Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 14:13:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438271.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_SRR8438271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438271_1.fastq.gz SRR8438271_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 14:13:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,310,430,866
Mapped reads	1,303,468,623 / 99.47%
Unmapped reads	6,962,243 / 0.53%
Mapped paired reads	1,303,468,623 / 99.47%
Mapped reads, first in pair	651,939,697 / 49.75%
Mapped reads, second in pair	651,528,926 / 49.72%
Mapped reads, both in pair	1,301,544,676 / 99.32%
Mapped reads, singletons	1,923,947 / 0.15%
Secondary alignments	0
Supplementary alignments	13,397,829 / 1.02%
Read min/max/mean length	28 / 151 / 133.41
Duplicated reads (estimated)	440,274,808 / 33.6%
Duplication rate	30.89%
Clipped reads	105,380,940 / 8.04%

2.2. ACGT Content

Number/percentage of A's	50,050,894,590 / 28.99%
Number/percentage of C's	36,550,476,902 / 21.17%
Number/percentage of T's	49,450,809,064 / 28.65%
Number/percentage of G's	36,565,852,514 / 21.18%
Number/percentage of N's	1,351,978 / 0%

GC Percentage	42.36%

2.3. Coverage

Mean	55.7755
Standard Deviation	785.9554

2.4. Mapping Quality

Mean Mapping Quality	54.48

2.5. Insert size

Mean	37,101.37
Standard Deviation	1,919,093.53
P25/Median/P75	136 / 212 / 290

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	737,304,507
Insertions	16,682,380
Mapped reads with at least one insertion	1.24%
Deletions	19,198,649
Mapped reads with at least one deletion	1.44%
Homopolymer indels	45.06%

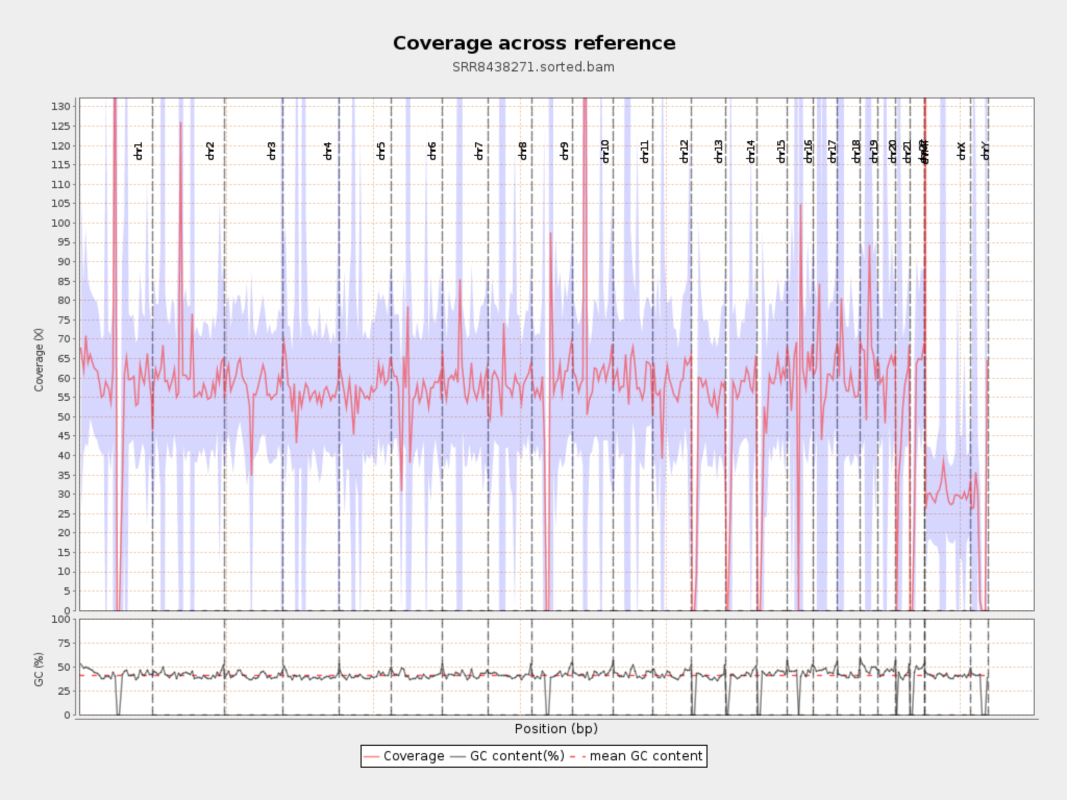
2.7. Chromosome stats

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

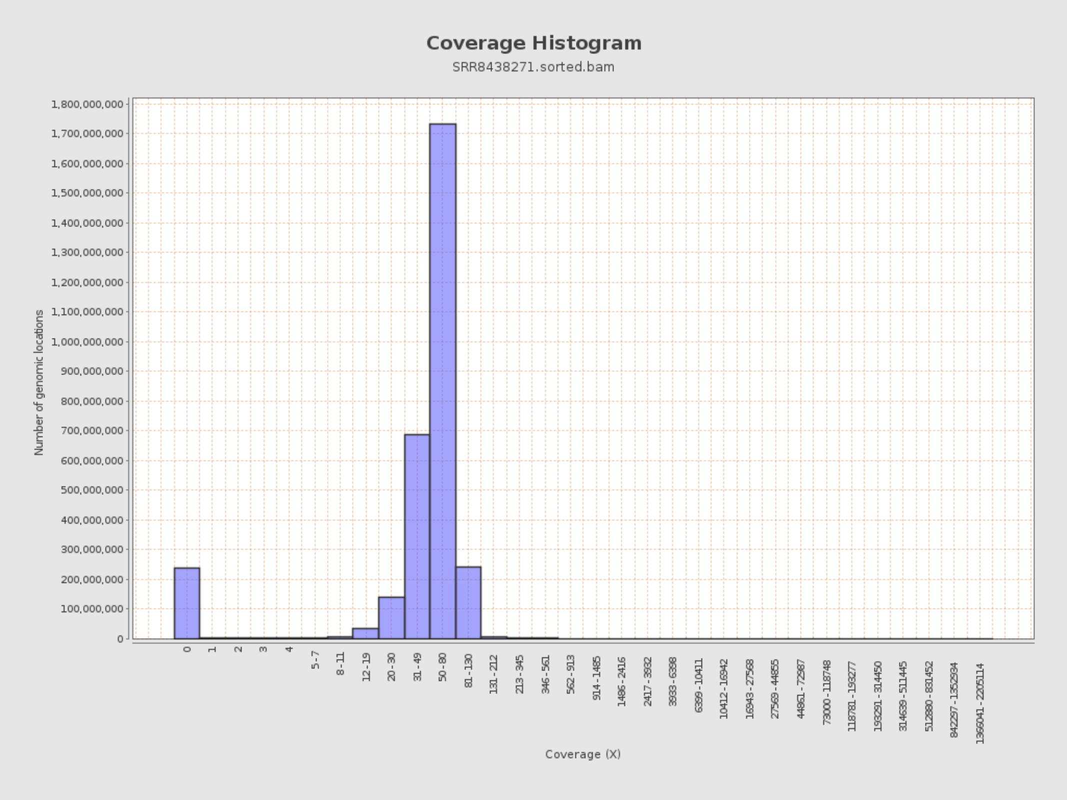
		bases	coverage	deviation
chr1	249250621	14747770362	59.1684	2,181.3166
chr2	243199373	15010736642	61.7219	508.6193
chr3	198022430	11445470746	57.7989	75.541
chr4	191154276	10747959106	56.2266	74.3034
chr5	180915260	10375621386	57.3507	38.5796
chr6	171115067	9704440184	56.7129	250.452
chr7	159138663	9571987921	60.1487	579.6994
chr8	146364022	8610507792	58.8294	200.2125
chr9	141213431	7713046025	54.6198	991.021
chr10	135534747	9217644024	68.0095	1,472.1567
chr11	135006516	8140565149	60.2976	253.9681
chr12	133851895	7785505024	58.1651	36.7692
chr13	115169878	5438485175	47.2214	27.6278
chr14	107349540	5286577802	49.2464	46.3032
chr15	102531392	4897765259	47.7684	34.3925
chr16	90354753	5561049553	61.5468	369.2157
chr17	81195210	4966469771	61.167	291.6466
chr18	78077248	4724982001	60.5168	673.8135
chr19	59128983	3982566764	67.3539	1,178.7878
chr20	63025520	3848986782	61.0703	64.126
chr21	48129895	2260634533	46.9694	106.4511
chr22	51304566	2331920505	45.4525	37.0197
chrMT	16571	264857128	15,983.1711	2,034.5944
chrX	155270560	4658602882	30.0031	104.5166

chrY	59373566	1369710463	23.0694	295.5862

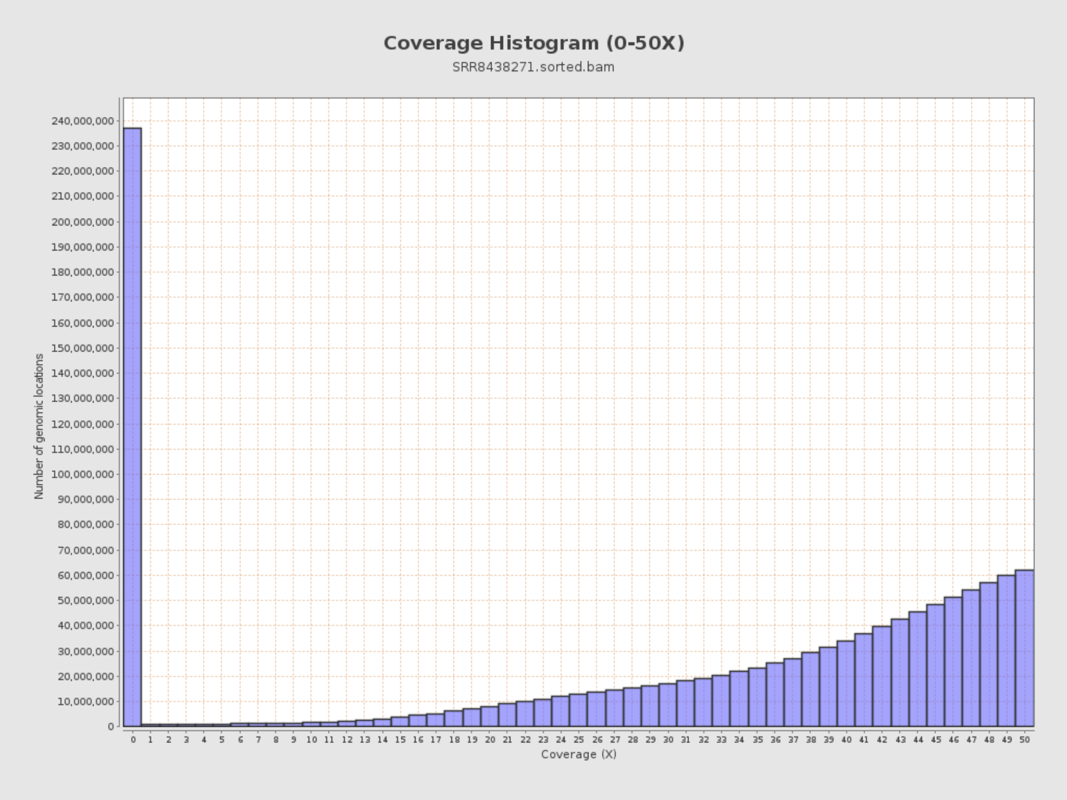
3. Results : Coverage across reference



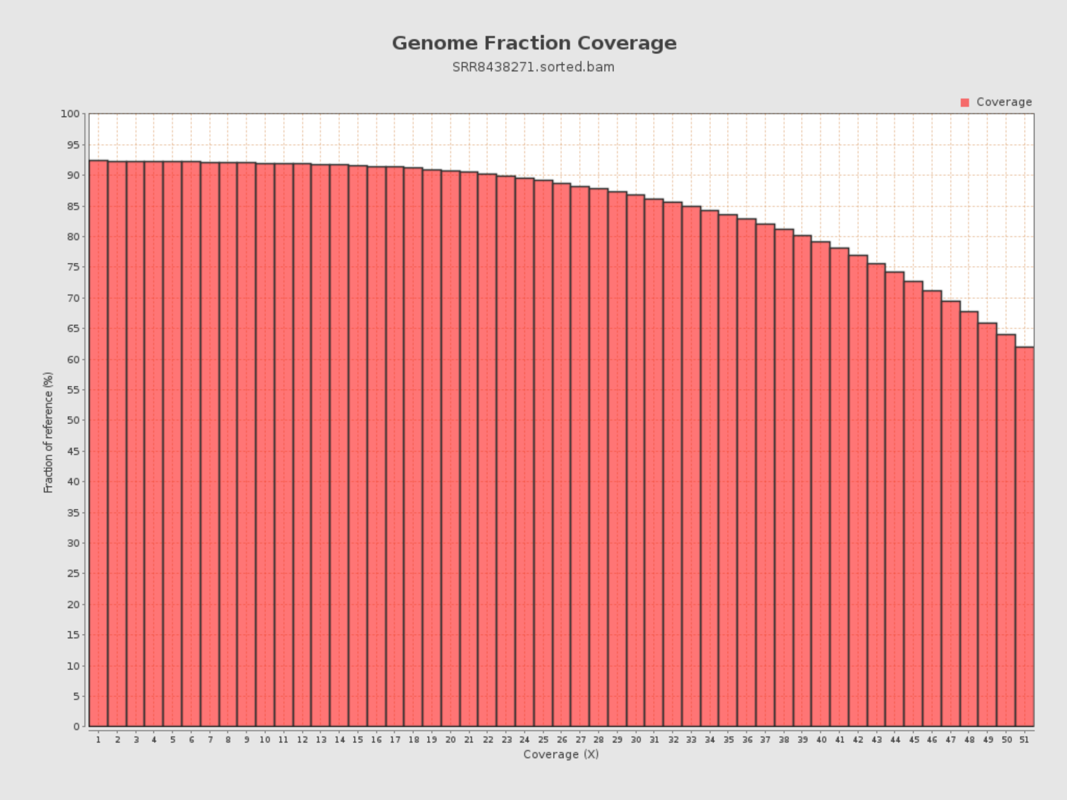
4. Results : Coverage Histogram



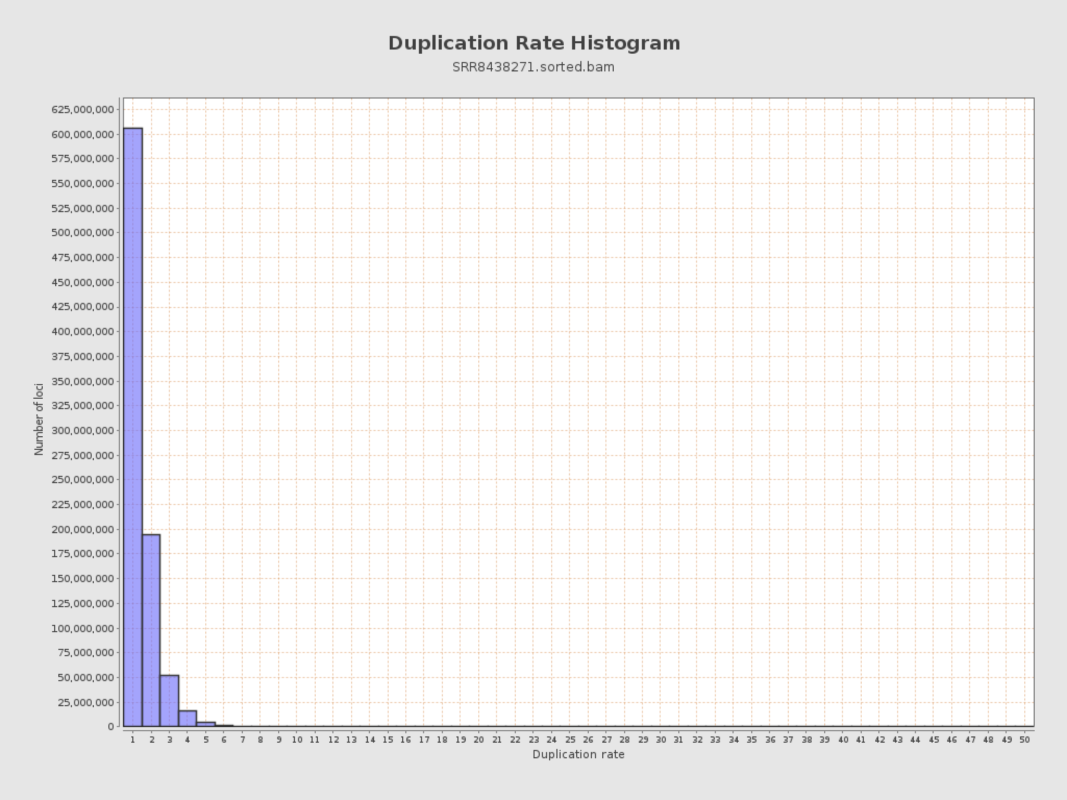
5. Results : Coverage Histogram (0-50X)



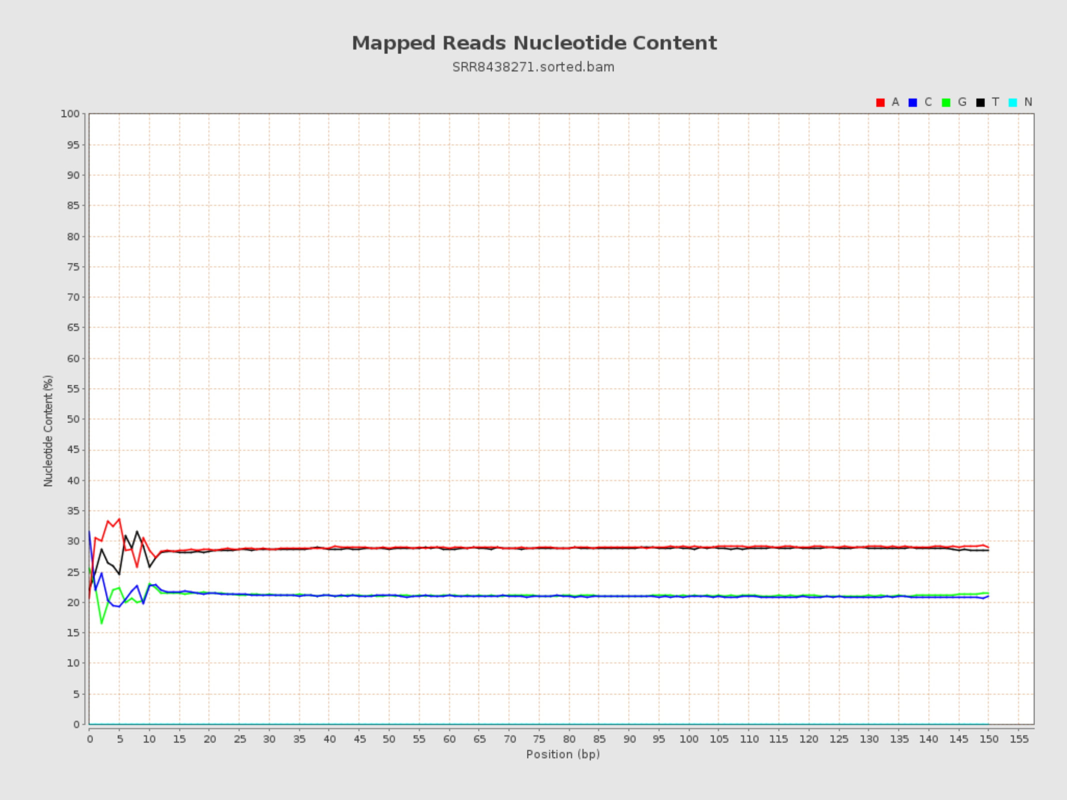
6. Results : Genome Fraction Coverage



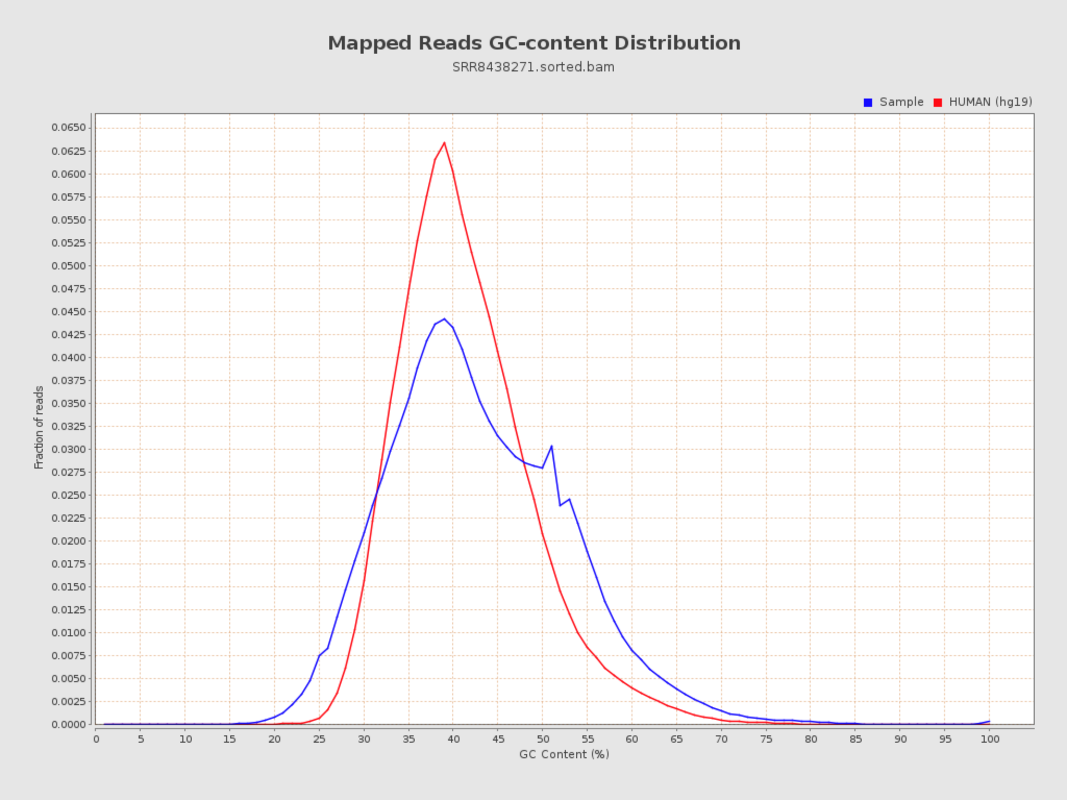
7. Results : Duplication Rate Histogram



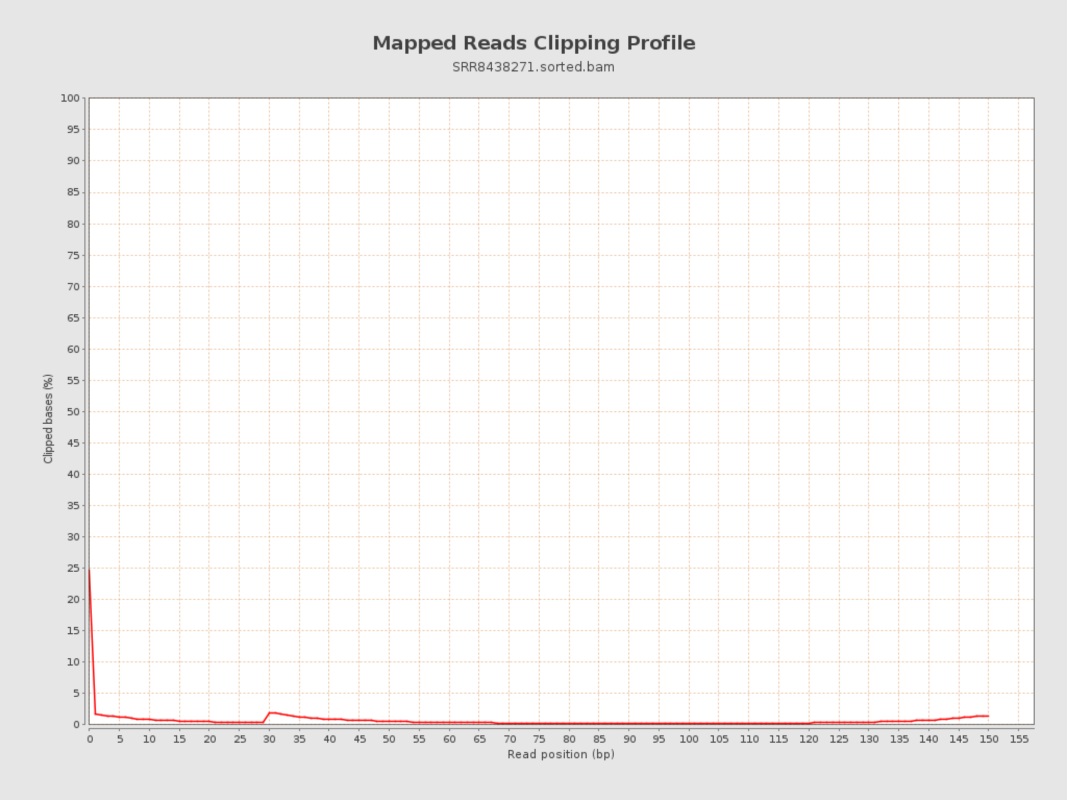
8. Results : Mapped Reads Nucleotide Content



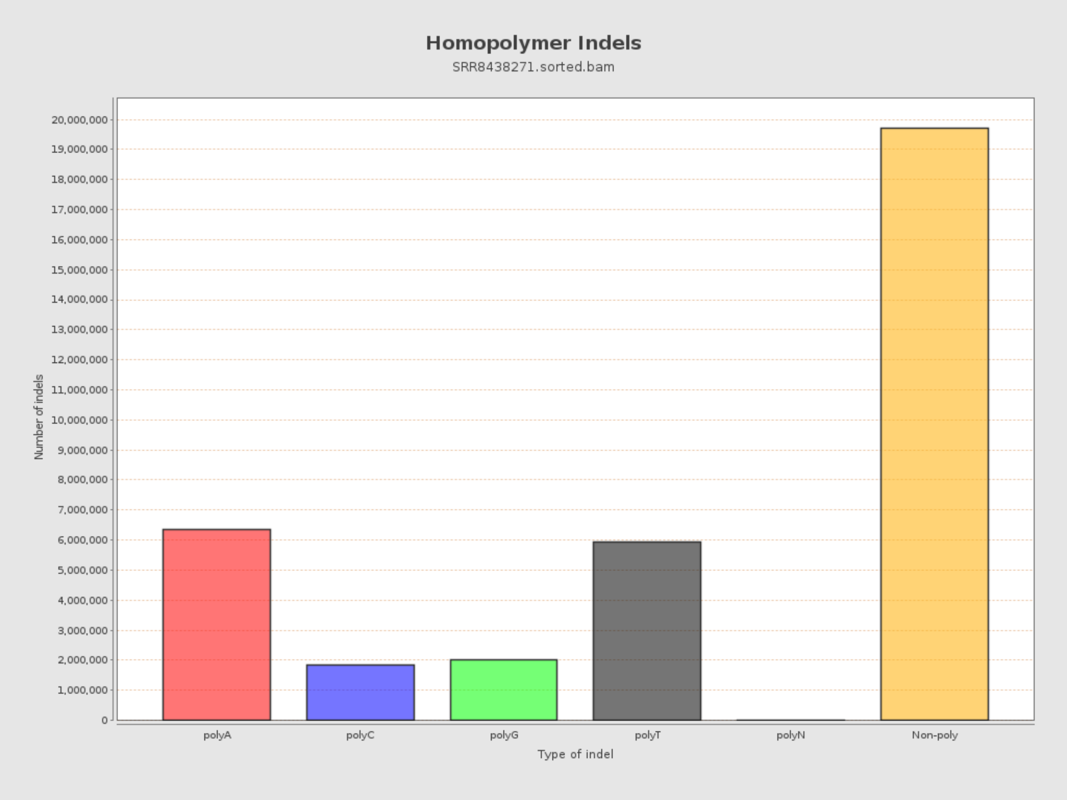
9. Results : Mapped Reads GC-content Distribution



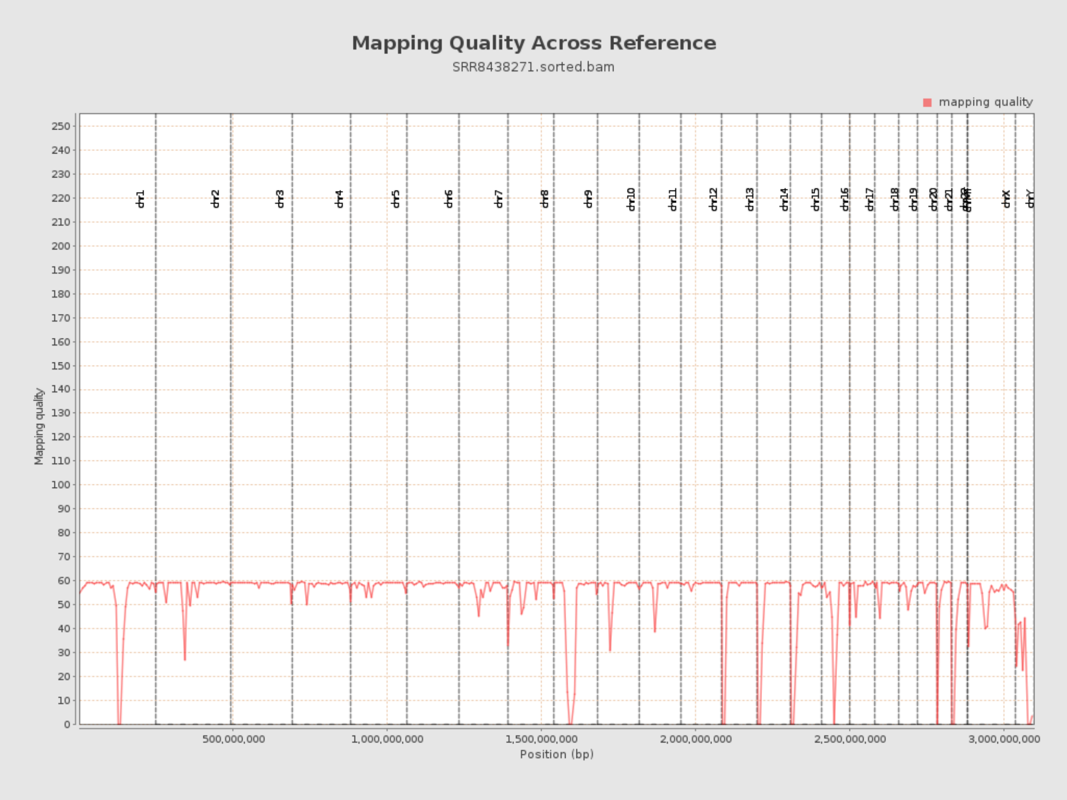
10. Results : Mapped Reads Clipping Profile



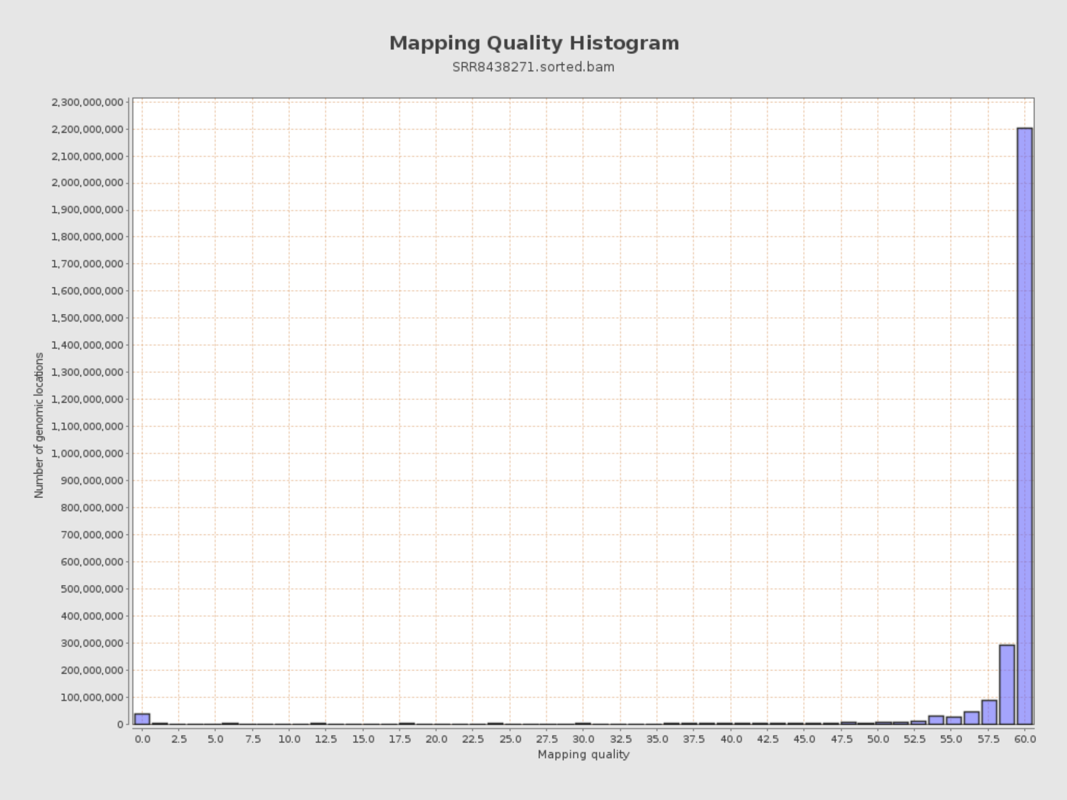
11. Results : Homopolymer Indels



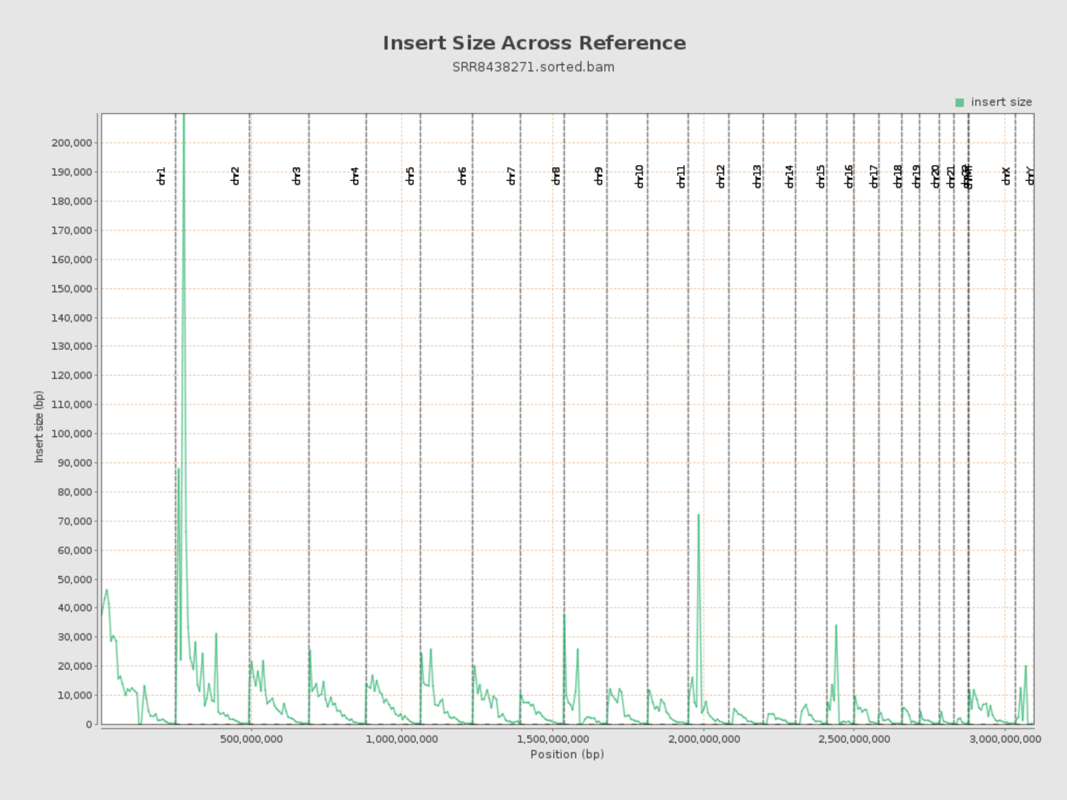
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram