

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 20:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264620.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_SRR1264620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264620_1.fastq.gz SRR1264620_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 20:06:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,609,813,856
Mapped reads	1,600,471,362 / 99.42%
Unmapped reads	9,342,494 / 0.58%
Mapped paired reads	1,600,471,362 / 99.42%
Mapped reads, first in pair	802,922,916 / 49.88%
Mapped reads, second in pair	797,548,446 / 49.54%
Mapped reads, both in pair	1,593,738,238 / 99%
Mapped reads, singletons	6,733,124 / 0.42%
Secondary alignments	0
Supplementary alignments	10,804,132 / 0.67%
Read min/max/mean length	30 / 101 / 101.28
Duplicated reads (estimated)	709,325,815 / 44.06%
Duplication rate	44.25%
Clipped reads	72,309,570 / 4.49%

2.2. ACGT Content

Number/percentage of A's	49,707,757,996 / 30.95%
Number/percentage of C's	30,620,923,718 / 19.06%
Number/percentage of T's	49,373,361,688 / 30.74%
Number/percentage of G's	30,891,488,076 / 19.23%
Number/percentage of N's	26,919,035 / 0.02%

GC Percentage	38.3%
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2.3. Coverage

Mean	51.897
Standard Deviation	52.3136

2.4. Mapping Quality

Mean Mapping Quality	54.47
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2.5. Insert size

Mean	88,591.41
Standard Deviation	2,850,953.98
P25/Median/P75	284 / 311 / 343

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	725,149,218
Insertions	17,613,950
Mapped reads with at least one insertion	1.09%
Deletions	16,493,267
Mapped reads with at least one deletion	1.01%
Homopolymer indels	48.4%

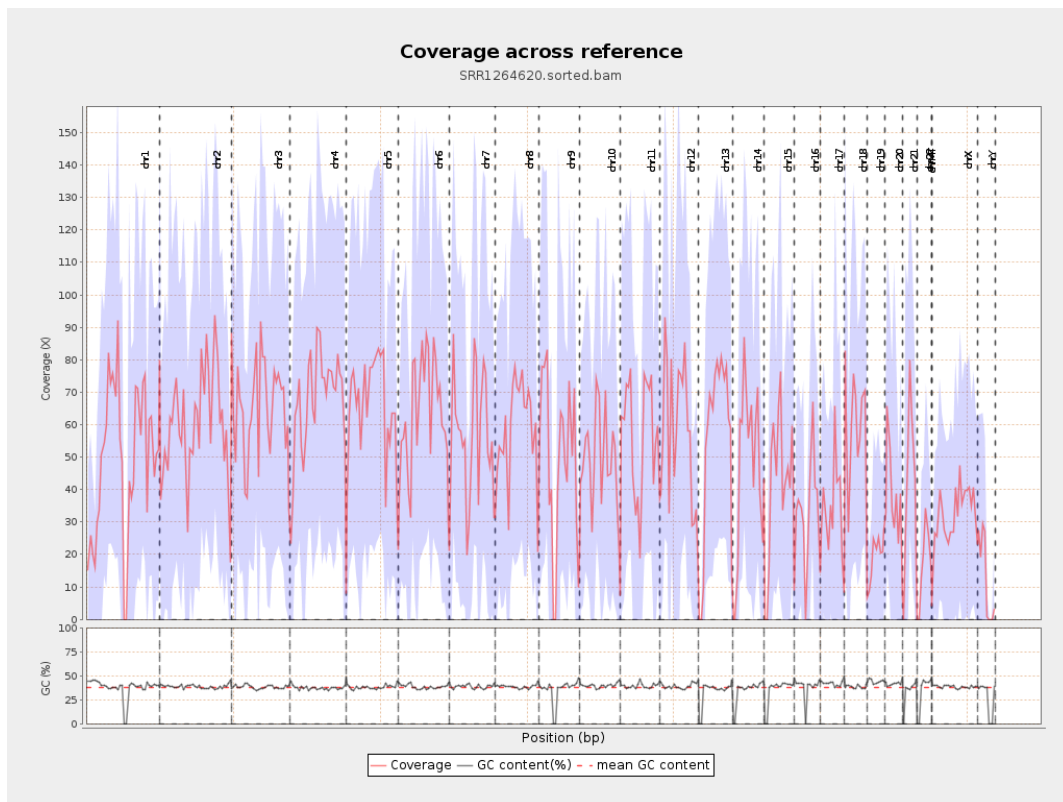
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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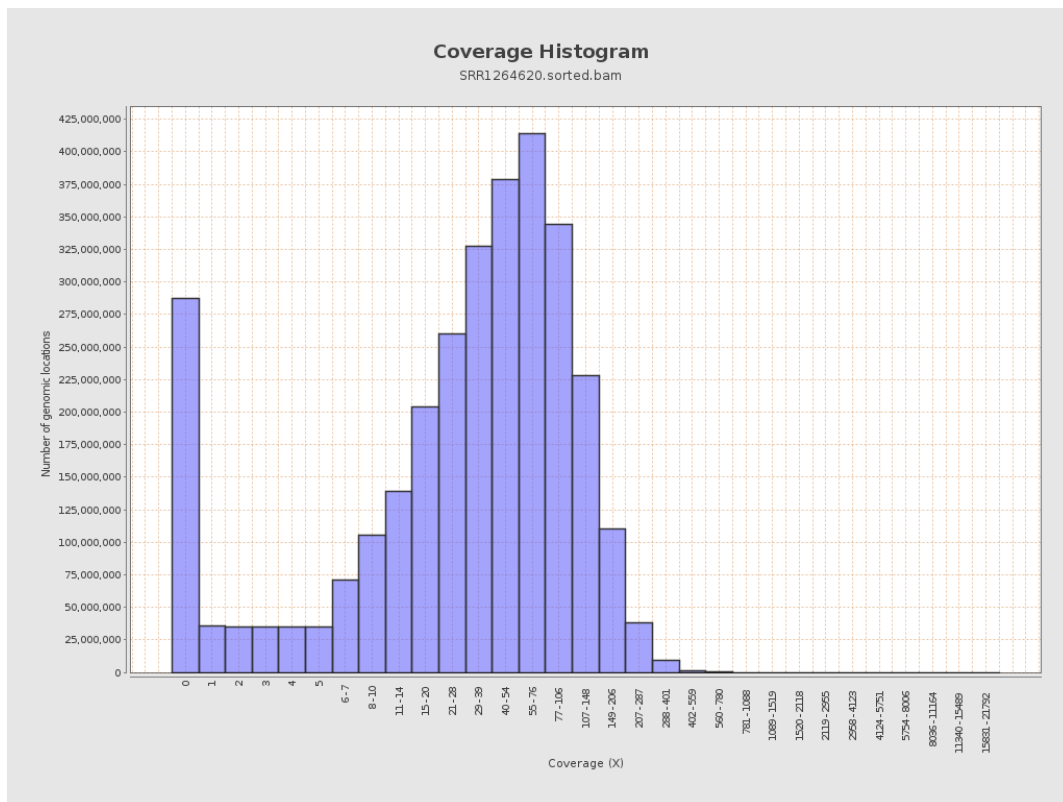
		bases	coverage	deviation
chr1	249250621	12324539417	49.4464	53.0548
chr2	243199373	14581101418	59.9553	53.5093
chr3	198022430	12874200055	65.0138	53.4661
chr4	191154276	12977002463	67.8876	53.8525
chr5	180915260	11818619287	65.3268	53.4682
chr6	171115067	11056731118	64.6158	55.3945
chr7	159138663	8949947589	56.2399	54.0582
chr8	146364022	8685466446	59.3415	50.7018
chr9	141213431	6753161300	47.8224	55.4462
chr10	135534747	6726513511	49.6294	45.9935
chr11	135006516	7579912078	56.1448	52.8008
chr12	133851895	7759166784	57.9683	57.1945
chr13	115169878	6538219808	56.7702	53.4977
chr14	107349540	5097772926	47.4876	51.6521
chr15	102531392	4295070772	41.8903	50.7163
chr16	90354753	2893707964	32.0261	38.7627
chr17	81195210	2746928419	33.8312	42.5913
chr18	78077248	4647753974	59.5276	50.0616
chr19	59128983	1126516561	19.0519	27.0646
chr20	63025520	2376407244	37.7055	48.871
chr21	48129895	2119196146	44.0308	56.8469
chr22	51304566	887747485	17.3035	29.0362
chrMT	16571	65946	3.9796	12.1617
chrX	155270560	5081125546	32.7243	34.2279

chrY	59373566	760322766	12.8057	28.9132
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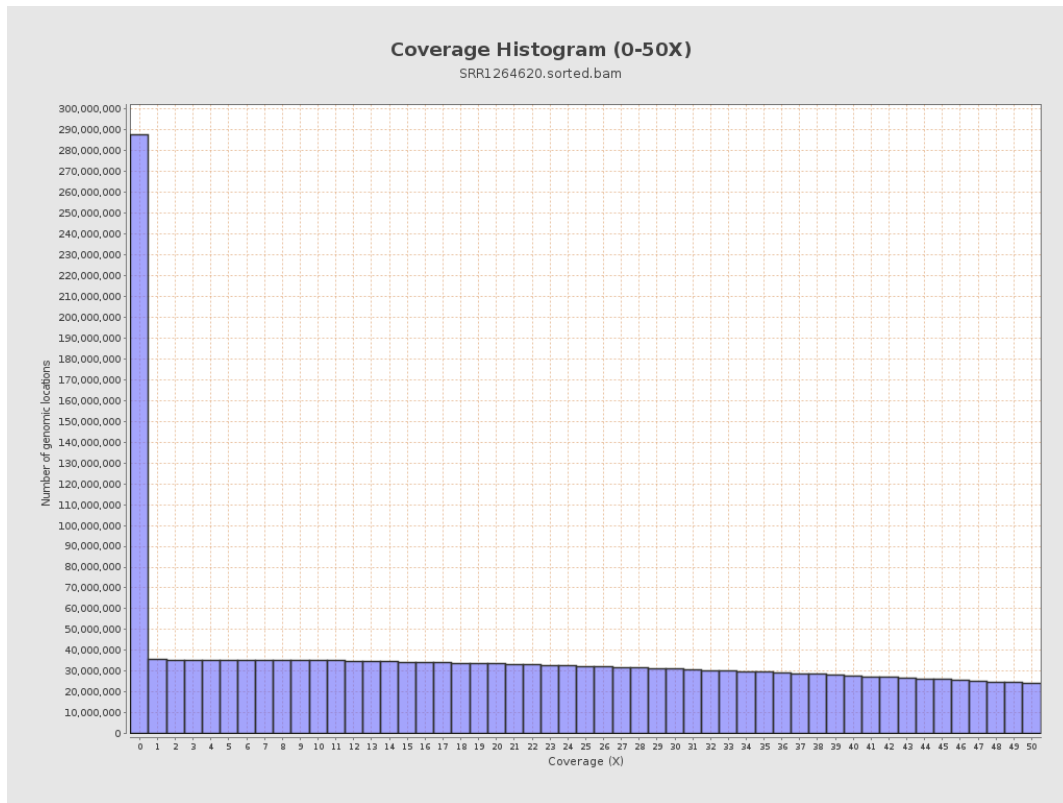
3. Results : Coverage across reference



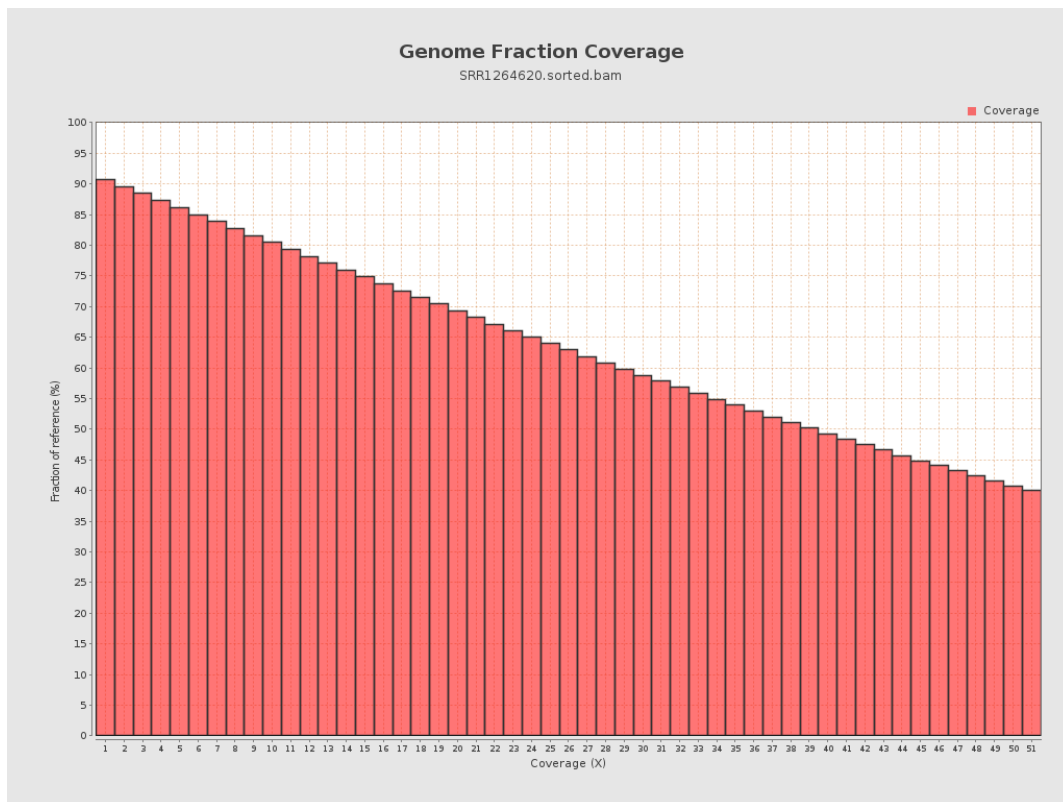
4. Results : Coverage Histogram



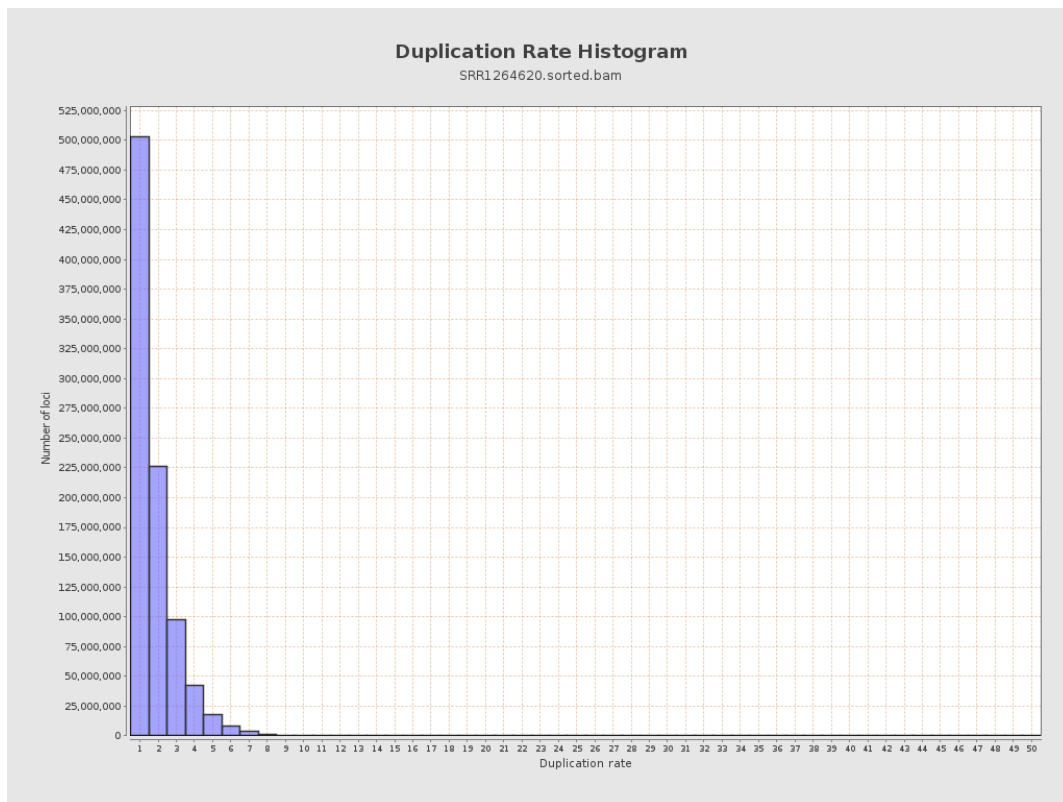
5. Results : Coverage Histogram (0-50X)



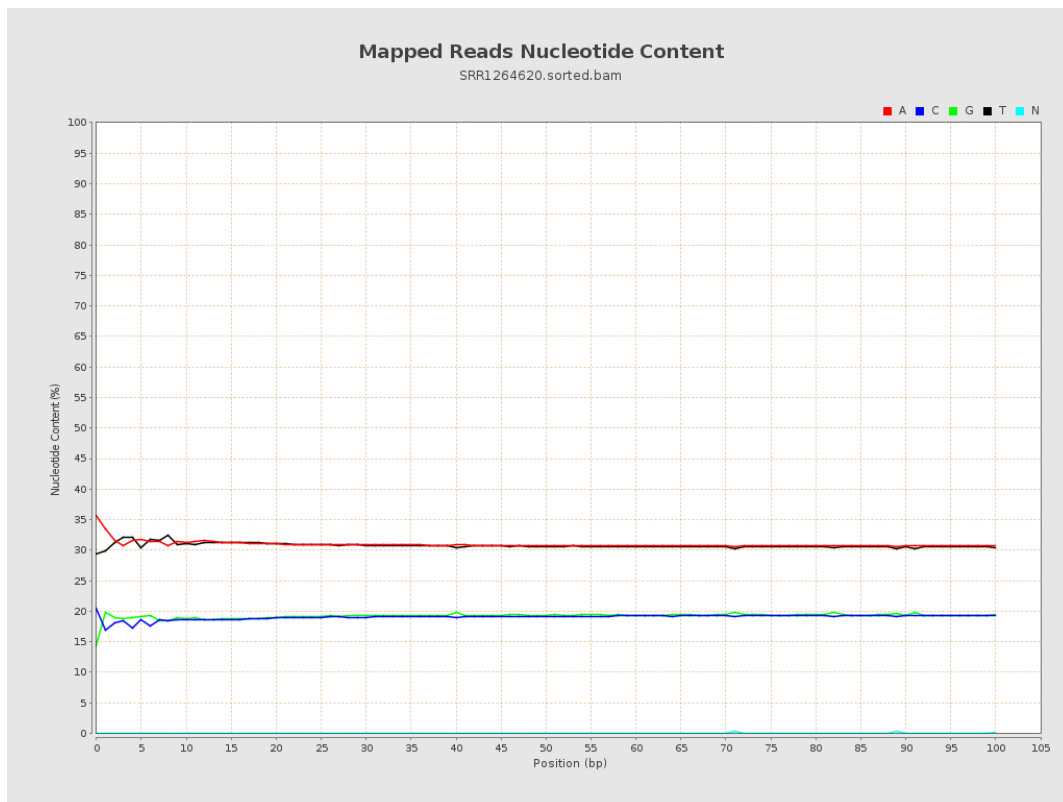
6. Results : Genome Fraction Coverage



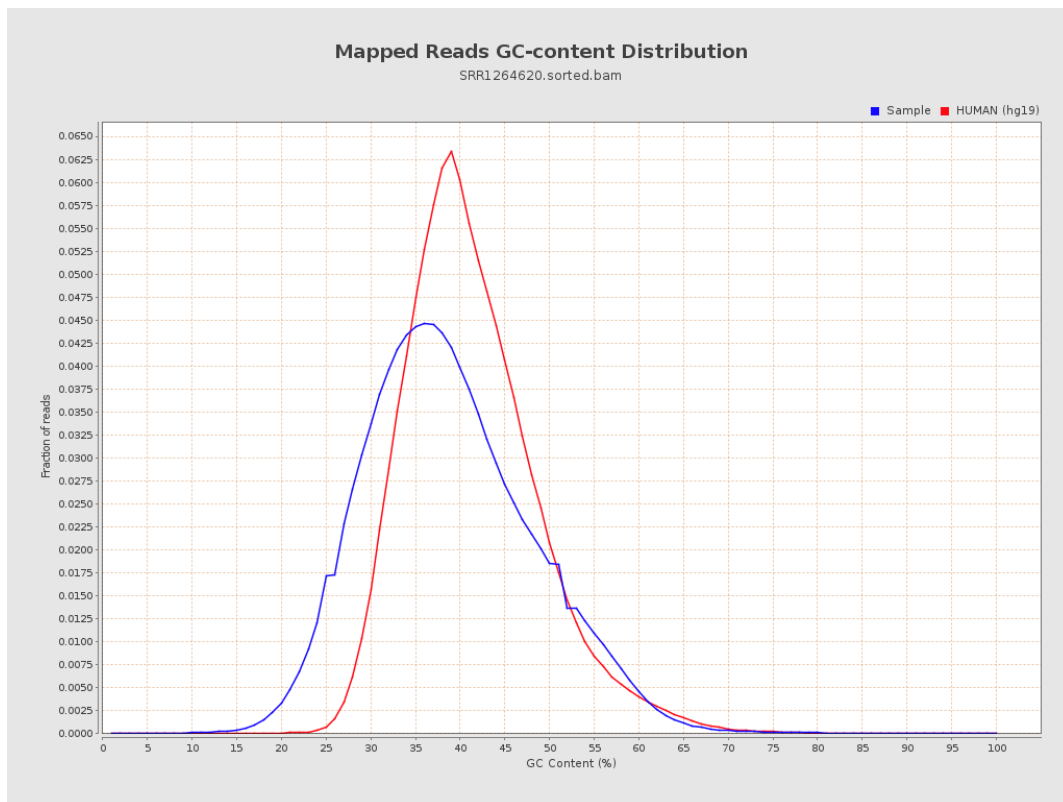
7. Results : Duplication Rate Histogram



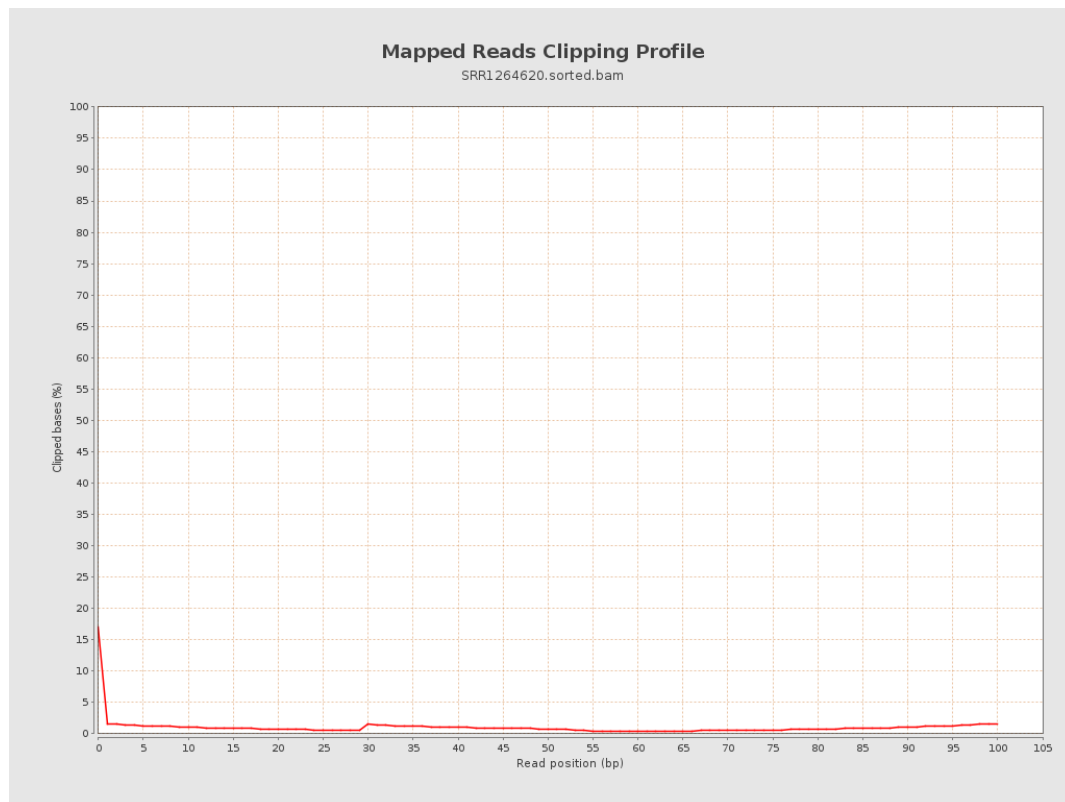
8. Results : Mapped Reads Nucleotide Content



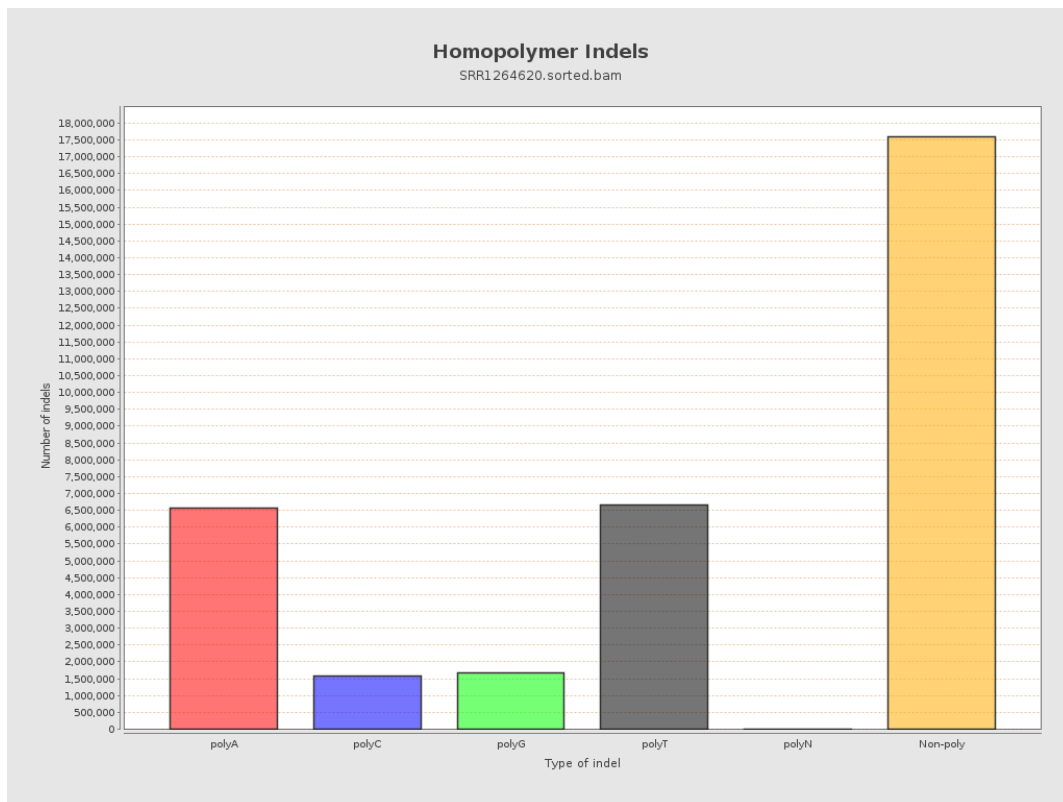
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



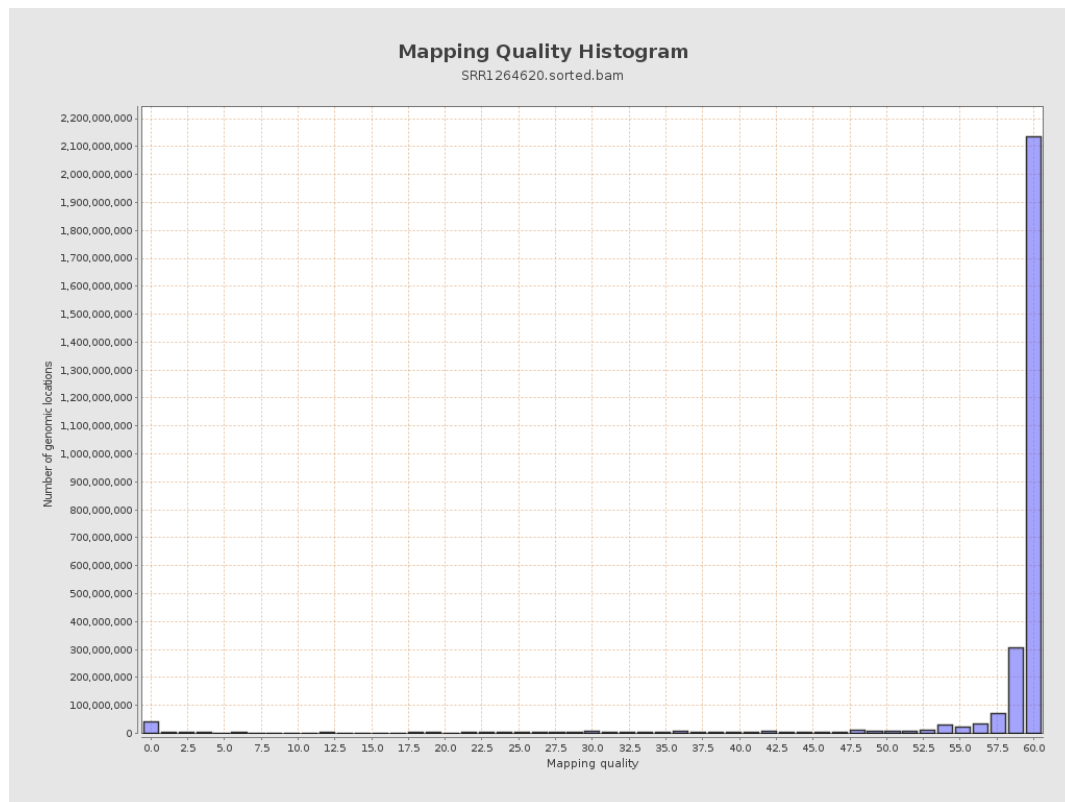
11. Results : Homopolymer Indels



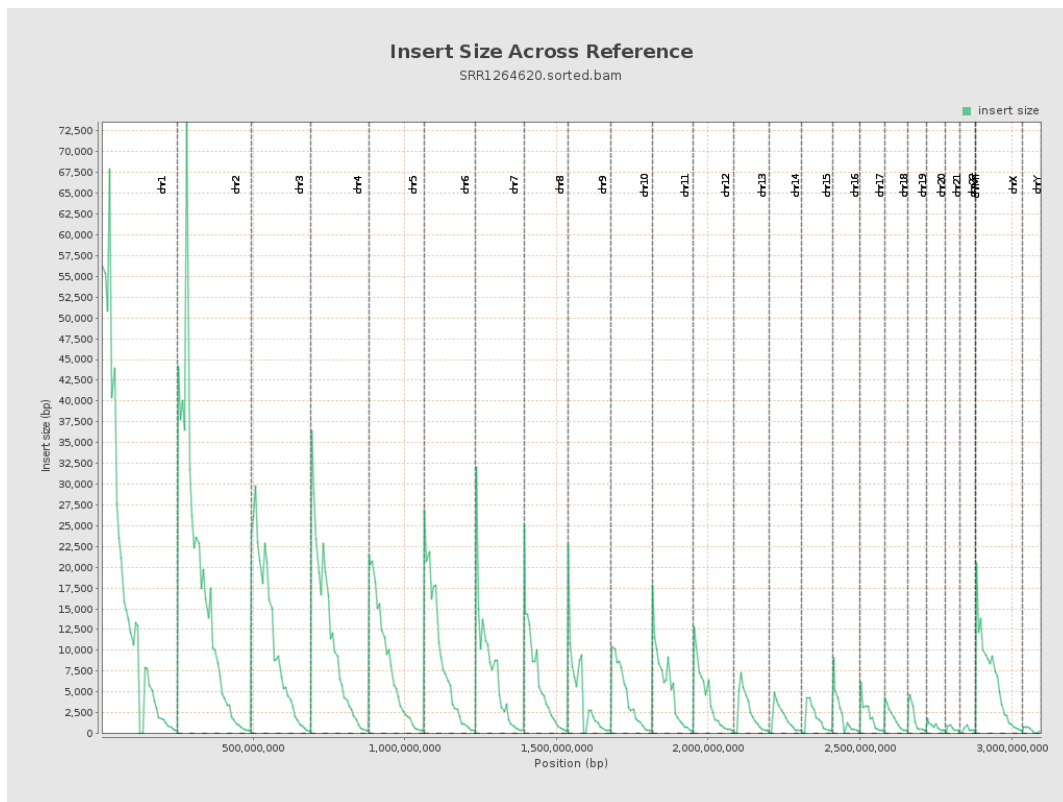
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

