SUPPLEMENTAL MATERIAL

Brd4 is required for chondrocyte differentiation and endochondral ossification

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Running Title: Brd4 and endochondral ossification

Genotyping Primer Pairs							
Gene	Forward Sequence	Reverse Sequence					
Brd4	CCTGTGTGCACTTGCTCCCGAGGAGAGA	GGAACCTCGCTATGTGTAACCA					
Cre	TCCAATTTACTGACCGTACACCAA	GGACTAGAAACCTCCCAAATGTCTACAA					
DNA Quantification Primer Pairs							
Gene	Forward Sequence	Reverse Sequence					
Brd4 exon 3 v1	CTGCCAGTAATGGGGGATGG	TGCAGTTGGTTTGTCTGTCTCT					
Brd4 exon 3 v2	GGACACTGGTGGTTAAGAGTTCA	CCTAGCCATCCTGACCAGTT					
Brd4 exon 6	AACTCACCCCTTTCCTGCTG	CAATGATGGGCGGGTGACT					
RT-qPCR Primer Pairs							
Gene	Forward Sequence	Reverse Sequence					
Acan	CCGCTTGCCAGGGGGGGGTTG	GATGATGGGCGCACGCCGTA					
Bglap	GCAATAAGGTAGTGAACAGACTCC	CCATAGATGCGTTTGTAGGCGG					
Brd4	GGAGGAAAGAAACAGGGGCA	GAGTCTGAAGTGGCTGAGGG					
Col10a1	GGGATGAAGTATTGTGTCTTGGG	TTCTGCTGCTAATGTTCTTGACC					
Col1a1	CCTCAGGGTATTGCTGGACAAC	CAGAAGGACCTTGTTTGCCAGG					
Col2a1	GCTGGTGAAGAAGGCAAACGAG	CCATCTTGACCTGGGAATCCAC					
Comp	TGCGAGAACTTCAGGAGACT	CTGCATTCCGCAAGCATCA					
Dcn	GCTCACGCAGTGAAACCTTAG	TTTCACGACCTTTTAATCCGGG					
Gapdh	CATCACTGCCACCCAGAAGACTG	ATGCCAGTGAGCTTCCCGTTCAG					
Hist2h4	AAGGTTCTCCGCGACAACATCC	GTCGCGGATCACATTCTCAAGG					
lbsp	GAATGGCCTGTGCTTTCTCG	CCGGTACTTAAAGACCCCGTT					
lhh	GCTTTCCTGCCGGAGCCCAG	GGTGGGGGTCCCATCCTCCC					
Mki67	CAGAGCTAACTTGCGCTGAC	ACTACAGGCAGCTGGATACG					
Mmp13	CTTCTGGCACACGCTTTTCC	TGGCTTTTGCCAGTGTAGGT					
Runx2	CCTGAACTCTGCACCAAGTCCT	TCATCTGGCTCAGATAGGAGGG					
Sox5	CGCCAGATGAAAGAGCAACTCAG	TGAGTCAGGCTCTCCAGTGTTG					
Sox6	GCATAAGTGACCGTTTTGGCAGG	GGCATCTTTGCTCCAGGTGACA					
Sox9	CACACGTCAAGCGACCCATGAA	TCTTCTCGCTCTCGTTCAGCAG					
Sp7	GGCTTTTCTGCGGCAAGAGGTT	CGCTGATGTTTGCTCAAGTGGTC					
Vegfa	AGAGGCTTGGGGCAGCCGAG	ACTCCCGGGCTGGTGAGTCC					

Supplemental Table 1: Primers used in this study.

Supplemental Table 2. Statistical evaluation of chondrogenic differentiation. For statistical evaluation of the impact of +JQ1 treatment throughout the chondrogenic differentiation time course, a mixed-effects model (REML) analysis was performed for each graph (alpha = 0.05). The p-value reported for the fixed effects was then assessed. For all datasets, the time variable had a statistically significant impact with a p-value < 0.001. The p-value calculated for the "treatment group" variable is reported on each graph. A follow-up multiple comparisons test was performed using the Tukey method (correct for multiple comparisons) to compare the means of each group.

Gene	Time	Treatment	Veh vs. JQ1	Veh vs JQ1	Veh vs. JQ1
	variable	variable	1X	cont.	late
	p-value	p-value	p-value	p-value	p-value
Sox5	< 0.0001	0.1506	0.4431	0.1226	0.7881
Sox6	< 0.0001	0.5107	0.8800	0.4383	0.8612
Sox9	< 0.0001	0.6933	0.9876	0.6567	0.9781
Col2a1	< 0.0001	0.9957	>0.9999	0.9992	0.9981
Acan	< 0.0001	0.9940	0.9976	0.9945	> 0.9999
Comp	< 0.0001	0.1099	0.7155	0.9931	0.4859
Runx2	< 0.0001	0.0001	0.4311	0.0003	0.9984
Sp7	< 0.0001	< 0.0001	0.4325	0.0004	>0.9999
Col10a1	< 0.0001	0.0459	0.3330	0.6484	0.5791
Mmp13	< 0.0001	.0107	0.9967	0.0148	0.1873
lhh	< 0.0001	<0.0001	0.2356	<0.0001	0.1945
Bglap	< 0.0001	0.3301	0.8996	0.9439	0.6232
lbsp	< 0.0001	<0.0001	0.9262	< 0.0001	0.2160

Supplemental Figure 1. Assessment of bone parameters in 3 week old cKO mice. Bone parameters were assessed by microcomputed tomography (μ CT) analysis of three week old CON (Brd4^{wt/wt}: Prrx1-Cre), HET (Brd4^{wt/fl}: Prrx1-Cre), and cKO (Brd4^{fl/fl}: Prrx1-Cre) female and male mice. The cortical thickness (Ct.Th), trabecular bone volume fraction of total volume (BV/TV), and trabecular total mineral density (TMD) were calculated in the femora of female mice (n = 8 to 9) (**A**). The length, trabecular bone volume to total volume (BV/TV), and trabecular thickness (Tb.Th) of L5 vertebrae of male mice (n = 7 to 9) (**B**). Boxplots indicate the median, interquartile range, and the minimum and maximum value in each dataset. Individual mice are represented by a single point on the graph. P-values shown on the graphs represent the results of a one-way ANOVA followed by a multiple comparisons test performed using the Tukey method (correct for multiple comparisons) to compare the means of the CON and cKO groups.



Supplemental Figure 2. Histologic assessment of Brd4 cKO femora. Trichrome staining of distal femora derived from one (**A**) and three (**B**) week old CON (Brd4^{wt/wt}: Prrx1-Cre), HET (Brd4^{wt/fl}: Prrx1-Cre), and cKO (Brd4^{fl/fl}: Prrx1-Cre) male mice. Data presented in panel A are higher magnification images of data presented in Fig 4F.



Supplemental Figure 3. Transcriptional profile of differentiating iMACs. iMACs were collected from five day-old wild-type C57BL/6J mice and cultured in three-dimensional micromass (3D- μ mass) conditions in chondrogenic differentiation media. Gene expression was assessed using RNA-sequencing (n = 1) and RT-qPCR (n = 3). RT-qPCR values (mean ± standard deviation) were normalized to day four (set at 1). Expression levels of key chondrogenic transcription factors (A and B), early chondrogenic markers (C and D), hypertrophic markers (E and F), and osteogenic markers (G and H).



Original Western Blot Images:

Fig. 2B





Gapdh



Figure 6B

Brd4



Gapdh

