Supplementary table 1

Gene name	Expression in *Barx2*$^{-/-}$/wildtype myoblasts P<0.01s
Cdh	0.0455
Vcan	0.1635
Ctgf	0.198
Ecm1	0.2496
Itga4	0.1662
Itga5	0.0967
Lama2	0.0579
Lamb2	0.0671
MMP3	0.4736
MMP7	0.2575
Sgce	0.0635
Sparc	0.1078
Spock1	0.3858
TnC	0.228
Vcam	0.2413

Supplementary Table 1. Gene expression analysis using the 'ECM & Adhesion PCR Array' reveals down-regulated genes in *Barx2-/-* myoblasts. Total RNA samples from wildtype and Barx2-/- primary myoblast cultures (prepared from P5 littermates) were assayed in triplicates, and the relative expression levels for each gene in the two samples were plotted against each other in a scatter plot. Genes encoding the matrix metallopeptidases (MMP3 & MMP7); integrins (Itga4 and Itga5); extracellular matrix molecules (ECM1, Lama2, Lamb2, TnC); cell contact and adhesion molecules (Vcan, Cad2, Vcam); proteoglycans (Sparc, Spock1, Sgce) and connective tissue growth factor (Ctgf) down-regulated, by more that two-fold in Barx2-/- myoblasts relative to wildtype myoblasts. Three independent experiments were performed ($p<0.05$).

Supplementary Table 2

Genotype	***Barx2+/+***	***Barx2+/-***	***Barx2-/-***
Observed	21	49	15
Expected	21.25	42.5	21.25

Supplementary Table 2. *Barx2-/-:mdx* pups are significantly underrepresented in litters derived from *Barx2+/-:mdx* crosses. After 6 generations of inbreeding, we collected and genotyped 16 litters (85 offspring) from crosses between *Barx2+/-:mdx* mice i.e. heterozygous for Barx2 and homozygous for the *mdx* allele of dystrophin. Mice were 4 weeks old when genotyped. The number of mice of each Barx2 genotype observed was compared to the expected 1:2:1 ratio. *Barx2-/-:mdx* mice are significantly underrepresented (exact bionomial test, p=0.07).