

1 **Supplementary data**

2 Suppl. Figure 1: Phoenix transfection and virus titration

3 (A) EGFP expression of uninfected (left) and MSNAIE transfected Phoenix cells (right). (B)  
4 EGFP expression of NIH/3T3 cells retrovirally infected with MSNAIE construct in different  
5 dilutions to determine virus titer. (C) EGFP and RFP expression of bone marrow cells  
6 retrovirally infected with MSNAIE vector (right) and uninfected control cells (left).

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8 Suppl. Figure 2: Primary MSNAIE transplantation

9 (A) Scheme of primary transplantation with MSNAIE infected BM. (B) EGFP expression of  
10 lymphatic organs and bone marrow of transplanted mice. (C) Flow cytometric dot plots of  
11 EGFP positive cells of spleen (Spl), lymph node (LN) and bone marrow (BM) cells of one  
12 representative MSNAIE transplanted mouse stained with anti-B220, anti-GR1, anti-CD11b  
13 and anti-Thy1.2. (D) Flow cytometric dot plots of EGFP positive cells of spleen (Spl), lymph  
14 node (LN) and bone marrow (BM) cells of one representative MSNAIE transplanted mouse  
15 stained with anti-CD4 and anti-CD8.

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17 Suppl. Figure 3: Primary MSNAIE transplantation and microarray analysis

18 (A) Flow cytometric histograms and dot blots showing ALK and Ki67 expression as well as  
19 CD4 and CD8 T cell sub-populations of lymphoma cells. (B) Gene expression levels of  
20 indicated genes comparing NPM-ALK+ (ALCL-like) and EL4 murine T cell lymphoma cells as  
21 well as Notch1-driven T cell lymphoma/leukemia cells (Tx17; Shoumariyeh et al.,  
22 unpublished data). Values represent duplicates. FDR adjusted \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ .

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24 Suppl. Figure 4: Immunophenotyping of CD4<sup>+</sup>/CD8<sup>-</sup> serial transplanted mice

25 (A) EGFP expression of lymphatic organs and bone marrow of CD4<sup>+</sup>/CD8<sup>-</sup> transplanted mice.

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27 Suppl. Figure 5: Immunophenotyping strategy of CD4<sup>+</sup>/CD8<sup>-</sup> serial transplanted mice

28 (A) Flow cytometric histograms showing isotype controls for immunophenotyping.

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30 Suppl. Figure 6: Microarray analysis of DN lymphoma sub-populations

31 (A) Venn diagram showing similar regulated genes comparing DN1 to DN4 lymphoma sub-  
32 population analysed by microarray with a qvalue cutoff <0.01. (B) Principle component  
33 analysis (PCA) separating lymphoma sub-populations DN1 to DN4 according to their  
34 variance of all genes analysed my microarray.

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36 Suppl. Figure 7: Immunophenotypic analysis of CD30 expression

37 (A) CD30 expression of different EGFP+ T cell sub-populations of thymus of MSNAIE Lck-  
38 Cre transgenic BM transplanted mice. n=2. (B) CD30 expression of different EGFP+ T cell  
39 sub-populations of lymph node of MSNAIE Lck-Cre transgenic BM transplanted mice. n=4.  
40 (C) CD30 expression of different EGFP+ T cell sub-populations of spleen of MSNAIE Lck-  
41 Cre transgenic BM transplanted mice. n=8.

42 \*p<0.05; \*\*\*p<0.001; \*\*\*\*p<0.0001. Data are represented as mean +SD.