Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 23:26:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038467.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_SRR5038467 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038467_1.fastq.gz SRR5038467_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 23:26:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038467.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,509,524
Mapped reads	18,917,042 / 96.96%
Unmapped reads	592,482 / 3.04%
Mapped paired reads	18,917,042 / 96.96%
Mapped reads, first in pair	9,564,821 / 49.03%
Mapped reads, second in pair	9,352,221 / 47.94%
Mapped reads, both in pair	18,654,738 / 95.62%
Mapped reads, singletons	262,304 / 1.34%
Secondary alignments	0
Supplementary alignments	279,986 / 1.44%
Read min/max/mean length	30 / 150 / 150.72
Duplicated reads (estimated)	3,856,712 / 19.77%
Duplication rate	14.5%
Clipped reads	8,737,358 / 44.79%

2.2. ACGT Content

Number/percentage of A's	733,183,414 / 28.64%
Number/percentage of C's	507,490,652 / 19.82%
Number/percentage of T's	746,976,430 / 29.18%
Number/percentage of G's	572,364,104 / 22.36%
Number/percentage of N's	202,439 / 0.01%

GC Percentage	42.18%

2.3. Coverage

Mean	0.8276
Standard Deviation	11.4756

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Insert size

Mean	77,914.85
Standard Deviation	2,704,201.41
P25/Median/P75	198 / 247 / 310

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	31,529,779
Insertions	428,170
Mapped reads with at least one insertion	2.15%
Deletions	868,190
Mapped reads with at least one deletion	4.43%
Homopolymer indels	47.47%

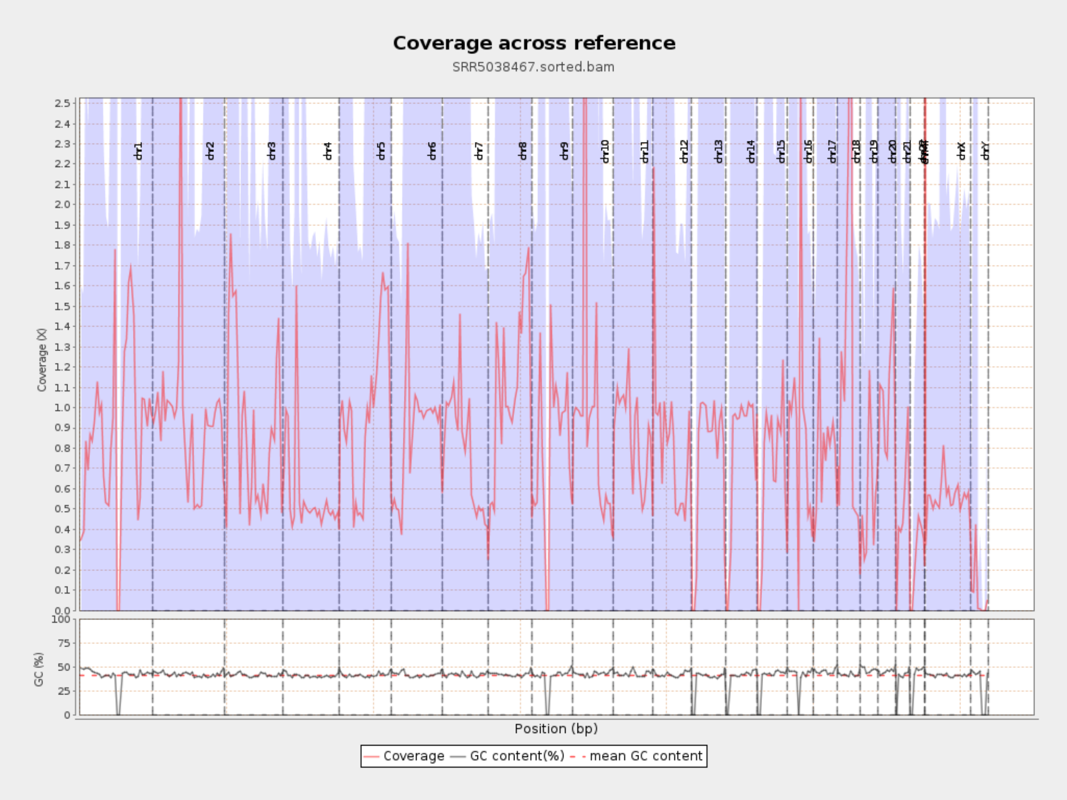
2.7. Chromosome stats

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

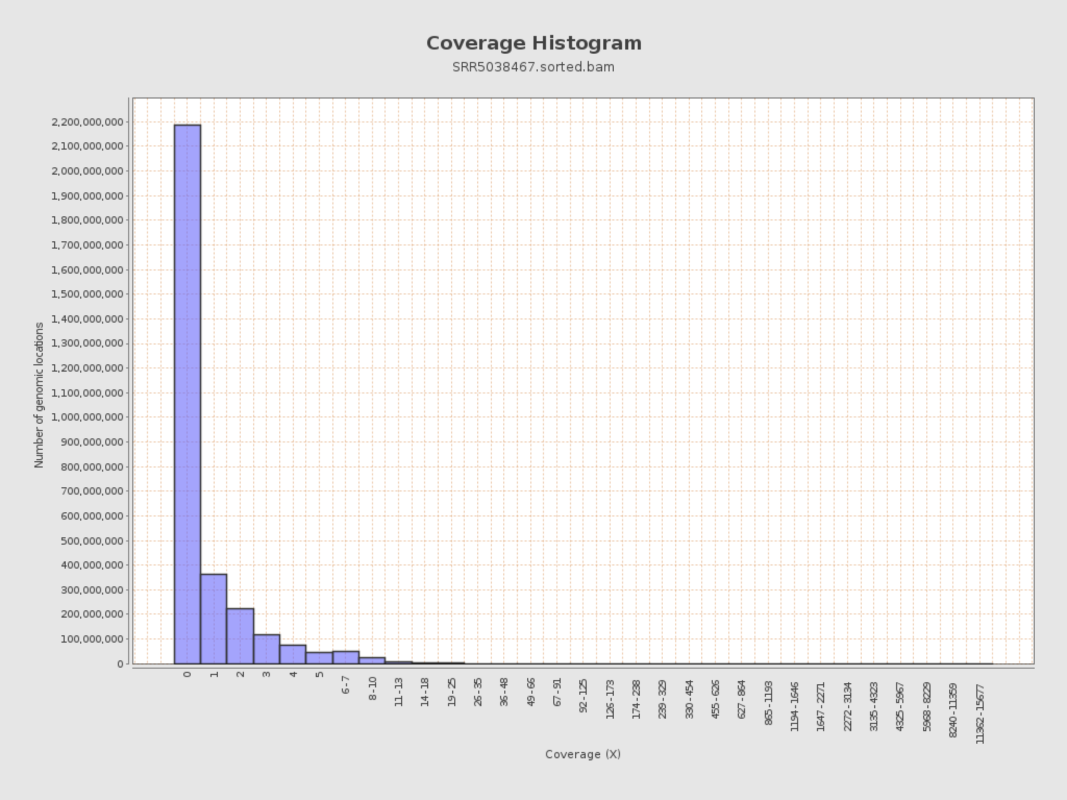
		bases	coverage	deviation
chr1	249250621	221049405	0.8869	15.6198
chr2	243199373	231998936	0.9539	12.6323
chr3	198022430	177682924	0.8973	2.0263
chr4	191154276	109971045	0.5753	9.2155
chr5	180915260	178305374	0.9856	1.983
chr6	171115067	153474105	0.8969	9.3858
chr7	159138663	125318457	0.7875	11.8423
chr8	146364022	164417797	1.1233	4.4877
chr9	141213431	110199392	0.7804	18.2061
chr10	135534747	140404560	1.0359	31.8948
chr11	135006516	117386837	0.8695	8.9477
chr12	133851895	112158431	0.8379	1.9573
chr13	115169878	87860343	0.7629	1.6879
chr14	107349540	84056129	0.783	1.8205
chr15	102531392	69146435	0.6744	1.6156
chr16	90354753	78634754	0.8703	11.761
chr17	81195210	62271443	0.7669	14.0661
chr18	78077248	103959897	1.3315	12.8359
chr19	59128983	32034869	0.5418	6.6055
chr20	63025520	67527733	1.0714	3.4778
chr21	48129895	24855269	0.5164	4.3299
chr22	51304566	13805094	0.2691	1.0067
chrMT	16571	3902624	235.5093	117.8329
chrX	155270560	86564106	0.5575	2.561

chrY	59373566	4936207	0.0831	9.1492

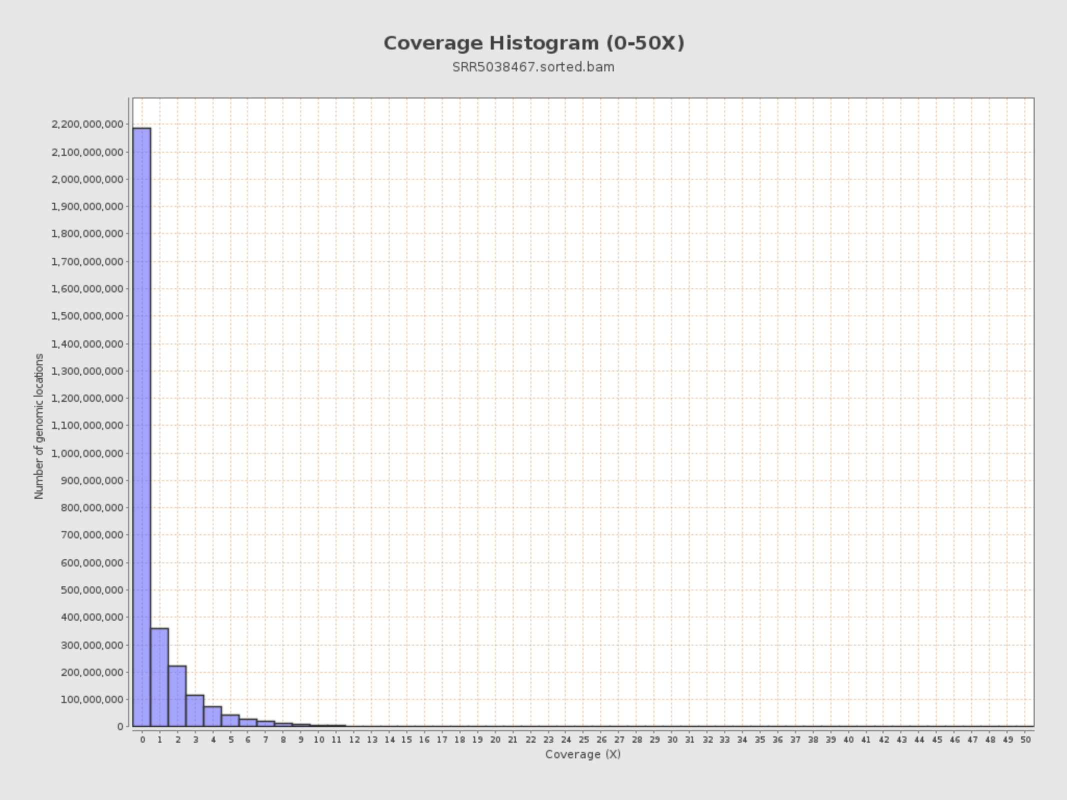
3. Results : Coverage across reference



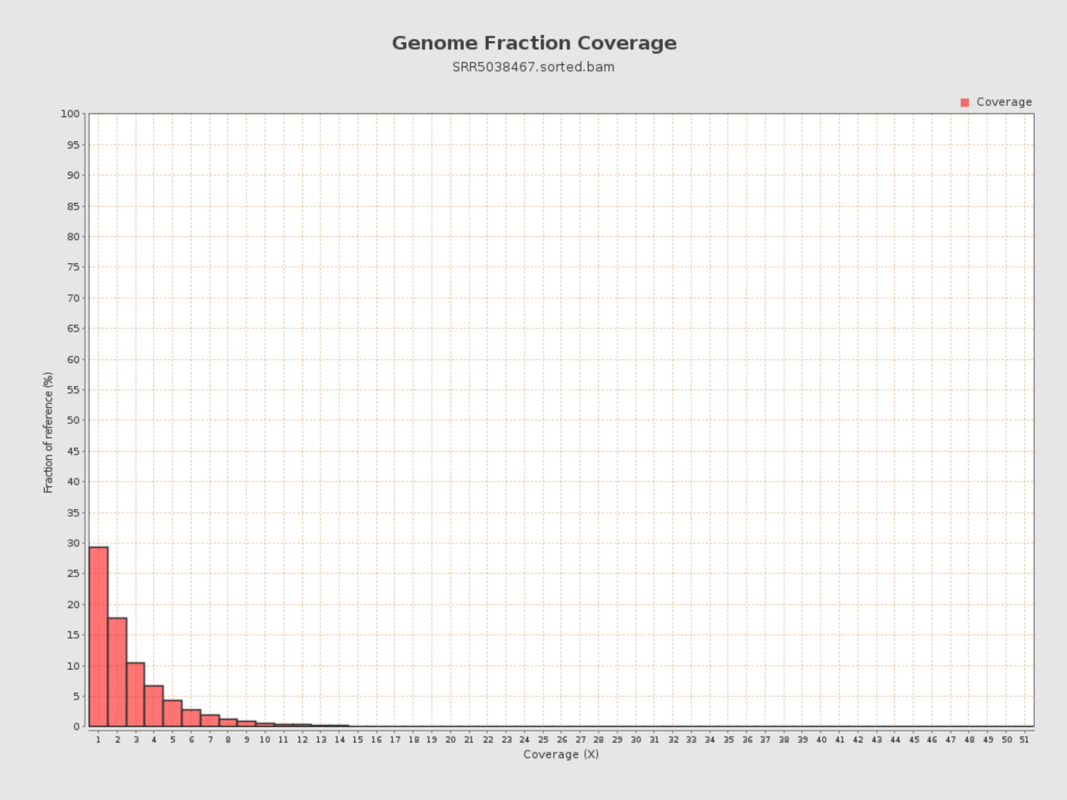
4. Results : Coverage Histogram



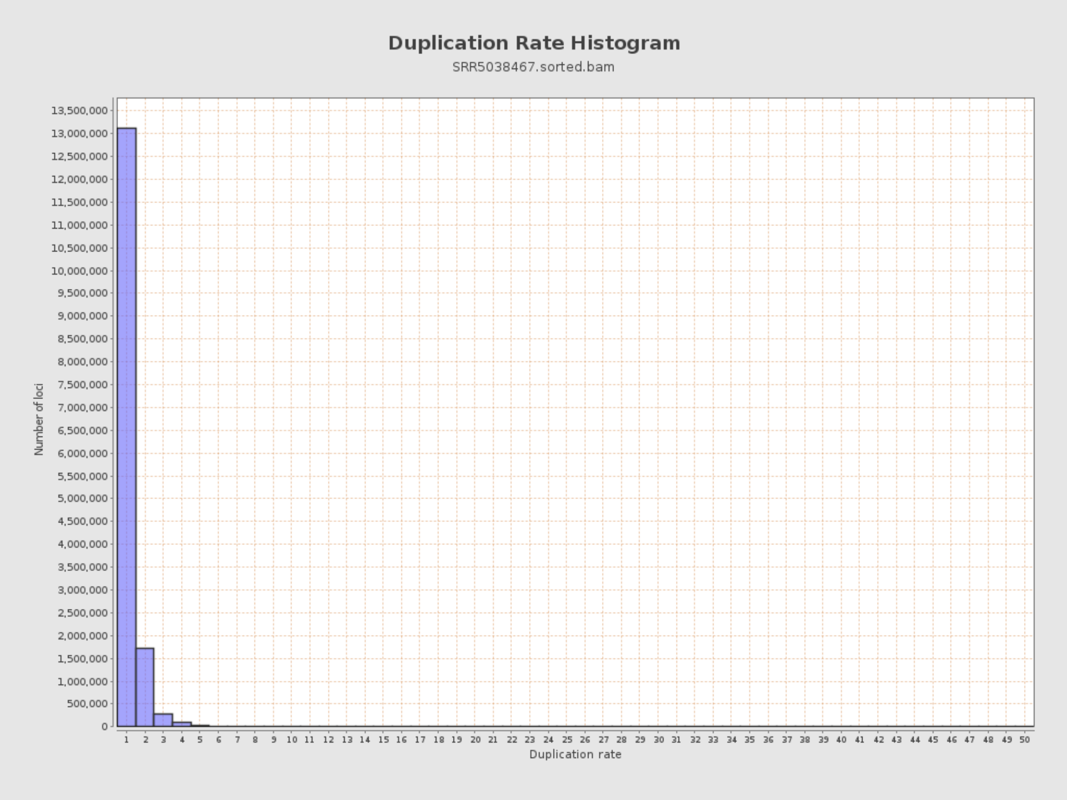
5. Results : Coverage Histogram (0-50X)



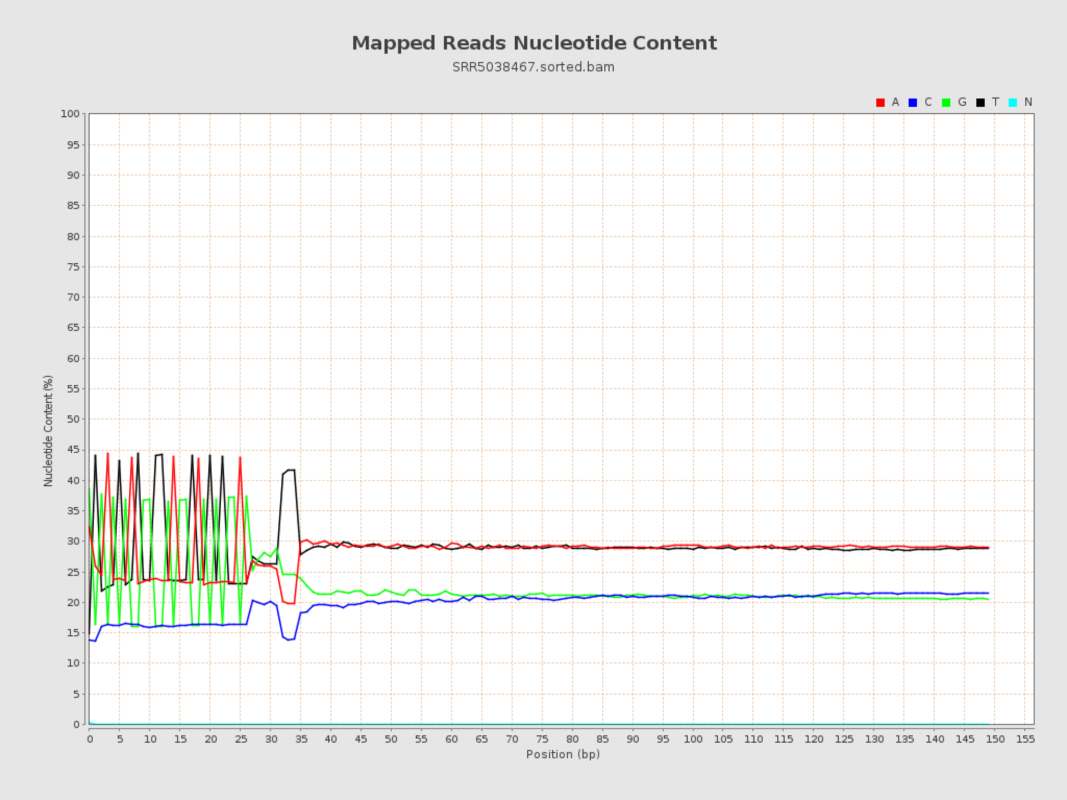
6. Results : Genome Fraction Coverage



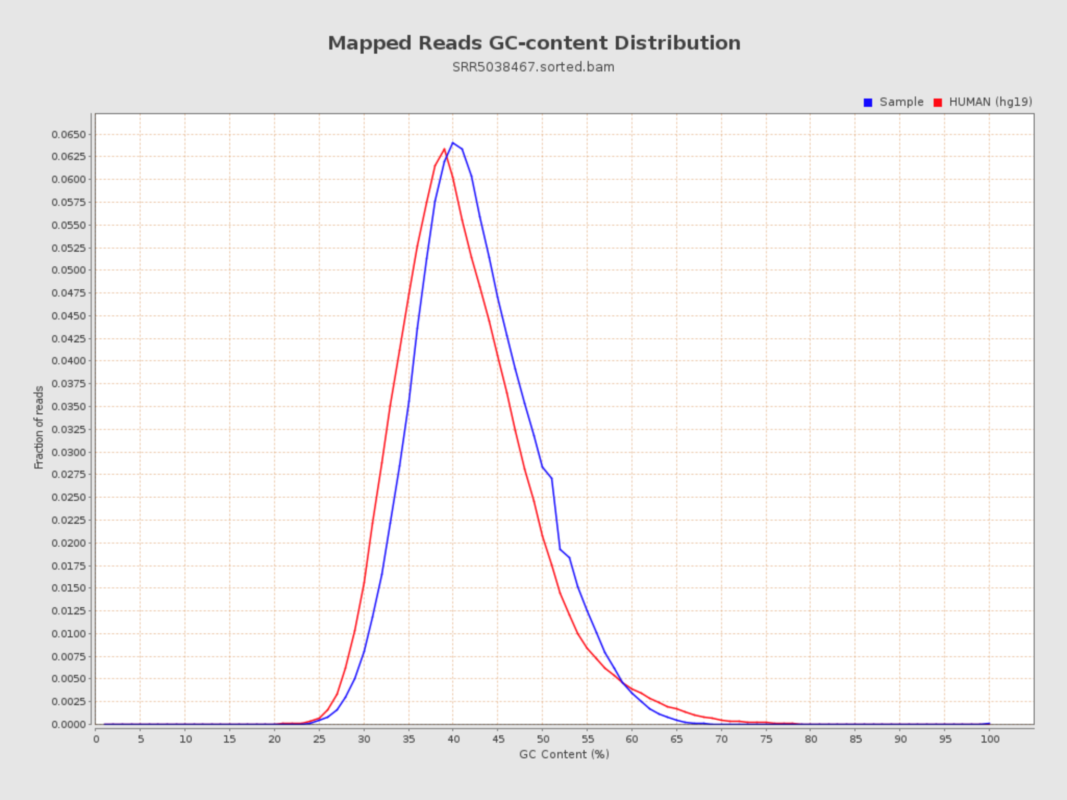
7. Results : Duplication Rate Histogram



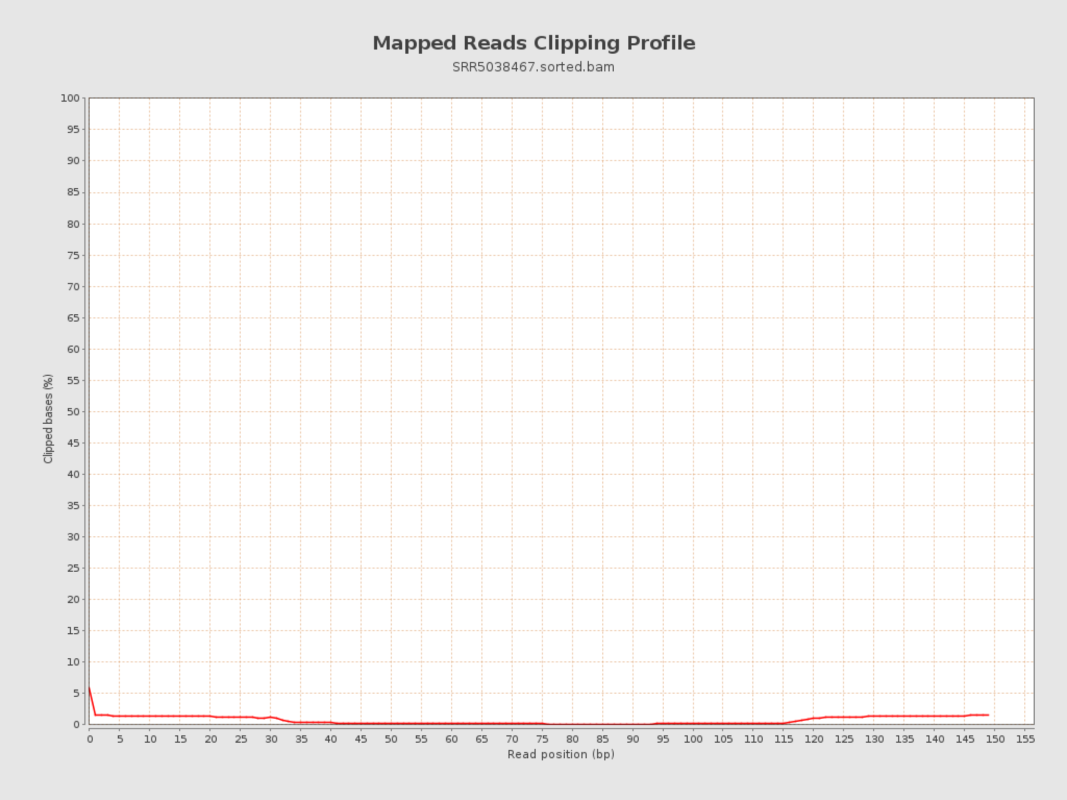
8. Results : Mapped Reads Nucleotide Content



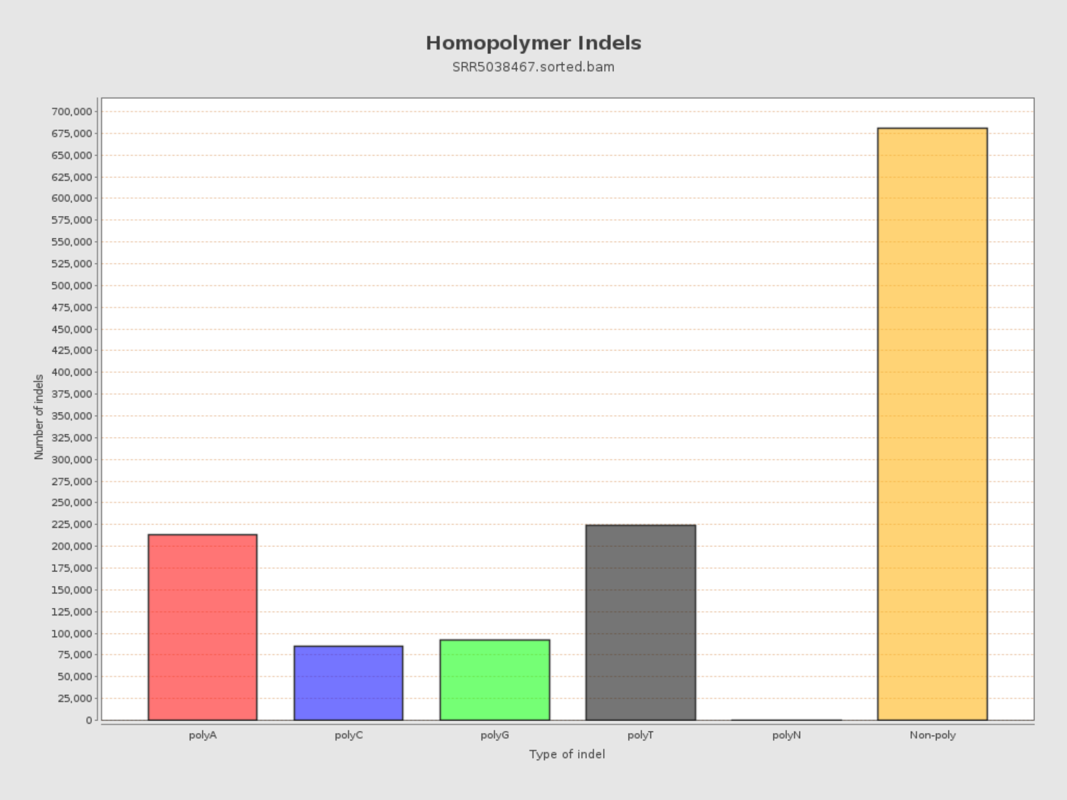
9. Results : Mapped Reads GC-content Distribution



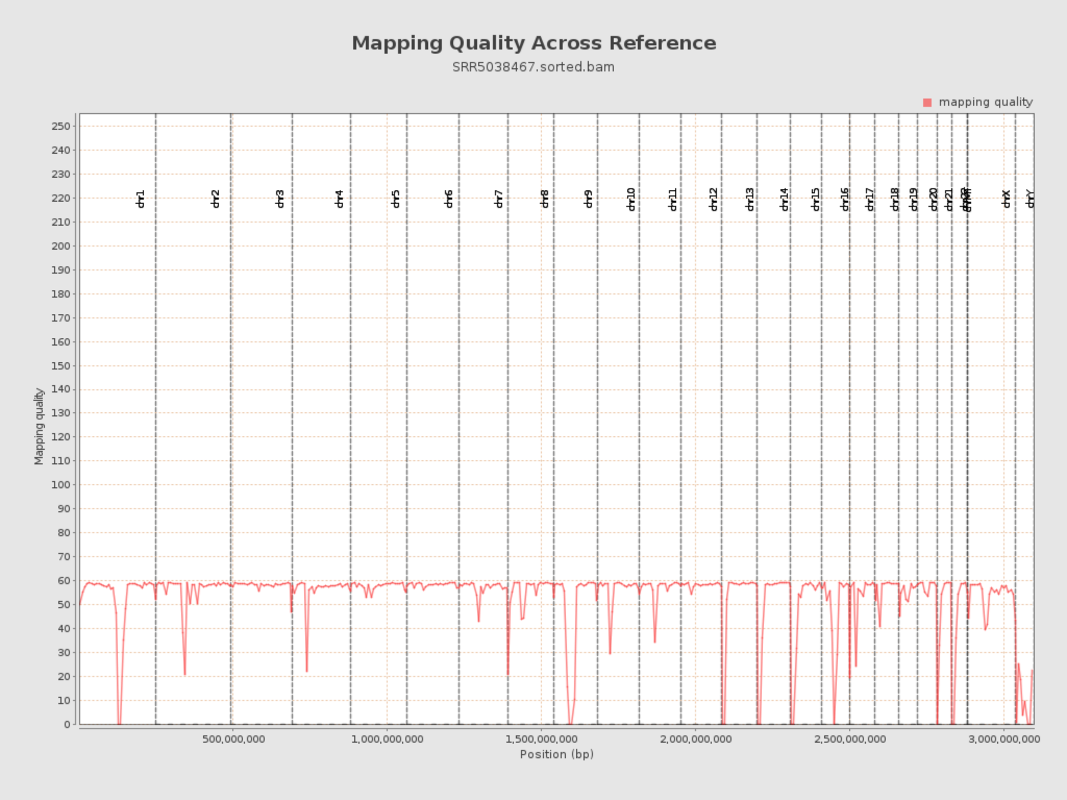
10. Results : Mapped Reads Clipping Profile



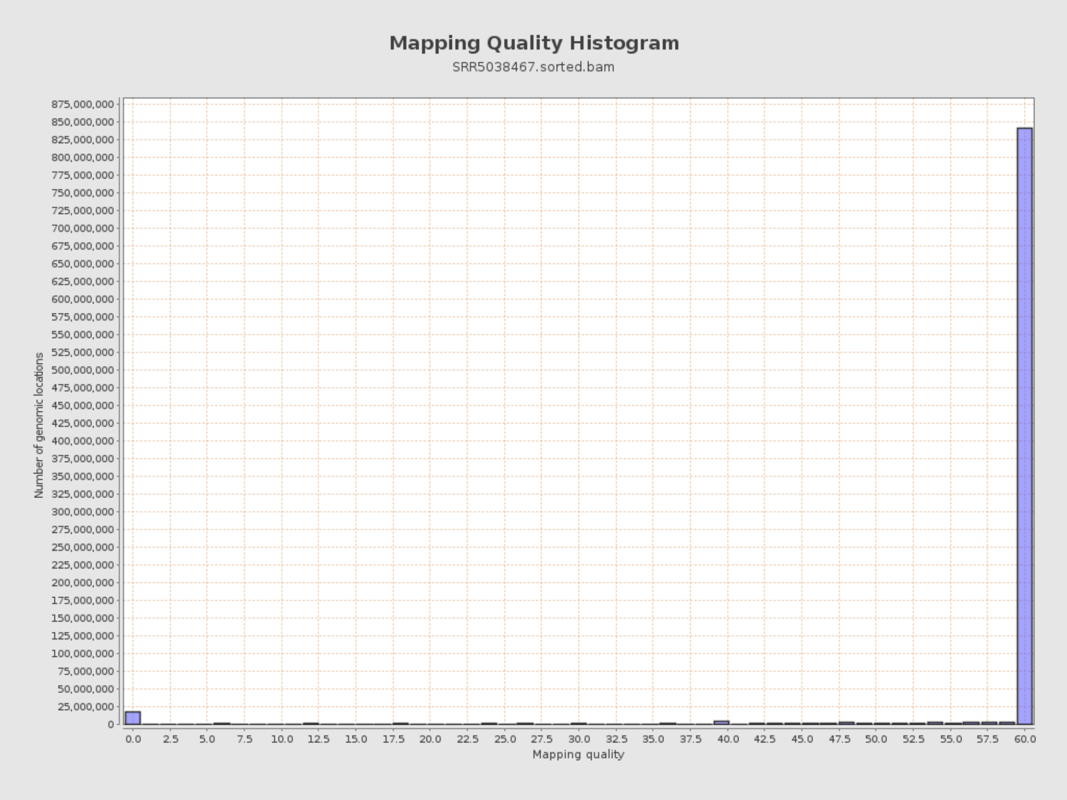
11. Results : Homopolymer Indels



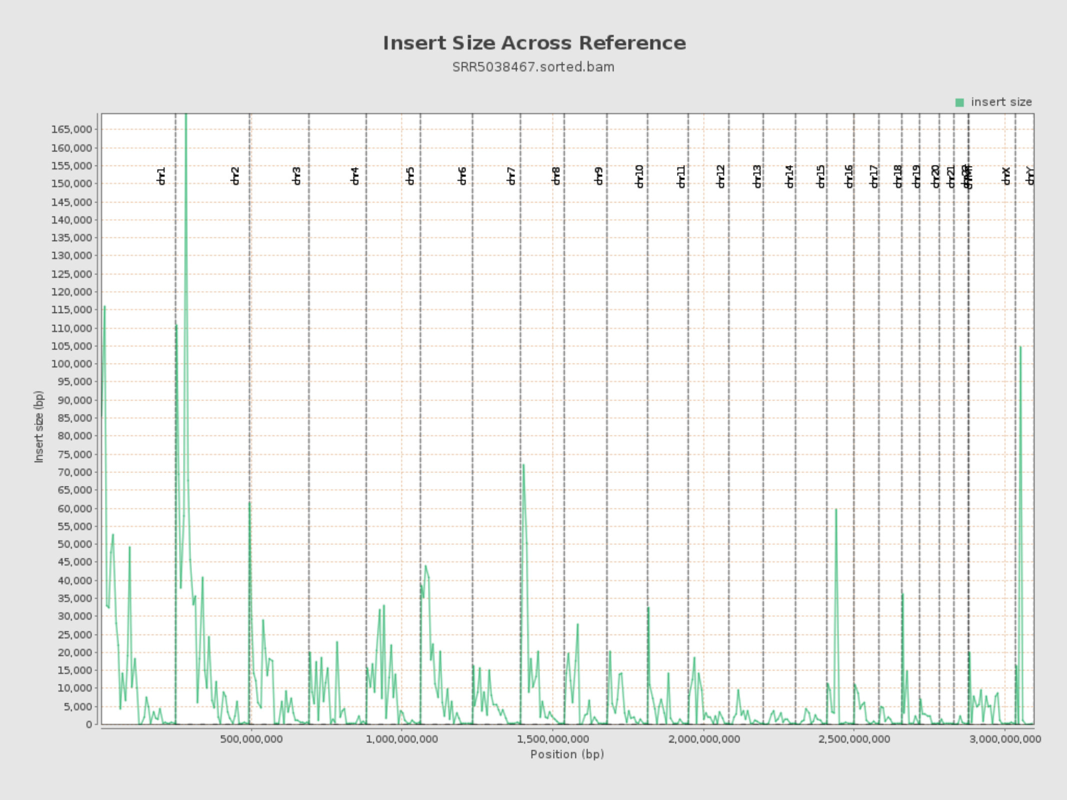
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram