Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:24:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089605.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_SRR089605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:24:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,146,282
Mapped reads	10,260,578 / 84.48%
Unmapped reads	1,885,704 / 15.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	380 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,057,612 / 25.17%
Duplication rate	20.89%
Clipped reads	1,001,446 / 8.24%

2.2. ACGT Content

Number/percentage of A's	155,103,221 / 32.08%
Number/percentage of C's	91,020,695 / 18.83%
Number/percentage of T's	132,041,658 / 27.31%
Number/percentage of G's	105,246,329 / 21.77%
Number/percentage of N's	17,213 / 0%
GC Percentage	40.6%

2.3. Coverage

Mean	0.1562

Standard Deviation	1.2441

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

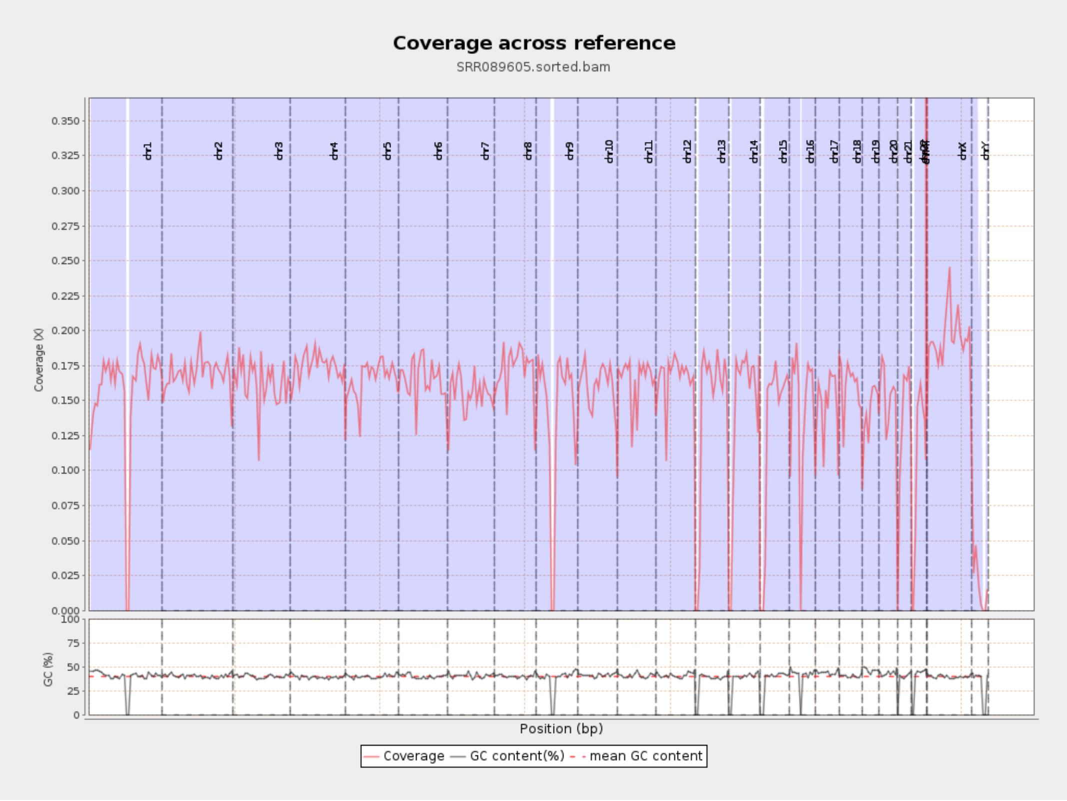
General error rate	0.5%
Mismatches	2,398,624
Insertions	19,361
Mapped reads with at least one insertion	0.19%
Deletions	63,157
Mapped reads with at least one deletion	0.61%
Homopolymer indels	46.6%

2.6. Chromosome stats

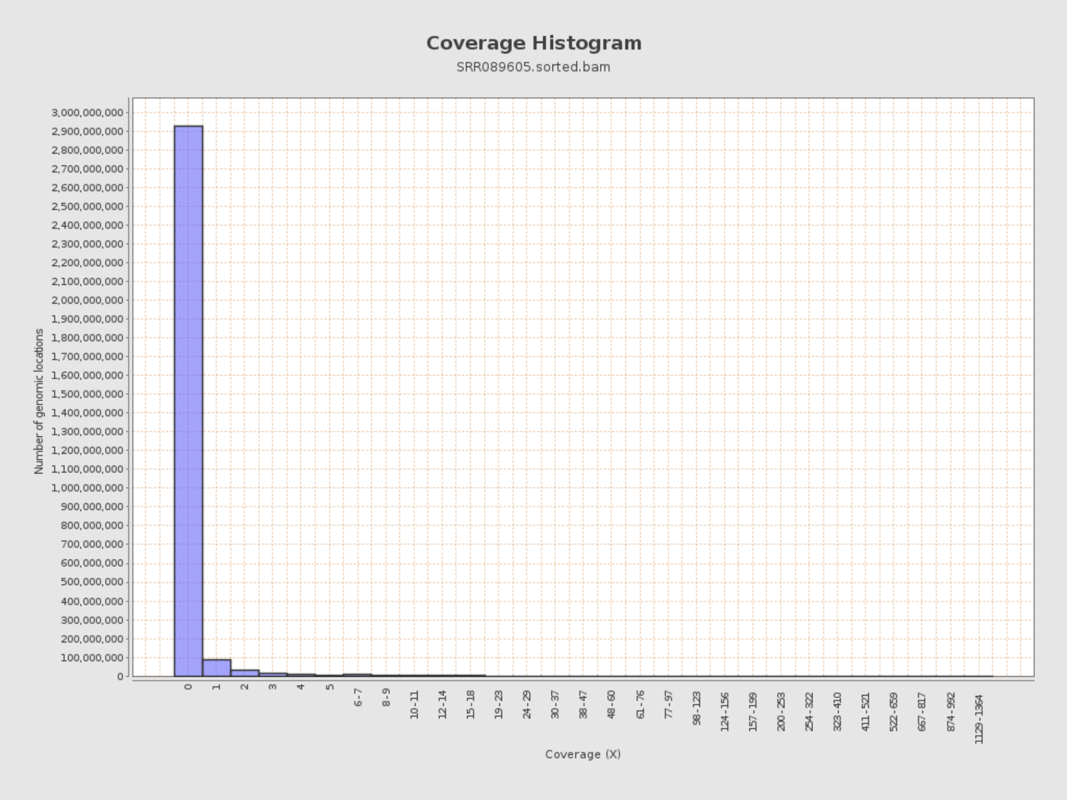
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38851360	0.1559	1.2923
chr2	243199373	41266809	0.1697	1.395
chr3	198022430	32386772	0.1636	1.2171
chr4	191154276	33393694	0.1747	1.291
chr5	180915260	30013252	0.1659	1.2064
chr6	171115067	28209887	0.1649	1.2723
chr7	159138663	24789114	0.1558	1.2352

chr8	146364022	25218516	0.1723	1.4601
chr9	141213431	19883913	0.1408	1.1333
chr10	135534747	22027979	0.1625	1.2445
chr11	135006516	22133196	0.1639	1.2942
chr12	133851895	22241499	0.1662	1.2066
chr13	115169878	16286172	0.1414	1.1323
chr14	107349540	15093180	0.1406	1.2421
chr15	102531392	13287218	0.1296	1.0417
chr16	90354753	13036168	0.1443	1.1428
chr17	81195210	11883227	0.1464	1.1295
chr18	78077248	12523563	0.1604	1.2692
chr19	59128983	8390956	0.1419	1.1817
chr20	63025520	9601566	0.1523	1.1748
chr21	48129895	6233963	0.1295	1.0984
chr22	51304566	5194999	0.1013	0.9383
chrMT	16571	265537	16.0242	30.6707
chrX	155270560	30113582	0.1939	1.4042
chrY	59373566	1197530	0.0202	0.416

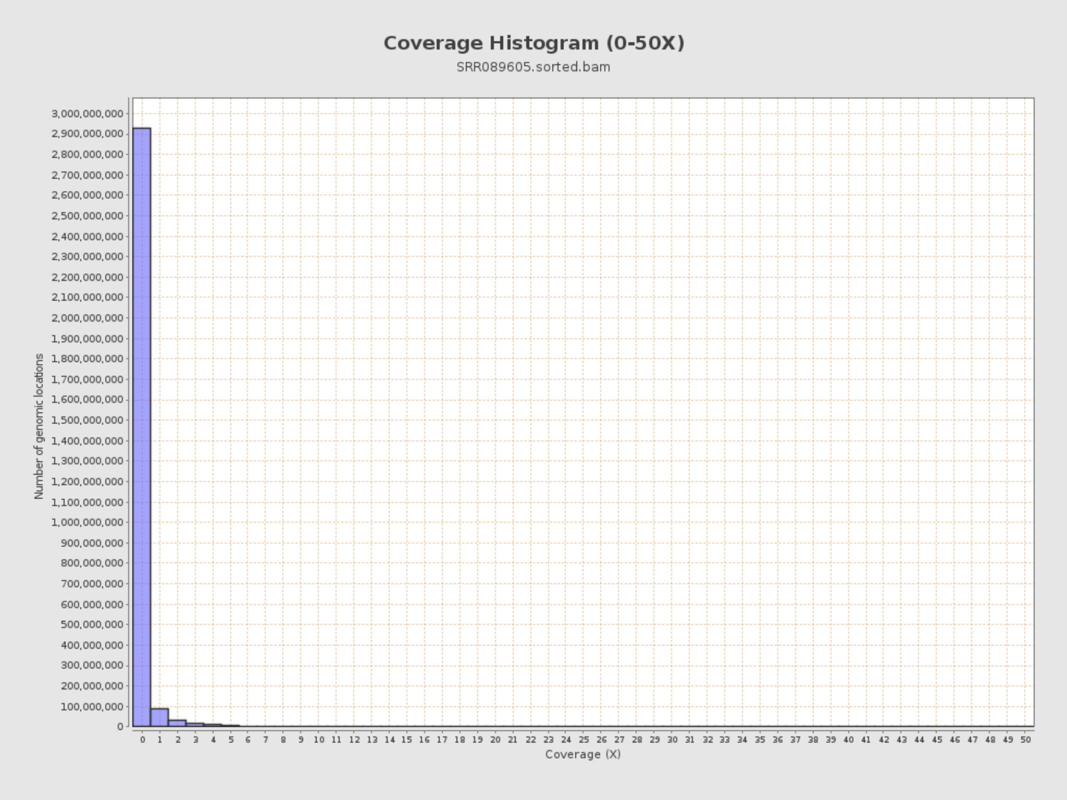
3. Results : Coverage across reference



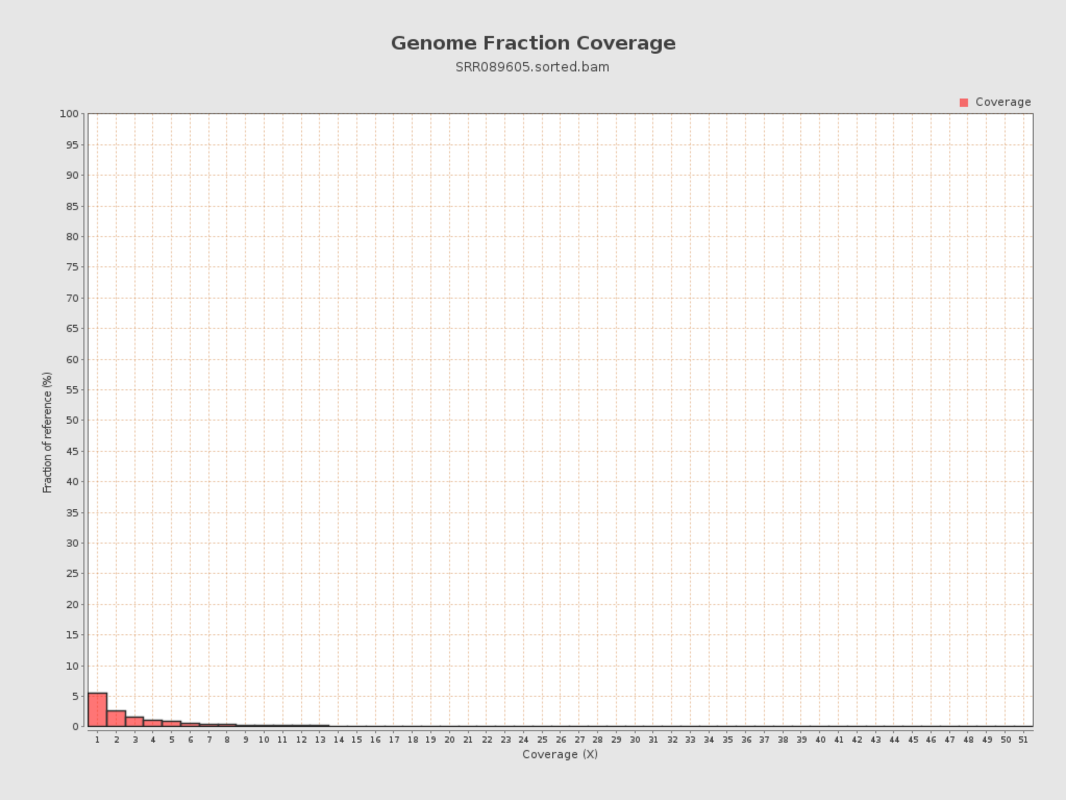
4. Results : Coverage Histogram



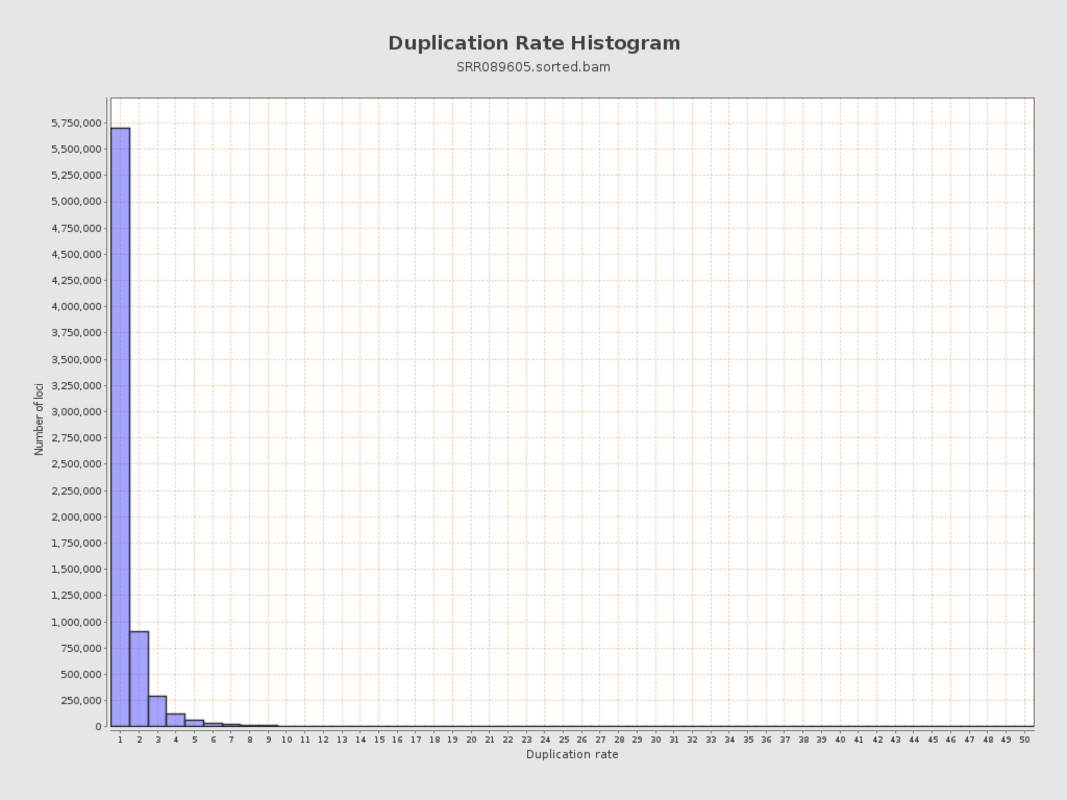
5. Results : Coverage Histogram (0-50X)



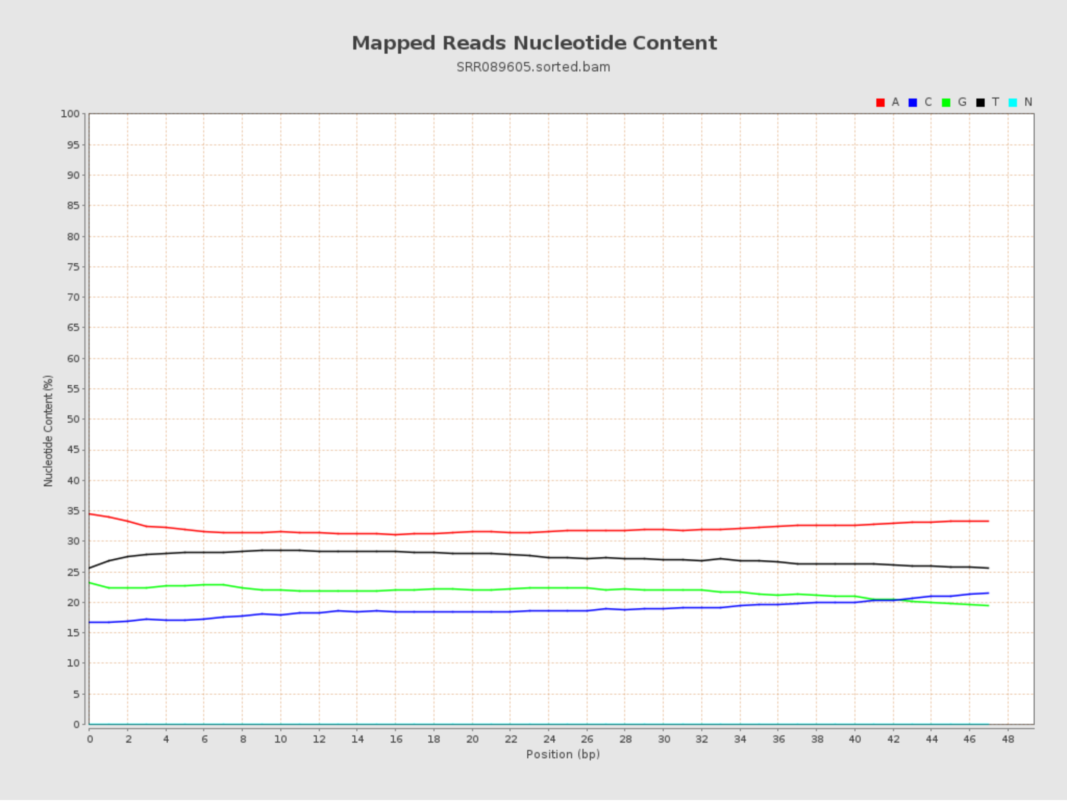
6. Results : Genome Fraction Coverage



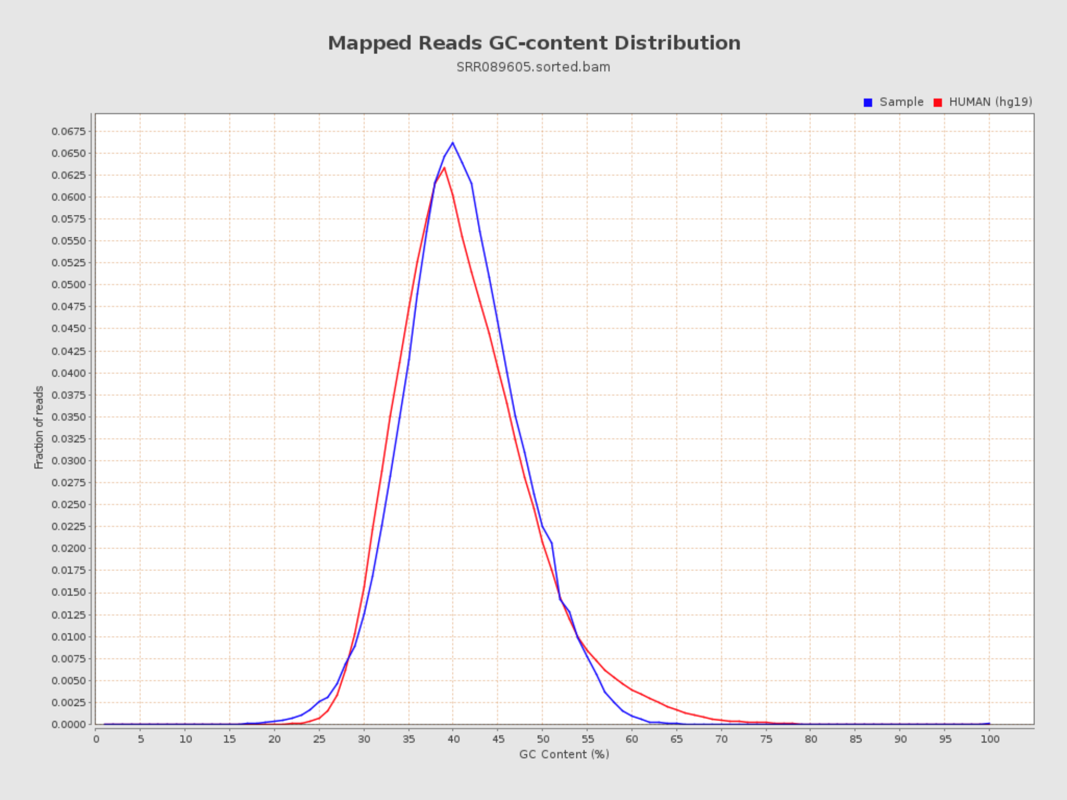
7. Results : Duplication Rate Histogram



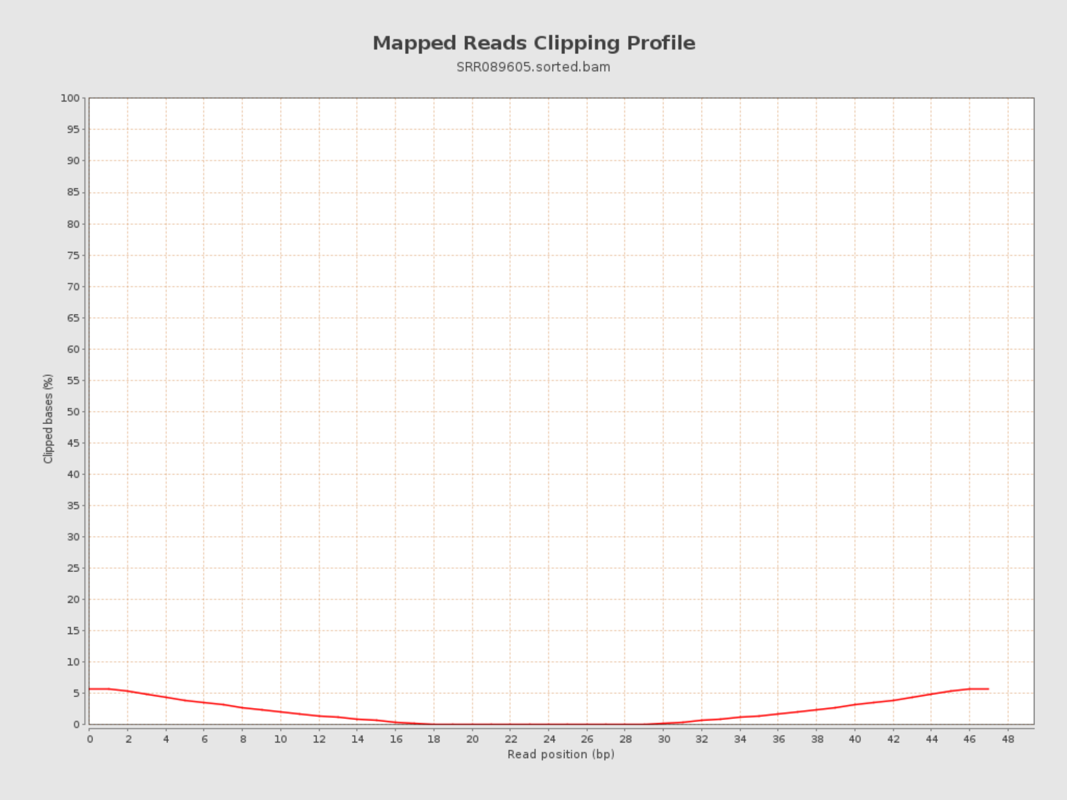
8. Results : Mapped Reads Nucleotide Content



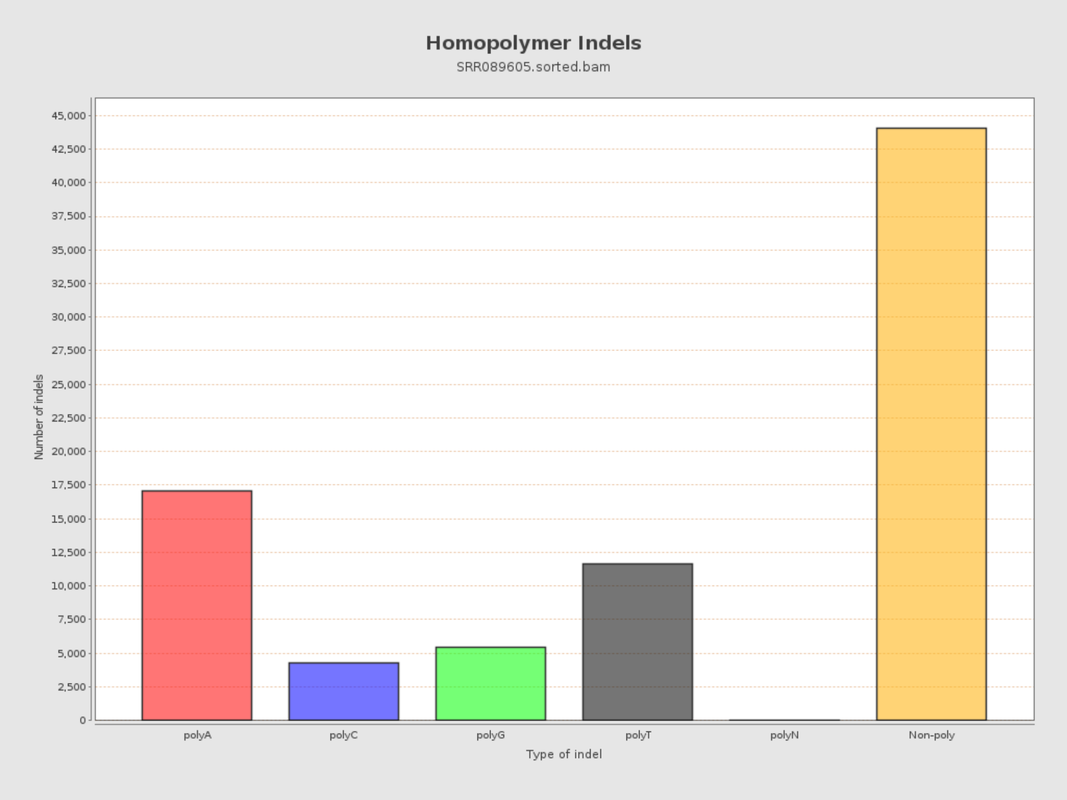
9. Results : Mapped Reads GC-content Distribution



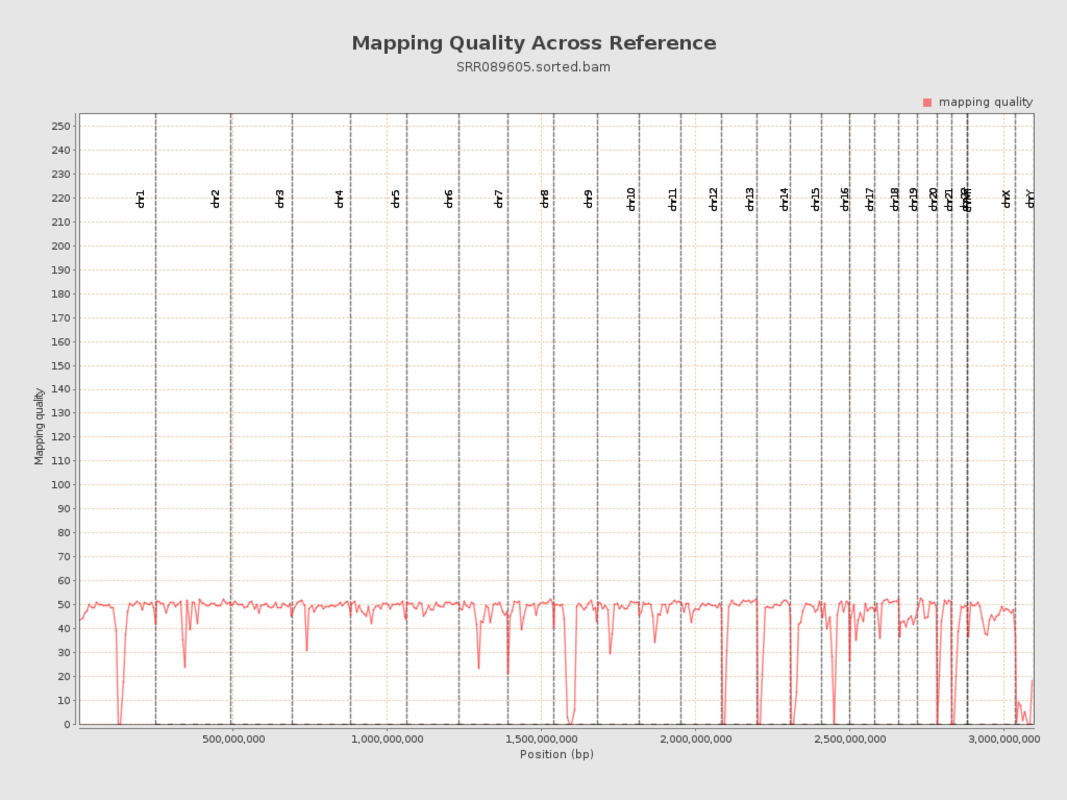
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram