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Effects of inhibitors of SLC9A-type sodium-proton exchangers on *Survival Motor Neuron 2* (*SMN2*) mRNA splicing and expression

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Running title: EIPA, HMA and *SMN2* gene regulation

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ABBREVIATIONS

ACTB, β-actin; ASIC1A, acid-sensing ionic channel 1A; ATXN1, ataxin-1; BLA, β-lactamase; COL3A, collagen IIIA; DHCR7, 7-dehydrocholesterol reductase; DMA, 5-(N,N-dimethyl)amiloride; EIPA, 5-(N-ethyl-N-isopropyl)amiloride; FABP3, fatty acid binding protein 3; FOXM1, forkhead box protein M1; GAPD, glyceraldehyde 3-phosphate dehydrogenase; HMA, 5-(N,N-hexamethylene)amiloride; hnRNPA1, heterogeneous nuclear ribonucleoprotein A1; NHE, sodium/proton exchanger; IPA, Ingenuity Pathways Analysis; PCA, principal component analysis; PRKAR2B, protein kinase cAMP-dependent type II regulatory subunit beta; RPLP0, large ribosomal protein P0; SaM68, Src-associated in mitosis 68 kDa; SF2/ASF, splicing factor 2 homolog/alternative-splicing factor; SI, splicing factor; SMA, spinal muscular atrophy; SMN1, survival motor neuron 1; SMN2, survival motor neuron 2; SRp20, serine/arginine-rich splicing factor 20 kDa; STRN3, striatin 3; TIA1, T cell-restricted intracellular antigen 1; Tra2β1, transformer 2 beta homolog; TRPP3, transient receptor potential cation channel subfamily P member 3; TRPV4, transient receptor potential cation channel subfamily V member 4; URA, upstream regulator analysis

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ABSTRACT

Spinal muscular atrophy (SMA) is an autosomal recessive, pediatric-onset disorder caused by the loss of spinal motor neurons thereby leading to muscle atrophy. SMA is caused by the loss of or mutations in the *survival motor neuron 1* (*SMN1*) gene. *SMN1* is duplicated in humans to give rise to the paralogous *SMN2* gene. This paralog is nearly identical except for a cytosine to thymine (C-to-T) transition within an exonic splicing enhancer (ESE) element within exon 7. As a result, the majority of *SMN2* transcripts lack exon 7 (SMNΔ7) which produces a truncated and unstable SMN protein. Since *SMN2* copy number is inversely related to disease severity, it is a well-established target for SMA therapeutics development. 5-(N-ethyl-N-isopropyl)amiloride (EIPA), an inhibitor of sodium/proton exchangers (NHEs), has previously been shown to increase exon 7 inclusion and SMN protein levels in SMA cells. In this study, NHE inhibitors were evaluated for their ability to modulate *SMN2* expression. EIPA as well as 5-(N,N-hexamethylene)amiloride (HMA) increase exon 7 inclusion in *SMN2* splicing reporter lines as well as in SMA fibroblasts. The EIPA-induced exon 7 inclusion occurs via a unique mechanism that does not involve previously identified splicing factors. Transcriptome analysis identified novel targets, including *TIA1* and *FABP3*, for further characterization. EIPA and HMA are more selective at inhibiting the NHE5 isoform, which is expressed in fibroblasts as well as in neuronal cells. These results show that NHE5 inhibition increases *SMN2* expression and may be a novel target for therapeutics development.

SIGNIFICANCE STATEMENT

This study demonstrates a molecular mechanism by which inhibitors of the sodium-protein exchanger increase the alternative splicing of *SMN2* in spinal muscular atrophy cells. NHE5 selective inhibitors increase the inclusion of full-length *SMN2* mRNAs by targeting *TIA1* and *FABP3* expression, which is distinct from other small molecule regulators of *SMN2* alternative splicing. This study provides a novel means to increase full-length *SMN2* expression and a novel target for therapeutics development.

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KEYWORDS

spinal muscular atrophy; *SMN2*; alternative splicing; drug discovery; EIPA; HMA; sodium-proton exchanger

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INTRODUCTION

Proximal spinal muscular atrophy (SMA) is an early-onset neurodegenerative disease characterized by the loss of α-motor neurons in the anterior horn of the spinal cord which leads to muscle weakness and atrophy (Crawford and Pardo, 1996; Tisdale and Pellizzoni, 2015). SMA is an autosomal recessive disease with an incidence of 1 in 6,000-10,000 births (Cuscó et al., 2002; Pearn, 1978). SMA results from the loss or mutation of *SMN1* (*survival motor neuron 1*) on chromosome 5q13 (Lefebvre et al., 1995). Uniquely in humans, a large tandem chromosomal duplication has led to a second copy of this gene known as *SMN2* (Lorson et al., 1999; Monani et al., 1999). *SMN2* is functionally distinguishable from *SMN1* by a single nucleotide difference (*SMN2 c.850C>T*) in exon 7 that disrupts an exonic splice enhancer. As a result, about 80-90% of *SMN2* mRNAs lack exon 7 (*SMNΔ7*) and produce a protein that is both unstable and not fully functional (Burnett et al., 2009; Cho and Dreyfuss, 2010; Lorson and Androphy, 2000). Because 10-20% of the *SMN2* gene product is fully functional (Lorson et al., 1999; Monani et al., 1999), increased genomic copies of *SMN2* inversely correlate with disease severity among individuals with SMA (Butchbach, 2016). Studies using transgenic mouse models for SMA have shown that increased *SMN2* copy number lessens the phenotypic severity of disease (Hsieh-Li et al., 2000; Michaud et al., 2010; Monani et al., 2000).

As *SMN2* is a major genetic modifier of SMA phenotype, it has become the primary target for the development of small molecule therapies for SMA (Cherry et al., 2014). *SMN2* gene expression can be regulated by increasing promoter activation, increasing inclusion of exon 7 in *SMN2* mRNA transcripts and including translational read-through of *SMNΔ7* mRNAs (Calder et al., 2016). Although there is currently no cure for SMA, a splice modifying oligonucleotide that increases *SMN2* exon 7 inclusion (nusinersen, Spinraza) recently received FDA approval for SMA patients (Finkel et al., 2017; Mercuri et al., 2018). Splice modifying oligonucleotides, however, have suboptimal properties including not being able to cross the blood-brain barrier, not being orally bioavailable, potentially being toxic at high doses and being expensive to manufacture (Sumner and Crawford, 2018). Despite these

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exciting advances, other therapies are needed, particularly if they are complementary to these current therapeutic options.

Small molecule inducers of *SMN2* exon 7 inclusion have been identified. NVS-SM1 (branaplam) is a small molecule *SMN2* exon 7 splicing modulator that is orally bioavailable and CNS penetrant (Palacino et al., 2015). The pyridopyrimidinone class of small molecule modulators of *SMN2* exon 7, including RG7800 and RG7916 (risdiplam), have also shown efficacy in cell culture as well as in animal models for SMA (Feng et al., 2016; Naryshkin et al., 2014; Ratni et al., 2018; Ratni et al., 2016; Sivaramakrishnan et al., 2017; Wang et al., 2018; Woll et al., 2016). Risdiplam (Evrysdi; Genetech and Roche) was recently approved by the FDA for treating SMA patients (Baranello et al., 2021). Other classes of small molecules have been identified as modulators of *SMN2* exon 7 splicing. EIPA (5-(N-ethyl-N-isopropyl)-amiloride), an inhibitor of Na^+/H^+ exchangers (NHEs, also known as SLC9A family), upregulates *SMN2* expression in SMA lymphoblastoid cells by increasing the inclusion of exon 7 in *SMN2* transcripts (Yuo et al., 2008). In this study, we examine the effects of other NHE inhibitors—both structurally related to EIPA as well as other classes of inhibitors—on *SMN2* alternative splicing at exon 7 and *SMN* expression in SMA cells. The modulatory effects of EIPA and its analogues are also compared against RG7800, a well-characterized *SMN2* exon 7 splicing modulator.

MATERIALS AND METHODS

Test Compounds

Amiloride, cariporide, 5-(N-ethyl-N-isopropyl)amiloride (EIPA), 5-(N,N dimethyl)amiloride (DMA), and zoniporide were obtained from Cayman Chemicals (Ann Arbor, MI) while 5-(N, N-hexamethylene)amiloride (HMA) was purchased from Sigma-Aldrich (St. Louis, MO). The structures of the amiloride test compounds are shown in **Figure 1**. RG7800 was obtained from MedKoo Biosciences, Inc (Morrisville, NC). All stock solutions were made by dissolving the compound in DMSO (Sigma-Aldrich).

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Cell Culture

Fibroblast cells derived from type II SMA patients (GM03813, GM22592, and AIDHC-SP22) have a homozygous deletion of *SMN1* and 3 copies of *SMN2* (Stabley et al., 2015; Stabley et al., 2017). GM03814 fibroblasts (Scudiero et al., 1986) were derived from the carrier mother of GM03813 with 1 copy of *SMN1* and 5 copies of *SMN2* (Stabley et al., 2015). GM03813, GM22592 and GM03814 fibroblasts were obtained from Coriell Cell Repositories (Camden, NJ) while the other fibroblast lines were generated at Nemours Children's Hospital Delaware (Stabley et al., 2017). All fibroblast lines were authenticated using short tandem repeat profiling and digital PCR (Stabley et al., 2017). The *SMN2* exon 7 splicing reporter cell line NSC-34:SMN2:Mg2:bla5.3 (Andreassi et al., 2001) was obtained from Vertex Pharmaceuticals (Boston, MA).

Fibroblast lines as well as NSC-34:SMN2:Mg2:bla5.3 cells were maintained in Dulbecco's modified essential medium (DMEM; Life Technologies, Grand Island, NY) containing 10% EquaFETAL (Atlas Biologicals; Fort Collins, CO), 2 mM L-glutamine (Life Technologies) and 1% penicillin- streptomycin (Life Technologies). All cell lines were maintained in a humidified chamber at 37°C with 5% CO_2.

***SMN2* Exon 7 Splicing Reporter Assay**

NSC-34:SMN2:Mg2:bla5.3 cells (Andreassi et al., 2001) were seeded onto a black-walled, clear bottom 96-well tissue culture plates (Santa Cruz Biotechnology, Dallas, TX) at a density of 5 x 10^4 cells/cm^2. Drug compounds (n = 4/dose) were added to serum-free medium at a dilution of 1:500. 100 µL of drug-containing medium was then added to maintenance medium over the seeded NSC-34 cells. After incubation for 19 hours, media containing drug compounds was aspirated and 100 µL of fresh maintenance medium was added to each well. 20 µL of 6X CCF2-AM Loading solution (GeneBlazer In Vivo Detection Kit, Life Technologies; containing 6 µM CCF2-AM and 12 mM probenecid) were added to each of the assay wells and plates were incubated at room temperature

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for 2 hours before the plates were read on a Victor X4 (Perkin Elmer, Waltham, MA) fluorescence plate reader (λ_{ex} = 405 nm, λ_{em} = 530 nm and λ_{em} = 460 nm). The 460 nm:530 nm fluorescence ratios were then calculated for each sample.

Drug Treatment of Cells

Fibroblasts were seeded 24 hours prior to drug treatment at a density of 3.2×10^4 cells/well in a 6-well plate for RNA analysis and of 4.0×10^5 cells/dish in a 10-cm dish for protein analysis. Test compounds were added to each sample at a 1:1000 dilution and compound-containing medium was replaced every 24 hours during the five-day treatment period. Cells were then harvested 24 hours after last drug compound treatment.

RNA Isolation

Total RNA was extracted from cell pellets using the RNeasy Mini kit (QIAGEN; Germantown, MD) per the manufacturer's instructions. RNA quality was assessed using a 2100 Bioanalyzer (Applied Biosystems).

***SMN* Exon 7 Inclusion Assay**

First-strand cDNA was synthesized from total RNA (500 ng) using the iScript™ cDNA Synthesis Kit (Bio-Rad, Hercules, CA, USA) as described previously (Gentillon et al., 2017). PCRs were run for sample cDNAs using GoTaq Green Polymerase Mix (Promega; Madison, WI) with the following primer sets (Integrated DNA Technologies; Coralville, IA): *SMN*, SMNex6 (F) 5'-cccatatgtccagattctcttgat-3'; SMNex8(R) 5'-ctacaacacccttctcacag-3'; *human collagen-IIIA* (*COL3A*), COL3A (F) 5'-gctctgcttcatcccactatt-3' and COL3A(R) 5'-ggaataccagggtcaccattt-3'. PCR products were resolved through a 2% agarose gels via electrophoresis. Images were captured with an AlphaImager gel documentation station (ProteinSimple, San Jose, CA) and band intensities were quantified using Image J 1.45s (National Institutes of Health, Bethesda, MD).

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Quantitative Reverse Transcriptase-Polymerase Chain Reaction (qPCR)

qPCR was completed for each treated sample using the iScript™ cDNA Synthesis Kit and the Bullseye EvaGreen qPCR MasterMix (Midsci, Valley Park, MO) as described previously (Gentillon et al., 2017). Each sample was assayed in triplicate. The following primer sets were used: *full-length SMN* (*FL-SMN*) (SMNex6F) 5'-ccatatgtccagattctcttgatga-3', (SMNex78R) 5'-atgccagcatttctccttaattta-3'; *SMNΔ7* (SMNex6F), (SMNex68R) 5'-atgccagcatttccatataatagc-3'; *full-length striatin-3* (*FL-STRN3*) (STRN3F) 5'-ggaagaaaggggtgaagagg-3', (STRN3R) 5'-tgattcctgaagggatgtgg-3'; *STRN3 lacking exons 8 and 9* (*STRN3Δ89*) (STRN3D89F) 5'-cagaatgggctgaaccaataa-3', (STRN3D89R) 5'-accgtcaagtctgcaaggtc-3'; *forkhead box protein M1A* (*FOXM1A*) (FOXM1AF) 5'-gaacatgaccatcaaaaccgaactc-3', (FOXM1AR) 5'-aaattaaacaagctggtgatgggtg-3'; (*FOXM1B*) (FOXM1BF) 5'-ggaccaggtgtttaagcagcag-3', (FOXM1BR) 5'-caatgcggactcgcttgctat-3'; (*FOXM1C*) (FOXM1CF) 5'-ttgcccgagcagttggaatca-3', (FOXM1CR) 5'-tcctcagctagcagcaccttg-3'; *heterogeneous nuclear ribonucleoprotein A1* (*hnRNPA1*) (hnRNPA1-F) 5'-agggcgaaggtaggctggca-3', (hnRNPA1-R) 5'-gcttcctcagctcttcgggct-3'; *transformer 2 beta homolog* (*hTra2β1*) (hTRA2bF) 5'-cacatcgaccggcgacagca-3' (hTRA2bR) 5'-ccccgatccgtgagcacttcc-3'; *splicing factor-2 homolog/alternative-splicing factor* (*SF2/ASF*) (hSF2ASF-F) 5'-cagagtggttgtctctg-3', (hSF2ASF-R) 5'-ctccacgacaccagtgcc-3'; *Src-associated in mitosis 68 kDa* (*SaM68*) (hSAM68F) 5'-atctctgtaattgggaaagggc-3', (hSAM68R) 5'-agagcataagcctcacatgg-3'; *serine/arginine-rich splicing factor 20 kDa* (*SRp20*) (hSRp20F) 5'-atgcatcgtgattcctg-3', (hSRp20R) 5'-ctgcgacgaggtggagg-3'; *T-cell-restricted intracellular antigen-1* (*TIA1*) (TIA1-F) 5'-cagcgttcacaagatcatttcc-3', (TIA1-R) 5'-tcccttagactttcctgttgc-3'; *fatty acid binding protein 3* (*FABP3*) (FABP3-F) 5'-aaatgggacgggcaagag-3', (FABP3-R) 5'-tgcctctttctcataagtgcg-3'; *7-dehydrocholesterol reductase* (*DHCR7*) (DHCR7-F) 5'-gcaacccaacattcccaaag-3', (DHCR7-R) 5'-agtgaaaaccagtccacctc-3'; *transient receptor potential cation channel subfamily V member 4* (*TRPV4*) (TRPV4-F) 5'-acctttccgattcctgctc-3', (TRPV4-R) 5'-tcctcattgcacaccttcatg-3'; *ataxin-1* (*ATXN1*) (ATXN1-F) 5'-catccagagtgcagagataagc-3', (ATXN1-R) 5'-

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ctctaccaaaacttcaacgctg-3' and *protein kinase cAMP-dependent type II regulatory subunit beta* (*PRKAR2B*) (PRKAR2B-F) 5'-tgatcaaggtgacgatggtg-3', (PRKAR2B-R) 5'-tgtacattaaggccagttcgc-3'. Primers for the human reference transcripts *β-actin (ACTB*), *large ribosomal protein P0* (*RPLP0*) and *glyceraldehyde 3-phosphate dehydrogenase* (*GAPD*) were purchased from Real Time Primers LLC (Elkins Park, PA).

The relative transcript levels were calculated using the efficiency-adjusted $2^{-\Delta\Delta Ct}$ method (Schmittgen and Livak, 2008; Yuan et al., 2008). The PCR efficiency (E) for each primer set was calculated from the slope of a Ct vs. $\log_{10}$(cDNA serial dilution) curve ($E = 10^{[-1/slope]}$) (Pfaffl, 2001). $\Delta C_{t,adjusted}$ is the difference between the adjusted C_t ($C_{t,measured} \times E$) for the target transcript and the geometric mean of the adjusted C_t values for the three reference genes and $\Delta\Delta C_t$ is defined as the difference between the ΔC_t for the SMA sample and the ΔC_t for the control sample.

Immunoblot

Protein extracts were generated from cell pellets as described previously (Gentillon et al., 2017). Protein extracts from treated cells (15 µg protein/lane) were resolved from miniPROTEAN TGX gradient precast acrylamide gels (BioRad) via electrophoresis as described previously (Gentillon et al., 2017). The resolved proteins were then transferred onto PVDF membranes via electroblotting. Immunoblotting was completed as described in (Gentillon et al., 2017). The following primary antibodies were used in this study: mouse anti-SMN mAb (1:2000; clone 8, BD Biosciences) and mouse anti-β-actin mAb (1:10,000; clone AC15, Sigma-Aldrich, St. Louis, MO). The horseradish peroxidase-conjugated anti-mouse and anti-rabbit secondary antibodies (1:5000); Rockland Immunochemicals, Inc., Gilbertsville, PA). After extensive washing, the bound antibody was detected by chemiluminescence using either Western Sure ECL Substrate (LiCor, Lincoln, NE) or SuperSignal West Femto (Thermo Scientific) kits and captured with the C-DiGit Blot Scanner (LiCor). Band intensities, defined as the band signal divided by the band area, were measured using the Image StudioTM Lite software (LiCor). The measured band areas were the same for each sample on a blot.

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Band intensities for the target protein (SMN) were divided by those for the reference protein (β-actin) to obtain normalized band intensities. To measure the relative protein level for a sample, the normalized band intensity for the drug-treated sample was divided by the normalized band intensity for the control sample (DMSO-treated cells).

Microarray

cDNAs from treated RNA samples—with RNA integrity numbers greater than 9.0—were prepared using the GeneChip WT PLUS Reagent Kit (Applied Biosystems, Foster City, CA). Double-stranded cDNA was synthesized from 100 ng total RNA using a random primer which incorporated a T7 promoter. This double-stranded cDNA was then used as a template to generate cRNA via a 16 hr in-vitro transcription reaction followed by purification with magnetic beads. Single stranded cDNA was regenerated from this cRNA through a random primed reverse transcription using a dNTP mix containing dUTP. After RNA hydrolysis with RNase H, the cDNA was purified using magnetic beads and then enzymatically fragmented with a mixture of uracil-DNA glycosylase (UDG) and apyrinic/apyrimidinic endonuclease 1 (APE1). This fragmented cDNA was then end-labeled with a biotinylated dideoxynucleotide using terminal transferase. Fragmented, biotinylated cDNA was added to a hybridization cocktail, denatured, loaded on a Clariom D human GeneChips and hybridized for 16 hours at 45 ºC and 60 rpm. Following hybridization, the chips were washed and stained using the pre-programmed FS450_0001 protocol. The stained chips were scanned at 532 nm with a GeneChip Scanner 3000 (Applied Biosystems).

The resultant data were analyzed with the TAC 4.0 software (Applied Biosystems). The raw data have been deposited into the NCBI Gene Expression Omnibus (GEO) (Barrett et al., 2013) under the accession number GSE179861. Identification of biological pathways and upstream regulators was completed using Ingenuity Pathway Analysis (IPA version 21901358; QIAGEN Redwood City, Inc., Redwood City, CA) as described previously (Maeda et al., 2014). Biological function and canonical pathways were determined to be over-represented using the Fisher exact test with a false discovery

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rate (FDR) correction ($p \leq 0.05$). Upstream regulators were considered as being activated if their z-scores were greater than or equal to 2.0 or inhibited if they were less than or equal to -2.0 (Krämer et al., 2014).

Statistical Analysis

Data are expressed as mean ± standard error. Parametric data were analyzed by ANOVA with a Holm-Sidak (expression analysis) *post hoc* test. Statistical significance was set at $p \leq 0.05$. Comparisons between data were performed with Sigma Plot v.12.0 or SPSS v.22.0.

RESULTS

Effects of NHE Inhibitors on *SMN2* Exon 7 Alternative Splicing

To determine the effect of NHE inhibitors on increasing *SMN2* expression, we first examined their effects on the inclusion of *SMN2* exon 7. Using a *SMN2* exon 7 splicing reporter assay established in motor neuron-like NSC-34 cells (Andreassi et al., 2001), we measured the effects of amiloride, DMA, EIPA, HMA, cariporide and zoniporide (**Figure 1**) on β-lactamase (BLA) activity—a marker for *SMN2* exon 7 inclusion. The EIPA and HMA significantly increased exon 7 inclusion, as shown by an increase in the λ_{460nm} to λ_{530nm} fluorescence ratio, in these reporter cells (**Figure 2A**). Amiloride, cariporide and zoniporide, on the other hand, significantly reduced BLA activity.

We also examined the effect of NHE inhibitors on the inclusion of exon 7 in *SMN2* mRNAs in a SMA intracellular environment by using patient-derived fibroblasts. GM03813 type II SMA fibroblasts (Scudiero et al., 1986) were treated with different concentrations of amiloride, DMA, EIPA, HMA, zoniporide or cariporide for 5 days. After treatment, *SMN2* exon 7 inclusion was measured via RT-PCR using primers spanning exons 6 through 8 of *SMN2*. *Collagen IIIA* (*COL3A*) transcript levels were used as a loading control as it is highly and constitutively expressed in fibroblast cells (Heier et al., 2007). As shown in **Figure 2B**, the proportion of *FL-SMN* (top band) relative to *SMNΔ7* (bottom band) transcripts was increased in SMA fibroblasts treated with EIPA and HMA but not in any of the

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other NHE inhibitors. HMA was more potent at increasing *SMN2* exon 7 inclusion than EIPA (**Figure 2C**).

There are 5 different isoforms of SLC9A-type Na^+/H^+ antiporters (*NHE1*, *NHE2*, *NHE3*, *NHE4* and *NHE5*) that are present on the plasma membrane (Masereel et al., 2003). Using RT-PCR, we determined the SLC9A isoform expression profiles for NSC-34 cells as well as for GM03813 and GM03814 fibroblasts. NSC-34 cells as well as fibroblast cell lines express predominantly *NHE1* and *NHE5* (**Supplemental Figure 1**).

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Effects of NHE Inhibitors on *SMN2* Expression in Type II SMA Fibroblasts

We treated GM03813 type II SMA fibroblasts with different concentrations (0.1 – 10 μM) of the NHE inhibitors for 5 days. *FL-SMN* and *SMNΔ7* transcript levels were measured by qPCR. EIPA and HMA significantly increase *FL-SMN* mRNA levels in GM03813 cells to about 80% of the amount of *FL-SMN* seen in carrier fibroblasts (GM03814) (**Figure 3A**). Amiloride, cariporide and zoniporide, however, reduced the abundance of *FL-SMN* transcripts in SMA fibroblasts. EIPA was the only NHE inhibitor that significantly reduced the levels of *SMNΔ7* mRNA in treated cells (**Figure 3B**). To demonstrate that these observations were not unique to a single SMA cell line, we measured the effects of the NHE inhibitors on *FL-SMN* and *SMNΔ7* transcript levels in two other type II SMA fibroblast lines— GM22592 and AIDHC-SP22. EIPA and HMA also increased *FL-SMN* transcripts in GM22592 and AIDHC-SP22 cells, indicating that their effects on *SMN2* mRNA regulation are cell-line independent (**Figure 3C**). *SMNΔ7* transcript levels were also reduced in AIDHC-SP22 and GM22592 fibroblasts treated with EIPA or HMA (**Figure 3D**).

We measured SMN protein levels of GM03813 type II SMA fibroblasts treated with the aforementioned NHE inhibitors for 5 days (**Figure 4**). Amiloride, cariporide and zoniporide had marginal effects on SMN protein levels in these cells. EIPA and HMA increased SMN protein levels in GM03813 fibroblasts with EIPA showing a maximal effect at 10 μM while the maximal effect of HMA was observed at 1 μM. Interestingly, DMA also increased SMA protein levels in SMA fibroblasts even

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though it had no effect on *FL-SMN* mRNA levels nor on exon 7 inclusion. This observation suggests that the DMA affects SMN gene regulation at a different level from EIPA and HMA.

Effects of NHE Inhibitors on Alternative Splicing of *Striatin-3* (*STRN3*) and *Forkhead Box Protein M1* (*FOXM1*) in SMA Fibroblasts

We measured the effects of the NHE inhibitors on the alternative splicing of other transcripts—aside from *SMN2*—that are affected by the pyridopyridinone RG7800 (Ratni et al., 2016; Woll et al., 2016) in order to determine if EIPA and HMA operate via a similar mechanism to promote exon 7 inclusion. *Striatin-3* (*STRN3*) has a similar pre-mRNA structure to the *SMN2* exon 7:intron 7 junction and RG7800 increases the inclusion of *STRN3* exons 8 and 9 (Naryshkin et al., 2014; Sivaramakrishnan et al., 2017). There are 3 isoforms of *forkhead box protein M1* (*FOXM1*) generated by alternative splicing of exons Va and VIIa: *FOXM1A* (which contains both exons Va and VIIa), *FOXM1B* (which contains neither exon) and *FOXM1C* (which contains only exon Va) (Liao et al., 2018). RG7800 increased the abundance of *FOXM1A* while reducing *FOXM1C* levels (Ratni et al., 2018).

The levels of *STRN3* and *FOXM1* splice variants were measured in GM03813 type II SMA fibroblasts treated with amiloride, EIPA, HMA or RG7800 for 5 days. EIPA and HMA had no effect on the amount of *FL-STRN3* mRNA while amiloride significantly increased *FL-STRN3* transcript levels (**Figure 5A**). RG7800 also increased the abundance of *FL-STRN3* transcripts in treated SMA fibroblasts. Interestingly, all NHE inhibitors tested increased *STRN3Δ89* mRNA levels (**Figure 5B**) while RG7800 reduced the amount of *STRN3Δ89* transcripts. None of the NHE inhibitors increased the levels of *FOXM1A* in SMA fibroblasts (**Figure 5C**). EIPA but not amiloride nor HMA significantly decreased *FOXM1C* transcript levels in SMA fibroblasts (**Figure 5D**). *FOXM1B* transcripts could not be detected in fibroblast samples (data not shown). Predictably, RG7800 increased relative *FOXM1A* levels and reduced the amount of *FOXM1C* transcript levels in treated cells (**Figures 5C** and **5D**). The

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mechanism of action of EIPA and HMA on the alternative splicing of *SMN2* exon 7, therefore, is distinct from that used by RG7800.

Effects of NHE Inhibitors on Expression of Regulators of *SMN2* Exon 7 Splicing

To understand the mechanism of action for the increased inclusion of exon 7 in *SMN2* transcripts induced by EIPA and HMA, we first examined the effects of NHE inhibitors on the expression of previously identified proteins that modulate the splicing of *SMN2* at exon 7. We focused on the following splicing regulators: hnRNP-A1 (Doktor et al., 2011; Harahap et al., 2012; Kashima et al., 2007a; Kashima et al., 2007b), SF2/ASF (SRSF1) (Cartegni et al., 2006; Cartegni and Krainer, 2002; Wee et al., 2014), hTra2β1 (SRSF10) (Chen et al., 2015; Helmken and Wirth, 2000; Hofmann et al., 2000; Hofmann and Wirth, 2002), SaM68 (KHDRBS1) (Pagliarini et al., 2015; Pedrotti et al., 2010) and SRp20 (SRSF3) (Helmken et al., 2003). The transcript levels of these splicing factors were measured in type II SMA fibroblasts treated with NHE inhibitors or DMSO for 5 days. *hnRNP-A1* transcript levels were significantly reduced in GM03813 cells treated with DMA, EIPA, HMA and zoniporide (**Figure 6A**). DMA, EIPA, HMA and cariporide reduced *SF2/ASF* levels in SMA fibroblasts (**Figure 6B**). Cariporide was the only NHE inhibitor to increase *hTra2β1* mRNA levels (**Figure 6C**). HMA significantly reduced *SaM68* transcript levels in SMA fibroblasts (**Figure 6D**). EIPA, HMA, cariporide and zoniporide decreased *SRp20* mRNA levels while DMA increased *SRp20* transcript levels (**Figure 6E**). Interestingly, *hrRNP-A1*, *hTra2β1* and *SRp20* mRNA levels are significantly elevated in GM03813 type II SMA fibroblasts relative to GM03814 carrier fibroblasts (**Figures 6A**, **6C** and **6E**). While the NHE inhibitors differentially regulate the expression of splicing factors which regulate *SMN2* exon 7 inclusion, there was no correlation between the differential expression of any of these splicing factors and the enhanced inclusion of *SMN2* exon 7 induced by EIPA or HMA in SMA fibroblasts.

Identification of Differentially Expressed Transcripts in SMA Fibroblasts Treated with EIPA

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To understand the molecular mechanisms by which EIPA enhances *SMN2* exon 7 inclusion, we compared the transcriptomes of GM03813 type II SMA fibroblasts treated with 10 μM EIPA against those treated with DMSO as well as against those treated with 10 μM amiloride, which did not increase *SMN2* exon 7 inclusion. Principal component analysis (PCA) correctly distributed each of the samples within their treatment groups (**Figure 7A**). Hierarchical clustering of the identified transcripts from amiloride-treated (**Figure 7B**) and EIPA-treated (**Figure 7C**) fibroblasts showed consistent differential expression between each treatment group. Amiloride treatment of GM03813 SMA fibroblasts altered the levels of 1269 transcripts when compared against DMSO-treated cells (**Figure 7D** and **Supplementary Table 1A**). There were 999 differentially expressed transcripts in SMA fibroblasts treated with 10 μM EIPA when compared against those cells exposed to DMSO (**Figure 7E** and **Supplementary Table 1B**). To identify those differentially expressed transcripts that may be relevant to *SMN2* alternative splicing, we compared the EIPA transcriptome against the amiloride transcriptome and identified 839 EIPA-unique differentially expressed transcripts (**Figure 7F** and **Supplementary Table 1C**).

Ingenuity Pathways Analysis (IPA) (Krämer et al., 2014) uses a manually curated literature database to determine the biological relevance of differentially expressed transcripts. There were 165 canonical pathways that were significantly overrepresented (Fisher's exact test p-value ≤ 0.05) in EIPA-treated SMA fibroblasts relative to amiloride-treated cells (**Supplementary Table 2**), with the top 12 overrepresented pathways shown in **Figure 7G**. Most of the top 12 overrepresented pathways contained Ras-family GTPases (*RAP2A*, *RAP1A* and *MRAS*) and subunits of the phosphatidylinositol-4-phosphate 3-kinase (*PIK3R1*, *PIK3C2G* and *PIK3CB*). Upstream Regulator Analysis (URA) (Krämer et al., 2014) can identify potential upstream molecules that may be responsible for EIPA-mediated differential gene expression. UPA identified 19 potential upregulators (10 of which were activated and 9 were inhibited) in EIPA-treated SMA fibroblasts relative to amiloride-treated fibroblasts (**Figure 7H** and **Supplementary Table 3**). Thrombospondin-1 (*THBS1*) and *DHCR7* are overrepresented target molecules in this analysis.

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Transcriptome arrays can also provide important information about differential splicing in response to drug treatment. There were 10307 splicing events that were differentially expressed in amiloride-treated GM03813 SMA fibroblasts while EIPA treatment showed 8307 differentially expressed splicing events. Of those events, only 352 were classifiable as either intron retention, alternative 5' donor, alternative 3' acceptor or cassette exon events in amiloride-treated cells and 251 in EIPA-treated cells (**Figure 7I**). The splicing index (SI) is a measure of exon expression that is normalized to the expression level of that gene (Clark et al., 2007). In EIPA-treated cells, there was an increase in the *SMN2* exons 6 and 7 splice junction (JUC0500051219; SI = +2.34, p = 0.0031) and a decrease in *SMN2* exons 6 and 8 splice junction (JUC0500051223; SI = -2.68; p = 0.0086). Amiloride treatment, however, did not significantly alter the abundance of either splice junction. The amount of *SMN2* exon 7 inclusion was, therefore, increased in EIPA-treated SMA fibroblasts.

To validate our microarray analysis, we used biological replicates of type II SMA fibroblasts (Fang and Cui, 2011) that were treated with either 10 μM EIPA, 10 μM HMA, 10 μM amiloride, 1 μM RG7800 or DMSO. We focused on the following transcripts: *TIA1* (**Figure 8A**; 2.06-fold decrease), *FABP3* (**Figure 8B**; 6.44-fold increase), *DHCR7* (**Figure 8C**; 2.07-fold decrease), *TRPV4* (**Figure 8D**; 2.13-fold decrease), *ATXN1* (**Figure 8E**; 2.58-fold decrease) and *PRKAR2B* (**Figure 8F**; 2.15-fold increase). The differential expressions of these transcripts, with respect to direction, in response to EIPA treatment were validated in the biological replicates. Transcripts that are differentially expressed only in EIPA- and HMA-treated SMA fibroblasts would potentially provide insights into the molecular mechanisms underlying EIPA- and HMA-induced *SMN2* exon 7 inclusion. *FABP3* (**Figure 8B**) transcript levels were markedly increased in cells treated with EIPA and HMA but not with amiloride or RG7800. EIPA and HMA as well as RG7800 reduced *TIA1* transcript levels (**Figure 8A**) in SMA fibroblasts. For the remaining transcripts, the direction of change in response to EIPA treatment was different from that to HMA, i.e. increased in EIPA-treated cells but decreased in HMA-treated cells.

DISCUSSION

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Because of the inverse relationship between SMA severity and *SMN2* copy number, *SMN2* is a primary target of SMA treatment and drug discovery through multiple mechanisms including promoter activation and increased exon 7 inclusion of *SMN2* pre-mRNA transcripts (Cherry et al., 2014). Many structurally distinct small molecules such as EIPA (Yuo et al., 2008), the pyridopyrimidinones RG7800 and RG7916 (Feng et al., 2016; Naryshkin et al., 2014; Ratni et al., 2018; Ratni et al., 2016; Sivaramakrishnan et al., 2017; Wang et al., 2018; Woll et al., 2016) and NVS-SM1 (Palacino et al., 2015) increase *SMN2* expression by enhancing exon 7 inclusion. EIPA is a derivative of amiloride and inhibits the activity of the SLC9A family of Na+/H+ antiporters (Kleyman and Cragoe Jr, 1988). In this study, we examined the effects of amiloride derivatives like EIPA and HMA as well as other NHE inhibitors on *SMN2* alternative splicing of exon 7. EIPA and HMA but none of the other SCL9A inhibitors tested increase *SMN2* exon 7 inclusion via a novel mechanism not involving previously identified regulators of SMN2 exon 7 splicing.

There are 5 different isoforms of SLC9A-type Na^+/H^+ antiporters that are localized to the plasma membrane in mammalian cells (Masereel et al., 2003). NHE1 is ubiquitously expressed in most mammalian cell types while NHE5 is primarily expressed in neurons and skeletal muscle (Donowitz et al., 2013). Tissue distribution profiles of *NHE1* and *NHE5* in humans and mice show strong expression in the tissues from which the cell lines used in this study were derived, i.e. brain and skin (Cheng et al., 2019; Fagerberg et al., 2014; Yue et al., 2014). EIPA and the related amiloride analogue HMA are potent inhibitors of the NHE1 and NHE5 isoforms (Kleyman and Cragoe Jr, 1988; Masereel et al., 2003; Szabó et al., 2000). Cariporide and zoniporide, on the other hand, are selective inhibitors of NHE1 (Masereel et al., 2003).

EIPA modulates neuronal plasticity and LTP in mice (Rönicke et al., 2009). NHE5 has been shown to be involved in neuronal excitation and long-term potentiation by negatively regulating dendrite spine growth in an a activity-dependent manner (Diering et al., 2011). NHE5 knockout mice display enhanced learning and memory and increased BDNF/TrkB-mediated signaling (Chen et al., 2017). NHE5 also regulates the membrane trafficking of the receptor tyrosine kinase Met and β1 integrins in

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glioma cells (Fan et al., 2016; Kurata et al., 2019). NHE5 is positively regulated by AMP-activated protein kinase (AMPK) in neuronal as well as non-neuronal cells (Jinadasa et al., 2014). NHE5 membrane localization is regulated by phosphatidylinositol 3-kinase (PI3K) activity and the actin cytoskeleton (Szászi et al., 2002). In addition to these roles in neuronal signaling, NHE5 regulates autophagy in neuronal cells (Togashi et al., 2013). Based on our observations, the selectivity of EIPA and HMA in increasing *SMN2* exon 7 inclusion may result from inhibition of a specific NHE isoform, in this case *NHE5*. The regulation of alternative splicing by *NHE5* has not been previously reported; future studies using gene knockdown approaches in SMA model systems will further elucidate the role of *NHE5* in *SMN2* exon 7 splicing. It is possible that selective inhibition of *NHE5* may not be sufficient to increase *SMN2* exon 7 inclusion. To address this possibility, future studies would determine if inhibition of other NHE isoforms, like *NHE1*, would be necessary for or would augment *SMN2* alternative splicing resulting from inhibition of *NHE5*.

The pyridopyridinone RG7800—which is undergoing clinical trials with SMA patients—increases *SMN2* exon 7 inclusion by binding to an exonic splice enhancer (ESE2) element present on the 5' splice site of the exon 7:intron 7 junction (Ratni et al., 2016; Sivaramakrishnan et al., 2017; Woll et al., 2016). Binding at these sites facilitates the binding of U1 snRNPs by dissociation of the inhibitory splicing factor hnRNP-G. *STRN3* has a similar pre-mRNA structure to the *SMN2* exon 7:intron 7 junction and RG7800 increases the inclusion of *STRN3* exons 8 and 9 (Naryshkin et al., 2014; Sivaramakrishnan et al., 2017). We show that EIPA and HMA have no effect on exon 8 and 9 inclusion in *STRN3* transcripts. Furthermore, EIPA and HMA do not modulate the alternative splicing of *FOXM1*, another transcript whose splicing is modulated by RG7800 (Ratni et al., 2018). These data suggest that EIPA and HMA modulate *SMN2* exon 7 alternative splicing via a mechanism that is distinct from the pyridopyridinones.

NHE antiporters regulate the cellular pH in mammalian cells (Masereel et al., 2003; Putney et al., 2002). Alterations in pH have been shown to affect the splicing of multiple mRNA transcripts including tenascin C and *SMN2* (Borsi et al., 1995; Chen et al., 2008). Low extracellular pH increases *SMN2*

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exon 7 skipping while a high extracellular pH promotes exon 7 inclusion (Chen et al., 2008). The decrease in exon 7 inclusion at low pH may be the result of diminished nuclear localization of hnRNP-A1, a splicing factor that prevents exon 7 inclusion via binding to an exonic enhancer element (Chen et al., 2008). EIPA (Yuo et al., 2008) and elevating extracellular pH (Chen et al., 2008) increase the nuclear localization of the splicing factor SRp20. In this study, we did not identify any relationship between the differential expression of any of these splicing factors and the enhanced inclusion of *SMN2* exon 7 induced by EIPA or HMA in SMA fibroblasts. Furthermore, the effects of EIPA and HMA on *SMN2* exon 7 alternative splicing may not be linked with regulation of cellular pH as other NHE1-selective inhibitors like cariporide and zoniporide do not alter *SMN2* exon 7 splicing. The effects of EIPA and HMA on *SMN2* alternative splicing may be mediated by a novel mechanism.

TIA1 is a splicing factor that has been shown to increase *SMN2* exon 7 levels (Singh et al., 2011). Loss of *Tia1* worsens disease progression in female, but not male, SMA-like mice (Howell et al., 2017). We show here that EIPA and HMA decrease *TIA1* mRNA levels in SMA fibroblasts even though these compounds increase *SMN2* exon 7 inclusion. Muscle biopsies from patients with Welander distal myopathy that harbor a point mutation in *TIA1* (TIA1(E384K)) have reduced *FL-SMN2* transcript levels but elevated *SMNΔ7* transcript levels (Klar et al., 2013); however, a recent report (Carrascoso et al., 2019) has shown that mutant TIA1 only modestly affects *SMN2* exon 7 alternative splicing in different cell types. Future studies will elucidate the role of NHE5 inhibition by EIPA and HMA on *TIA1* expression and the regulation of *TIA1* expression on the modulation *SMN2* exon 7 alternative splicing.

FABP3 transcript levels were markedly elevated in SMA fibroblasts treated with EIPA or HMA but not by other NHE inhibitors. *FABP3* is robustly expressed in neurons, as well as other non-neural tissues, and is responsible for intracellular transport of long chain polyunsaturated fatty acids (Falomir-Lockhart et al., 2019; Liu et al., 2010). FABP3 increases the aggregation of α-synuclein within dopaminergic neurons of the substantia nigra pars compacta, which leads to cell death and neurodegeneration (Shioda et al., 2014). In murine GABAergic neurons within the anterior cingulate

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cortex, FABP3 modulates the expression of glutamic acid decarboxylase (*Gad67*) by differential promoter methylation (Yamamoto et al., 2018). Further studies examining the effect of increased *FABP3* expression on *SMN2* alternative splicing would provide important insights into a novel mechanism of gene regulation.

While EIPA and HMA are potent inhibitors of NHE-type antiporters (Masereel et al., 2003), it is possible their mode of action with respect to *SMN2* exon 7 inclusion may be separate from NHE inhibition. Certain amilorides can also inhibit different types of Ca^{2+}-activated non-specific cation channels like ASIC1A (acid-sensing ion channel 1A) or TRPP3 (transient receptor potential P3, also known as polycystin-2) (Dai et al., 2007; Leng et al., 2016). It is possible that the effects of EIPA and HMA on *SMN2* alternative splicing may be mediated by inhibition of these other channels. To address this possibility, SMA fibroblasts and other cellular models can be treated with more specific ASIC1A or TRPP3 inhibitors, like phenamil and benzamil (Dai et al., 2007; Leng et al., 2016) to monitor their effects on *SMN2* exon 7 inclusion.

SMA can now be considered an actionable disease since there are currently 3 therapies approved by the FDA for SMA patients: nusinersen (Finkel et al., 2017; Mercuri et al., 2018), risdiplam (Baranello et al., 2021) and onasemnogene abeparvovec (Mendell et al., 2017). Despite these exciting advances, other therapies are needed, particularly if they are complementary to current therapeutic options. Traditional small molecule therapies have been the mainstay of the pharmaceutical industry for several important reasons. Small molecule inducers of *SMN2* expression could serve as complementary therapies for SMA patients who are either not good candidates or poor responders to biologic therapies. NHE5 inhibitors like EIPA and HMA may be able to serve this complementary role but they will need to be tested in animal models for SMA. The identification of more precisely targets for therapeutic development will ultimately lead to additional drug candidates for the treatment of SMA which can be used either alone or in combination with existing SMA therapies.

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AUTHORSHIP CONTRIBUTIONS

Participated in research design: Kanda and Butchbach

Conducted experiments: Kanda and Moulton

Contributed new reagents or analytic tools: Butchbach

Performed data analysis: Kanda, Moulton and Butchbach

Wrote or contributed to the writing of the manuscript: Kanda, Moulton and Butchbach

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FOOTNOTES

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FIGURE LEGENDS

Figure 1. Chemical structures of the SLC9A-type sodium-proton exchanger (NHE) inhibitors tested.

Figure 2. Effects of NHE inhibitors on *SMN2* alternative splicing. (A) *SMN2* exon 7 inclusion reporter cells (NSC-34:SMN2:Mg2:bla5.3) were treated with varying concentrations of the NHE inhibitors amiloride, DMA, EIPA, HMA, cariporide or zoniporide (1 nM - 10 μM; n=4/dose) or DMSO for 19 hours. β-Lactamase (BLA) activity was measured fluorimetrically. **(B-C)** Effect of NHE inhibitors on *SMN2* exon 7 inclusion in type II SMA fibroblasts. Type II SMA fibroblasts (GM03813) were treated with varying concentrations (100 nM – 10 μM; n=3/group) of NHE inhibitors or DMSO for 5 days (n=3/treatment group). After total RNA isolation, samples were analyzed for relative amounts of *FL-SMN* and *SMNΔ7* transcripts by RT-PCR and agarose gel electrophoresis. *COL3A* served as a loading control in this assay. The relative amounts of *FL-SMN* and *SMNΔ7* transcripts were also measured on carrier fibroblasts (GM03814). The asterisk (*) denoted a statistically significant ($p < 0.05$) difference between NHE inhibitor- and vehicle-treated cells.

Figure 3. Effects of NHE inhibitors on expression of *FL-SMN* and *SMNΔ7* mRNA transcripts in SMA patient-derived fibroblasts. GM03813 type II SMA fibroblasts were treated with different concentrations of NHE inhibitors (100 nM – 10 μM; n=3/dose) or DMSO for 5 days. Changes in *FL-SMN* **(A)** or *SMNΔ7* **(B)** transcript levels were measured via quantitative RT-PCR with *ACTB*, *GAPDH*, and *RPLP0* serving as reference transcripts. *FL-SMN* and *SMNΔ7* transcript levels were also measured in GM03814 carrier fibroblasts. Changes in *FL-SMN* **(C)** or *SMNΔ7* **(D)** transcript levels were measured in two other type II SMA fibroblast lines (GM22592 and AIDHC-SP22) treated with NHE inhibitors (10 μM; n=3/inhibitor) for 5 days. All transcript levels were expressed relative to

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DMSO-treated GM03813 cells (dashed line). The asterisk (*) denoted a statistically significant ($p < 0.05$) difference between NHE inhibitor- and vehicle-treated cells.

Figure 4. Effects of NHE inhibitors on SMN protein levels in SMA fibroblasts. GM03813 type II SMA fibroblasts were treated with different concentrations of NHE inhibitors (100 nM – 10 μM; n=3/dose) or DMSO for 5 days. Changes in SMN protein levels were measured via immunoblot using β-actin as a reference protein. SMN protein levels were also measured in GM03814 carrier fibroblasts.

Figure 5. Effects of the NHE inhibitors on alternative splicing of *striatin-3* (*STRN3*) and *forkhead box protein M1* (*FOXM1*) in type II SMA fibroblasts. GM03813 type II SMA fibroblasts were treated with 10 μM amiloride, 10 μM EIPA, 10 μM HMA, 1 μM RG7800 or DMSO (n=3/group) for 5 days. The levels of *full-length STRN3* (*FL-STRN3*; **A**), *STRN3* lacking exons 8 and 9 (*STRN3Δ89*; **B**), *FOXM1* containing exons Va and VIIa (*FOXM1A*; **C**) and *FOXM1* containing exon Va (*FOXM1C*; **D**) transcripts were measured in total RNA extracted from treated cells by quantitative RT-PCR. All transcript levels were expressed relative to DMSO-treated GM03813 cells (dashed line). The asterisk (*) denoted a statistically significant ($p < 0.05$) difference between drug- and vehicle-treated cells.

Figure 6. Effects of NHE inhibitors on the expression of splicing regulators involved in *SMN2* exon 7 alternative splicing. GM03813 type II SMA fibroblasts were treated with 10 μM NHE inhibitors (amiloride, DMA, EIPA, HMA, cariporide or zoniporide) or DMSO (n=3/group) for 5 days. *hnRNP-A1* (**A**), *SF2/ASF* (**B**), *hTRA2β1* (**C**), *SaM68* (**D**) and *SRp20* (**E**) transcript levels were measured in total RNA extracted from treated cells by quantitative RT-PCR. Transcript levels were also measured in GM03814 carrier fibroblasts. All transcript levels were expressed relative to DMSO-treated GM03813 cells (dashed line). The asterisk (*) denoted a statistically significant ($p < 0.05$) difference between drug- and vehicle-treated cells.

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Figure 7. Identification of differentially expressed transcripts in type II SMA fibroblasts treated with amiloride or EIPA. GM03813 type II SMA fibroblasts were treated with 10 μM amiloride, 10 μM EIPA or DMSO (n=3/group) for 5 days and their RNA pools were analyzed for differential transcript expression using Clariom D human transcriptome arrays. (**A**) Principal component analysis (PCA) of samples treated with amiloride (purple), EIPA (red) or DMSO (blue). Hierarchical clustering analysis of amiloride vs. DMSO (**B**) and EIPA vs. DMSO (**C**). Volcano plots of amiloride vs. DMSO (**D**) and EIPA vs. DMSO (**E**) type II SMA fibroblast transcriptomes. Significantly upregulated transcripts are shown in red while significantly downregulated transcripts are shown in blue. (**F**) Venn diagram showing the similarities and differences between the amiloride vs. DMSO (red) and EIPA vs. DMSO (blue) transcriptomes. The overlap between these two transcriptomes is shown in purple. (**G**) The top dozen canonical pathways—out of 165—that were significantly over-represented in the EIPA-unique transcriptome. The numbers next to the pathway lines represent the number of differentially expressed molecules for each pathway. (**H**) The upstream regulators that are significantly and uniquely differentially regulated in EIPA-treated type II SMA fibroblasts. (**I**) Distributions of the categorized differential splicing events between amiloride vs. DMSO and EIPA vs. DMSO transcriptomes.

Figure 8. Validation of EIPA- and HMA-responsive transcripts in type II SMA fibroblasts. GM03813 type II SMA fibroblasts were treated with 10 μM amiloride, 10 μM EIPA, 10 μM HMA, 1 μM RG7800 or DMSO (n=3/group) for 5 days. *TIA1* (**A**), *FABP3* (**B**), *DHCR7* (**C**), *TRPV4* (**D**), *ATXN1* (**E**) and *PRKARB2* (**F**) transcript levels were measured in total RNA extracted from treated cells by quantitative RT-PCR. All transcript levels were expressed relative to DMSO-treated GM03813 cells (dashed line). The asterisk (*) denoted a statistically significant ($p < 0.05$) difference between drug- and vehicle-treated cells.

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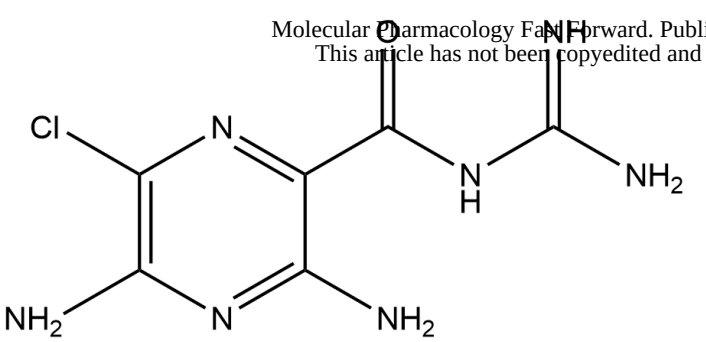
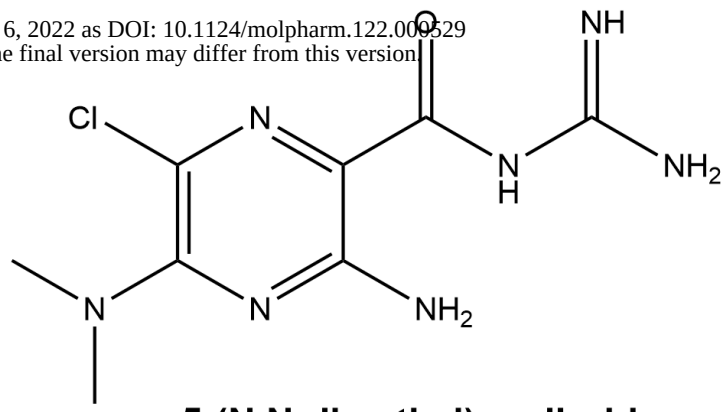
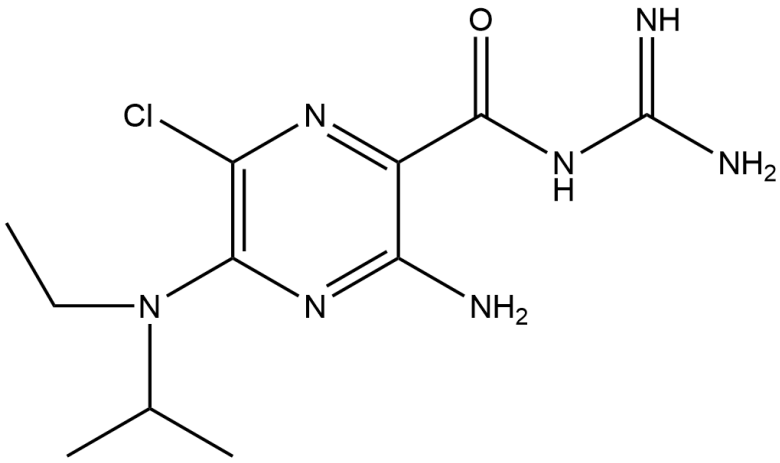


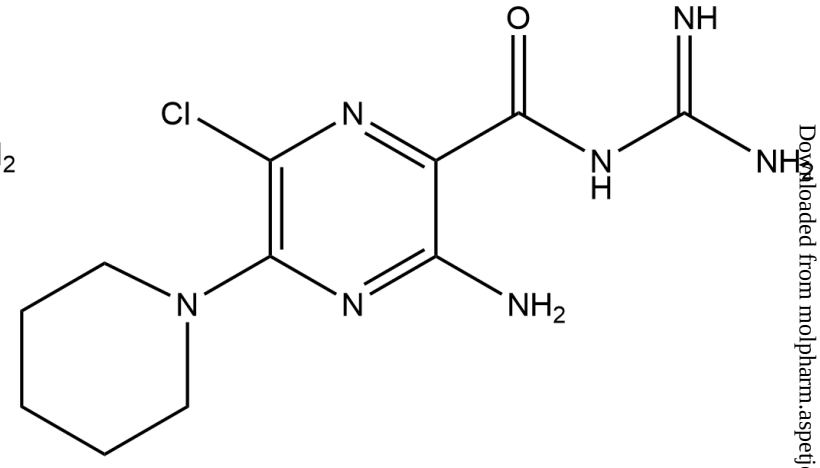
amiloride



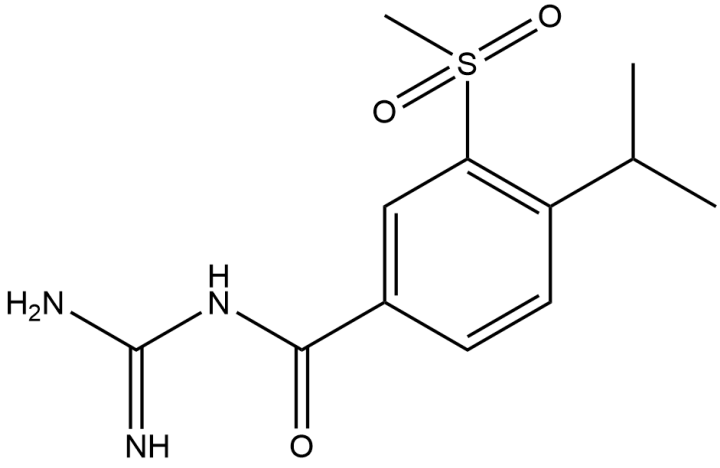
5-(N,N-dimethyl)-amiloride
(DMA)



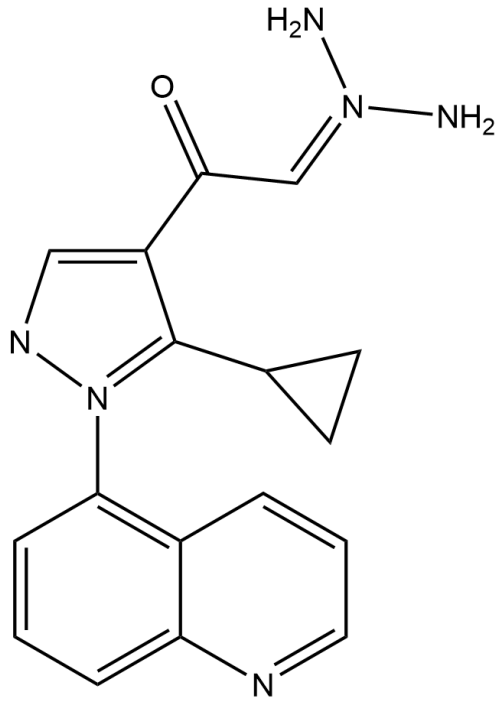
5-(N-ethyl-N-isopropyl)-amiloride
(EIPA)



5-(N,N-hexamethylene)-amiloride
(HMA)



cariporide



zoniporide

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Figure 1

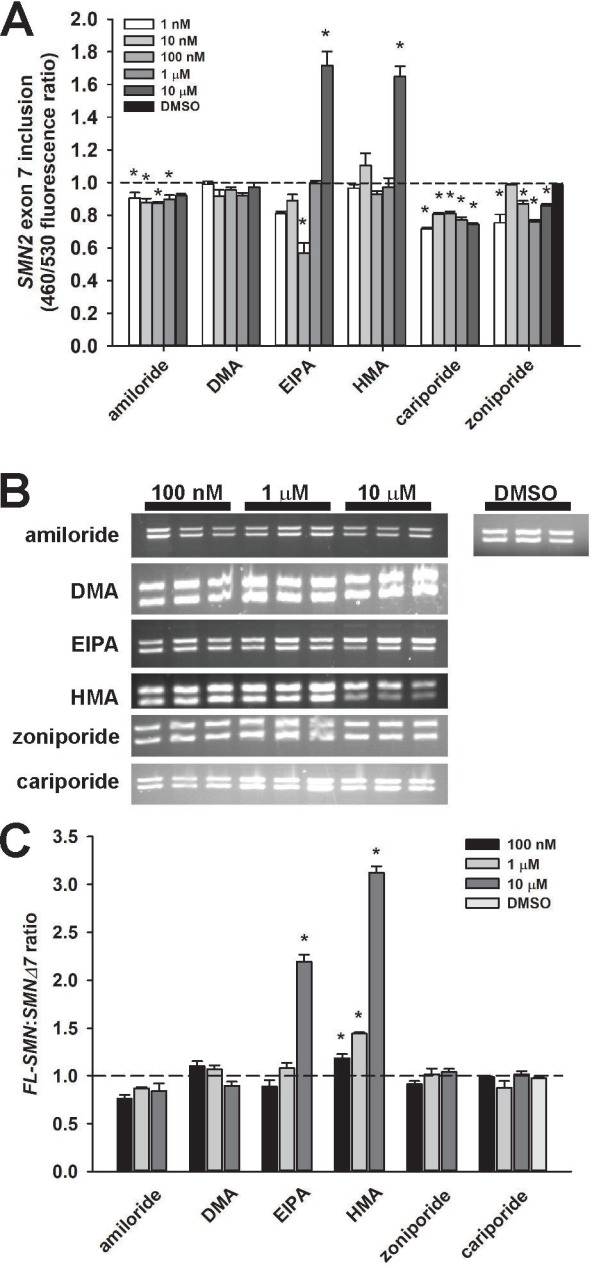
A
SMN2 exon 7 inclusion (460/530 fluorescence ratio)
1 nM
10 nM
100 nM
1 μM
10 μM
DMSO
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
B
100 nM
1 μM
10 μM
DMSO
amiloride
DMA
EIPA
HMA
zoniporide
cariporide
C
FL-SMN:SMNΔ7 ratio
100 nM
1 μM
10 μM
DMSO
amiloride
DMA
EIPA
HMA
zoniporide
cariporide

Figure 2

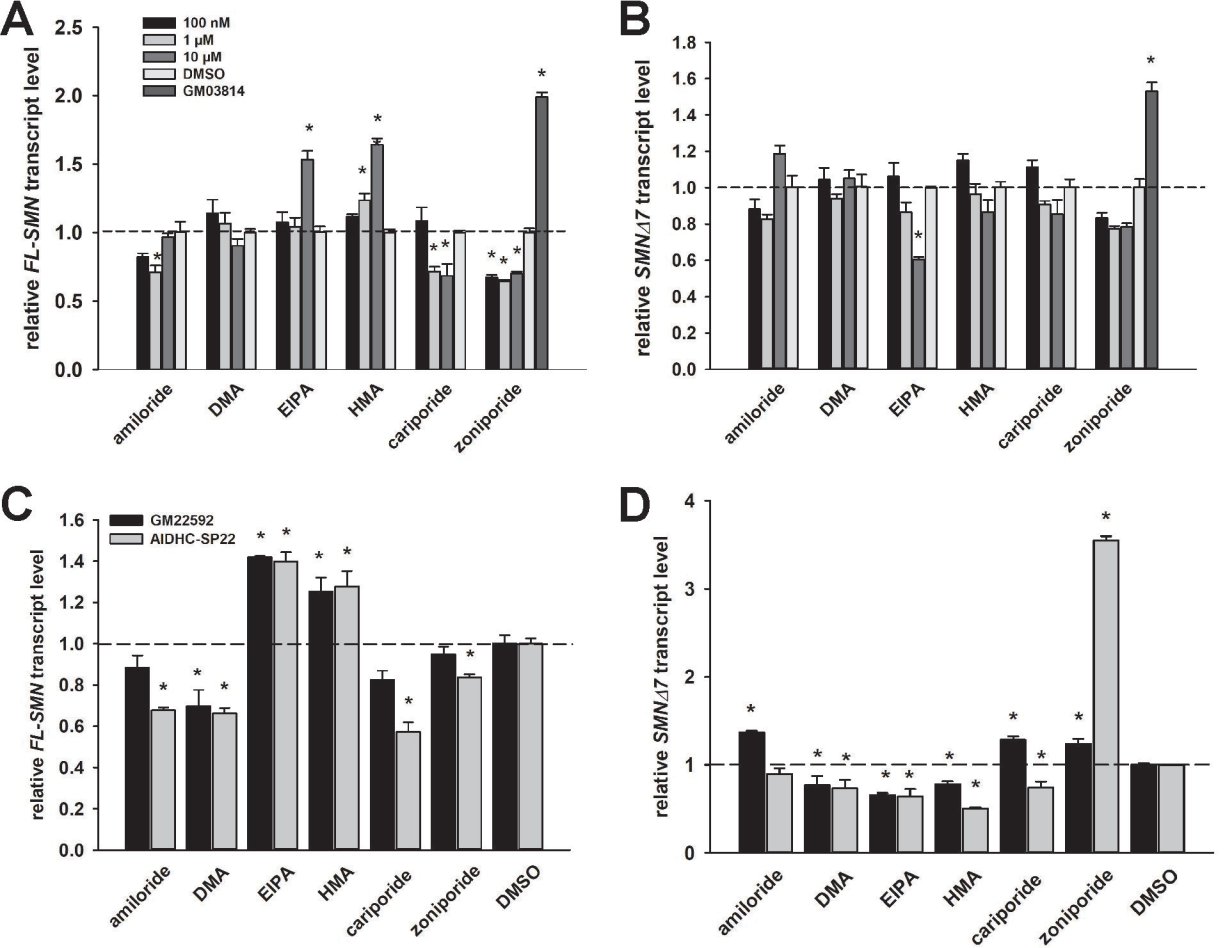
A
100 nM
1 μM
10 μM
DMSO
GM03814
relative FL-SMN transcript level
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
B
relative SMNΔ7 transcript level
C
GM22592
AIDHC-SP22
DMSO
D

Figure 3

Molecular Pharmacology Fast Forward. Published on June 6, 2022 as DOI: 10.1124/molpharm.122.000529
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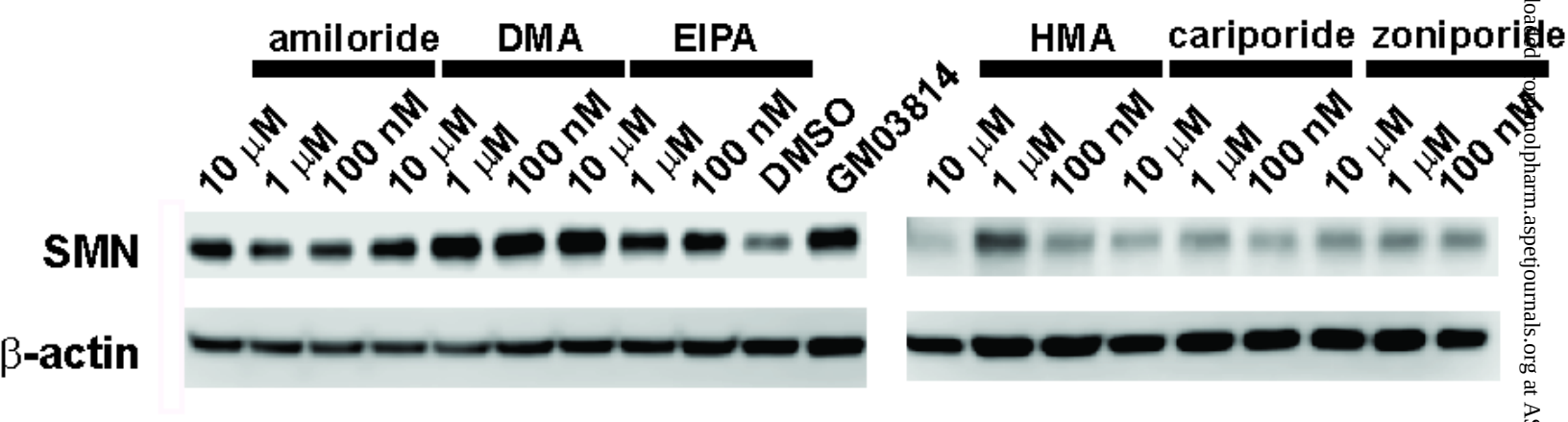

Figure 4

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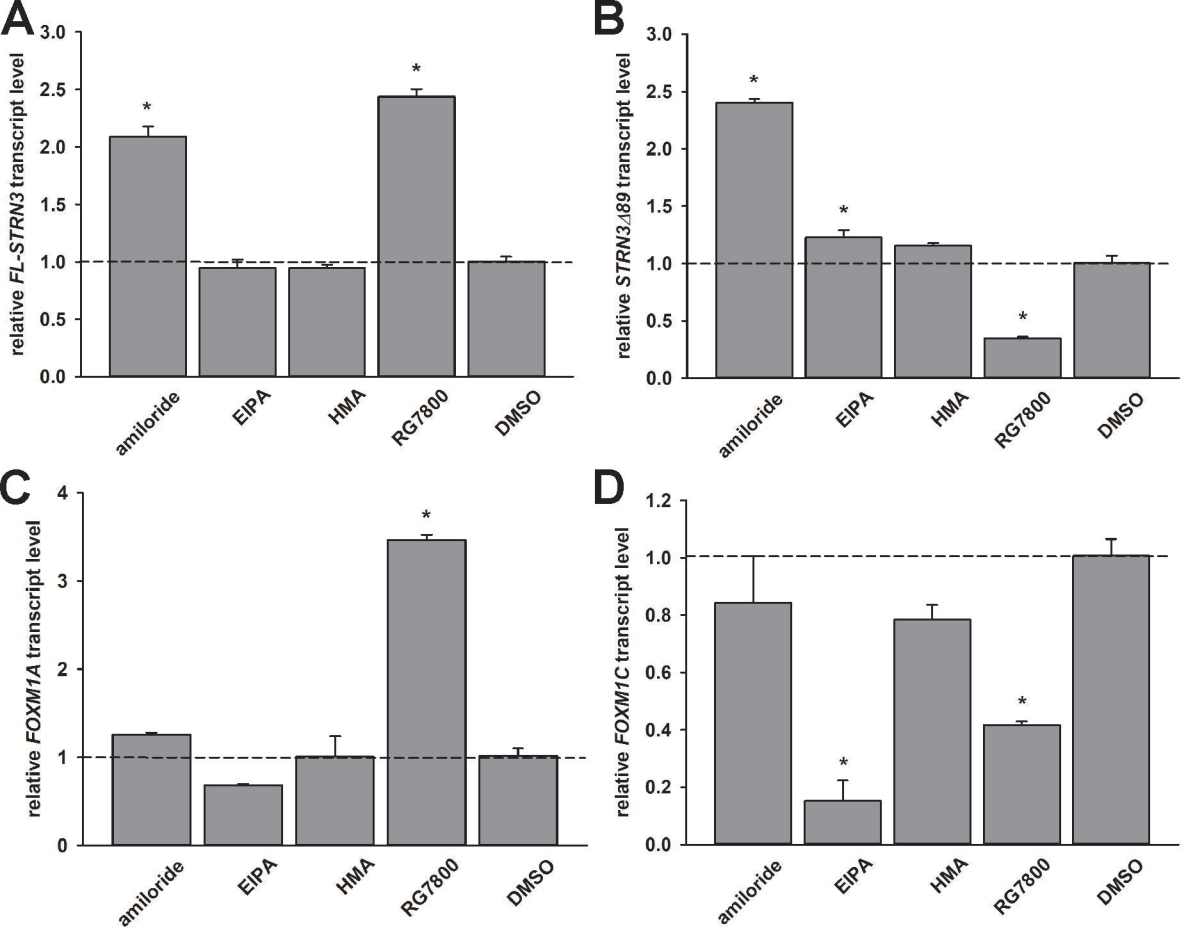
A
relative FL-STRN3 transcript level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
*
*
amiloride
EIPA
HMA
RG7800
DMSO
B
relative STRN3Δ89 transcript level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
*
*
*
amiloride
EIPA
HMA
RG7800
DMSO
C
relative FOXM1A transcript level
4
3
2
1
0
*
amiloride
EIPA
HMA
RG7800
DMSO
D
relative FOXM1C transcript level
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
*
amiloride
EIPA
HMA
RG7800
DMSO

Figure 5

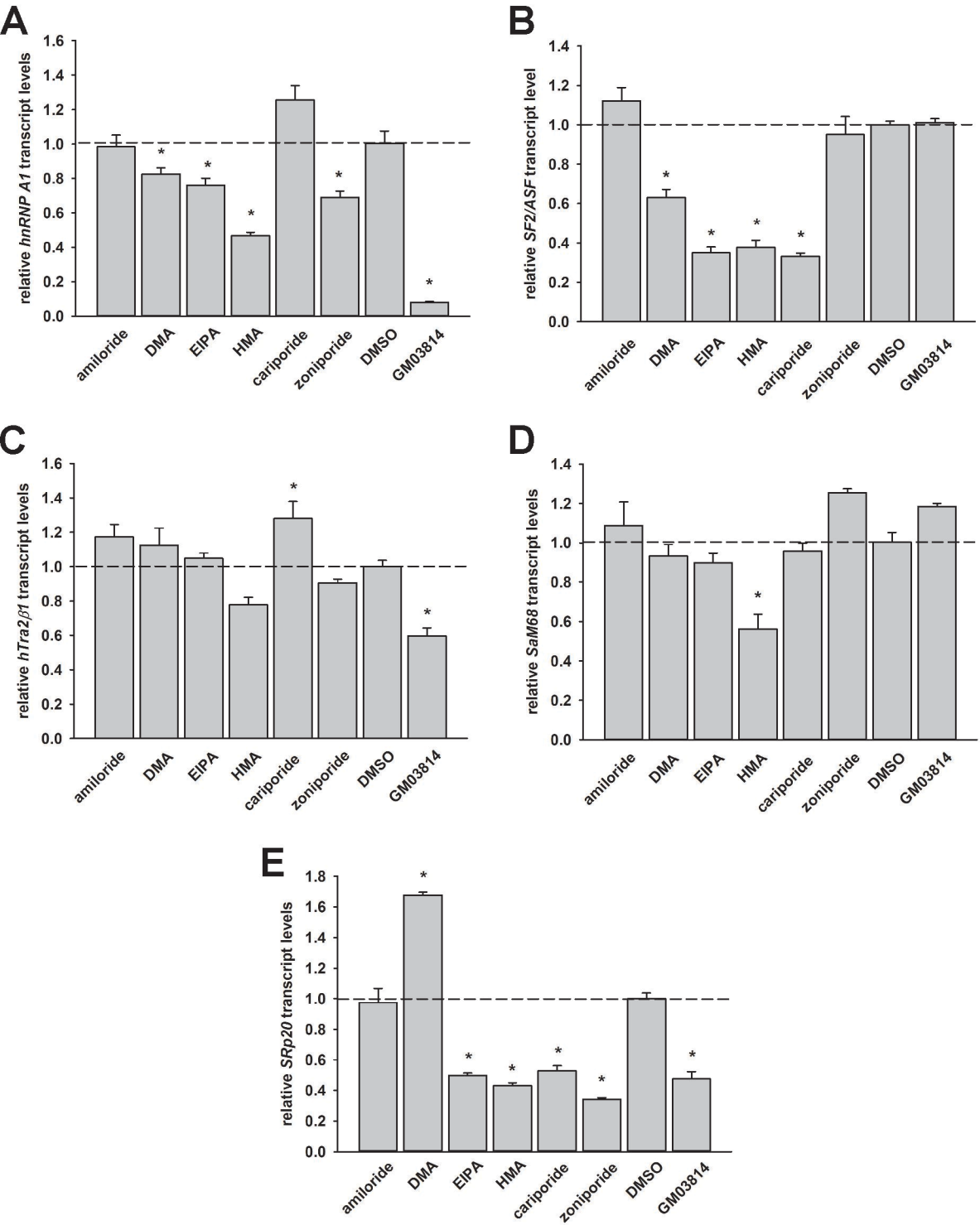
A
relative hnRNP A1 transcript levels
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
DMSO
GM03814
B
relative SF2/ASF transcript level
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
DMSO
GM03814
C
relative hTra2β1 transcript levels
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
DMSO
GM03814
D
relative SaM68 transcript levels
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
DMSO
GM03814
E
relative SRp20 transcript levels
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
amiloride
DMA
EIPA
HMA
cariporide
zoniporide
DMSO
GM03814

Figure 6

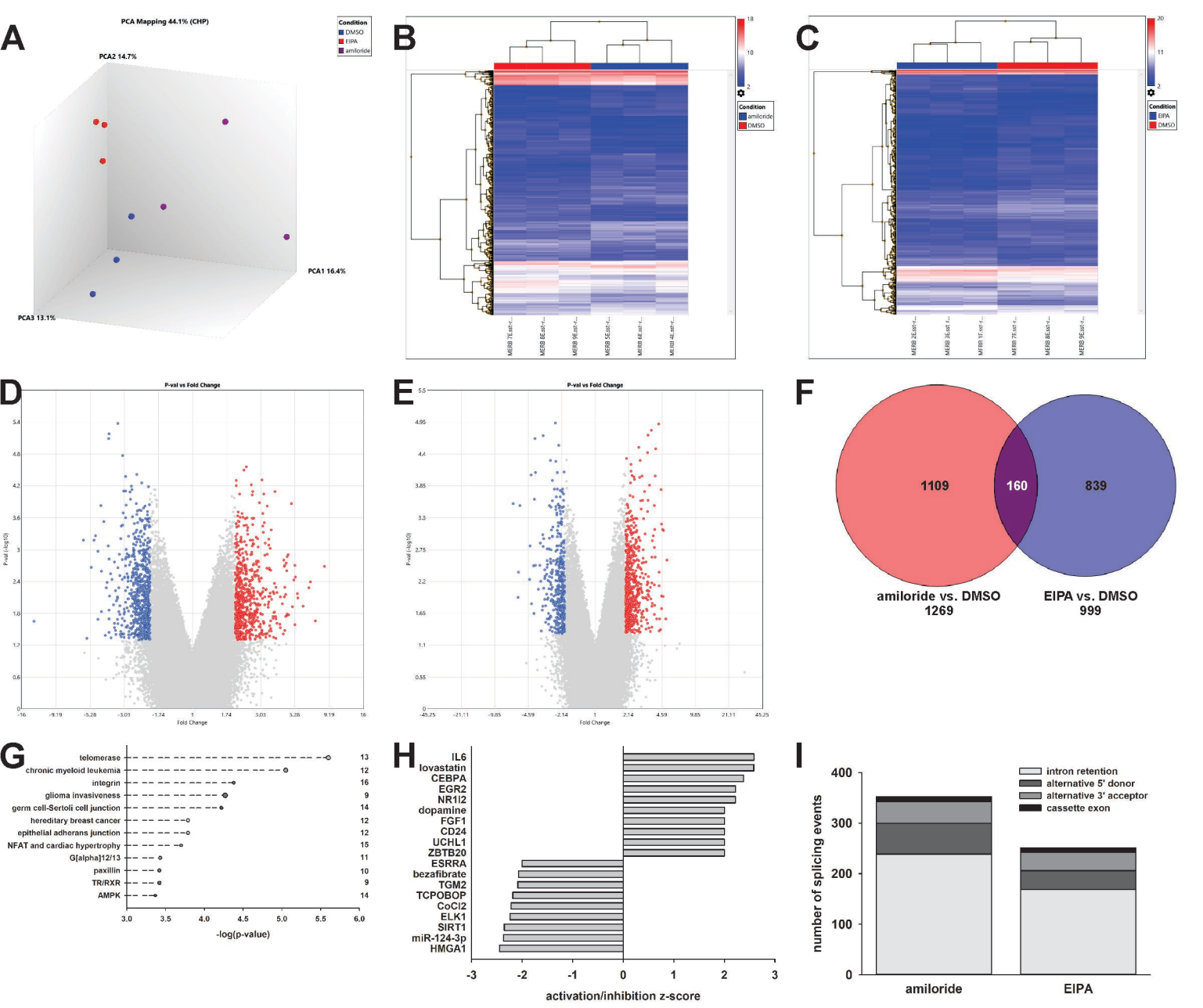
A
PCA Mapping 44.1% (CHP)
Condition
DMSO
EIPA
amiloride
PCA2 14.7%
PCA1 16.4%
PCA3 13.1%
B
Condition
amiloride
DMSO
C
Condition
EIPA
DMSO
D
P-val vs Fold Change
P-val (-log10)
Fold Change
E
P-val vs Fold Change
P-val (-log10)
Fold Change
F
1109
160
839
amiloride vs. DMSO
1269
EIPA vs. DMSO
999
G
telomerase 13
chronic myeloid leukemia 12
integrin 16
glioma invasiveness 9
germ cell-Sertoli cell junction 14
hereditary breast cancer 12
epithelial adherans junction 12
NFAT and cardiac hypertrophy 15
G[alpha]12/13 11
paxillin 10
TR/RXR 9
AMPK 14
-log(p-value)
H
IL6
lovastatin
CEBPA
EGR2
NR1I2
dopamine
FGF1
CD24
UCHL1
ZBTB20
ESRRA
bezafibrate
TGM2
TCPOBOP
CoCl2
ELK1
SIRT1
miR-124-3p
HMGA1
activation/inhibition z-score
I
intron retention
alternative 5' donor
alternative 3' acceptor
cassette exon
number of splicing events
amiloride
EIPA

Figure 7

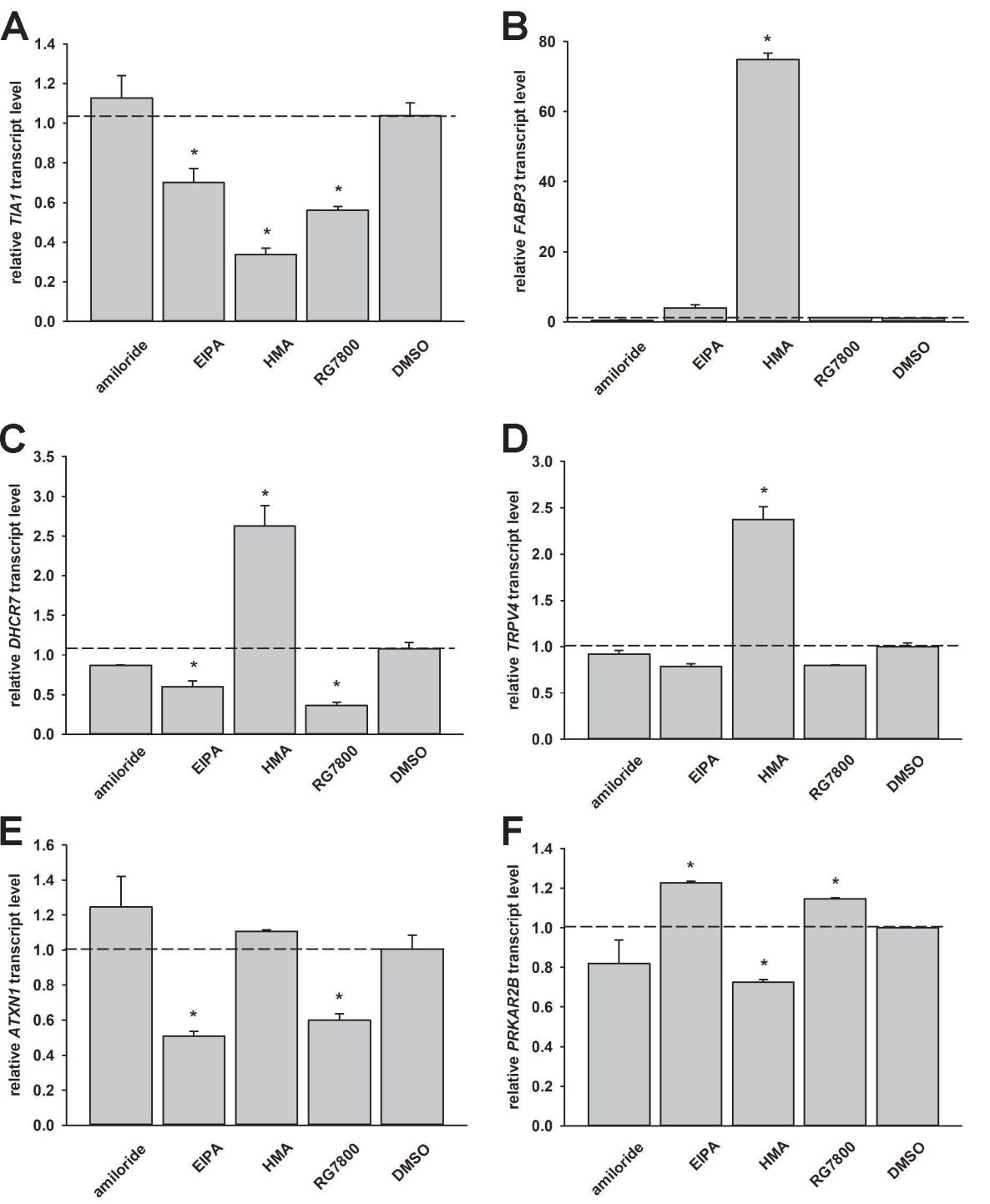
A
relative TIA1 transcript level
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
*
*
amiloride
EIPA
HMA
RG7800
DMSO
B
relative FABP3 transcript level
80
60
40
20
0
*
amiloride
EIPA
HMA
RG7800
DMSO
C
relative DHCR7 transcript level
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
*
*
*
amiloride
EIPA
HMA
RG7800
DMSO
D
relative TRPV4 transcript level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
*
amiloride
EIPA
HMA
RG7800
DMSO
E
relative ATXN1 transcript level
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
*
amiloride
EIPA
HMA
RG7800
DMSO
F
relative PRKAR2B transcript level
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
*
*
amiloride
EIPA
HMA
RG7800
DMSO

Figure 8