Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/06 14:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR611532.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_SRR611532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR611532_1.fastq.gz SRR611532_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 06 14:24:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR611532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,235,385,080
Mapped reads	1,220,911,799 / 98.83%
Unmapped reads	14,473,281 / 1.17%
Mapped paired reads	1,220,911,799 / 98.83%
Mapped reads, first in pair	611,950,661 / 49.54%
Mapped reads, second in pair	608,961,138 / 49.29%
Mapped reads, both in pair	1,212,733,824 / 98.17%
Mapped reads, singletons	8,177,975 / 0.66%
Secondary alignments	0
Supplementary alignments	2,148,935 / 0.17%
Read min/max/mean length	30 / 90 / 90.07
Duplicated reads (estimated)	323,487,087 / 26.19%
Duplication rate	22.93%
Clipped reads	55,845,224 / 4.52%

2.2. ACGT Content

Number/percentage of A's	30,974,165,631 / 28.5%
Number/percentage of C's	23,272,193,842 / 21.42%
Number/percentage of T's	30,976,663,005 / 28.51%
Number/percentage of G's	23,434,592,616 / 21.57%
Number/percentage of N's	6,642,814 / 0.01%

GC Percentage	42.98%

2.3. Coverage

Mean	35.1103
Standard Deviation	308.7805

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	29,998.85
Standard Deviation	1,571,658.79
P25/Median/P75	175 / 181 / 187

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	617,438,710
Insertions	9,092,653
Mapped reads with at least one insertion	0.73%
Deletions	11,093,037
Mapped reads with at least one deletion	0.89%
Homopolymer indels	40.56%

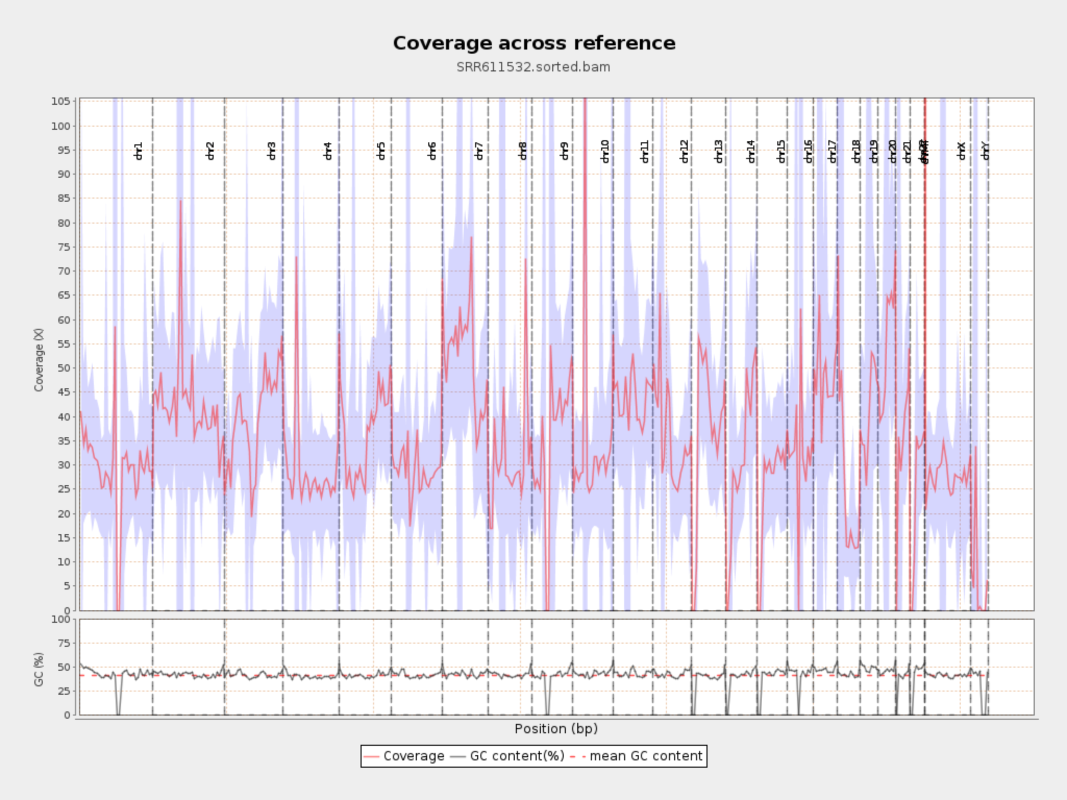
2.7. Chromosome stats

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

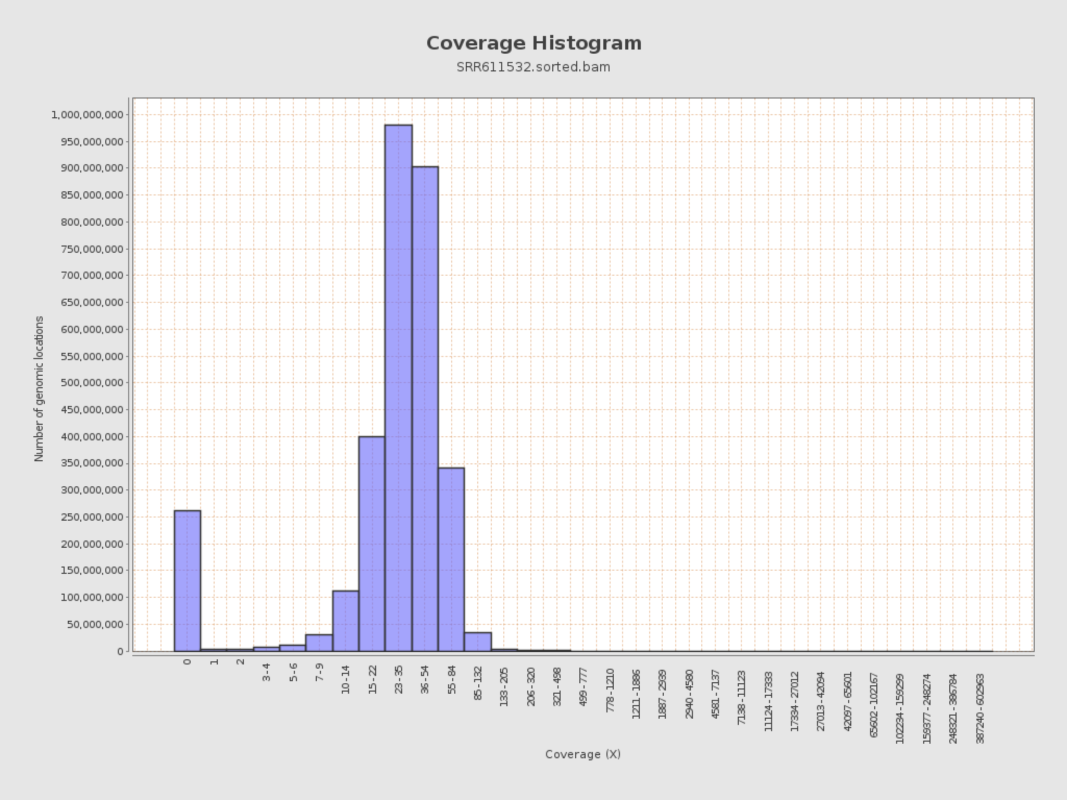
		bases	**coverage**	**deviation**
chr1	249250621	7327130546	29.3966	618.4806
chr2	243199373	10370246707	42.6409	278.9149
chr3	198022430	7819344400	39.4872	23.7528
chr4	191154276	5478085485	28.6579	212.1329
chr5	180915260	6645796538	36.7343	35.1219
chr6	171115067	4933767183	28.833	112.3843
chr7	159138663	8356883095	52.5132	332.1581
chr8	146364022	4560915751	31.1615	200.0809
chr9	141213431	4893438635	34.6528	387.704
chr10	135534747	4642285182	34.2516	718.1881
chr11	135006516	5945172932	44.0362	184.494
chr12	133851895	4832105621	36.1004	31.3845
chr13	115169878	4274962987	37.1188	24.7803
chr14	107349540	3277518848	30.5313	39.6293
chr15	102531392	2582723626	25.1896	19.2208
chr16	90354753	2972174162	32.8945	245.3783
chr17	81195210	3914164283	48.2068	219.6319
chr18	78077248	1906805145	24.422	457.3947
chr19	59128983	2466098043	41.7071	296.1949
chr20	63025520	3452235817	54.7752	112.483
chr21	48129895	1702798007	35.3792	133.0332
chr22	51304566	1237535260	24.1213	23.9161
chrMT	16571	408804694	24,669.8868	4,951.4065
chrX	155270560	4292897219	27.6479	96.6831

chrY	59373566	396996709	6.6864	305.6131

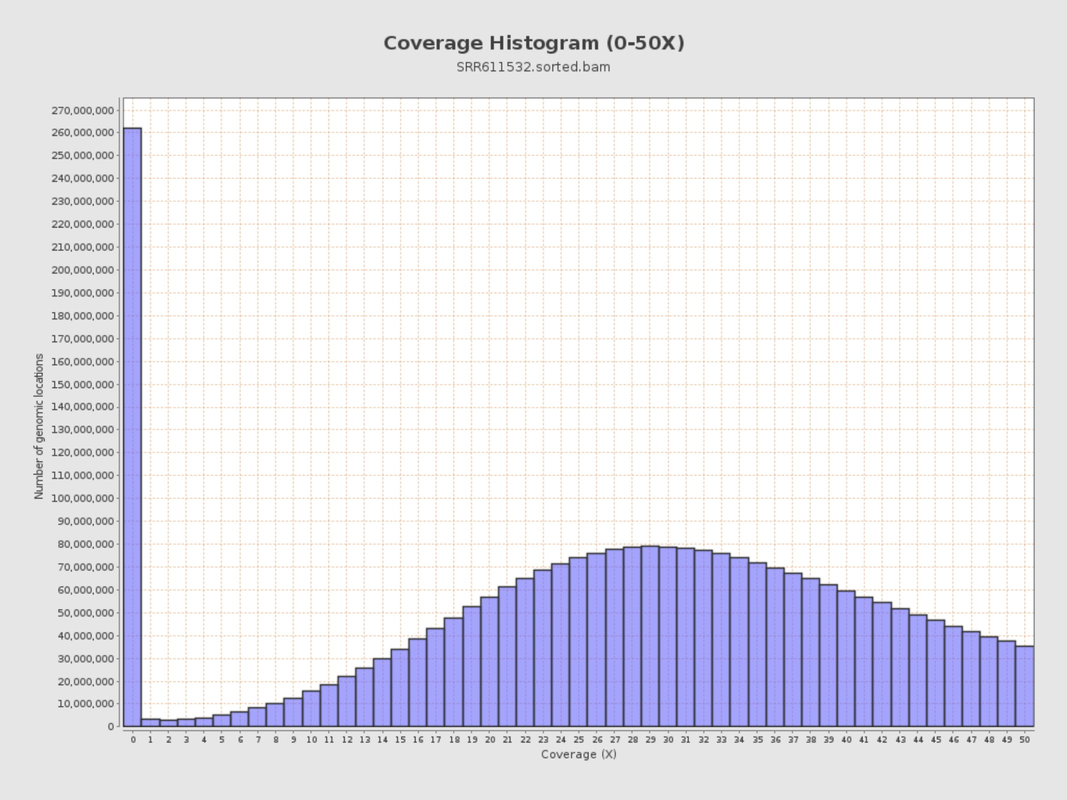
3. Results : Coverage across reference



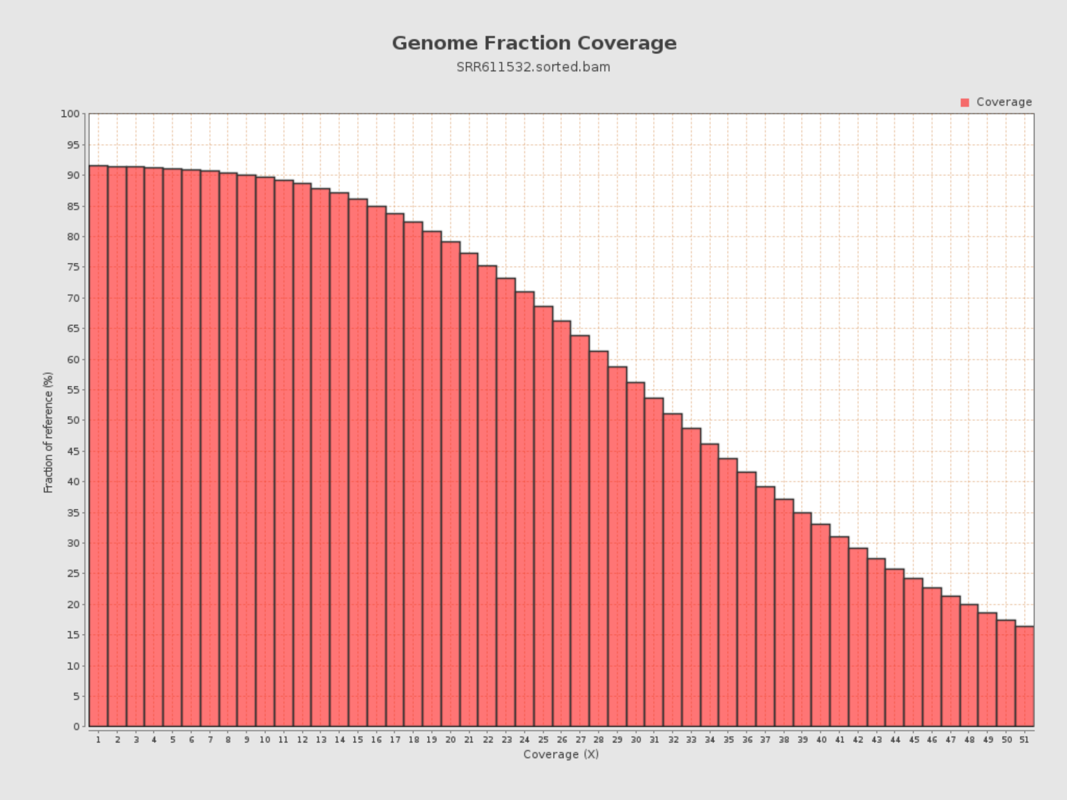
4. Results : Coverage Histogram



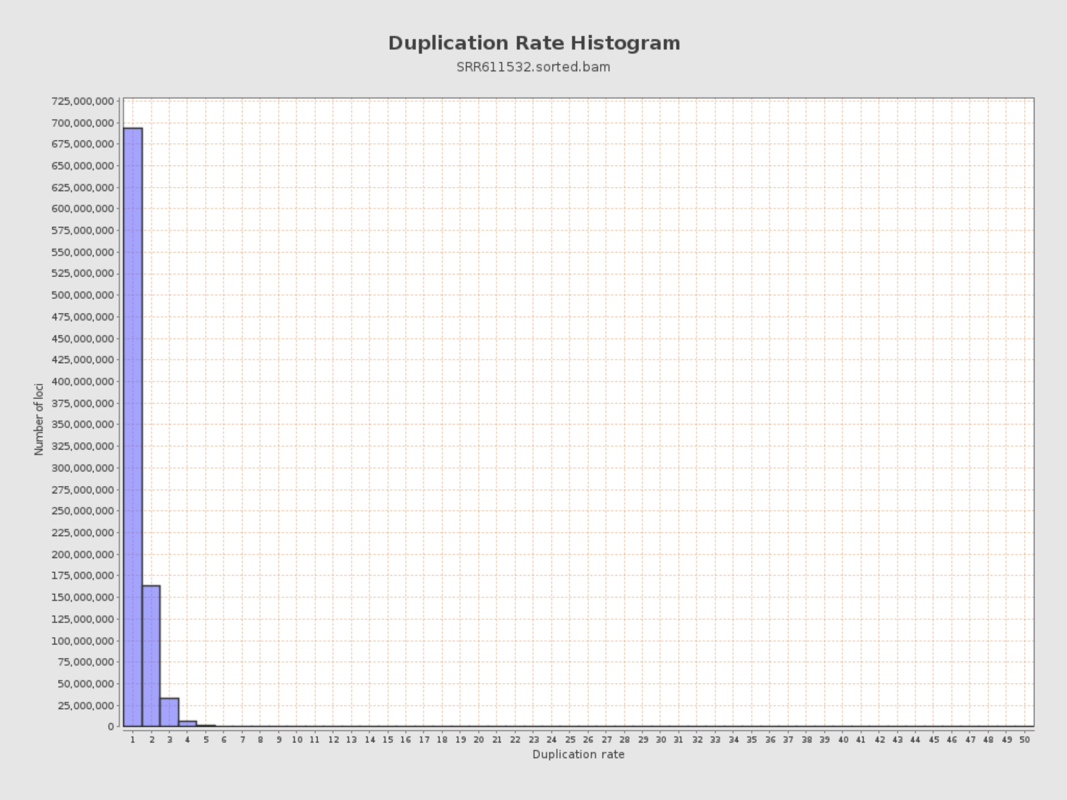
5. Results : Coverage Histogram (0-50X)



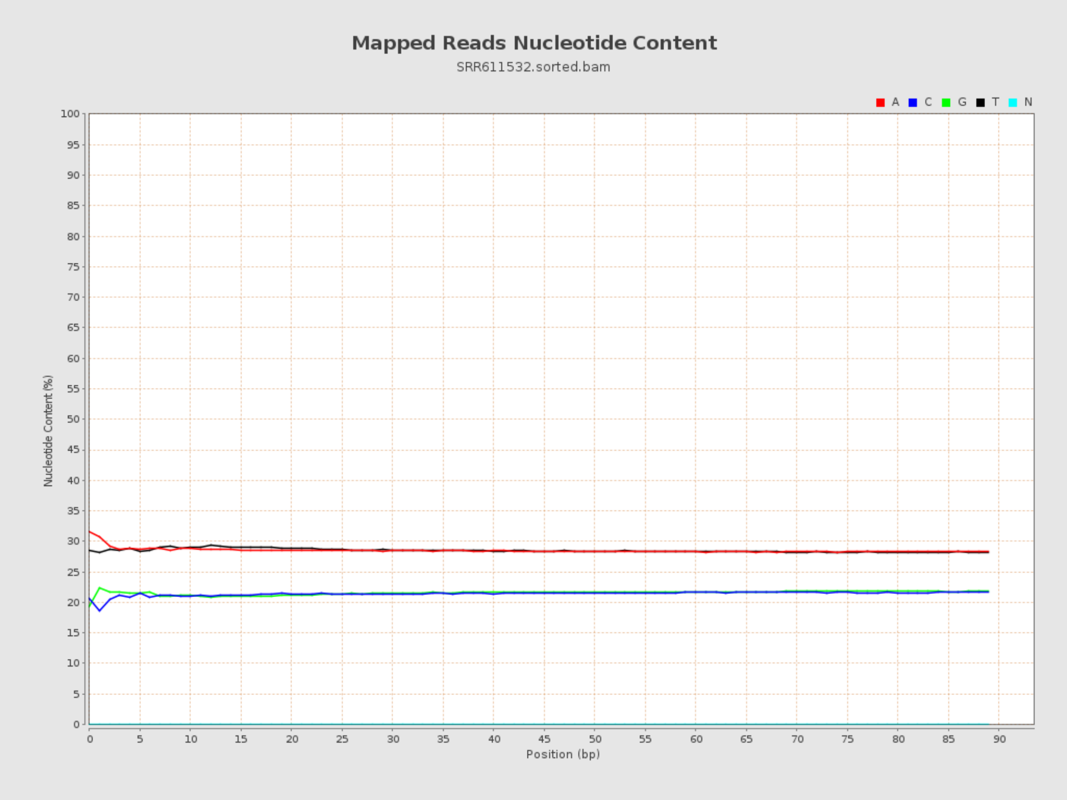
6. Results : Genome Fraction Coverage



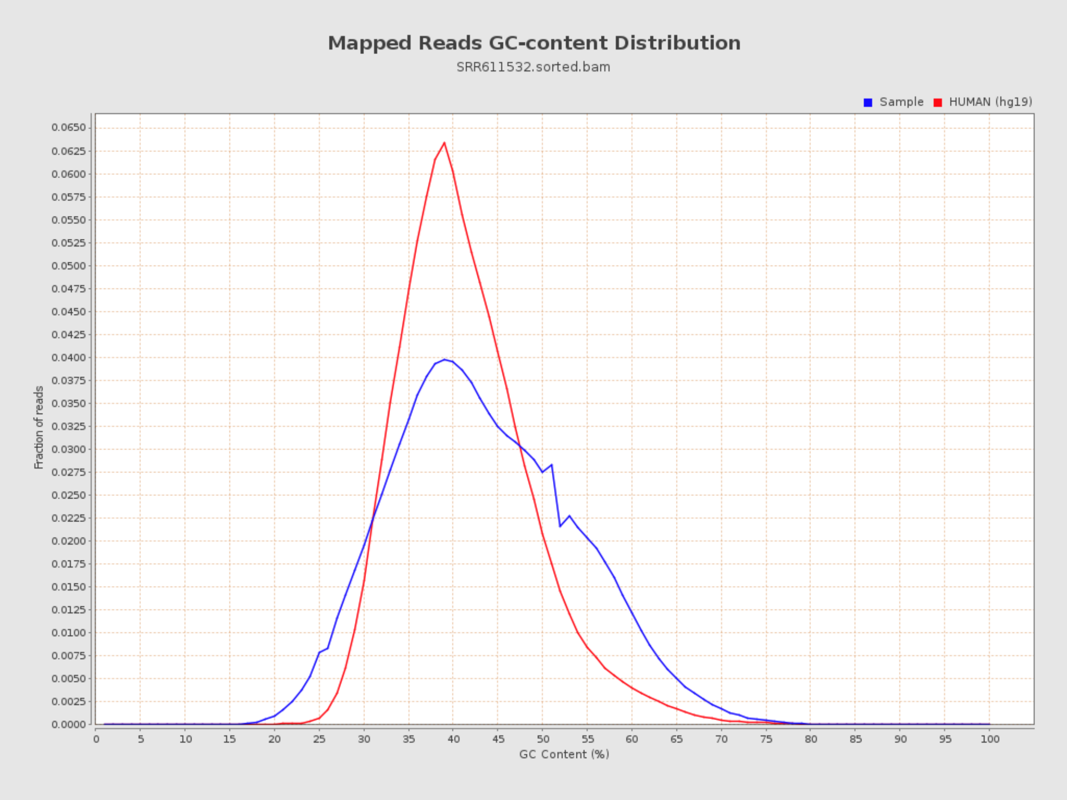
7. Results : Duplication Rate Histogram



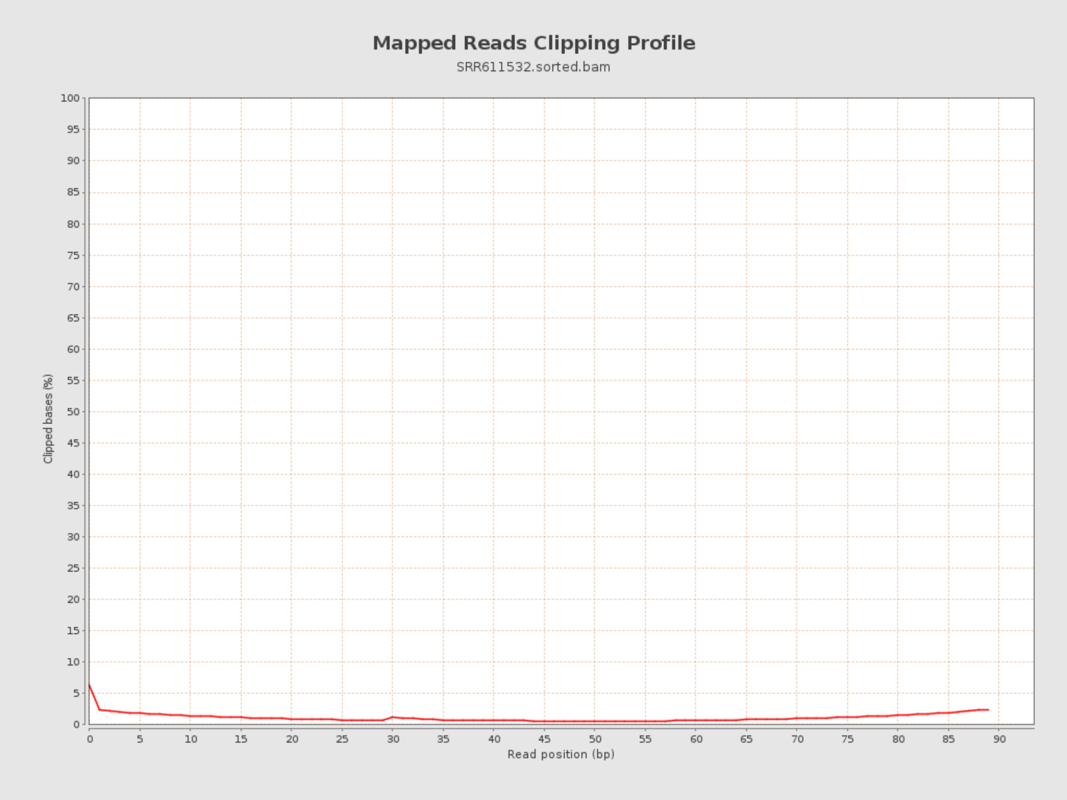
8. Results : Mapped Reads Nucleotide Content



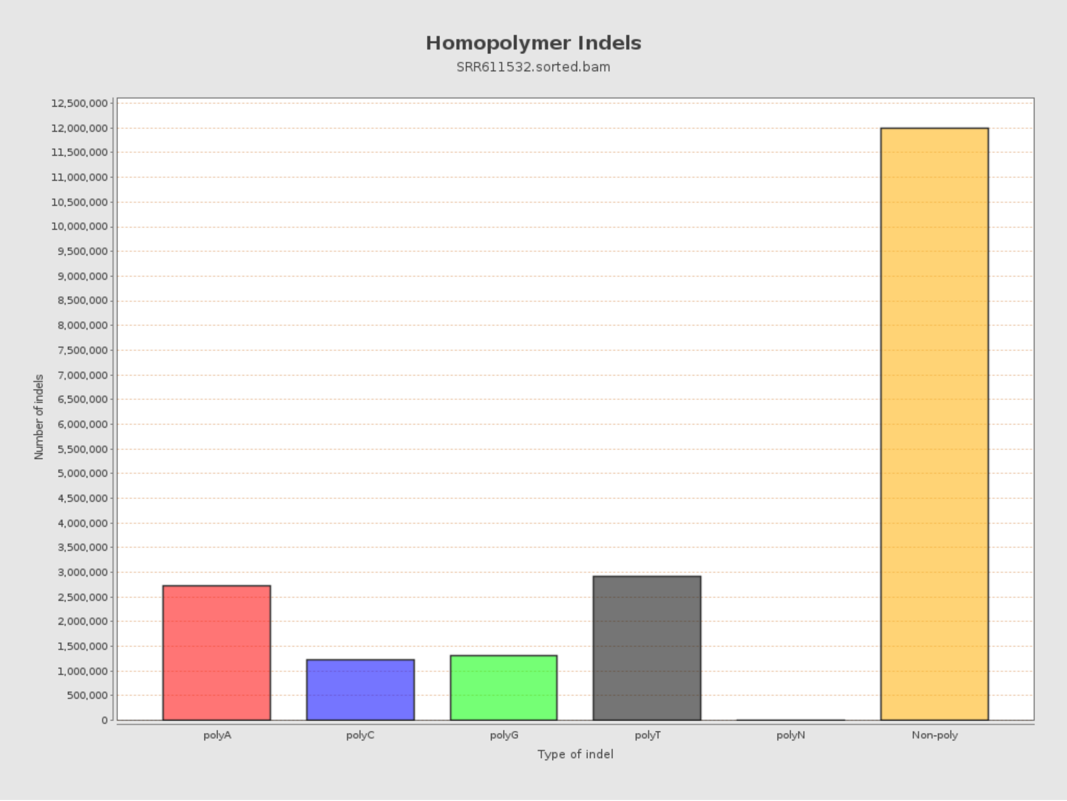
9. Results : Mapped Reads GC-content Distribution



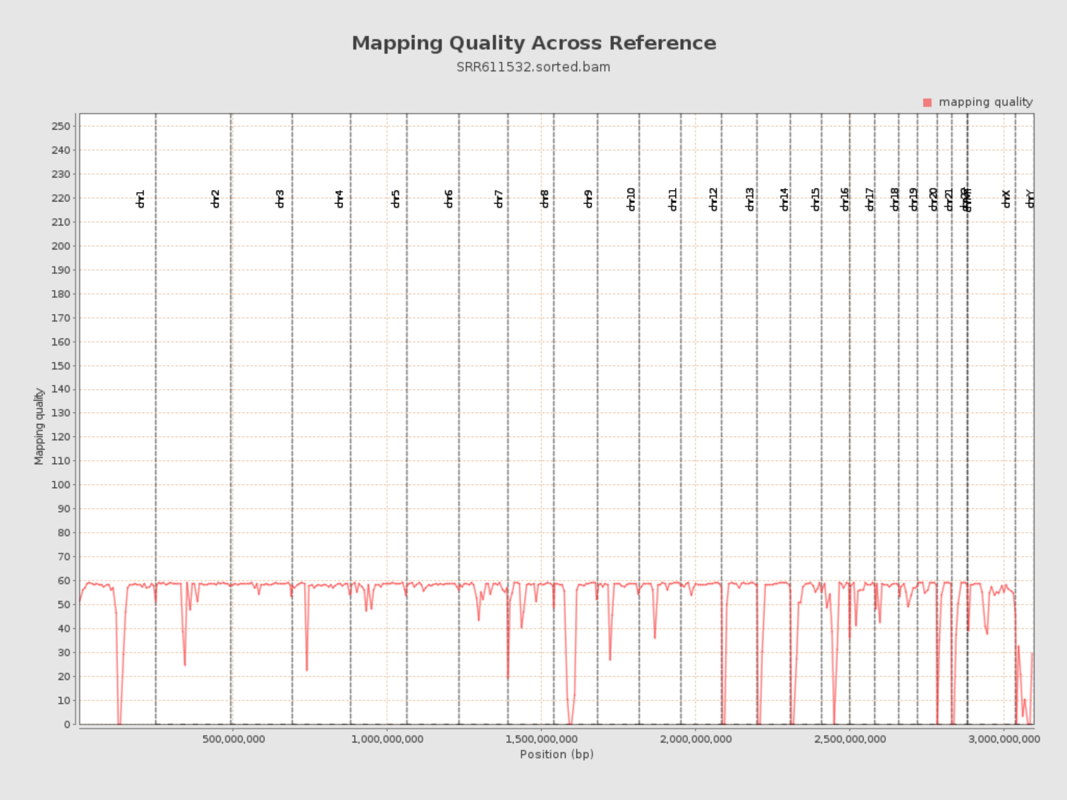
10. Results : Mapped Reads Clipping Profile



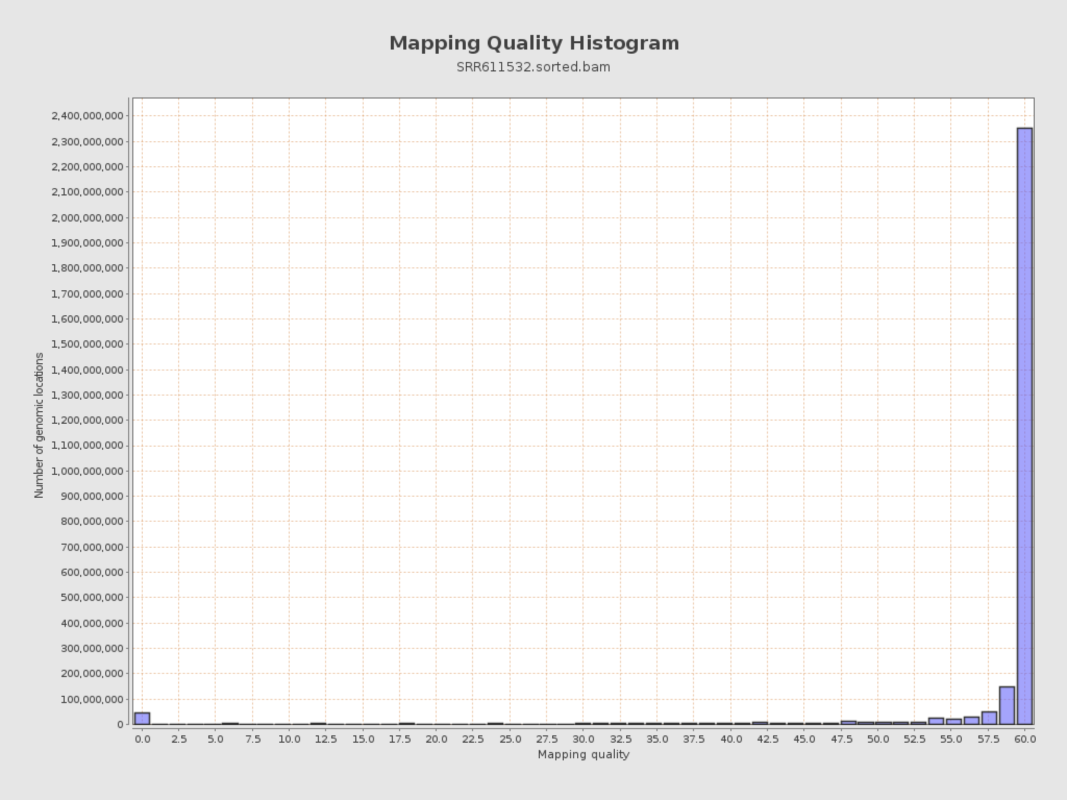
11. Results : Homopolymer Indels



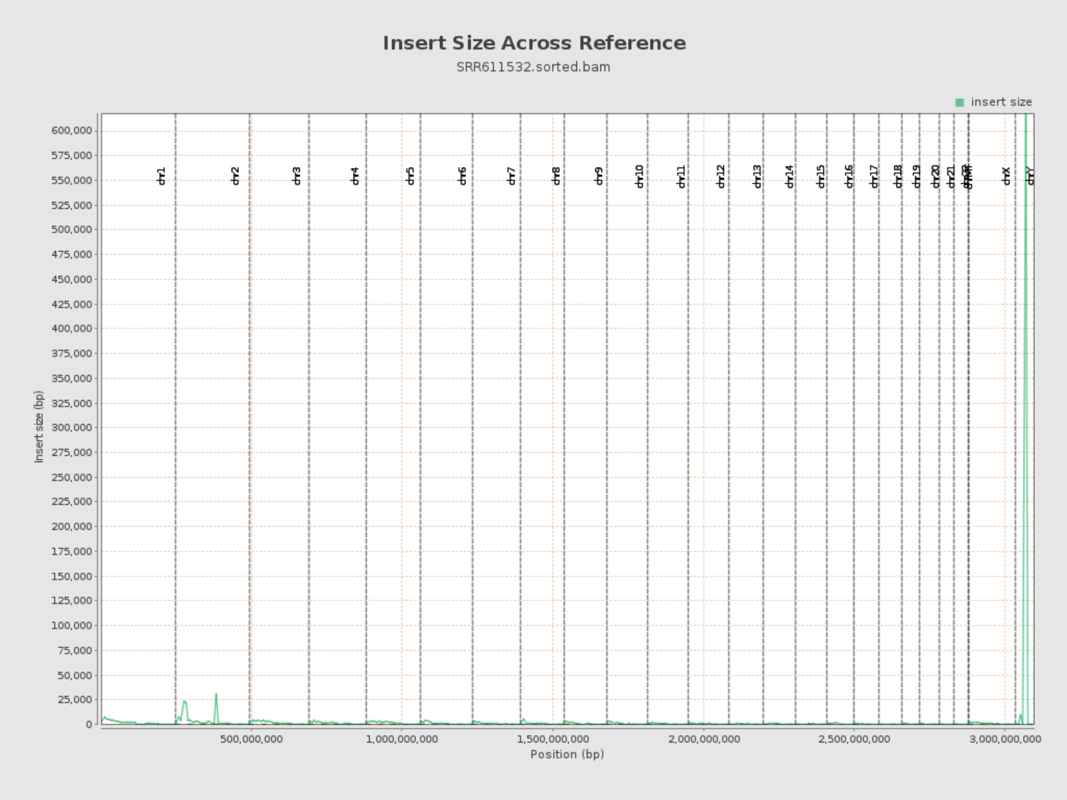
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram