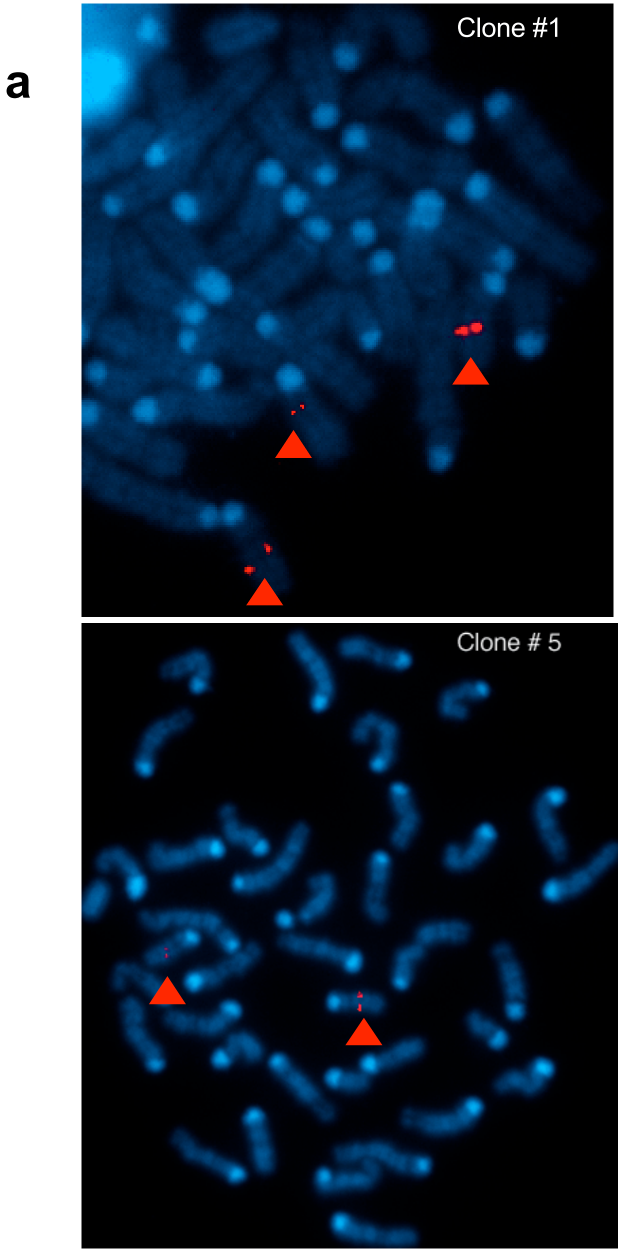

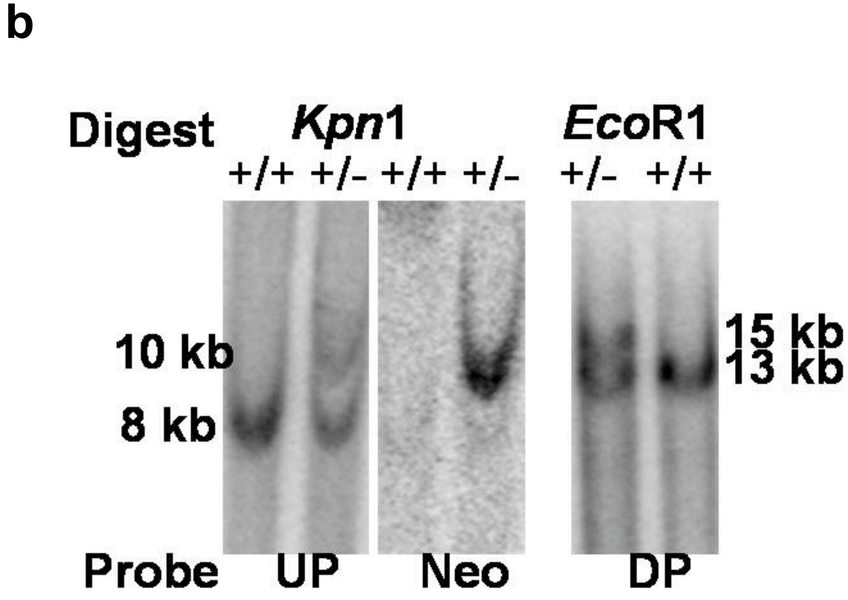

Supplemental Figure 1: Construction of the TLT-1$^{-/-}$ null mouse - (a) Fluorescent *in situ* hybridization of ES cell clones using the whole BAC as a probe. Arrows are just below the chromosomes that demonstrated probe hybridization. Clone 1 (top) demonstrated three regions of hybridization and clone 5 (bottom) demonstrated only two. Clone 5 was ultimately chosen for further studies. (b) Southern analysis of *Kpn*1 and *Eco*R1 digested genomic DNA from a representative ES cell clone. The Kpn1 digest is probed with the upstream probe (UP) and the neo-cassette and the EcoR1 digest is probed with the downstream probe (DP).

Supplementary Table 1: Characteristics of the Initial Study Population

Parameter	Value
Age	49.5 ± 14.6
Sex, Male (%)	77%
SOFA Score	2.6 ± 1.9
APACHE II Score	10.5 ± 4.7
Length of Hospital Stay (Days)	14.5 ± 10.7
Length of Stay in ICU (days)	1.5 ± 3.2
Death	0.1 ± 0.3
Temperature	37.6 ± 1.0
PaO_2:FiO_2	315.5 ± 69.3
WBC	20.1 ± 11.7
Platelets x1000/ml	299.6 ± 142.4
sTLT-1 μg/ml	328.8 ± 76.06

Patients with sepsis have increased levels of soluble TLT-1. Values are means ±SD, PaO_2:FO_2 denotes the ratio of the partial pressure of arterial oxygen to the fraction of inspired oxygen , sTLT-1 – soluble Trem-like transcript-1. The Sepsis-related Organ Failure Assessment (SOFA) score can range from 0-24, with higher scores indicating more abnormal organ function. The Acute Physiology and Chronic Evaluation II (APACHE II) score can range from 0- 71 with the higher scores indicating more abnormal organ function.

Supplemental Table 2: Clinical and Biological Parameters at Admission from a Longitudinal Study of sTLT-1 in Sepsis.

Parameter	Overall (n=46)	Survivors (n=24)	Non Survivors (n=22)	P value
Age, mean (SD) yrs	62 (17)	59 (20)	65 (12)	0.15
Sex, male (%)	66	71	64	0.41
SAPSII, mean (SD)	65 (19)	65 (22)	66 (18)	0.93
SOFA score, median (IQR)	13 (12-15)	13 (12-15)	13 (11-16)	0.55
Corticosteroids (%)	74	75	73	0.47
rhaPC (%)	15	20	9	0.12
Bacteremia (%)	26	29	23	0.55
Lactate, median (IQR) mmol/L	3.1 (1.8-4.6)	2.8 (1.7-4.2)	3.6 (2.1-4.9)	0.22
Procalcitonin, median (IQR) ng/mL	12.4 (3.5-40.2)	12.8 (3.8-111.6)	12.6 (3.4-38.4)	0.50
C-Reactive Protein, median (IQR) mg/L	164 (87-251)	144 (65-222)	158 (115-274)	0.32
sTLT-1, median (IQR) µg/mL	36.6 (16.5-79.8)	36.1 (19.8-69.7)	37.1 (11.3-104.3)	0.83

Supplemental Table 3 : Microorganism distribution in the Longitudinal Study of sTLT-1 in Sepsis.*

Microorganism	Overall (n=46)	Survivors (n=24)	Non Survivors (n=22)	P value
Bacilli, n (%)				
Escherichia coli	8 (17)	5 (21)	3 (14)	0.18
Haemophilus species	3 (6)	2 (8)	1 (5)	0.29
Pseudomonas aeriginosa	1 (2)		1 (5)	0.12
Cocci, n (%)				
Streptococcus species	15 (33)	8 (33)	7 (32)	0.85
Staphylococcus species	3 (6)	2 (8)	1 (5)	0.29
Enterococcus species	2 (4)	1 (4)	1 (5)	0.62
Unknown	14 (30)	6 (25)	8 (36)	0.16

* Due to rounding, percentages do not add up to 100.