

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:08:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238315.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_SRR6238315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:08:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,718,845
Mapped reads	3,376,152 / 90.78%
Unmapped reads	342,693 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,482 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	139,655 / 3.76%
Duplication rate	3.17%
Clipped reads	1,922,820 / 51.7%

2.2. ACGT Content

Number/percentage of A's	58,860,515 / 27.19%
Number/percentage of C's	41,437,055 / 19.14%
Number/percentage of T's	65,763,959 / 30.38%
Number/percentage of G's	50,387,298 / 23.27%
Number/percentage of N's	55,427 / 0.03%
GC Percentage	42.41%

2.3. Coverage

Mean	0.07

Standard Deviation	0.4801
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2.4. Mapping Quality

Mean Mapping Quality	43.67
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2.5. Mismatches and indels

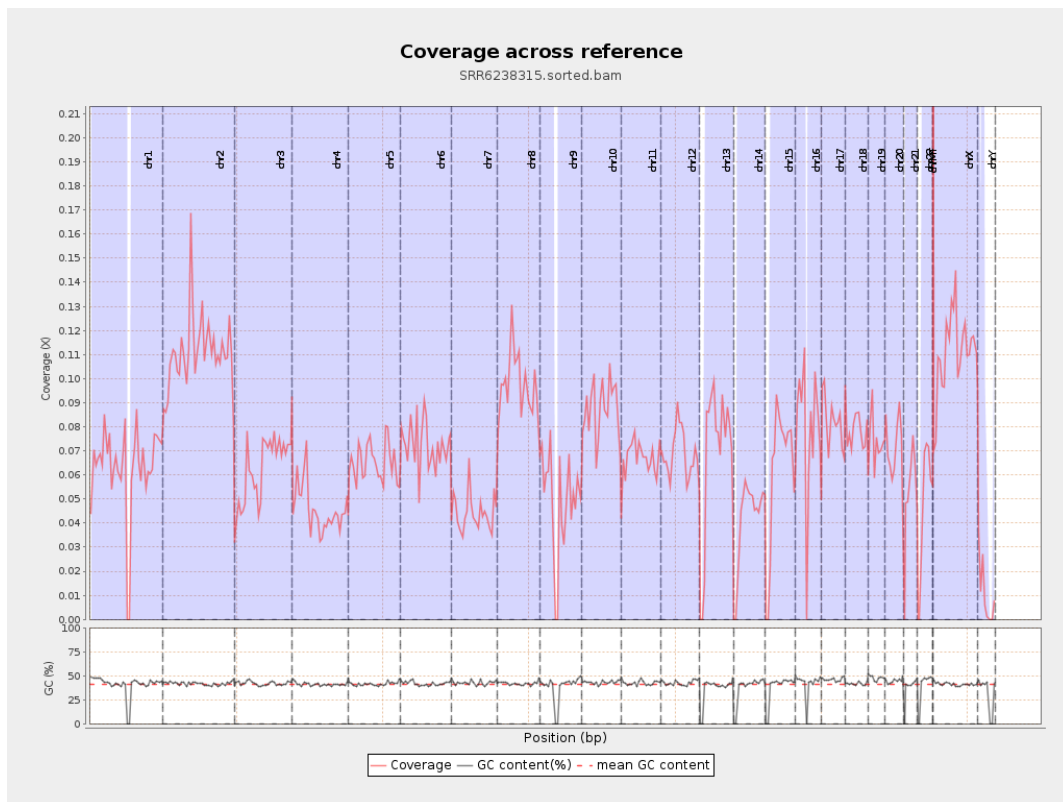
General error rate	0.85%
Mismatches	1,819,310
Insertions	16,822
Mapped reads with at least one insertion	0.49%
Deletions	62,431
Mapped reads with at least one deletion	1.83%
Homopolymer indels	44.73%

2.6. Chromosome stats

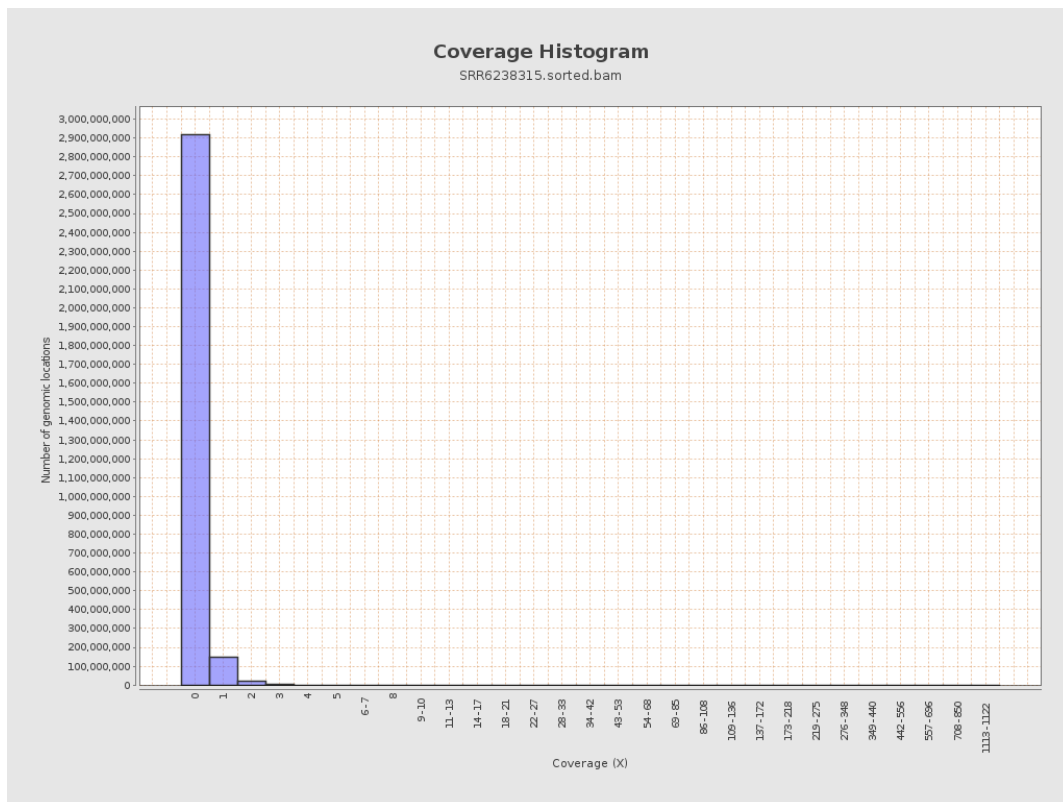
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15738134	0.0631	0.7042
chr2	243199373	27050258	0.1112	0.7536
chr3	198022430	12364234	0.0624	0.2925
chr4	191154276	8734212	0.0457	0.2777
chr5	180915260	11800846	0.0652	0.3018
chr6	171115067	12355908	0.0722	0.4237
chr7	159138663	7069560	0.0444	0.4273

chr8	146364022	14238469	0.0973	0.6713
chr9	141213431	6889490	0.0488	0.4375
chr10	135534747	11874309	0.0876	0.4853
chr11	135006516	9074279	0.0672	0.4401
chr12	133851895	9221480	0.0689	0.3142
chr13	115169878	7933217	0.0689	0.3101
chr14	107349540	4515506	0.0421	0.2921
chr15	102531392	6212259	0.0606	0.3032
chr16	90354753	6989111	0.0774	0.3634
chr17	81195210	6714653	0.0827	0.3822
chr18	78077248	6117776	0.0784	0.8308
chr19	59128983	4387146	0.0742	0.5879
chr20	63025520	4496288	0.0713	0.3318
chr21	48129895	2556776	0.0531	0.3075
chr22	51304566	2424719	0.0473	0.2557
chrMT	16571	13007	0.7849	1.0628
chrX	155270560	17225997	0.1109	0.464
chrY	59373566	608537	0.0102	0.189

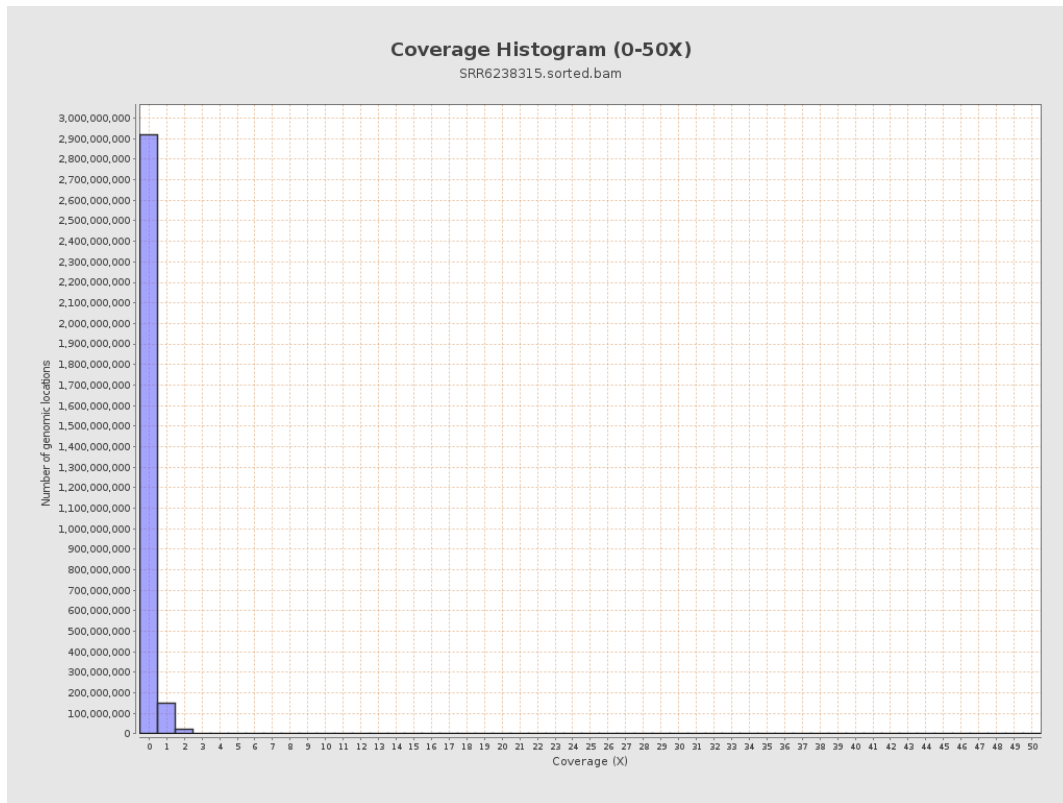
3. Results : Coverage across reference



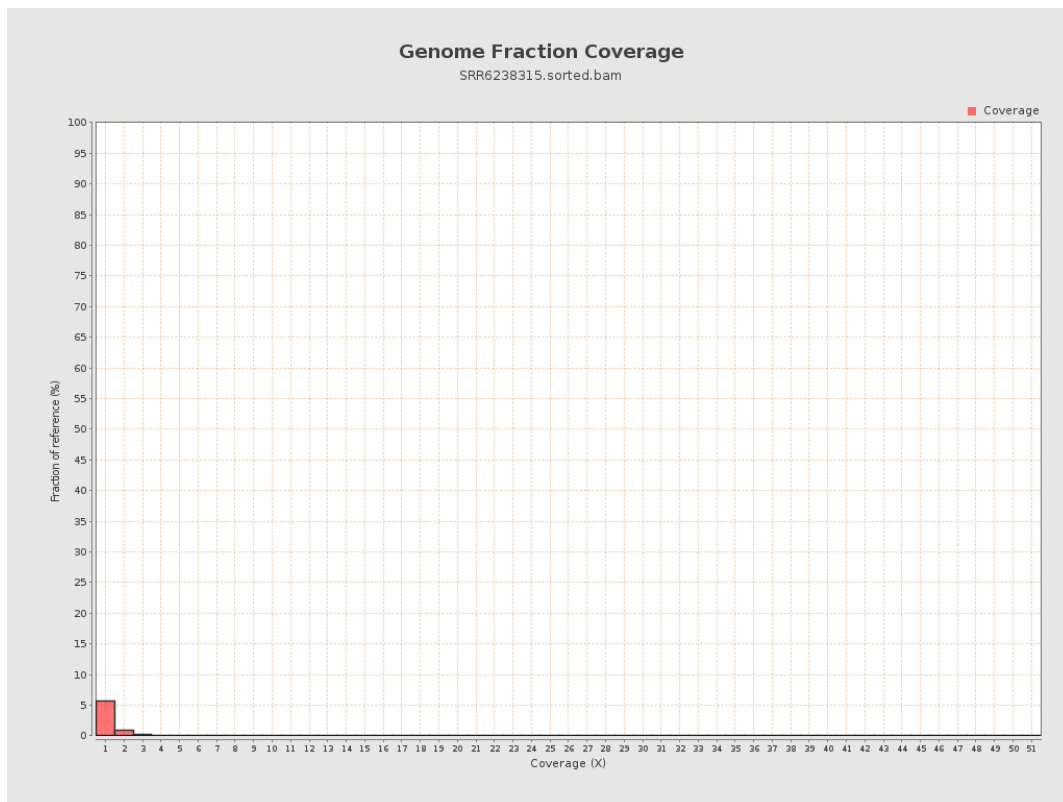
4. Results : Coverage Histogram



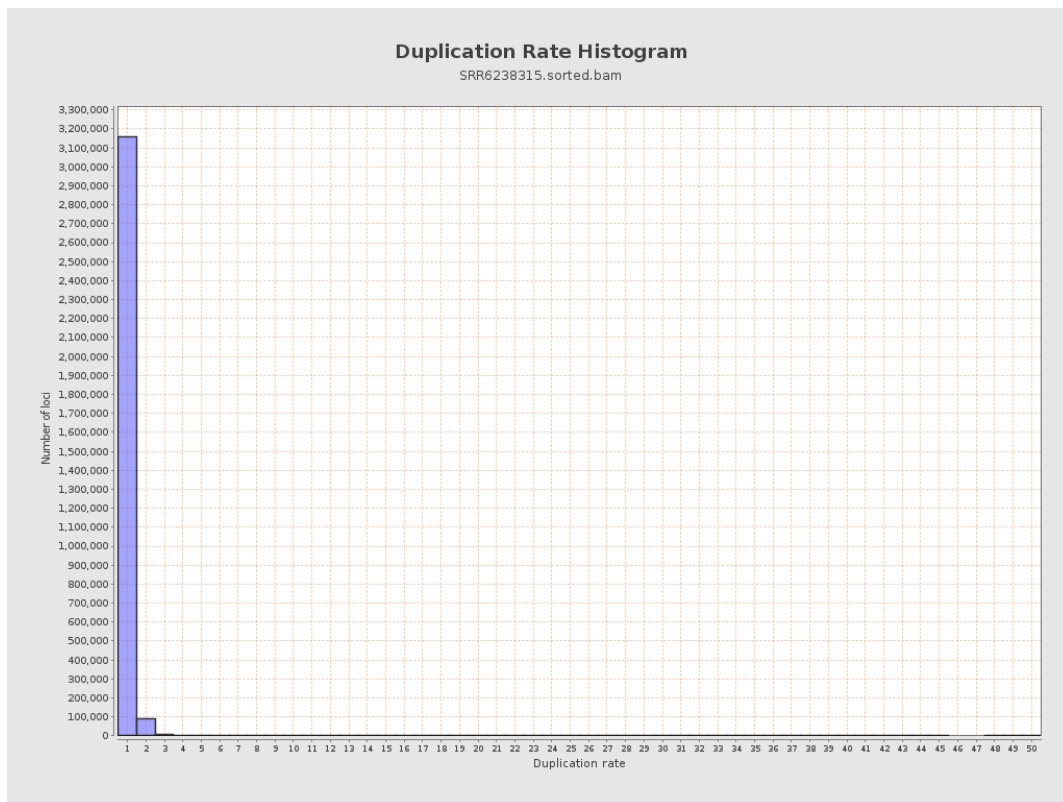
5. Results : Coverage Histogram (0-50X)



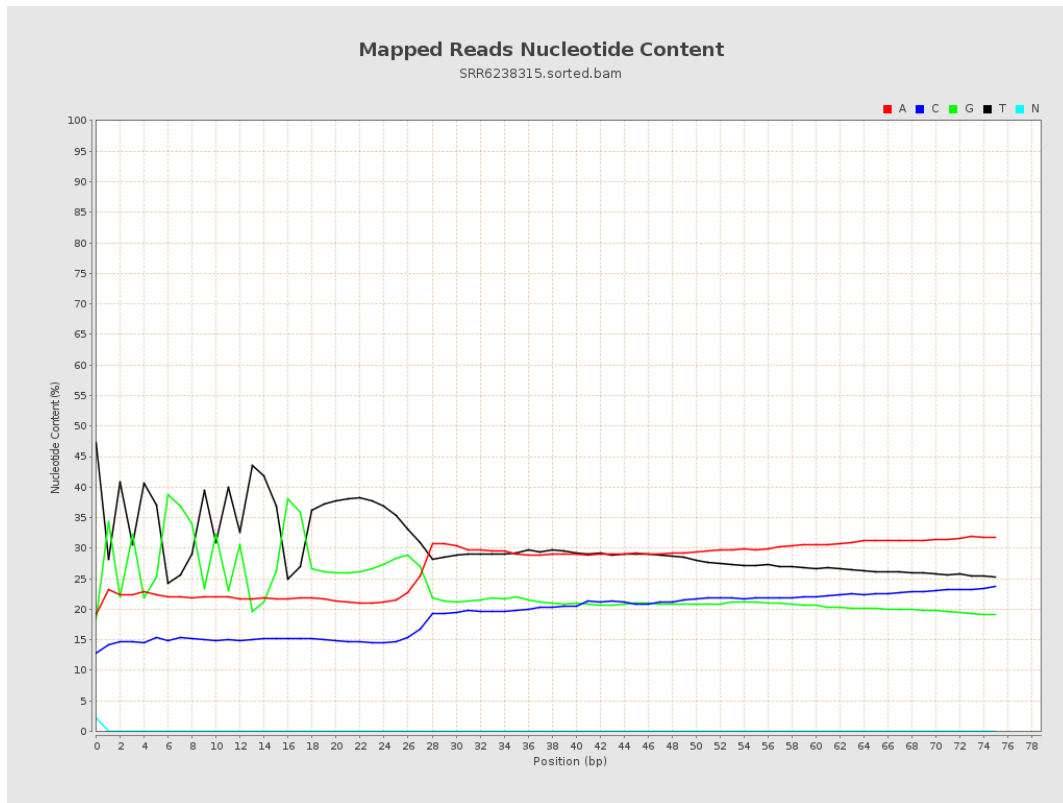
6. Results : Genome Fraction Coverage



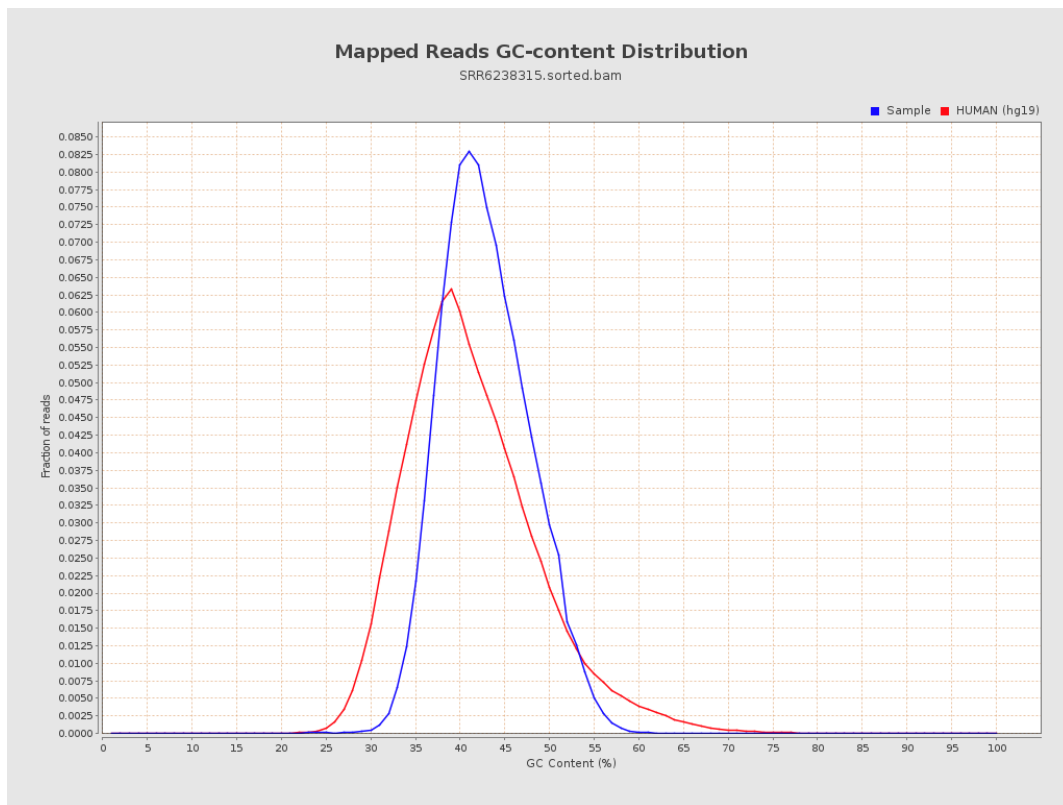
7. Results : Duplication Rate Histogram



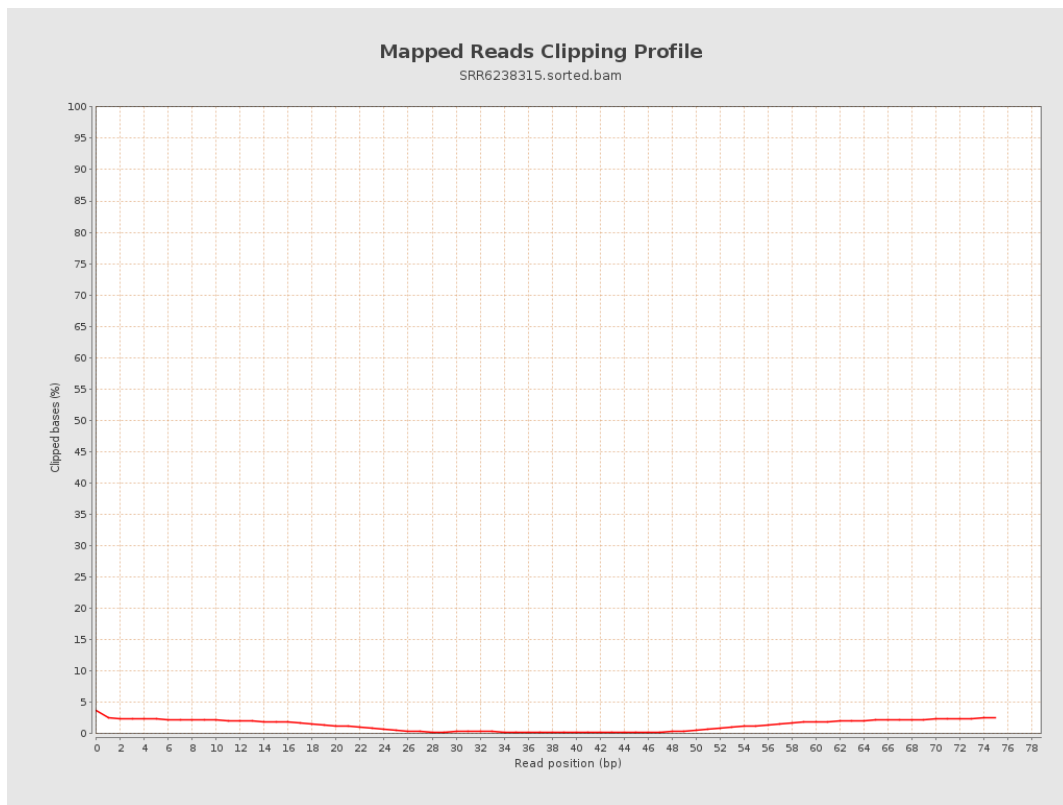
8. Results : Mapped Reads Nucleotide Content



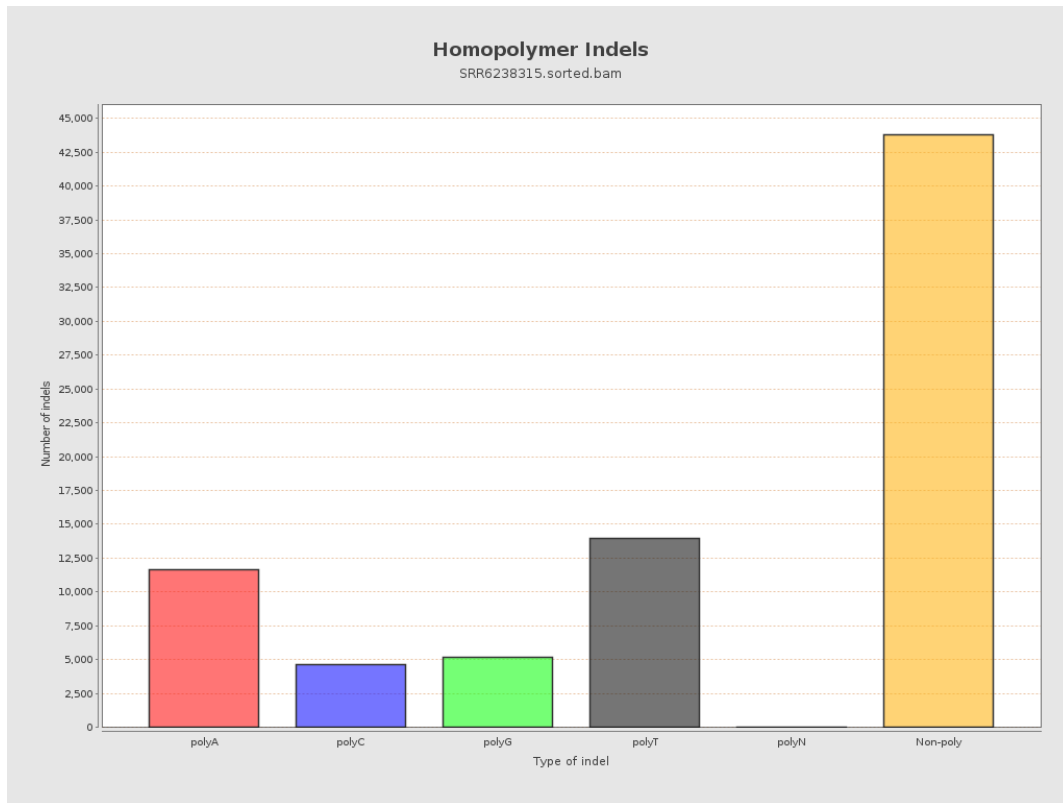
9. Results : Mapped Reads GC-content Distribution



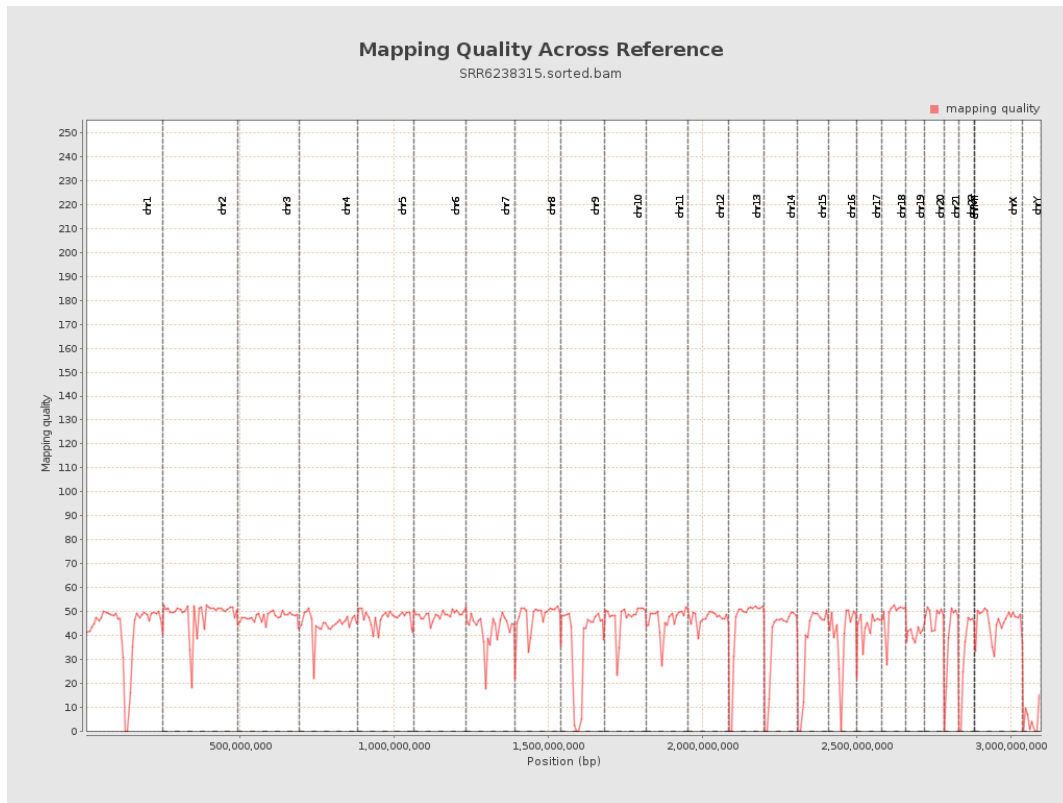
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

