Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:29:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237613.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_SRR6237613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:29:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	709,723
Mapped reads	499,674 / 70.4%
Unmapped reads	210,049 / 29.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,302 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	49,322 / 6.95%
Duplication rate	8.37%
Clipped reads	341,397 / 48.1%

2.2. ACGT Content

Number/percentage of A's	7,688,532 / 25.46%
Number/percentage of C's	5,127,631 / 16.98%
Number/percentage of T's	10,016,782 / 33.17%
Number/percentage of G's	7,313,626 / 24.22%
Number/percentage of N's	53,843 / 0.18%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.142

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

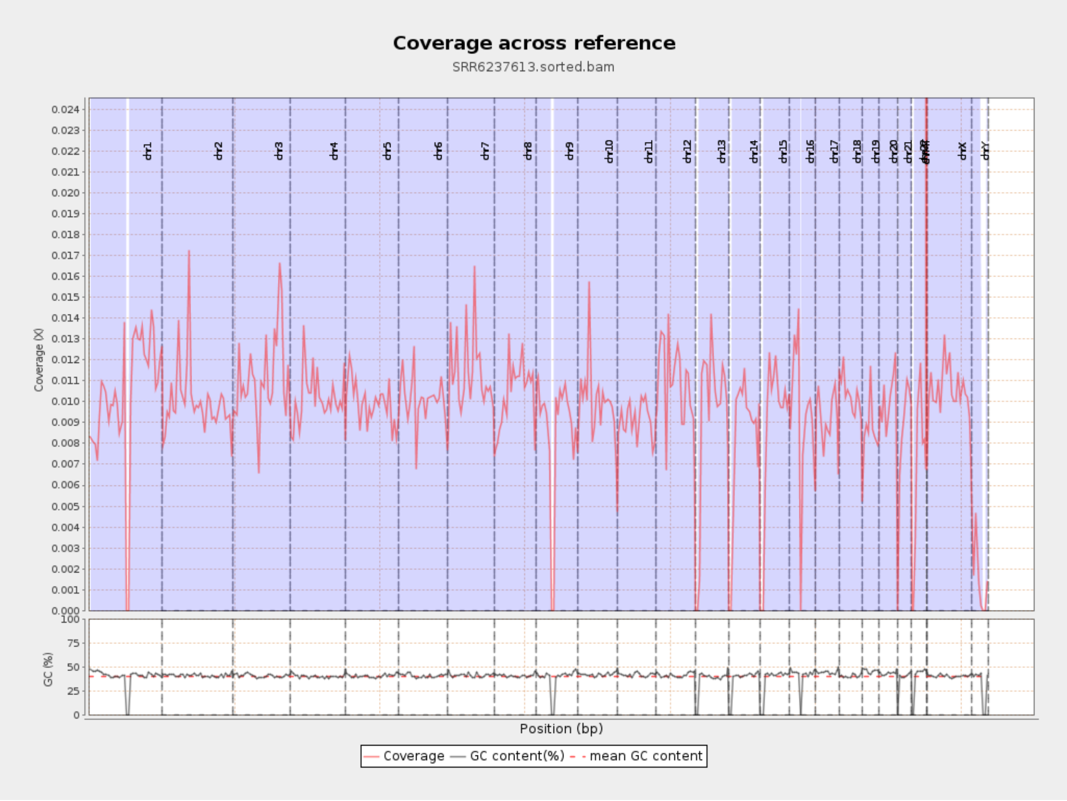
General error rate	1.02%
Mismatches	303,567
Insertions	2,576
Mapped reads with at least one insertion	0.51%
Deletions	11,579
Mapped reads with at least one deletion	2.29%
Homopolymer indels	48.6%

2.6. Chromosome stats

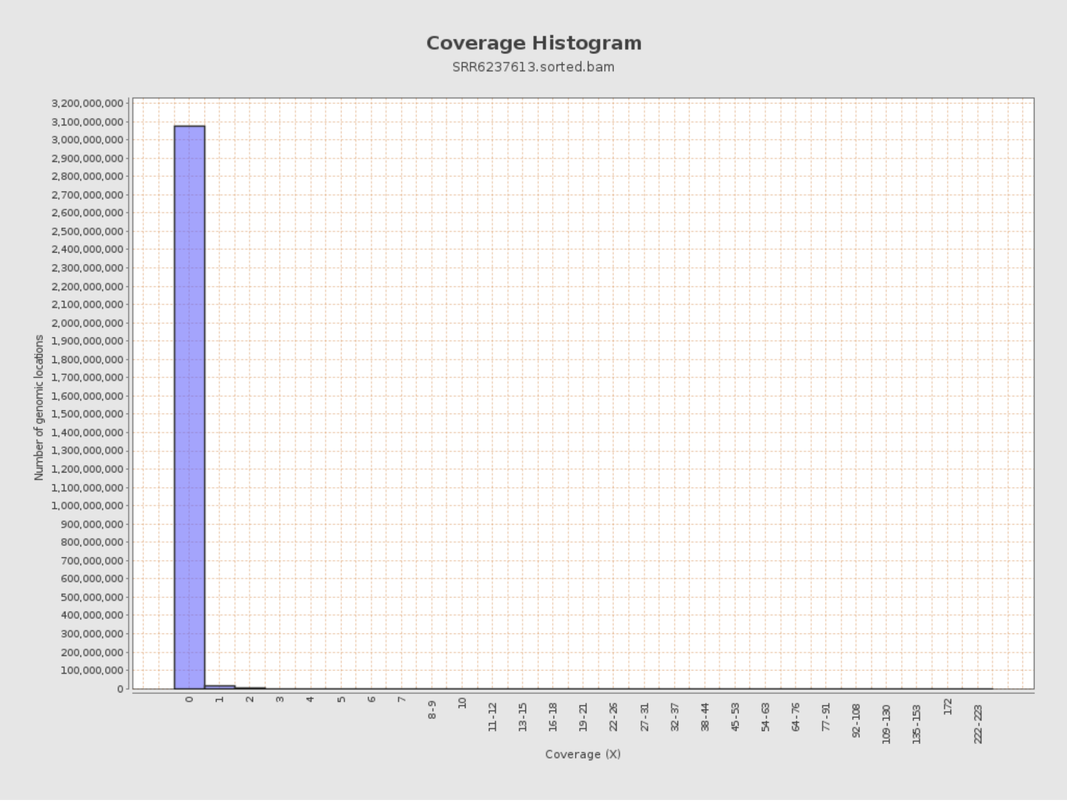
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2554713	0.0102	0.1739
chr2	243199373	2437135	0.01	0.1643
chr3	198022430	2199437	0.0111	0.1365
chr4	191154276	1942448	0.0102	0.1307
chr5	180915260	1793722	0.0099	0.1271
chr6	171115067	1730289	0.0101	0.1367
chr7	159138663	1822554	0.0115	0.1586

chr8	146364022	1524282	0.0104	0.1411
chr9	141213431	1203927	0.0085	0.1267
chr10	135534747	1367205	0.0101	0.1393
chr11	135006516	1217552	0.009	0.1324
chr12	133851895	1461563	0.0109	0.1361
chr13	115169878	1061898	0.0092	0.1249
chr14	107349540	865420	0.0081	0.1155
chr15	102531392	899522	0.0088	0.1215
chr16	90354753	844639	0.0093	0.1248
chr17	81195210	742049	0.0091	0.123
chr18	78077248	808574	0.0104	0.1978
chr19	59128983	514638	0.0087	0.1396
chr20	63025520	631417	0.01	0.1285
chr21	48129895	402146	0.0084	0.117
chr22	51304566	332373	0.0065	0.1003
chrMT	16571	141668	8.5492	6.4609
chrX	155270560	1630164	0.0105	0.1328
chrY	59373566	89257	0.0015	0.0494

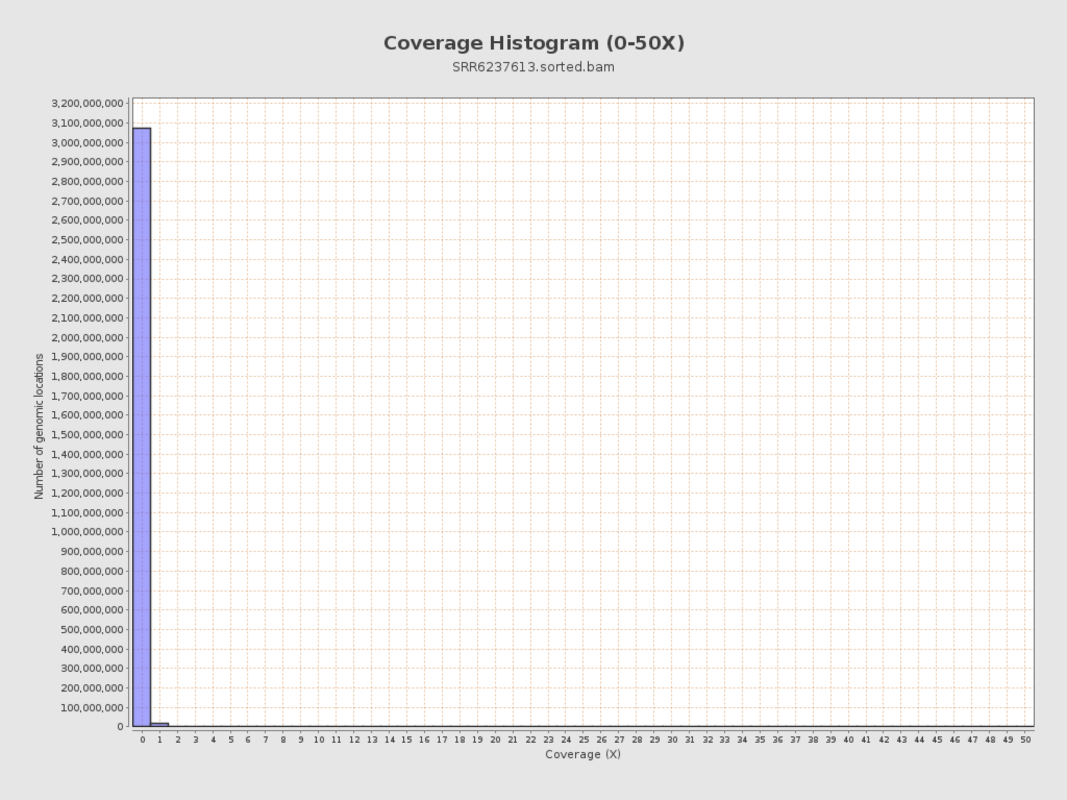
3. Results : Coverage across reference



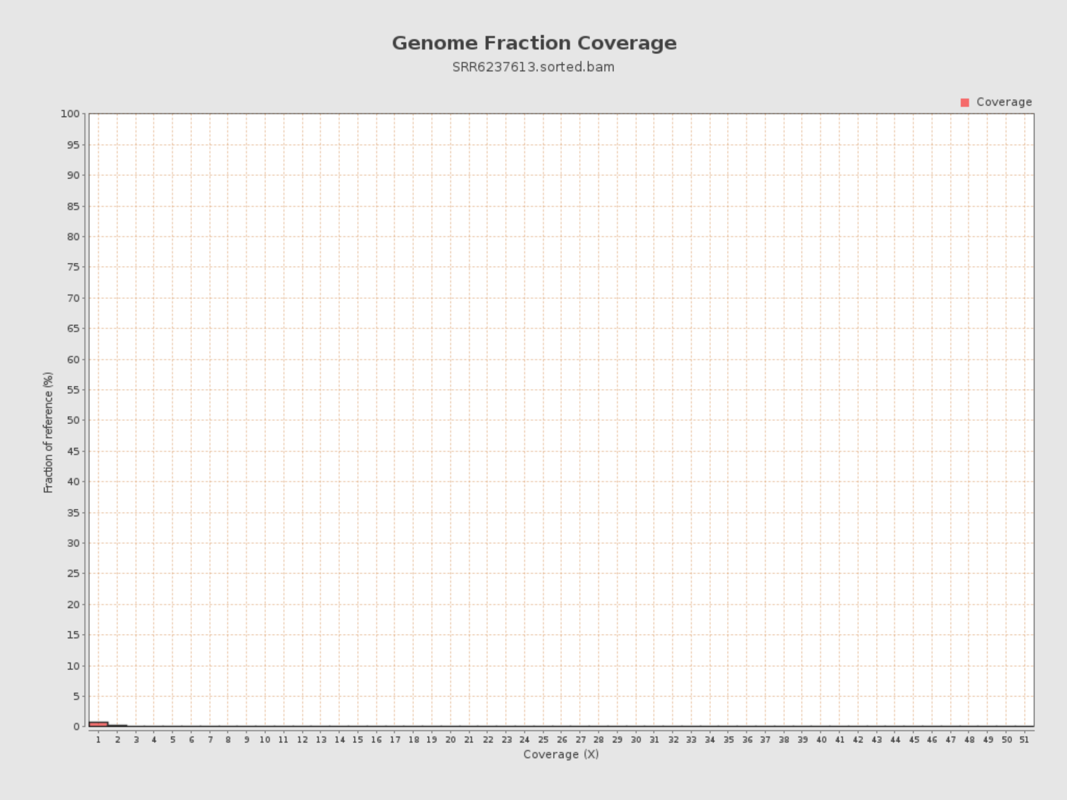
4. Results : Coverage Histogram



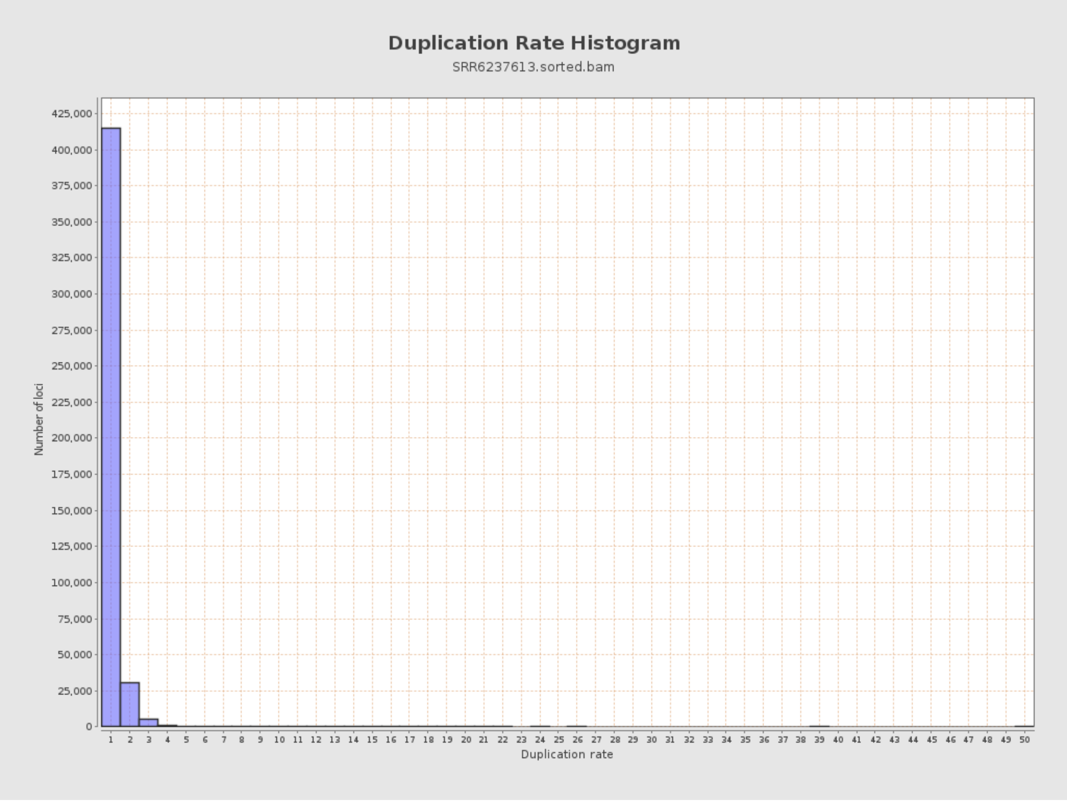
5. Results : Coverage Histogram (0-50X)



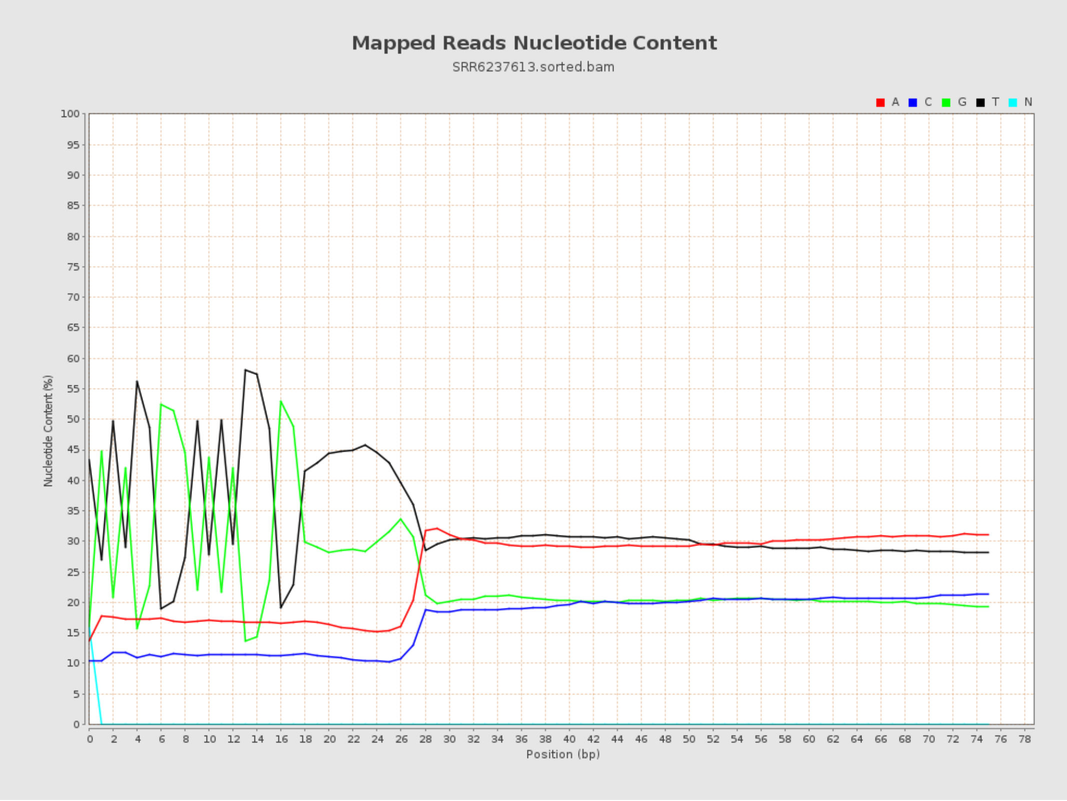
6. Results : Genome Fraction Coverage



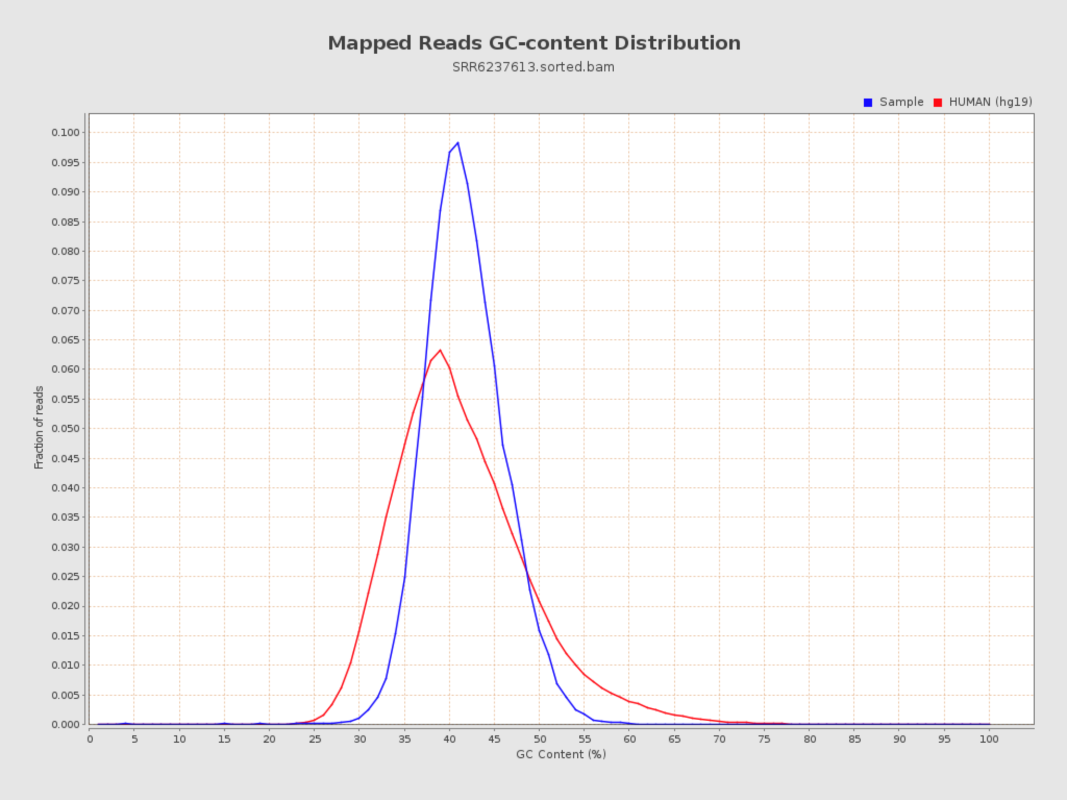
7. Results : Duplication Rate Histogram



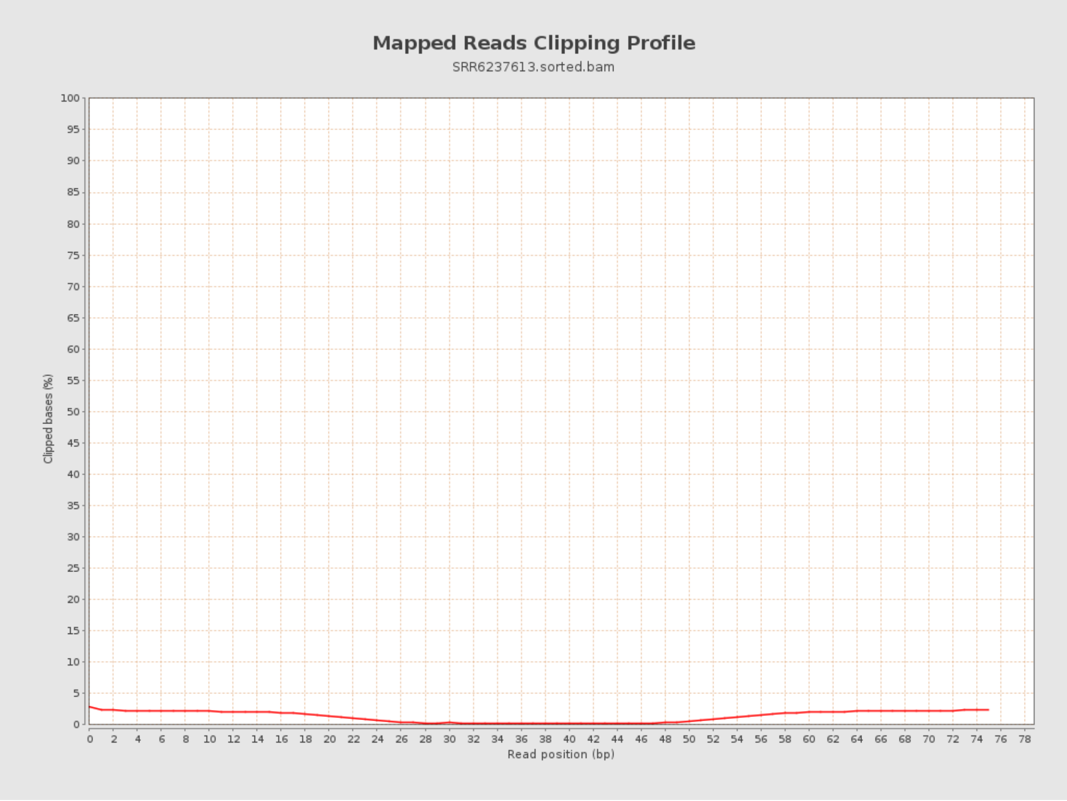
8. Results : Mapped Reads Nucleotide Content



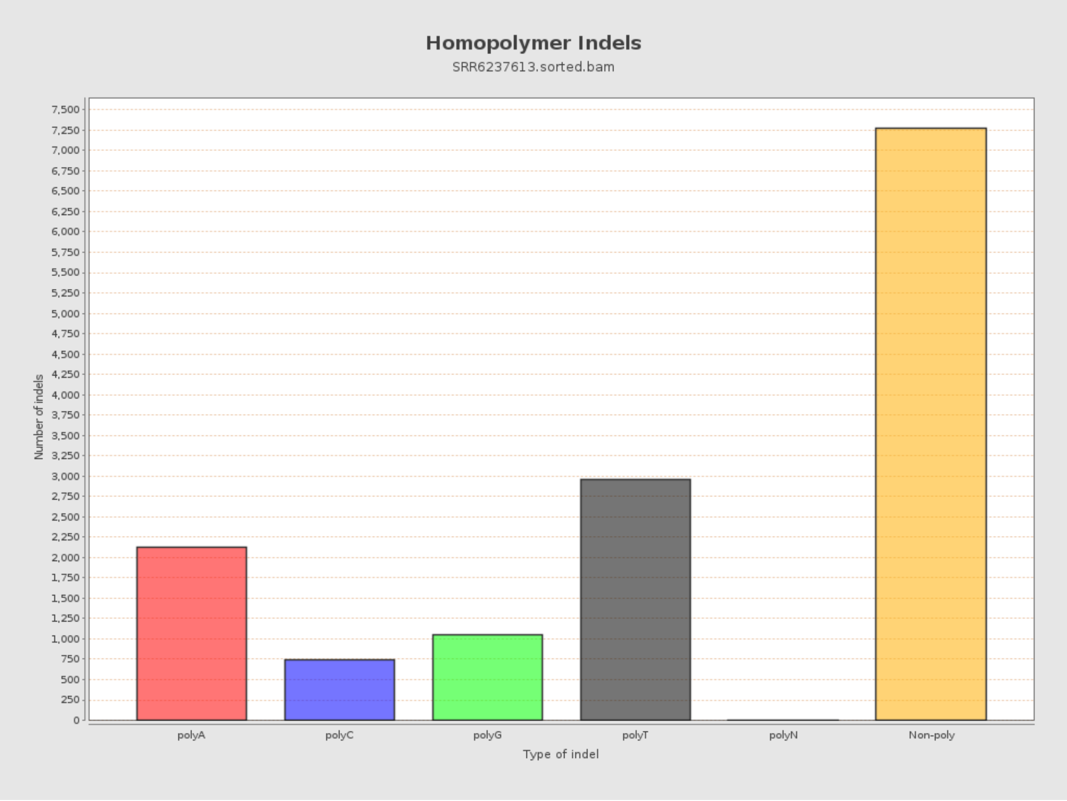
9. Results : Mapped Reads GC-content Distribution



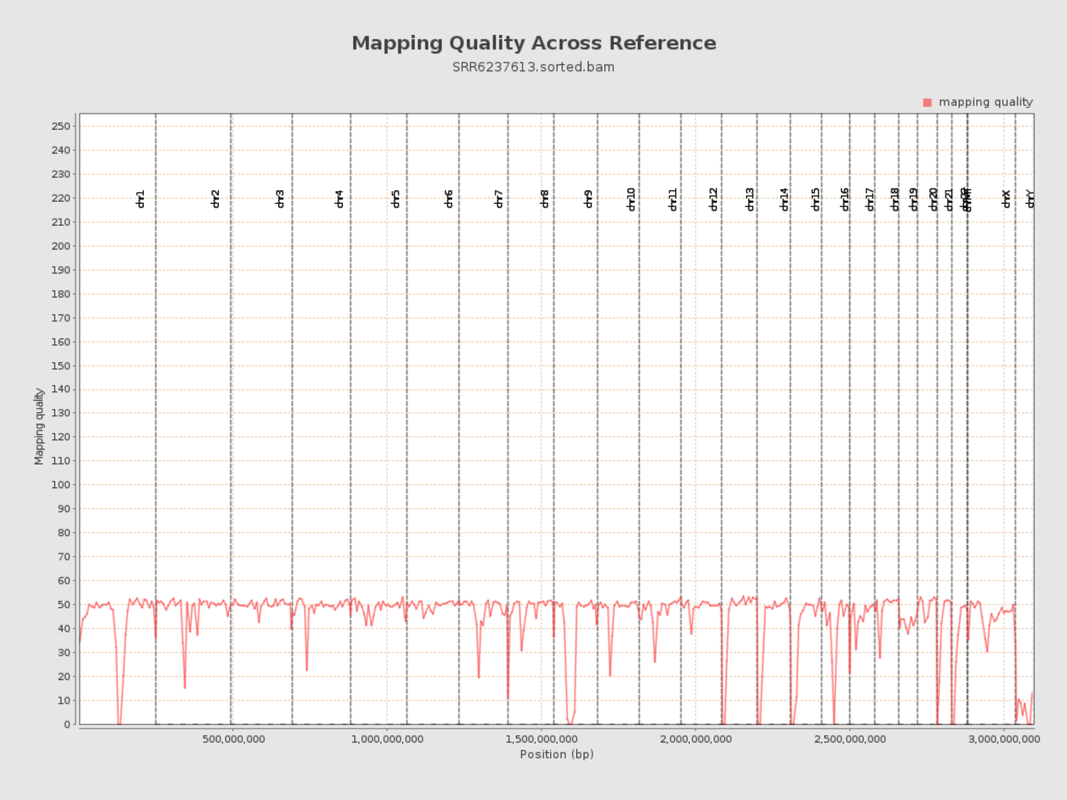
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram