

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:51:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006137.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_SRR1006137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006137_1.fastq.gz SRR1006137_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:51:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,252,404
Mapped reads	17,827,910 / 88.03%
Unmapped reads	2,424,494 / 11.97%
Mapped paired reads	17,827,910 / 88.03%
Mapped reads, first in pair	9,075,576 / 44.81%
Mapped reads, second in pair	8,752,334 / 43.22%
Mapped reads, both in pair	16,269,988 / 80.34%
Mapped reads, singletons	1,557,922 / 7.69%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	2,090,234 / 10.32%
Duplication rate	10.36%
Clipped reads	1,298,795 / 6.41%

2.2. ACGT Content

Number/percentage of A's	187,434,051 / 27.21%
Number/percentage of C's	149,522,783 / 21.7%
Number/percentage of T's	193,563,870 / 28.1%
Number/percentage of G's	158,399,296 / 22.99%
Number/percentage of N's	29,130 / 0%
GC Percentage	44.69%

2.3. Coverage

Mean	0.2226
Standard Deviation	1.1133

2.4. Mapping Quality

Mean Mapping Quality	47.12
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2.5. Insert size

Mean	64,800.32
Standard Deviation	2,484,980.3
P25/Median/P75	81 / 118 / 158

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	3,282,641
Insertions	22,001
Mapped reads with at least one insertion	0.12%
Deletions	59,978
Mapped reads with at least one deletion	0.34%
Homopolymer indels	46.16%

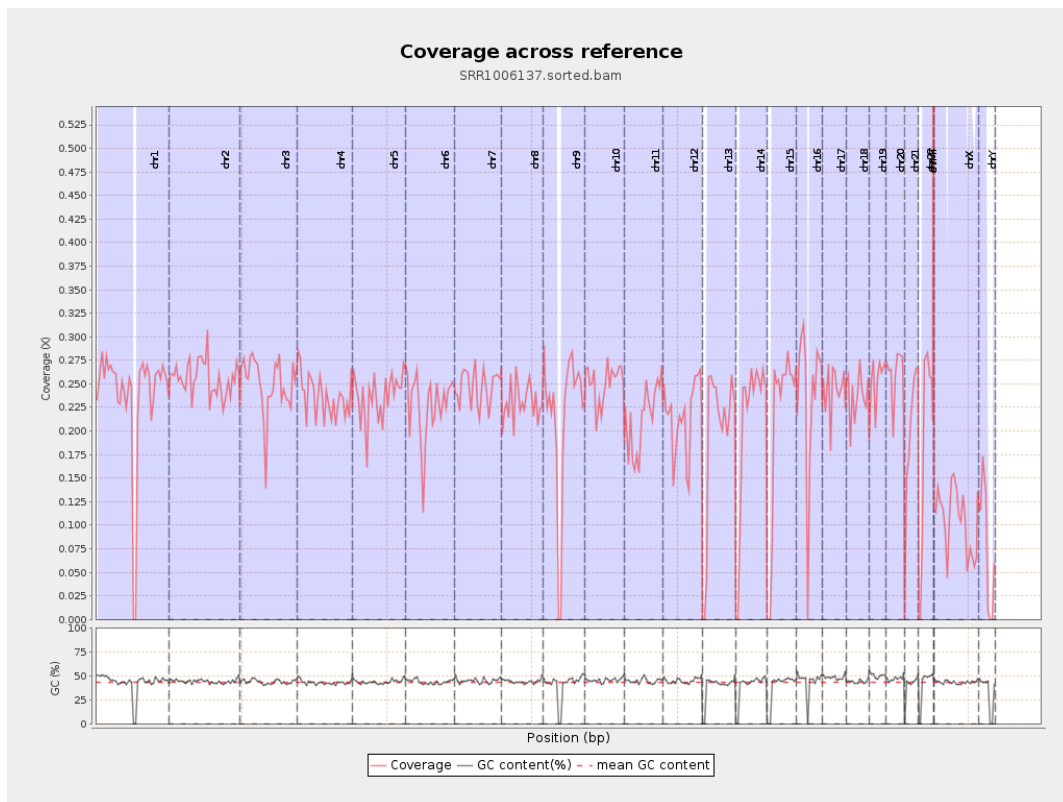
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

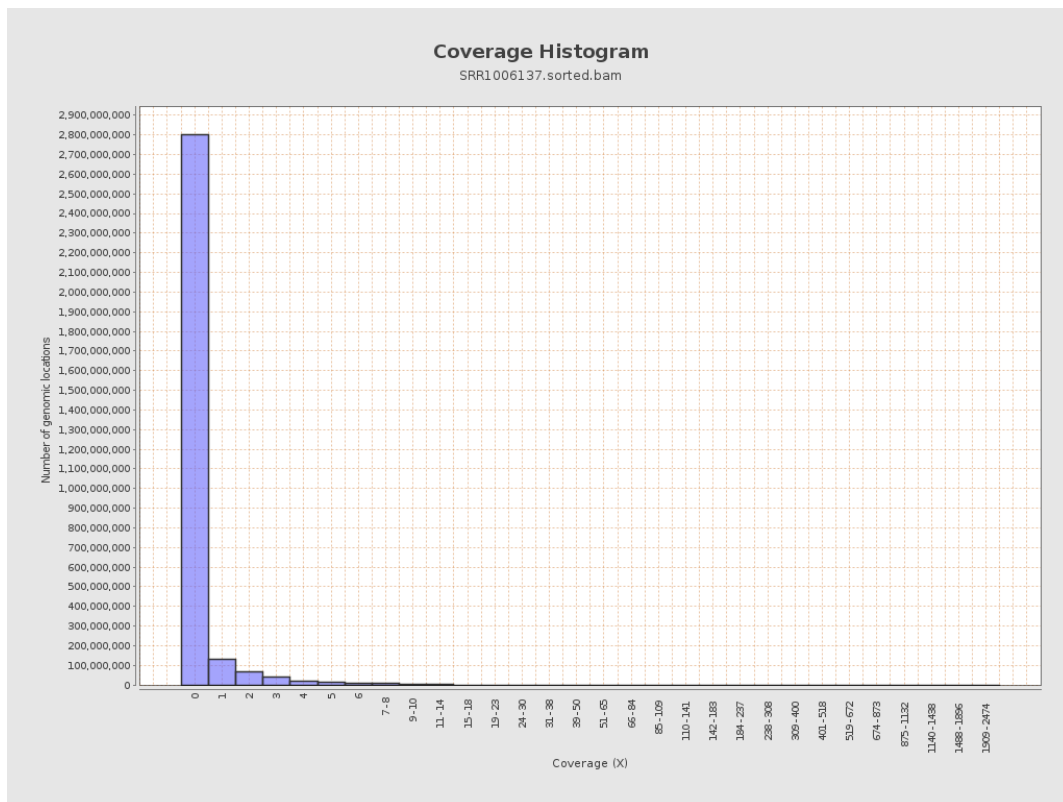
chr1	249250621	59275360	0.2378	1.2706
chr2	243199373	62179634	0.2557	1.2009
chr3	198022430	49358122	0.2493	0.9574
chr4	191154276	45103648	0.236	0.9936
chr5	180915260	42752674	0.2363	0.9321
chr6	171115067	38878232	0.2272	1.0161
chr7	159138663	39244447	0.2466	1.5081
chr8	146364022	33597961	0.2296	1.5667
chr9	141213431	30140397	0.2134	1.0135
chr10	135534747	34083368	0.2515	1.017
chr11	135006516	28877922	0.2139	1.5295
chr12	133851895	28565341	0.2134	0.8871
chr13	115169878	22326243	0.1939	0.8549
chr14	107349540	22200253	0.2068	0.9039
chr15	102531392	21406759	0.2088	0.8978
chr16	90354753	21821953	0.2415	1.0503
chr17	81195210	19809175	0.244	1.0772
chr18	78077248	18573315	0.2379	1.4402
chr19	59128983	14986595	0.2535	1.2463
chr20	63025520	16350886	0.2594	1.0141
chr21	48129895	9494567	0.1973	0.9765
chr22	51304566	9366571	0.1826	0.94
chrMT	16571	22997	1.3878	2.4429
chrX	155270560	16174379	0.1042	0.669

chrY	59373566	4434687	0.0747	0.5763
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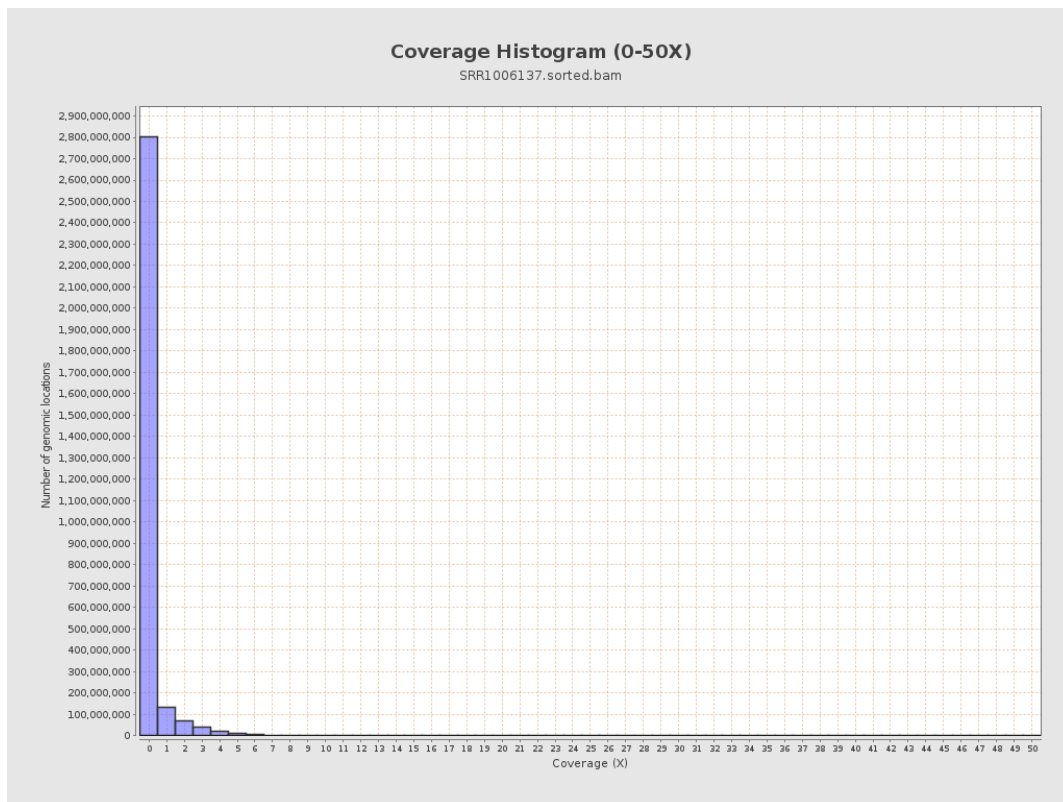
3. Results : Coverage across reference



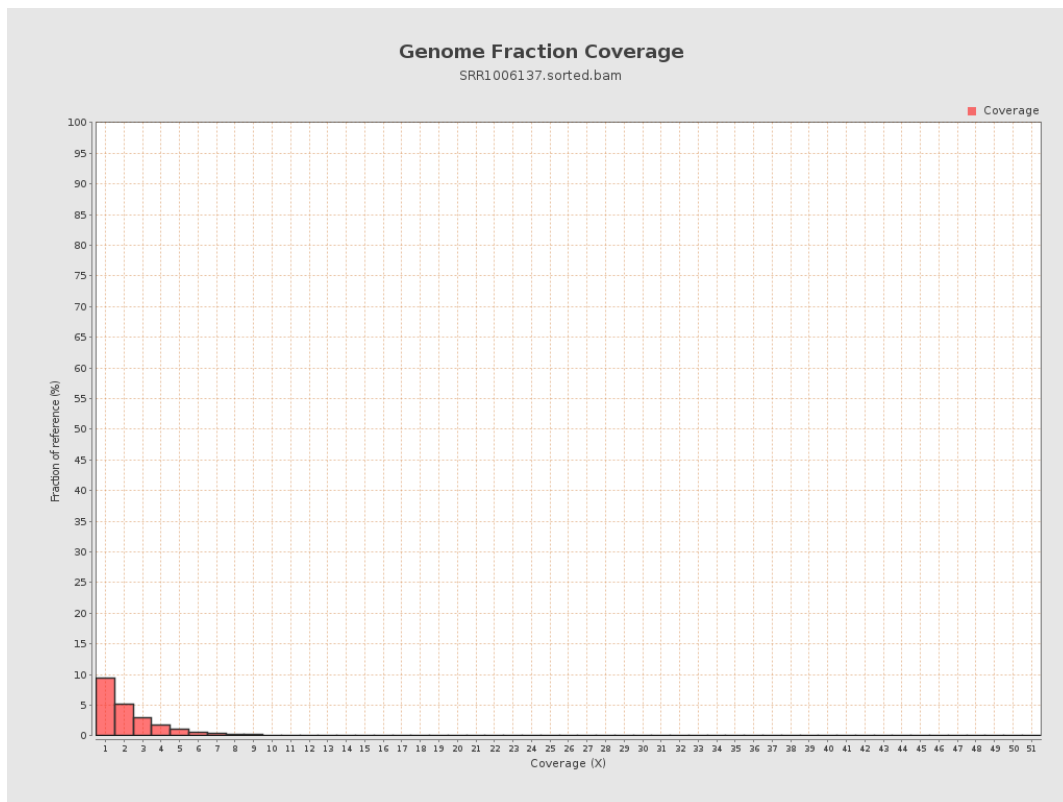
4. Results : Coverage Histogram



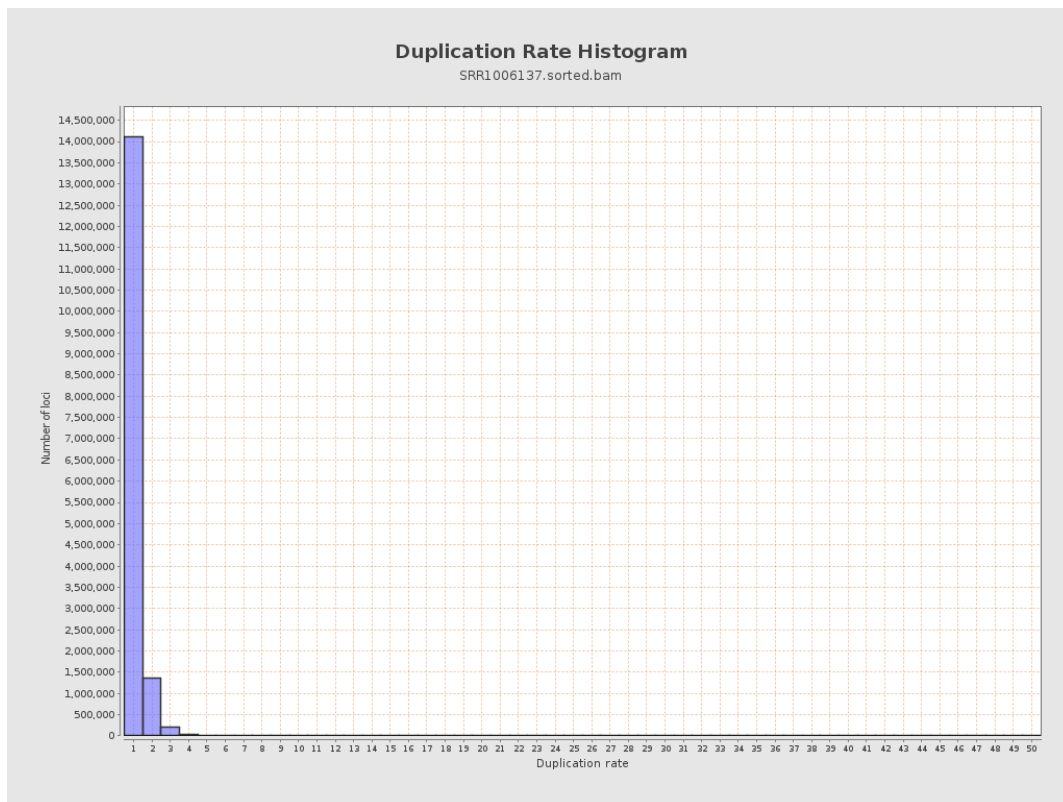
5. Results : Coverage Histogram (0-50X)



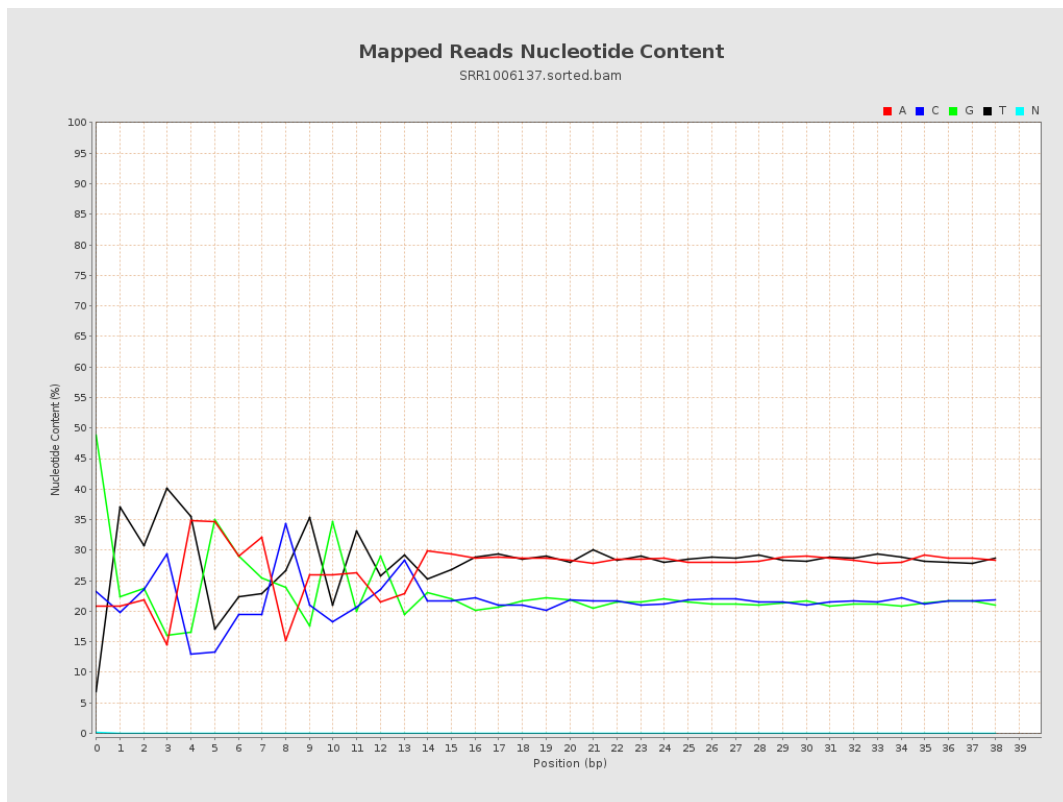
6. Results : Genome Fraction Coverage



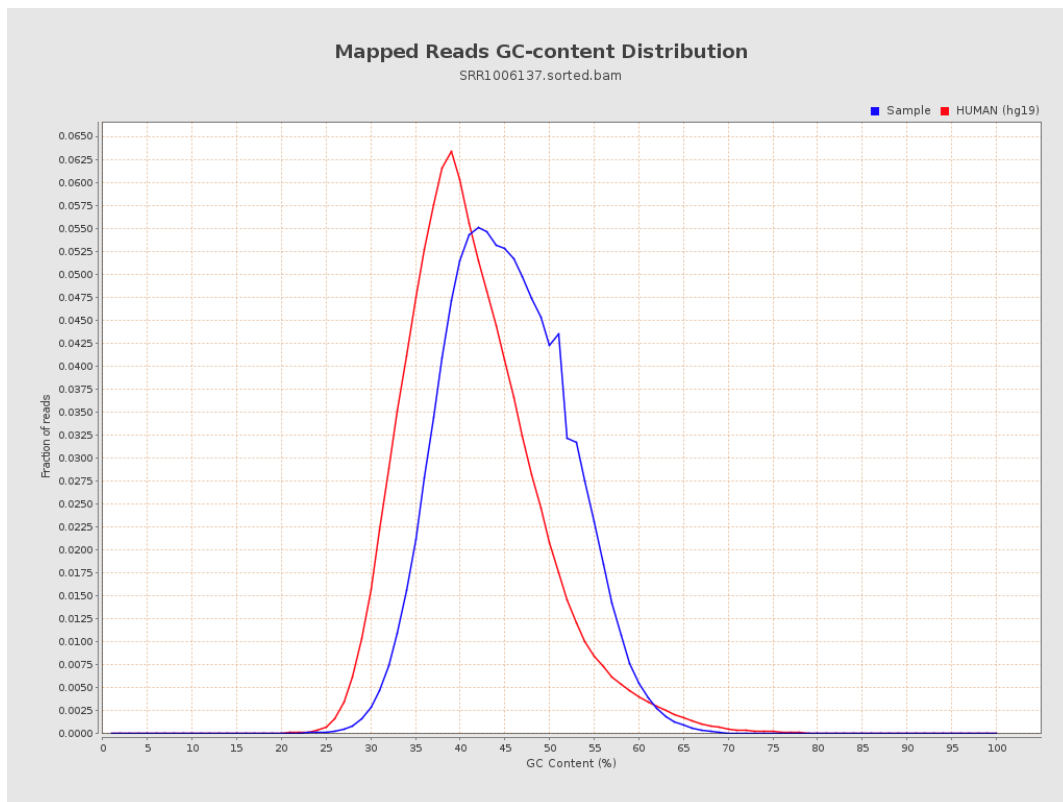
7. Results : Duplication Rate Histogram



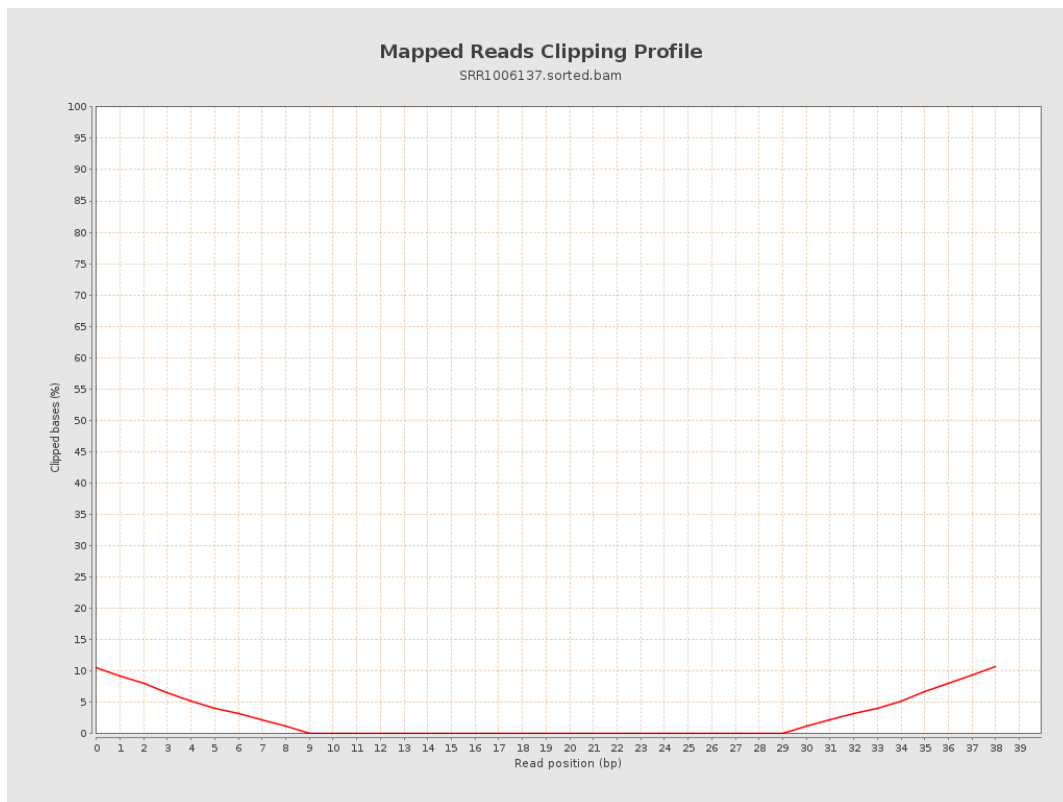
8. Results : Mapped Reads Nucleotide Content



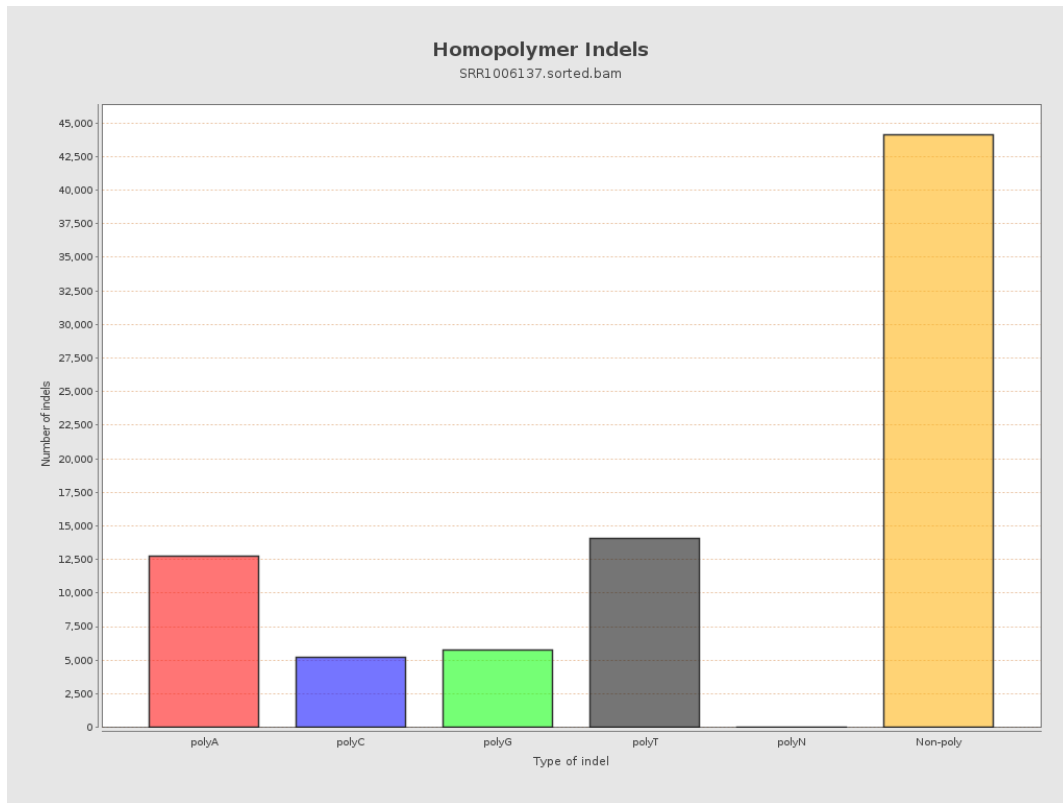
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



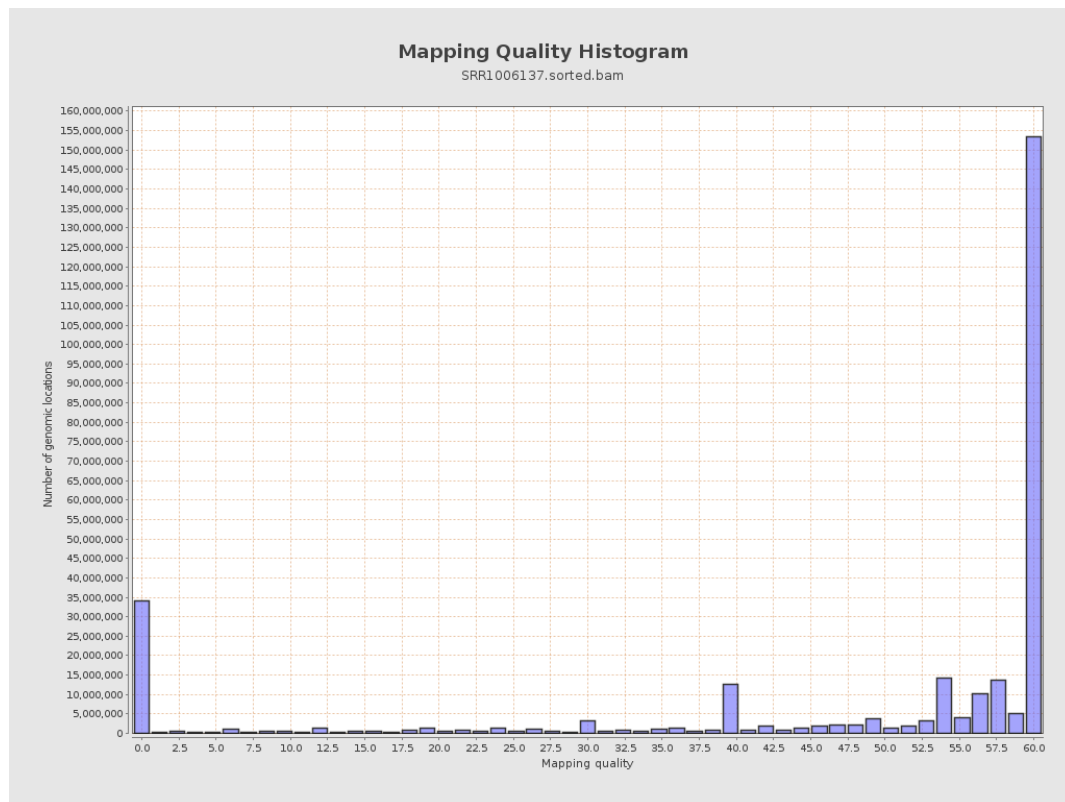
11. Results : Homopolymer Indels



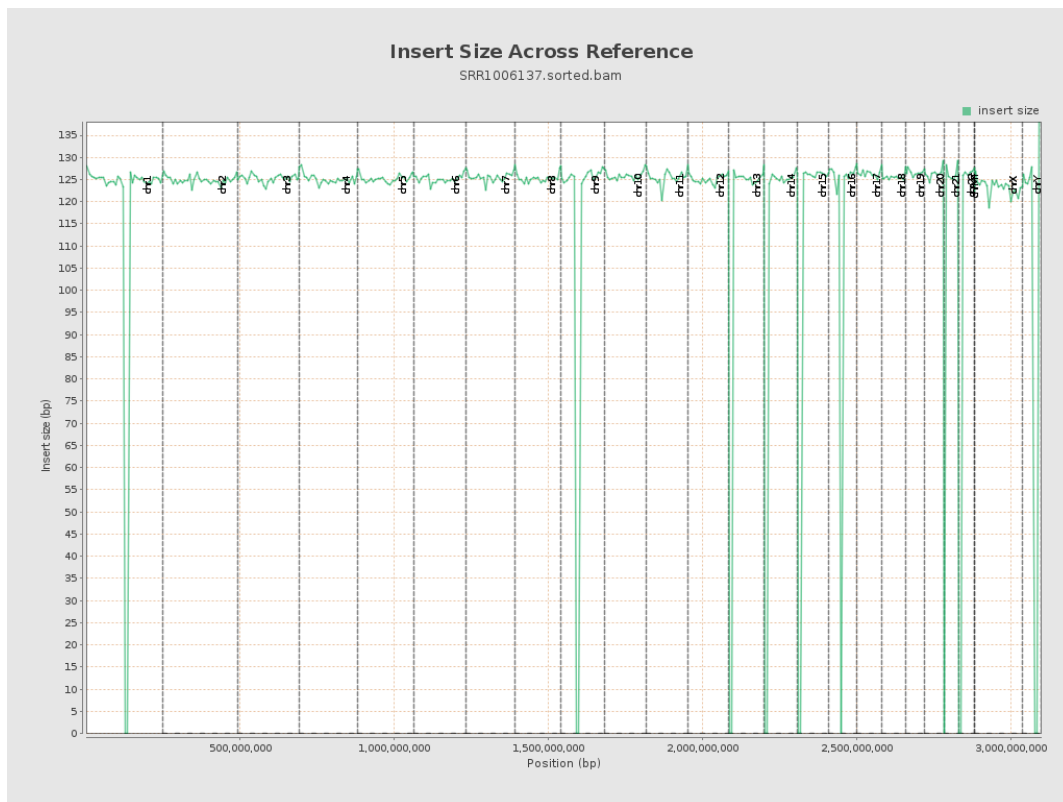
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

