

**Additional file 1 - Table of NIP data**

nt	FBgn (FlyBase gene ID)	Plesiomorphic intron (confirmed by ESTs if bold)	Apomorphic intron (confirmed by ESTs if bold)	Intron-less	Apomorphic subtree node	RT-PCR	origin	Gene name conservation score
2	0031216		1927-1: vir, moj, gri 1928-0: mel, sim, sec, yak, ere, ana, per, pse, wil	Aga, Cpi, Aae			Unknown	CG11376 0.932
2	0036142		456-2: vir, moj, gri 456-0: wil, per, pse, ana, ere, yak, sec, sim, mel	Aga, Cpi, Phu, Gmo (457-2)			Putative sliding	CG7616 0.955
3	003607	117-1: <b>gri</b> , vir, moj, <b>wil</b> , <b>ana</b>	118-1: <b>mel</b> , <b>sim</b> , sec, <b>yak</b> , ere, pse, per		(5, 9)		Sliding	Su(var)2-5, CG8409 0.887
3	0015572	5-2: <b>mel</b> , sim, ere, yak, ana, wil, moj, vir	4-2: per, pse		9	pse, per	Putative sliding	Alpha-esterase 4, CG1082 0.779
3	0032087	20-1: mel, sec, sim, yak,ere, ana, per, pse, wil, moj, vir	19-1: <b>gri</b>		D.grimshawi		Putative sliding	CG9568 0.783
3	0032261	56-0: wil, gri, vir, moj	55-0: <b>ana</b> , per, pse, ( <b>mel</b> , sim, sec, yak, ere)		3		Sliding	CG6094 0.916
3	0032504	198-2: mel, sim, ere 199-2: pse, per		ana, wil, vir			Unknown	CG16970 1.000
3	0037757	615-1: per, pse, wil, moj, vir, gri	616-1: mel, sec, ere, yak, ana		4		Sliding	CG8516 0.843
3	0052081	4-2: ana 5-2: mel, sim, yak, ere		(wil, vir, moj excluded from alignment)			Putative sliding	CG32081 0.868

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5	0046689	15-0: <b>mel</b> , sim, sec, per, pse, yak, ere	16-2: ana	(ere annotation manually improved)	D.ananassae	ana	Putative sliding	Tak1-like 1, CG31421 0.752
6	0019809	253-0: moj, vir, gri, wil, sec, sim, <b>mel</b> , yak, ere, ana	255-0: pse, per		9		Sliding	gcm2, CG3858 0.958
6	0031395	40-0: mel, sim, sec, yak, ere, ana, pse, per, wil 42-0: gri, moj, vir					Putative sliding	CG10874 0.891
6	0035879	103-1: <b>pse</b> , per, ere, yak, sim, sec, mel	105-1: ana	(wil vir moj gri excluded from alignment)			Sliding	CG7112 0.851
9	0032821	1197-0: <b>mel</b> , sim, sec, yak, ere, ana, pse, per, wil, <b>vir</b> , gri	1200-0: moj		D.mojavensis		Sliding	CdGAPr, CG10538 0.814
9	0034221	396-1: yak 399-1: mel, sim sec					Sliding	CG10764 0.809
9	0038302	68-2: mel, sim, sec, yak, ere, ana, per, pse, gri, moj, vir	65-2: wil		D.willistoni		Putative sliding	CG4210 0.783
10	0030661	211-0: ana 214-1: wil		mel, sim, sec, yak, ere, pse, per, vir, moj			Exon duplication	CG8105 0.852

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12	0033734	420-0: ana, pse, per, <b>wil</b> , Phu, Bmo	419-0: mel, sim, sec, yak, ere 423-0: vir, moj, gri	Aga, Aae, Cpi	5 10		Sliding	CG8520 0.897
14	0035965	48-2: <b>gri, moj</b> , vir, Aga, Aae, Cpi, Gmo, Phu, Bmo	44-0: wil	mel, sim sec, yak, ere, ana, per, pse	D.willistoni		Unknown	Use1, CG14181 0.866
15	0001124	119-0: <b>sec, sim, mel</b> , ere, yak, ana, per, <b>pse</b> , gri, vir, moj, Bmo, Phu, Tca, Gmo	124-0: <b>wil</b>		D.willistoni		Sliding	CG8430, Got1 1.000
16	0033686		53-2: gri, moj, vir 59-0: wil	mel, sim, sec, yak, ere, ana, pse, per			Unknown	piRNA methyltransferase, CG12367 0.836
21	0029747	200-0: mel, sim, sec, yak, ere, wil 207-0: vir, moj, (gri)		pse, per, ana			Exon duplication	CG5062 0.810
21	0030055	87-0: mel, sim, ere, sec, yak, ana, wil (pse,per) 94-0: gri, moj, vir		(manually aligned)			Putative sliding	CG12772 0.770
22	0032517	213-2: sec, sim, mel, ere, yak, ana, pse, moj, vir, gri	221-0: wil		D.willistoni		Unknown	CG7099 0.832

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23	0033247	38-0: sec, sim, <b>mel</b> , ere, yak, <b>ana</b> , <b>pse</b> , per, moj, vir, <b>gri</b> , Isc, Gmo, Bmo, Aga, Aae, Cpi, Phu, Tca	45-2: <b>wil</b>		D.willistoni		Unknown	CG8722, Nup44A 0.949
24	0034793	21-0: <b>sec</b> , <b>mel</b> , ere, yak, ana, pse, per, <b>moj</b> , vir, <b>gri</b>	29-0: <b>wil</b>		D.willistoni		Putative sliding	asrij, CG13533 0.870
27	0001185	44-2: wil 53-2: ana		mel, sim, sec, yak, ere, pse, per, vir, moj, gri			Unknown	hermaphrodite, CG4694 0.775
28	0031773	155-0: <b>mel</b> , sim, sec, yak, ere, ana, pse, per, wil, Aae, Aga, Cpi, Tca	164-1: vir, moj, gri		10		Unknown	CG9144 1.000
30	0038300	44-0: wil 54-0: gri, moj, vir		mel, (sim), sec, yak, ere, ana, pse, per, Isc, Aga, Aae, Gmo, Bmo, Phu, Tca			Exon duplication	CG4203 0.979
30	0050101	241-0: sec, sim, <b>mel</b> , ere, yak, ana, pse, per, moj, vir, gri	251-0: wil		D.willistoni		Exon duplication	CG30101 0.993

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31	0002526	1460-0: mel, sim, sec, yak 1449-2: gri, moj, vir		ere, ana, pse, per, wil, Api, Tca, Aga, Cpi, Nvi, Ame, Aae, Bmo			Exon duplication	Laminin A, CG10236 0.940

Intron positions with species names in bold letters indicate that these positions are supported by EST hits.

Abbreviations: mel=Drosophila melanogaster, sim=D. simulans, sec=D. sechellia, yak=D. yakuba, ere=D. erecta, ana= D. ananassae, pse= D. pseudoobscura, per=D. persimilis, wil= D. willistoni, vir=D. virilis, moj=D. mojavensis, gri=D. grimshawi, Aae=Aedes aegypti, Aga=Anopheles gambiae, Api=Acyrtosiphon pisum, Cpi=Culex pipiens, Bmo=Bombyx mori, Tca=Tribolium castaneum, Ame=Apis mellifera, Nvi=Nasonia vitripennis, Phu=Pediculus humanus, Gmo=Glossina morsitans