

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:03:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548989.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_SRR1548989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:03:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,351,606
Mapped reads	8,062,584 / 86.22%
Unmapped reads	1,289,022 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	745,011 / 7.97%
Duplication rate	6.6%
Clipped reads	695,375 / 7.44%

2.2. ACGT Content

Number/percentage of A's	94,601,382 / 29.71%
Number/percentage of C's	64,563,799 / 20.28%
Number/percentage of T's	94,538,449 / 29.69%
Number/percentage of G's	64,715,789 / 20.32%
Number/percentage of N's	2,888 / 0%
GC Percentage	40.6%

2.3. Coverage

Mean	0.1029
Standard Deviation	1.3225

2.4. Mapping Quality

Mean Mapping Quality	37.31
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2.5. Mismatches and indels

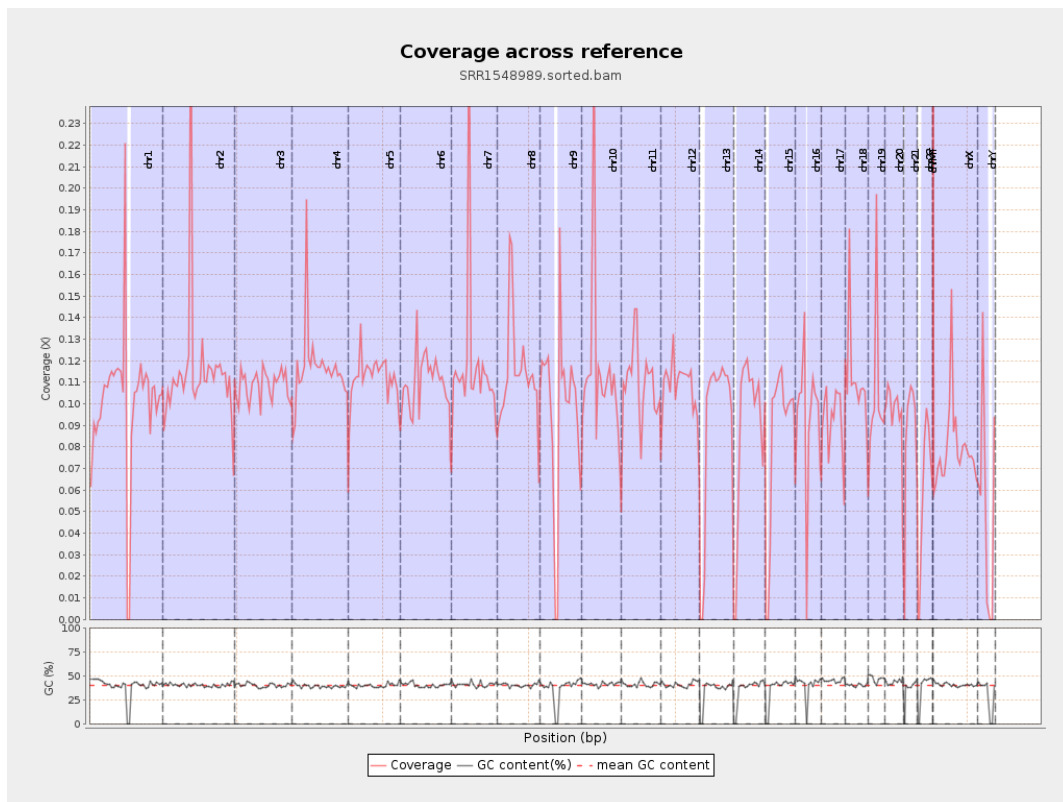
General error rate	0.4%
Mismatches	1,268,443
Insertions	12,926
Mapped reads with at least one insertion	0.16%
Deletions	27,251
Mapped reads with at least one deletion	0.34%
Homopolymer indels	39.48%

2.6. Chromosome stats

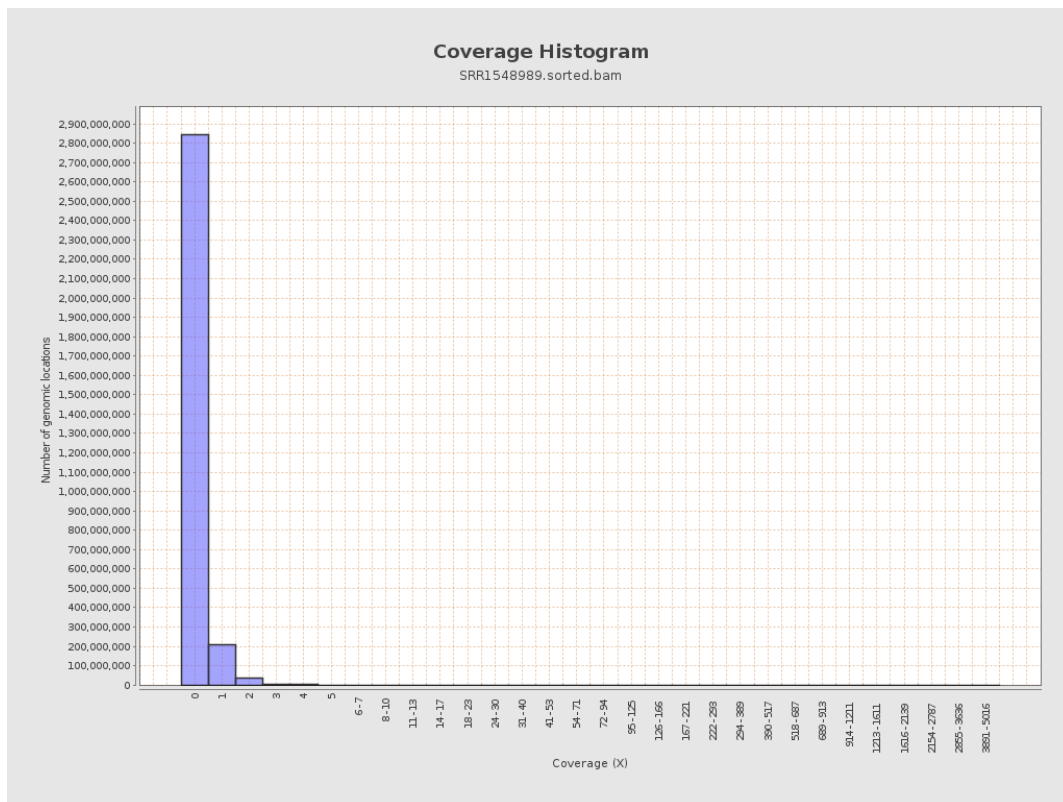
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25103989	0.1007	2.3108
chr2	243199373	28078083	0.1155	1.3862
chr3	198022430	21523500	0.1087	0.4151
chr4	191154276	22325029	0.1168	0.5644
chr5	180915260	20198338	0.1116	0.4786
chr6	171115067	18857365	0.1102	0.5656
chr7	159138663	18728399	0.1177	1.7729
chr8	146364022	16708238	0.1142	2.5546

chr9	141213431	13797963	0.0977	1.349
chr10	135534747	15491200	0.1143	1.1502
chr11	135006516	14796302	0.1096	0.9379
chr12	133851895	14480190	0.1082	0.5288
chr13	115169878	10467524	0.0909	0.3492
chr14	107349540	9607006	0.0895	0.7747
chr15	102531392	8597172	0.0838	0.3547
chr16	90354753	8257407	0.0914	0.6374
chr17	81195210	7595209	0.0935	0.4771
chr18	78077248	8822792	0.113	3.0734
chr19	59128983	6199961	0.1049	2.2834
chr20	63025520	6090536	0.0966	0.5374
chr21	48129895	4102559	0.0852	0.7416
chr22	51304566	3076418	0.06	0.3241
chrMT	16571	8947	0.5399	0.9458
chrX	155270560	12315537	0.0793	0.8391
chrY	59373566	3226663	0.0543	0.6413

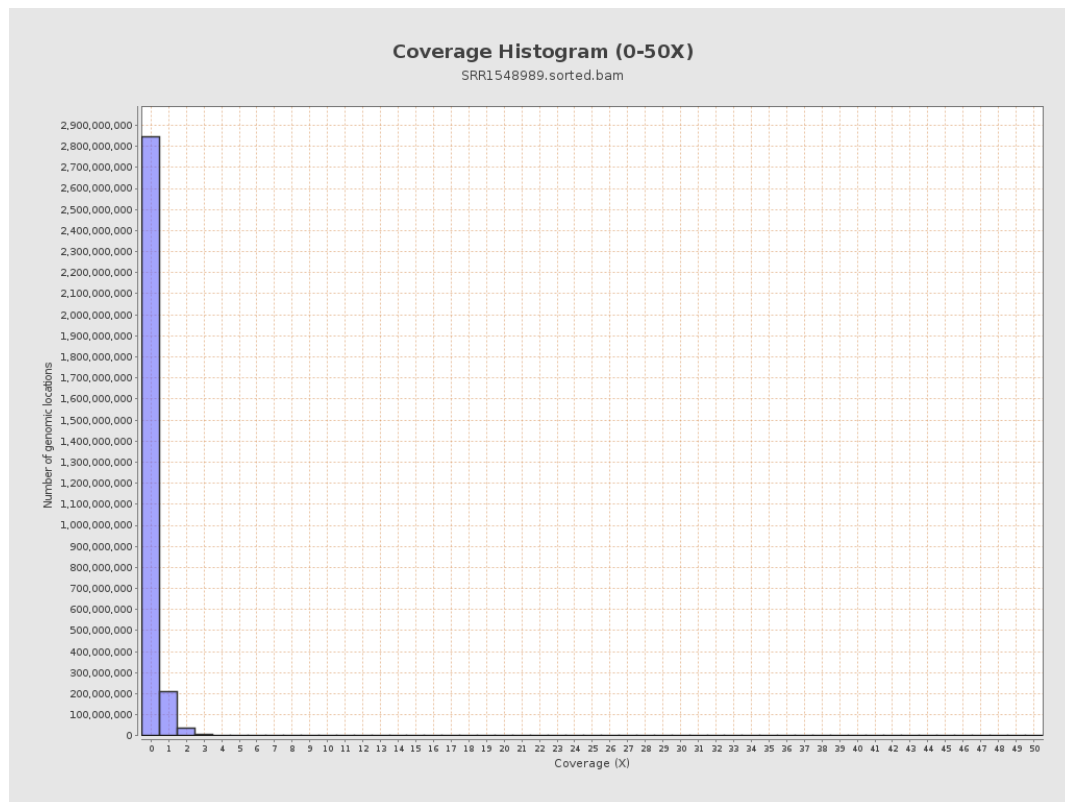
3. Results : Coverage across reference



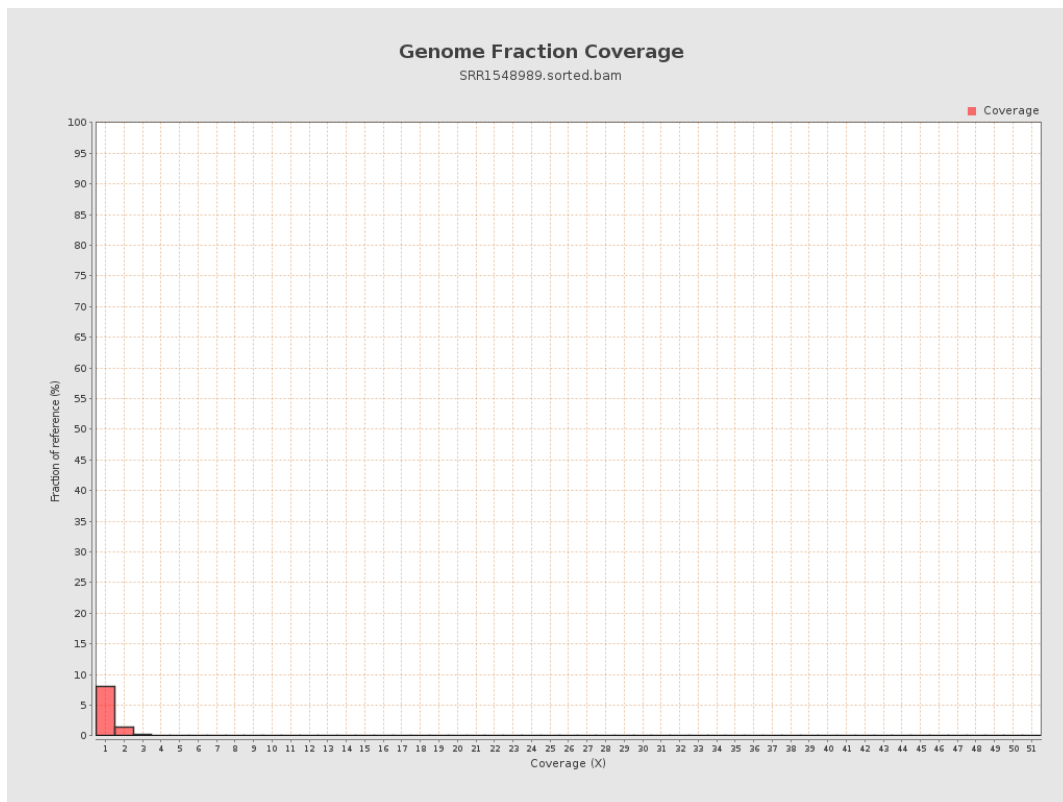
4. Results : Coverage Histogram



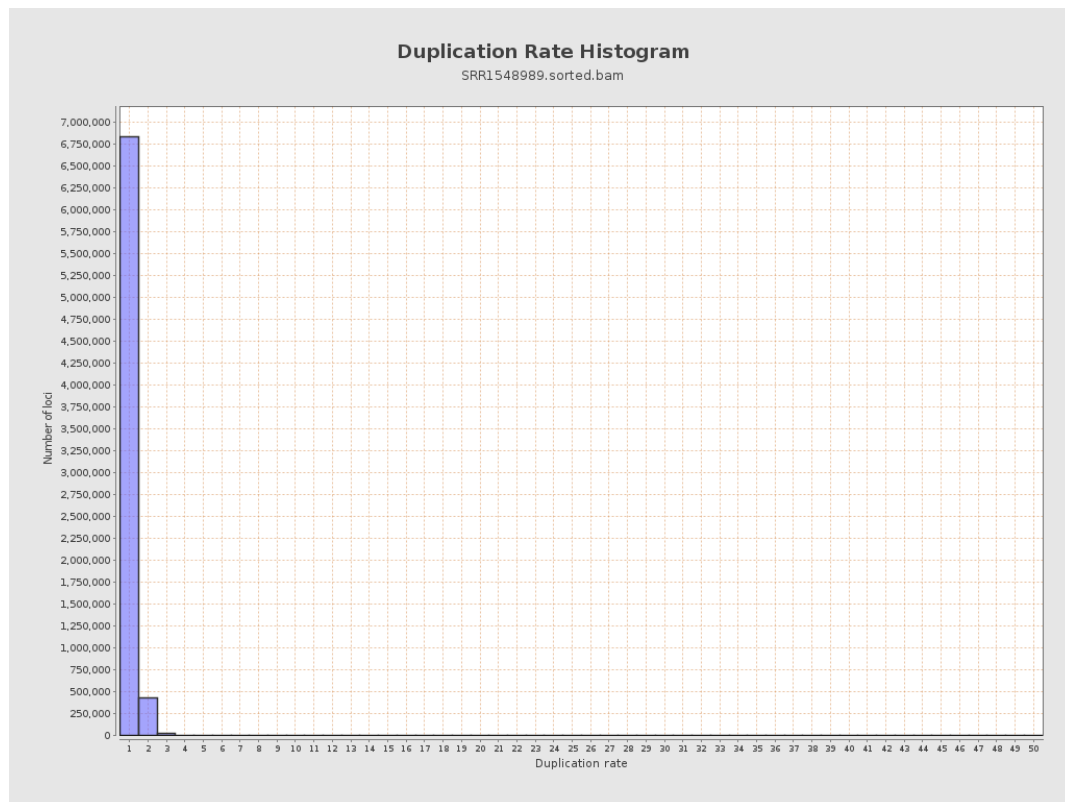
5. Results : Coverage Histogram (0-50X)



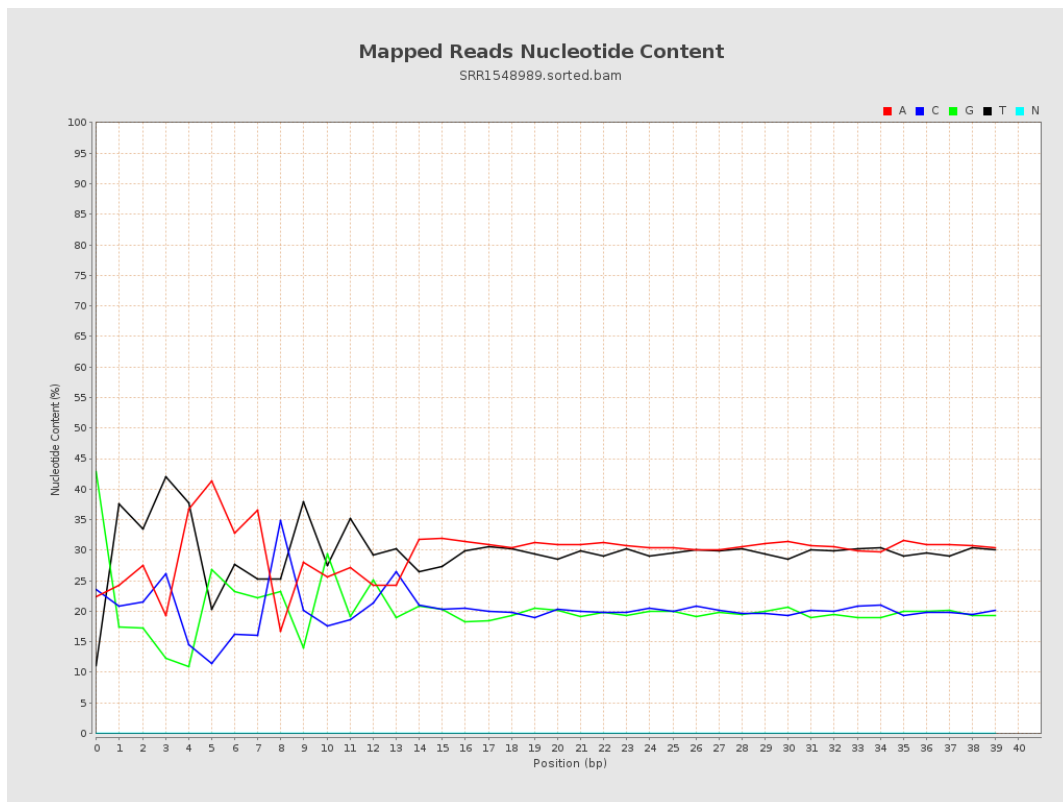
6. Results : Genome Fraction Coverage



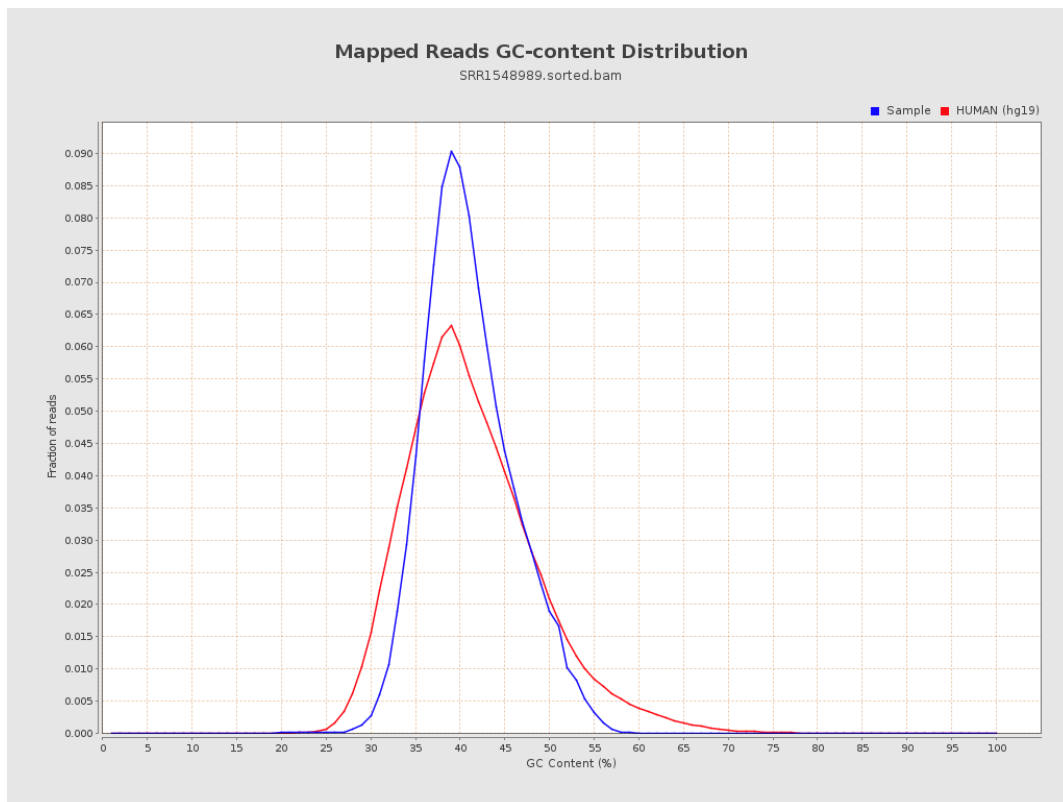
7. Results : Duplication Rate Histogram



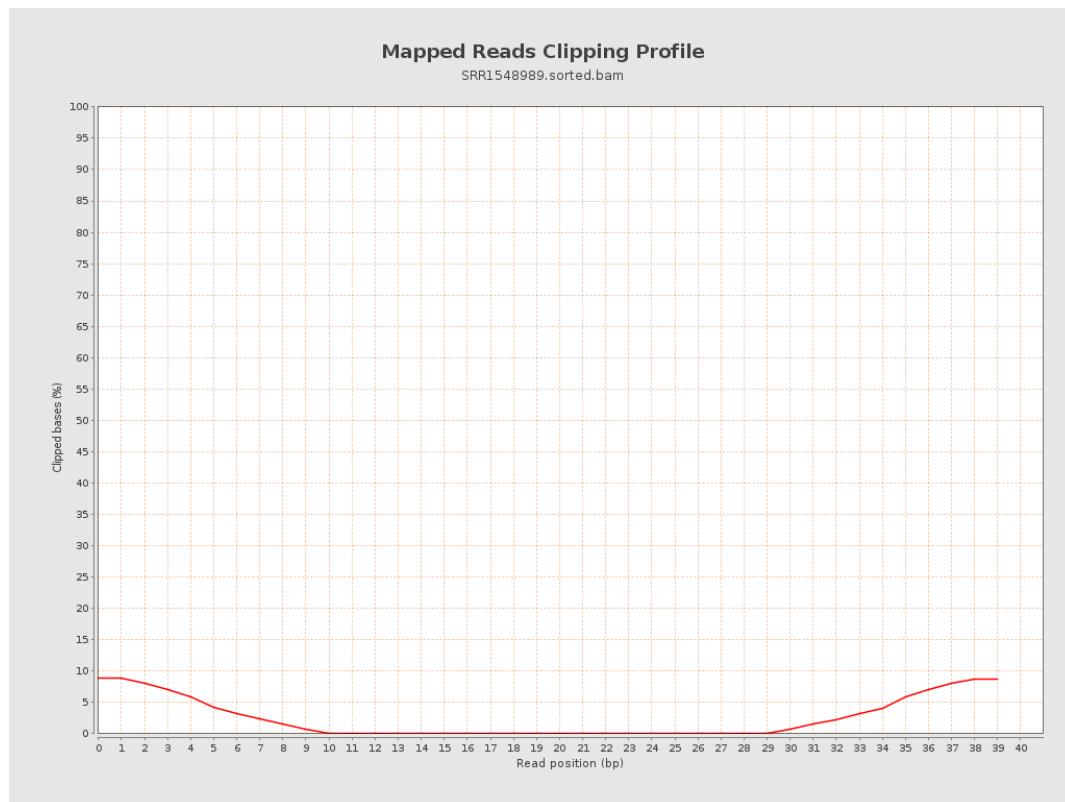
8. Results : Mapped Reads Nucleotide Content



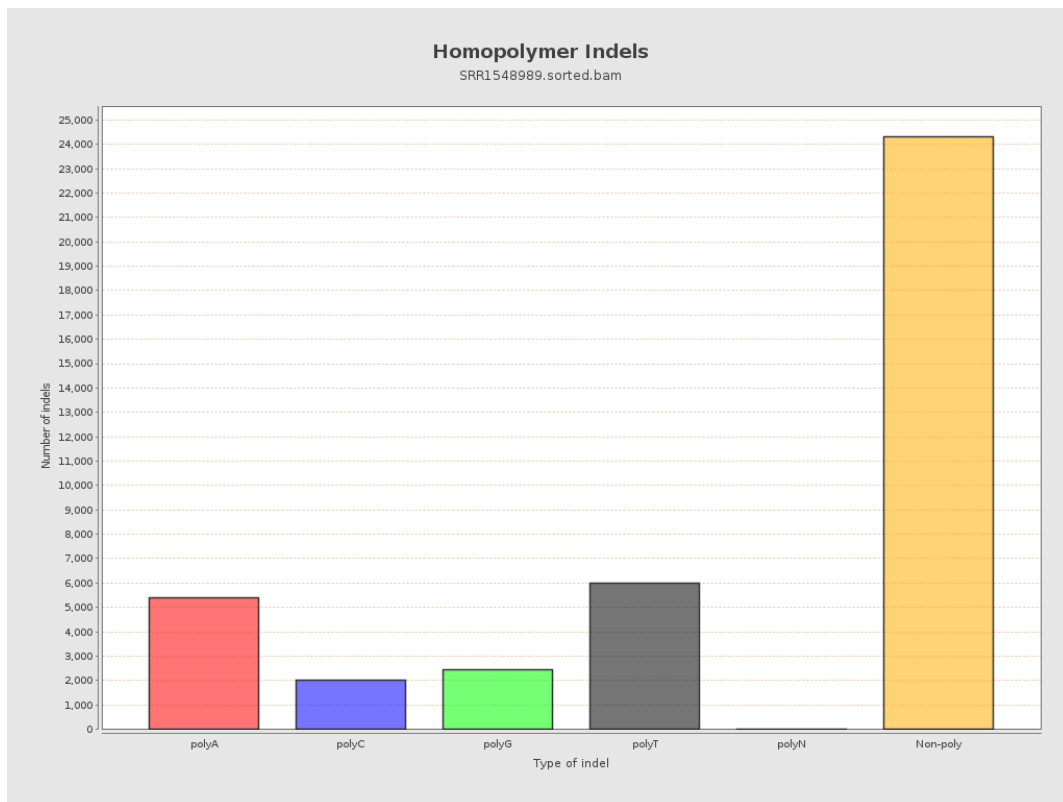
9. Results : Mapped Reads GC-content Distribution



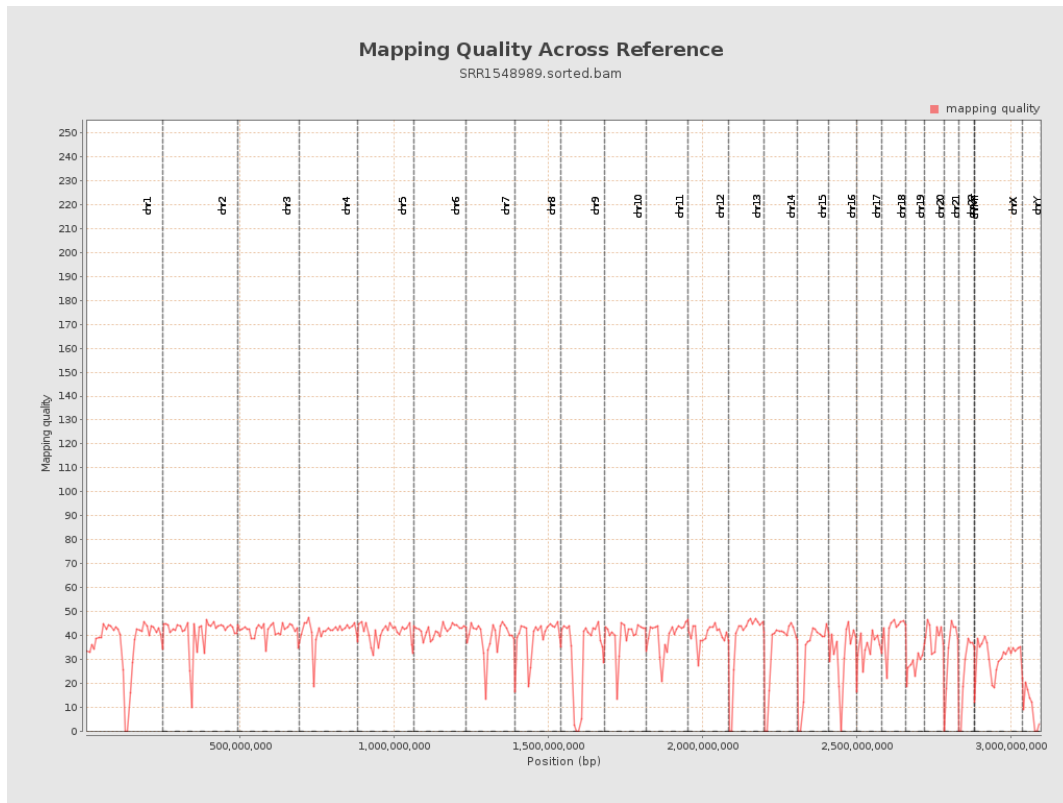
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

