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Supplemental Information

Mouse Genetic Analysis of Bone Marrow Stem Cell Niches: Technological Pitfalls, Challenges, and Translational Considerations

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Table S1. Developmental Stage-Related Marker Gene Expression in Bone Marrow Stem Cell Lineages: Conditions and Constrains in Murine Models

Stages	Mouse strains/cells	Major findings & descriptions	CFU -F	Authors' comments	References
E8.5-, E10.5-, E18.5	<i>Nes-CreER^{T2}</i> : RCE-loxP	Tamoxifen induction at E8.5 & E10.5, chase to E18.5: <i>Nes-Cre⁺</i> cells, not found in proliferating and hypertrophic chondrocytes, infiltrate over osteochondral junction and into the trabecular bone.	0.8%	BM <i>Nes-Cre⁺</i> cells do not contribute to fetal endochondrogenesis.	(Isern et al., 2014)
E9.5	<i>Sox10-CreER^{T2}</i>	Among 18% of <i>Sox10-Cre⁺</i> cells, 72% of them were <i>Nes-GFP⁺/PDGFRα⁺</i> cells.	NA	Evidence of <i>Nes-GFP⁺</i> cells' neural crest association	(Isern et al., 2014)
E10.5	<i>Nes-GFP⁺/CD31⁺</i> cells	Represent 8% of endothelial cells at limb buds	NA	Appeared at the endochondral condensation stage	(Ono et al., 2014)
E11.5	<i>Nes-GFP⁺/CD31⁺</i> cells	Observed at the perichondrium	NA	<i>Nes-GFP⁺</i> cells are rarely found within the mesenchymal condensation region.	(Ono et al., 2014)
E11.5-P0, P21	<i>Nes-CreER^{T2}</i> : Rosa26 tomato	Tamoxifen induction (from E11.5) before the formation the POC and chase to P0 and P21: only few <i>Nes-Cre⁺</i> cells found in bone at P0 and P21	NA	After the POC, <i>Nes-Cre⁺</i> cells do not commit to neonatal and postnatal bone development.	(Ono et al., 2014)
E12.5	<i>Nes-GFP⁺/CD31⁻</i> cells	1 st appearance at the perichondrium	NA	None	(Ono et al., 2014)
E13.5	<i>Nes-GFP⁺/CD31^{+/-}</i> cells	<ul style="list-style-type: none"> ▶ Overlap with <i>Col2⁺</i> cells at the perichondrium ▶ Some <i>Nes-GFP⁺</i> cells are likely derived from collagen II-expressing (chondrogenic) cells. ▶ Perichondral <i>Nes-GFP⁺CD31^{+/-}</i> cells are regulated by both <i>lhh</i> and <i>Runx2</i>. 	NA	<i>Nes-GFP⁺/CD31⁻</i> non-endothelial cells become osteoprogenitor cells upon <i>lhh</i> and <i>Runx2</i> induction.	(Ono et al., 2014)
E13.5	<i>Nes-CreER^{T2}</i> : RCE-loxP	Similar to <i>Nes-GFP⁺</i> cells: detected near the chondral-perichondral interface and the osteo-chondral junction	NA	Consistent with the dynamic nature of <i>Nes-GFP⁺</i> cells	(Isern et al., 2014)
E13.5-P0, P21	<i>Nes-CreER^{T2}</i> : Rosa26 tomato	Tamoxifen induction and chase from E13.5: only few <i>Nes-Cre⁺</i> cells found in bone at P0 and P21	NA	After the POC, <i>Nes-Cre⁺</i> cells do not commit to neonatal and postnatal bone development.	(Ono et al., 2014)
E14.5	<i>Nes-GFP⁺/CD31^{+/-}</i> cells	Both types of <i>Nes⁺</i> cells occupied at the inner perichondrium, with <i>Nes-GFP⁺/CD31⁻</i> cells aligned on the innermost portion.	NA	None	(Ono et al., 2014)
E15.5	<i>Nes-GFP⁺/CD31^{+/-}</i> cells	<ul style="list-style-type: none"> ▶ Infiltrate into the cartilage template along vascular invasion ▶ Increase in <i>Nes-GFP⁺/CD31^{+/-}</i> cell numbers ▶ <i>Nes-GFP⁺CD31^{+/-}</i> closely associated at the POC 	NA	<i>Nes-GFP⁺/CD31⁺</i> cells show (at least 3-fold) stronger GFP signals than <i>Nes-GFP⁺/CD31⁻</i> cells at E15.5, suggesting that <i>Nes-GFP</i> transcription is positively regulated by endothelial cell signaling.	(Ono et al., 2014)
E15.5	<i>Lepr-Cre</i>	Absence of <i>Lepr-Cre⁺</i> cells at the POC at this stage		<i>Nes-GFP⁺</i> and <i>Osx-Cre⁺</i> emerged in the POC	(Mizoguchi et al., 2014)
E15.5	<i>Nes-creER^{T2}</i> : iDTR mice	Deletion of <i>Nes-Cre⁺</i> cells in this double transgenic mice resulted in 4-fold decrease in HSC activity in fetal BM within 48 hours, concomitantly with 8-fold increase in HSCs in fetal liver	NA	These data suggest that <i>Nes-GFP</i> transcriptome positively regulates the migration of HSC niches from the embryonic liver to the BM.	(Isern et al., 2014)
E16.5-P7, P21	<i>Nes-CreER^{T2}</i> : Rosa26 tomato	Tamoxifen induction at E16.5, the time that the marrow space starts to form, and chase to P7 and P21: see larger numbers of <i>Nes-Cre⁺</i> in bone	0.3%	<i>Nes-CreER</i> transcription is repressed before the formation of POC, but derepressed after the formation of the POC and marrow cavity.	(Ono et al., 2014)
E17.5	<i>Lepr-Cre⁺</i> cells	<ul style="list-style-type: none"> ▶ 1st appearance of <i>Lepr-Cre⁺</i> cells ▶ Found in the primary spongiosa and the periosteum 	NA	<i>Lepr-Cre⁺</i> cells in the periosteum might be originated from <i>Nes-GFP⁺/CD31^{+/-}</i> cells as described by Ono et al. 2014.	(Mizoguchi et al., 2014)
E17.5	<i>Nes-GFP⁺</i> cells	Display 3-fold lower CFU-Fs than <i>Nes-GFP⁻</i> cells, but higher capacity to form "mesospheres"	0.1%	Higher SCC potential in <i>Nes-GFP⁺</i> cells than <i>Nes-GFP⁻</i> cells	(Isern et al., 2014)

E17.5	<i>Nes</i> -GFP ⁺ cells	Not associated with <i>Col2.3</i> -Cre ⁺ cells and chondrocytes	0.1%	Distinction from osteoblastic cells	(Isern et al., 2014)
E18.5	<i>Nes</i> -GFP ⁺ cells	Frequently associated with arterioles and nascent CD31 ⁺ endothelial cells within the osteochondral junction; but not with osterix (by antibody staining);	0.8%	<ul style="list-style-type: none"> ▶ Express endogenous <i>Nes</i> mRNAs at this stage ▶ CFU-F frequency 6-fold lower than <i>Nes</i>-GFP⁺ cells 	(Isern et al., 2014)
E18.5-P1, Peri-natal	<i>Nes</i> -GFP ⁺ cells	<ul style="list-style-type: none"> ▶ <i>Nes</i>-GFP⁺ cells, likely derived from neural crest ▶ Secrete the HSC niche factor <i>Cxcl12</i> ▶ Distinguished from mesoderm derived “MSCs” ▶ Do not generate fetal chondrocytes 	0.2%	<ul style="list-style-type: none"> ▶ Perinatal stages: from E18.5 to postnatal day 1 (www.jax.org) ▶ “MSCs” are an incorrect terminology that depicts BM SSCs. 	(Isern et al., 2014)
E19.5	<i>Lepr</i> -Cre: dTomato; <i>Col2.3</i> -GFP	<i>Lepr</i> -Cre ⁺ cells were rare and had no contribution to bone development at this stage.	NA	Used for explicitly identifying osteoblastic bone-lining cells	(Zhou et al., 2014)
P0	<i>Nes</i> -GFP ⁺ cells	Belong to BM CD45 ⁻ /CD31 ⁻ /Ter119 ⁻ stromal cells	0.2%	P0, neonatal stage	(Isern et al., 2014)
P0	<i>Nes</i> -GFP ⁺ /PDGFR α ⁻ cells	<ul style="list-style-type: none"> ▶ <i>Nes</i>-GFP⁺ cells are close to HSCs (within 20 μm) in the neonatal BM. ▶ Express mRNAs (e.g., <i>Sox10</i>, <i>Plp1</i>, <i>ErbB3</i>, and <i>Dhh</i>), typically presented in Schwann cell precursors ▶ No <i>Gfap</i> found in mature Schwann cells 	0.2%	<ul style="list-style-type: none"> ▶ Give rise to distinct HSC niche-forming stromal cells <i>in vivo</i> ▶ Have a high glial differentiation propensity <i>in vitro</i> 	(Isern et al., 2014)
P0	<i>Nes</i> -GFP ⁺ /PDGFR α ⁻ cells	<ul style="list-style-type: none"> ▶ Enriched mRNA transcripts associated with HSC niche maintenance genes (e.g. <i>Cxcl12</i>, <i>KitL</i>, <i>Angpt1</i>, and <i>Lepr</i>), may have a role in HSC maintenance ▶ Have an <i>in vitro</i> mesodermal (adipocyte) differentiation propensity 	0.2%	<ul style="list-style-type: none"> ▶ <i>Nes</i>-GFP⁺ cells show physical proximity to the HSC niche. ▶ Osteoblastic differentiation genes were selectively inhibited during enforced HSC mobilization or <i>Adrb3</i> activation (Mendez-Ferrer et al. 2010). 	(Isern et al., 2014)
P0.5	<i>Lepr</i> -Cre: dTomato; <i>Col2.3</i> -GFP	<ul style="list-style-type: none"> ▶ A drastic increase in the number of <i>Lepr</i>-Cre⁺ cells in metaphysis ▶ The emergence of few <i>Lepr</i>-Cre⁺/<i>Col2.3</i>-GFP⁺ osteoblasts in trabecular bone 	NA	This probably is the earliest osteogenic contribution made by <i>Lepr</i> -Cre ⁺ cells, highlighting the 1 st plausible postnatal SSC niche at the metaphyseal and trabecular regions.	(Zhou et al., 2014)
P0-P7	<i>Nes</i> -CreER ^{T2}	Tamoxifen induction at P0 and chase to P7: highly colocalized with BM <i>Nes</i> -GFP ⁺ cells	0.3%	Two transcriptional mechanisms for <i>Nes</i> -GFP are consistent at this stage, suggesting the two reporter systems might share an enhancer complex at the intron 2 of the <i>Nes</i> gene.	(Isern et al., 2014)
P0-P14	<i>Nes</i> -GFP: <i>Nes</i> -CreER ^{T2}	Tamoxifen induction at the neonatal stage (P0): <i>Nes</i> -GFP ⁺ cells overlap with <i>Nes</i> -CreER ^{T2} ⁺ cells.	0.3%	It appears that <i>Nes</i> -Cre ⁺ cells partially overlay with <i>Nes</i> -GFP ⁺ cells at BM blood vessels, but not in <i>Nes</i> -GFP ⁺ perivascular pericytes.	(Isern et al., 2014)
P3	<i>Nes</i> -GFP ⁺ cells	CFU-F activity much lower than <i>Nes</i> -GFP ⁺ cells	0.3%	None	(Isern et al., 2014)
P3	<i>Nes</i> -GFP: <i>Tie2</i> -Cre	94% <i>Nes</i> -GFP ⁺ / <i>Tie2</i> -Cre ⁺ /CD45 ⁻ cells	NA	<i>Nes</i> -GFP ⁺ cells have a role in specifying endothelial cells.	(Ono et al., 2014)
P3-P5	<i>Nes</i> -GFP: <i>Nes</i> -CreER ^{T2}	<p>Tamoxifen induction at P3 and chase to P5:</p> <ul style="list-style-type: none"> ▶ Almost 100% <i>Nes</i>-GFP⁺/<i>Nes</i>-Cre⁺ cells ▶ 81% <i>Nes</i>-Cre⁺/CD31⁺ cells at the primary spongiosa and BM ▶ 34% <i>Nes</i>-GFP⁺/CD31⁺ endothelial cells ▶ <i>Nes</i>-GFP⁺/<i>Nes</i>-CreER⁺ cells also express endogeneous <i>Nes</i> mRNAs and the nestin protein (detected by flow cytometry using ab6142). ▶ <i>Nes</i> mRNA (by quantitative PCR) increased by 82-, 263-, and 414-fold in <i>Nes</i>-GFP⁺/<i>Nes</i>-Cre⁻CD31⁻, <i>Nes</i>-GFP⁺/<i>Nes</i>-Cre⁺CD31⁺, and <i>Nes</i>- 	NA	<ul style="list-style-type: none"> ▶ <i>Nes</i>-Cre is inducible at 48 hours after tamoxifen administration ▶ Both <i>Nes</i>-GFP⁺ and <i>Nes</i>-Cre⁺ cells likely share a transcriptional mechanism at this stage. ▶ <i>Nes</i>-Cre transcriptional activity is dominant over <i>Nes</i>-GFP in CD31⁺ endothelial cells. ▶ Additional transcriptional activators from endothelial cells are needed to drive endogenous <i>Nes</i> mRNA expression to a high level. 	(Ono et al., 2014)

		GFP ⁺ / <i>Nes</i> -Cre ⁺ , respectively, relative to <i>Nes</i> -GFP negative control			
P3-P5, P10, P17, P24, 4w	<i>Nes</i> -creER ^{T2} : Rosa26 tomato: Col1(2.3kb)-GFP	Tamoxifen induction at P3 and chase up to 1 month (4 weeks or 4w): ▶ 10% <i>Nes</i> -Cre ⁺ osteoblasts expressing Col1 at P5 ▶ <i>Nes</i> -Cre ⁺ cells increased up to 26% and 23% at P10 and P17 respectively ▶ <i>Nes</i> -Cre ⁺ decreased to 5% and 3% at P24 and 4w respectively	NA	<i>Nes</i> -Cre ⁺ cells have limited contribution to osteoblasts at the postnatal stage (within one month).	(Ono et al., 2014)
P3-P10	<i>Nes</i> -GFP: <i>Osx</i> -CreER	Tamoxifen induction at P3 and chase to P10: 96% of cells targeted by <i>Osx</i> -CreER were positive for <i>Nes</i> -GFP (i.e. <i>Nes</i> -GFP ⁺ / <i>Osx</i> -CreER ⁺).	NA	<i>Nes</i> -GFP ⁺ cells might have a major role in specifying osteoblasts at this stage.	(Ono et al., 2014)
P3-P10	<i>Nes</i> -GFP: Col1(3.2kb)-CreER	Tamoxifen induction at P3 and chase to P10: 92% <i>Nes</i> -GFP ⁺ /Col1(3.2kb)-CreER ⁺	NA	The same comment as above	(Ono et al., 2014)
P3-P10	<i>Nes</i> -GFP: <i>Ocn</i> -CreER	Tamoxifen induction at P3 and chase to P10: 93% <i>Nes</i> -GFP ⁺ / <i>Ocn</i> -Cre ⁺	NA	The same comment as above	(Ono et al., 2014)
P3-24w	<i>Nes</i> -CreER ^{T2} : Rosa26 tomato	Tamoxifen induction at P3 and chase 6 months (24 weeks or 24w): ▶ <i>Nes</i> -Cre ⁺ cells distributed from the BM to the growth plate; 84% <i>Nes</i> -CreER ⁺ /CD31 ⁺ cells; ▶ <i>Nes</i> -Cre ⁺ descendant cells form reticular sinusoidal endothelial cells for at least 24 weeks. ▶ <i>Nes</i> -Cre ⁺ cells generate few osteoblasts, osteocytes, and chondrocytes; but no adipocytes	NA	In adult BM, <i>Nes</i> -Cre ⁺ cells mainly contribute to sinusoidal endothelial cells.	(Ono et al., 2014)
P5-P6	<i>Nes</i> -GFP: iOsx/Tomato	Tamoxifen induction at P5 and chase to P6: ~38% of iOsx ⁺ cells were <i>Nes</i> -GFP ⁺ in bone tissues.	NA	P5-iOsx ⁺ BM cells exhibit a trilineage differentiation potential.	(Mizoguchi et al., 2014)
P5-4w	iOsx/Tomato	Tamoxifen induction at P5: increased CFU-F frequency of sorted iOsx/Tomato ⁺ cells in the BM stroma harvested at 4 weeks after tamoxifen injection	0.5% at 4w	None	(Mizoguchi et al., 2014)
P5-15w	<i>Nes</i> -GFP: iOsx/Tomato;	Tamoxifen induction at P5 and chase to 15w in CD45 ⁺ /Ter119 ⁺ /CD31 ⁺ /iOsx ⁺ BM stromal cells: 78% <i>Nes</i> -GFP ⁺ /Lepr ⁺ (using anti-Lepr), in which 89% of cells were PDGFR α ⁺ and 83% of cells PDGFR β ⁺	NA	▶ Regulation of <i>Nes</i> -GFP and <i>Lepr</i> is converged at this stage, apparently for the maturation of bone development. ▶ No Western blots used to define the size of the Lepr protein in this and other studies.	(Mizoguchi et al., 2014)
P5-15w, 16w, 19w	<i>Lepr</i> -Cre: <i>Osx</i> -Cre /Tomato	<i>Osx</i> -Cre/Tomato mice pulsed at P5 and fracture wound started in 15w-old <i>Lepr</i> -Cre/Tomato mice: ▶ Observed freshly made chondrogenic zones of the fracture callus at day 8 (total 16w) ▶ No <i>Osx</i> -Cre ⁺ chondrocytes observed after 3w chase (total 19w)	NA	See comments to P5-32w below.	(Mizoguchi et al., 2014)
P5-32w-33w	<i>Lepr</i> -Cre: <i>Osx</i> -Cre /Tomato	<i>Osx</i> -Cre/Tomato mice pulsed at P5 and fracture wound started in 32w-old mice: ▶ Some <i>Lepr</i> -Cre ⁺ cells, identified as Sox9 ⁺ cells in the fractured callus, contributed to progenitors of osteocytes, chondrocytes, and adipocytes <i>in vivo</i> . ▶ <i>Lepr</i> -Cre ⁺ cells not colocalized well with the Lepr protein in the non-fracture callus region ▶ No Lepr protein detected (by an antibody from R&D Systems) in the fracture callus at day 8 (33w)	NA	These data suggest the Lepr protein is not required for the skeletal repair, thus reinforcing the role of <i>Lepr</i> transcriptomes as pivotal indicators of skeletal development.	(Mizoguchi et al., 2014)
P7	<i>Nes</i> -GFP ⁺	~2.4-fold decrease in <i>Nes</i> mRNAs relative	0.3%	Evidence of a dynamic <i>Nes</i>	(Isern et al.,

	cells	to E18.5		transcriptome	2014)
P7	<i>Lepr-Cre</i> ⁺ cells	<ul style="list-style-type: none"> ▶ Distributed throughout the BM cavity ▶ ~92% <i>Lepr-Cre</i>⁺ cells also positive for <i>Nes-GFP</i> in the BM ▶ Positive for <i>Nes-GFP</i> and <i>Osx-Cre</i> in the primary spongiosa 	NA	The emergence of <i>Lepr-Cre</i> dominance (in the developing bone and BM) coincides with the decrease of <i>Nes-GFP</i> transcriptional activity, suggesting a coordinate regulation between the <i>Lepr</i> and <i>Nes</i> genes.	(Mizoguchi et al., 2014)
P7	<i>Gfap</i> ⁺ cells	Schwann cells expressing <i>Gfap</i> detected in the BM	0.3%	<i>Gfap</i> : a marker for non-myelin-forming Schwann cells	(Isern et al., 2014)
P7	<i>Nes-GFP</i> : <i>Wnt1-Cre2</i>	Increase in <i>Wnt1-Cre2</i> -traced osteochondral cells; partially overlap with <i>Nes-GFP</i> ⁺ cells, including perivascular <i>Nes-GFP</i> ⁺ cells	0.3%	<i>Wnt1</i> is not a specific marker for neural crest cells.	(Isern et al., 2014)
P7	<i>Nes-GFP</i>	<ul style="list-style-type: none"> ▶ <i>Nes-GFP</i>⁺ cells distributed at the diaphysis and metaphysis (close to the growth plate) in endochondral bones ▶ <i>Nes-GFP</i>^{high} cells traced perivascular cells in the primary spongiosa and pericytes of the arterioles in diaphysis ▶ <i>Nes-GFP</i>^{low} cells in osteoblasts on the bone surface, osteocytes, and endothelial cells 	NA	See comments on <i>Nes-GFP</i> expression at 8w described by Ono et al., 2014	(Ono et al., 2014)
P7	<i>Nes-GFP</i> : <i>Lepr-Cre</i>	97% <i>Nes-GFP</i> ⁺ / <i>Lepr-Cre</i> ⁺ / <i>CD45</i> ⁻ cells	NA	<i>Nes-GFP</i> ⁺ cells may have a role in specifying <i>Lepr-Cre</i> ⁺ SSCs.	(Ono et al., 2014)
P7	<i>Nes-GFP</i> : <i>Osx-Cre</i>	98% <i>Nes-GFP</i> ⁺ / <i>Osx-Cre</i> ⁺ / <i>CD45</i> ⁻ cells	NA	<i>Nes-GFP</i> ⁺ cells are associated with osteoblast development.	(Ono et al., 2014)
P7 & more stages	<i>Mx1-Cre</i>	<ul style="list-style-type: none"> ▶ <i>Mx1-Cre</i> labels non-hematopoietic and non-endothelial osteogenic cells in the bone. ▶ <i>Mx1-Cre</i>⁺ cells are highly enriched at the postnatal day 7. ▶ <i>Mx1-Cre</i>⁺ cells are resided at the perivascular niche and enriched in the <i>CD105</i>⁺/<i>CD140a</i>⁺ subset (43%) and calvarial sutures. ▶ 59% <i>Nes-GFP</i>⁺ cells overlap with <i>Mx-1</i>⁺ cells. ▶ <i>Mx1-Cre</i>⁺ stromal cells are lineage-restricted, essential for supplying new osteoblasts, and for fracture healing <i>in vivo</i>. ▶ <i>Mx1-Cre</i>⁺ cells are clonogenic, having tripotent differentiation potential <i>in vitro</i> and <i>in vivo</i>. ▶ <i>Mx1-Cre</i> labels mature osteogenic cells that express osterix, osteopontin, and osteocalcin. 	High	<ul style="list-style-type: none"> ▶ <i>Nes-GFP</i>⁺ cells may be the precursor of <i>Mx1-cre</i>⁺ cells. ▶ <i>Mx1-Cre</i>⁺ cells may contribute to pre-osteoblasts. ▶ No chondrogenesis is required for adult bone fracture repair. ▶ <i>Mx1-Cre</i>-labeled cells partially overlap with <i>nestin</i>⁺ cells detected by an anti-<i>nestin</i> antibody (Millipore, clone rat-401). ▶ <i>Mx1-Cre</i> can be used to distinguish long-term osteogenic cells from other bone-forming cells. ▶ The osteoblastic turnover rates vary at different developmental stages. 	(Park et al., 2012)
P14	<i>Nes-GFP</i> ⁻ cells	More than 100-fold decrease in CFU-F activity in <i>Nes-GFP</i> ⁻ BM stromal cells compared with E18.5 cells	~0%	Unknown mechanisms to regulate this critical transition	(Isern et al., 2014)
P21	<i>Nes-GFP</i> ⁺ cells	Maintain steady CFU-F activity	0.3%	None	(Isern et al., 2014)
P21	<i>Lepr-Cre</i> ⁺ cells	Distributed throughout the BM cavity, but not on the endosteum	NA	See comments on <i>Lepr-Cre</i> ⁺ cells at 15w	(Mizoguchi et al., 2014)
P28	<i>Wnt1-Cre2</i> ⁺ cells	CFU-F activity was much higher in <i>Wnt1-Cre2</i> ⁺ cells than in <i>Wnt1-Cre2</i> ⁻ BM stromal cells.	0.2%	See above comments.	(Isern et al., 2014)
5w	<i>Nes-GFP</i>	<i>Nes-GFP</i> ⁺ cells clustered, but not colocalized, with <i>osterix</i> ⁺ cells (by immunostaining) in trabecular bone sections	NA	None	(Mendez-Ferrer et al., 2010)
7w-12w	<i>Nes-GFP</i> ^{high} cells	<ul style="list-style-type: none"> ▶ Exceptionally low, 0.002% of BM cells ▶ Quiescent, only along arterioles ▶ <i>NG2</i>⁺ and α-smooth muscle actin⁺ 	High	<ul style="list-style-type: none"> ▶ Likely have an HSC-niche-supporting role ▶ Neither <i>Nes-GFP</i>^{high} nor <i>Nes-</i> 	(Kunisaki et al., 2013)

		pericytes ▶ Physically associated with tyrosine hydroxylase (HT) positive sympathetic nerves and GFAP ⁺ Schwann cells ▶ Do not overlap with <i>Lepr-Cre</i> ⁺ cells		GFP ^{low} BM stromal cells seem to express endogenous <i>Nes</i> mRNAs by microarray (Mendez-Ferrer et al., 2010) and by RNA sequencing (Kunisaki et al., 2013).	
7w-12w	<i>Nes-GFP</i> ^{low} cells	Abundant, reticular in shape, mainly associated with perisinusoids and overlap with <i>Lepr-Cre</i> ⁺ cells	Low	Likely pericytes for SSCs	(Kunisaki et al., 2013)
7w-12w	<i>Nes-GFP</i> ^{high} / <i>Lepr-Cre</i> ⁻ cells	▶ <i>Nes-GFP</i> ^{high} / <i>Lepr-cre</i> ⁻ cells express the highest level of <i>Scf</i> and <i>Cxcl12</i> . ▶ RNA-seq data showed that <i>Nes-GFP</i> ^{high} / <i>Lepr-cre</i> ⁻ cells were negative for <i>Nes</i> and positive for <i>Lepr</i> expression (GSE48764).	NA	▶ Discrepancy between transcriptome and transcriptional activity ▶ Evidence of a putative inverse regulation between the <i>Nes</i> and <i>Lepr</i> genes	(Kunisaki et al., 2013)
7w-12w	<i>Nes-GFP</i> : <i>NG2-CreER</i>	<i>Nes-GFP</i> ^{high} cells (~30%), not <i>Nes-GFP</i> ^{low} cells, colocalized with <i>NG2-Cre</i> ⁺ cells	NA	None	(Kunisaki et al., 2013)
7w-12w	<i>NG2-CreER</i> : iDTR	▶ Tamoxifen induction and diphtheria toxin treatment depleted ~55% of <i>Nes-GFP</i> ^{high} cells. ▶ Depletion of <i>NG2</i> ⁺ cells expelled quiescent HSCs from arteriolar to perisinusoidal niches.	NA	<i>NG2-Cre</i> ⁺ cells are believed to be part of HSC niches, which endorses HSC for quiescence.	(Kunisaki et al., 2013)
8w	<i>Nes-GFP</i>	In endochondral bones: ▶ <i>Nes-GFP</i> ^{high} cells were decreased in the primary spongiosa and BM. ▶ <i>Nes-GFP</i> ^{low} cells were further decreased in osteoblasts (on bone surfaces), osteocytes, but still observable at this stage.	NA	From P7 to 8w, <i>Nes-GFP</i> ^{high/low} cells continue to decrease without a conclusive mechanism.	(Ono et al., 2014)
8w	<i>Lepr-Cre</i> ⁺ / <i>Col2.3-GFP</i> ⁻	<i>Lepr-Cre</i> ⁺ / <i>Col2.3-GFP</i> ⁻ / <i>CD45</i> ⁻ / <i>Ter119</i> ⁻ / <i>CD31</i> ⁻ BM cells ▶ Cell frequency stabilized near 0.2% ▶ Quiescent at 8w, reactivable under stress conditions ▶ Intrafemoral injection of 500 of these cells generated adipocytes, osteocytes, and chondrocytes at 4w.	NA	These data suggest that <i>Lepr-Cre</i> ⁺ / <i>Col2.3-GFP</i> ⁻ cells are a progenitor cell source for adipocytes and osteolineage cells.	(Zhou et al., 2014)
8w	<i>Nes-CreER</i> ^{T2} : <i>Scf</i> ^{fl/-}	Deletion of <i>Scf</i> from <i>Nes-Cre</i> ⁺ cells did not affect HSC frequency in BM.	NA	HSC niche maintenance does not require SCF from <i>Nes-Cre</i> ⁺ cells.	(Ding and Morrison, 2013)
8w	<i>Nes-GFP</i>	<i>Nes-GFP</i> ^{high} along larger vessels in BM; <i>Nes-GFP</i> ^{low} in perisinusoidal stromal cells similar to <i>Scf-GFP</i> ⁺ cells	NA	<i>Nes-GFP</i> expression patterns in this study are consistent with the report by Mendez-Ferrer et al. 2010.	(Ding and Morrison, 2013)
8w	<i>Nes-Cre</i> ⁺ cells	Only found around larger blood vessels in BM	NA	<i>Nes</i> expression discrepancies	(Ding and Morrison, 2013)
8w	<i>Nes-Cherry</i> : <i>Nes-GFP</i>	<i>Nes-Cherry</i> ⁺ cells were around larger vessels but not around sinusoids, whereas <i>Nes-GFP</i> ⁺ cells were detected around both regions.	NA	<i>Nes-Cherry</i> has a similar expression pattern to that of <i>Nes-Cre</i> . However, the detail information about <i>Nes-Cherry</i> mice is not available.	(Ding and Morrison, 2013)
8w (2m)	<i>Lepr-Cre</i> : dTomato: <i>Col2.3-GFP</i>	<i>Lepr-Cre</i> ⁺ cells were filled with metaphysis and diaphysis of the BM,	NA	The emergence of 3-10% <i>Lepr-Cre</i> ⁺ / <i>Col2.3-GFP</i> ⁺ osteoblasts in bone	(Zhou et al., 2014)
8w-16w	<i>Wnt1-CreER</i>	<i>Wnt1-CreER</i> ⁺ / <i>CD45</i> ⁻ / <i>Ter119</i> ⁻ BM stromal cells	0.5%	<i>Wnt1-Cre</i> ⁺ neural crest derivatives minimally contribute to CFU-F colonies at this stage.	(Zhou et al., 2014)
8w-12w	<i>Nes-GFP</i> : <i>Lepr</i>	70% of <i>Lepr</i> ⁺ cells (by flow cytometric analysis) in BM mainly overlap with <i>Nes-GFP</i> ⁺ cells.	NA	None	(Pinho et al., 2013)
8w-12w	<i>PDGFR</i> α ⁺ / <i>CD51</i> ⁺	<i>PDGFR</i> α ⁺ / <i>CD51</i> ⁺ cells represent a small subset of <i>Nes-GFP</i> ⁺ cells. <i>Nes</i> mRNAs are expressed in this cell population.	NA	Expression of <i>CD51</i> (the integrin subunit α V) enhances <i>Nes</i> mRNA expression and might enable to convert <i>Nes-GFP</i> ⁺ / <i>PDGFR</i> α ⁺	(Pinho et al., 2013)

				/CD146 ⁺ cells into perivascular pericytes.	
8w-12w	α -catulin-GFP ⁺ cells	<ul style="list-style-type: none"> ▶ Represent 0.02% of BM hematopoietic cells, located at the central perisinusoids ▶ Restricted to HSC niche cells, adjacent to <i>Lepr</i>⁺ and <i>Cxcl12</i>⁺ cells, ▶ Distant from arterioles and endosteal surface ▶ HSCs located within the 10 μm sinusoidal vessels with an HSC frequency of 1/6 	NA	These data are inconsistent with periarteriolar HSC-niches supported by <i>NG2</i> -CreER ⁺ cells in a previous report (Kunisaki et al. 2013).	(Acar et al., 2015)
8w-12w	Gfap ⁺ cells	Gfap ⁺ non-myelinating Schwann cells associated with nerve fibers tend to localize in the central BM.	NA	Indirect evidence of an HSC-niche supporting role by neural crest lineage cells	(Acar et al., 2015)
8w-12w	<i>NG2</i> -CreER ⁺ cells	<ul style="list-style-type: none"> ▶ Not detected in <i>Scf</i>-GFP⁺ or <i>Cxcl12</i>-DsRed⁺ cells ▶ <i>NG2</i>-CreER mediated conditional deletion of <i>Scf</i> in <i>Scf</i>^{GFP/fl} mice or <i>Cxcl12</i> in <i>NG2</i>-CreER: <i>Cxcl12</i>^{-fl} mice did not affect HSC frequency. 	NA	<i>Nes</i> -Cre mediated deletion of <i>Scf</i> also shows no effects on HSC function (Ding et al. 2012).	(Acar et al., 2015)
8w-12w	HSCs	Higher HSC density, marked by α -catulin-GFP ⁺ /c-kit ⁺ , found in the diaphysis than in metaphysis	NA	An unexpected result that might provide insights into HSC niche dynamics	(Acar et al., 2015)
8w-16w	BM stromal cells	CD45 ⁺ /Ter119 ⁻ non-hematopoietic BM cells	1.4%	None	(Zhou et al., 2014)
8w-16w	PDFFR α ⁺	PDGFR α ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	10%	None	(Zhou et al., 2014)
8w-16w	PDFFR α ⁺ /Sca-1 ⁺	The PDGFR α ⁺ /Sca-1 ⁺ /CD45 ⁻ /Ter119 ⁻ cell population	16%	Reside mainly around arterioles, but does not express the HSC niche factor <i>Cxcl12</i>	(Zhou et al., 2014)
8w-16w	PDFFR α ⁺ /Sca-1 ⁻	The PDGFR α ⁺ /Sca-1 ⁻ /CD45 ⁻ /Ter119 ⁻ cell population, known as CXCL12-abundant reticular (CAR) cells	8%	Exist primarily around sinusoids and express high levels of <i>Cxcl12</i>	(Zhou et al., 2014)
8w-16w	<i>Lepr</i> -Cre/Tomato ⁺ /CD105 ⁺	<ul style="list-style-type: none"> ▶ 0.3% <i>Lepr</i>-Cre⁺/CD45⁻/Ter119⁻ cells ▶ 98% PDFFRα⁺, 98% CD51⁺, 69% CD105⁺ ▶ Around sinusoids and arterioles ▶ High levels of <i>Lepr</i> mRNAs ▶ The <i>Lepr</i> protein detected by immunostaining ▶ Considered as a major source of BM SSCs 	14%	<ul style="list-style-type: none"> ▶ Tripotent cells from 9% of CFU-F colonies ▶ Ossicles from 30% CFC-F colonies ▶ CD105, known as endoglin, a plasma membrane and extracellular glycoprotein of vascular endothelial cells, used as an "MSC" marker 	(Zhou et al., 2014)
8w-16w	<i>Lepr</i> -Cre/Tomato ⁻ /CD105 ⁻	<i>Lepr</i> -Cre/Tomato ⁻ /CD105 ⁻ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	1%	14-fold decrease in CFU-F colonies compared with <i>Lepr</i> -Cre/Tomato ⁺ /CD105 ⁺ cells	(Zhou et al., 2014)
8w-16w	<i>Lepr</i> -Cre/Tomato ⁺	<i>Lepr</i> -Cre/Tomato ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	11%	Around sinusoids and arterioles	(Zhou et al., 2014)
8w-16w	<i>Lepr</i> -Cre/Tomato ⁻	<i>Lepr</i> -Cre/Tomato ⁻ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	0.1%	Depletion of CFU-F capacity	(Zhou et al., 2014)
8w-16w	<i>Lepr</i> -Cre ⁺ /Scf-GFP ⁺	<i>Lepr</i> -Cre/Tomato ⁺ /Scf-GFP ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	NA	Around sinusoids only	(Zhou et al., 2014)
8w-16w	<i>Prx1</i> -Cre/Tomato ⁺	<i>Prx1</i> -Cre/Tomato ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	10%	A positive marker for BM stromal cells, tightly associated with <i>Lepr</i> -Cre	(Zhou et al., 2014)
8w-16w	<i>Scf</i> -GFP ⁺	<i>Scf</i> -GFP ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	10%	A positive marker for BM stromal cells	(Zhou et al., 2014)
8w-16w	<i>Cxcl12</i> -DsRed ^{high}	<i>Cxcl12</i> -DsRed ^{high} /CD45 ⁻ /Ter119 ⁻ BM stromal cells	12%	A positive marker for BM stromal cells	(Zhou et al., 2014)
8w-16w	<i>Nes</i> -GFP ^{low}	<i>Nes</i> -GFP ^{low} /CD45 ⁻ /Ter119 ⁻ BM stromal cells	8%	A positive marker for BM stromal cells	(Zhou et al., 2014)
8w-16w	<i>Nes</i> -GFP ^{high}	<i>Nes</i> -GFP ^{high} /CD45 ⁻ /Ter119 ⁻ BM stromal cells	3%	See comments on <i>NG2</i> -CreER ⁺ cells	(Zhou et al., 2014)
8w-16w	<i>Nes</i> -CreER ⁺	<i>Nes</i> -CreER ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	0	A negative marker for BM stromal cells	(Zhou et al., 2014)

8w-16w	NG2-CreER ⁺	NG2-CreER ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	2%	NG2-Cre ⁺ and Nes-GFP ⁺ cells show similar low CFU-F activity.	(Zhou et al., 2014)
8w-16w	Mx1-CreER ⁺	Mx1-CreER ⁺ /CD45 ⁻ /Ter119 ⁻ BM stromal cells	2%	Mx1-Cre seems a weaker marker for osteoblastic lineage at this stage.	(Zhou et al., 2014)
12w-16w	Prx1-Cre; Jak2 ^{V617F}	► Jak2 mutant cells had a 3-fold decrease in CFU-F activity compared with the wild-type cells. ► Increase in adipocytes	Low	Genetic evidence indicates Jak2/Stat3 is underlying the regulation of both adipogenesis and osteogenesis.	(Yue et al., 2016)
12w-16w	Nes-creER ^{T2} : RCE-loxP	Pulsed with tamoxifen at 3 months and chased for 4w (1 month): No Nes-Cre ⁺ osteoblasts, osteocytes, and chondrocytes (collagen α 1 type 2 ⁺)	NA	Nes-Cre mediates slow turnover of osteolineage cells.	(Mendez-Ferrer et al., 2010)
12w-44w	Nes-creER ^{T2} : RCE-loxP	Pulsed with tamoxifen at 3 months (12w) and chased for 8 months (44w): see GFP ⁺ osteoblasts, osteocytes, and chondrocytes (collagen α 1 type 2 ⁺)	NA	Adult Nes-Cre ⁺ cells are likely an SSC source.	(Mendez-Ferrer et al., 2010)
15w	Lepr-Cre ⁺ cells	Distributed not only in the BM cavity, but also along the cortical bone as Lepr-Cre ⁺ /Ocn ⁺ /DMP1 ⁺ osteoblasts and osteocytes	NA	This study suggests a migration route of Lepr-Cre ⁺ cells during osteogenesis: BM cavity → endosteum → trabecular bone → cortical bone.	(Mizoguchi et al., 2014)
24w	Prx1-Cre /Lepr ^{fl/fl}	Conditional deletion of Lepr in SSCs: increased osteogenesis and down-regulated adipogenesis	NA	The Lepr protein is likely an inhibitor of adult osteogenesis.	(Yue et al., 2016)
24w, 40w, 56w	Lepr-Cre: dTomato: Col2.3-GFP	Age-dependent contribution of Lepr-Cre ⁺ cells to bone development: 24w: 10%–23% of Col2.3-GFP ⁺ cells, 40w: 43%–67% of Col2.3-GFP ⁺ cells, 56w: 61%–81% of Col2.3-GFP ⁺ cells	NA	Accordingly, no Lepr protein expression was detected by IF (at 10w or 40w), which suggests that Lepr-Cre functions as an independent transcriptional reporter in these stages	(Zhou et al., 2014)

ABBREVIATIONS:

Adrb3, β 3 adrenoreceptor; BM, bone marrow; CFU-F, Colony forming unit-fibroblastic, an assay based on freshly isolated single cells from an intact tissue, in which single cells are able to initiate clonal growth of fibroblastic cells at low density; Col1, collagen I; DMP1, dentin matrix protein 1; HSC, hematopoietic stem cell; iDTA, diphtheria toxin; iDTAR, diphtheria toxin receptor; IF, immunofluorescence; m, month(s); MSC, “mesenchymal stem cells”; NA, not available; Nes-CreER^{T2}, tamoxifen-inducible transgenic mouse described by Balordi and Fishell (2007); Ocn, osteocalcin; Osx, osterix; POC, primary ossification center; SSC, skeletal stem cell; Tripotent: osteochondrogenic, osteogenic, and adipogenic; wk, week

REREFERNCES

Acar, M., Kocherlakota, K.S., Murphy, M.M., Peyer, J.G., Oguro, H., Inra, C.N., Jaiyeola, C., Zhao, Z., Luby-Phelps, K., and Morrison, S.J. (2015). Deep imaging of bone marrow shows non-dividing stem cells are mainly perisinusoidal. *Nature* 526, 126-130.

Balordi, F., and Fishell, G. (2007). Mosaic removal of hedgehog signaling in the adult SVZ reveals that the residual wild-type stem cells have a limited capacity for self-renewal. *J Neurosci* 27, 14248-59.

Ding, L., and Morrison, S.J. (2013). Haematopoietic stem cells and early lymphoid progenitors occupy distinct bone marrow niches. *Nature* 495, 231-235.

Isern, J., García-García, A., Martín, A.M., Arranz, L., Martín-Pérez, D., Torroja, C., Sánchez-Cabo, F., Méndez-Ferrer, S. (2014). The neural crest is a source of mesenchymal stem cells with specialized hematopoietic stem cell niche function. *Elife* 25; 3:e03696.

Kunisaki, Y., Bruns, I., Scheiermann, C., Ahmed, J., Pinho, S., Zhang, D., Mizoguchi, T., Wei, Q., Lucas, D., Ito, K., et al. (2013). Arteriolar niches maintain haematopoietic stem cell quiescence. *Nature* 502, 637-643.

Mendez-Ferrer, S., Michurina, T.V., Ferraro, F., Mazloom, A.R., Macarthur, B.D., Lira, S.A., Scadden, D.T., Ma'ayan, A., Enikolopov, G.N., and Frenette, P.S. (2010). Mesenchymal and haematopoietic stem cells form a unique bone marrow niche. *Nature* 466, 829-834.

Mizoguchi, T., Pinho, S., Ahmed, J., Kunisaki, Y., Hanoun, M., Mendelson, A., Ono, N., Kronenberg, H.M., and Frenette, P.S. (2014). Osterix marks distinct waves of primitive and definitive stromal progenitors during bone marrow development. *Dev Cell* 29, 340-349.

Ono, N., Ono, W., Mizoguchi, T., Nagasawa, T., Frenette, P.S., and Kronenberg, H.M. (2014). Vasculature-associated cells expressing nestin in developing bones encompass early cells in the osteoblast and endothelial lineage. *Dev Cell* 29, 330-339.

Park, D., Spencer, J.A., Koh, B.I., Kobayashi, T., Fujisaki, J., Clemens, T.L., Lin, C.P., Kronenberg, H.M., and Scadden, D.T. (2012). Endogenous bone marrow MSCs are dynamic, fate-restricted participants in bone maintenance and regeneration. *Cell Stem Cell* 10, 259-72.

Pinho, S., Lacombe, J., Hanoun, M., Mizoguchi, T., Bruns, I., Kunisaki, Y., and Frenette, P.S. (2013). PDGFRalpha and CD51 mark human nestin+ sphere-forming mesenchymal stem cells capable of hematopoietic progenitor cell expansion. *J Exp Med* 210, 1351-1367.

Yue, R., Zhou, B.O., Shimada, I.S., Zhao, Z., and Morrison, S.J. (2016). Leptin Receptor Promotes Adipogenesis and Reduces Osteogenesis by Regulating Mesenchymal Stromal Cells in Adult Bone Marrow. *Cell Stem Cell* 18, 782-796.

Zhou, B.O., Yue, R., Murphy, M.M., Peyer, J.G., and Morrison, S.J. (2014). Leptin-receptor-expressing mesenchymal stromal cells represent the main source of bone formed by adult bone marrow. *Cell Stem Cell* 15, 154-168.

