Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:05:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237333.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_SRR6237333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:05:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,259,342
Mapped reads	3,029,625 / 92.95%
Unmapped reads	229,717 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,301 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	267,077 / 8.19%
Duplication rate	7.03%
Clipped reads	1,617,062 / 49.61%

2.2. ACGT Content

Number/percentage of A's	52,421,977 / 27%
Number/percentage of C's	34,054,271 / 17.54%
Number/percentage of T's	63,758,411 / 32.84%
Number/percentage of G's	43,906,654 / 22.61%
Number/percentage of N's	21,625 / 0.01%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0628

Standard Deviation	0.7092

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

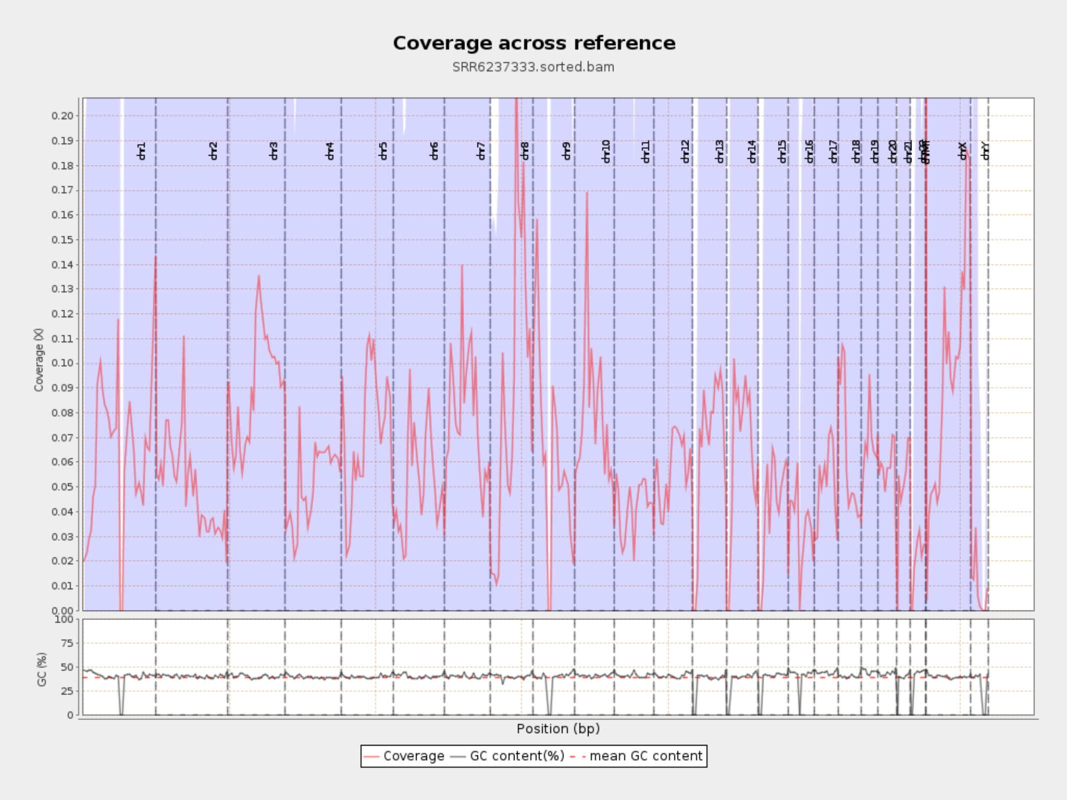
General error rate	0.61%
Mismatches	1,150,968
Insertions	13,755
Mapped reads with at least one insertion	0.45%
Deletions	58,641
Mapped reads with at least one deletion	1.91%
Homopolymer indels	43.22%

2.6. Chromosome stats

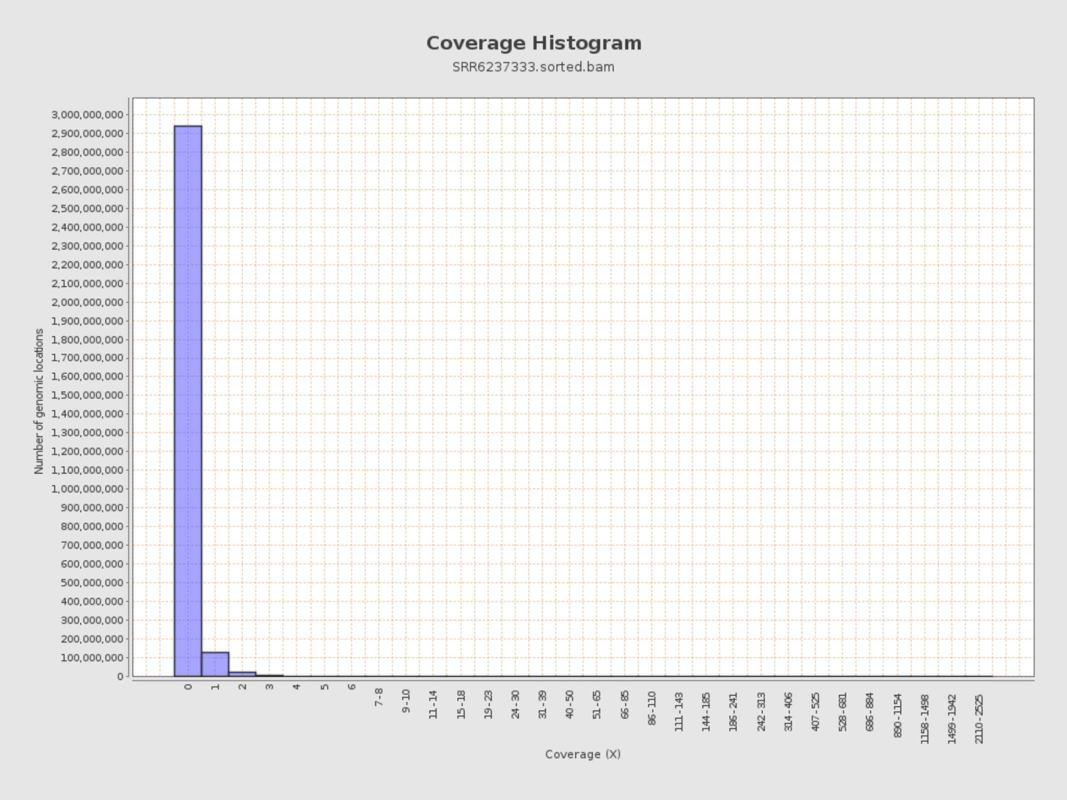
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16048635	0.0644	1.25
chr2	243199373	12224031	0.0503	0.8963
chr3	198022430	18017530	0.091	0.363
chr4	191154276	9870031	0.0516	0.3762
chr5	180915260	13106981	0.0724	0.3295
chr6	171115067	8990834	0.0525	0.4222
chr7	159138663	12566937	0.079	0.8398

chr8	146364022	13021194	0.089	1.6162
chr9	141213431	9070454	0.0642	0.5695
chr10	135534747	10753820	0.0793	0.7757
chr11	135006516	5648712	0.0418	0.3399
chr12	133851895	7695180	0.0575	0.3233
chr13	115169878	7624853	0.0662	0.3245
chr14	107349540	6984957	0.0651	0.337
chr15	102531392	4224464	0.0412	0.264
chr16	90354753	2920765	0.0323	0.3098
chr17	81195210	4224075	0.052	0.3466
chr18	78077248	5014395	0.0642	1.0118
chr19	59128983	3949050	0.0668	0.8245
chr20	63025520	3694505	0.0586	0.3039
chr21	48129895	2476939	0.0515	0.3351
chr22	51304566	1039013	0.0203	0.166
chrMT	16571	13547	0.8175	1.165
chrX	155270560	14533535	0.0936	0.428
chrY	59373566	553137	0.0093	0.295

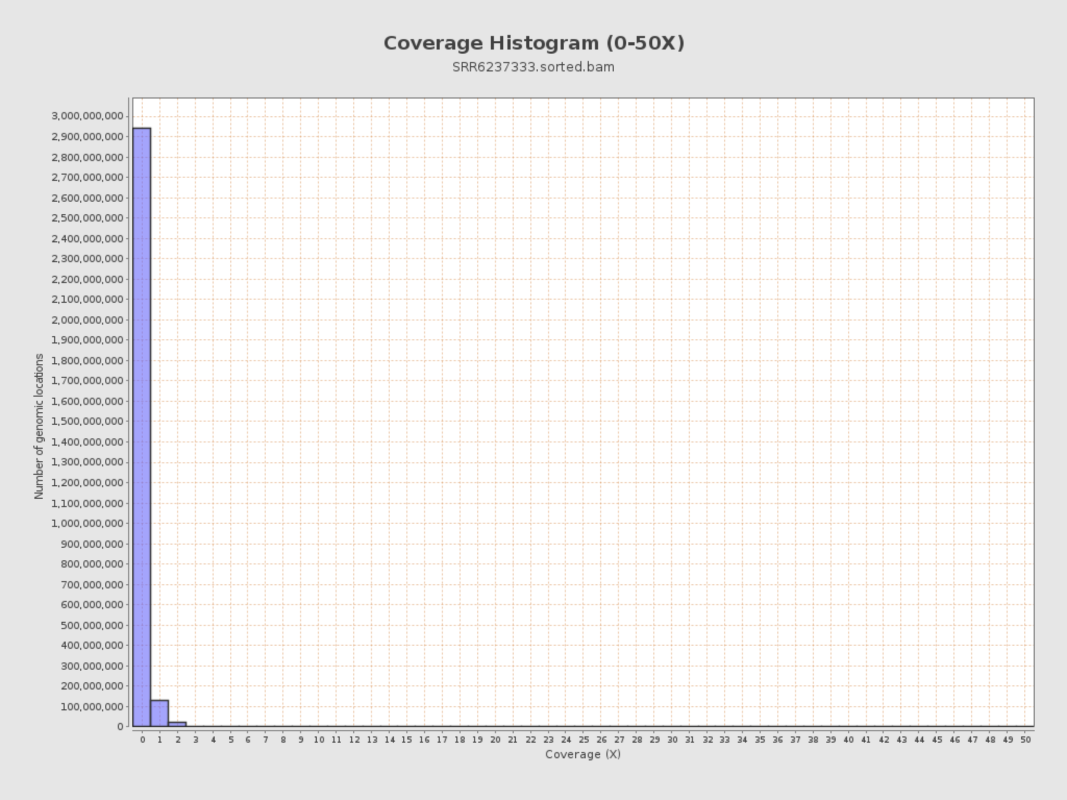
3. Results : Coverage across reference



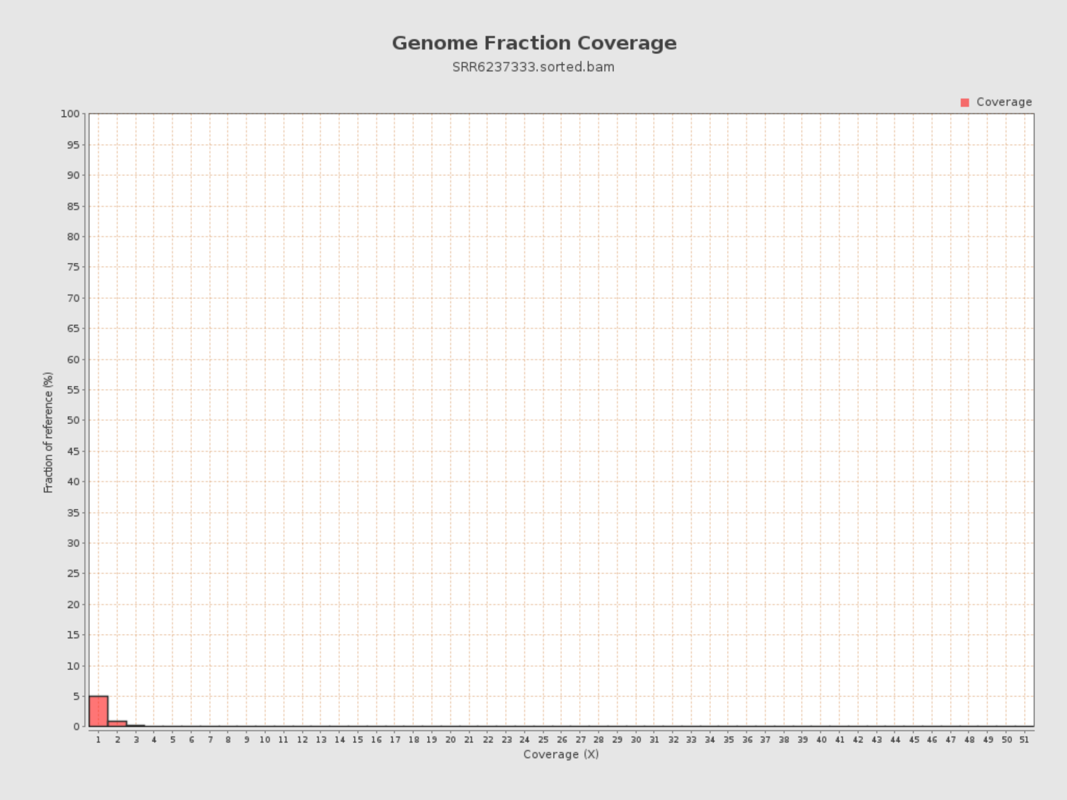
4. Results : Coverage Histogram



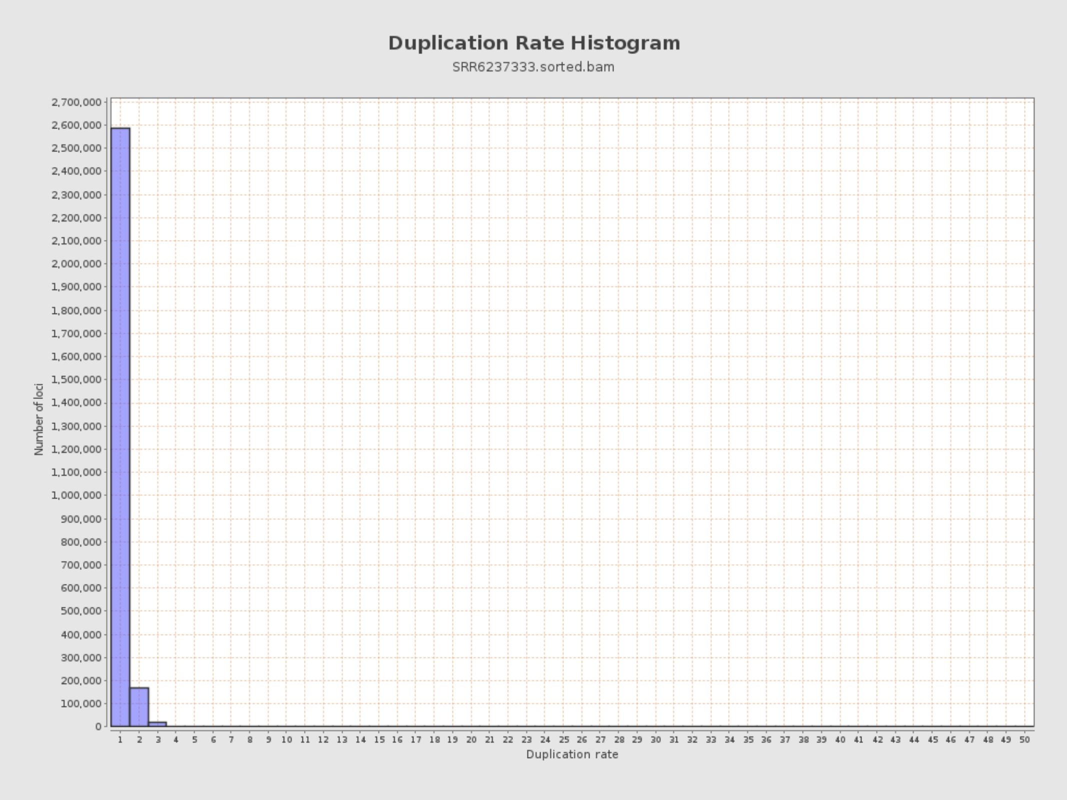
5. Results : Coverage Histogram (0-50X)



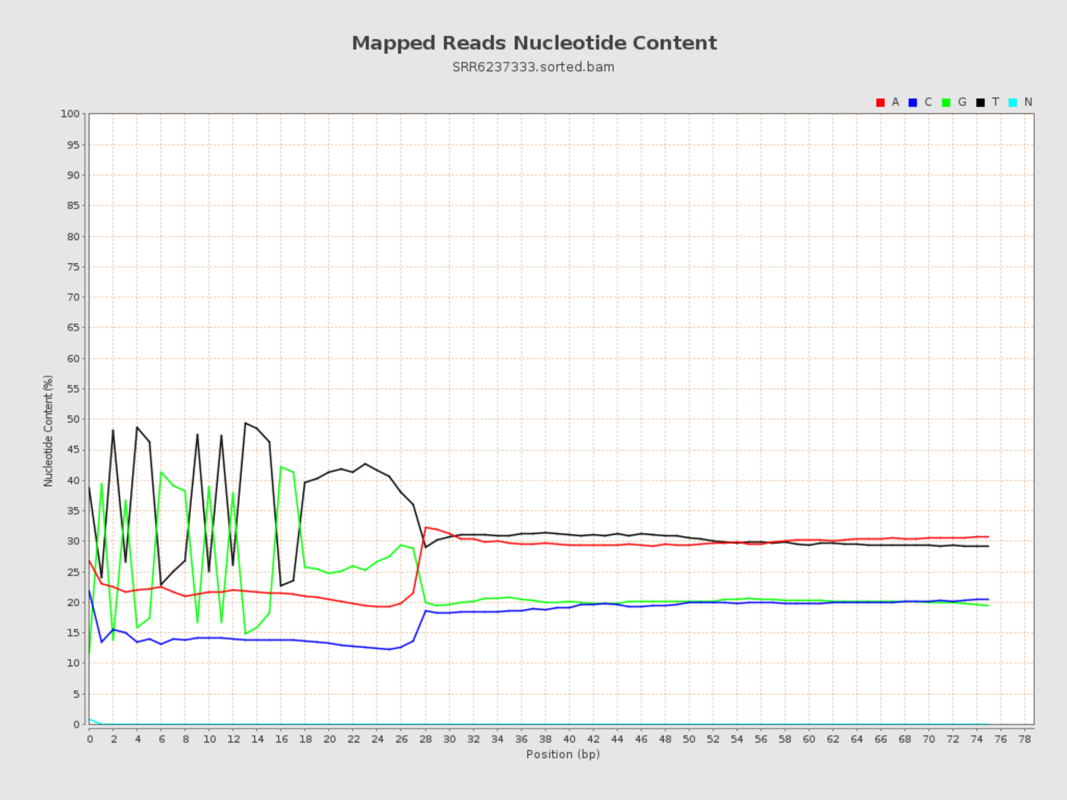
6. Results : Genome Fraction Coverage



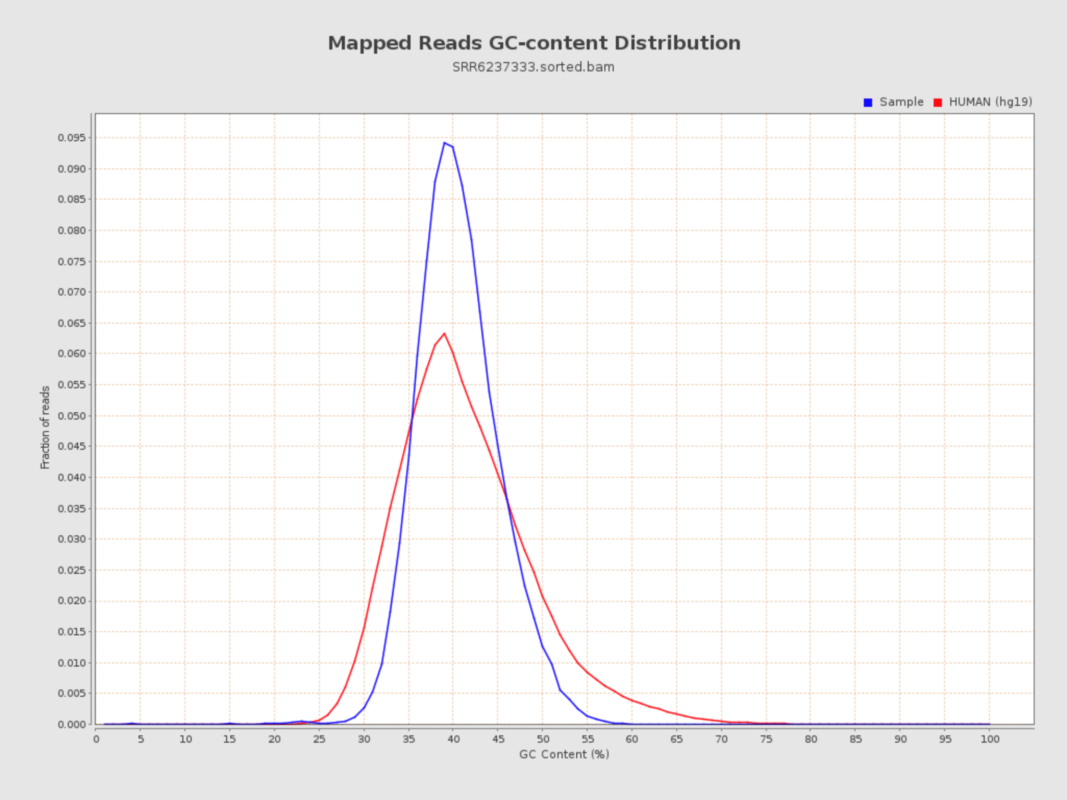
7. Results : Duplication Rate Histogram



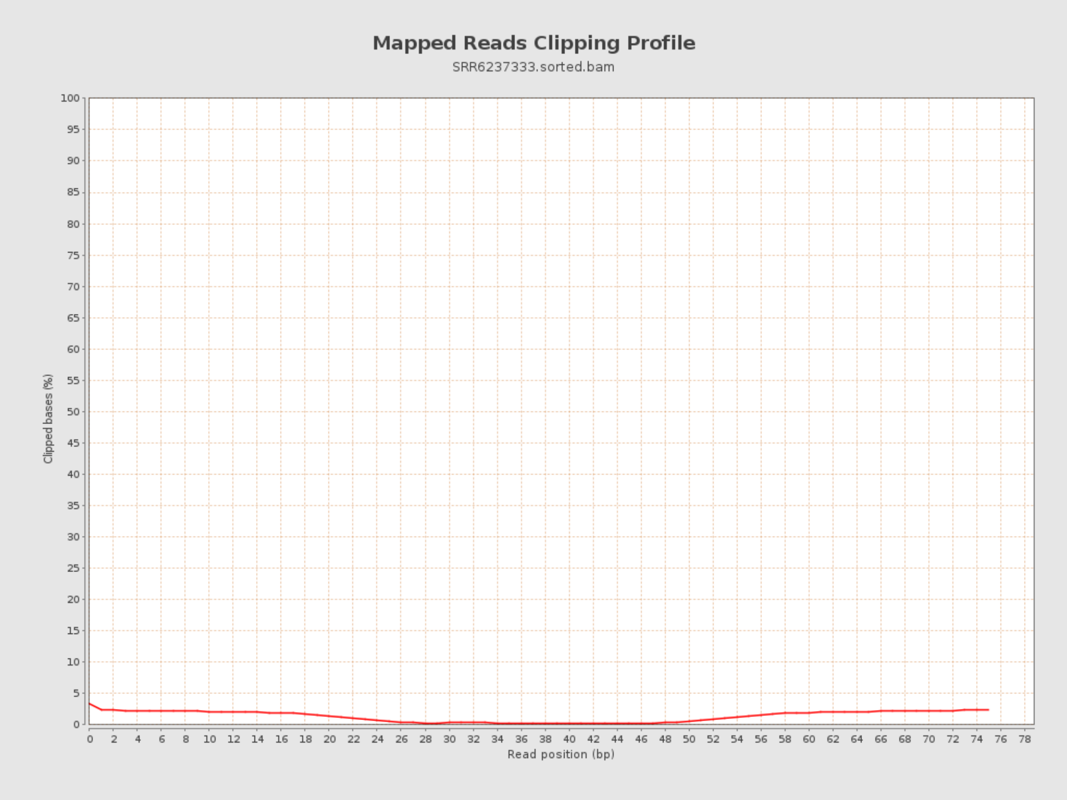
8. Results : Mapped Reads Nucleotide Content



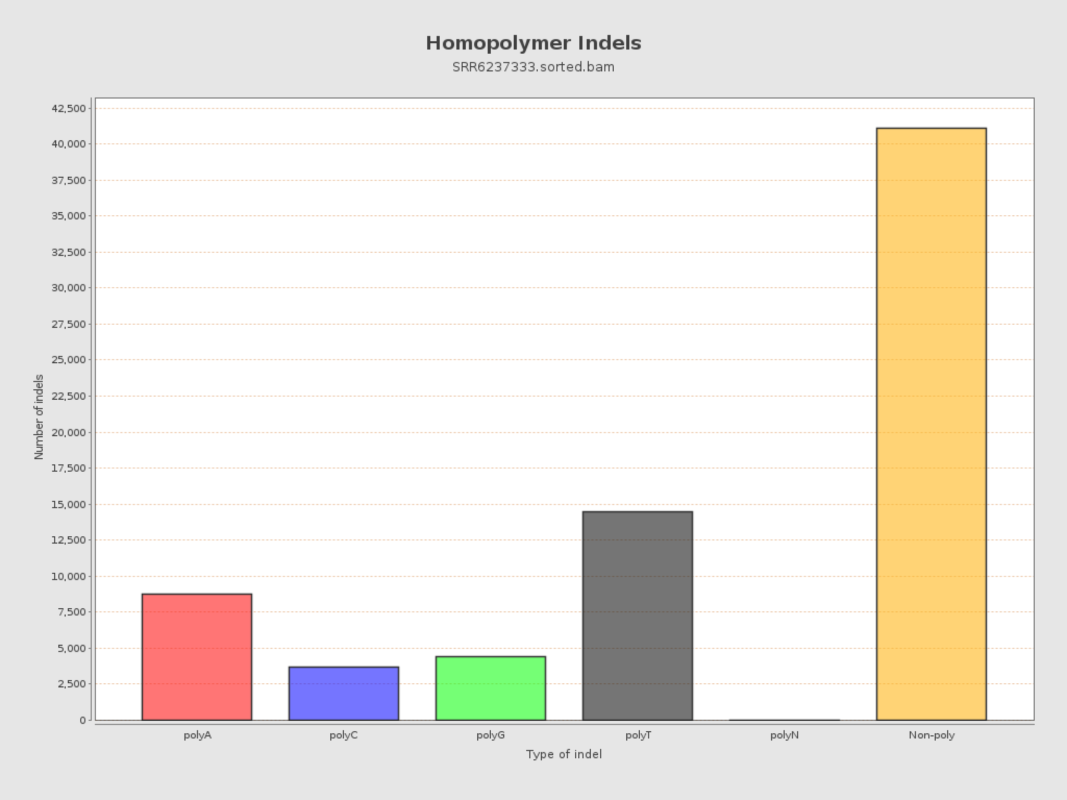
9. Results : Mapped Reads GC-content Distribution



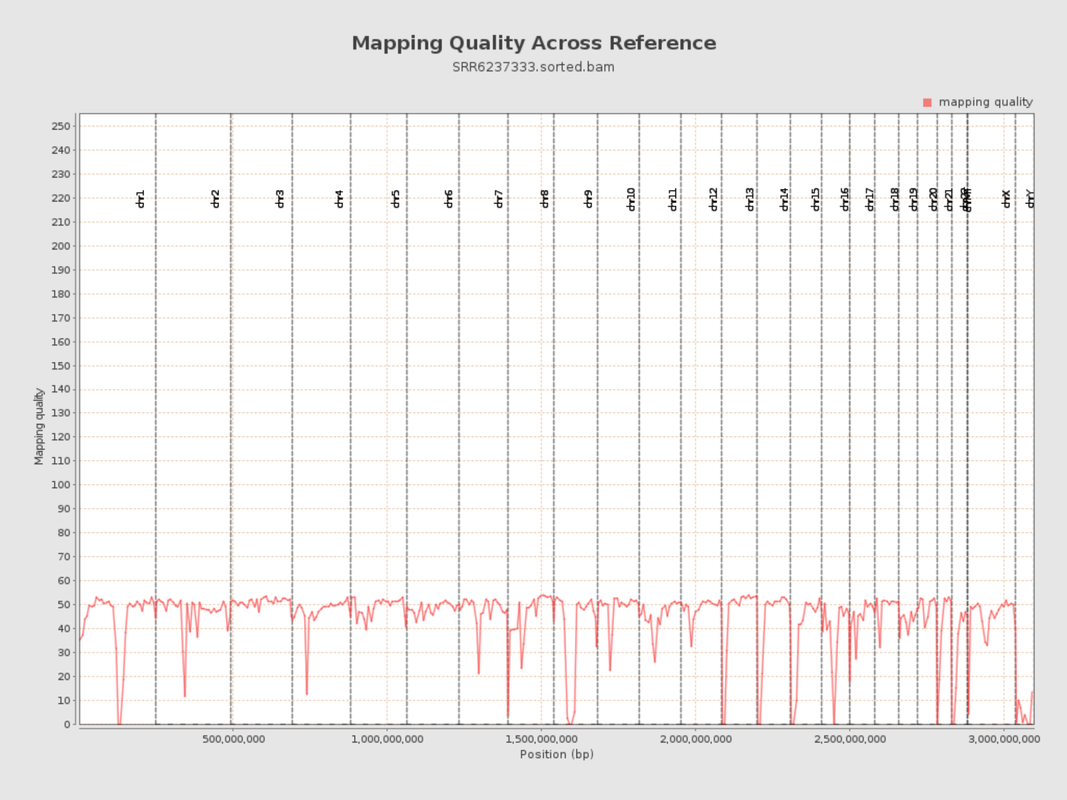
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram