Supplemental Materials and Methods:

Mice and Infection

At least one male and four female *B.malayi* parasites were surgically implanted into the peritoneal cavity of recipient mice in a total volume of 0.5 mL RPMI supplemented with 0.25 U/mL Penicillin and 100 mg/mL Streptomycin (Gibco). Control mice underwent sham surgery with an equal volume of medium but no parasites. Three days prior to necropsy control mice were additionally injected i.p. with 800 μL 4% Brewer modified thioglycollate medium (BD Biosciences). Three to 21 days post surgery mice were killed and the peritoneal cavity flushed with 10mL cold medium. For *in vitro* experiments mice were injected with 800 μL 4% thioglycollate three days prior to necropsy without prior surgery.

RNA-isolation

Total RNA was isolated from MΦ lysed in Qiazol using the miRNEasy-kit (Qiagen) according to manufacturers instructions. Briefly the RNA from lysed cells was precipitated using Phenol-Chloroform-extraction and the aqueous supernatant purified over a spin-column. RNA-content was determined using a NanoDrop (Thermo Scientific).

Quantitative RT-PCR

For the analysis of miRNA expression by qRT-PCR the TaqMan® MicroRNA Reverse Transcription Kit with miRNA-specific TaqMan® MicroRNA Assays (Applied Biosystems) was used following the manufacturer's instructions. Briefly 5-10 ng of total

RNA were coincubated with 2-3 μL miRNA-specific Primers (Assay-ID miR-16: 000391; miR-125b: 000449; miR-146a: 000468; miR-199b: 001131; miR-378: 002243; snoRNA135: 001230; snoRNA234: 001234) and cDNA generated in the presence of RNase-inhibitors. Detection of successfully transcribed products was carried out using TaqMan®2x Universal PCR Mix (no AmpErase® UNG; Applied Biosystems) in combination with miRNA-specific primers and TaqMan®-probes and quantified on a Lightcycler® 480 (Roche Applied Sciences). Fold change over medium/naïve controls was calculated using the ΔΔct method utilizing expression of miR-16 as the house keeping gene.

For the measurement of mRNA-expression, total RNA was converted to cDNA utilizing BioScript™ Reverse Transcriptase (Bioline) and $p(dT)_{15}$ Primers (Roche Applied Science). Expression levels were quantified using LightCycler® 480 SYBR Green I Master (Roche Applied Science). A list of sequences of mRNA-specific, intron-spanning primers used can be found in supplementary table S1. Measurements were performed on a Lightcycler® 480 (Roche Applied Science). Expression was normalized against *Gapdh* or *Anxa-6* expression and is depicted as fold change over medium/naïve controls.

Dual-Luciferase Reporter Assay

Transfected cells were lysed in 50 μL passive lysis buffer and firefly luciferase activity assessed by mixing 10 μL lysate with 50 μL Luciferase Assay Reagent II and resulting luminescence measured on a LumiStar luminometer (BMG Labtechnologies). Subsequently 50 μL per sample Stop&Glo® Reagent were added and *Renilla* luciferase activity assessed using the same luminometer.

Flow cytometry

For the analysis of STAT-6 phosphorylation thioglycollate-elicited peritoneal MΦ were stimulated with rIL-4 or medium for 24 hours as described above. Subsequently remaining stimulus was washed off and the cells incubated without stimulus for 1 hour prior to re-stimulation with rIL-4 for 5 – 60 min. Afterwards cells were fixed with 2% paraformaldehyde (Sigma Aldrich) for 10 min at RT, subjected to surface staining for F4/80 and CD11b (Biolegend) and permeabilised with methanol (Sigma Aldrich) at 4 °C for 30 min prior to staining with anti-phosphoSTAT-6 antibodies (BD Phosflow™ STAT6 (pY641), BD Pharmingen). As negative control appropriate isotype staining was performed. Samples were acquired on a BD FACSCanto™ II (BD Pharmingen) and post-acquisition analysis performed using FlowJo v8.8.6 (Tree Star Inc.). Data are depicted as median fluorescence intensity.

Protein extraction and Western blotting

For the determination of Akt-1 and Grb2 protein levels RAW264.7 cells were transfected as described above and 12 hours post transfection cells were lysed using passive lysis buffer (Promega) supplemented with 1% protease inhibitor cocktail (Sigma Aldrich). Protein concentrations were determined using the Coomassie Plus Bradford reagent assay (Thermo Scientific) and equal amounts separated on NuPage® 4-12% Bis-Tris gels (Life Technologies). Proteins were transferred to Hybond ECL membranes (GE Healthcare) and specific protein bands detected using monoclonal antibodies against Grb2 or Akt-1 simultaneously with β-actin (all Abs from Cell Signaling Technology). Hybridisations

were done 1:1000 in 5% milk, 1x TBS, 0.1% Tween-20 overnight at 4ºC. Anti-rabbit IgG (H+L) DyLight800™ Ab (Thermo Scientific) was added 1:1000 for 2 hours at room temperature. Signals were visualized utilizing the Odyssey® Imager (Li-Cor) and densitometric analysis carried out using ImageJ (http://rsb.info.nih.gov/ij/index.html) following the method described by Luke Miller (http://lukemiller.org/index.php/2010/11/analyzing-gels-and-western-blots-with-image-j/).

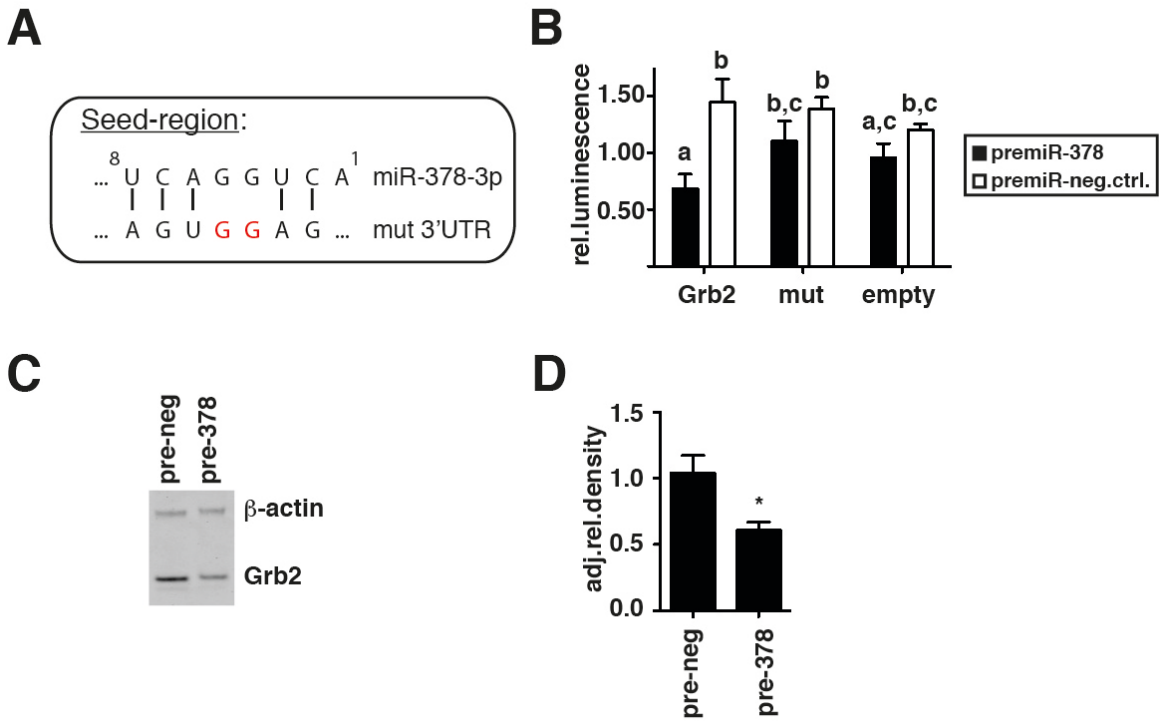
Table S1: List of Primers used for quantitative RT-PCR

Gene-Symbol	direction	Primer-sequence
Akt1	fwd	5'-CATGAACGACGTAGCCATTG-3'
	rev	5'-CCATCGTTCTTGAGGAGGAA-3'
Arg1	fwd	5'-CAGAAGAATGGAAGAGTCAG-3'
	rev	5'-CAGATATGCAGGGAGTCACC-3'
Bactin	fwd	5'-TGGAATCCTGTGGCATCCATGAAAC-3'
	rev	5'-TAAAACGCAGCTCAGTAACAGTCCG
Ccna2	fwd	5'-CTTGGCTGCACCAACAGTAA-3'
	rev	5'-CAAACTCAGTTCTCCCAAAAACA-3'
Cd36	fwd	5'-TGGCCTTACTTGGGATTGG-3'
	rev	5'-CCAGTGTATATGTAGGCTCATCCA-3'
Chi3l3	fwd	5'-TCACAGGTCTGGCAATTCTTCTG-3'
	rev	5'-TTGTCCTTAGGAGGGCTTCCTC-3'
Gapdh	fwd	5'-ATGACATCAAGAAGGTGGTG-3'
	rev	5'-CATACCAGGAAATGAGCTTG-3'
Grb2	fwd	5'-TGACCCCCAGGAGGATGGCG-3'
	rev	5'-AACATGCCGGTCTGCCCGTG-3'
Nos2	fwd	5'-CCCGGAAGGTTTGTACAGC-3'
	rev	5'-AAGGGGACGAACTCAGTGG-3'
Ppargc1b	fwd	5'-GACGTGGACGAGCTTTCACT-3'
	rev	5'-GAGCGTCAGAGCTTGCTGTT-3'
pan-Pparg	fwd	5'-TTATAGCTGTCATTATTCTCAGTGGAG-3'
	rev	5'-GACTCTGGGTGATTCAGCTTG-3'
Retnla	fwd	5'-TATGAACAGATGGGCCTCCT-3'
	rev	5'-GGCAGTTGCAAGTATCTCCAC-3'

Table S2: microRNA-array results. Log2 ratio of microRNAs found to be significantly differentially expressed in BALB/c NeMΦ as compared to Thio-MΦ (left column) or IL-4Rα$^{-/-}$ NeMΦ (right column). y: microRNA selected for qRT-PCR verification. – no significant change or not chosen for validation.

microRNA-ID (Array) miRBase 13	microRNA-ID (current) miRBase 18	Log2 NeMΦ/ThioMΦ	Log2 BALB/c / IL-4Rα$^{-/-}$	Selected for qRT-validation
miR-18a	miR-18a-5p	-1.31	-	y
miR-20a	miR-20a-5p	-	-0.60	-
miR-125a-5p	miR-125a-5p	-	-1.09	-
miR-125b-5p	miR-125b-5p	-	1.91	y
miR-141	miR-141-3p	-1.14	-	-
miR-146a	miR-146a-5p	-1.46	-	y
miR-150	miR-150-5p	-	-1.97	y
miR-199b*	miR-199b-5p	-	2.04	y
miR-221	miR-221-3p	-1.53	-	y
miR-222	miR-222-3p	-1.27	-	y
miR-223	miR-223-3p	-	1.22	-
miR-291a-5p	miR-291a-5p	-	-0.75	-
miR-342-3p	miR-342-3p	-1.51	-	y
miR-378	miR-378-3p	2.10	2.28	y
miR-467b	miR-476b-5p	-1.10	-	-
miR-689	-	-	-2.56	y
miR-710	miR-710	-	-1.06	-
miR-720	miR-720	-	1.03	-
miR-744	miR-744-5p	-	-0.85	-

Suppl. Fig.1



Suppl.Figure 1: miR-378-3p targets the IL-4R/PI3K/Akt-signaling pathway.
(A) Schematic depiction of the mutated miR-378-3p binding site in 3'UTR-sequences used in this study.
(B) Luciferase-assay using the 3'UTR of wildtype Grb2 (Grb2) or constructs with mutated seed-region binding sites for both predicted miR-378-3p binding sites (mut) or without insert (empty). Data indicates cotransfection with a miR-378-3p mimic (black bars) or a scrambled control (open bars). Data is pooled from 4 separate experiments and depicted as relative luminescence compared to no-RNA transfected controls. Bars not connected by the same letters are statistically significantly different.
(C) Representative WesternBlot analysis of RAW264.7 cells 12h post transfection with a mimic (pre-378) of miR-378-3p or appropriate negative controls (pre-neg). Samples were separated on a 4-12% Gradient gel and stained for Grb2 and b-actin at the same time.
(D) Densitometric analysis of the samples analysed in (C). Data representative of four separate experiments. *P< .05