

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:18:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173937.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_SRR10173937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173937_1.fastq.gz SRR10173937_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:18:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,703,104
Mapped reads	6,564,541 / 97.93%
Unmapped reads	138,563 / 2.07%
Mapped paired reads	6,564,541 / 97.93%
Mapped reads, first in pair	3,285,972 / 49.02%
Mapped reads, second in pair	3,278,569 / 48.91%
Mapped reads, both in pair	6,477,156 / 96.63%
Mapped reads, singletons	87,385 / 1.3%
Secondary alignments	0
Supplementary alignments	843,934 / 12.59%
Read min/max/mean length	30 / 133 / 124.95
Duplicated reads (estimated)	5,378,803 / 80.24%
Duplication rate	66.81%
Clipped reads	3,226,778 / 48.14%

2.2. ACGT Content

Number/percentage of A's	221,803,432 / 29.82%
Number/percentage of C's	148,205,188 / 19.92%
Number/percentage of T's	219,963,107 / 29.57%
Number/percentage of G's	153,873,493 / 20.69%
Number/percentage of N's	5,642 / 0%

GC Percentage	40.61%
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2.3. Coverage

Mean	0.2405
Standard Deviation	4.4118

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	1,231,947.64
Standard Deviation	10,676,355.08
P25/Median/P75	105 / 153 / 237

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	6,218,297
Insertions	81,379
Mapped reads with at least one insertion	1.2%
Deletions	216,847
Mapped reads with at least one deletion	3.23%
Homopolymer indels	41.41%

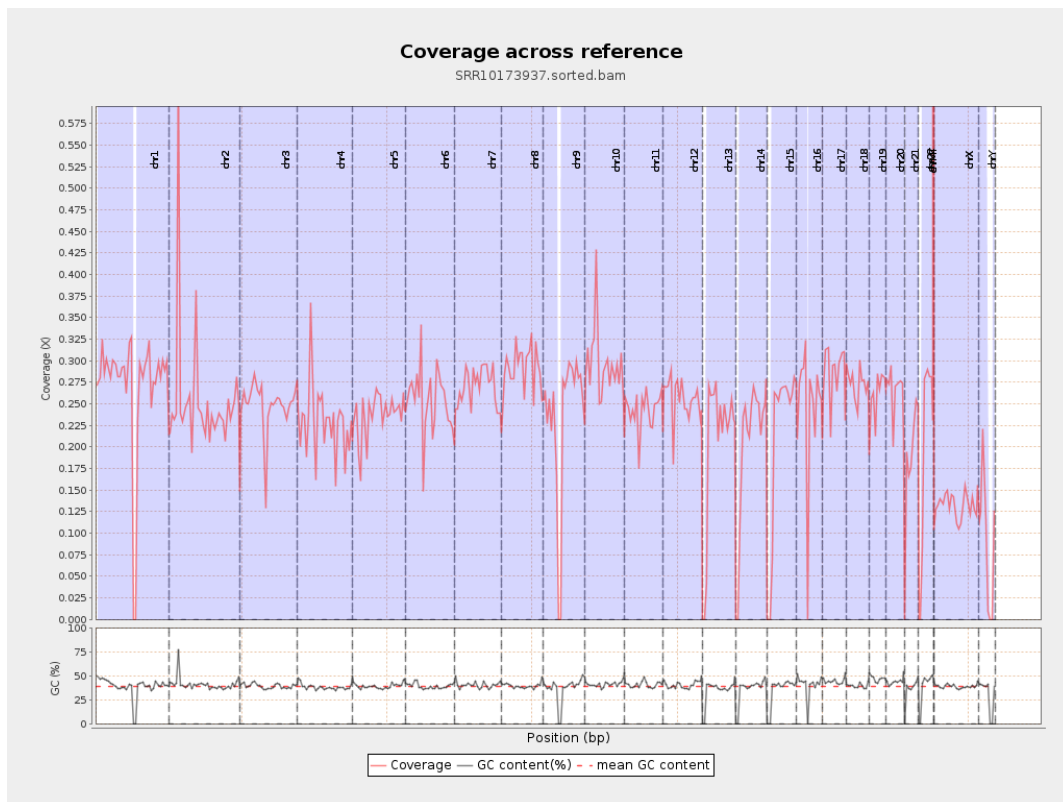
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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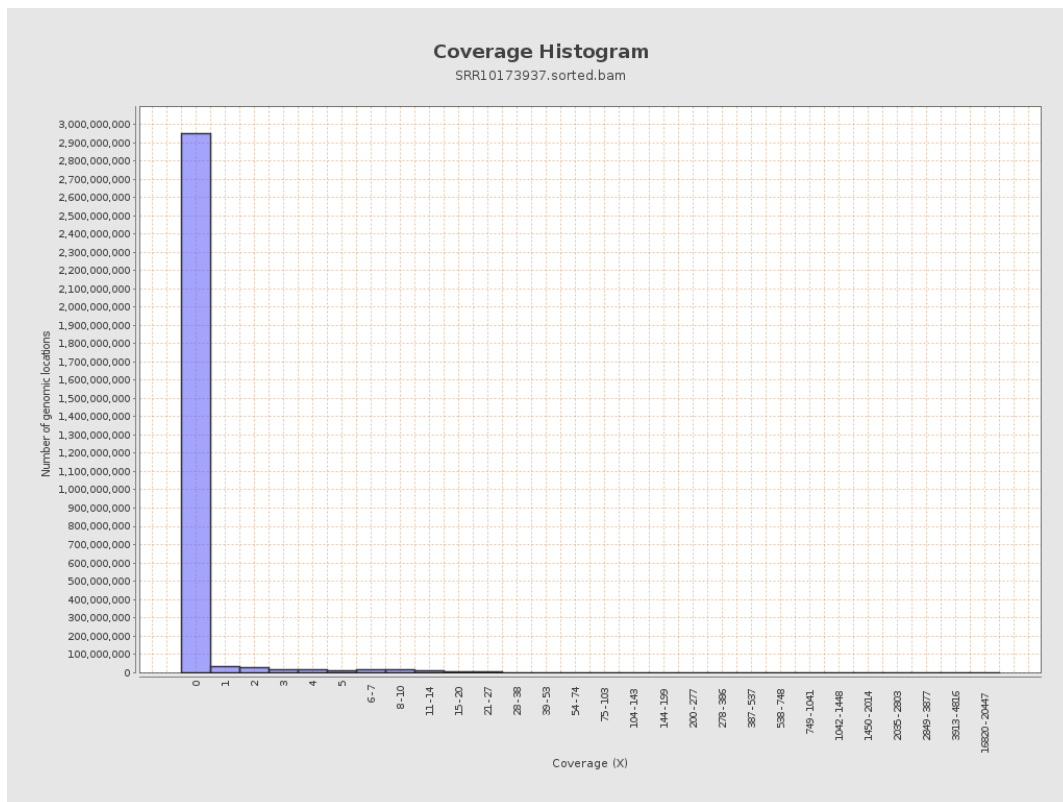
		bases	coverage	deviation
chr1	249250621	67545767	0.271	2.3012
chr2	243199373	61925179	0.2546	14.366
chr3	198022430	48861337	0.2467	1.5536
chr4	191154276	43403594	0.2271	1.9114
chr5	180915260	42902303	0.2371	1.5302
chr6	171115067	43368009	0.2534	1.8832
chr7	159138663	43111960	0.2709	2.2341
chr8	146364022	42606895	0.2911	2.3692
chr9	141213431	33031373	0.2339	2.1364
chr10	135534747	40110351	0.2959	2.4645
chr11	135006516	32720475	0.2424	1.612
chr12	133851895	34158160	0.2552	1.6292
chr13	115169878	23465912	0.2038	1.413
chr14	107349540	21604194	0.2013	1.4393
chr15	102531392	21765439	0.2123	1.4671
chr16	90354753	22201265	0.2457	1.7565
chr17	81195210	23090704	0.2844	1.8073
chr18	78077248	21406570	0.2742	2.6911
chr19	59128983	15414652	0.2607	1.9414
chr20	63025520	16663987	0.2644	1.6166
chr21	48129895	9093552	0.1889	1.7008
chr22	51304566	9866458	0.1923	1.4431
chrMT	16571	406847	24.5517	22.8945
chrX	155270560	20418079	0.1315	1.1266

chrY	59373566	5217883	0.0879	1.3553
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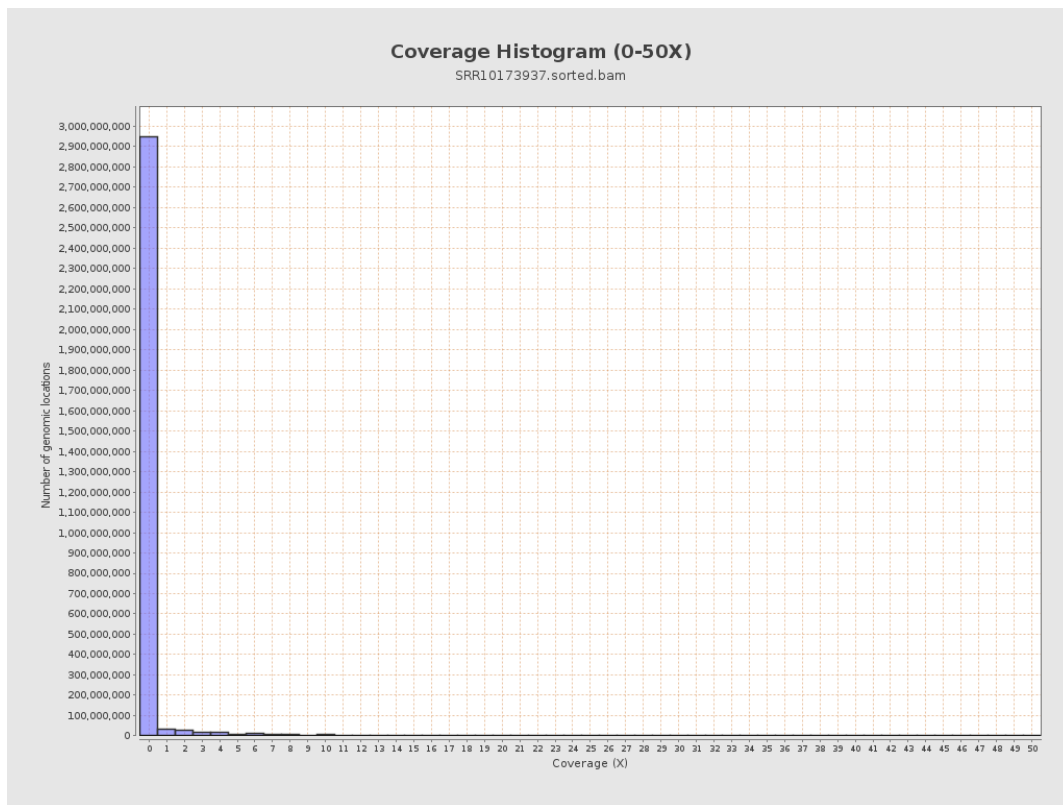
3. Results : Coverage across reference



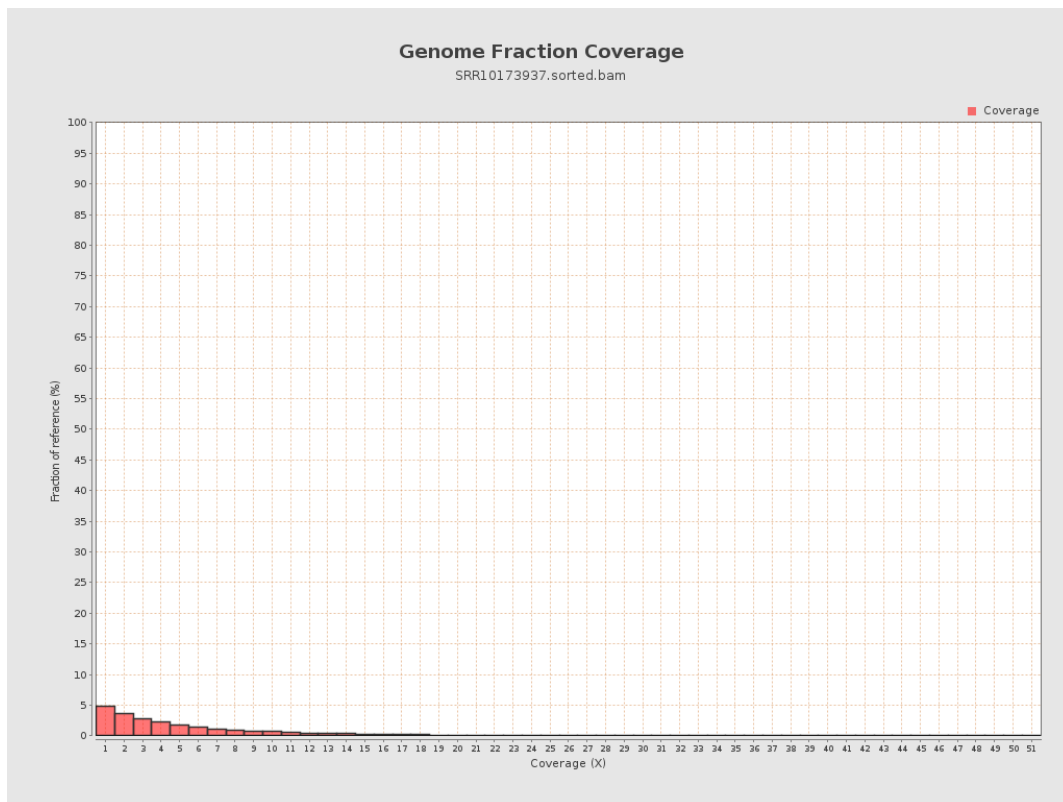
4. Results : Coverage Histogram



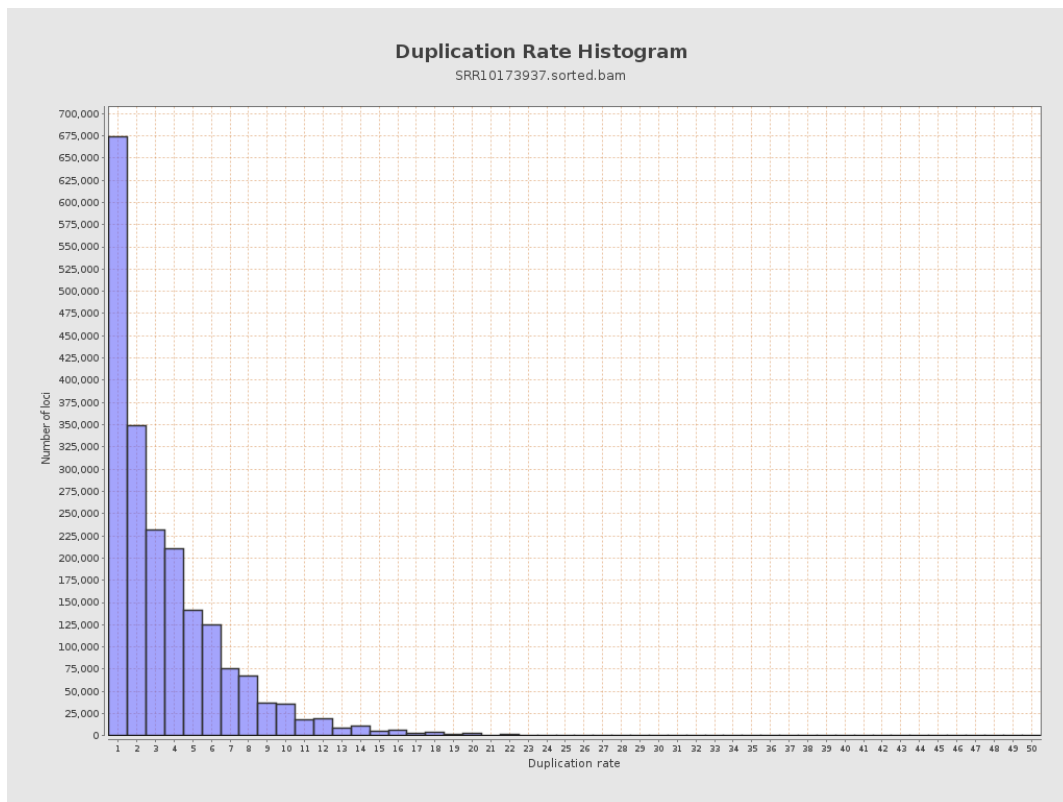
5. Results : Coverage Histogram (0-50X)



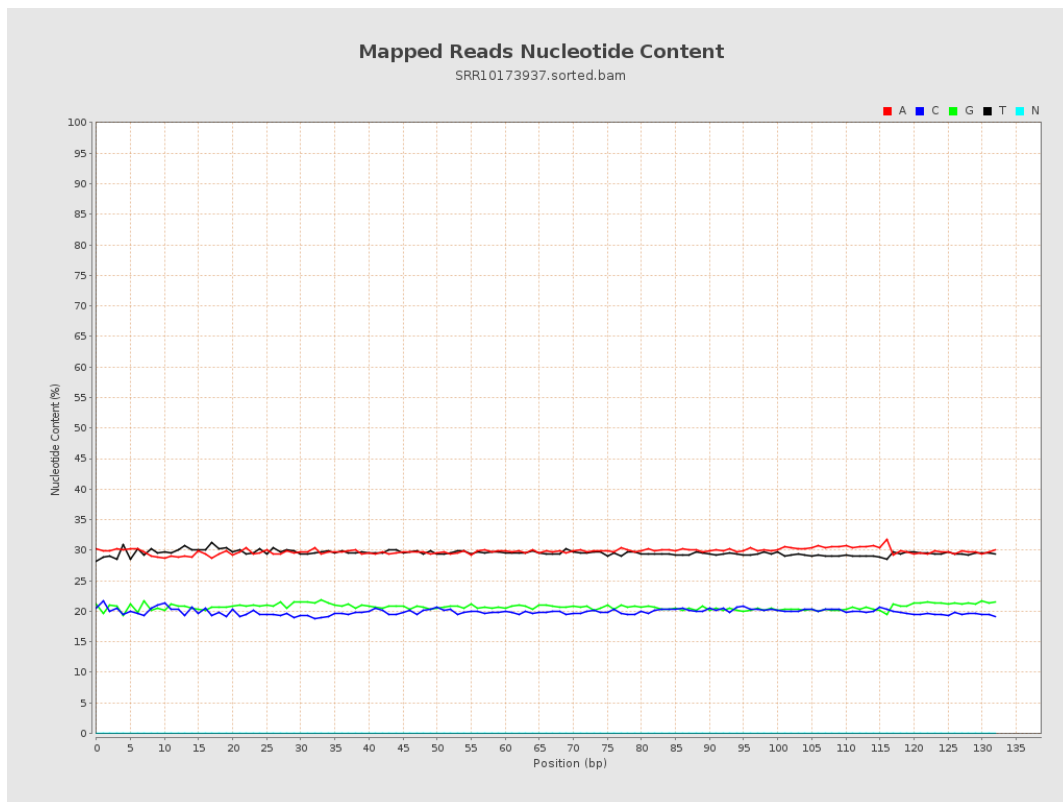
6. Results : Genome Fraction Coverage



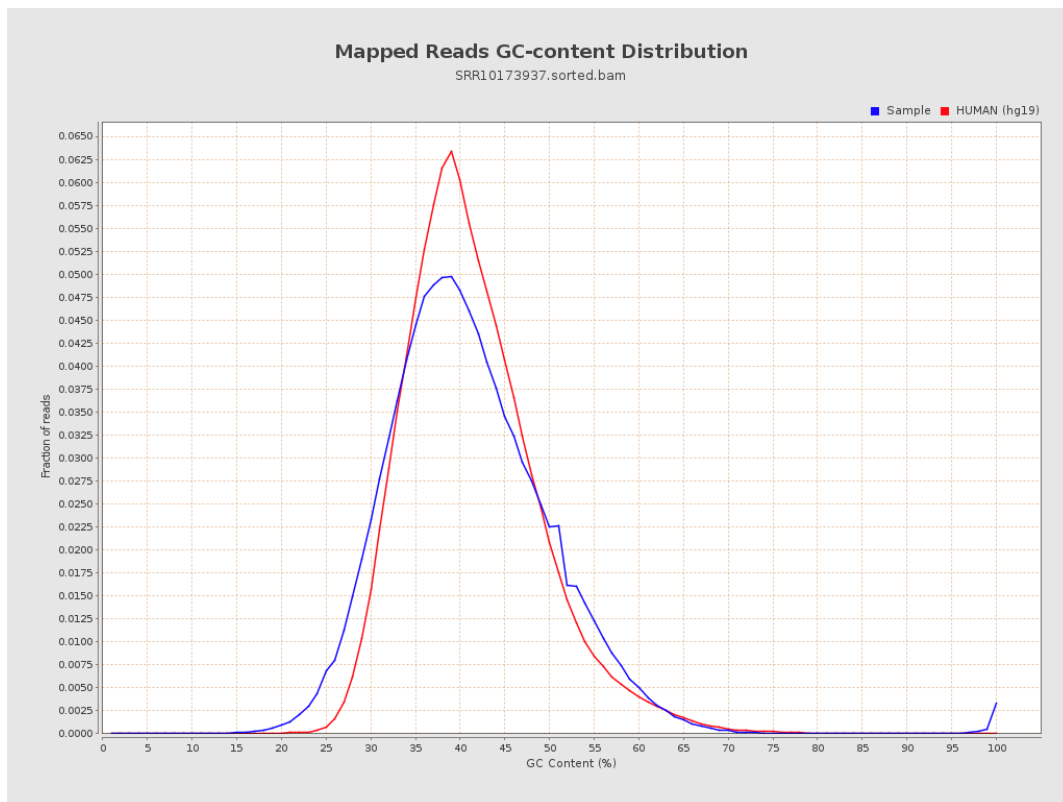
7. Results : Duplication Rate Histogram



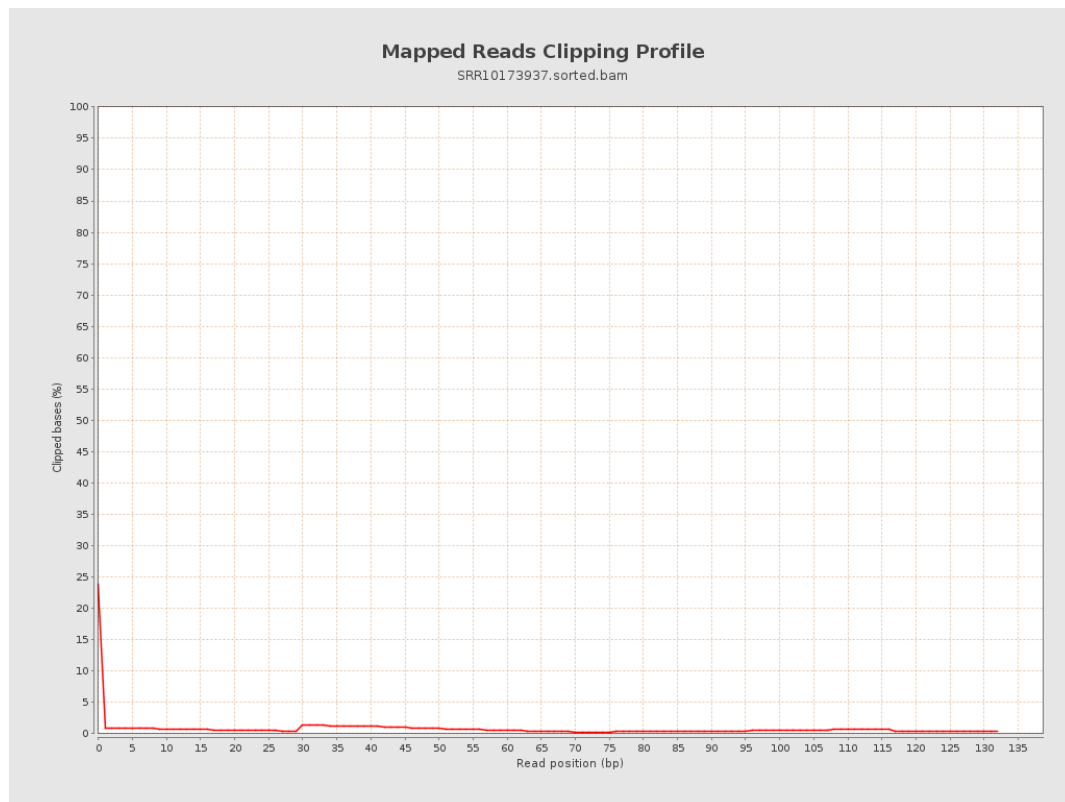
8. Results : Mapped Reads Nucleotide Content



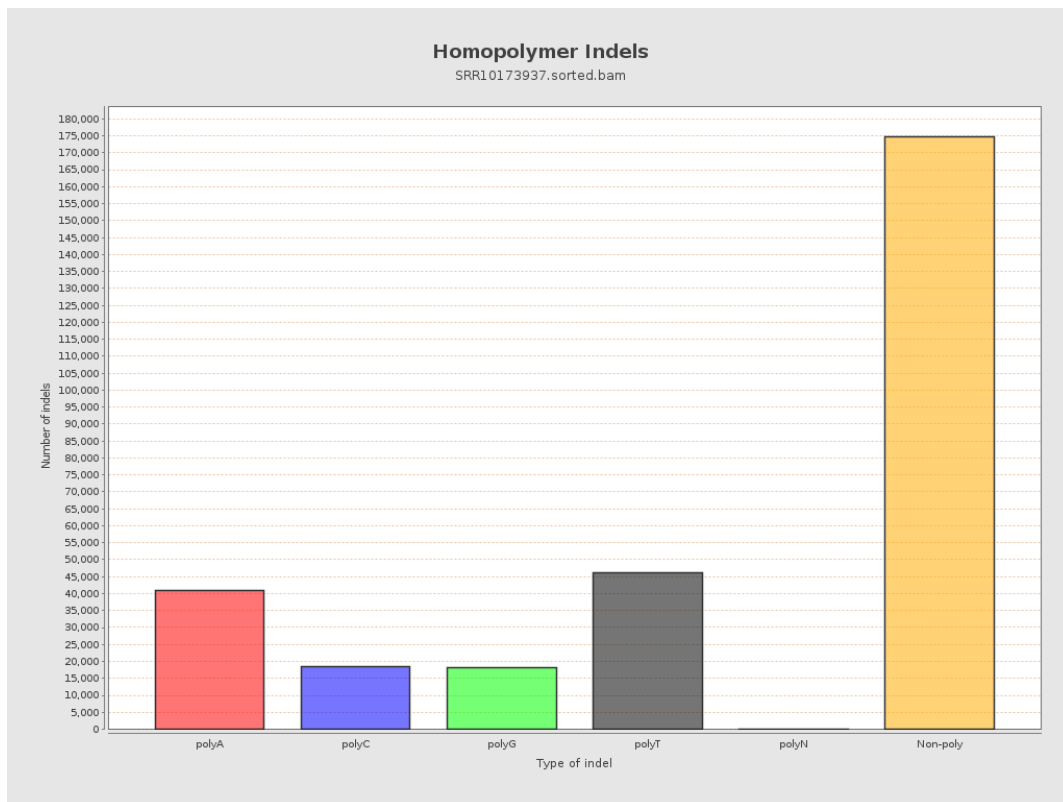
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



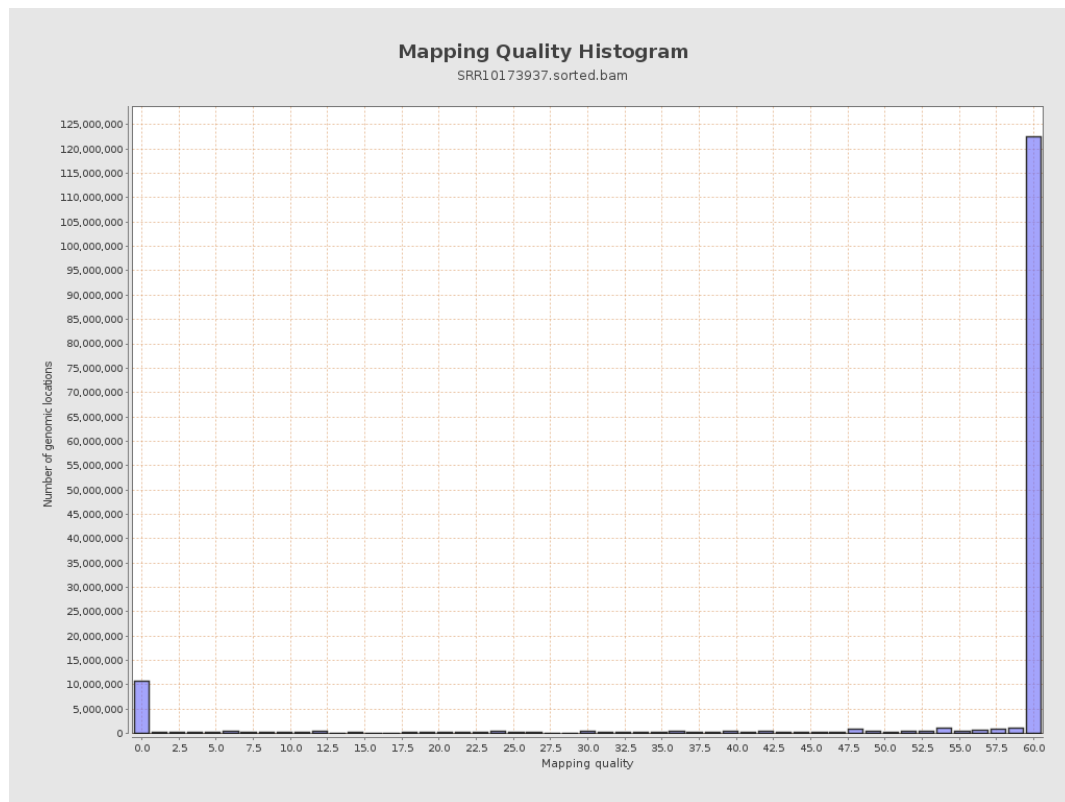
11. Results : Homopolymer Indels



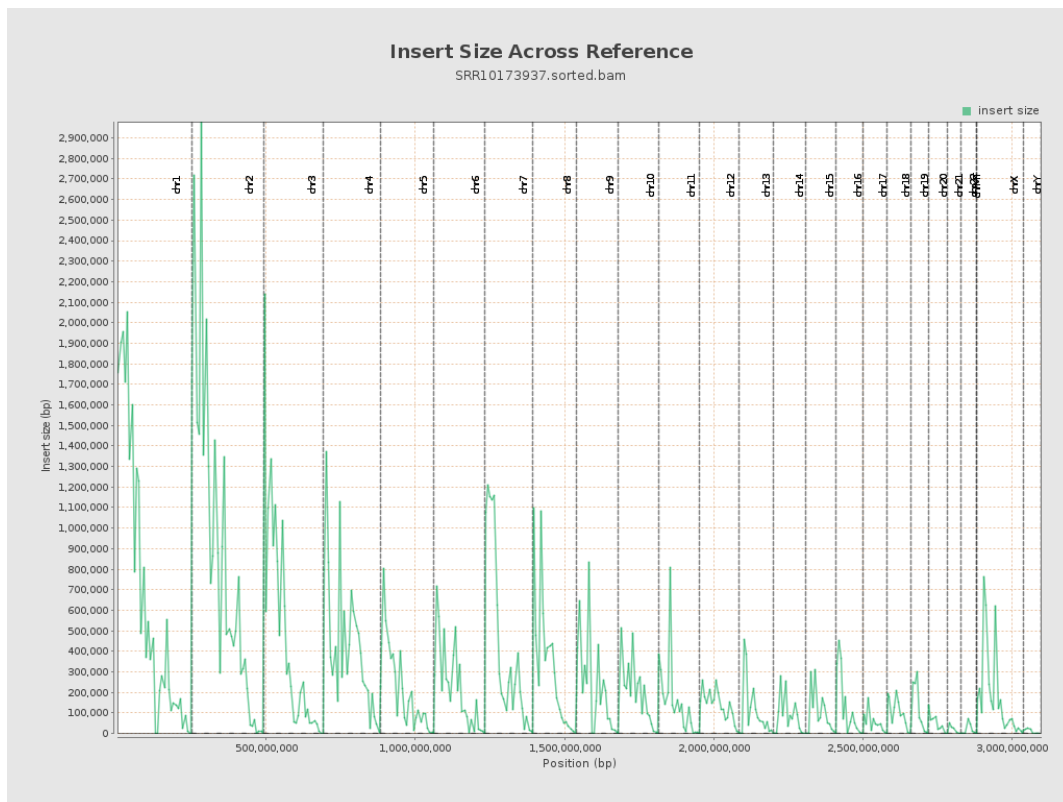
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

