

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:00:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237315.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_SRR6237315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:59:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,751,345
Mapped reads	2,296,697 / 83.48%
Unmapped reads	454,648 / 16.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,445 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	103,928 / 3.78%
Duplication rate	3.69%
Clipped reads	945,752 / 34.37%

2.2. ACGT Content

Number/percentage of A's	43,571,731 / 28.1%
Number/percentage of C's	28,315,403 / 18.26%
Number/percentage of T's	49,276,963 / 31.77%
Number/percentage of G's	33,919,245 / 21.87%
Number/percentage of N's	2,725 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.3832
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2.4. Mapping Quality

Mean Mapping Quality	42.86
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2.5. Mismatches and indels

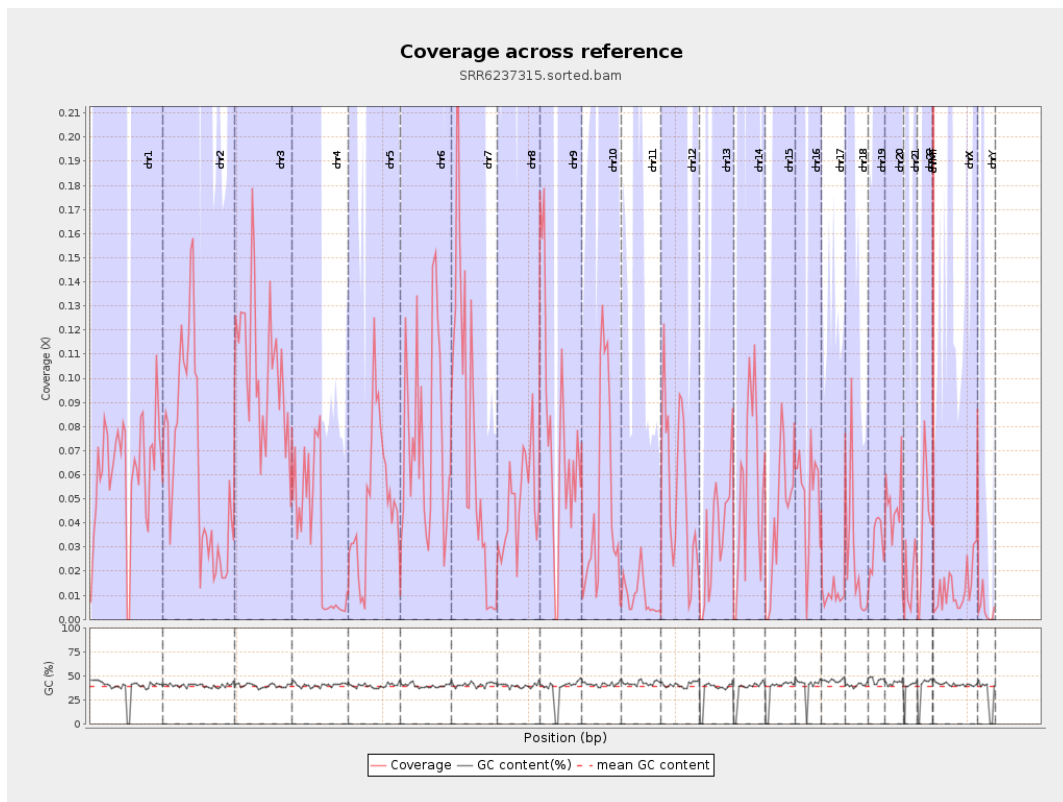
General error rate	0.79%
Mismatches	1,193,829
Insertions	12,826
Mapped reads with at least one insertion	0.55%
Deletions	38,595
Mapped reads with at least one deletion	1.66%
Homopolymer indels	47.5%

2.6. Chromosome stats

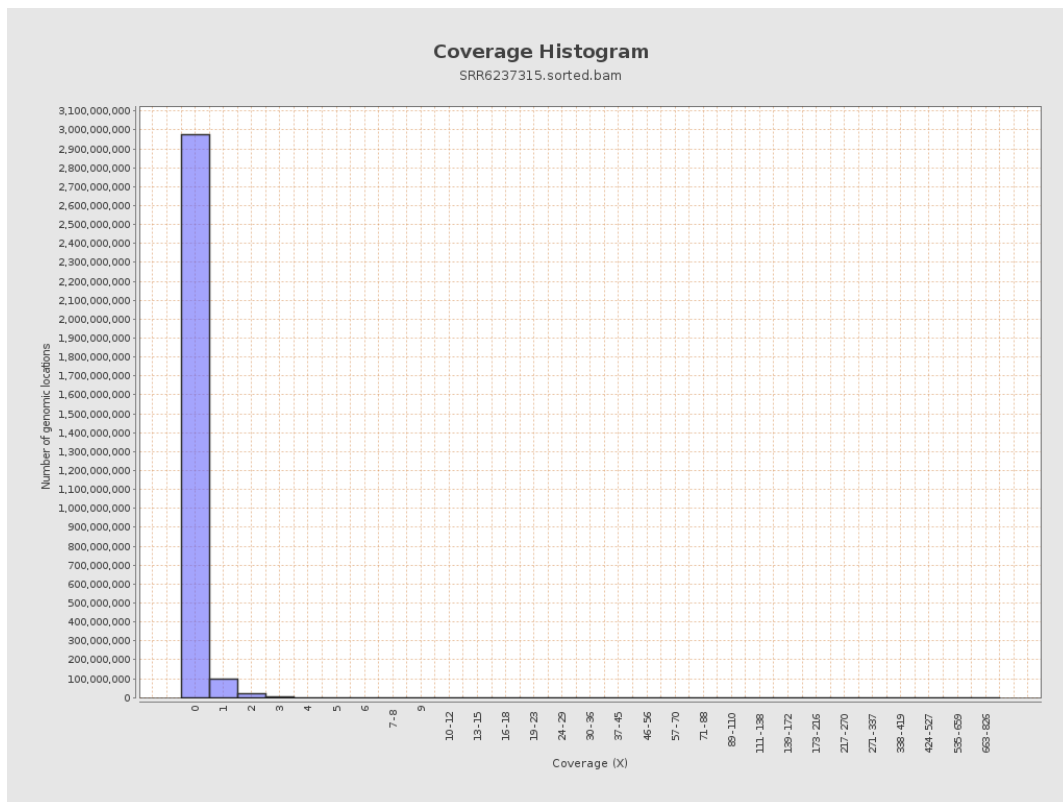
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15156132	0.0608	0.5373
chr2	243199373	15436648	0.0635	0.4966
chr3	198022430	20532895	0.1037	0.392
chr4	191154276	6180578	0.0323	0.2494
chr5	180915260	8861852	0.049	0.2674
chr6	171115067	12971341	0.0758	0.4034
chr7	159138663	11471632	0.0721	0.3793

chr8	146364022	7166606	0.049	0.5948
chr9	141213431	10283587	0.0728	0.4558
chr10	135534747	6509211	0.048	0.3617
chr11	135006516	1343927	0.01	0.2226
chr12	133851895	7213992	0.0539	0.2885
chr13	115169878	4094476	0.0356	0.228
chr14	107349540	5905909	0.055	0.3108
chr15	102531392	4337396	0.0423	0.2556
chr16	90354753	4650827	0.0515	0.2938
chr17	81195210	795857	0.0098	0.1183
chr18	78077248	2066587	0.0265	0.73
chr19	59128983	1852466	0.0313	0.3954
chr20	63025520	2960334	0.047	0.2645
chr21	48129895	871402	0.0181	0.2094
chr22	51304566	2037234	0.0397	0.2364
chrMT	16571	34100	2.0578	1.9804
chrX	155270560	2155937	0.0139	0.1701
chrY	59373566	258451	0.0044	0.1436

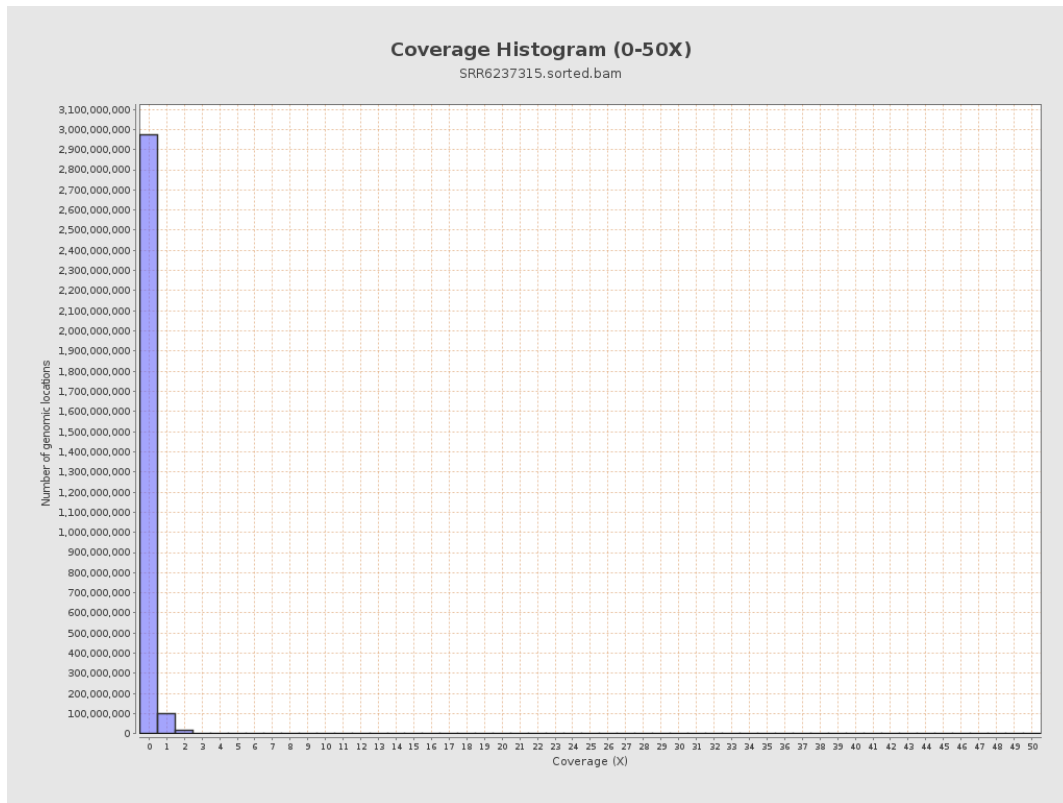
3. Results : Coverage across reference



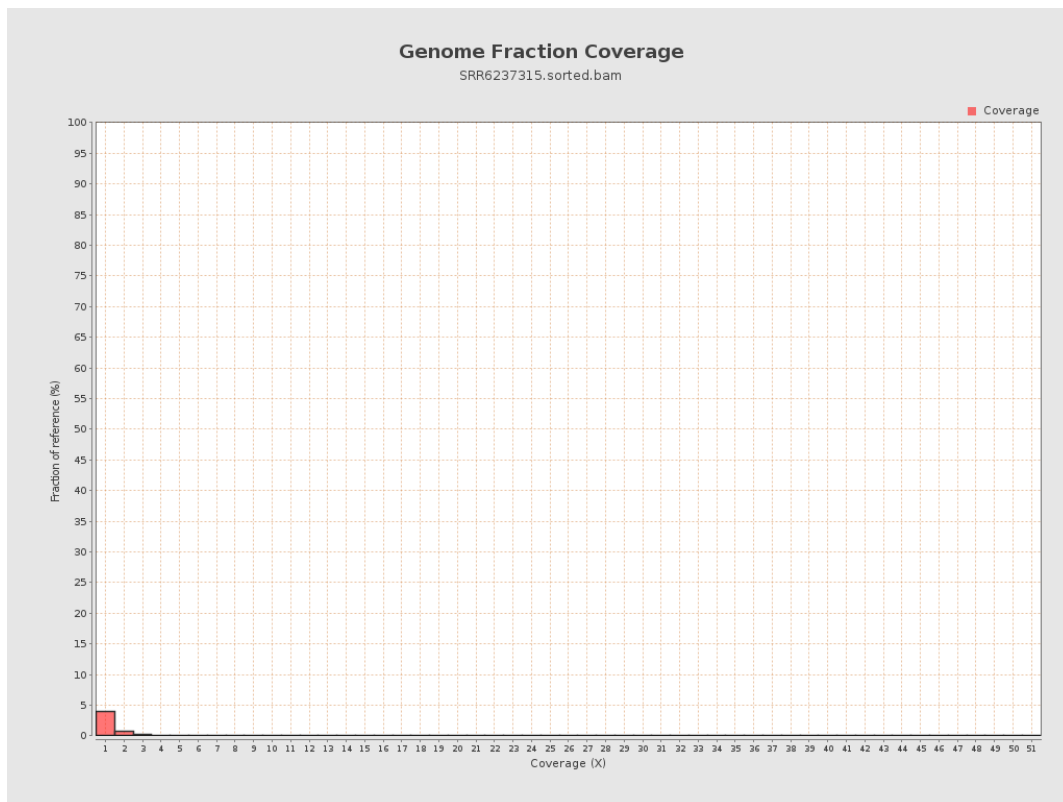
4. Results : Coverage Histogram



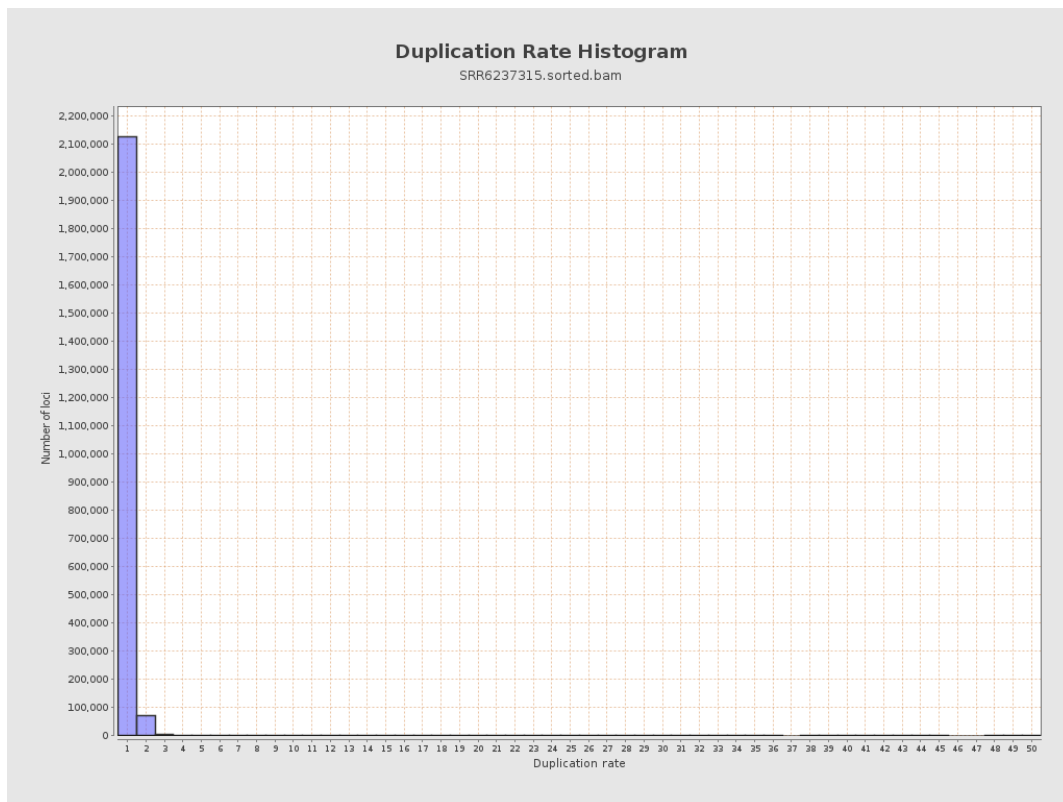
5. Results : Coverage Histogram (0-50X)



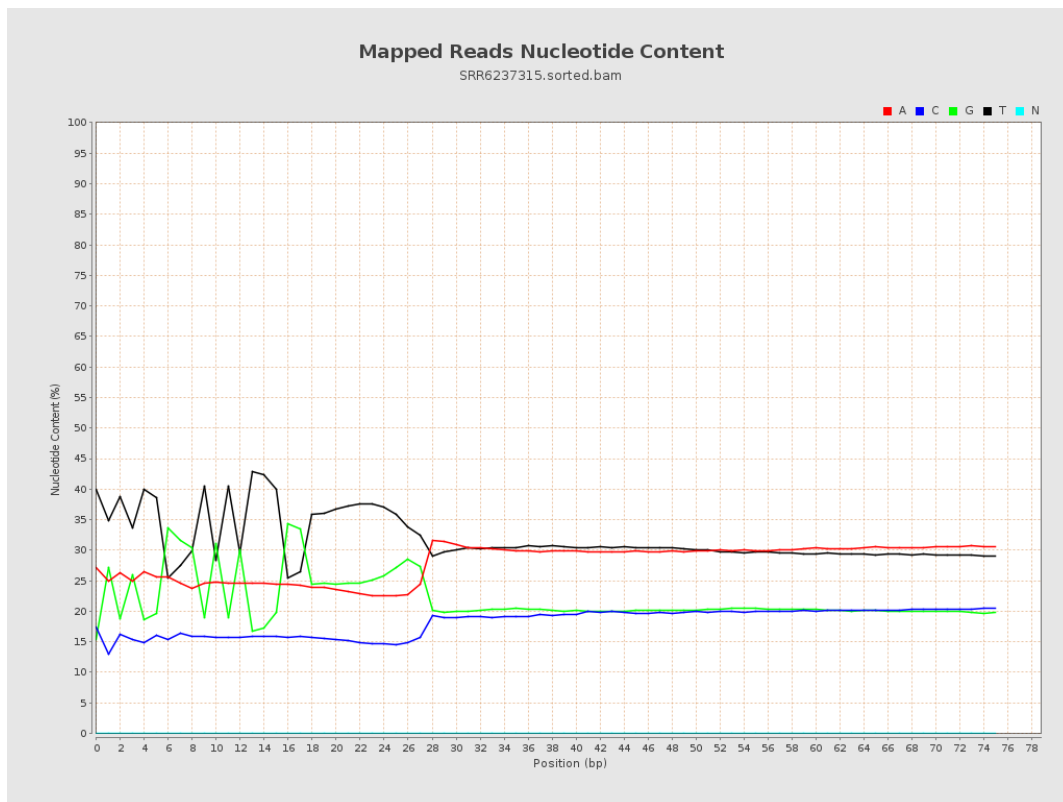
6. Results : Genome Fraction Coverage



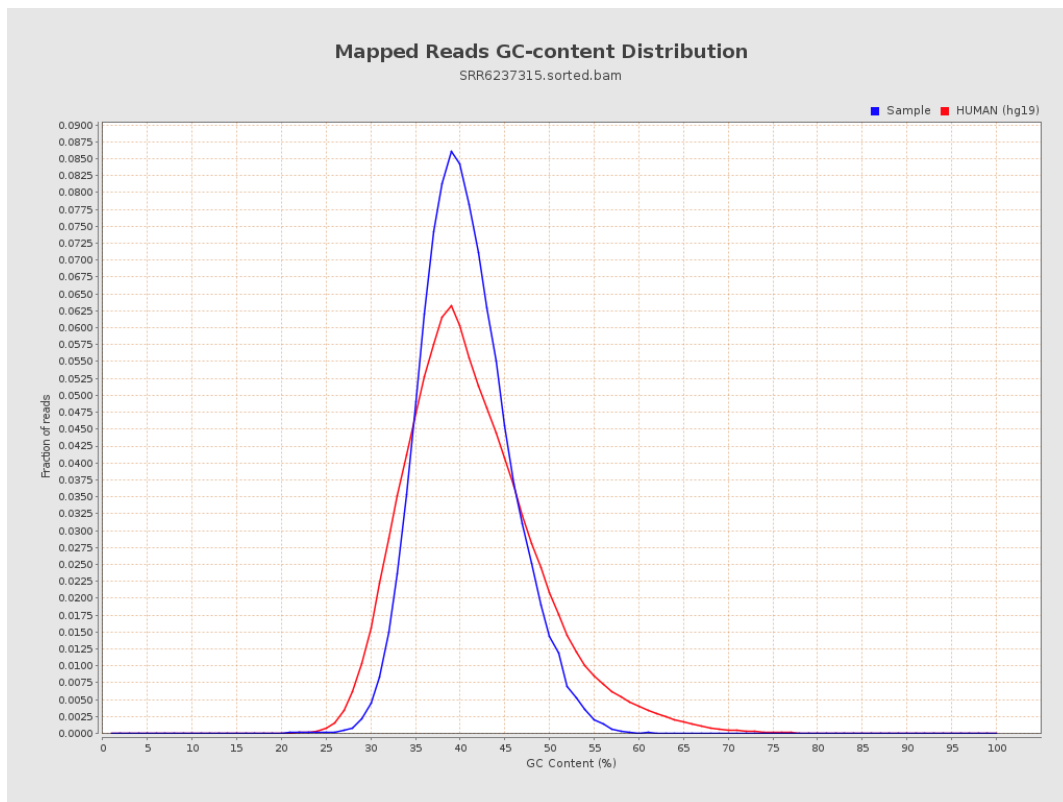
7. Results : Duplication Rate Histogram



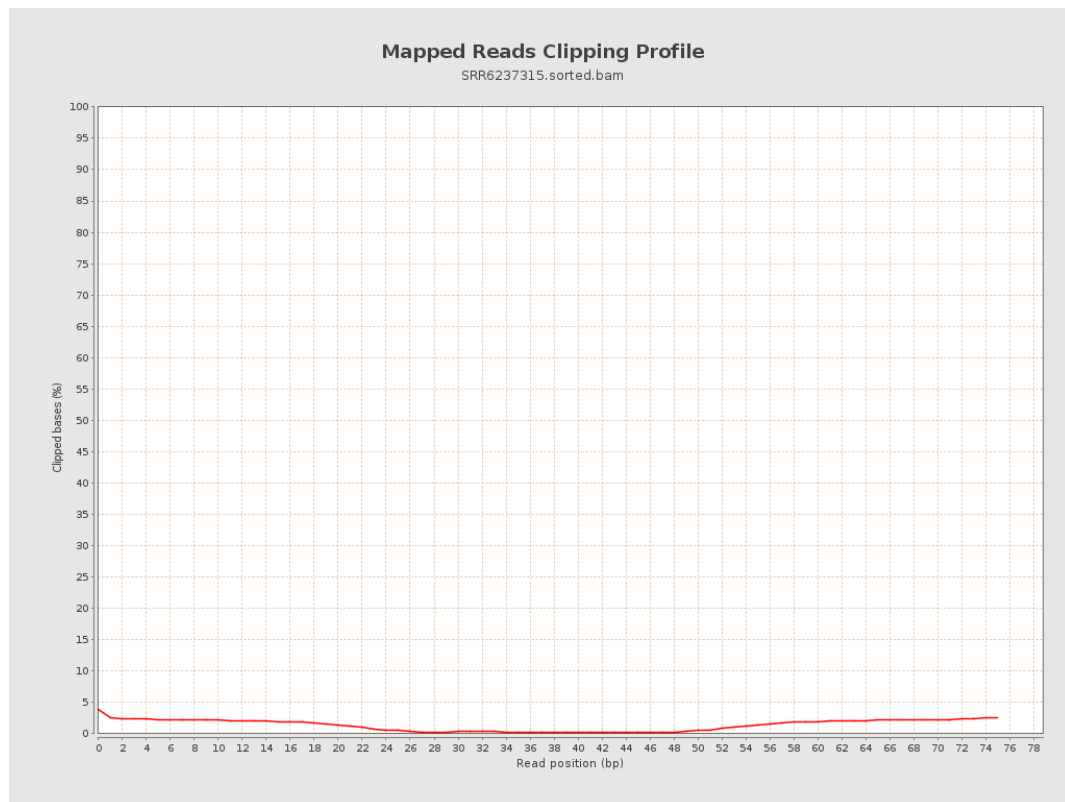
8. Results : Mapped Reads Nucleotide Content



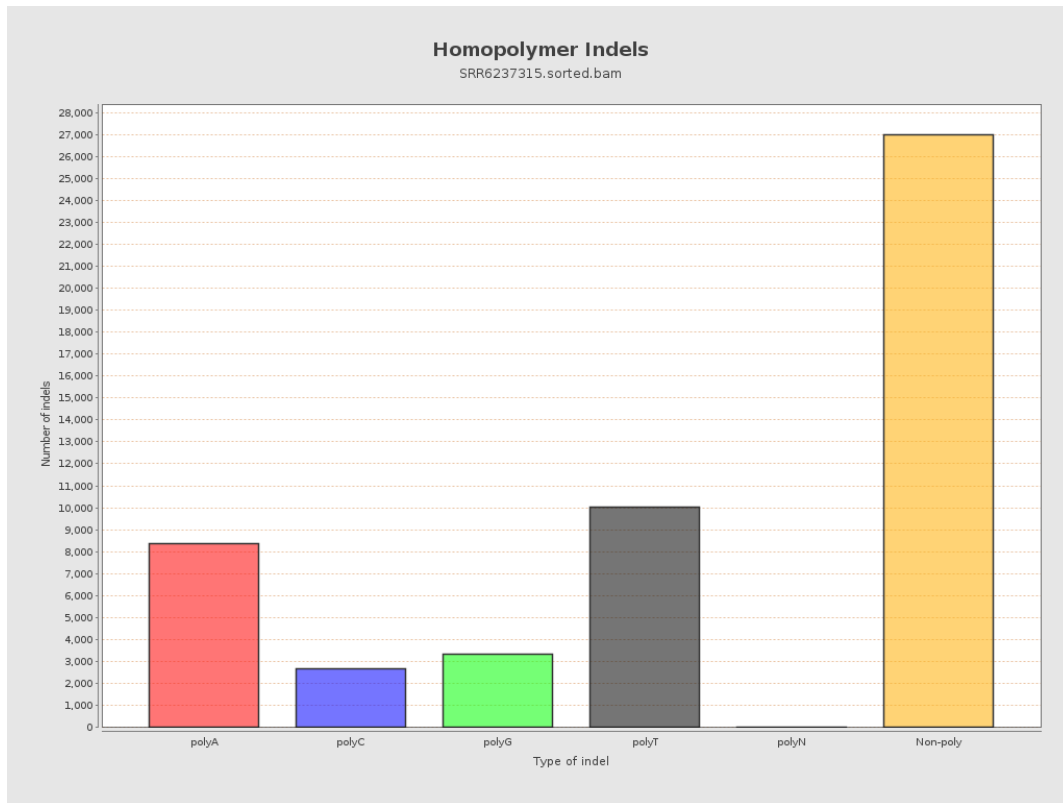
9. Results : Mapped Reads GC-content Distribution



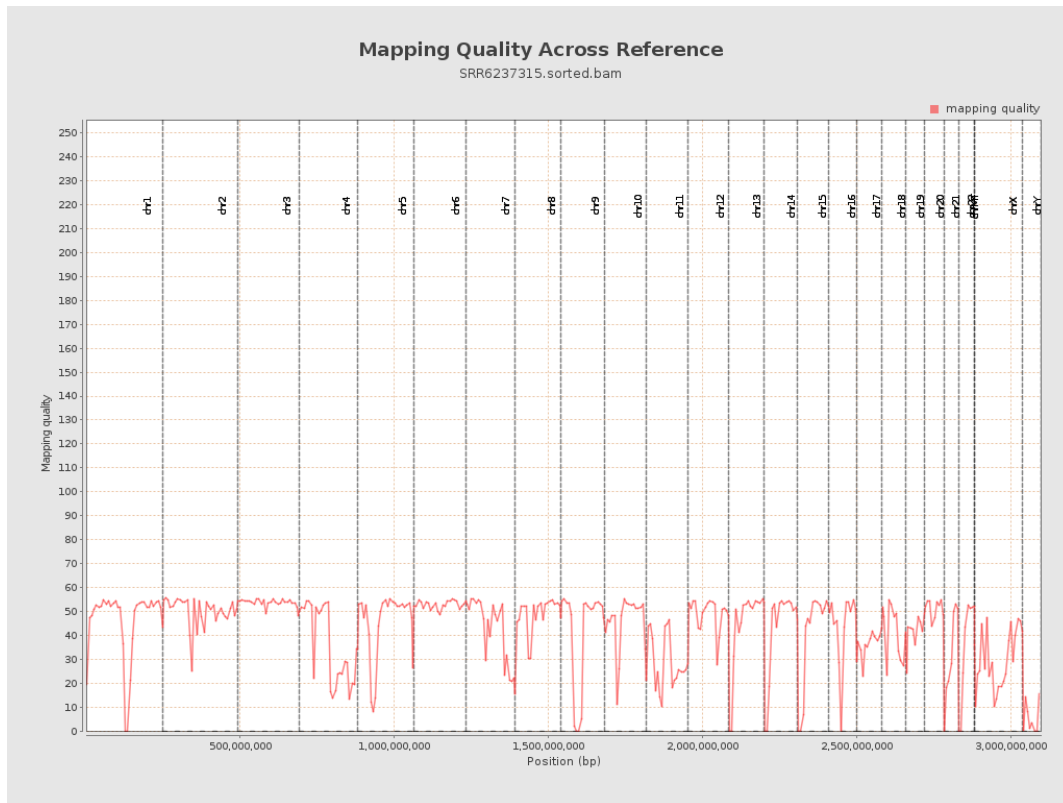
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

