Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 16:21:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038404.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_SRR5038404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038404_1.fastq.gz SRR5038404_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 16:21:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,668,008
Mapped reads	16,394,642 / 92.79%
Unmapped reads	1,273,366 / 7.21%
Mapped paired reads	16,394,642 / 92.79%
Mapped reads, first in pair	8,320,732 / 47.09%
Mapped reads, second in pair	8,073,910 / 45.7%
Mapped reads, both in pair	16,090,192 / 91.07%
Mapped reads, singletons	304,450 / 1.72%
Secondary alignments	0
Supplementary alignments	219,096 / 1.24%
Read min/max/mean length	30 / 150 / 150.62
Duplicated reads (estimated)	3,257,605 / 18.44%
Duplication rate	14.21%
Clipped reads	7,754,849 / 43.89%

2.2. ACGT Content

Number/percentage of A's	632,401,450 / 28.65%
Number/percentage of C's	436,067,141 / 19.75%
Number/percentage of T's	644,041,642 / 29.17%
Number/percentage of G's	494,917,493 / 22.42%
Number/percentage of N's	174,500 / 0.01%

GC Percentage	42.17%

2.3. Coverage

Mean	0.7136
Standard Deviation	8.8507

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	74,022.04
Standard Deviation	2,646,990.01
P25/Median/P75	201 / 252 / 319

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	27,723,992
Insertions	370,222
Mapped reads with at least one insertion	2.16%
Deletions	762,638
Mapped reads with at least one deletion	4.5%
Homopolymer indels	48.18%

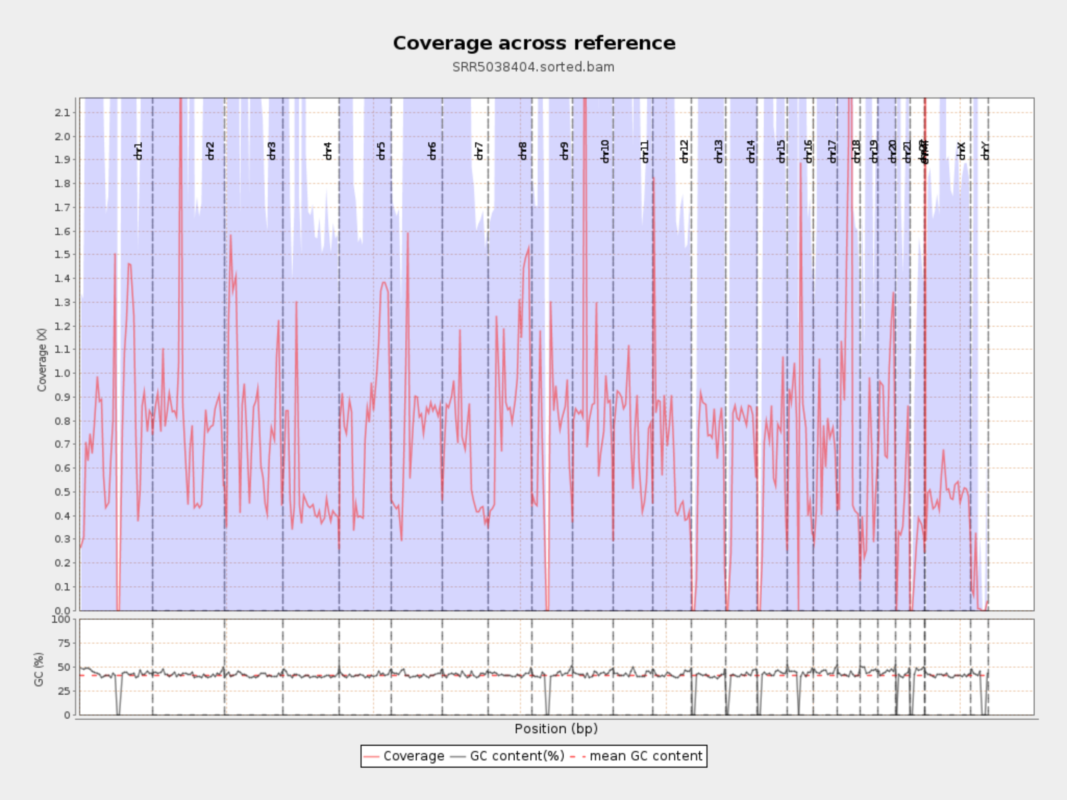
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

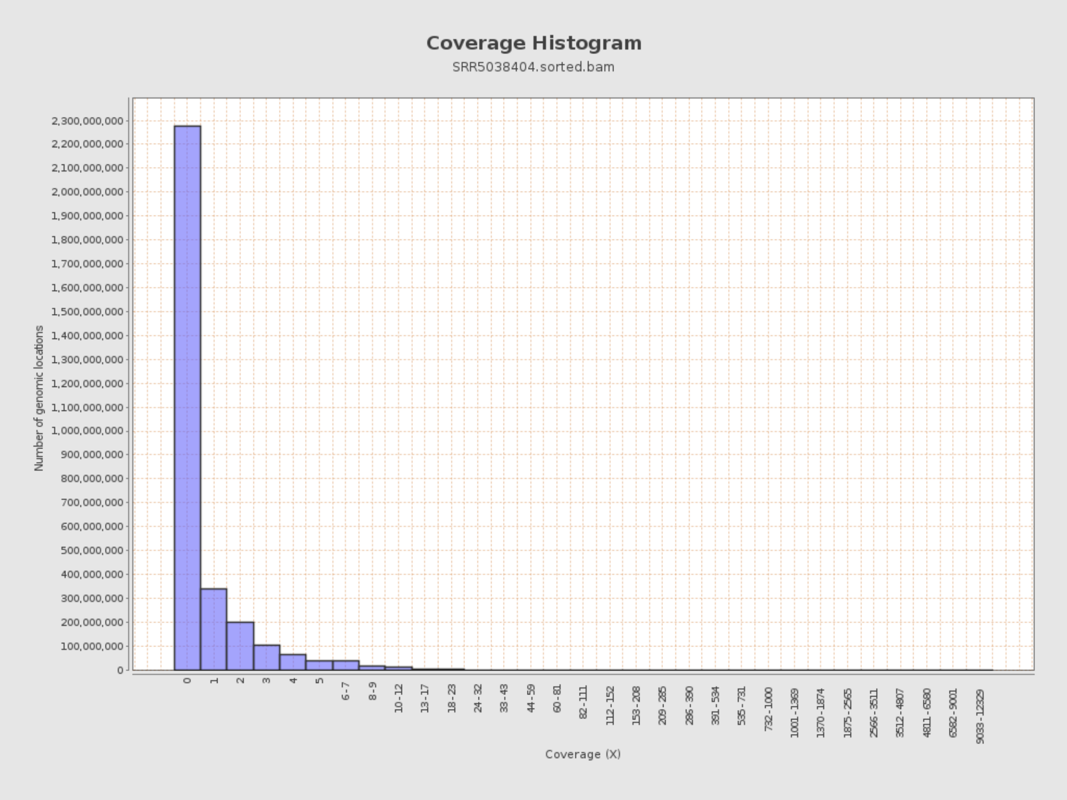
		bases	coverage	deviation
chr1	249250621	189661642	0.7609	12.5046
chr2	243199373	197987089	0.8141	10.7898
chr3	198022430	163647177	0.8264	1.8652
chr4	191154276	94672978	0.4953	7.7991
chr5	180915260	152202073	0.8413	1.818
chr6	171115067	130832940	0.7646	7.9997
chr7	159138663	106462277	0.669	9.2099
chr8	146364022	141995562	0.9702	3.7687
chr9	141213431	94007131	0.6657	16.1146
chr10	135534747	131322049	0.9689	20.2263
chr11	135006516	100480308	0.7443	7.6965
chr12	133851895	91668812	0.6849	1.7991
chr13	115169878	74524226	0.6471	1.5406
chr14	107349540	71423970	0.6653	1.6671
chr15	102531392	59096512	0.5764	1.4954
chr16	90354753	66219345	0.7329	8.3958
chr17	81195210	52364032	0.6449	10.9346
chr18	78077248	88486041	1.1333	11.3384
chr19	59128983	27474942	0.4647	5.2614
chr20	63025520	58446355	0.9273	3.1589
chr21	48129895	20741741	0.431	3.8417
chr22	51304566	11972757	0.2334	0.932
chrMT	16571	3400157	205.1872	117.7466
chrX	155270560	76031838	0.4897	2.1003

chrY	59373566	3923681	0.0661	7.7578

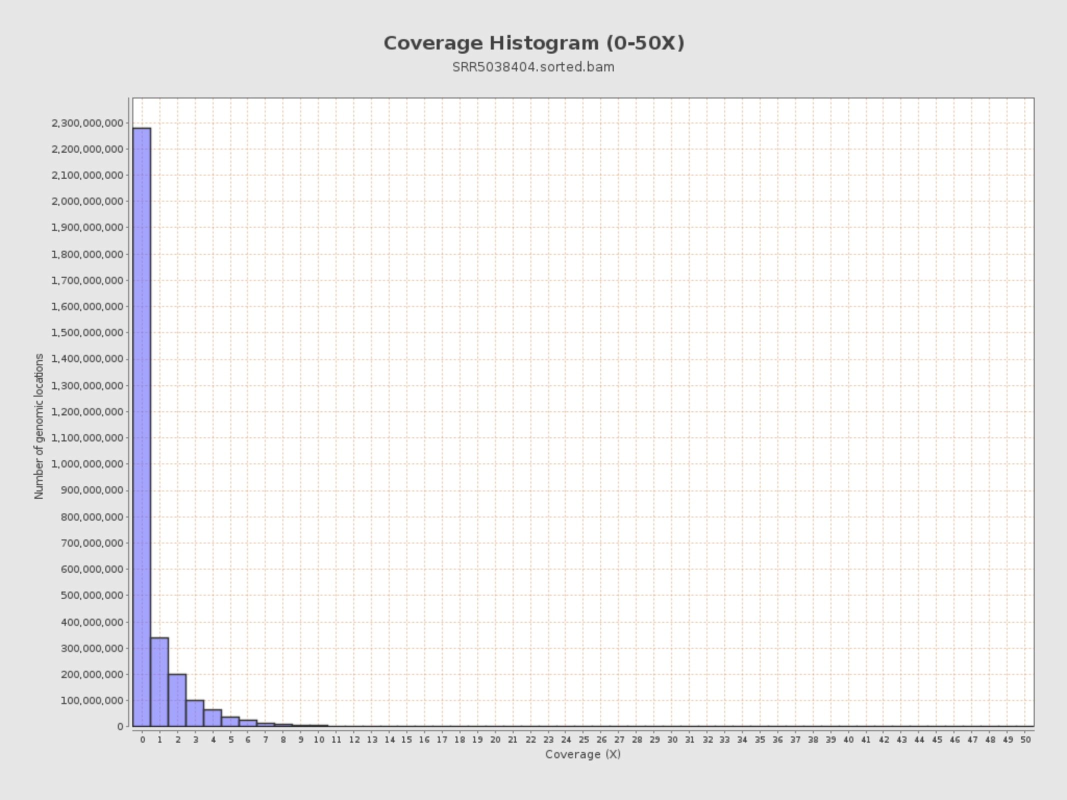
3. Results : Coverage across reference



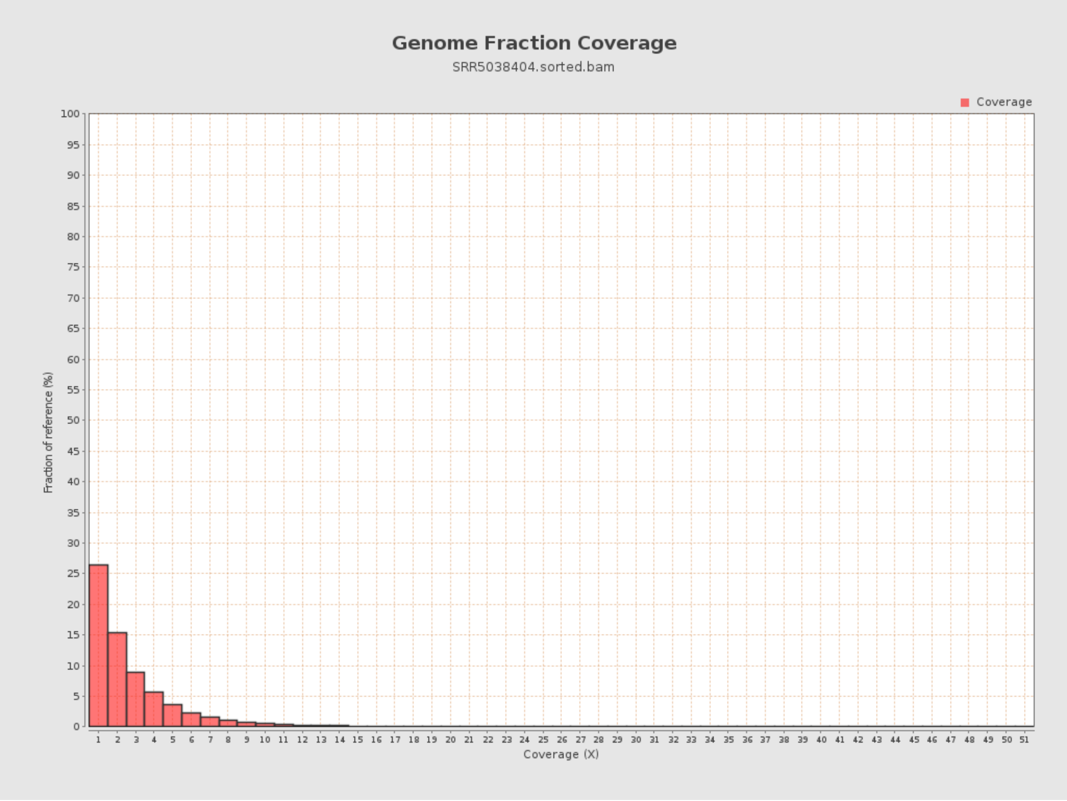
4. Results : Coverage Histogram



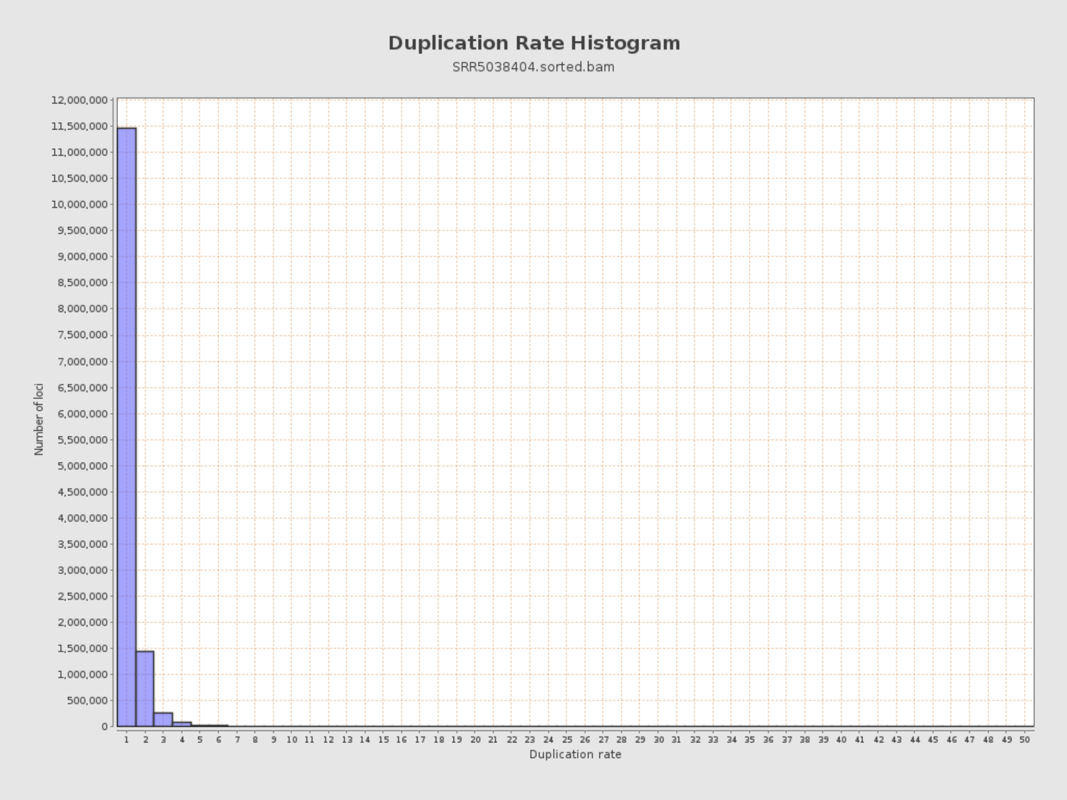
5. Results : Coverage Histogram (0-50X)



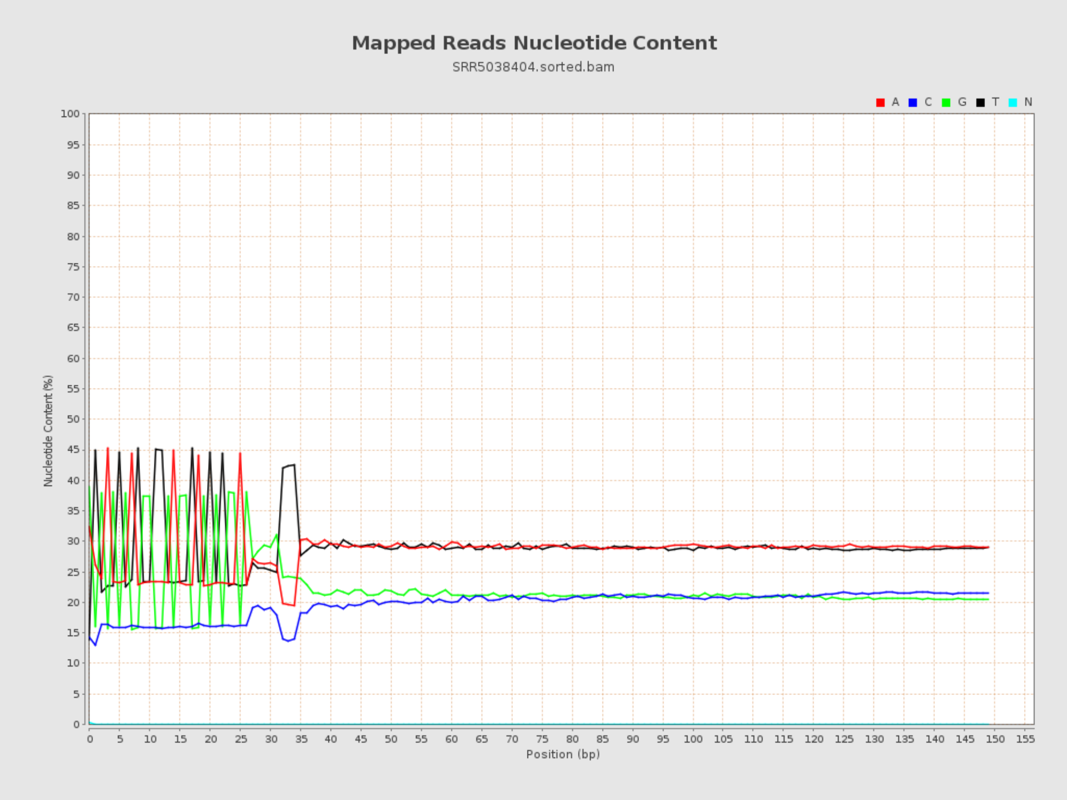
6. Results : Genome Fraction Coverage



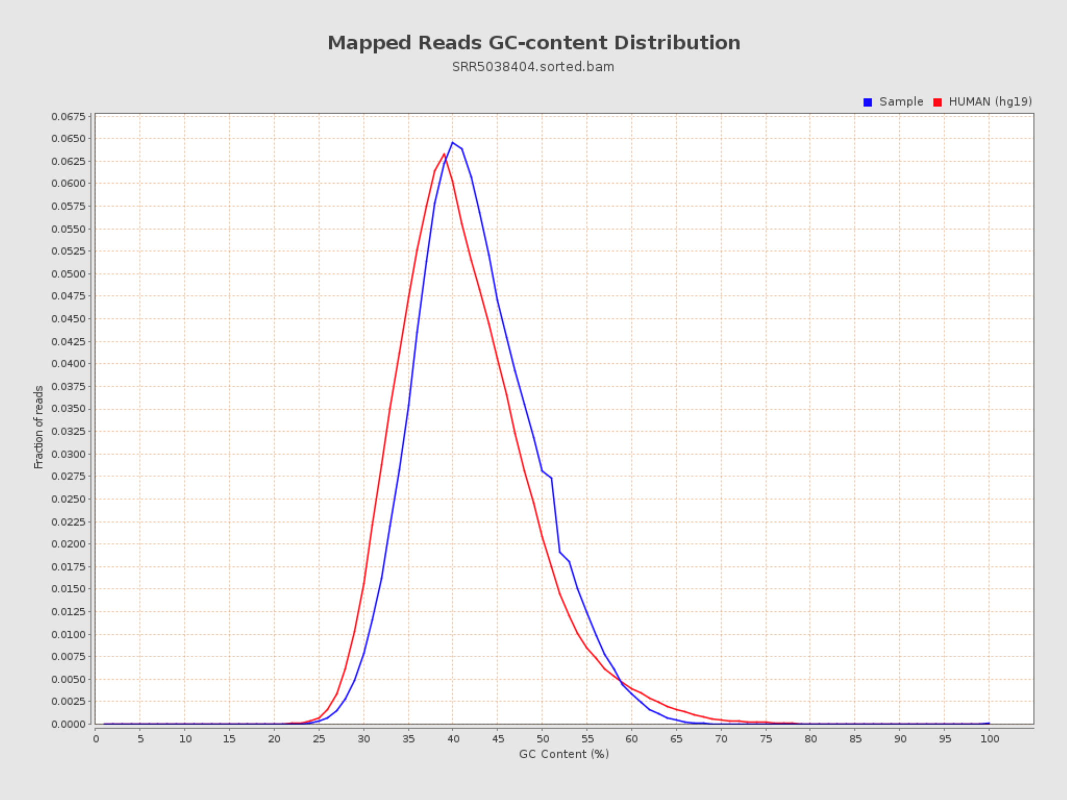
7. Results : Duplication Rate Histogram



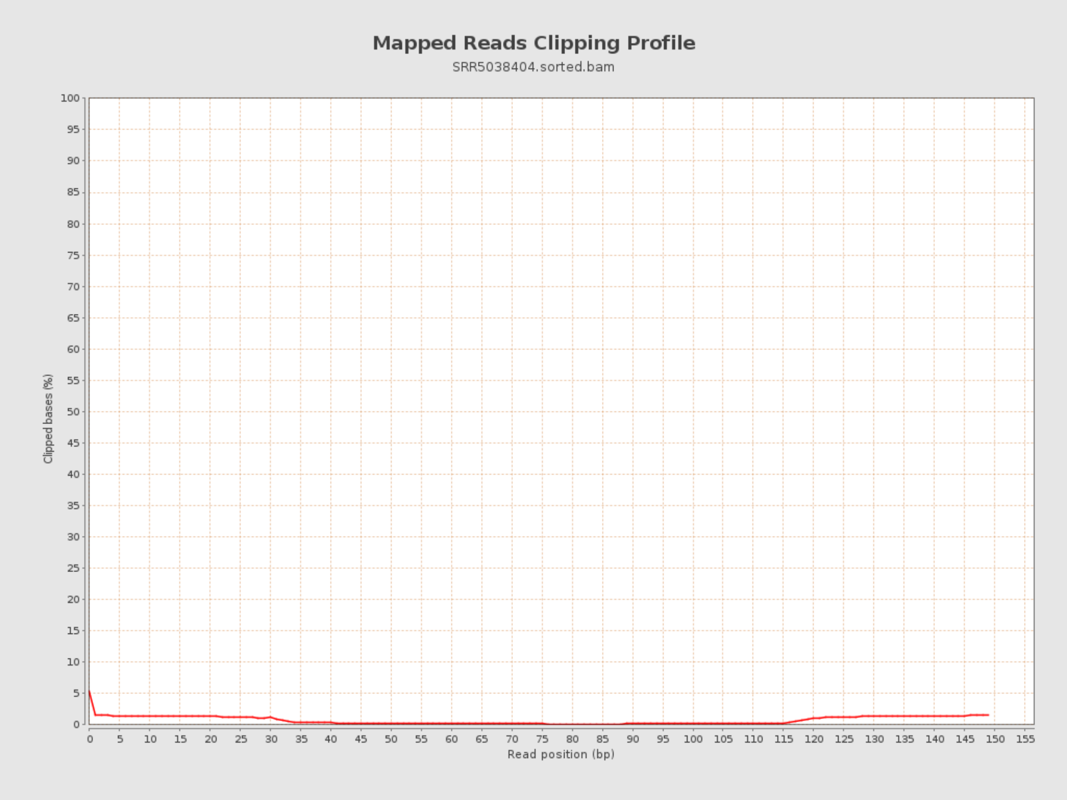
8. Results : Mapped Reads Nucleotide Content



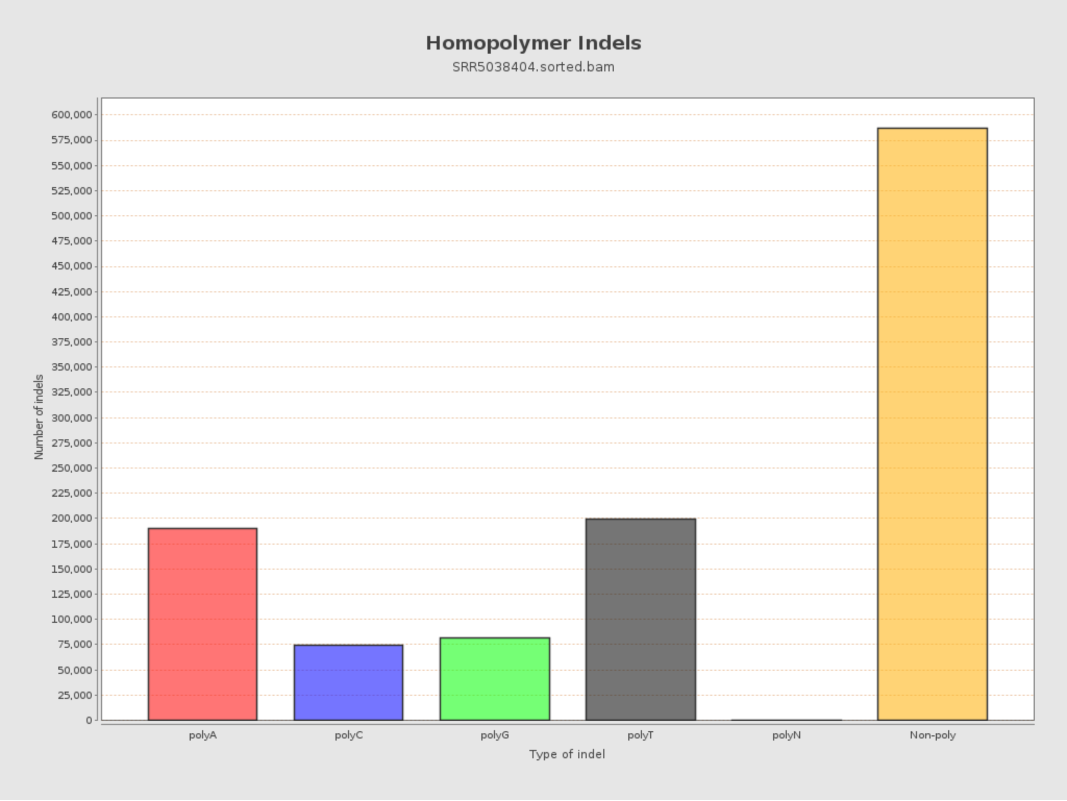
9. Results : Mapped Reads GC-content Distribution



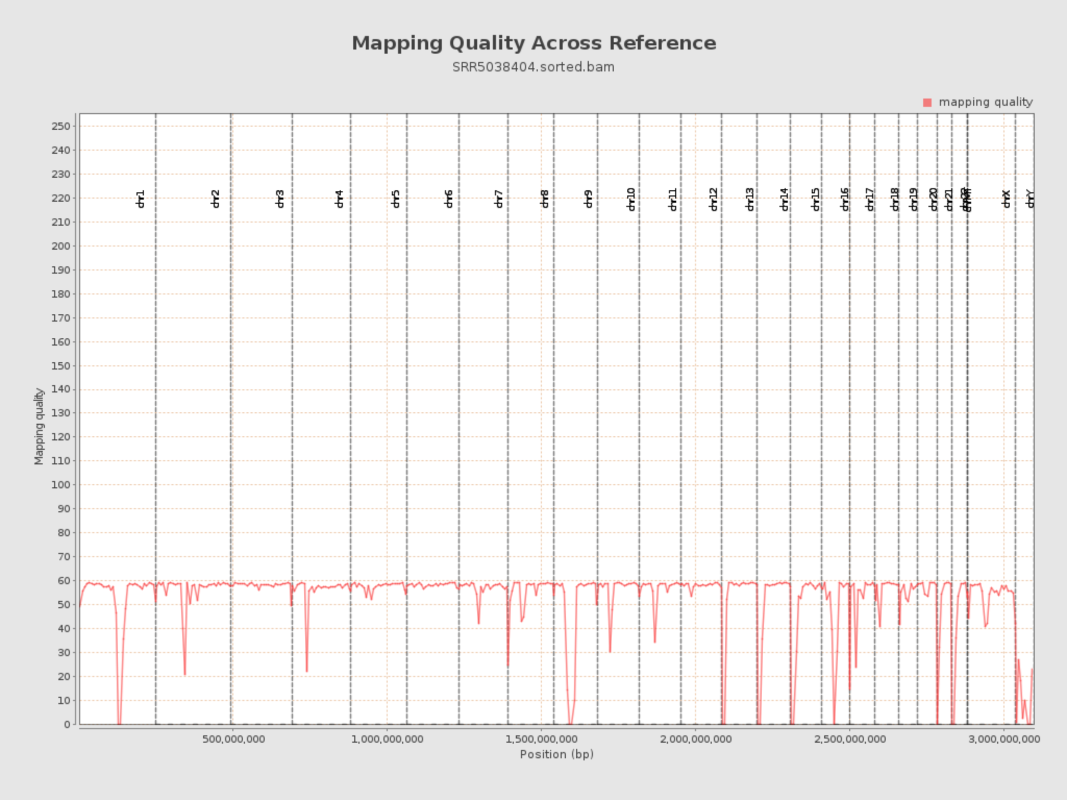
10. Results : Mapped Reads Clipping Profile



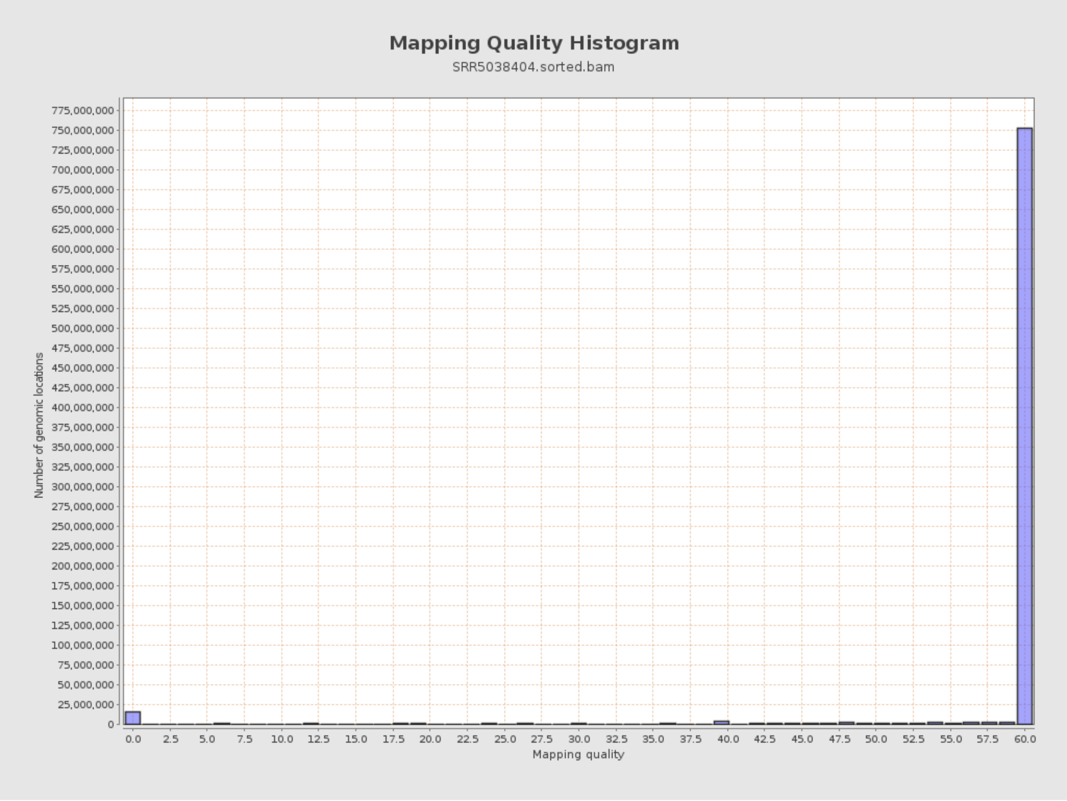
11. Results : Homopolymer Indels



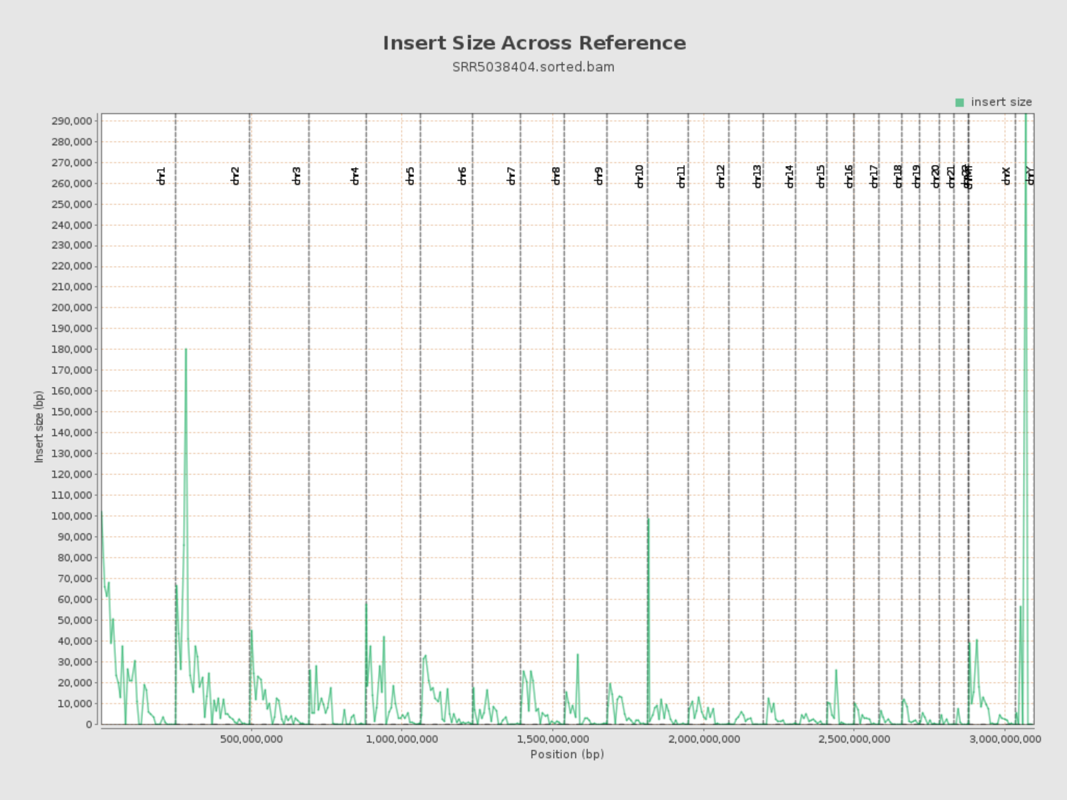
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



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15. Results : Insert Size Histogram