Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 09:23:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038489.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_SRR5038489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038489_1.fastq.gz SRR5038489_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 09:23:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038489.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,913,612
Mapped reads	13,560,845 / 97.46%
Unmapped reads	352,767 / 2.54%
Mapped paired reads	13,560,845 / 97.46%
Mapped reads, first in pair	6,838,597 / 49.15%
Mapped reads, second in pair	6,722,248 / 48.31%
Mapped reads, both in pair	13,428,080 / 96.51%
Mapped reads, singletons	132,765 / 0.95%
Secondary alignments	0
Supplementary alignments	133,679 / 0.96%
Read min/max/mean length	30 / 150 / 150.49
Duplicated reads (estimated)	1,327,584 / 9.54%
Duplication rate	7.12%
Clipped reads	1,443,082 / 10.37%

2.2. ACGT Content

Number/percentage of A's	576,503,032 / 28.91%
Number/percentage of C's	423,721,004 / 21.25%
Number/percentage of T's	571,270,794 / 28.65%
Number/percentage of G's	422,319,920 / 21.18%
Number/percentage of N's	45,367 / 0%

GC Percentage	42.43%

2.3. Coverage

Mean	0.6443
Standard Deviation	6.7255

2.4. Mapping Quality

Mean Mapping Quality	54.44

2.5. Insert size

Mean	89,865.6
Standard Deviation	3,001,664.1
P25/Median/P75	220 / 268 / 333

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	20,471,304
Insertions	249,812
Mapped reads with at least one insertion	1.73%
Deletions	263,251
Mapped reads with at least one deletion	1.86%
Homopolymer indels	44.32%

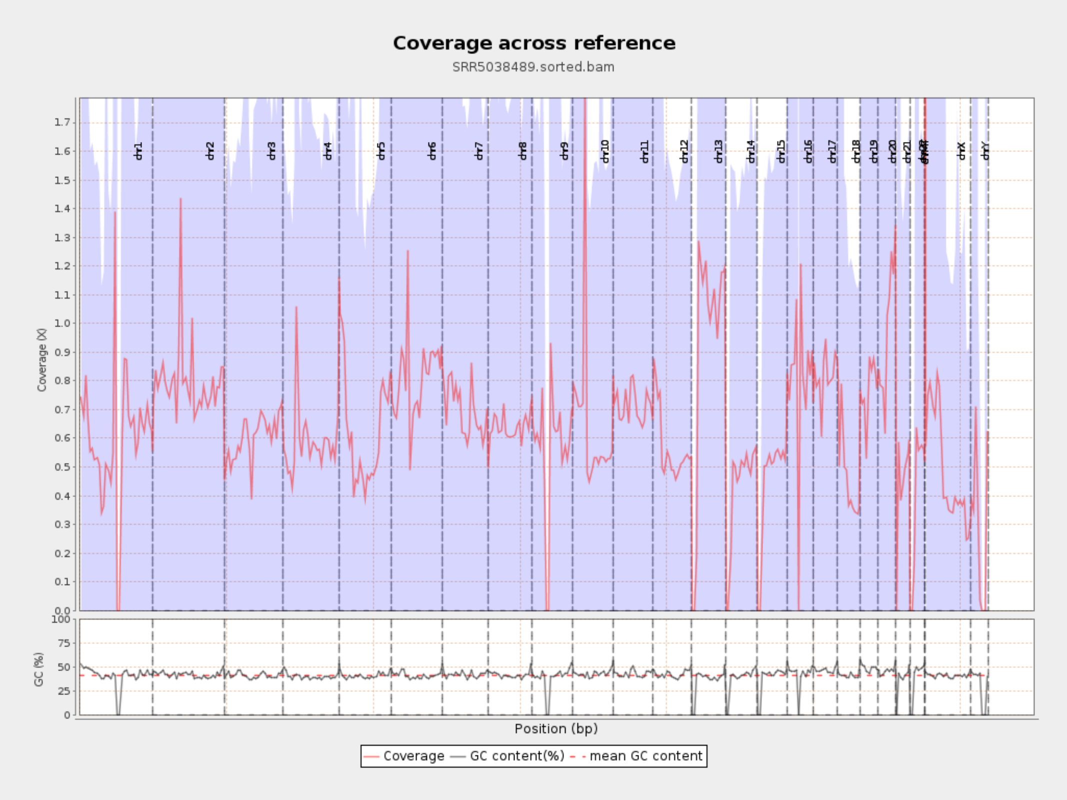
2.7. Chromosome stats

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

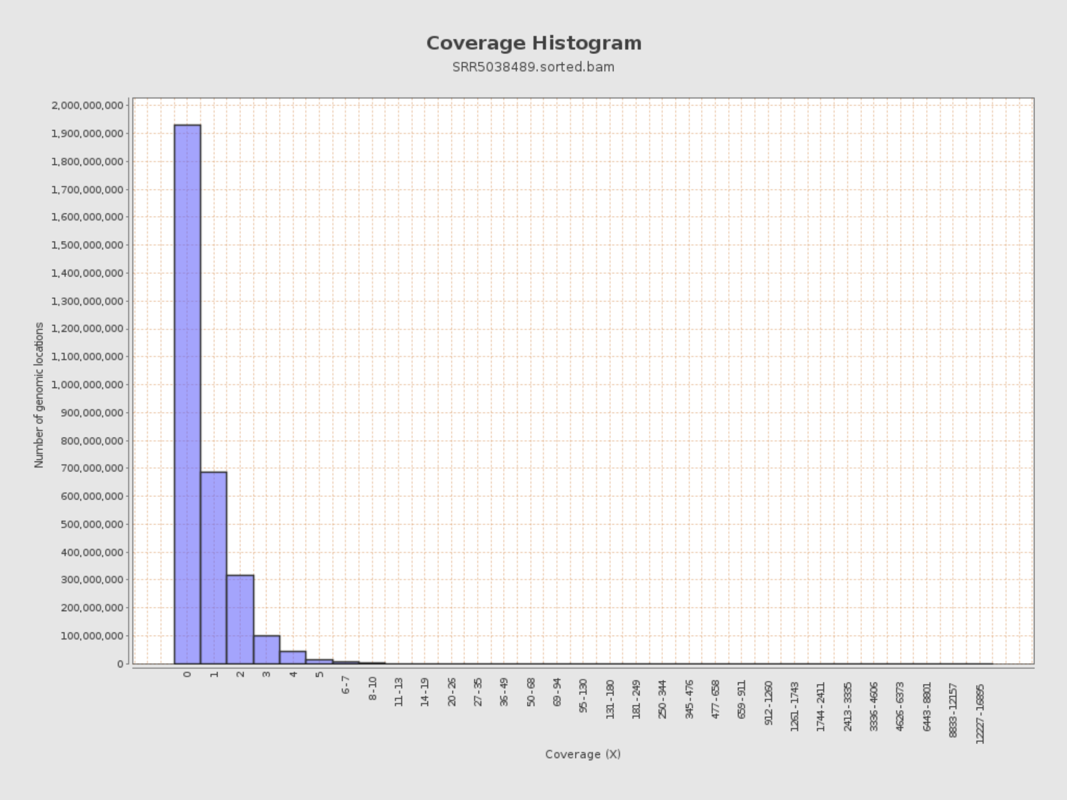
		bases	coverage	deviation
chr1	249250621	149141435	0.5984	17.5796
chr2	243199373	194755280	0.8008	5.2985
chr3	198022430	119115098	0.6015	0.9943
chr4	191154276	111184666	0.5816	4.5202
chr5	180915260	113468467	0.6272	1.0835
chr6	171115067	138325972	0.8084	5.5913
chr7	159138663	111352397	0.6997	4.217
chr8	146364022	93674470	0.64	4.7382
chr9	141213431	79096071	0.5601	7.5869
chr10	135534747	88568132	0.6535	10.3676
chr11	135006516	96996973	0.7185	3.5716
chr12	133851895	76885029	0.5744	1.0065
chr13	115169878	108275524	0.9401	1.2948
chr14	107349540	45290743	0.4219	0.9304
chr15	102531392	44617874	0.4352	0.8484
chr16	90354753	73093775	0.809	4.3033
chr17	81195210	66514399	0.8192	3.6793
chr18	78077248	36126759	0.4627	7.738
chr19	59128983	45671038	0.7724	7.978
chr20	63025520	61071826	0.969	1.951
chr21	48129895	21887353	0.4548	2.8015
chr22	51304566	20386713	0.3974	2.1847
chrMT	16571	4392576	265.0761	32.4367
chrX	155270560	76538844	0.4929	1.2678

chrY	59373566	18155033	0.3058	5.6763

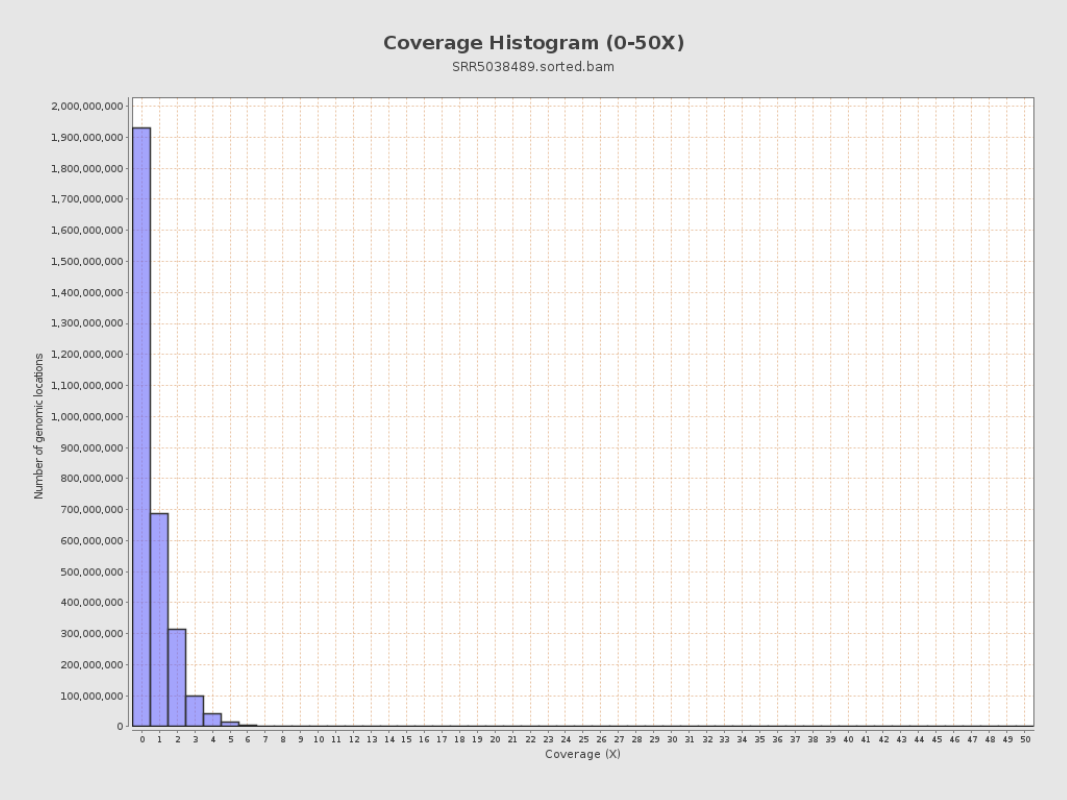
3. Results : Coverage across reference



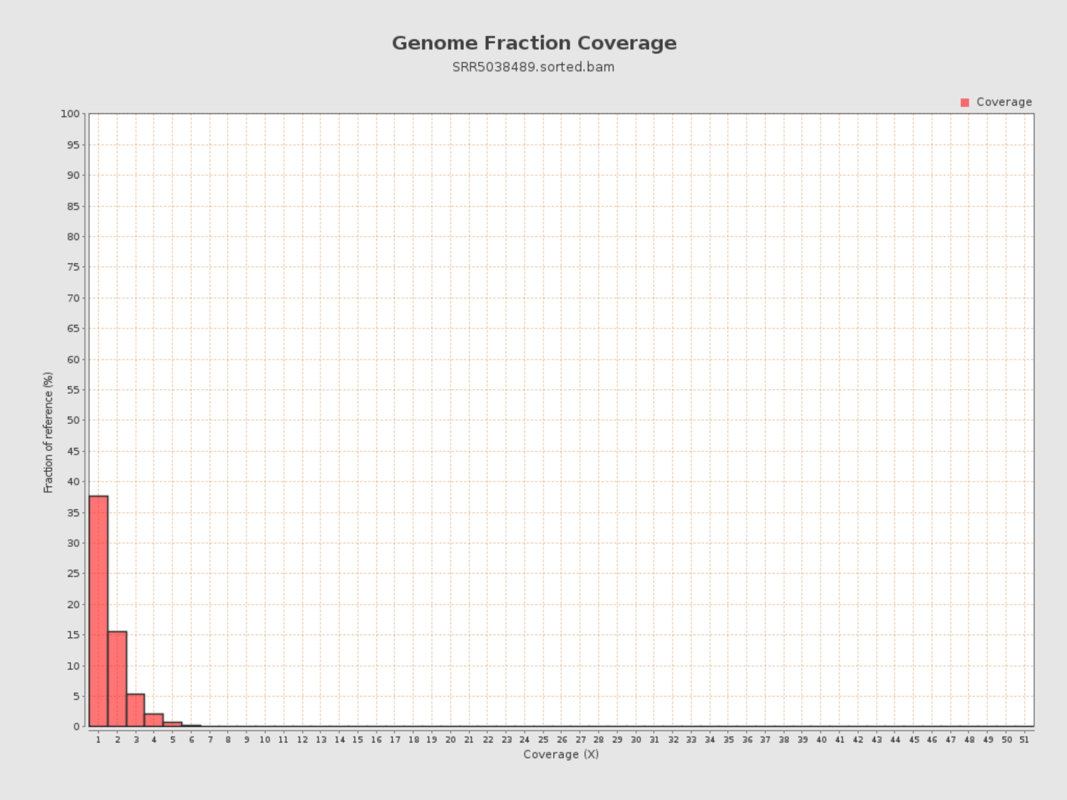
4. Results : Coverage Histogram



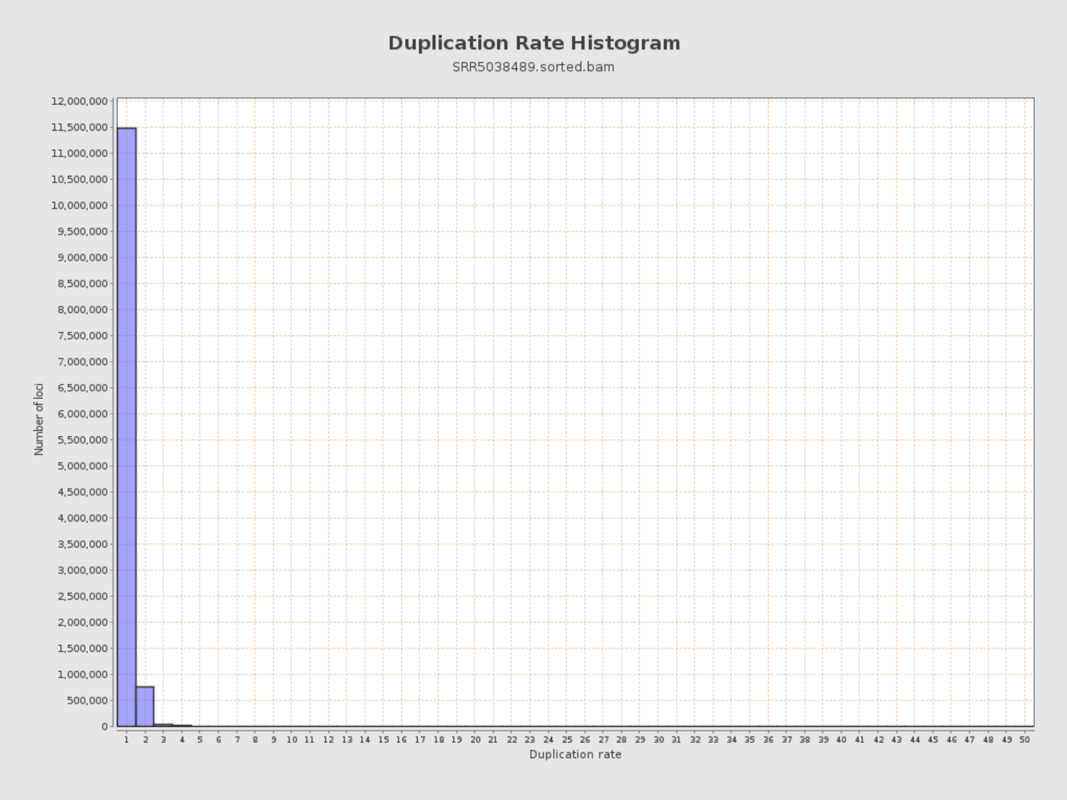
5. Results : Coverage Histogram (0-50X)



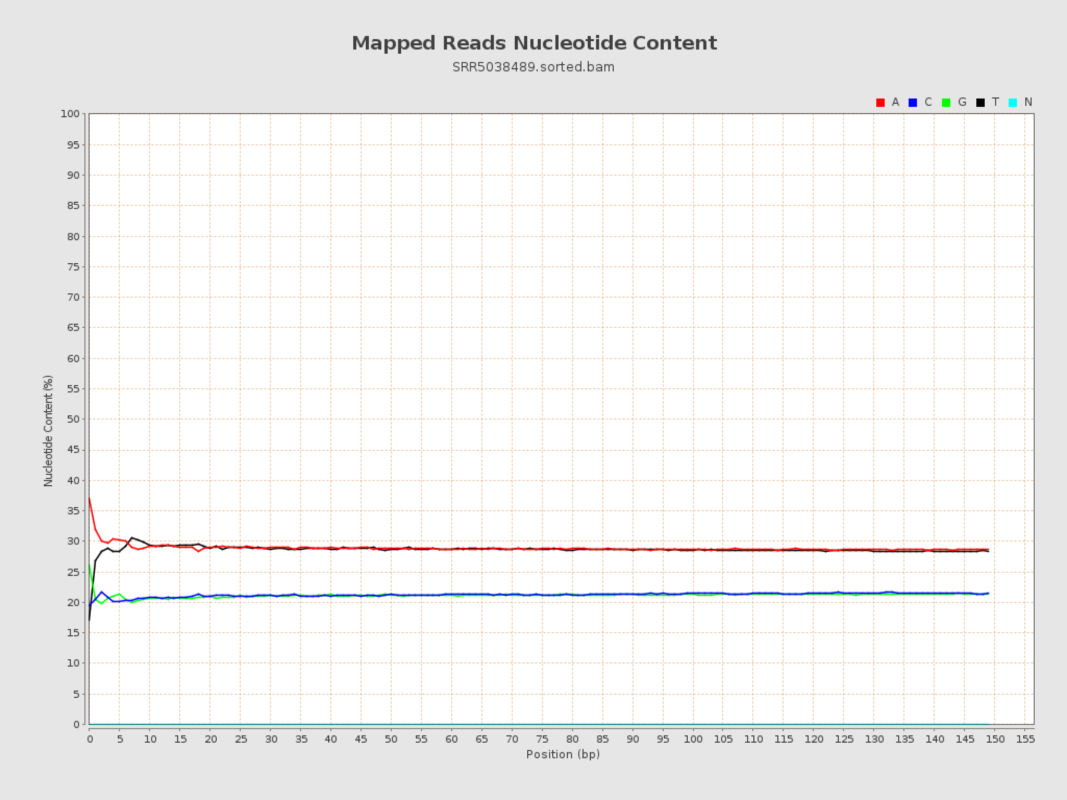
6. Results : Genome Fraction Coverage



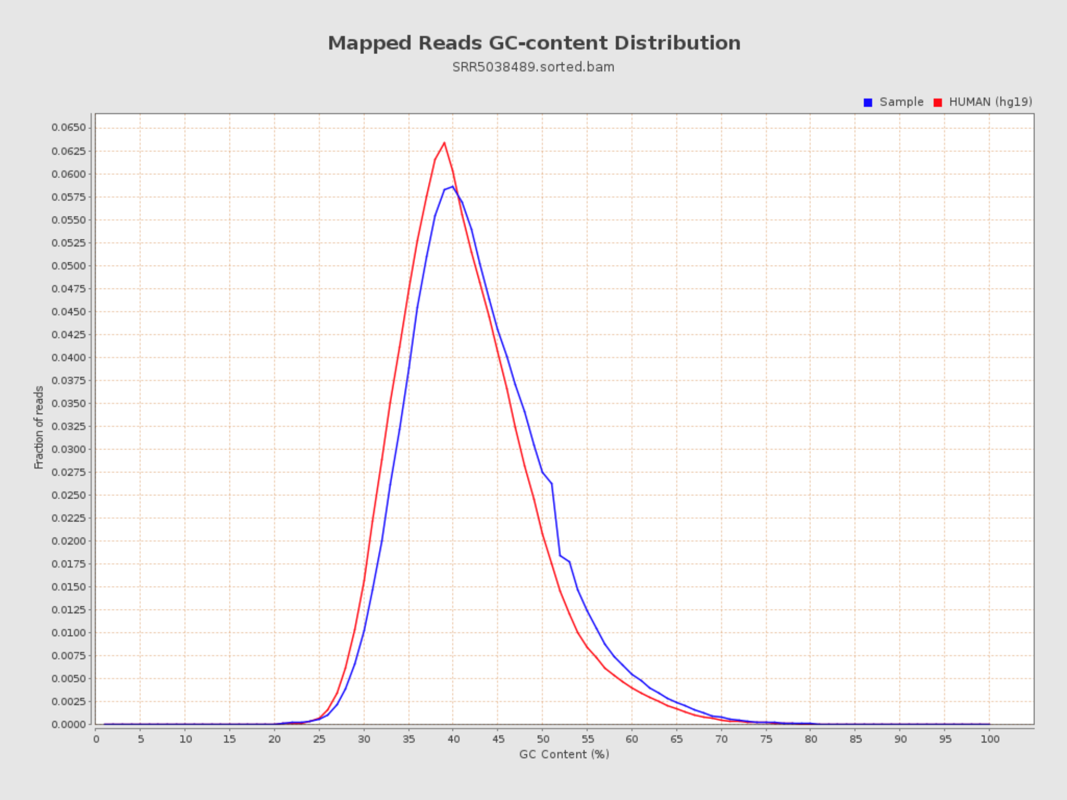
7. Results : Duplication Rate Histogram



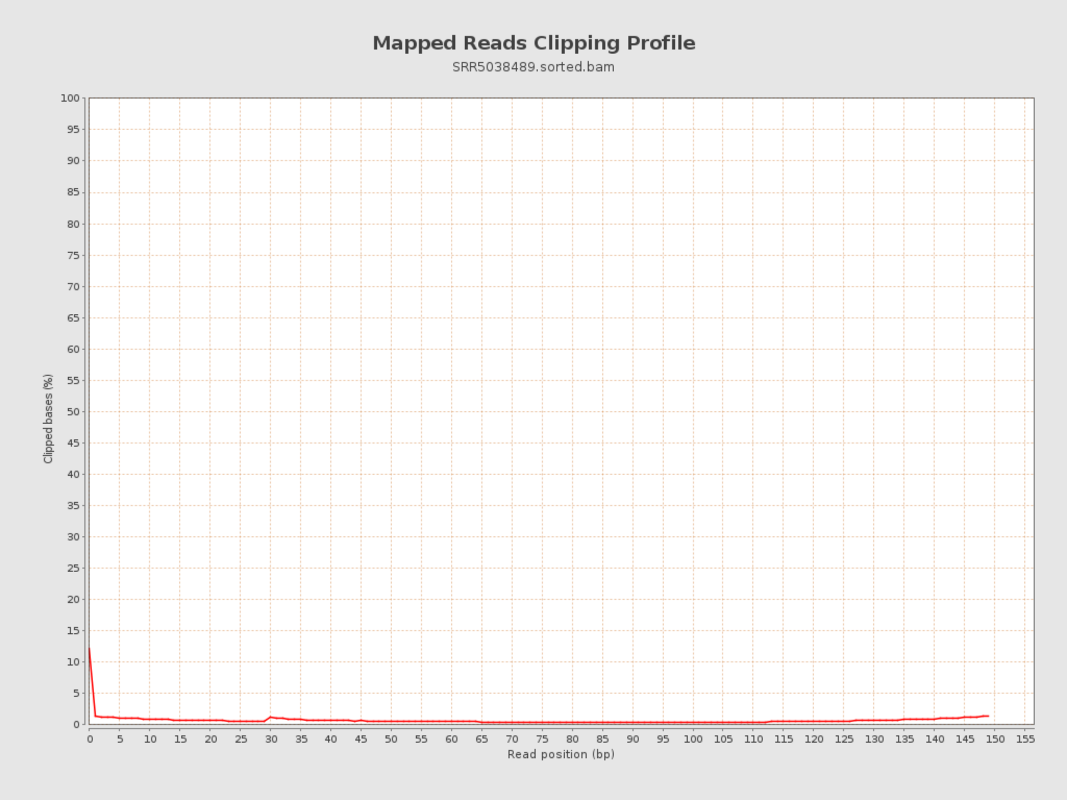
8. Results : Mapped Reads Nucleotide Content



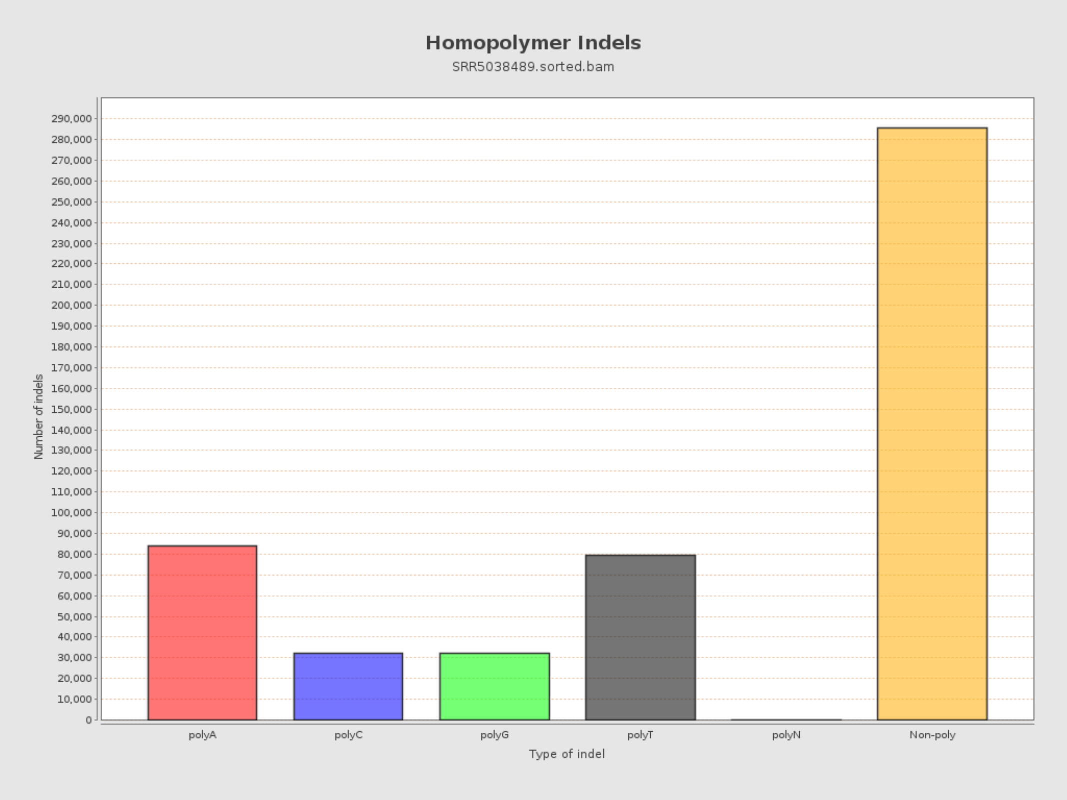
9. Results : Mapped Reads GC-content Distribution



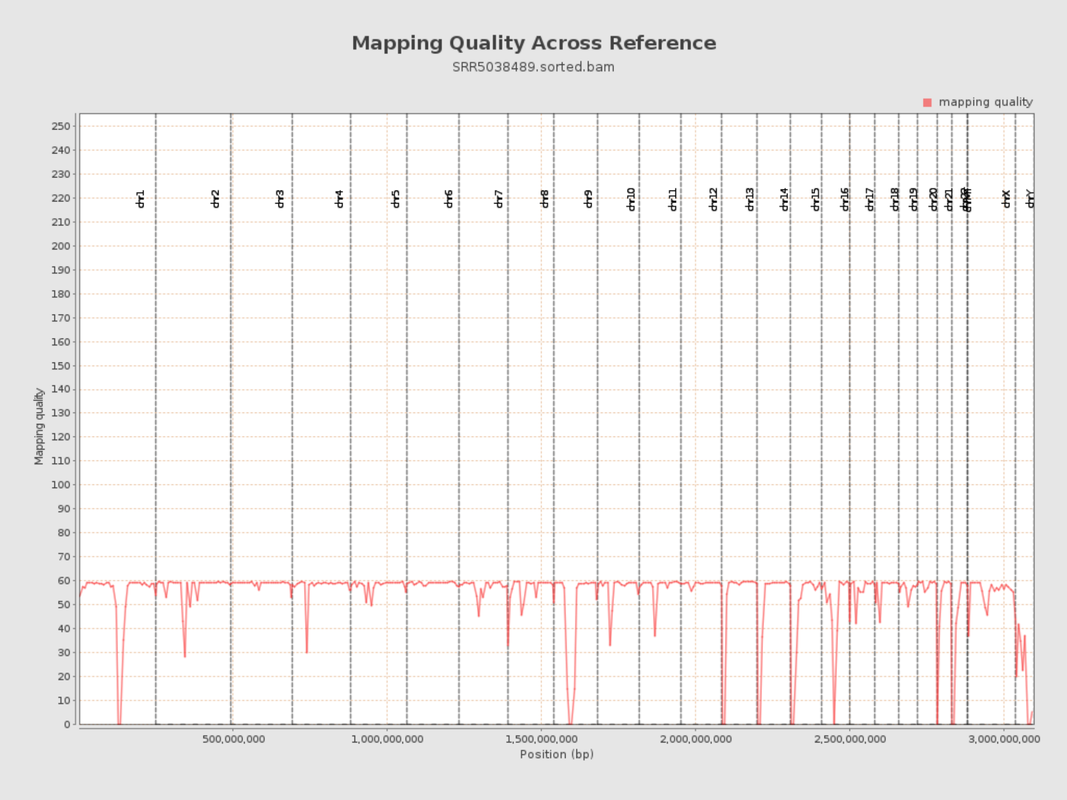
10. Results : Mapped Reads Clipping Profile



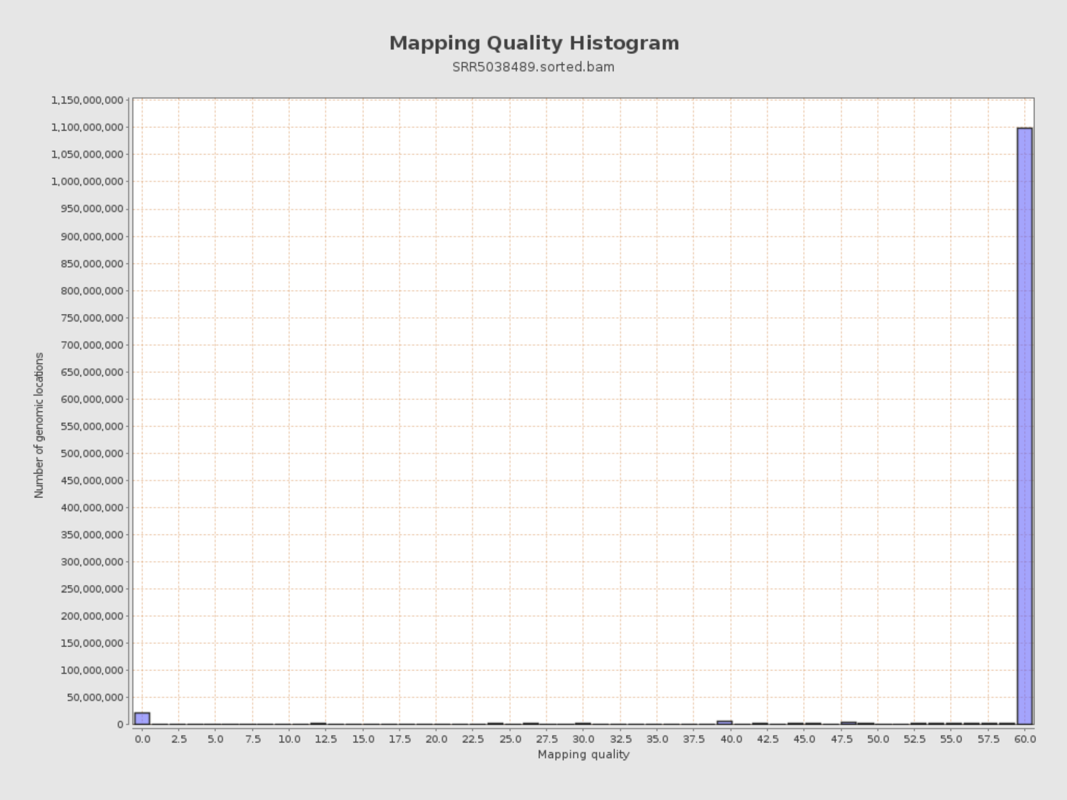
11. Results : Homopolymer Indels



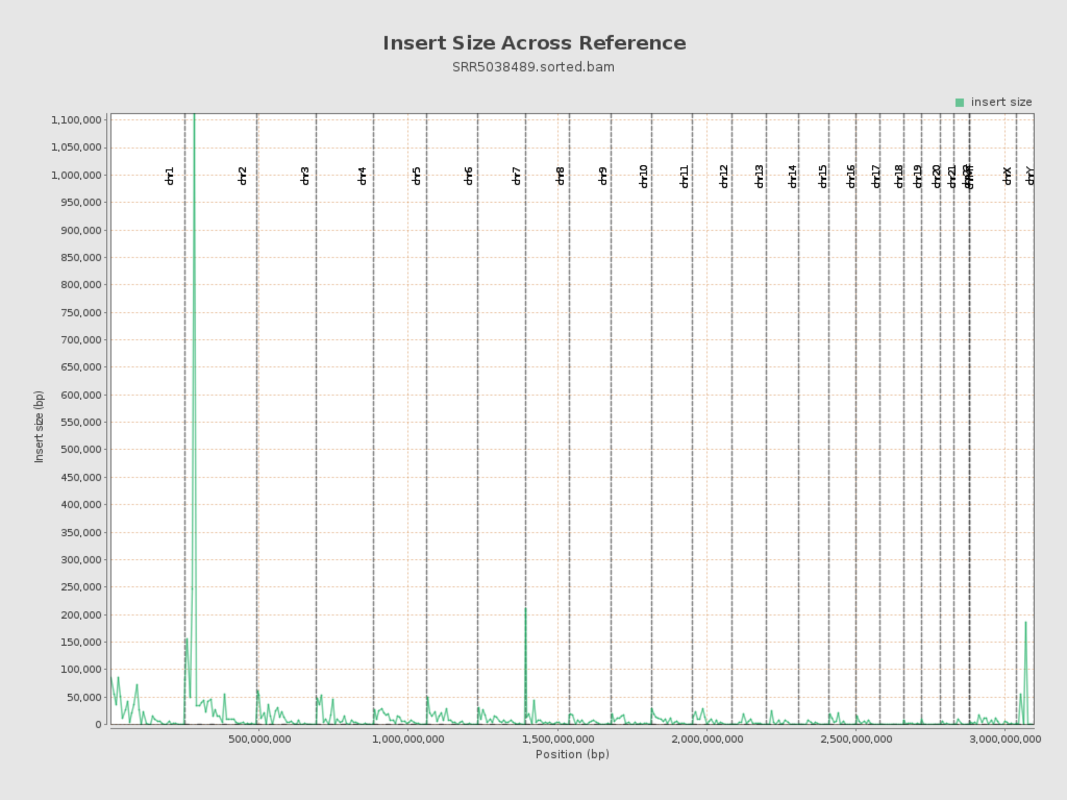
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram