Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:32:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237588.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_SRR6237588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237588.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:31:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,280,309
Mapped reads	1,029,487 / 80.41%
Unmapped reads	250,822 / 19.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,518 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	56,101 / 4.38%
Duplication rate	3.87%
Clipped reads	640,783 / 50.05%

2.2. ACGT Content

Number/percentage of A's	16,702,901 / 25.85%
Number/percentage of C's	11,643,156 / 18.02%
Number/percentage of T's	19,784,842 / 30.62%
Number/percentage of G's	16,431,671 / 25.43%
Number/percentage of N's	41,536 / 0.06%
GC Percentage	43.46%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.2292

2.4. Mapping Quality

Mean Mapping Quality	40.06

2.5. Mismatches and indels

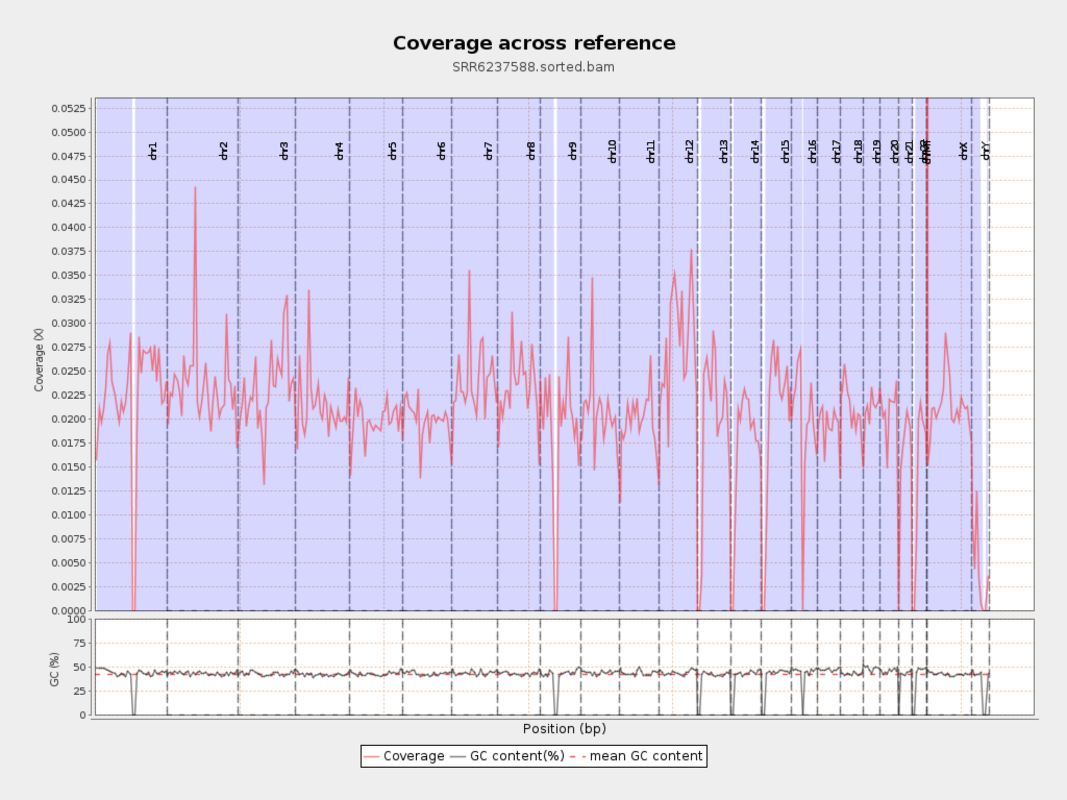
General error rate	1.02%
Mismatches	644,616
Insertions	6,264
Mapped reads with at least one insertion	0.6%
Deletions	23,693
Mapped reads with at least one deletion	2.27%
Homopolymer indels	45.99%

2.6. Chromosome stats

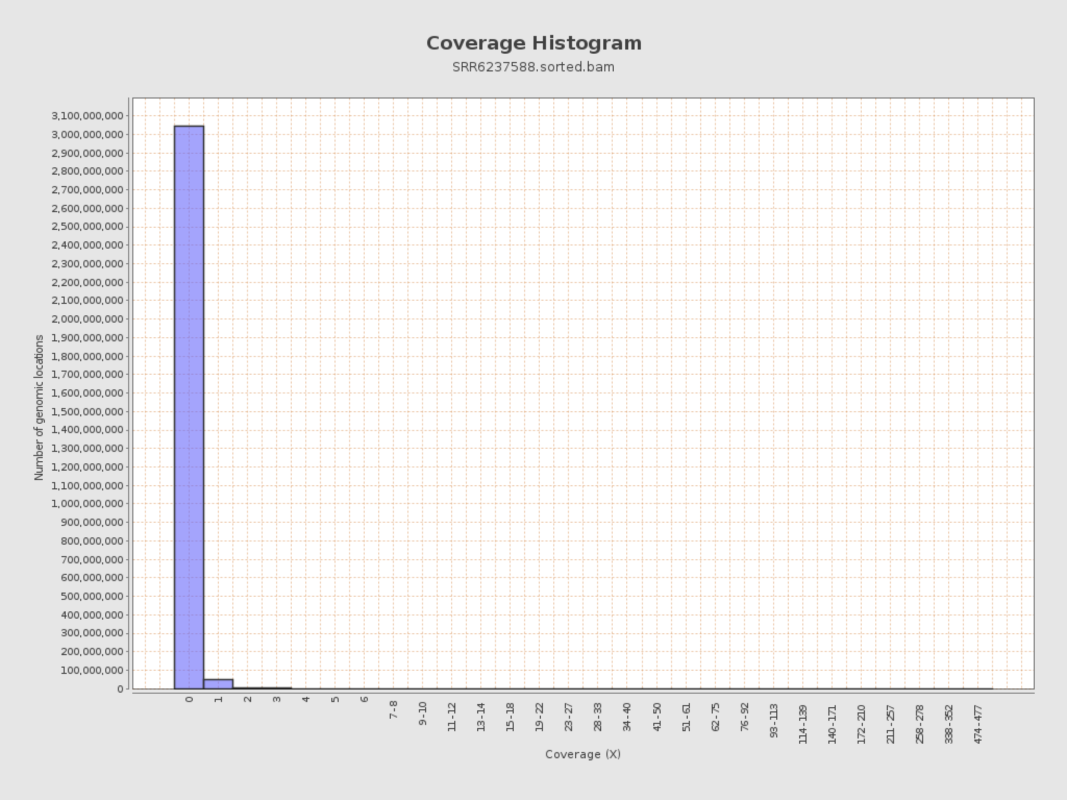
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5548460	0.0223	0.274
chr2	243199373	5732475	0.0236	0.3314
chr3	198022430	4555218	0.023	0.1902
chr4	191154276	4076785	0.0213	0.1913
chr5	180915260	3612603	0.02	0.1713
chr6	171115067	3398560	0.0199	0.1881
chr7	159138663	3823635	0.024	0.3179

chr8	146364022	3407391	0.0233	0.2238
chr9	141213431	2618045	0.0185	0.2459
chr10	135534747	2788492	0.0206	0.2186
chr11	135006516	2691875	0.0199	0.2361
chr12	133851895	3775632	0.0282	0.2196
chr13	115169878	2184749	0.019	0.1732
chr14	107349540	1795534	0.0167	0.1762
chr15	102531392	2020333	0.0197	0.1808
chr16	90354753	1751968	0.0194	0.1913
chr17	81195210	1571970	0.0194	0.182
chr18	78077248	1658355	0.0212	0.3391
chr19	59128983	1248298	0.0211	0.2231
chr20	63025520	1293976	0.0205	0.1827
chr21	48129895	781198	0.0162	0.1687
chr22	51304566	703986	0.0137	0.1468
chrMT	16571	50776	3.0641	2.7115
chrX	155270560	3317526	0.0214	0.1919
chrY	59373566	235306	0.004	0.1046

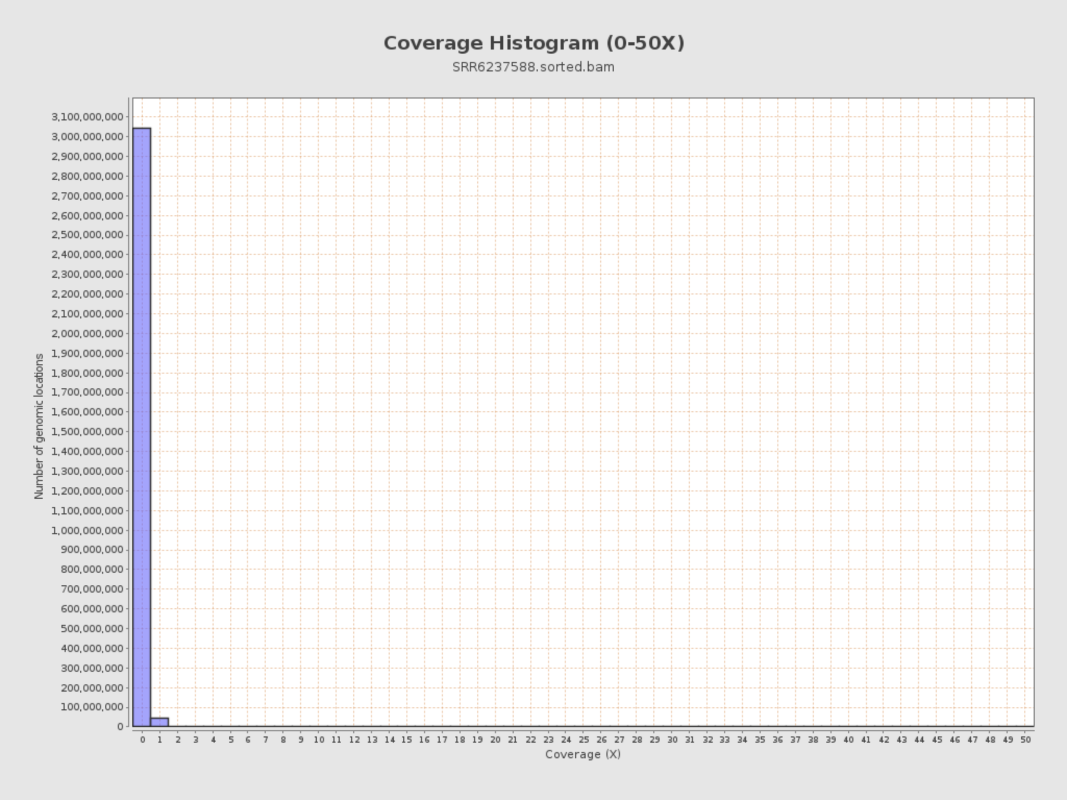
3. Results : Coverage across reference



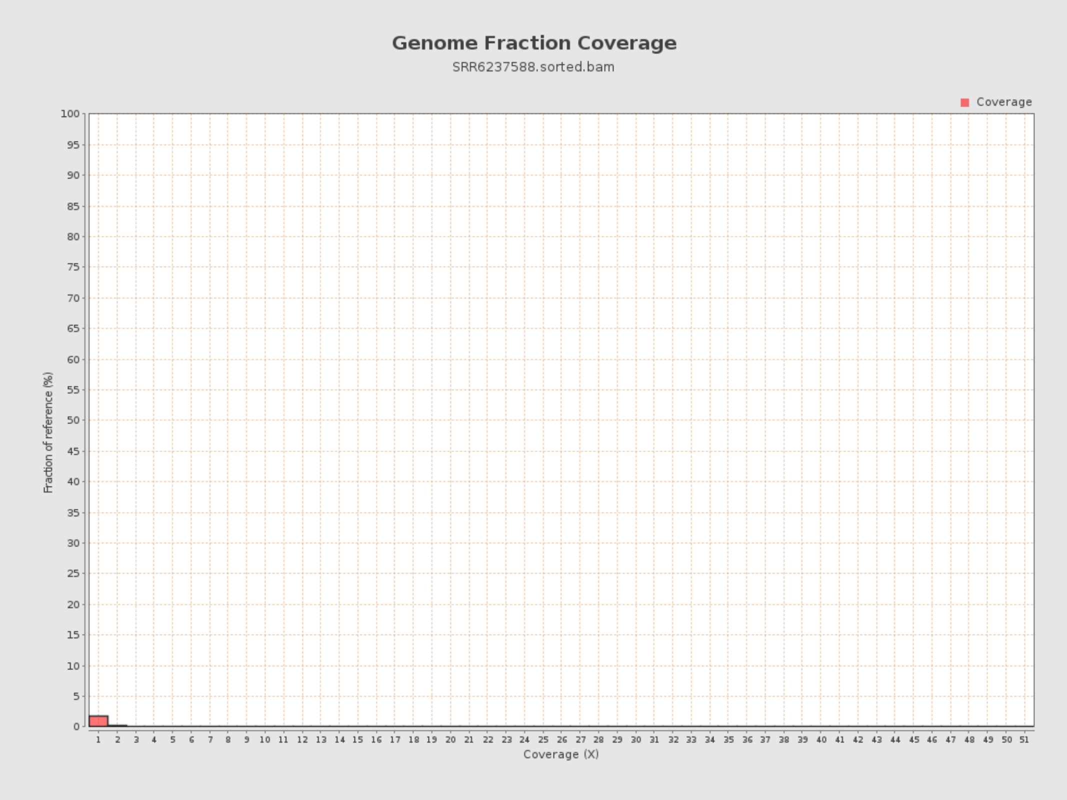
4. Results : Coverage Histogram



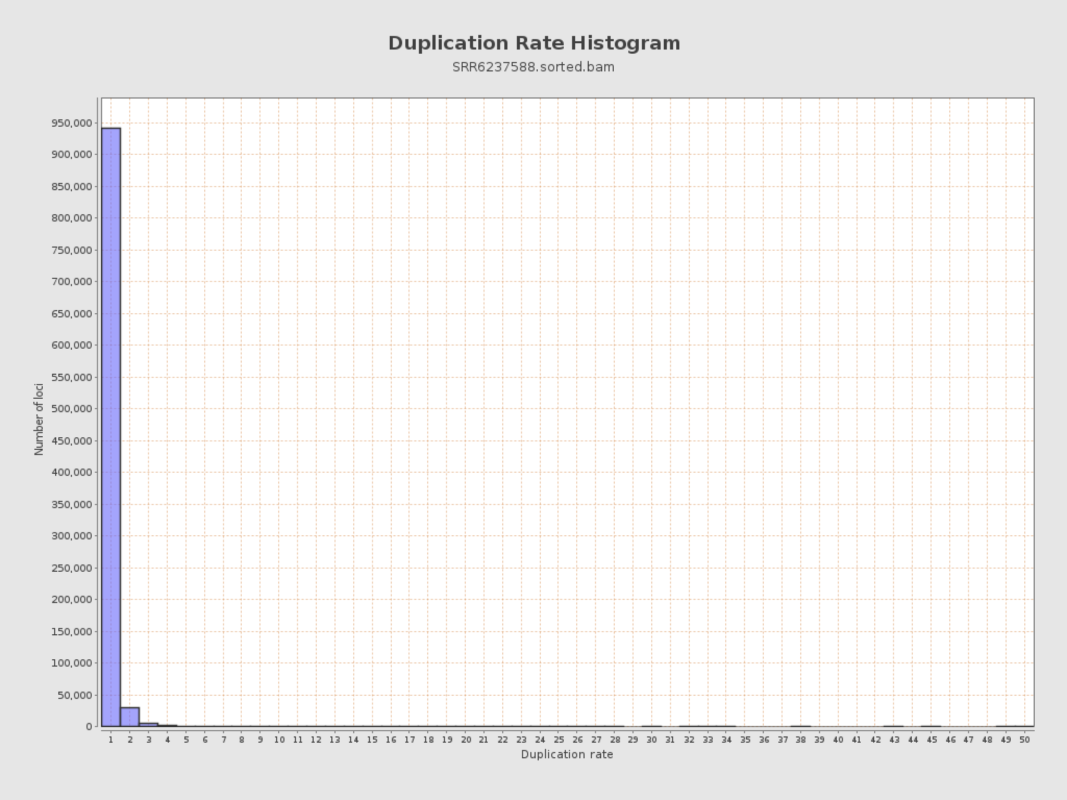
5. Results : Coverage Histogram (0-50X)



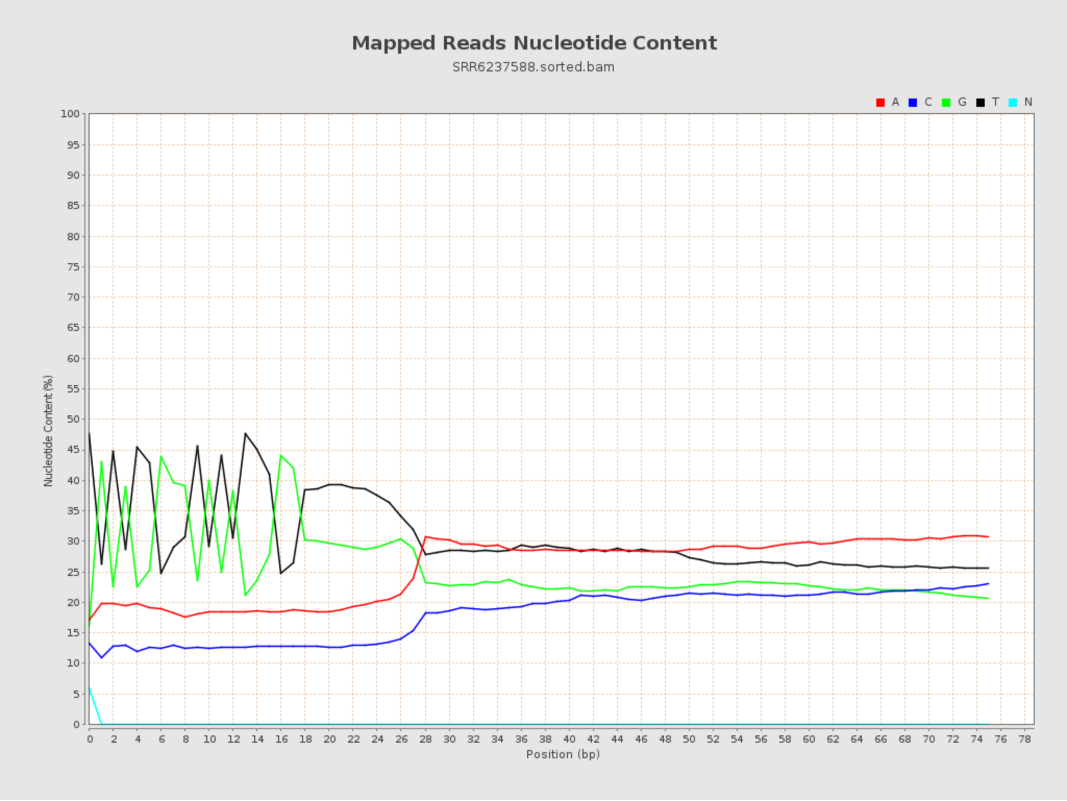
6. Results : Genome Fraction Coverage



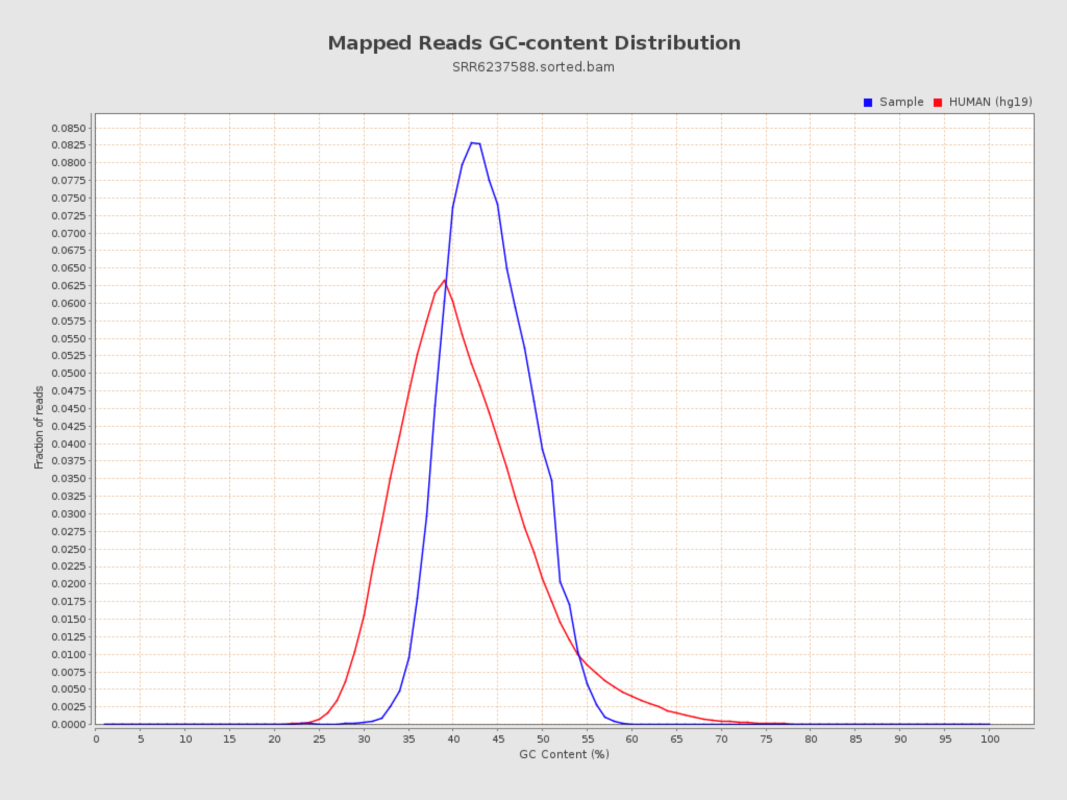
7. Results : Duplication Rate Histogram



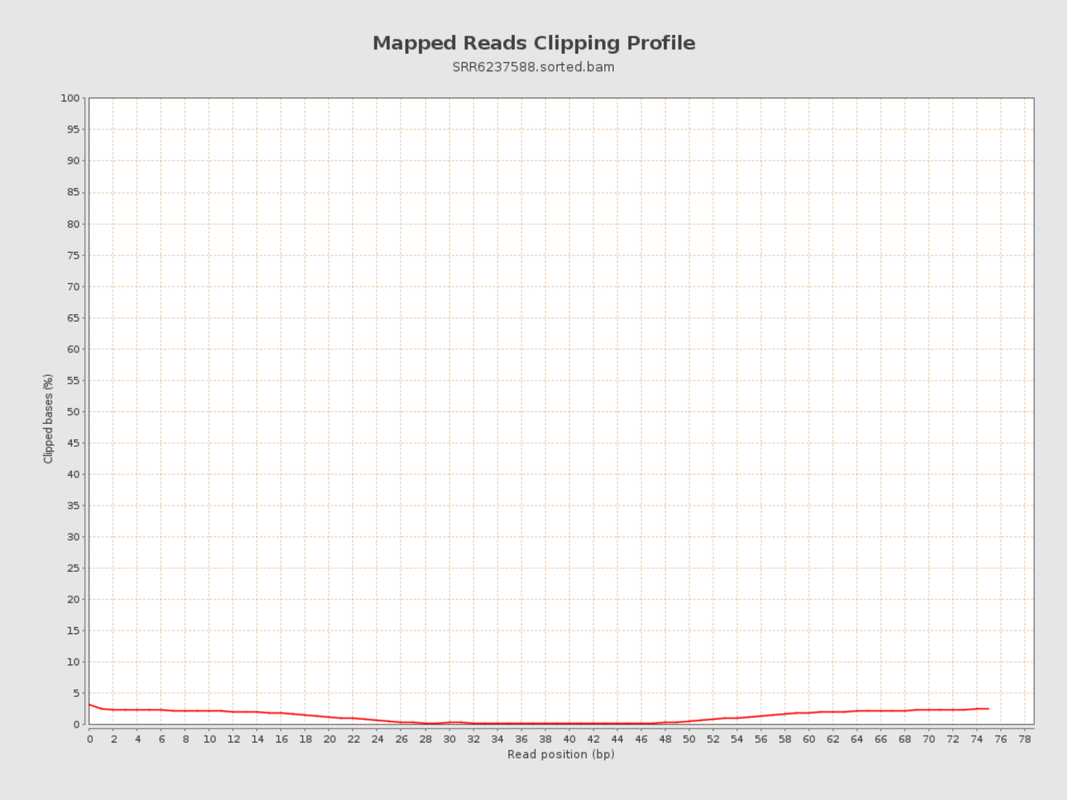
8. Results : Mapped Reads Nucleotide Content



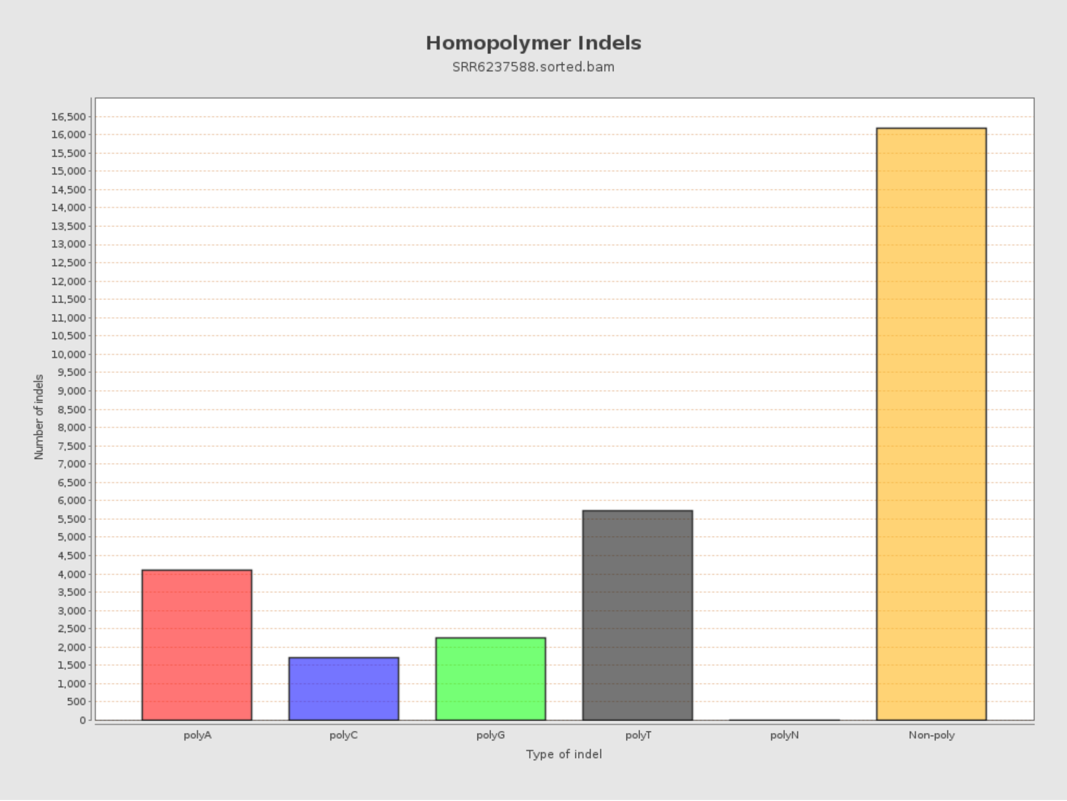
9. Results : Mapped Reads GC-content Distribution



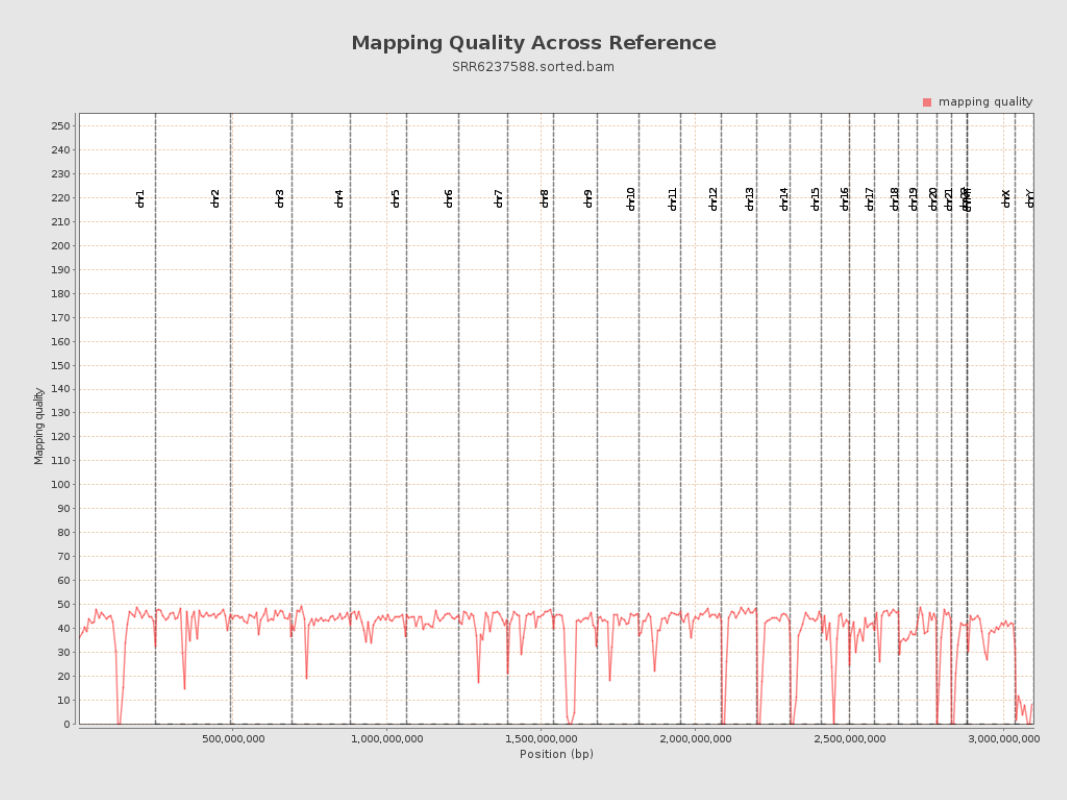
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram