Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:29:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054618.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_SRR054618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:29:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,057,382
Mapped reads	11,572,882 / 82.33%
Unmapped reads	2,484,500 / 17.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	335 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,699,140 / 19.2%
Duplication rate	16.95%
Clipped reads	903,166 / 6.42%

2.2. ACGT Content

Number/percentage of A's	158,291,004 / 28.92%
Number/percentage of C's	107,306,353 / 19.61%
Number/percentage of T's	160,168,353 / 29.26%
Number/percentage of G's	120,921,321 / 22.09%
Number/percentage of N's	618,992 / 0.11%
GC Percentage	41.7%

2.3. Coverage

Mean	0.1768

Standard Deviation	1.1875

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

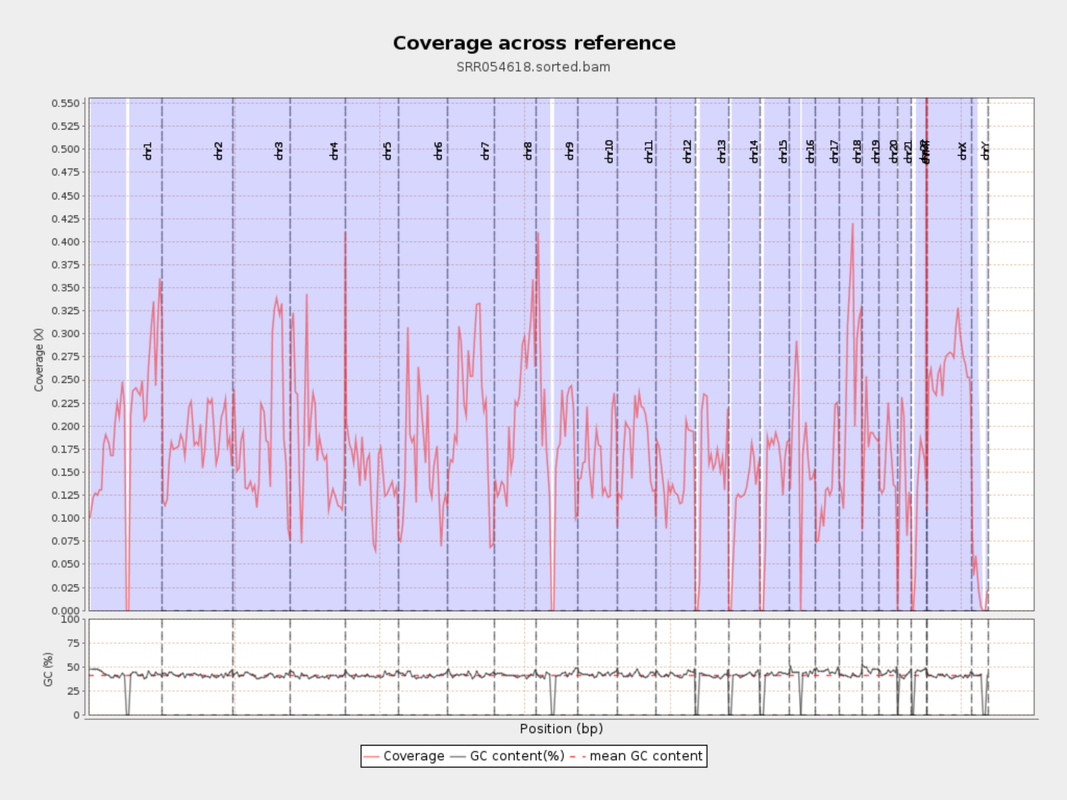
General error rate	0.59%
Mismatches	3,219,371
Insertions	21,303
Mapped reads with at least one insertion	0.18%
Deletions	73,346
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.39%

2.6. Chromosome stats

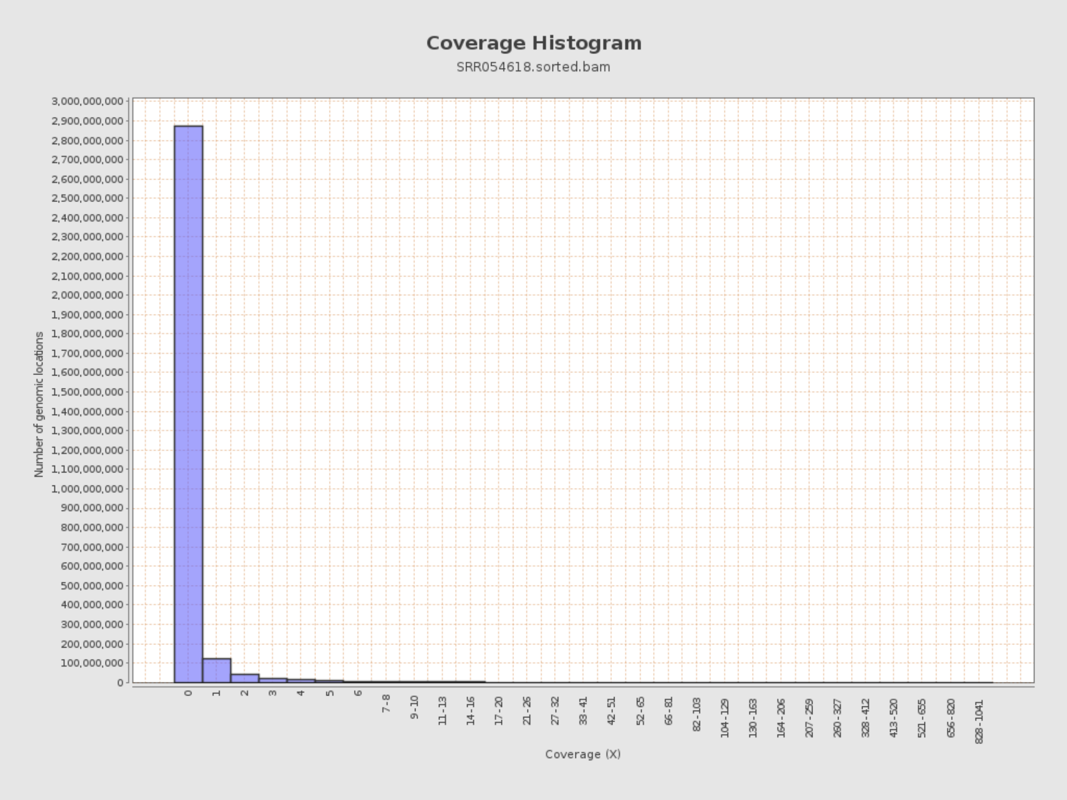
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49949253	0.2004	1.3784
chr2	243199373	44796839	0.1842	1.3647
chr3	198022430	38197575	0.1929	1.1344
chr4	191154276	34033448	0.178	1.1478
chr5	180915260	26845149	0.1484	0.9372
chr6	171115067	26962548	0.1576	1.0628
chr7	159138663	35167857	0.221	1.4715

chr8	146364022	31214322	0.2133	1.269
chr9	141213431	26681704	0.1889	1.2295
chr10	135534747	22423541	0.1654	1.0967
chr11	135006516	24250382	0.1796	1.1877
chr12	133851895	20042212	0.1497	0.9467
chr13	115169878	17178673	0.1492	0.9684
chr14	107349540	12546422	0.1169	0.983
chr15	102531392	14496060	0.1414	0.9126
chr16	90354753	15916788	0.1762	1.2037
chr17	81195210	11088956	0.1366	0.8934
chr18	78077248	20258343	0.2595	1.5973
chr19	59128983	11176750	0.189	1.25
chr20	63025520	9695936	0.1538	1.0699
chr21	48129895	6577225	0.1367	1.1866
chr22	51304566	5685192	0.1108	0.7917
chrMT	16571	22851	1.379	3.4581
chrX	155270560	40711392	0.2622	1.4661
chrY	59373566	1497560	0.0252	0.5368

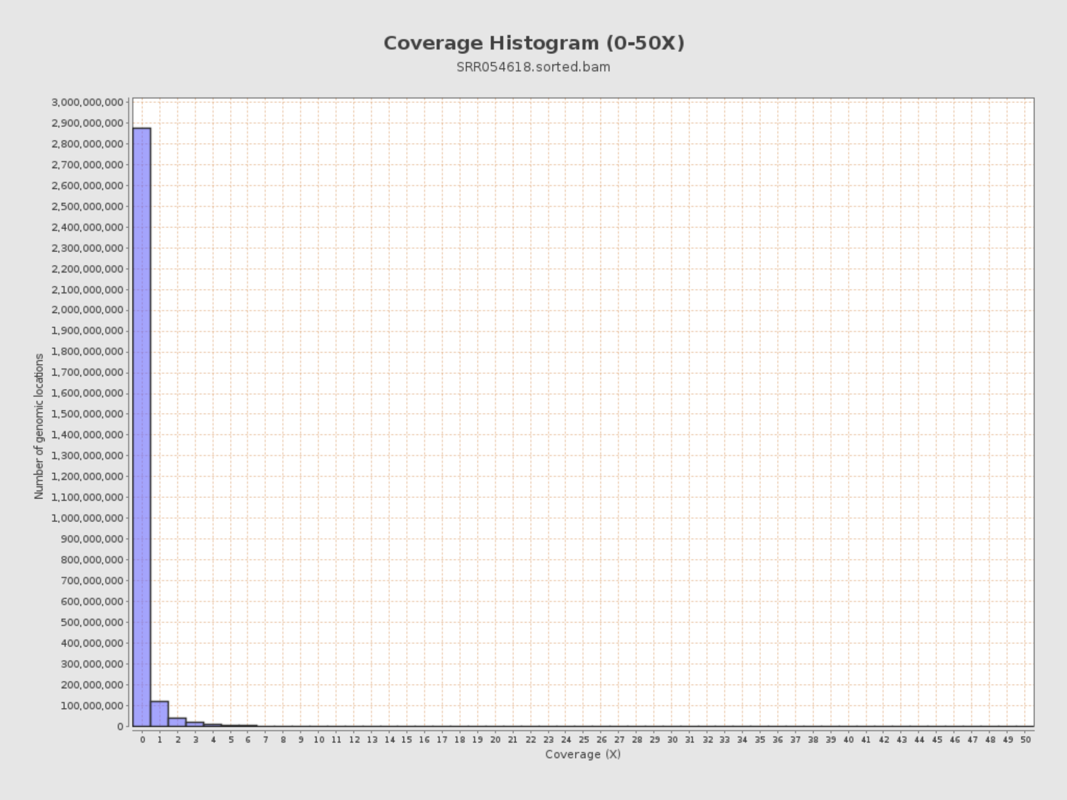
3. Results : Coverage across reference



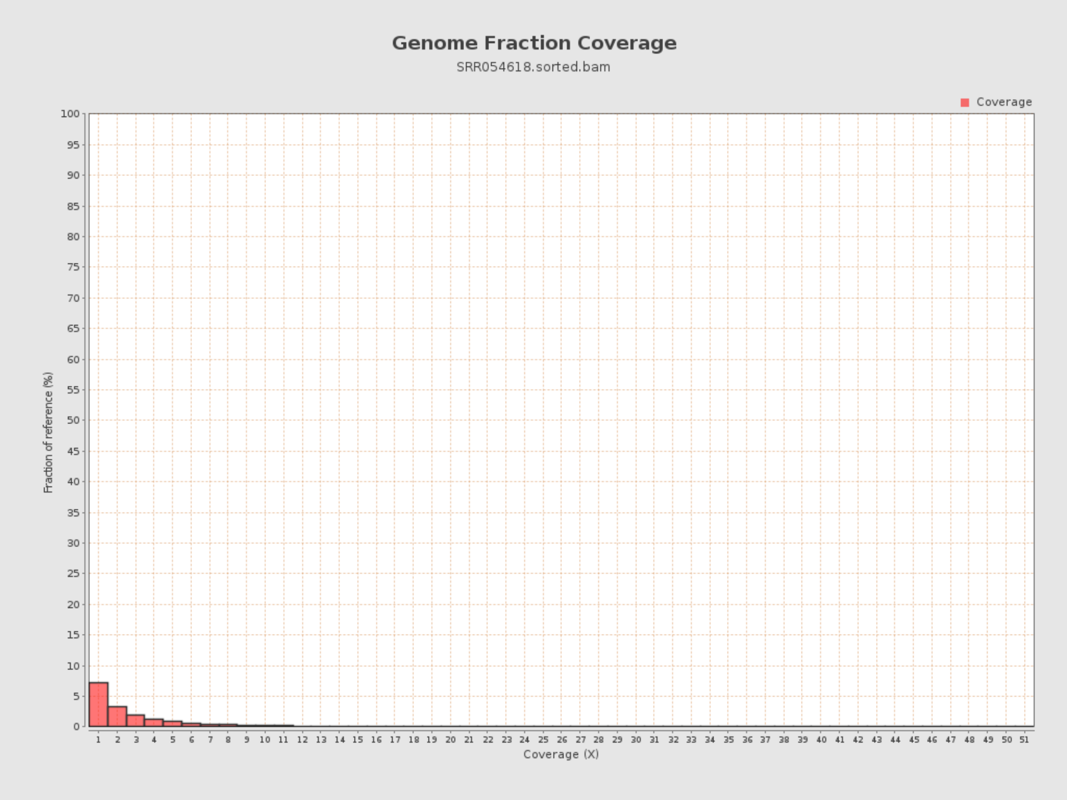
4. Results : Coverage Histogram



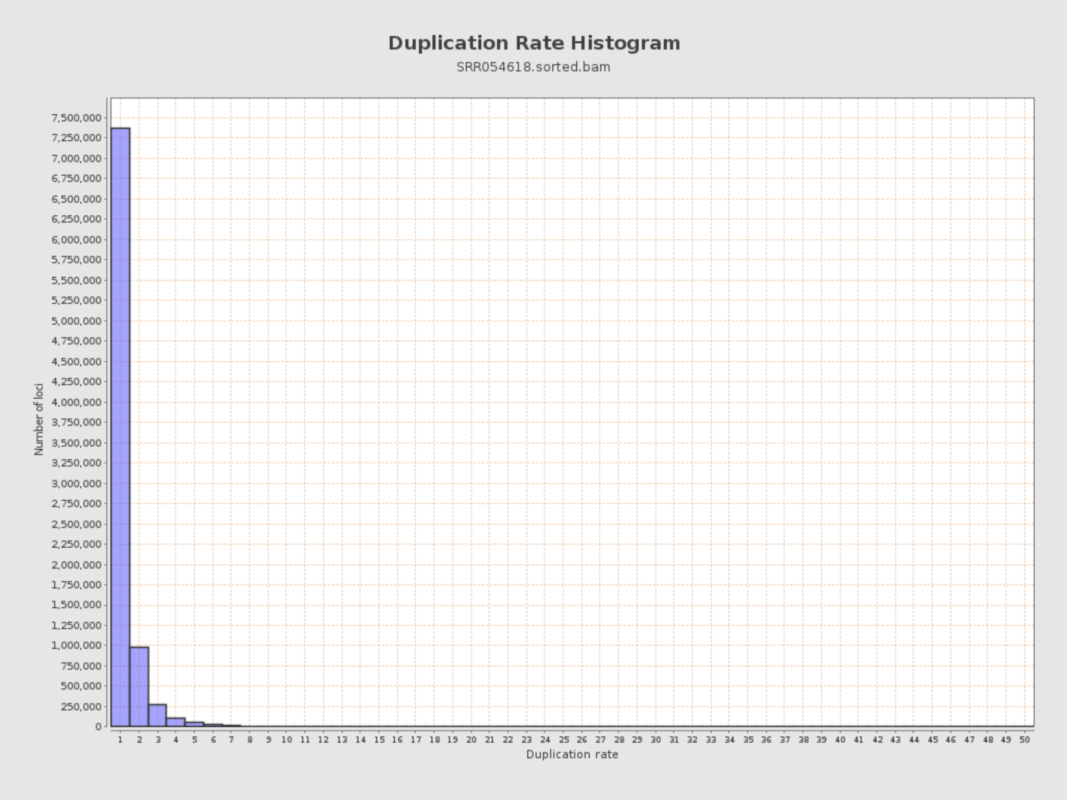
5. Results : Coverage Histogram (0-50X)



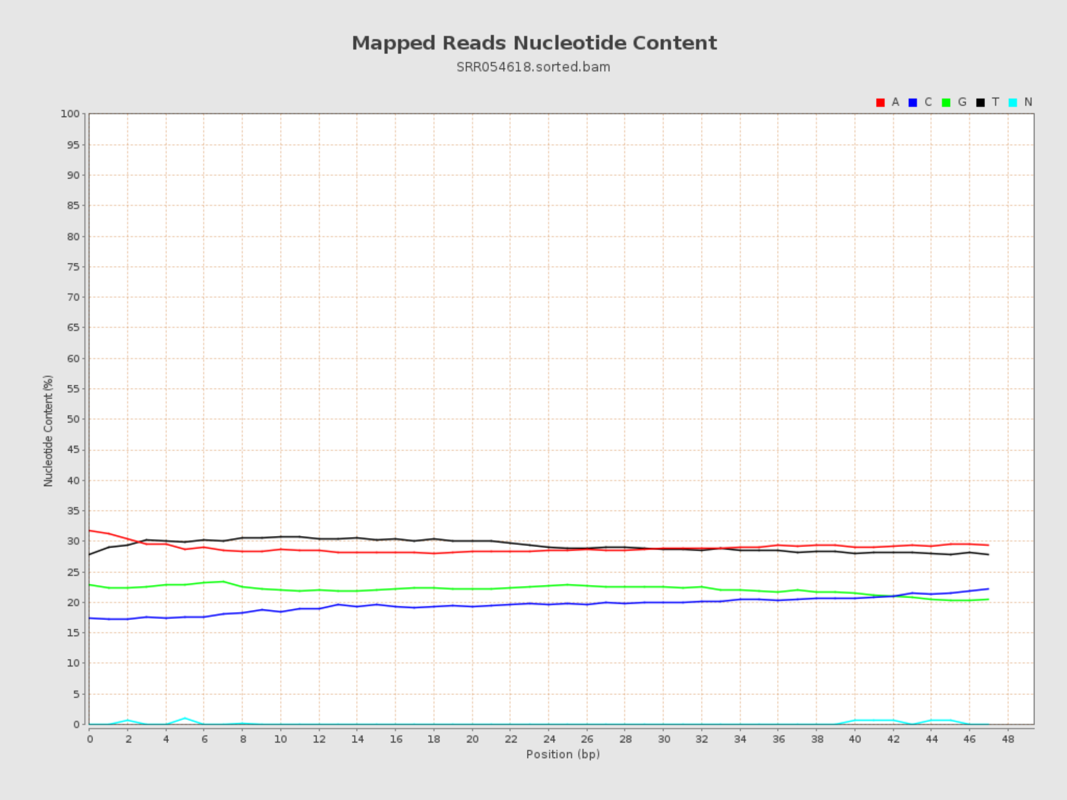
6. Results : Genome Fraction Coverage



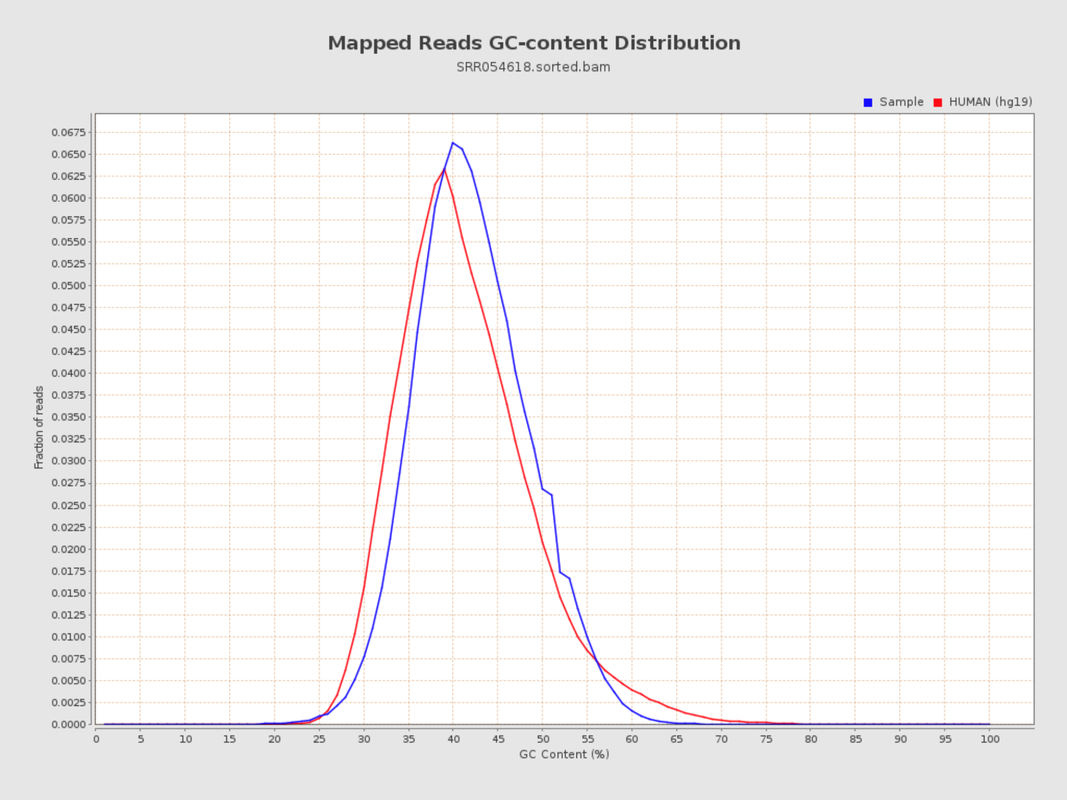
7. Results : Duplication Rate Histogram



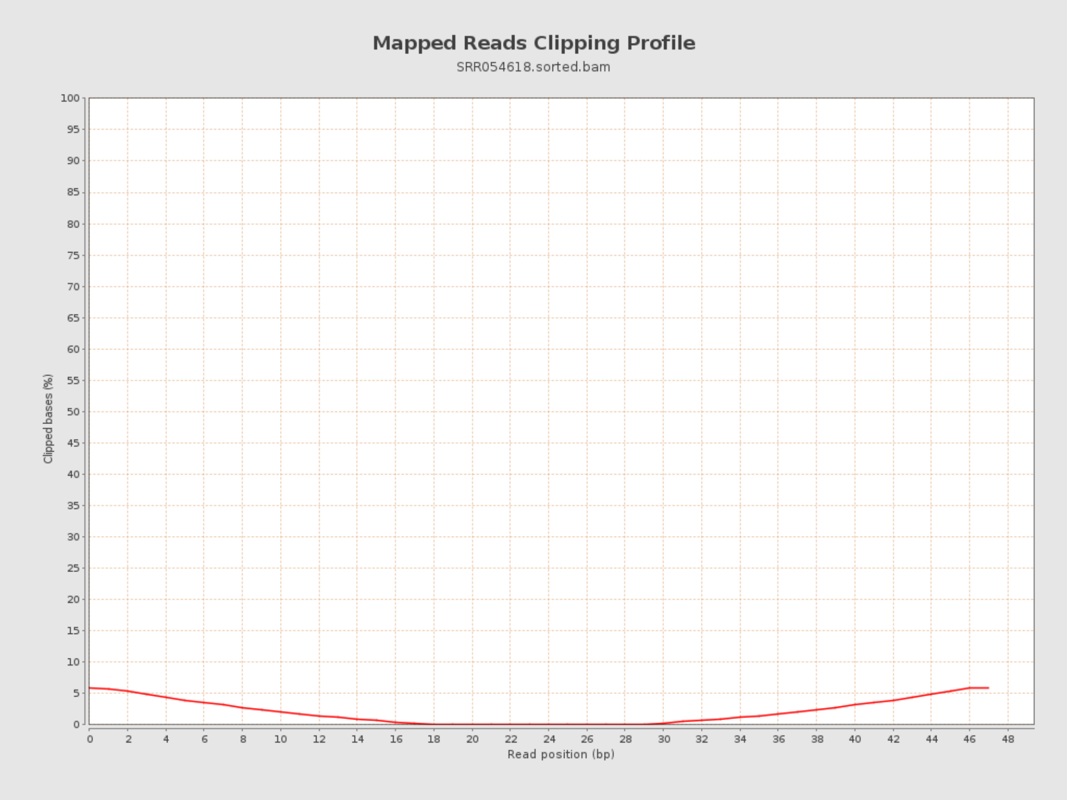
8. Results : Mapped Reads Nucleotide Content



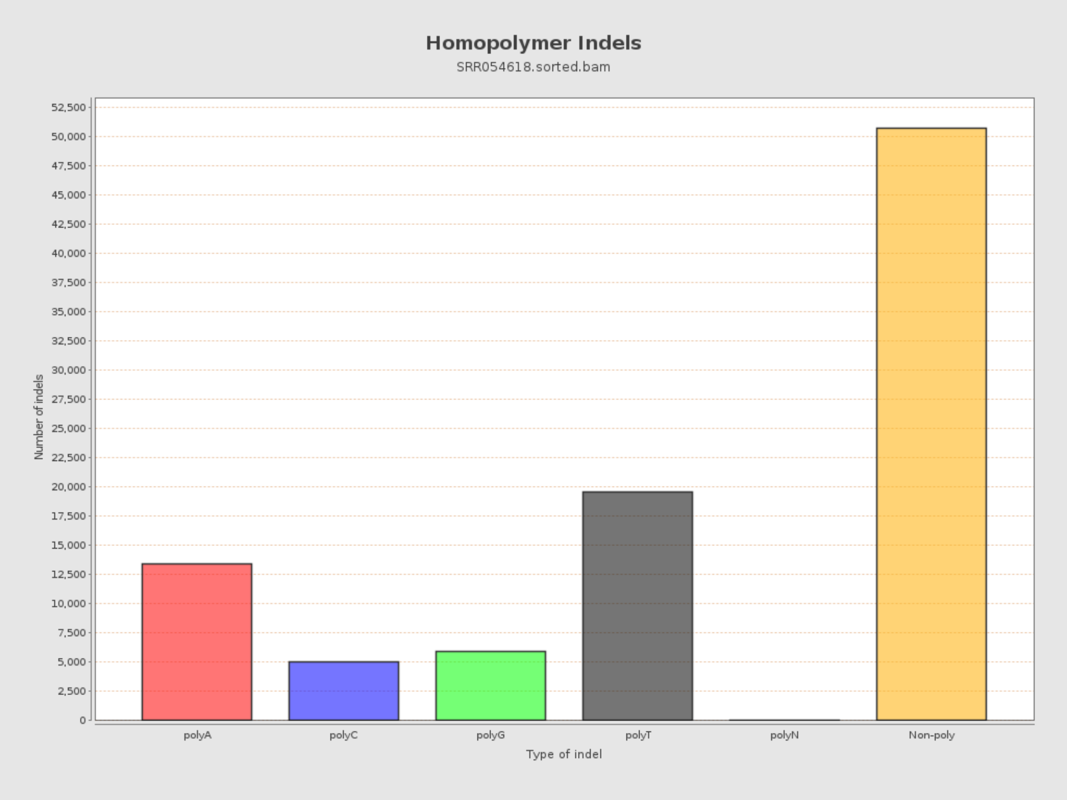
9. Results : Mapped Reads GC-content Distribution



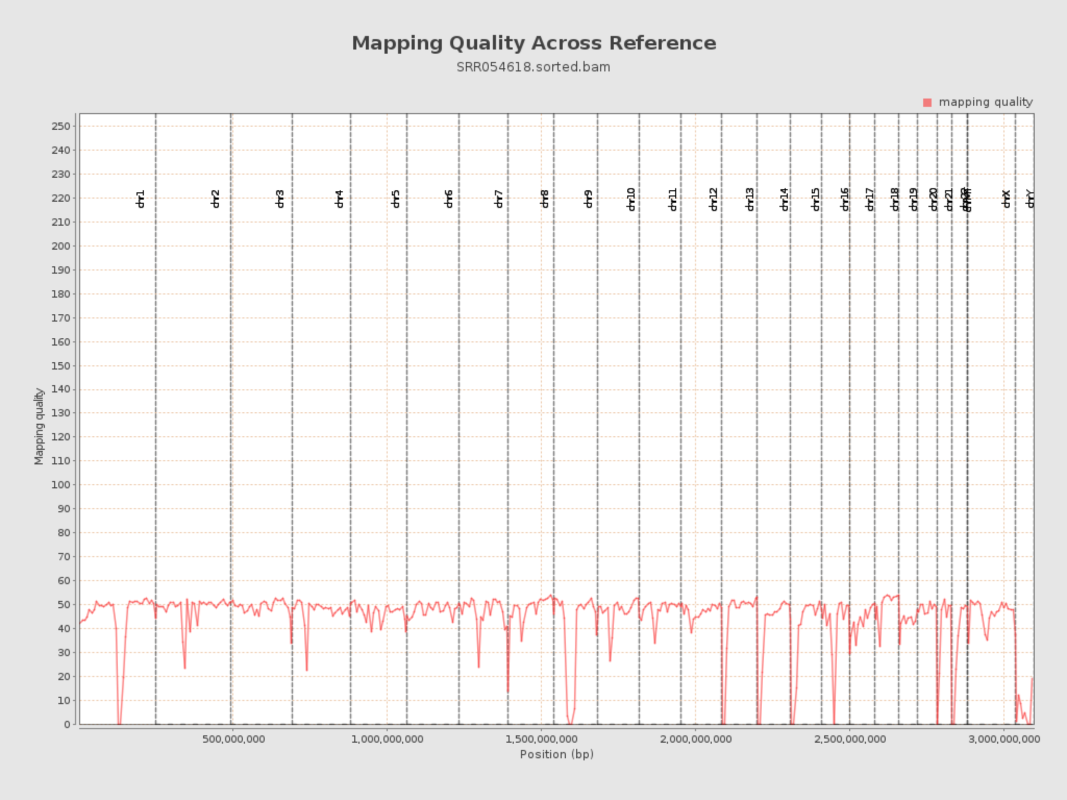
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram