

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 19:53:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630576.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_SRR630576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630576_1.fastq.gz SRR630576_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 19:53:38 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,315,180
Mapped reads	33,887,777 / 98.75%
Unmapped reads	427,403 / 1.25%
Mapped paired reads	33,887,777 / 98.75%
Mapped reads, first in pair	17,012,251 / 49.58%
Mapped reads, second in pair	16,875,526 / 49.18%
Mapped reads, both in pair	33,696,938 / 98.2%
Mapped reads, singletons	190,839 / 0.56%
Secondary alignments	0
Supplementary alignments	57,305 / 0.17%
Read min/max/mean length	30 / 101 / 101.06
Duplicated reads (estimated)	4,434,188 / 12.92%
Duplication rate	11.05%
Clipped reads	3,812,605 / 11.11%

2.2. ACGT Content

Number/percentage of A's	953,961,097 / 28.73%
Number/percentage of C's	685,869,438 / 20.66%
Number/percentage of T's	959,920,152 / 28.91%
Number/percentage of G's	720,166,541 / 21.69%
Number/percentage of N's	503,168 / 0.02%

GC Percentage	42.35%
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2.3. Coverage

Mean	1.0734
Standard Deviation	5.1571

2.4. Mapping Quality

Mean Mapping Quality	54.05
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2.5. Insert size

Mean	30,001.03
Standard Deviation	1,741,192.75
P25/Median/P75	156 / 199 / 263

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	29,189,393
Insertions	627,636
Mapped reads with at least one insertion	1.82%
Deletions	1,856,858
Mapped reads with at least one deletion	5.32%
Homopolymer indels	54.49%

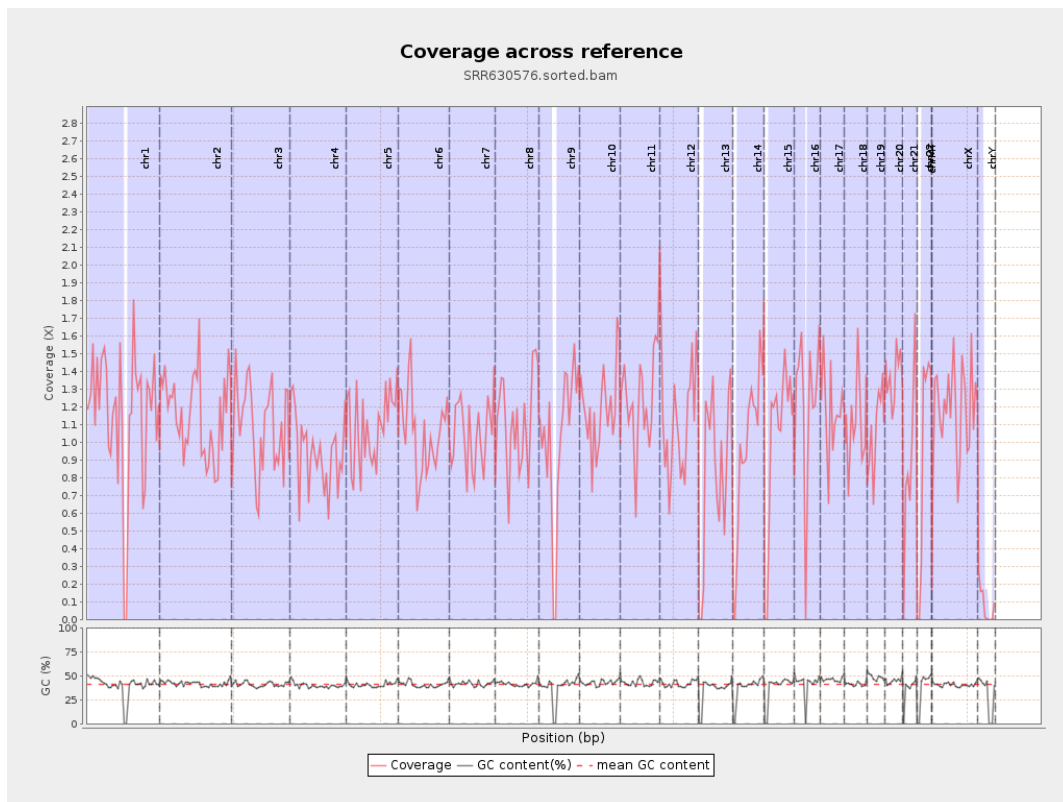
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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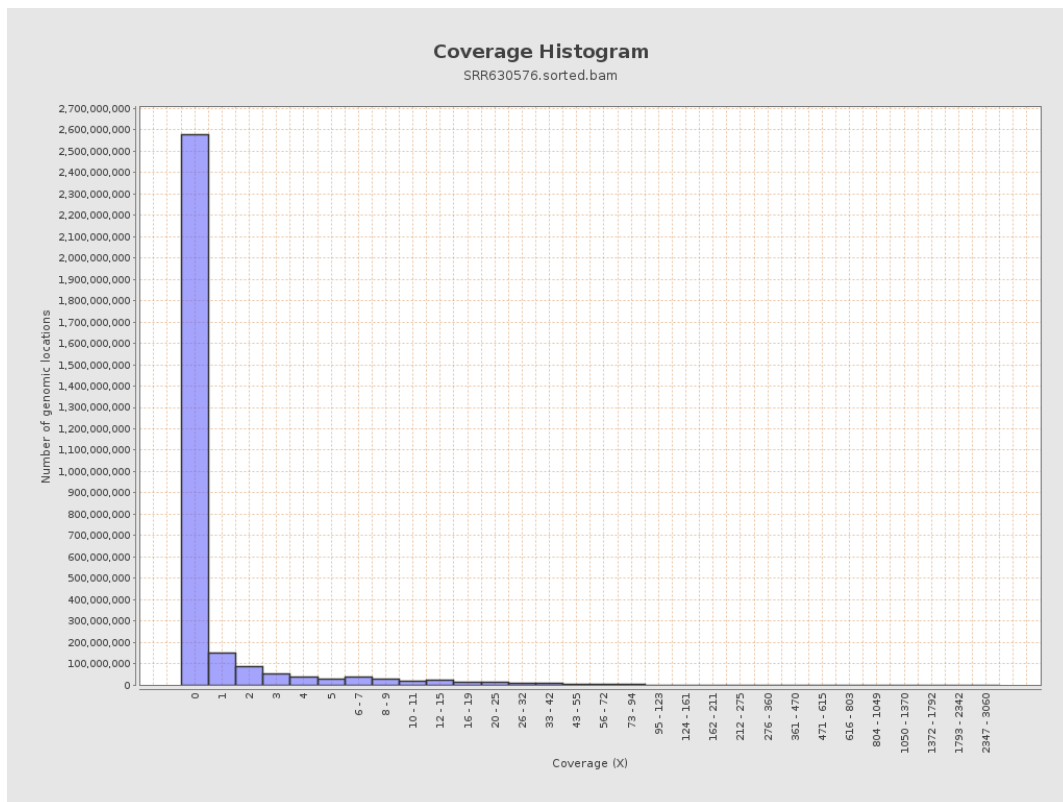
		bases	coverage	deviation
chr1	249250621	287673298	1.1542	5.6355
chr2	243199373	281415947	1.1571	6.0705
chr3	198022430	217708385	1.0994	4.7445
chr4	191154276	179269388	0.9378	4.5575
chr5	180915260	196175204	1.0843	4.6883
chr6	171115067	180775896	1.0565	4.7518
chr7	159138663	166814808	1.0482	4.6765
chr8	146364022	164435888	1.1235	5.0111
chr9	141213431	144467789	1.023	5.1965
chr10	135534747	160925984	1.1873	5.1287
chr11	135006516	166793069	1.2354	5.5265
chr12	133851895	149936601	1.1202	5.0244
chr13	115169878	96176196	0.8351	4.1344
chr14	107349540	103447631	0.9637	4.5097
chr15	102531392	104179579	1.0161	4.7613
chr16	90354753	108740896	1.2035	7.3655
chr17	81195210	94381269	1.1624	5.3294
chr18	78077248	87570473	1.1216	5.1846
chr19	59128983	64129472	1.0846	5.4134
chr20	63025520	86329449	1.3698	6.0011
chr21	48129895	44355598	0.9216	5.7919
chr22	51304566	48453217	0.9444	5.0414
chrMT	16571	2658	0.1604	0.9177
chrX	155270560	184058965	1.1854	5.0441

chrY	59373566	4710812	0.0793	2.6052
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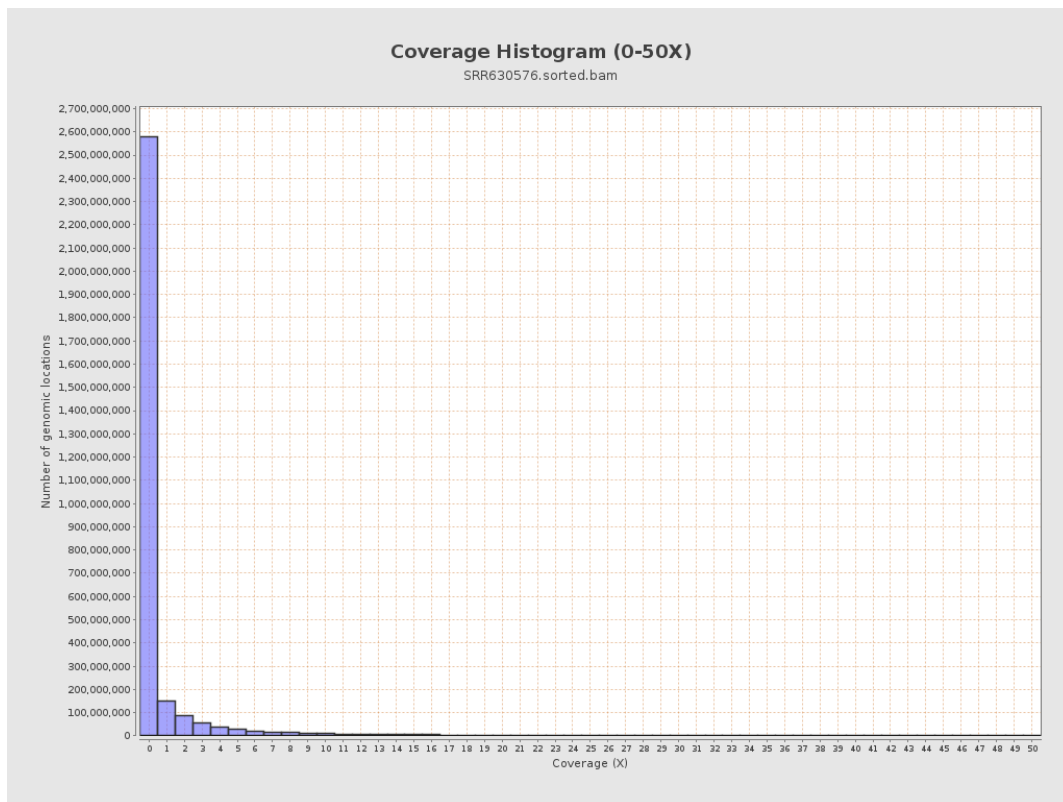
3. Results : Coverage across reference



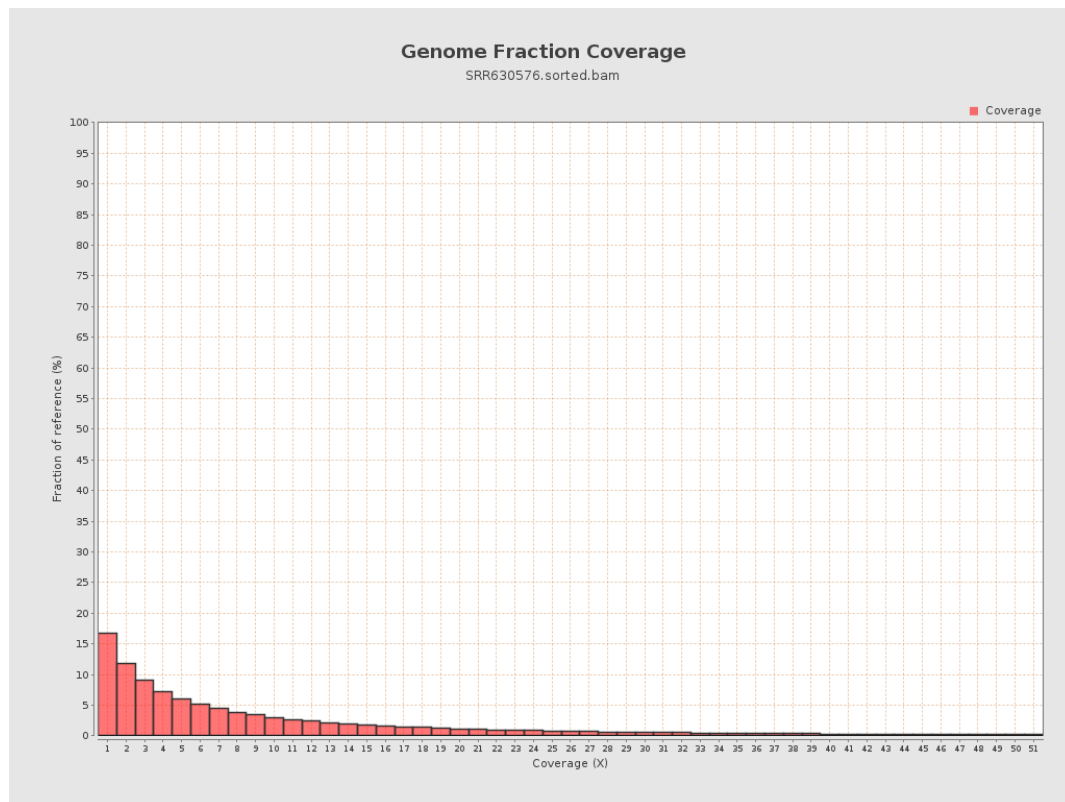
4. Results : Coverage Histogram



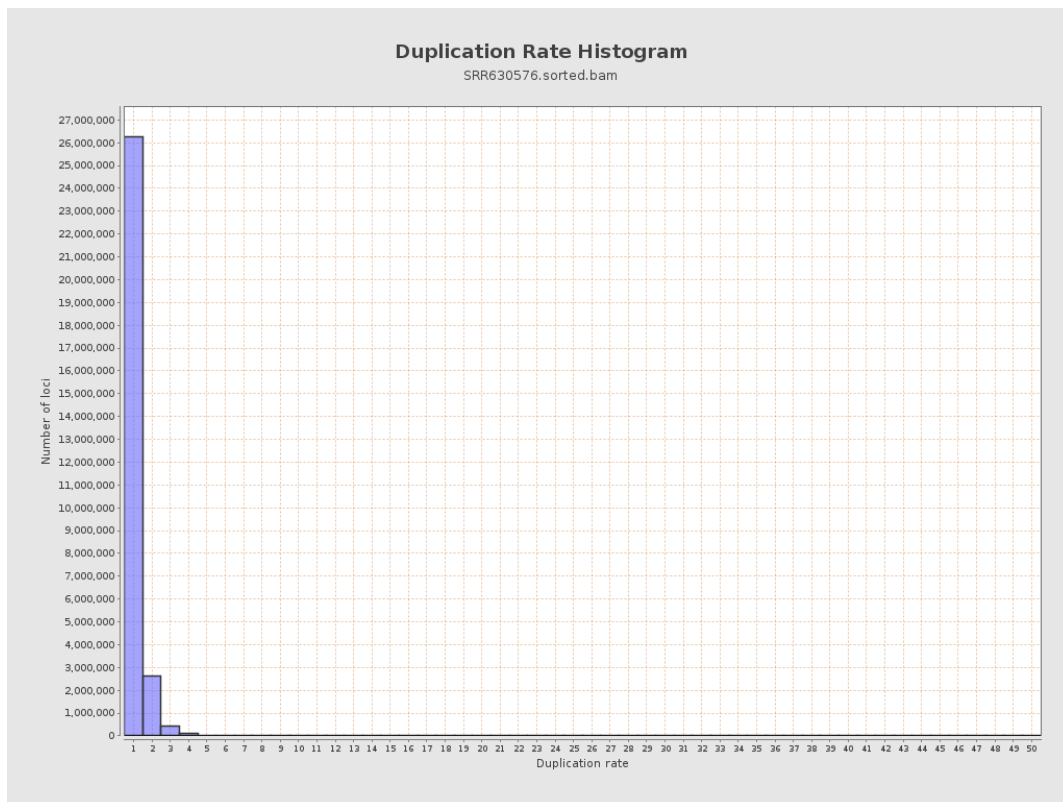
5. Results : Coverage Histogram (0-50X)



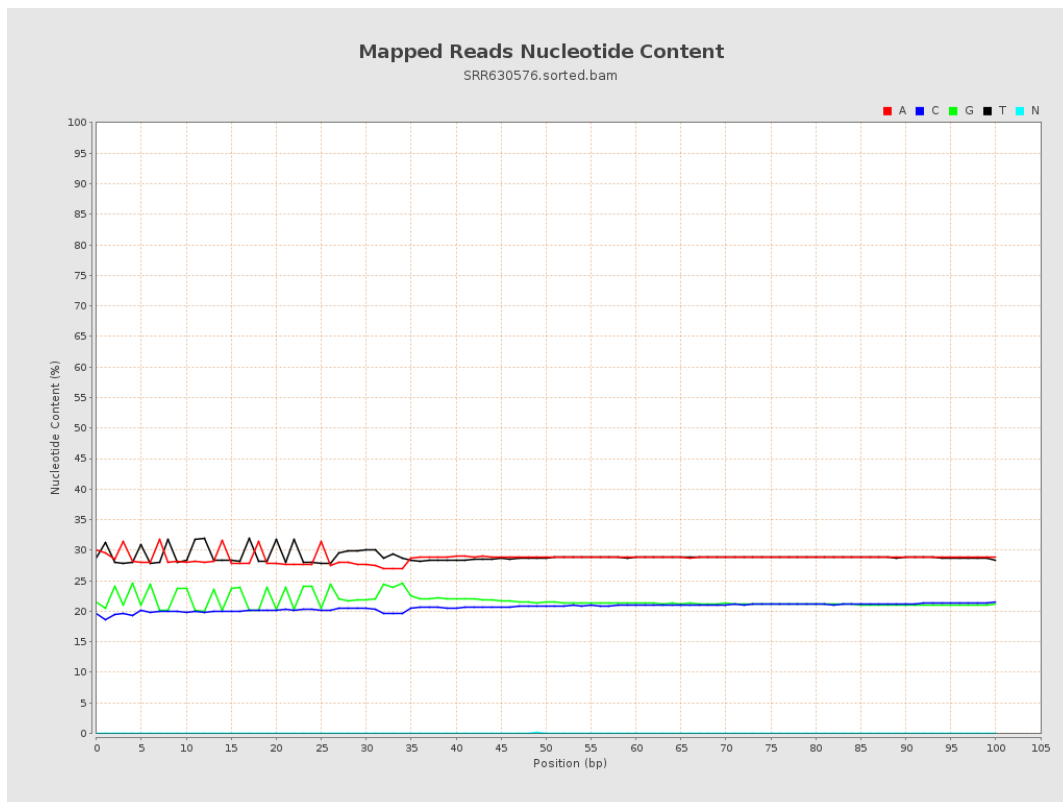
6. Results : Genome Fraction Coverage



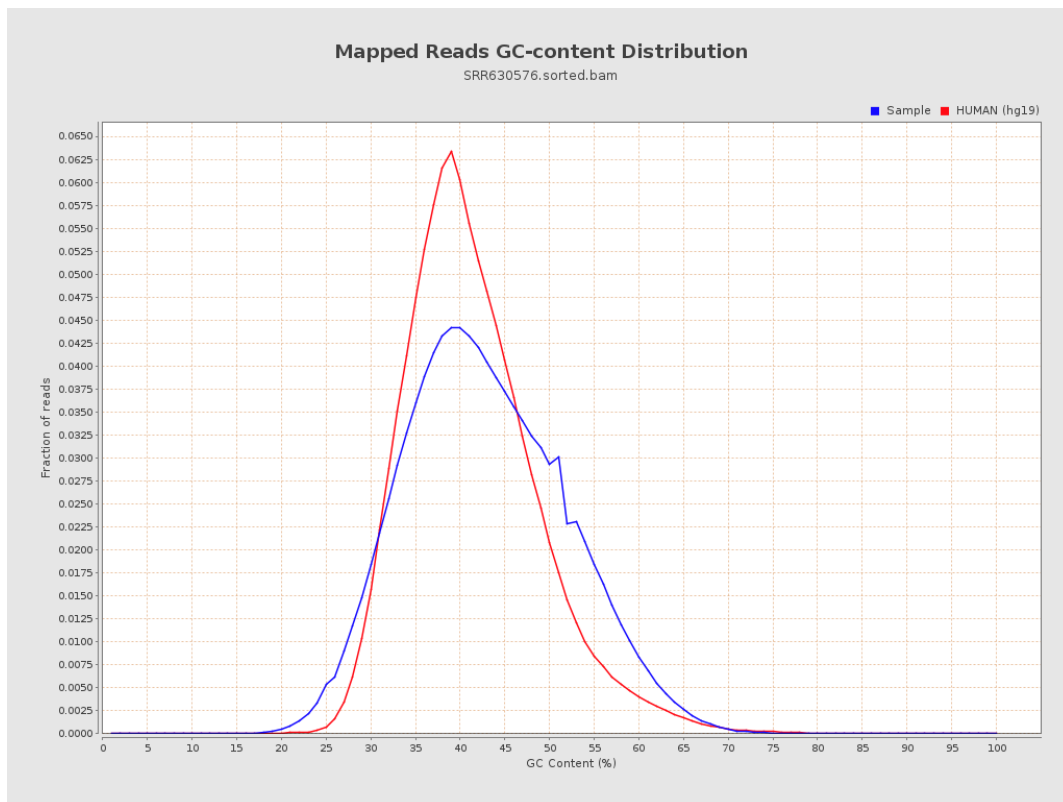
7. Results : Duplication Rate Histogram



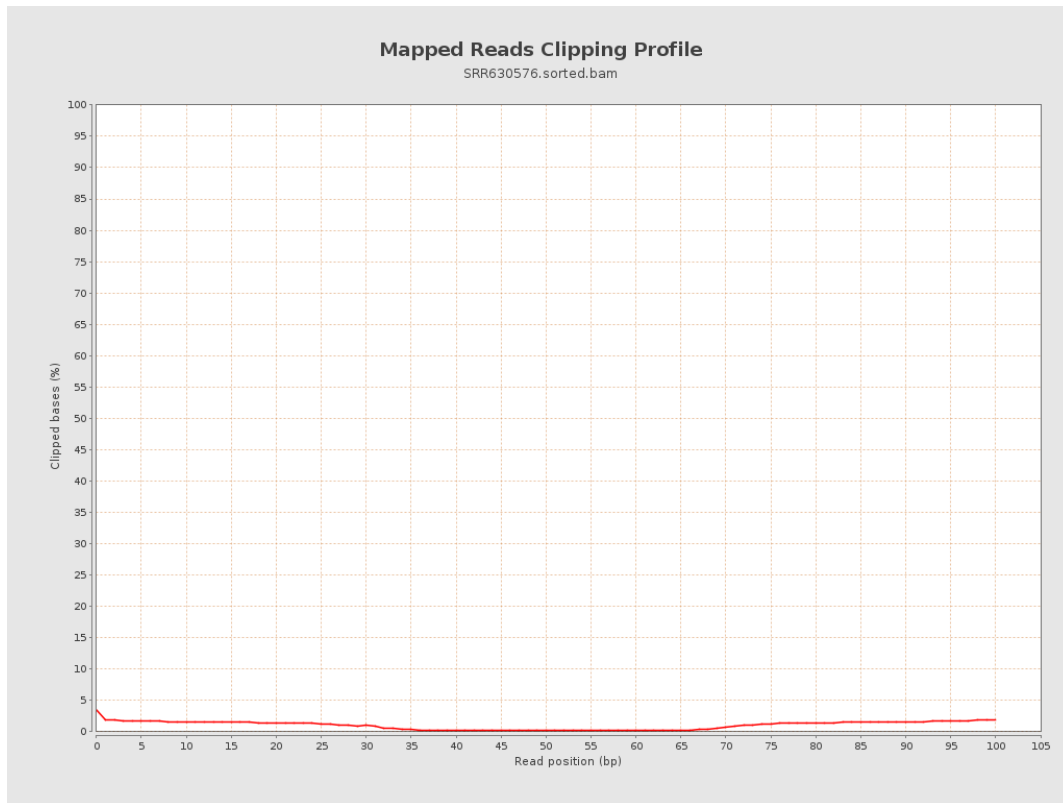
8. Results : Mapped Reads Nucleotide Content



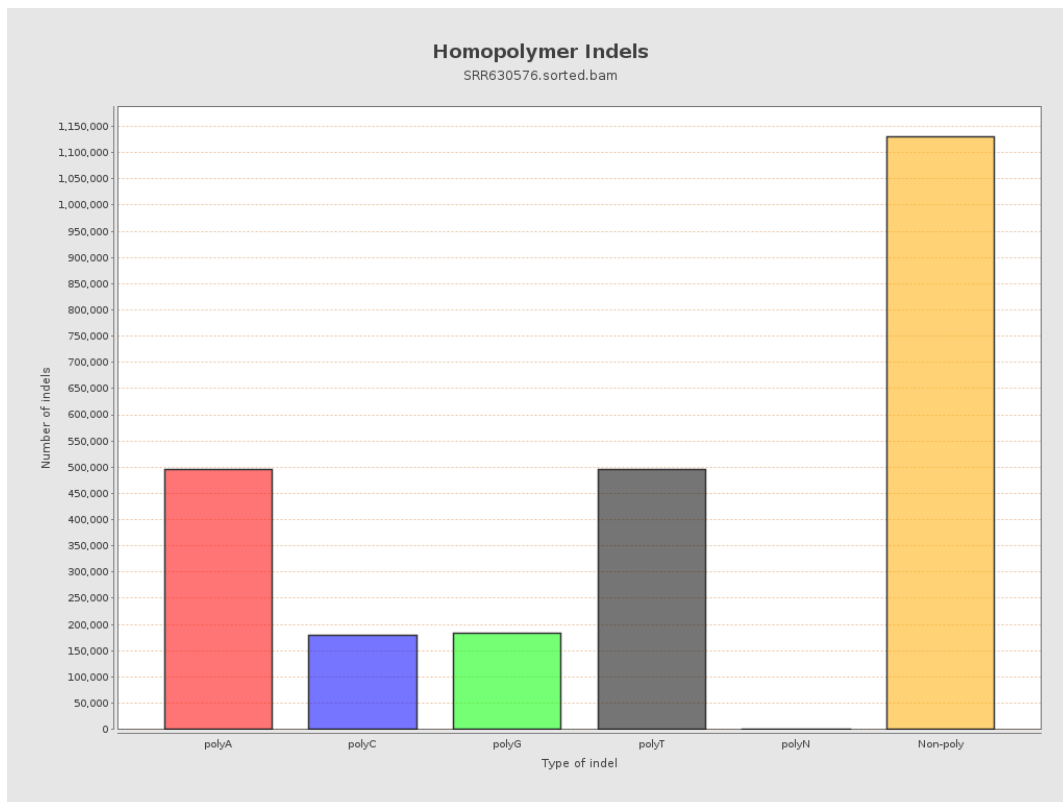
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



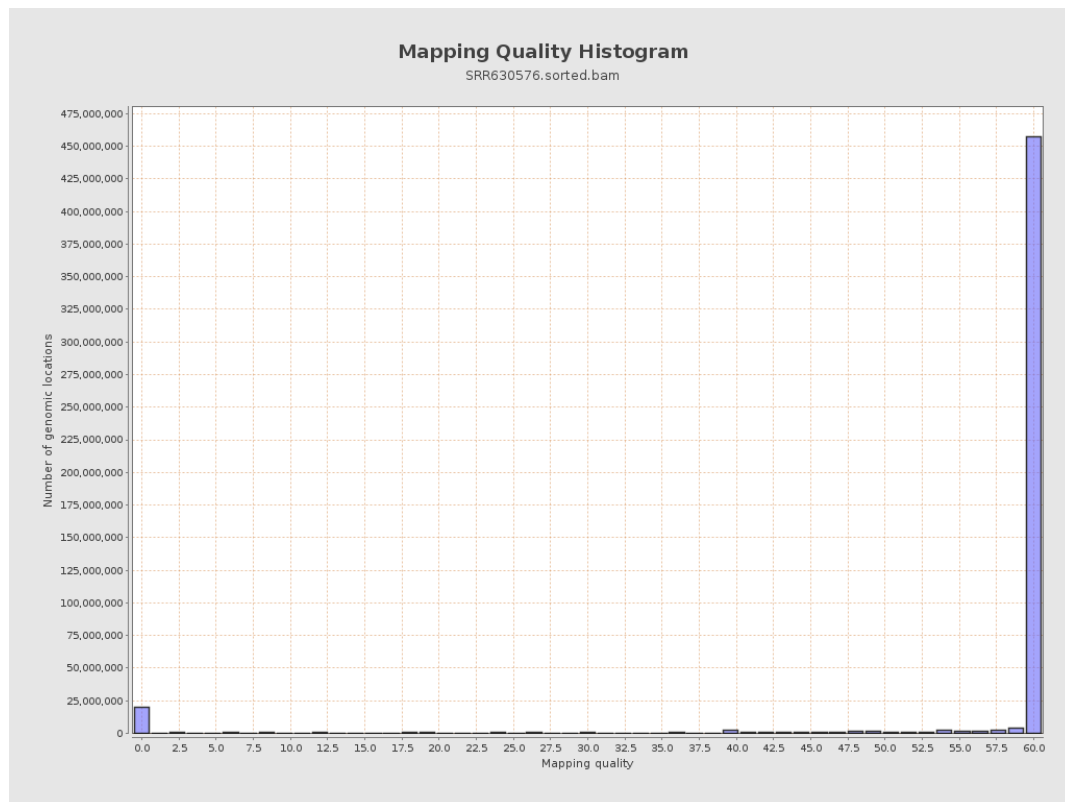
11. Results : Homopolymer Indels



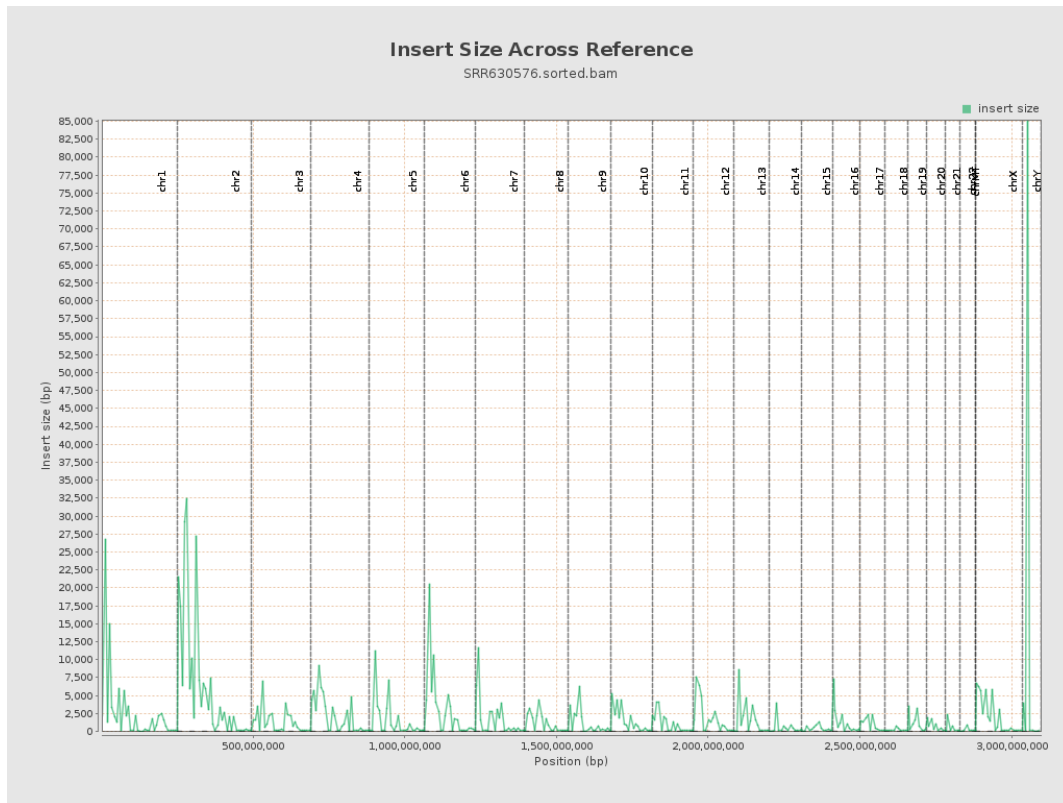
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

