Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:44:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054613.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_SRR054613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:44:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,117,844
Mapped reads	10,044,085 / 76.57%
Unmapped reads	3,073,759 / 23.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	304 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,392,173 / 18.24%
Duplication rate	16.98%
Clipped reads	864,569 / 6.59%

2.2. ACGT Content

Number/percentage of A's	139,545,284 / 29.41%
Number/percentage of C's	92,842,299 / 19.57%
Number/percentage of T's	141,075,489 / 29.74%
Number/percentage of G's	100,686,103 / 21.22%
Number/percentage of N's	268,182 / 0.06%
GC Percentage	40.79%

2.3. Coverage

Mean	0.1533

Standard Deviation	1.0859

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

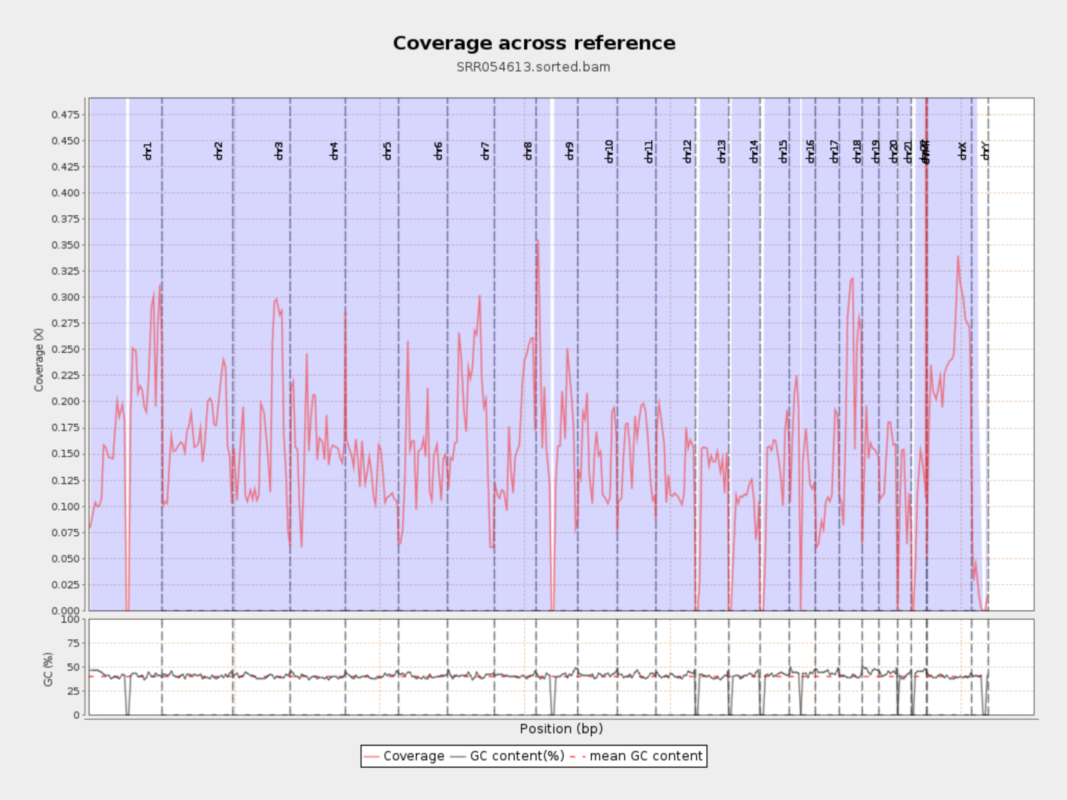
General error rate	0.66%
Mismatches	3,100,344
Insertions	19,181
Mapped reads with at least one insertion	0.19%
Deletions	63,500
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.24%

2.6. Chromosome stats

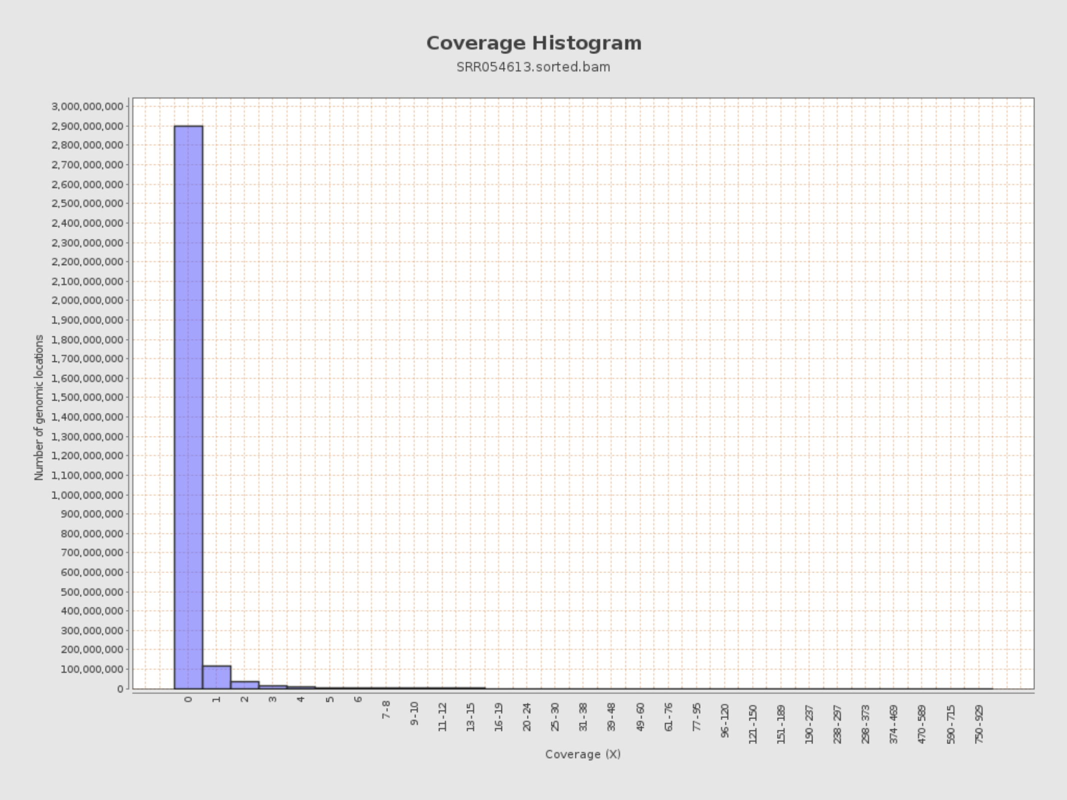
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43640930	0.1751	1.2252
chr2	243199373	40599775	0.1669	1.2497
chr3	198022430	32602508	0.1646	1.0807
chr4	191154276	30805489	0.1612	1.1074
chr5	180915260	23880754	0.132	0.8939
chr6	171115067	23890812	0.1396	1.0111
chr7	159138663	30492916	0.1916	1.2692

chr8	146364022	24634321	0.1683	1.1399
chr9	141213431	23728631	0.168	1.1246
chr10	135534747	20142499	0.1486	1.043
chr11	135006516	20564421	0.1523	1.0457
chr12	133851895	18503266	0.1382	0.9304
chr13	115169878	13898556	0.1207	0.8556
chr14	107349540	9408382	0.0876	0.894
chr15	102531392	12665117	0.1235	0.8903
chr16	90354753	13057498	0.1445	1.0325
chr17	81195210	9195930	0.1133	0.8485
chr18	78077248	16851643	0.2158	1.3339
chr19	59128983	8946985	0.1513	1.1082
chr20	63025520	8996180	0.1427	1.014
chr21	48129895	4897350	0.1018	0.9235
chr22	51304566	4640481	0.0904	0.7237
chrMT	16571	48507	2.9272	5.9464
chrX	155270560	37298352	0.2402	1.4156
chrY	59373566	1120841	0.0189	0.3788

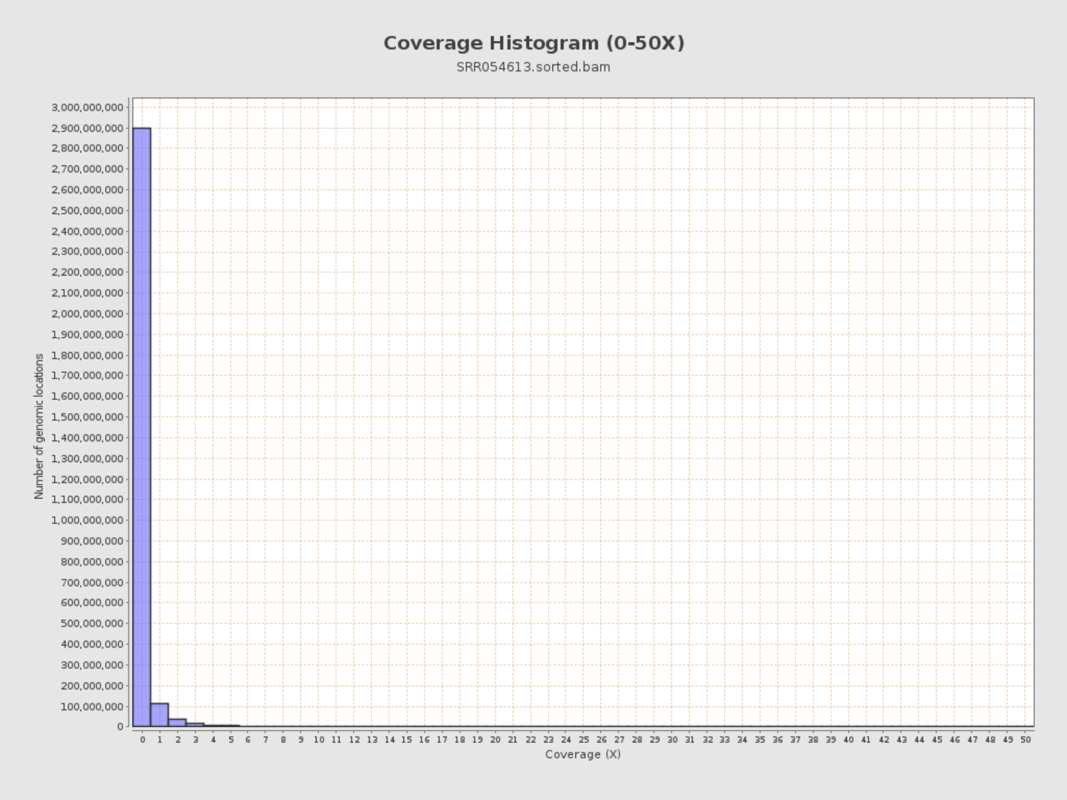
3. Results : Coverage across reference



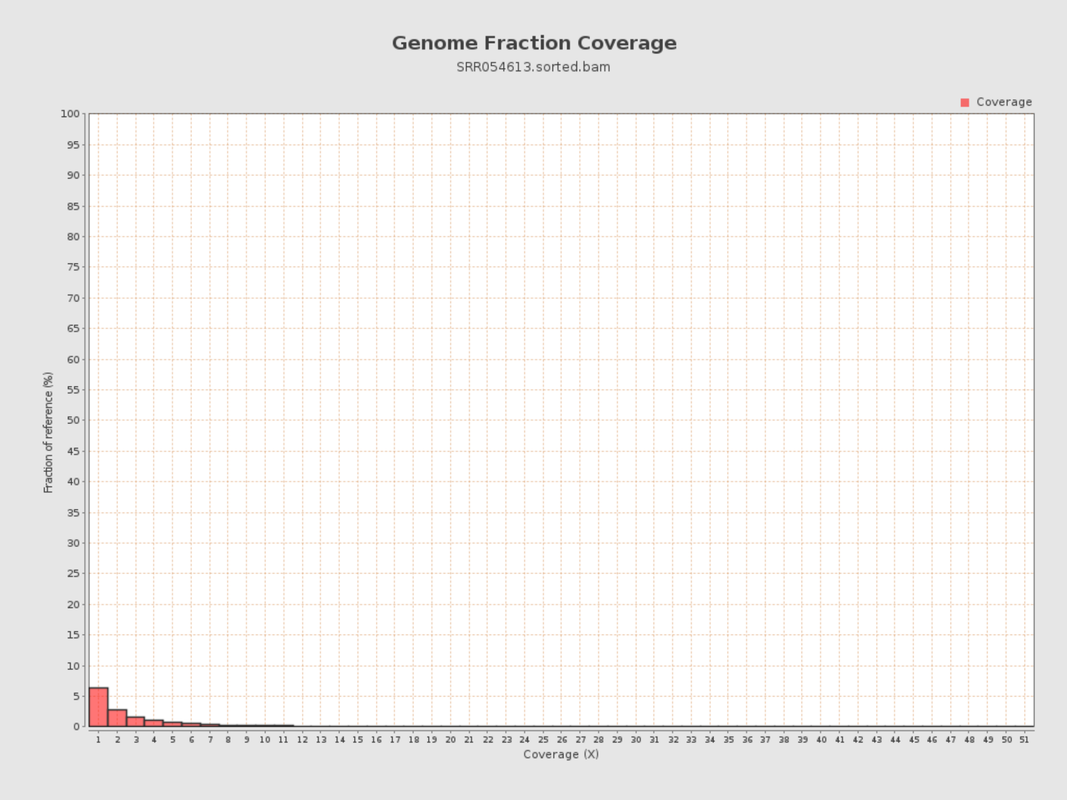
4. Results : Coverage Histogram



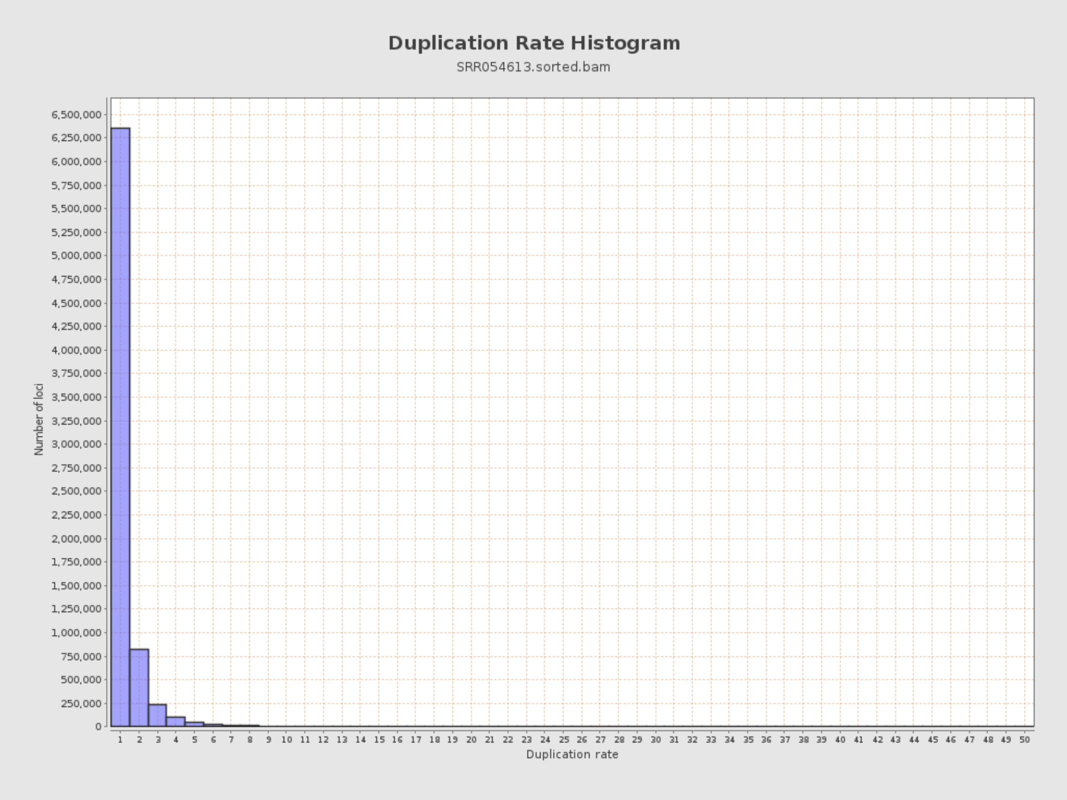
5. Results : Coverage Histogram (0-50X)



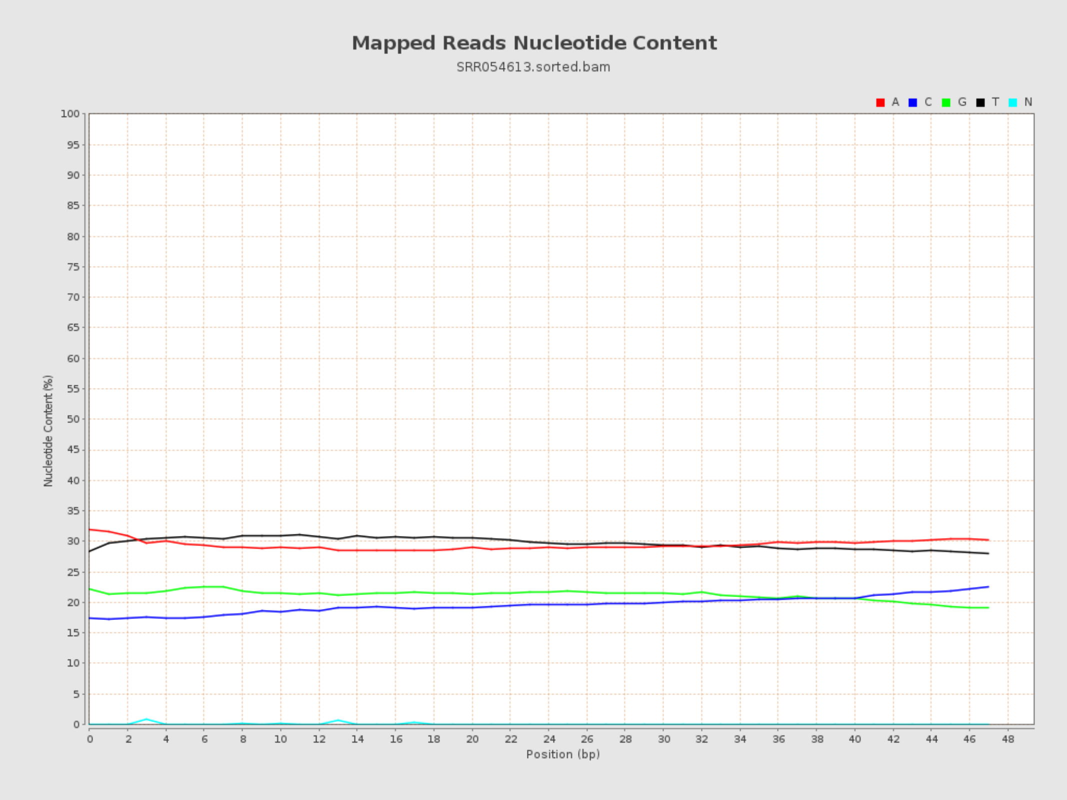
6. Results : Genome Fraction Coverage



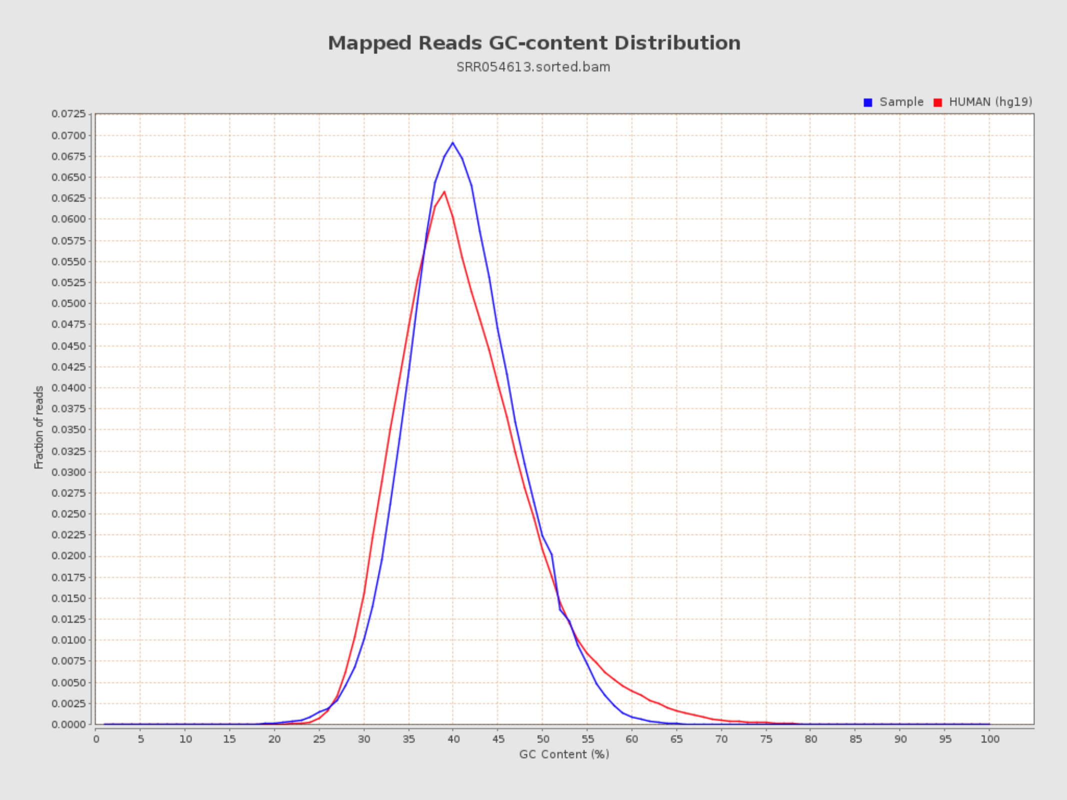
7. Results : Duplication Rate Histogram



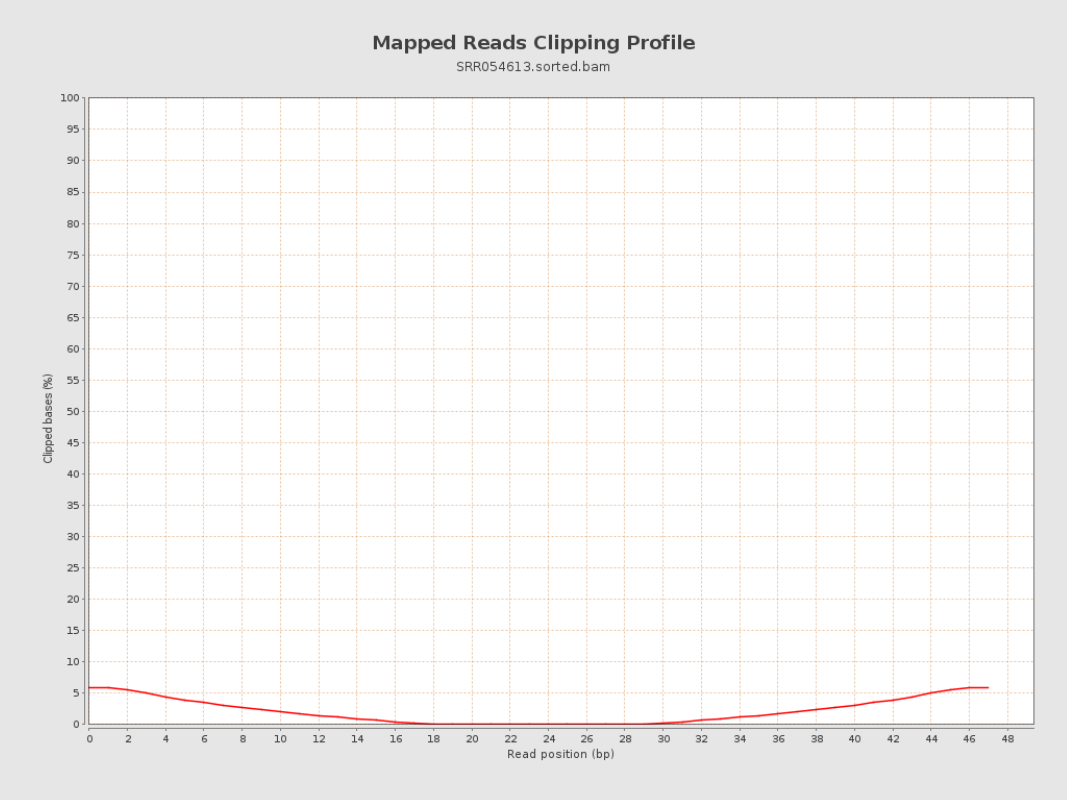
8. Results : Mapped Reads Nucleotide Content



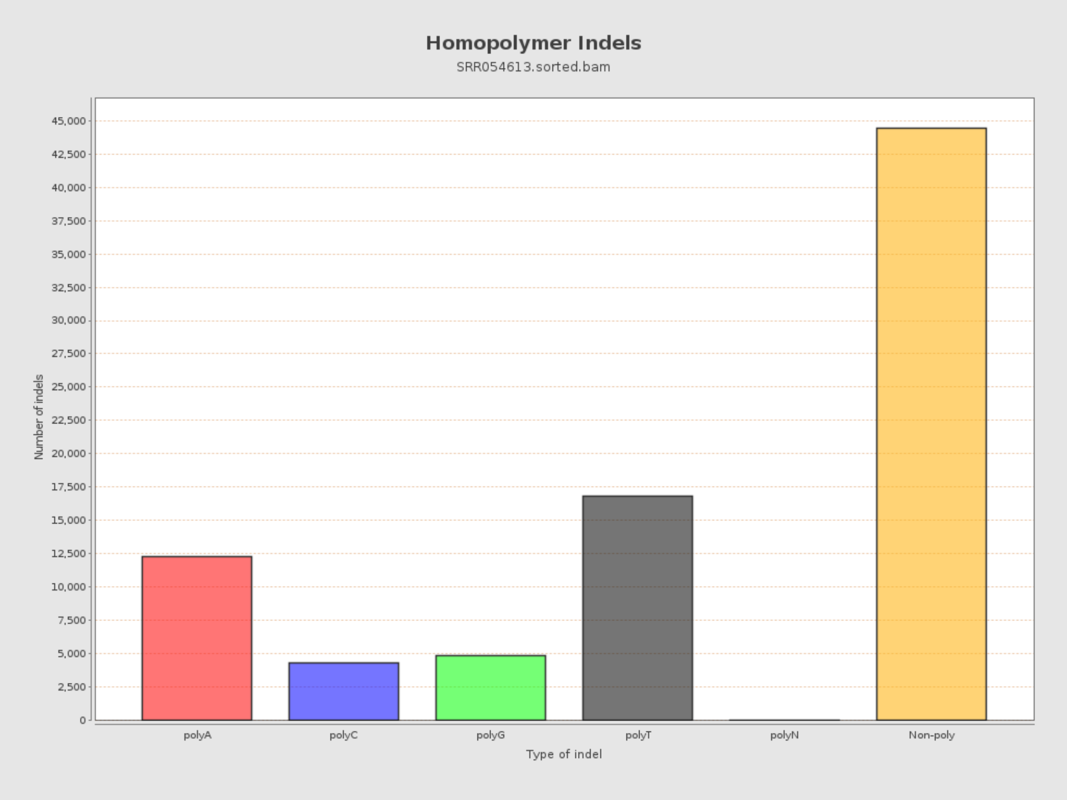
9. Results : Mapped Reads GC-content Distribution



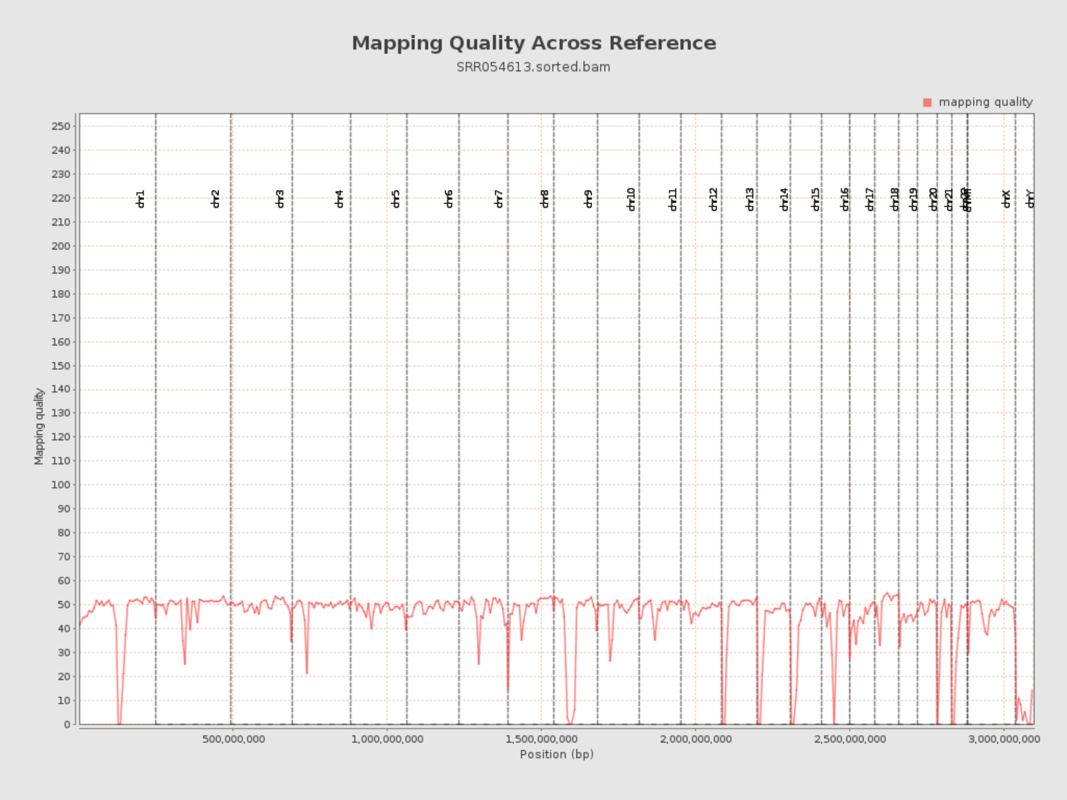
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram