

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/output2/results/variants/c
Warnings	3,802
Errors	39
Number of lines (input file)	5,433
Number of variants (before filter)	5,433
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	5,433
Number of known variants (i.e. non-empty ID)	4,739 (87.226%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of annotations	179,385
Genome total length	143,726,002
Genome effective length	138,694,329
Variant rate	1 variant every 25,528 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
AE013599.5	25,286,936	1,020	24,791
AE014134.6	23,513,712	963	24,417
AE014135.4	1,348,131	54	24,965
AE014296.5	28,110,227	1,084	25,931
AE014297.3	32,079,331	1,221	26,272
AE014298.5	23,542,271	847	27,794
CP007075.1	11,983	6	1,997
CP007076.1	87,365	2	43,682
CP007077.1	36,913	12	3,076
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	3	15,040
CP007091.1	20,763	2	10,381
CP007095.1	25,560	1	25,560
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	6	611,225
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
DS483641.1	14,503	10	1,450
DS483650.1	13,906	1	13,906
DS483655.1	13,549	3	4,516
DS483659.1	13,416	7	1,916
DS483660.1	13,394	2	6,697

DS483680.1	12,399	1	12,399
DS483695.1	11,743	1	11,743
DS483707.1	25,840	1	25,840
DS483724.1	13,501	2	6,750
DS483746.1	9,341	7	1,334
DS483751.1	7,314	5	1,462
DS483753.1	7,123	1	7,123
DS483758.1	6,860	1	6,860
DS483770.1	6,193	1	6,193
DS483781.1	5,952	1	5,952
DS483783.1	5,891	3	1,963
DS483792.1	5,465	1	5,465
DS483793.1	5,463	1	5,463
DS483817.1	4,933	2	2,466
DS483818.1	4,917	2	2,458
DS483821.1	4,879	3	1,626
DS483828.1	4,785	1	4,785
DS483843.1	4,515	1	4,515
DS483851.1	4,395	1	4,395
DS483865.1	4,289	1	4,289
DS483880.1	4,150	2	2,075
DS483885.1	4,085	3	1,361
DS483886.1	4,081	1	4,081
DS483905.1	3,926	1	3,926
DS483908.1	3,913	1	3,913
DS483913.1	3,871	1	3,871
DS483918.1	3,818	3	1,272
DS483920.1	3,806	2	1,903
DS483923.1	3,775	3	1,258
DS483928.1	3,730	1	3,730
DS483940.1	3,648	1	3,648
DS483944.1	3,622	2	1,811
DS483956.1	3,553	2	1,776
DS483971.1	3,478	1	3,478
DS484000.1	3,302	1	3,302
DS484004.1	3,277	1	3,277
DS484012.1	3,254	1	3,254
DS484022.1	3,209	1	3,209
DS484023.1	3,206	1	3,206
DS484054.1	3,080	1	3,080
DS484060.1	3,065	1	3,065
DS484064.1	3,044	1	3,044
DS484077.1	2,984	1	2,984
DS484089.1	2,928	1	2,928
DS484116.1	2,860	3	953
DS484140.1	2,819	1	2,819
DS484148.1	2,795	1	2,795
DS484153.1	2,793	1	2,793
DS484185.1	2,686	1	2,686
DS484187.1	2,671	2	1,335
DS484202.1	2,636	1	2,636
DS484216.1	2,603	1	2,603
DS484244.1	2,536	2	1,268
DS484255.1	2,516	1	2,516
DS484267.1	2,476	1	2,476
DS484268.1	2,475	1	2,475
DS484271.1	2,470	2	1,235
DS484277.1	2,442	1	2,442
DS484279.1	2,438	2	1,219
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
DS484343.1	2,325	2	1,162
DS484345.1	2,318	2	1,159
DS484361.1	2,282	1	2,282
DS484382.1	2,223	1	2,223
DS484396.1	2,198	2	1,099
DS484397.1	2,196	2	1,098
DS484417.1	2,139	1	2,139

DS484421.1	2,129	1	2,129
DS484450.1	2,087	1	2,087
DS484472.1	2,046	1	2,046
DS484487.1	2,010	1	2,010
DS484540.1	1,935	1	1,935
DS484556.1	1,916	3	638
DS484588.1	1,863	1	1,863
DS484601.1	1,832	2	916
DS484632.1	1,775	1	1,775
DS484718.1	1,586	1	1,586
DS484782.1	1,484	1	1,484
DS484817.1	1,445	1	1,445
DS484822.1	1,436	1	1,436
DS484869.1	1,391	1	1,391
DS484894.1	1,375	3	458
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
DS485376.1	1,155	1	1,155
DS485572.1	1,107	1	1,107
DS485597.1	1,100	2	550
DS485599.1	1,100	1	1,100
DS485656.1	1,083	1	1,083
DS485703.1	1,071	1	1,071
DS485797.1	1,049	1	1,049
DS485801.1	1,048	1	1,048
DS485802.1	1,048	1	1,048
DS485848.1	1,040	2	520
DS485887.1	1,029	2	514
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	8	2,440
Total	138,694,329	5,433	25,528

Number variants by type

Type	Total
SNP	0
MNP	0
INS	842
DEL	2,172
MIXED	1,494
INV	0
DUP	231
CNV	0
BND	694
INTERVAL	0
Total	5,433

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	58,286	32.492%
LOW	5,520	3.077%
MODERATE	90,849	50.645%
MODIFIER	24,730	13.786%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
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Number of annotaitons and region counts

Annotation			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
3_prime_UTR_truncation	11	0.006%	CHROMOSOME	39	0.022%
3_prime_UTR_variant	465	0.256%	DOWNSTREAM	5,949	3.316%
5_prime_UTR_truncation	55	0.03%	EXON	2,292	1.278%
5_prime_UTR_variant	164	0.09%	GENE	27,282	15.209%
bidirectional_gene_fusion	1,971	1.086%	INTERGENIC	7,343	4.093%
chromosome_number_variation	22	0.012%	INTRON	9,015	5.026%
conservative_inframe_deletion	55	0.03%	SPLICE_SITE_ACCEPTOR	85	0.047%
conservative_inframe_insertion	10	0.006%	SPLICE_SITE_DONOR	119	0.066%
disruptive_inframe_deletion	43	0.024%	SPLICE_SITE_REGION	246	0.137%
disruptive_inframe_insertion	12	0.007%	TRANSCRIPT	120,094	66.948%
downstream_gene_variant	5,951	3.278%	UPSTREAM	6,381	3.557%
duplication	91,253	50.259%	UTR_3_PRIME	428	0.239%
exon_loss_variant	1,465	0.807%	UTR_5_PRIME	112	0.062%
feature_ablation	6,488	3.573%			
feature_fusion	5,122	2.821%			
frameshift_variant	1,313	0.723%			
gene_fusion	1,963	1.081%			
intergenic_region	2,221	1.223%			
intragenic_variant	281	0.155%			
intron_variant	9,245	5.092%			
missense_variant	24	0.013%			
non_coding_transcript_exon_variant	134	0.074%			
non_coding_transcript_variant	253	0.139%			
splice_acceptor_variant	95	0.052%			
splice_donor_variant	161	0.089%			
splice_region_variant	548	0.302%			
start_lost	62	0.034%			
stop_gained	71	0.039%			
stop_lost	23	0.013%			
stop_retained_variant	1	0.001%			
synonymous_variant	22	0.012%			
transcript_ablation	45,681	25.159%			
upstream_gene_variant	6,381	3.514%			



Quality:

Min	10
Max	999
Mean	670.858
Median	797
Standard deviation	351.065
Values	10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57
Count	1,6,6,6,3,6,6,9,6,3,6,4,4,3,6,5,4,8,2,2,4,10,6,4,6,5,3,4,4,2,7,4,5,3,8,1,1,5,2,7,8,4,7,4,6,3,5,6,8,5,8,3,4,5,5,6,7,4,10,2,2,5,1,5,3,6,4,10,7,5,1,4,4,4,2,4,3,2



Insertions and deletions length:

Min	1
Max	596
Mean	26.16
Median	1
Standard deviation	65.231
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	2172,228,20,14,10,12,22,18,17,20,11,3,12,11,13,8,9,15,8,7,6,13,2,6,8,8,6,4,7,6,4,5,6,6,2,2,6,4,1,2,2,6,2,2,2,1,5,8,1,3,3,3,3,2,3,2,1,1,1,3,3,2,4,5,2,1,1,



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	25
Max	100
Mean	58.881
Median	50
Standard deviation	27.608
Values	25,50,75,100
Count	1299,2296,447,1391

Allele Count



Min	1
Max	4
Mean	2.355
Median	2
Standard deviation	1.104
Values	1,2,3,4
Count	1299,2296,447,1391

Hom/Het per sample



Sample_names , X, X
Reference , 932, 437
Het , 2993, 3205
Hom , 1508, 1791
Missing , 0, 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).

	-	A>S	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACN	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATN	ATT	CAA	C
-			3,389	2,234	2,133	2,153	2,445	1,734	1,653		2,009	2,317	2,649	2,791	1,795	1,707	2,012	1,978	2	2,126	3,426	2
A>S																						
AAA	221		59	20	19	55	17	25	22		38	46	78	14	46	44	40	18		52	68	
AAC	191		41	72	36	19	55	51	42		57	50	39	63	13	24	63	31		33	38	
AAG	390		61	52	62	92	58	51	70		99	24	59	109	117	43	30	94		62	111	
AAT	295		64	21	27	24	39	22	86		13	34	81	89	68	35	20	83		19	42	
ACA	766	1	60	12	22	44	45	24	18		19	37	45	41	16	10	44	31		21	12	
ACC	474		53	59	22	30	67	82	61		35	39	60	24	71	17	27	49		35	125	
ACG	319		45	21	19	34	41	23	6		45	20	60	28	30	12	28	24		10	20	
ACN																						
ACT	880		39	7	26	8	18	52	23		82	21	17	37	19	17	26			6	16	
AGA	299		15	11	8	5	2		14		16	6	9	10	19	3		6		17	10	
AGC	226		55	21	77	41	31	48	30		24	16	60	21	79	13	71	18		47	29	
AGG	142		24		8	45	17	25	32		12	16	50	33		12	12	10		13	32	
AGT	251		60	16	13	20	18	12	35		31	32	45	22	52	6	17	7		52	32	
ATA	172		53	34	40	8	27	22			10	16	11	8	7	4	12	16		12	4	
ATC	233		21	35	29	45	65	45	96		63	38	64	28	63	32	33	51		46	69	

	-	A>S	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACN	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATN	ATT	CAA	C
ATG	201		88	52	72	52	78	15	34		74	67	58	36	12	37	47	46		25	77	
ATN																						
ATT	260		28	21	56	36	60	22	46		26	45	34	33	17	25	47	36		40	33	
CAA	383		32	60	57	37	23	32	44		32	78	44	31	6	22	21	32		53	14	
CAC	157		50	56	18	19	33	17	28		49	17	81	50	42	14	31	30		7	31	
CAG	430		34	48	25	44	131	112	84		89	93	67	77	106	11	79	124		54	71	
CAT	115		13	11	5	17	20	10	21		28	14	38	12	10	8	46	48		30	22	
CCA	605		31	13	46	21	33	56	26		42	17	33	32	31	16	27	16		26	32	
CCC	311		15	23	42	77	44	29	22	4	44	4	61	15	12	8	25	27		77	44	
CCG	212		34	14	28	32	23	45	38		32	33	42	13	38	13	20	45		26	70	
CCT	335		28	29	59	11	7	25	2		32	2	21	6	15	30	16	2		22	4	
CGA	95		17	4	12	15	19	12	2		10	2	15	41		29	28	13		8	35	
CGC	114		11	29	3	8	42	29	2		38	79	35	42	33	8	49	76		24	38	
CGG	110		4	4	30	13	14	24	13		13	11	13	4	4	6	18			8	19	
CGN																						
CGT	82			16	12	29	9	12	4		14	48	13	19	10	17	26	2			26	
CTA	126		15		9	4	17	3	8		15	18	39	14	10		15	11		23	33	
CTC	120		14	18	38	14	16	12	23		27	7	6	37	13	17	29	26		28	40	
CTG	266		53	67	77	77	118	77	68		69	143	77	54	60	66	103	82		56	96	
CTN																						
CTT	131		71	12	17	19	9	2	5		23	11	13	37	23	14	25	16		19	17	
G>S																						
GAA	616		94	29	87	28	47	48	30		69	46	44	52	28	13	29	40		55	45	
GAC	290		70	29	41	51	86	93	26		48	36	62	88	30	16	49	25		42	53	
GAG	403		138	143	178	64	75	100	87		102	72	79	141	72	50	80	103		99	99	
GAT	342		84	92	44	67	64	22	54		52	69	98	114	41	25	74	76		70	78	
GCA	254		40	49	26	13	22	15	8		24	18	18	8	33	6	24	24		37	32	
GCC	251		100	64	42	68	106	51	95		118	94	104	118	38	27	92	49		40	78	
GCG	110		20	31	20	24	26	34	48		23	21	37	1	17	36	78	5		30	61	
GCT	238		22	24	67	27	42	31	41		50	11	37	28	24	10	26	31		30	28	
GGA	372		69	40	37	51	66	36	43		19	25	58	61	30	20	5	86		74	47	
GGC	181		68	38	64	61	66	49	57		43	59	98	75	43	57	96	74		67	33	
GGG	89			10	11	28	6		2			37	4	4	4		16	5		9	10	
GGT	277		33	19	10	14	34	5	19		18	19	30	49	17	12	30	25		19	73	
GNN																						
GT>																						
GTA	147		16	16	22	10	14	15	6		19	15	5	4		17	3	9		3	14	
GTC	166		27	12	46	52	26	39	19		24	34	39	57	20	9	41	25		28	45	
GTG	264		52	50	25	46	49	59	112		49	44	120	92	67	27	56	56		43	80	
GTT	358		23	62	23	22	46	18	12		22	9	59	16	12	22	53	25		42	16	
NAC																						
NI<																						
NNN																						
NTT																						
SNI																						
TAA	36		3			13		3			4						1	12			3	
TAC	163		67	36	35	56	32	32	27		32	46	49	38	27	43	53	52		36	66	
TAG	14		4						3				4									
TAT	138		17	16	15	14	29	5	8		32	35	26	25	7		44	15		23	24	
TCA	469		32	5	6	13	40	41	16		29	18	27	8	6		9	38		9	46	
TCC	216		37	73	33	43	56	72	33		64	47	90	65	52	46	31	15		73	71	
TCG	150		50	37	32	20	49	37	25		32	35	65	28	57	38	17	58		38	52	
TCT	321		35	17	34	7	35	4	7		33	6	29	4	23	3	15	4		24	11	
TGA	21			3			3									3						
TGC	133		33	28	15	21	11	32	17		6	79	25	45	17	23	69	61		43	21	
TGG	125		26	6	19	41	22	20	2		25	8	41	10	24	26	8	30		13	11	
TGN																						
TGT	98		17		1	4	5	22	6		17	5	57	9	4	10	3	3		6	7	
TNN																						
TTA	143		53		22	14	47		4		11	10	8	4	2	19	12	10		24	5	
TTC	244		25	18	21	22	50	17	79		43	50	18	31	24	34	65	45		41	57	
TTG	157		30	56	21	37	67	20	45		18	45	38	117	31	6	39	20		36	54	
TTT	206		30	31	19	23	23	42	5		28	19	30	22	29	14	21	36		42	12	

Amino acid changes

How to read this table:

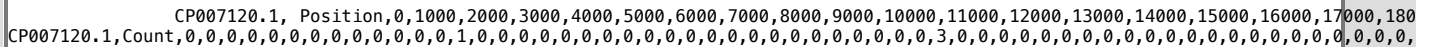
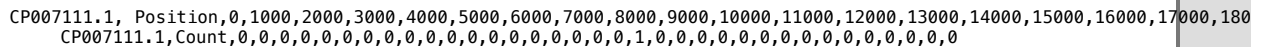
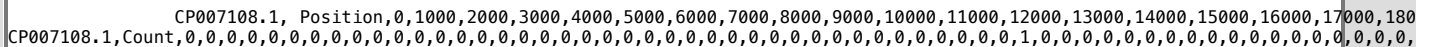
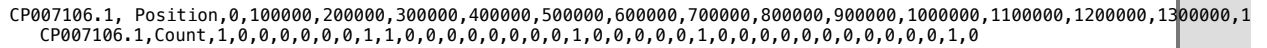
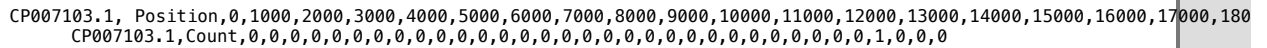
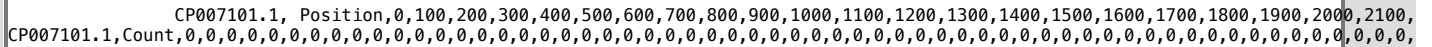
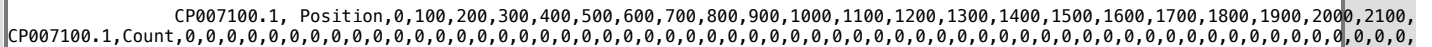
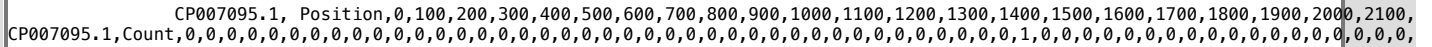
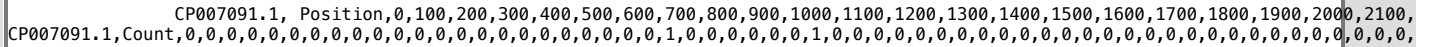
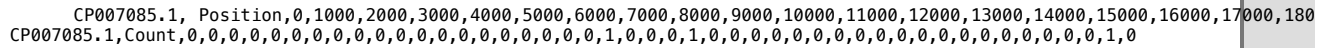
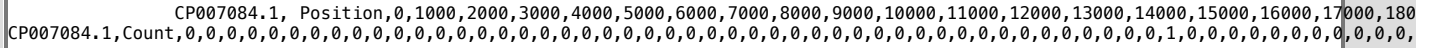
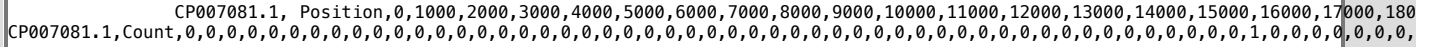
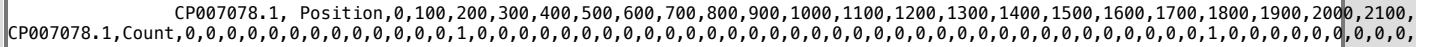
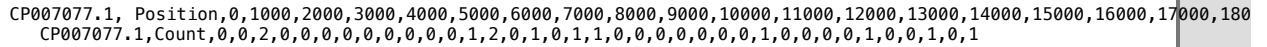
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).

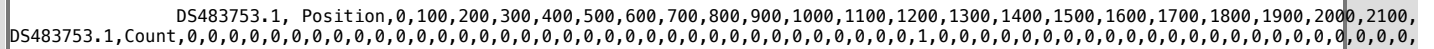
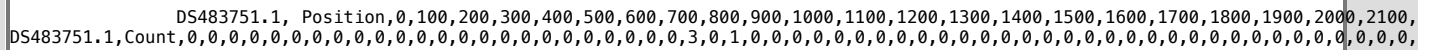
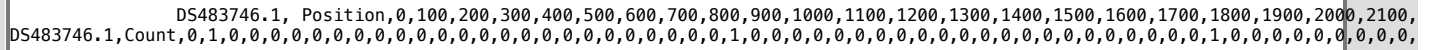
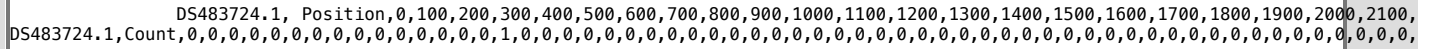
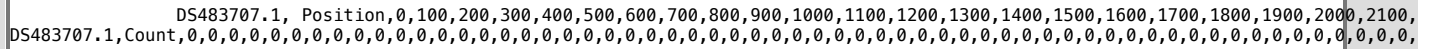
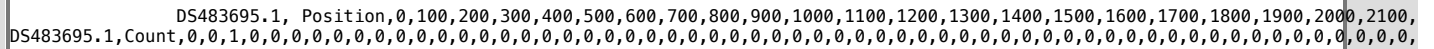
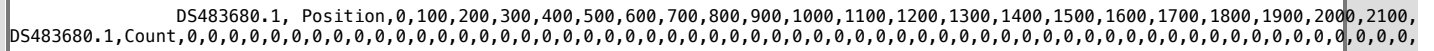
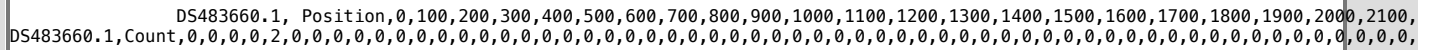
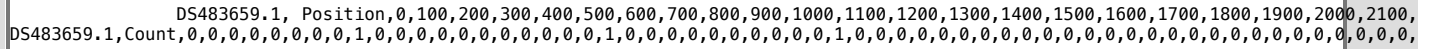
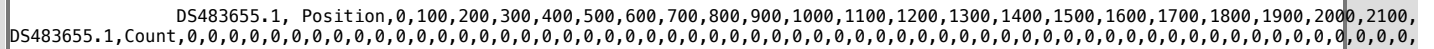
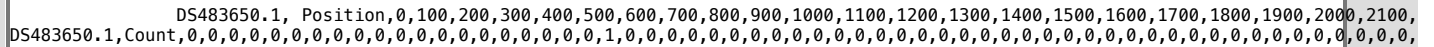
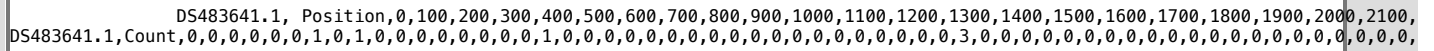
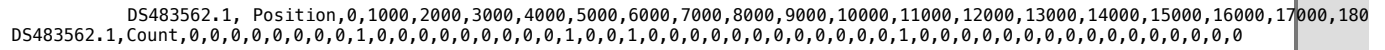
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

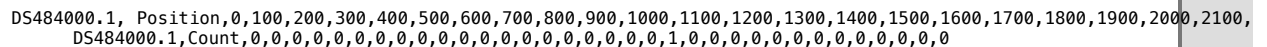
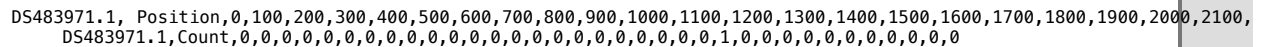
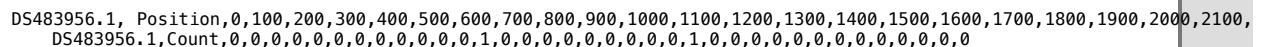
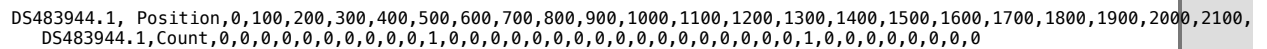
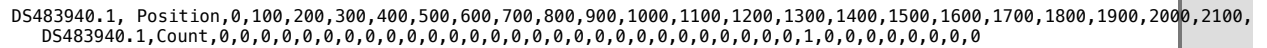
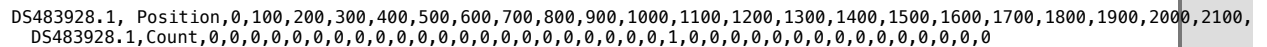
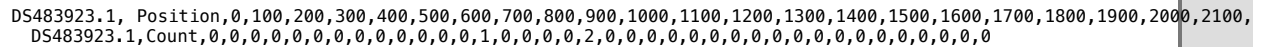
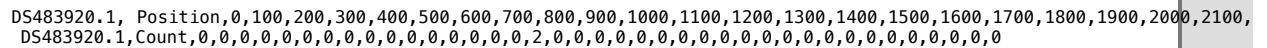
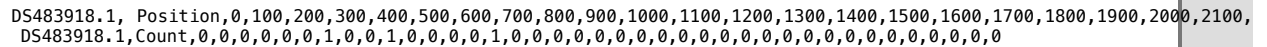
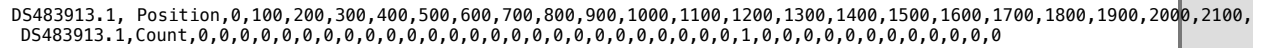
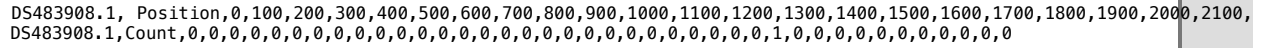
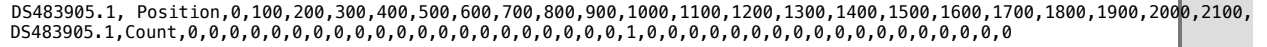
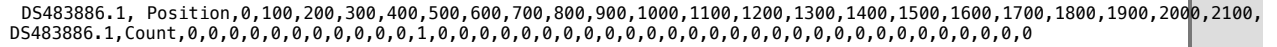
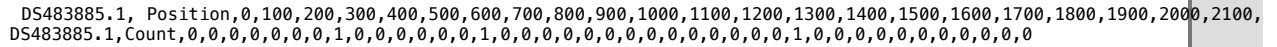
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*	32	71	6	15	9	7	2	12	9	11	4	7	18	12	16	13	15	2	14	13	
-	5,511		1,579	10,373	4,802	3,551	4,372	4,280	9,257	4,750	5,845	5,522	10,756	1,978	4,387	9,861	6,013	12,859	11,417	7,841	6,511
?	2	4																			
A	239	850	17	713	338	316	470	195	677	327	436	337	775	109	300	647	407	827	851	734	411
C	51	231	8	221	101	54	54	83	138	48	154	66	97	64	53	168	55	280	213	116	
D	169	627	12	502	208	228	302	158	363	166	276	239	404	101	239	510	248	610	565	445	311
E	283	1,019	14	739	287	310	521	207	505	219	326	497	657	143	264	771	269	829	759	558	412
F	105	449	7	357	125	127	88	101	310	118	217	95	265	81	94	230	113	350	361	287	213
G	265	916	19	726	348	258	334	165	538	268	405	292	386	190	261	620	279	778	632	463	311
H	115	272	8	289	67	111	107	118	192	116	136	86	275	78	103	197	78	279	416	206	
I	155	664	9	445	208	184	231	182	317	138	251	227	341	103	179	464	187	449	468	482	211
K	201	610	25	484	123	200	283	143	411	211	271	201	417	112	219	547	283	502	722	380	311
L	349	943	15	920	408	247	328	330	715	254	531	420	729	165	318	778	478	1,183	949	704	411
M	65	199	10	184	88	30	96	107	158	97	109	160	155	46	104	193	104	242	229	201	111
N	116	485	11	533	216	197	189	106	216	170	194	168	402	114	136	325	113	543	427	365	111
P	266	1,460	21	613	237	219	333	119	351	302	306	283	383	90	220	542	290	503	733	500	311
Q	181	813	12	564	205	185	290	100	513	232	240	148	432	156	189	481	183	650	528	547	211
R	272	838	22	683	317	309	275	149	414	189	278	144	380	107	179	571	279	738	607	375	211
S	509	1,629	16	1,297	310	323	415	353	754	343	509	464	626	140	313	778	437	1,042	1,250	802	511
T	321	2,436	20	603	197	318	415	182	420	148	253	286	479	104	215	587	327	592	770	641	411
V	192	935	29	641	229	240	272	242	446	116	344	234	498	115	270	501	253	708	724	529	361
W	58	125	8	164	49	23	39	38	61	14	47	45	77	30	47	85	25	101	116	69	
Y	78	300	1	316	133	76	142	60	201	93	199	134	236	67	122	250	139	337	313	197	111

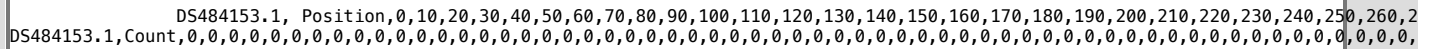
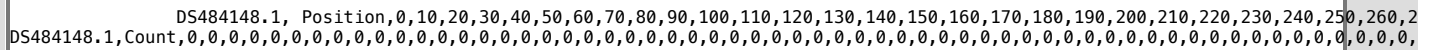
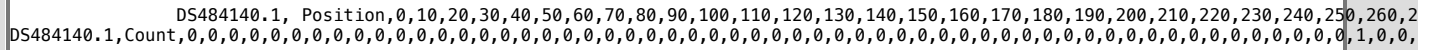
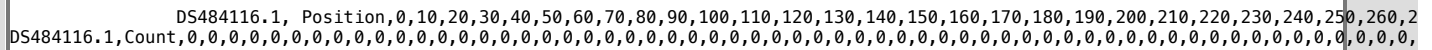
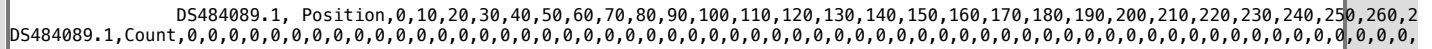
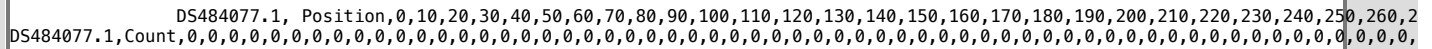
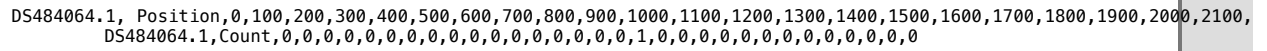
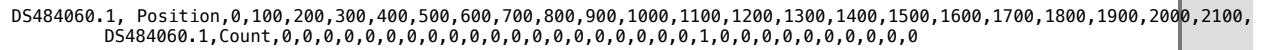
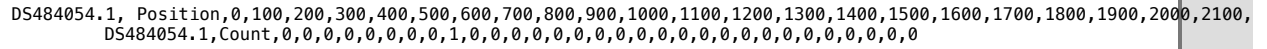
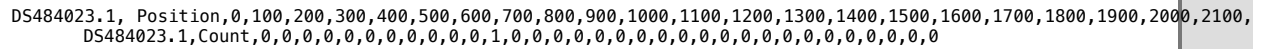
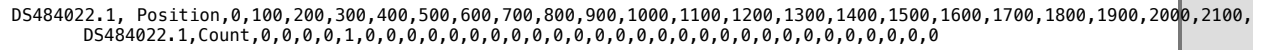
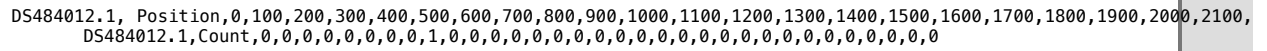
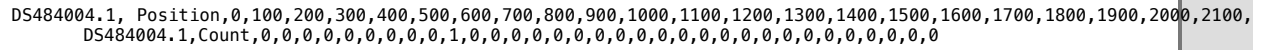


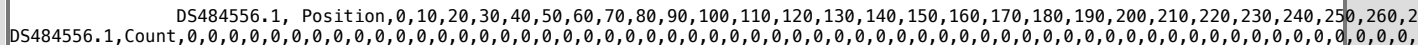
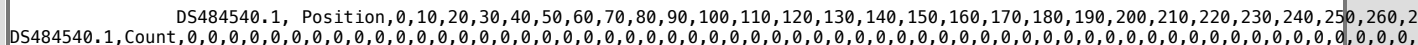
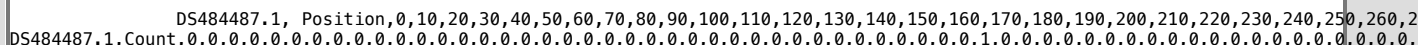
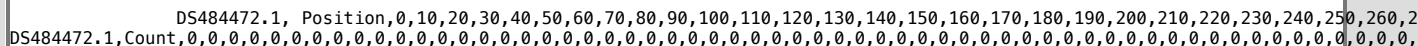
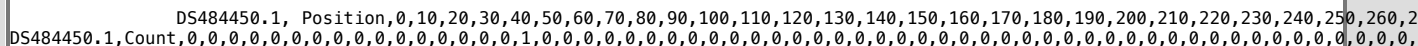
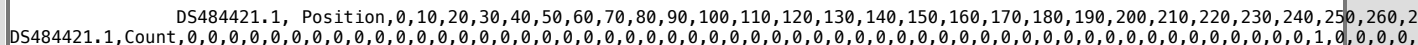
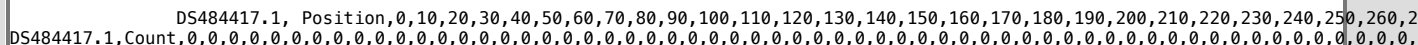
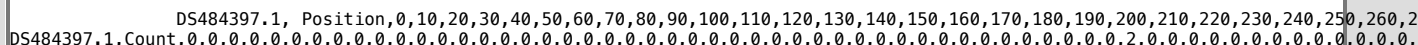
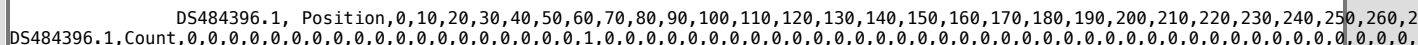
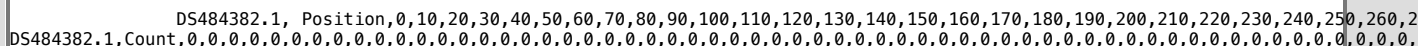
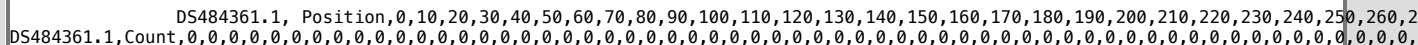
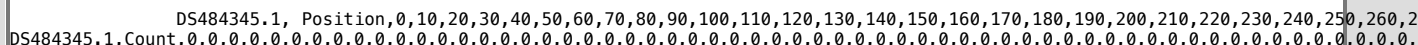
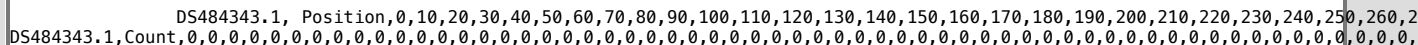
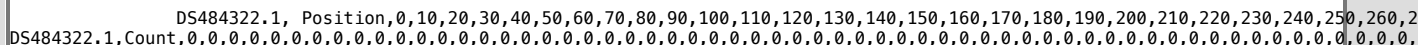
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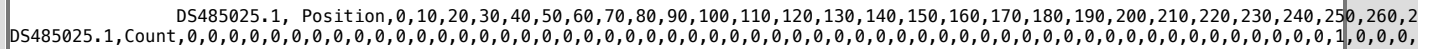
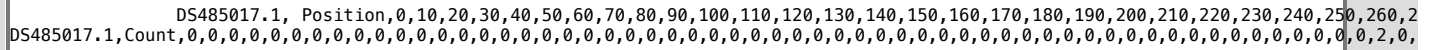
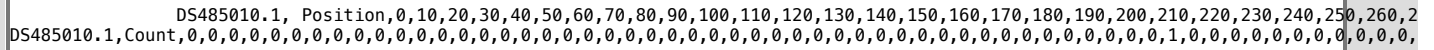
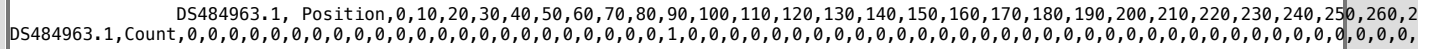
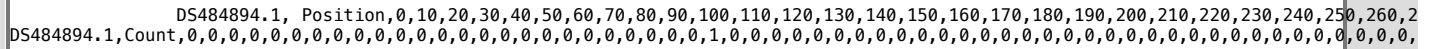
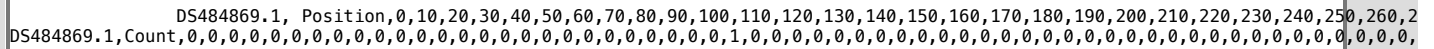
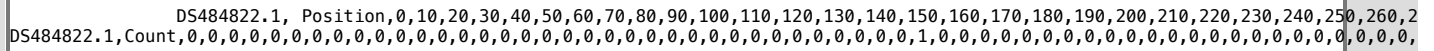
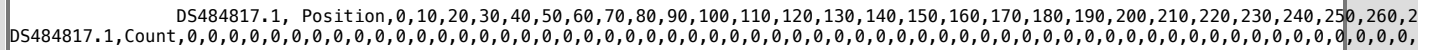
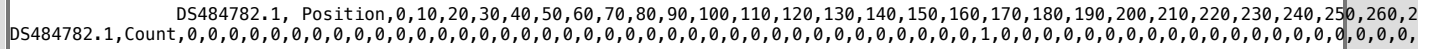
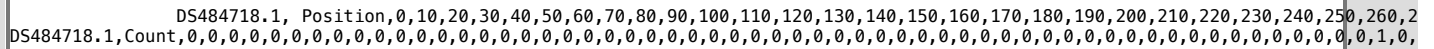
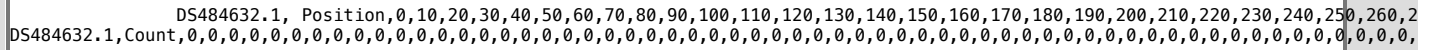
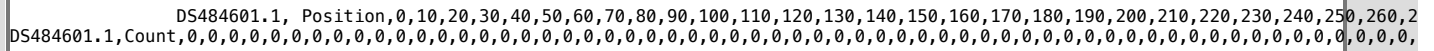
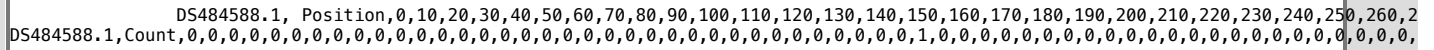


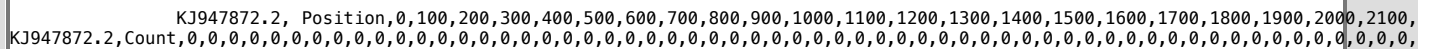
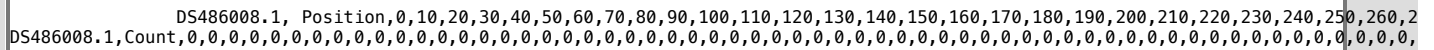
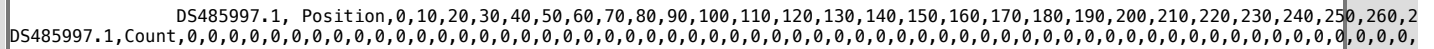
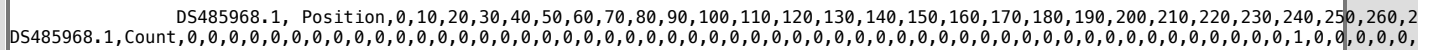
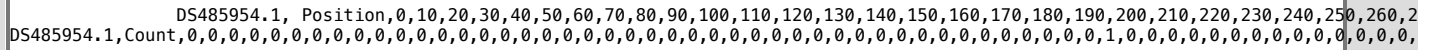
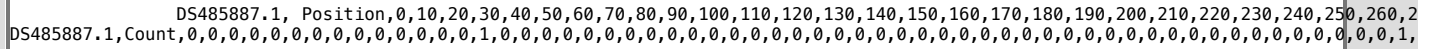
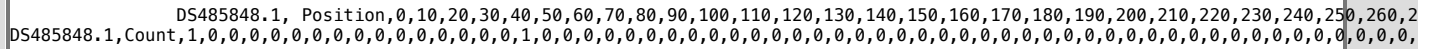
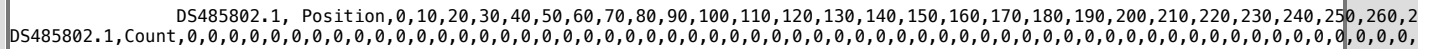












Details by gene

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