

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:59:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013188.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_SRR6013188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:59:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,196,835
Mapped reads	2,925,355 / 91.51%
Unmapped reads	271,480 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,586 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	107,392 / 3.36%
Duplication rate	2.09%
Clipped reads	1,466,507 / 45.87%

2.2. ACGT Content

Number/percentage of A's	52,495,339 / 27.46%
Number/percentage of C's	37,259,697 / 19.49%
Number/percentage of T's	57,143,511 / 29.89%
Number/percentage of G's	44,257,792 / 23.15%
Number/percentage of N's	21,549 / 0.01%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0618

Standard Deviation	0.6237
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2.4. Mapping Quality

Mean Mapping Quality	43.35
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2.5. Mismatches and indels

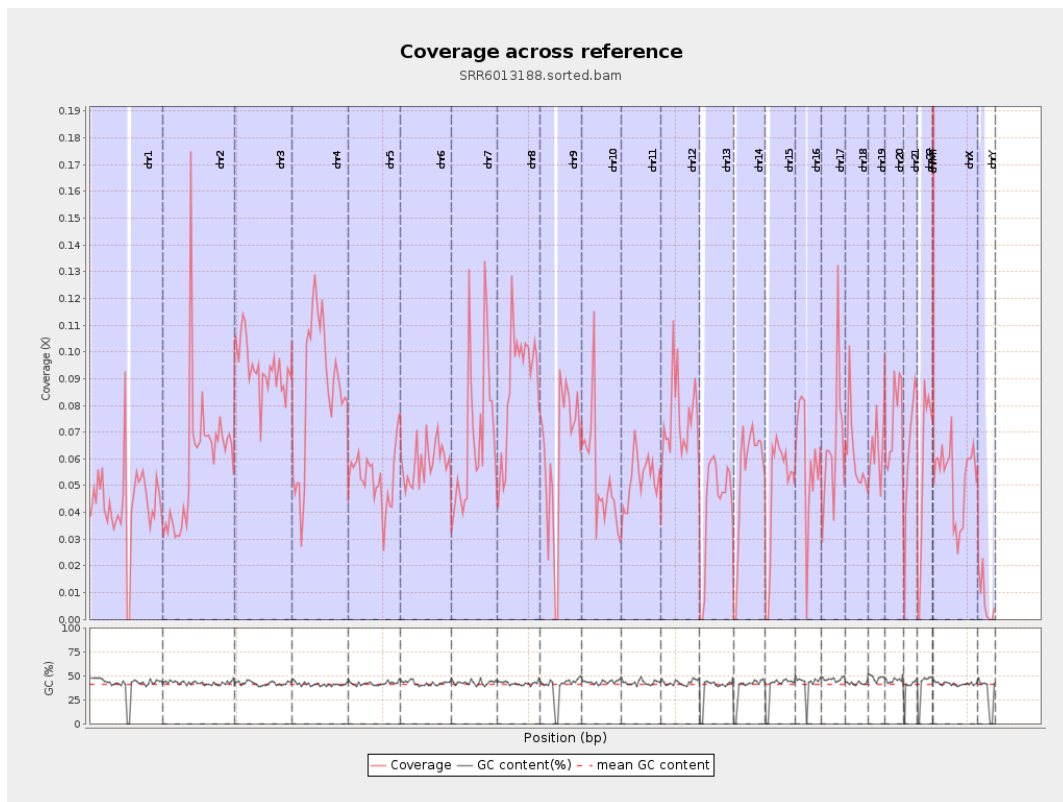
General error rate	0.8%
Mismatches	1,498,503
Insertions	14,846
Mapped reads with at least one insertion	0.5%
Deletions	49,850
Mapped reads with at least one deletion	1.68%
Homopolymer indels	44.15%

2.6. Chromosome stats

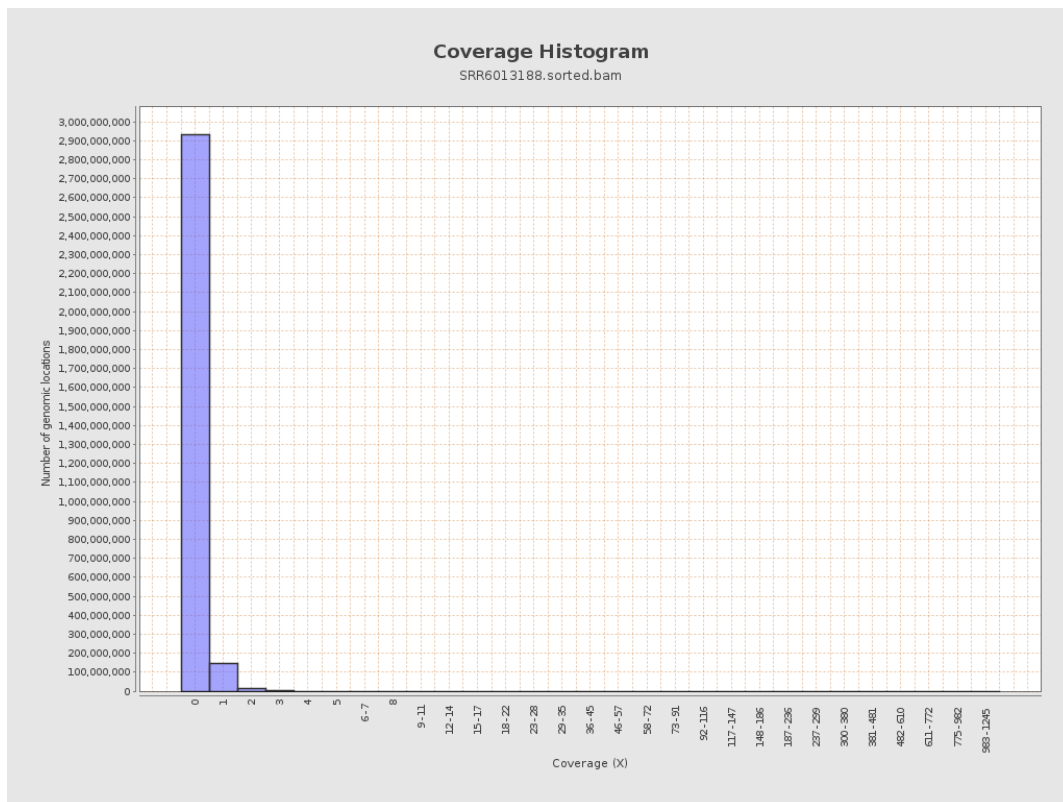
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10753110	0.0431	1.0179
chr2	243199373	14375090	0.0591	0.8974
chr3	198022430	18626742	0.0941	0.3433
chr4	191154276	16557139	0.0866	0.3654
chr5	180915260	9677994	0.0535	0.2653
chr6	171115067	10082866	0.0589	0.3543
chr7	159138663	10856924	0.0682	1.0348

chr8	146364022	12871525	0.0879	0.6323
chr9	141213431	8770619	0.0621	0.6807
chr10	135534747	7114993	0.0525	0.6304
chr11	135006516	7090691	0.0525	0.4792
chr12	133851895	10057760	0.0751	0.3259
chr13	115169878	4967583	0.0431	0.2299
chr14	107349540	5861238	0.0546	0.3604
chr15	102531392	4966619	0.0484	0.2639
chr16	90354753	5340795	0.0591	0.3685
chr17	81195210	5247672	0.0646	0.3466
chr18	78077248	4825742	0.0618	1.3518
chr19	59128983	3819486	0.0646	0.8276
chr20	63025520	4656035	0.0739	0.3327
chr21	48129895	3058952	0.0636	0.3291
chr22	51304566	2916676	0.0569	0.267
chrMT	16571	141057	8.5123	5.2063
chrX	155270560	8192688	0.0528	0.362
chrY	59373566	434118	0.0073	0.2056

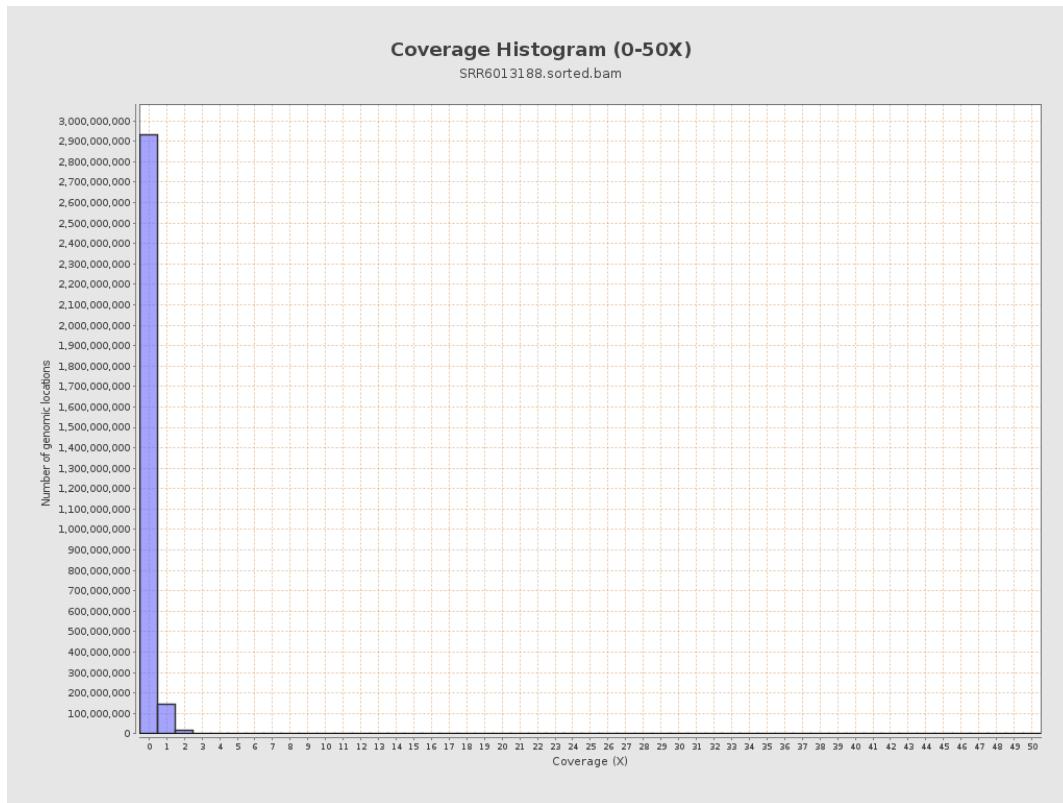
3. Results : Coverage across reference



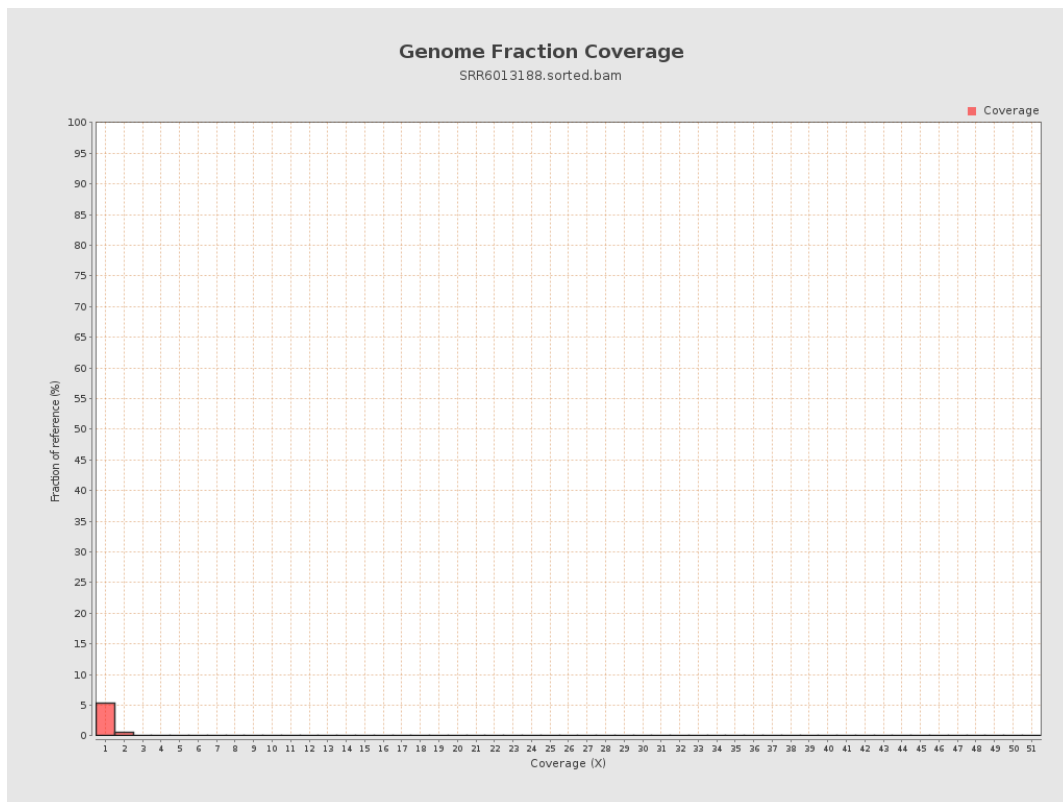
4. Results : Coverage Histogram



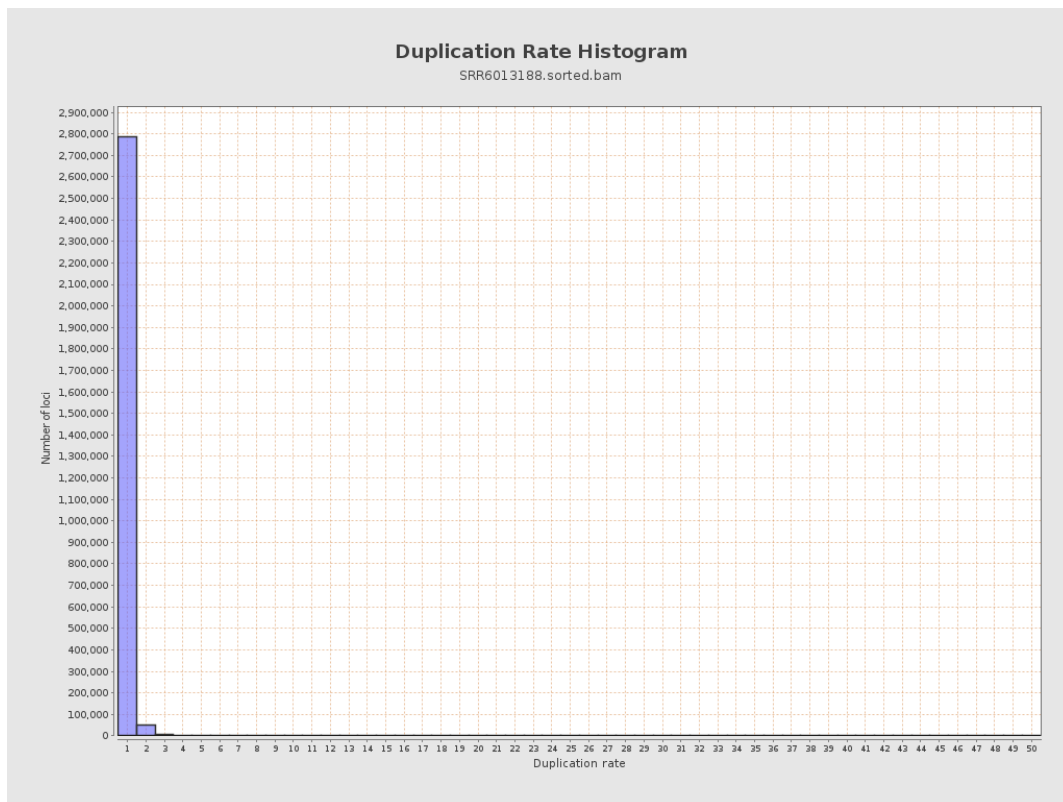
5. Results : Coverage Histogram (0-50X)



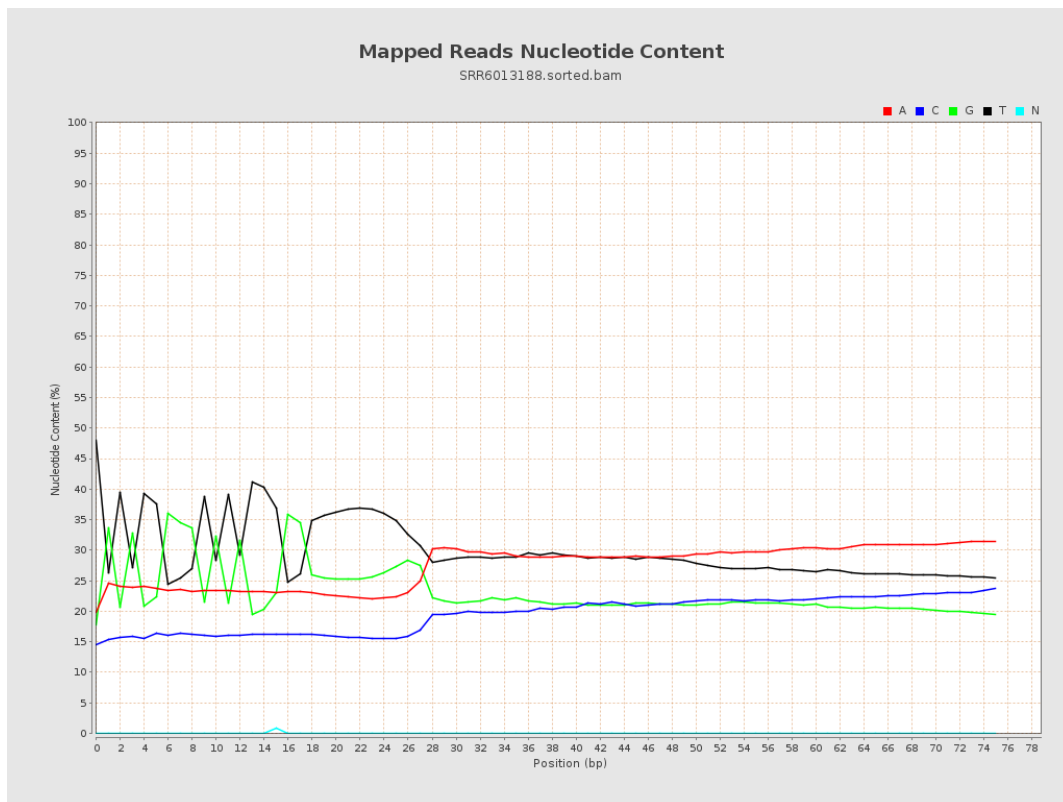
6. Results : Genome Fraction Coverage



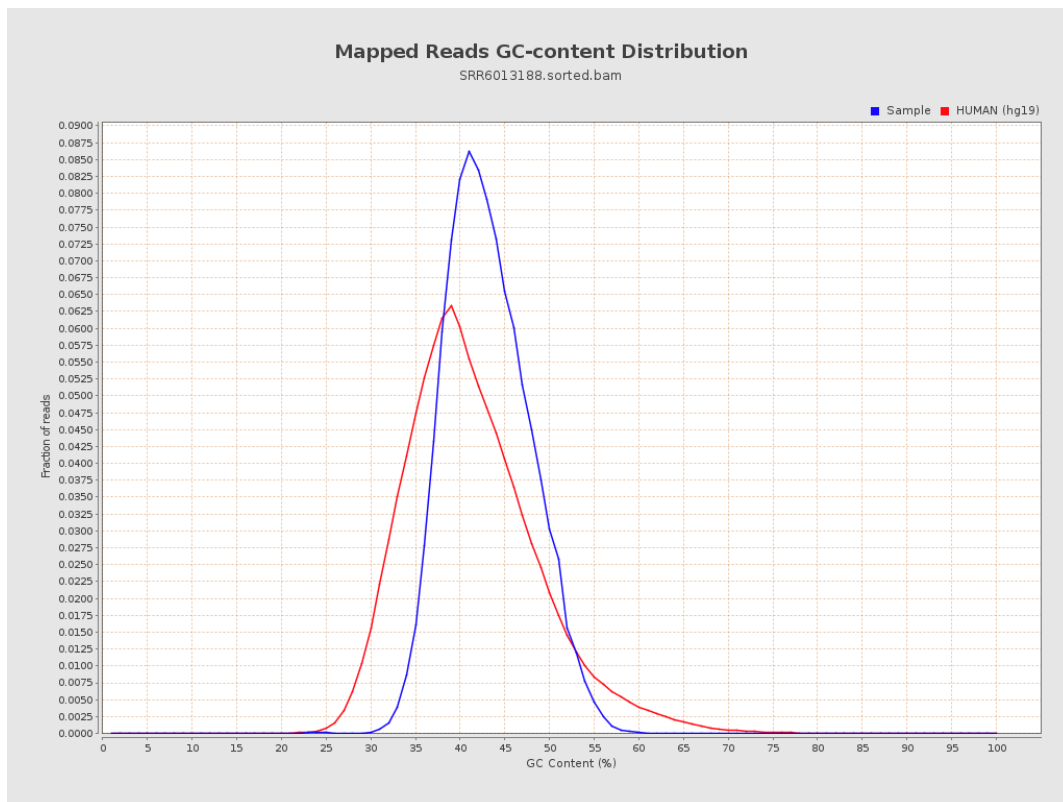
7. Results : Duplication Rate Histogram



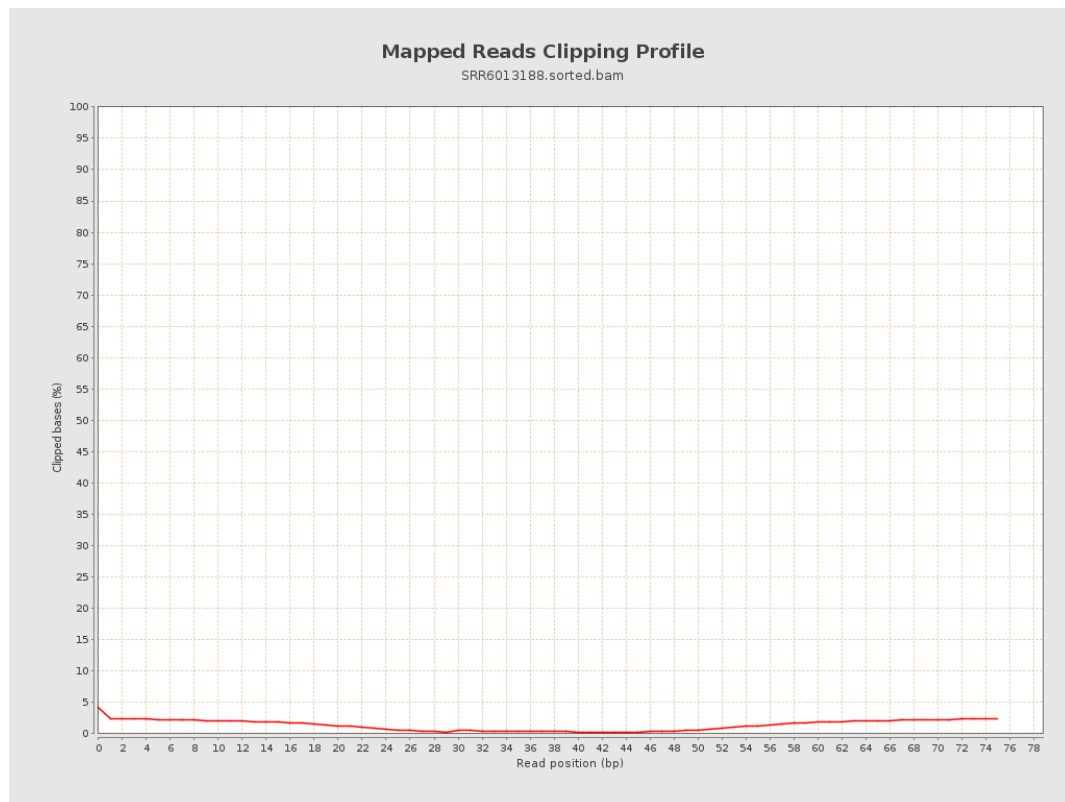
8. Results : Mapped Reads Nucleotide Content



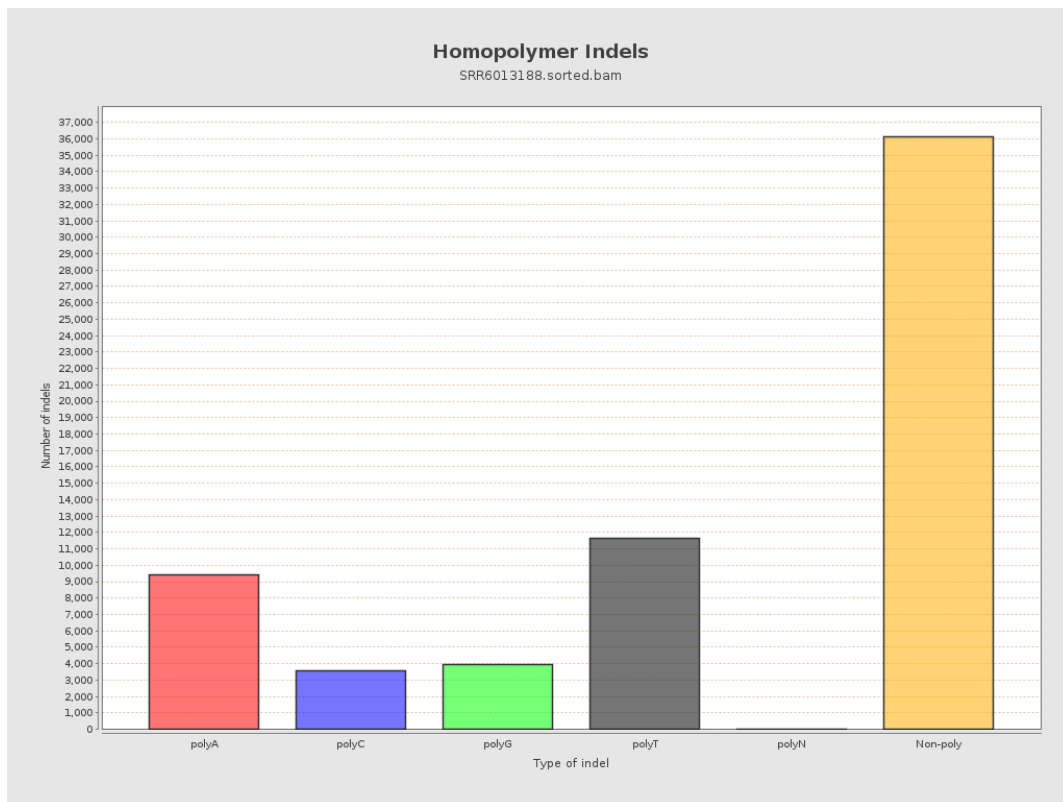
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

