

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 07:44:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777267.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_SRR1777267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777267_1.fastq.gz SRR1777267_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 07:44:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	68,870,482
Mapped reads	68,577,783 / 99.58%
Unmapped reads	292,699 / 0.42%
Mapped paired reads	68,577,783 / 99.58%
Mapped reads, first in pair	34,290,042 / 49.79%
Mapped reads, second in pair	34,287,741 / 49.79%
Mapped reads, both in pair	68,476,258 / 99.43%
Mapped reads, singletons	101,525 / 0.15%
Secondary alignments	0
Supplementary alignments	2,309,261 / 3.35%
Read min/max/mean length	30 / 101 / 102.38
Duplicated reads (estimated)	38,557,781 / 55.99%
Duplication rate	48.97%
Clipped reads	8,149,249 / 11.83%

2.2. ACGT Content

Number/percentage of A's	1,893,813,795 / 27.52%
Number/percentage of C's	1,553,217,373 / 22.57%
Number/percentage of T's	1,884,736,391 / 27.39%
Number/percentage of G's	1,548,616,750 / 22.51%
Number/percentage of N's	85,119 / 0%

GC Percentage	45.08%
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2.3. Coverage

Mean	2.2229
Standard Deviation	20.5777

2.4. Mapping Quality

Mean Mapping Quality	54.7
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2.5. Insert size

Mean	331,562.86
Standard Deviation	5,665,890.56
P25/Median/P75	189 / 239 / 301

2.6. Mismatches and indels

General error rate	0.22%
Mismatches	13,846,329
Insertions	1,188,533
Mapped reads with at least one insertion	1.71%
Deletions	470,542
Mapped reads with at least one deletion	0.68%
Homopolymer indels	52.19%

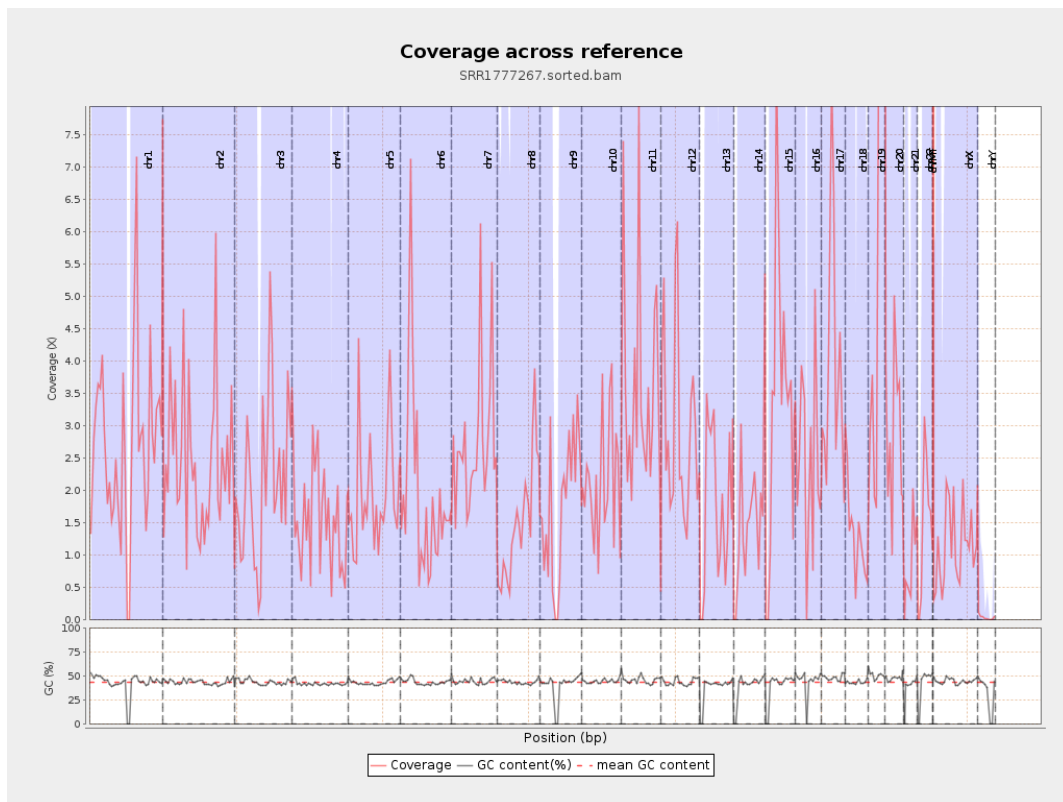
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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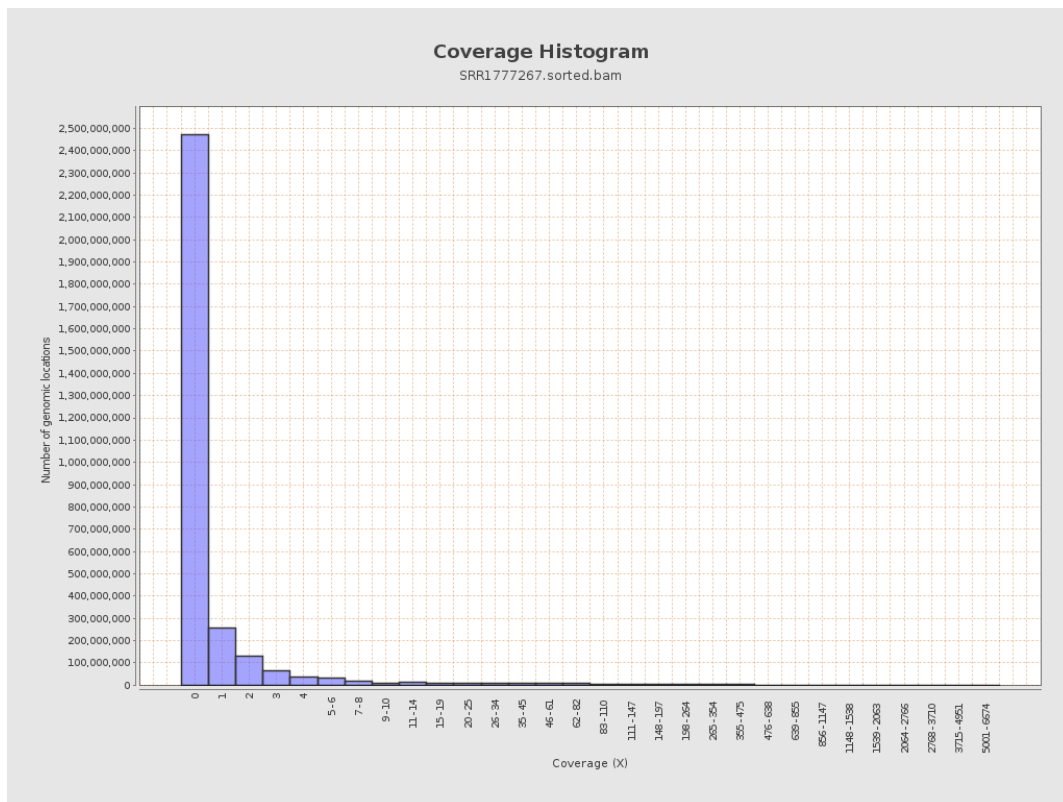
		bases	coverage	deviation
chr1	249250621	678391338	2.7217	22.301
chr2	243199373	596035193	2.4508	21.268
chr3	198022430	417198237	2.1068	19.4763
chr4	191154276	292988465	1.5327	16.244
chr5	180915260	360105162	1.9905	19.1568
chr6	171115067	324340807	1.8955	19.3064
chr7	159138663	433286500	2.7227	23.5088
chr8	146364022	223921139	1.5299	17.0376
chr9	141213431	241138989	1.7076	17.1673
chr10	135534747	292790159	2.1603	19.6779
chr11	135006516	485160155	3.5936	30.4905
chr12	133851895	401955747	3.003	23.8108
chr13	115169878	197401225	1.714	18.003
chr14	107349540	154272792	1.4371	14.5685
chr15	102531392	333767553	3.2553	27.3971
chr16	90354753	216660153	2.3979	19.8135
chr17	81195210	318578547	3.9236	28.5336
chr18	78077248	102881400	1.3177	13.616
chr19	59128983	330881566	5.5959	33.4885
chr20	63025520	181525917	2.8802	22.5183
chr21	48129895	43475125	0.9033	11.8453
chr22	51304566	75830193	1.478	13.1729
chrMT	16571	1521390	91.8104	29.4515
chrX	155270560	175689835	1.1315	12.8136

chrY	59373566	1696151	0.0286	0.9375
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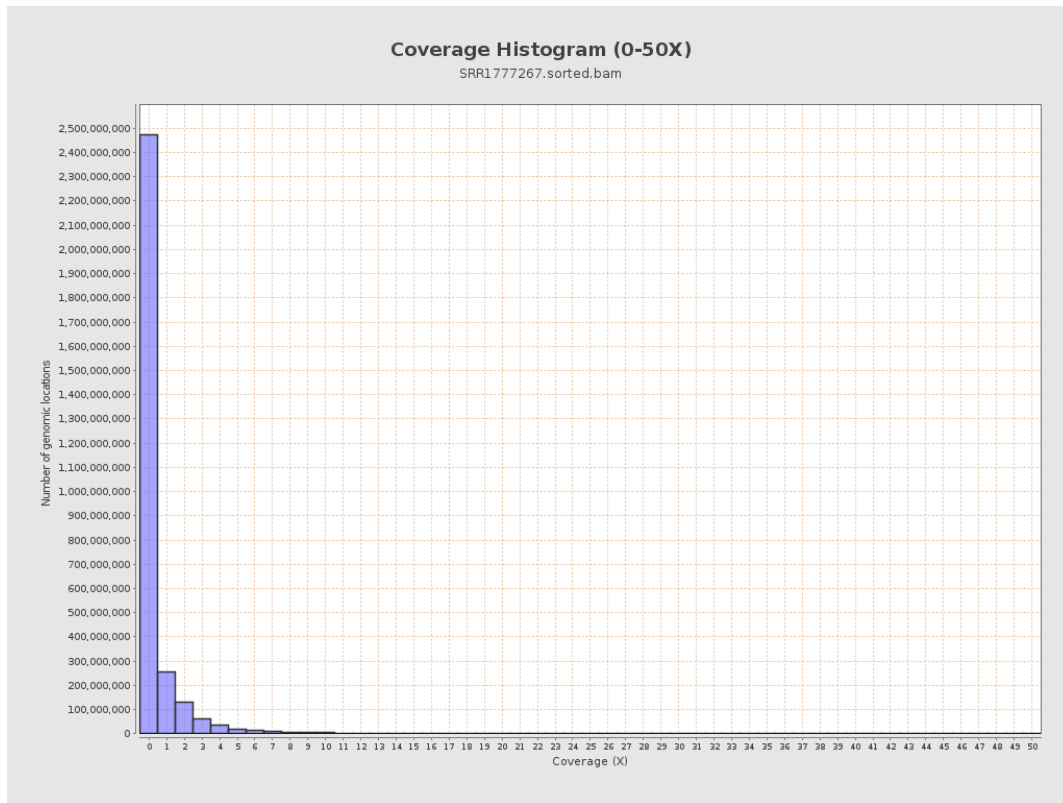
3. Results : Coverage across reference



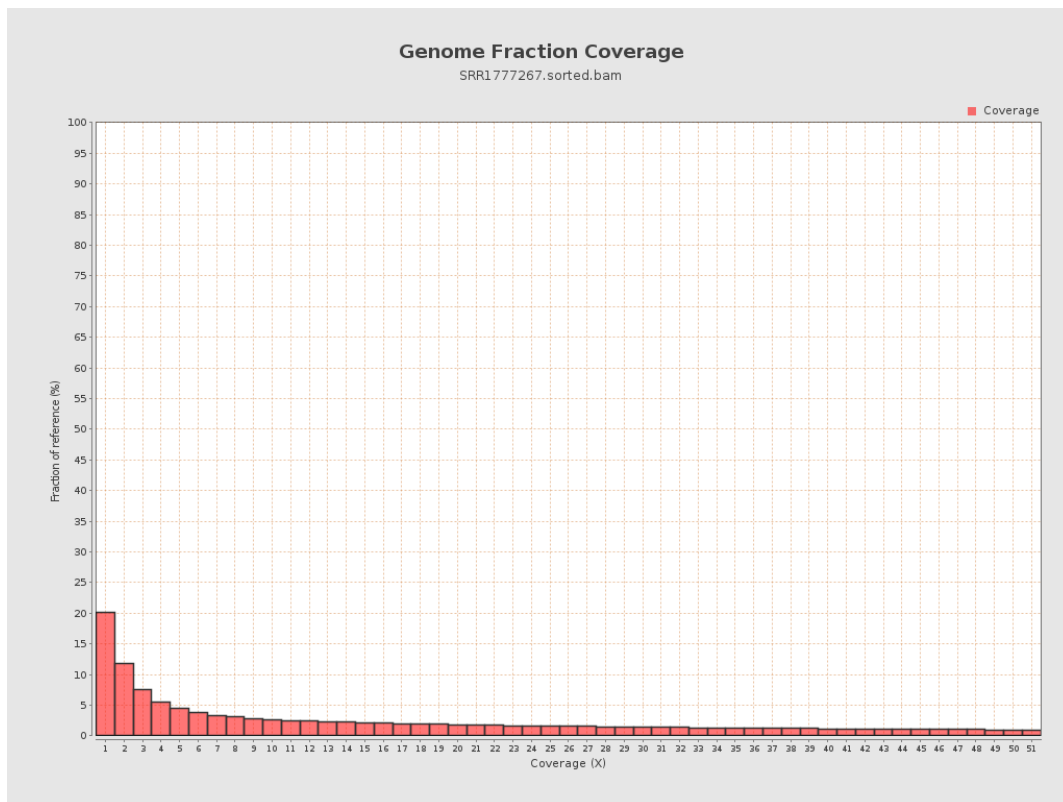
4. Results : Coverage Histogram



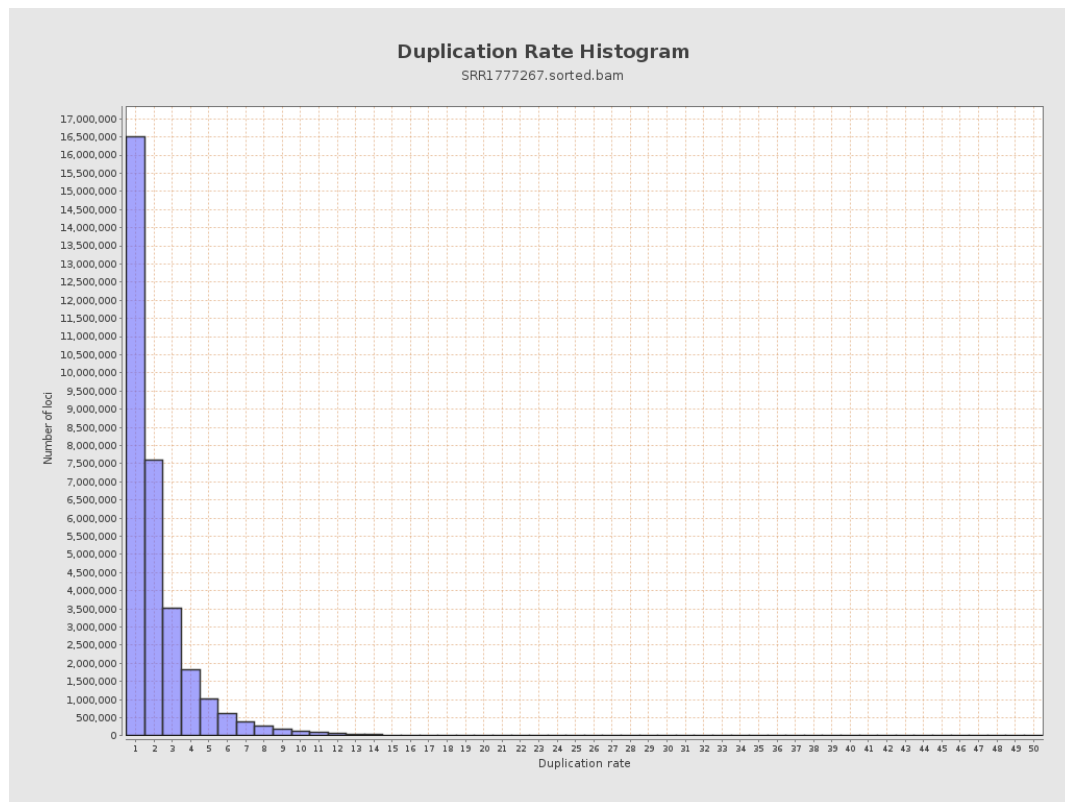
5. Results : Coverage Histogram (0-50X)



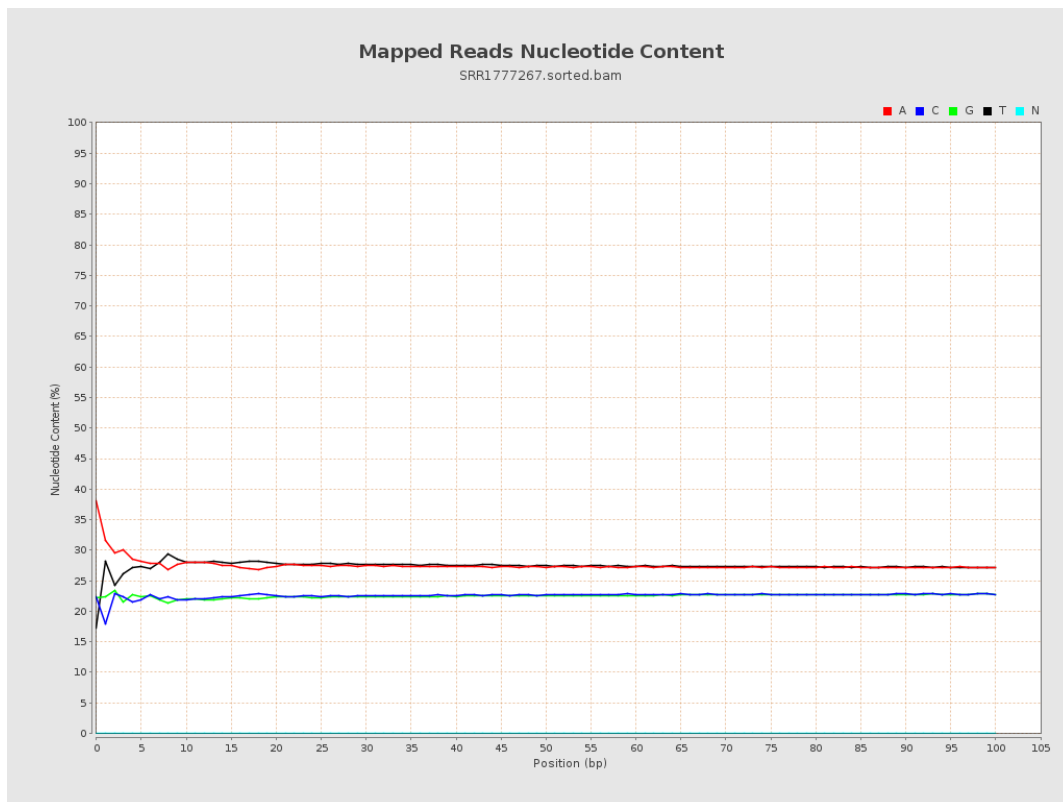
6. Results : Genome Fraction Coverage



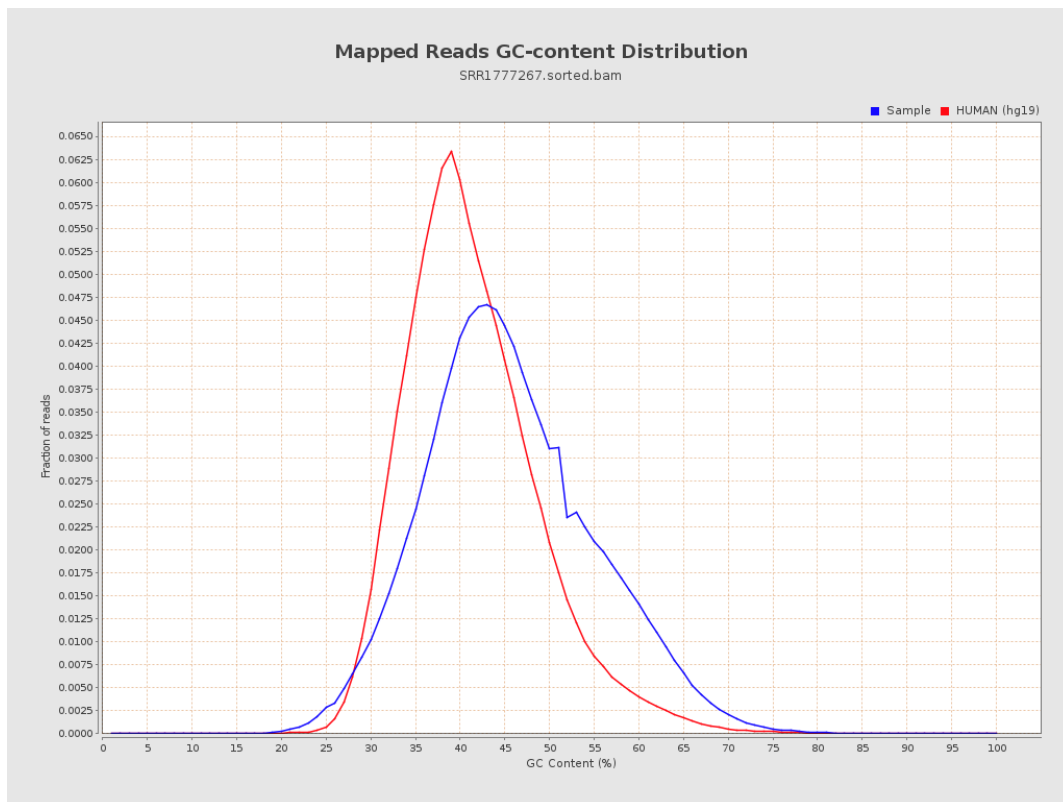
7. Results : Duplication Rate Histogram



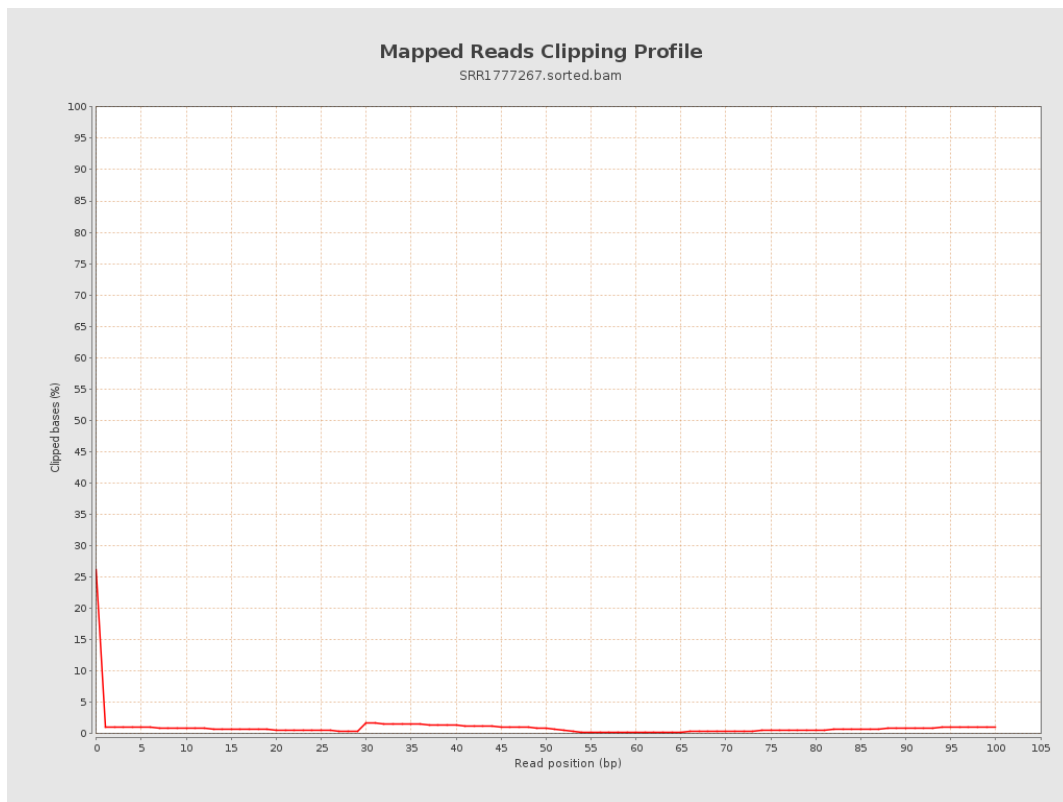
8. Results : Mapped Reads Nucleotide Content



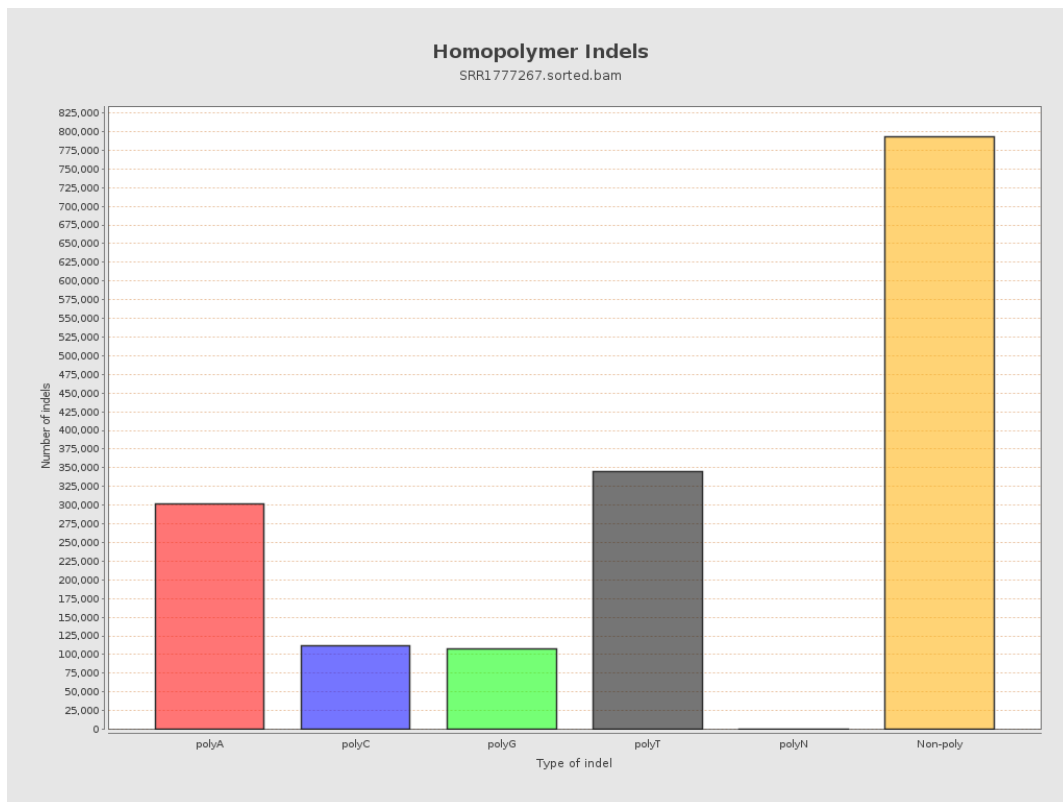
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



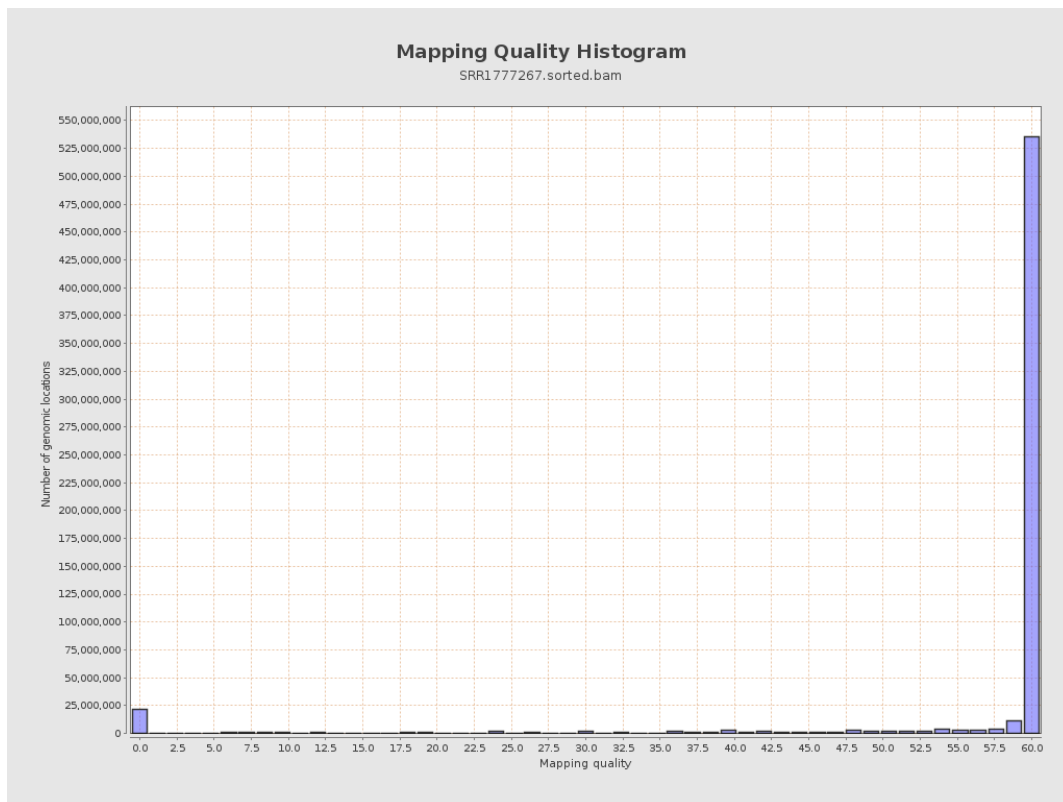
11. Results : Homopolymer Indels



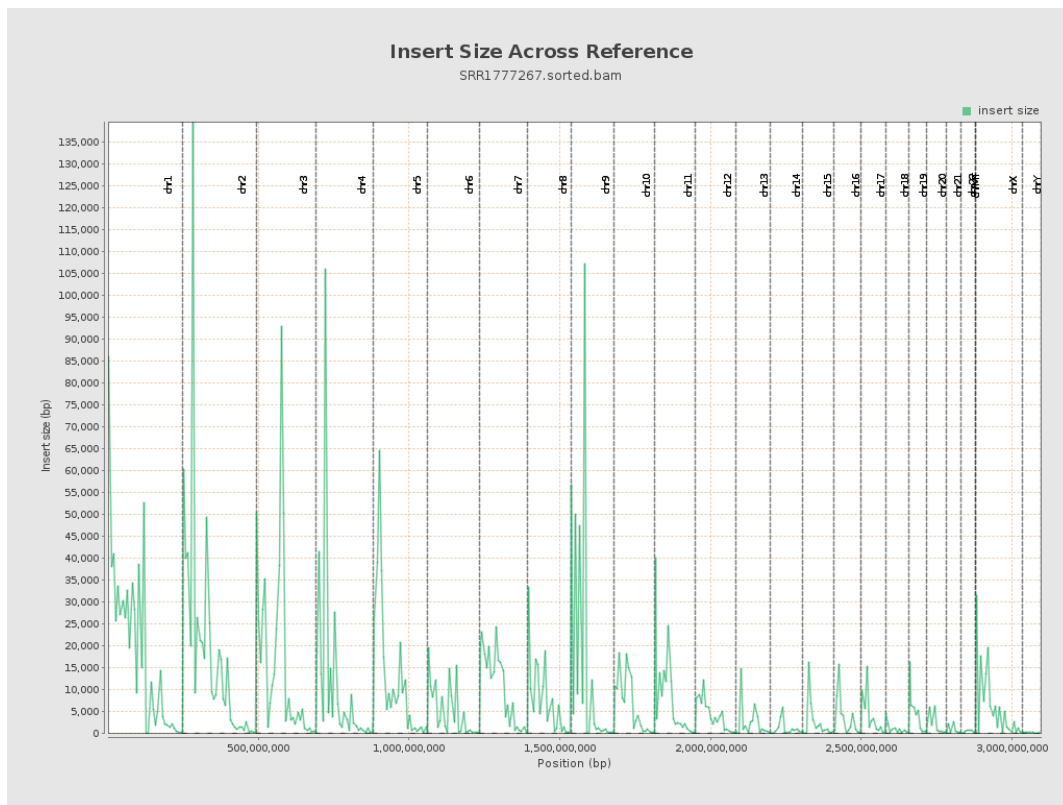
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

