

Supplemental Figure Legends

Supplemental Figure 1. Survival curve demonstrating that co-culture on VeraVec results in more aggressive leukemic cells. 50,000 leukemic cells cultured without feeder layers in 10% serum and co-cultured with VeraVec in serum free + 50 ng/mL of sKitL were injected into sublethally irradiated mice (650 Rads) and after 20 days, all mice transplanted with leukemic cells co-cultured on VeraVec were moribund and sacrificed. The bone marrow (BM) and spleen were collected and analyzed by flow cytometry (n=10 per cohort, 2 independent experiments from 2 different clones used for Figure 1). The remaining mice that were either transplanted or not transplanted with leukemic cells cultured in 10% serum were allowed to survive to generate the survival curve. Significance of Survival Curve was determined by Log Rank Test (*P<0.05. **P<0.001).

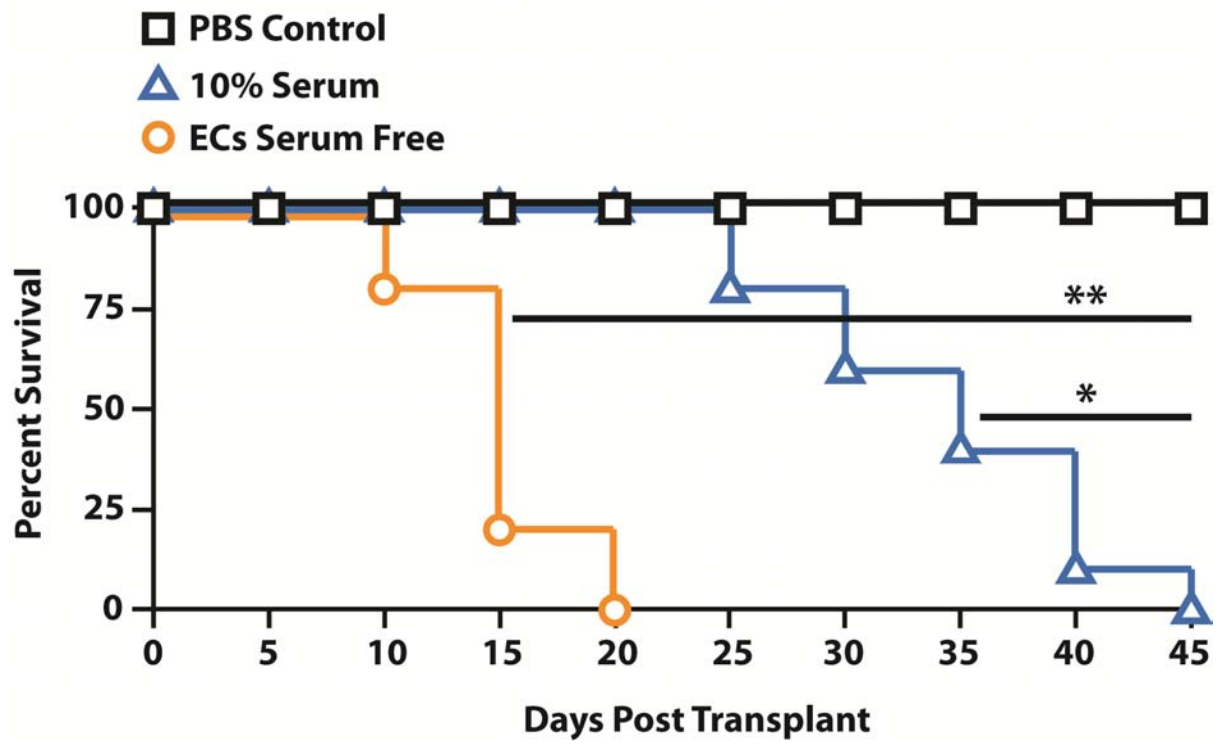
Supplemental Figure 2. VEGF-A does not directly affect the expansion of MLL-AF9 LICs. MLL-AF9 GFP⁺ clones were cultured in 10% serum supplemented with either 50 ng/mL sKitL or with 50 ng/mL sKitL plus 20 ng/mL VEGF-A for 14 days (all culture conditions were without the support of VeraVec). The addition of VEGF-A to LICs did not increase the cumulative expansion of LICs generated from any clones.

Supplemental Figure 3. Schematic for *in vivo* experiments. A) On day 0, animals were sublethally irradiated (650 Rads) and were transplanted with 5×10^5 GFP⁺ AML cells that were cultured in 10% serum supplemented with 50 ng/mL sKitL for 7 days. On day 15 post transplant, 5 mice from each cohort were sacrificed and the BM and spleen were analyzed for GFP⁺ AML leukemia. The remaining 15 mice were allowed to live to

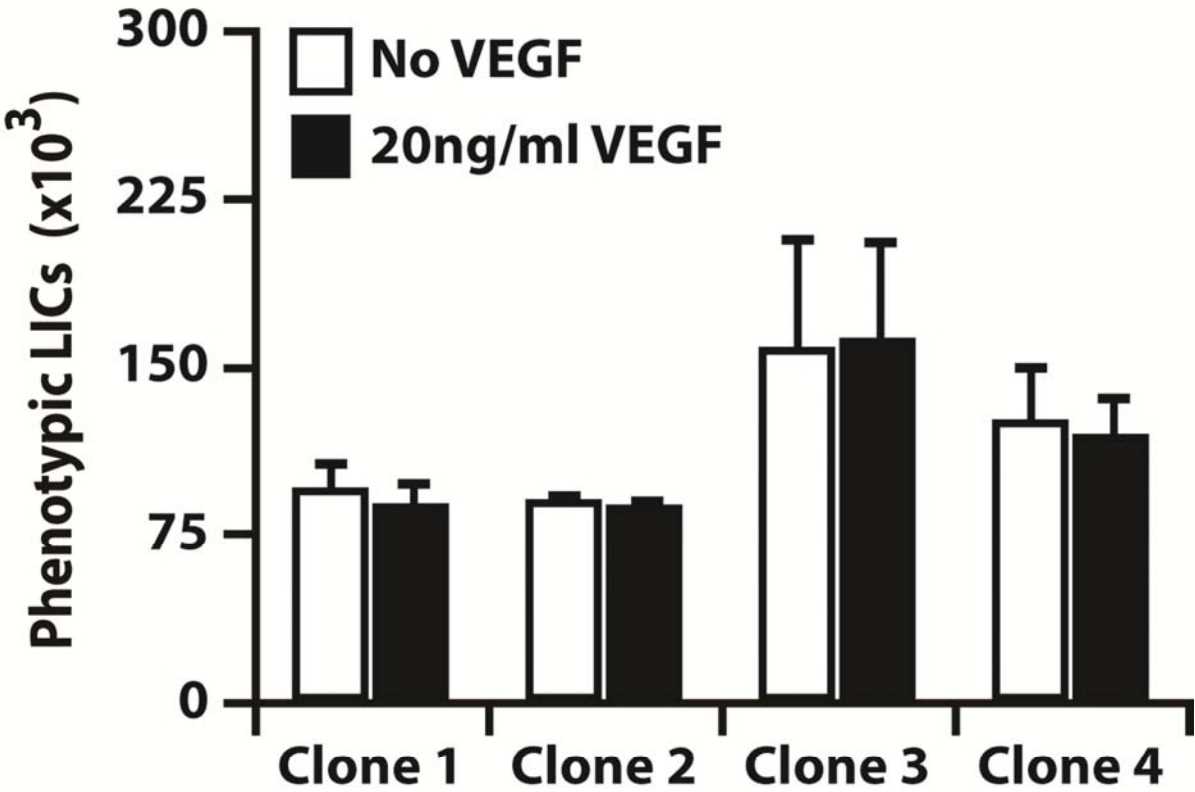
generate survival curves. Three individual MLL-AF9 clones were used in 3 independent experiments. B) VEGF-A, α VEGFR2, and Ara-C dosing schedule.

Supplemental Figure 4. MLL-AF9 LICs do not express VEGF receptors. Lineage⁻ cKit⁺CD16/32⁺CD34⁺ GMPs were isolated from mice and MLL-AF9 GFP⁺ transduced GMPs were generated (5 clones). MLL-AF9 GFP⁺ cell lines were transplanted into sublethally irradiated mice (650 Rads; 1 cell line/5 mice). **A-B)** Mice were allowed to generate GFP⁺ leukemia as demarcated by peripheral blood analysis (60-80% GFP⁺). Bone marrow was isolated and underwent flow cytometric analysis. Lineage⁻ CD16/32⁺CD34⁺ cells were divided into cKit⁺ and cKit⁺GFP⁺ groups and were analyzed for expression of VEGFR1 and VEGFR2 and each receptor from each fraction was compared to IgG controls. **A)** The cKit⁺GFP⁻ fraction did not express VEGFR2, but did express high levels of VEGFR1 when compared with cKit⁻GFP⁻. **B)** The cKit⁺GFP⁺ fraction did not express either VEGFR1 or VEGFR2. **C)** Representative histograms and dot plots. All data represents mean \pm s.d. (***)P<0.0001, n.s.=not significant).

Supplemental Figure 1



Supplemental Figure 2



14 day cumulative expansion
(10% serum + 50ng/ml kitL)

Supplemental Figure 3

A

Day 0 (n=20/cohort)

3 independent experiments

1. Sublethally Irradiate (650 Rads)
2. Transplant 50,000 GFP+AML cells

Day 15 (n=5/cohort)

1. Sacrifice mice to analyze BM and Spleen for % of GFP+ AML cells
2. Harvest organs for IF and flow cytometry

Survival (n=15/cohort)

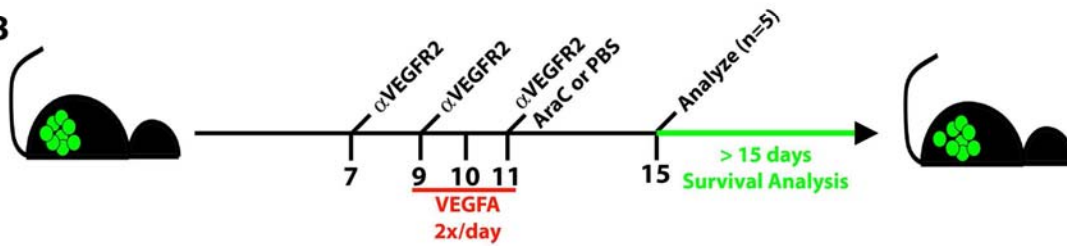
1. Analyze survival of each cohort to generate a survival curve.



6 cohorts:

1. PBS (Day 11)
2. 125mg/kg AraC (Day 11)
3. 25ng VEGFA 2x/day (Days 9,10,11)
4. 800ug α -VEGFR2 (Days 7, 9, 11)
5. AraC + VEGF
6. AraC + α VEGFR2

B



Supplemental Figure 4

