

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 06:33:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617668.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_SRR8617668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617668_1.fastq.gz SRR8617668_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 06:33:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,425,380
Mapped reads	10,337,446 / 99.16%
Unmapped reads	87,934 / 0.84%
Mapped paired reads	10,337,446 / 99.16%
Mapped reads, first in pair	5,169,959 / 49.59%
Mapped reads, second in pair	5,167,487 / 49.57%
Mapped reads, both in pair	10,309,940 / 98.89%
Mapped reads, singletons	27,506 / 0.26%
Secondary alignments	0
Supplementary alignments	79,437 / 0.76%
Read min/max/mean length	30 / 101 / 101.32
Duplicated reads (estimated)	423,811 / 4.07%
Duplication rate	1.52%
Clipped reads	5,416,354 / 51.95%

2.2. ACGT Content

Number/percentage of A's	291,433,224 / 28.98%
Number/percentage of C's	211,151,351 / 21%
Number/percentage of T's	286,097,998 / 28.45%
Number/percentage of G's	216,852,104 / 21.56%
Number/percentage of N's	68,048 / 0.01%

GC Percentage	42.56%
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2.3. Coverage

Mean	0.325
Standard Deviation	3.5297

2.4. Mapping Quality

Mean Mapping Quality	53.34
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2.5. Insert size

Mean	141,510.67
Standard Deviation	3,521,190.76
P25/Median/P75	154 / 189 / 240

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	4,450,080
Insertions	149,150
Mapped reads with at least one insertion	1.41%
Deletions	144,385
Mapped reads with at least one deletion	1.36%
Homopolymer indels	39.66%

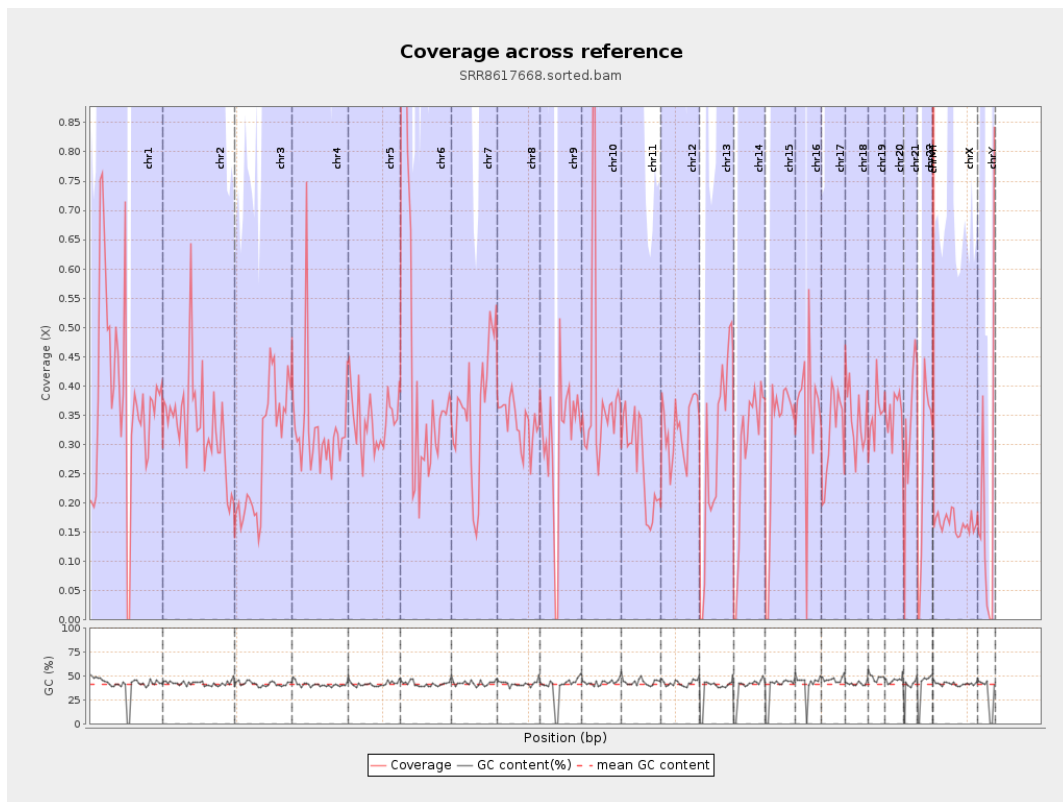
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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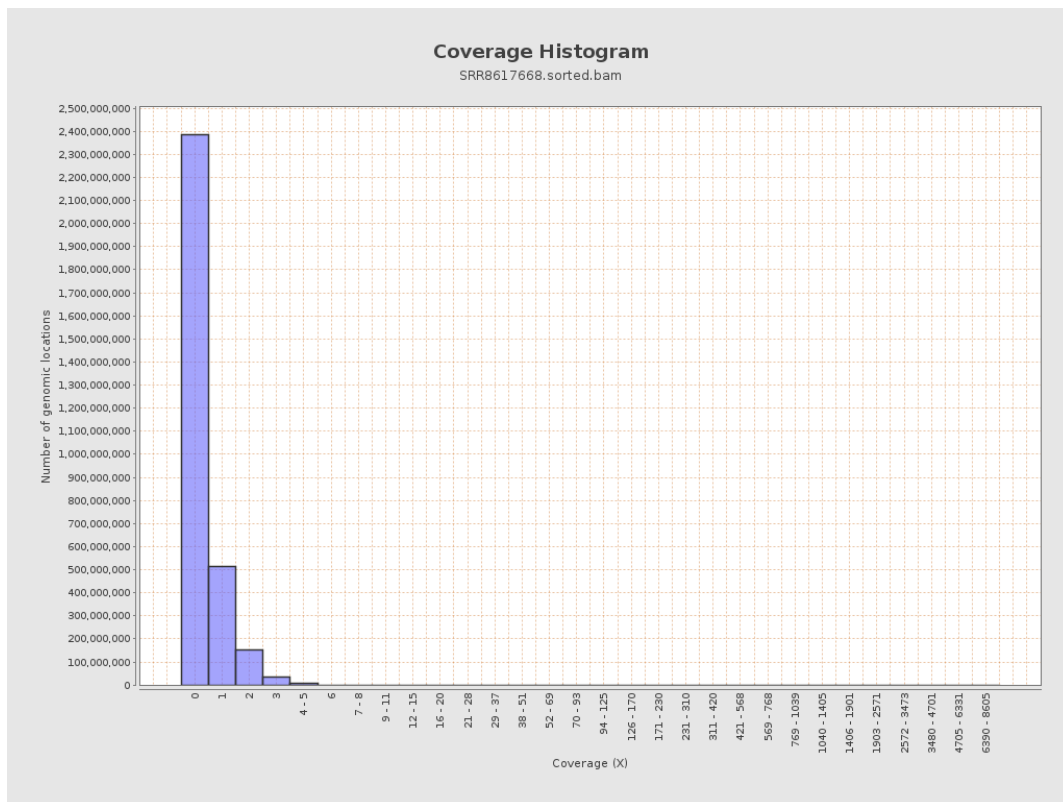
		bases	coverage	deviation
chr1	249250621	95251398	0.3822	8.619
chr2	243199373	80795279	0.3322	2.2161
chr3	198022430	56392014	0.2848	0.8053
chr4	191154276	62201259	0.3254	3.1582
chr5	180915260	61898352	0.3421	0.6941
chr6	171115067	74559777	0.4357	1.3724
chr7	159138663	57651943	0.3623	2.6828
chr8	146364022	49174050	0.336	3.5407
chr9	141213431	43482571	0.3079	3.7359
chr10	135534747	52352016	0.3863	6.9978
chr11	135006516	35505773	0.263	1.4282
chr12	133851895	44352866	0.3314	0.6842
chr13	115169878	33670249	0.2924	0.6457
chr14	107349540	31011115	0.2889	0.6836
chr15	102531392	31214083	0.3044	0.6448
chr16	90354753	32161045	0.3559	1.9575
chr17	81195210	25590071	0.3152	1.0005
chr18	78077248	26877247	0.3442	3.4489
chr19	59128983	20830488	0.3523	4.3015
chr20	63025520	22094856	0.3506	1.037
chr21	48129895	16279191	0.3382	2.2709
chr22	51304566	13617734	0.2654	2.3368
chrMT	16571	1118276	67.4839	24.18
chrX	155270560	25551222	0.1646	0.7896

chrY	59373566	12313044	0.2074	4.3211
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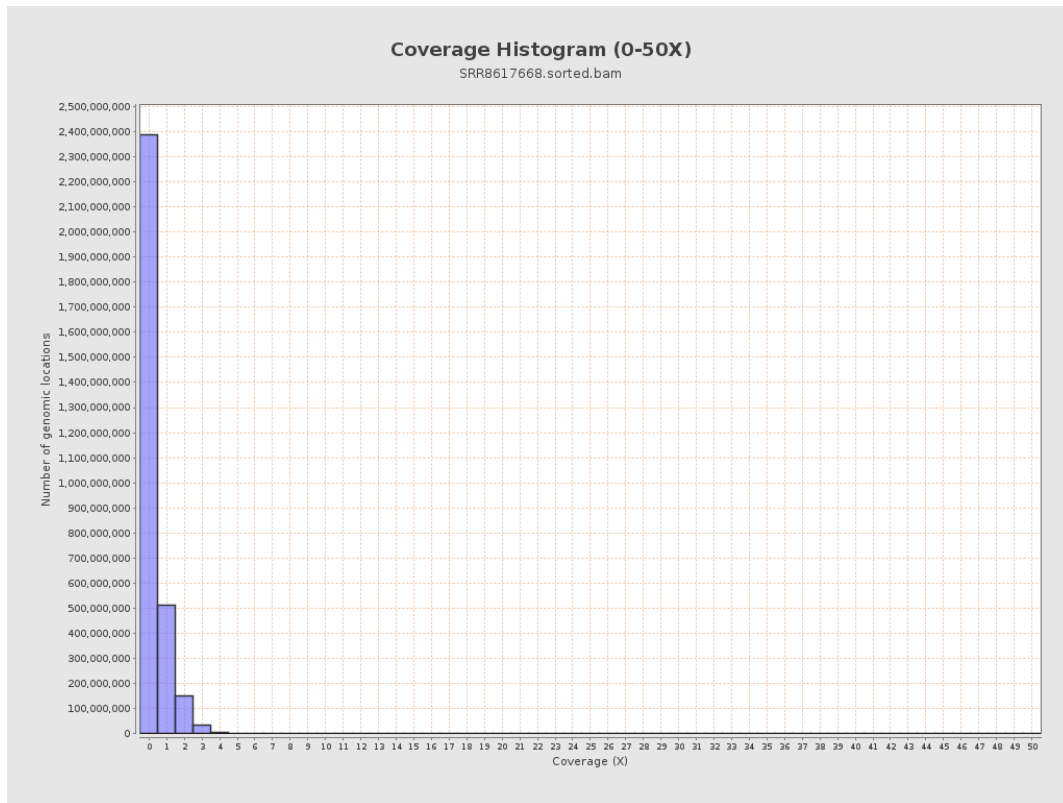
3. Results : Coverage across reference



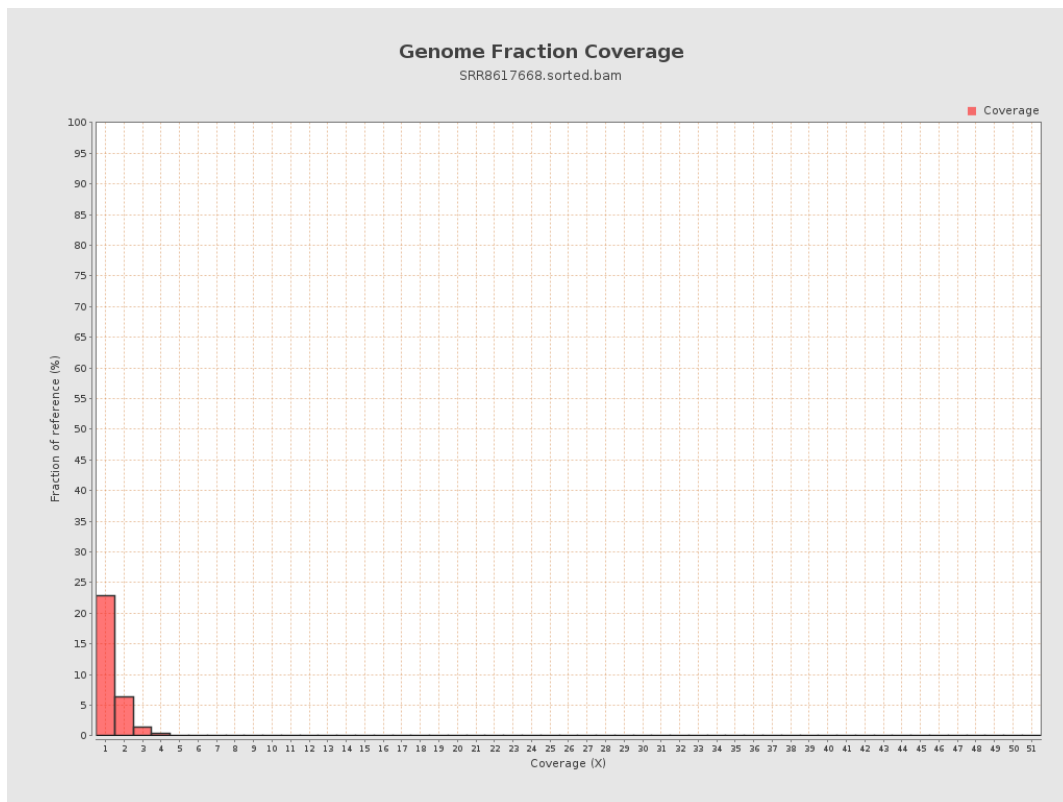
4. Results : Coverage Histogram



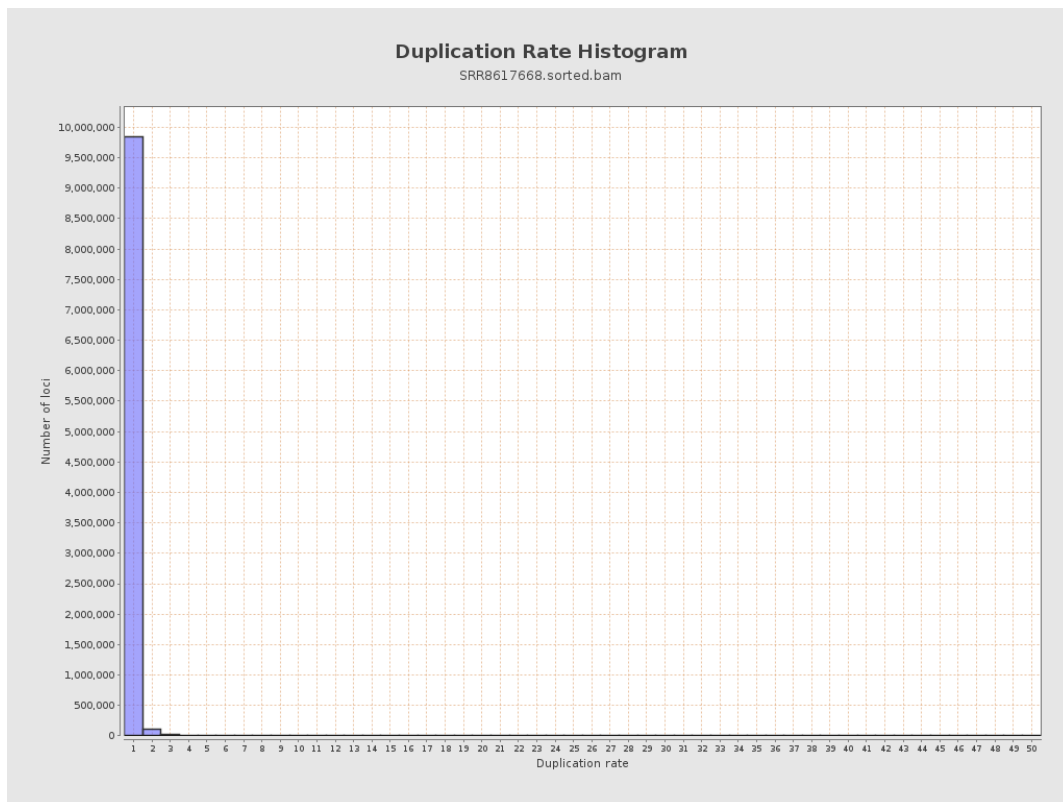
5. Results : Coverage Histogram (0-50X)



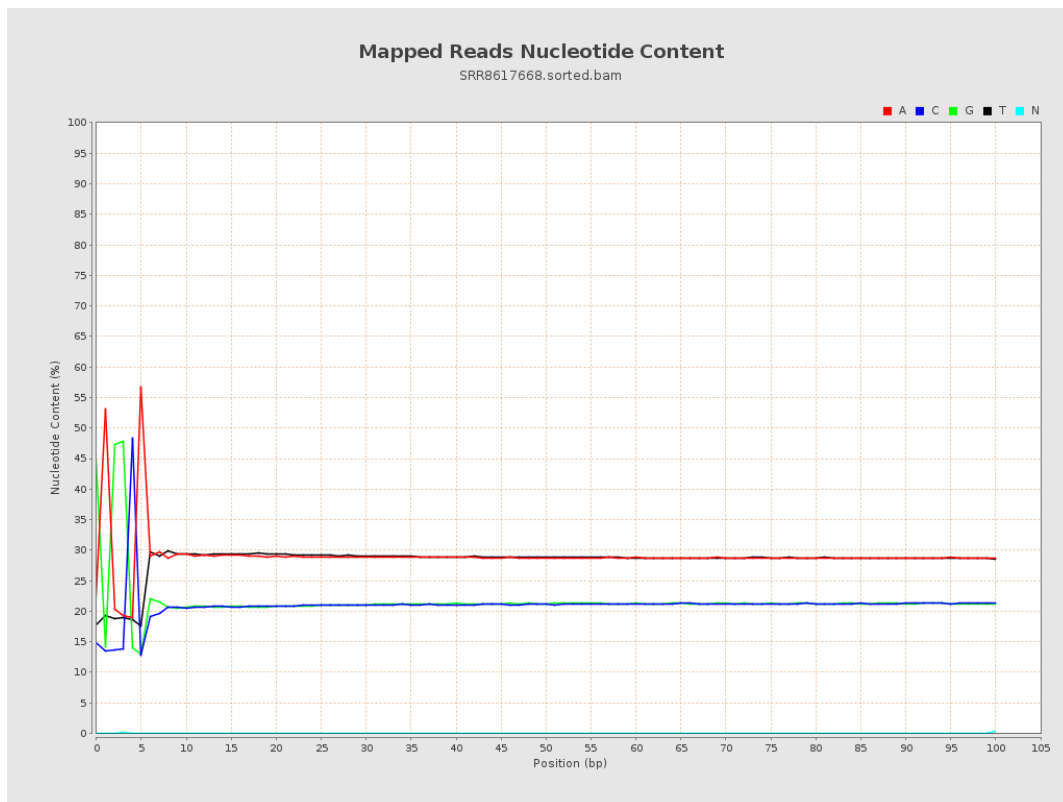
6. Results : Genome Fraction Coverage



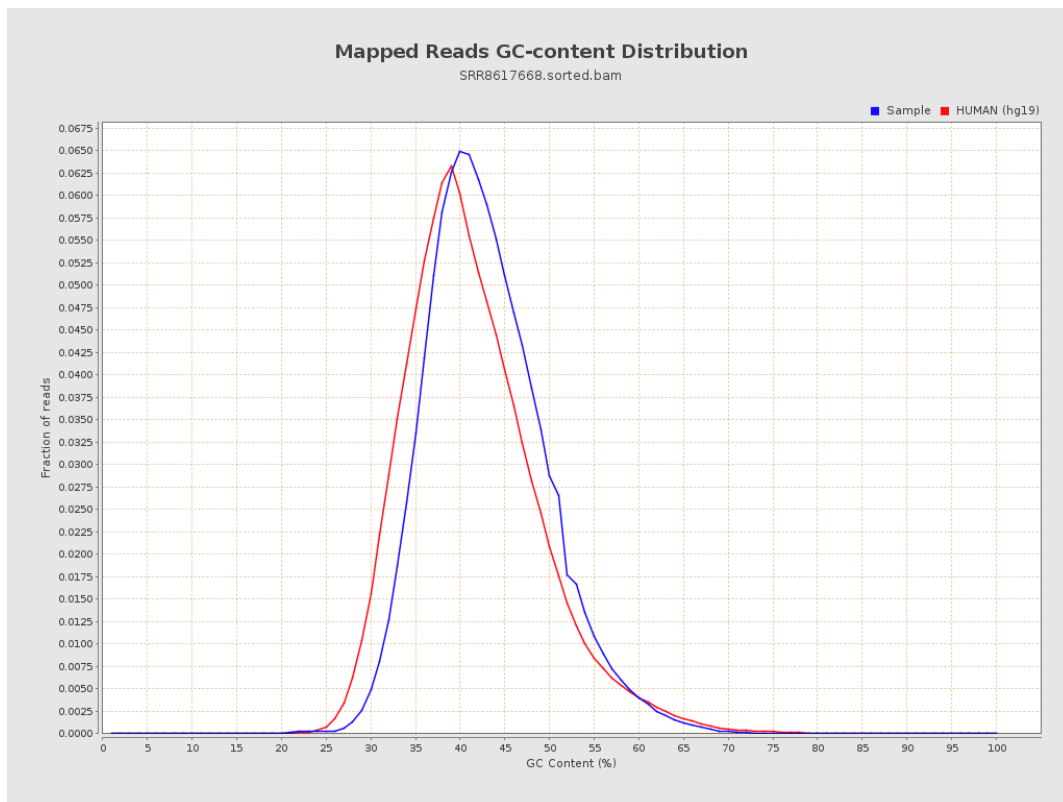
7. Results : Duplication Rate Histogram



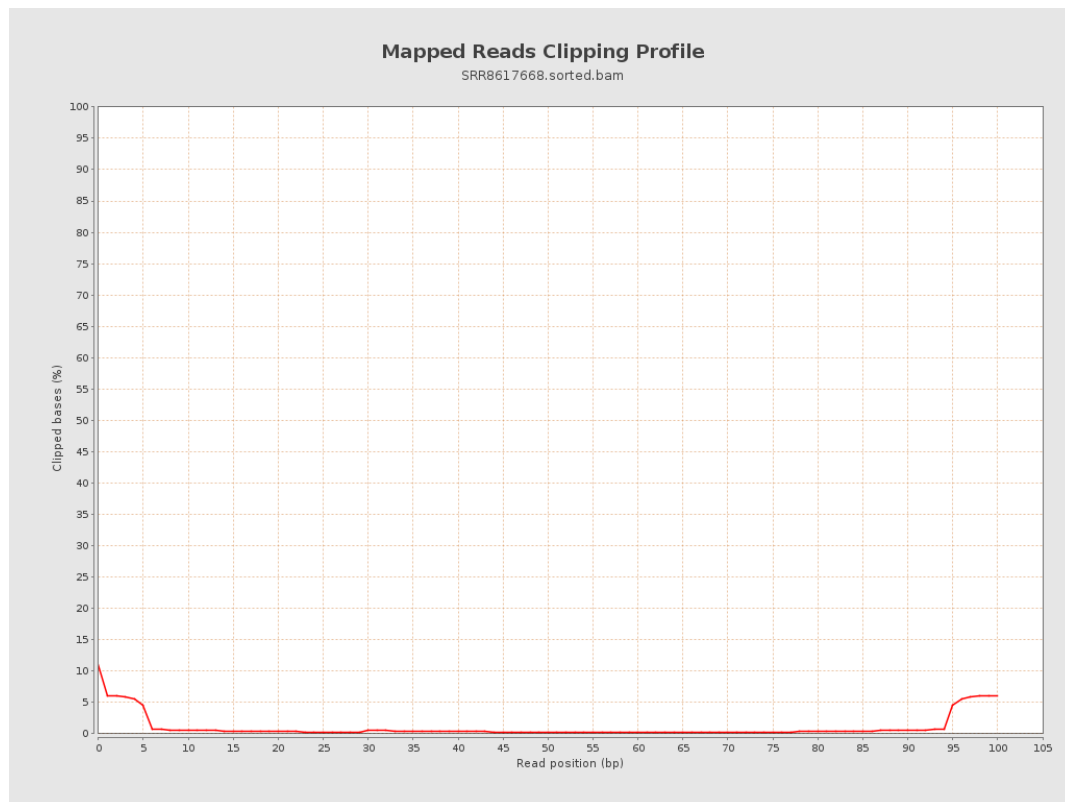
8. Results : Mapped Reads Nucleotide Content



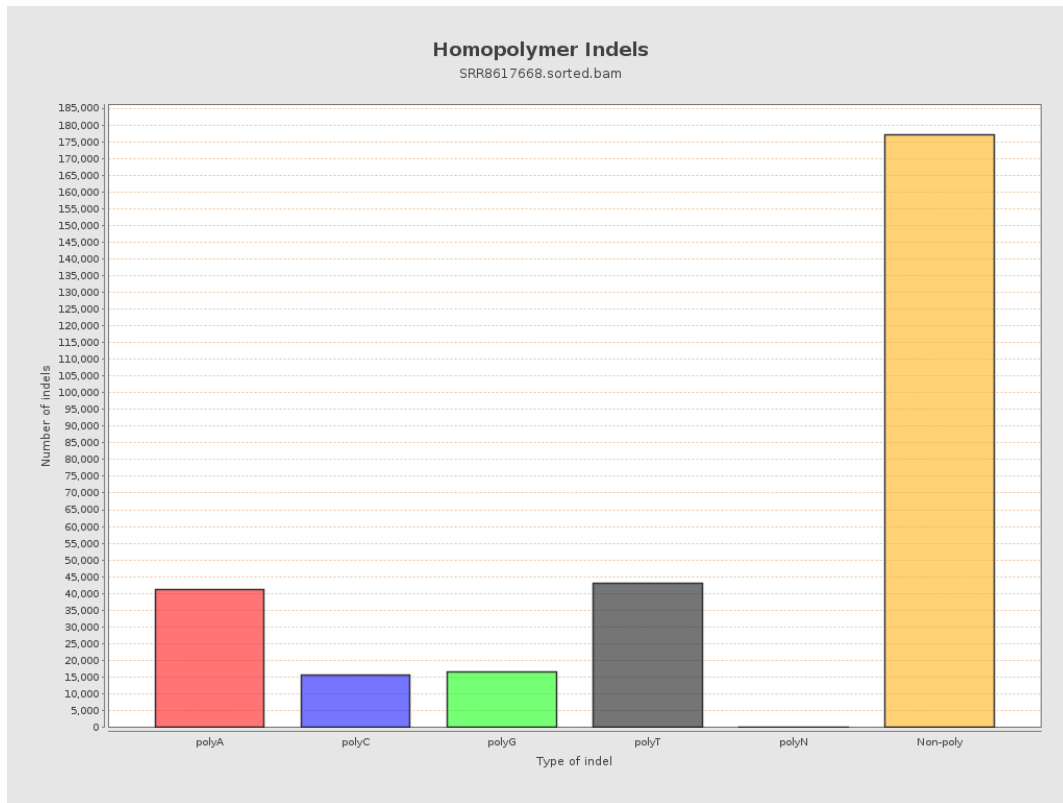
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



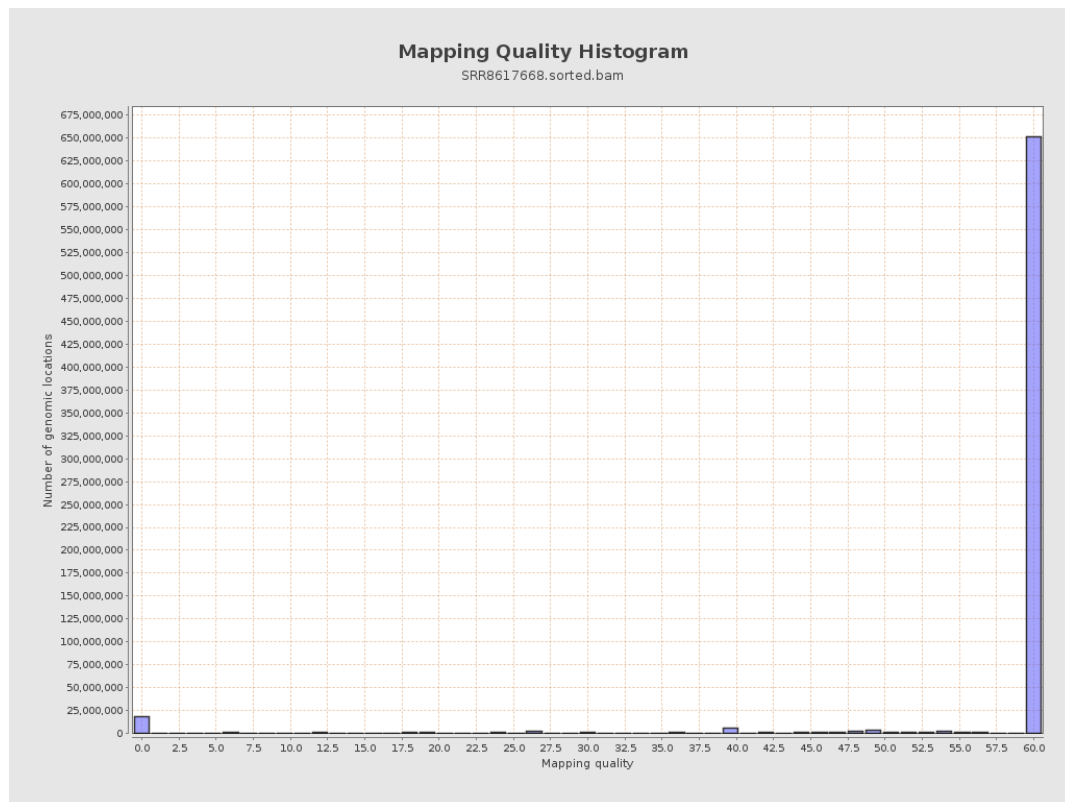
11. Results : Homopolymer Indels



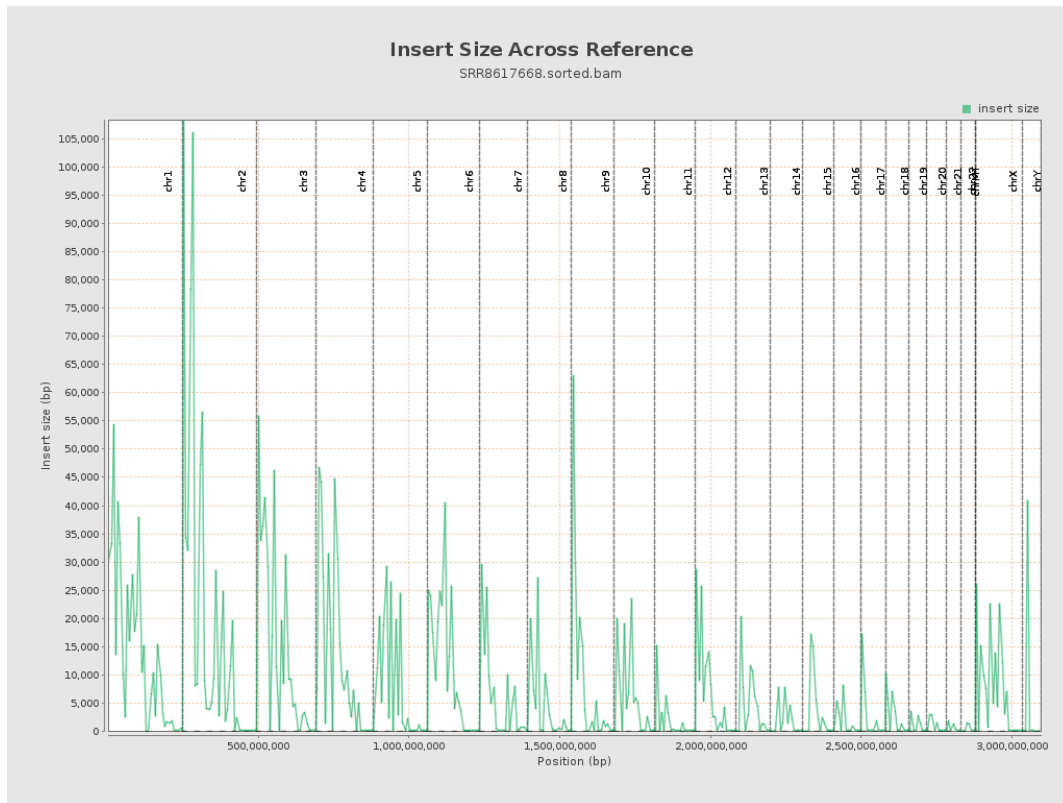
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

