

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:01:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173848.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_SRR10173848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173848_1.fastq.gz SRR10173848_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:01:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,055,734
Mapped reads	12,693,166 / 97.22%
Unmapped reads	362,568 / 2.78%
Mapped paired reads	12,693,166 / 97.22%
Mapped reads, first in pair	6,365,623 / 48.76%
Mapped reads, second in pair	6,327,543 / 48.47%
Mapped reads, both in pair	12,449,390 / 95.36%
Mapped reads, singletons	243,776 / 1.87%
Secondary alignments	0
Supplementary alignments	1,286,718 / 9.86%
Read min/max/mean length	30 / 133 / 128.43
Duplicated reads (estimated)	9,949,359 / 76.21%
Duplication rate	64.69%
Clipped reads	5,240,952 / 40.14%

2.2. ACGT Content

Number/percentage of A's	450,696,018 / 30.04%
Number/percentage of C's	294,883,509 / 19.65%
Number/percentage of T's	449,486,344 / 29.96%
Number/percentage of G's	305,349,244 / 20.35%
Number/percentage of N's	17,105 / 0%

GC Percentage	40%
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2.3. Coverage

Mean	0.485
Standard Deviation	6.6742

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	867,430.85
Standard Deviation	8,490,993.3
P25/Median/P75	150 / 210 / 302

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	15,822,243
Insertions	161,365
Mapped reads with at least one insertion	1.23%
Deletions	354,542
Mapped reads with at least one deletion	2.73%
Homopolymer indels	42.8%

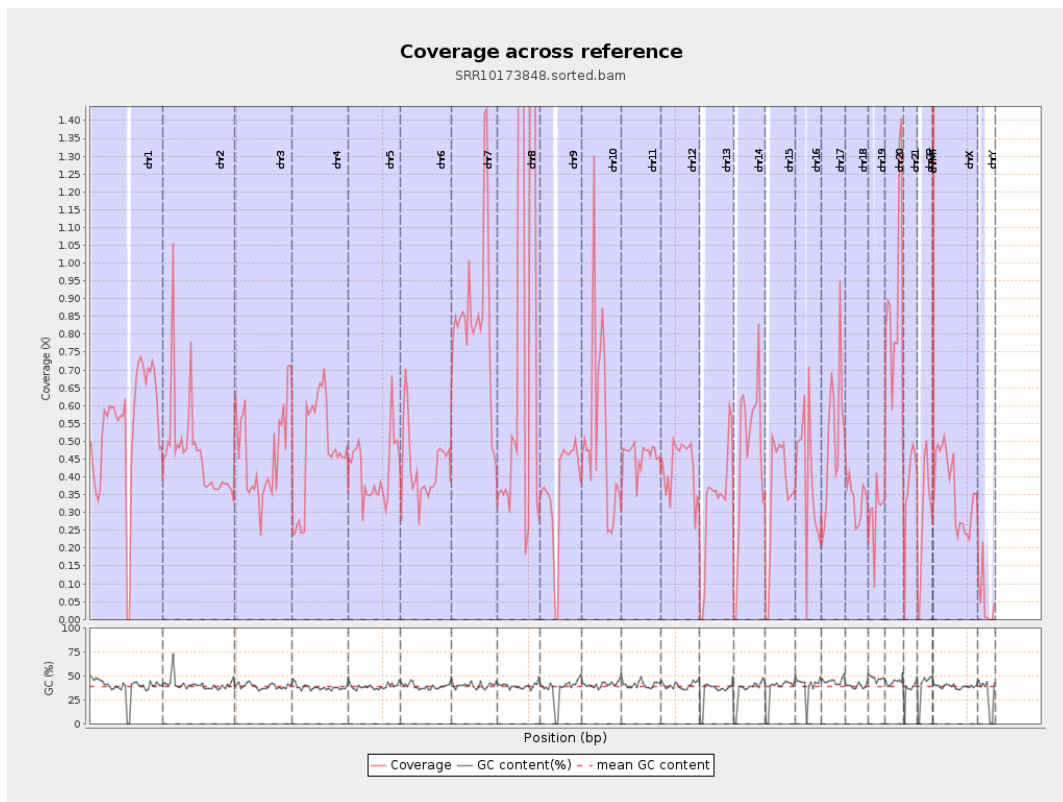
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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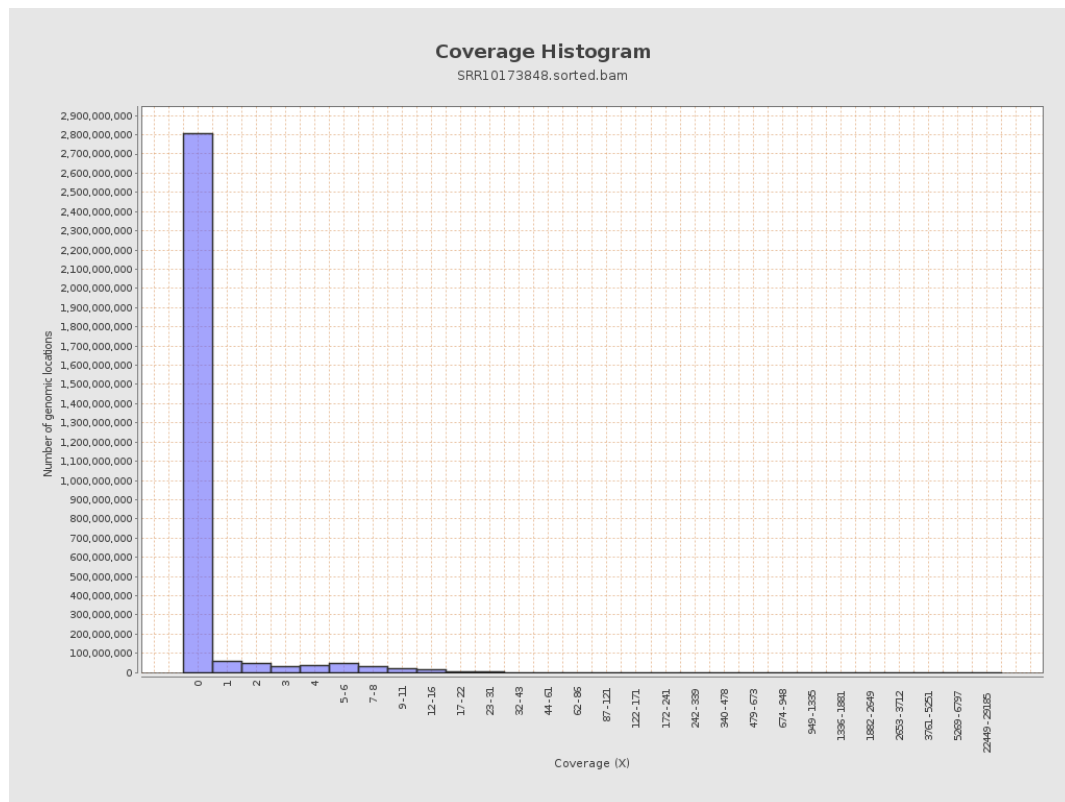
		bases	coverage	deviation
chr1	249250621	134738751	0.5406	3.4673
chr2	243199373	112692104	0.4634	20.3473
chr3	198022430	92735319	0.4683	2.0081
chr4	191154276	91628125	0.4793	3.3615
chr5	180915260	75617672	0.418	1.8617
chr6	171115067	73475336	0.4294	2.1085
chr7	159138663	132500448	0.8326	7.1039
chr8	146364022	145318147	0.9929	4.0967
chr9	141213431	52339860	0.3706	2.8056
chr10	135534747	69941485	0.516	8.4057
chr11	135006516	61879077	0.4583	2.1741
chr12	133851895	57398211	0.4288	1.9151
chr13	115169878	38585120	0.335	1.6815
chr14	107349540	50508869	0.4705	2.0292
chr15	102531392	36385747	0.3549	1.7251
chr16	90354753	35749432	0.3957	3.2044
chr17	81195210	41127394	0.5065	2.5531
chr18	78077248	26878459	0.3443	4.3128
chr19	59128983	17538136	0.2966	2.6878
chr20	63025520	57990735	0.9201	2.9438
chr21	48129895	18233716	0.3788	2.1433
chr22	51304566	14712382	0.2868	1.5164
chrMT	16571	3976129	239.945	164.2793
chrX	155270560	56311796	0.3627	1.7936

chrY	59373566	3037495	0.0512	2.1441
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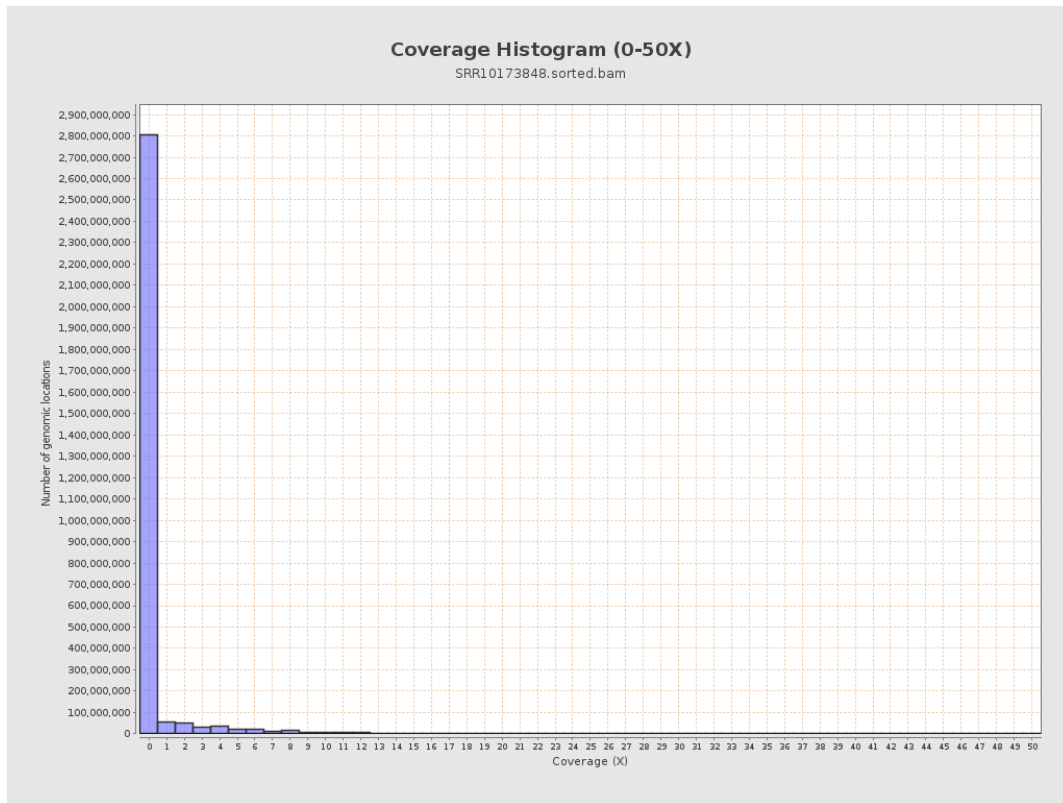
3. Results : Coverage across reference



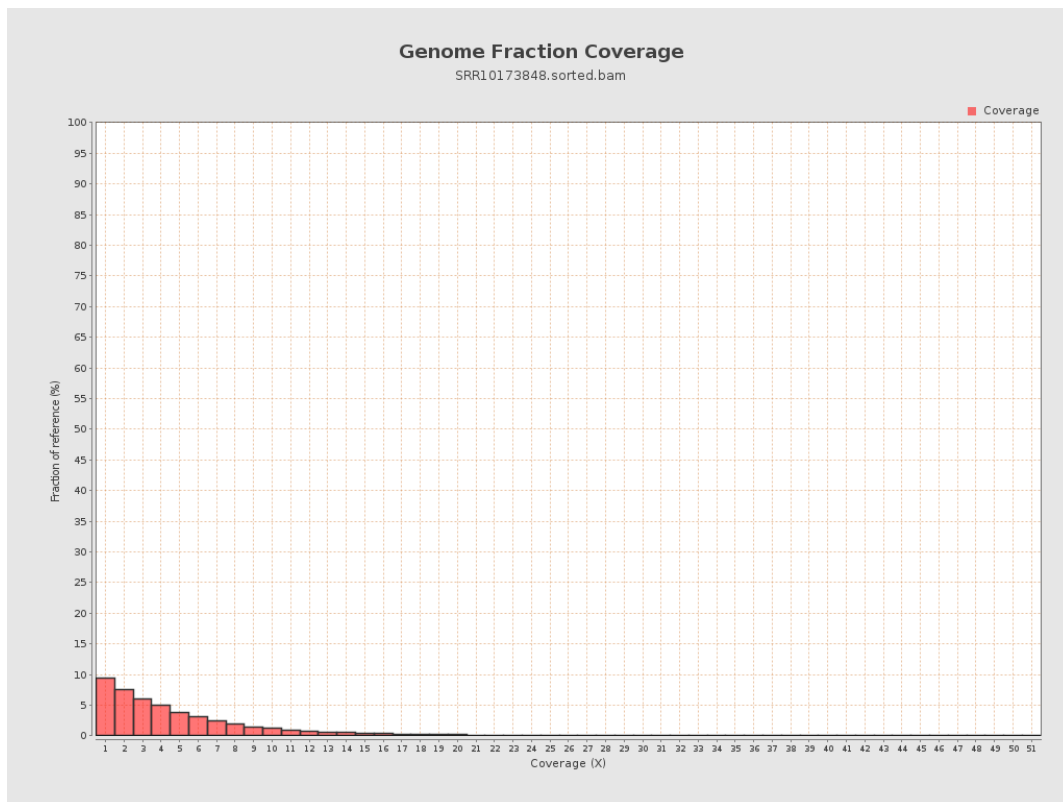
4. Results : Coverage Histogram



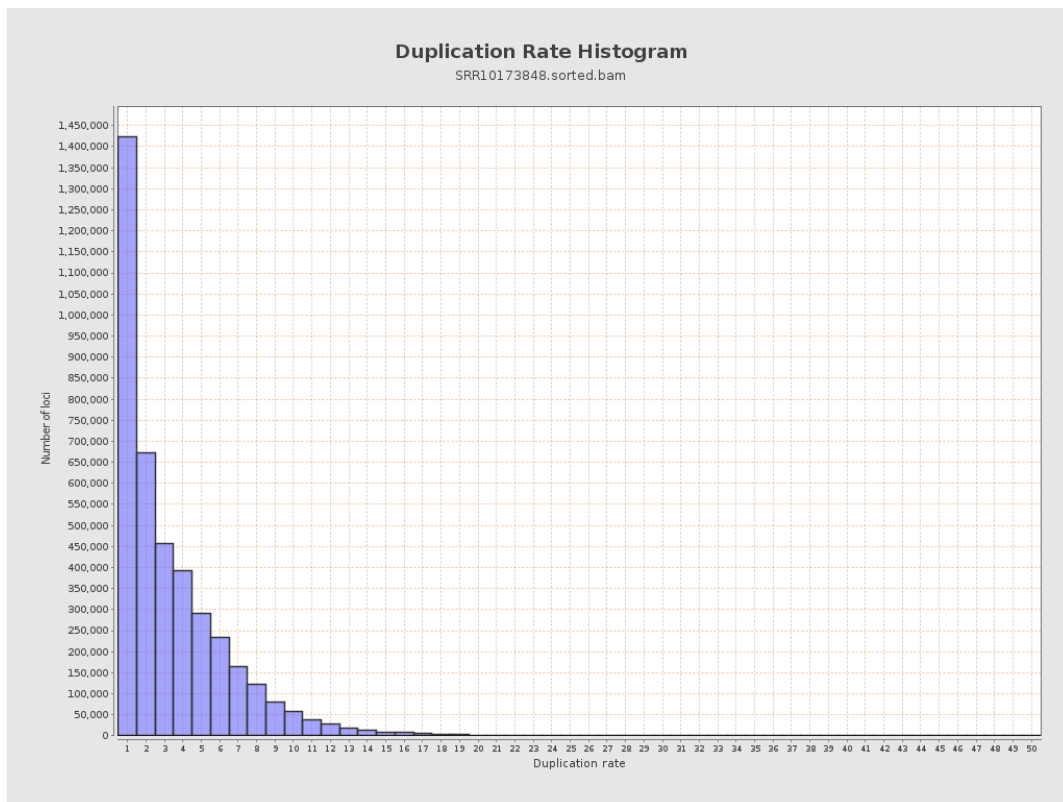
5. Results : Coverage Histogram (0-50X)



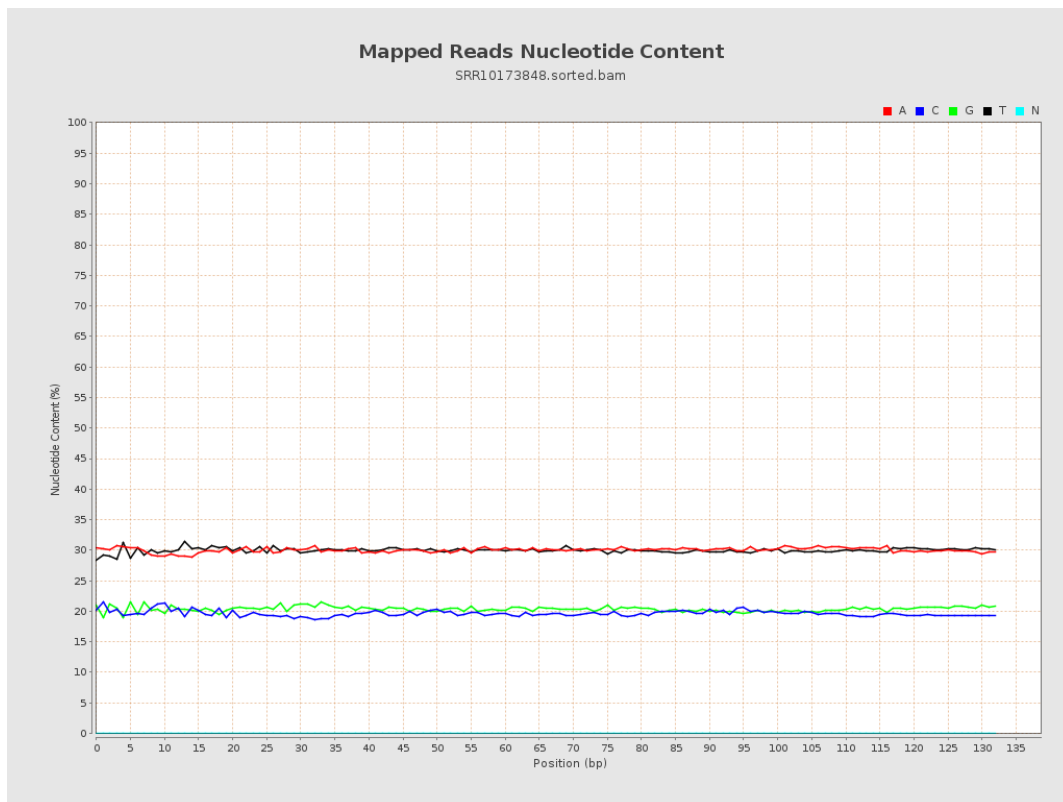
6. Results : Genome Fraction Coverage



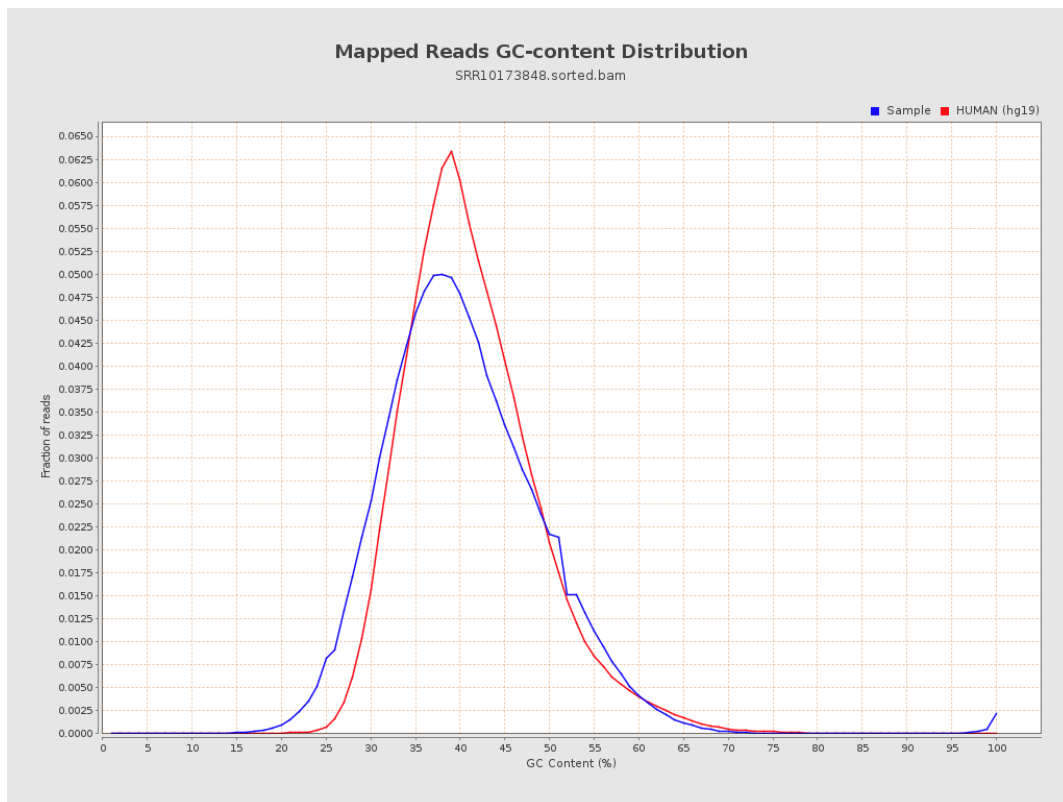
7. Results : Duplication Rate Histogram



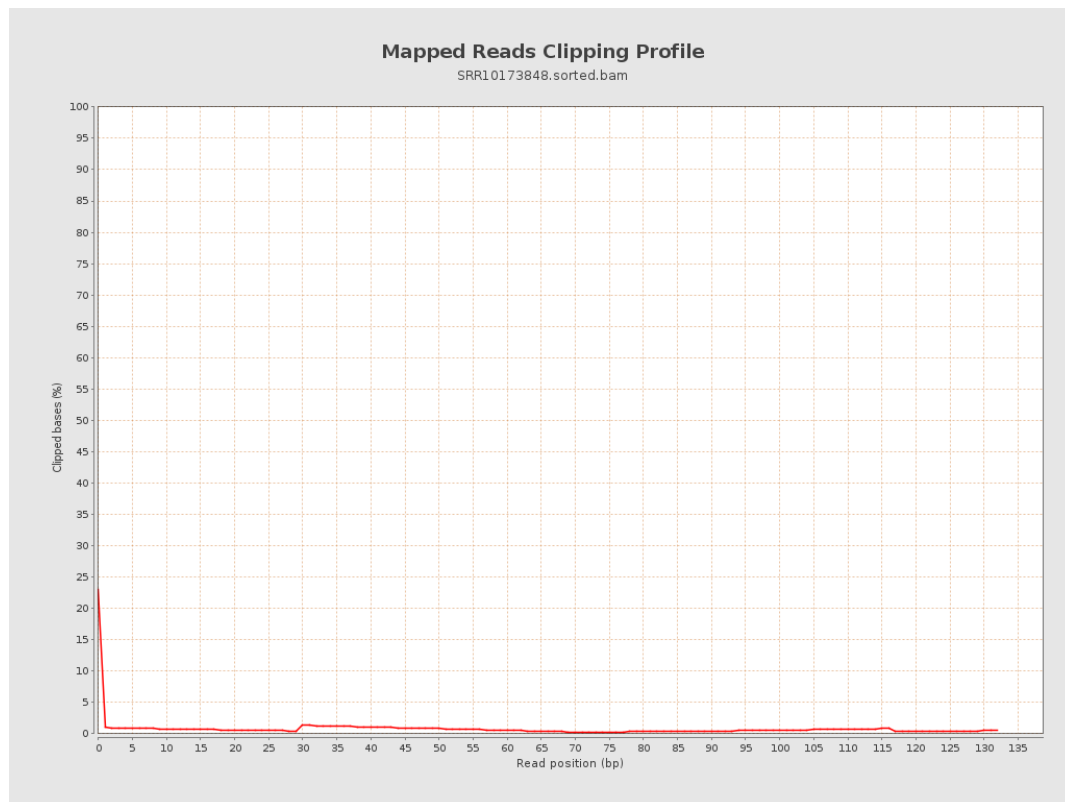
8. Results : Mapped Reads Nucleotide Content



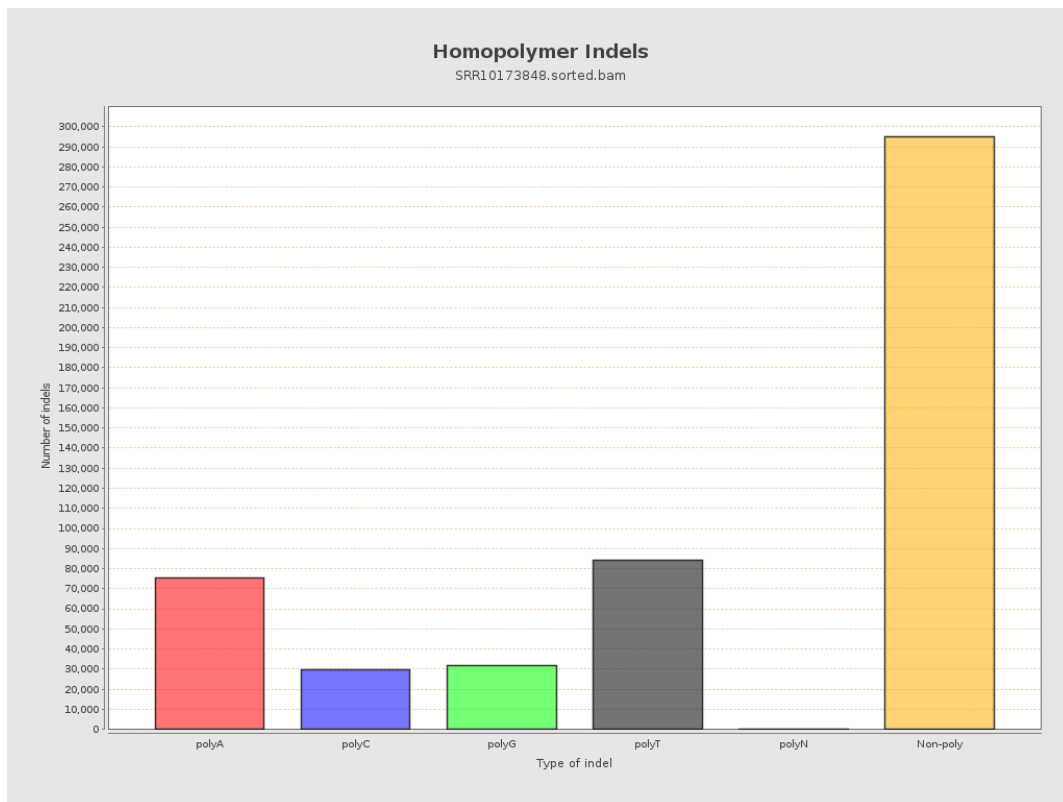
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



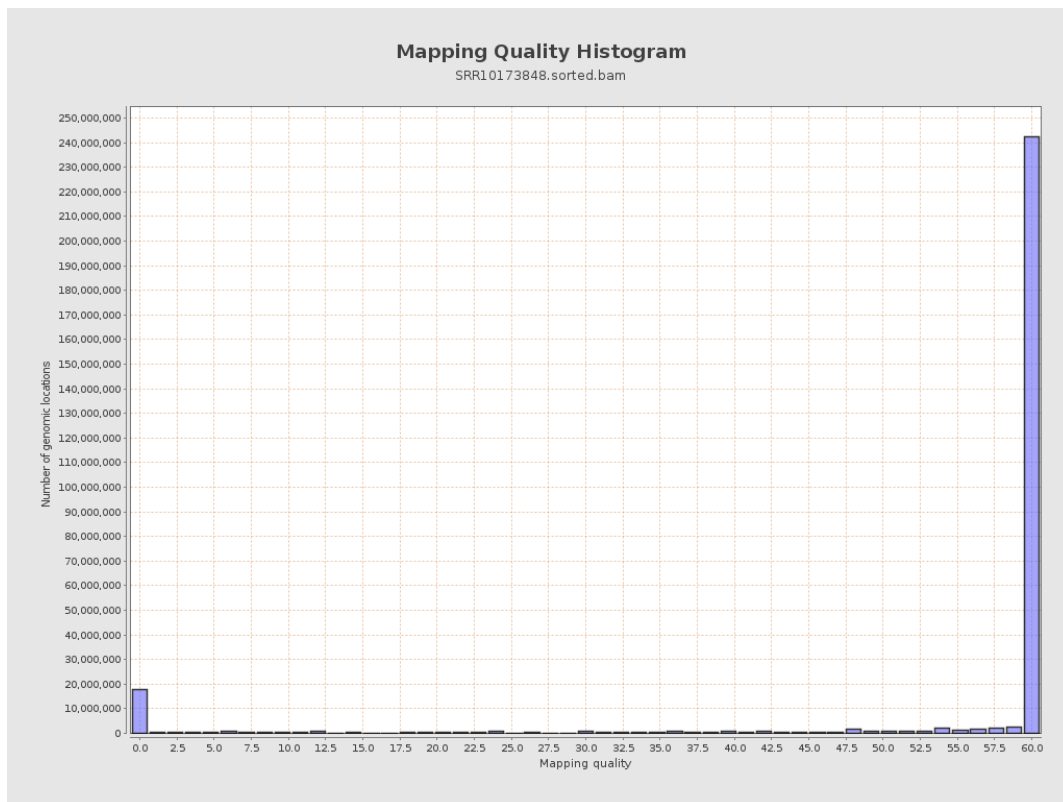
11. Results : Homopolymer Indels



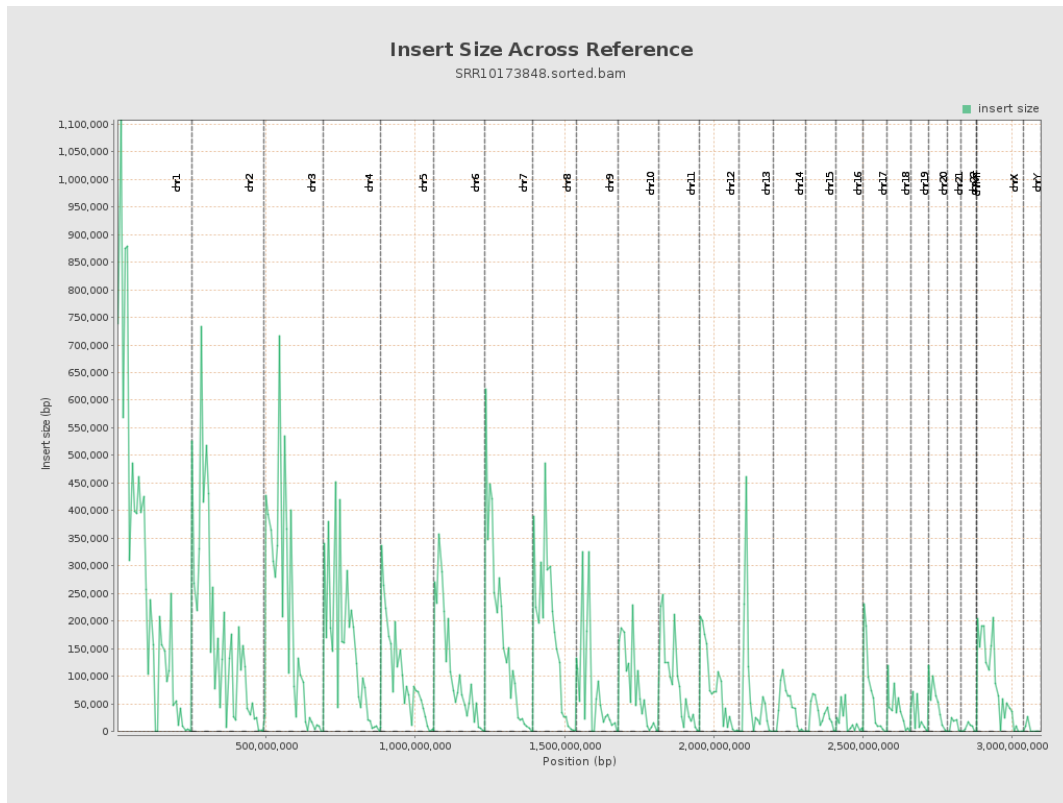
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

