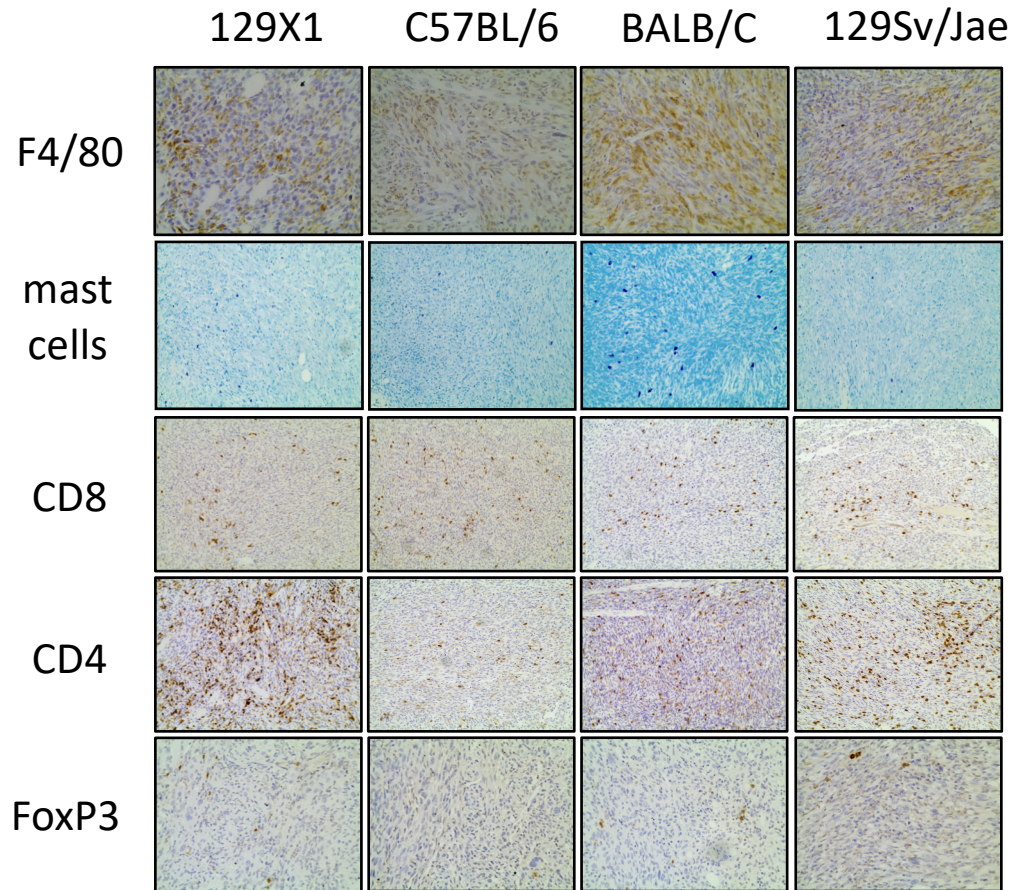


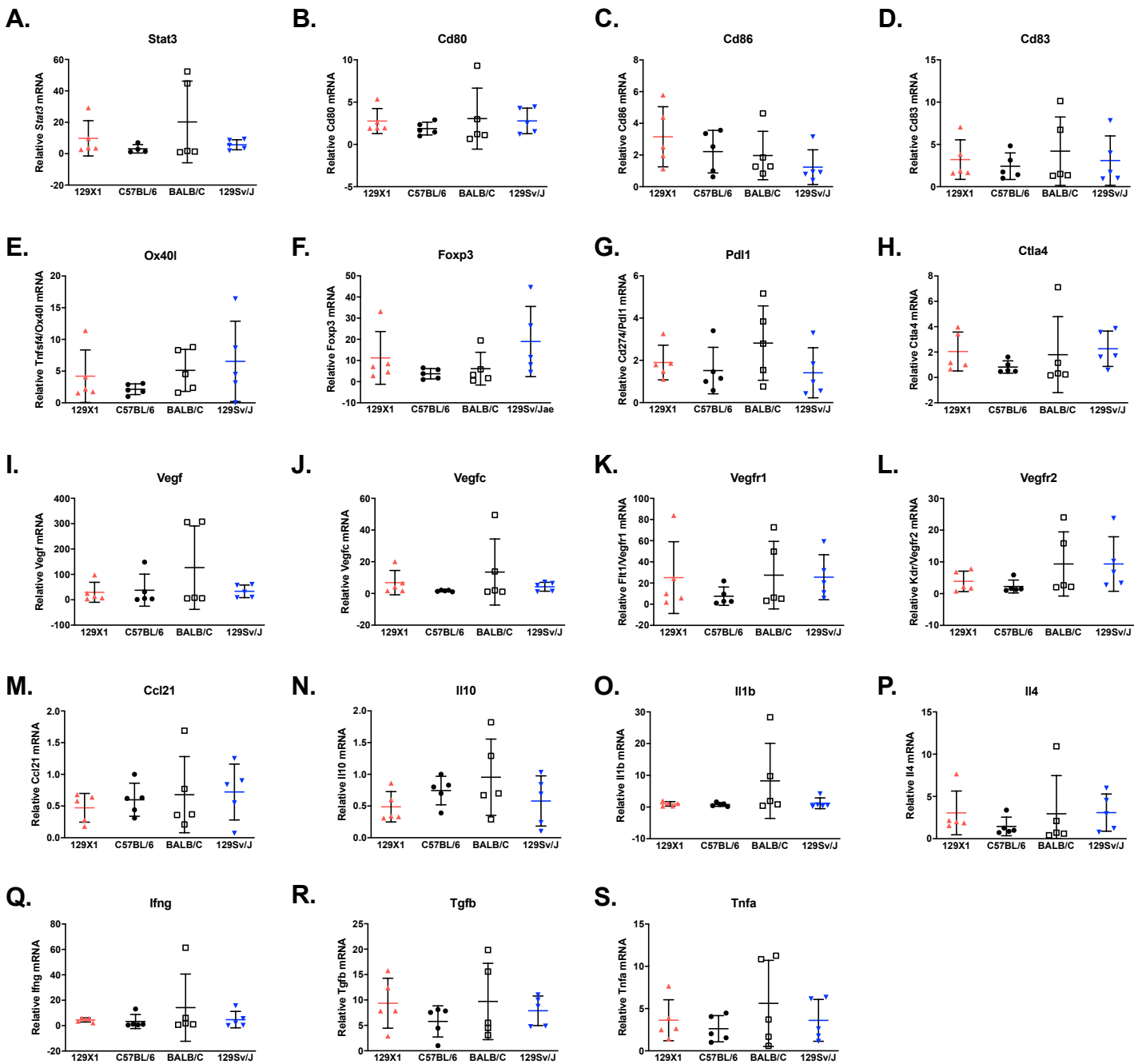
Table S1: Primer and guide RNA sequences

<b>Primer/gRNA Name</b>	<b>Sequence (5' to 3')</b>	<b>Use</b>
gNf1	GGACATCTCCAAGGATGTGGTGG	gRNA targeting Nf1
gTrp53	GATGGTAAGGATAGGTCCGCGG	gRNA targeting Trp53
Nf1 fw	TAGCAATTTTGGGGGAACGC	PCR for Indel Analysis
Nf1 rv	GTCAGAGCCTTTCAGTCATG	
Trp53 fw	TGCCGAACAGGTGGAATATC	PCR for Indel Analysis
Trp53 rv	CATCCTGACTGTGTGTAAGCTAGGCCCC	
Arg1 fw	AGAGATTATCGGAGCGCCTT	RT-qPCR
Arg1 rv	TTTTTCCAGCAGACCAGCTT	
Nos2 fw	CACTTGGATCAGGAACCTGAAGCCC	RT-qPCR
Nos2 rv	CTTTGTGCTGGGAGTCATGGAGCCG	
Stat3 fw	CAATACCATTGACCTGCCGAT	RT-qPCR
Stat3 rv	GAGCGACTCAAACCTGCCCT	
Cd80 fw	CTCTTTGTGCTGCTGATTCG	RT-qPCR
Cd80 rv	GGCAAGGCAGCAATACCTTA	
Cd86 fw	CTTACGGAAGCACCCATGAT	RT-qPCR
Cd86 rv	TCTCCACGGAACAGCATCT	
Cd83 fw	GCTCTCCTATGCAGTGCCTG	RT-qPCR
Cd83 rv	TCGAAGGAGCTGTTTTGCTT	
OX40L (Tnfsf4) fw	CTAAGGCTGGTGGTCTCTGG	RT-qPCR
OX40L (Tnfsf4) rv	CTTTGGATTGGAGGGTCCTT	
Foxp3 fw	TGGCAGAGAGGTATTGAGGG	RT-qPCR
Foxp3 rv	CTCGTCTGAAGGCAGAGTCA	
PD-L1 (CD274) fw	GCTCCAAAGGACTTGTACGTG	RT-qPCR
PD-L1 (CD274) rv	TGATCTGAAGGGCAGCATTC	
Ctla-4 fw	GCCTTCTAGGACTTGGCCTT	RT-qPCR
Ctla-4 rv	CACTGAAGGTTGGGTACCT	
Vegfa fw	GCTTCCTACAGCACAGCAGA	RT-qPCR
Vegfa rv	AATGCTTTCTCCGCTCTGAA	

VEGFR1 (Flt1) fw	CTGCTCGGGTGTCTGCTT	RT-qPCR
VEGFR1 (Flt1) rv	AAGAGAGTCTGGCCTGCTTG	
VEGFR2 (Kdr) fw	AAACCTCCTGCAAGCAAATG	RT-qPCR
VEGFR2 (Kdr) rv	TCCAGAATCCTCTTCCATGC	
Ccl21 fw	CCCTGCTTCAACCATTACATCTGC	RT-qPCR
Ccl21 rv	CCTGCTGTCTCCTTCCTCATTCC	
Il10 fw	ATCGATTCTCCCCTGTGAA	RT-qPCR
Il10 rv	TGTCAAATTCATTCATGGCCT	
Il1b fw	GAAATGCCACCTTTTGACAGTG	RT-qPCR
Il1b rv	CTGGATGCTCTCATCAGGACA	
Il4 fw	GGATGTGCCAAACGTCCTC	RT-qPCR
Il4 rv	GAGTTCTTCTTCAAGCATGGAG	
Ifng fw	TCTGGAGGAACTGGCAAAG	RT-qPCR
Ifng rv	TTCAAGACTTCAAAGAGTCTGAGG	
Tgfb1 fw	GGAGAGCCCTGGATACCAAC	RT-qPCR
Tgfb1 rv	CAACCCAGGTCCTTCCTAAA	
Tnfa fw	CTTCTGTCTACTGAACCTCGGG	RT-qPCR
Tnfa rv	CACTTGGTGGTTTGCTACGAC	
B2M fw	GGTCTTTCTGGTGCTTGTCTC	RT-qPCR
B2M rv	G TTCAGTATGTTCGGCTTCCC	



Supplemental Figure 1: IHC of innate and adaptive immune cells in CRISPR/Cas9-generated MPNSTs. Macrophages (F4/80 staining; 40x) and mast cells (toluidine blue staining; 20x) are enriched in MPNSTs from BALB/c mice. Cytotoxic T cells (CD8 staining; 20x) are similar across all strains. Helper T cells (CD4 staining; 20x) are enriched in 129X1 and 129Sv/Jae tumors. Regulatory T cells (FoxP3 staining, 40x) are enriched in 129X1 tumors.



Supplemental Figure 2: Quantitative RT-PCR data from heatmap.  
 Expression levels of genes in the MPNST microenvironment  
 examining macrophages (A), adaptive immunity (B-H), angiogenesis  
 and lymphangiogenesis (I-L), and cytokines (M-S).