

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:57:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779288.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_SRR1779288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779288_1.fastq.gz SRR1779288_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:57:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,724,452
Mapped reads	12,329,113 / 96.89%
Unmapped reads	395,339 / 3.11%
Mapped paired reads	12,329,113 / 96.89%
Mapped reads, first in pair	6,232,178 / 48.98%
Mapped reads, second in pair	6,096,935 / 47.92%
Mapped reads, both in pair	12,174,772 / 95.68%
Mapped reads, singletons	154,341 / 1.21%
Secondary alignments	0
Supplementary alignments	31,028 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	315,516 / 2.48%
Duplication rate	2.26%
Clipped reads	401,762 / 3.16%

2.2. ACGT Content

Number/percentage of A's	302,876,402 / 30.87%
Number/percentage of C's	186,478,191 / 19.01%
Number/percentage of T's	302,045,571 / 30.79%
Number/percentage of G's	189,502,197 / 19.32%
Number/percentage of N's	185,556 / 0.02%

GC Percentage	38.32%
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2.3. Coverage

Mean	0.317
Standard Deviation	1.3429

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	41,883.1
Standard Deviation	1,927,562.77
P25/Median/P75	147 / 193 / 259

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	3,620,544
Insertions	71,214
Mapped reads with at least one insertion	0.57%
Deletions	91,043
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.73%

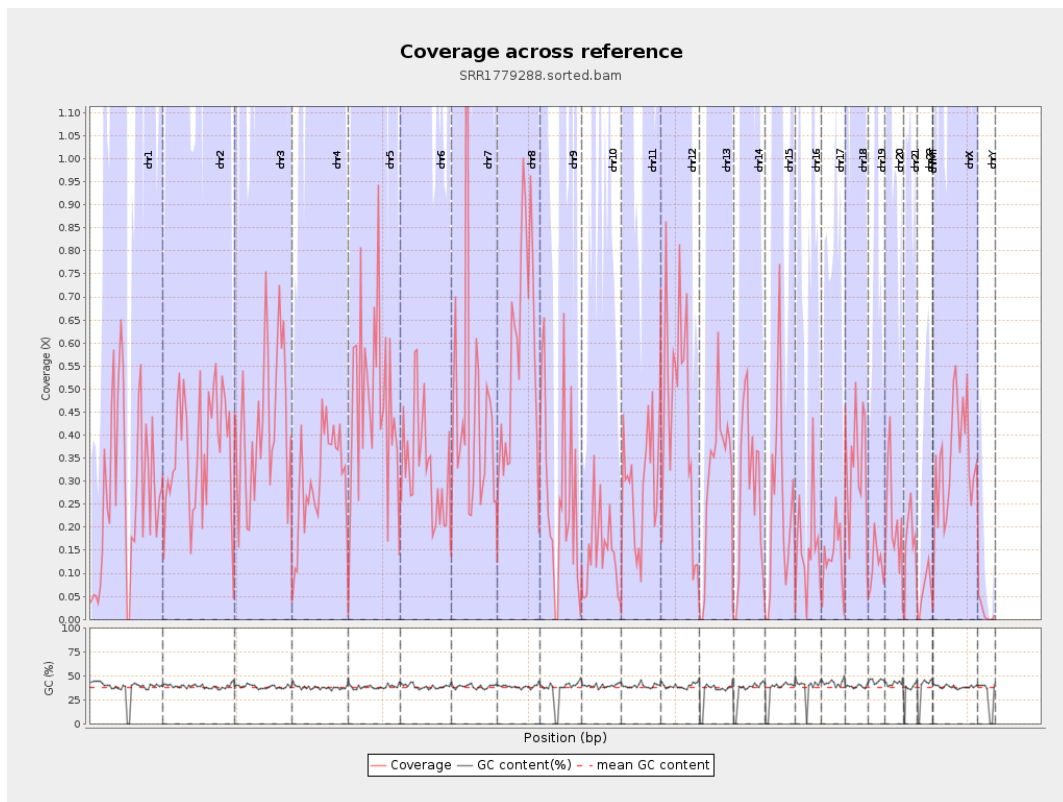
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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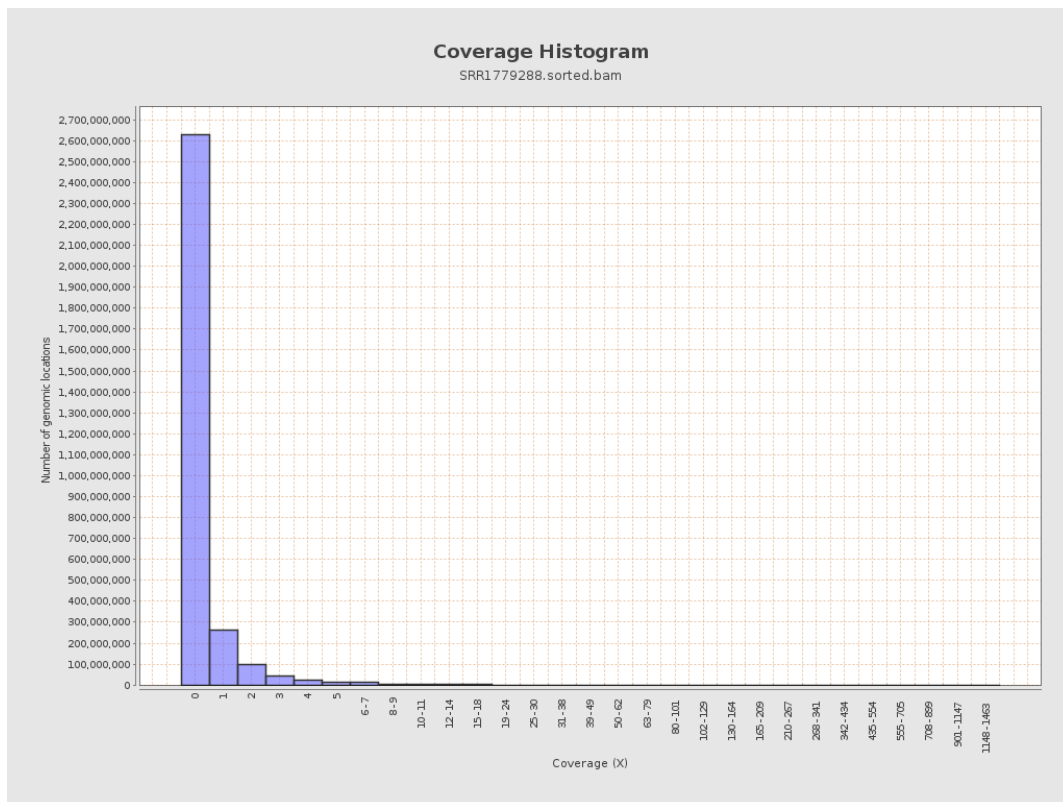
		bases	coverage	deviation
chr1	249250621	68318175	0.2741	1.7786
chr2	243199373	88236134	0.3628	1.1505
chr3	198022430	82915795	0.4187	1.2646
chr4	191154276	58282895	0.3049	1.0732
chr5	180915260	84070268	0.4647	1.3539
chr6	171115067	56839181	0.3322	1.0749
chr7	159138663	72425078	0.4551	1.9161
chr8	146364022	84340422	0.5762	1.6411
chr9	141213431	37700438	0.267	1.0765
chr10	135534747	19715941	0.1455	2.7123
chr11	135006516	39844802	0.2951	1.0444
chr12	133851895	58353524	0.436	1.3103
chr13	115169878	36127971	0.3137	1.0489
chr14	107349540	30090834	0.2803	1.0119
chr15	102531392	24809615	0.242	1.0008
chr16	90354753	14107585	0.1561	0.6909
chr17	81195210	11126125	0.137	0.6019
chr18	78077248	26168754	0.3352	1.0494
chr19	59128983	7092335	0.1199	0.9452
chr20	63025520	13996316	0.2221	0.781
chr21	48129895	7871842	0.1636	0.7143
chr22	51304566	3374357	0.0658	0.3743
chrMT	16571	240	0.0145	0.1347
chrX	155270560	54621745	0.3518	1.1935

chrY	59373566	844892	0.0142	0.2175
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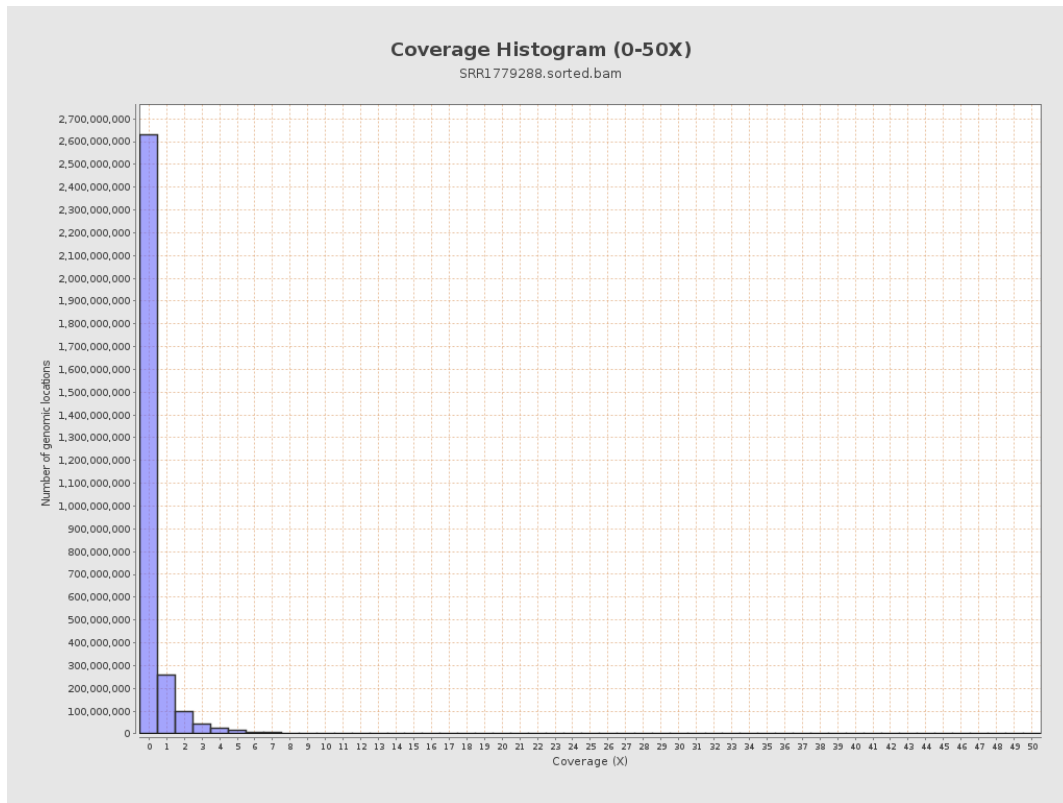
3. Results : Coverage across reference



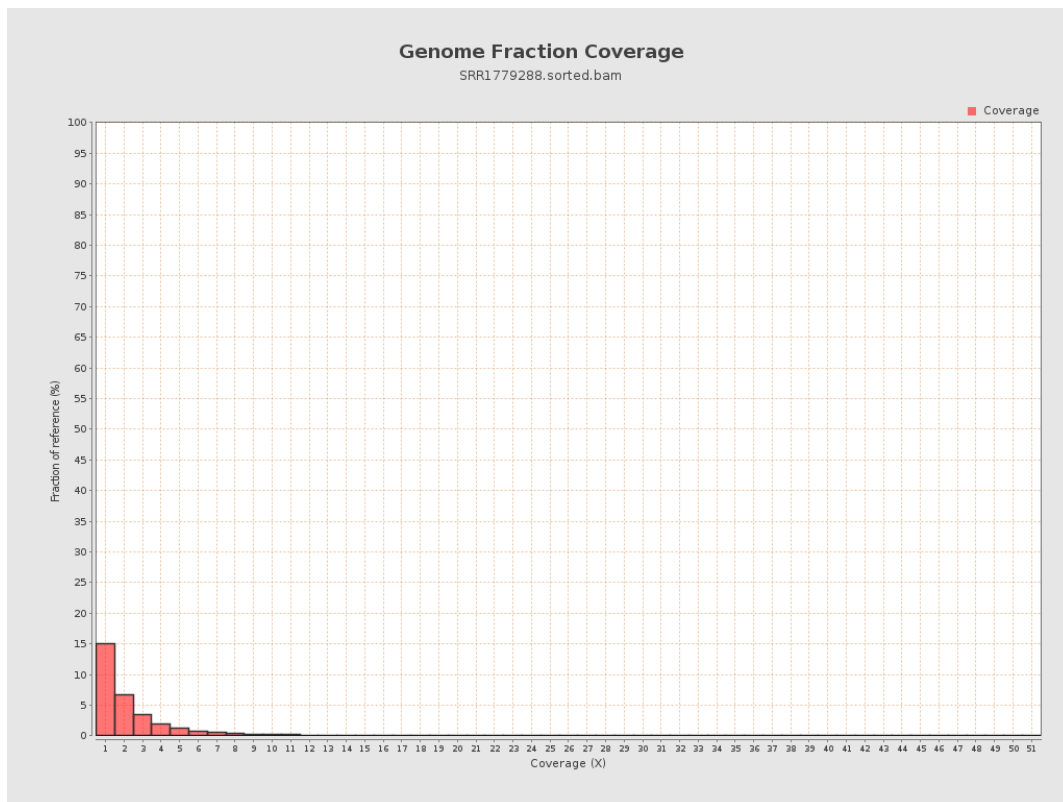
4. Results : Coverage Histogram



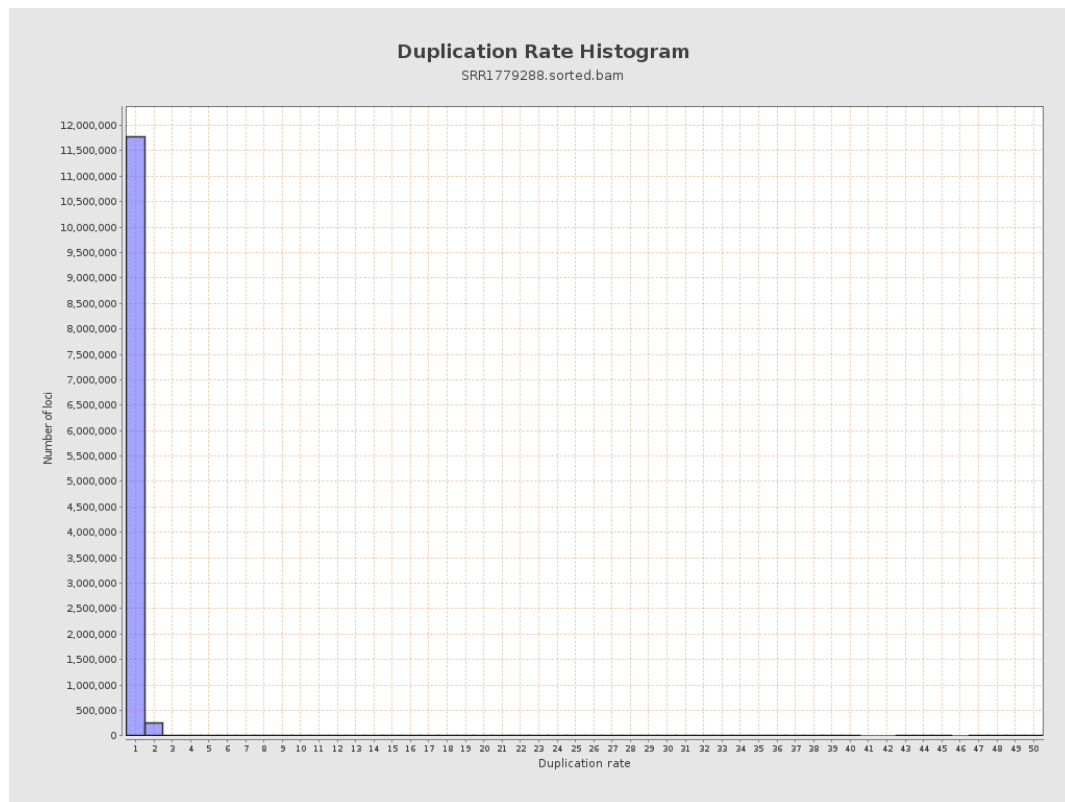
5. Results : Coverage Histogram (0-50X)



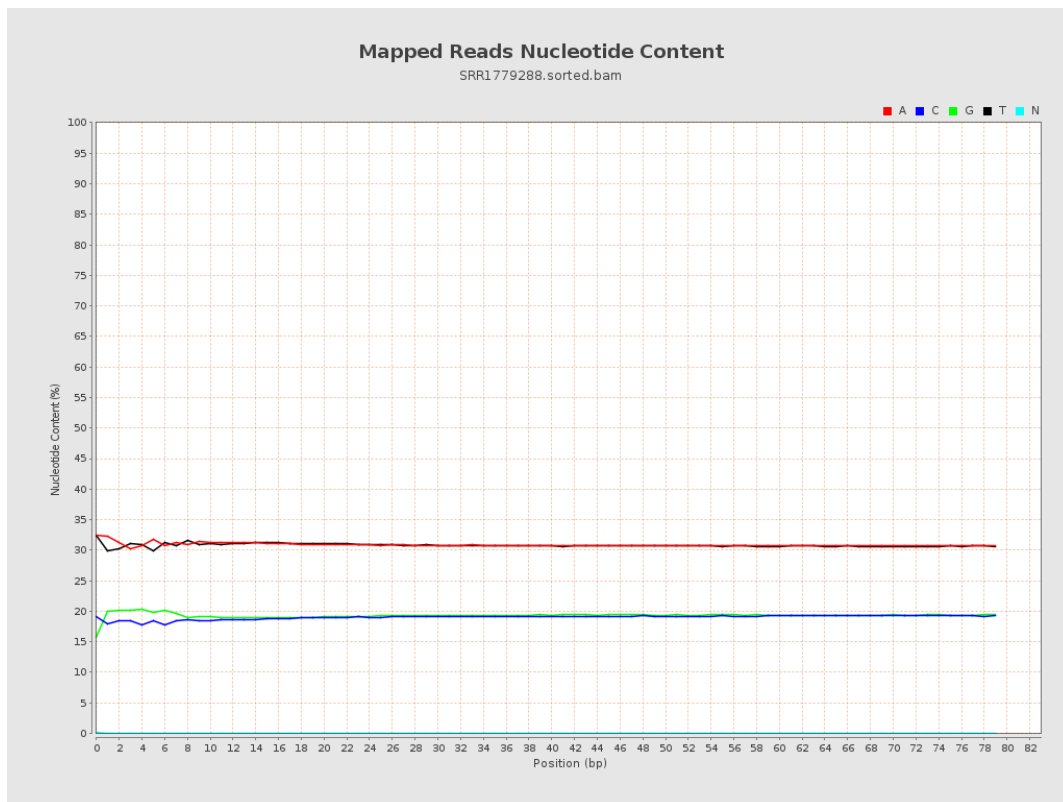
6. Results : Genome Fraction Coverage



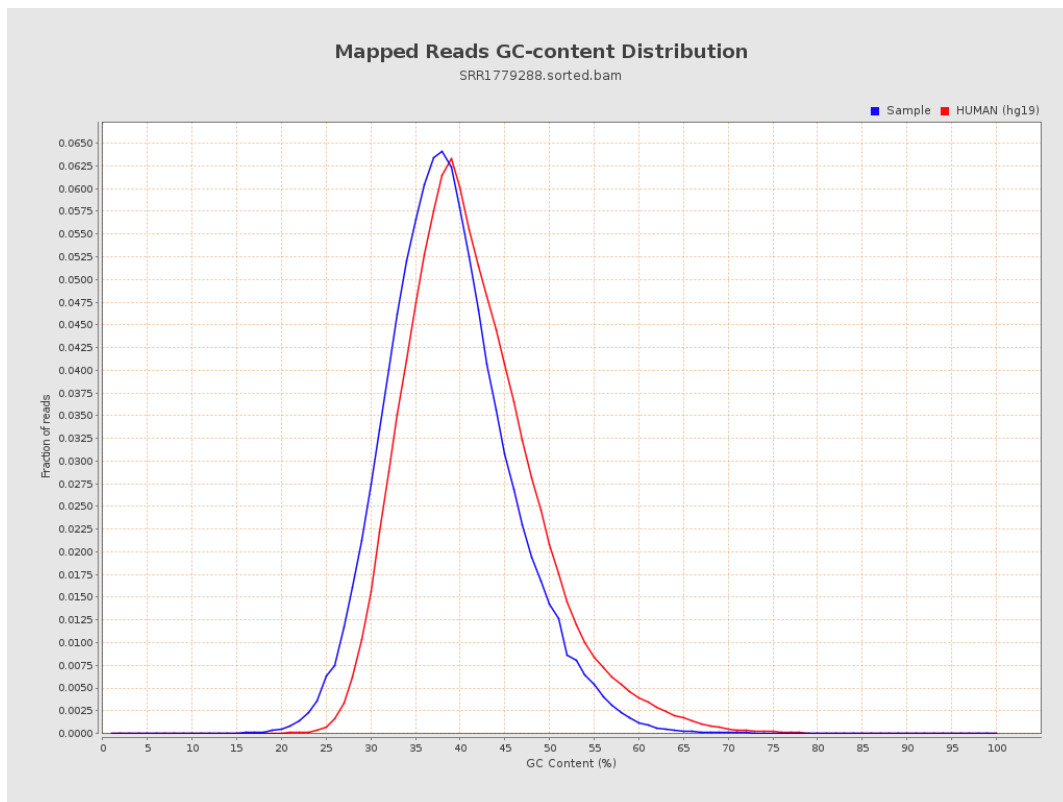
7. Results : Duplication Rate Histogram



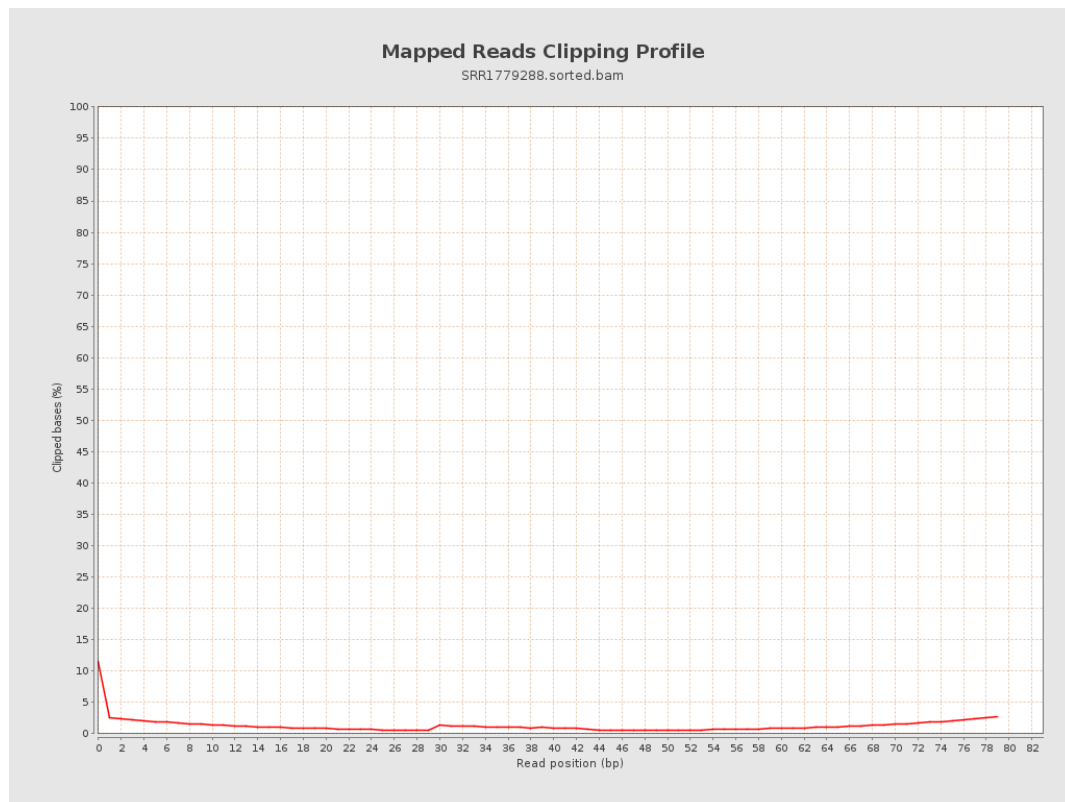
8. Results : Mapped Reads Nucleotide Content



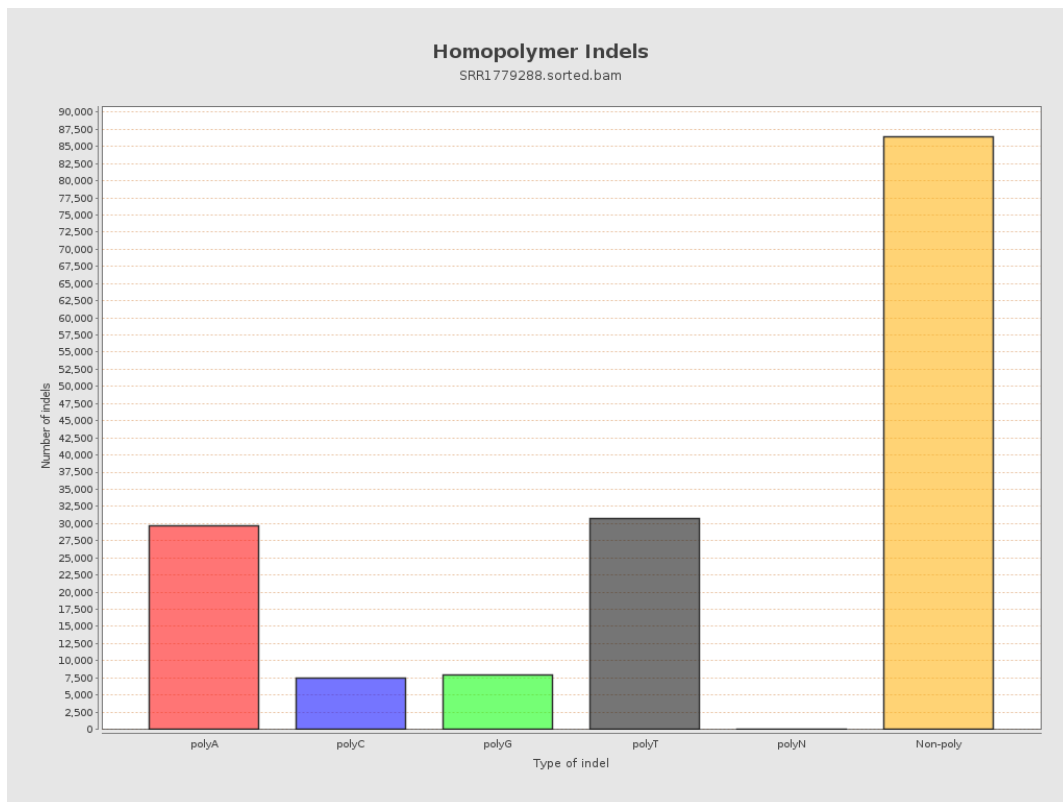
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



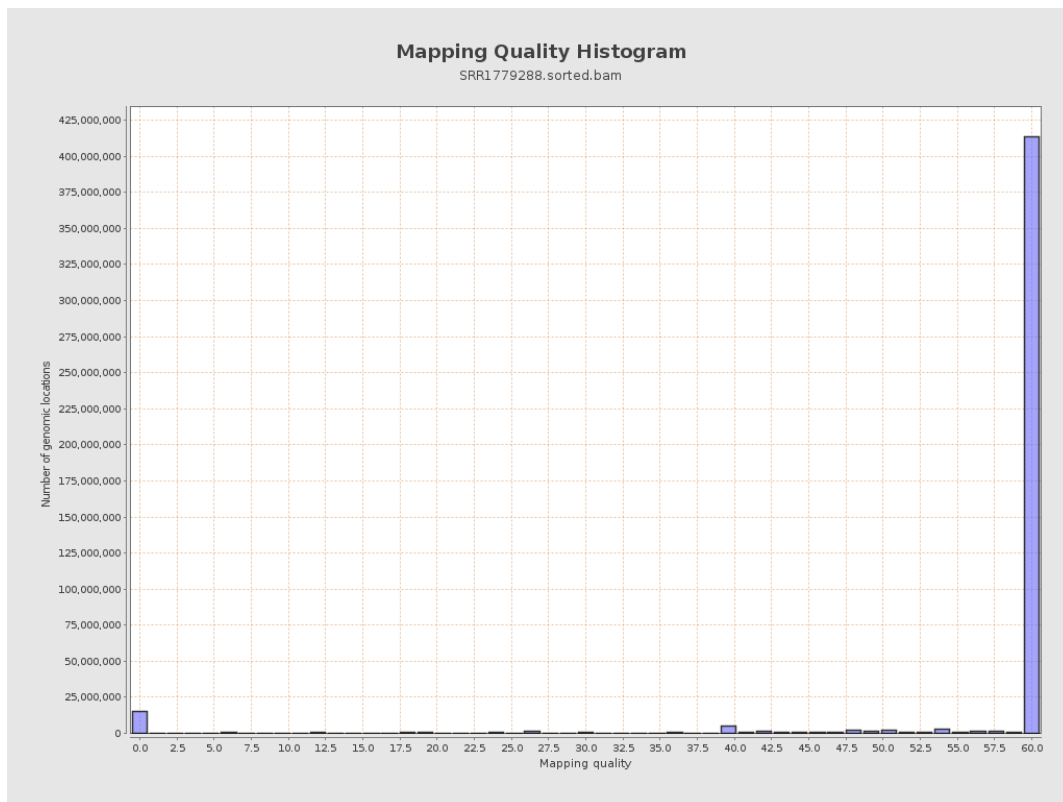
11. Results : Homopolymer Indels



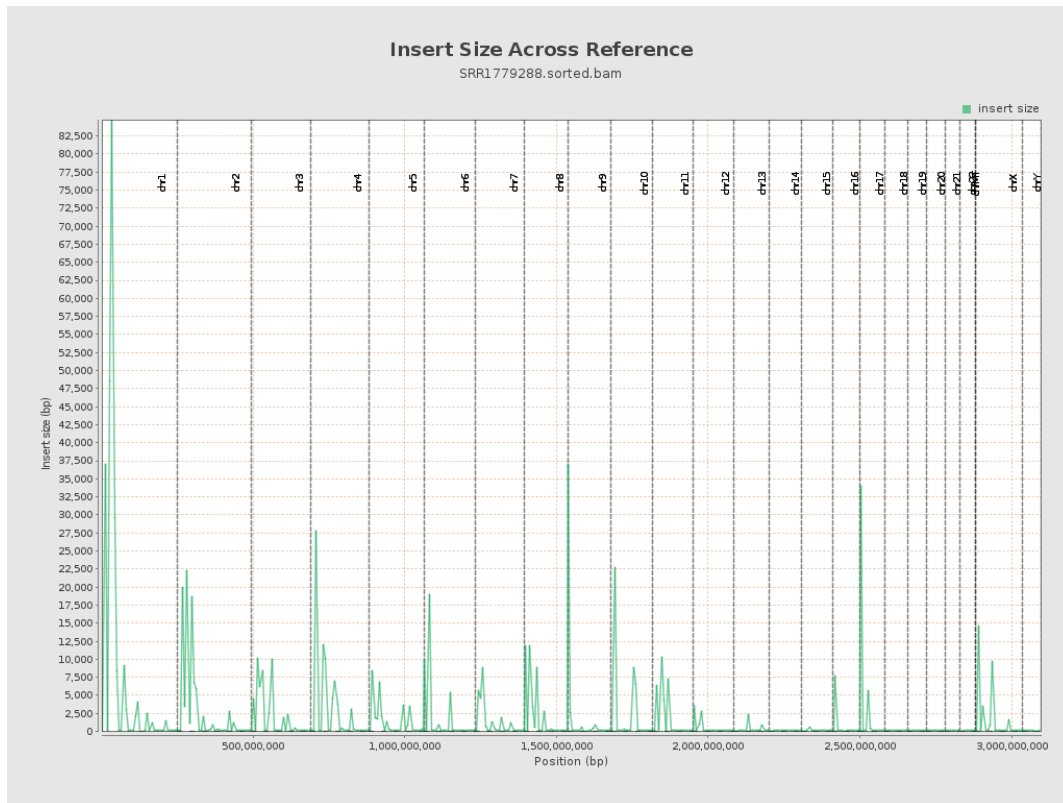
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

