Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:46:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053616.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_SRR053616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:46:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,780,602
Mapped reads	3,857,380 / 56.89%
Unmapped reads	2,923,222 / 43.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	185 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	553,974 / 8.17%
Duplication rate	11.87%
Clipped reads	724,012 / 10.68%

2.2. ACGT Content

Number/percentage of A's	56,052,394 / 31.46%
Number/percentage of C's	33,559,512 / 18.83%
Number/percentage of T's	53,544,343 / 30.05%
Number/percentage of G's	35,034,226 / 19.66%
Number/percentage of N's	4,106 / 0%
GC Percentage	38.49%

2.3. Coverage

Mean	0.0576

Standard Deviation	0.425

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

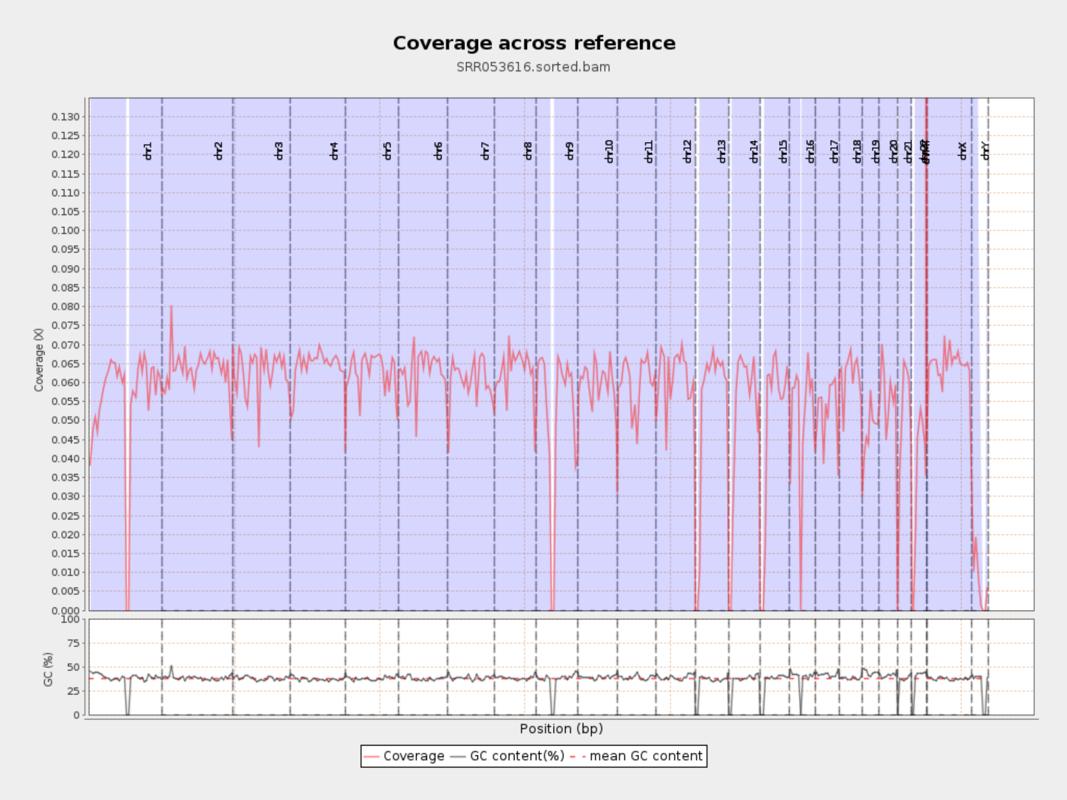
General error rate	0.74%
Mismatches	1,303,046
Insertions	9,030
Mapped reads with at least one insertion	0.23%
Deletions	27,590
Mapped reads with at least one deletion	0.71%
Homopolymer indels	45.71%

2.6. Chromosome stats

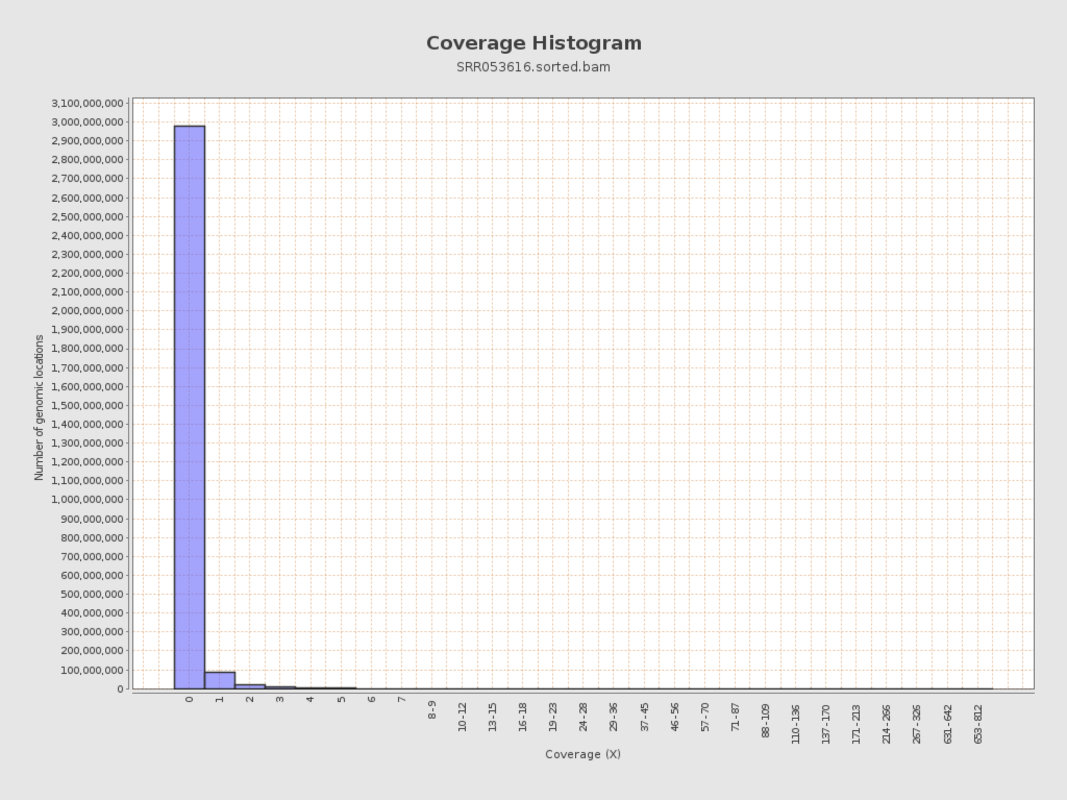
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13845418	0.0555	0.4261
chr2	243199373	15509519	0.0638	0.7229
chr3	198022430	12487007	0.0631	0.3805
chr4	191154276	12352353	0.0646	0.3957
chr5	180915260	11376356	0.0629	0.3782
chr6	171115067	10777141	0.063	0.4203
chr7	159138663	9720822	0.0611	0.4379

chr8	146364022	9235381	0.0631	0.4325
chr9	141213431	7373262	0.0522	0.3691
chr10	135534747	8205049	0.0605	0.4028
chr11	135006516	8055495	0.0597	0.4166
chr12	133851895	8204679	0.0613	0.3762
chr13	115169878	6052614	0.0526	0.3493
chr14	107349540	5460702	0.0509	0.3671
chr15	102531392	5025441	0.049	0.3321
chr16	90354753	4615974	0.0511	0.3655
chr17	81195210	4226129	0.052	0.339
chr18	78077248	4839131	0.062	0.4378
chr19	59128983	2800907	0.0474	0.3888
chr20	63025520	3534151	0.0561	0.3594
chr21	48129895	2350523	0.0488	0.3495
chr22	51304566	1700519	0.0331	0.2618
chrMT	16571	70195	4.236	6.2612
chrX	155270560	9960277	0.0641	0.4071
chrY	59373566	455114	0.0077	0.1271

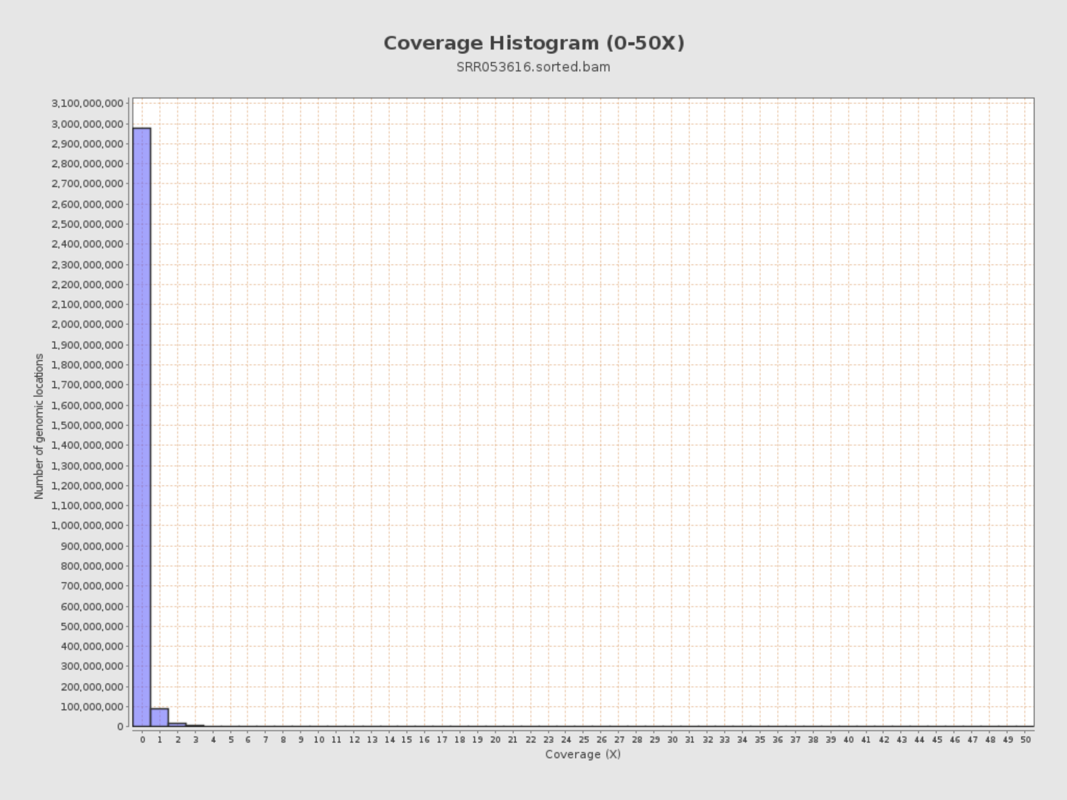
3. Results : Coverage across reference



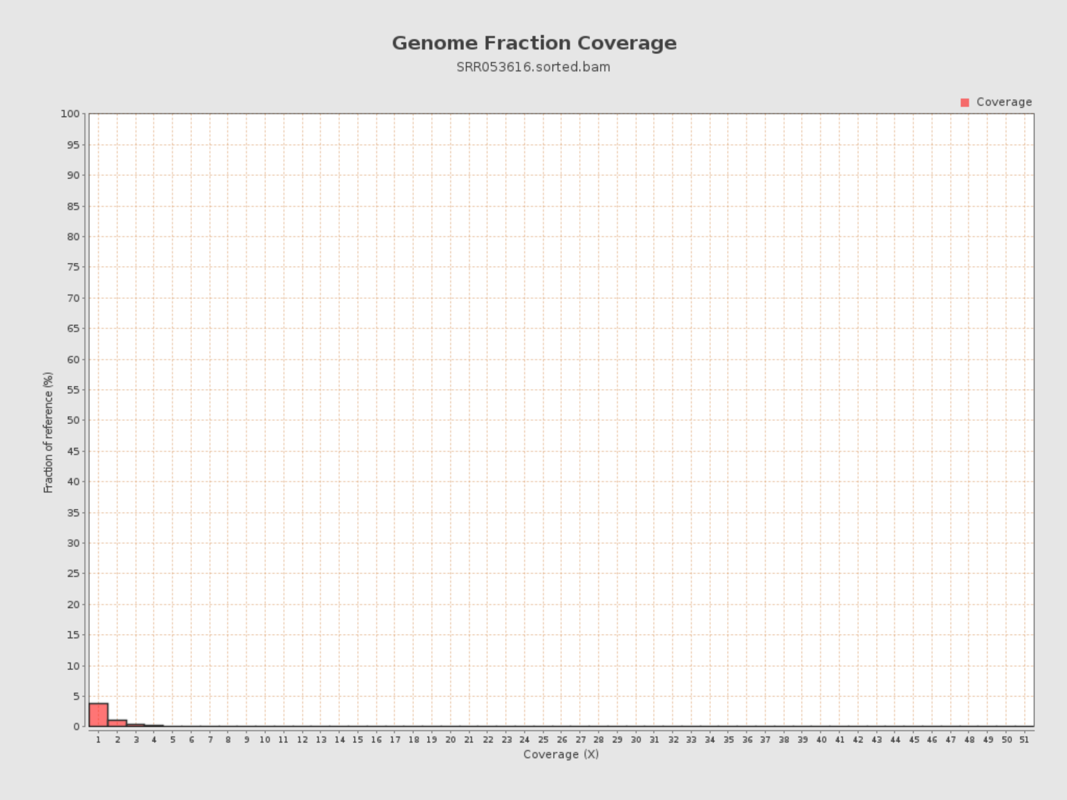
4. Results : Coverage Histogram



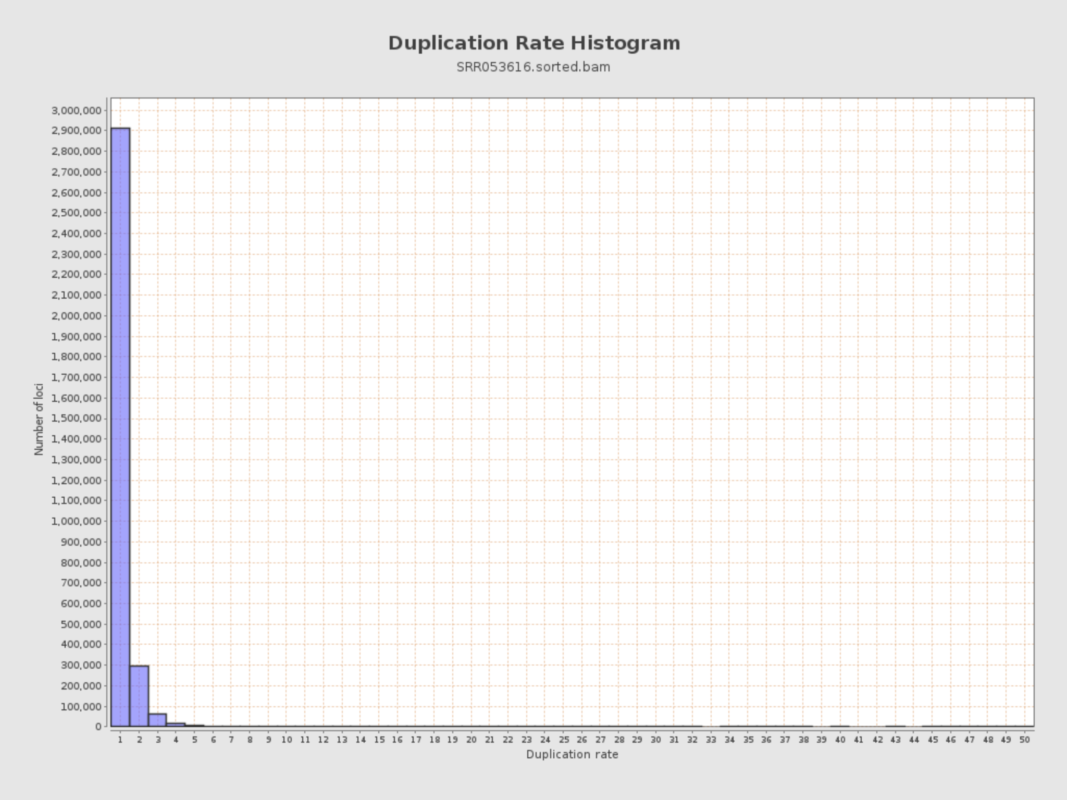
5. Results : Coverage Histogram (0-50X)



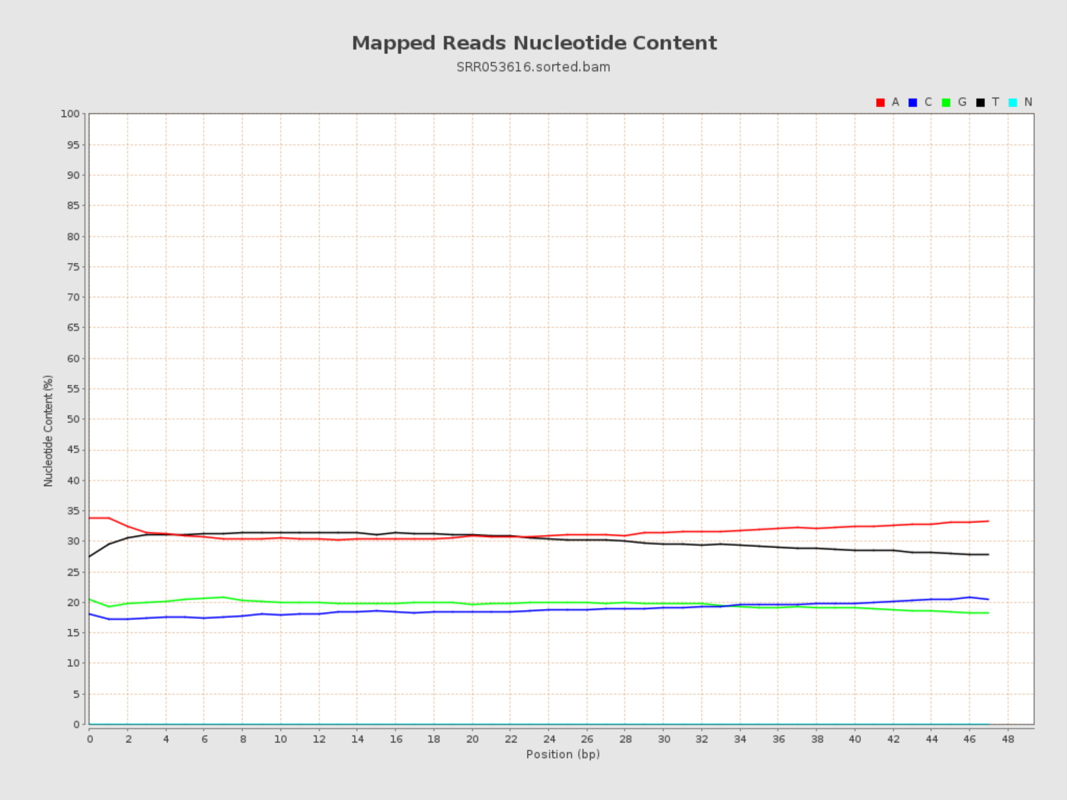
6. Results : Genome Fraction Coverage



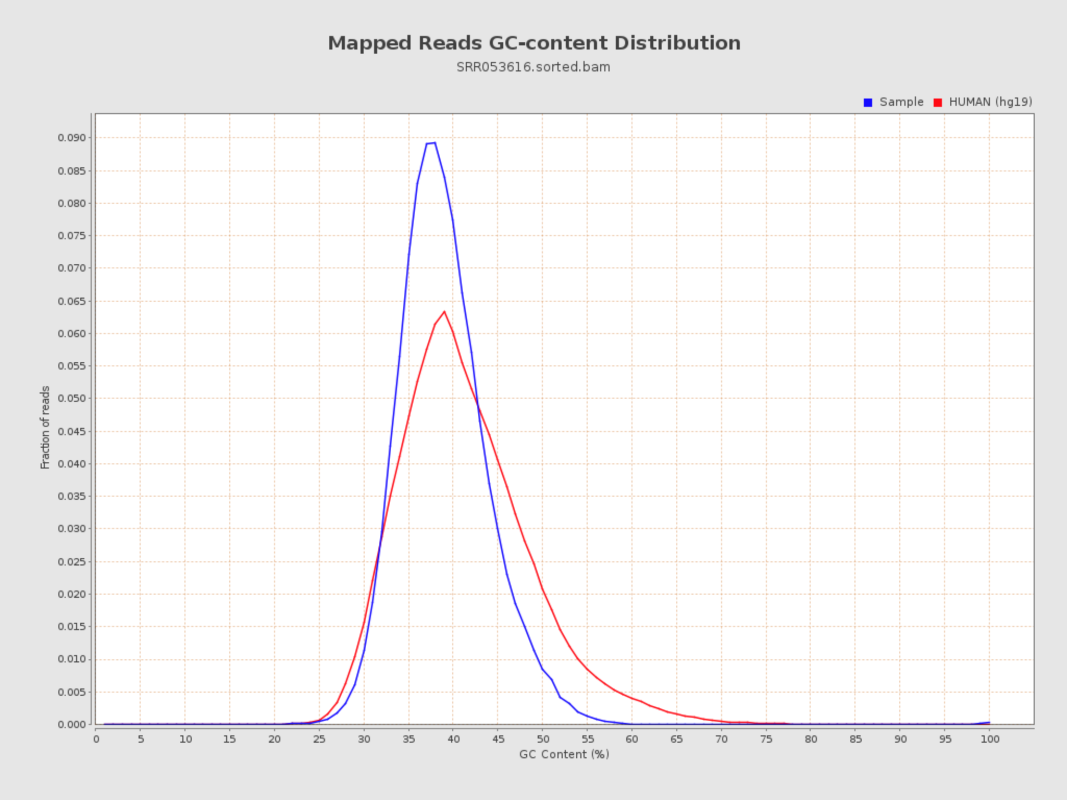
7. Results : Duplication Rate Histogram



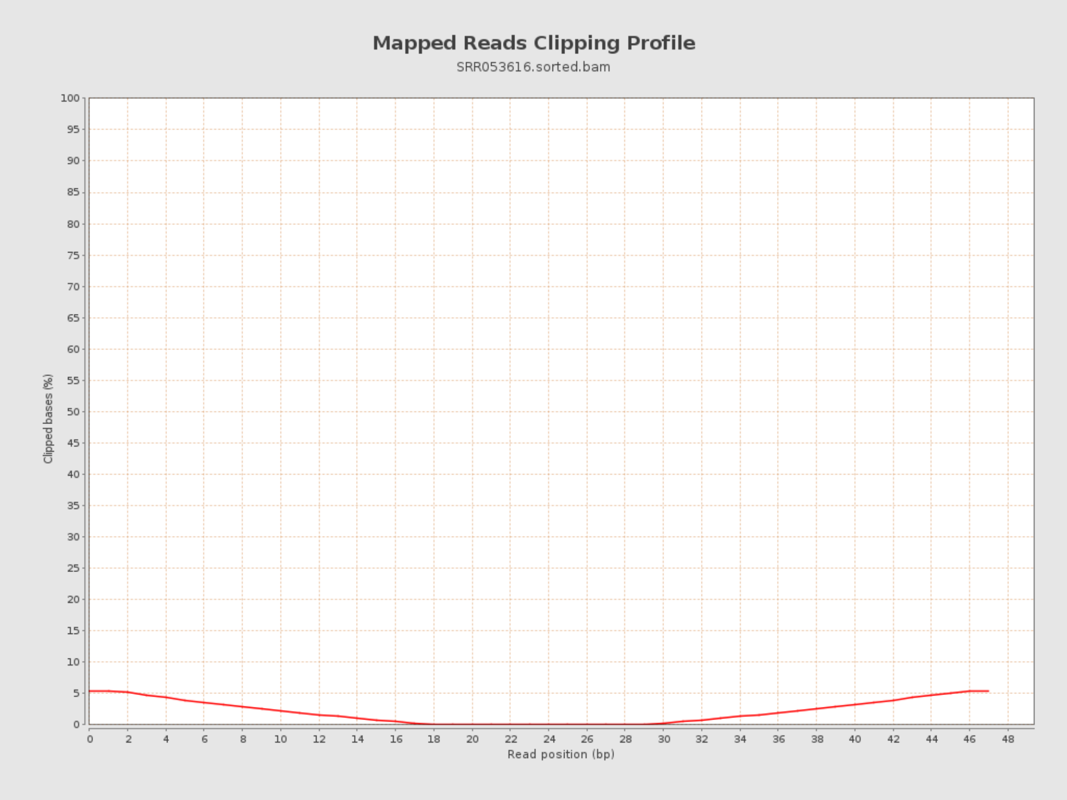
8. Results : Mapped Reads Nucleotide Content



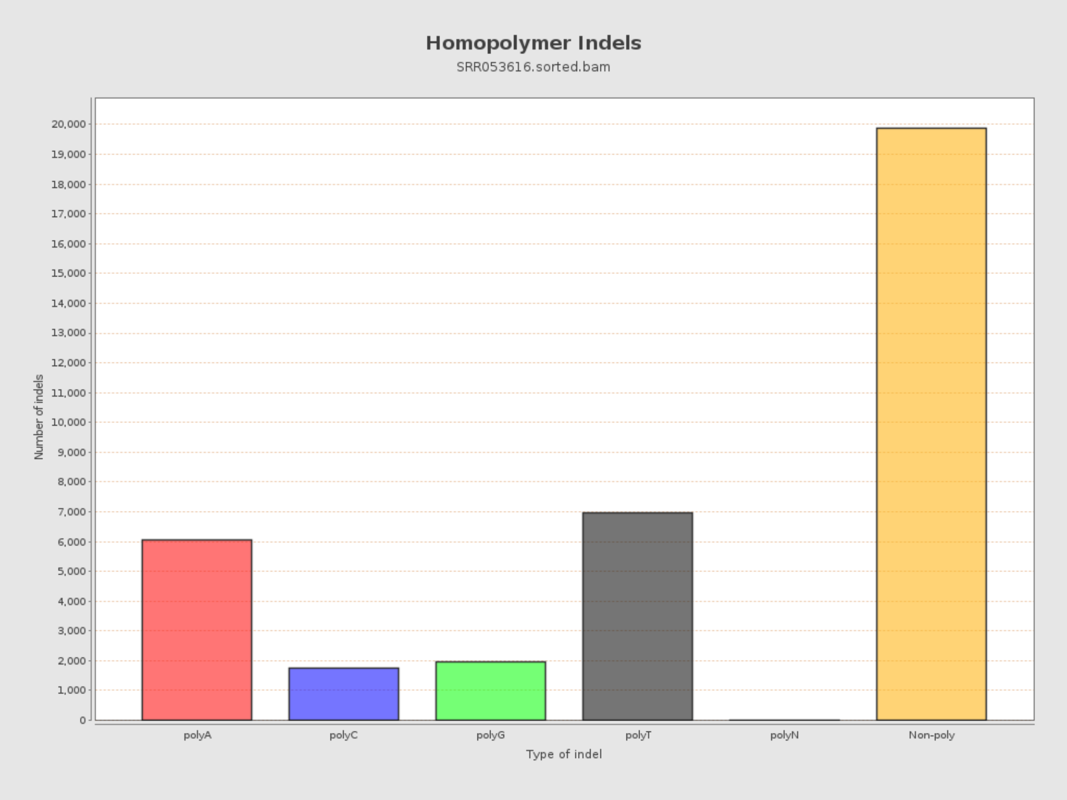
9. Results : Mapped Reads GC-content Distribution



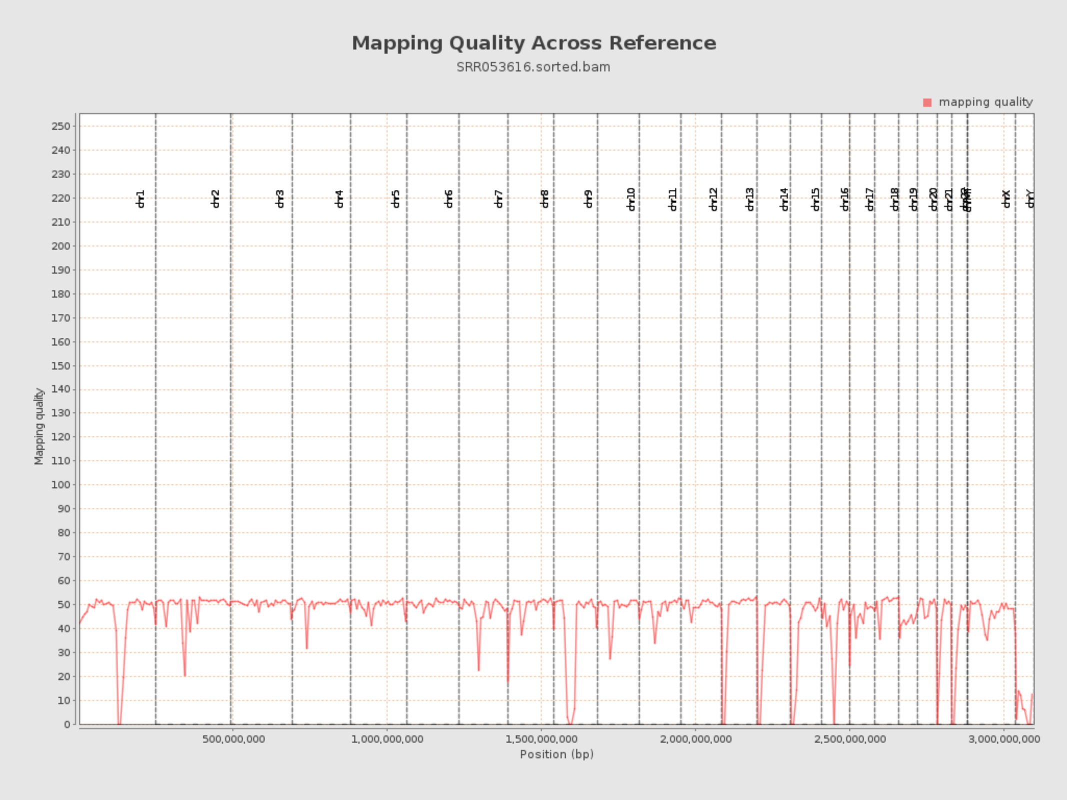
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram