Gene BLAST

Gene name	Gene name (in D. melanogaster)	Gene length (full gene list) (bp)	Gene length (wil + mel files) (bp)	NDN-Full — BLAST (tblastn) — Full gene list — Filter: alignment length > 60*(1/3)% of gene length (when multiple hits - all in same region): contig	% id	alignment length (protein)	NDN-FLYE-DCA: BLAST (tblastn) — Filter >60*(1/3)% (No hits left after filtering!)	NDN-Full — BLAST (blastn) — Full gene list — Filter: alignment length > 60*(1/3)% of gene length: contig	% id	alignment length	NDN-Full — BLAST (blastn) — gene list with only wil + mel hits: contig	% id	alignment length	% of gene length	CANU-Full — BLAST (tblastn) — Full gene list (when multiple hits - all in same region): contig	% id	alignment length	CANU-Full — BLAST (blastn) — gene list with only wil + mel hits: contig	% id	alignment length	% of gene length	CANU-FLYE-DCA: BLAST (blastn) — gene list with only wil + mel hits: contig	% id	alig len	% of gene length	CANU-FLYE-DCA-mix0: contig	% id	alig len	% of gene length	CANU-FLYE-DCA-mix0-GF: contig	% id	alig len	% of gene length
Found in melanogaster and willistoni, used as Y specific																																	
kl-2		91086	13350															tig00000535	95,076-97,143	105-4082	31%	contig_443	94,51	1858	14%	contig_77	94,93	1854	14%	contig_223	94,93	1854	14%
																		tig00000461	94,714	1854	14%												
																		tig00000358	92,78	651	4.90%												
kl-3		226785	13785								contig 36	96,332	518					tig00000552	91,603-95,324	131-1387	27%												
											contig 78	95,023	221					tig00000530	94,083-98,113	106-1112	19%												
ORY		56595	2724								contig 1305	95,680 (95,679-)	324-625					tig00000659	92,744-93,939	317-627	35%	contig_442	95,046-95,312	192-646	31%	contig_27	91,346	312	11%	contig_99	91,346	312	11%
											contig 1077	95,157 (92,121-)	165-351					tig00000324	92,593-95,362	162-345	19%	contig_379	91,346	312	11,00%								
											contig 1509	91,346	312					tig00000224	91,346	312	11%												
											contig 577	95,344	2470					tig00000364	91,254	606	16%												
PRY		45929	3711															tig00000422	95,088	285	17%												
Ppr-Y		248273	1716																			contig_869	91,254	606	16%	contig_346	91,254	606	19%				
CCY		16933	3597																			contig_188	84,238-95,652	46-755	21%+1,3%	contig_75	95,775	284	17%				
ARY		1619	1053					6 hits, ctg000300	92,746- 98,824	170-345				67%				tig00000597	92,228-97,647	170-345	67%	contig_592	92,228-98,235	170-345	67%	contig_368	92,746- 98,824	170-345	67%	contig_23	92,746- 98,824	170-345	67%
Expected in paulistorum and willistoni																																	
JYalpa		4161																															
Novel finding in willistoni, expected in paulistorum																																	
GK21041	CG18155	1884						ctg000890	90,292 (83,62-)	1782-1978					tig00000222	90,174-01,098	1781-1831															
GK27406	Piezo-like	7074																															
GK20609	CG15580	2334		ctg000660	79,065	492		ctg000660	91,731	2334																							
YOgnWI000172	CG14339	3123																															
Novel finding in willistoni, not expected in paulistorum																																	
GK13929	CG10588	3246		ctg000330	91,61	1037		ctg000330	93,262	3250					tig00000698	93,262	3250															
GK28041	CG32650	960		ctg000190	71,160- 77,407	270-320		ctg000190	87,11	962					tig00000707	87,11	962															
GK27472	CG15359	813																															
YOgnWI030283	CG34277	819						ctg000200	80,314	828																							
GK21220	CG6052	5370						ctg000330	90,201	5378					tig00000698	90,182	5378															
GK28211	Ran-like	657						ctg000330	81,238	501					tig00000698	81,238	501															
GK18510	ProtA	582						ctg000330	78,705	587	contig 268	78,929	579		tig00000345	78,223-79,066	574-578	contig_272	78,929	579												
								ctg000410	78,694	582	contig 145	78,585	579		tig00000698	78,705	587	contig_37	78,305	590												
											contig 165	78,141	581		tig00000208	78,238	579	contig_533	78,584	579												
											contig 138	76,087	598		tig00000893	78,103	580	contig_659	78,238	579												
															tig00000310	78,313	581	contig_23	78,141	581												
															tig00000889	78,066	579	contig_47	77,211	588												
															tig00000585	76,831	587	contig_89	77,119	590												
															tig00000734	76,206	601															
GK28591	CG6888	591		ctg000480	30,469-100	128-197		ctg000480	96,447	591					tig00000030	76,447	591															
YOgnWI018045	CG34175	303		ctg000330	80,328	61		ctg000330	90,323	248					tig00000698	90,323	248															
GK20618, GK20619	Prox-beta-6	690 *4		ctg000330	79,565- 87,773	139-230		ctg000330	91,884 (91,319-)	690					tig00000698	91,739-92,319	690															

Notes within column groups:
- **NDN-FLYE-DCA:** BLAST (tblastn), Full gene list, Filter: alignment length > 60*(1/3)% of gene length — *No hits (left after filtering)!*
- **NDN-FLYE-DCA** BLAST (blastn), Full gene list, Filter: alignment length > 60% of gene length
- **NDN-FLYE-DCA** BLAST (blastn), gene list with only wil + mel hits
- **NDN-FLYE-DCA-GF** BLAST (blastn), gene list with only wil + mel hits — *No hits!*
- **NDN-FLYE-DCA-increased threshold:** BLAST (blastn), gene list with only wil + mel hits — *No hits!*
- **CANU-Full** BLAST (tblastn), Full gene list, Filter: alignment length > 60*(1/3)% of gene length — *No hits (left after filtering)!*
- **CANU-FLYE-DCA:** BLAST (tblastn), Full gene list, Filter: alignment length > 60*(1/3)% of gene length — *No hits (left after filtering)!*
- **CANU-FLYE-DCA** BLAST (blastn), Full gene list, Filter: alignment length > 60% of gene length