Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 03:14:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038426.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_SRR5038426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038426_1.fastq.gz SRR5038426_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 03:14:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,645,748
Mapped reads	12,834,027 / 94.05%
Unmapped reads	811,721 / 5.95%
Mapped paired reads	12,834,027 / 94.05%
Mapped reads, first in pair	6,494,783 / 47.6%
Mapped reads, second in pair	6,339,244 / 46.46%
Mapped reads, both in pair	12,656,800 / 92.75%
Mapped reads, singletons	177,227 / 1.3%
Secondary alignments	0
Supplementary alignments	252,584 / 1.85%
Read min/max/mean length	30 / 150 / 150.96
Duplicated reads (estimated)	1,928,742 / 14.13%
Duplication rate	8.53%
Clipped reads	3,661,891 / 26.84%

2.2. ACGT Content

Number/percentage of A's	526,595,601 / 29.04%
Number/percentage of C's	369,630,830 / 20.38%
Number/percentage of T's	527,785,018 / 29.1%
Number/percentage of G's	389,606,590 / 21.48%
Number/percentage of N's	37,908 / 0%

GC Percentage	41.86%

2.3. Coverage

Mean	0.5863
Standard Deviation	10.2086

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	92,500.58
Standard Deviation	2,840,262.41
P25/Median/P75	224 / 264 / 315

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	25,917,097
Insertions	327,370
Mapped reads with at least one insertion	2.41%
Deletions	635,455
Mapped reads with at least one deletion	4.76%
Homopolymer indels	46.98%

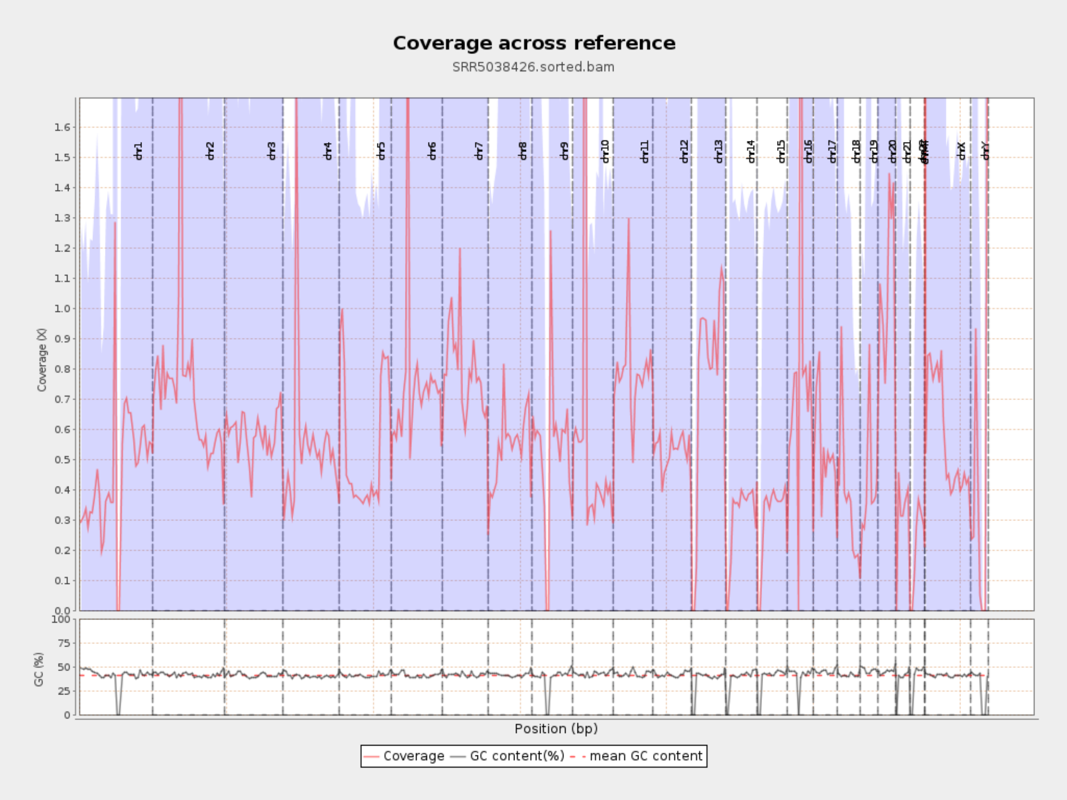
2.7. Chromosome stats

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

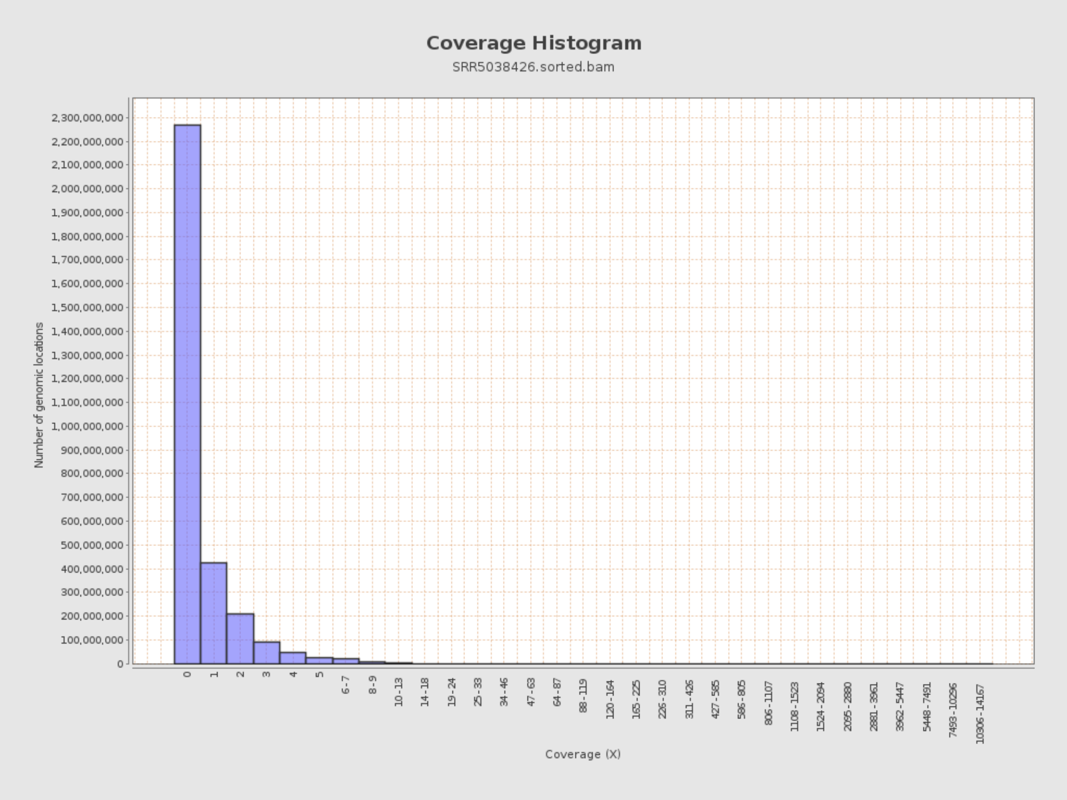
		bases	coverage	deviation
chr1	249250621	112577216	0.4517	14.5682
chr2	243199373	182831037	0.7518	11.296
chr3	198022430	115658696	0.5841	1.3174
chr4	191154276	104039538	0.5443	9.2998
chr5	180915260	98316611	0.5434	1.299
chr6	171115067	131050054	0.7659	16.4062
chr7	159138663	126098595	0.7924	8.9632
chr8	146364022	79612113	0.5439	2.3638
chr9	141213431	73115366	0.5178	14.7866
chr10	135534747	80328913	0.5927	21.9433
chr11	135006516	105146000	0.7788	9.5193
chr12	133851895	70612863	0.5275	1.1991
chr13	115169878	88702558	0.7702	1.5087
chr14	107349540	32659557	0.3042	0.9902
chr15	102531392	31302961	0.3053	0.8471
chr16	90354753	73842647	0.8173	14.522
chr17	81195210	42637669	0.5251	8.2749
chr18	78077248	28968770	0.371	11.2898
chr19	59128983	23543958	0.3982	8.1416
chr20	63025520	67495524	1.0709	3.3373
chr21	48129895	15407064	0.3201	3.9915
chr22	51304566	10922648	0.2129	0.7578
chrMT	16571	3061477	184.7491	130.9568
chrX	155270560	88937067	0.5728	2.3489

chrY	59373566	28087354	0.4731	13.6524

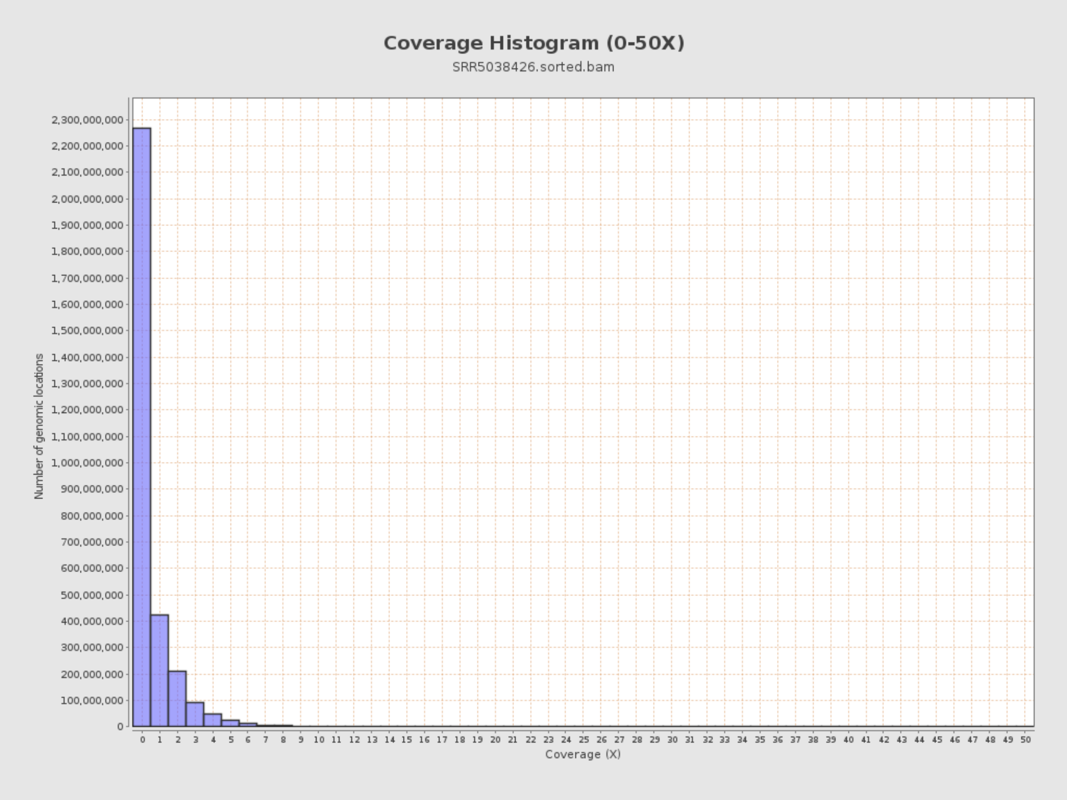
3. Results : Coverage across reference



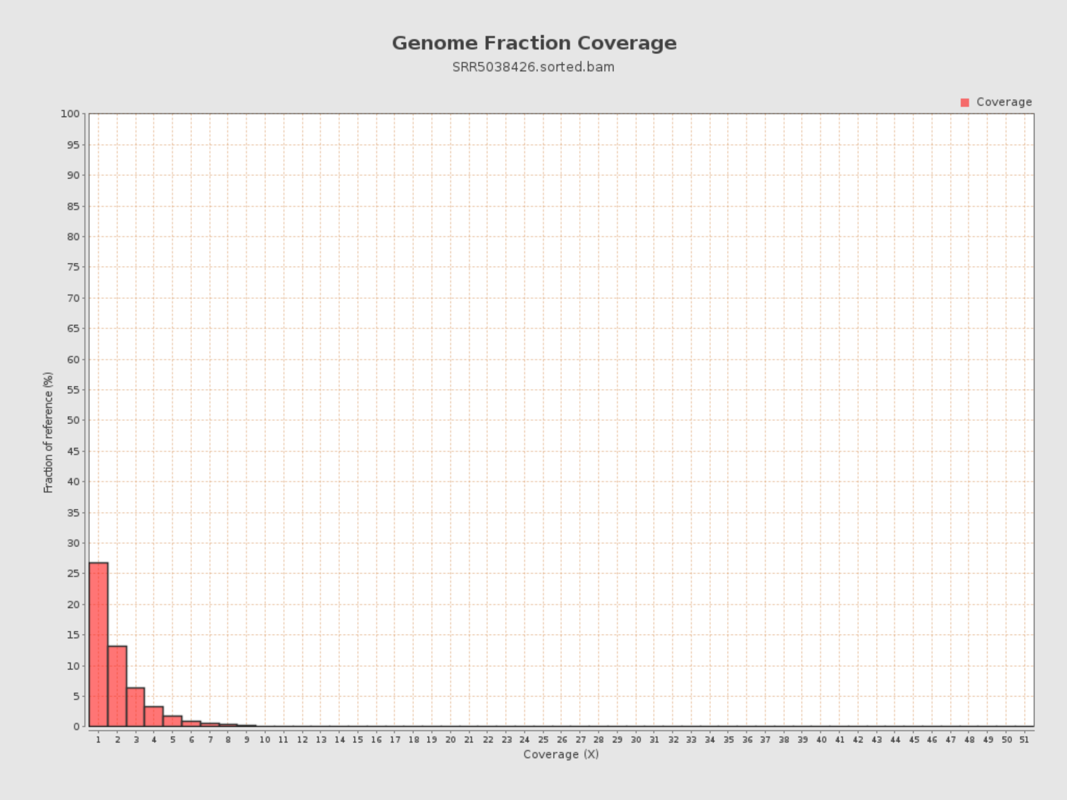
4. Results : Coverage Histogram



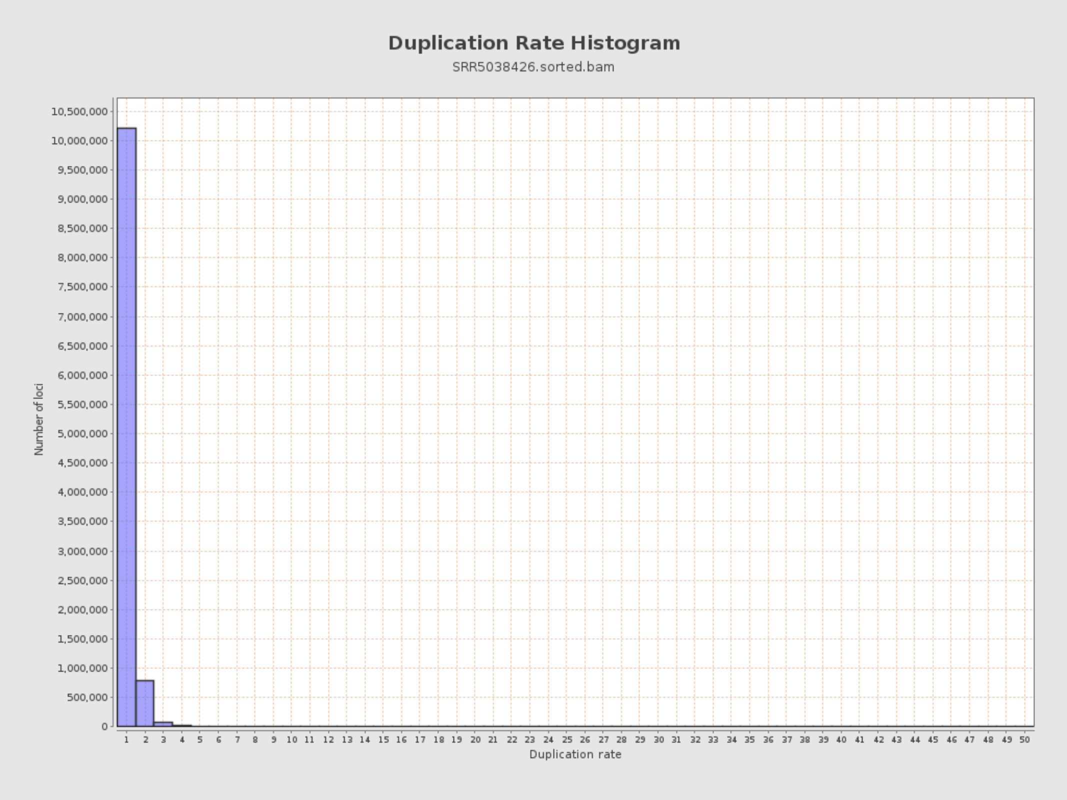
5. Results : Coverage Histogram (0-50X)



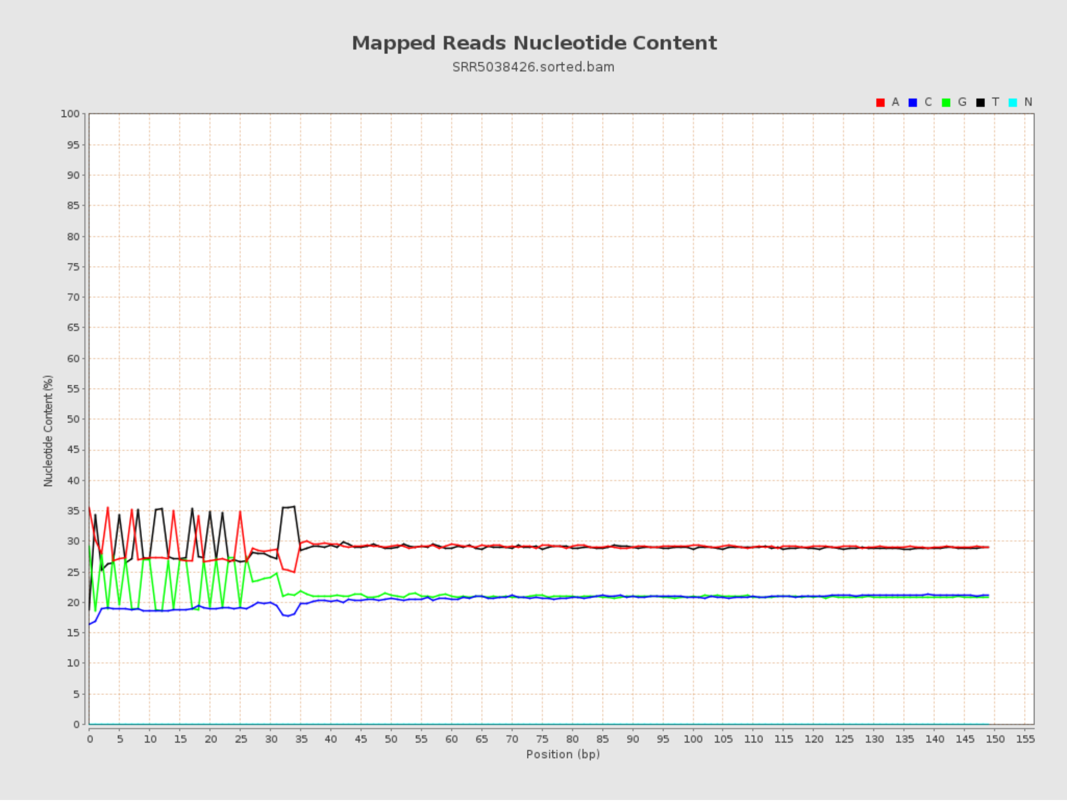
6. Results : Genome Fraction Coverage



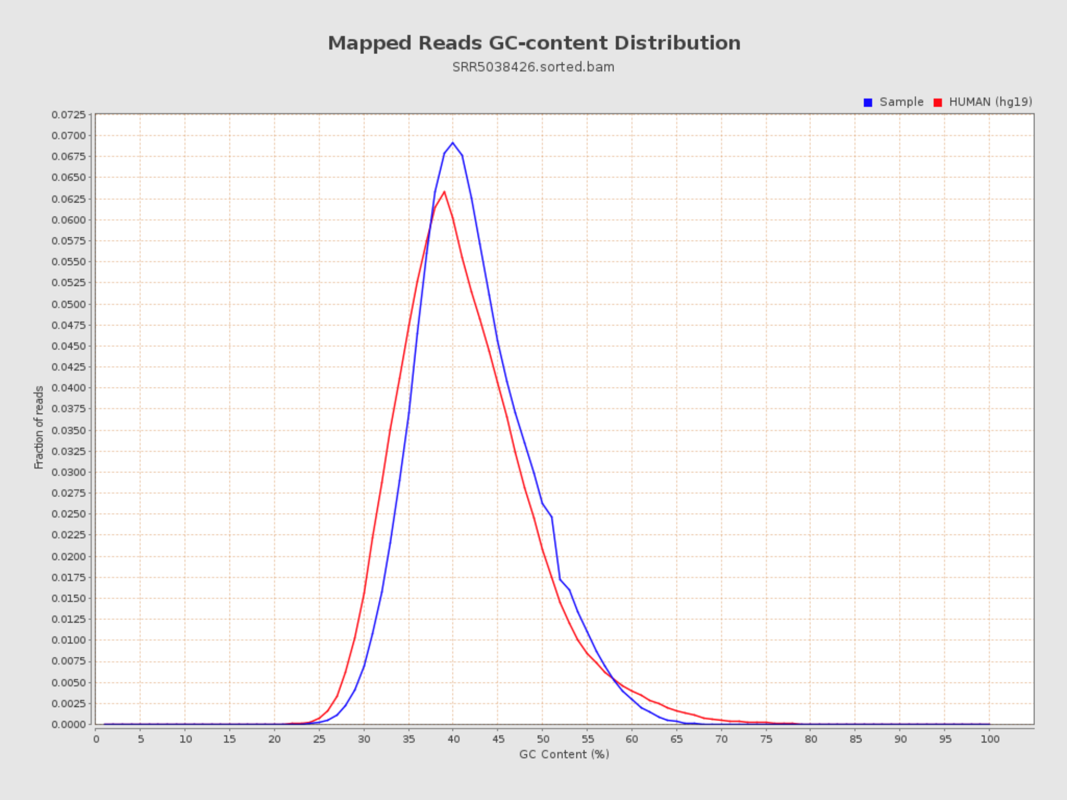
7. Results : Duplication Rate Histogram



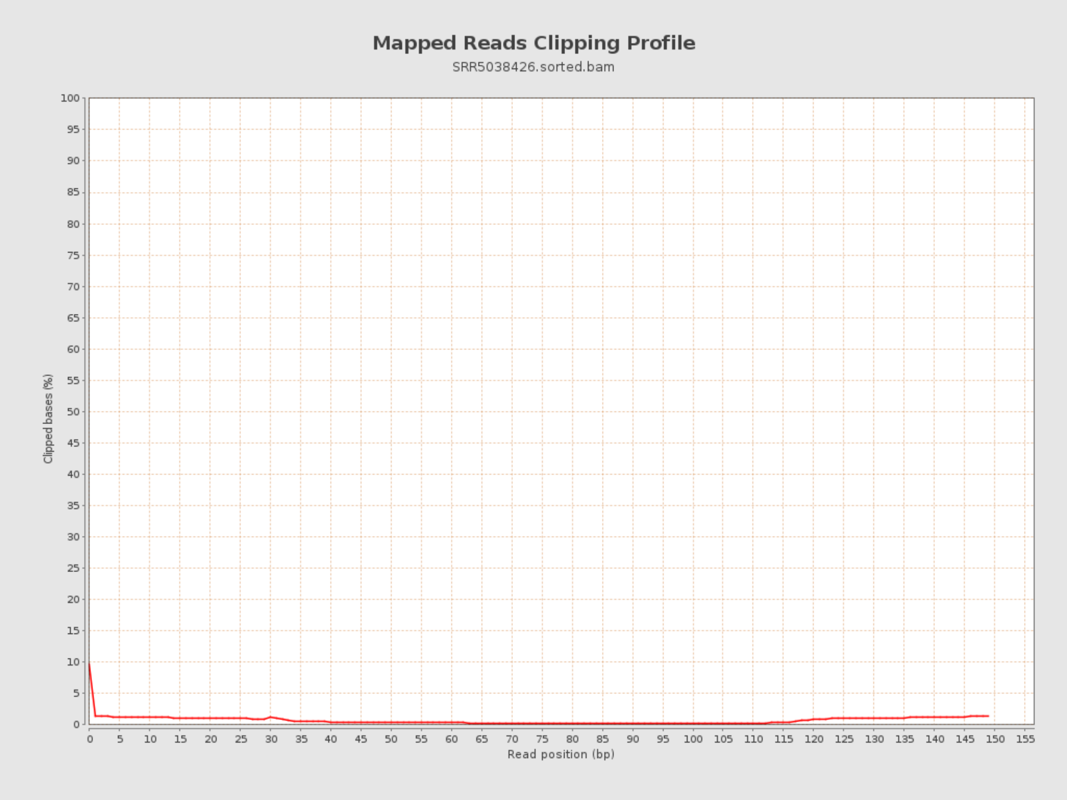
8. Results : Mapped Reads Nucleotide Content



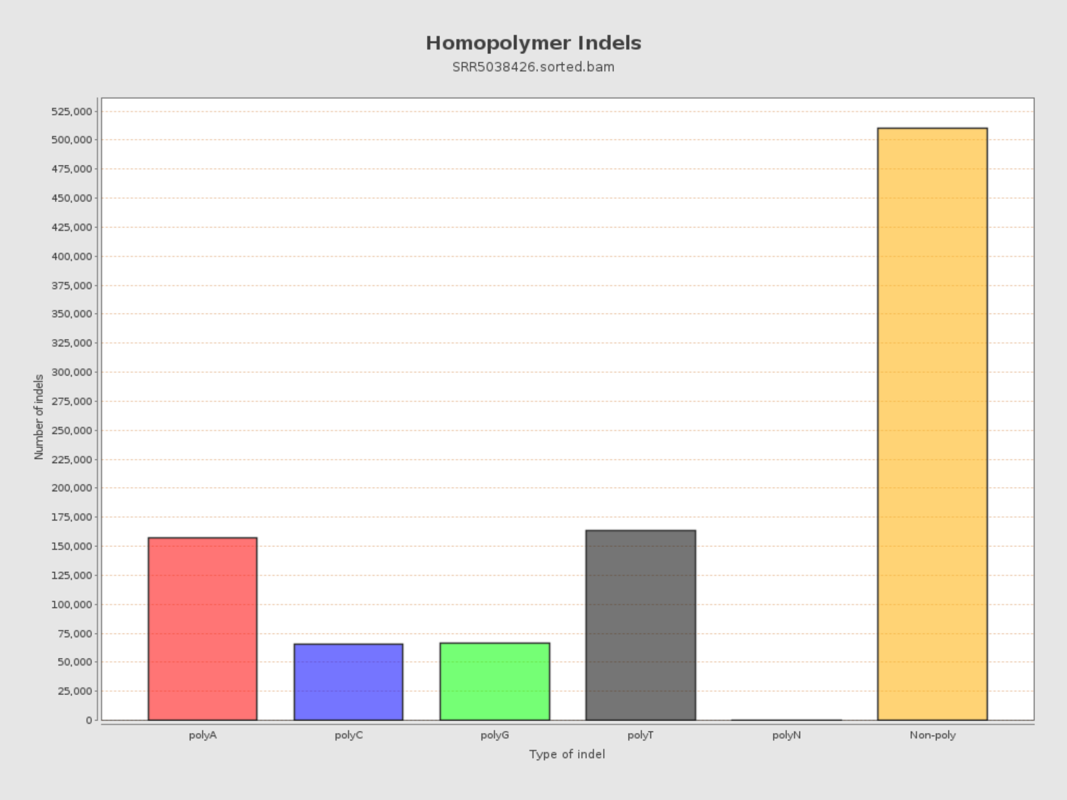
9. Results : Mapped Reads GC-content Distribution



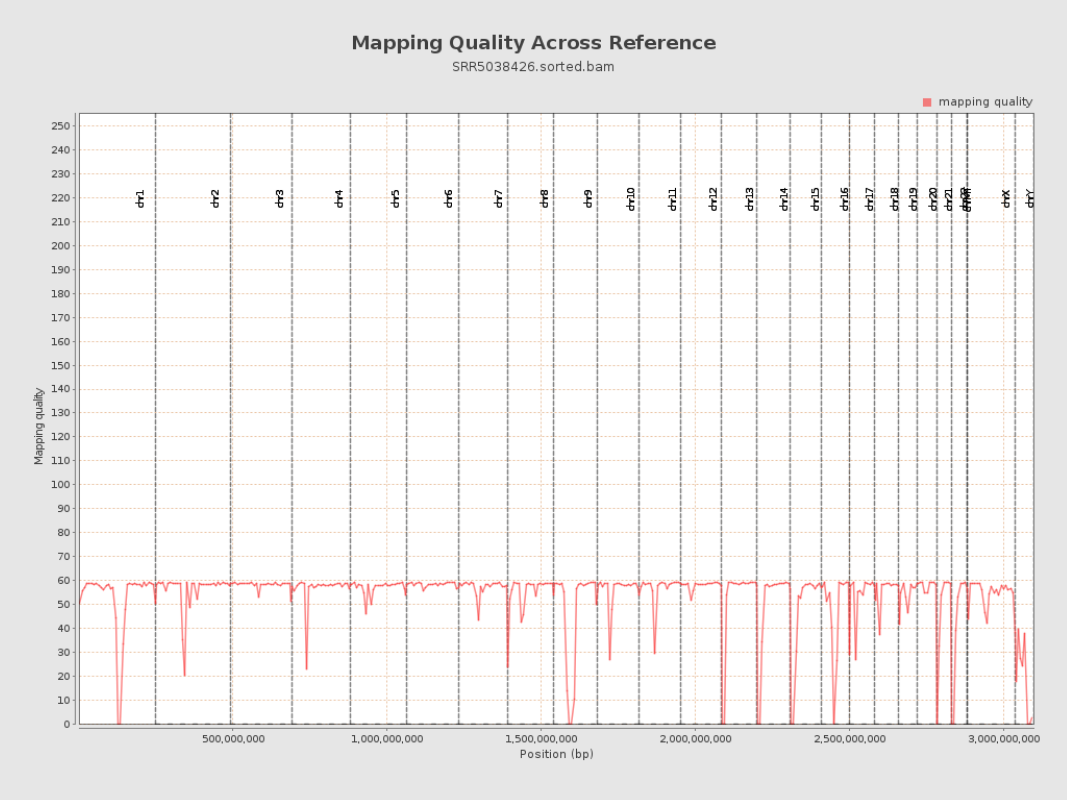
10. Results : Mapped Reads Clipping Profile



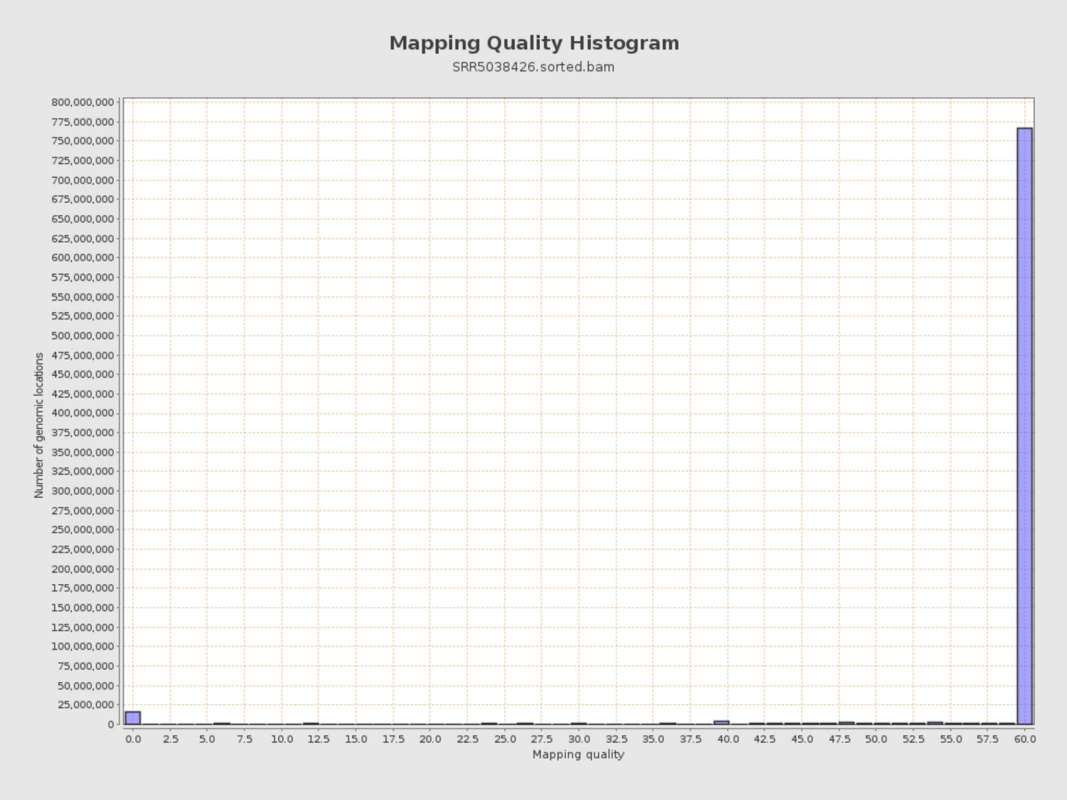
11. Results : Homopolymer Indels



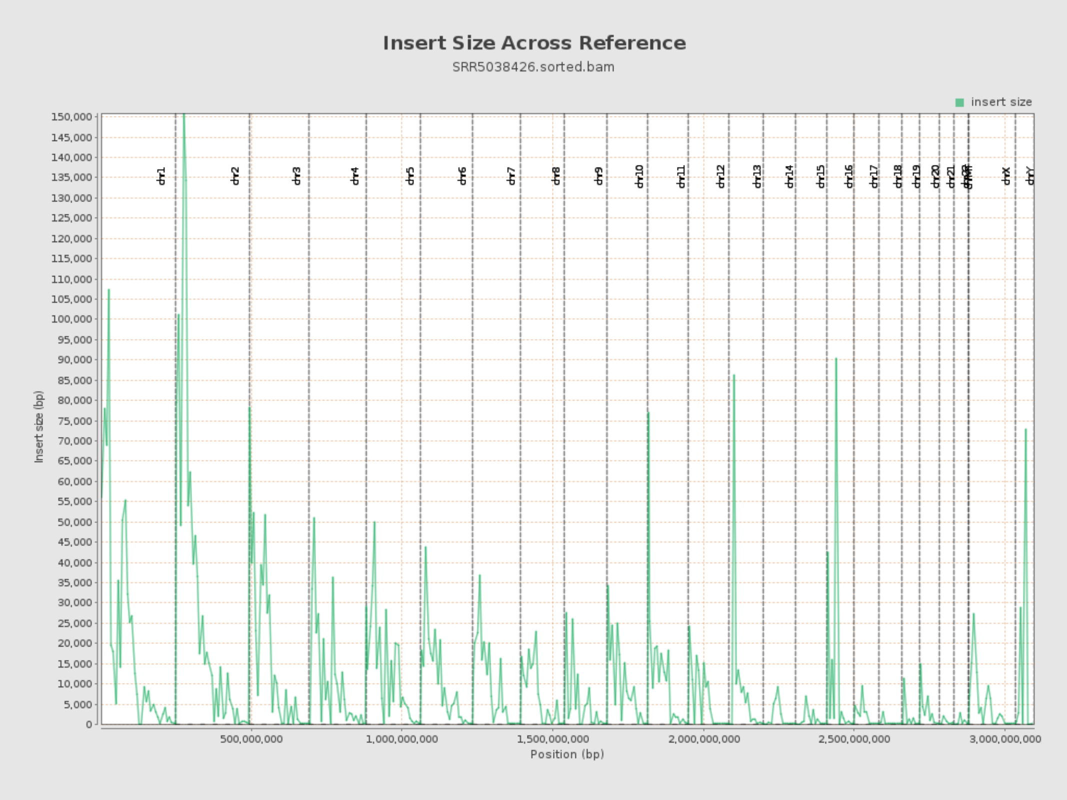
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram