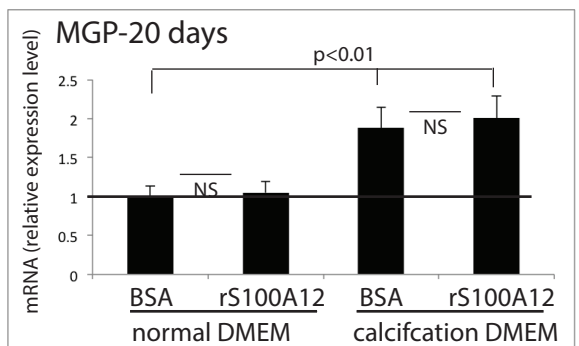
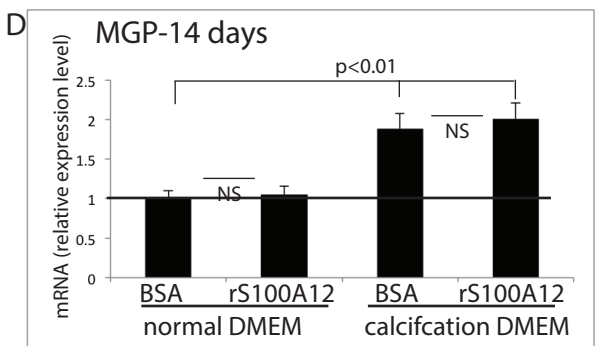
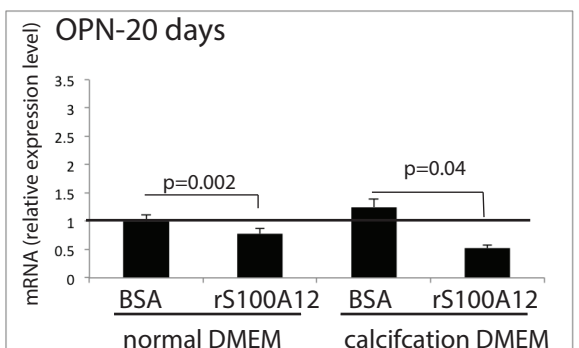
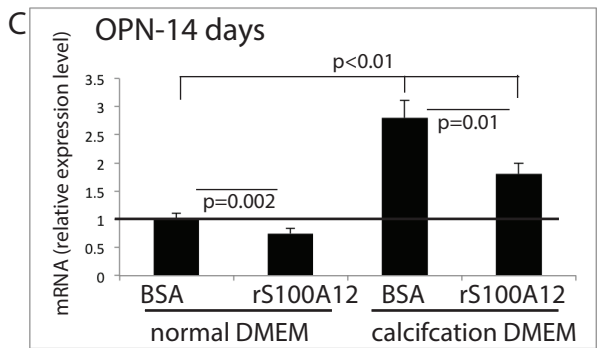
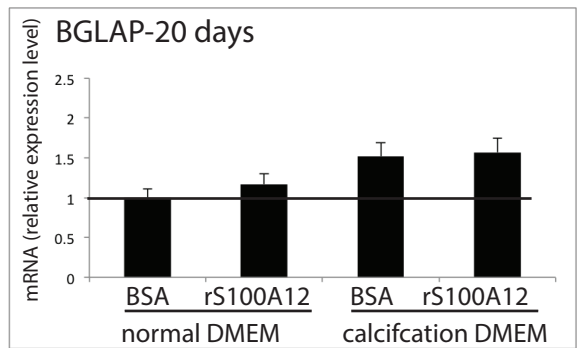
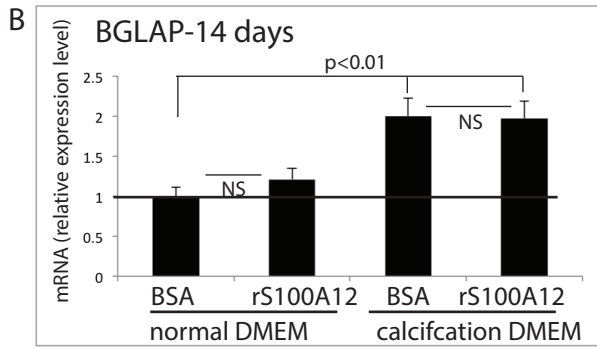
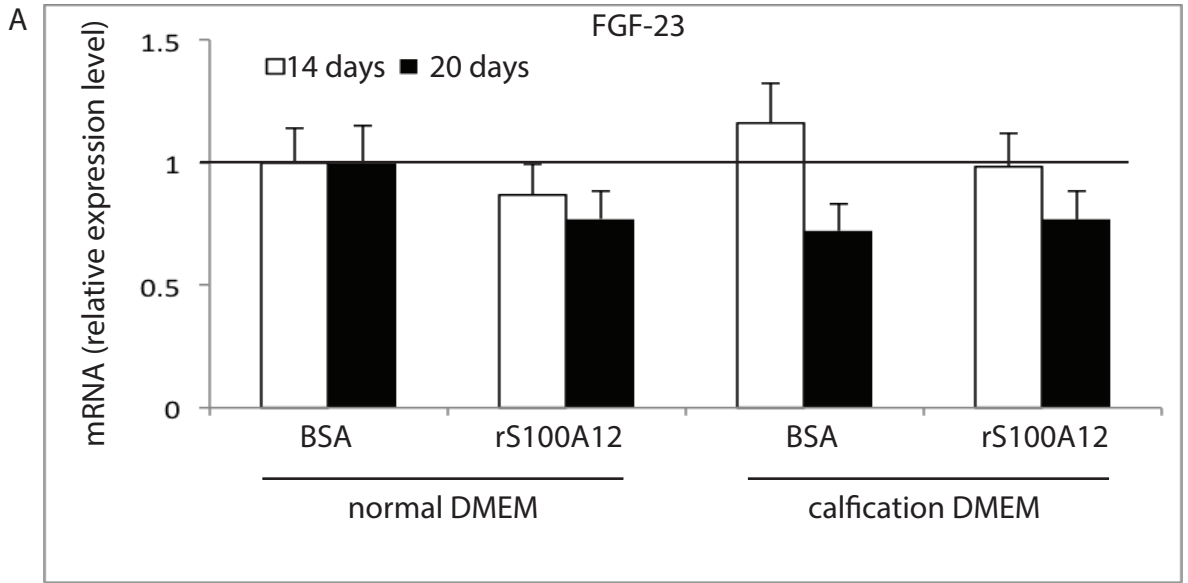


Figure legend:

Supplement Figure I. Recombinant S100A12 protein does not induce FGF23 mRNA in cultured neonatal cardiac fibroblasts. Neonatal cardiac fibroblasts were cultured for 14 and 20 days in either control medium (DMEM) or high phosphate calcification medium supplemented with either rS100A12 protein (1 μ g/ml) or control (bovine serum albumin, BSA). **A)** FGF23 mRNA was similar in all groups. **B)** mRNA for Bone Gla Protein (BGLAP, osteocalcin) increased in response to 14-day-calcification medium, but S100A12 had no effect on BGLAP. **C)** mRNA for OPN (osteopontin) increased in response to 14-day and 20-day treatment with calcification medium, and was significantly attenuated in S100A12-treated cells. **D)** mRNA for Matrix Gla Protein (MGP) increased in response to 14-day and 20-day treatment with calcification medium, but S100A12 had no effect on MGP.

Supplement TABLE I. Expression fold change of the top 50 genes significantly up and down regulated in blood cDNA isolated from 6-weeks old hBAC-S100 mice and WT littermate mice and analyzed on IlluminaWG-6v2 microarray.



Supplement Table I A. Expression fold change of the top 50 genes up-regulated in blood cDNA of hBAC-S100 mice.

Gene Description	Gene Symbol	Fold Change
lactotransferrin (Ltf)	Ltf	7.3305
neutrophilic granule protein (Ngp)	Ngp	6.7347
cathelicidin antimicrobial peptide (Camp)	Camp	6.2200
myeloperoxidase (Mpo)	Mpo	5.1112
proteinase 3 (Prtn3)	Prtn3	3.6874
elastase 2, neutrophil (Ela2)	Ela2	3.2735
lipocalin 2 (Lcn2)	Lcn2	3.0721
chitinase 3-like 4 (Chi3l4)	Chi3l4	2.7760
chitinase 3-like 3 (Chi3l3)	Chi3l3	2.7506
proteoglycan 2, bone marrow (Prg2)	Prg2	2.5456
CD177 antigen (Cd177)	Cd177	2.3458
cathepsin G (Ctsg)	Ctsg	2.2901
	F830002E14Rik	2.0120
protease, serine, 34 (Prss34)	Prss34	1.9825
ficolin A (Fcna)	Fcna	1.9210
histone cluster 1, H2an (Hist1h2an)	Hist1h2an	1.8723
erythroid associated factor (Eraf)	Eraf	1.8451
histone cluster 1, H2ak (Hist1h2ak)	Hist1h2ak	1.8247
histone cluster 1, H2ao (Hist1h2ao)	Hist1h2ao	1.8082
histone cluster 1, H2ad (Hist1h2ad)	Hist1h2ad	1.8075
carbonic anhydrase 1 (Car1), transcript variant 1	Car1	1.7330
PREDICTED: similar to monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain (LOC674110)	LOC674110	1.7165
metallothionein 1 (Mt1)	Mt1	1.7108
annexin A3 (Anxa3)	Anxa3	1.6924
interferon induced transmembrane protein 6 (Ifitm6)	Ifitm6	1.6730
similar to Immunoglobulin heavy chain (LOC100043991)	LOC100043991	1.6685
ficolin B (Fcnb)	Fcnb	1.6490
	IGHV10S3_AF064446_Ig_heavy_variable_10S3_9	1.6306
complement component 1, q subcomponent, beta polypeptide (C1qb)	C1qb	1.6247
complement component 3 (C3)	C3	1.6137
chitinase 3-like 1 (Chi3l1)	Chi3l1	1.5927

ADP-dependent glucokinase (Adpgk)	Adpgk	1.5862
splicing factor, arginine/serine-rich 5 (SRp40, HRS) (Sfrs5), transcript variant 2	Sfrs5	1.5759
myosin, light polypeptide 4 (Myl4)	Myl4	1.5524
integrin beta 2-like (Itgb2l)	Itgb2l	1.5510
glycophorin A (Gypa)	Gypa	1.5498
olfactomedin-like 2B (Olfml2b)	Olfml2b	1.5393
similar to high mobility group nucleosomal binding domain 2 (LOC100042405)	LOC100042405	1.5392
histone cluster 1, H2ah (Hist1h2ah)	Hist1h2ah	1.5327
RIKEN cDNA 6430706D22 gene (6430706D22Rik)	6430706D22Rik	1.5305
high mobility group nucleosomal binding domain 2 (Hmgn2)	Hmgn2	1.5299
	IGKV4- 53_AJ231231_Ig_kappa_v ariable_4-53_12	1.5241
similar to immunoglobulin light chain variable region (LOC232067)	LOC232067	1.5100
similar to Hmgn2 protein (LOC100047827)	LOC100047827	1.5014
CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe)	Cebpe	1.4976
solute carrier family 4 (anion exchanger), member 1 (Slc4a1)	Slc4a1	1.4761
	5930418K15Rik	1.4759
pre-B lymphocyte gene 1 (Vpreb1)	Vpreb1	1.4660
similar to Ig heavy chain V-III region VH26 precursor (LOC637337)	LOC637337	1.4621
complement component 1, q subcomponent, C chain (C1qc)	C1qc	1.4571

Values were obtained after clustering analysis on microarray performed in blood cDNA of WT and hBAC-S100 mice. n = 3 samples/group. Values are expressed as fold change compared to the WT control value. Genes were selected based on a *P* value threshold of 0.05.

Supplement Table I B. Expression fold change of selected up-regulated genes confirmed by RT-PCR in blood cDNA of hBAC-S100 mice.

Gene Description	Gene Symbol	Microarray Fold Change	RT-PCR Fold Change
lactotransferrin (Ltf)	Ltf	7.3305	20.8767
myeloperoxidase (Mpo)	Mpo	5.1112	31.8178
proteinase 3 (Prtn3)	Prtn3	3.6874	44.1915
lipocalin 2 (Lcn2)	Lcn2	3.0721	4.4896
chitinase 3-like 3 (Chi3l3)	Chi3l3	2.7506	4.6739
proteoglycan 2, bone marrow (Prg2)	Prg2	2.5456	22.5033
CD177 antigen (Cd177)	Cd177	2.3458	3.8180
cathepsin G (Ctsg)	Ctsg	2.2901	24.4727
carbonic anhydrase 1 (Car1), transcript variant 1	Car1	1.7330	7.4500
CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe)	Cebpe	1.4976	6.4035
vascular cell adhesion molecule 1 (Vcam1)	Vcam1	1.3354	22.4915
lipopolysaccharide binding protein (Lbp)	Lbp	1.1382	5.0199

Values are expressed as fold change compared to the WT value. n = 3 samples/group. Comparisons were performed using Student T test. $P < 0.05$ vs WT.

Supplement Table I C. Expression fold change of the top 50 genes down-regulated in blood cDNA of hBAC-S100 mice.

Gene Description	Gene Symbol	Fold Change
	IGHV1S135_AF304556_Ig_heavy_v ariable_1S135_43	0.2623
immunoglobulin kappa variable 4-50 (LOC381782)	LOC381782	0.3271
	LOC384415	0.4140
hypothetical protein LOC673501 (LOC673501)	LOC673501	0.5009
	IGHV1S30_X02462_Ig_heavy_varia ble_1S30_12	0.5100
dual specificity phosphatase 1 (Dusp1)	Dusp1	0.5296
similar to monoclonal antibody 17-1A, light chain (LOC100047132)	LOC100047132	0.5498
similar to Ig H-chain V-JH1-region (LOC100048770)	LOC100048770	0.5569
	IGKV2- 137_AJ231263_Ig_kappa_variable_ 2-137_15	0.5701
similar to Ig kappa V-region 24B (LOC100046496)	LOC100046496	0.5703
similar to Igh-VJ558 protein (LOC380799)	LOC380799	0.6111
DNA segment, Chr 6, Massachusetts Institute of Technology 97 (D6Mit97)	D6Mit97	0.6167
serine (or cysteine) peptidase inhibitor, clade B, member 6a (Serpib6a)	Serpib6a	0.6198
	IGHV5S18_AF290972_Ig_heavy_va riable_5S18_125	0.6227
Immunoglobulin heavy chain (gamma polypeptide), transcript variant 1 (Ighg)	Ighg	0.6245
RIKEN cDNA 2410146L05 gene (2410146L05Rik)	2410146L05Rik	0.6328
hypothetical LOC385068	LOC385068	0.6449
E26 avian leukemia oncogene 2, 3' domain (Ets2)	Ets2	0.6468
RIKEN cDNA 4930486L24 gene (4930486L24Rik)	4930486L24Rik	0.6491
arginase type II (Arg2)	Arg2	0.6507
similar to Ig heavy chain V region 1B43 precursor (LOC630337)	LOC630337	0.6514
RIKEN cDNA 1700081H05 gene	1700081H05Rik	0.6588
RAS related protein 2a (Rap2a)	Rap2a	0.6840
coagulation factor XIII, A1 subunit (F13a1)	F13a1	0.6882
arrestin domain containing 3 (Arrdc3)	Arrdc3	0.6901
C-type lectin domain family 7, member a	Clecsf12	0.6922

leucine rich repeat protein 3, neuronal (Lrrn3)	Lrrn3	0.6938
RIKEN cDNA 2210039O17 gene	2210039O17Rik	0.6945
	scl0015365.1_6	0.6966
cDNA sequence AK157302 (AK157302)	AK157302	0.6978
DnaJ (Hsp40) homolog, subfamily B, member 1 (Dnajb1)	Dnajb1	0.6979
	E430033B07Rik	0.6986
period homolog 1 (Drosophila) (Per1)	Per1	0.6991
aspartic peptidase, retroviral-like 1 (Asprv1)	Asprv1	0.6997
similar to Ig kappa chain V-V region MPC11 precursor (LOC637227)	LOC637227	0.7002
predicted gene, OTTMUSG00000000971 (OTTMUSG00000000971)	OTTMUSG00000000971	0.7003
LSM12 homolog (S. cerevisiae)	2600001B17Rik	0.7022
RIKEN cDNA 4732429D16 gene (4732429D16Rik)	4732429D16Rik	0.7024
G protein-coupled receptor 109A (Gpr109a)	Gpr109a	0.7036
potassium voltage gated channel, Shaw-related subfamily, member 4 (Kcnc4)	Kcnc4	0.7076
similar to integrin-linked kinase ILK (LOC621824), misc RNA.	LOC621824	0.7081
RAS-related C3 botulinum substrate 1 (Rac1)	Rac1	0.7086
similar to idiotypic anti-NP IgG(1) heavy chain V-D-J (LOC544904)	LOC544904	0.7119
similar to idiotypic anti-NP IgG(1) heavy chain V-D-J (LOC380805)	LOC380805	0.7147
	IGKV8-31_AJ235957_Ig_kappa_variable_8-31_3	0.7160
similar to Ig H chain V region (clone 1E10) (LOC630305), misc RNA.	LOC630305	0.7160
solute carrier family 44, member 1 (Slc44a1)	Slc44a1	0.7177
C-type lectin domain family 4, member g (Clec4g)	Clec4g	0.7188
Chemokine (C-C motif) ligand 6 (Ccl6)	Ccl6	0.7192
similar to LRRGT00183 (LOC619973)	LOC619973	0.7199

Values were obtained after clustering analysis on microarray performed in blood cDNA of WT and hBAC-S100 mice. n = 3 samples/group. Values are expressed as fold change compared to the WT control value. Genes were selected based on a *P* value threshold of 0.05.