

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 15:29:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354867.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_SRR22354867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354867_1.fastq.gz SRR22354867_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 15:29:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,485,170
Mapped reads	20,168,237 / 98.45%
Unmapped reads	316,933 / 1.55%
Mapped paired reads	20,168,237 / 98.45%
Mapped reads, first in pair	10,092,610 / 49.27%
Mapped reads, second in pair	10,075,627 / 49.18%
Mapped reads, both in pair	20,129,266 / 98.26%
Mapped reads, singletons	38,971 / 0.19%
Secondary alignments	0
Supplementary alignments	781,469 / 3.81%
Read min/max/mean length	30 / 150 / 151.38
Duplicated reads (estimated)	10,961,229 / 53.51%
Duplication rate	54.23%
Clipped reads	9,279,740 / 45.3%

2.2. ACGT Content

Number/percentage of A's	722,219,840 / 28.03%
Number/percentage of C's	544,553,036 / 21.13%
Number/percentage of T's	731,752,804 / 28.39%
Number/percentage of G's	578,484,240 / 22.45%
Number/percentage of N's	41,736 / 0%

GC Percentage	43.58%
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2.3. Coverage

Mean	0.8329
Standard Deviation	37.0562

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	339,899.11
Standard Deviation	6,712,907.26
P25/Median/P75	111 / 179 / 272

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	15,134,947
Insertions	427,663
Mapped reads with at least one insertion	1.98%
Deletions	452,821
Mapped reads with at least one deletion	2.14%
Homopolymer indels	45.03%

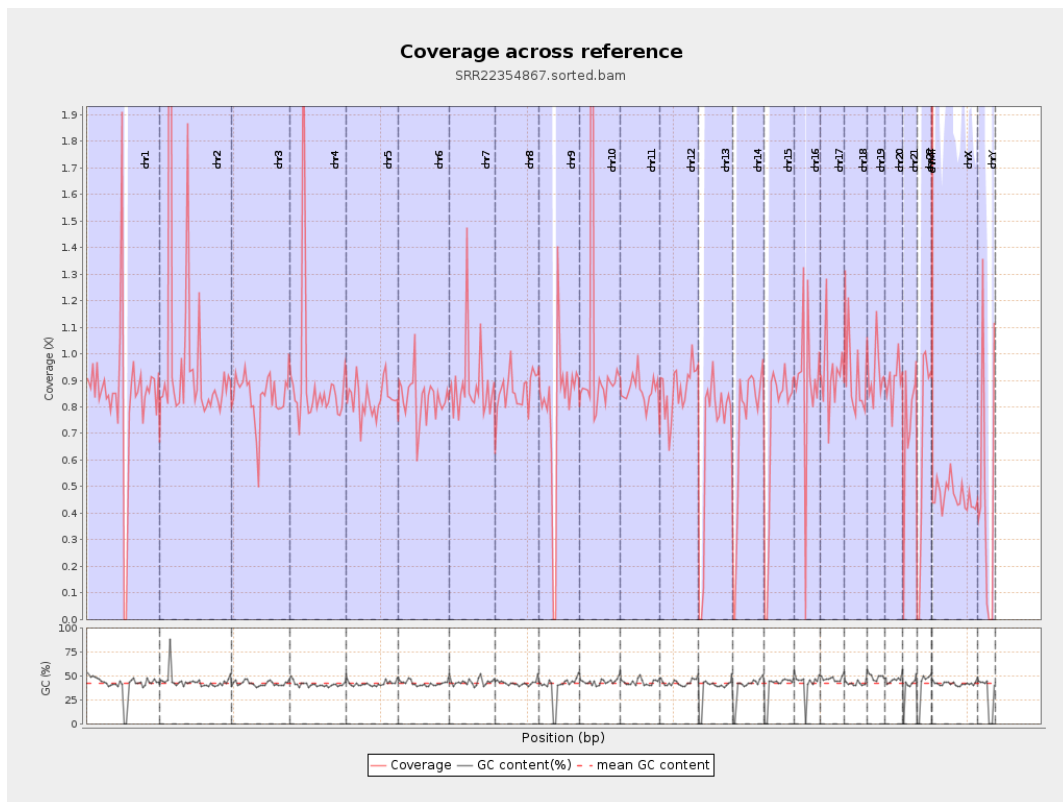
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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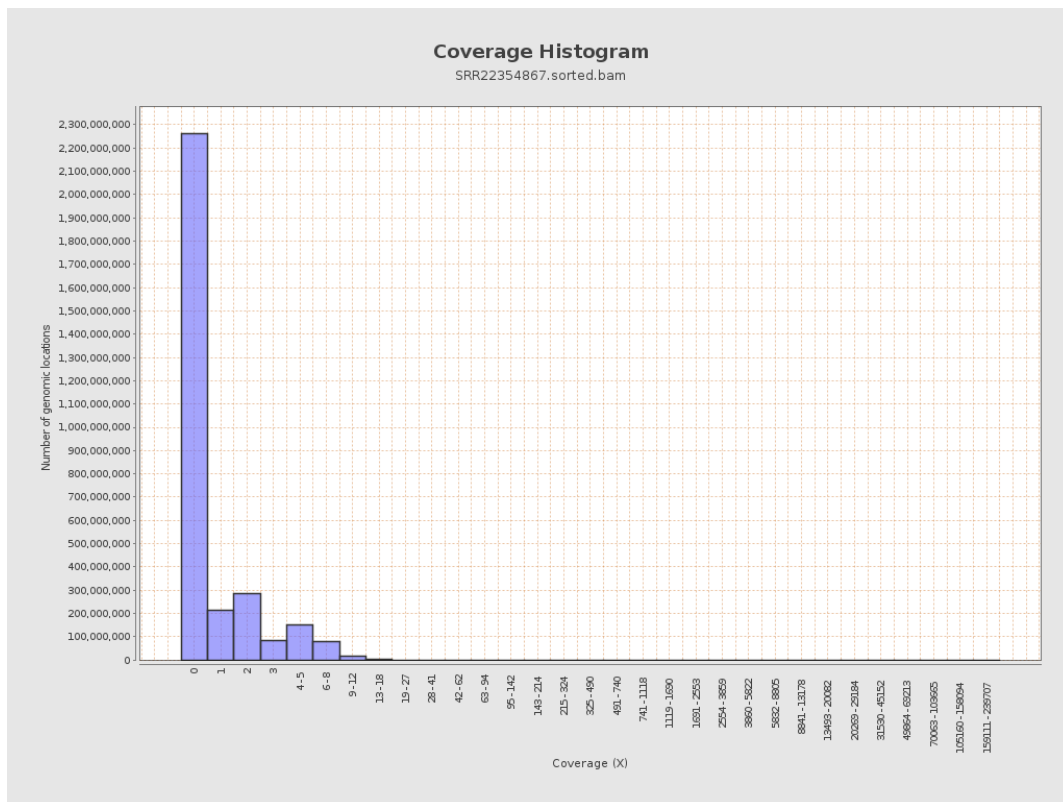
		bases	coverage	deviation
chr1	249250621	210734713	0.8455	23.6726
chr2	243199373	247306064	1.0169	125.0649
chr3	198022430	166283117	0.8397	2.0525
chr4	191154276	170342029	0.8911	10.9959
chr5	180915260	149667961	0.8273	1.8309
chr6	171115067	142653145	0.8337	3.3481
chr7	159138663	140488802	0.8828	28.5118
chr8	146364022	127083839	0.8683	6.2387
chr9	141213431	111328930	0.7884	13.2624
chr10	135534747	139658863	1.0304	23.9915
chr11	135006516	117121306	0.8675	4.7737
chr12	133851895	115933584	0.8661	1.8599
chr13	115169878	78605079	0.6825	1.6085
chr14	107349540	77700661	0.7238	3.1712
chr15	102531392	72752721	0.7096	1.6483
chr16	90354753	80616068	0.8922	4.8608
chr17	81195210	74825519	0.9216	5.2411
chr18	78077248	70814919	0.907	10.9328
chr19	59128983	54723280	0.9255	12.4881
chr20	63025520	56454113	0.8957	3.7007
chr21	48129895	35698723	0.7417	5.7617
chr22	51304566	34565202	0.6737	2.8951
chrMT	16571	2902910	175.1801	36.1544
chrX	155270560	71572146	0.461	2.0283

chrY	59373566	28488879	0.4798	13.3994
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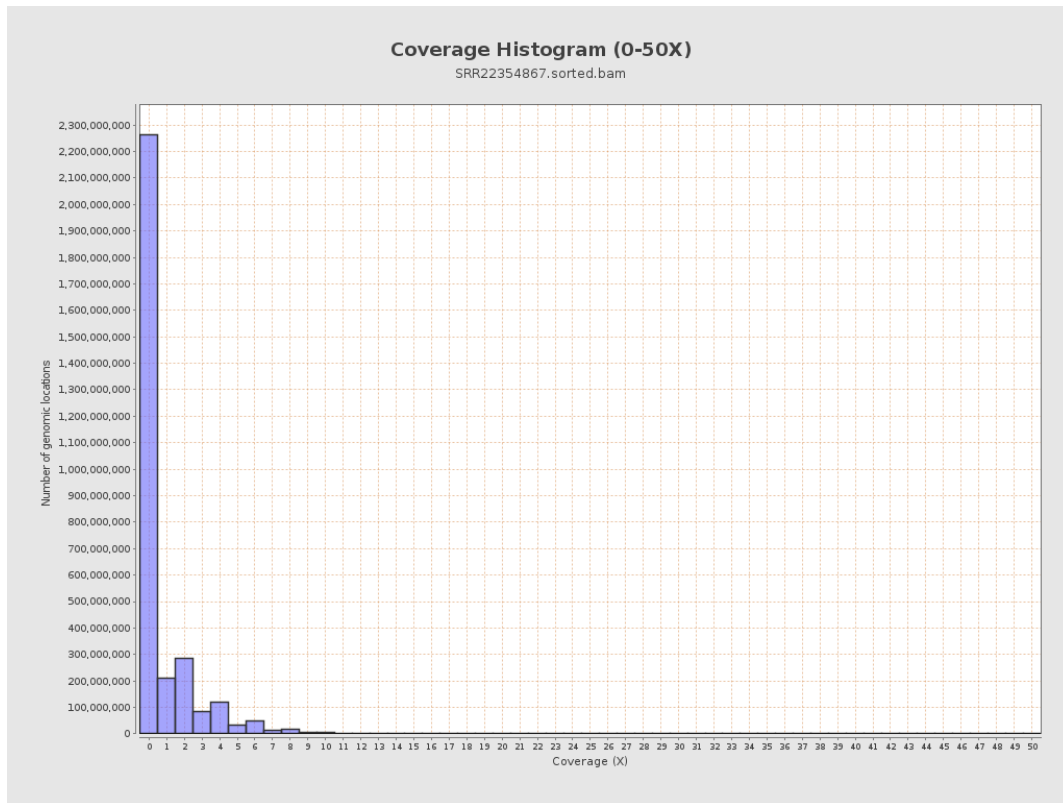
3. Results : Coverage across reference



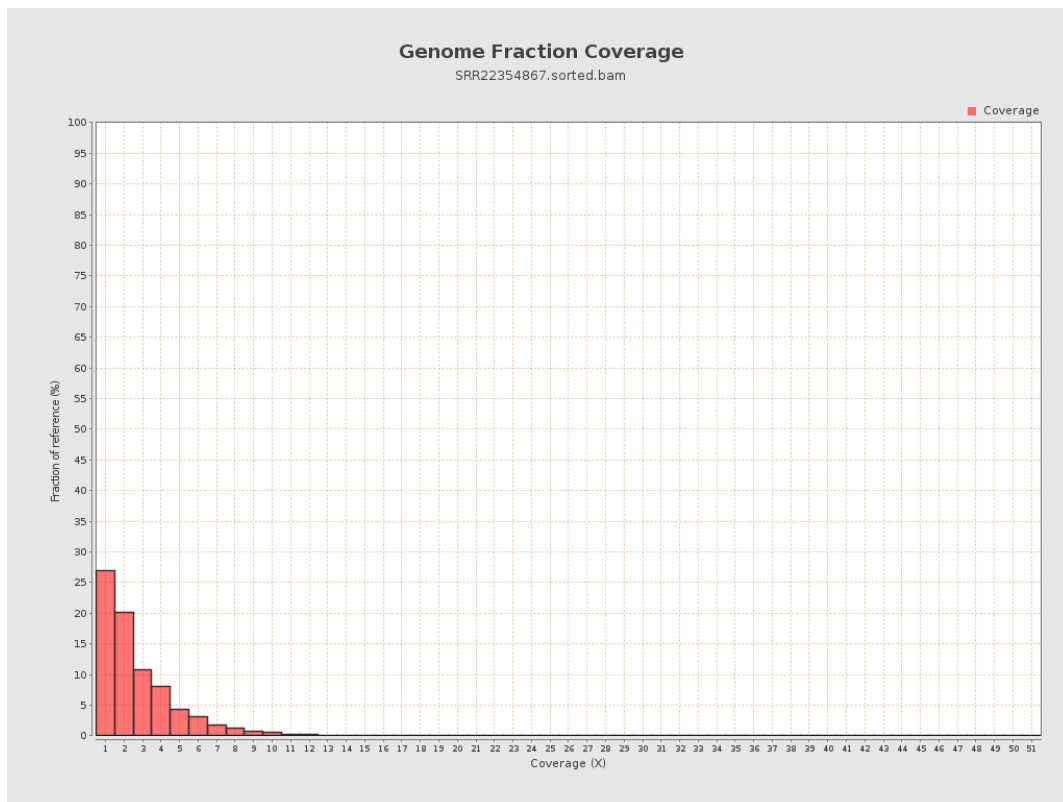
4. Results : Coverage Histogram



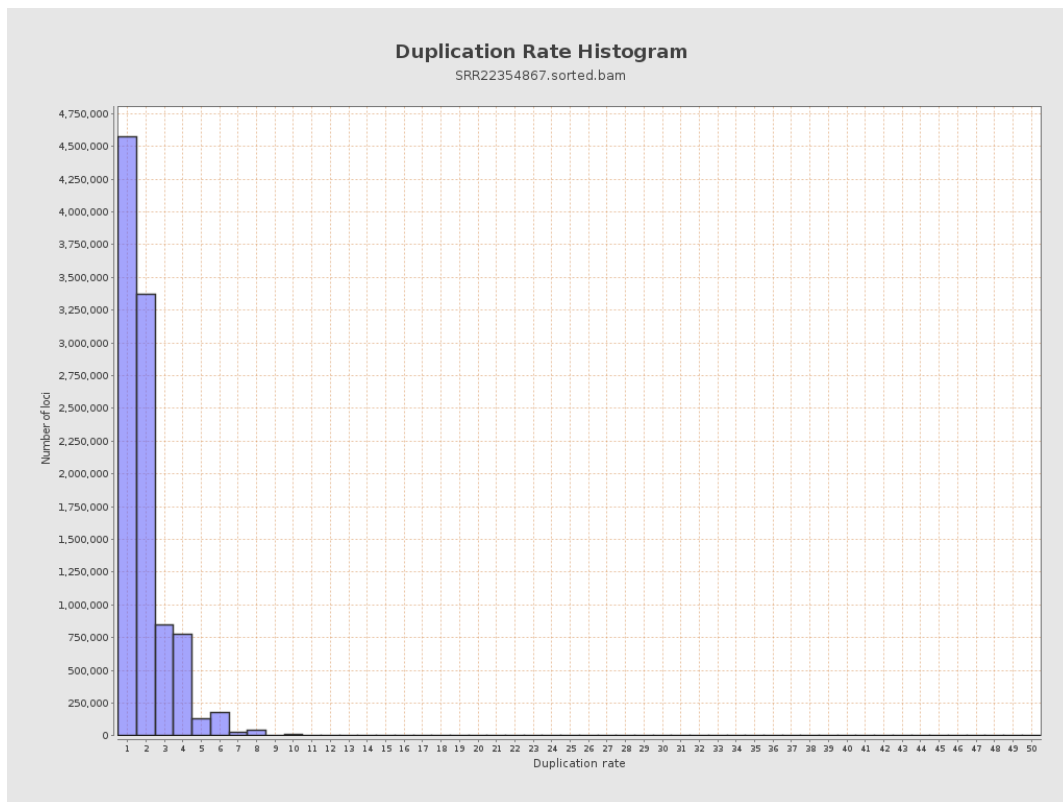
5. Results : Coverage Histogram (0-50X)



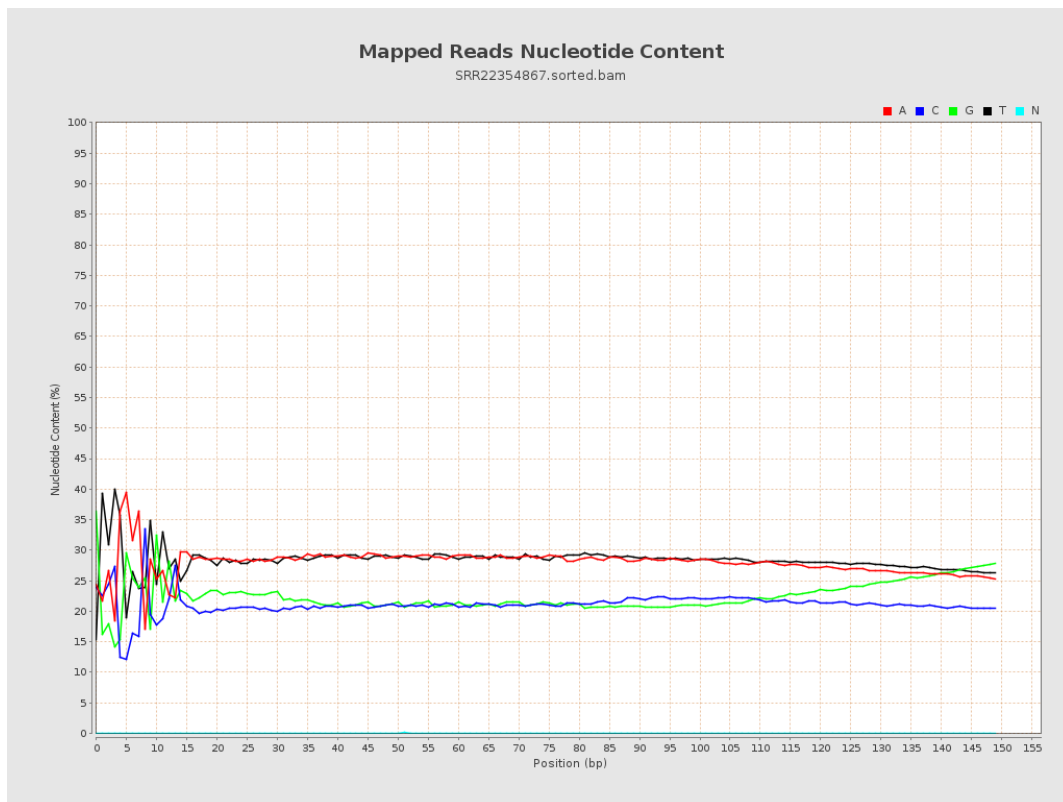
6. Results : Genome Fraction Coverage



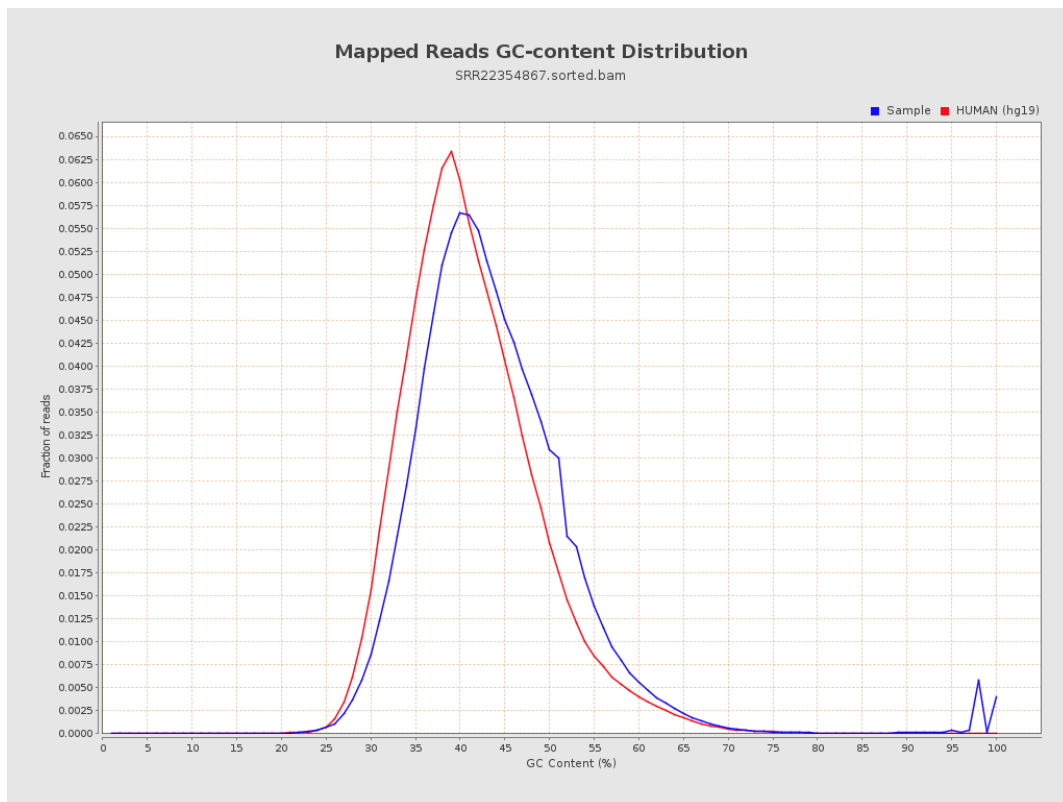
7. Results : Duplication Rate Histogram



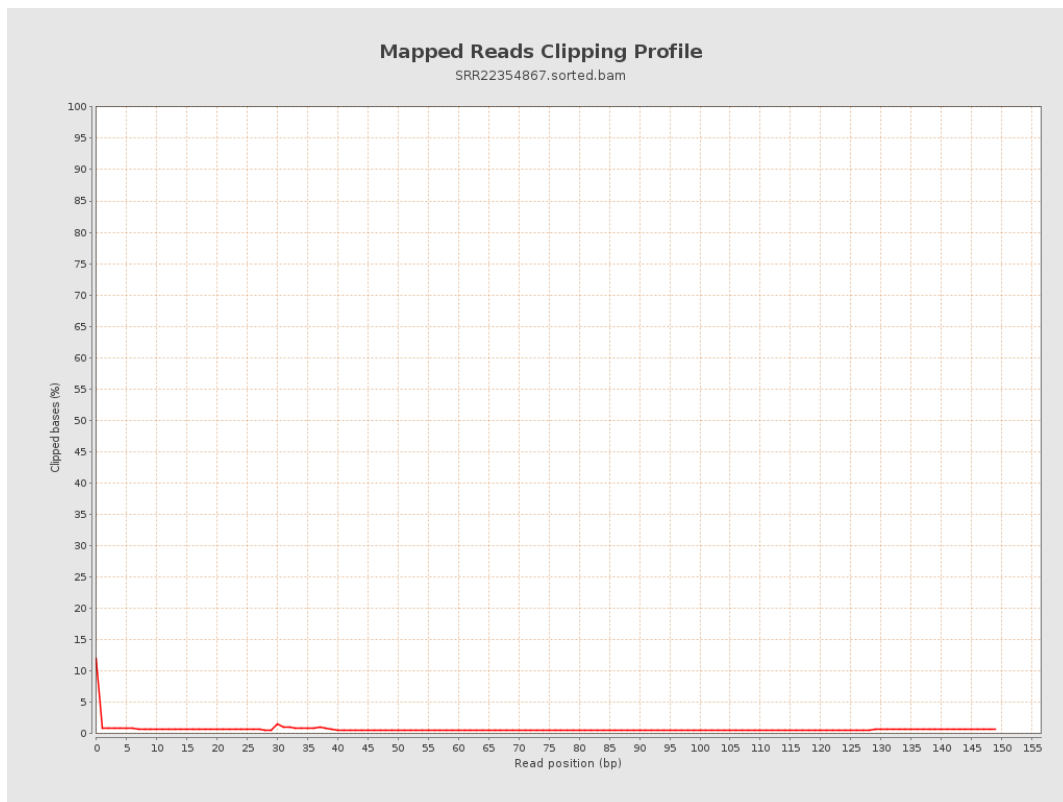
8. Results : Mapped Reads Nucleotide Content



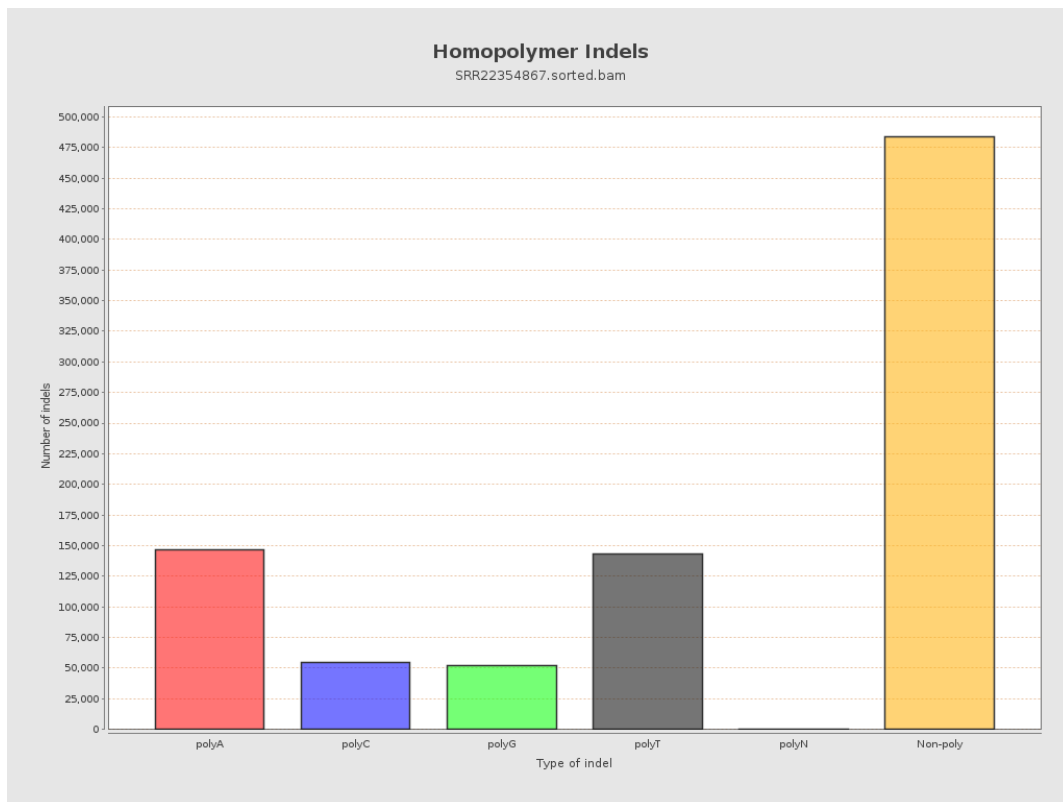
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



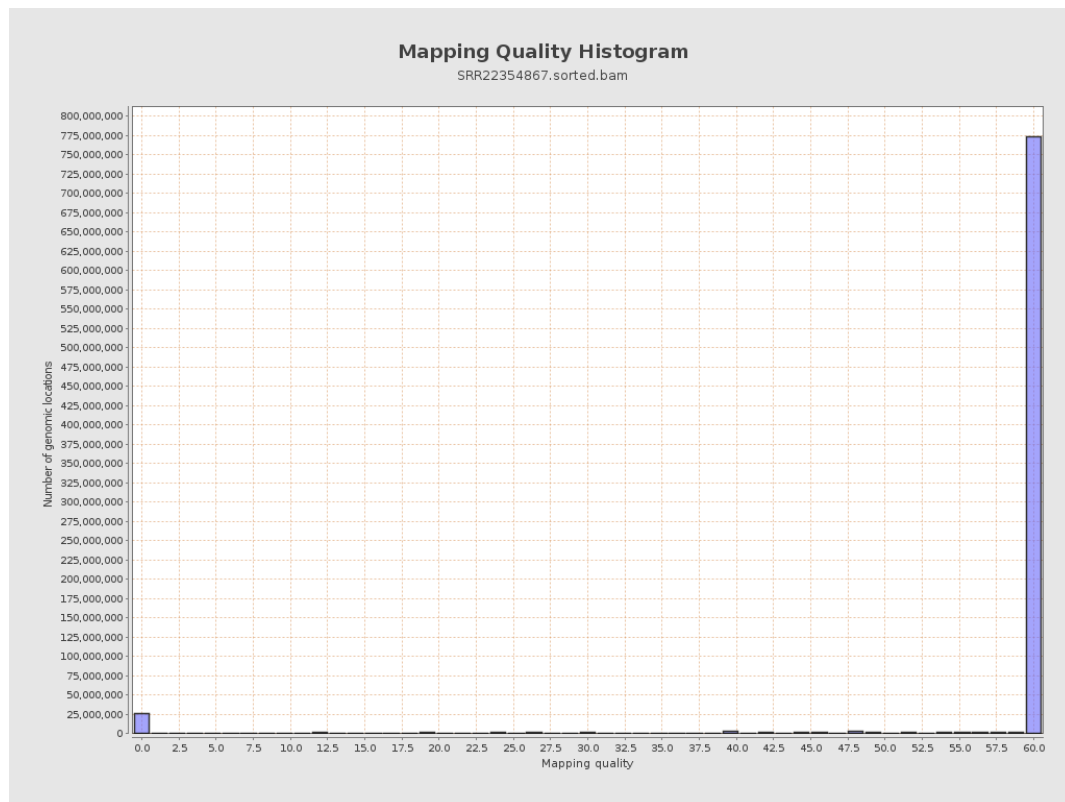
11. Results : Homopolymer Indels



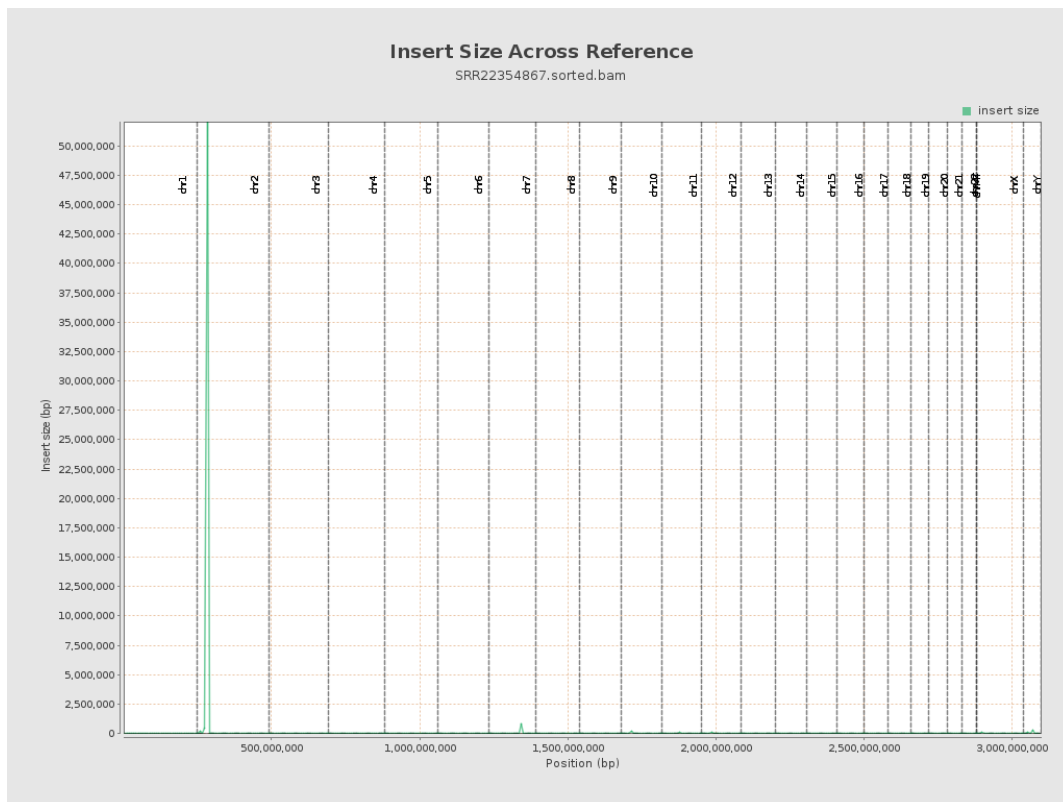
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

