

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 08:44:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779318.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_SRR1779318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779318_1.fastq.gz SRR1779318_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 08:44:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,416,760
Mapped reads	12,466,194 / 86.47%
Unmapped reads	1,950,566 / 13.53%
Mapped paired reads	12,466,194 / 86.47%
Mapped reads, first in pair	6,318,017 / 43.82%
Mapped reads, second in pair	6,148,177 / 42.65%
Mapped reads, both in pair	12,260,592 / 85.04%
Mapped reads, singletons	205,602 / 1.43%
Secondary alignments	0
Supplementary alignments	33,618 / 0.23%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	412,435 / 2.86%
Duplication rate	3.06%
Clipped reads	426,595 / 2.96%

2.2. ACGT Content

Number/percentage of A's	303,605,757 / 30.62%
Number/percentage of C's	190,305,873 / 19.2%
Number/percentage of T's	303,524,324 / 30.62%
Number/percentage of G's	193,719,047 / 19.54%
Number/percentage of N's	254,683 / 0.03%

GC Percentage	38.74%
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2.3. Coverage

Mean	0.3203
Standard Deviation	1.3565

2.4. Mapping Quality

Mean Mapping Quality	53.24
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2.5. Insert size

Mean	43,045.82
Standard Deviation	1,964,853.02
P25/Median/P75	184 / 240 / 314

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	3,768,080
Insertions	73,318
Mapped reads with at least one insertion	0.58%
Deletions	92,027
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.98%

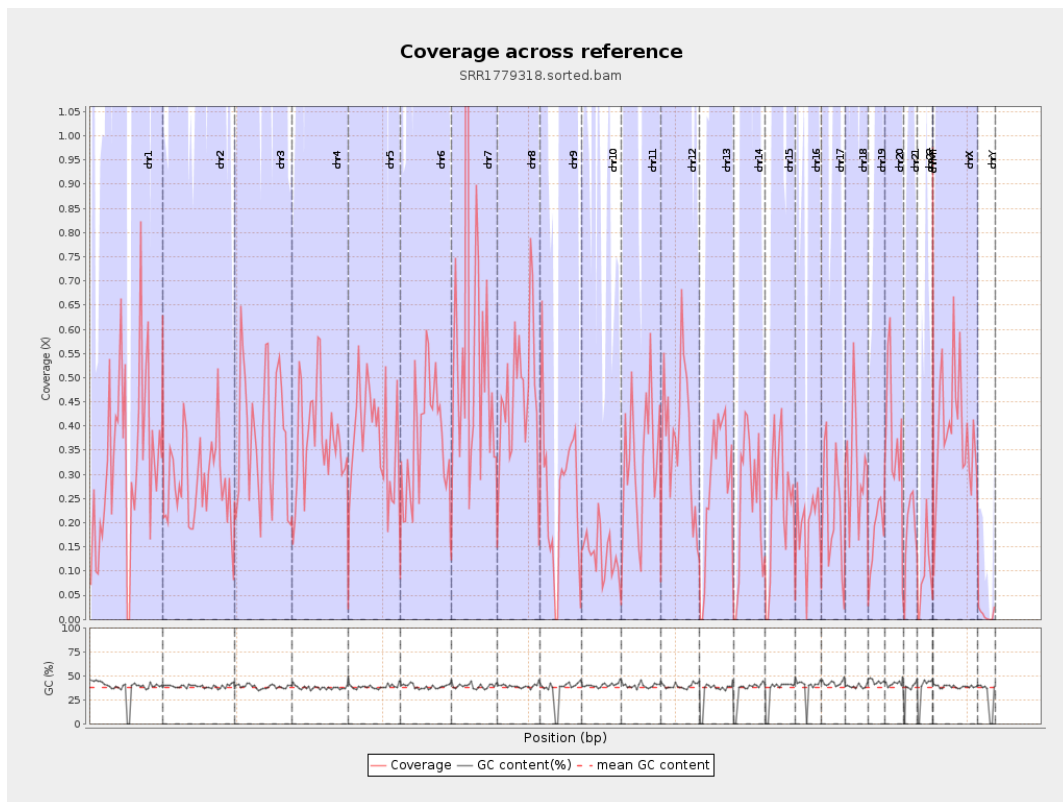
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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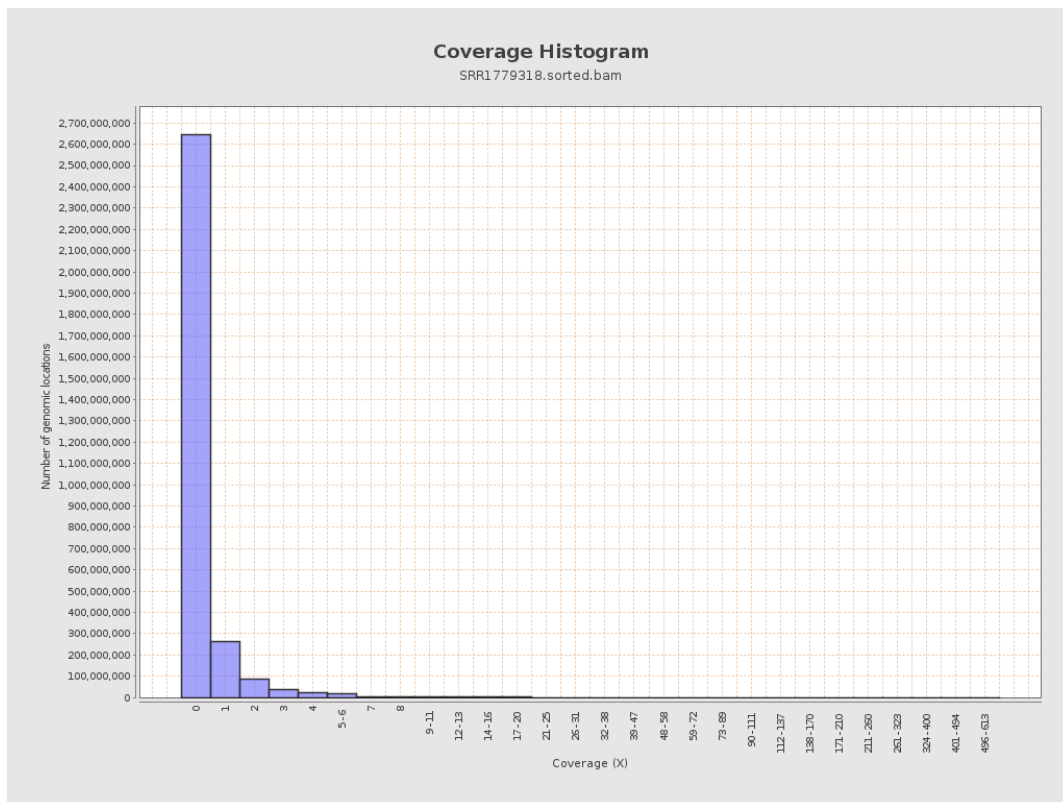
		bases	coverage	deviation
chr1	249250621	81255872	0.326	1.5683
chr2	243199373	67985972	0.2795	1.0387
chr3	198022430	75345991	0.3805	1.4149
chr4	191154276	71454124	0.3738	1.4307
chr5	180915260	66885026	0.3697	1.3913
chr6	171115067	63927460	0.3736	1.3448
chr7	159138663	92266266	0.5798	2.3468
chr8	146364022	68551884	0.4684	1.4531
chr9	141213431	36812098	0.2607	1.1949
chr10	135534747	18464136	0.1362	1.1138
chr11	135006516	44742230	0.3314	1.3778
chr12	133851895	50016288	0.3737	1.3284
chr13	115169878	32350837	0.2809	1.0819
chr14	107349540	26392092	0.2459	1.0858
chr15	102531392	24422074	0.2382	1.1033
chr16	90354753	17137819	0.1897	0.8115
chr17	81195210	18754846	0.231	1.1655
chr18	78077248	25041271	0.3207	1.2279
chr19	59128983	10758453	0.1819	0.8824
chr20	63025520	24537465	0.3893	1.7292
chr21	48129895	8883554	0.1846	0.7643
chr22	51304566	5015674	0.0978	0.4969
chrMT	16571	16184	0.9766	1.0597
chrX	155270560	59969762	0.3862	1.4744

chrY	59373566	614040	0.0103	0.1782
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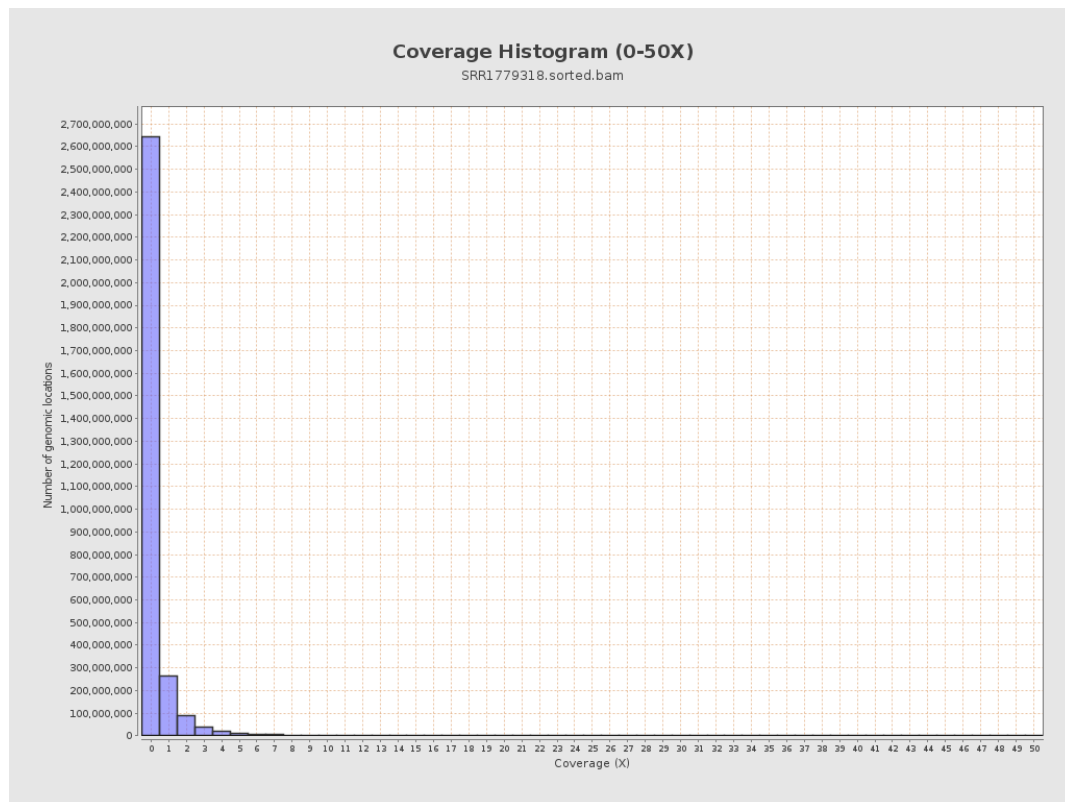
3. Results : Coverage across reference



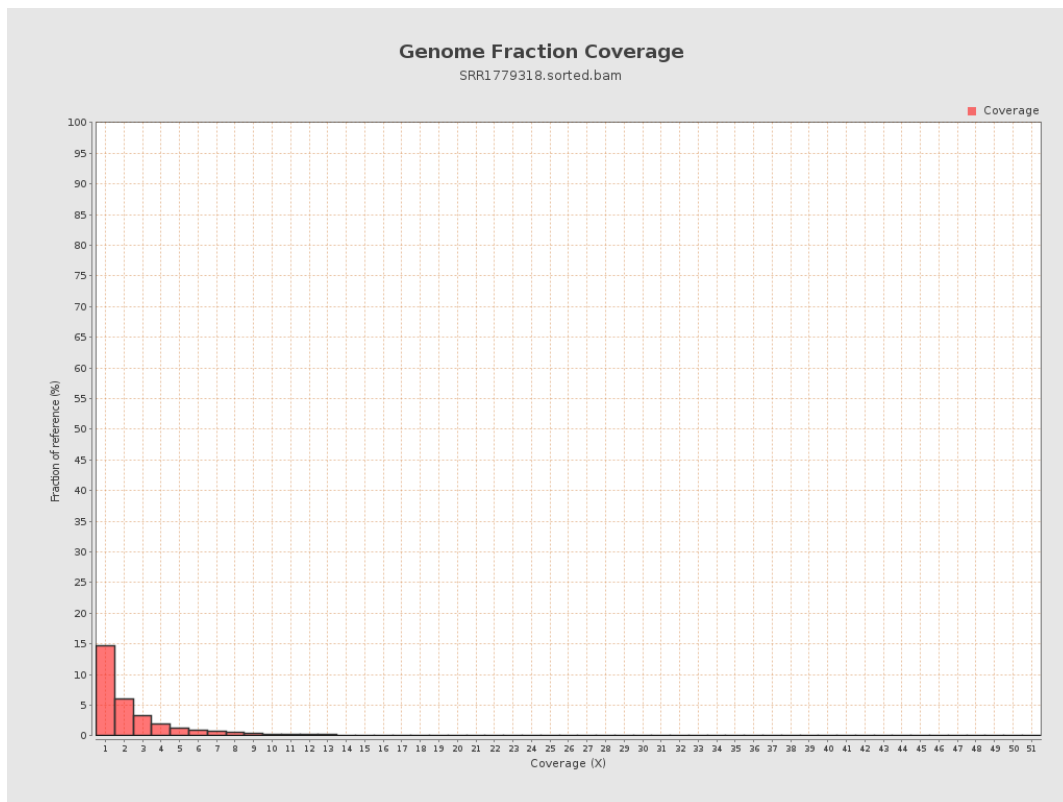
4. Results : Coverage Histogram



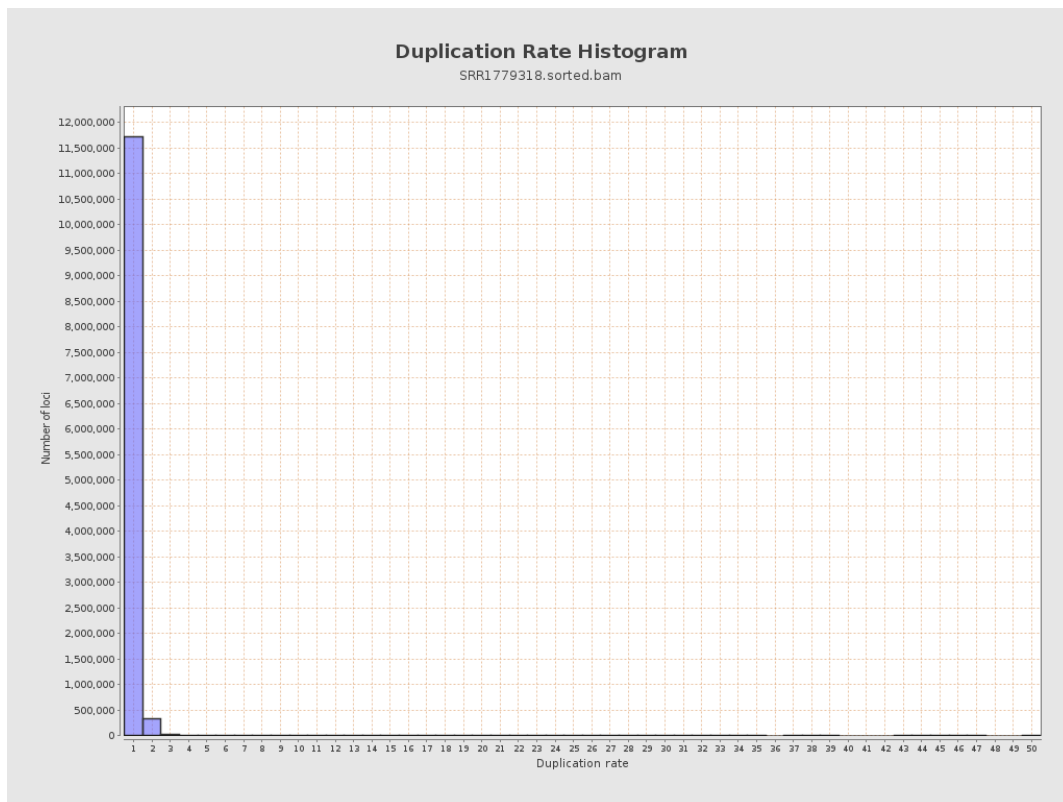
5. Results : Coverage Histogram (0-50X)



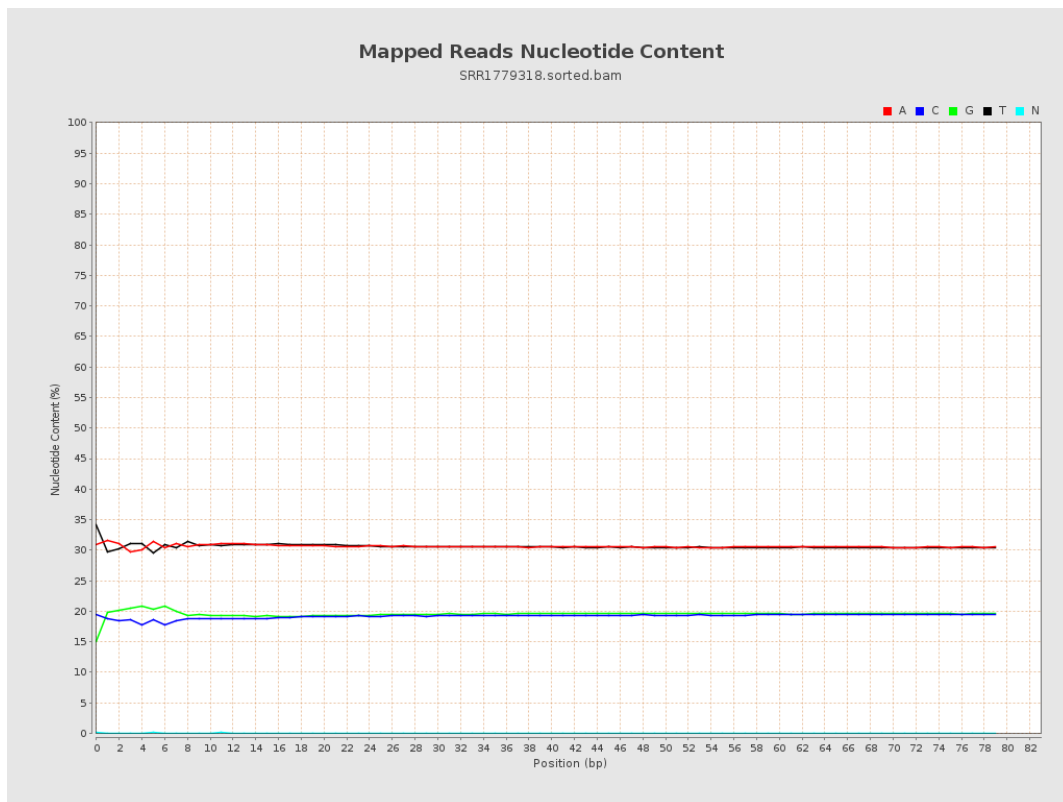
6. Results : Genome Fraction Coverage



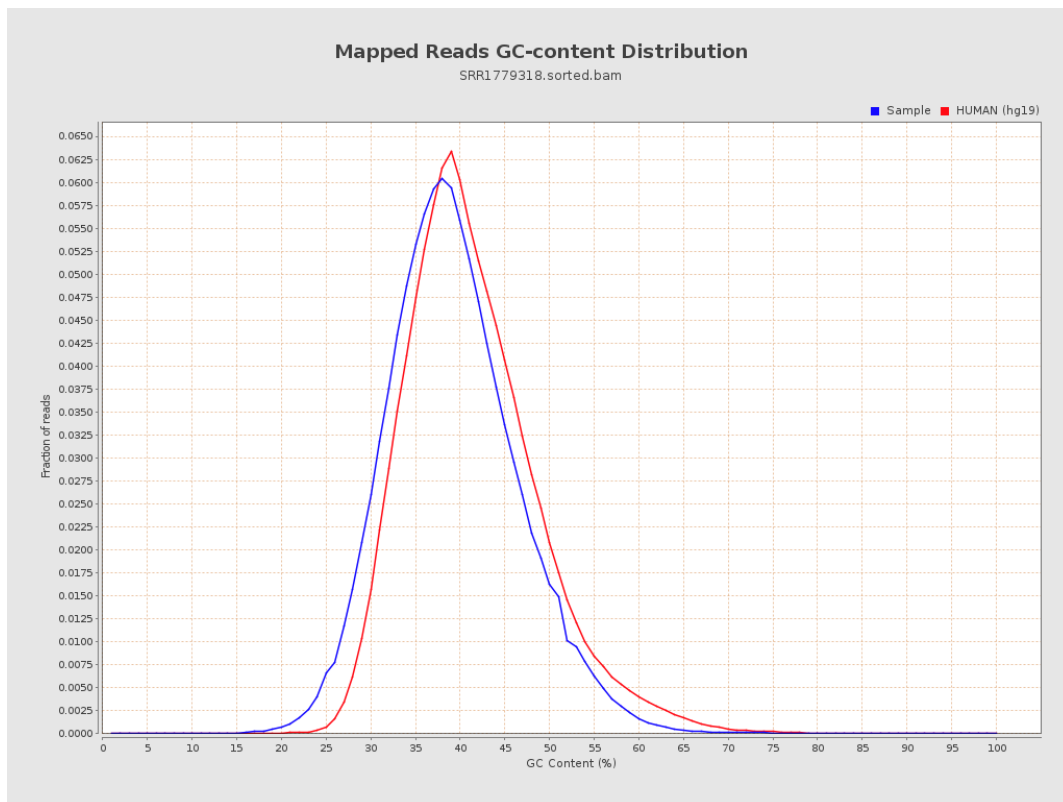
7. Results : Duplication Rate Histogram



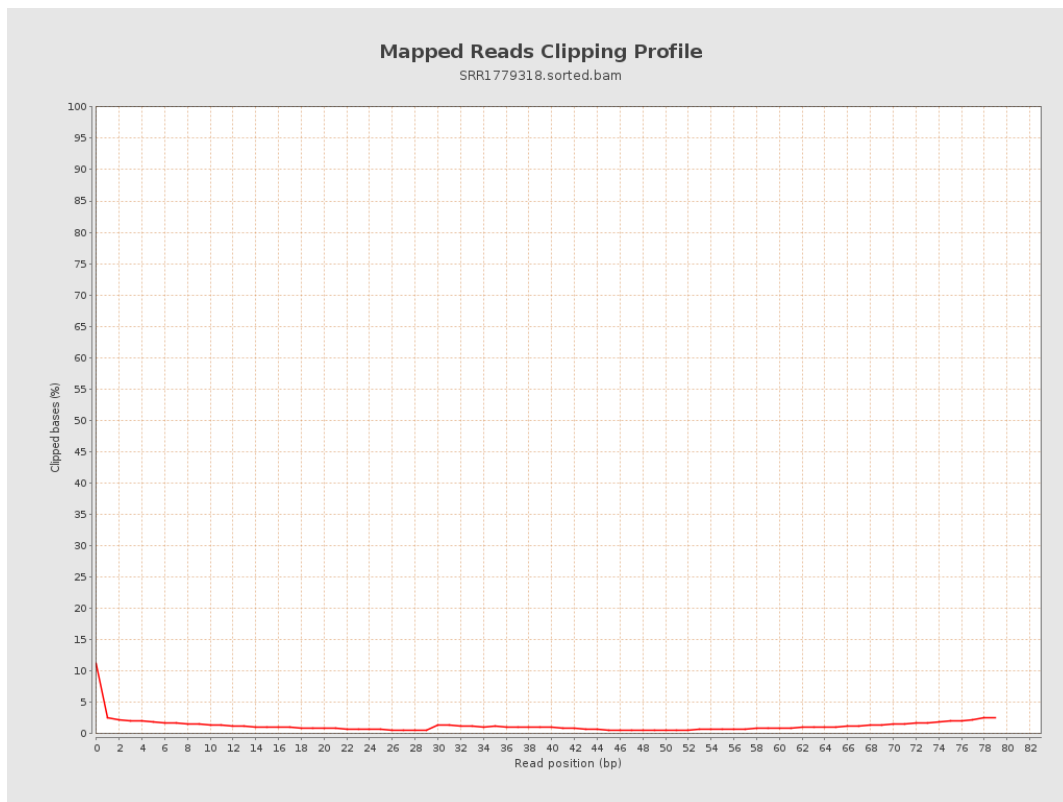
8. Results : Mapped Reads Nucleotide Content



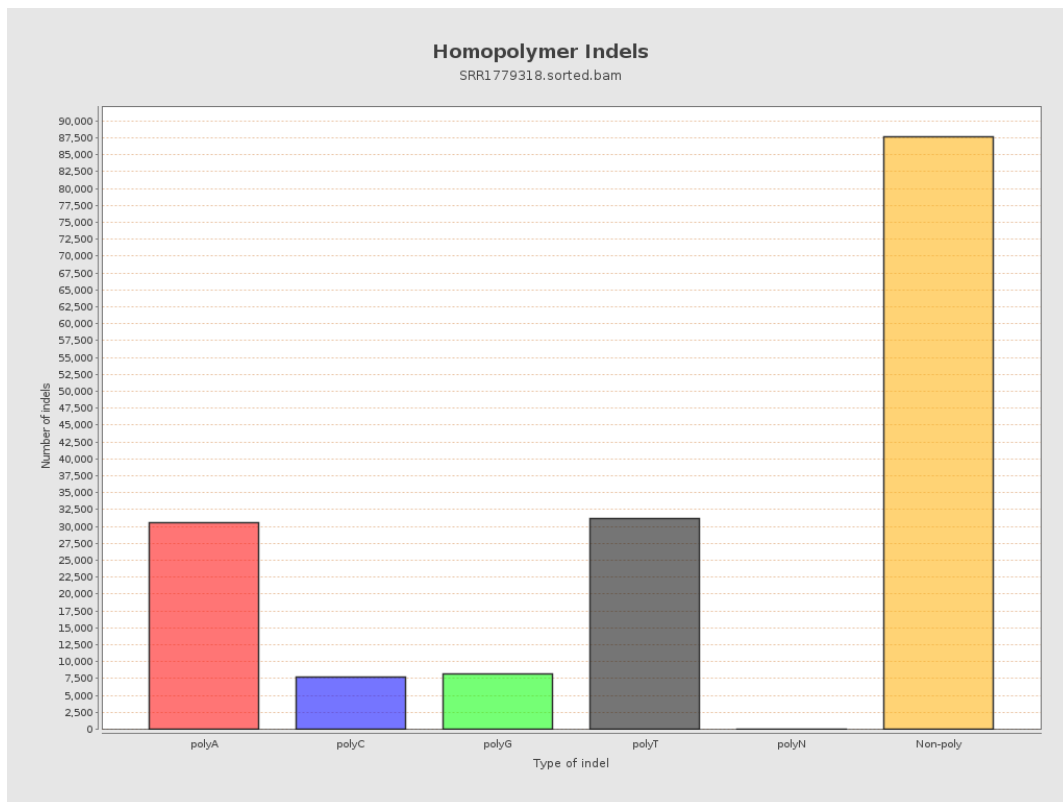
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



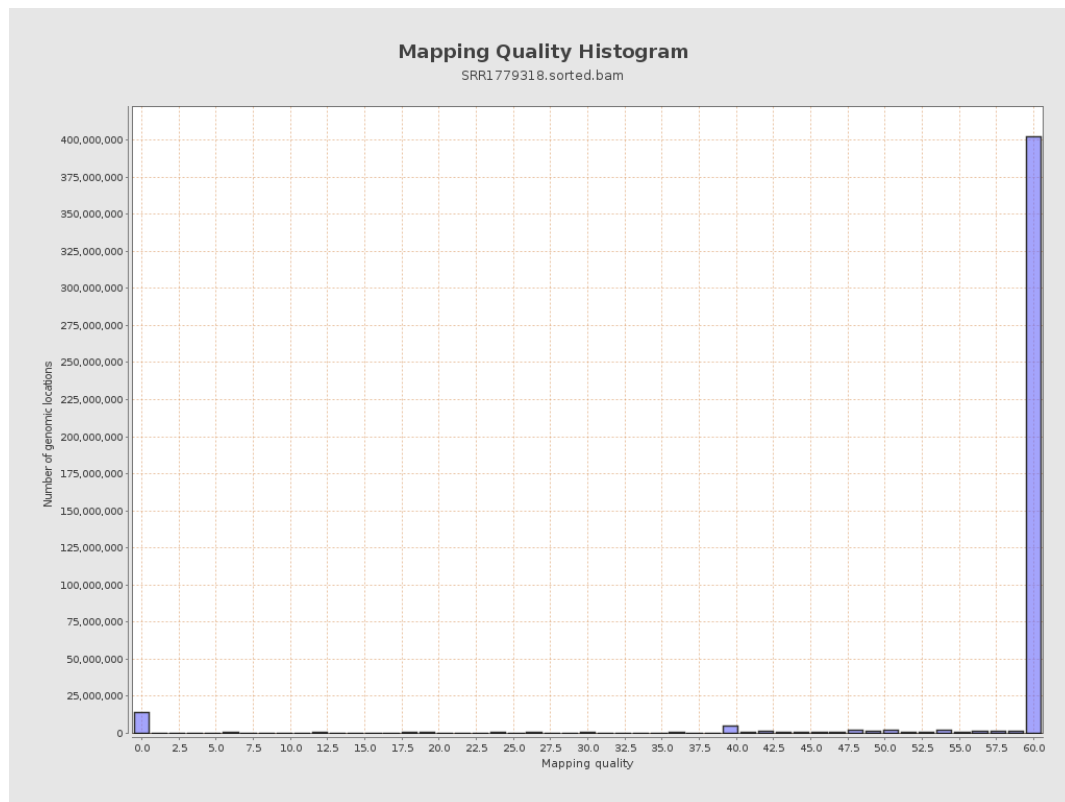
11. Results : Homopolymer Indels



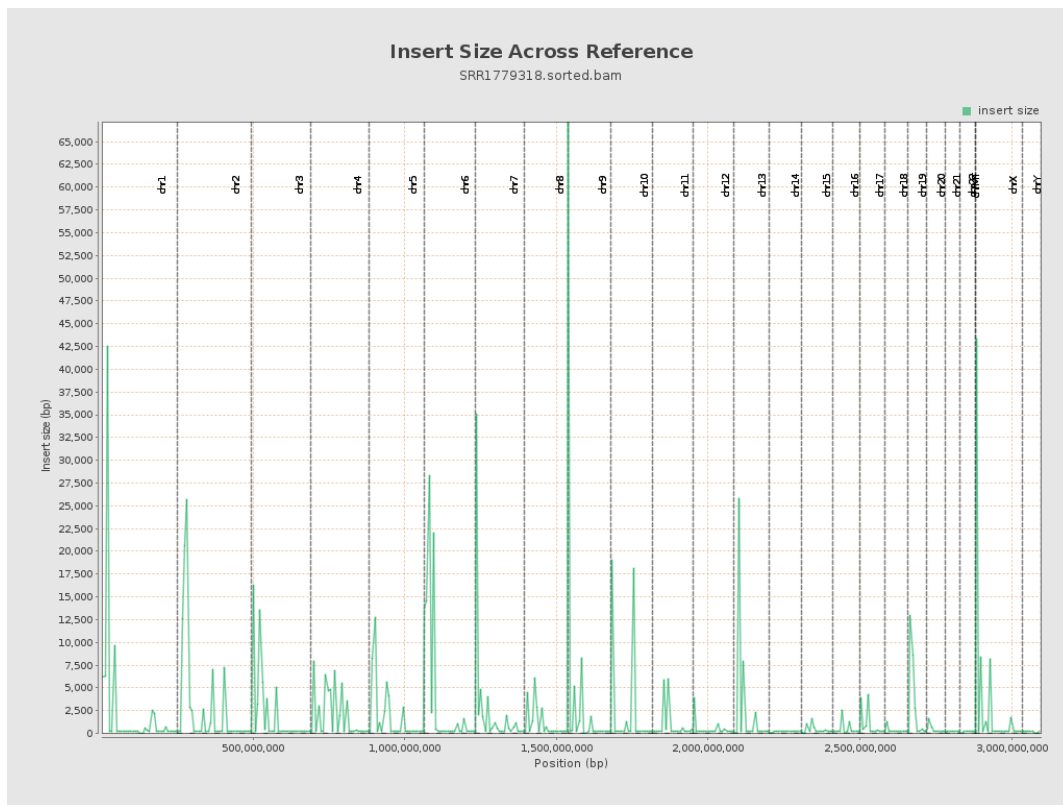
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

