

SnpEff: Variant analysis

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Summary

| | |
|--|---|
| Genome | ncbi_drosophila |
| Date | 2025-12-29 00:17 |
| SnpEff version | SnpEff 5.3a (build 2025-09-02 10:24), by Pablo Cingolani |
| Command line arguments | SnpEff -stats smallIndels_annotation_summary.html ncbi_drosophila /Volumes/Crucial X9/Manta-Output-Processing/MantaTestOutput/output/results/variants/d: |
| Warnings | 3,167 |
| Errors | 32 |
| Number of lines (input file) | 4,535 |
| Number of variants (before filter) | 4,535 |
| Number of non-variants (i.e. reference equals alternative) | 0 |
| Number of variants processed (i.e. after filter and non-variants) | 4,535 |
| Number of known variants (i.e. non-empty ID) | 3,933 (86.725%) |
| Number of multi-allelic VCF entries (i.e. more than two alleles) | 0 |
| Number of annotations | 141,432 |
| Genome total length | 143,726,002 |
| Genome effective length | 138,604,427 |
| Variant rate | 1 variant every 30,563 bases |

Variants rate details

| Chromosome | Length | Variants | Variants rate |
|------------|------------|----------|---------------|
| AE013599.5 | 25,286,936 | 852 | 29,679 |
| AE014134.6 | 23,513,712 | 791 | 29,726 |
| AE014135.4 | 1,348,131 | 28 | 48,147 |
| AE014296.5 | 28,110,227 | 923 | 30,455 |
| AE014297.3 | 32,079,331 | 1,047 | 30,639 |
| AE014298.5 | 23,542,271 | 693 | 33,971 |
| CP007075.1 | 11,983 | 4 | 2,995 |
| CP007076.1 | 87,365 | 1 | 87,365 |
| CP007077.1 | 36,913 | 10 | 3,691 |
| CP007078.1 | 22,604 | 2 | 11,302 |
| CP007081.1 | 88,768 | 1 | 88,768 |
| CP007084.1 | 62,570 | 1 | 62,570 |
| CP007085.1 | 45,120 | 2 | 22,560 |
| CP007091.1 | 20,763 | 2 | 10,381 |
| CP007095.1 | 25,560 | 2 | 12,780 |
| CP007100.1 | 10,091 | 2 | 5,045 |
| CP007101.1 | 24,503 | 1 | 24,503 |
| CP007103.1 | 33,320 | 1 | 33,320 |
| CP007106.1 | 3,667,352 | 2 | 1,833,676 |
| CP007108.1 | 66,731 | 1 | 66,731 |
| CP007111.1 | 34,521 | 1 | 34,521 |
| CP007120.1 | 76,973 | 4 | 19,243 |
| DS483562.1 | 50,625 | 4 | 12,656 |
| DS483629.1 | 15,417 | 1 | 15,417 |
| DS483641.1 | 14,503 | 7 | 2,071 |
| DS483655.1 | 13,549 | 2 | 6,774 |
| DS483659.1 | 13,416 | 7 | 1,916 |
| DS483660.1 | 13,394 | 2 | 6,697 |

| | | | |
|------------|--------|---|--------|
| DS483680.1 | 12,399 | 1 | 12,399 |
| DS483746.1 | 9,341 | 3 | 3,113 |
| DS483751.1 | 7,314 | 4 | 1,828 |
| DS483770.1 | 6,193 | 1 | 6,193 |
| DS483781.1 | 5,952 | 1 | 5,952 |
| DS483783.1 | 5,891 | 1 | 5,891 |
| DS483793.1 | 5,463 | 1 | 5,463 |
| DS483803.1 | 5,232 | 1 | 5,232 |
| DS483817.1 | 4,933 | 2 | 2,466 |
| DS483818.1 | 4,917 | 4 | 1,229 |
| DS483821.1 | 4,879 | 3 | 1,626 |
| DS483828.1 | 4,785 | 1 | 4,785 |
| DS483843.1 | 4,515 | 1 | 4,515 |
| DS483865.1 | 4,289 | 1 | 4,289 |
| DS483880.1 | 4,150 | 2 | 2,075 |
| DS483885.1 | 4,085 | 2 | 2,042 |
| DS483886.1 | 4,081 | 1 | 4,081 |
| DS483905.1 | 3,926 | 1 | 3,926 |
| DS483913.1 | 3,871 | 1 | 3,871 |
| DS483920.1 | 3,806 | 2 | 1,903 |
| DS483923.1 | 3,775 | 3 | 1,258 |
| DS483928.1 | 3,730 | 1 | 3,730 |
| DS483944.1 | 3,622 | 1 | 3,622 |
| DS483955.1 | 3,553 | 1 | 3,553 |
| DS483956.1 | 3,553 | 2 | 1,776 |
| DS483971.1 | 3,478 | 1 | 3,478 |
| DS484000.1 | 3,302 | 1 | 3,302 |
| DS484023.1 | 3,206 | 1 | 3,206 |
| DS484060.1 | 3,065 | 1 | 3,065 |
| DS484064.1 | 3,044 | 3 | 1,014 |
| DS484070.1 | 3,009 | 1 | 3,009 |
| DS484077.1 | 2,984 | 1 | 2,984 |
| DS484138.1 | 2,822 | 1 | 2,822 |
| DS484140.1 | 2,819 | 1 | 2,819 |
| DS484148.1 | 2,795 | 1 | 2,795 |
| DS484185.1 | 2,686 | 1 | 2,686 |
| DS484187.1 | 2,671 | 3 | 890 |
| DS484188.1 | 2,670 | 1 | 2,670 |
| DS484202.1 | 2,636 | 1 | 2,636 |
| DS484205.1 | 2,629 | 1 | 2,629 |
| DS484216.1 | 2,603 | 2 | 1,301 |
| DS484244.1 | 2,536 | 1 | 2,536 |
| DS484267.1 | 2,476 | 1 | 2,476 |
| DS484268.1 | 2,475 | 1 | 2,475 |
| DS484277.1 | 2,442 | 1 | 2,442 |
| DS484279.1 | 2,438 | 1 | 2,438 |
| DS484280.1 | 2,438 | 1 | 2,438 |
| DS484282.1 | 2,435 | 1 | 2,435 |
| DS484285.1 | 2,431 | 1 | 2,431 |
| DS484303.1 | 2,390 | 1 | 2,390 |
| DS484322.1 | 2,366 | 1 | 2,366 |
| DS484345.1 | 2,318 | 2 | 1,159 |
| DS484348.1 | 2,308 | 1 | 2,308 |
| DS484361.1 | 2,282 | 1 | 2,282 |
| DS484382.1 | 2,223 | 2 | 1,111 |
| DS484383.1 | 2,221 | 1 | 2,221 |
| DS484394.1 | 2,200 | 1 | 2,200 |
| DS484396.1 | 2,198 | 3 | 732 |
| DS484397.1 | 2,196 | 1 | 2,196 |
| DS484417.1 | 2,139 | 1 | 2,139 |
| DS484450.1 | 2,087 | 1 | 2,087 |
| DS484454.1 | 2,084 | 1 | 2,084 |
| DS484487.1 | 2,010 | 1 | 2,010 |
| DS484496.1 | 1,998 | 1 | 1,998 |
| DS484556.1 | 1,916 | 3 | 638 |
| DS484588.1 | 1,863 | 1 | 1,863 |
| DS484601.1 | 1,832 | 1 | 1,832 |
| DS484632.1 | 1,775 | 1 | 1,775 |
| DS484644.1 | 1,747 | 1 | 1,747 |
| DS484782.1 | 1,484 | 1 | 1,484 |

| | | | |
|--------------|--------------------|--------------|---------------|
| DS484817.1 | 1,445 | 1 | 1,445 |
| DS484869.1 | 1,391 | 1 | 1,391 |
| DS484894.1 | 1,375 | 2 | 687 |
| DS484963.1 | 1,315 | 1 | 1,315 |
| DS485010.1 | 1,286 | 1 | 1,286 |
| DS485017.1 | 1,281 | 2 | 640 |
| DS485025.1 | 1,278 | 1 | 1,278 |
| DS485077.1 | 1,258 | 2 | 629 |
| DS485102.1 | 1,240 | 2 | 620 |
| DS485190.1 | 1,211 | 1 | 1,211 |
| DS485260.1 | 1,189 | 1 | 1,189 |
| DS485360.1 | 1,159 | 2 | 579 |
| DS485362.1 | 1,158 | 3 | 386 |
| DS485547.1 | 1,112 | 1 | 1,112 |
| DS485572.1 | 1,107 | 1 | 1,107 |
| DS485597.1 | 1,100 | 3 | 366 |
| DS485599.1 | 1,100 | 2 | 550 |
| DS485703.1 | 1,071 | 1 | 1,071 |
| DS485797.1 | 1,049 | 1 | 1,049 |
| DS485801.1 | 1,048 | 1 | 1,048 |
| DS485848.1 | 1,040 | 2 | 520 |
| DS485887.1 | 1,029 | 1 | 1,029 |
| DS485954.1 | 1,014 | 1 | 1,014 |
| DS485968.1 | 1,011 | 2 | 505 |
| DS485997.1 | 1,004 | 2 | 502 |
| DS486008.1 | 1,001 | 1 | 1,001 |
| KJ947872.2 | 19,524 | 4 | 4,881 |
| Total | 138,604,427 | 4,535 | 30,563 |

Number variants by type

| Type | Total |
|--------------|--------------|
| SNP | 0 |
| MNP | 0 |
| INS | 724 |
| DEL | 1,827 |
| MIXED | 1,208 |
| INV | 0 |
| DUP | 174 |
| CNV | 0 |
| BND | 602 |
| INTERVAL | 0 |
| Total | 4,535 |

Number of effects by impact

| Type (alphabetical order) | Count | Percent |
|---------------------------|--------|---------|
| HIGH | 45,074 | 31.87% |
| LOW | 3,802 | 2.688% |
| MODERATE | 71,971 | 50.887% |
| MODIFIER | 20,585 | 14.555% |

Number of effects by functional class

| Type (alphabetical order) | Count | Percent |
|---------------------------|-------|---------|
|---------------------------|-------|---------|

Missense / Silent ratio: 0

Number of annotations and region counts

| Annotation | | | Region | | |
|--------------------------------|-------|---------|---------------------------|--------|---------|
| Type (alphabetical order) | Count | Percent | Type (alphabetical order) | Count | Percent |
| 3_prime_UTR_truncation | 11 | 0.008% | CHROMOSOME | 32 | 0.023% |
| 3_prime_UTR_variant | 413 | 0.288% | DOWNSTREAM | 4,963 | 3.509% |
| 5_prime_UTR_truncation | 49 | 0.034% | EXON | 1,990 | 1.407% |
| 5_prime_UTR_variant | 126 | 0.088% | GENE | 22,342 | 15.797% |
| bidirectional_gene_fusion | 1,867 | 1.303% | INTERGENIC | 5,247 | 3.71% |
| chromosome_number_variation | 19 | 0.013% | INTRON | 7,625 | 5.391% |
| conservative_inframe_deletion | 33 | 0.023% | SPLICE_SITE_ACCEPTOR | 79 | 0.056% |
| conservative_inframe_insertion | 11 | 0.008% | SPLICE_SITE_DONOR | 107 | 0.076% |
| disruptive_inframe_deletion | 33 | 0.023% | SPLICE_SITE_REGION | 219 | 0.155% |

| Type (alphabetical order) | Count | Percent | Type (alphabetical order) | Count | Percent |
|------------------------------------|--------|---------|---------------------------|--------|---------|
| disruptive_inframe_insertion | 10 | 0.007% | TRANSCRIPT | 93,111 | 65.834% |
| downstream_gene_variant | 4,965 | 3.465% | UPSTREAM | 5,254 | 3.715% |
| duplication | 72,298 | 50.46% | UTR_3_PRIME | 378 | 0.267% |
| exon_loss_variant | 1,365 | 0.953% | UTR_5_PRIME | 85 | 0.06% |
| feature_ablation | 4,941 | 3.449% | | | |
| feature_fusion | 3,452 | 2.409% | | | |
| frameshift_variant | 1,067 | 0.745% | | | |
| gene_fusion | 1,644 | 1.147% | | | |
| intergenic_region | 1,795 | 1.253% | | | |
| intragenic_variant | 203 | 0.142% | | | |
| intron_variant | 7,836 | 5.469% | | | |
| missense_variant | 16 | 0.011% | | | |
| non_coding_transcript_exon_variant | 104 | 0.073% | | | |
| non_coding_transcript_variant | 221 | 0.154% | | | |
| splice_acceptor_variant | 89 | 0.062% | | | |
| splice_donor_variant | 146 | 0.102% | | | |
| splice_region_variant | 495 | 0.345% | | | |
| start_lost | 33 | 0.023% | | | |
| stop_gained | 66 | 0.046% | | | |
| stop_lost | 21 | 0.015% | | | |
| stop_retained_variant | 1 | 0.001% | | | |
| synonymous_variant | 9 | 0.006% | | | |
| transcript_ablation | 34,686 | 24.209% | | | |
| upstream_gene_variant | 5,254 | 3.667% | | | |



Quality:

| | |
|--------------------|---|
| Min | 10 |
| Max | 999 |
| Mean | 662.315 |
| Median | 734 |
| Standard deviation | 337.04 |
| Values | 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,55,56,57,58,59,60 |
| Count | 2,4,3,3,2,2,3,5,5,2,3,4,3,2,1,2,2,1,1,6,7,1,3,6,4,1,6,2,3,2,3,3,2,3,3,2,9,4,2,3,1,1,3,4,7,5,6,3,2,3,3,2,6,4,6,5,2,1,3,2,3,3,13,2,4,1,2,5,2,3,2,4,1,2,1,2,1,1, |



Insertions and deletions length:

| | |
|--------------------|---|
| Min | 1 |
| Max | 509 |
| Mean | 24.762 |
| Median | 1 |
| Standard deviation | 60.349 |
| Values | 1,4,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,86,87,88,89,90,91,92,93,94,95,96 |
| Count | 1827,195,21,13,10,10,22,17,15,15,9,3,12,12,9,8,7,10,8,4,7,14,2,4,7,7,7,4,6,5,4,4,6,4,1,4,5,3,2,2,1,5,2,2,1,1,5,6,1,2,4,3,3,1,3,2,2,1,1,3,2,2,4,4,2,1,2,1, |



Base changes (SNPs)

| | A | C | G | T |
|---|---|---|---|---|
| A | 0 | 0 | 0 | 0 |
| C | 0 | 0 | 0 | 0 |
| G | 0 | 0 | 0 | 0 |
| T | 0 | 0 | 0 | 0 |

Ts/Tv (transitions / transversions)

Note: Only SNPs are used for this statistic.
Note: This Ts/Tv ratio is a 'raw' ratio (ratio of observed events).

| | |
|---------------|---|
| Transitions | 0 |
| Transversions | 0 |
| Ts/Tv ratio | 0 |

All variants:

No results available (empty input?)

Only known variants (i.e. the ones having a non-empty ID field):

No results available (empty input?)

Allele frequency



| | |
|--------------------|-----------|
| Min | 50 |
| Max | 100 |
| Mean | 68.721 |
| Median | 50 |
| Standard deviation | 24.201 |
| Values | 50,100 |
| Count | 2837,1698 |

Allele Count



| | |
|--------------------|-----------|
| Min | 1 |
| Max | 2 |
| Mean | 1.374 |
| Median | 1 |
| Standard deviation | 0.484 |
| Values | 1,2 |
| Count | 2837,1698 |

Hom/Het per sample



Sample_names , X
Reference , 0
Het , 2837
Hom , 1698
Missing , 0

Codon changes

How to read this table:

- Rows are reference codons and columns are changed codons. E.g. Row 'AAA' column 'TAA' indicates how many 'AAA' codons have been replaced by 'TAA' codons.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

| | - | AA< | AAA | AAC | AAG | AAT | ACA | ACC | ACG | ACN | ACT | AGA | AGC | AGG | AGT | ATA | ATC | ATG | ATN | ATT | CAA | CAU |
|-----|-----|-----|-------|-------|-------|-------|-------|-------|-------|-----|-------|-------|-------|-------|-------|-----|-------|-------|-----|-------|-------|-------|
| - | | | 2,167 | 1,445 | 1,316 | 1,243 | 1,704 | 1,204 | 1,195 | | 1,447 | 1,746 | 2,004 | 2,192 | 1,295 | 827 | 1,394 | 1,331 | 2 | 1,236 | 2,337 | 1,698 |
| AA< | | | | | | | | | | | | | | | | | | | | | | |
| AAA | 210 | | 55 | 13 | 16 | 51 | 11 | 25 | 12 | | 13 | 38 | 79 | 4 | 28 | 44 | 20 | 15 | | 31 | 60 | |
| AAC | 149 | 3 | 26 | 55 | 17 | 9 | 55 | 18 | 29 | | 56 | 38 | 35 | 45 | 10 | 16 | 53 | 28 | | 31 | 38 | |
| AAG | 358 | | 45 | 31 | 56 | 83 | 41 | 30 | 50 | | 87 | 16 | 40 | 100 | 102 | 40 | 21 | 92 | | 55 | 88 | |
| AAT | 219 | | 40 | 19 | 21 | 8 | 29 | 16 | 87 | | 9 | 27 | 63 | 67 | 48 | 17 | 13 | 68 | | 9 | 24 | |
| ACA | 222 | | 51 | 2 | 16 | 22 | 36 | 20 | 19 | | 12 | 33 | 39 | 36 | 7 | 10 | 18 | 10 | | 18 | 12 | |
| ACC | 262 | | 40 | 24 | 22 | 29 | 60 | 61 | 42 | | 28 | 35 | 56 | 24 | 67 | 11 | 27 | 36 | | 29 | 96 | |
| ACG | 168 | | 15 | 13 | 19 | 11 | 25 | 23 | 7 | | 40 | 21 | 50 | 10 | 18 | 7 | 24 | 21 | | 10 | 13 | |
| ACN | | | | | | | | | | | | | | | | | | | | | | |
| ACT | 240 | | 27 | 4 | 22 | 5 | 11 | 43 | 22 | | 62 | 18 | 14 | 29 | 19 | 3 | 18 | | | 3 | 16 | |
| AGA | 75 | | 5 | 7 | 6 | 4 | 2 | 1 | 14 | | 16 | 6 | 9 | 10 | 19 | 2 | | 7 | | 16 | 11 | |
| AGC | 144 | | 40 | 21 | 54 | 41 | 30 | 45 | 31 | | 24 | 15 | 44 | 15 | 71 | 12 | 47 | 18 | | 40 | 13 | |
| AGG | 80 | | 9 | 1 | 9 | 33 | 14 | 17 | 32 | | 9 | 16 | 38 | 32 | | 8 | 12 | 10 | | 12 | 19 | |
| AGT | 151 | | 44 | 17 | 13 | 7 | 8 | 8 | 32 | | 31 | 30 | 27 | 17 | 51 | 7 | 17 | 5 | | 33 | 22 | |
| ATA | 106 | | 46 | 22 | 32 | | 26 | 9 | | | 8 | 16 | 12 | 4 | 7 | 5 | 11 | 17 | | 11 | 4 | |
| ATC | 159 | | 12 | 29 | 23 | 30 | 65 | 15 | 84 | | 62 | 31 | 45 | 25 | 38 | 18 | 33 | 37 | | 46 | 44 | |
| ATG | 175 | | 42 | 51 | 64 | 52 | 66 | 14 | 34 | | 51 | 58 | 48 | 32 | 8 | 31 | 18 | 32 | | 21 | 65 | |
| ATN | | | | | | | | | | | | | | | | | | | | | | |
| ATT | 182 | | 28 | 7 | 37 | 16 | 49 | 14 | 14 | | 26 | 42 | 28 | 33 | 14 | 17 | 24 | 34 | | 40 | 24 | |
| CAA | 212 | | 18 | 56 | 59 | 18 | 23 | 30 | 41 | | 22 | 58 | 40 | 29 | 6 | 21 | 17 | 22 | | 35 | 10 | |
| CAC | 105 | | 35 | 38 | 18 | 13 | 33 | 17 | 11 | | 37 | 11 | 67 | 37 | 44 | 15 | 33 | 17 | | 5 | 20 | 4 |
| CAG | 306 | | 30 | 42 | 18 | 33 | 113 | 92 | 79 | | 73 | 77 | 51 | 67 | 89 | 8 | 48 | 112 | | 54 | 56 | |
| CAT | 107 | | 11 | 11 | 5 | 16 | 16 | 6 | 14 | | 28 | 9 | 26 | 6 | 10 | 4 | 43 | 45 | | 21 | 16 | |
| CCA | 229 | | 28 | 12 | 31 | 10 | 15 | 42 | 26 | | 40 | 10 | 24 | 16 | 23 | 7 | 23 | 13 | | 28 | 15 | |
| CCC | 162 | | 15 | 23 | 38 | 60 | 40 | 16 | 22 | 4 | 35 | | 55 | 15 | 8 | 7 | 19 | 12 | | 66 | 36 | |
| CCG | 103 | | 30 | 14 | 21 | 26 | 20 | 45 | 26 | | 28 | 19 | 30 | 6 | 31 | 10 | 13 | 43 | | 26 | 45 | |
| CCT | 130 | | 15 | 22 | 59 | 5 | | 18 | 2 | | 34 | 2 | 22 | 2 | 9 | 29 | 16 | 2 | | 20 | 2 | |
| CGA | 78 | | 18 | 2 | 12 | 10 | 6 | 9 | 2 | | 10 | 2 | 15 | 41 | | 16 | 24 | 13 | | 8 | 31 | |
| CGC | 99 | | 6 | 20 | 3 | 9 | 18 | 23 | 2 | | 27 | 69 | 28 | 38 | 33 | 5 | 49 | 67 | | 24 | 31 | |

| | - | AA< | AAA | AAC | AAG | AAT | ACA | ACC | ACG | ACN | ACT | AGA | AGC | AGG | AGT | ATA | ATC | ATG | ATN | ATT | CAA | C/ |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| CGG | 69 | | 7 | 4 | 30 | 10 | 12 | 18 | 13 | | 4 | 8 | 13 | 4 | 4 | 6 | 19 | | | 8 | 14 | |
| CGT | 64 | | | 16 | 8 | 29 | 10 | 13 | | | 8 | 43 | 13 | 19 | 10 | 4 | 26 | 2 | | | 25 | |
| CTA | 87 | | 16 | | 9 | | 17 | | 8 | | 15 | 11 | 39 | 10 | 8 | 1 | 15 | 11 | | 15 | 34 | |
| CTC | 112 | | 4 | 18 | 26 | 9 | 17 | 10 | 23 | | 27 | 7 | 6 | 25 | 13 | 3 | 29 | 13 | | 17 | 36 | |
| CTG | 235 | | 36 | 62 | 29 | 50 | 98 | 50 | 71 | | 59 | 124 | 66 | 35 | 46 | 52 | 70 | 64 | | 43 | 82 | |
| CTN | | | | | | | | | | | | | | | | | | | | | | |
| CTT | 91 | | 71 | 12 | 15 | 10 | 2 | 2 | 5 | | 16 | 11 | 6 | 37 | 9 | 5 | 18 | 16 | | 10 | 17 | |
| G>S | | | | | | | | | | | | | | | | | | | | | | |
| GAA | 223 | | 84 | 12 | 80 | 23 | 40 | 46 | 17 | | 65 | 46 | 34 | 42 | 15 | 12 | 26 | 22 | | 38 | 37 | |
| GAC | 182 | | 64 | 25 | 37 | 47 | 83 | 71 | 23 | | 41 | 32 | 50 | 77 | 30 | 13 | 43 | 25 | | 38 | 45 | |
| GAG | 298 | | 129 | 124 | 172 | 45 | 63 | 77 | 74 | | 92 | 66 | 79 | 114 | 67 | 46 | 62 | 92 | | 92 | 67 | |
| GAT | 209 | | 79 | 56 | 44 | 52 | 44 | 7 | 52 | | 52 | 58 | 78 | 98 | 31 | 21 | 46 | 72 | | 60 | 48 | |
| GCA | 125 | | 26 | 42 | 21 | 13 | 10 | 14 | 2 | | 13 | 1 | 6 | 6 | 33 | 4 | 24 | 24 | | 24 | 19 | |
| GCC | 254 | | 70 | 50 | 18 | 54 | 78 | 47 | 66 | | 108 | 94 | 90 | 118 | 38 | 19 | 63 | 26 | | 38 | 62 | |
| GCG | 91 | | 10 | 23 | 16 | 24 | 10 | 34 | 48 | | 23 | 16 | 20 | | 12 | 35 | 63 | 3 | | 26 | 42 | |
| GCT | 178 | | 20 | 20 | 67 | 8 | 34 | 20 | 41 | | 36 | 11 | 21 | 15 | 23 | 8 | 22 | 15 | | 22 | 9 | |
| GGA | 330 | | 58 | 27 | 21 | 35 | 29 | 20 | 35 | | 16 | 23 | 53 | 53 | 26 | 8 | 4 | 87 | | 38 | 29 | |
| GGC | 168 | | 61 | 26 | 56 | 45 | 50 | 31 | 57 | | 42 | 43 | 84 | 75 | 39 | 51 | 84 | 69 | | 46 | 23 | |
| GGG | 44 | | | 6 | 7 | 8 | 6 | | 2 | | | 31 | 4 | 4 | 4 | | 16 | 5 | | | 2 | |
| GGT | 140 | | 18 | 19 | 9 | 14 | 32 | 5 | 16 | | 18 | 19 | 19 | 47 | 13 | | 25 | 25 | | 15 | 42 | |
| GT> | | | | | | | | | | | | | | | | | | | | | | |
| GTA | 77 | | 11 | 4 | 12 | 10 | 14 | 6 | 3 | | 20 | 15 | 5 | 4 | | 10 | | 8 | | 2 | 14 | |
| GTC | 94 | | 27 | 8 | 30 | 34 | 26 | 23 | 19 | | 24 | 34 | 38 | 44 | 20 | 9 | 38 | 22 | | 20 | 42 | |
| GTG | 179 | | 49 | 37 | 22 | 27 | 43 | 55 | 97 | | 49 | 44 | 69 | 65 | 64 | 21 | 28 | 50 | | 27 | 68 | |
| GTT | 141 | | 15 | 26 | 20 | 22 | 35 | 18 | 12 | | 18 | 2 | 53 | 16 | 12 | 15 | 40 | 17 | | 39 | 10 | |
| INS | | | | | | | | | | | | | | | | | | | | | | |
| NI< | | | | | | | | | | | | | | | | | | | | | | |
| NNN | | | | | | | | | | | | | | | | | | | | | | |
| NTT | | | | | | | | | | | | | | | | | | | | | | |
| SNI | | | | | | | | | | | | | | | | | | | | | | |
| TAA | 38 | | 1 | | | 14 | 1 | | | | 1 | | | | | 1 | | | | | 6 | |
| TAC | 157 | | 55 | 33 | 32 | 48 | 25 | 32 | 20 | | 12 | 45 | 46 | 37 | 18 | 43 | 40 | 30 | | 19 | 58 | |
| TAG | 16 | | | | 1 | | | | | | | | 2 | | | | | | | | | |
| TAT | 128 | | 7 | 16 | 16 | 12 | 22 | 4 | 8 | | 18 | 34 | 22 | 22 | 6 | | 32 | 6 | | 16 | 19 | |
| TCA | 114 | | 29 | 6 | 6 | 8 | 40 | 40 | 11 | | 28 | 16 | 19 | 8 | 7 | | 11 | 38 | | 7 | 38 | |
| TCC | 158 | | 14 | 42 | 32 | 38 | 42 | 34 | 34 | | 62 | 42 | 80 | 43 | 40 | 21 | 7 | 13 | | 63 | 56 | |
| TCG | 109 | | 41 | 16 | 18 | 8 | 49 | 20 | 21 | | 30 | 35 | 56 | 20 | 44 | 14 | | 29 | | 36 | 37 | |
| TCT | 84 | | 35 | 11 | 18 | | 35 | | | | 24 | 5 | 25 | 4 | 20 | 2 | 4 | | | 24 | 7 | |
| TG> | | | | | | | | | | | | | | | | | | | | | | |
| TGA | 21 | | | 3 | 1 | | 3 | | | | | 1 | | | | 1 | | | | | 1 | |
| TGC | 117 | | 24 | 26 | 14 | 20 | 11 | 15 | 12 | | 6 | 76 | 26 | 41 | 17 | 23 | 34 | 61 | | 43 | 15 | |
| TGG | 96 | | 26 | 6 | 17 | 37 | 10 | 21 | 2 | | 14 | 8 | 28 | 8 | 22 | 21 | 8 | 22 | | 13 | 11 | |
| TGN | | | | | | | | | | | | | | | | | | | | | | |
| TGT | 80 | | 12 | | | 1 | 2 | 9 | 8 | | 13 | 4 | 52 | 10 | 4 | 10 | 3 | | | 3 | 7 | |
| TTA | 67 | | 36 | 1 | 4 | 15 | 29 | | 4 | | 2 | 11 | 8 | 4 | 3 | 12 | 14 | 2 | | 8 | 4 | |
| TTC | 189 | | 22 | 18 | 21 | 18 | 41 | 17 | 79 | | 43 | 37 | 15 | 28 | 20 | 15 | 31 | 32 | | 35 | 49 | |
| TTG | 148 | | 15 | 35 | 19 | 16 | 46 | 8 | 31 | | 17 | 36 | 34 | 108 | 22 | 6 | 35 | 20 | | 22 | 36 | |
| TTT | 143 | | 31 | 18 | 19 | 16 | 24 | 7 | 5 | | 15 | 19 | 20 | 16 | 29 | 14 | 18 | 14 | | 17 | 7 | |

Amino acid changes

How to read this table:

- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

| | * | - | ? | A | C | D | E | F | G | H | I | K | L | M | N | P | Q | R | S | T | V |
|---|-------|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| * | 33 | 75 | 4 | 17 | 3 | 4 | 2 | 7 | 5 | 14 | 2 | 3 | 7 | | 17 | 6 | 20 | 1 | 4 | 5 | 9 |
| - | 3,628 | | 1,330 | 8,085 | 3,285 | 2,539 | 3,149 | 2,598 | 7,141 | 3,443 | 3,457 | 3,483 | 7,109 | 1,331 | 2,688 | 7,754 | 4,208 | 9,645 | 8,234 | 5,550 | 4,471 |
| ? | 2 | 5 | | | | | | | | | | | | | | | | | | | |
| A | 204 | 645 | 11 | 563 | 297 | 261 | 370 | 134 | 475 | 188 | 348 | 248 | 528 | 68 | 234 | 550 | 287 | 699 | 697 | 584 | 321 |
| C | 42 | 197 | 1 | 167 | 84 | 53 | 34 | 66 | 97 | 26 | 116 | 50 | 84 | 61 | 47 | 159 | 45 | 243 | 192 | 76 | 52 |
| D | 145 | 386 | 6 | 454 | 159 | 170 | 283 | 107 | 269 | 135 | 221 | 224 | 285 | 97 | 180 | 465 | 175 | 521 | 455 | 373 | 270 |
| E | 246 | 521 | | 649 | 250 | 268 | 465 | 151 | 365 | 170 | 276 | 465 | 541 | 114 | 204 | 695 | 211 | 726 | 619 | 474 | 405 |
| F | 82 | 331 | 1 | 309 | 94 | 109 | 66 | 71 | 239 | 71 | 130 | 93 | 159 | 46 | 70 | 203 | 88 | 302 | 287 | 231 | 182 |
| G | 212 | 679 | 8 | 631 | 292 | 198 | 221 | 147 | 384 | 179 | 287 | 230 | 248 | 186 | 180 | 564 | 156 | 649 | 537 | 359 | 299 |
| H | 89 | 212 | | 274 | 45 | 95 | 81 | 84 | 174 | 111 | 121 | 69 | 223 | 62 | 78 | 178 | 57 | 225 | 369 | 162 | 67 |
| I | 131 | 447 | | 359 | 177 | 150 | 186 | 100 | 214 | 104 | 205 | 178 | 188 | 88 | 104 | 415 | 131 | 374 | 355 | 372 | 249 |

| | * | - | ? | A | C | D | E | F | G | H | I | K | L | M | N | P | Q | R | S | T | V | |
|---|-----|-----|----|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|--|
| K | 149 | 567 | 5 | 398 | 98 | 137 | 211 | 91 | 260 | 100 | 211 | 172 | 317 | 107 | 178 | 476 | 217 | 379 | 550 | 269 | 202 | |
| L | 326 | 740 | 1 | 799 | 362 | 219 | 260 | 265 | 521 | 213 | 375 | 280 | 577 | 126 | 228 | 666 | 393 | 997 | 741 | 557 | 436 | |
| M | 49 | 174 | 9 | 153 | 76 | 30 | 82 | 85 | 98 | 90 | 70 | 106 | 112 | 32 | 103 | 171 | 76 | 196 | 192 | 165 | 148 | |
| N | 92 | 367 | 4 | 412 | 174 | 126 | 130 | 85 | 132 | 121 | 139 | 104 | 311 | 96 | 91 | 299 | 83 | 413 | 339 | 299 | 98 | |
| P | 207 | 621 | 7 | 477 | 204 | 185 | 284 | 66 | 265 | 195 | 264 | 237 | 279 | 70 | 172 | 465 | 204 | 329 | 617 | 409 | 234 | |
| Q | 151 | 518 | 8 | 493 | 170 | 157 | 215 | 91 | 397 | 171 | 183 | 125 | 317 | 134 | 149 | 419 | 154 | 542 | 432 | 473 | 209 | |
| R | 254 | 462 | 11 | 593 | 244 | 265 | 215 | 127 | 347 | 156 | 239 | 113 | 297 | 99 | 145 | 525 | 202 | 654 | 541 | 280 | 171 | |
| S | 464 | 758 | 6 | 1,119 | 257 | 259 | 326 | 245 | 529 | 257 | 345 | 344 | 369 | 103 | 215 | 673 | 281 | 837 | 1,044 | 679 | 414 | |
| T | 282 | 891 | 5 | 472 | 176 | 233 | 327 | 112 | 292 | 68 | 178 | 212 | 312 | 67 | 110 | 528 | 220 | 494 | 629 | 511 | 340 | |
| V | 157 | 491 | 13 | 555 | 181 | 179 | 203 | 140 | 327 | 89 | 249 | 186 | 352 | 97 | 168 | 447 | 204 | 566 | 596 | 462 | 261 | |
| W | 45 | 96 | | 139 | 46 | 23 | 31 | 28 | 48 | 14 | 42 | 43 | 64 | 22 | 43 | 73 | 25 | 86 | 96 | 47 | 78 | |
| Y | 69 | 284 | 1 | 246 | 112 | 67 | 107 | 39 | 140 | 77 | 150 | 110 | 120 | 36 | 109 | 217 | 110 | 306 | 250 | 141 | 98 | |

Variants by chromosome



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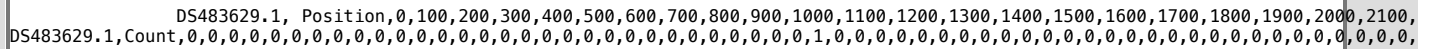
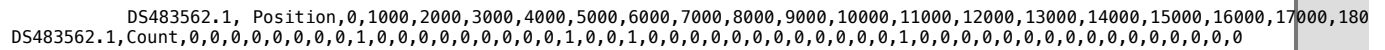
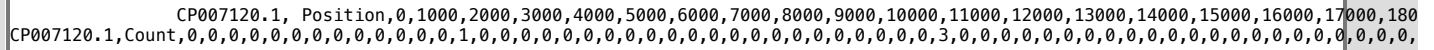
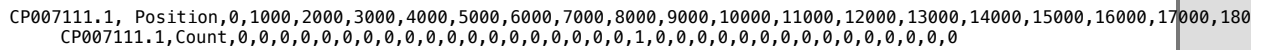
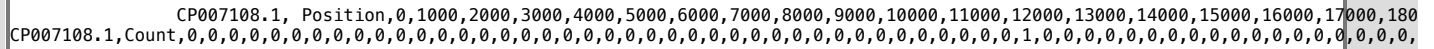
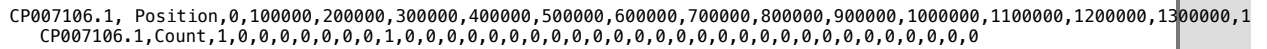
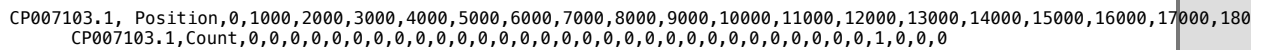
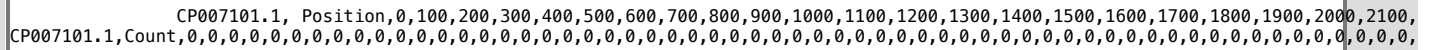
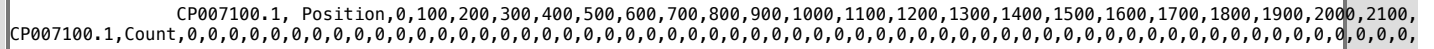
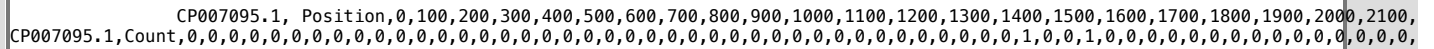
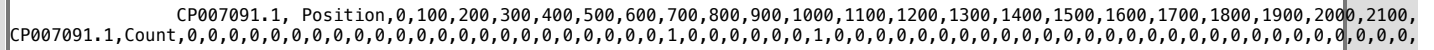
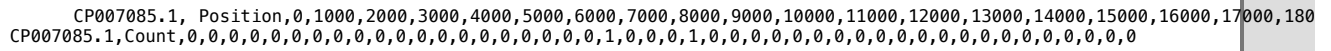
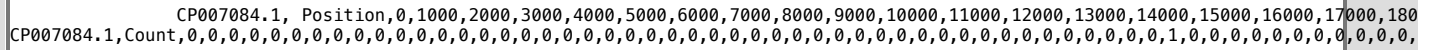


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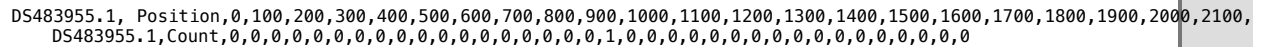
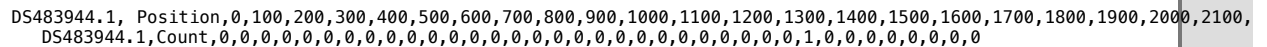
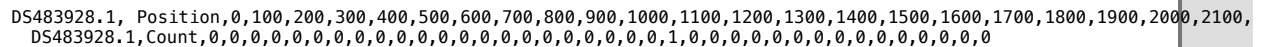
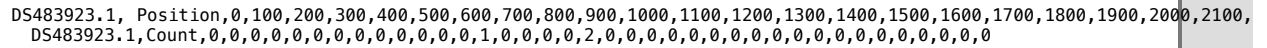
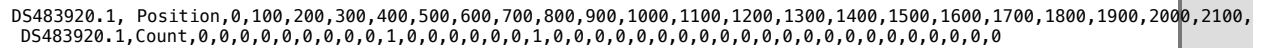
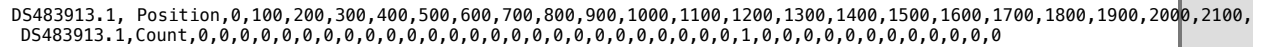
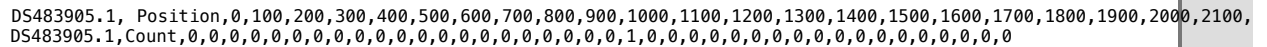
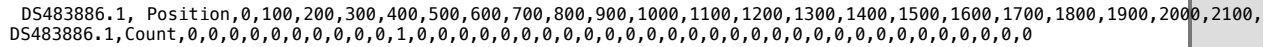
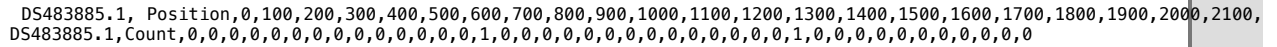
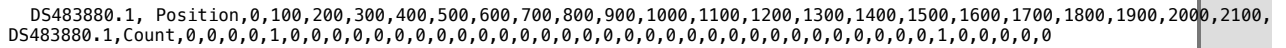
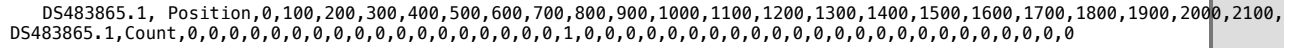
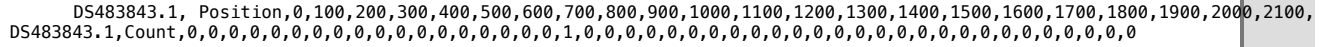
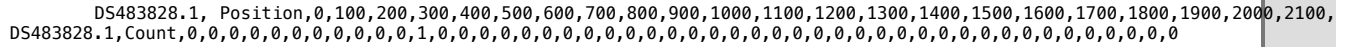
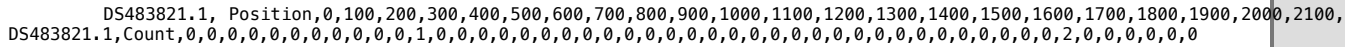
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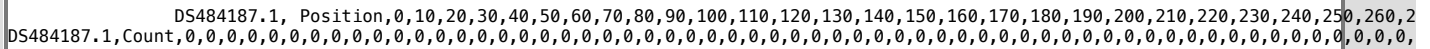
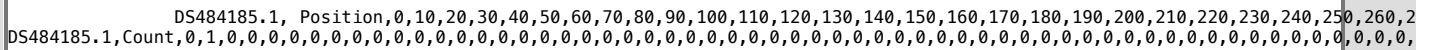
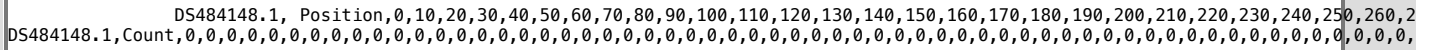
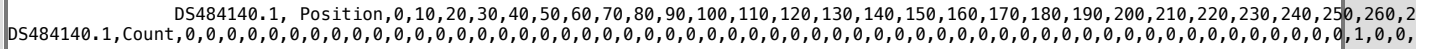
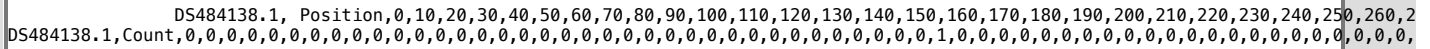
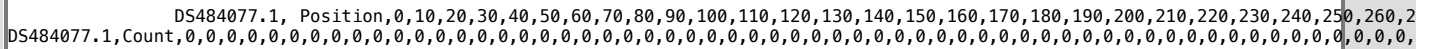
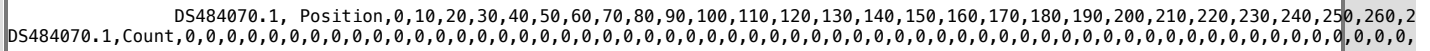
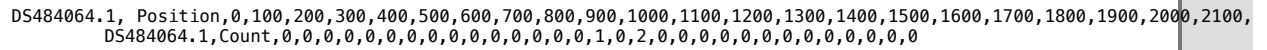
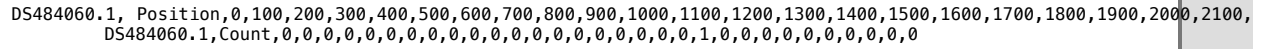
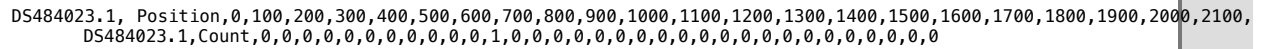
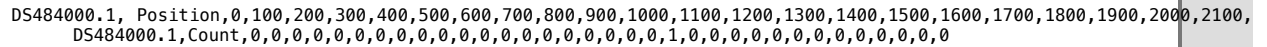
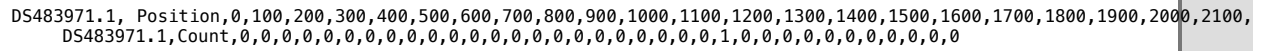
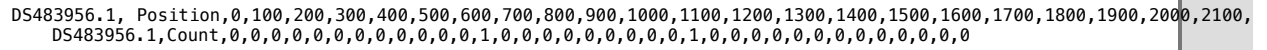


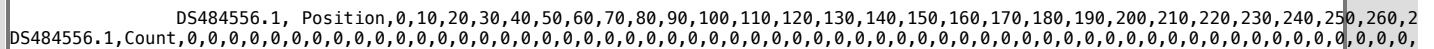
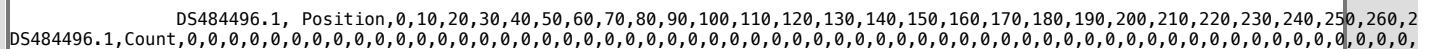
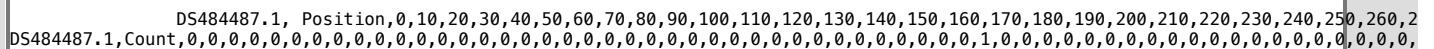
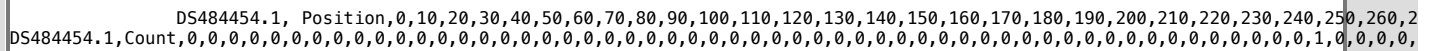
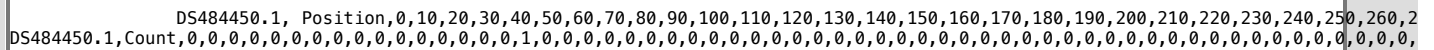
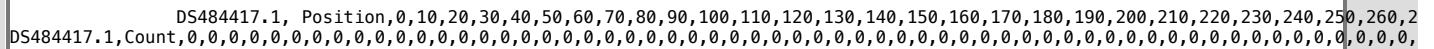
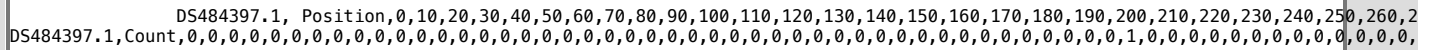
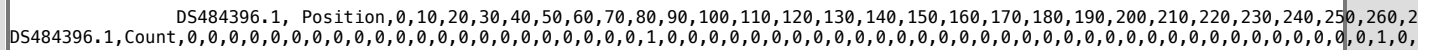
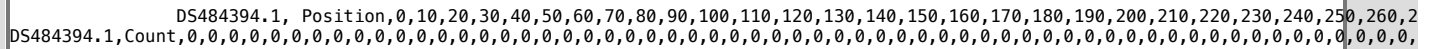
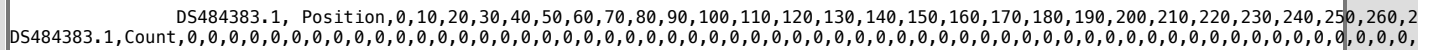
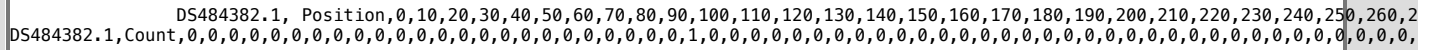
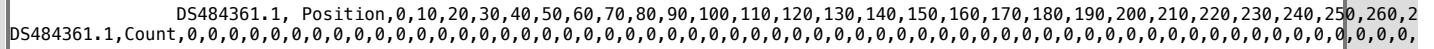
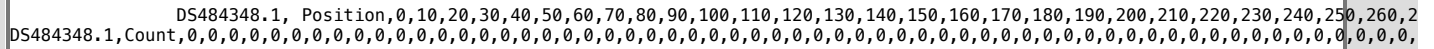
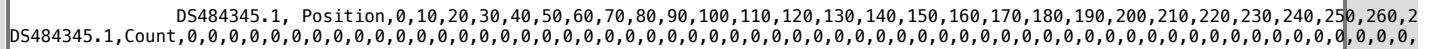
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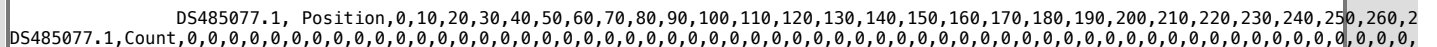
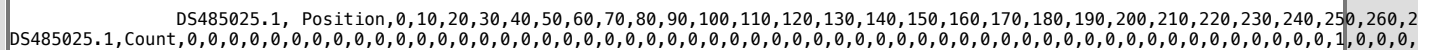
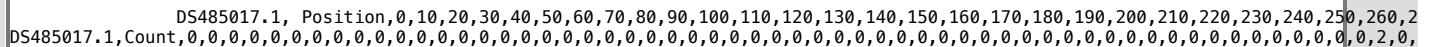
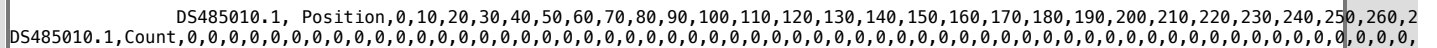
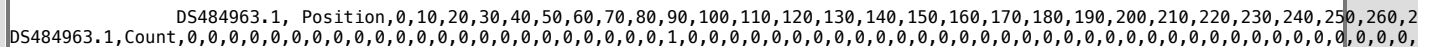
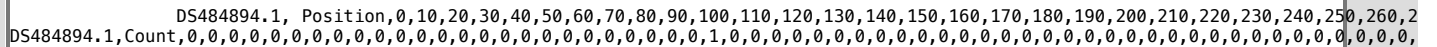
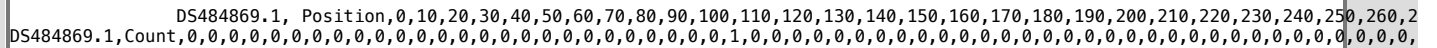
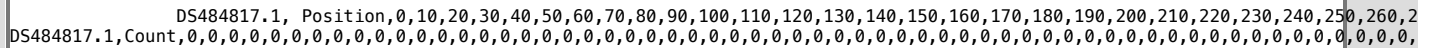
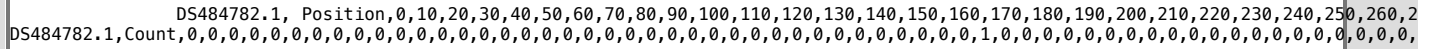
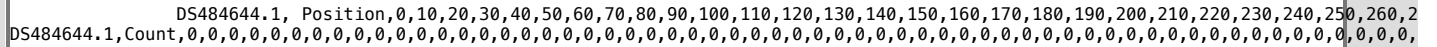
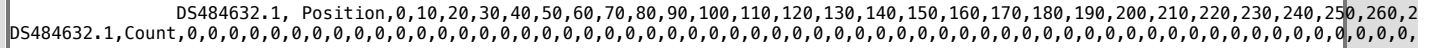
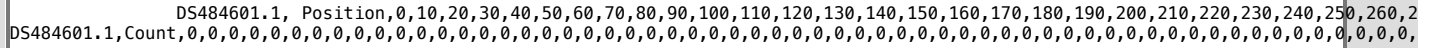
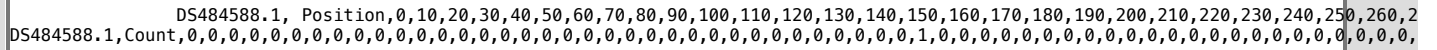
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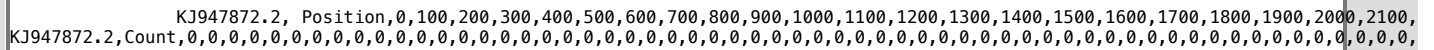
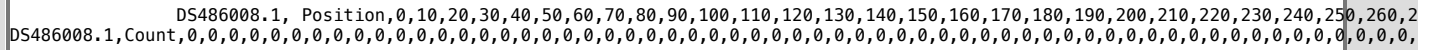
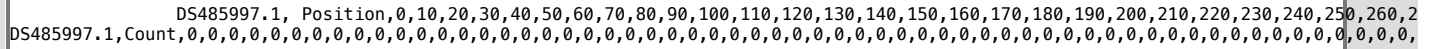
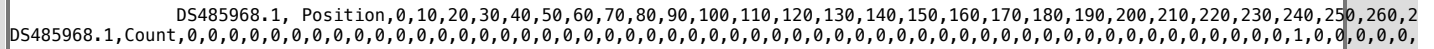
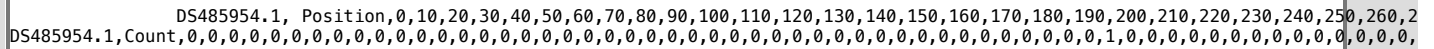
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Details by gene

[Here](#) you can find a tab-separated table.

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