Supplementary Material

Figure S1 Phylogenetic tree of *NlFOXO* and its homologues.
Aa, *Aedes aegypti*, ABK76646.1; *Ad*, *Apis dorsata*, XP_006623461.1; *Af, Apis florea*, XP_00369 2941.1; *Amel*, *Apis mellifera*, XP_001122804.2;*Amex*, *Astyanax mexicanus*, XP_007258711.1; *Ap*, *Acyrthosiphon pisum*, XP_001944722.2; *Bg*, *Blattella germanica*,CCF23214.1;*Bi, Bombus impatie ns*,XP_003487689.1; *Bm, Bombyx mori*,AFD99125.1; *Bt, Bos Taurus*,NP_001193012.1; *Ca,Chryso chloris asiatica*,XP_006873780.1;*Cca, Ceratitis capitata*,XP_004531037.1; *Ccr, Condylura cristata*, XP_004680393.1;*Ce,Caenorhabditis elegans*,O16850.3; *Cg, Crassostrea gigas*, EKC23646.1;*Ch, C lytia hemisphaerica*,ABG21226.1;*Ci, Ciona intestinalis*, NP_001071717.1;*Clf, Canis lupus familiar is*, XP_003639448.1;*Cp, Culex pipiens*, AEI86721.1; *Css, Ceratotherium simum*,XP_004443237.1; *Dm, Drosophila melanogaster*, NP_996205.1; Dr, Danio rerio,NP_571160.1; Ee, Elephantulus ed wardii, XP_006879673.1; *Gg, Gallus gallus*, XP_001234496.2;Gmm, Glossina morsitans morsitan s,AFQ01085.1; *Hg, Heterocephalus glaber*, XP_004889213.1; *Hsal, Harpegnathos saltator*, EFN8 4381.1; *Hsap, Homo sapiens*, NP_001446.1; *Lc, Latimeria chalumnae*, XP_005993189.1; *Mb, M yotis brandtii*, XP_005862824.1; *Md, Musca domestica*, XP_005190128.1; *Mmul, Macaca mulatt a*, XP_001093593.1; *Mmus, Mus musculus*, NP_062714.1; Mo, *Metaseiulus occidentalis*, XP_003 741272.1; *Mr, Megachile rotundata*, XP_003705281.1; *Nl, Nilaparvata lugens*, KM250122; *Nv, N asonia vitripennis*, XP_001607658.2;*Pa, Pteropus alecto*, XP_006909082.1; *Pmb, Peromyscus ma niculatus bairdii*, XM_006977605.1; Pt, *Pan troglodytes*, XP_003311562.1; *Rn, Rattus norvegicus*, NP_001099865.1; *Sh, Sarcophilus harrisii*, XP_003769392.1; *Sk, Saccoglossus kowalevskii*, NP_ 001158440.1; *Sm, Schistosoma mansoni*, ABG78546.1; *Sp, Strongylocentrotus purpuratus*, ABB89 484.1; *Ss, Sus scrofa*, NP_999179.2;*Tca, Tribolium castaneum*, XP_975200.1; *Tch, Tupaia chinen sis*, XP_006154300.1; *Tml, Trichechus manatus latirostris*,XP_004388138.1; *Ts, Trichinella spirali s*, XP_003372811.1; *Tt, Tursiops truncates*, XP_004315811.1; *Xl, Xenopus laevis*,ACO24747.1; *X m, Xiphophorus maculatus*,AAK74186.1.

Figure S2 Phylogenetic tree of *NlAkt* and its homologues.
Am, Alligator mississippiensis, XM_006257899.1; *As, Alligator sinensis*, XM_006031384.1; *Ag, Anopheles gambiae*, XM_003435996; *Bas,Balaenoptera acutorostrata scammoni*,XM_007176250.1; *Bm, Bos mutus*, XM_005890586.1; *Bt, Bos Taurus*, XM_005218981.1; *Bb, Bubalus bubalis*, XM _006050047.1;*Cf, Camelus ferus*, XM_006177926.1; *Clf, Canis lupus familiaris*,XM_005623876.1; *Ch, Capra hircus*, XM_005692409.1; *Cl, Chinchilla lanigera*, XM_005410843.1; *Ca, Chrysochlo ris asiatica*, XM_006839485.1; *Cc, Condylura cristata*, XM_004694120.1; *Cq, Culex quinquefasc iatus*, XM_001849205.1; *Dm, Drosophila melanogaster*,NM_169706.2; *Ef, Eptesicus fuscus*, XM_ 008139592.1; *Ec, Equus caballus*, XM_001492713.4; *Ep, Equus przewalskii*, XM_008506799.1; *Ee, Erinaceus europaeus*, XM_007518365.1; *Fc, Felis catus*, XM_006933187.1; *Ggg, Gorilla go rilla gorilla*, XM_004055779.1; *Hl, Haemaphysalis longicornis*, AB601888.1; *Ha, Helicoverpa ar migera*, N399217.1; *Hs, Homo sapiens*, KJ890652.1; *Lo, Lepisosteus oculatus*, XM_006627598.1; *Lw, Leptonychotes weddellii*, XM_006738332.1; *La, Loxodonta Africana*, XM_003408651.1; *Md, Musca domestica*, XM_005186450.1; *Mp, Mustela putorius*, XM_004796606.1; *Mb, Myotis brand tii*, XM_005868806.1; *Ml, Myotis lucifugus*, XM_006096753.1; *Nl, Nilaparvata lugens*, KM2501

21; *Nle, Nomascus leucogenys*, XM_003276210.2; Op,Ochotona princeps, XM_004584261.1; *Or, Odobenus rosmarus*, XM_004395604.1; *Pp, Pan paniscus*, XM_003806999.1; *Pa, Pteropus alecto*, XM_006925608.1; *Sa, Sorex araneus*, XM_004603607.1; *Sp, Stegastes partitus*, XM_008284966.1; *Ss, Sus scrofa*, HQ687753.1; *Tml, Trichechus manatus latirostris*, XM_004376758.1.

Figure S3 Phylogenetic tree of *NlPI3K* and its homologues.
Ap, Anas platyrhynchos, XM_005024480.1; *Ad, Apis dorsata*, XM_006623134.1; *Af, Apis florea*, XM_003697036.1; *Am, Astyanax mexicanus*, XM_007228848.1; *Bt, Bombus terrestris*, XM_003392868.1; *Cm, Callorhinchus milii*, XM_007889678.1; *Can,Calypte anna*, XM_008496003.1; *Cm, Chelonia mydas*, XM_007064298.1; *Cla, Chinchilla lanigera*, XM_005406860.1; *Cpb, Chrysemys picta belli*, XM_005278661.2; *Cas, Chrysochloris asiatica*, XM_006846635.1; *Cli, Columba livia*,XM_005505585.1; *Cb, Corvus brachyrhynchos*, XM_008633983.1; *Dm, Drosophila melanogaster*,NM_057785.5; *Et, Echinops telfairi*, XM_004704007.1; *Ef, Eptesicus fuscus*, XM_008153234.1; *Ec, Equus caballus*, XM_001496778.2; *Fc,Falco cherrug*, XM_005445871.1; *Fp, Falco peregrinus*, XM_005242248.1; *Fa,Ficedula albicollis*, XM_005041237.1; *Gg, Gallus gallus*, XM_001235240.2; *Gf, Geospiza fortis*, XM_005423953.1; *Hs, Homo sapiens*, NM_014602.2; *Lo, Lepisosteus oculatus*, XM_006635531.1; *Lv, Lipotes vexillifer*, XM_007462423.1; *La, Loxodonta Africana*, XM_003420917.1; *Mr, Megachile rotundata*, XM_003703820.1; *Mg, Meleagris gallopavo*, XM_003207226.1; *Mu, Melopsittacus undulates*, XM_005141305.1; *Mde, Microplitis demolitor*, XM_008547450.1; *Mdo, Monodelphis domestica*, XM_003342097.2; *Mb, Myotis brandtii*, XM_005863585.1; *Mda,Myotis davidii*, XM_006770215.1; *Ml, Myotis lucifugus*, XM_006083684.1; *Nl, Nilaparvata lugens*, KM373311; *Nv, Nasonia vitripennis*, XM_008204184.1; *Op, Ochotona princeps*, XM_004588388.1; *Oaa, Orycteropus aferafer*, XM_007936842.1; *Og, Otolemur garnettii*, XM_003781713.1; *Pt, Pan troglodytes*, XM_516746.3; *Phc,Pediculus humanus corporis*, XM_002429885.1; *Pc, Physeter catodon*, XM_007115466.1; *Pr, Poecilia reticulate*, XM_008430629.1; *Ph, Pseudopodoces humilis*, XM_005518997.1; *Pb,Python bivittatus*, XM_007433030.1; *St, Spermophilus tridecemlineatus*, XM_005327000.1; *Sp,Stegastes partitus*, XM_008297967.1; *Tg, Taeniopygia guttata*, XM_002198545.1; *Tc, Tribolium castaneum*, XM_965590.2; *Tm, Trichechus manatus*, XM_004381391.1; *Za, Zonotrichia albicollis*, XM_005480995.1.

Figure S4 Phylogenetic tree of *NlPDK* and its homologues.
Ap, Acyrthosiphon pisum, XM_001950984.3; *Ad, Apis dorsata*, XM_006608687.1; *Af, Apis florea*, XM_003697518.1; *Am, Apis mellifera*, XM_006567943.1; *At, Arabidopsis thaliana*, AF132742.1; *Bi, Bombus impatiens*, XM_003487039.1; *Bt, Bombus terrestris*, XM_003396474.1; *Dm, Drosophila melanogaster*, NM_080382.4; *Hl, Haemaphysalis longicornis*, AB617886.1; *Hb, Haplochromis burtoni*, XM_005939509.1; *Hs, Homo sapiens*, AF017995.1; *Le, Lycopersicon esculentum*, AY849915.1; *Mz, Maylandia zebra*, XM_004562456.1; *Mr, Megachile rotundata*, XM_003708447.1; *Md, Microplitis demolitor*, XM_008560785.1; *Nb, Neolamprologus brichardi*, XM_006801043.1; *Nl, Nilaparvata lugens*, KM373312; *Nv, Nasonia vitripennis*, XM_008204995.1; *On, Oreochromis niloticus*, XM_003438771.2; *Oa, Orycteropus afer*, XM_007939543.1; *Ol, Oryzias latipes*, XM_004080354.1; *Pf, Poecilia Formosa*, XM_007576622.1; *Pr, Poecilia reticulate*, XM_008436325.1; *Pb, Python bivittatus*, XM_007439249.1; *Sp, Stegastes partitus*, XM_008303696.1; *Tr, Takifugu rubripes*, XM_003961305.1; *Xm, Xiphophorus maculatus*, XM_005803239.1.

Figure S5 QRT-PCR measurement of the expression of *NlPI3K, NlAkt, NlPDK1* and *NlFOXO* after dsRNA knockdown /double knockdown of *PI3K*/*Akt*/*FOXO* Signaling.

Figure S1

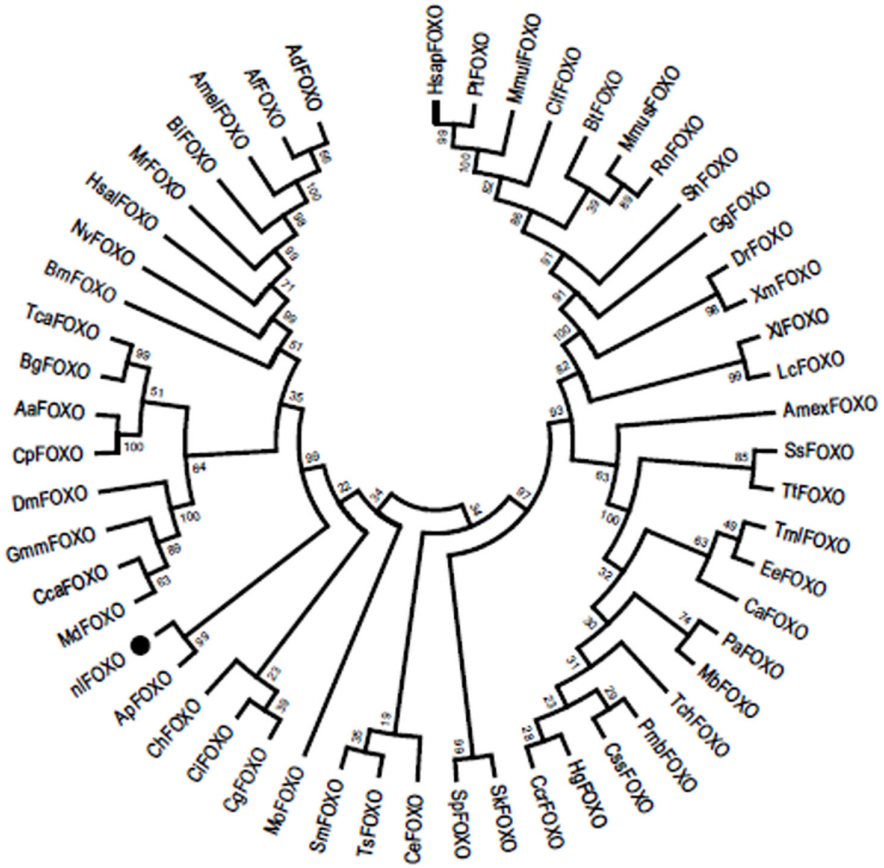
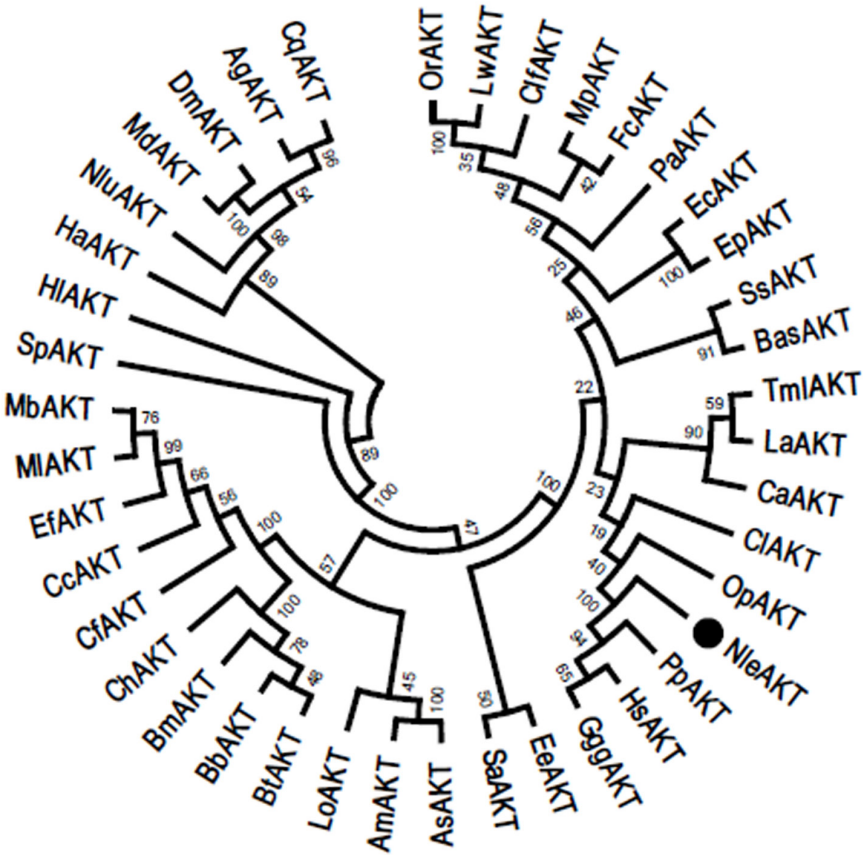


Figure S2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MdAKT
NluAKT
HaAKT
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SpAKT
MbAKT
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CcAKT
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ChAKT
BmAKT
BbAKT
BtAKT
LoAKT
AmAKT
AsAKT
SeAKT
EeAKT
GggAKT
HsAKT
PpAKT
NleAKT
OpAKT
ClAKT
CaAKT
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BasAKT
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EcAKT
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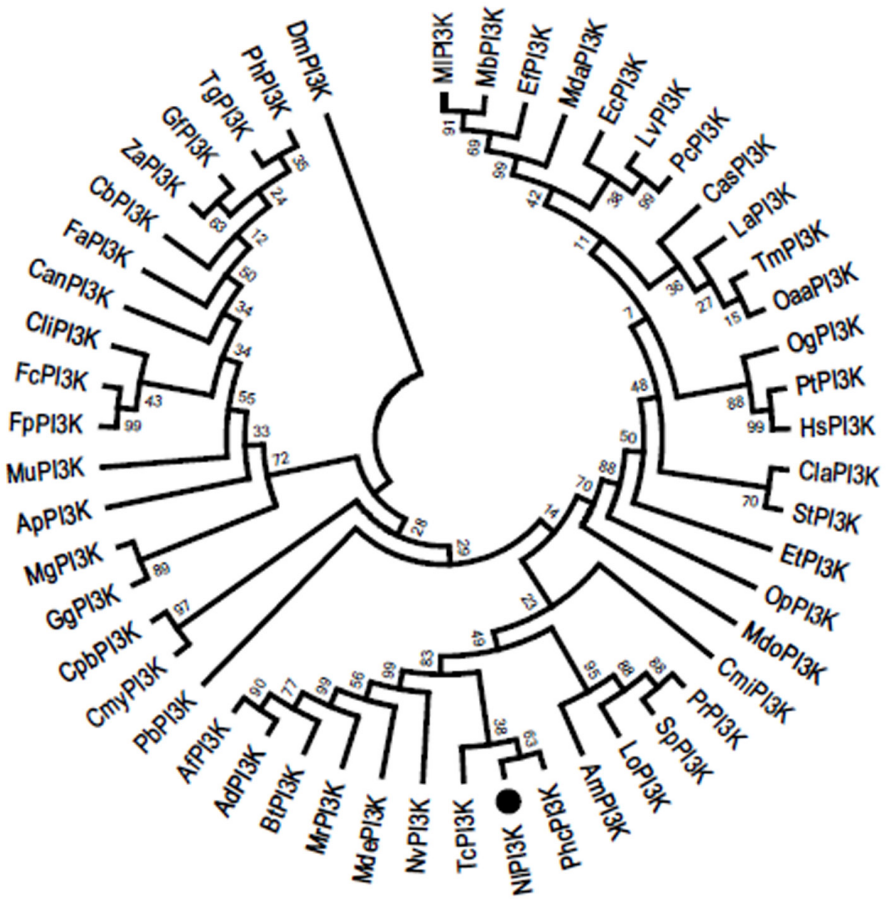
FcAKT
MpAKT
ClfAKT
LwAKT
OrAKT

Figure S3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GfPI3K
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CbPI3K
FaPI3K
CanPI3K
CliPI3K
FcPI3K
FpPI3K
MuPI3K
ApPI3K
MgPI3K
GgPI3K
CpbPI3K
CmyPI3K
PbPI3K
AfPI3K
AdPI3K
BtPI3K
MrPI3K
MdePI3K
NvPI3K
TcPI3K
NlPI3K
PhcPI3K
AmPI3K
LoPI3K
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PrPI3K
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TmPI3K
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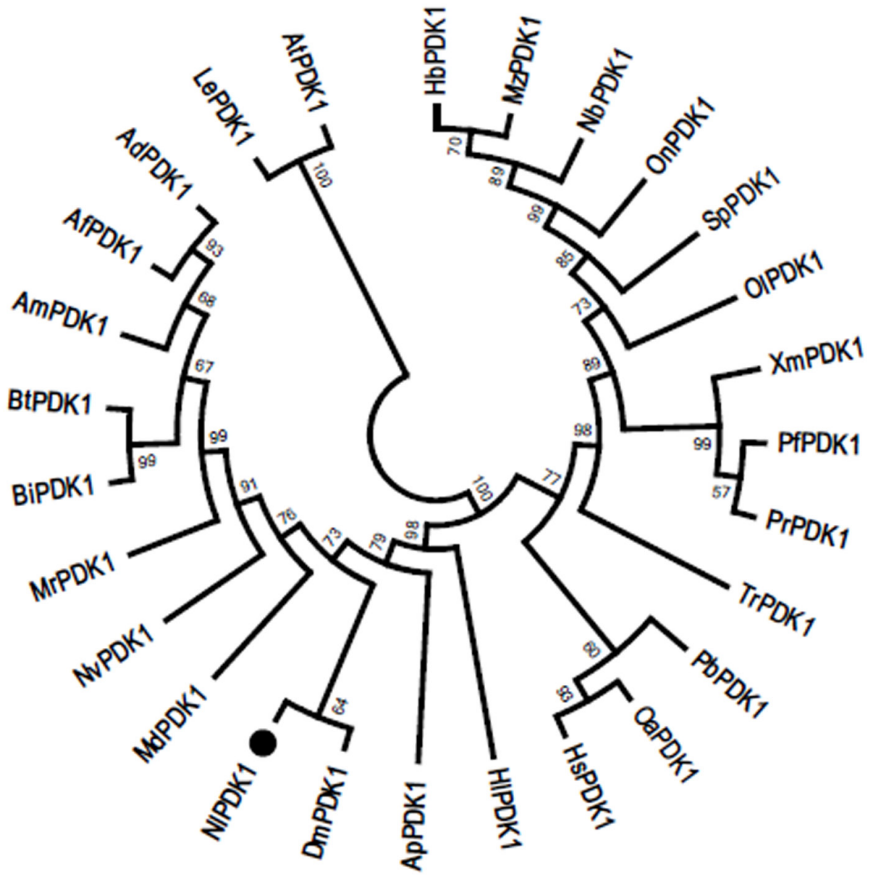
Figure S4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AdPDK1
AfPDK1
AmPDK1
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85
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76
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99
99
67
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93
64
88

Figure S5

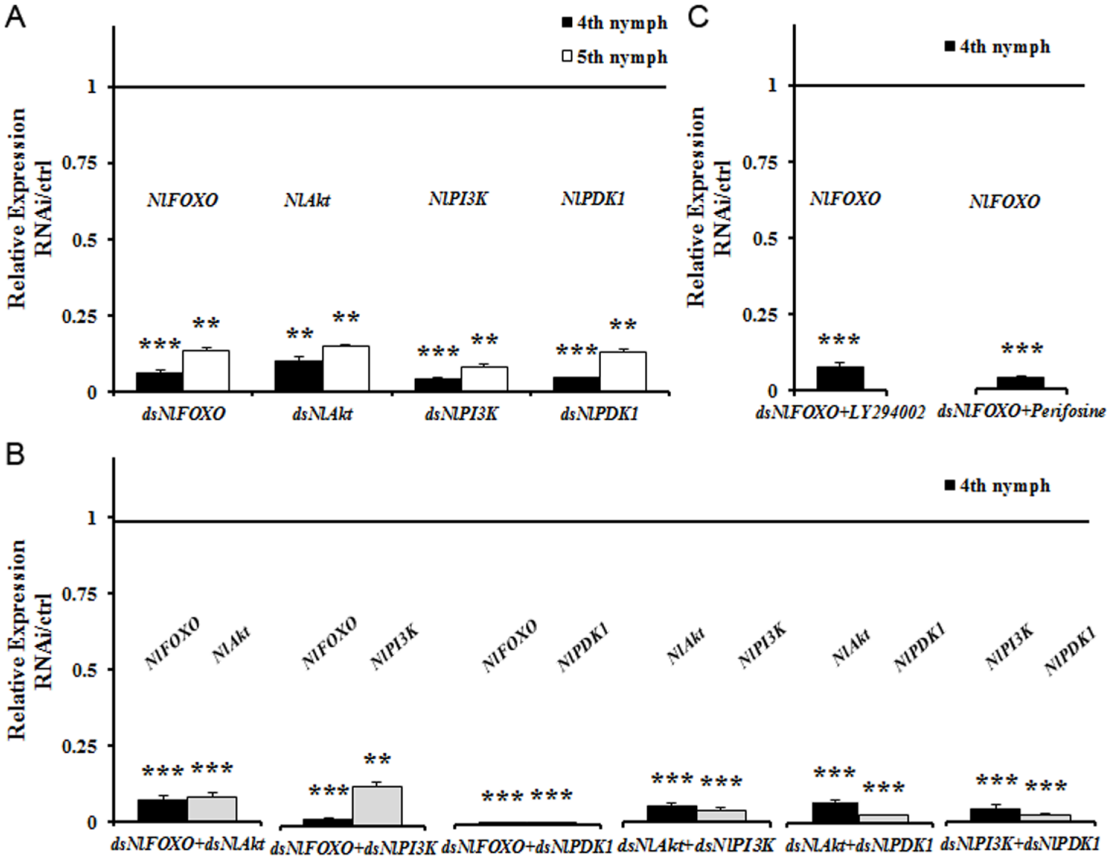
A
4th nymph
5th nymph
Relative Expression RNAi/ctrl
1
0.75
0.5
0.25
0
NlFOXO
NlAkt
NlPI3K
NlPDK1
dsNlFOXO
dsNlAkt
dsNlPI3K
dsNlPDK1
C
4th nymph
NlFOXO
NlFOXO
dsNlFOXO+LY294002
dsNlFOXO+Perifosine
B
4th nymph
NlFOXO
NlAkt
NlFOXO
NlPI3K
NlFOXO
NlPDK1
NlAkt
NlPI3K
NlAkt
NlPDK1
NlPI3K
NlPDK1
dsNlFOXO+dsNlAkt
dsNlFOXO+dsNlPI3K
dsNlFOXO+dsNlPDK1
dsNlAkt+dsNlPI3K
dsNlAkt+dsNlPDK1
dsNlPI3K+dsNlPDK1

Table S1 Parameters measured and calculated for cluster analysis.

Catatory	Treatment	Body length (10^{-3}m)	Body weight(10^{-3}g)	Bristle number/wing area(bristle/$10^{-6}m^2$)
SWF	NC	3.25	2.45	144.20
	dsGFP	3.41	1.80	157.78
	dsNlAkt	3.16	1.44	160.62
	dsNlPI3K	3.22	2.41	185.46
	dsNlPDK1	3.18	1.70	196.99
	LY294002	3.41	2.14	137.81
	Perifosine(SWF)	3.36	1.76	172.09
	dsNlFOXO+dsNlAkt	3.29	1.76	150.01
	dsNlFOXO+dsNlPI3K	3.06	2.09	193.79
	dsNlAkt+dsNlPI3K	3.12	2.03	180.16
	dsNlAkt+dsNlPDK1	3.19	1.79	196.01
	dsNlPI3K+dsNlPDK1	3.14	1.73	160.86
SWM	NC	2.87	1.01	202.80
	dsGFP	2.50	0.93	216.28
	dsNlAkt	2.37	0.75	243.33
	dsNlPI3K	2.78	1.36	209.15
	dsNlPDK1	2.39	0.73	246.97
	LY294002	2.50	1.02	211.02
	Perifosine	2.41	1.06	159.80
	dsNlFOXO+dsNlAkt	2.60	1.20	234.37
	dsNlAkt+dsNlPI3K	2.53	1.10	199.94
	dsNlAkt+dsNlPDK1	2.47	0.92	236.72
	dsNlPI3K+dsNlPDK1	2.41	0.93	214.00
LWF	NC	3.42	2.27	69.78
	dsGFP	3.47	2.17	67.20
	dsNlFOXO	3.55	2.07	75.77
	dsNlPDK1	3.07	1.63	79.03
	LY294002	3.50	2.70	64.76
	Perifosine	3.38	2.40	76.73
	dsNlFOXO+dsNlAkt	3.31	1.78	90.73
	dsNlFOXO+dsNlPI3K	3.42	2.24	99.36
	dsNlFOXO+dsNlPDK1	3.34	2.02	93.87
	dsNlFOXO+LY294002	3.19	2.08	79.38
	dsNlFOXO+Perifosine	3.16	1.82	98.98
LWM	NC	2.99	1.11	78.06
	dsGFP	2.53	1.10	78.44
	dsNlFOXO	2.54	1.02	102.74
	dsNlAkt	2.41	1.42	102.25
	dsNlPI3K	2.70	1.08	89.00
	dsNlPDK1	2.50	1.07	81.64
	LY294002	2.56	1.17	71.71

Perifosine	2.77	1.57	77.07
dsNlFOXO+dsNlAkt	2.52	0.93	90.49
dsNlFOXO+dsNlPI3K	2.59	1.13	91.09
dsNlFOXO+dsNlPDK1	2.54	1.40	78.44
dsNlAkt+dsNlPI3K	2.47	1.17	101.56
dsNlAkt+dsNlPDK1	2.47	0.95	84.68
dsNlPI3K+dsNlPDK1	2.39	0.98	78.60
dsNlFOXO+LY294002	2.63	1.06	76.12
dsNlFOXO+Perifosine	2.53	0.99	84.32