

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:43:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173902.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_SRR10173902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173902_1.fastq.gz SRR10173902_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:43:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,475,214
Mapped reads	16,978,682 / 97.16%
Unmapped reads	496,532 / 2.84%
Mapped paired reads	16,978,682 / 97.16%
Mapped reads, first in pair	8,499,853 / 48.64%
Mapped reads, second in pair	8,478,829 / 48.52%
Mapped reads, both in pair	16,638,896 / 95.21%
Mapped reads, singletons	339,786 / 1.94%
Secondary alignments	0
Supplementary alignments	1,909,695 / 10.93%
Read min/max/mean length	30 / 133 / 128.96
Duplicated reads (estimated)	13,742,031 / 78.64%
Duplication rate	65.58%
Clipped reads	7,609,013 / 43.54%

2.2. ACGT Content

Number/percentage of A's	599,285,332 / 29.95%
Number/percentage of C's	393,080,784 / 19.65%
Number/percentage of T's	598,983,327 / 29.94%
Number/percentage of G's	409,328,941 / 20.46%
Number/percentage of N's	23,503 / 0%

GC Percentage	40.11%
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2.3. Coverage

Mean	0.6467
Standard Deviation	9.0127

2.4. Mapping Quality

Mean Mapping Quality	52.46
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2.5. Insert size

Mean	1,037,351.2
Standard Deviation	9,110,984.44
P25/Median/P75	149 / 210 / 307

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	21,310,131
Insertions	218,603
Mapped reads with at least one insertion	1.24%
Deletions	502,917
Mapped reads with at least one deletion	2.89%
Homopolymer indels	42.55%

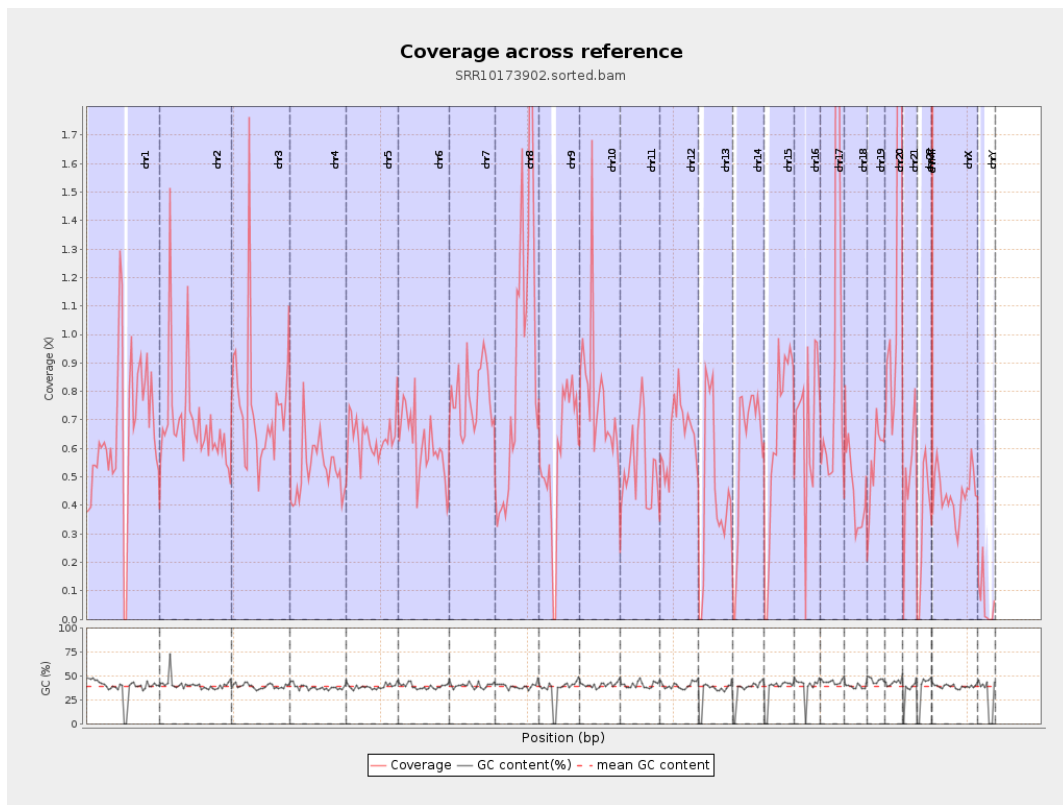
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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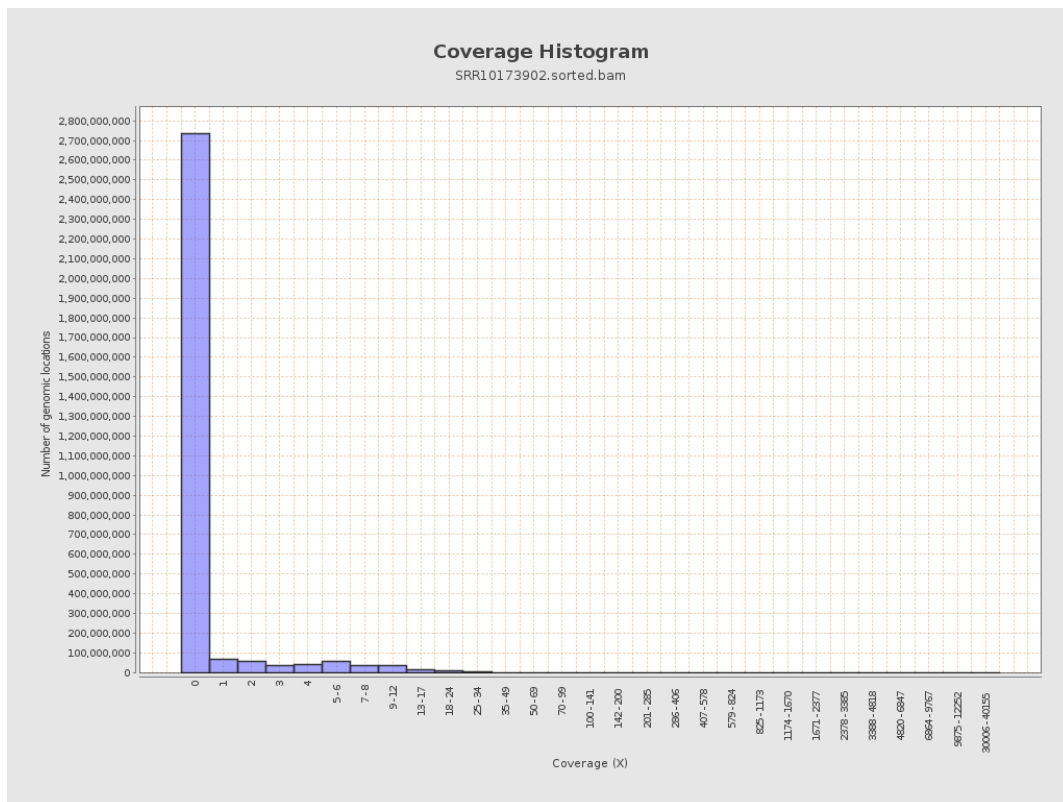
		bases	coverage	deviation
chr1	249250621	163981324	0.6579	6.3731
chr2	243199373	167593908	0.6891	28.0629
chr3	198022430	147068649	0.7427	2.691
chr4	191154276	100738842	0.527	3.6595
chr5	180915260	116043380	0.6414	2.4161
chr6	171115067	104808954	0.6125	3.3771
chr7	159138663	123901655	0.7786	5.9331
chr8	146364022	132617415	0.9061	5.1818
chr9	141213431	80887277	0.5728	4.6168
chr10	135534747	106038666	0.7824	9.9518
chr11	135006516	73032148	0.541	2.4879
chr12	133851895	86741606	0.648	2.499
chr13	115169878	51127103	0.4439	2.0406
chr14	107349540	64679751	0.6025	2.4449
chr15	102531392	65661100	0.6404	2.471
chr16	90354753	63001904	0.6973	4.6749
chr17	81195210	79093480	0.9741	4.0442
chr18	78077248	35248045	0.4515	7.4334
chr19	59128983	33002723	0.5581	4.8169
chr20	63025520	88114031	1.3981	4.4148
chr21	48129895	25066015	0.5208	2.6263
chr22	51304566	17417687	0.3395	1.7096
chrMT	16571	4246242	256.2454	179.5407
chrX	155270560	68038128	0.4382	2.0911

chrY	59373566	3774859	0.0636	2.3343
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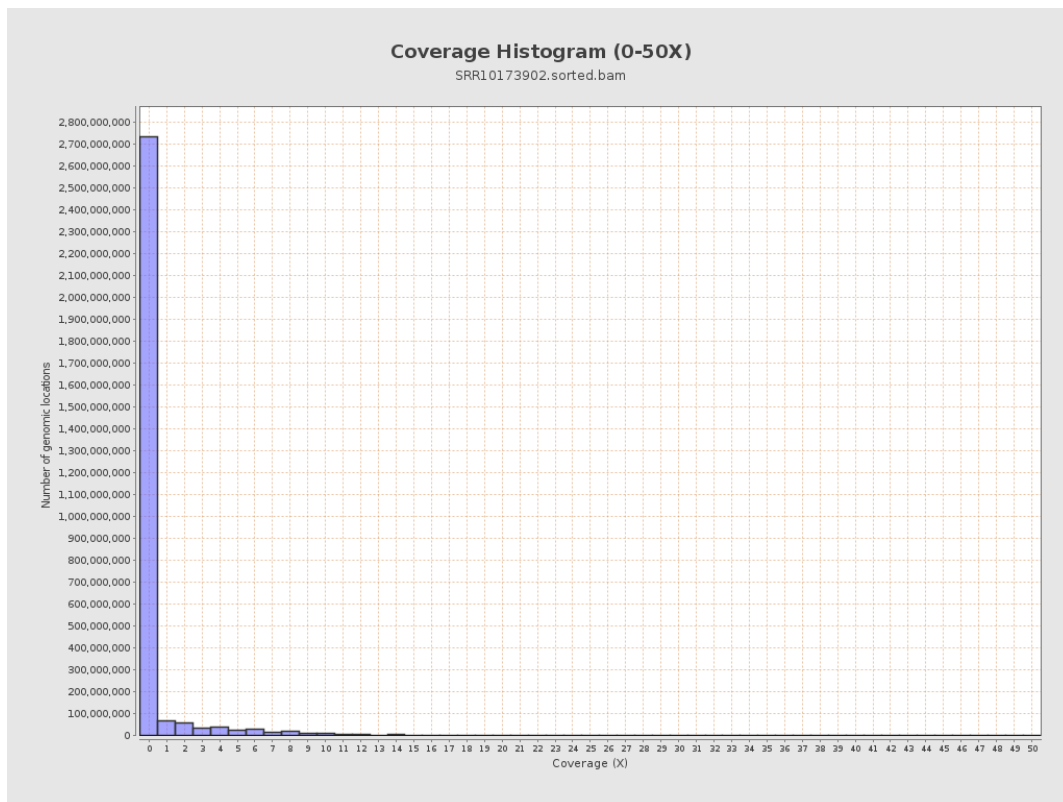
3. Results : Coverage across reference



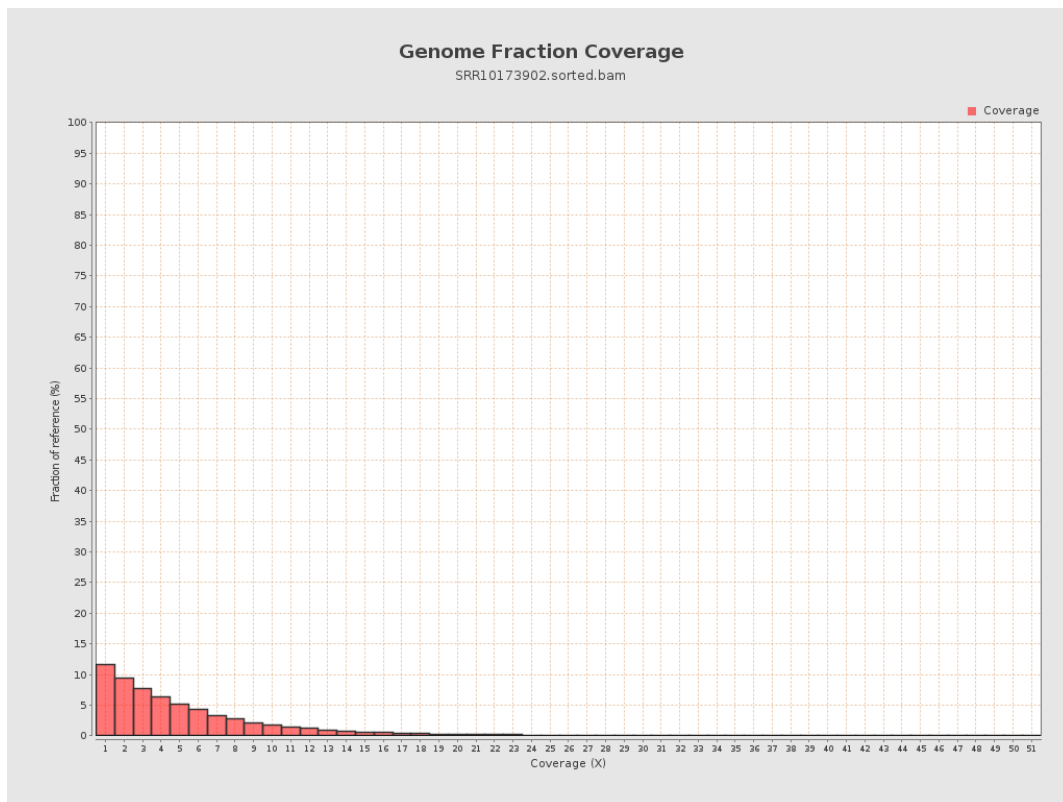
4. Results : Coverage Histogram



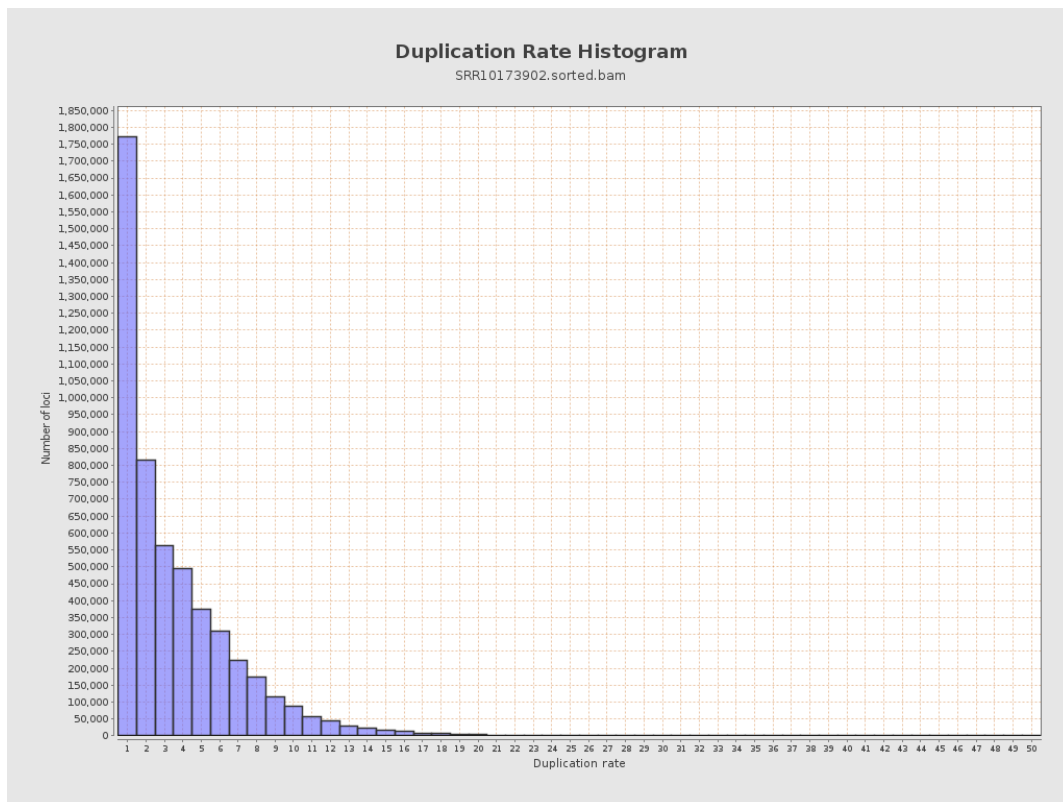
5. Results : Coverage Histogram (0-50X)



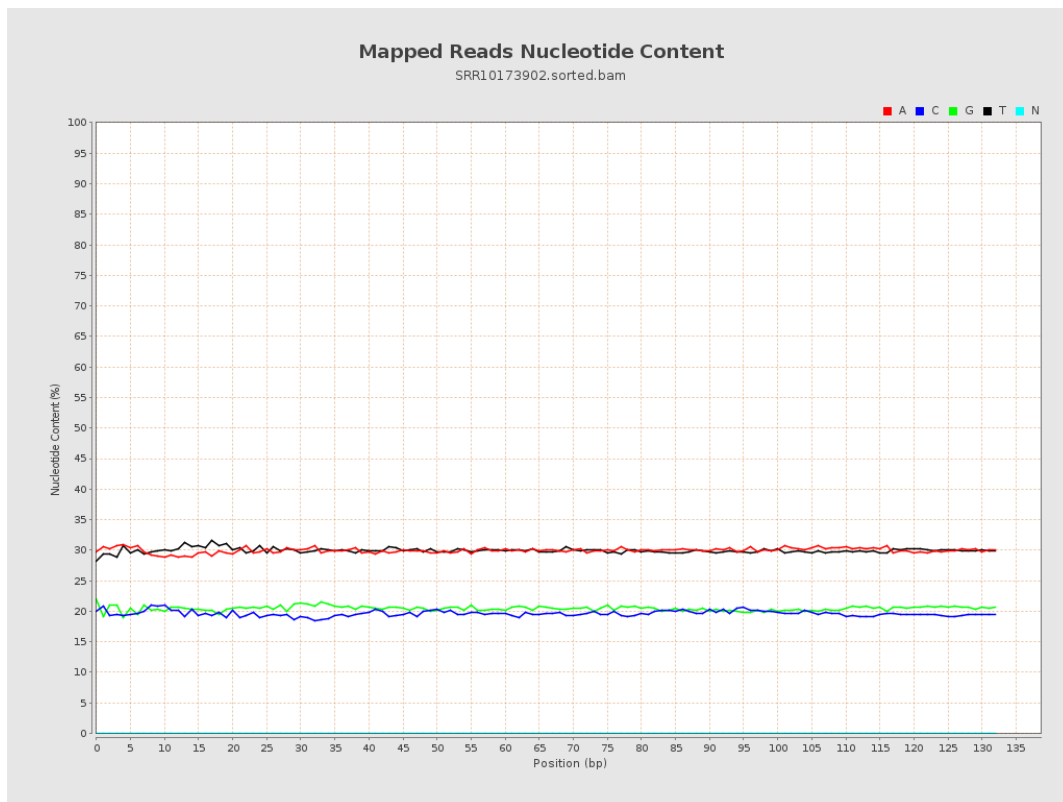
6. Results : Genome Fraction Coverage



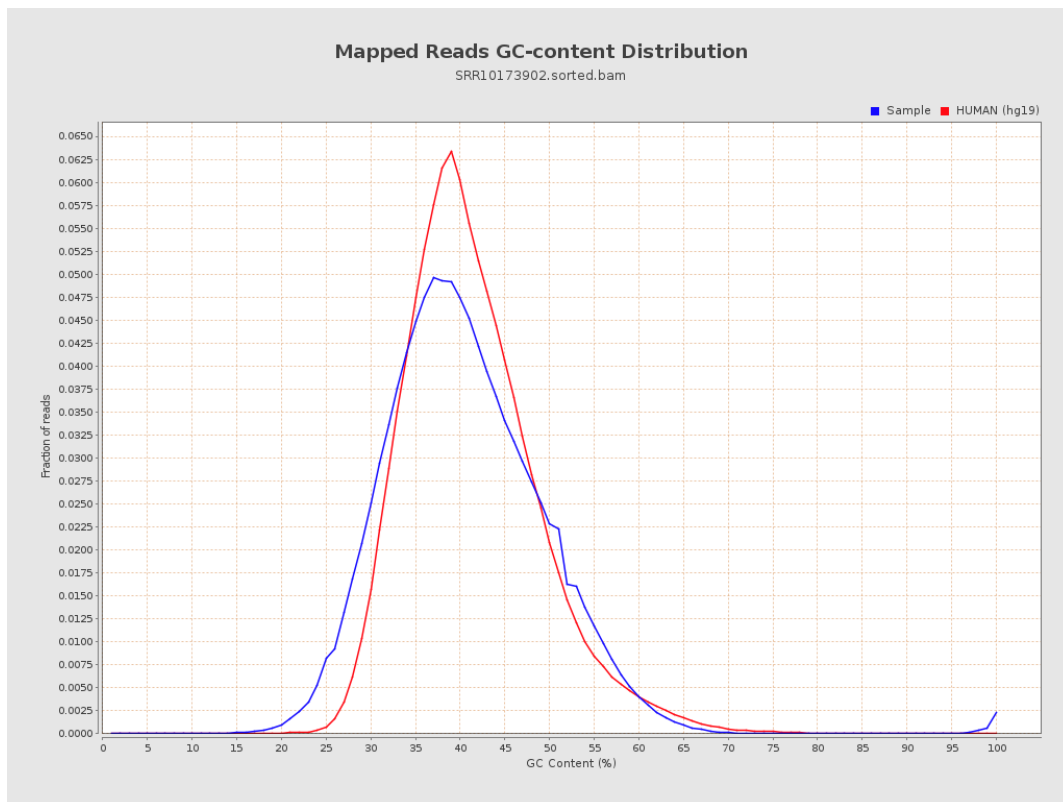
7. Results : Duplication Rate Histogram



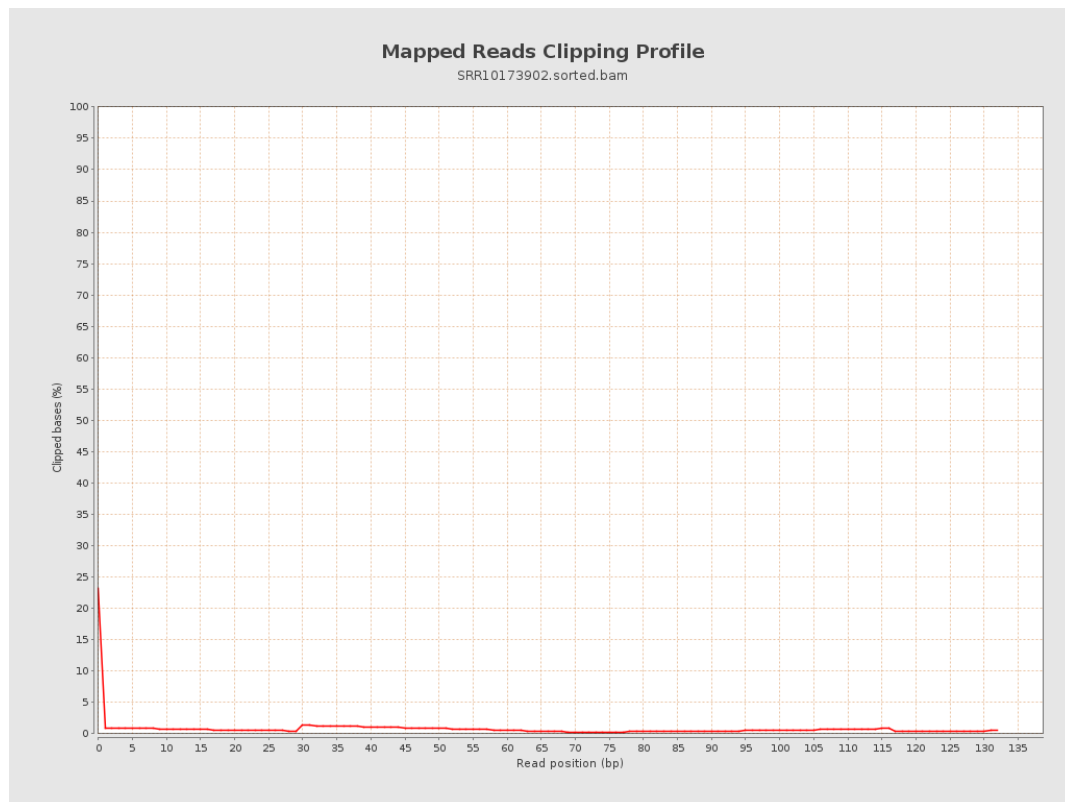
8. Results : Mapped Reads Nucleotide Content



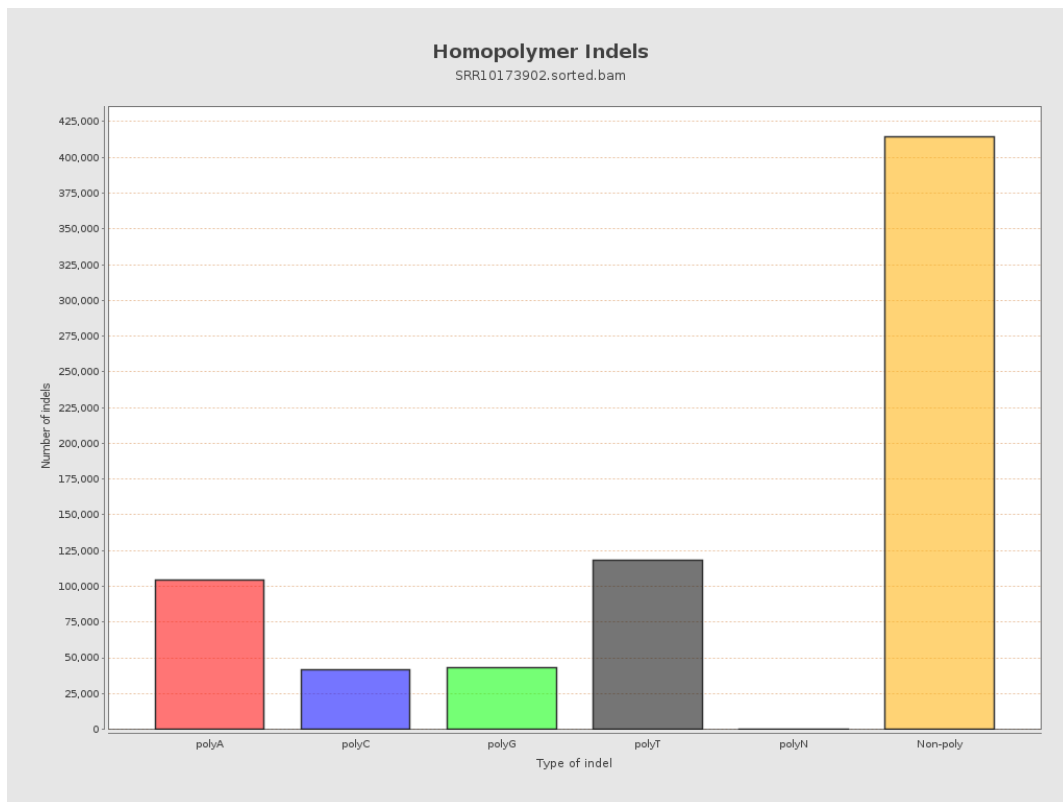
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



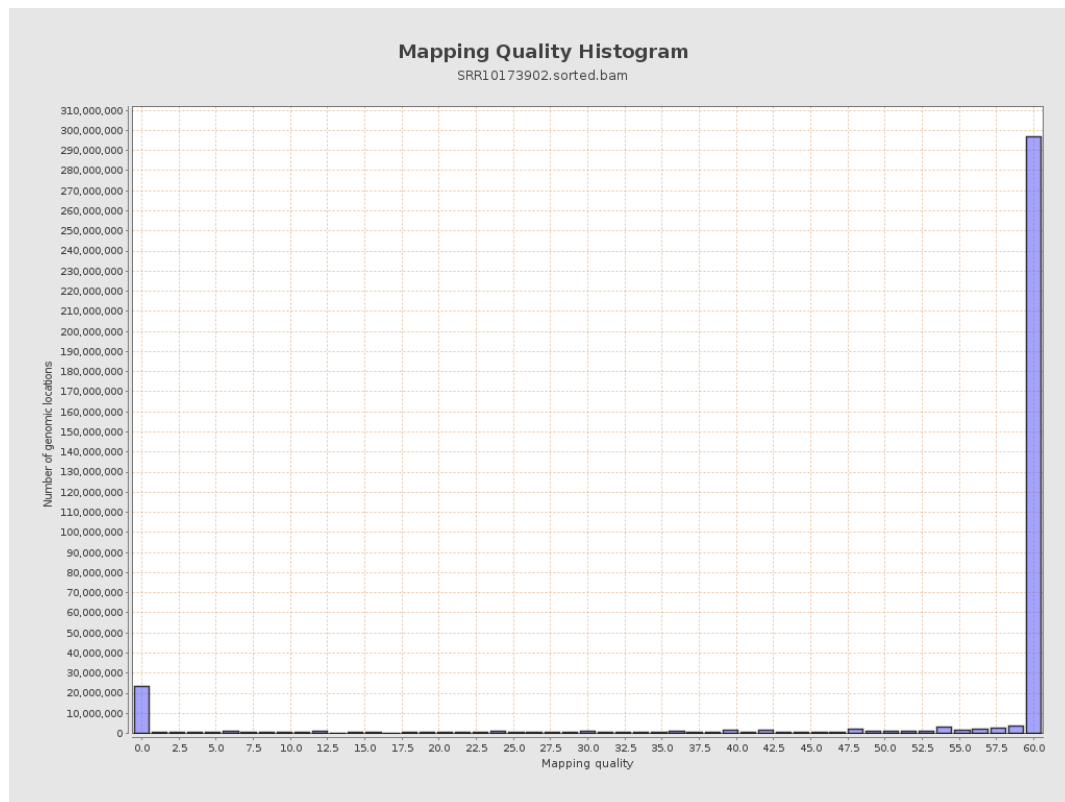
11. Results : Homopolymer Indels



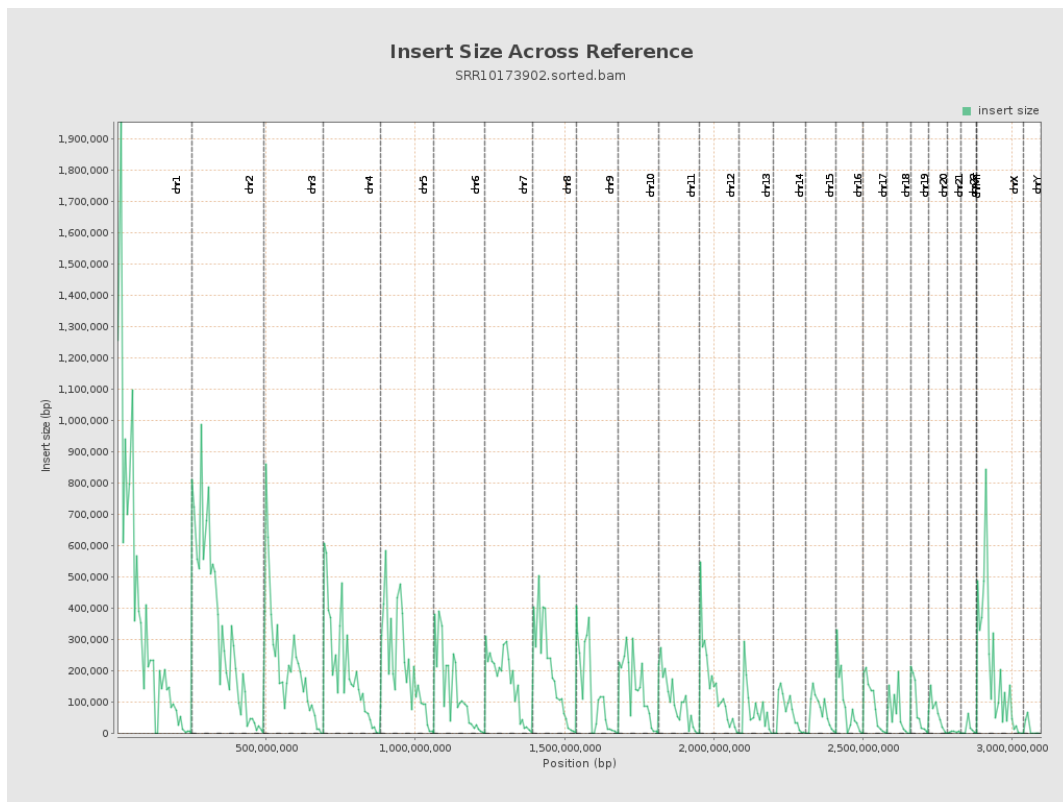
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

