

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:15:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472444.sorted.bam -c -nw 400 -hm 3
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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_SRR3472444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472444_1.fastq.gz SRR3472444_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:15:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472444.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,046,172
Mapped reads	17,869,933 / 99.02%
Unmapped reads	176,239 / 0.98%
Mapped paired reads	17,869,933 / 99.02%
Mapped reads, first in pair	8,958,505 / 49.64%
Mapped reads, second in pair	8,911,428 / 49.38%
Mapped reads, both in pair	17,777,078 / 98.51%
Mapped reads, singletons	92,855 / 0.51%
Secondary alignments	0
Supplementary alignments	64,092 / 0.36%
Read min/max/mean length	30 / 100 / 99.18
Duplicated reads (estimated)	11,327,708 / 62.77%
Duplication rate	48.05%
Clipped reads	1,367,520 / 7.58%

2.2. ACGT Content

Number/percentage of A's	473,054,471 / 27.09%
Number/percentage of C's	401,488,906 / 22.99%
Number/percentage of T's	473,455,949 / 27.12%
Number/percentage of G's	397,835,398 / 22.78%
Number/percentage of N's	216,300 / 0.01%

GC Percentage	45.78%
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2.3. Coverage

Mean	0.5641
Standard Deviation	17.7382

2.4. Mapping Quality

Mean Mapping Quality	54.78
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2.5. Insert size

Mean	16,839.89
Standard Deviation	1,292,623.43
P25/Median/P75	148 / 208 / 282

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	9,550,446
Insertions	100,472
Mapped reads with at least one insertion	0.56%
Deletions	87,310
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46.3%

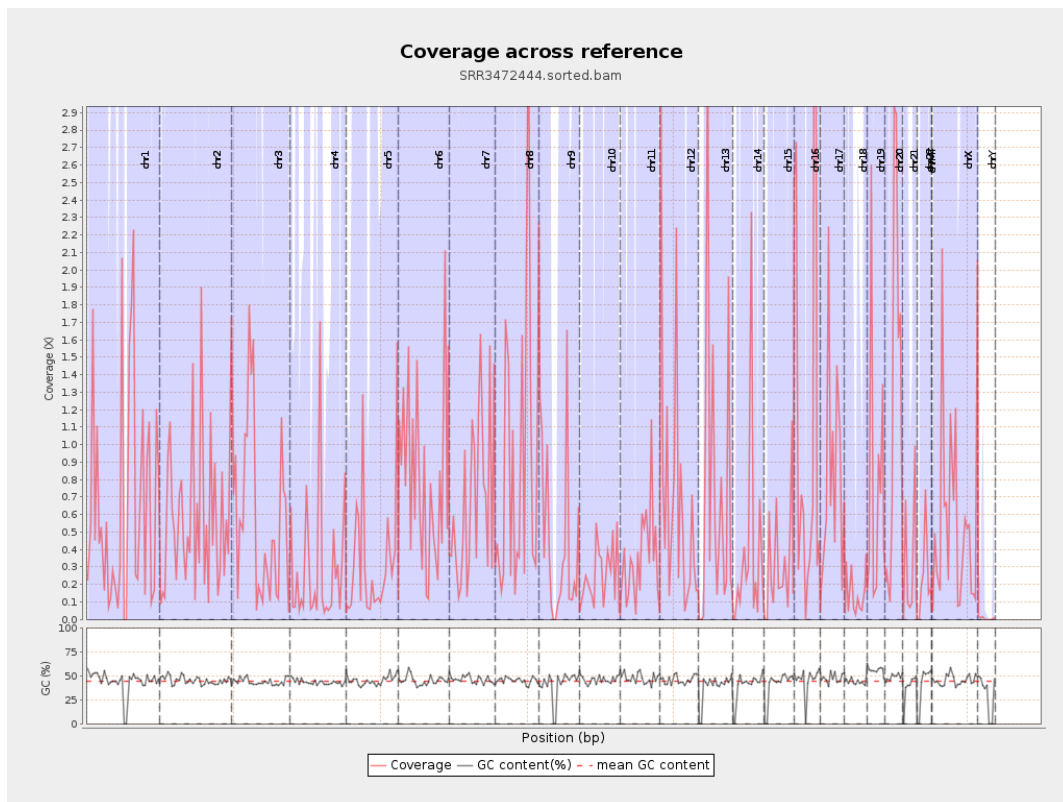
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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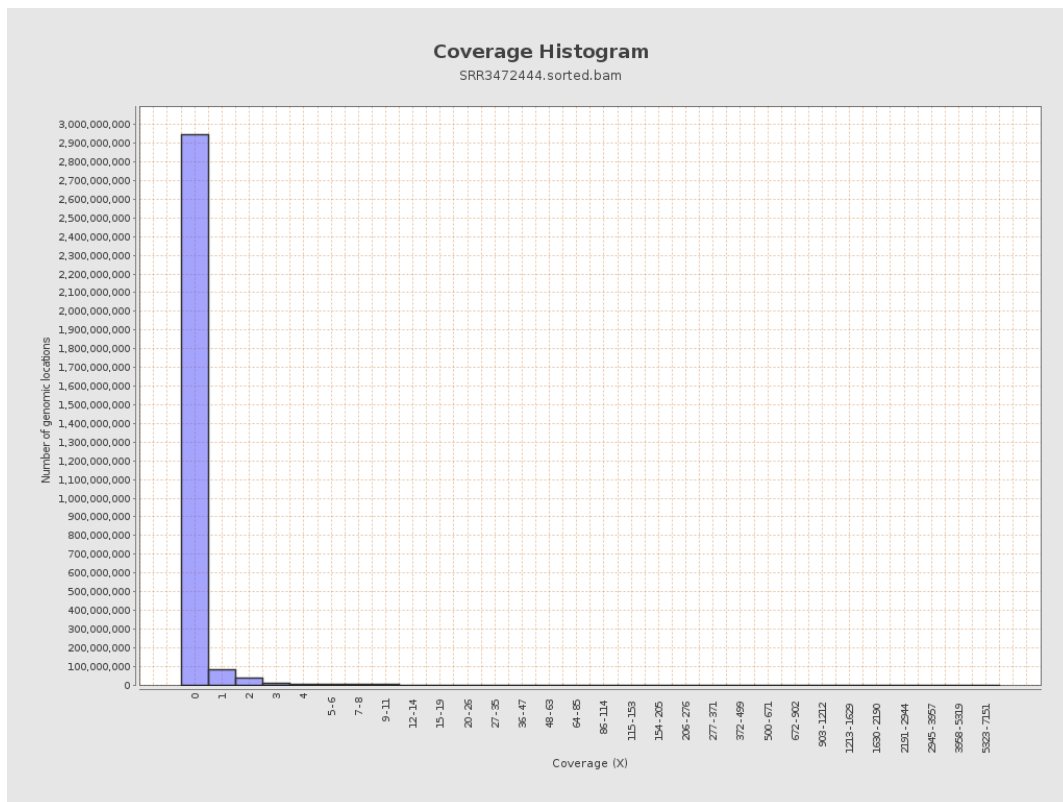
		bases	coverage	deviation
chr1	249250621	167145582	0.6706	20.208
chr2	243199373	138455719	0.5693	17.0397
chr3	198022430	120702490	0.6095	14.294
chr4	191154276	53817789	0.2815	12.1371
chr5	180915260	61242794	0.3385	11.9747
chr6	171115067	134816504	0.7879	17.4266
chr7	159138663	108933995	0.6845	19.8858
chr8	146364022	133597540	0.9128	24.8217
chr9	141213431	63522742	0.4498	11.7993
chr10	135534747	34728810	0.2562	9.2416
chr11	135006516	48814537	0.3616	9.6089
chr12	133851895	95270784	0.7118	20.7026
chr13	115169878	85648176	0.7437	25.9245
chr14	107349540	38687888	0.3604	11.9314
chr15	102531392	33149819	0.3233	9.8478
chr16	90354753	107495915	1.1897	32.9178
chr17	81195210	66320276	0.8168	19.6391
chr18	78077248	11326288	0.1451	5.4865
chr19	59128983	49710986	0.8407	17.071
chr20	63025520	80959777	1.2846	37.9706
chr21	48129895	15713012	0.3265	14.986
chr22	51304566	11851467	0.231	6.4617
chrMT	16571	4721	0.2849	0.6506
chrX	155270560	83948985	0.5407	17.1095

chrY	59373566	383904	0.0065	0.5183
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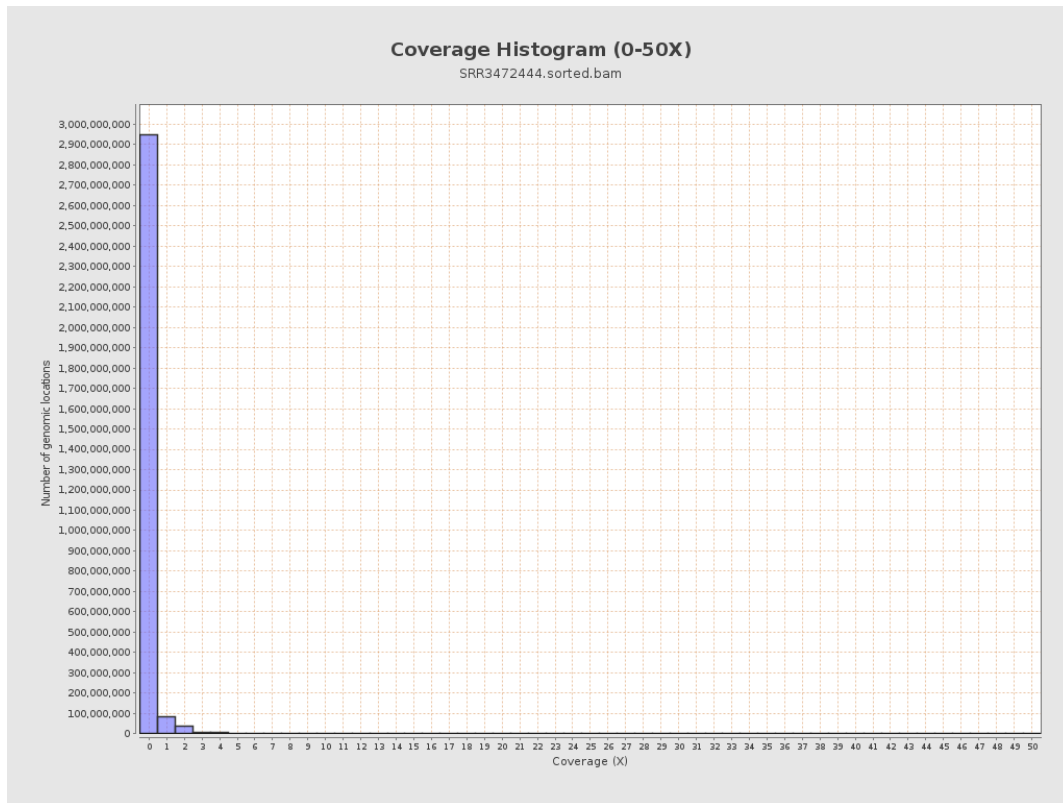
3. Results : Coverage across reference



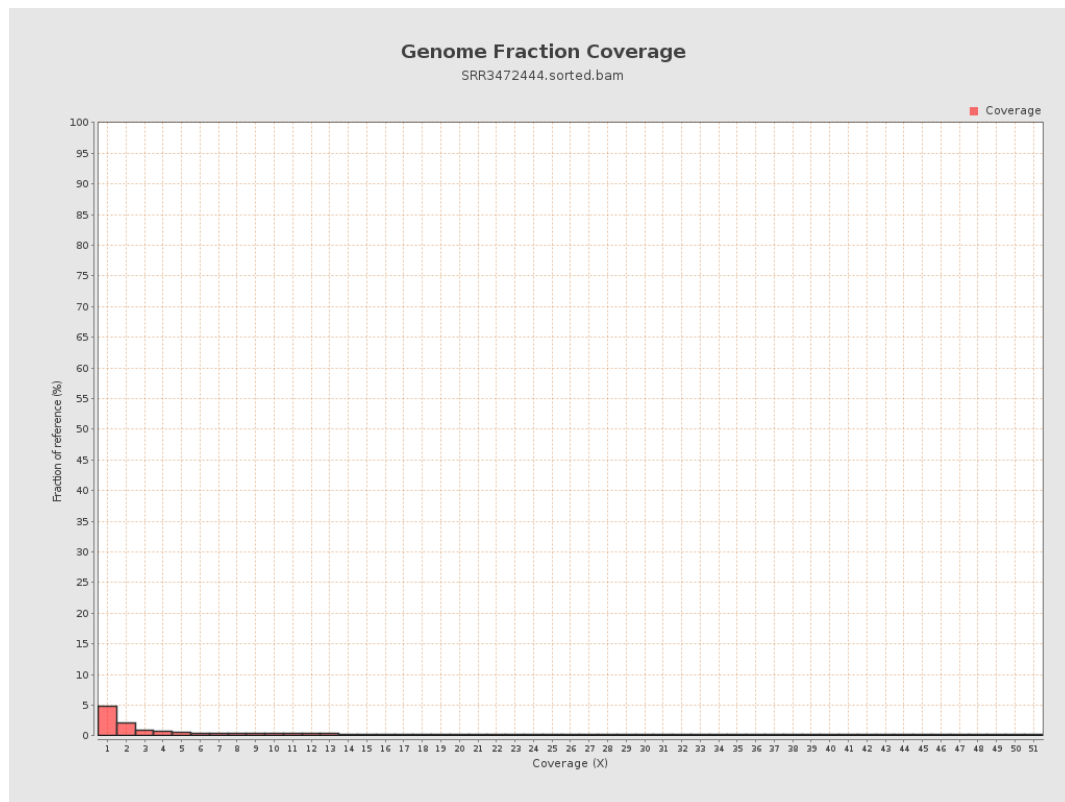
4. Results : Coverage Histogram



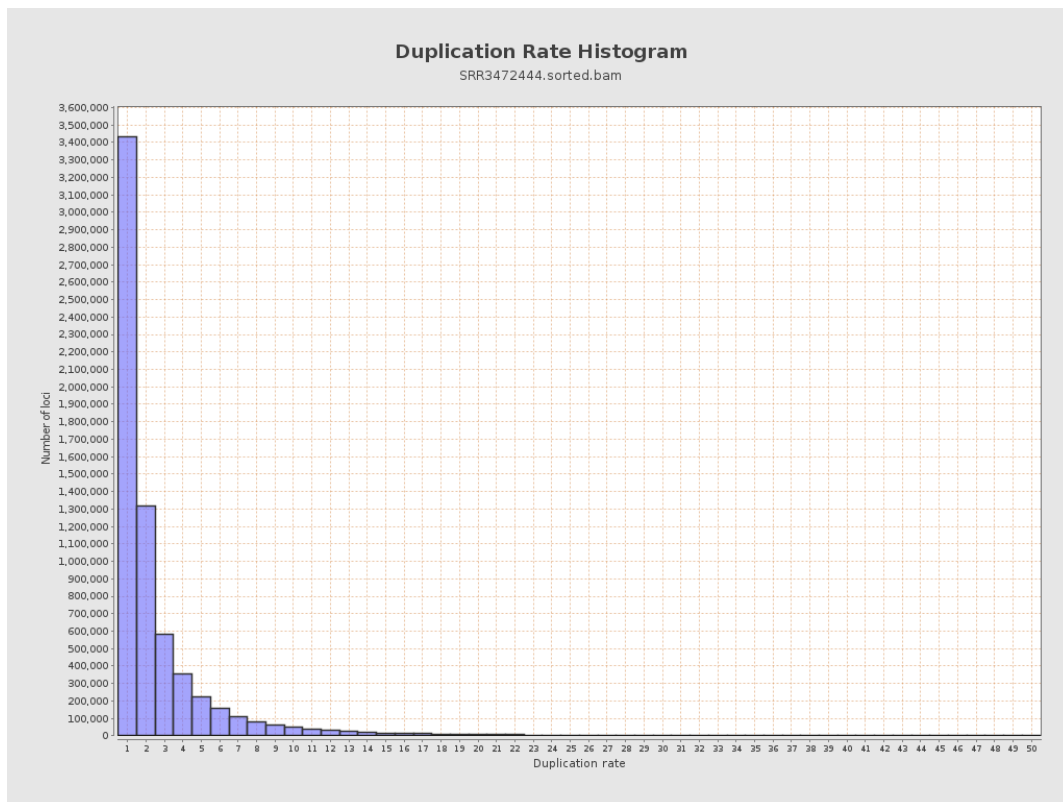
5. Results : Coverage Histogram (0-50X)



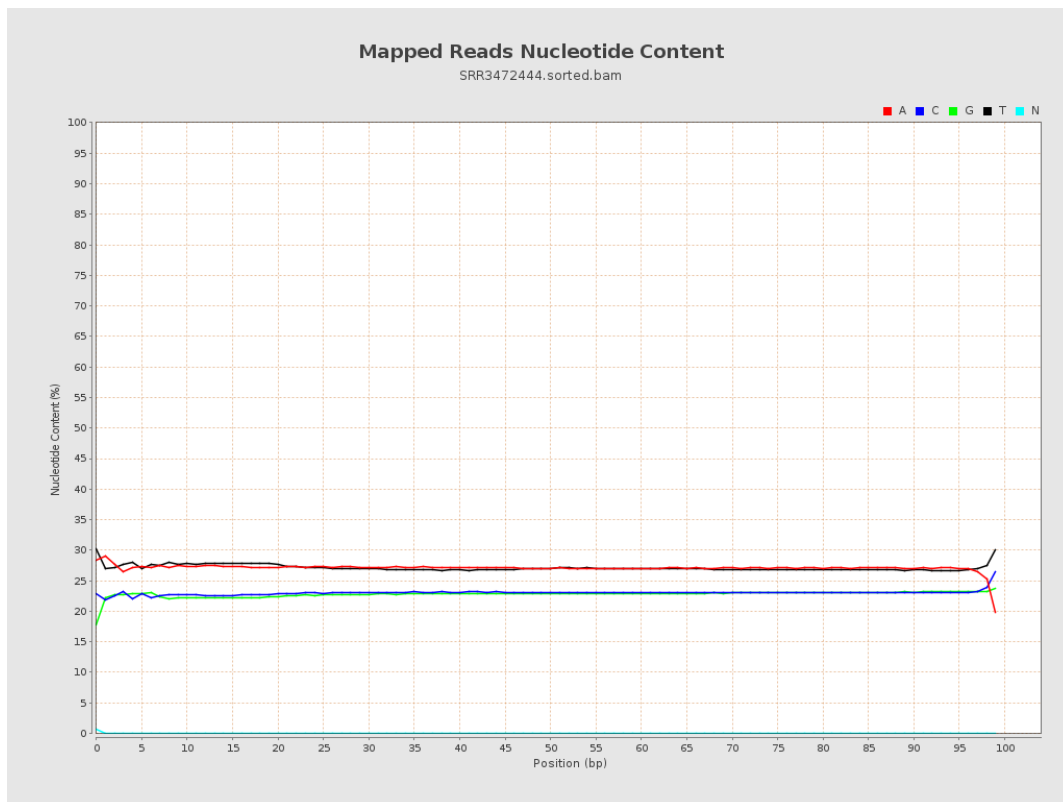
6. Results : Genome Fraction Coverage



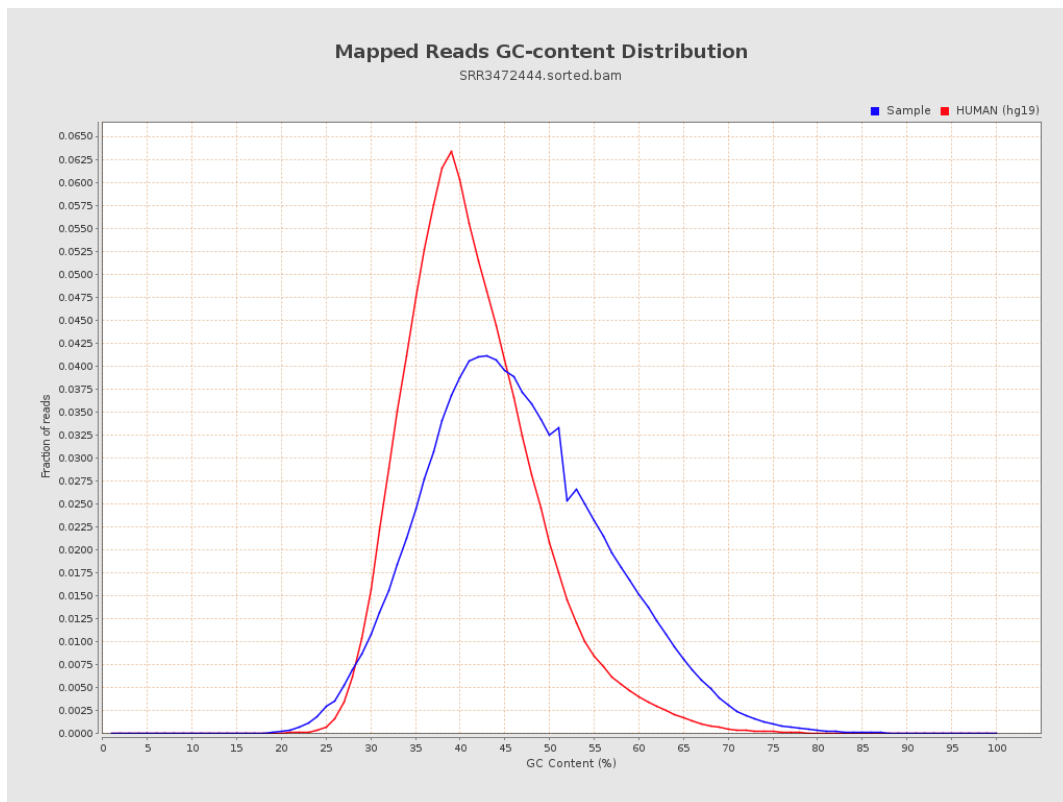
7. Results : Duplication Rate Histogram



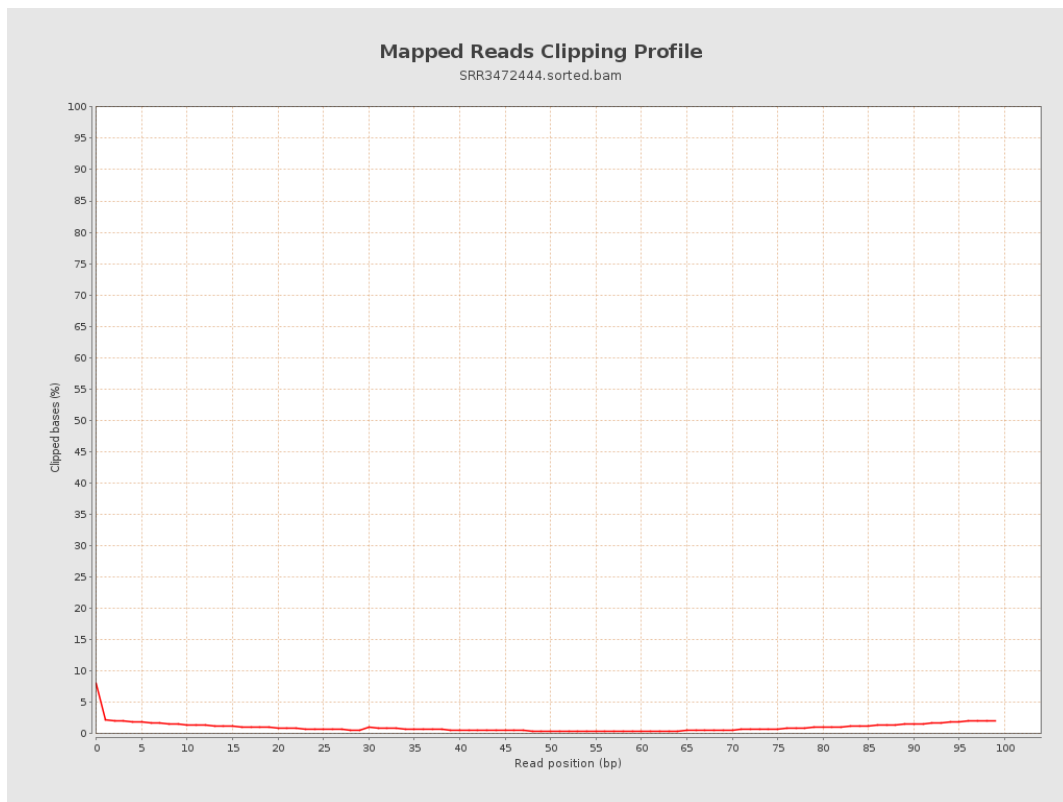
8. Results : Mapped Reads Nucleotide Content



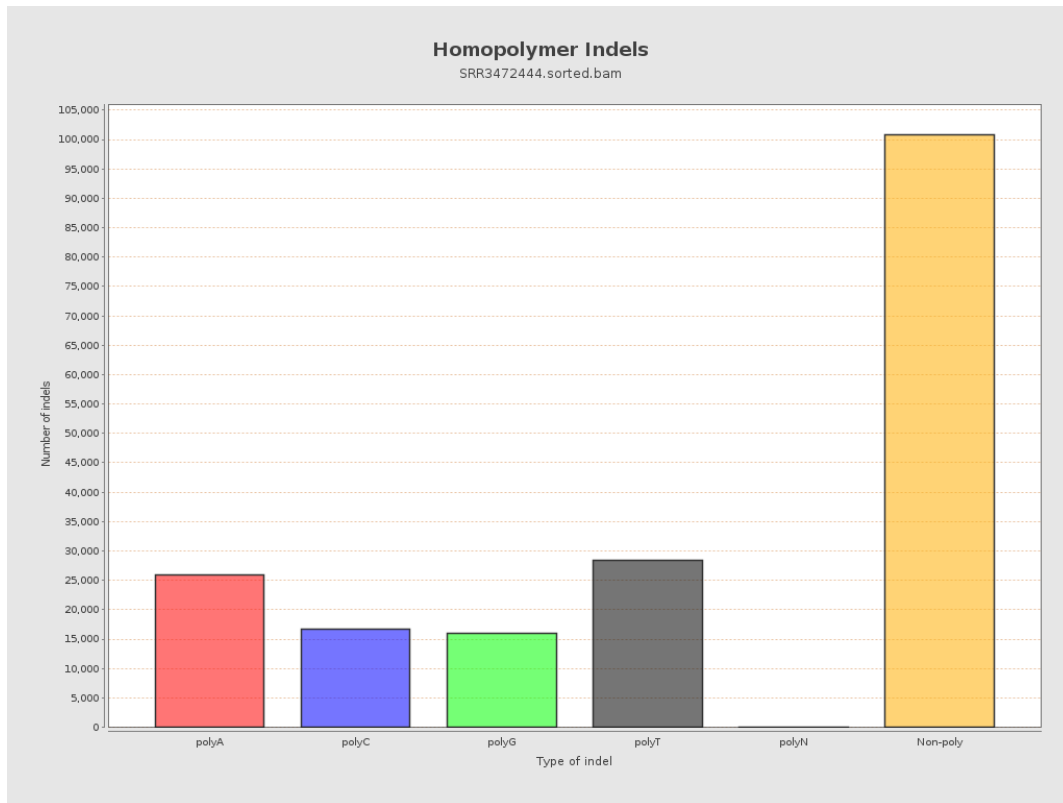
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



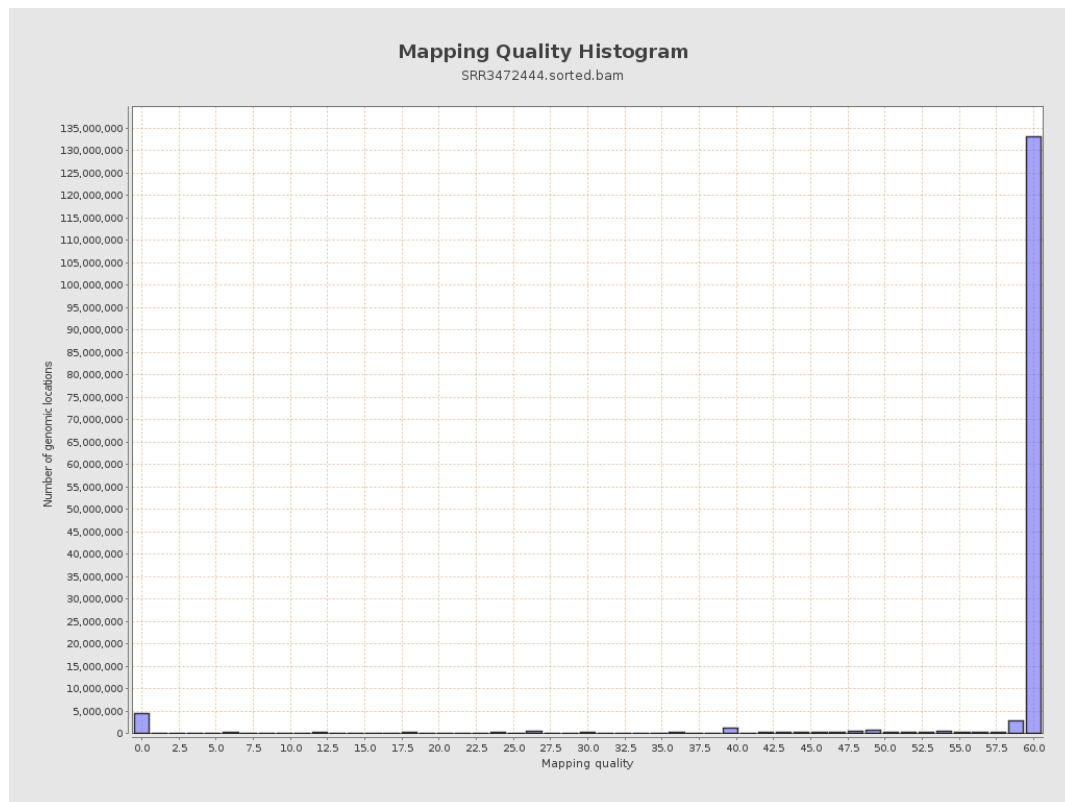
11. Results : Homopolymer Indels



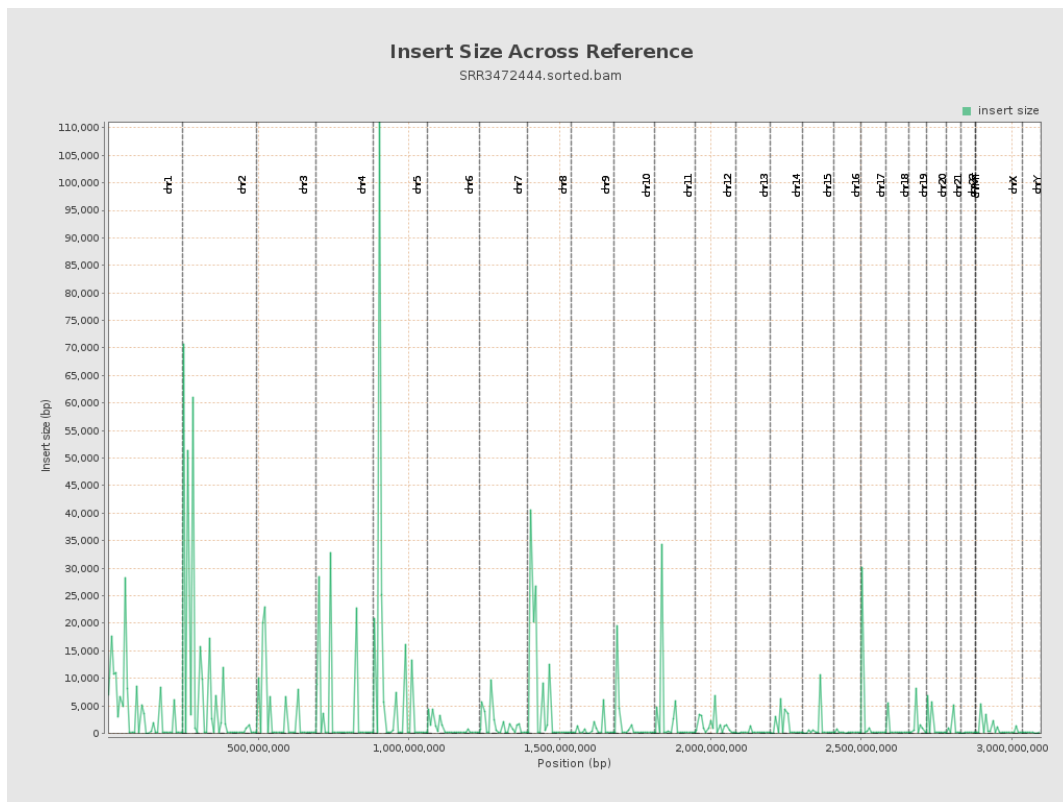
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

