

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:37:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006432.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_SRR1006432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006432.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:37:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006432.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,365,167
Mapped reads	1,256,577 / 92.05%
Unmapped reads	108,590 / 7.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,466 / 0.25%
Read min/max/mean length	30 / 59 / 59.08
Duplicated reads (estimated)	52,327 / 3.83%
Duplication rate	3.67%
Clipped reads	201,470 / 14.76%

2.2. ACGT Content

Number/percentage of A's	20,236,857 / 28.23%
Number/percentage of C's	15,187,571 / 21.18%
Number/percentage of T's	20,747,550 / 28.94%
Number/percentage of G's	15,521,164 / 21.65%
Number/percentage of N's	2,689 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2151
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2.4. Mapping Quality

Mean Mapping Quality	46.47
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2.5. Mismatches and indels

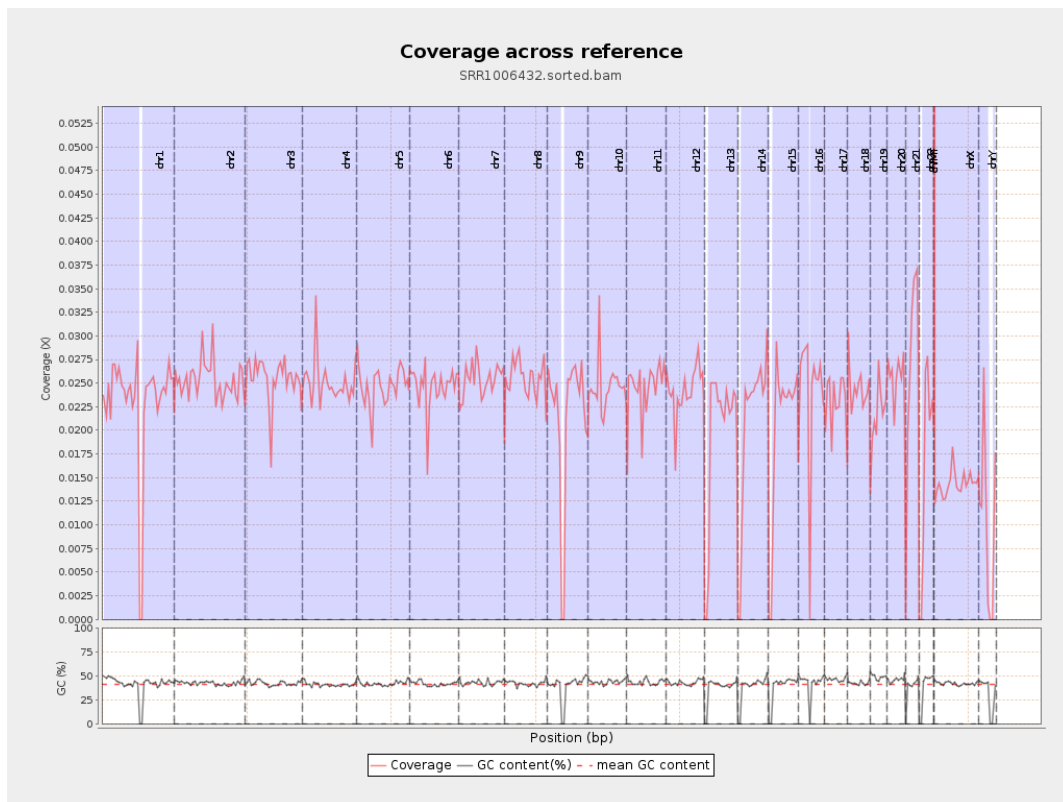
General error rate	0.43%
Mismatches	297,247
Insertions	4,611
Mapped reads with at least one insertion	0.37%
Deletions	12,846
Mapped reads with at least one deletion	1.02%
Homopolymer indels	45.96%

2.6. Chromosome stats

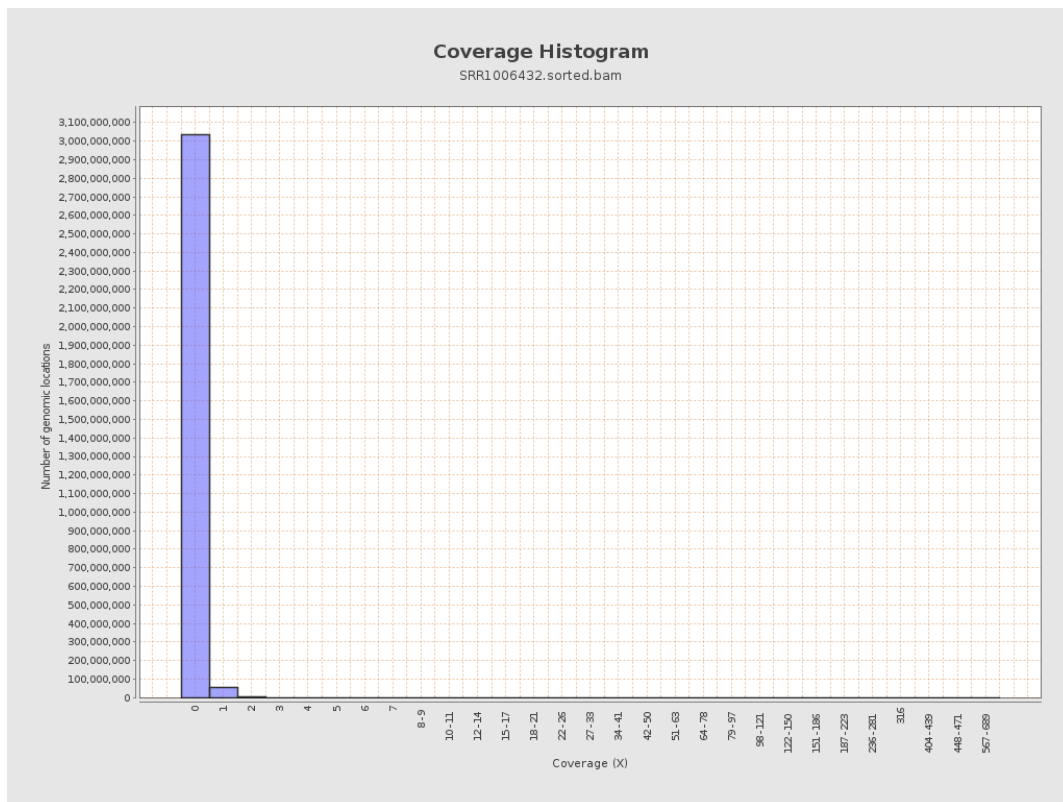
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5738669	0.023	0.2466
chr2	243199373	6171253	0.0254	0.2004
chr3	198022430	5047643	0.0255	0.1771
chr4	191154276	4790438	0.0251	0.182
chr5	180915260	4462524	0.0247	0.1744
chr6	171115067	4212250	0.0246	0.1801
chr7	159138663	4041669	0.0254	0.2124

chr8	146364022	3739194	0.0255	0.4281
chr9	141213431	3029957	0.0215	0.1801
chr10	135534747	3342556	0.0247	0.2054
chr11	135006516	3330634	0.0247	0.1871
chr12	133851895	3231361	0.0241	0.1732
chr13	115169878	2242810	0.0195	0.1554
chr14	107349540	2243211	0.0209	0.3344
chr15	102531392	2073199	0.0202	0.1579
chr16	90354753	2142915	0.0237	0.1857
chr17	81195210	1865791	0.023	0.1783
chr18	78077248	1917068	0.0246	0.2311
chr19	59128983	1296680	0.0219	0.2093
chr20	63025520	1611094	0.0256	0.1924
chr21	48129895	1310205	0.0272	0.1943
chr22	51304566	870965	0.017	0.1564
chrMT	16571	156403	9.4384	6.2022
chrX	155270560	2233283	0.0144	0.1357
chrY	59373566	615634	0.0104	0.1536

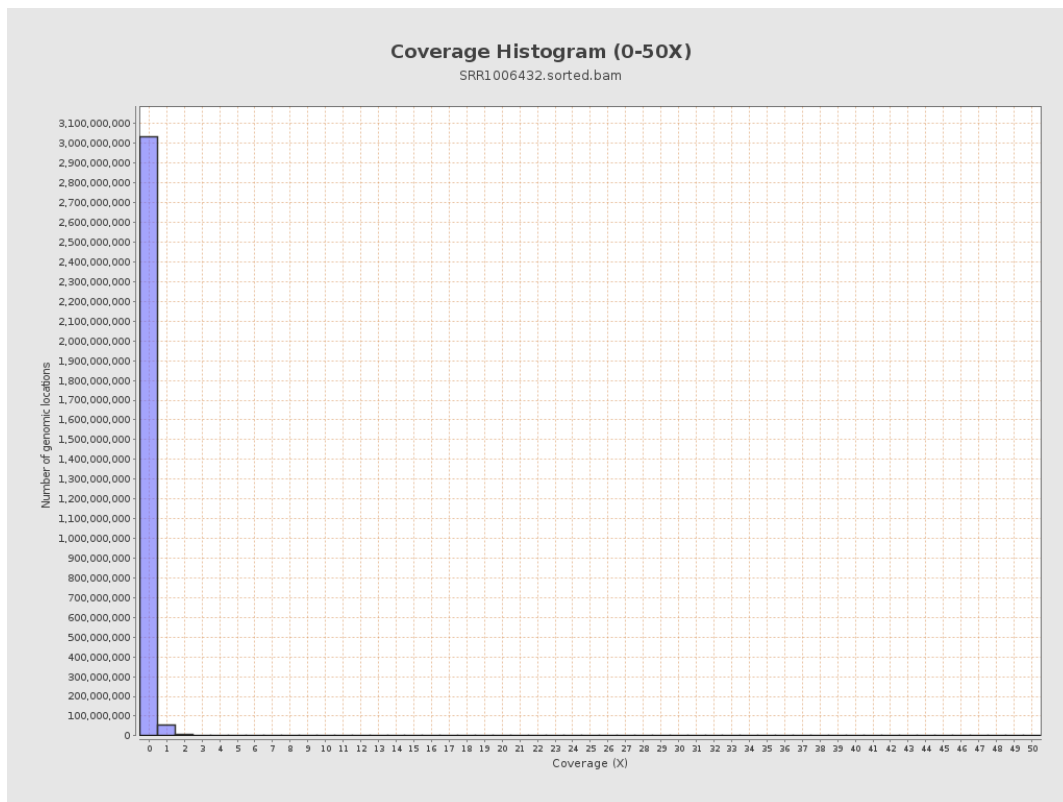
3. Results : Coverage across reference



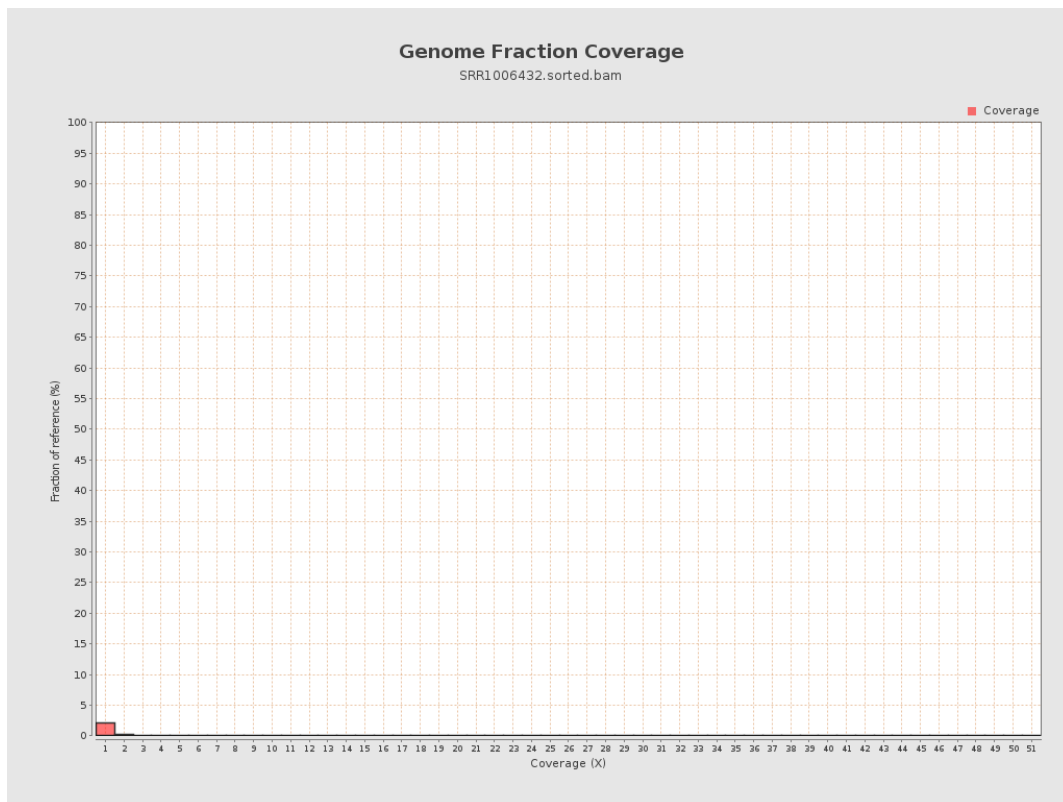
4. Results : Coverage Histogram



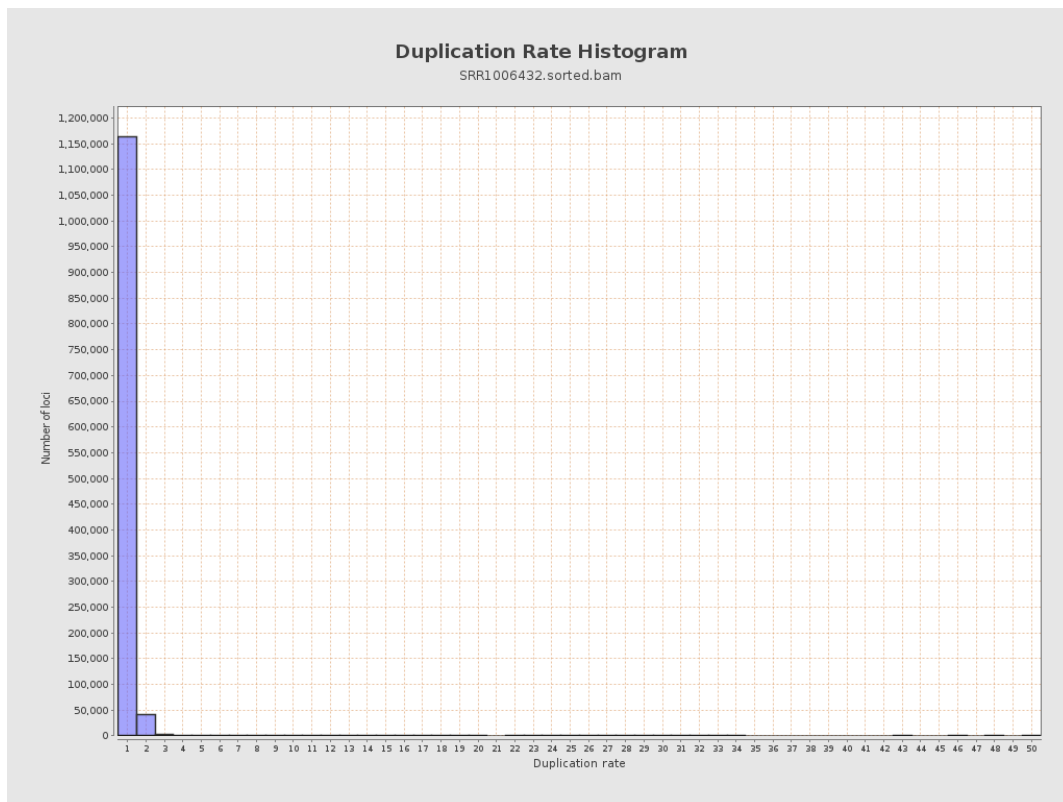
5. Results : Coverage Histogram (0-50X)



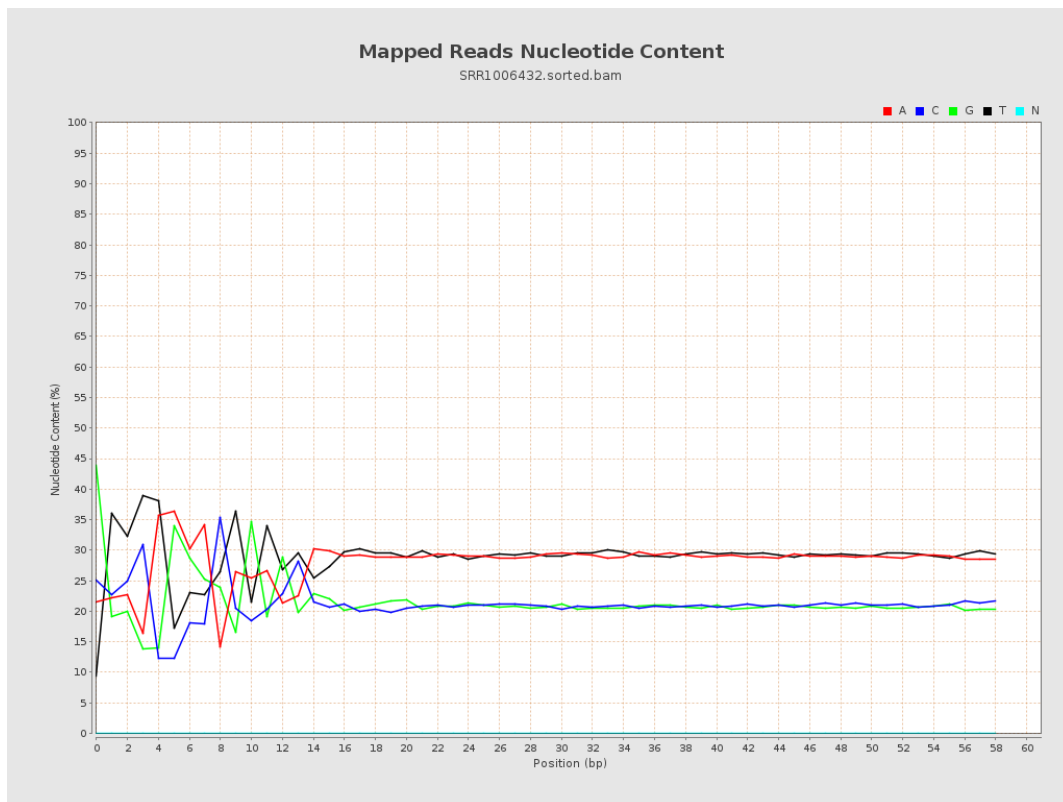
6. Results : Genome Fraction Coverage



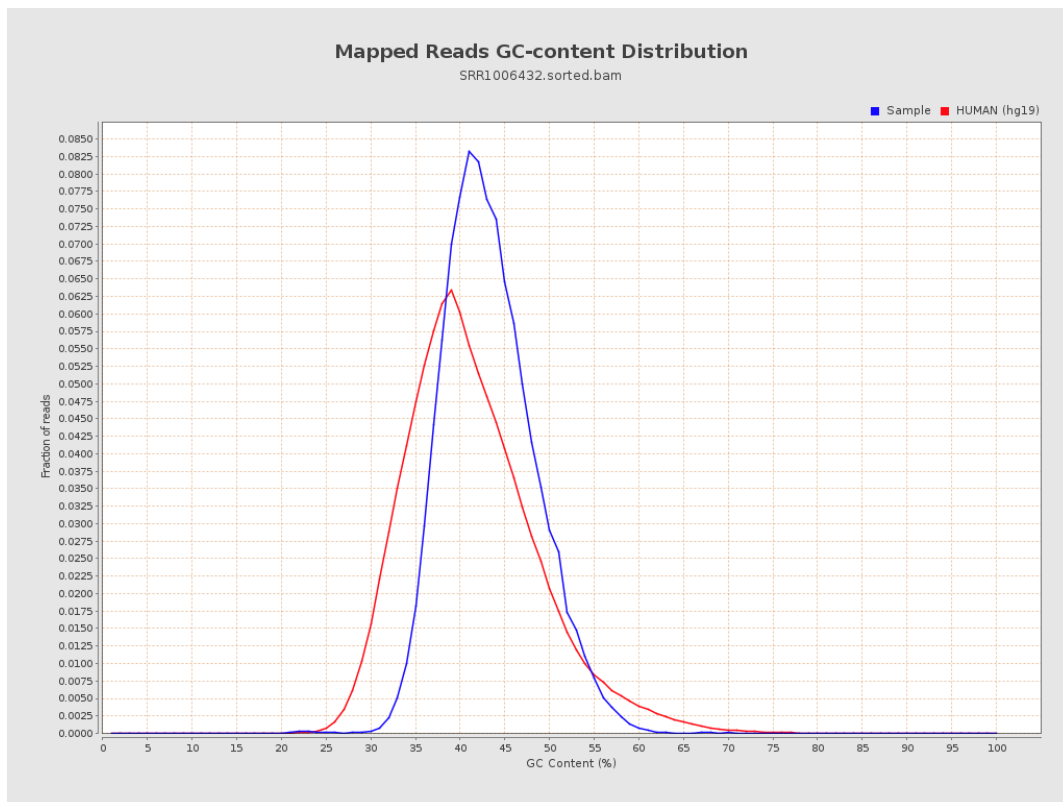
7. Results : Duplication Rate Histogram



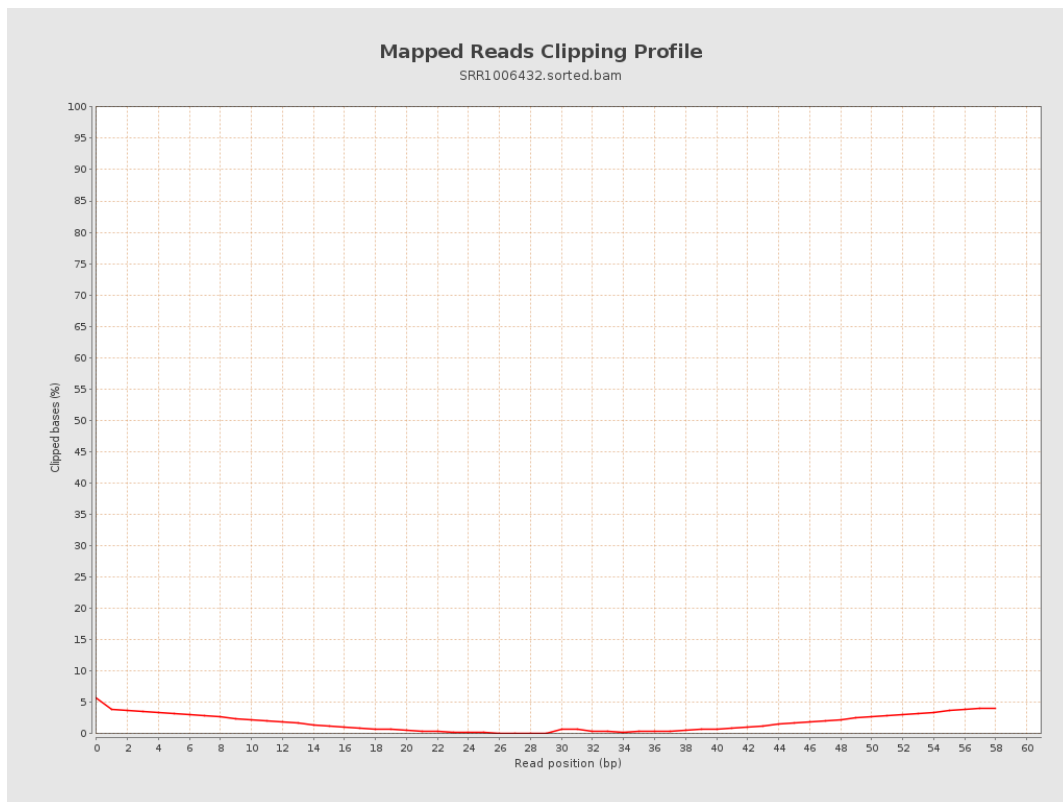
8. Results : Mapped Reads Nucleotide Content



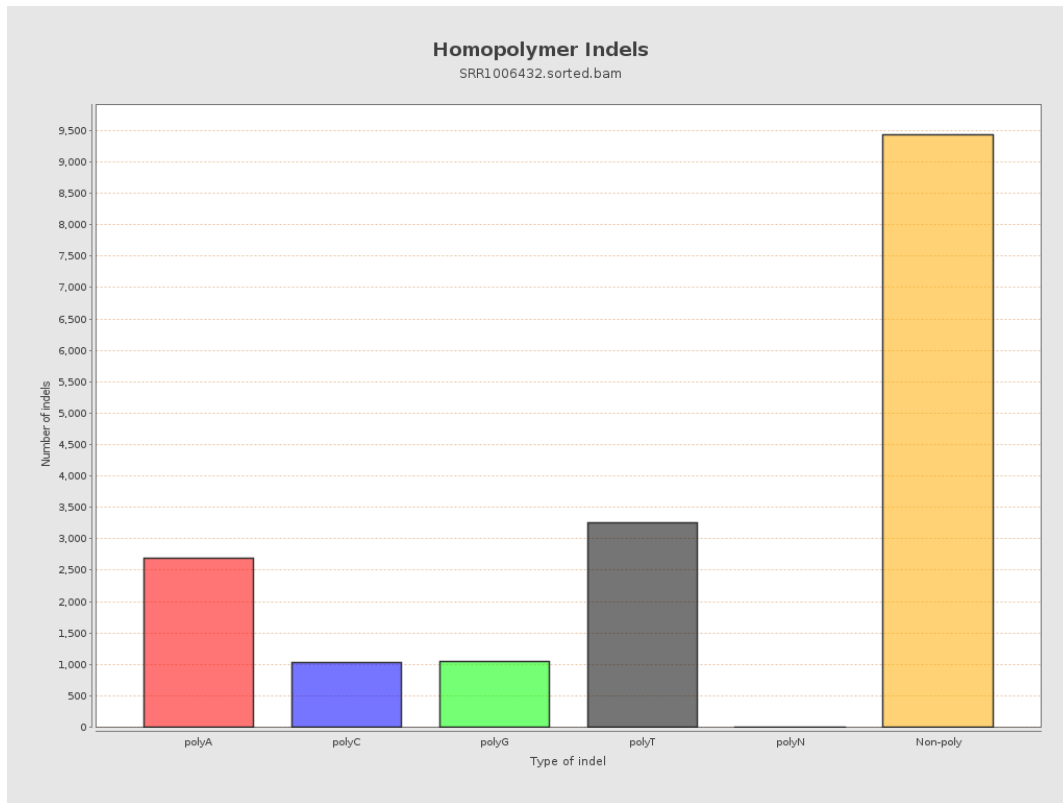
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

