

Genotype	(N)	Animals That Developed Tumors	Confirmed RMS	Penetrance (%)
Experimental Lines				
<i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{F/F} ; <i>Myf6</i> ^{ICN/any}	56	19	12/15	27
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{F/F} ; <i>Myf6</i> ^{ICN/any}	37	35	13/14	88
MST^{WT} Control Lines				
<i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{+/+} ; <i>Myf6</i> ^{ICN/any}	17	1	0/1	0
<i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{F/+} ; <i>Myf6</i> ^{ICN/any}	46	0	-	0
<i>Pax3</i> ^{PF/+} ; <i>Cdkn2a</i> ^{+/+} ; <i>Myf6</i> ^{ICN/any}	15	0	-	0
<i>Pax3</i> ^{PF/+} ; <i>Cdkn2a</i> ^{F/+} ; <i>Myf6</i> ^{ICN/any}	2	0	-	0
MST^{Null} Control Lines				
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax7</i> ^{CE/+} (+IP Tamoxifen)	8	0	-	0
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax3</i> ^{+/+} ; <i>Cdkn2a</i> ^{+/+} ; <i>Myf6</i> ^{ICN/any}	27	1	0/1	0
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax3</i> ^{PF/+} ; <i>Cdkn2a</i> ^{+/+} ; <i>Myf6</i> ^{ICN/any}	8	0	-	0
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{+/+} ; <i>Myf6</i> ^{ICN/any}	22	0	-	0
<i>Stk3</i> ^{F/F} ; <i>Stk4</i> ^{F/F} ; <i>Pax3</i> ^{PF/PF} ; <i>Cdkn2a</i> ^{F/+} ; <i>Myf6</i> ^{ICN/any}	26	0	-	0

Supplementary Table 3. Experimental genotypes generated and tumor penetrance. MST1/2-floxed (*Stk3*^{F/F}; *Stk4*^{F/F}) mice were crossed with an established MST^{WT} aRMS GEMM based on conditional expression of Pax3:Foxo1 from the endogenous *Pax3* locus and conditional loss of *Cdkn2a* in *Myf6*-expressing cells. Red font indicates point of divergence from aRMS model genotype. Penetrance is calculated as (animals with tumors/total animals) x (confirmed RMS tumors/total analyzed tumors).