

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 01:48:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779421.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_SRR1779421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779421_1.fastq.gz SRR1779421_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 01:48:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,284,056
Mapped reads	14,126,753 / 92.43%
Unmapped reads	1,157,303 / 7.57%
Mapped paired reads	14,126,753 / 92.43%
Mapped reads, first in pair	7,116,832 / 46.56%
Mapped reads, second in pair	7,009,921 / 45.86%
Mapped reads, both in pair	13,971,794 / 91.41%
Mapped reads, singletons	154,959 / 1.01%
Secondary alignments	0
Supplementary alignments	70,467 / 0.46%
Read min/max/mean length	30 / 80 / 80.17
Duplicated reads (estimated)	1,053,375 / 6.89%
Duplication rate	5.83%
Clipped reads	705,248 / 4.61%

2.2. ACGT Content

Number/percentage of A's	350,246,990 / 31.22%
Number/percentage of C's	210,170,760 / 18.73%
Number/percentage of T's	345,141,658 / 30.76%
Number/percentage of G's	216,161,566 / 19.27%
Number/percentage of N's	251,481 / 0.02%

GC Percentage	38%
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2.3. Coverage

Mean	0.3625
Standard Deviation	3.4747

2.4. Mapping Quality

Mean Mapping Quality	52.91
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2.5. Insert size

Mean	46,375.63
Standard Deviation	2,035,031.11
P25/Median/P75	155 / 199 / 252

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	4,369,274
Insertions	106,644
Mapped reads with at least one insertion	0.75%
Deletions	121,002
Mapped reads with at least one deletion	0.85%
Homopolymer indels	47.07%

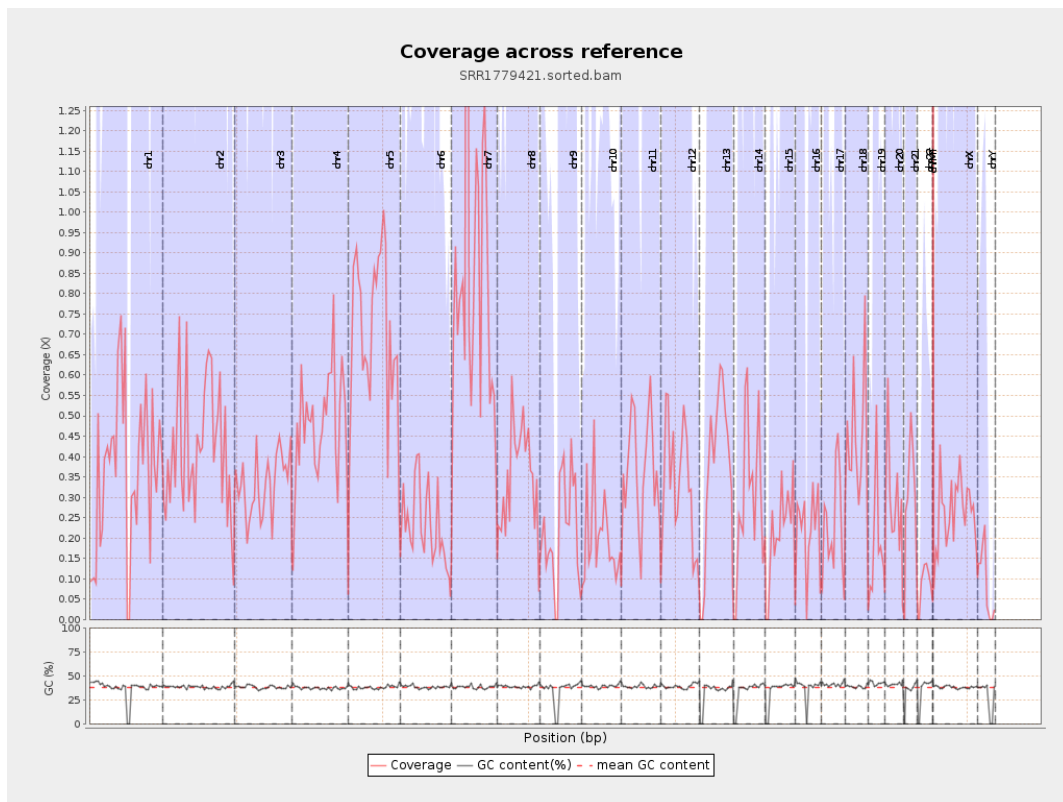
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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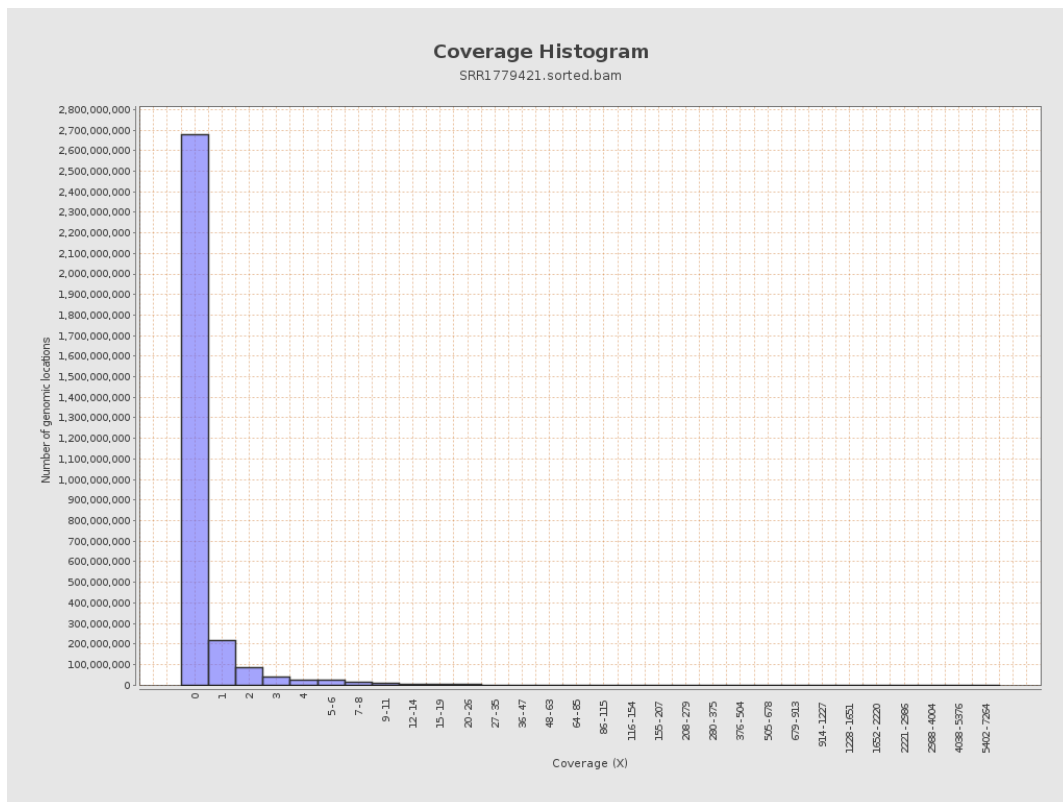
		bases	coverage	deviation
chr1	249250621	91427649	0.3668	8.0577
chr2	243199373	102314619	0.4207	2.2042
chr3	198022430	65536105	0.331	2.5296
chr4	191154276	90742337	0.4747	1.9495
chr5	180915260	125349119	0.6929	2.2499
chr6	171115067	40395900	0.2361	4.2134
chr7	159138663	138297962	0.869	5.7899
chr8	146364022	51415990	0.3513	1.8883
chr9	141213431	31250023	0.2213	1.8879
chr10	135534747	26666878	0.1968	4.8139
chr11	135006516	49584428	0.3673	1.7597
chr12	133851895	43906978	0.328	1.6362
chr13	115169878	43117356	0.3744	1.5755
chr14	107349540	32507130	0.3028	1.5748
chr15	102531392	21851623	0.2131	1.0755
chr16	90354753	18898825	0.2092	1.2538
chr17	81195210	19196791	0.2364	1.5596
chr18	78077248	35235268	0.4513	2.7707
chr19	59128983	11148062	0.1885	5.1232
chr20	63025520	18488141	0.2933	1.3444
chr21	48129895	14184648	0.2947	1.3543
chr22	51304566	4477388	0.0873	0.5547
chrMT	16571	46876	2.8288	1.9337
chrX	155270560	40708951	0.2622	1.3683

chrY	59373566	5466541	0.0921	0.6462
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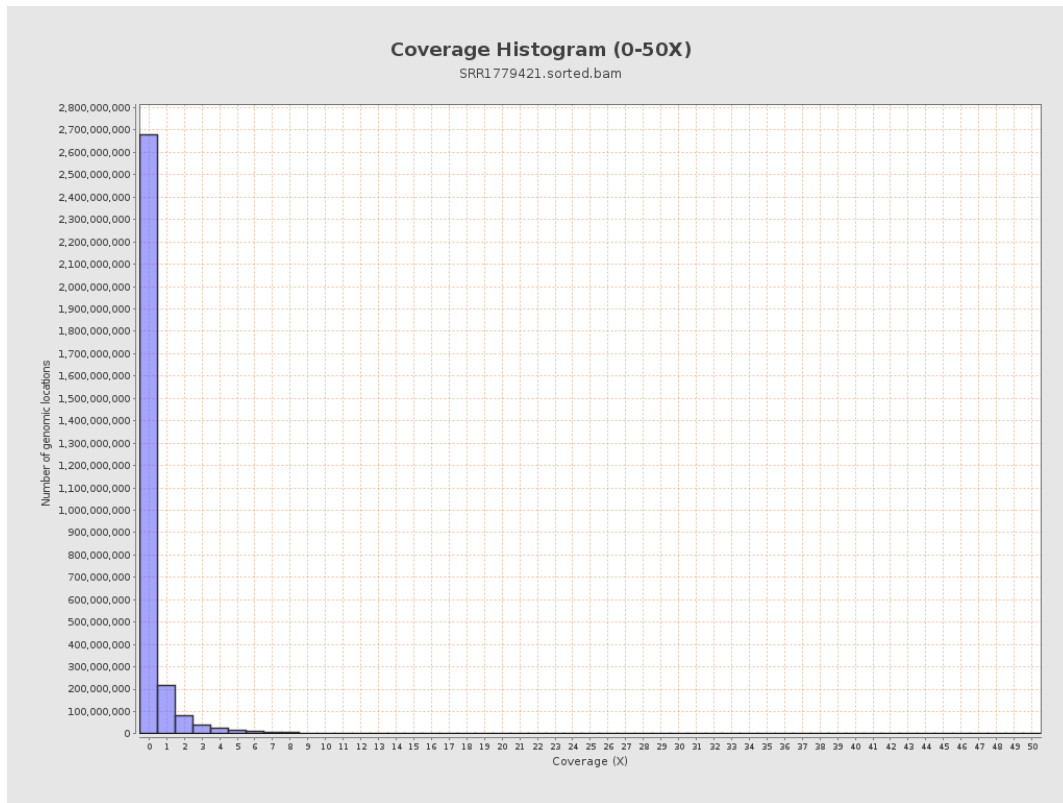
3. Results : Coverage across reference



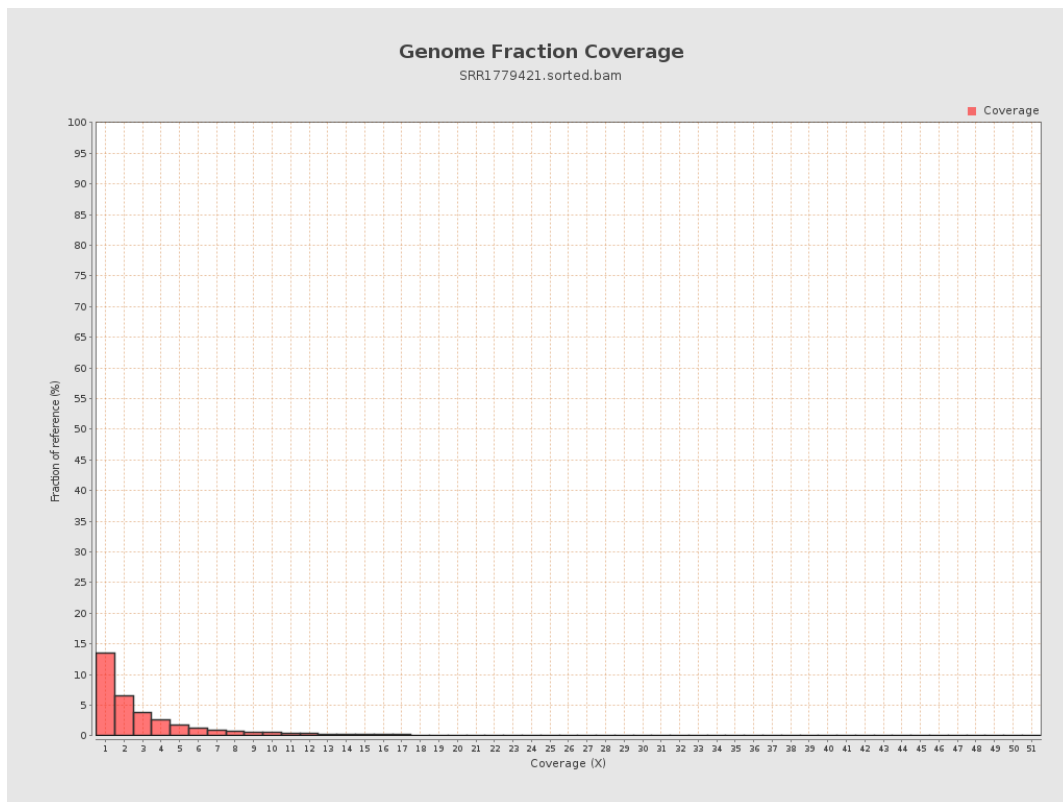
4. Results : Coverage Histogram



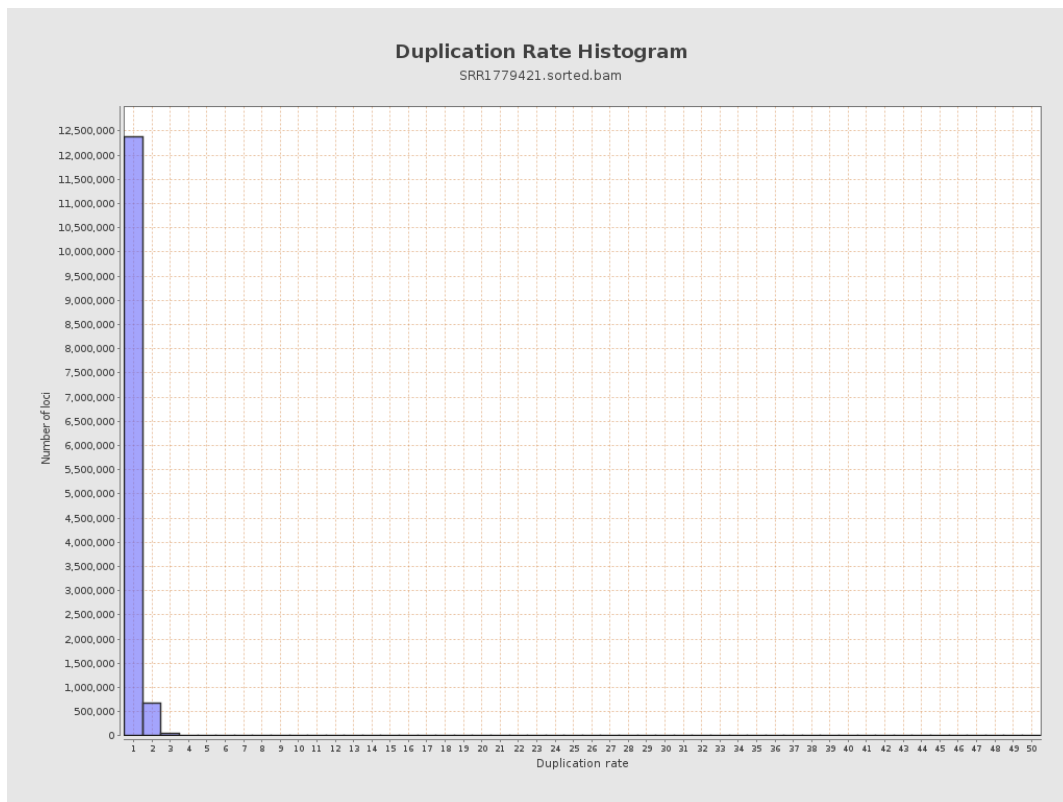
5. Results : Coverage Histogram (0-50X)



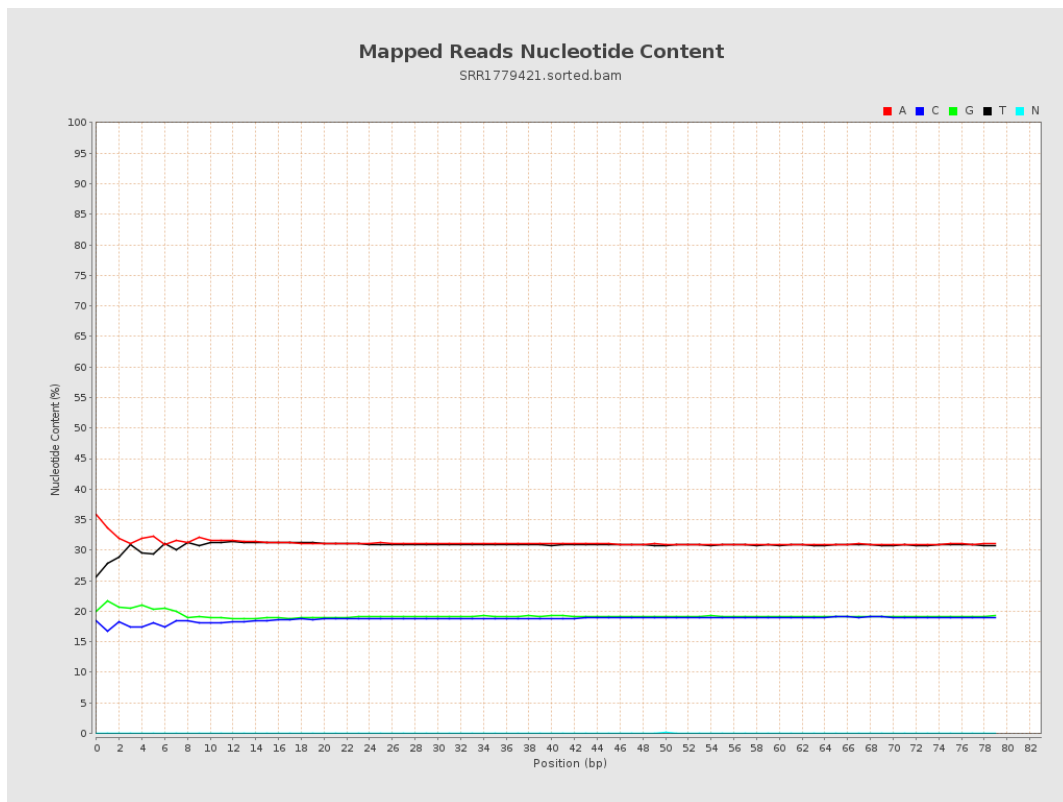
6. Results : Genome Fraction Coverage



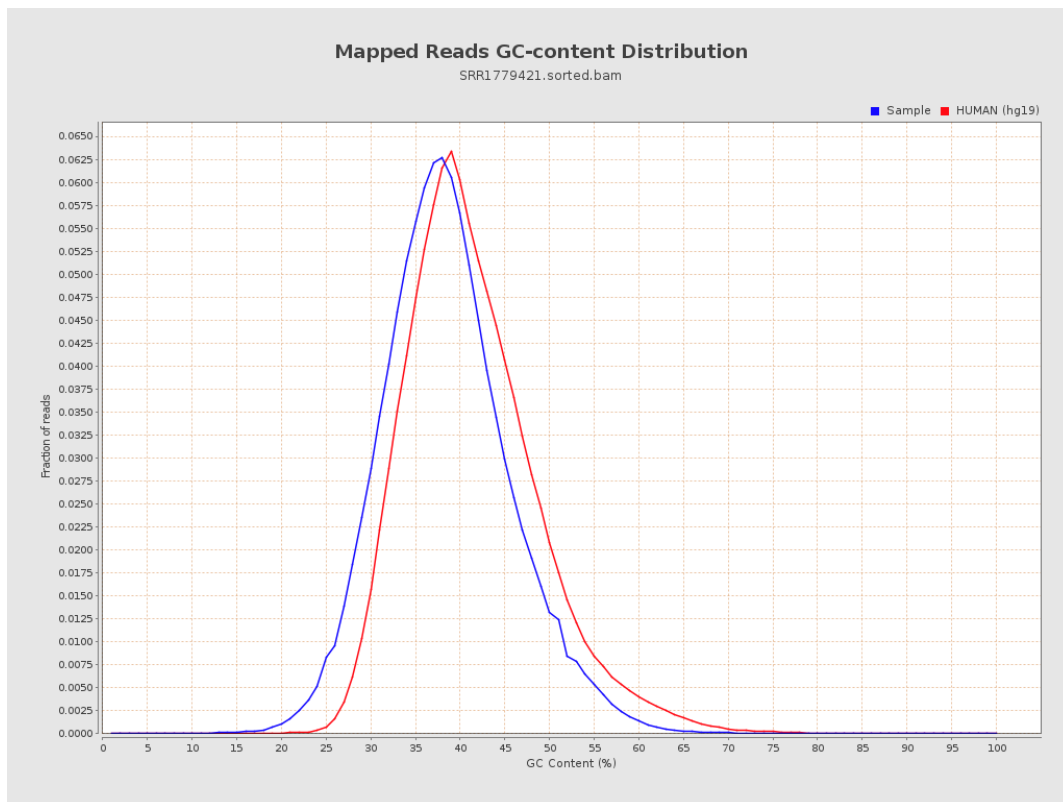
7. Results : Duplication Rate Histogram



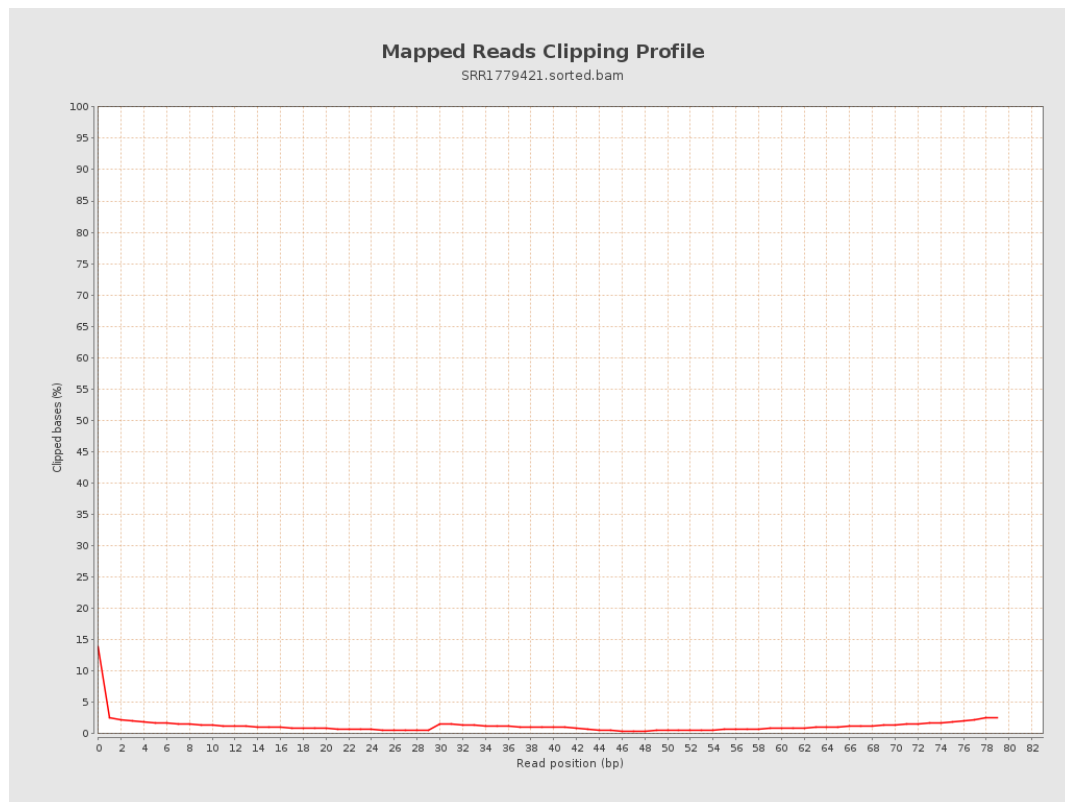
8. Results : Mapped Reads Nucleotide Content



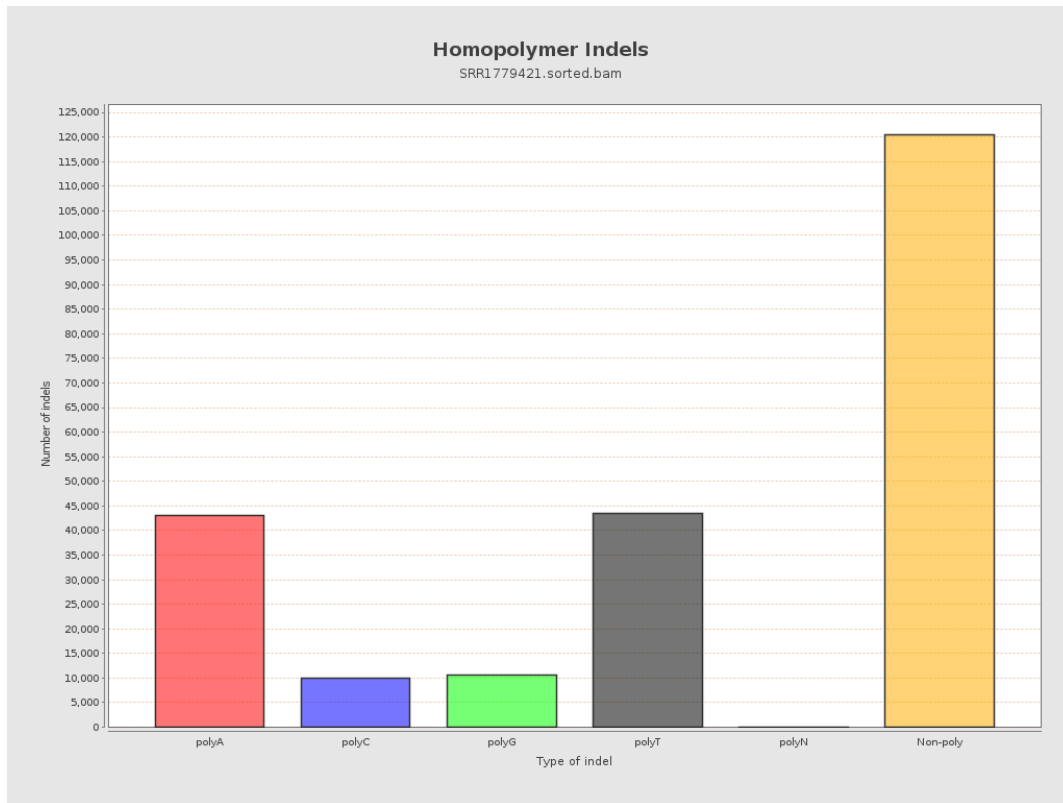
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



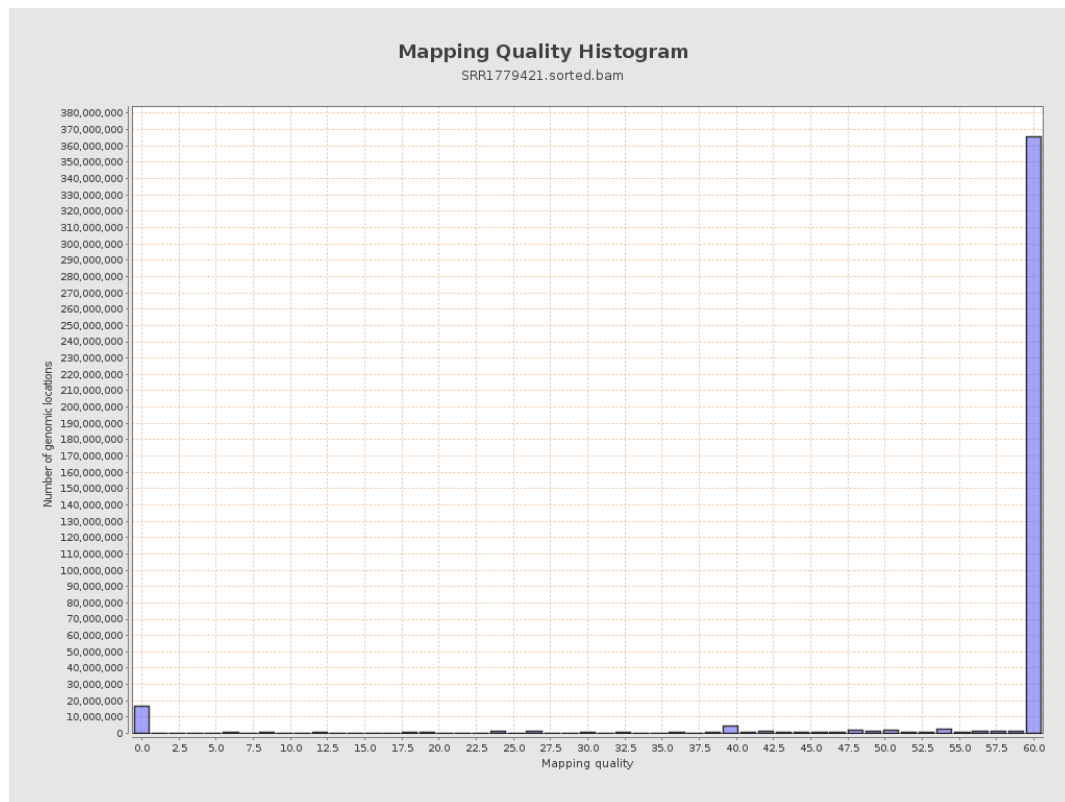
11. Results : Homopolymer Indels



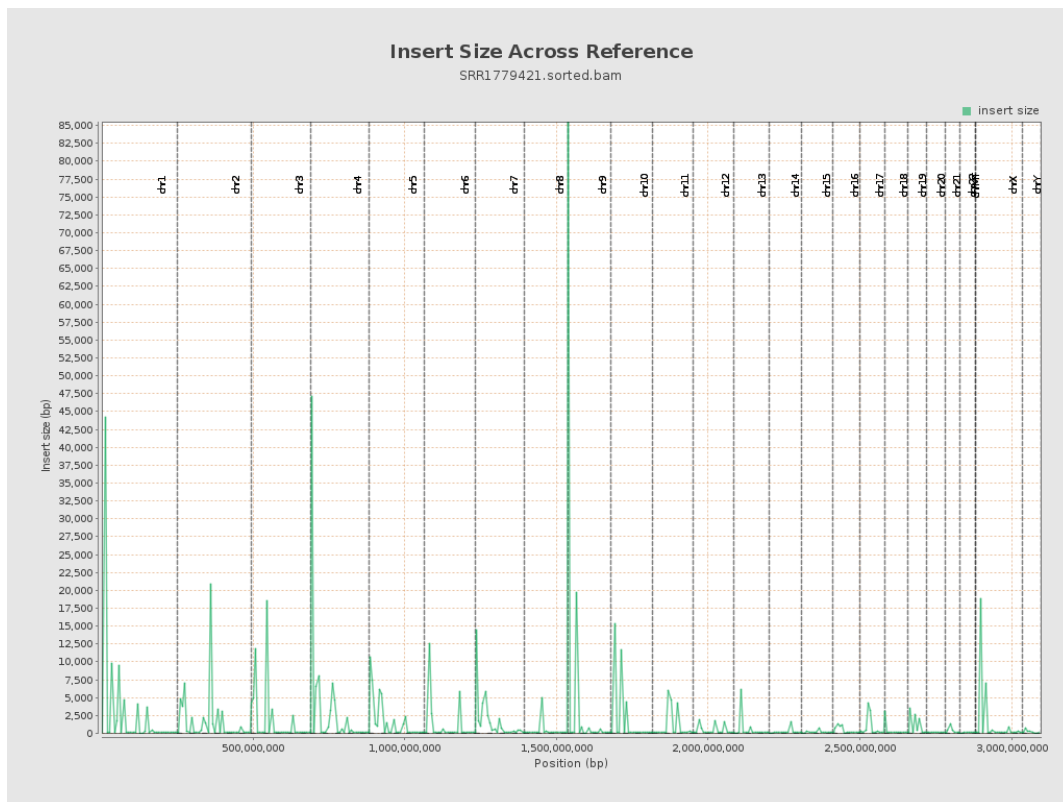
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

