

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 18:15:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779329.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_SRR1779329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779329_1.fastq.gz SRR1779329_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 18:15:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	141,133,976
Mapped reads	138,972,224 / 98.47%
Unmapped reads	2,161,752 / 1.53%
Mapped paired reads	138,972,224 / 98.47%
Mapped reads, first in pair	69,857,691 / 49.5%
Mapped reads, second in pair	69,114,533 / 48.97%
Mapped reads, both in pair	138,105,702 / 97.85%
Mapped reads, singletons	866,522 / 0.61%
Secondary alignments	0
Supplementary alignments	494,768 / 0.35%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	10,582,193 / 7.5%
Duplication rate	7.28%
Clipped reads	8,120,392 / 5.75%

2.2. ACGT Content

Number/percentage of A's	4,289,835,667 / 30.81%
Number/percentage of C's	2,688,682,562 / 19.31%
Number/percentage of T's	4,180,913,655 / 30.03%
Number/percentage of G's	2,760,843,838 / 19.83%
Number/percentage of N's	3,315,224 / 0.02%

GC Percentage	39.14%
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2.3. Coverage

Mean	4.4987
Standard Deviation	7.0182

2.4. Mapping Quality

Mean Mapping Quality	53.82
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2.5. Insert size

Mean	155,637.63
Standard Deviation	3,762,201.1
P25/Median/P75	168 / 233 / 316

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	41,219,674
Insertions	1,125,753
Mapped reads with at least one insertion	0.8%
Deletions	1,421,372
Mapped reads with at least one deletion	1%
Homopolymer indels	47.38%

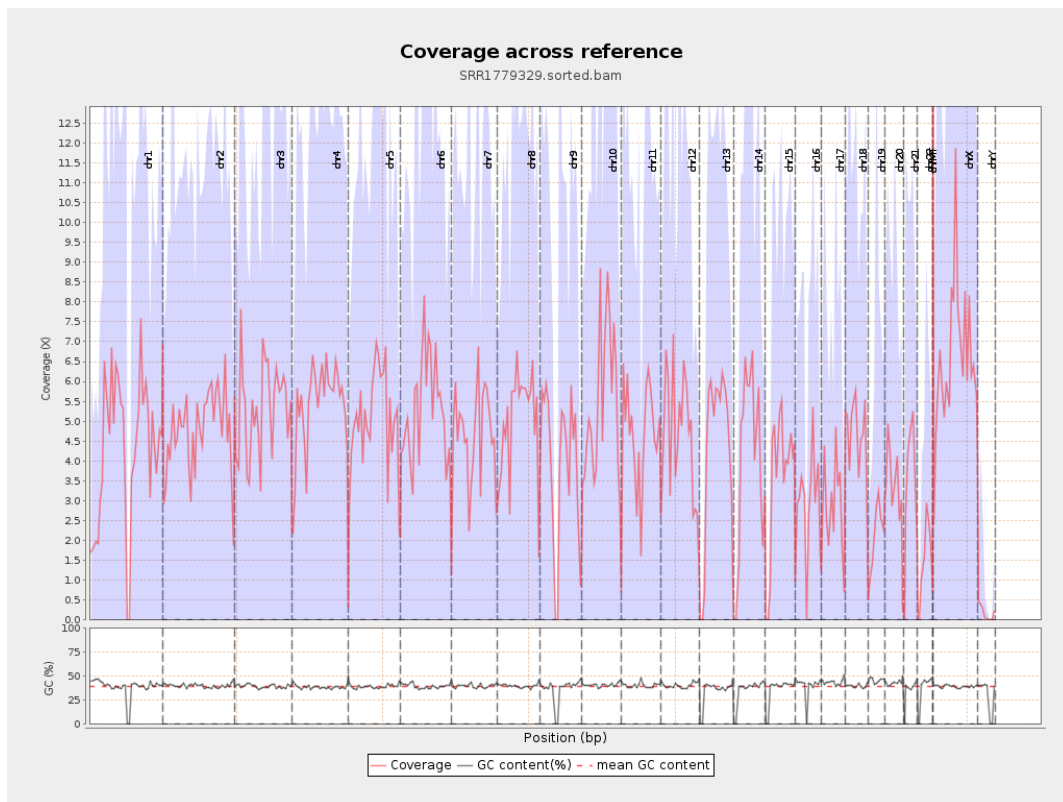
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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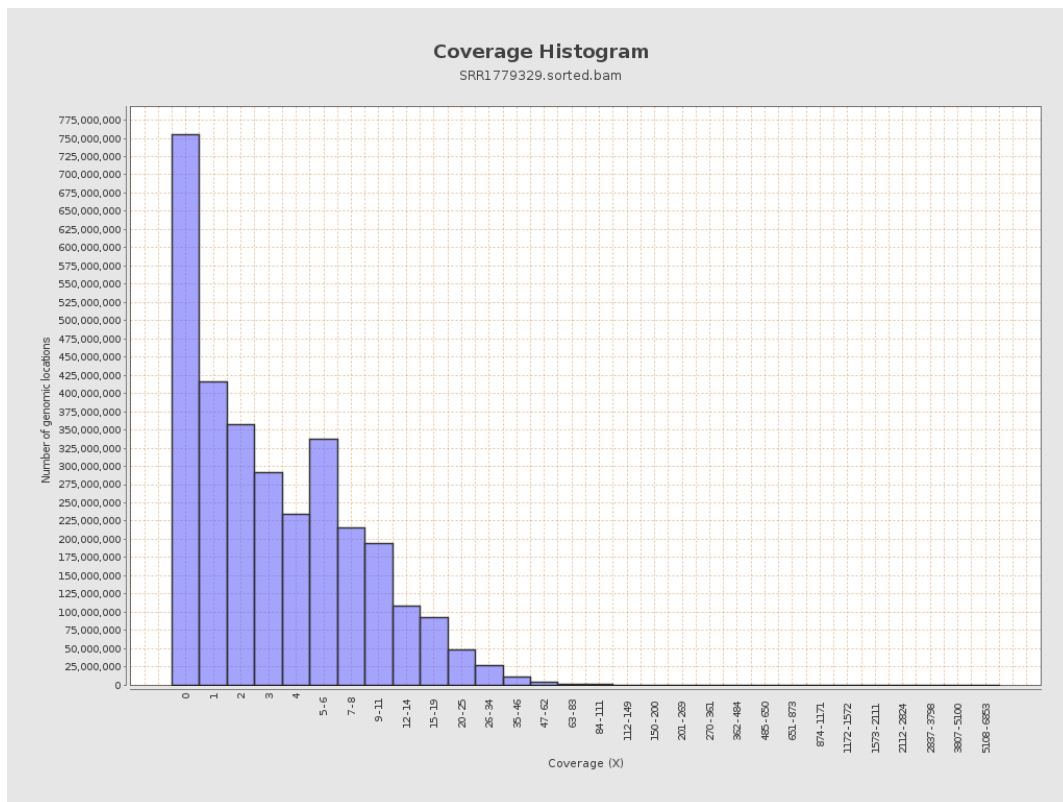
		bases	coverage	deviation
chr1	249250621	1067544164	4.283	8.3324
chr2	243199373	1155458641	4.7511	6.3009
chr3	198022430	1050283794	5.3039	6.6262
chr4	191154276	1040255500	5.442	6.5329
chr5	180915260	906287577	5.0095	6.1608
chr6	171115067	904656006	5.2868	6.679
chr7	159138663	733724243	4.6106	6.7684
chr8	146364022	738049565	5.0426	6.11
chr9	141213431	557372034	3.947	6.5729
chr10	135534747	742161690	5.4758	13.7103
chr11	135006516	629808101	4.665	6.4314
chr12	133851895	617714561	4.6149	6.3829
chr13	115169878	495337890	4.3009	5.84
chr14	107349540	440030379	4.099	6.1525
chr15	102531392	358621604	3.4977	5.4121
chr16	90354753	257967888	2.8551	4.7829
chr17	81195210	236508003	2.9128	4.7968
chr18	78077248	368357927	4.7179	6.4034
chr19	59128983	128320321	2.1702	5.3646
chr20	63025520	212679391	3.3745	5.4461
chr21	48129895	169046573	3.5123	6.1055
chr22	51304566	78594744	1.5319	3.6033
chrMT	16571	374368	22.5918	8.4029
chrX	155270560	1028214832	6.6221	8.2034

chrY	59373566	9364604	0.1577	1.7447
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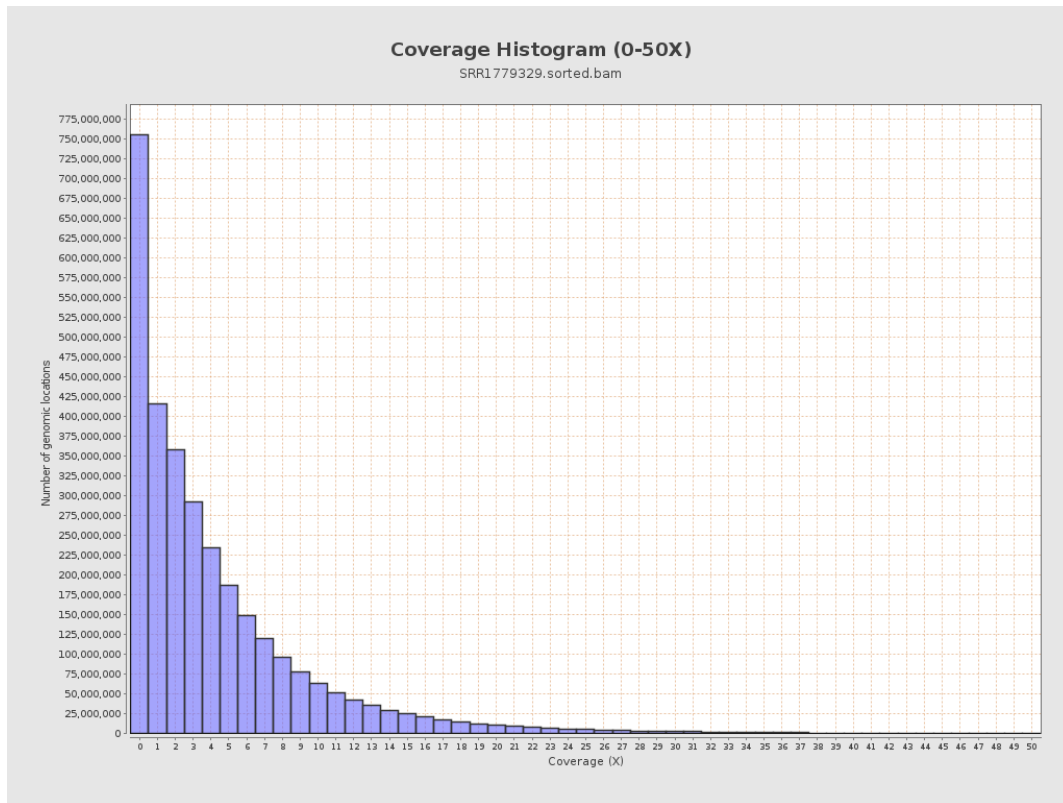
3. Results : Coverage across reference



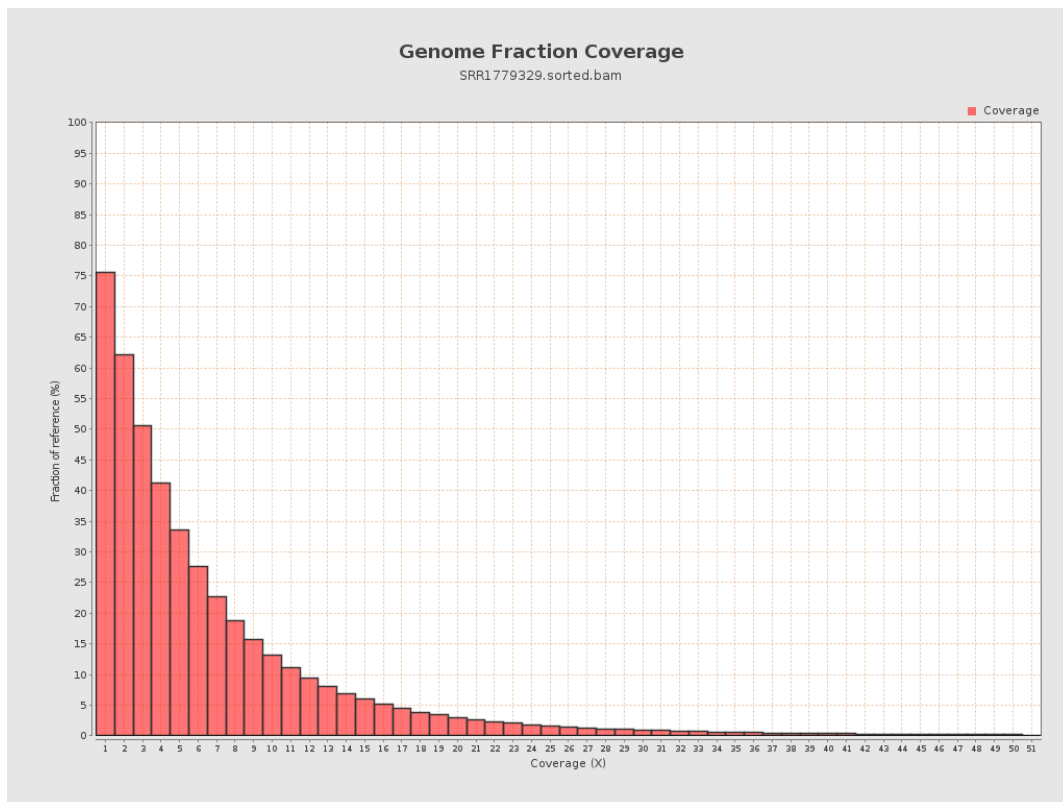
4. Results : Coverage Histogram



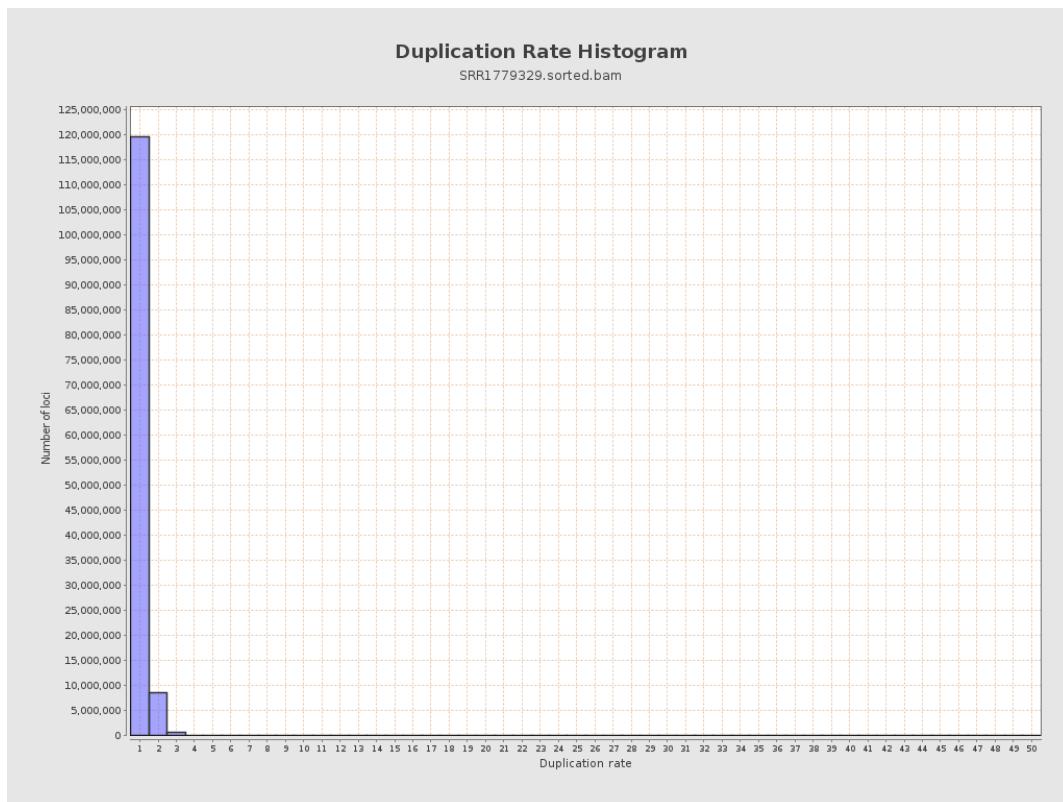
5. Results : Coverage Histogram (0-50X)



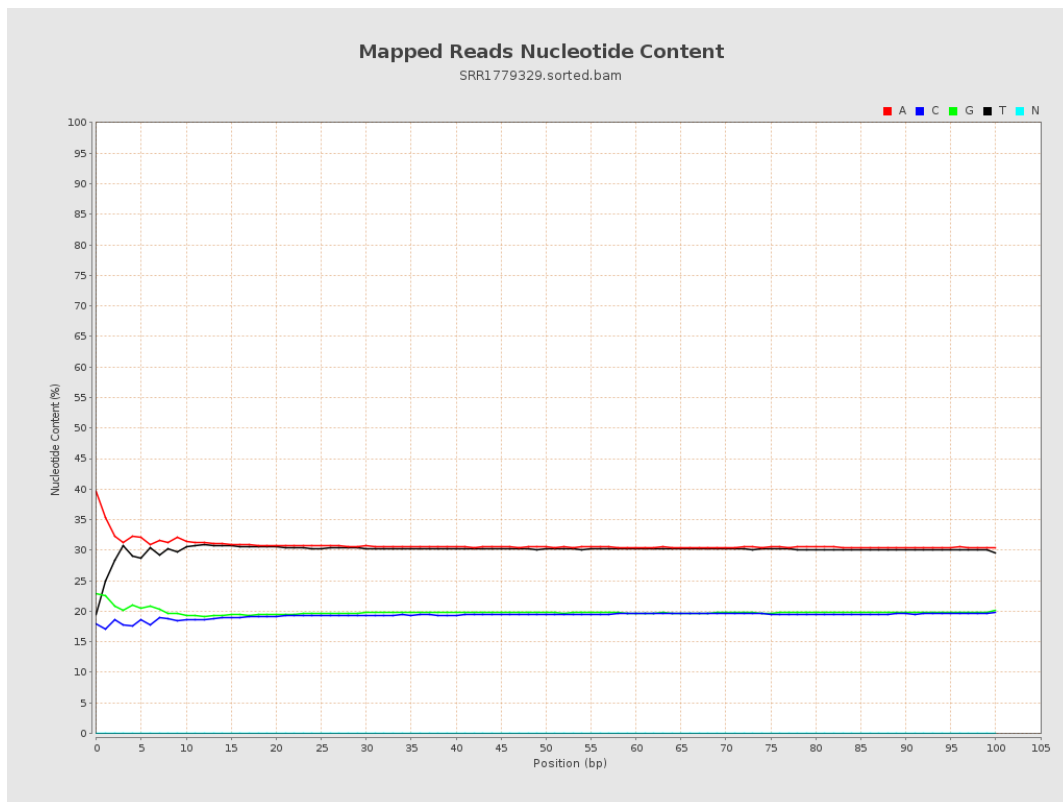
6. Results : Genome Fraction Coverage



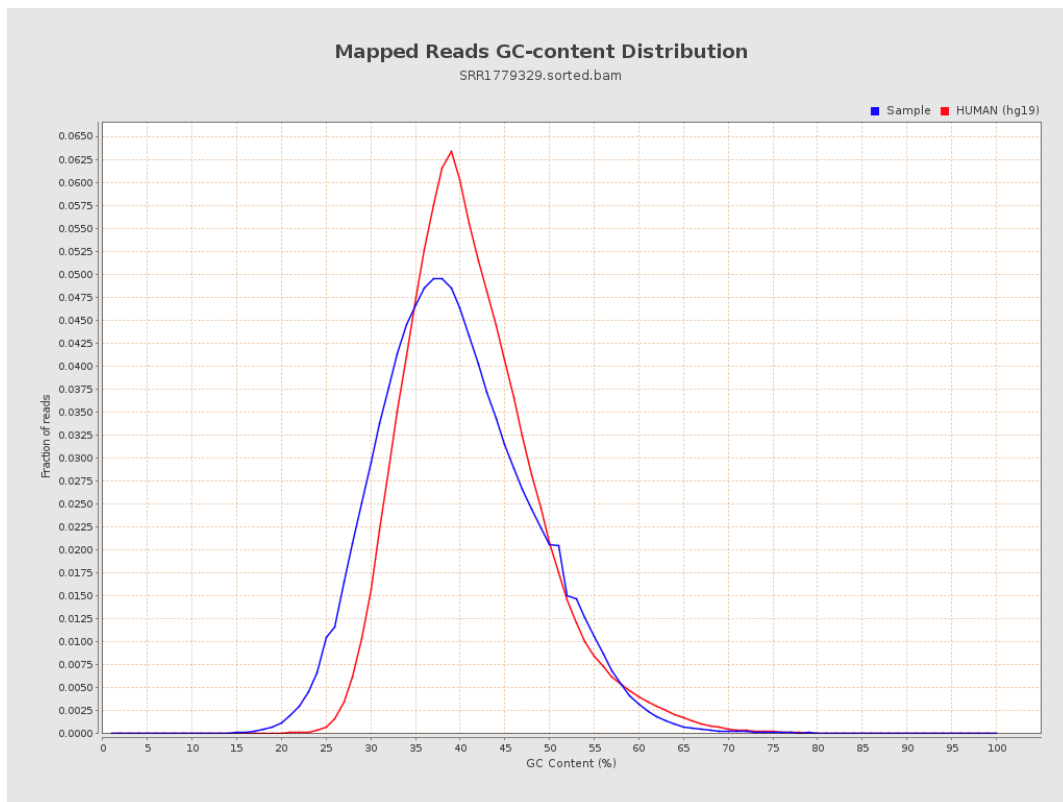
7. Results : Duplication Rate Histogram



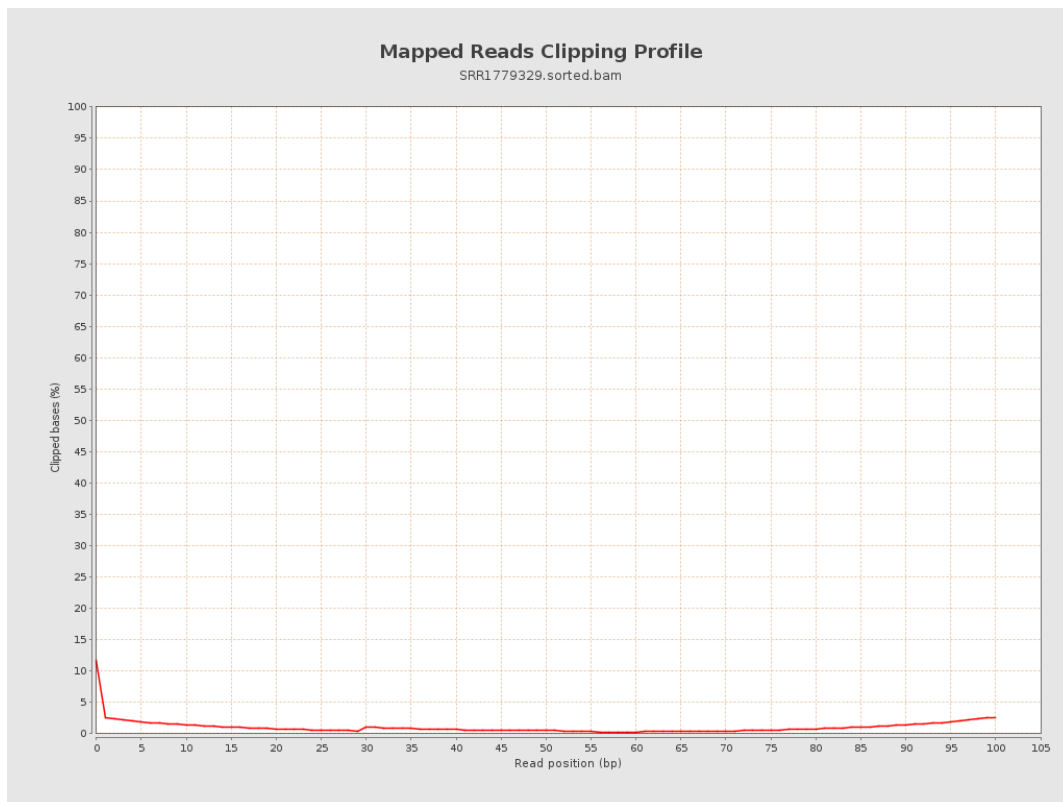
8. Results : Mapped Reads Nucleotide Content



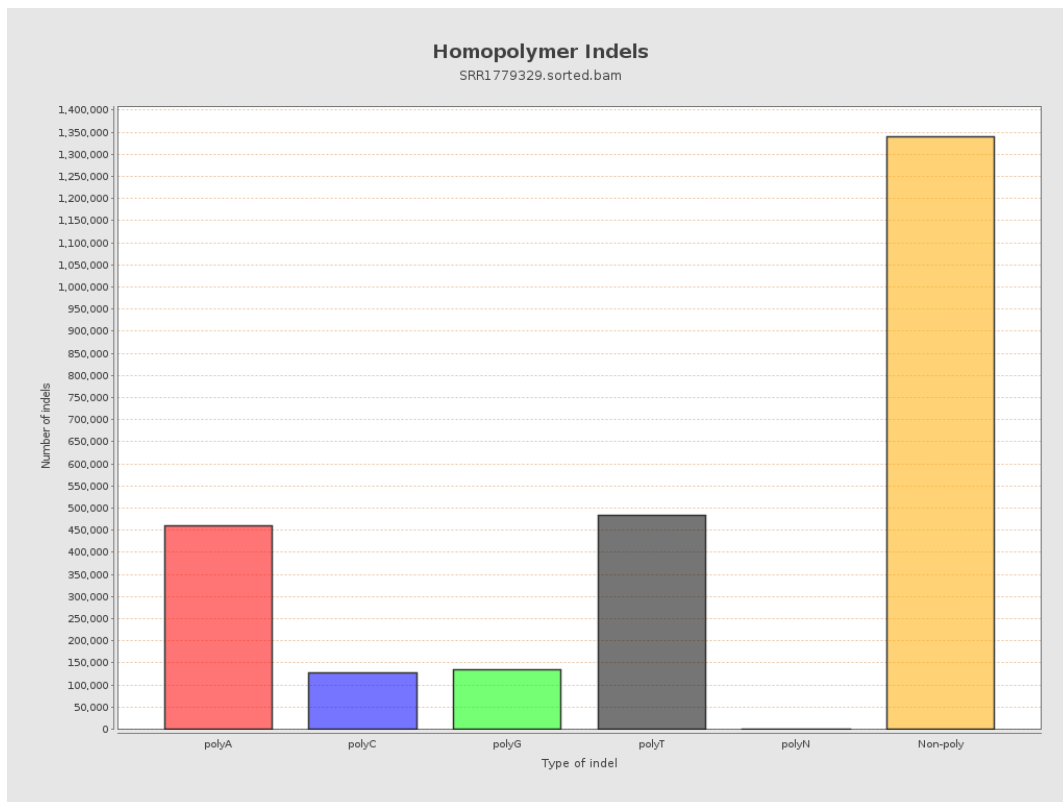
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



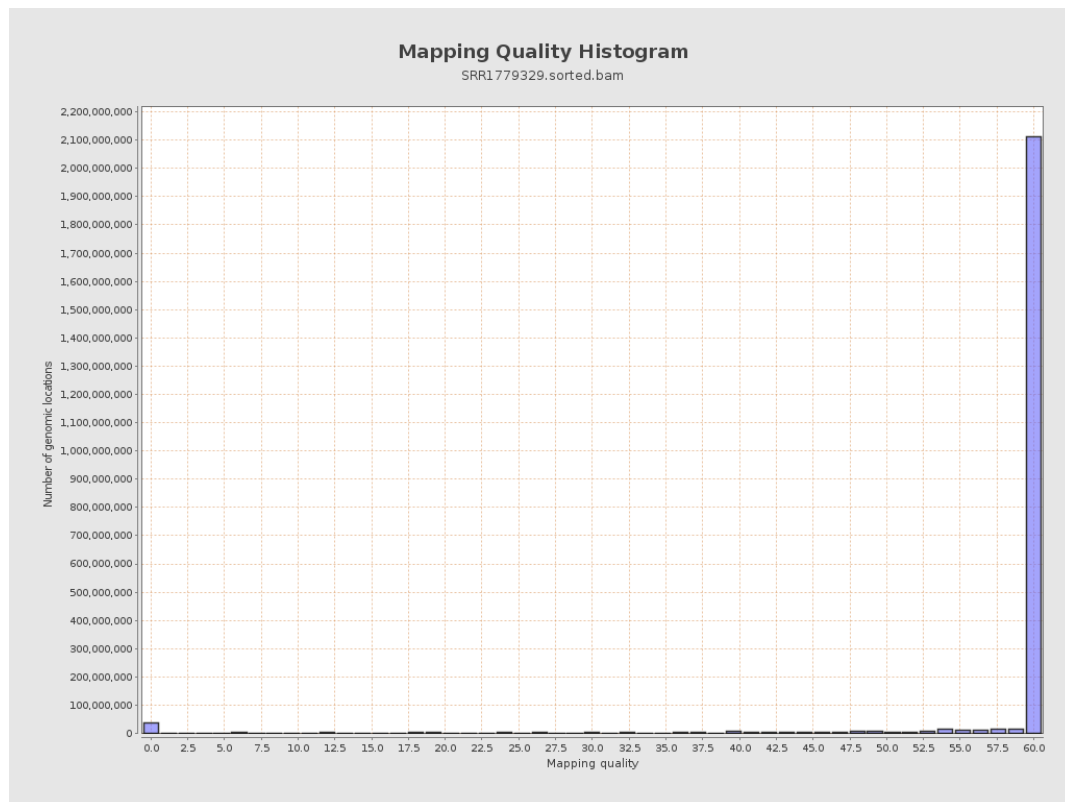
11. Results : Homopolymer Indels



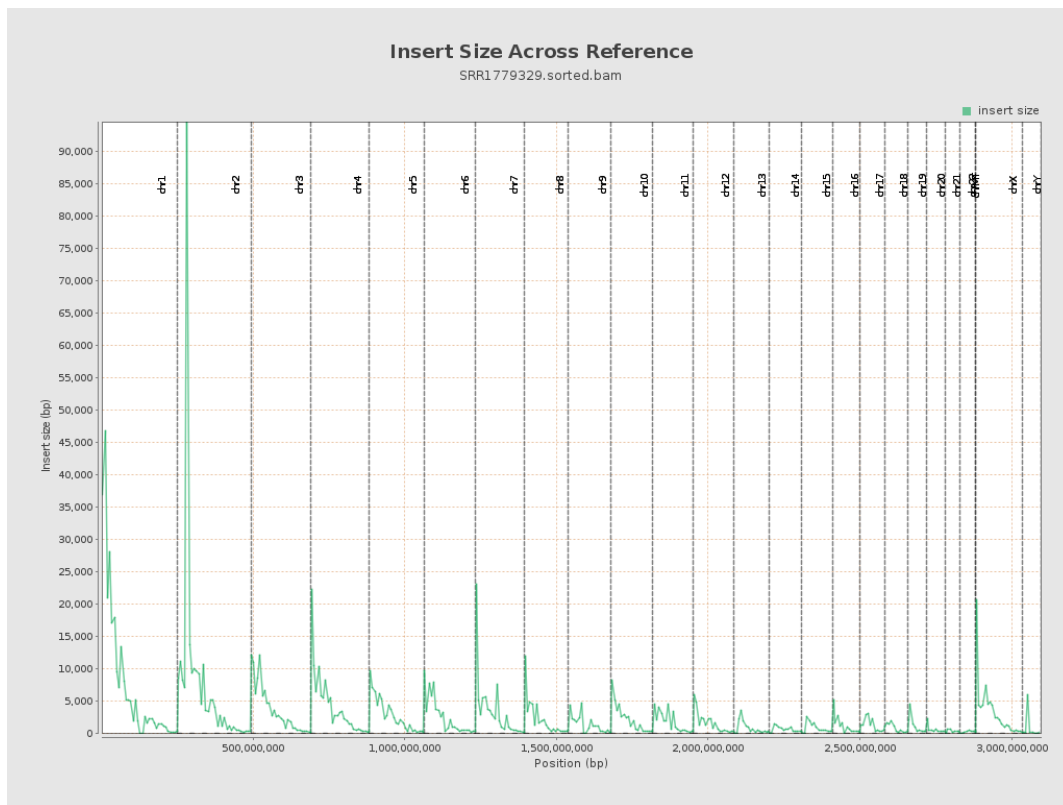
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

