SUPPLEMENTAL MATERIAL

Supplemental Table 1. Medians of miRNAs expression values from qRT-PCR experiment

	2$^{-\Delta CT}$ (MEDIAN)		
	Healty control	**LL**	**TT**
miR-101	0.000158	0.000085	0.000032
miR-125b	0.062728	0.025480	0.006089
miR-196b	0.034144	0.005964	0.000370
miR-26a	0.194189	0.095560	0.016690
miR-27a	0.007599	0.002923	0.002834
miR-27b	0.024220	0.007198	0.001648
miR-29c	0.000318	0.000194	0.000012
miR-34c	0.032532	0.006924	0.008581
miR-425-5p	0.012199	0.026915	0.004551
miR-452	0.037138	0.025655	0.003609
miR-455-3p	0.001856	0.000507	0.000386

miR-502-3p	0.000419	0.000303	0.000024
miR-539	0.002949	0.000485	0.001431
miR-660	0.009529	0.004937	0.002680
miR-92a	0.008199	0.004379	0.002393
miR-99a	0.081285	0.109929	0.018840

$2^{-\Delta Ct}$ median of each miRNAs from validation experiment.
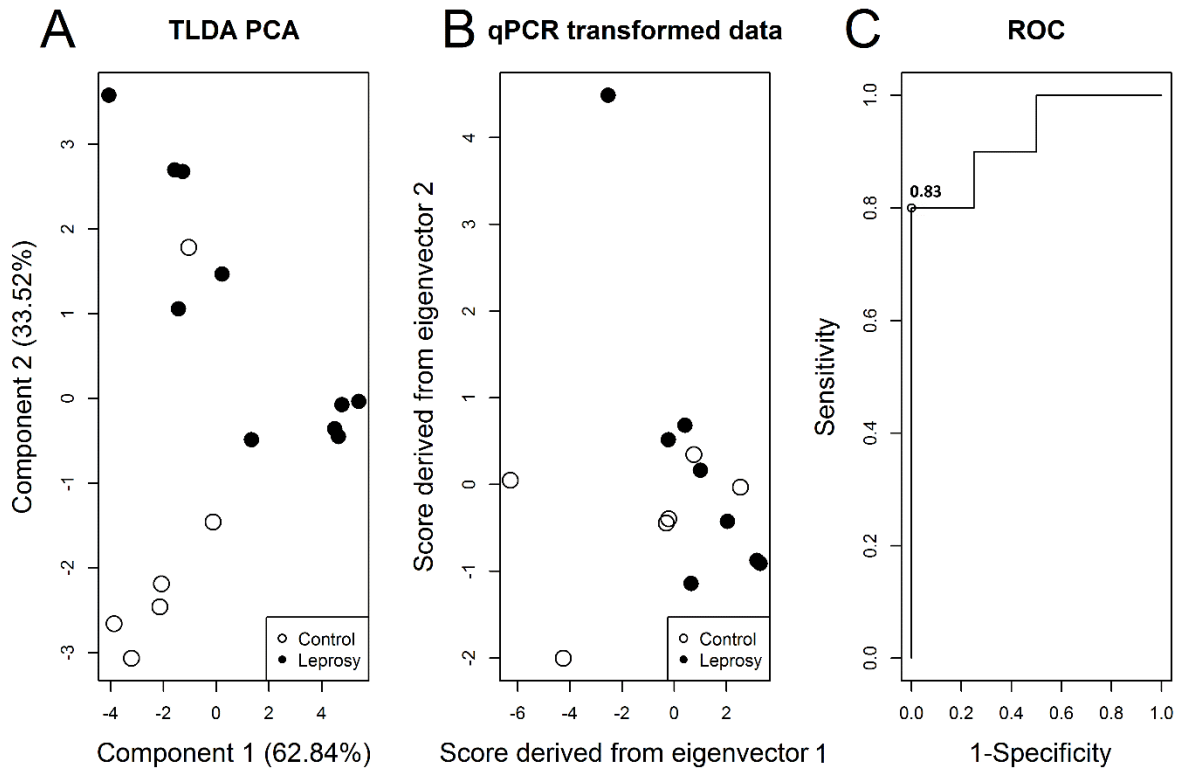
Figure SF1. Diagnostic power evaluation of miRNAs for discrimination between leprosy patients and healthy controls using sixteen miRNAs.

Principal components scores of TLDA expression data of miR-539, miR-125b, miR-196b, miR-26a, miR-27a, miR-27b, miR-92a, miR-99a, miR-101, miR-29c, miR-34c, miR-425-5p, and miR-660 indicate separation between leprosy group and healthy control group (A). Normalized eigenvectors were used to transform qRT-PCR data revealing a separation between the groups and high correlation of the data (B). The first qRT-PCR transformed score was evaluated in a ROC analyses after a logistic regression revealing 70% sensitivity and 100% specificity with the cutoff of 0.83 and AUC 92.5% (95% CI: 78.4%-100.0%) for discrimination of leprosy patients and healthy control (C).
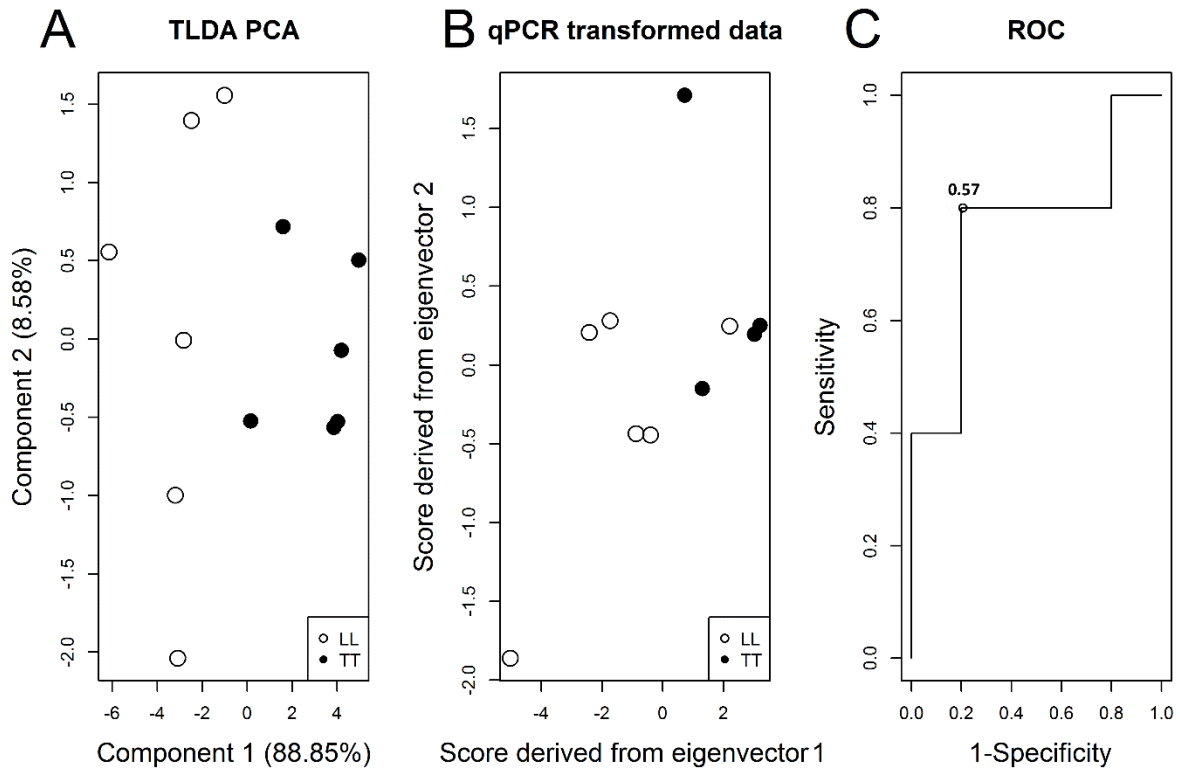
Figure SF2. Diagnostic power evaluation of miRNAs for discrimination between LL and TT patients using sixteen miRNAs.

Principal components scores of TLDA expression data of miR-539, miR-125b, miR-196b, miR-26a, miR-27a, miR-27b, miR-92a, miR-99a, miR-101, miR-29c, miR-34c, miR-425-5p, and miR-660 indicates separation between LL and TT groups (A). Normalized eigenvectors were used to transform qRT-PCR data revealing a separation between the groups (B). The first qRT-PCR transformed score was evaluated in a ROC analyses after a logistic regression revealing 80% sensitivity and 80% specificity with the cutoff of 0.57 and AUC 76% (95% CI: 41.4%-100.0%) for discrimination of LL and TT patients (C).