Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:20:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237608.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_SRR6237608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:20:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,478,962
Mapped reads	1,305,436 / 88.27%
Unmapped reads	173,526 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,085 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	50,264 / 3.4%
Duplication rate	3.05%
Clipped reads	714,739 / 48.33%

2.2. ACGT Content

Number/percentage of A's	22,241,761 / 26.73%
Number/percentage of C's	14,224,576 / 17.1%
Number/percentage of T's	27,435,834 / 32.97%
Number/percentage of G's	19,158,441 / 23.03%
Number/percentage of N's	144,242 / 0.17%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2641

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

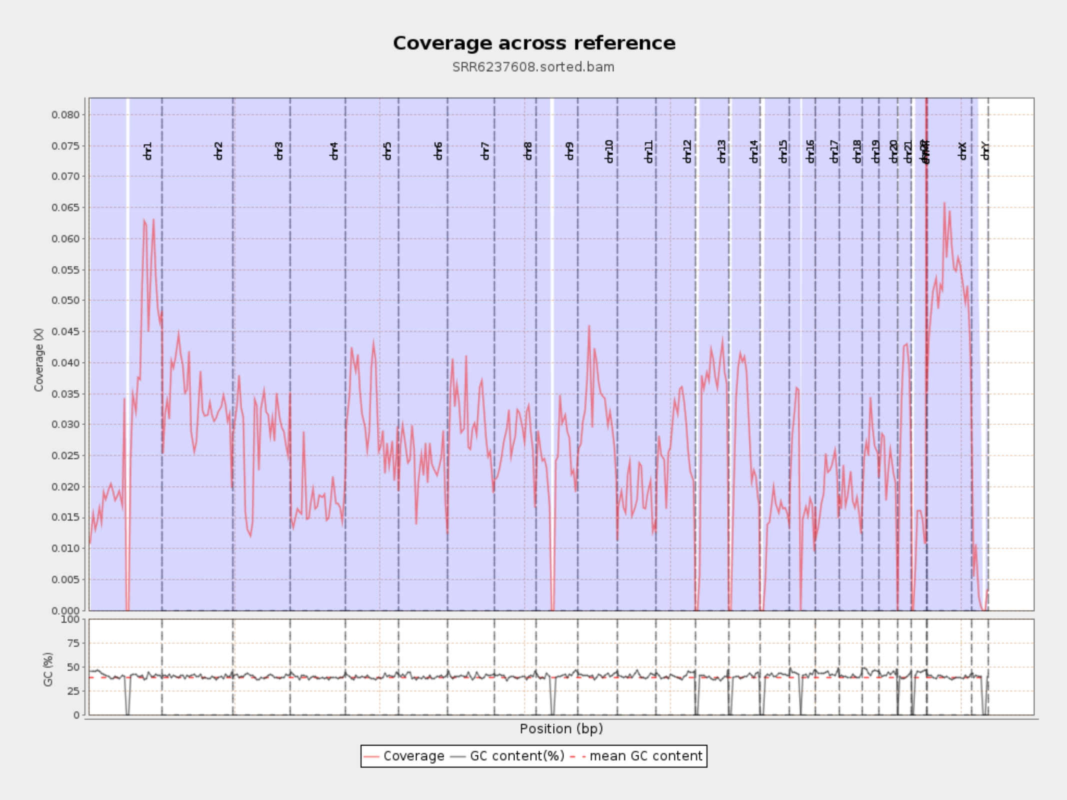
General error rate	0.91%
Mismatches	743,689
Insertions	7,071
Mapped reads with at least one insertion	0.54%
Deletions	31,729
Mapped reads with at least one deletion	2.4%
Homopolymer indels	45.14%

2.6. Chromosome stats

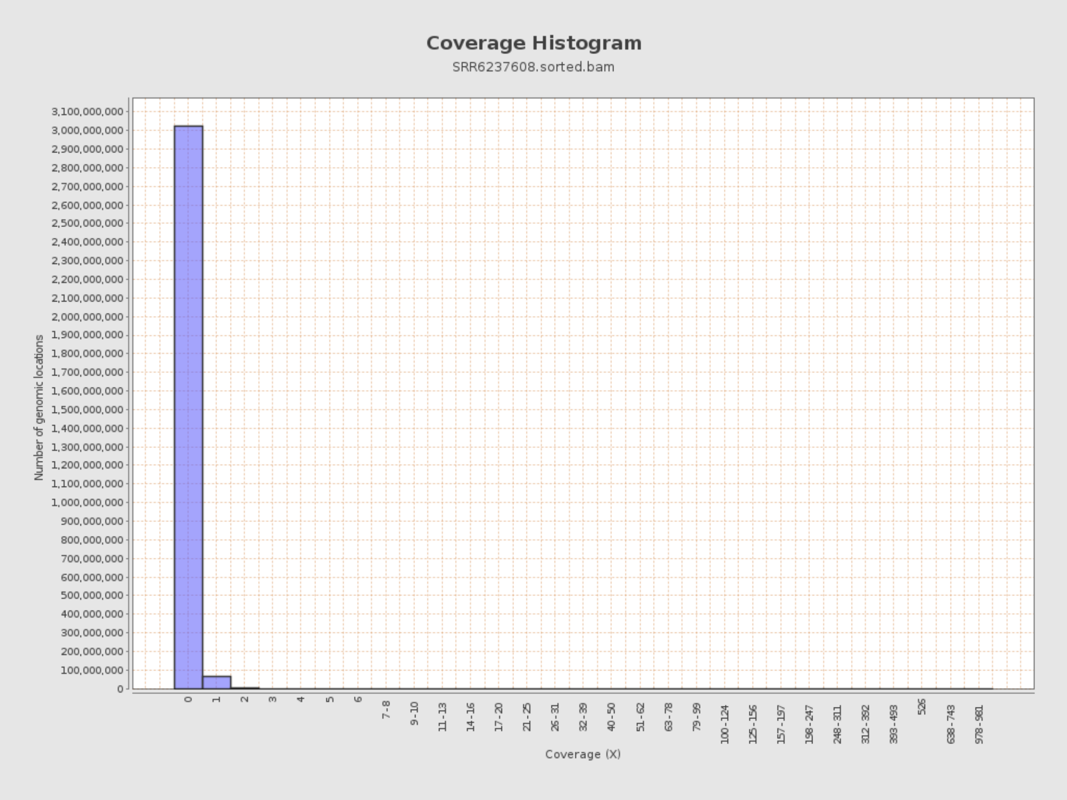
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7406966	0.0297	0.3912
chr2	243199373	8186565	0.0337	0.4703
chr3	198022430	5589719	0.0282	0.1846
chr4	191154276	3278718	0.0172	0.1546
chr5	180915260	5722668	0.0316	0.196
chr6	171115067	4070038	0.0238	0.2312
chr7	159138663	4922042	0.0309	0.2972

chr8	146364022	3987550	0.0272	0.3399
chr9	141213431	3219937	0.0228	0.2033
chr10	135534747	4493405	0.0332	0.2519
chr11	135006516	2445575	0.0181	0.1645
chr12	133851895	3657780	0.0273	0.1826
chr13	115169878	3688170	0.032	0.2024
chr14	107349540	2806243	0.0261	0.1832
chr15	102531392	1351230	0.0132	0.1303
chr16	90354753	1836250	0.0203	0.182
chr17	81195210	1629335	0.0201	0.1586
chr18	78077248	1411944	0.0181	0.2881
chr19	59128983	1586123	0.0268	0.2931
chr20	63025520	1451414	0.023	0.1726
chr21	48129895	1536356	0.0319	0.2011
chr22	51304566	521469	0.0102	0.1085
chrMT	16571	5020	0.3029	0.6301
chrX	155270560	8186826	0.0527	0.268
chrY	59373566	266277	0.0045	0.1008

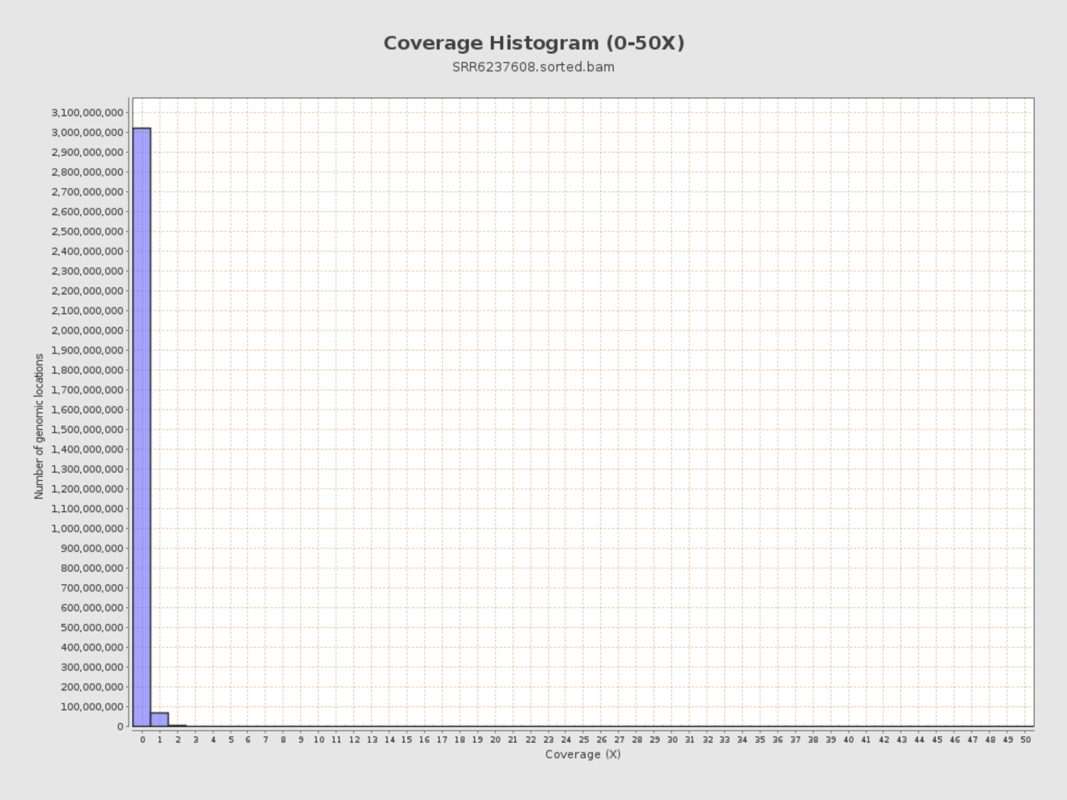
3. Results : Coverage across reference



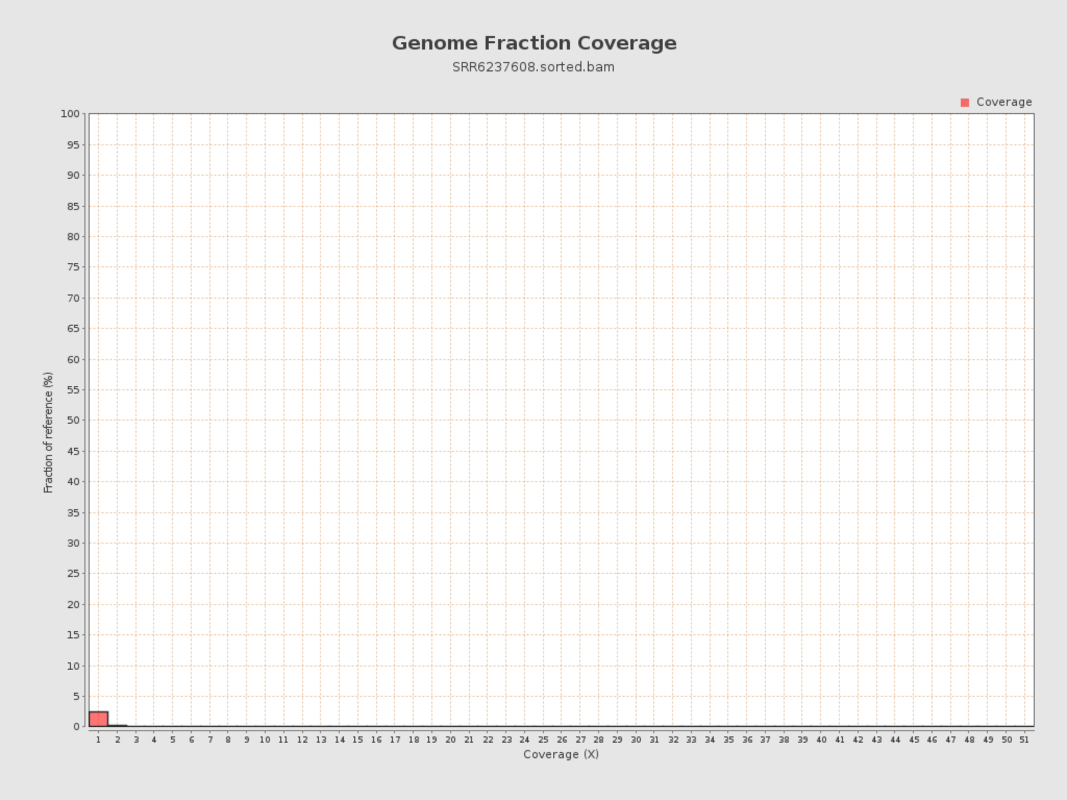
4. Results : Coverage Histogram



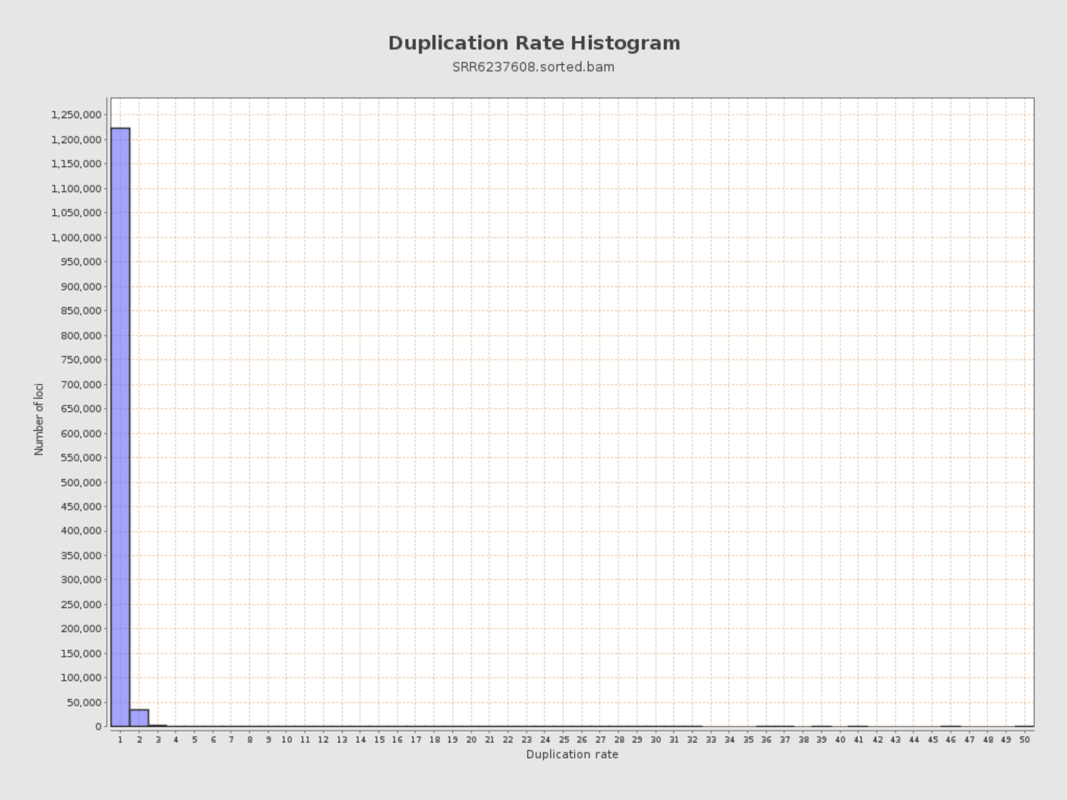
5. Results : Coverage Histogram (0-50X)



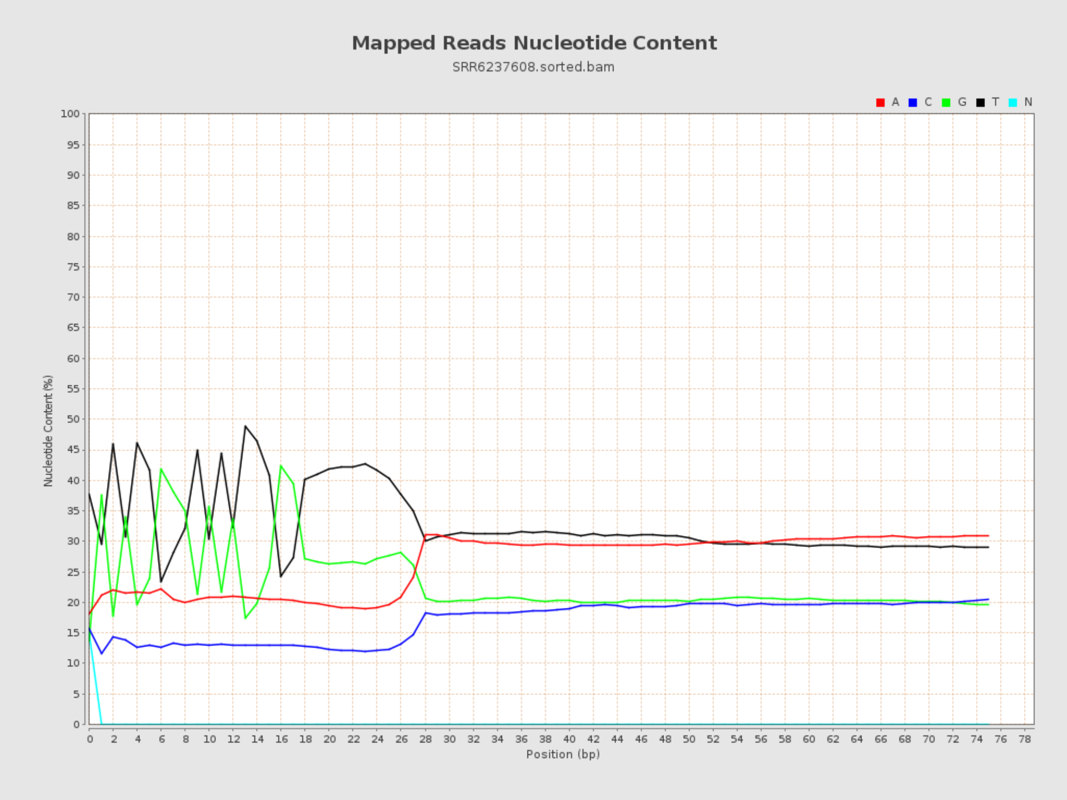
6. Results : Genome Fraction Coverage



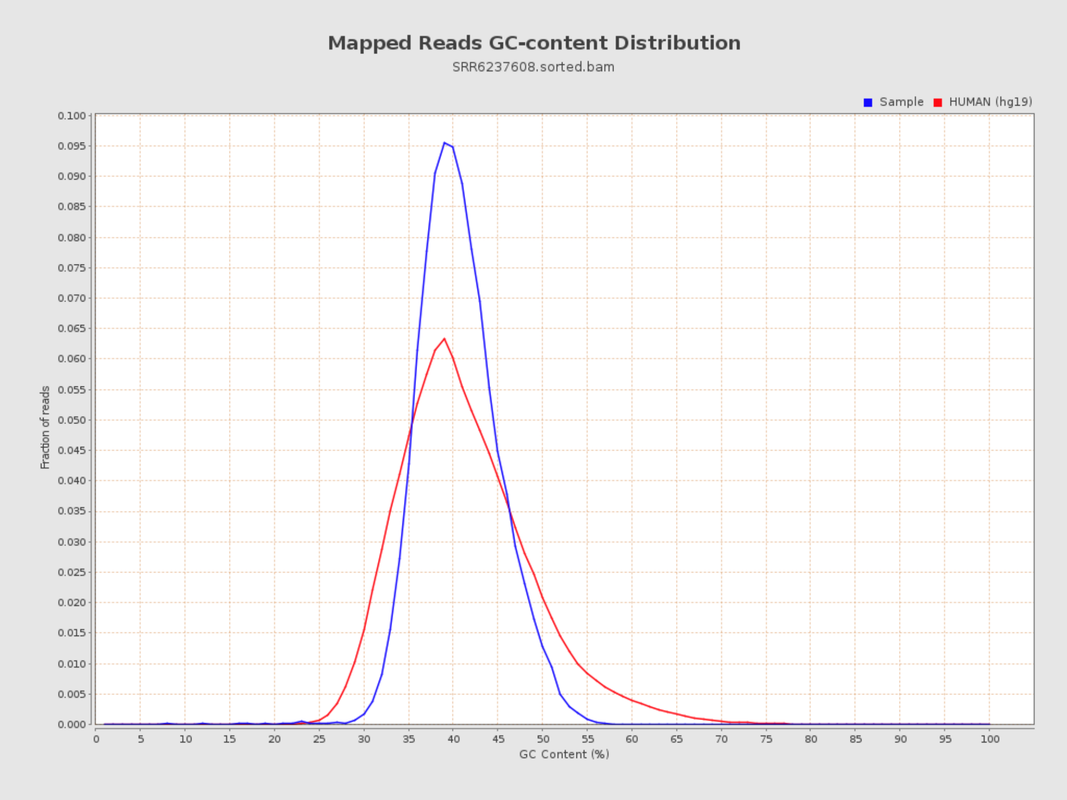
7. Results : Duplication Rate Histogram



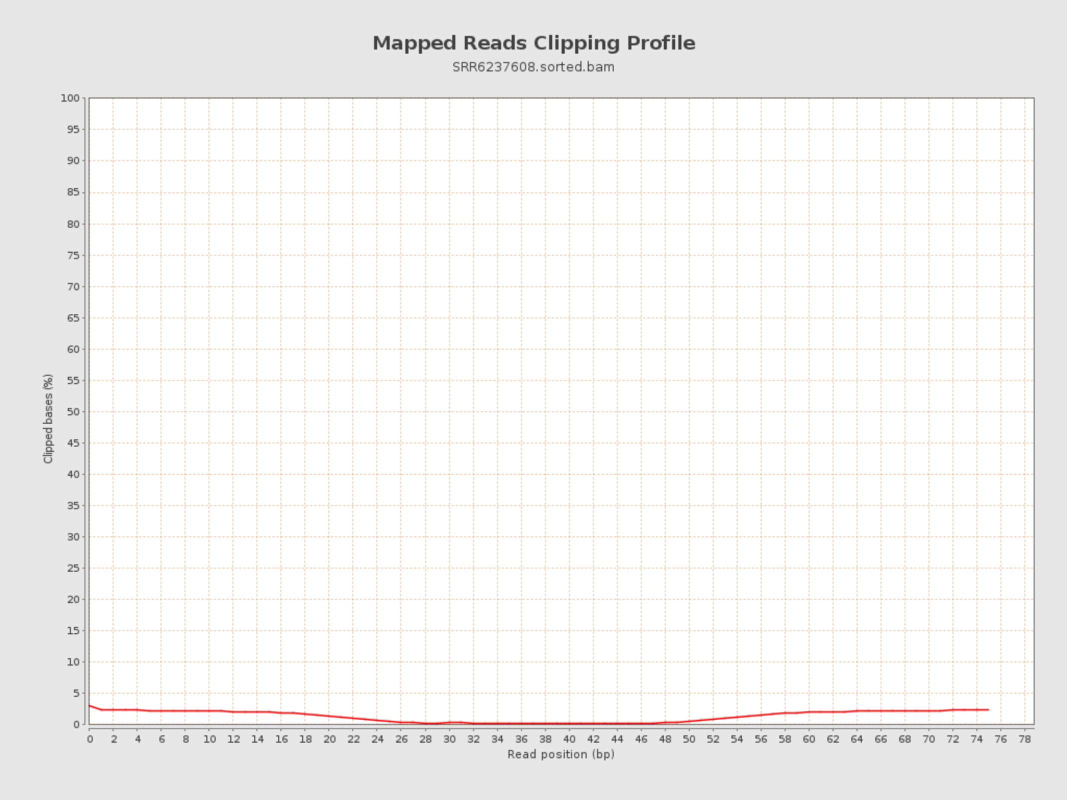
8. Results : Mapped Reads Nucleotide Content



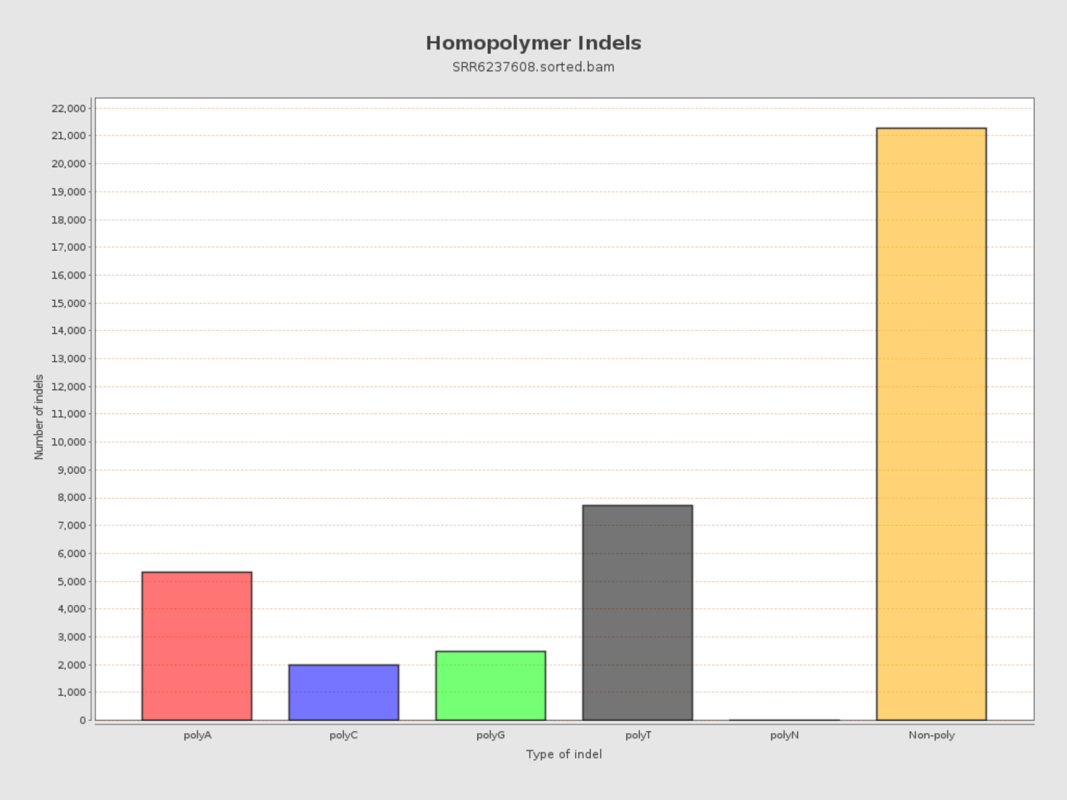
9. Results : Mapped Reads GC-content Distribution



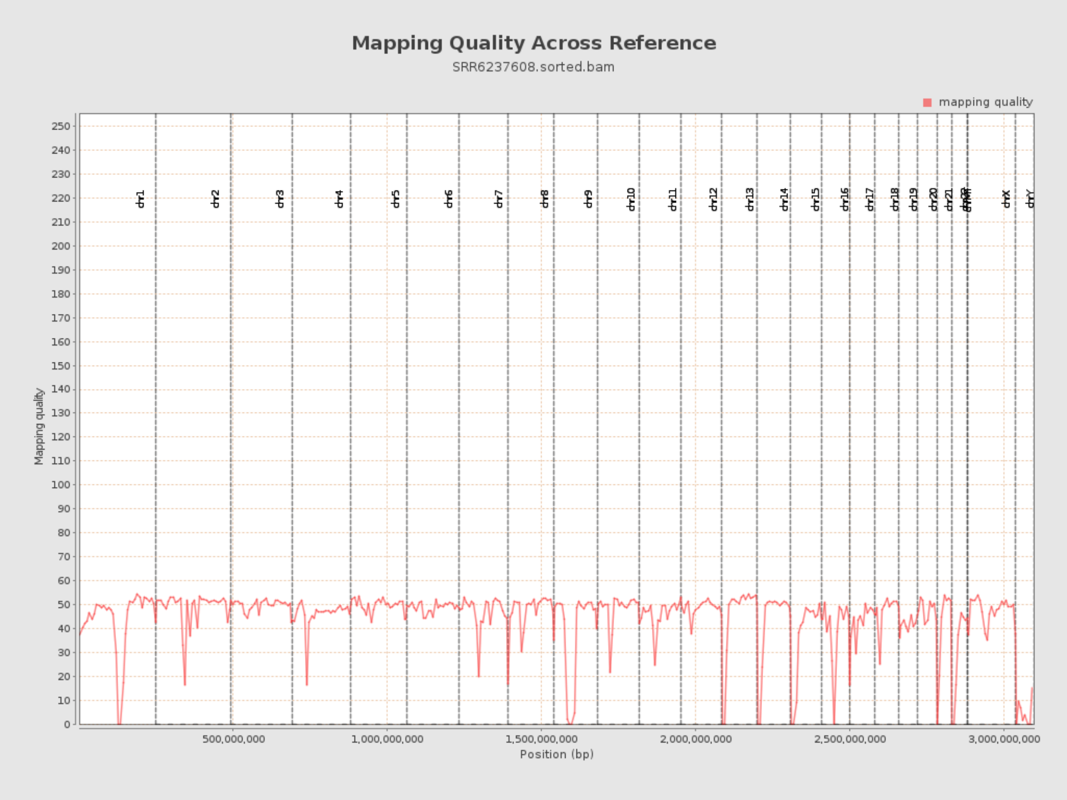
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram