Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:32:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237804.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_SRR6237804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:32:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,173
Mapped reads	1,450,250 / 58.17%
Unmapped reads	1,042,923 / 41.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,746 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	120,836 / 4.85%
Duplication rate	7.02%
Clipped reads	898,768 / 36.05%

2.2. ACGT Content

Number/percentage of A's	24,324,941 / 27.1%
Number/percentage of C's	17,542,755 / 19.54%
Number/percentage of T's	27,192,987 / 30.29%
Number/percentage of G's	20,628,606 / 22.98%
Number/percentage of N's	75,628 / 0.08%
GC Percentage	42.52%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2853

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

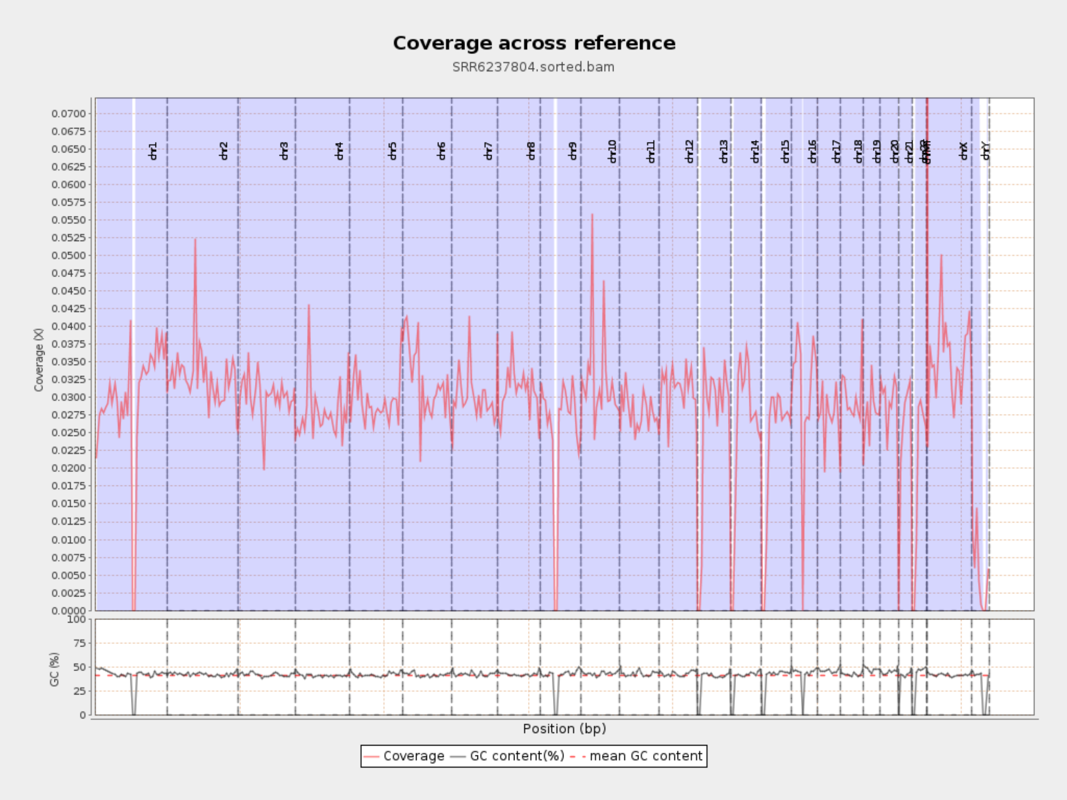
General error rate	0.85%
Mismatches	747,492
Insertions	6,566
Mapped reads with at least one insertion	0.45%
Deletions	24,853
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.49%

2.6. Chromosome stats

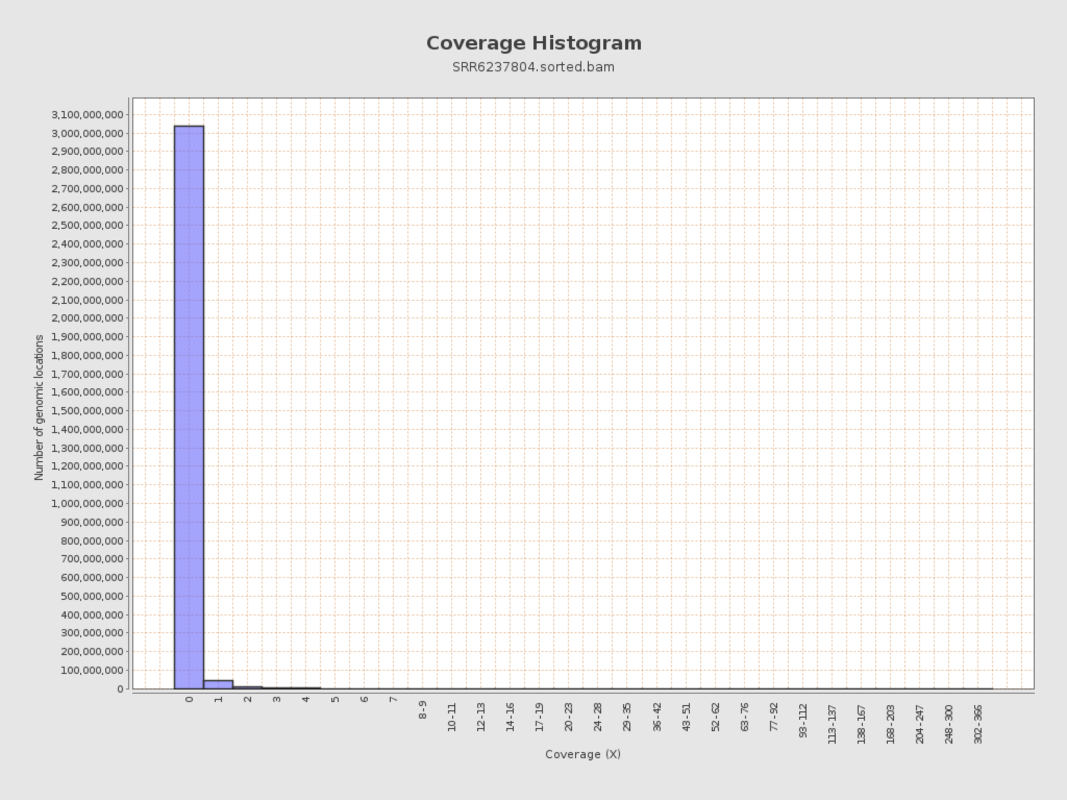
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7406518	0.0297	0.3929
chr2	243199373	8072697	0.0332	0.321
chr3	198022430	5964959	0.0301	0.2484
chr4	191154276	5358555	0.028	0.2484
chr5	180915260	5349545	0.0296	0.245
chr6	171115067	5503451	0.0322	0.279
chr7	159138663	4767646	0.03	0.3214

chr8	146364022	4530836	0.031	0.291
chr9	141213431	3572137	0.0253	0.2535
chr10	135534747	4427003	0.0327	0.3504
chr11	135006516	3790807	0.0281	0.2625
chr12	133851895	4171588	0.0312	0.2498
chr13	115169878	2991953	0.026	0.2267
chr14	107349540	2730469	0.0254	0.2337
chr15	102531392	2341755	0.0228	0.2141
chr16	90354753	2740982	0.0303	0.2632
chr17	81195210	2224786	0.0274	0.2467
chr18	78077248	2347689	0.0301	0.3997
chr19	59128983	1652627	0.0279	0.3168
chr20	63025520	1848205	0.0293	0.2505
chr21	48129895	1181954	0.0246	0.2265
chr22	51304566	987193	0.0192	0.2013
chrMT	16571	39237	2.3678	2.5137
chrX	155270560	5502064	0.0354	0.2808
chrY	59373566	300099	0.0051	0.1226

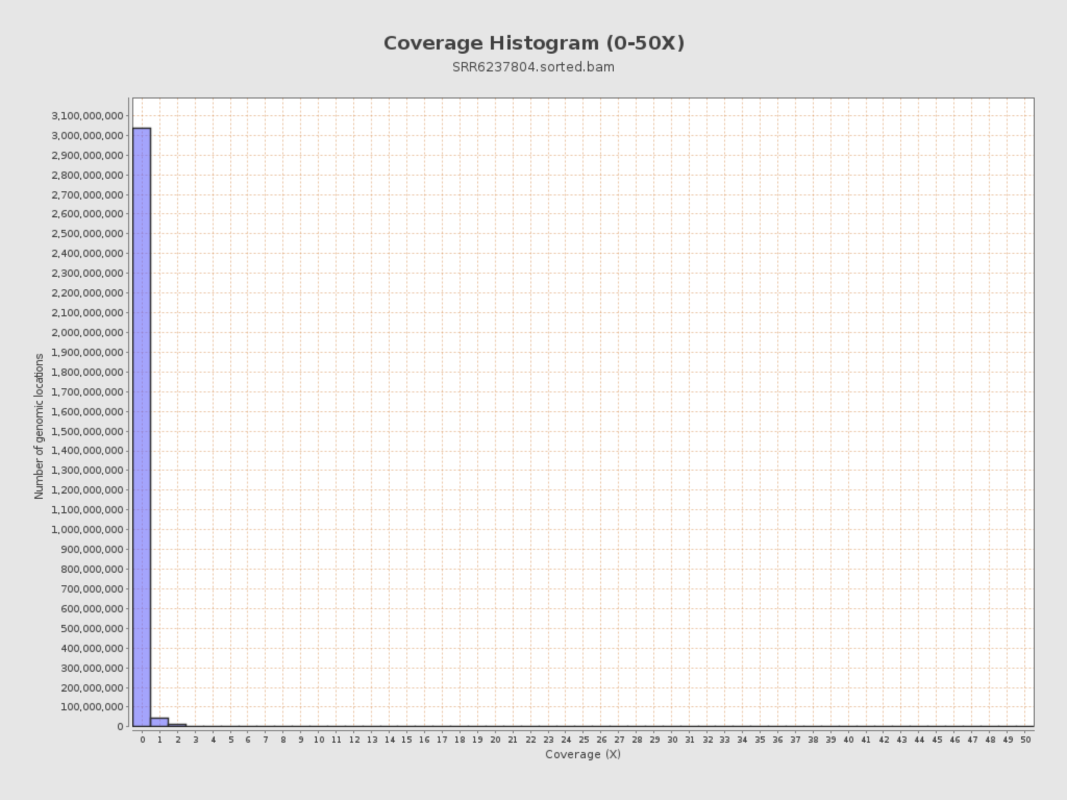
3. Results : Coverage across reference



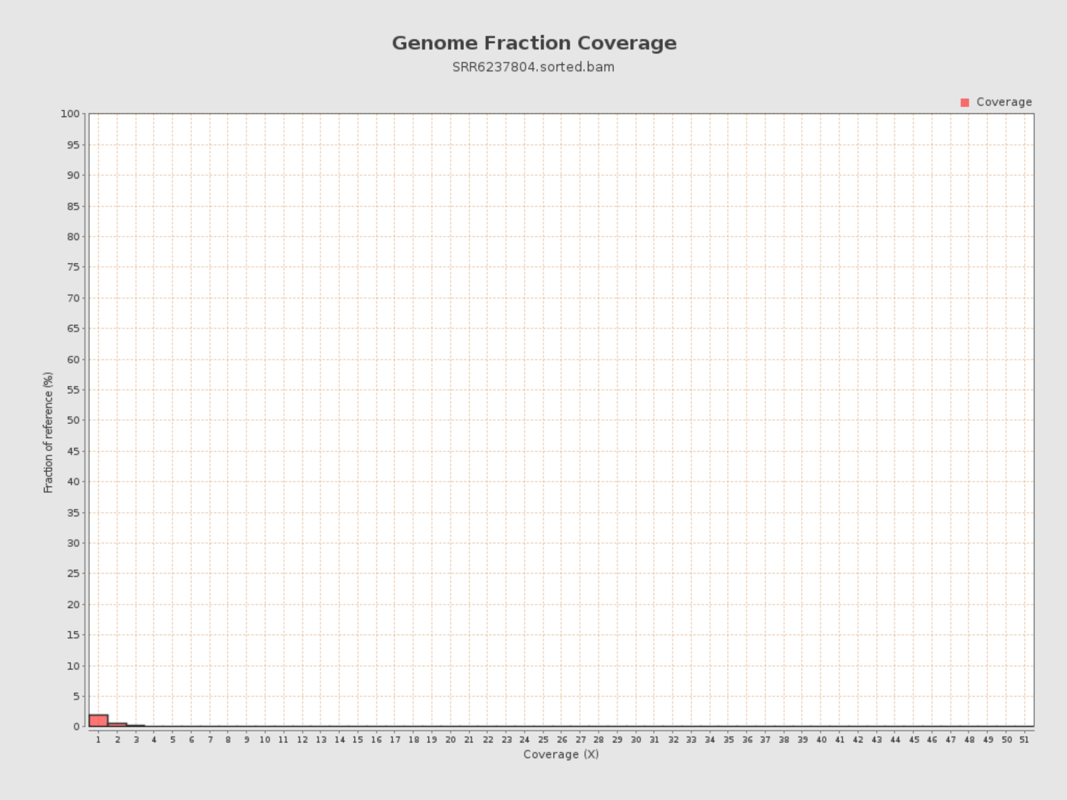
4. Results : Coverage Histogram



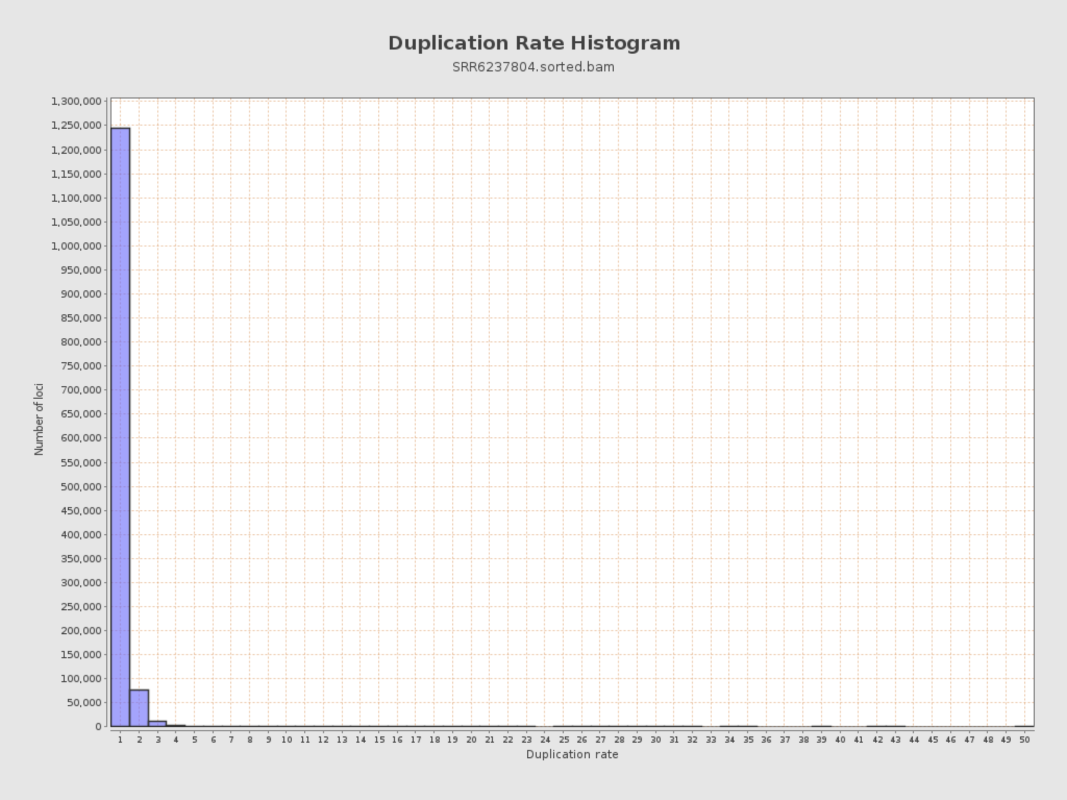
5. Results : Coverage Histogram (0-50X)



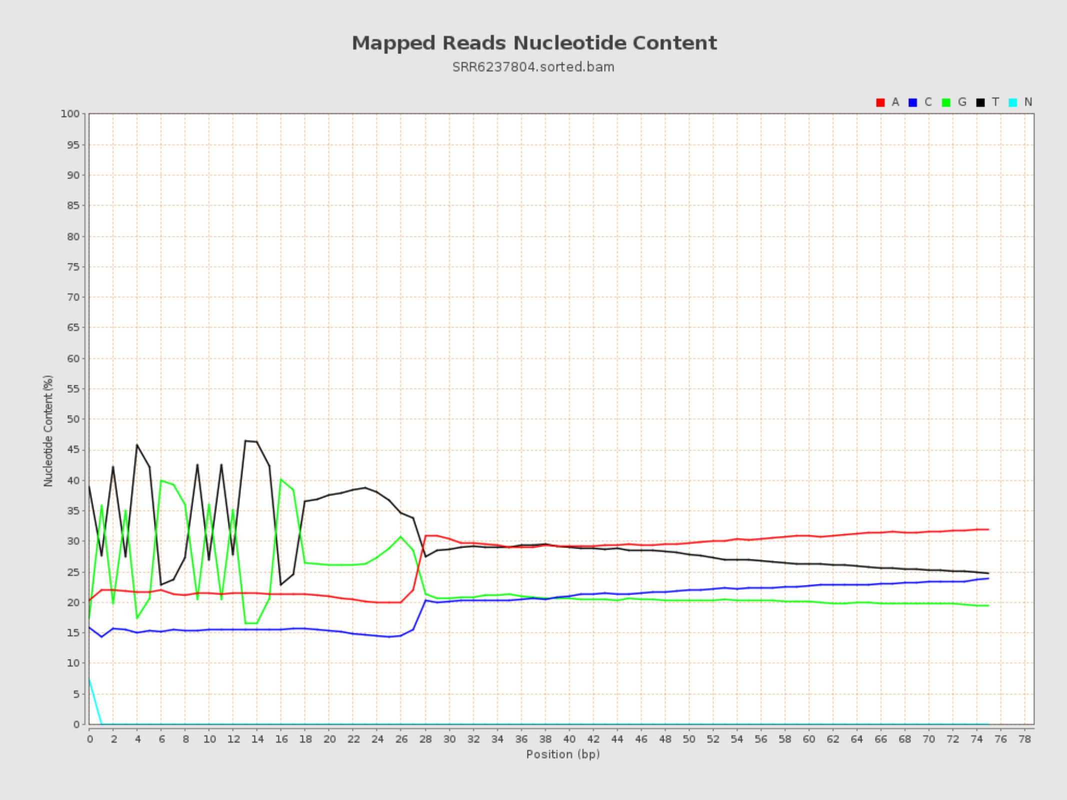
6. Results : Genome Fraction Coverage



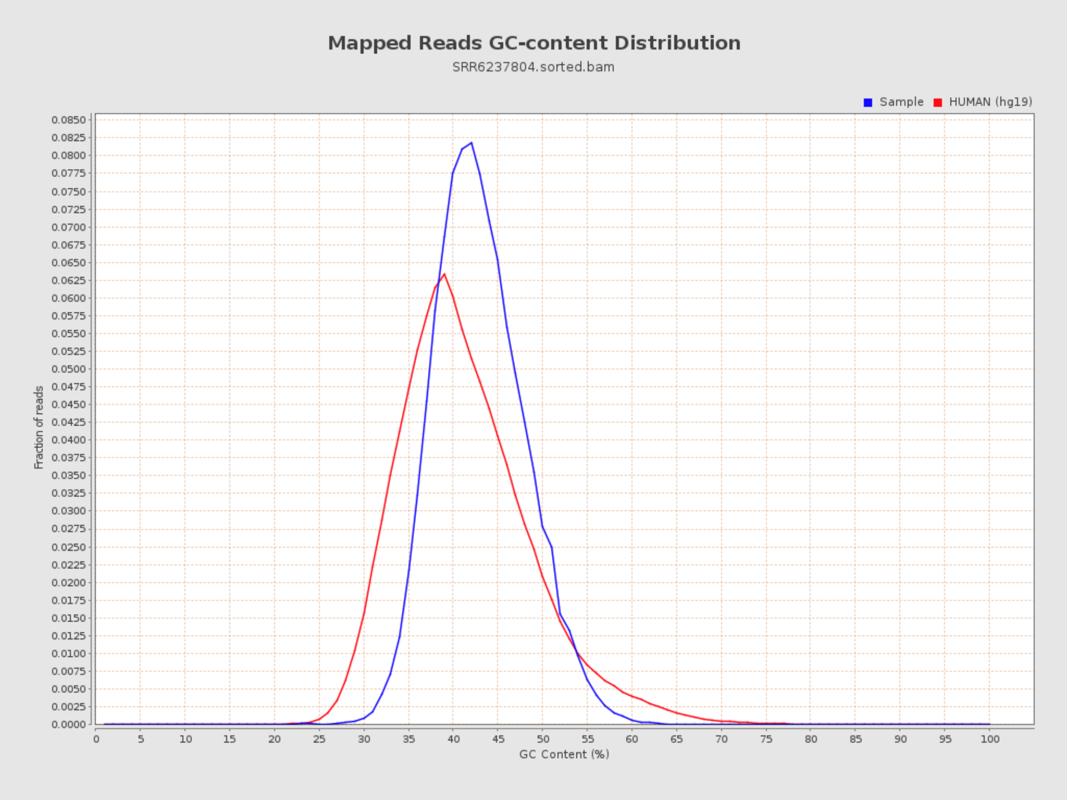
7. Results : Duplication Rate Histogram



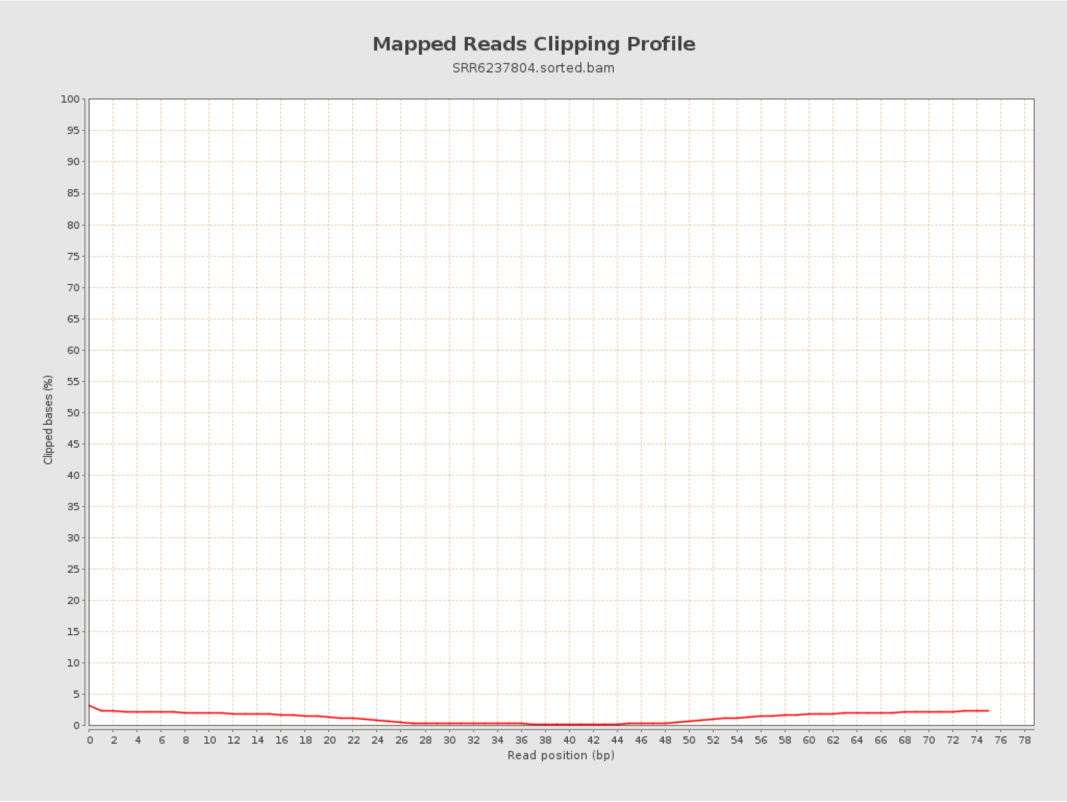
8. Results : Mapped Reads Nucleotide Content



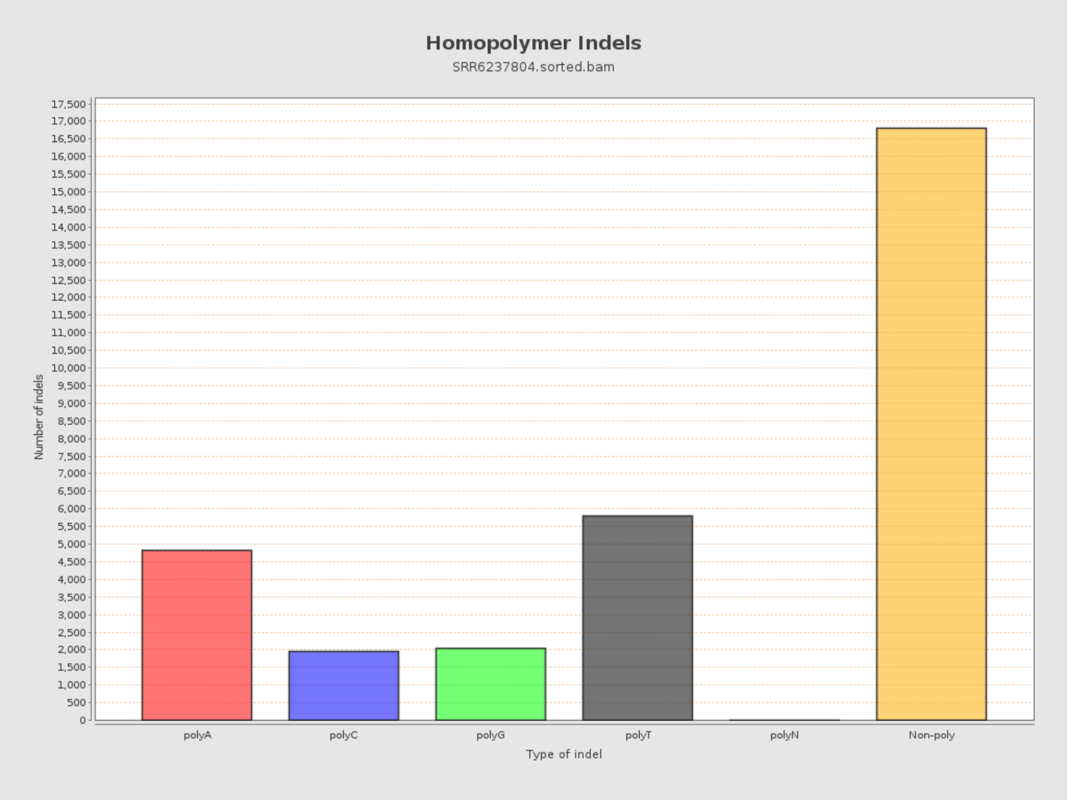
9. Results : Mapped Reads GC-content Distribution



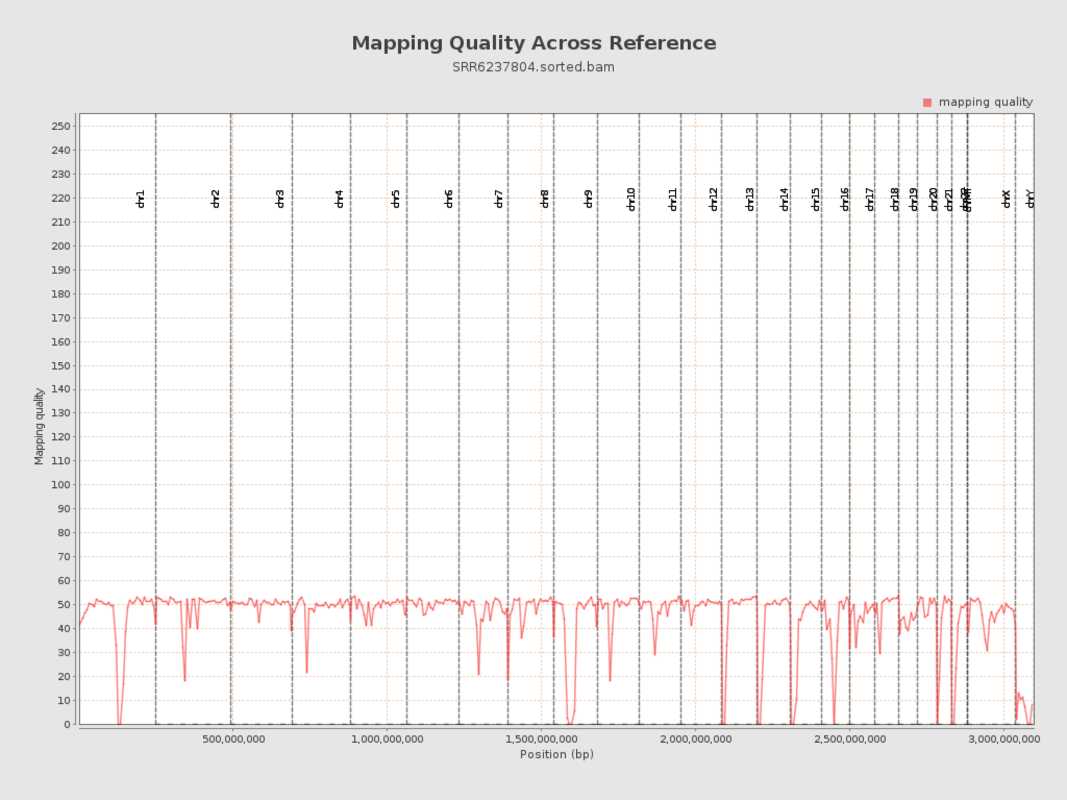
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram