Supplemental Data:

Table S1. Primers and probes used for RT-qPCR analysis

Gene		**Taqman Primer/probe sequence**
α-Tubulin84B	F	GTATCTCTATCCATGTTGGTCAGG
	R	AGACGGCATCTGGCCATCG
	P	ACGCCTGCTGGGAGCTCTACTGC
miple	F	GGAAAGTCCAAGGACAAAAGTG
	R	AATCGAGTTCGATATCACTTAAACG
	P	AACAAAGATAAAGCTGCTCGCAAAGGAC
CG32373	F	ACACACCGGACTTTGGTCTAGT
	R	ATTATTGCAGCTTGCAGGATAGA
	P	AAGTGCGTGGAATCCCTCGCA
mthl8	F	TTATTACGGCTCTAGGCTCATCTT
	R	CACGAAAACAGGAGCGTAAAAATA
	P	CTGGTTTGATCCACGCAATTGGTC
unc-13-4A	F	CAACTTTCATGGACTGAAACAAATC
	R	AAAGTCCTGAGCCTGCTTGTC
	P	CAAAAGGATAAATGCAATCCCATTTTGCA
Gene		**Primer sequence for Sybr green analysis**
nmo	F	CCTTCTCGGTGCTCTACACA
	R	ACGCCCCTCATCCAGATAC
α-Tubulin84B	F	CACTACACCATCGGCAAGGA
	R	GCAGACCGGTGCACTGATC

F, forward; R, reverse; P,probe

Table S2. List of genes significantly up-regulated in *arm*-GFP, *nmo*^{P1} imaginal eye discs in a microarray analysis

Up-regulated genes		
Biological process	**Adjusted *p-value****	**Fold change****
General metabolism		
RFeSP	0.0000005432	3.00
Mgstl	0.0000052169	1.72
CG3788	0.0000495427	1.71
CG8607	0.000419257	1.66
CG6414	0.000988570	1.47
Wwox	0.003878009	0.71
Aprt	0.004341881	0.69
Cyp9c1	0.007195249	0.85
CG10175	0.010326191	0.64
veil	0.026866680	0.48
GS	0.027082857	0.44
Fmo-1	0.033828278	0.47
Protein metabolism		
CG7722	0.002798614	0.70
Usp36	0.009133010	0.58
CG32640	0.010095192	0.54
Topors	0.016110128	0.46
CG6357	0.023230661	0.65
Carbohydrate metabolism		
CG11357	4.74424E-06	4.08
sfl	0.0000687907	2.69
CG11594	0.001206152	2.01
CG18278	0.009590515	1.00
CG3253	0.011079780	0.62
Ch7	0.022853142	0.84
pgant5	0.030908713	0.54
CG15661	0.005202531	1.13
Ion transport		
CG9826	0.001347469	1.23
CG12455	0.022527347	0.50
Nach	0.038025986	0.69
Cytoskeleton biogenesis and organization		
hts	0.0000410873	1.62
shi	0.0000419885	1.74
Tektin A	0.030870819	0.61
Aplip	0.039368893	0.89
rib	0.045443021	0.38
Signaling		

miple	0.0000002411	4.29
mthl8	0.0000002411	3.62
	0.0000002551	4.27
Gr64a	0.000335219	1.38
fwd	0.000988570	1.47
Arr1	0.001519850	1.07
Gr64d/e	0.003878009	0.86
CG7787	0.005202531	0.59
Spred	0.009658771	0.87
Gr64c/e	0.016886397	0.79
Rh6	0.022853142	0.84
Pvf2	0.025250662	0.49
Phk-3	0.025818298	0.45
Obp83g	0.032014350	0.50
daw	0.035694755	0.47
CG9593	0.047404591	0.77
Adhesion		
mspo	0.000421616	1.47
off-track	0.012004949	0.58
dumpy	0.024129666	0.63
ndl	0.029566669	0.41
Transcription, translation and nucleic acid metabolism		
XRCC1	0.000335219	0.95
Ribosomal protein L28	0.000340665	2.05
CG32281	0.003115307	0.90
GV1	0.002438683	0.69
	0.003878009	0.68
CG32364	0.005924707	0.78
CG300080	0.010095192	1.13
CG6961	0.011330326	0.69
lola	0.013326317	0.77
TBPH	0.016712839	0.46
RpL22-like	0.026590207	0.39
CG10306	0.032077400	0.41
Unkown function		
CG17669	0.0000002411	3.43
CG30190	0.0000002843	2.75
CG15449	0.0000584923	2.11
CG42351	0.0000989489	2.72
	0.002634764	1.16
CG15747	0.0002114938	1.21
CG15785	0.000335219	1.10
CG30217	0.000433933	1.29
CG16885	0.000489149	2.15

	0.001519850	1.31
CG11073	0.000507278	0.88
yellow-d	0.001422267	1.14
CG15786	0.001533364	0.93
CG1317	0.002386336	0.64
CG10344	0.002684763	0.63
	0.025250662	0.58
CG11854	0.003878009	0.70
CG7231	0.009658771	0.49
CG15879	0.015364244	1.08
CG9192	0.016380643	1.30
CG32278	0.017369068	0.52
Gmap	0.020560697	0.50
CG11550	0.022789551	0.46
CG34035	0.024129666	0.65
CG30101	0.026133796	0.73
	0.028708881	0.86
CG1368	0.026133796	0.45
CG13791	0.026133796	0.50
CG17841	0.026368928	0.45
CG30017	0.027082857	0.52
CG30118	0.027945128	0.93
CG1344	0.027945128	0.39
CG34057	0.032014350	0.65
c11.1	0.033533835	0.45
mam	0.037080238	0.43
CG9021	0.040526287	1.79
CG3880	0.046911478	0.53
CG30222	0.047965582	0.44
CG13335	0.049876980	0.52
CG7016	0.049876980	0.50
Others		
CG15313	0.000480655	1.58
CG11170	0.003878009	0.75
bip1	0.006465021	0.80
Cpr47Ea	0.010326191	0.64
CG3530	0.011079780	0.62

* Benjamini–Hochberg-adjusted *p-value*s are shown. ** Fold change expressed as the $\log_2$ of the ratio of the two compared mean intensities. A fold change of 2 represents a 2^2-times increase in the expression in nmo^{P1} mutants. Two Adjusted *p-value* and Fold change represent different probes in the array for the same gene.

Table S3. List of genes significantly down-regulated in *arm*-GFP, *nmo*^{P1} imaginal eye discs in a microarray analysis

Down-regulated		
Biological process	**Adjusted *p-value* ***	**Fold change *,****
nmo	**0.000000241**	**-4.43**
Signaling		
PGRP-LE	0.000008500	-3.07
CG6701	0.006136463	-0.68
mthl2	0.008026766	-1.14
CkIIbeta	0.009658771	-0.51
Ptp99A	0.020420963	-0.48
Klp54D	0.025250662	-0.76
Tie	0.025818298	-0.83
mthl4	0.027409617	-0.58
EDTP	0.027409617	-0.58
Nplp2	0.040173584	-1.26
Pde9	0.048475136	-0.60
General metabolism		
CG31809	0.012004949	-1.04
Cyp4p1	0.014199627	-0.53
GstE5	0.015586534	-0.68
CG13325	0.016855433	-0.49
CG11200/CG13868	0.022129718	-0.47
ssp3	0.027082857	-0.41
CG15343	0.027794711	-1.10
Gpo-1	0.031037805	-0.56
phm	0.035454899	-1.20
CG8193	0.046287086	-1.28
CG8889	0.047965582	-0.86
Carbohydrate metabolism		
CG10924	0.004907708	-0.57
cracked	0.010588946	-0.89
CG13937	0.026133796	-0.42
CG4351	0.032014350	-0.43
CG18135	0.047404591	-1.08
Protein metabolism		
CG17739	0.003878009	-0.88
CG32412 (DromeQC)	0.004907708	-0.96
CG40072	0.025250662	-0.78
fat spondin	0.027409617	-0.58
CG4408	0.036613926	-0.97
Lipid metabolism		
CG13890	0.000218244	-1.14

Reg-2	0.017373919	-0.73
CG9009	0.021055261	-0.47
CG10131	0.044462459	-0.77
Exocytosis		
sec6	0.017240975	-0.48
Transcription, translation and nucleic acid metabolism		
scribbler	0.000241820	-1.49
msl-3	0.000342548	-1.38
	0.003675677	-0.87
krimper	0.001347469	-1.11
CG10630	0.007809501	-1.01
CG12605	0.014131140	-0.56
CG11883	0.017015276	-0.44
CG13895	0.029968609	-0.73
dre4	0.034335820	-0.47
mutator 2	0.046333660	-0.38
CG32006	0.047404591	-0.43
Su(z)12	0.047404591	-0.49
Cytoskeleton biogenesis and organization		
Kap3	0.047594869	-0.44
Transport		
Glut1	0.000208607	-1.09
CG30392	0.001869396	-0.87
Trn	0.006049149	-0.98
Mdr65	0.017256934	-0.81
Tom70	0.031037805	-0.39
CG5535	0.046298994	-0.43
CG9864	0.046368006	-0.53
Unknown function		
CG32373	0.000001675	-3.05
CG12643	0.000034931	-1.81
pst	0.000246204	-1.03
CG15784	0.000284751	-1.23
CG8209	0.000376479	-1.01
CG12607	0.001983851	-1.09
CG14960	0.005008857	-0.75
CG42272	0.005493316	-0.67
CG6701	0.006136463	-0.68
CG32368	0.007942964	-0.90
CG1092	0.008944602	-0.98
CG13516	0.009993200	-0.87
CG15312	0.010588946	-0.89
CG6579	0.011809099	-0.72
CG10855	0.012919961	-0.74
CG34342	0.012919961	-0.72

CG13679	0.013938244	-0.64
small non-messenger RNA 60Cb/snoRNA:Or-CD9b	0.014083209	-0.85
CG30380	0.014131140	-0.98
CG8501	0.014199627	-0.80
CG42565/CG42566	0.014365537	-1.09
CG34331	0.016855433	-0.94
Fie	0.017170357	-0.79
CG33494	0.018713506	-0.61
CG15073	0.022763693	-0.57
CG13896	0.024325182	-0.54
CG7852	0.026133796	-0.52
CG11475	0.026133796	-0.41
CG32663	0.026133796	-0.41
CG2469	0.031037805	-0.38
CG13531	0.034675021	-0.50
CG14962	0.039533382	-0.66
CG13679	0.042359317	-0.55
	0.044111239	-0.58
CG5704	0.044924698	-0.58
Adhesion		
unc-13-4A	0.000021273	-2.54
lectin-28C	0.018550832	-1.24
del	0.026133796	-0.55
Cht6	0.042359317	-0.42
Others		
Spinophilin	0.000218244	-1.77
MtnA	0.003171962	-0.97
CG15021	0.023240118	-1.36
ssp3	0.027082857	-0.41
CG13398	0.028632409	-0.60
CG1240	0.033257010	-0.37
MtnB	0.047404591	-1.08

* Benjamini–Hochberg-adjusted *p-value*s are shown. ** Fold change expressed as the $\log_2$ of the ratio of the two compared mean intensities. A fold change of -2 represents a 2^2-times decrease in the expression in *nmo*^{P1} mutants. Two Adjusted *p-value* and Fold change represent different probes in the array for the same gene.