

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 01:52:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777248.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_SRR1777248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777248_1.fastq.gz SRR1777248_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 01:52:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,009,904
Mapped reads	9,530,396 / 95.21%
Unmapped reads	479,508 / 4.79%
Mapped paired reads	9,530,396 / 95.21%
Mapped reads, first in pair	4,783,970 / 47.79%
Mapped reads, second in pair	4,746,426 / 47.42%
Mapped reads, both in pair	9,443,502 / 94.34%
Mapped reads, singletons	86,894 / 0.87%
Secondary alignments	0
Supplementary alignments	468,787 / 4.68%
Read min/max/mean length	30 / 101 / 102.83
Duplicated reads (estimated)	1,642,466 / 16.41%
Duplication rate	14.62%
Clipped reads	6,400,187 / 63.94%

2.2. ACGT Content

Number/percentage of A's	229,410,413 / 28.18%
Number/percentage of C's	156,749,714 / 19.25%
Number/percentage of T's	246,922,206 / 30.33%
Number/percentage of G's	181,025,179 / 22.24%
Number/percentage of N's	14,708 / 0%

GC Percentage	41.49%
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2.3. Coverage

Mean	0.2631
Standard Deviation	2.9486

2.4. Mapping Quality

Mean Mapping Quality	51.03
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2.5. Insert size

Mean	329,549.08
Standard Deviation	5,604,290.91
P25/Median/P75	89 / 127 / 177

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	5,434,352
Insertions	86,299
Mapped reads with at least one insertion	0.89%
Deletions	234,823
Mapped reads with at least one deletion	2.42%
Homopolymer indels	47.88%

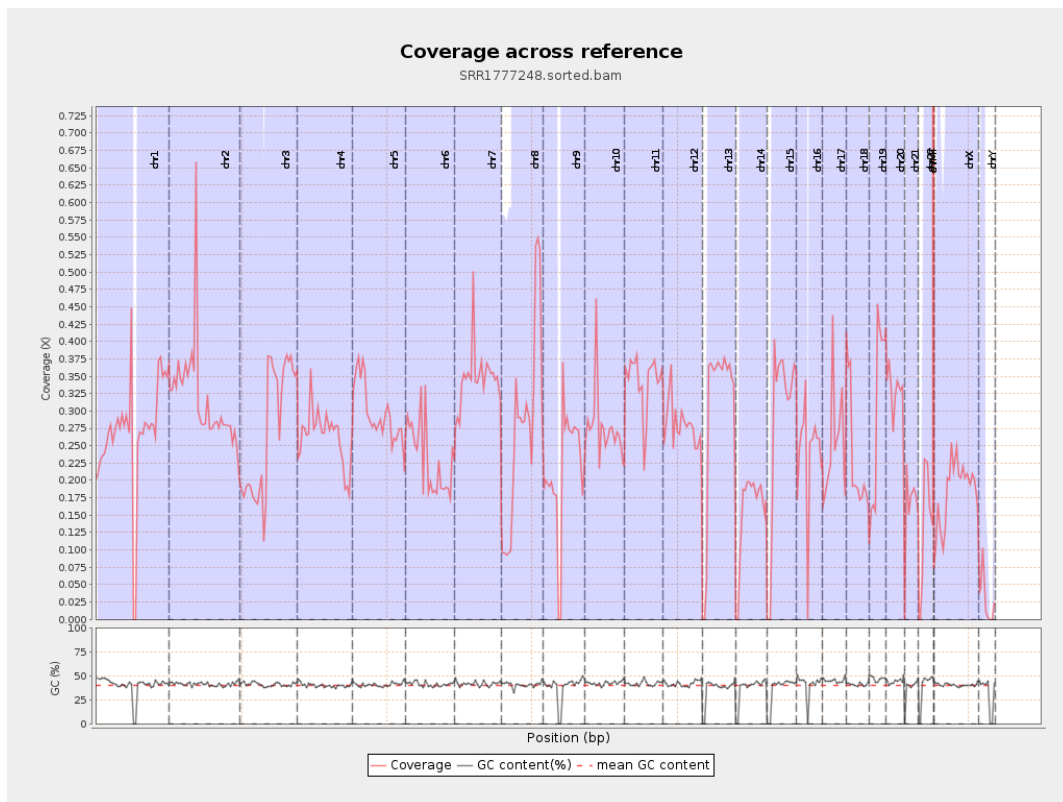
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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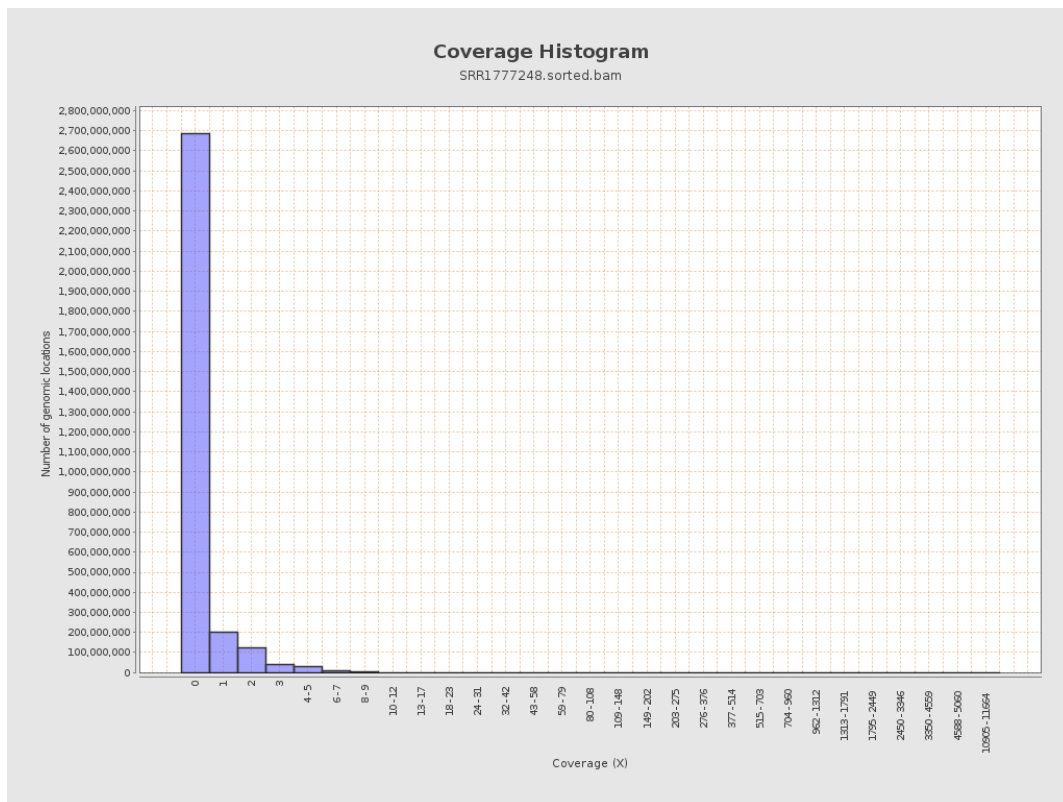
		bases	coverage	deviation
chr1	249250621	67536672	0.271	3.9544
chr2	243199373	77375843	0.3182	2.6015
chr3	198022430	53310341	0.2692	0.8477
chr4	191154276	50304436	0.2632	1.1004
chr5	180915260	53781132	0.2973	0.8995
chr6	171115067	39446736	0.2305	8.3817
chr7	159138663	55404161	0.3482	3.1548
chr8	146364022	40593674	0.2773	3.9737
chr9	141213431	30261442	0.2143	2.8873
chr10	135534747	37457246	0.2764	2.1261
chr11	135006516	46130528	0.3417	1.8223
chr12	133851895	37227925	0.2781	1.2262
chr13	115169878	34483101	0.2994	0.8957
chr14	107349540	16557427	0.1542	0.7507
chr15	102531392	29638589	0.2891	0.8911
chr16	90354753	21669444	0.2398	1.3135
chr17	81195210	20276996	0.2497	1.0779
chr18	78077248	18001587	0.2306	3.534
chr19	59128983	17871558	0.3022	2.6319
chr20	63025520	20554303	0.3261	0.9746
chr21	48129895	7854817	0.1632	0.8333
chr22	51304566	6618552	0.129	0.5855
chrMT	16571	1961634	118.3775	65.5262
chrX	155270560	28596110	0.1842	0.9503

chrY	59373566	1629690	0.0274	1.0123
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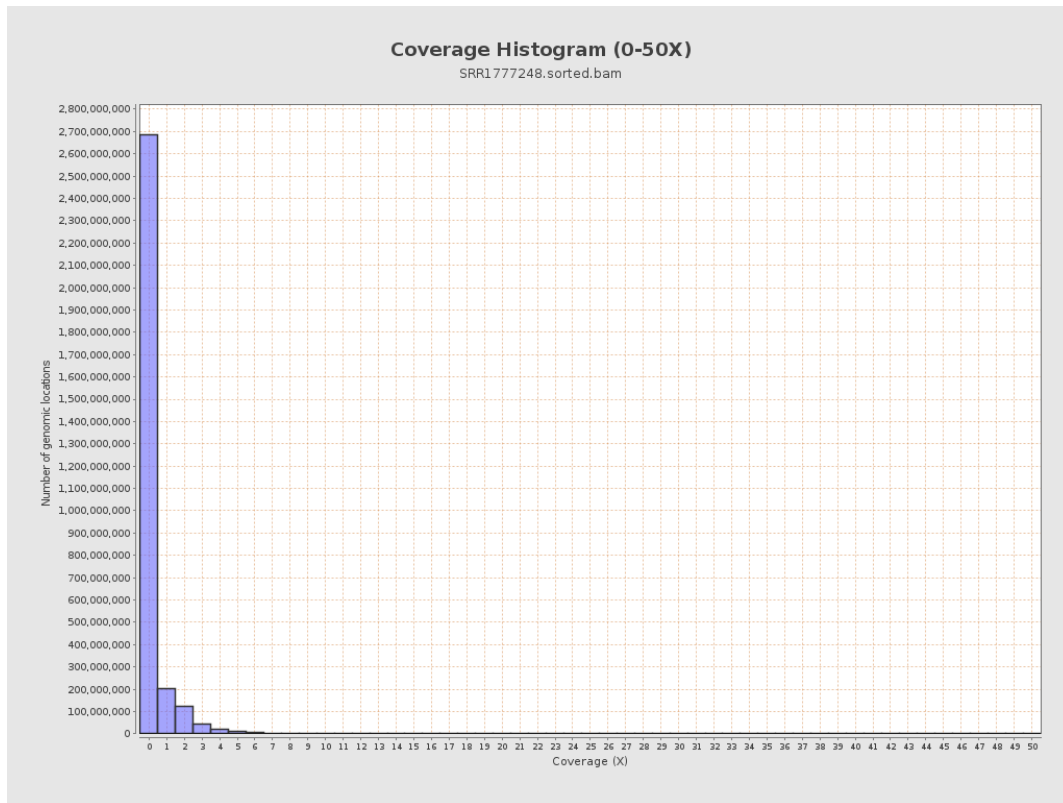
3. Results : Coverage across reference



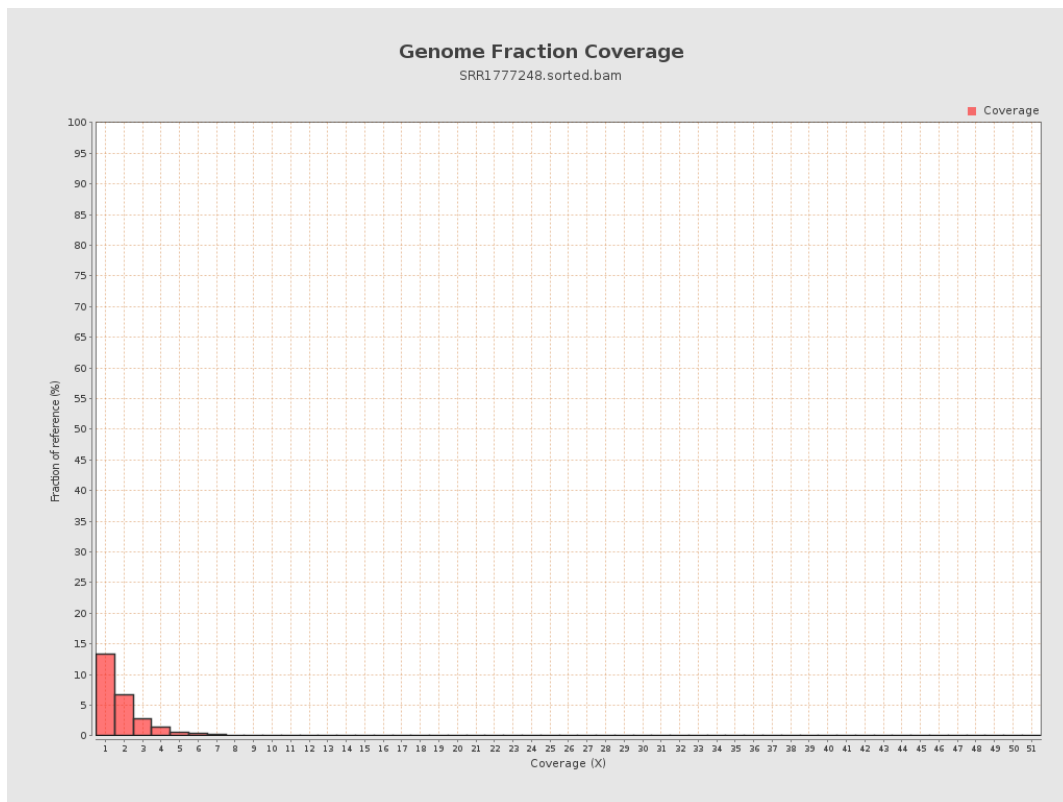
4. Results : Coverage Histogram



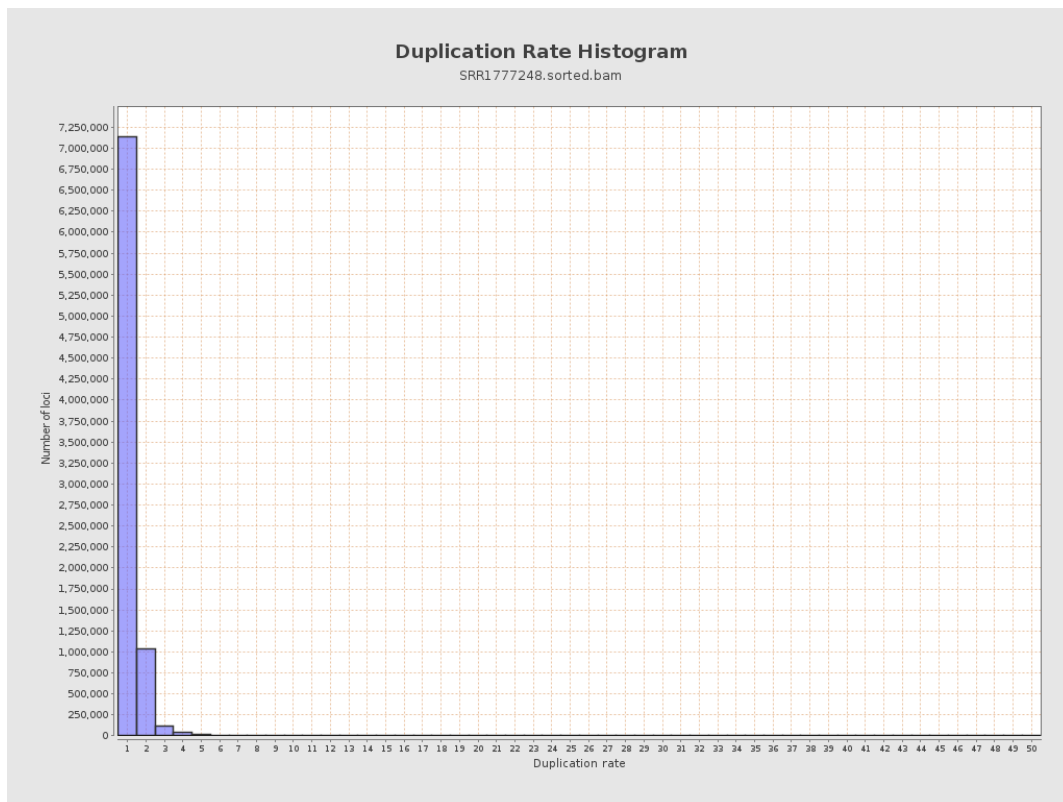
5. Results : Coverage Histogram (0-50X)



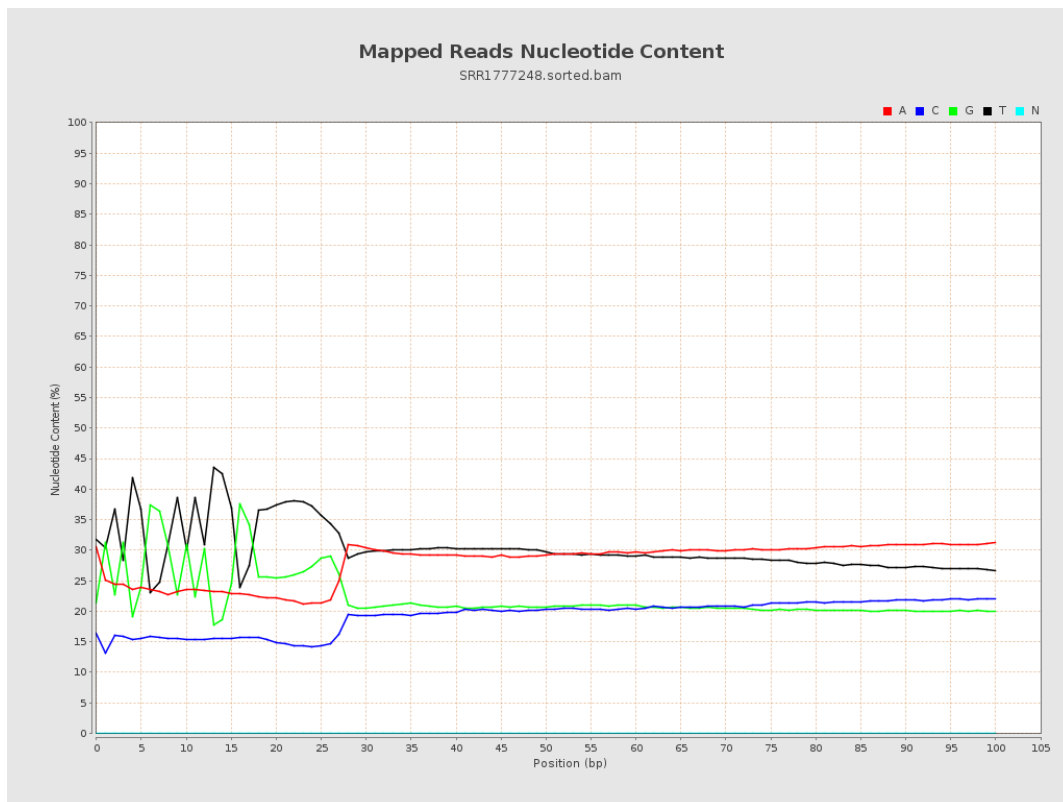
6. Results : Genome Fraction Coverage



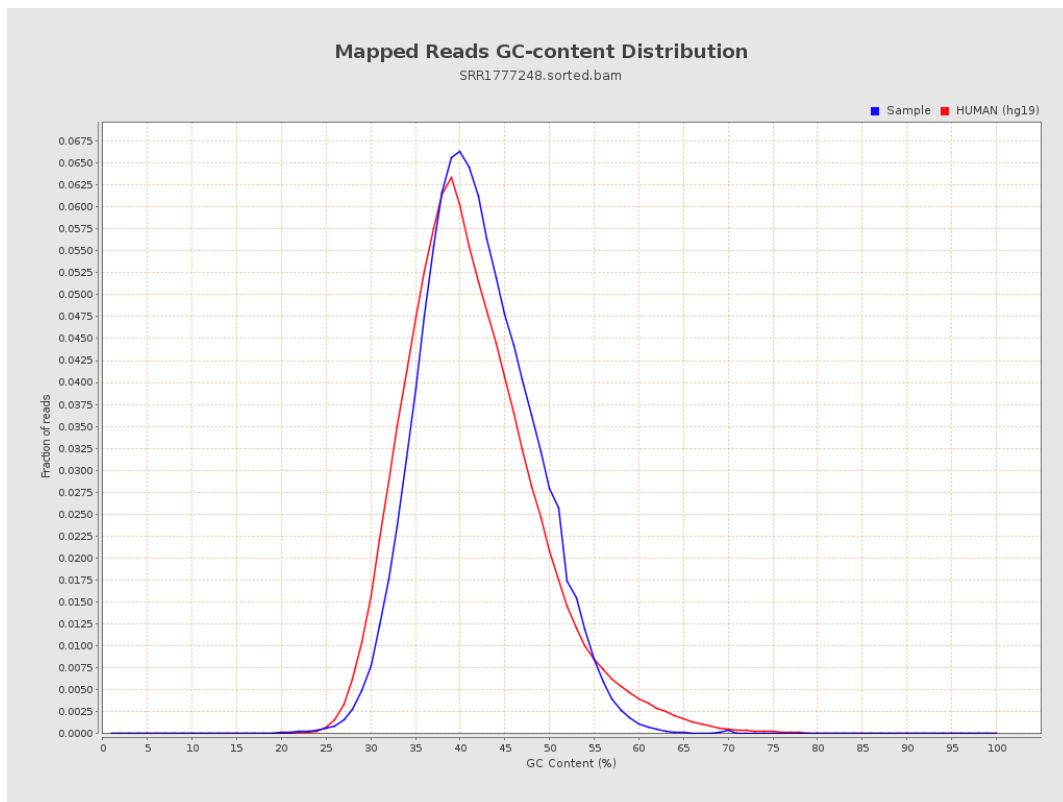
7. Results : Duplication Rate Histogram



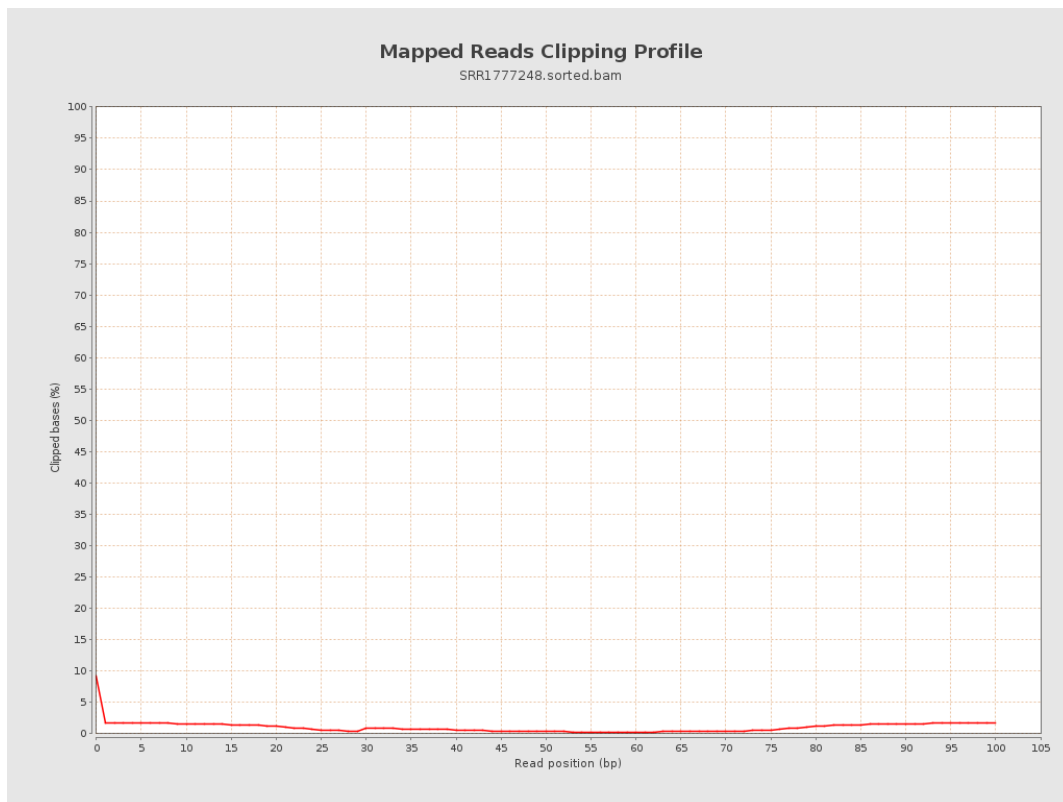
8. Results : Mapped Reads Nucleotide Content



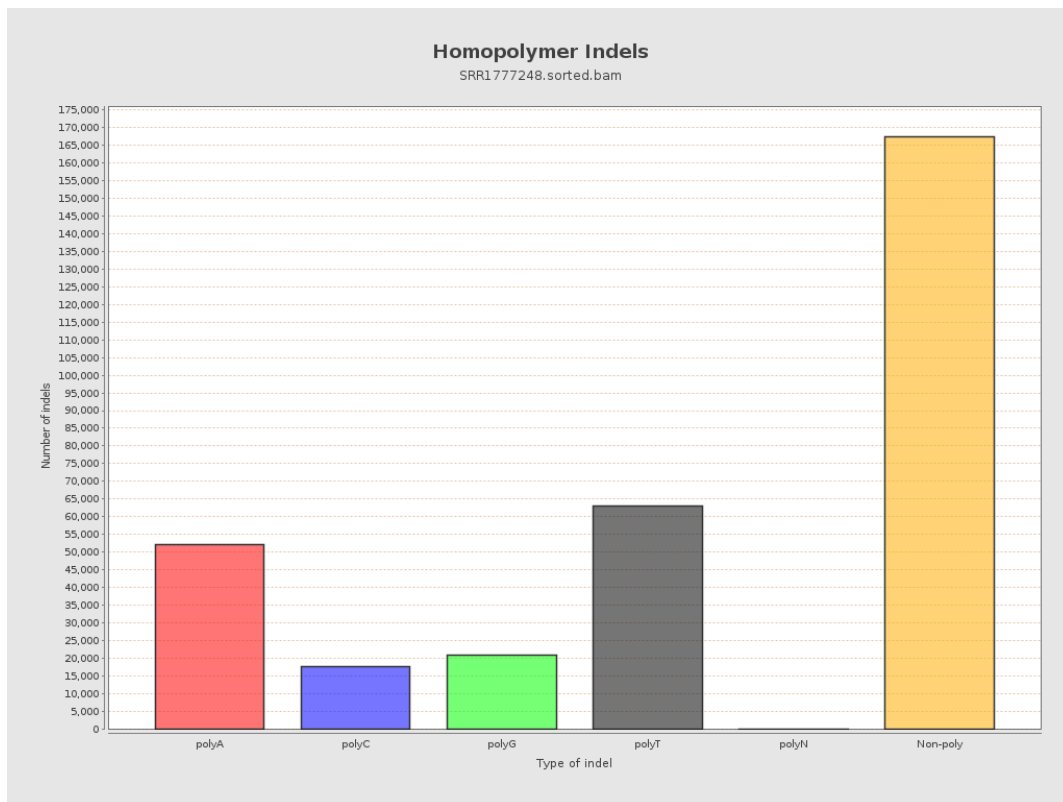
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



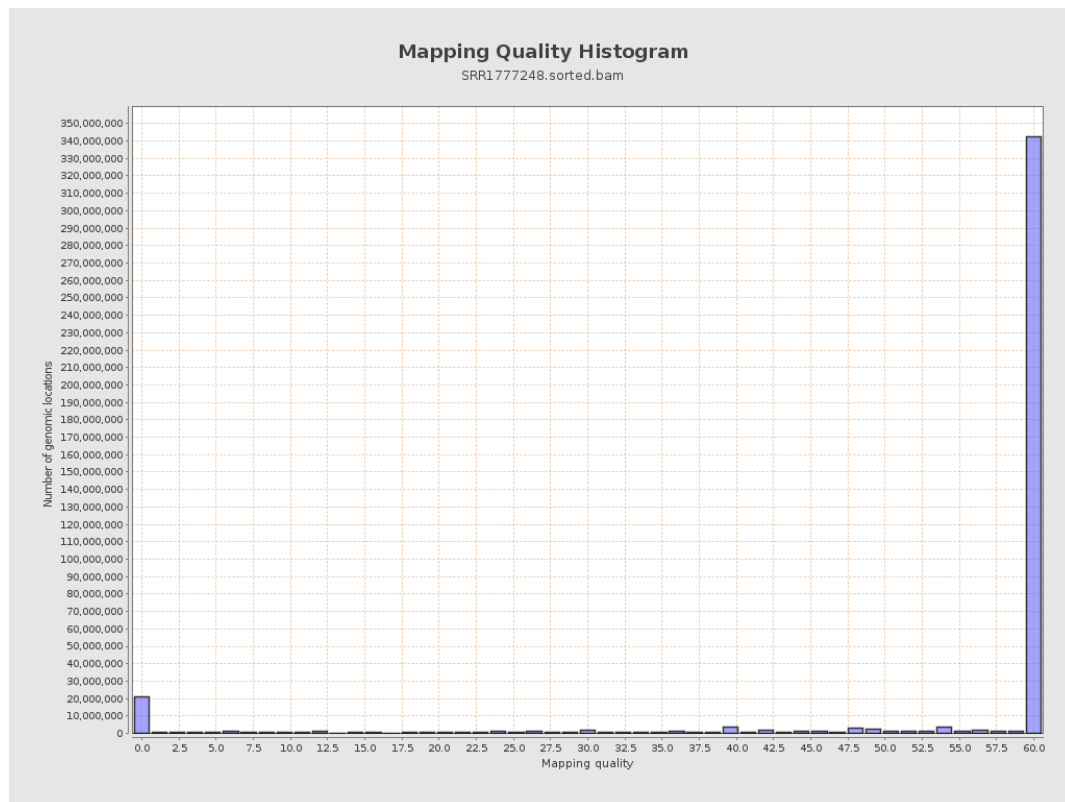
11. Results : Homopolymer Indels



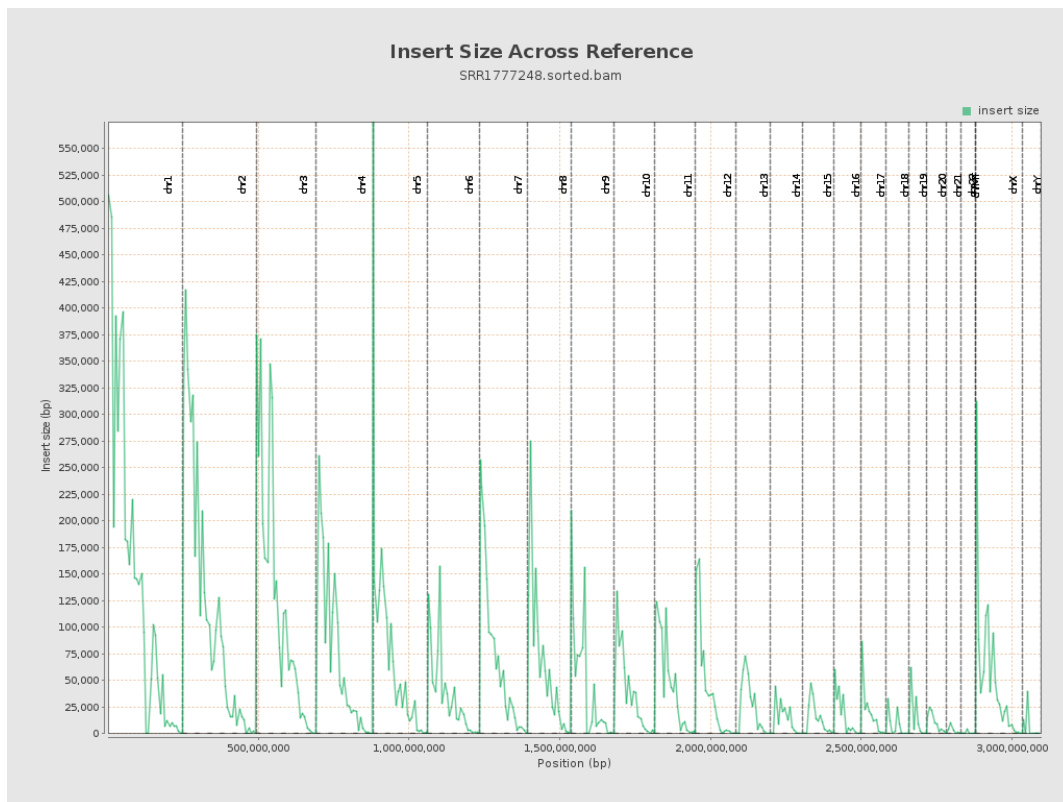
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

