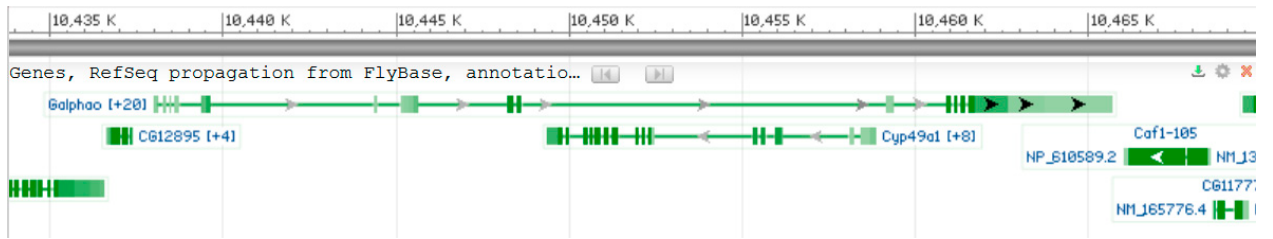
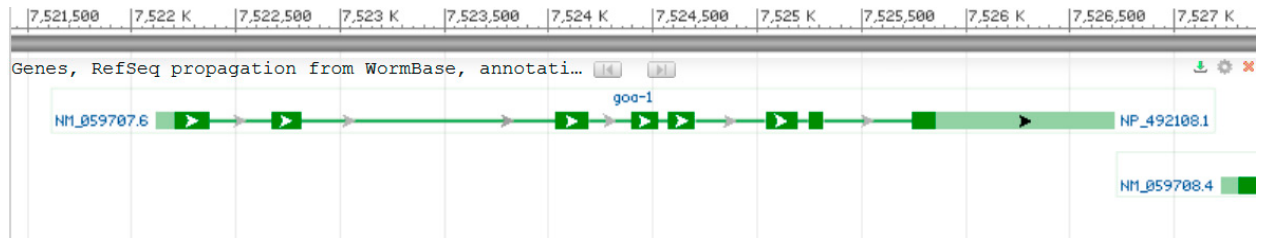


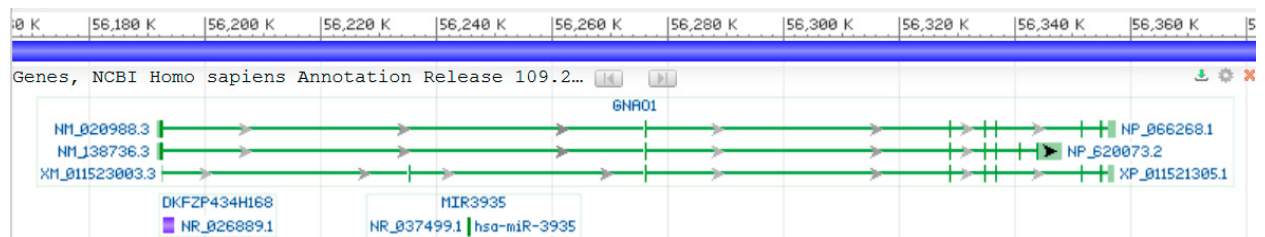
D.melanogaster *Gao*



C.elegans *goa-1*



H.sapiens *GNAO1*



Supplementary Figure S1. Loci of *Gao* genes have variable size but similar exon-intron structures (see also Fig. 1B). NCBI Gene ID: 36104 (primary source [FLYBASE:FBgn0001122](https://www.ncbi.nlm.nih.gov/nuccore/FLYBASE:FBgn0001122)) for *D. melanogaster*; 172505 (primary source [WormBase:WBGene00001648](https://www.ncbi.nlm.nih.gov/nuccore/WormBase:WBGene00001648)) for *C. elegans*; 2775 (primary source [HGNC:4389](https://www.ncbi.nlm.nih.gov/nuccore/HGNC:4389)) for *H. sapiens*.

A

dGao-PA	1	MGCAQSAEERAAARSRLIERNLKEDGIQAAKDIKLLLLG
dGao-PB	1	MGCTTSAEERAAIQRSKQIEKNLKEDGIQAAKDIKLLLLG
hGao	1	MGCTL SAEERAA LE RSKA IEKNLKEDGISAAKDVKLLLLG
		.**.***.***.*****.****.*****

B

hGαoA	242	NRMHESIMLFDSICNNKFFIDTSIILFLNKKDLFGEKIKKSPLTICFPEYTGPN TY EDAA
dGαo	242	NRMQESLKLFD SI CNNKWF TD TSIILFLNKKDLFEEKIRKSPLTICFPEYTGQ EY GEAA
hGαoB	242	NRMHESLKLFD SI CNNKWF TD TSIILFLNKKDLFEEKIKKSPLTICFPEYTGPSA FT EAV
hGαoA	302	AYIQAQFESKNRSPNKEIYCHMTCATDTNNIQVFDAVTDIIIAN N LRGCGLY
dGαo	302	AYIQAQFEAKNKS TS KEIYCHMTCATDTNNIQFVDAVTDV II AN N LRGCGLY
hGαoB	302	AYIQAQYESKNKSAHKEIYTHVTCATDTNNIQFVDAVTDV II AK N LRGCGLY

Supplementary Figure S2. A. Alignment of Gao proteins (amino acids are coded by 1st exons). *D. melanogaster* has splice variants with variable 1st coding sequence-containing exons. Most non-conservative amino acids between two *Drosophila* isoforms overlap non-conservative amino acids between *Drosophila* and human. B. Alignment of Gao proteins (amino acids are coded by two last exons). *Human* has splice variants with variable two last exons. hGaoA (settled as reference sequences here) has more identity with *Drosophila*'s sequences than with hGaoB (17 mismatches vs 20). There are 16 mismatches between dGao and hGaoB.

Supplementary Table S1. Sequence of primers used in the molecular analysis and cloning.

Primer	Sequence
dGaomRNAfw	GGTGAGTCGGGCAAGAGCACAATA
dGaomRNArev	GGCCTGGAATCCATCTTAGTACAGTCCA
LHAdGao23fw	cacctgcgaatccgatTGTGGACTTTTTCAAGTGGTGA
LHAdGao23rev	GAAGCCGTCCTCGTGAATGATTTTC
RHAdGao23fw	gactatctttctAGGGTTAACGATTCCGCAAATAGTAAGTACCAAATCA
RHAdGao23rev	atggctctctttcCCGGAACTAACGCTGAGGGACGAGTG
LdGao23fw (1)	CGCTGCTGCTCTTGAGTTTTCCA
RdGao23rev (2)	TCGTGAGTTTGCCCTTTGGCTTT
LHAdGao47fw	tagtgtcttcggggccGAAAATTGAGAATGGACGGGTGGA
LHAdGao47rev	ttatctttctagggTTAATCTTCTCCCCGAACAAATCCT
RHAdGao47fw	ctatctttctagggTTAAGAAGAGTCCCCTGACGATT
RHAdGao47rev	atggctctctttcccGGTTACGGTGTTCCTGCTAA
LdGao47fw (5)	AAGCTGTTTGCATAGCCAAGTGAG
RdGao47rev (6)	ACAACGTATGCAATGTTGGCGCTTG TG
pUC-L (7)	GCGCCTGTCACCTTTGCTTGATA
pUC-R (8)	CGATGGTAGTGTGGGGACTCC
pBac_rev (4)	GAGAGAGCAATATTTCAAGAATGC
pBacWTlong (3)	CCGATAAAACACATGCGTCAATT

Lowercase letters designate overlap sequences, required for the assembly of adjacent fragments upon cloning using the NEBuilder HiFi DNA Assembly Cloning Kit (New England Biolabs). Numbers in brackets after the primers' names represent how they are designated in Fig. 2B.