| Supplementary Table 1: MassARRAY primer sequences	
Name	Sequence (5'-3')
FCCG3A-1F	GGATATGTAATTTATAGGAGTTATTG
FCCG3A-1R	TTCTAATAAAAAACCCTAAAACCCC
FCCG3B-1F	GGATATGTAATTTATAGGAGTTGAT
FCCG3B-1R	CCCTAAAACCCTAAAACCCTAAA
FCGR3A-3F	AGTTTTATTTTGGTTTGTTTTAGGAG
FCGR3A-3R	CCAAACTCTTTCCTTCCTAATC
FCGR3B-3F	TTTAGTTTTATTTTGGTTTGTTTTGGT
FCGR3B-3R	CTCCAAACTCTTTCCTTCCTAT
FCGR3A-4F	GGGGTTTTAGGGTTTTTTATTAG
FCGR3A-4R	TAAAATAACTACCTAAATTCATTTCC
FCGR3B-4F	TAGGGTTTTAGGGTTTTTTATTAGAA
FCGR3B-4R	ACCTAAATTCATTTCTATTATCCAATC
FCGR3A-5F	TATATTAAAAAGTTAGTAGTTTTTGTGG
FCGR3A-5R	TACCAAAATATACCCTCAACCA
FCGR3B-5F	TATATTAAAAAGTTAGTTTTTGTGGATTA
FCGR3B-5R	CTACCAAAATATACCCTCAACTT
FCGR3A-6F	TGGGGTAAGTATTTTGGGATG
FCGR3A-6R	CTTCTCCCTCAACCAAAAAAAC
FCGR3B-6F	TGGGGGTAAGTATTTTGGGAAA
FCGR3B-6R	ACTTCTCCCTCAACCAAAAAAAT

Supplementary Figure 1

A — Adult axillary lymph node (Lin-)
B — Adult peripheral blood (Lin-)
C — Adult axillary lymph node (Lin-CD56+)
D — Adult peripheral blood (Lin-CD56+)
E — Adult peripheral blood (Lin-)
F
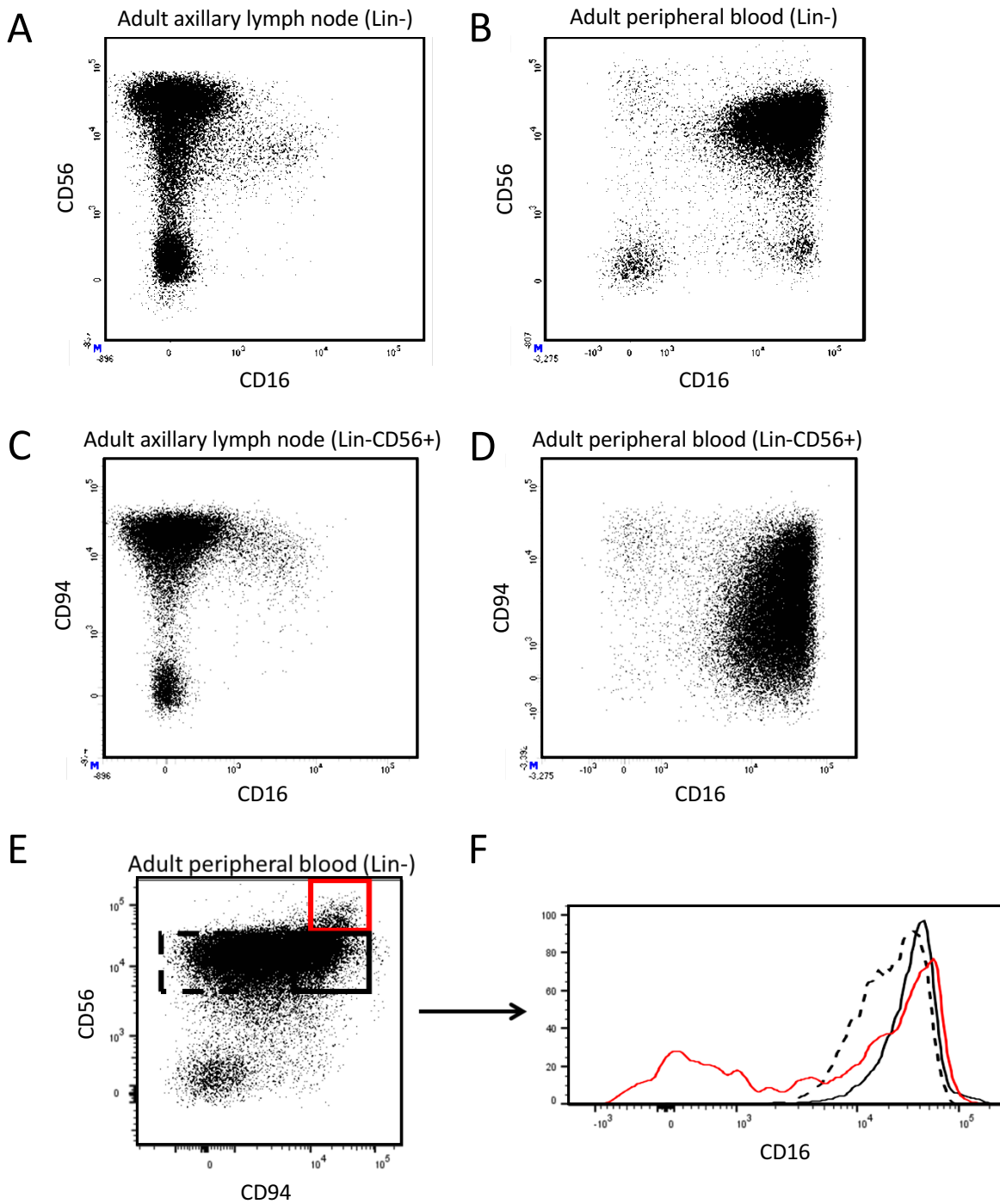
Supplementary Figure 1: The CD94high/CD56bright NK population corresponds to a CD16low NK population. Mononuclear cells (MNCs) from adult axillary lymph node (A and C) and adult peripheral blood (B, D, E, and F) from representative donors were analyzed by flow cytometry by gating on Lin- cells and then NK cell markers. Both axillary and peripheral blood NK cell CD16 expression was described in the context of NK markers CD56 (A and B) and CD94 (C and D). CD16 expression was also described in populations using both CD56 and CD94 (E and F).

Supplementary Figure 2

A
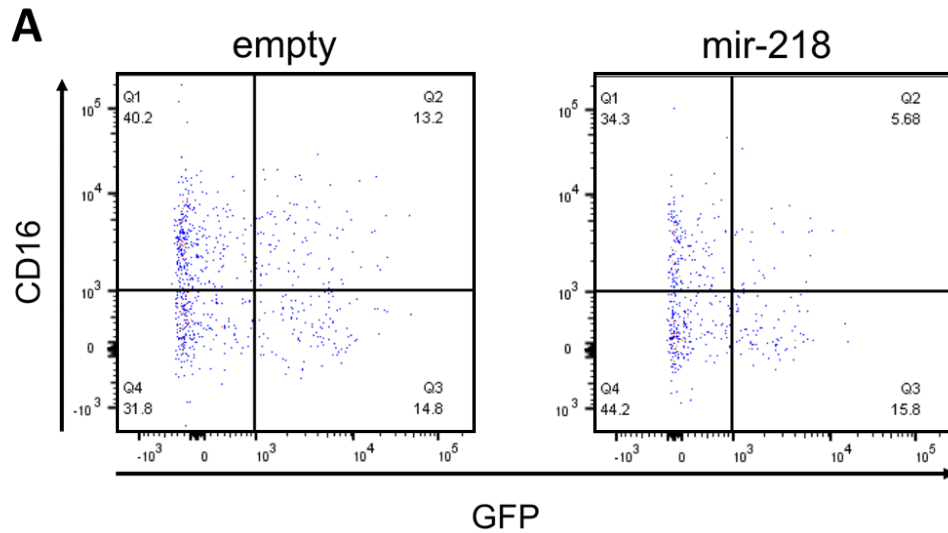
B

		empty	**mir-218**
Total cells	**%GFP+**	58.0±23.9	13.8±9.2
GFP+ cells	**%CD16+**	35.2±19.8	16.1±9.4
	%CD16-	64.8±19.8	83.9±9.4
CD16- cells	**%GFP+**	63.9±24.8	16.5±8.5

Supplementary Figure 2: Transduction of primary NK cells. Primary human NK cells were enriched from peripheral blood by negative selection. NK cells were transduced with lentivirus for either mir-218 or empty vector. (A) Cells were analyzed 2 days after infection by flow cytometry. Live cells were gated, followed by doublet discrimination and a lymphocyte gate. The population was further gated on CD3-CD56+ cells. The cut off for the GFP gate was determined by mock infection. One of six donors is shown. (B) Summary of data from six donors shown as average ± standard deviation.