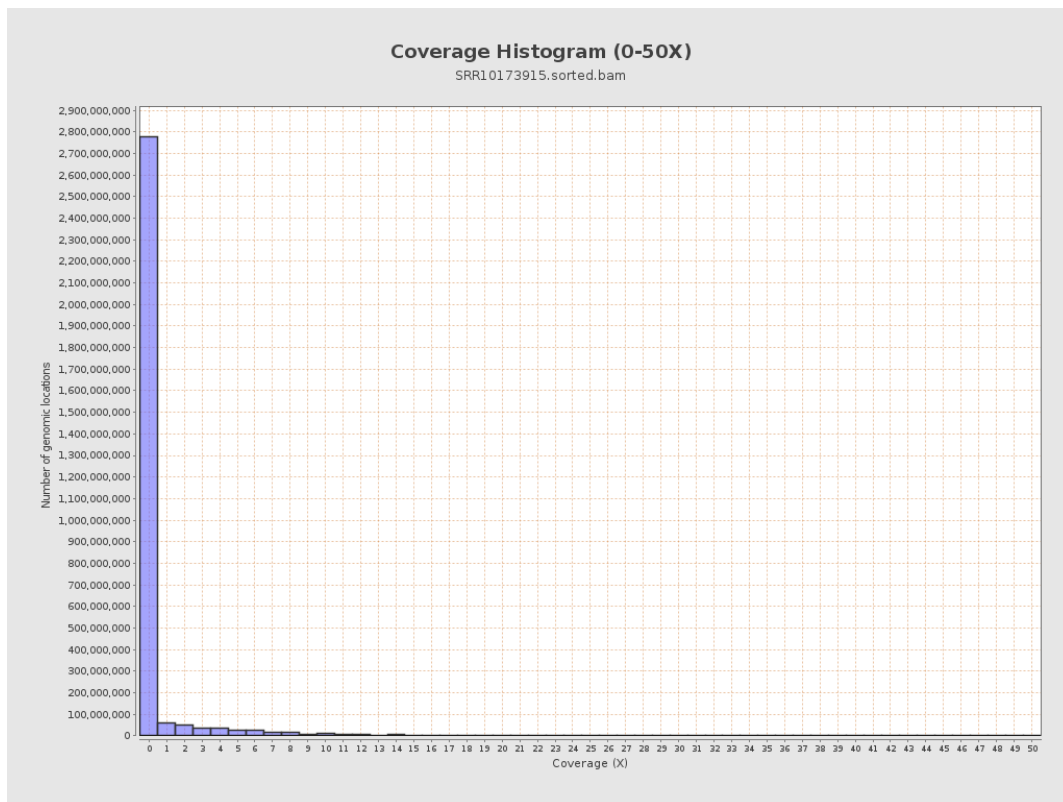
3. Results : Coverage across reference



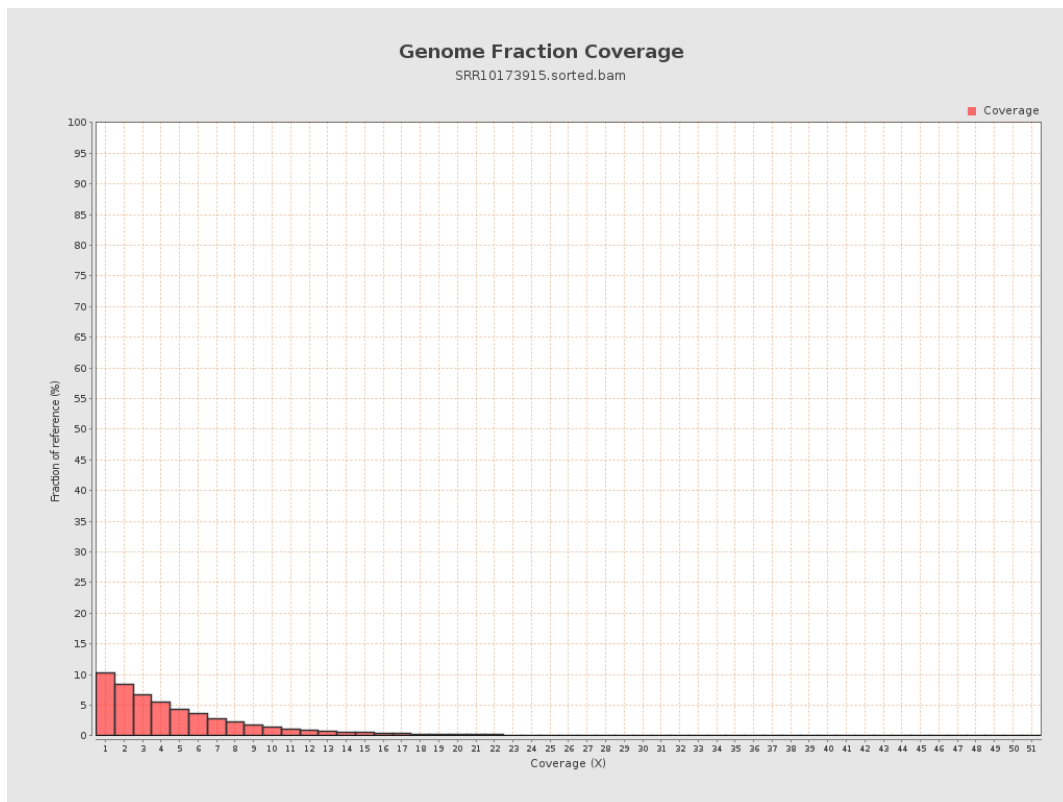
4. Results : Coverage Histogram



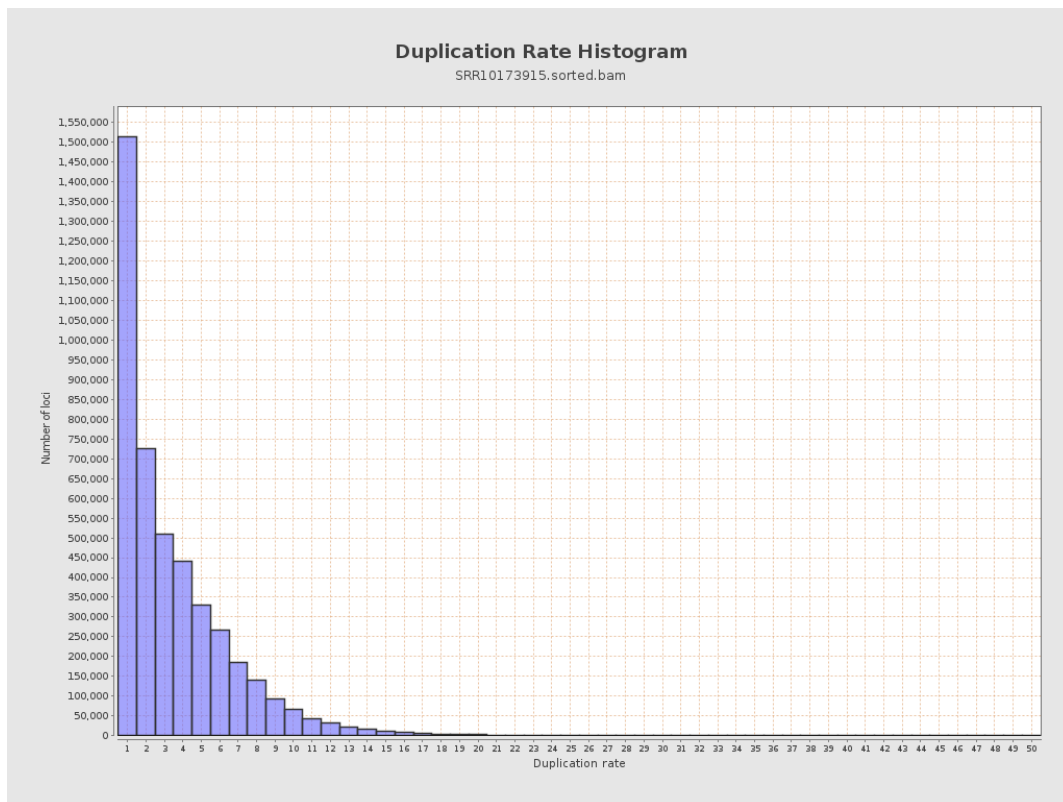
5. Results : Coverage Histogram (0-50X)



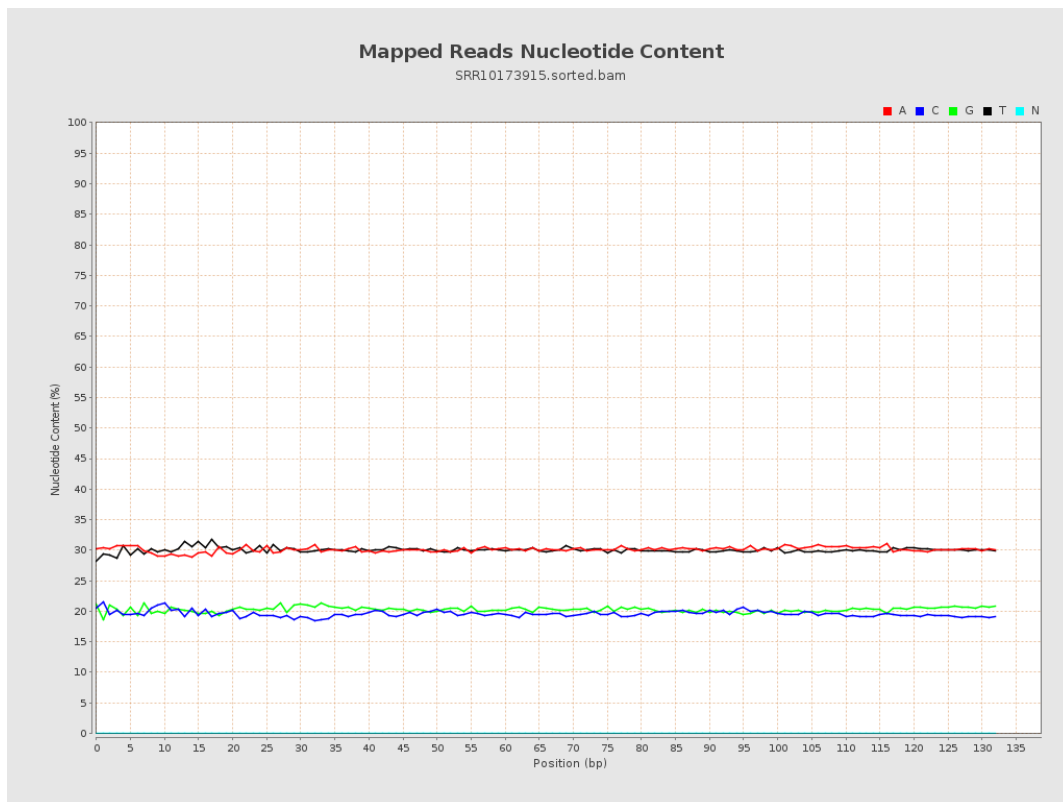
6. Results : Genome Fraction Coverage



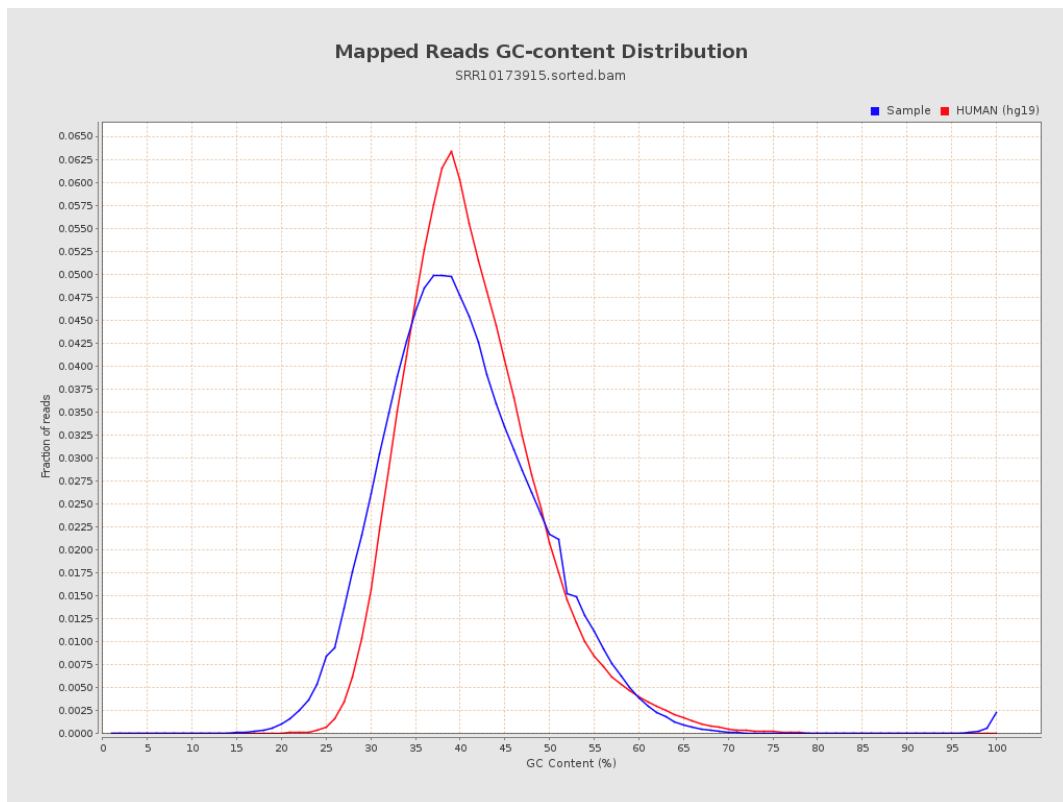
7. Results : Duplication Rate Histogram



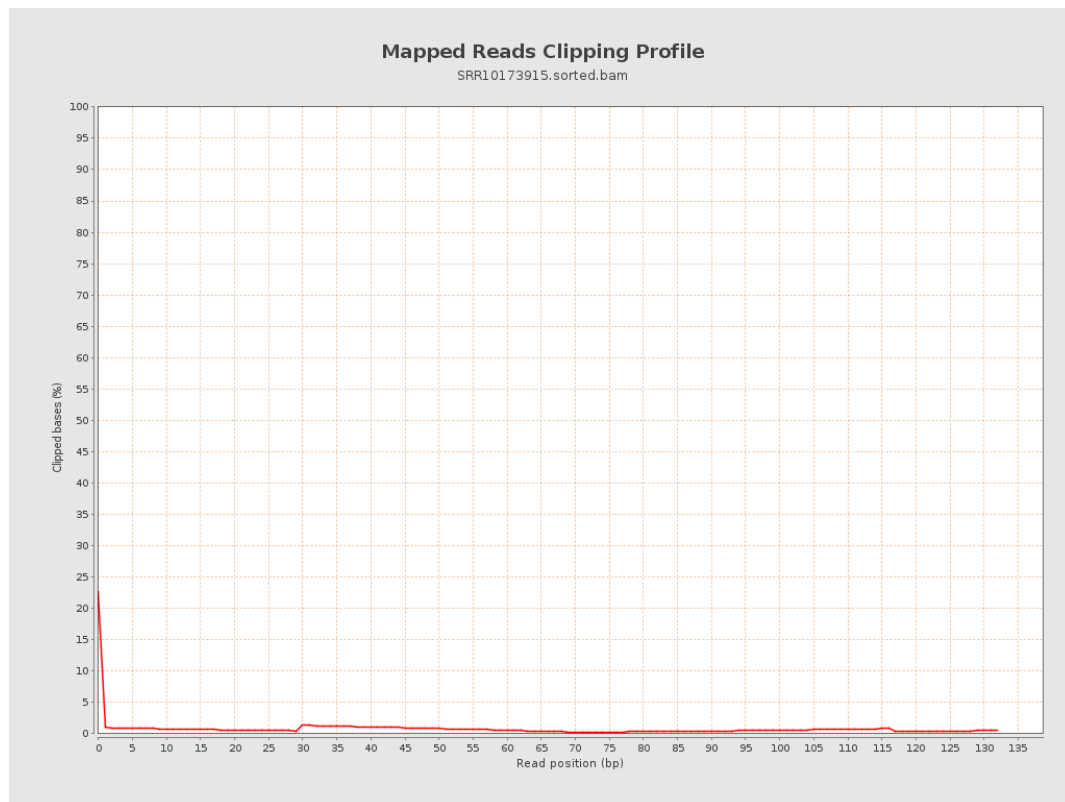
8. Results : Mapped Reads Nucleotide Content



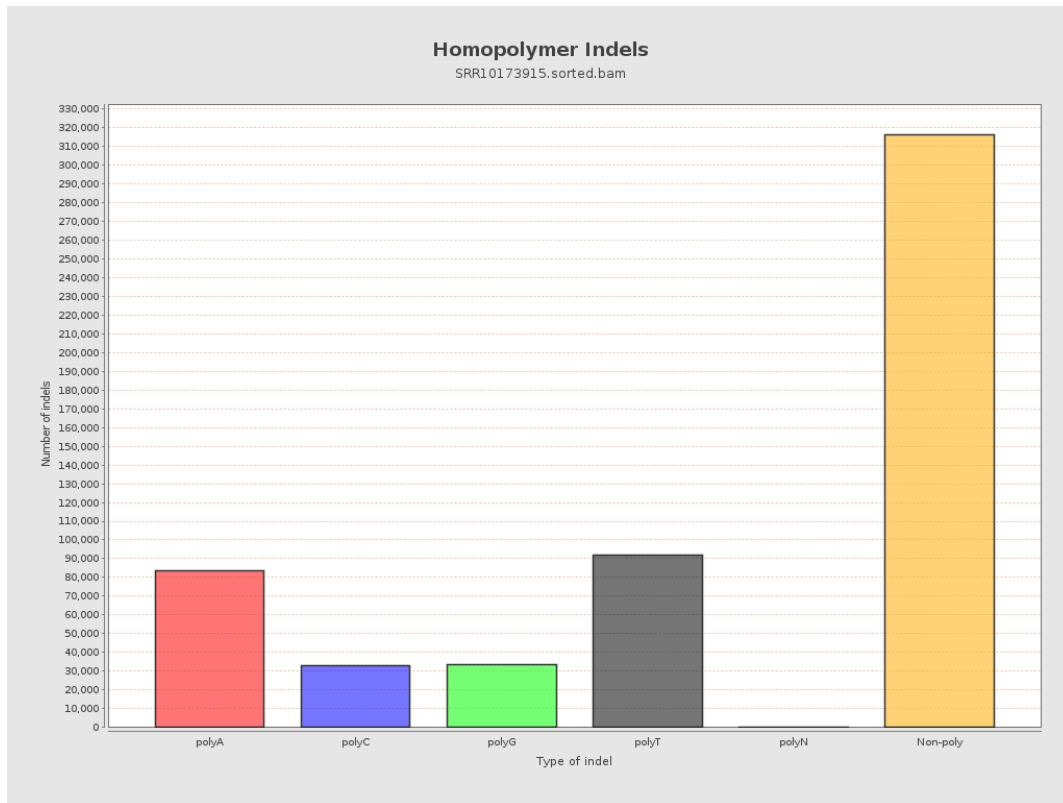
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



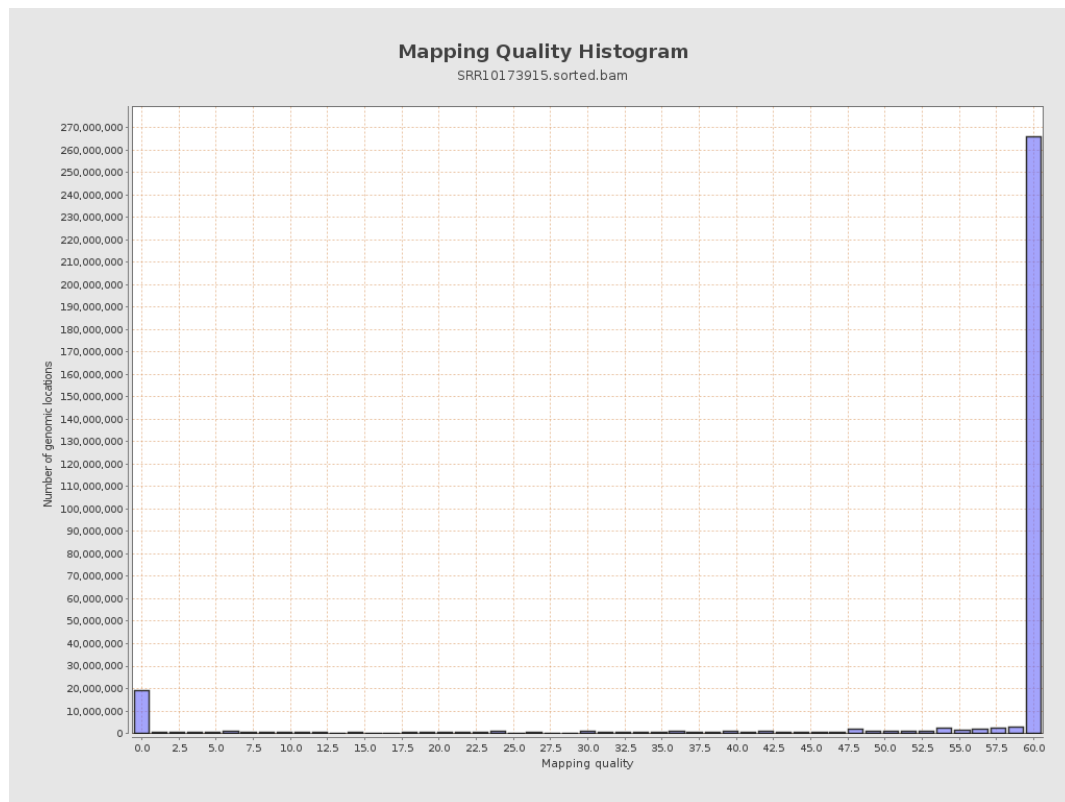
11. Results : Homopolymer Indels



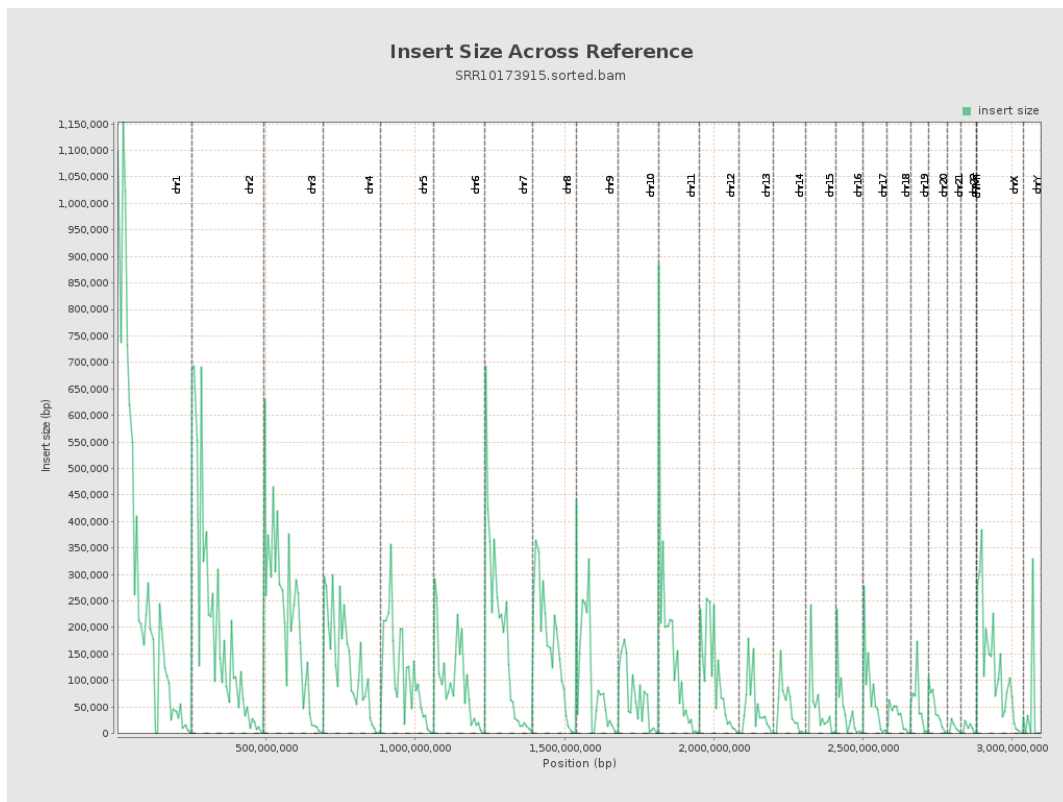
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

