

SnpEff: Variant analysis

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Summary

Genome	ncbi_drosophila
Date	2025-12-29 00:12
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/c
Warnings	52,483
Errors	0
Number of lines (input file)	67,764
Number of variants (before filter)	67,764
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	67,764
Number of known variants (i.e. non-empty ID)	67,764 (100%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of annotations	354,454
Genome total length	143,726,002
Genome effective length	139,177,133
Variant rate	1 variant every 2,053 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
AE013599.5	25,286,936	12,149	2,081
AE014134.6	23,513,712	13,878	1,694
AE014135.4	1,348,131	102	13,216
AE014296.5	28,110,227	14,025	2,004
AE014297.3	32,079,331	14,040	2,284
AE014298.5	23,542,271	12,232	1,924
CP007074.1	76,224	2	38,112
CP007075.1	11,983	14	855
CP007077.1	36,913	61	605
CP007078.1	22,604	3	7,534
CP007079.1	23,238	12	1,936
CP007081.1	88,768	5	17,753
CP007084.1	62,570	1	62,570
CP007085.1	45,120	8	5,640
CP007086.1	22,882	1	22,882
CP007087.1	46,986	5	9,397
CP007089.1	16,157	1	16,157
CP007091.1	20,763	6	3,460
CP007103.1	33,320	31	1,074
CP007104.1	27,447	6	4,574
CP007106.1	3,667,352	26	141,052
CP007108.1	66,731	2	33,365
CP007111.1	34,521	1	34,521
CP007120.1	76,973	16	4,810
DS483562.1	50,625	15	3,375
DS483629.1	15,417	33	467
DS483641.1	14,503	25	580
DS483646.1	14,098	1	14,098

DS483648.1	13,940	2	6,970
DS483655.1	13,549	5	2,709
DS483659.1	13,416	34	394
DS483660.1	13,394	17	787
DS483670.1	12,827	4	3,206
DS483675.1	12,536	1	12,536
DS483677.1	12,513	2	6,256
DS483681.1	12,368	1	12,368
DS483711.1	14,687	1	14,687
DS483724.1	13,501	23	587
DS483736.1	14,006	1	14,006
DS483746.1	9,341	45	207
DS483749.1	8,007	16	500
DS483751.1	7,314	22	332
DS483753.1	7,123	5	1,424
DS483758.1	6,860	1	6,860
DS483770.1	6,193	6	1,032
DS483773.1	6,062	6	1,010
DS483776.1	6,000	1	6,000
DS483781.1	5,952	11	541
DS483783.1	5,891	3	1,963
DS483784.1	5,832	1	5,832
DS483789.1	5,555	7	793
DS483803.1	5,232	1	5,232
DS483808.1	5,060	4	1,265
DS483809.1	5,057	3	1,685
DS483817.1	4,933	22	224
DS483818.1	4,917	3	1,639
DS483819.1	4,903	1	4,903
DS483833.1	4,701	2	2,350
DS483843.1	4,515	6	752
DS483845.1	4,465	3	1,488
DS483851.1	4,395	3	1,465
DS483853.1	4,381	16	273
DS483854.1	4,378	1	4,378
DS483866.1	4,273	6	712
DS483870.1	4,231	1	4,231
DS483880.1	4,150	7	592
DS483885.1	4,085	4	1,021
DS483892.1	4,013	5	802
DS483893.1	4,012	1	4,012
DS483897.1	3,984	4	996
DS483903.1	3,941	2	1,970
DS483905.1	3,926	5	785
DS483906.1	3,924	5	784
DS483907.1	3,921	1	3,921
DS483908.1	3,913	1	3,913
DS483918.1	3,818	2	1,909
DS483920.1	3,806	11	346
DS483927.1	3,737	1	3,737
DS483928.1	3,730	2	1,865
DS483940.1	3,648	13	280
DS483944.1	3,622	7	517
DS483951.1	3,574	8	446
DS483954.1	3,554	4	888
DS483956.1	3,553	6	592
DS483961.1	3,527	5	705
DS483970.1	3,490	2	1,745
DS483971.1	3,478	1	3,478
DS483974.1	3,473	2	1,736
DS483982.1	3,402	2	1,701
DS483992.1	3,365	1	3,365
DS484000.1	3,302	12	275
DS484002.1	3,290	2	1,645
DS484004.1	3,277	8	409
DS484022.1	3,209	6	534
DS484039.1	3,162	1	3,162
DS484041.1	3,157	8	394
DS484042.1	3,156	17	185
DS484046.1	3,123	1	3,123

DS484051.1	3,100	2	1,550
DS484057.1	3,076	3	1,025
DS484058.1	3,073	27	113
DS484060.1	3,065	2	1,532
DS484061.1	3,059	2	1,529
DS484064.1	3,044	9	338
DS484068.1	3,013	1	3,013
DS484069.1	3,010	4	752
DS484070.1	3,009	7	429
DS484084.1	2,956	1	2,956
DS484089.1	2,928	5	585
DS484099.1	2,910	4	727
DS484102.1	2,903	3	967
DS484116.1	2,860	19	150
DS484124.1	2,846	6	474
DS484125.1	2,844	2	1,422
DS484130.1	2,834	3	944
DS484131.1	2,833	2	1,416
DS484138.1	2,822	1	2,822
DS484140.1	2,819	5	563
DS484143.1	2,814	1	2,814
DS484148.1	2,795	23	121
DS484153.1	2,793	4	698
DS484159.1	2,784	1	2,784
DS484178.1	2,698	3	899
DS484180.1	2,697	4	674
DS484185.1	2,686	2	1,343
DS484187.1	2,671	3	890
DS484197.1	2,642	1	2,642
DS484198.1	2,641	4	660
DS484202.1	2,636	1	2,636
DS484203.1	2,635	2	1,317
DS484216.1	2,603	2	1,301
DS484219.1	2,591	1	2,591
DS484225.1	2,577	5	515
DS484235.1	2,557	1	2,557
DS484244.1	2,536	19	133
DS484246.1	2,529	6	421
DS484258.1	2,510	2	1,255
DS484260.1	2,505	1	2,505
DS484263.1	2,487	1	2,487
DS484268.1	2,475	4	618
DS484272.1	2,464	1	2,464
DS484276.1	2,447	3	815
DS484277.1	2,442	11	222
DS484278.1	2,439	1	2,439
DS484279.1	2,438	16	152
DS484280.1	2,438	1	2,438
DS484281.1	2,438	1	2,438
DS484282.1	2,435	9	270
DS484285.1	2,431	2	1,215
DS484289.1	2,425	4	606
DS484296.1	2,417	1	2,417
DS484297.1	2,413	3	804
DS484300.1	2,400	2	1,200
DS484316.1	2,379	1	2,379
DS484319.1	2,372	5	474
DS484322.1	2,366	2	1,183
DS484330.1	2,353	1	2,353
DS484343.1	2,325	6	387
DS484345.1	2,318	1	2,318
DS484346.1	2,317	3	772
DS484348.1	2,308	1	2,308
DS484354.1	2,293	1	2,293
DS484358.1	2,286	1	2,286
DS484361.1	2,282	1	2,282
DS484367.1	2,259	1	2,259
DS484369.1	2,253	14	160
DS484371.1	2,247	1	2,247
DS484377.1	2,232	2	1,116

DS484382.1	2,223	4	555
DS484383.1	2,221	3	740
DS484387.1	2,210	1	2,210
DS484388.1	2,209	1	2,209
DS484393.1	2,201	3	733
DS484394.1	2,200	6	366
DS484396.1	2,198	4	549
DS484417.1	2,139	1	2,139
DS484419.1	2,132	1	2,132
DS484429.1	2,113	2	1,056
DS484431.1	2,113	1	2,113
DS484447.1	2,089	1	2,089
DS484450.1	2,087	1	2,087
DS484454.1	2,084	7	297
DS484462.1	2,068	1	2,068
DS484469.1	2,060	1	2,060
DS484472.1	2,046	4	511
DS484486.1	2,014	1	2,014
DS484507.1	1,978	1	1,978
DS484526.1	1,956	1	1,956
DS484528.1	1,947	1	1,947
DS484533.1	1,944	1	1,944
DS484552.1	1,920	1	1,920
DS484556.1	1,916	2	958
DS484563.1	1,903	1	1,903
DS484566.1	1,900	11	172
DS484568.1	1,899	1	1,899
DS484578.1	1,872	1	1,872
DS484588.1	1,863	2	931
DS484593.1	1,849	3	616
DS484594.1	1,843	1	1,843
DS484600.1	1,841	1	1,841
DS484601.1	1,832	7	261
DS484608.1	1,818	1	1,818
DS484609.1	1,818	1	1,818
DS484610.1	1,813	3	604
DS484611.1	1,813	1	1,813
DS484614.1	1,806	1	1,806
DS484632.1	1,775	3	591
DS484644.1	1,747	1	1,747
DS484646.1	1,747	4	436
DS484672.1	1,703	1	1,703
DS484673.1	1,696	2	848
DS484697.1	1,636	1	1,636
DS484702.1	1,623	1	1,623
DS484718.1	1,586	4	396
DS484719.1	1,586	1	1,586
DS484722.1	1,577	4	394
DS484724.1	1,575	1	1,575
DS484725.1	1,573	1	1,573
DS484737.1	1,550	2	775
DS484739.1	1,549	10	154
DS484748.1	1,538	1	1,538
DS484751.1	1,533	1	1,533
DS484765.1	1,516	1	1,516
DS484768.1	1,509	1	1,509
DS484777.1	1,489	1	1,489
DS484779.1	1,487	1	1,487
DS484787.1	1,475	1	1,475
DS484789.1	1,473	1	1,473
DS484803.1	1,461	1	1,461
DS484817.1	1,445	3	481
DS484857.1	1,402	3	467
DS484869.1	1,391	3	463
DS484904.1	1,366	2	683
DS484907.1	1,361	2	680
DS484913.1	1,355	1	1,355
DS484948.1	1,328	2	664
DS484963.1	1,315	4	328
DS484970.1	1,310	2	655

DS484978.1	1,306	2	653
DS484982.1	1,304	4	326
DS484990.1	1,301	1	1,301
DS485010.1	1,286	4	321
DS485015.1	1,283	1	1,283
DS485017.1	1,281	4	320
DS485025.1	1,278	3	426
DS485031.1	1,275	4	318
DS485044.1	1,271	1	1,271
DS485050.1	1,268	3	422
DS485054.1	1,265	1	1,265
DS485056.1	1,263	1	1,263
DS485064.1	1,262	4	315
DS485077.1	1,258	2	629
DS485119.1	1,235	2	617
DS485141.1	1,228	2	614
DS485148.1	1,227	9	136
DS485172.1	1,220	1	1,220
DS485176.1	1,219	8	152
DS485255.1	1,190	1	1,190
DS485260.1	1,189	6	198
DS485262.1	1,189	1	1,189
DS485266.1	1,186	1	1,186
DS485268.1	1,186	1	1,186
DS485278.1	1,184	1	1,184
DS485281.1	1,184	2	592
DS485299.1	1,178	3	392
DS485303.1	1,175	3	391
DS485310.1	1,173	2	586
DS485331.1	1,165	4	291
DS485345.1	1,161	2	580
DS485360.1	1,159	2	579
DS485371.1	1,156	3	385
DS485384.1	1,153	3	384
DS485411.1	1,146	1	1,146
DS485422.1	1,144	1	1,144
DS485454.1	1,135	1	1,135
DS485464.1	1,133	2	566
DS485465.1	1,133	1	1,133
DS485476.1	1,130	1	1,130
DS485504.1	1,123	1	1,123
DS485509.1	1,123	1	1,123
DS485528.1	1,117	4	279
DS485535.1	1,116	1	1,116
DS485543.1	1,114	1	1,114
DS485549.1	1,112	2	556
DS485592.1	1,102	1	1,102
DS485597.1	1,100	4	275
DS485606.1	1,097	1	1,097
DS485647.1	1,086	1	1,086
DS485651.1	1,084	1	1,084
DS485656.1	1,083	2	541
DS485664.1	1,081	8	135
DS485703.1	1,071	2	535
DS485707.1	1,071	2	535
DS485753.1	1,059	1	1,059
DS485757.1	1,058	1	1,058
DS485771.1	1,055	1	1,055
DS485773.1	1,054	1	1,054
DS485775.1	1,053	1	1,053
DS485801.1	1,048	2	524
DS485876.1	1,032	1	1,032
DS485879.1	1,031	9	114
DS485887.1	1,029	5	205
DS485933.1	1,019	2	509
DS485940.1	1,018	1	1,018
DS485941.1	1,018	1	1,018
DS485952.1	1,014	3	338
DS485962.1	1,012	1	1,012
DS485968.1	1,011	1	1,011

DS485981.1	1,007	1	1,007
DS486004.1	1,001	1	1,001
KJ947872.2	19,524	8	2,440
Total	139,177,133	67,764	2,053

Number variants by type

Type	Total
SNP	0
MNP	259
INS	19,041
DEL	25,070
MIXED	23,394
INV	0
DUP	0
CNV	0
BND	0
INTERVAL	0
Total	67,764

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	364	0.103%
LOW	868	0.245%
MODERATE	3,346	0.944%
MODIFIER	349,876	98.708%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
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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	1	0%	DOWNSTREAM	76,118	21.475%
3_prime_UTR_variant	5,737	1.612%	EXON	5,158	1.455%
5_prime_UTR_variant	2,641	0.742%	GENE	82	0.023%
bidirectional_gene_fusion	52	0.015%	INTERGENIC	25,147	7.095%
conservative_inframe_deletion	627	0.176%	INTRON	156,173	44.06%
conservative_inframe_insertion	556	0.156%	SPLICE_SITE_ACCEPTOR	63	0.018%
disruptive_inframe_deletion	1,317	0.37%	SPLICE_SITE_DONOR	46	0.013%
disruptive_inframe_insertion	865	0.243%	SPLICE_SITE_REGION	868	0.245%
downstream_gene_variant	76,124	21.387%	TRANSCRIPT	387	0.109%
exon_loss_variant	1	0%	UPSTREAM	82,073	23.155%
frameshift_variant	162	0.046%	UTR_3_PRIME	5,733	1.617%
gene_fusion	30	0.008%	UTR_5_PRIME	2,606	0.735%
intergenic_region	25,147	7.065%			
intragenic_variant	126	0.035%			
intron_variant	156,856	44.068%			
missense_variant	303	0.085%			
non_coding_transcript_exon_variant	1,693	0.476%			
non_coding_transcript_variant	261	0.073%			
splice_acceptor_variant	72	0.02%			
splice_donor_variant	57	0.016%			
splice_region_variant	986	0.277%			
start_lost	14	0.004%			
start_retained_variant	6	0.002%			
stop_gained	21	0.006%			
stop_lost	28	0.008%			
stop_retained_variant	5	0.001%			
synonymous_variant	183	0.051%			
upstream_gene_variant	82,073	23.058%			



Quality:



Insertions and deletions length:

Min	1
Max	48
Mean	6.59
Median	1
Standard deviation	8.258
Values	1,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48
Count	25070,2866,2140,1877,1407,1979,939,998,811,759,434,656,354,368,346,282,245,283,239,160,171,196,140,136,129,128,117,108,118,97,66,75,75,46



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



Allele Count



Min	1
Max	1
Mean	1
Median	1
Standard deviation	0
Values	1
Count	67764

Hom/Het per sample



Sample_names
Reference
Het
Hom
Missing

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).

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT	CCA	CCC
-		87	257	137	103	146	107	60	107	45	141	36	90	30	40	90	31	554	92	1,578	115	145	85
AAA	73		2	4	1					1	1		9			2							2
AAC	276		1	2	33	1	13				10	9			8			2				1	

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT	CCA	CCC
AAG	140	21	2	3	2						2	2		2									
AAT	151	4	17	2	9	2	1		1		1			1									
ACA	183					13	12	1	19		14			9	4	1			1			4	
ACC	247		12			7		9	5		9		20		1								1
ACG	61					3	4		6					1				8		14			
ACT	132		1		2	14	11	6	5												1		
AGA	36		1									4	2							6			
AGC	272		33	3	2	2	14		12		1		11		8	2							
AGG	31	4								5	3												
AGT	91		5	2	3		6	12			14			3			3	2				4	
ATA	40		2				2								5		1						
ATC	94		1	2		2				2	1					1							
ATG	93		7	1						4	3	2	1	2	4				2				
ATT	44		1		1		2		6		1			1			9						
CAA	788																		55	268	20	4	
CAC	153																	11	2	33	12		
CAG	2,302																	233	29	47	48	8	8
CAT	202																	20	3	18			
CCA	218																	7		30	3	11	3
CCC	147												2							6		5	4
CCG	163							1										10	2	10		5	9
CCT	137					2														2		8	9
CGA	32									4									1	2			
CGC	45																						
CGG	52			1																16			
CGT	38	2																	5	2			
CTA	18																	1					
CTC	60																	2			1		2
CTG	172								26										1	15	2		
CTT	31																			3	2	1	
GAA	164																	1					
GAC	109	1																	2				
GAG	238			4				1															
GAT	119								1														
GCA	389					2																2	
GCC	180																						
GCG	126			4																			
GCT	199					1			2												4		
GGA	278																						
GGC	320																						
GGG	59																						
GGT	202												2										
GTA	32																	1					
GTC	69					2																	
GTG	135										1												
GTT	95	1																					
TAA	7	1																					
TAC	55		3																	1	3		
TAG	7																						
TAT	58																				1		
TCA	120					2				2								4					
TCC	249		6		2																		
TCG	129																3				4		4
TCT	94	2				1																	
TGA	10							1															
TGC	28													1						1			
TGG	24		2		1																		
TGT	37																	1					
TTA	36					2																	
TTC	36												1		3								2
TTG	99															2			3	4			
TTT	30							8															

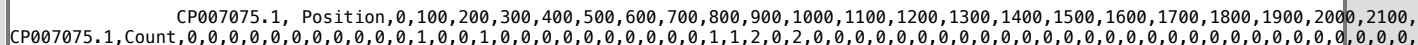
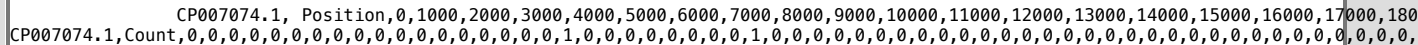
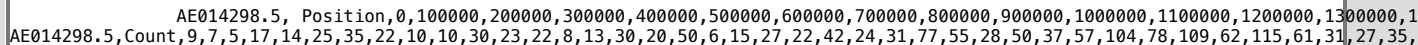
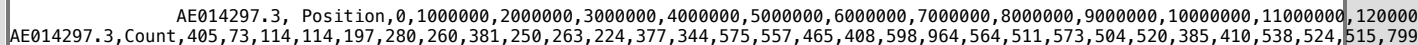
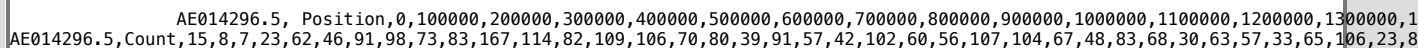
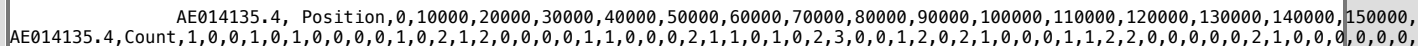
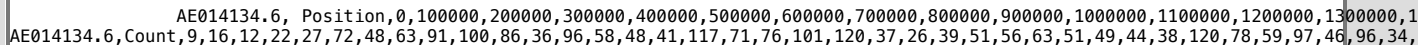
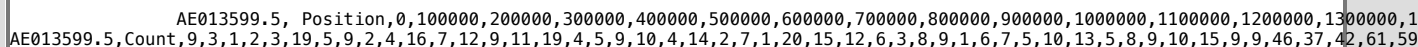
Amino acid changes

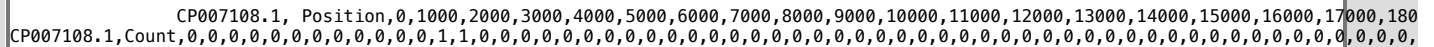
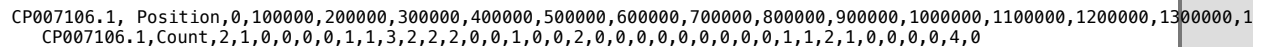
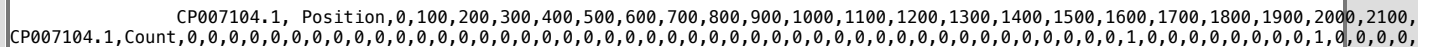
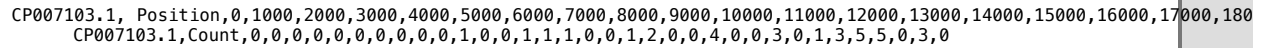
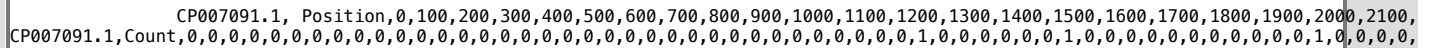
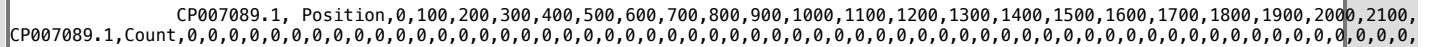
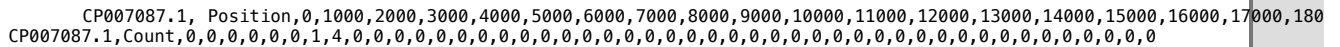
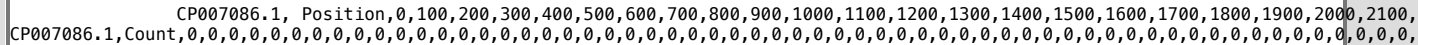
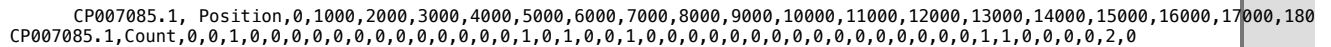
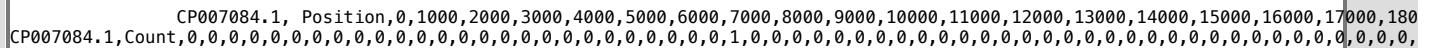
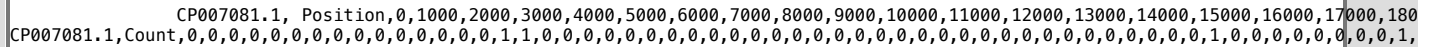
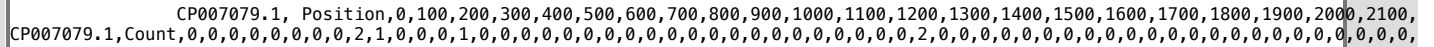
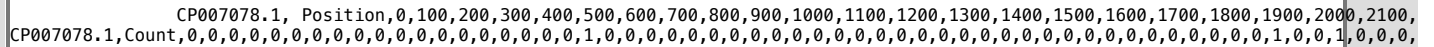
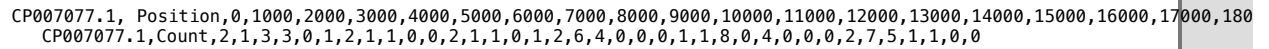
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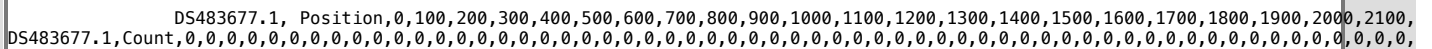
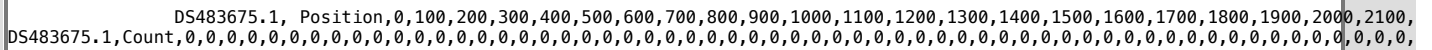
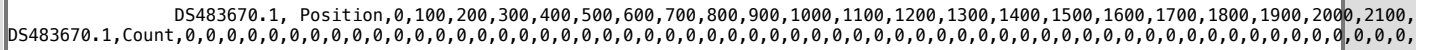
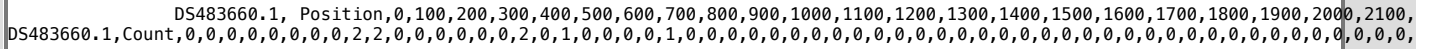
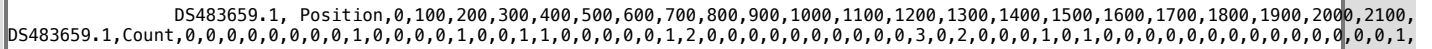
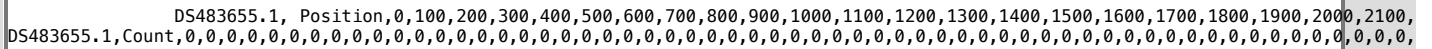
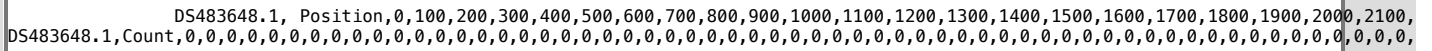
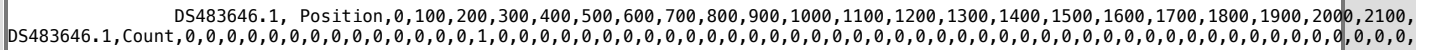
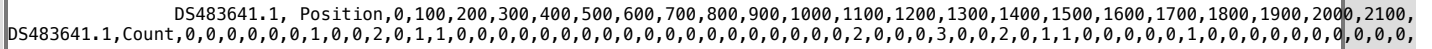
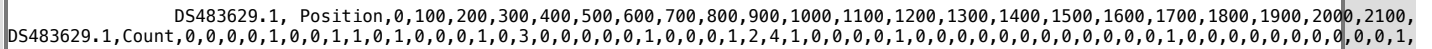
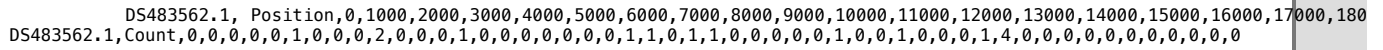
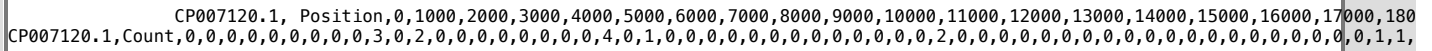
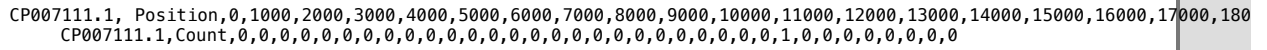
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).

- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

Variants by chromosome







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DS483724.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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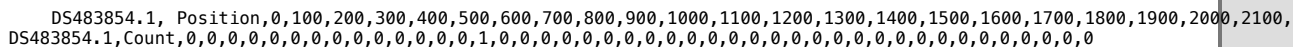
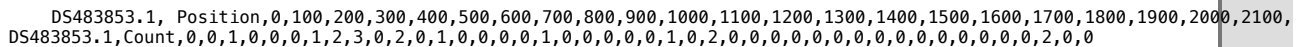
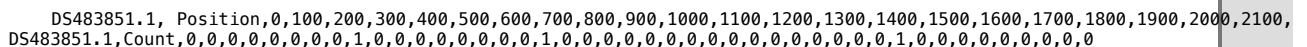
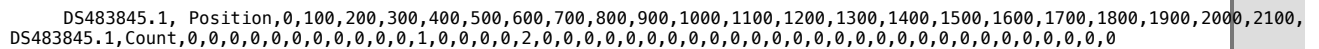
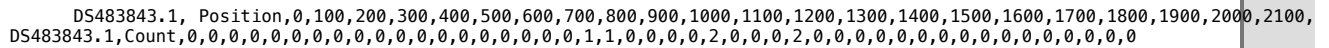
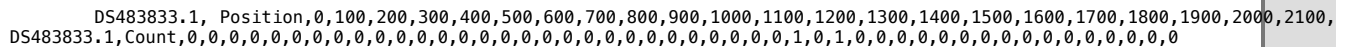
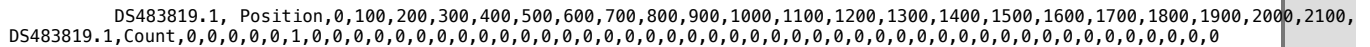
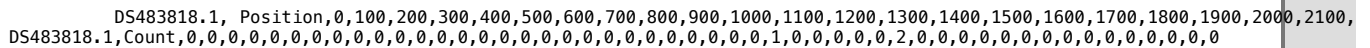
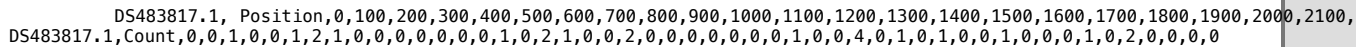
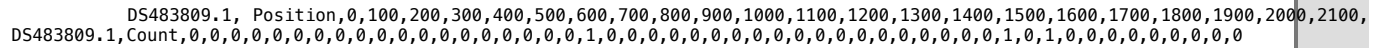
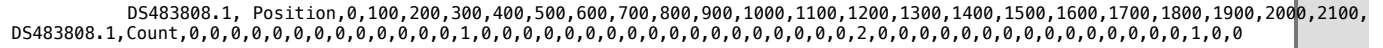
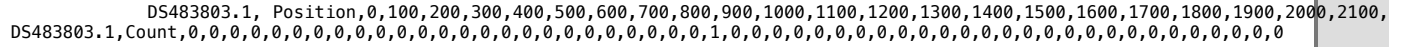
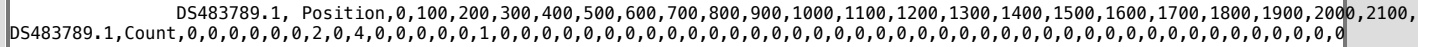
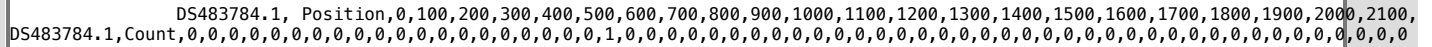
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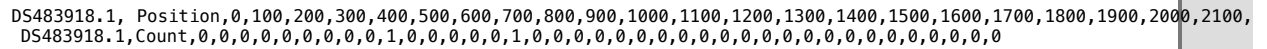
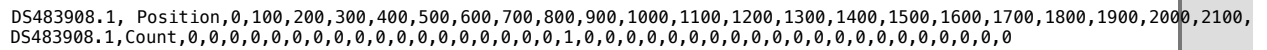
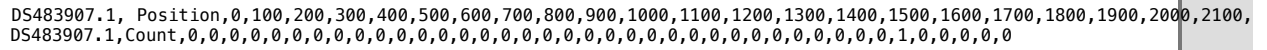
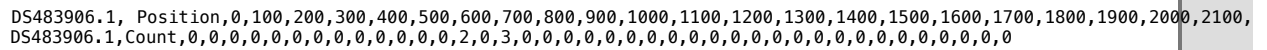
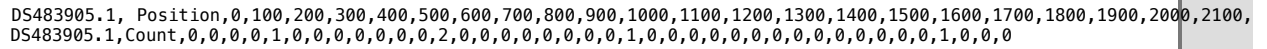
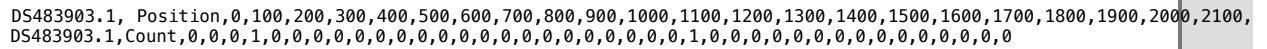
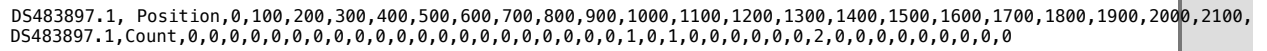
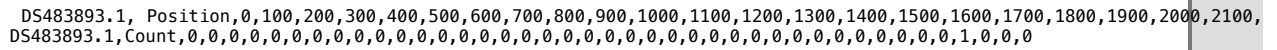
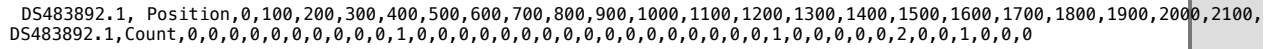
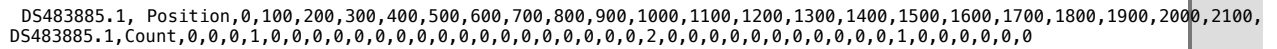
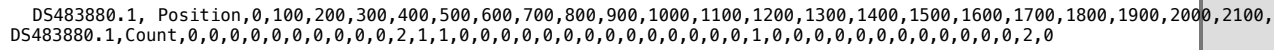
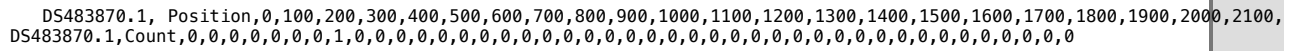
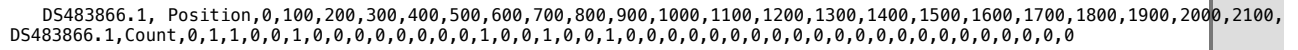
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DS483773.1,Count,0,1,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,1,0,

[illegible][illegible][illegible]







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DS484002.1,Count,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0



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DS484042.1,Count,0,0,0,0,0,0,2,0,0,4,4,0,0,0,2,0,3,0,2,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0



DS484046.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
DS484046.1,Count,0,1,0,0,0,0,0,0



DS484051.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS484057.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS484058.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
DS484058.1,Count,0,3,4,6,0,5,3,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,2,2,0,0,0,0,0



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DS484061.1,Count,0,0,0,0,0,1,0,1,0,0,0,0,0



DS484064.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS484068.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
DS484068.1,Count,0,0,0,0,0,0,1,0



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DS484070.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484070.1,Count,0,2,0,0,0,0,



DS484084.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484084.1,Count,0,



DS484089.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484089.1,Count,0,1,0,0,0,



DS484099.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484099.1,Count,0,



DS484102.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484102.1,Count,0,



DS484116.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484116.1,Count,0,



DS484124.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484124.1,Count,0,



DS484125.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484125.1,Count,0,



DS484130.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484130.1,Count,0,

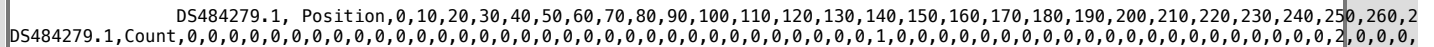
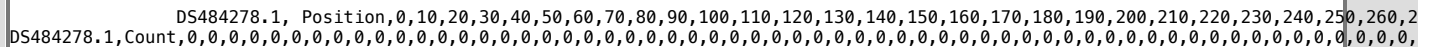
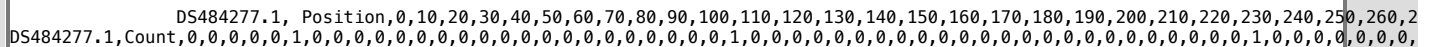
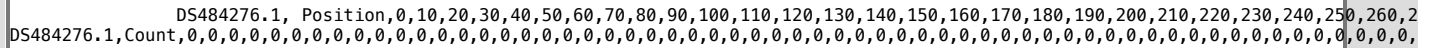
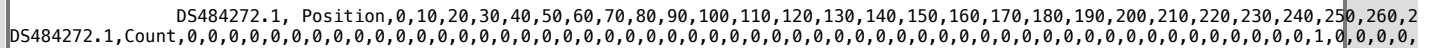
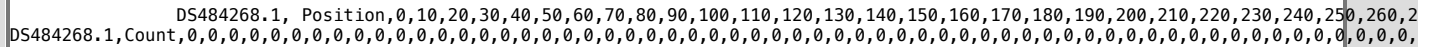
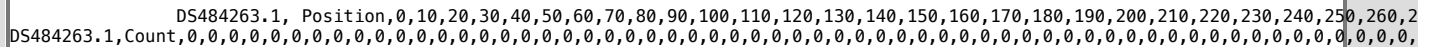
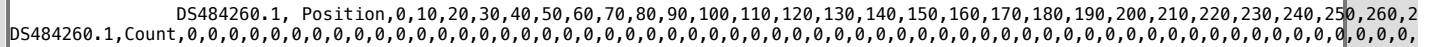
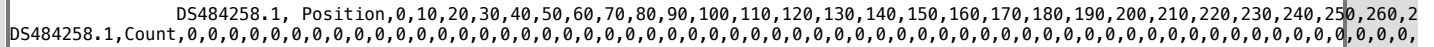
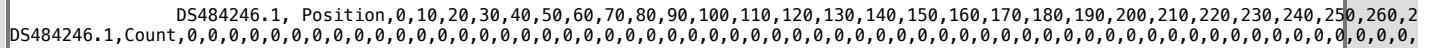
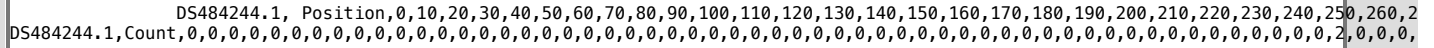
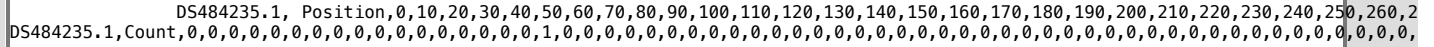
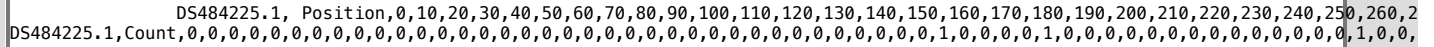
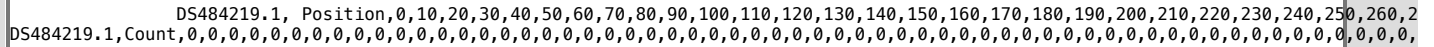


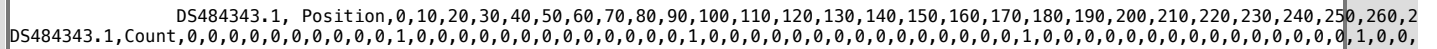
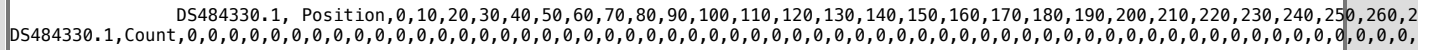
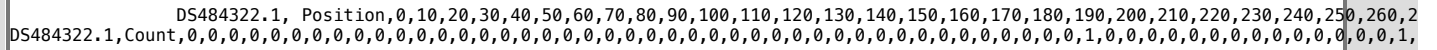
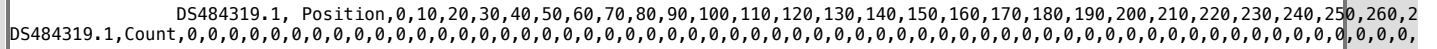
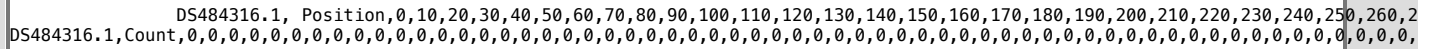
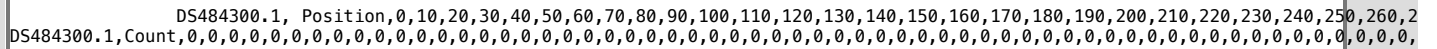
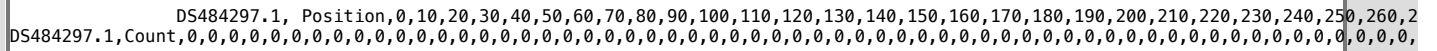
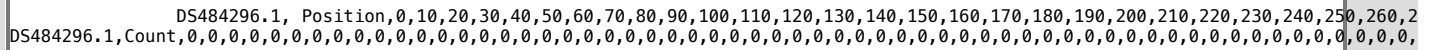
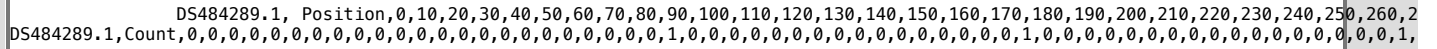
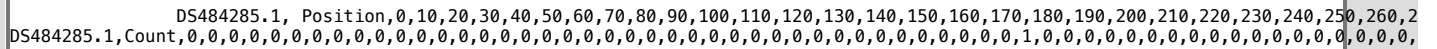
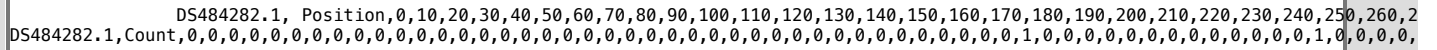
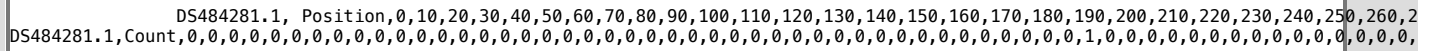
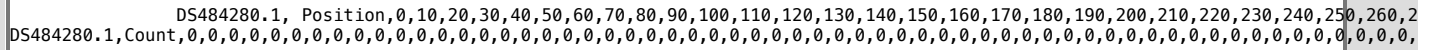
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DS484131.1,Count,0,



DS484138.1, Position,0,10,20,30,40,50,60,70,80,90,100,110,120,130,140,150,160,170,180,190,200,210,220,230,240,250,260,2
DS484138.1,Count,0,

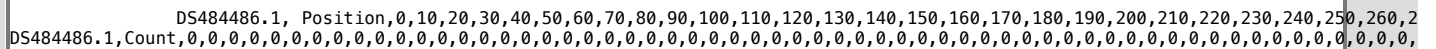
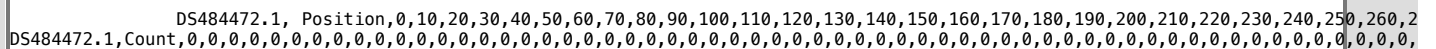
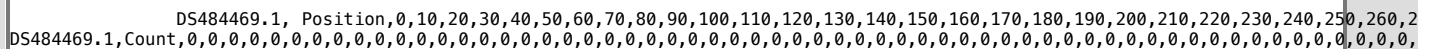
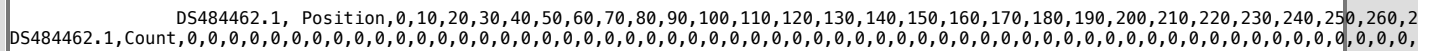
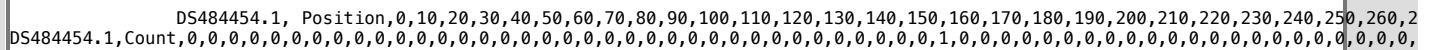
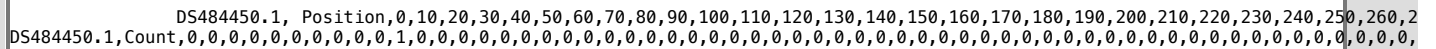
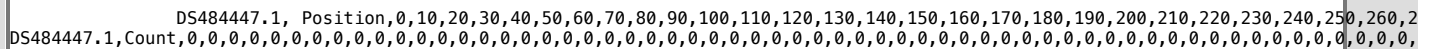
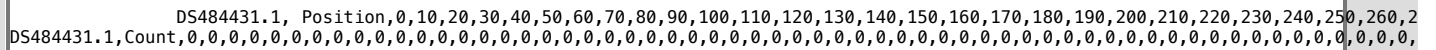
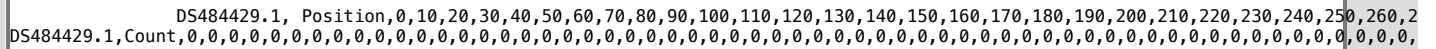
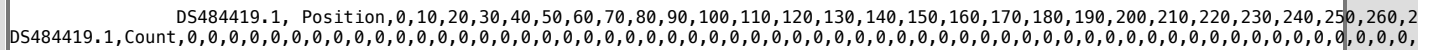
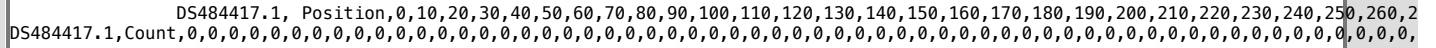
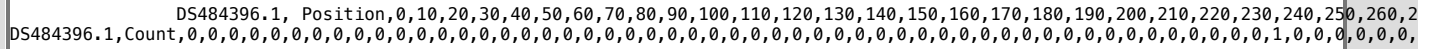
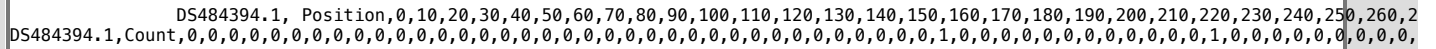
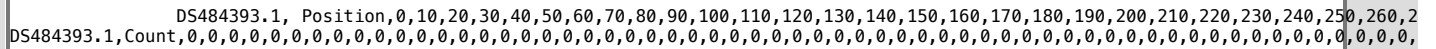


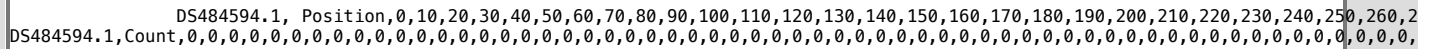
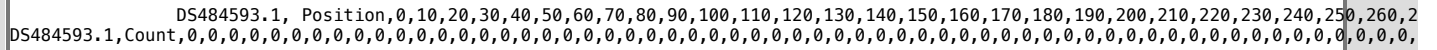
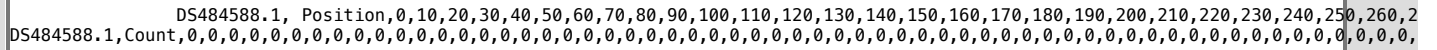
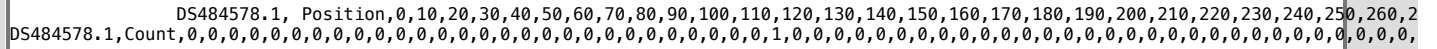
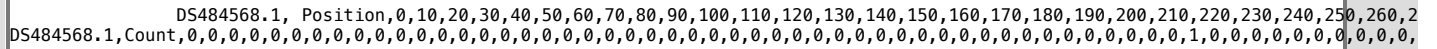
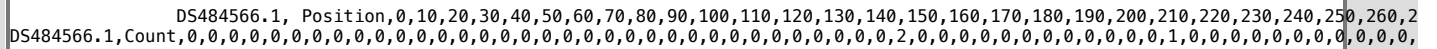
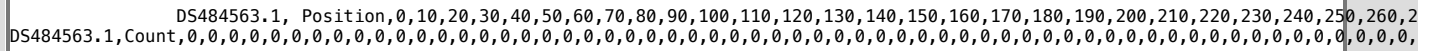
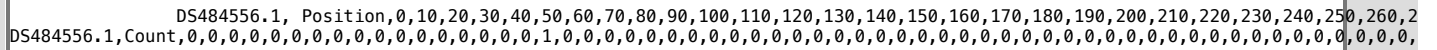
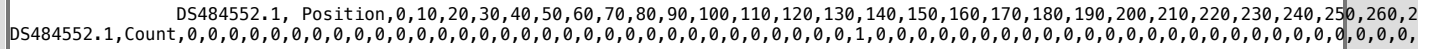
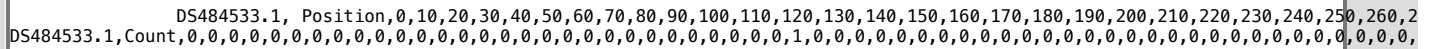
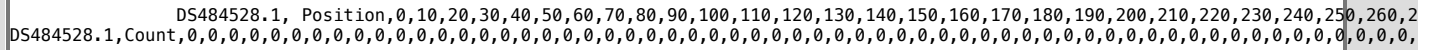
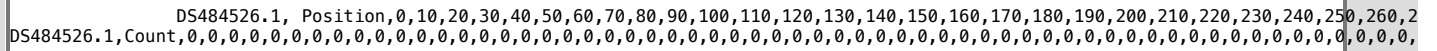
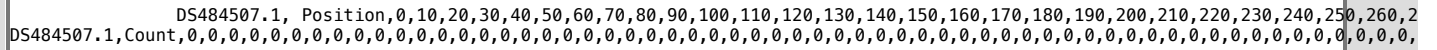




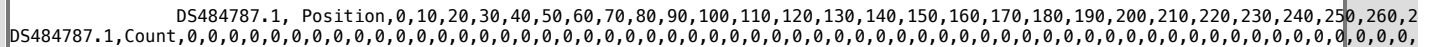
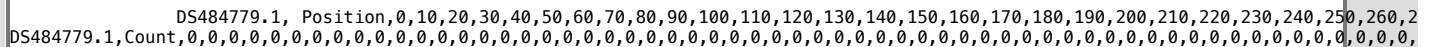
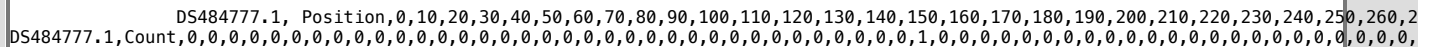
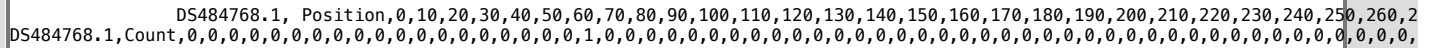
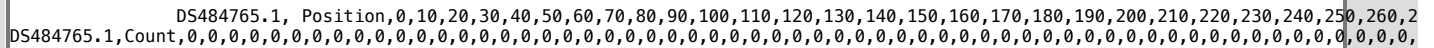
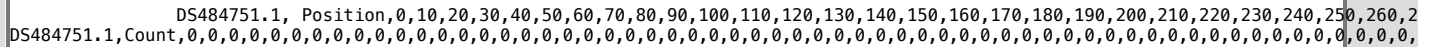
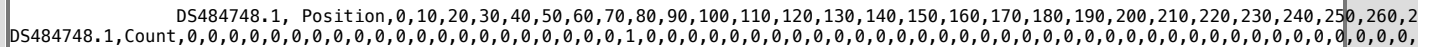
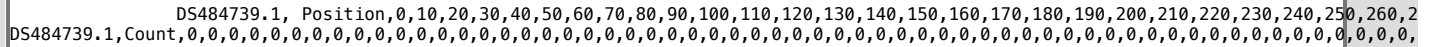
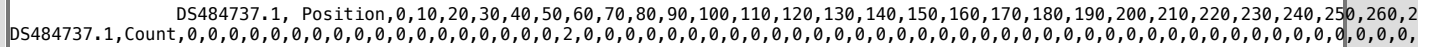
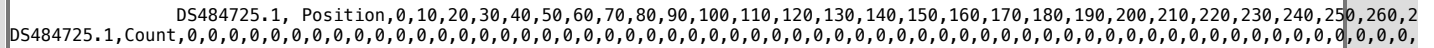
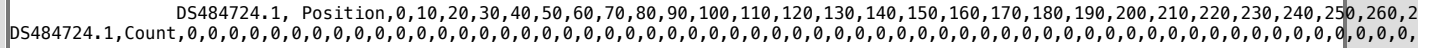
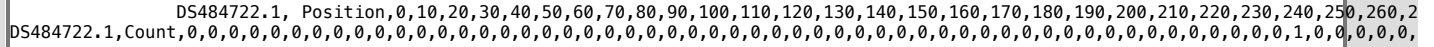
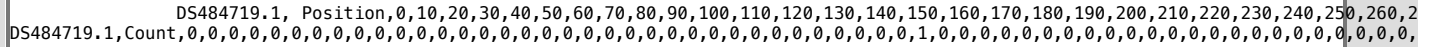
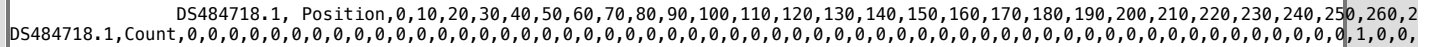
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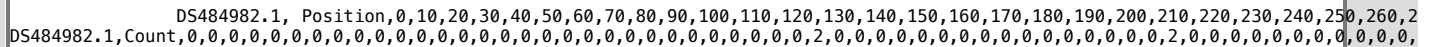
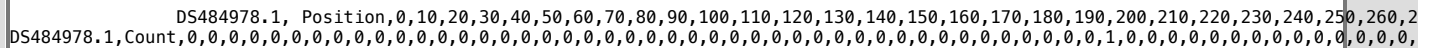
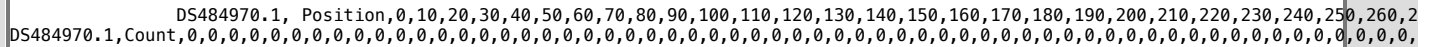
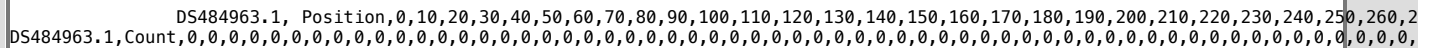
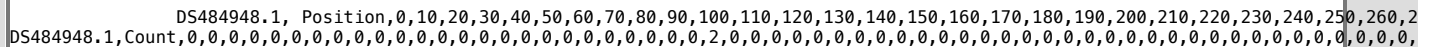
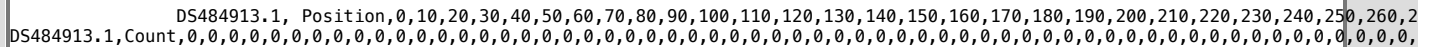
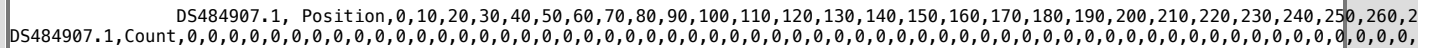
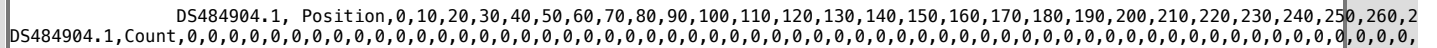
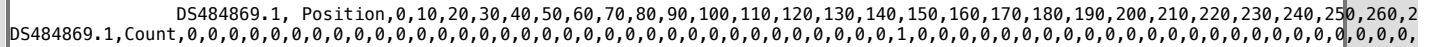
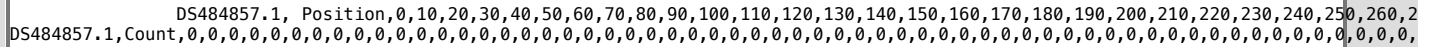
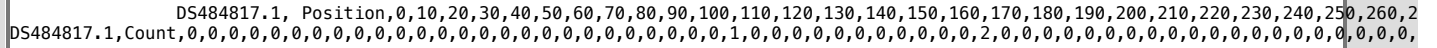
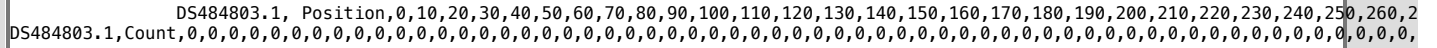
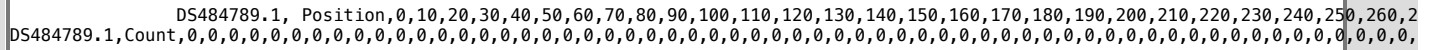


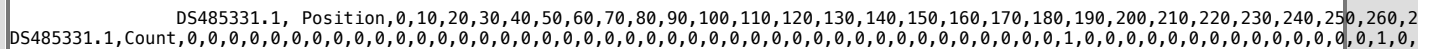
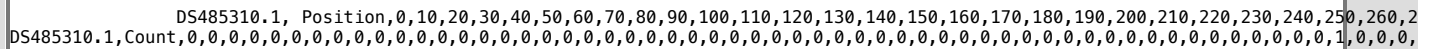
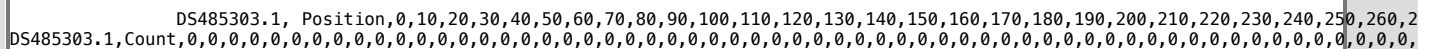
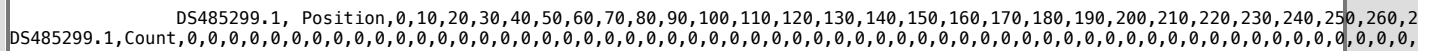
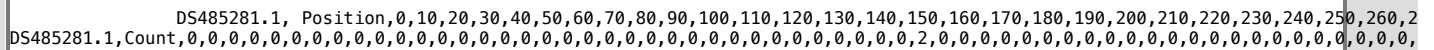
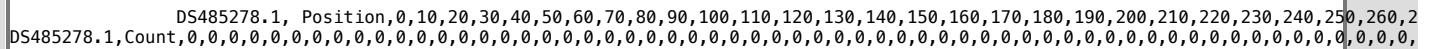
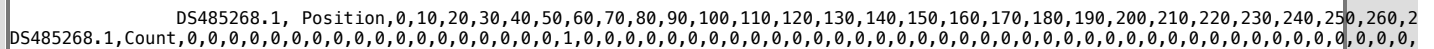
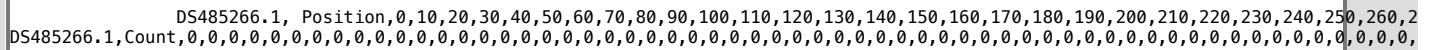
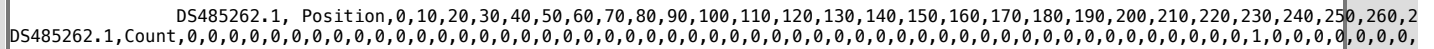
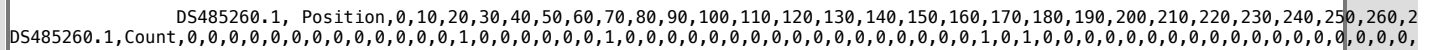
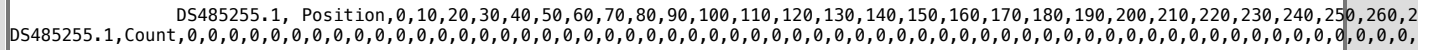
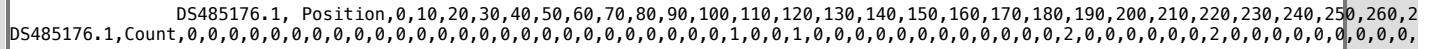
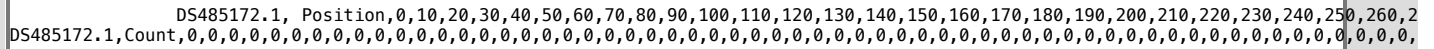
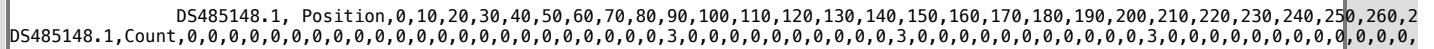


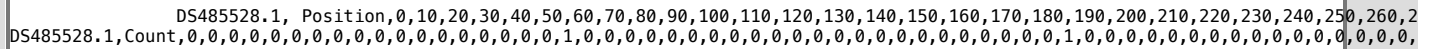
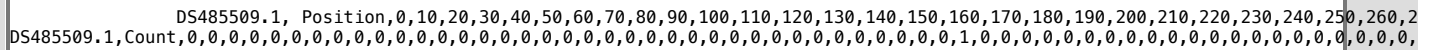
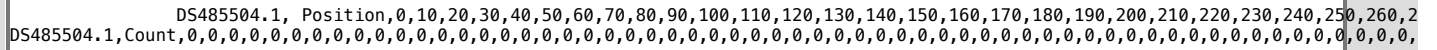
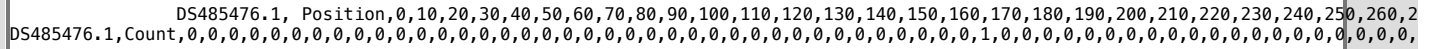
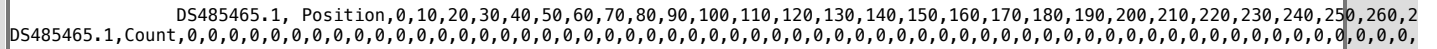
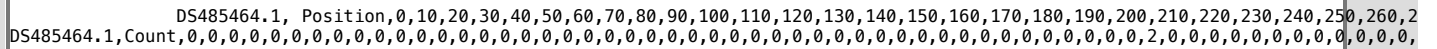
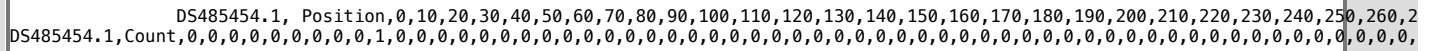
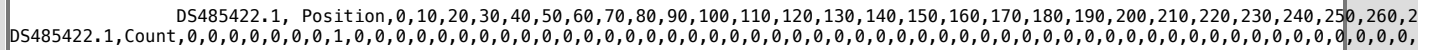
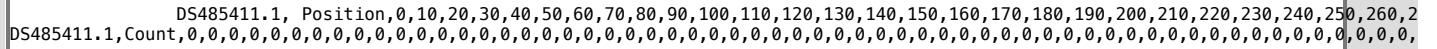
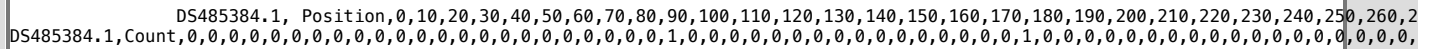
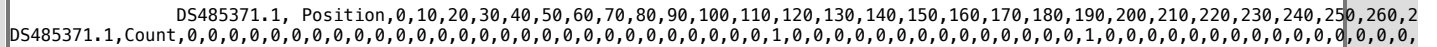
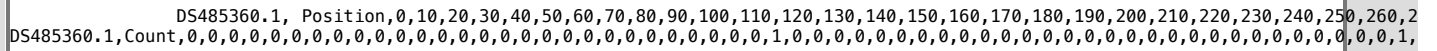
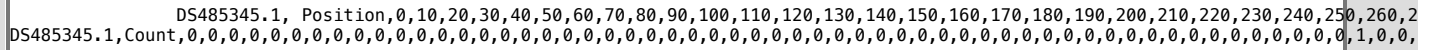


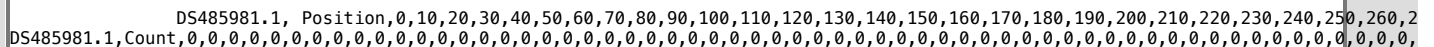
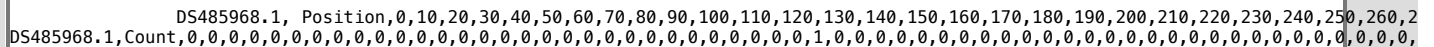
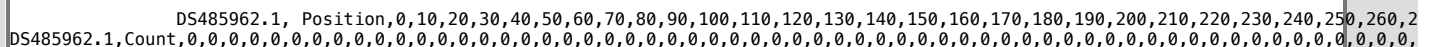
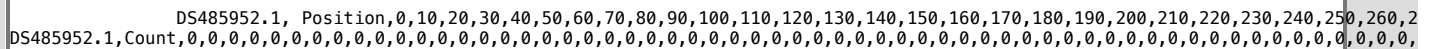
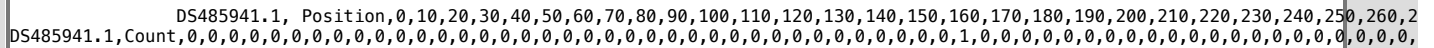
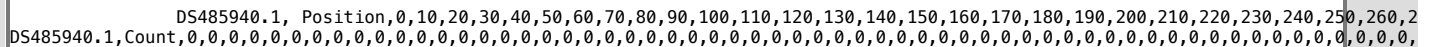
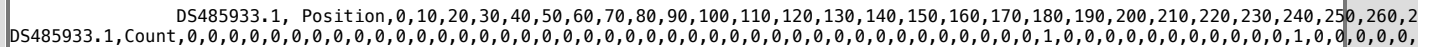
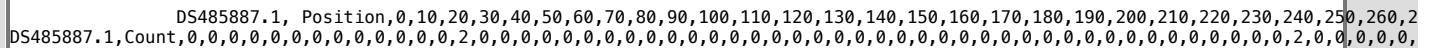
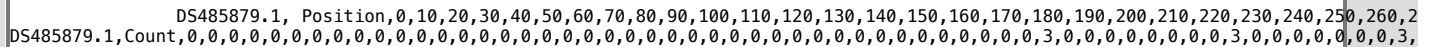
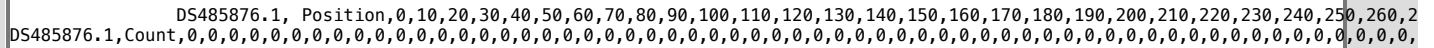
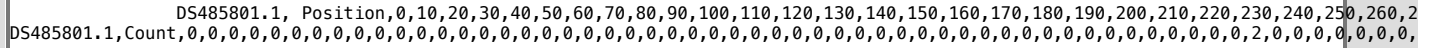
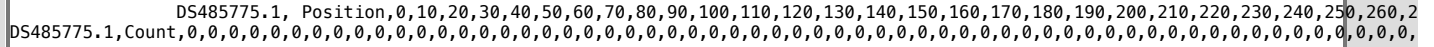
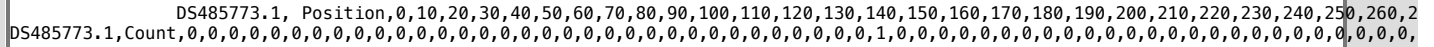
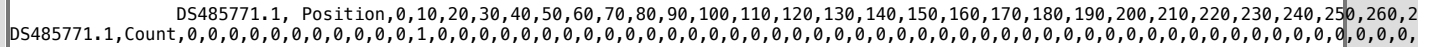


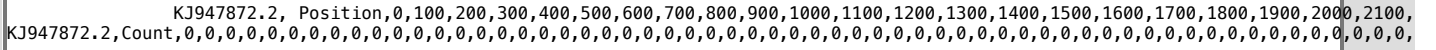
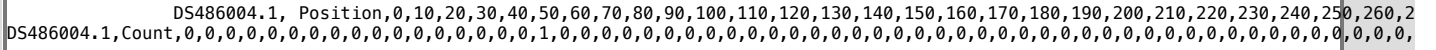












Details by gene

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