

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 08:15:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038486.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_SRR5038486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038486_1.fastq.gz SRR5038486_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 08:15:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,921,602
Mapped reads	10,198,942 / 93.38%
Unmapped reads	722,660 / 6.62%
Mapped paired reads	10,198,942 / 93.38%
Mapped reads, first in pair	5,179,998 / 47.43%
Mapped reads, second in pair	5,018,944 / 45.95%
Mapped reads, both in pair	10,020,652 / 91.75%
Mapped reads, singletons	178,290 / 1.63%
Secondary alignments	0
Supplementary alignments	164,910 / 1.51%
Read min/max/mean length	30 / 150 / 150.78
Duplicated reads (estimated)	1,190,450 / 10.9%
Duplication rate	7.39%
Clipped reads	2,323,927 / 21.28%

2.2. ACGT Content

Number/percentage of A's	419,073,606 / 28.72%
Number/percentage of C's	305,021,133 / 20.9%
Number/percentage of T's	419,144,520 / 28.73%
Number/percentage of G's	315,889,499 / 21.65%
Number/percentage of N's	31,827 / 0%

GC Percentage	42.55%
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2.3. Coverage

Mean	0.4717
Standard Deviation	5.6773

2.4. Mapping Quality

Mean Mapping Quality	53.84
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2.5. Insert size

Mean	98,439.02
Standard Deviation	2,999,074.65
P25/Median/P75	229 / 271 / 323

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	20,558,068
Insertions	242,133
Mapped reads with at least one insertion	2.23%
Deletions	489,866
Mapped reads with at least one deletion	4.62%
Homopolymer indels	47.14%

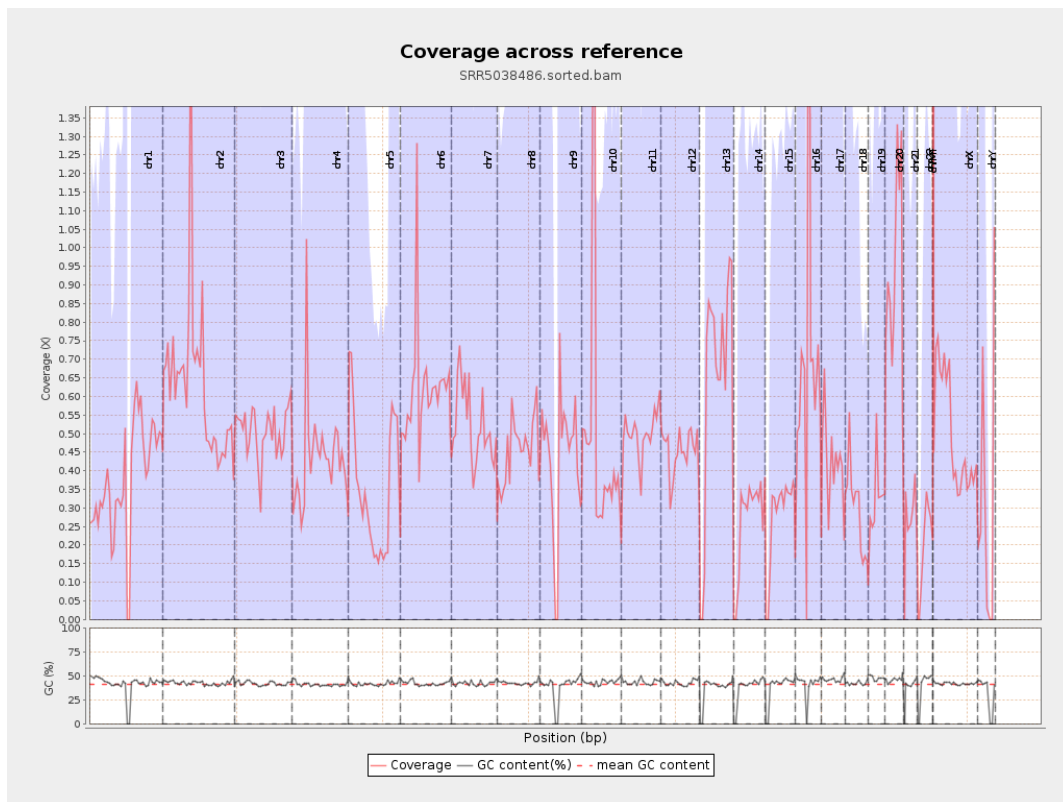
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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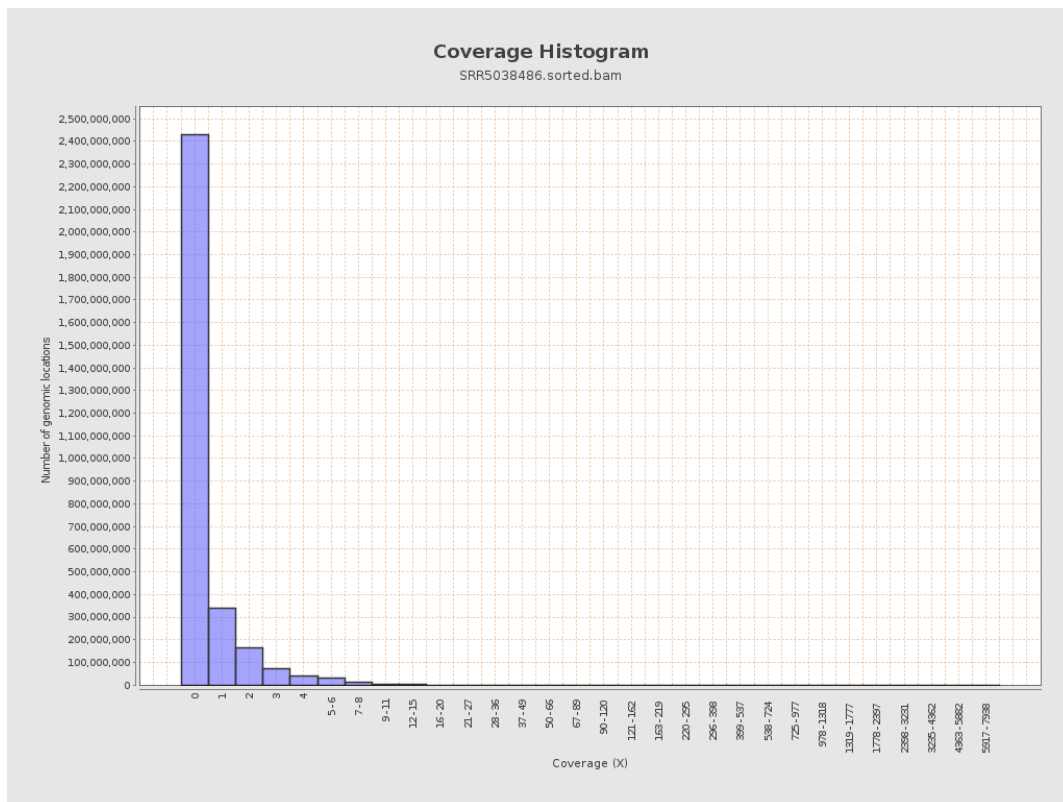
		bases	coverage	deviation
chr1	249250621	94073294	0.3774	3.3859
chr2	243199373	153940586	0.633	7.024
chr3	198022430	99747983	0.5037	1.2367
chr4	191154276	83512023	0.4369	4.6921
chr5	180915260	63751947	0.3524	1.0399
chr6	171115067	105839368	0.6185	7.3056
chr7	159138663	83049972	0.5219	4.9914
chr8	146364022	67072510	0.4583	1.6253
chr9	141213431	61430189	0.435	7.7048
chr10	135534747	65378760	0.4824	15.6868
chr11	135006516	66757587	0.4945	2.7518
chr12	133851895	60738323	0.4538	1.1603
chr13	115169878	75333209	0.6541	1.4972
chr14	107349540	28672091	0.2671	0.9065
chr15	102531392	27979067	0.2729	0.845
chr16	90354753	64007004	0.7084	12.2484
chr17	81195210	35002210	0.4311	3.149
chr18	78077248	23435280	0.3002	6.1224
chr19	59128983	19012130	0.3215	2.1235
chr20	63025520	60973075	0.9674	2.4023
chr21	48129895	12836698	0.2667	2.451
chr22	51304566	10190224	0.1986	0.7975
chrMT	16571	1037556	62.6128	28.744
chrX	155270560	76799976	0.4946	1.4066

chrY	59373566	19576796	0.3297	8.8909
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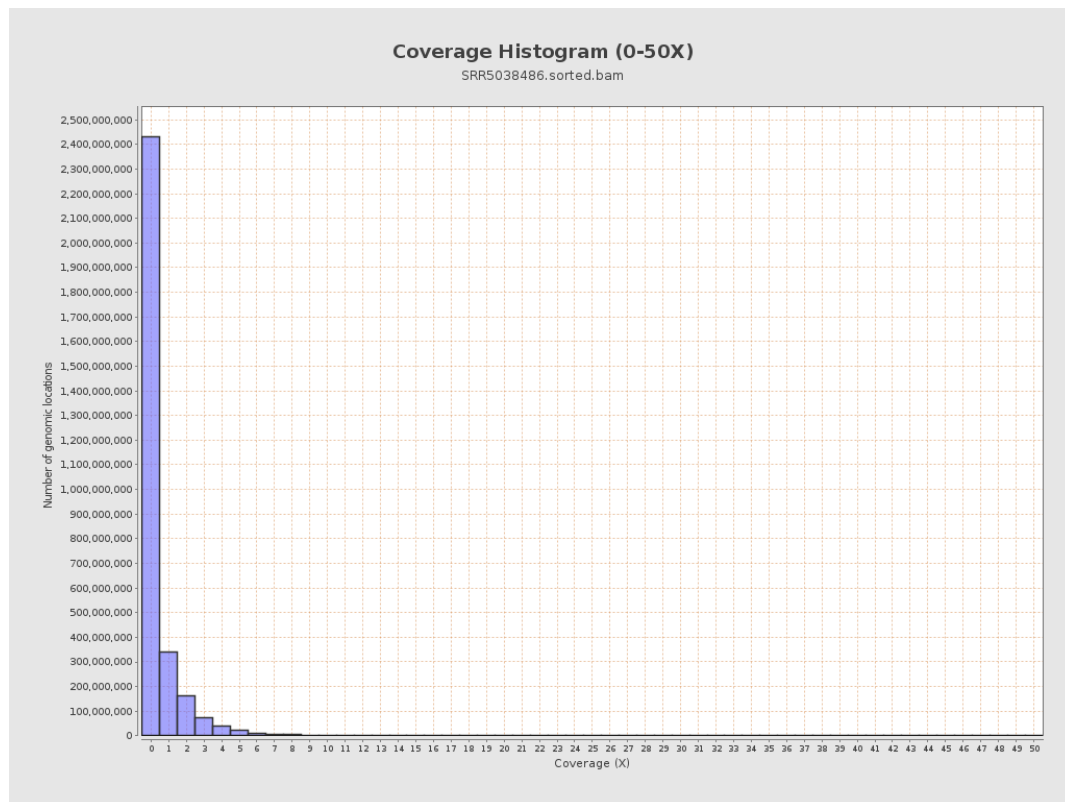
3. Results : Coverage across reference



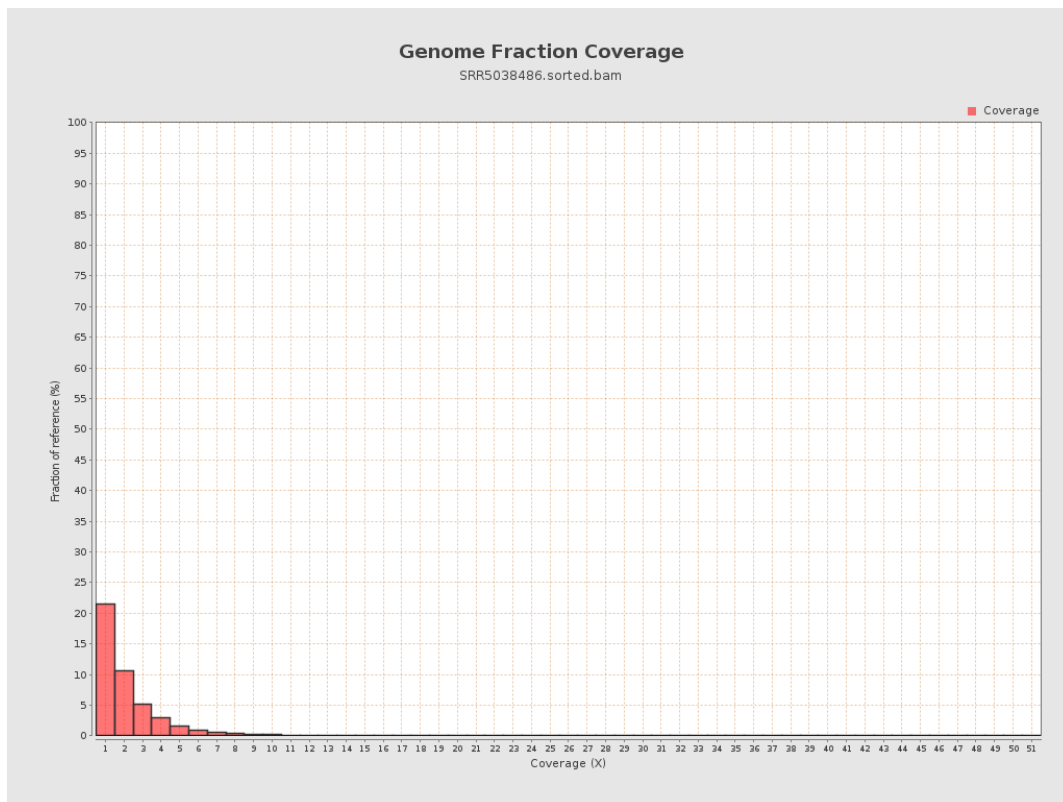
4. Results : Coverage Histogram



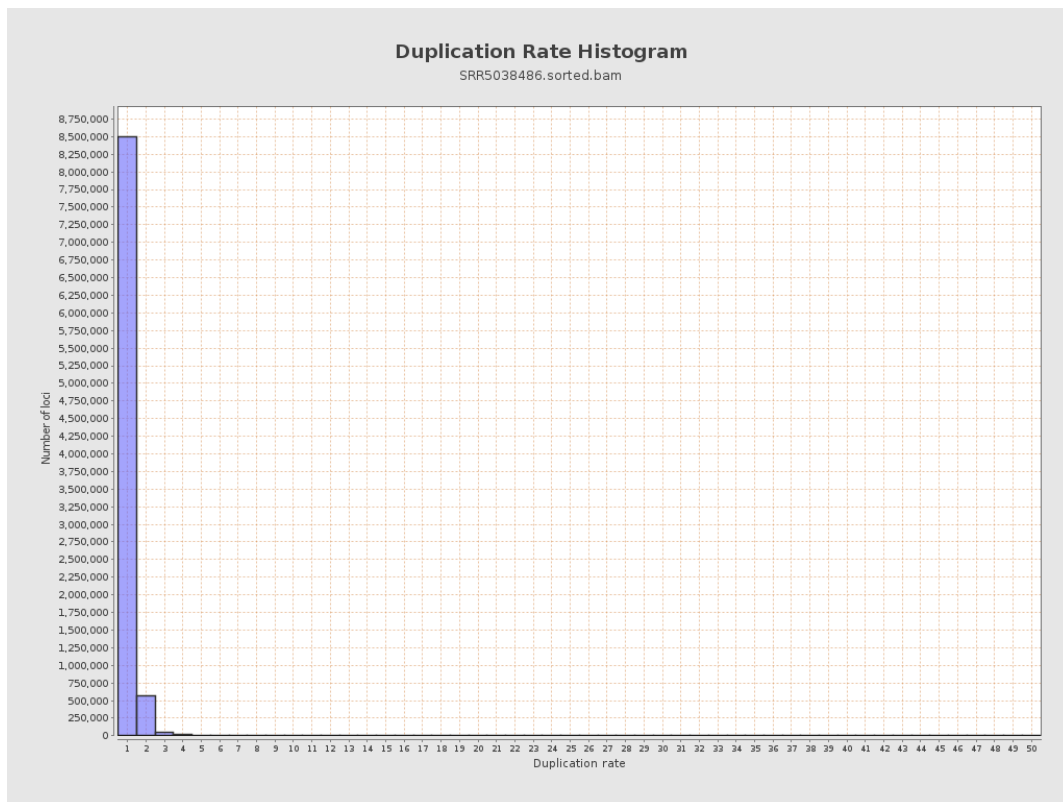
5. Results : Coverage Histogram (0-50X)



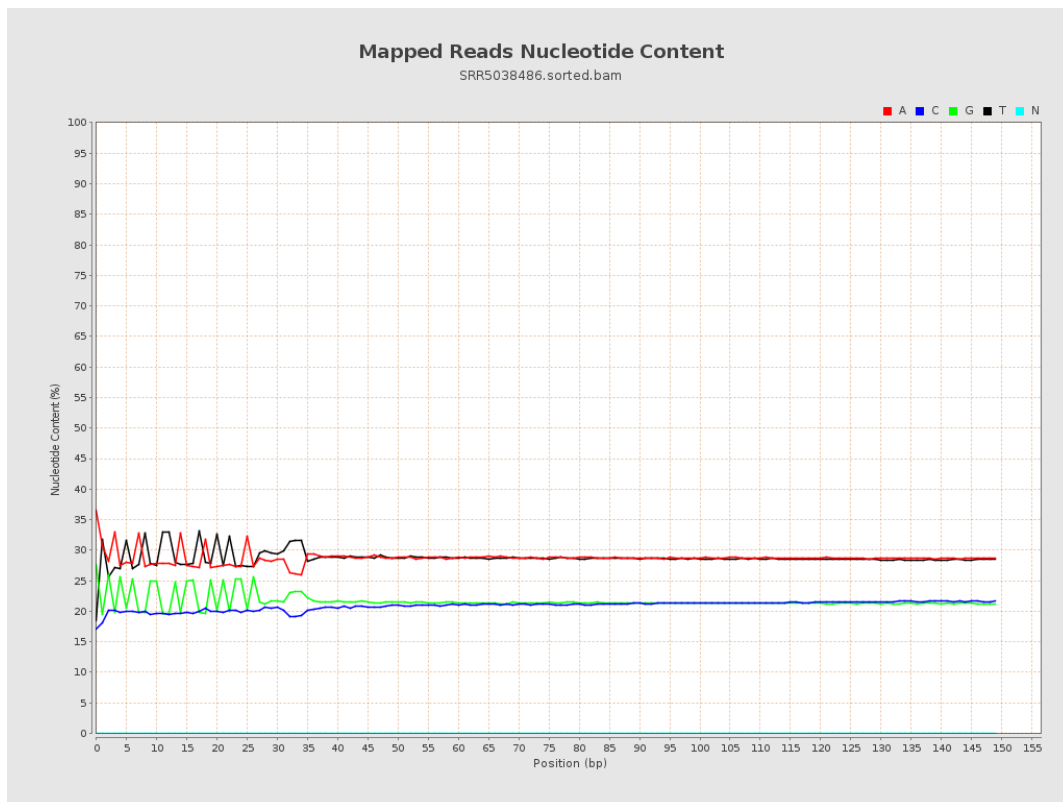
6. Results : Genome Fraction Coverage



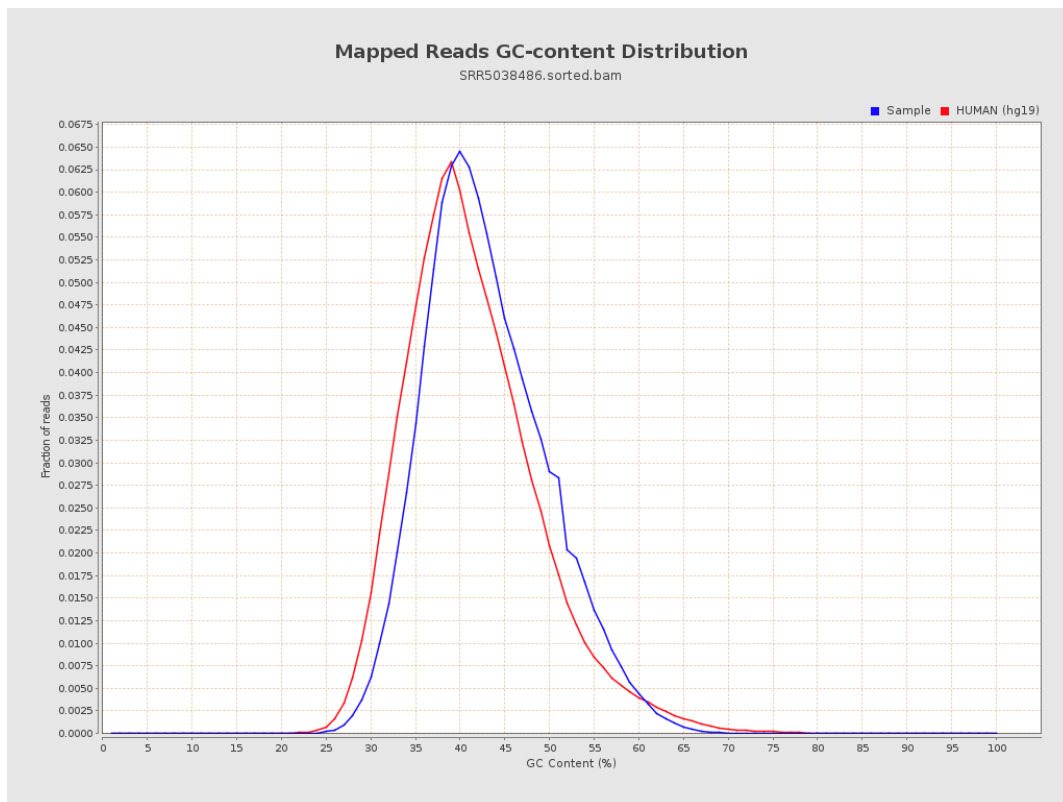
7. Results : Duplication Rate Histogram



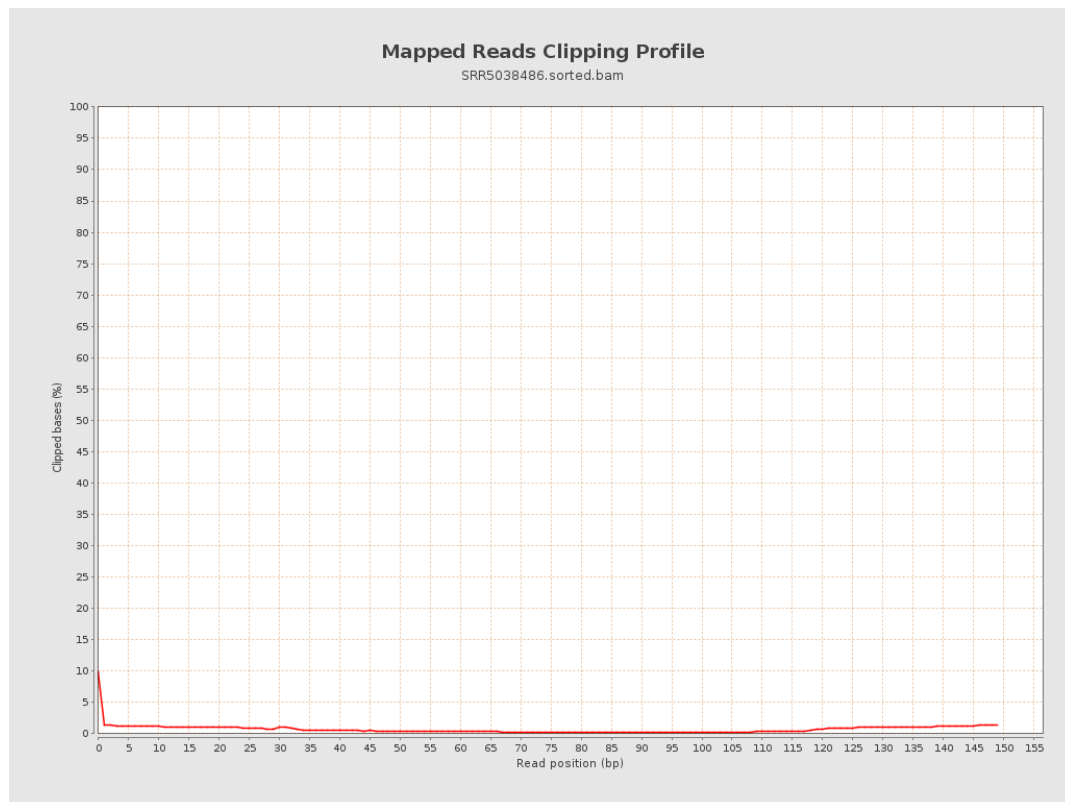
8. Results : Mapped Reads Nucleotide Content



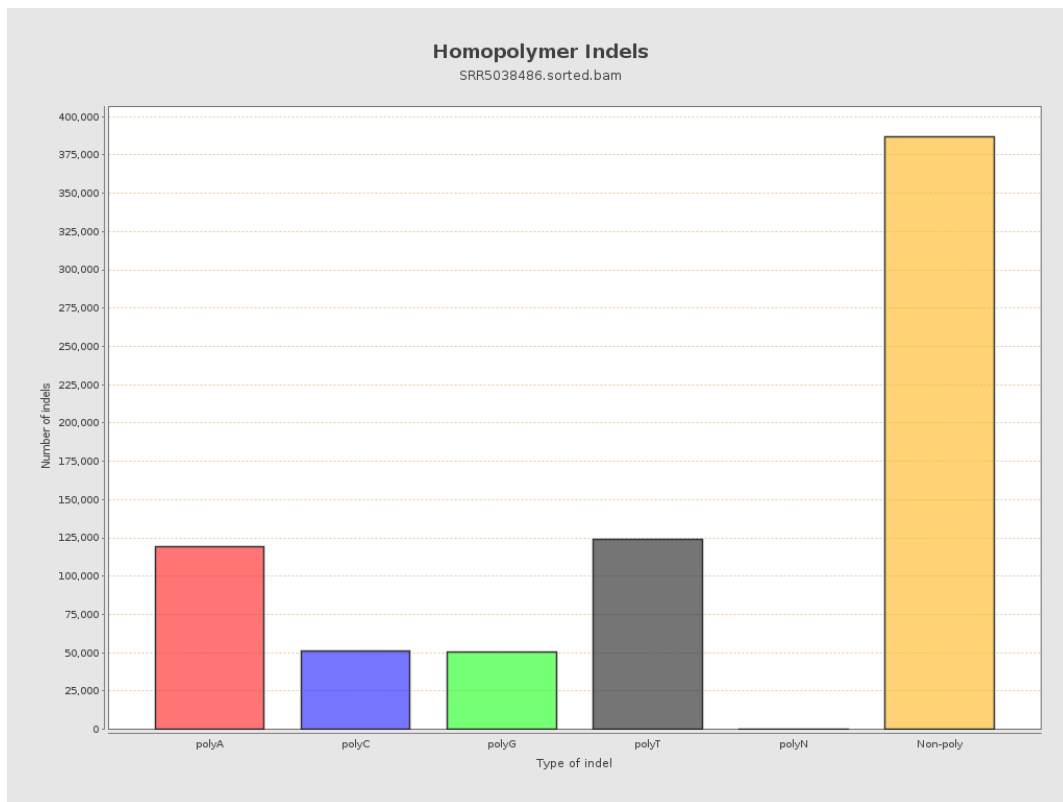
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



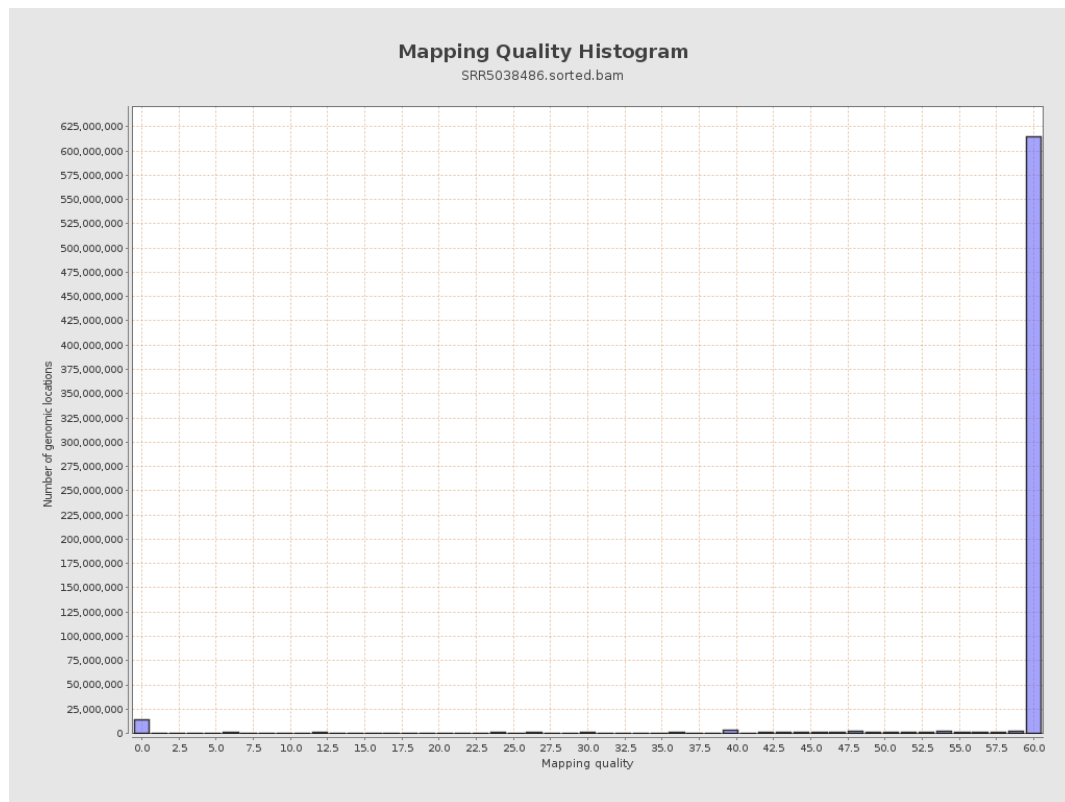
11. Results : Homopolymer Indels



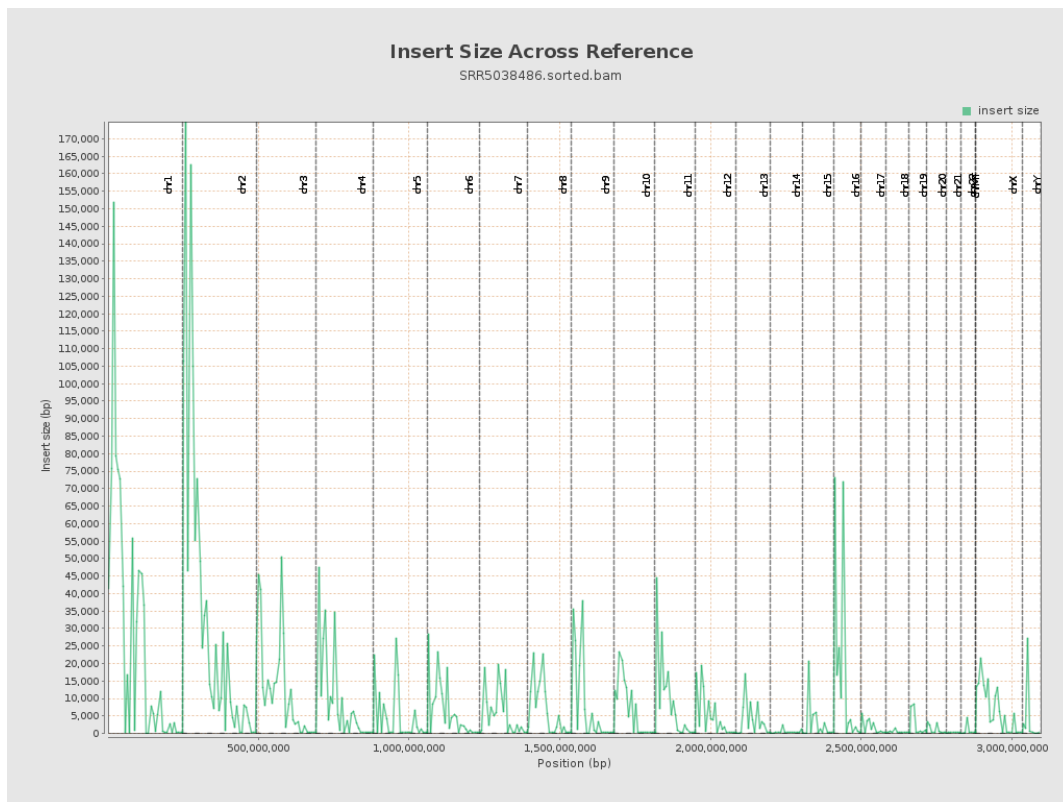
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

