

Chemotherapy Induced Sensory Neuropathy Depends on Non-Linear Interactions with Cancer

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Chemotherapy Induced Sensory Neuropathy Depends on Non-Linear Interactions with Cancer

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This work is dedicated to my wife, Emily.

You empower me to be my best in all endeavors.

This work would not be possible without you.

I owe you a lifetime of gratitude

For your unwavering love and support.

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Summary

For the constellation of neurological disorders known as chemotherapy induced neuropathy, mechanistic understanding, and treatment remain deficient. In **project one**, I leveraged a multi-scale experimental approach to provide the first evidence that chronic sensory neuropathy depends on non-linear interactions between cancer and chemotherapy. Global transcriptional profiling of dorsal root ganglia revealed amplified differential expression, notably in regulators of neuronal excitability, metabolism and inflammatory responses, all of which were unpredictable from effects observed with either chemotherapy or cancer alone. Systemic interactions between cancer and chemotherapy also determined the extent of deficits in sensory encoding *in vivo* and ion channel protein expression by single mechanosensory neurons, with the potassium ion channel Kv3.3 emerging as candidate mechanisms explaining sensory neuron dysfunction. The sufficiency of this novel molecular mechanism was tested in an *in silico* biophysical model of mechanosensory function. Finally, validated measures of sensorimotor behavior in awake behaving animals confirmed that dysfunction after chronic chemotherapy treatment is exacerbated by cancer. Notably, errors in precise fore-limb placement emerged as a novel behavioral deficit unpredicted by our previous study of chemotherapy alone. These original findings identify novel contributors to peripheral neuropathy, and emphasize the fundamental dependence of neuropathy on the systemic interaction between chemotherapy and cancer across multiple levels of biological control.

In **project two**, I extend study to multiple classes of mechanosensory neurons that are necessary for generating the information content (population code) needed for proprioception. I first tested the hypothesis that exacerbated neuronal dysfunction is conserved across multiple classes of mechanosensory neurons. Results revealed co-

suppression of specific signaling parameters across all neuronal classes. To understand the consequences of corrupt population code, I employed a long-short-term memory neural network (LSTM), a deep-learning algorithm, to test how decoding of spatiotemporal features of movement are altered after chemotherapy treatment of cancer. Results indicate that spiking activity from the population of neurons in animals with cancer, treated by chemotherapy contain significantly less information about key features of movement including, e.g. timing, magnitudes, and velocity. I then modeled the central nervous systems (CNS) capacity to compensate for this information loss. Even under optimal learning conditions, the inability to fully restore predictive power suggests that the CNS would not be able to compensate and restore full function. Our results support our proposal that lasting deficits in mobility and perception experienced by cancer survivors can originate from sensory information that is corrupted and un-interpretable by CNS neurons or networks.

Collectively, I present the first evidence that chronic cancer neuropathy cannot be explained by the effects of chemotherapy alone but instead depend on non-linear interactions with cancer. This understanding is a prerequisite for designing future studies and for developing effective treatments or preventative measures.

CHAPTER 1. INTRODUCTION

Societal Burden of Cancer

Cancer diagnoses represent an ever-increasing burden on global society which is expected to grow to over 20 million new cases annually by 2025 (Ferlay, Soerjomataram *et al.* 2015). While the incidence of cancer diagnoses expands (Center, Jemal *et al.* 2009), increased screening and advanced treatment strategies, such as chemotherapies are extending disease-free lifespans (André, Boni *et al.* 2004; Edwards, Ward *et al.* 2010; Bosetti, Levi *et al.* 2011; Avan, Postma *et al.* 2015).

Chemotherapy's Benefit to Survival

One such example, platinum-based chemotherapies, are central pillars of contemporary cancer treatment. Oxaliplatin (OX), a third-generation platinum-based agent, has been shown to extend lifespans by improving disease free survival up to 80%, reduce toxicity and improve tolerability, especially for older patients (Galanski, Jakupec *et al.* 2005; Montagnani, Turrisi *et al.* 2011; Johnstone, Park *et al.* 2014). This superior efficacy as a first-line treatment for the 1.4 million new diagnoses of colorectal cancer (Torre, Bray *et al.* 2015) and adjunctive therapy for millions of bladder, ovarian and testicular cancers patients (Andre *et al.* 2009; de Gramont, Et *al.* 2000; Taylor *et al.* 2014; Fu *et al.* 2006) helps explain why it is estimated that approximately 50% of all patients diagnosed with cancer undergoing chemotherapeutic treatment receive a platinum-based chemotherapy such as OX (Galanski, Jakupec *et al.* 2005; (Johnstone, Park *et al.* 2014).

Dark side of chemotherapy

Despite impressive efficacy, nearly all patients treated with OX and other platinum-based drugs are afflicted by severe off-target, neurotoxic side-effects such as pain, sensory

abnormalities, fatigue, mobility and balance deficits (Bennett, Park *et al.* 2012). This constellation dose-limiting side effects is collectively referred to as Chemotherapy-Induced Peripheral Neuropathy (CIPN), diminishes quality of life and limits functional capacity (Cavaletti, Bogliun *et al.* 1995; Quasthoff and Hartung 2002; André, Boni *et al.* 2004; Argyriou, Polychronopoulos *et al.* 2008; Alcindor and Beauger 2011; Mols, Beijers *et al.* 2013; Tofthagen, Donovan *et al.* 2013; Argyriou, Kyritsis *et al.* 2014; Beijers, Mols *et al.* 2014; Avan, Postma *et al.* 2015). While, acute CIPN symptoms may decline after caseation of treatment, they frequently persist, leaving many patients with chronic CIPN that does not improve even years after treatment (Dietrich, Han *et al.* 2006; Park, Lin *et al.* 2011; Park, Goldstein *et al.* 2013; Aaronson, Mattioli *et al.* 2014; Seretny, Currie *et al.* 2014; Marshall, Zipp *et al.* 2017).

Seeking Treatments for CIPN

Various approaches to prevent acute and ameliorate chronic CIPN have been attempted (Adelsberger, Quasthoff *et al.* 2000; Webster, Brain *et al.* 2005; Ishibashi, Okada *et al.* 2010; Saif, Syrigos *et al.* 2010; Sittl, Lampert *et al.* 2012; Kagiava, K Kosmidis *et al.* 2013). However, these approaches have yet to show efficacy in large randomized control trials, leaving cancer patients' symptoms essentially unabated (Loprinzi, Qin *et al.* 2013; Hershman, Lacchetti *et al.* 2014; Sisignano, Baron *et al.* 2014). Given the lack of supporting evidence, The American Society of Clinical Oncologists recently published clinical practice guidelines that concluded, few, if any, therapeutic strategies are recommended (Hershman, Lacchetti *et al.* 2014).

Knowledge gaps and motivations

Abject failure of these clinical trials to lessen symptoms of CIPN present prima fascia evidence of knowledge gaps (Hershman, Lacchetti *et al.* 2014), promulgated by problems with preclinical study we correct in this work, notably 1) focus on transient

(acute) CIPN signs and symptoms at the expense of understanding lasting chronic effects, 2) flawed experimental methodologies, and 3) failure to consider role of cancer in pathophysiology of CIPN.

Focus on Acute CIPN

While it is clear that platinum-based drugs have the potential to disrupt neuronal excitability (Sittl, Lampert *et al.* 2012), the majority of studies have focused on elucidating underlying mechanisms of acute CIPN symptomology that do not persist, e.g. cold-induced pain, muscle spasms and cramps (Alcindor and Beauger 2011; Seretny, Currie *et al.* 2014). Acute CIPN symptoms that are readily attributable to neural hyperexcitability. This has been verified by axon-excitability testing in peripheral nerves (Quasthoff and Hartung 2002; Krishnan, Goldstein *et al.* 2006; Argyriou, Polychronopoulos *et al.* 2008; Alcindor and Beauger 2011; Seretny, Currie *et al.* 2014) along with numerous demonstrations of disrupted ion channels, e.g. Na, K, and Ca ion channels, Ca chelation, and TRP channels, all of which have the potential to increase neuronal excitability (Grolleau, Gamelin *et al.* 2001; Sittl, Lampert *et al.* 2012; Sittl, Lampert *et al.* 2012; Kagiava, K Kosmidis *et al.* 2013; Sisignano, Baron *et al.* 2014; Kanat, Ertas *et al.* 2017).

However, many fewer studies have examined chronic CIPN, which results in lasting impairments to cancer survivors. These impairments are associated with functional movement disorders e.g. reduced sensation, impaired balance, discoordination (Saif, Syrigos *et al.* 2010; Marshall, Zipp *et al.* 2017) and are commonly attributed to dying-back, length-dependent axon degeneration (Argyriou, Kyritsis *et al.* 2014; Avan, Postma *et al.* 2015). However, given that physical evidence from nerve-conduction studies suggest that axon degeneration is typically minimal <25% (Burakgazi, Messersmith *et al.* 2011), additional mechanisms must be at play. Chronic CIPN can occur even in cases

where no detectable reduction in either nerve-evoked action potentials or epidermal nerve density exist (Burakgazi, Messersmith *et al.* 2011). Based on reports from our lab (Vincent, Wiczerzak *et al.* 2016), we speculated that rather than by structural degeneration alone, chronic CIPN symptoms might depend on functional impairment of sensory neurons attributable to neuronal hypo-excitability based on a failure to maintain firing in response to fixed levels of stimulation (Vincent, Nardelli *et al.* 2015; Vincent, Wiczerzak *et al.* 2016). Discovering no receptor or axonal degeneration provides further evidence for this hypothesis, despite this being the pervasive explanation in the literature (Vincent, Nardelli *et al.* 2015; Vincent, Wiczerzak *et al.* 2016).

Methodology

Another limitation is that the effects of platinum-based chemotherapy on neuronal excitability have been examined almost exclusively using experimental methodologies, which themselves alter neuronal excitability (Button, Kalmar *et al.* 2008; Yamamoto, Tsuboi *et al.* 2016; Yamamoto, Ono *et al.* 2016). With neuronal excitability influenced by a myriad of factors (Desai, Rutherford *et al.* 1999; Rekling, Funk *et al.* 2000; Kuo, Siddique *et al.* 2005; Grubb and Burrone 2010; Panatier and Robitaille 2012), experimental effects confound identification of the actual mechanisms by which platinum-based chemotherapy alone alter neuronal excitability (Devor, Govrin-Lippmann *et al.* 1993). For example, neuronal excitability is altered by damage, which is an inevitable consequence with tissue extraction used during in vitro study, a common experimental approach utilized and a likely contributor to abnormal neuronal excitability without platinum-based chemotherapy (Tulleuda, Cokic *et al.* 2011). Investigations also fall short when failing to reproduce the in vivo milieu, including interaction with systemic changes induced by platinum-based chemotherapy, e.g. inflammatory and oxidative responses known to impact excitability (Pardillo-Díaz, Carrascal *et al.* 2015; Vezzani and

Viviani 2015; Barbosa, Xiao *et al.* 2017; Tzour, Leibovich *et al.* 2017; Wang, Zhang *et al.* 2017).

Cancer

Experimental investigations of CIPN also fall short when failing to reproduce the clinically relevant condition when platinum-based chemotherapy effects coexist cancer effects (Cain, Wacnik *et al.* 2001; Klampfer 2011; Zheng, Fang *et al.* 2012; Cai, Fang *et al.* 2015; Pardillo-Díaz, Carrascal *et al.* 2015; Vezzani and Viviani 2015; West, McCuaig *et al.* 2015; Mager, Wasmer *et al.* 2016; Barbosa, Xiao *et al.* 2017; Kovalchuk, Ilnytskyy *et al.* 2017; Tzour, Leibovich *et al.* 2017; Wang, Zhang *et al.* 2017).

To date, cancer is excluded in preclinical studies of CIPN. However, since the clinical utility of chemotherapy rest solely on treating cancer, we must consider how cancer contributes to CIPN independent of or in combination with chemotherapy (Ahles 2012; Boyette-Davis, Eng *et al.* 2012; van Erning, Janssen-Heijnen *et al.* 2016). Patients with tumors located outside the nervous system can exhibit subclinical peripheral neuropathy even before chemotherapy or surgical intervention (Ahles 2012; Boyette-Davis, Eng *et al.* 2012; van Erning, Janssen-Heijnen *et al.* 2016). These observations are consistent with cancer's effect on signaling pathways known to affect neuronal excitability (Cain, Wacnik *et al.* 2001; Klampfer 2011; Zheng, Fang *et al.* 2012; Cai, Fang *et al.* 2015; Pardillo-Díaz, Carrascal *et al.* 2015; Vezzani and Viviani 2015; West, McCuaig *et al.* 2015; Mager, Wasmer *et al.* 2016; Barbosa, Xiao *et al.* 2017; Kovalchuk, Ilnytskyy *et al.* 2017; Tzour, Leibovich *et al.* 2017; Wang, Zhang *et al.* 2017). Several signaling pathways intersect with ones affected by chemotherapy, thereby opening the possibility for dynamical interaction. For example, the frequency and gain of neuronal repetitive firing is impaired by oxidative stress (Pardillo-Díaz, Carrascal *et al.* 2015). Because colorectal cancer and chemotherapy treatment each induce oxidative stress (Boyette-

Davis, Walters *et al.* 2015), their combination may amplify neuronal dysfunction. The prototypical inflammatory cytokines, e.g. IL-1 β , TNF- α , IL-6 are activated by chemotherapy and colorectal cancer (Klampfer 2011; West, McCuaig *et al.* 2015; Mager, Wasmer *et al.* 2016). These pathways present additional sites where dynamical interactions may disrupt neuronal excitability (Vezzani and Viviani 2015; Barbosa, Xiao *et al.* 2017; Tzour, Leibovich *et al.* 2017). Alternatively, cancer and chemotherapy may act through pathways that are hidden from investigations of chemotherapy alone. These data provide strong rationale to suspect that cancer and chemotherapy may dynamically interact to exacerbate CIPN. While chemotherapy alone may be necessary to induce neuronal dysfunction in preclinical models, it may not be sufficient to capture the mechanistic underpinnings of the clinically relevant CIPN condition when cancer is present (Sisignano, Baron *et al.* 2014).

Overall Objectives

My overall objective was to investigate the role of cancer in the development of chronic neuropathy in living animals. By doing so, I correct many of the limitations of previous preclinical studies to gain mechanistic understanding of the clinically relevant *chronic* CIPN to meet the urgent and unmet need of cancer survivors globally. To accomplish these objectives, I employed a multi-scale experimental approach centered on *in vivo* electrophysiologic recordings from intact neurons. Further utilization of high-throughput, whole transcriptome analysis, protein expression studies, validated measures of sensorimotor behavior in awake behaving animals, *in silico* biophysical modeling, and deep-learning decoding algorithms afforded comprehensive insight into establishing the independent and combinatorial effects of chemotherapy and cancer on the sensory nervous system.

CHAPTER 2. GENERAL METHODS

Animal Care

All procedures and experiments were approved by the Georgia Institute of Technology Institutional Animal Care and Use Committee. Adult male rats (250-350g) were studied in terminal experiments only and were not subject to any other experimental procedures. All animals were housed in clean cages and provided food and water ad libitum in a temperature- and light-controlled environment in Georgia Institute of Technology's Animal facility.

Rat model of Colorectal Cancer

We studied the rat model of colorectal cancer developed in Fisher 344 (F344) rats and known as polyposis in rat colon ($Apc^{Pirc/+}$) (Amos-Landgraf, Kwong *et al.* 2007). Pirc rats were generated from a germline mutation in the Apc gene ($Apc^{1137/+}$). This mutation is shared by 80% of patients with colorectal cancer (Kwong and Dove 2009). We studied age-matched male rats (4 months). This age has been previously validated to result in 100% incidence of animals (Irving, Yoshimi *et al.* 2014) developing colon cancer and was consistent with our population. $Apc^{Pirc/+}$ rats exhibit: regional distribution of tumors that best represents that seen in human colorectal cancer (Irving, Yoshimi *et al.* 2014); histopathology and morphology closely resembling human tumors (adenocarcinomas) (Washington, Powell *et al.* 2013; Femia, Luceri *et al.* 2015), up-regulation of well-established pro-growth factors, e.g. β -catenin and EGFR and proliferative markers Ki-67 seen in human carcinogenesis (Amos-Landgraf, Kwong *et al.* 2007), dramatic increases in Wnt signaling believed to be a key factor in human colorectal carcinogenesis (Bienz and Clevers 2000), presence of apoptotic resistant cells unique to carcinogenesis (Figure 1) (Amos-Landgraf, Kwong *et al.* 2007; Irving, Yoshimi *et al.* 2014), oxaliplatin

(OX)-induction of apoptosis in colon tumors, survivability (12-15 months) enabling long-term investigation of OX's chronic effects (Amos-Landgraf, Kwong *et al.* 2007).

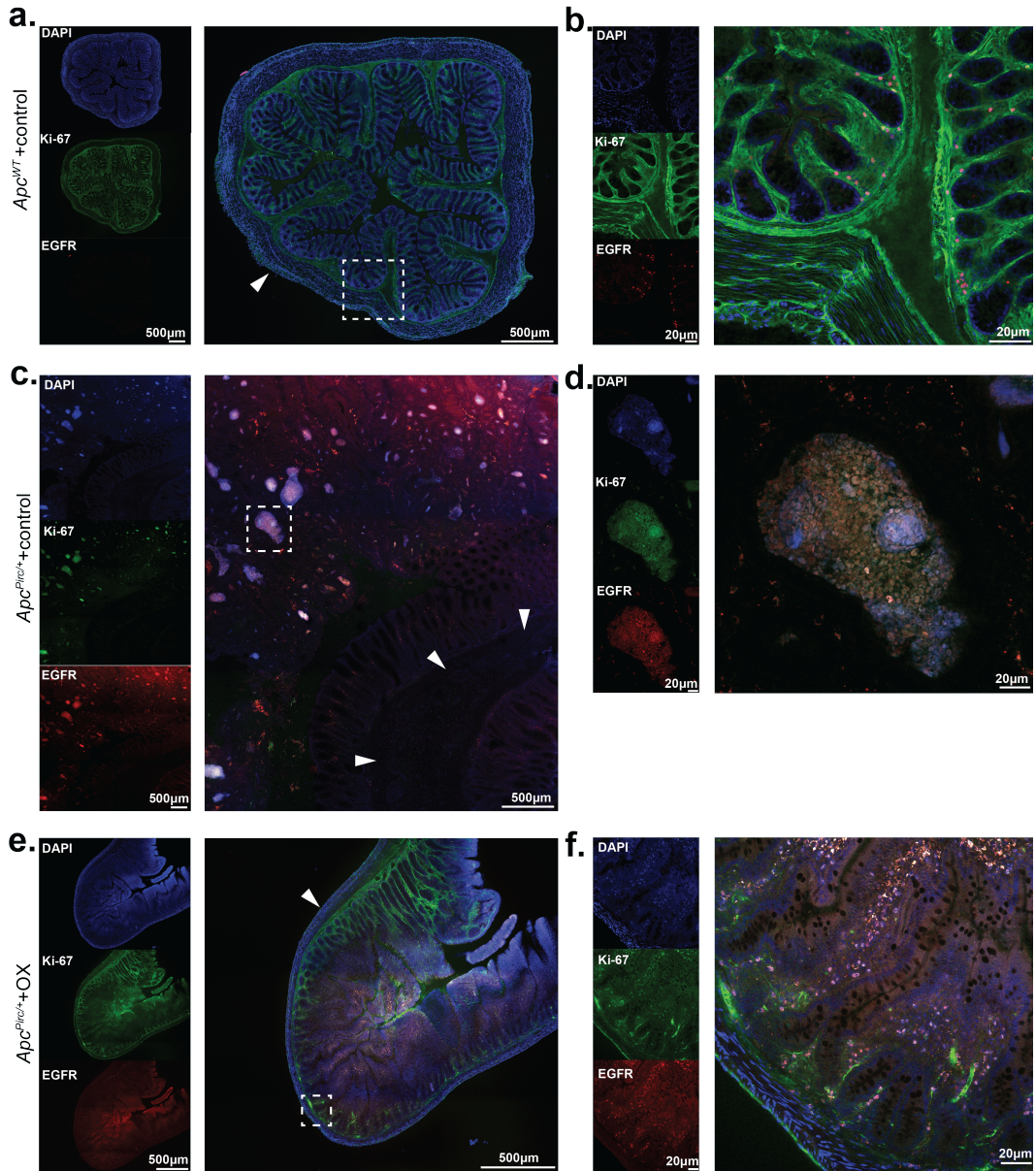


Figure 1.

Immunohistochemical and morphological analyses of healthy and tumor bearing colons. a-f, Confocal images of a colon from *Apc*^{WT}+control rat (a, b) and colon and colon tumors from *Apc*^{Pirc/+}+control (c, d) and *Apc*^{Pirc/+}+ OX rats (e, f). Immunolabeling shows expression of DAPI and Ki-67, and EGFR a measure proliferative growth associated with tumor progression. White dotted boxes in wide-field images (a, c, e) outline region of interest (b, d, f). White arrows indicate smooth muscle boundary used as anatomical reference.

Chemotherapy treatment

OX (Cyclohexane-1,2-diamine; oxalate; platinum(2+)) was injected intraperitoneal (i.p.) once a week (10mg/Kg, 1 ml 5% dextrose in DMSO) in aged matched rats (4 months) to achieve a cumulative dose of 70 mg/Kg over 7 weeks, which scales to a human dose of 420mg/m² (conversion based on rat body surface area and Km= 6) (Reagan-Shaw, Nihal *et al.* 2008; Nair and Jacob 2016). Further, this dose minimizes nerve degeneration in patients (Grisold, Cavaletti *et al.* 2012; Park, Goldstein *et al.* 2013). Rats in each group were randomized to receive injections of oxaliplatin (OX), a platinum based compound known to induce neuropathy in patients with cancer and shown in our previous studies to induce chronic movement disorders (Vincent, Wiczerzak *et al.* 2016). OX was administered by intraperitoneal injection on a human-scaled dose schedule (Vincent, Wiczerzak *et al.* 2016). The OX treatment schedule resulted in four experimental groups used for all studies: Apc^{WT} +control, Apc^{WT} +OX, Apc^{Pirc1+} +control and Apc^{Pirc1+} + OX (Figure 2).

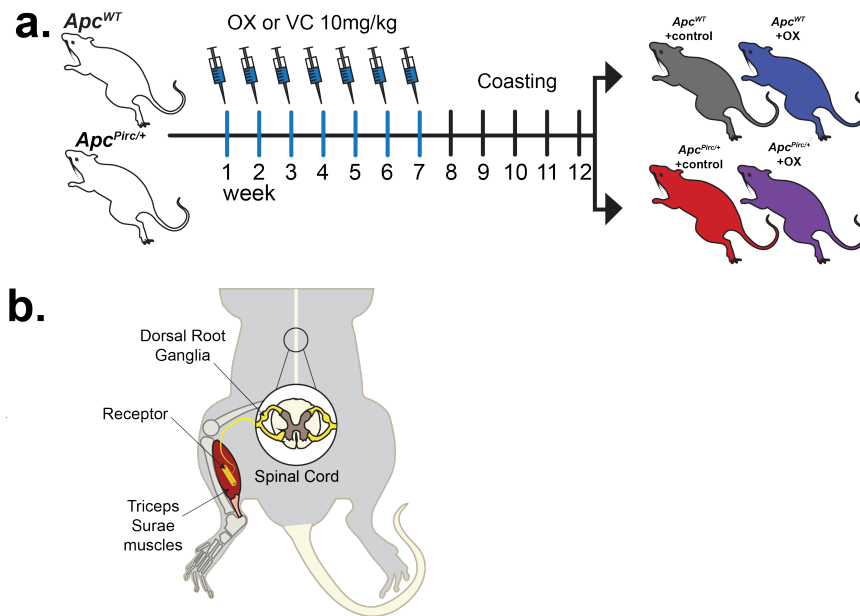


Figure 2.

Treatment Schedule and Targets. a, Schematic of treatment schedule of oxaliplatin (OX) and vehicle control (VC) generating four independent experimental groups in wild-type (Apc^{WT}) and autosomal dominant mutation of the adenomatous polyposis coli gene ($Apc^{Pirc/+}$): Apc^{WT} +control, Apc^{WT} +OX, $Apc^{Pirc/+}$ +control, and $Apc^{Pirc/+}$ +OX rats. b, Diagram of experimental targets of lumbosacral dorsal root ganglia (DRG) and muscle for assaying transcriptomes and/or cell-specific protein expression in rat models.

Clinical dose extrapolation, e.g. converting human OX doses to rat OX doses was based on body surface area, which is a better representation of metabolic rate than mass. Metabolic rate is a key determinant of drug pharmacokinetic and pharmacodynamics and scales non-linearly with animal size, e.g. the body surface area in relation to body weight decreases. In other words, larger animals have lower specific metabolic rate (the metabolic rate per unit mass) whereas metabolic rate to surface area remains relatively conserved (Sharma and McNeill 2009; Nair and Jacob 2016).

Throughout treatment, rats were frequently monitored for pain or distress. No individual rat reached set criteria established for early removal from the study: greater than 10% weight loss, pain or distress assessed by vocalization, absence of grooming, and rats show normal exploratory and feeding behaviors.

Surgical Procedures

Terminal in vivo experiments were performed 5 weeks after achieving clinically relevant chemotherapy doses. They were designed to measure the firing of individual intact sensory neurons in response to physiologically relevant muscle contraction and stretch with electrophysiological techniques. All in vivo procedures are well established in our lab and have been extensively described in previous publications (Haftel, Bichler *et al.* 2004; Bullinger, Nardelli *et al.* 2011; Vincent, Wiczerzak *et al.* 2016; Nardelli, Powers *et al.* 2017; Vincent, Gabriel *et al.* 2017). Briefly, rats were deeply anesthetized by inhalation of isoflurane (5% in 100% O₂), intubated via a tracheal cannula, then maintained for the remainder of the experiment (up to 12 hours by 1.5–2.5% in 100% O₂). Respiratory rate, pCO₂, core temperature, pulse rate and pO₂ were continuously monitored and maintained by adjusting anesthesia and adjusting heat sources. Dorsal roots (lumbar L4–6), muscles, and nerves in the left hindlimb were prepared for stimulation and recording with the rat fixed in a rigid frame at the snout, vertebral bodies, distal tibia, and distal femur (knee angle 120°). Triceps surae muscles (lateral and medial gastrocnemii and soleus) were partially freed of surrounding connective tissue and marked for their resting length (L₀) at ankle angle 90° before their common Achilles tendon was severed at the calcaneus and tied directly to the lever arm of a force- and length-sensing servomotor (model 305B-LR; Aurora Scientific). Triceps surae nerves were loosely positioned in continuity on a unipolar silver stimulating electrode, and all other hindlimb nerves were crushed to reduce extraneous neuronal activity. Dorsal

rootlets were freed in continuity from overlying connective tissue and supported on bipolar hook electrodes positioned close to the rootlet's entry into the dorsal spinal cord. Exposed tissues were covered with warm mineral oil in pools formed by attaching the edges of severed skin to the recording frame (*Figure 3*).

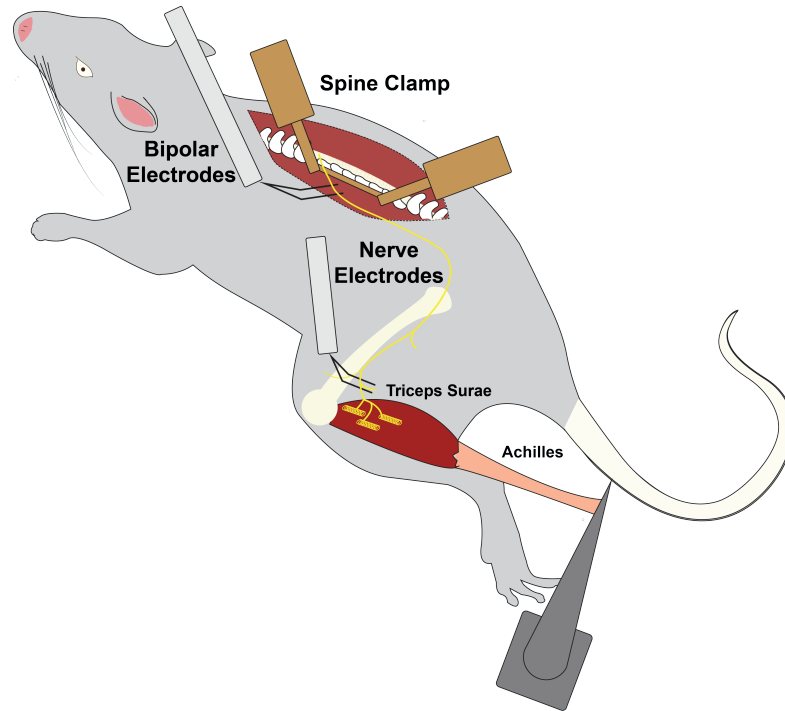


Figure 3.

In Vivo Design. Diagram of anesthetized rat stabilized in spine clamps for physiological recordings. Experiments focus on the triceps surae muscles (soleus and medial and lateral gastrocnemius), triceps surae nerves, and intra-axonally from single sensory neurons in dorsal roots in the lumbosacral (L4-S2) spinal cord.

Bayesian Data Analysis

General Approach

To determine the effect of cancer and/or chemotherapy on various parameters, e.g. neuronal signaling, sensorimotor behavioral factors, etc., we employed Bayesian data

analytic approaches to empirically derive the full joint posterior probability distribution of parameters on which inferences were applied. Bayesian analytic techniques were chosen because they present noteworthy advantages over frequentist analysis such as null hypothesis statistical testing e.g. t -test and ANOVA. Bayesian analytics do not require making assumptions that traditional ANOVA necessitates (e.g. normally distributed data, heteroscedasticity, multiple-test correction) (Kruschke 2013; Kruschke 2014). There is no need to generate sampling distributions, e.g. t , F , χ^2 , and determine whether the probability that fictitious data generated from the null distribution would be more extreme than the observed data i.e. formal definition of p -values. In addition to their ambiguity, p values provide an incoherent framework for reallocation of evidential support because of their high sensitivity to stopping and testing intentions (Wagenmakers 2007; Kruschke 2013). Instead, Bayesian estimation derives the entire joint posterior distribution of all parameters simultaneously (Eq. 1) and provides the ability to examine individual parameters, such as the threshold of spindle firing and peak firing rate in chemotherapy treated animals compared to control without the need to correct for multiple tests on the data. In other words, there is no need for p values and p value-based confidence intervals (e.g. 95%CI). Instead, Bayesian inference and decision making provides a simpler and more intuitive interpretation of the evidence by directly examining the posterior distribution to see which parameter values and ranges are most credible. Further, unlike null hypothesis statistical testing, that can only reject or fail to reject a null hypothesis, by reallocating credibility across the parameter space, Bayesian inference generates evidence and uncertainty in that evidence to support or refute the null or alternative hypothesis (when a region of practical equivalence (ROPE) is defined). While parameter estimation is not unique to Bayesian approaches (e.g. maximum likelihood estimation) uncertainty in parameter

estimates are typically expressed in the form of confidence intervals which rests on the p value along with the limitations discussed above.

$$P(\theta|x) = \frac{P(x|\theta) P(\theta)}{P(x)}, \quad \theta_j \sim N(\mu, \sigma), x_{i,j} \sim f(\theta_j)$$

Where $\theta = (\mu, \sigma)$ is a set of all unknown model parameters as defined above, x denotes a set of mean-centered and standardized dynamic conditioned stretch reflex (cSR) response measurements. The conditional distribution of θ given data (i.e. $P(\theta|x)$) denotes the posterior distribution. The $P(x|\theta)$ is the distribution of x , which is a likelihood function when viewed as a function of model parameters, assuming that θ is known. The $P(\theta)$ is the distribution of θ without any knowledge on data, referred to as a prior distribution. The equation above demonstrates that the posterior distribution of θ is proportional to the product of the likelihood of θ given x and the prior distribution of $P(\theta)$.

Inferences

Bayesian inference, e.g. analogous to traditional hypothesis testing, was performed by analyzing the probability mass of the parameter region in question we defined as the 95% highest posterior density interval (HDI) hereinafter referred to as the HDI. Value contained within the HDI are more credible than values outside. The HDI was used to make unbiased inferences by directly comparing the posterior probability distributions between two (or more) contrasts of interests e.g. mean-comparisons testing. For example, when performing a mean comparison test, an HDI of a credible difference distribution that does not span zero indicates that the model predictions for the two conditions of interest are different from each other. This provides strong unbiased evidential support to simultaneously support the alternative and refute the null hypothesis that the parameters for both populations are equal. Alternatively, if an HDI of

a credible difference distribution spans zero, that indicates the model predictions for the two conditions do not differ. Unlike null hypothesis statistical testing, Bayesian techniques afford the ability to accept the null hypothesis by defining a ROPE (region of practical equivalence) range, e.g. values between -0.1 and 0.1. When the 95% HDI falls completely within the ROPE region we declare the ROPE value accepted. We report the expected value for the parameter alongside 95% credible intervals using the HDI unless otherwise noted.

Models

All models were developed in a fully hierarchical Bayesian framework with the *rstanarm* package (2.18.1) (Gabry and Goodrich 2018) in the R environment (3.5.0) (Team 2018). *Rstanarm* implements regression models in *stan* (Carpenter, Gelman *et al.* 2017), which are fit using Hamiltonian Markov Chain Monte Carlo sampling to compute credible parameter values (Brooks, Gelman *et al.* 2011; Hoffman and Gelman 2014). For intercepts and predictors, we use Student's *t*-distribution with mean zero and four degrees of freedom as the prior distribution. The scale of the prior distribution is 10 for the intercept and 2.5 for the predictors. Each model was run with four independent chains for 400 warm-up, 4,000 sampling steps and every second sample (thinning) was discarded. For all parameters, the number of effective (n_{eff}) samples was >500. Convergence was assessed and assumed to have reached the stationary distribution by ensuring that the Gelman–Rubin shrinkage statistic (rhat, \hat{R}) statistic for all reported parameters was <1.05 and Monte Carlo standard error of the parameter means was <0.002 (Gelman and Rubin 1992) . We report the expected mean parameter values alongside 95% credible intervals using the HDI. For clarity, an example 'Kruschke style' hierarchical model diagram is included and should be interpreted as the graphical representation of mathematical model used for analysis (*Figure 4*). Reading the

diagrams should start at the bottom with a description and nature of the data being modeled, then described the likelihood function, then described the prior (top). Diagrams were created in LibreOffice (Version: 6.0.6.2).

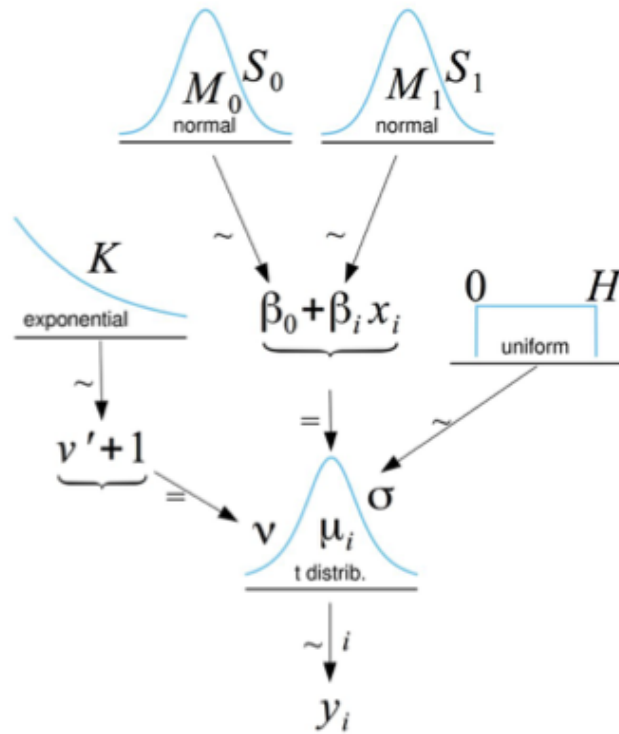


Figure 4.

'Kruschke style' hierarchical model graphical diagram. Robust Bayesian linear regression was used to model the data y_i as a t-distributed random value around the central tendency $\mu_i = \beta_0 + \beta_1 x_i$. The intercept β_0 and slope β_1 were given broad normal priors that are vague to the scale of data. σ was given an uninformative uniform prior, and the normality parameter ν was given a broad exponential prior.

Model Validation

To estimate and validate model performance of our fitted Bayesian models, for the purposes of model comparison and model selection (Geisser and Eddy 1979; Vehtari and Lampinen 2002; Ando and Tsay 2010; Vehtari and Ojanen 2012), we estimated the

out-of-sample predictive accuracy (Figure 5) using Pareto-smoothed importance sampling (PSIS (Vehtari, Gelman *et al.* 2017)) to perform leave-one-out cross (LOO) validation. Exact cross-validation requires refitting models with different training data; however, one can approximate LOO by importance sampling (Gelfand, Dey *et al.* 1992; Gelfand 1996). Importance sampling is a simple statistical procedure for computing/estimating expectations, e.g. of a particular distribution, while only having samples generated from a different, approximating distribution than from the target distribution. Expectations with respect to the target distribution can be estimated by weighting the importance samples by the ratio of their densities. However, importance sampling can result in noisy estimates (Epifani, MacEachern *et al.* 2008), when the approximating distribution is narrower than the target distribution or when the approximating distribution is a poor fit, resulting in the distribution having a heavy right tail and unstable estimates.

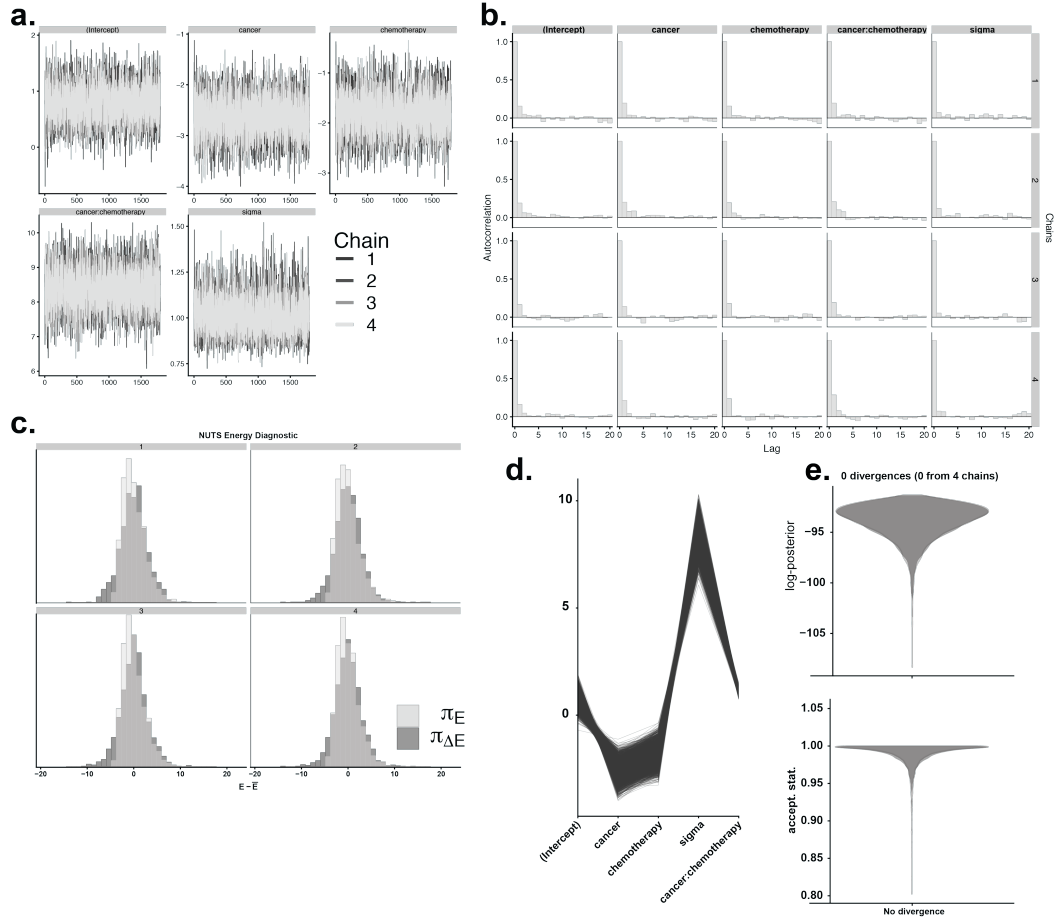


Figure 5.

Exemplar Graphical Bayesian Model Validation. **a**, Time series trace plot of the Markov chains ($n=4$ overlaid) shows the evolution of parameter ($n=5$) vectors over the all iterations and indicate chains explored the full parameter space. **b**, Autocorrelation of paramters (columns) illustrate the degree of correlation between MCMC samples separated by different lags (x -axis). For example, a lag of 0 represents the degree of correlation between each MCMC sample and itself (correlation of 1). A lag of 1 represents the degree of correlation between each Markov chain Monte Carlo (MCMC) sample and the next sample along the chains (rows). Independent (uncorrelated) samples (autocorrelation of 0) indicate unbiased estimates of parameters. No parameters violate autocorrelation. **c**, Shows overlaid histograms of the (centered) marginal energy distribution π_E and the first-differenced distribution $\pi_{\Delta E}$. The MCMC No-U-Turn Sampler (NUTS) Energy diagnostic identifies overly heavy tails that are also challenging for sampling and quantifies the heaviness of the tails of the posterior distribution. The two distributions are well-matched, meaning the random walk will explore the marginal energy distribution extremely efficiently. **d**, Plot shows one line per

iteration connecting parameter values at iterations and identifies global patterns to detect divergences if present (divergences will be colored in the plot (by default in red). No divergent transitions were detected. e, NUTS divergence plot in the top panel shows the distribution of the log-posterior and indicates no divergences for all chains. This provides evidential support that chains adequately explore all parts of the posterior. The bottom panel shows the distribution of NUTS acceptance statistic approaches 1.

PSIS is a new approach that provides a more accurate and reliable estimate by fitting a Pareto distribution to the upper tail of the distribution of the importance weights. PSIS allows the computation of LOO using importance weights that would otherwise be unstable (PSIS-LOO). Although alternative validation strategies, e.g. Watanabe-Akaike information criterion (Watanabe 2010), are asymptotically equal to LOO, PSIS-LOO provides a more accurate and stable estimate of model performance and is more robust in the finite cases with diffuse priors (weakly informative), as is true for models in this proposal when little is known previously about the cancer and chemotherapy interactions.

PSIS-LOO was quantified by computing standard errors for predictions and for comparison of predictive errors between models to definitively test and rank models based on predictive accuracy ($elpd$ = expected log pointwise predictive density) (Vehtari, Gelman *et al.* 2017).

CHAPTER 3. PROJECT 1

Introduction

Chemotherapy can achieve high rates of survival in patients with common cancers (André, Boni *et al.* 2004) but often causes severe side effects, including neuropathy, that can limit its use (Cavaletti and Marmiroli 2010; Alcindor and Beauger 2011; Stone and DeAngelis 2016). Debilitating sensory disorders, including pain, paraesthesia, and somatosensory loss, reduce quality of life for many patients and can persist for months or years after discontinuing chemotherapy (Quasthoff and Hartung 2002; Seretny, Currie *et al.* 2014; Sisignano, Baron *et al.* 2014). These neurological disorders occur for up to 80% of patients receiving commonly used antineoplastic agents, notably antitubulins and proteasome inhibitors, as well as platinum-based compounds (Sisignano, Baron *et al.* 2014; Avan, Postma *et al.* 2015), which are the prescribed adjuvant treatment in 50% of cancer cases worldwide (Galanski, Jakupiec *et al.* 2005; Johnstone, Park *et al.* 2014). There are few options available for the prevention or treatment of sensory disorders and those that exist largely focus on symptomatic management (Hershman, Lacchetti *et al.* 2014). Thus, there is an urgent need to better understand the pathogenesis of sensory dysfunction to aid development of mechanism-based therapies.

Preclinical studies of chronic neuropathy in experimental models of cancer are unavailable, possibly because of presumption that chemotherapy alone is sufficient to explain the neuropathology. A recently published meta-analysis identified 341 preclinical studies of chemotherapy induced neuropathy, and none assessed interaction between chemotherapy and cancer (Currie, Angel-Scott *et al.* 2018). Omitting cancer from preclinical study produces a fundamental gap in knowledge that may explain why treatments for neuropathic side effects of chemotherapy have been unsuccessful in

patients with cancer. Cancerous tumors located outside the nervous system can induce cognitive disability and peripheral nervous system dysfunction independent of chemotherapy, surgery, or co-morbidities (Ahles 2012; Boyette-Davis, Eng *et al.* 2012). Moreover, cancer provokes dysregulation in immune, metabolic, oxidative and neuronal excitability (Reuter, Gupta *et al.* 2010; Zheng, Fang *et al.* 2012), all of which are identified as targets through which chemotherapy produces neuropathy (Cavaletti and Marmiroli 2010). Convergence of cancer and chemotherapy on the same biological processes seems likely to yield non-linear interactions, leading us to hypothesize that clinically relevant neuropathy emerges from codependent actions of cancer and chemotherapy.

We tested our hypothesis by uncoupling the independent and combinatorial effects of cancer and chemotherapy on sensory neurons in studies of rats that are not feasible in human patients. Here we present original findings to show that sensory neuropathy depends on complex systemic interactions between cancer and chemotherapy. By combining cancer and chemotherapy, we reproduce the relevant clinical condition in preclinical study of rats to produce the first transcriptional profile of nervous tissue, to discover recurrent metabolic reprogramming and perturbed inflammatory and ion channel processes distinct from the independent effects of cancer or chemotherapy. Parallel codependency is found in novel neuropathic responses of mechanosensory neurons, both in their immunohistochemistry for selected voltage-gated potassium ion channels and in electrophysiological measures of encoding naturalistic stimuli *in vivo*. Collectively, our data show for the first time that sensory neuropathy emerges from codependencies between the systemic effects of cancer and chemotherapy. Apart from identifying new molecular targets for restoring function to mechanosensory neurons, our findings provide the fundamental insight that accounting for chemotherapy-cancer

combinatorial effects on the somatosensory nervous system is prerequisite for developing meaningful treatment or prevention of neuropathy.

Aim 1: Test the hypothesis that cancer exacerbates chemotherapy induced gene dysregulation in the sensory nervous system.

Aim 1 Introduction

To gain comprehensive and unbiased understanding of treatment effects, we first profiled the transcriptomes of lumbosacral (L4-S1) dorsal root ganglia, where sensory neurons (Figure 2b) are known to be particularly vulnerable to chemotherapy (Cavaletti and Marmiroli 2010). We studied wild-type (Apc^{WT}) rats and rats carrying an *Apc* gene mutation ($Apc^{Pirc/+}$) (Amos-Landgraf, Kwong *et al.* 2007) associated with development of colon cancer (Kwong and Dove 2009), not only in these rats, but also in 80% of patients with colorectal cancer (Kwong and Dove 2009). This allowed us to simulate clinical treatment of colorectal cancer in a rat model. We employed the standard-of-care, platinum-based chemotherapy agent oxaliplatin (OX), in a human-scaled, dose-equivalent treatment schedule. This experimental approach provided the best available approximation of human colorectal cancer treatment, while enabling controlled experimental manipulations and analysis of molecular and functional properties of sensory neurons (Irving, Yoshimi *et al.* 2014).

Aim Specific Methods

Tissue Collection

At the conclusion of in vivo experiments, three to four animals from each of four groups were selected for whole-transcriptome analysis alone and did not undergo further

analysis. Dorsal root ganglia (DRG) from the lumbosacral (L5-S2) spinal cord were surgically removed (4-6 per animal), washed with sterile saline and immediately flash frozen (fresh) in 2-methylbutane (isopentane) pre-chilled in liquid nitrogen. DRG were then stored at -80°C for further analysis (see below).

RNA Extraction and Amplification

RNA extraction and amplification were performed according to our previously described methods (Lili, Matyunina *et al.* 2013). Briefly, RNAs were isolated and purified from sensory neurons of DRG (L5-S2) using the mRNeasy Micro KIT (Qiagen, Germantown, MD). Total RNA concentration and integrity was assessed on the Bioanalyzer RNA Pico Chip (Agilent Technologies, Santa Clara, CA). Labeling of RNAs was performed with the FlashTag Biotin HSR RNA Labeling Kit (Affymetrix, ThermoFisher). Gene expression was determined by microarray analysis on the Affymetrix platform (Rat Transcriptome Array 2.0).

Microarray data analysis

In total, 13 (four groups with biologic triplicates per group (4 biologic replicates from *Apc^{Pirc/+}*+OX group) global transcriptional expression data sets were generated in this study. Raw mRNA expression data were processed using Affymetrix Expression Console (EC) software Version 1.4. Raw data probes were normalized using SST-RMA algorithm. Differentially expressed genes (DEG) were determined through a linear fixed effects model (*limma* (Smyth 2004; Smyth 2005)) with a robust empirical Bayes (eBayes) framework (Phipson, Lee *et al.* 2016) to moderate the residual variances (Smyth 2004; Smyth 2005). This has the effect of increasing the effective degrees of freedom by which gene-wise variances are estimated, thus reduces the number of false

positives for genes with small variances and improves power to detect DEG with larger variances (Ritchie, Silver *et al.* 2007).

Unsupervised multivariate analysis

DEGs were subjected to paired multivariate analyses to discover latent data structure. We serially linking two analytic techniques, Principal Components Analysis (PCA) and Hierarchical clustering. This stabilized clustering performance and reduced dimensionality to a more tractable number of continuous variables containing the most important information on which clustering algorithms are focused which leads to a better clustering solution (Husson, Josse *et al.* 2010; Argüelles, Benavides *et al.* 2014). PCA and visualization was applied to DEGs with the *factoextra* (Kassambara and Mundt 2016) and *FactoMineR* (Husson, Josse *et al.* 2010) packages. PCs capturing high-level structure were then employed to drive hierarchical clustering. Hierarchical clustering and heatmaps were visualization with the *gplots* package (*heatmap.2*) (Warnes, Bolker *et al.* 2016) in the R environment (3.5.0) (Team 2018). Hierarchical-clustering, using the ward.D2 method (Murtagh and Legendre 2014) were applied to the eBayes-filtered gene set to obtain unsupervised visualization of the gene clusters coordinately expressed among the different experimental groups. Prior to hierarchical clustering, genes were standardized across the samples to a mean of zero and an s.d. of 1. Subclusters were derived using the R function *cutree* (Becker, Chambers *et al.* 1988).

Pathway and Gene Set Enrichment Analysis

To extract biological meaning from large lists of differentially expressed genes acquired through high-throughput technologies, e.g. transcriptomics, one must utilize bioinformatic support. Pathway enrichment analysis is one such analytic approach through which high-throughput, typically -omics, data are analyzed to uncover a variety of biological

mechanisms associated with a physiological process, e.g. diseases, development, etc. Detailed descriptions and protocols have been described previously (Huang, Sherman *et al.* 2008; Huang, Sherman *et al.* 2008); therefore, only a brief description follows.

Pathway enrichment analysis was conducted on subclusters of named genes using DAVID (Database for Annotation, Visualization, and Integrated Discovery) and g:Profiler to pinpoint significantly enriched pathways or biological processes (Huang, Sherman *et al.* 2008; Huang, Sherman *et al.* 2008). Biological processes and pathways are composed of group of genes as opposed to individual genes and are derived from the collective knowledgebase of published literature e.g. annotation database Gene Ontology (GO). Biological processes link individual genes to a broader biological concept or pathway and typically contain many tens to hundreds of genes. It should be noted that different biological processes can have some degree of redundancy of their composition.

The foundations of pathway enrichment analysis rest on the idea that if a biological process or pathway is truly abnormal in a disease, the co-functioning genes should have a higher potential to be selected for as a relevant group by the high-throughput screening technologies as opposed to studying individual genes. This shift from focus on individual genes to large gene lists increases the likelihood of identifying correct biological processes most pertinent to the disease or biological phenomena under study and reduces the likelihood of false positive findings. We further increase statistical power by submitting subclusters, co-regulated (up or down) probe sets, for testing that were previously separated during our initial multivariate approach (Hong, Zhang *et al.* 2014). All biological processes with adjusted $P < 0.05$ were considered significantly enriched. g:Profiler 3-500 (min-max) Benjamini Hochberg FDR correction intersection terms (2) only annotated genes were searched.

Parallel identification of pathways enrichment was performed by GSEA (gene-set enrichment analysis). GSEA underlying statistical construct is independent of DAVID. GSEA can uncover novel sets of functionally related genes by focusing on all detected (above-background) genes. GSEA is unbiased in this regard in that it reduces arbitrary cut-off factors in the typical gene selection step utilized in traditional analyses; and it uses all information by allowing genes with even minimal change that would otherwise not pass the selection threshold. These advantages afford the detection of even subtle enrichment signals. GSEA accomplishes this by leveraging list rank information without using a threshold typically applied in overlap statistics like hypergeometric testing to define genes as members at the top or bottom of a ranked list of genes.

The Molecular Signature Database v 6.2 (C2-CP: canonical pathways; C3- MIR: microRNA targets; C3- TFT: transcription factor targets; C5-BP: GO biological process; C5- CC: GO cellular component; C5- MF: GO molecular function C7: immunologic signatures gene sets) with the permutation type set to 'gene set,' 15-500 (min-max), to calculate statistical significance, as suggested for fewer than seven replicates; default settings were applied to all the other options. For GSEA, a false discovery rate (FDR) of <0.2 was considered statistically significant. Selecting appropriate reference background for pathway analyses is a potential pitfall since the different gene reference background settings may greatly impact the enrichment scores. Even though there is no 'gold' standard for the reference background, we followed the widely utilized procedure of setting the reference background to the pool of genes that could be potentially be selected, e.g. total genes evaluated in an -omics study. Specifically, all pathway analyses performed utilized the same Affymetrix platform Rat Transcriptome Array 2.0 as the background list of genes.

Targeted Transcriptional Analysis

Complementary supervised analysis of DEGs leveraged knowledge of proteins known to be expressed at sensory neuron receptor endings that directly (Simon, Shenton *et al.* 2010; Woo, Lukacs *et al.* 2015; Carrasco, Vincent *et al.* 2017) or indirectly (Bewick and Banks 2015; de Nooij, Simon *et al.* 2015) regulate excitability. In addition, due to incomplete knowledge of the full suite of proteins that are necessary and sufficient for normal function (Bewick and Banks 2015), we expand targeted transcriptional analysis to incorporate gene families, including: ion channels, GPCRs, and channel regulators.

Results

Transcriptional profiling of sensory neurons

We employed an empirical Bayesian (eBayes) linear model (Smyth 2004) to modify residual variances on a total of 31,042 (22,875 named) genes and identified 3,426 differentially expressed genes (DEG) across all groupwise contrasts ($P_{\text{eBayesAdj}} < 0.005$). Subsequent *post hoc* analysis identified DEG from all possible contrasts (fold-change (FC) ≥ 1.2 and ≤ -1.2). Overlap between DEGs retrieved from individual comparisons is illustrated in (Figure 6a). In keeping with the notion that chemotherapy and cancer act through similar molecular mechanisms, we found overlap of 112 DEG affected independently by cancer and chemotherapy (Figure 6a). Of note, we found that 73.8% (n=1,704) of all DEG (n=2,307) were uniquely affected when cancer and chemotherapy interacted (*ApC*^{Pirc/+}+OX) Figure 6a). This finding demonstrates the first evidence that cancer exacerbates genetic dysregulation induced by chemotherapy, unmasking a more than four-fold increase in DEG.

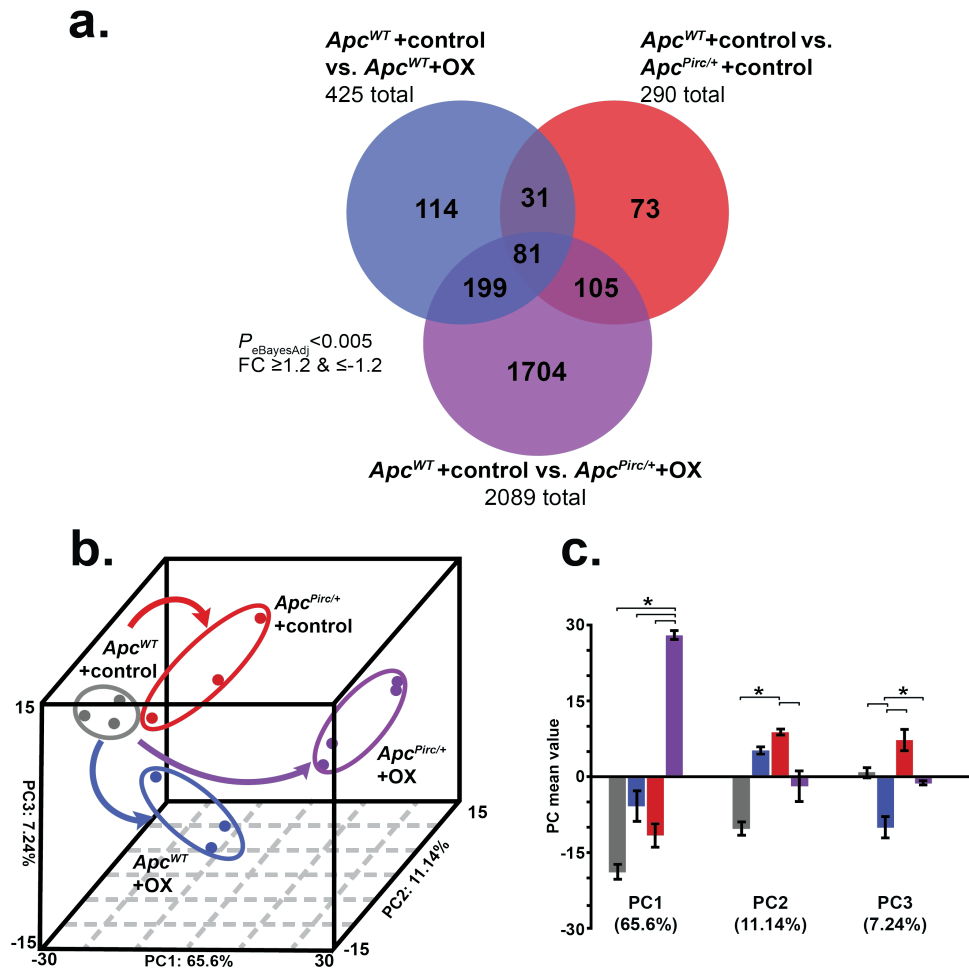


Figure 6.

Cancer-chemotherapy codependence amplifies transcriptional dysregulation.

c. Venn-diagram distribution of significantly differentially expressed genes from the lumbosacral DRG among all groupwise contrasts. Significance determined by both $P < 0.005$ and fold-change (FC) ≥ 1.2 and ≤ -1.2 using a Bayesian moderated linear fixed effects model ($eBayes_{Adj}$). **d.** Group correlation determined by principal-component (PC) analysis of significantly differentially expressed genes. Genes were visualized in the new 3D composite space created by PC1-3. Effects of independent chemotherapy ($Apc^{WT}+OX$) or cancer ($Apc^{Pirc/+}+control$) and their combinatorial ($Apc^{Pirc/+}+OX$) treatment are indicated by curved arrows; dots represent individual animals. **e.** Bar graphs of the mean values of PC1, PC2, and PC2. Error bars represent s.e.m. * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model ($stan_glm$).

Next, we performed two independent downstream analyses (Figure 7) to test for interaction and determine which biologic processes might be involved in pathogenesis of sensory disorders. First, we subjected the eBayes filtered database to unsupervised principal component (PC) analysis. DEG were visualized in the new 3D composite space created by PC1-3 (Figure 6b) that explained 83.98% of the variance and clearly segregated the four experimental groups. Inspection of individual PCs revealed significant evidence of non-linear interactions between cancer and chemotherapy captured in PC1 (65.6% of explained variance), whereas PC2 (11.14%) and PC3 (7.24%) separated the effects of cancer and chemotherapy, respectively (Figure 6c). Second, we drove unsupervised hierarchical clustering onto the PC1 solution to identify groups of coregulated genes that express interaction (Argüelles, Benavides *et al.* 2014) (Figure 8a). Analysis identified two clusters of genes displaying distinct, but internally consistent expression profiles clearly representing patterns of interaction (Figure 8a, C1 and C2; Table 1).

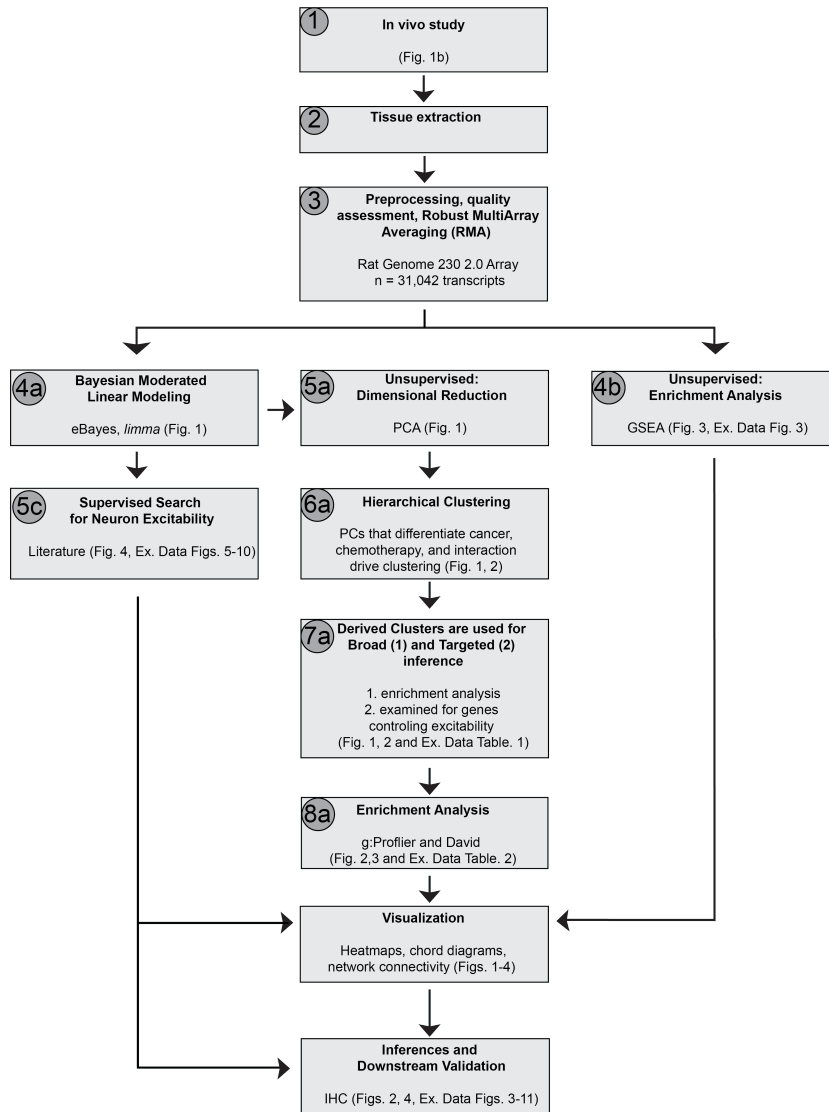


Figure 7.

Steps outlining parallel independent transcriptome analyses. Data analysis flowchart depicts the multi-step (split into a, b, and c streams) approach utilized for transcriptome analysis, inferences and downstream protein level validation. A detailed description of each step is available in the **Online Methods Sections**. Each box highlights specific analytic techniques, statistical packages (when relevant), and corresponding figures as reference. Principal component analysis, PCA; gene set enrichment analysis, GSEA; principal components, PC; Database for Annotation, Visualization and Integrated Discovery, DAVID; immunohistochemistry, IHC.

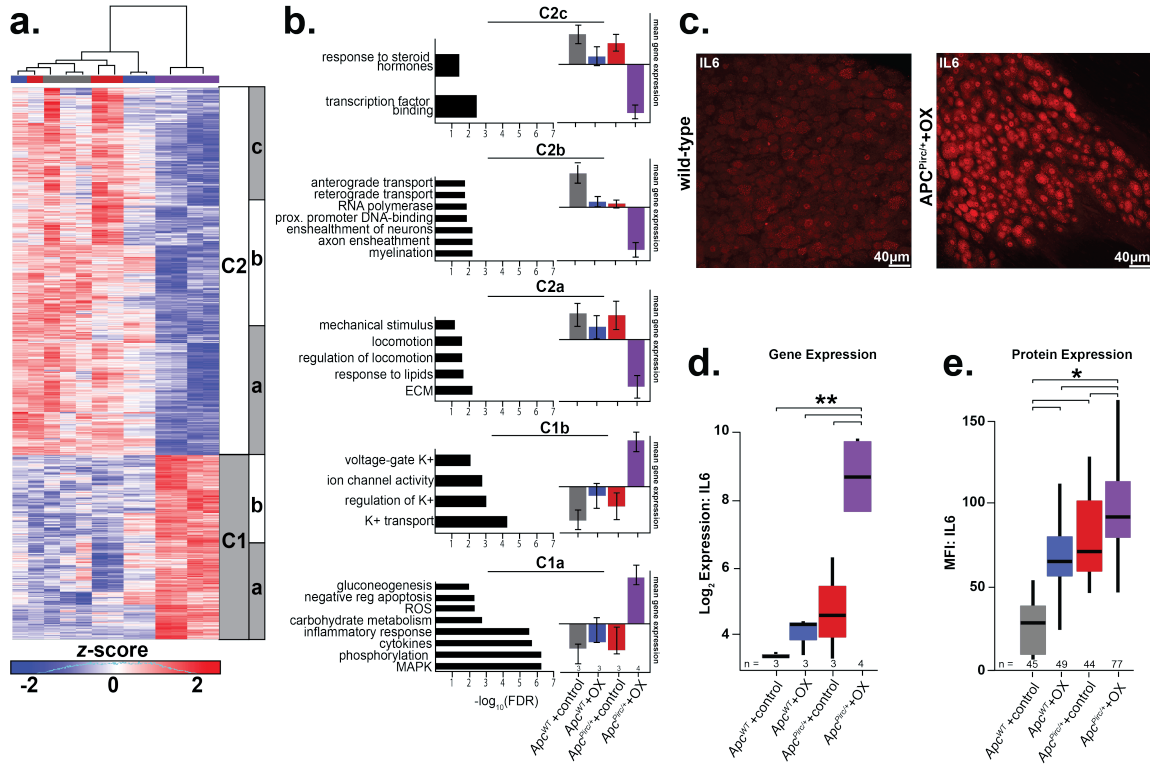


Figure 8.

Cancer-chemotherapy interaction disrupts distinct biological processes. a, Heatmap of the top differentially expressed genes in the sensory neurons identified by PC1 driven hierarchical-clustering (biological triplicates $n = 3$ for $Apc^{WT}+control$, $Apc^{WT}+OX$, $Apc^{Pirc/+}+control$ and four biologic replicates for $Apc^{Pirc/+}+OX$). Data were mean-centered and s.d. normalized before clustering; upregulated and downregulated genes (row) are shown in red and blue, respectively. White and grey bars (C1 and C2 respectively) display the main clusters from gene level hierarchical-clustering and were chosen for clarity, while subclusters (a-c) highlight unique biologic characteristics within the main clusters. b, Clusters showing distinct up- or downregulation of key biological processes (Gene Ontology (GO) terms) and pathways (Kyoto Encyclopedia of Genes and Genomes (KEGG)). Selected pathway and gene ontology terms significantly associated (false discovery rate [FDR] ≤ 0.25) with misregulated transcripts in individual clusters are listed on the left of each gene cluster with significance indicated by horizontal bars ($-\log_{10}(FDR)$). The vertical bar graphs on the right compare mean \pm s.d. of gene expression levels in each subcluster (Table S1). c, Confocal image of a dorsal root ganglia immunostained against interleukin 6 (IL6). Scale bar, 40 μ m. Gene expression (d) and receptor protein expression (e, mean fluorescence intensity (MFI)) of IL6 as determined by transcriptional profiling and cell-specific immunohistochemistry of large diameter sensory neurons

(>30 μ m). Numbers (n) identify sample size for each group. * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (stan_glm). ** indicates $e_{\text{BayesAdj}} < 0.005$ and fold-change (FC) >1.5 using a Bayesian moderated linear fixed effects model. Data presented as mean \pm s.d.

We then subjected clusters of named genes (Table S1) to pathway-enrichment analysis (Reimand, Kull *et al.* 2007; Huang, Sherman *et al.* 2008) and identified unique subclusters (Figure 8a) expressing dysregulation in distinct biological processes (Figure 8b, see Methods: Pathway and Gene Set Enrichment Analysis). In keeping with the notion that combinatorial effects of cancer and chemotherapy (OX) reflect convergence onto shared signaling pathways, genes mediating inflammatory response, e.g. interleukin 6 (*Il6*) ($P_{e_{\text{BayesAdj}}} = 7.82 \times 10^{-6}$), *Ptgs2* ($P_{e_{\text{BayesAdj}}} = 0.0028$) and *Cxcr4* ($P_{e_{\text{BayesAdj}}} = 3.74 \times 10^{-7}$), and reactive oxygen species processes, e.g. *Hmbox1* ($P_{e_{\text{BayesAdj}}} = 0.001$), were found to be among the most upregulated in cluster 1a (C1a) (Figure 8b). Notably, we observed substantial induction of genes encoding glycolytic and carbohydrate metabolic processes ($\text{FDR} \leq 1.83 \times 10^{-3}$, C1a; Figure 8b) in the *Apc*^{Pirc/+}+OX neurons. Coincident with these changes was a statistically significant down-regulation of genes mediating lipid metabolism (C2a), suggestive of pervasive metabolic dysfunction beyond the small subset of dysregulated mitochondrial related processes that we found in response to *Apc*^{WT}+OX or *Apc*^{Pirc/+}+control alone (Figure 8b; Figure 9a,b) and similar to dysfunctional effects previously suggested (Cavaletti and Marmioli 2010). Among additional unique transcripts downregulated in *Apc*^{Pirc/+}+OX neurons, Figure 8b highlights multiple deficits in processes related to extracellular matrix control, mechanical stimulus transduction (C2a), DNA-binding, RNA polymerization (C2b), transcription factor activity, hormone signal transduction (C2c and Table. S1). Furthermore, we observed genes in C1b and 2a that represent specific dysregulation of neuronal and sensorimotor function,

e.g. ion-channel genes determining neuronal excitability along with coincident down-regulation of locomotion. These data provide the first evidence that codependent neuropathy induces broad metabolic reprogramming, e.g. increased glycolytic and decreased lipid metabolism, consistent with cancers capacity to corrupt metabolic processes (DeBerardinis, Lum *et al.* 2008; Hay 2016), which extends knowledge beyond the limited impairment observed in mitochondria.

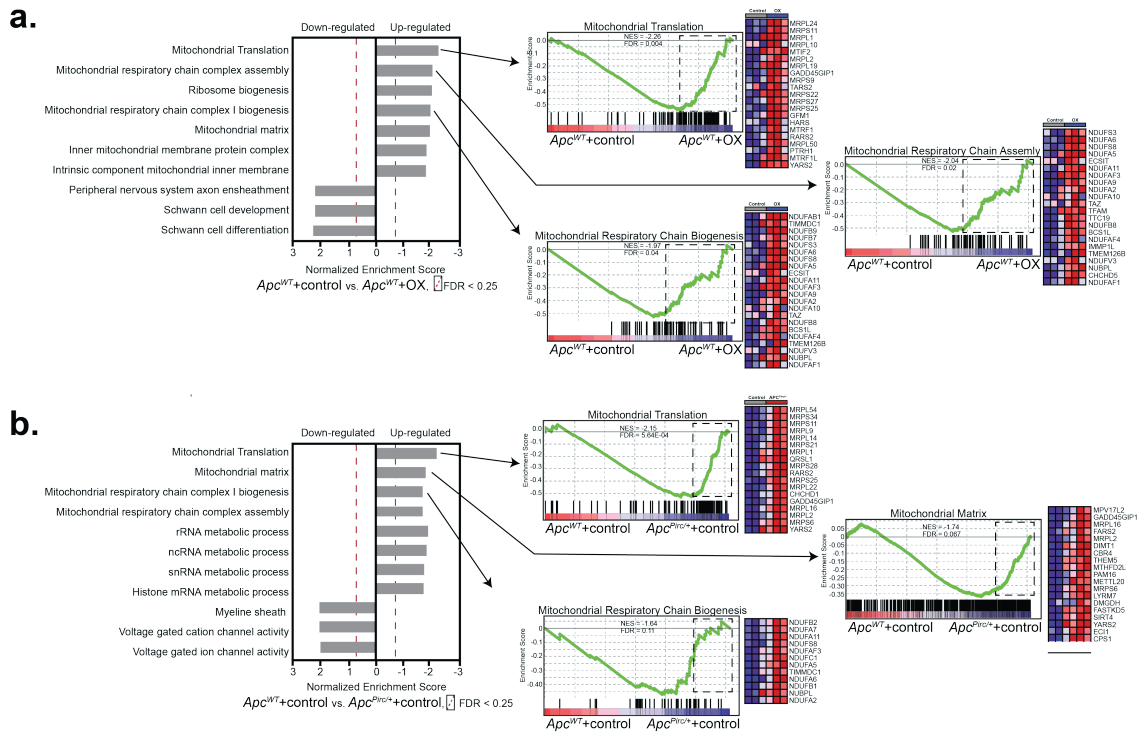


Figure 9.

Pathway analysis and GSEA based comparison of the independent effects of cancer and chemotherapy show convergence of mitochondrial dysfunction. List of enriched gene sets in sensory neurons identified by GSEA (queried against MSigDB, C2-CP: canonical pathways; C3- MIR: microRNA targets; C3- TFT: transcription factor targets; C5-BP: GO biological process; C5- CC: GO cellular component; C5- MF: GO molecular function C7: immunologic signatures gene sets from the comparison of a, $Apc^{WT}+control$ and $Apc^{WT}+OX$ and b, $Apc^{WT}+control$ and $Apc^{Pirc/+}+control$ groups. Individual frames identify functional related groups of gene sets expressing distinct up- or downregulation as compared with control. Representative enrichment plots are shown on the right. Heat-map representation of leading-edge genes are shown on the right of each enrichment plot highlight key mitochondrion-related proc, such as translation and biogenesis in both $Apc^{WT}+OX$ and $Apc^{Pirc/+}+control$ neurons, and key neuron myelination-related processes. Statistical significance was determined by permutation testing with normalized enrichment score (NES) and Benjamini–Hochberg false discovery rate (FDR) < 0.25.

Markers for nerve degeneration, inconsistently observed in patients treated with antineoplastic drugs (Burakgazi, Messersmith *et al.* 2011) exhibited mixed results. While we observed few significantly downregulated genes associated with myelination processes (C2b; $P \leq 7.12 \times 10^{-3}$, Figure 8b), we also found significant induction of processes involved in the preservation of neurons (e.g. enrichment of negative regulation of apoptosis $P \leq 5.96 \times 10^{-3}$) in C1a that is related to the synergistic effects of cancer and chemotherapy, i.e. where cancer and chemotherapy impart influence in the same direction. Mixed results from these data suggests heterogeneous neuronal populations in the DRG may contain discrete subpopulations with selective vulnerability whereas others are resistant to degeneration, which is consistent with mixed results seen in human studies (Burakgazi, Messersmith *et al.* 2011) and highlights the need for future cell-type specific investigations that are currently unavailable.

Global dysregulation of neuron transcriptomes

We then used gene-set enrichment analysis (GSEA) as a second independent tool to investigate the cellular processes underlying codependent neuropathy. We initially focused on the comparison of $Apc^{WT}+OX$ and $Apc^{Pirc/+}+OX$ (Figure 10a: how cancer alters the independent effects of chemotherapy) and $Apc^{Pirc/+}+control$ and $Apc^{Pirc/+}+OX$ (Figure 10b: how chemotherapy alters the independent effects of cancer) and interrogated entire data sets against the Molecular Signatures Database (Table S2). Two novel conclusions can be drawn from the GSEA findings. First, GSEA independently validated codependencies of cancer and chemotherapy in the DEG identified by transcriptional profiling using paired unsupervised analysis (Figure 10a, b). GSEA corroborated downregulation of lipid metabolic pathways (normalized enrichment score (NES)=1.73) and upregulation of glycolytic pathways (NES=-1.94) in $Apc^{Pirc/+}+OX$ sensory neurons when compared with either chemotherapy (Figure 10a) or cancer alone

(Figure 10b). Focusing analysis on pathways directly involved in neuronal signaling confirmed dysfunction in peripheral neuron ensheathment in the absence of evidence supporting neuron specific apoptotic response (FDR>0.83) (Figure 10a). Second, GSEA exposed dysregulation of genes relevant to neuronal excitability particularly potassium ion channels and transporters, and others participating in synaptic communication, e.g. SNARE and glutamatergic transmission (Figure 10a, b). Dysregulation of these and other gene sets (e.g. proinflammatory chemokines) was not predicted from the independent effects of cancer or chemotherapy alone. (Table S2). Unlike previous studies that consistently report dysregulated voltage-gated sodium channels (Sittl, Lampert *et al.* 2012), we find little evidence of differentially expressed sodium channels or disrupted regulatory pathways (Sittl, Lampert *et al.* 2012). Instead, we find targeted DEG related to potassium ion channels unlike those previously identified. We draw two conclusions from these data. First, ion channel clusters are differentially vulnerable to codependent neuropathy. Second, chronic neuropathy may be mechanistically linked to dysregulation of ion channels distinct from those identified in acute preparations.

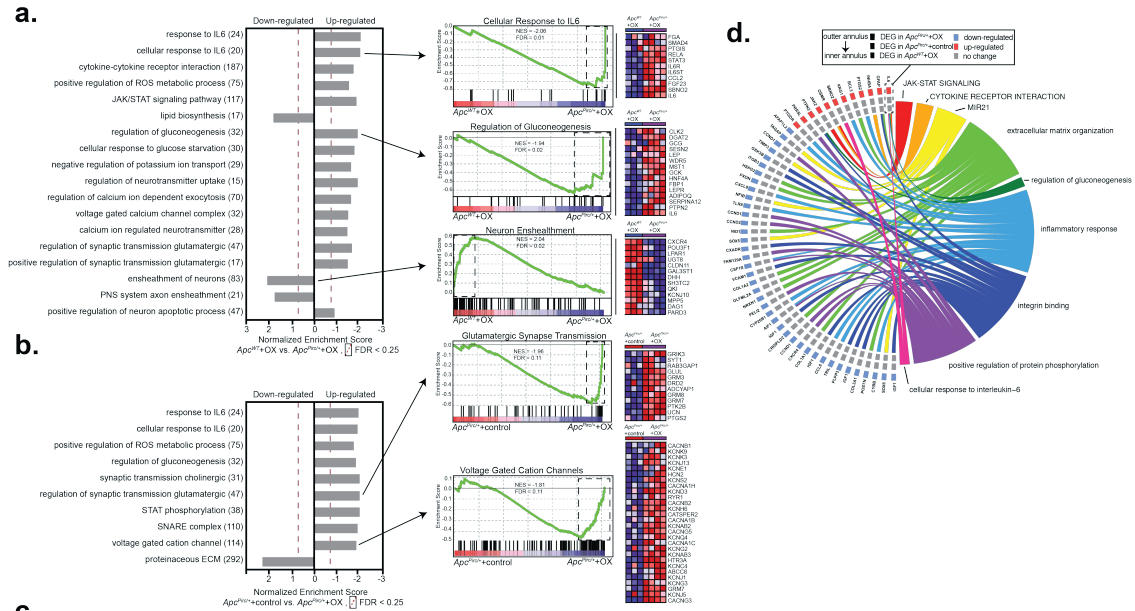


Figure 10.

GSEA and pathway analyses test codependence of cancer and chemotherapy. Enriched gene sets in sensory neurons identified by gene set enrichment analysis (GSEA: MSigDB, C2-CP: canonical pathways; C3- MIR: microRNA targets; C3- TFT: transcription factor targets; C5-BP: GO biological process; C5- CC: GO cellular component; C5- MF: GO molecular function C7: immunologic signatures gene sets from the comparison of a, *Apc*^{WT}+OX and *Apc*^{Pirc/+}+OX and b, *Apc*^{Pirc/+}+control and *Apc*^{Pirc/+}+OX groups. Individual frames (horizontal grey bars) identify functional related (internally consistent) groups of gene sets expressing distinct up- or downregulation as compared with *Apc*^{WT}+OX. Number of overlapping genes displayed in parentheses to the right of the corresponding GO term. Representative enrichment plots are shown in the middle column. Heat-map representation of leading-edge genes is shown on right. c, Heat-map representation of enriched individual gene sets, identified by GSEA, in sensory neurons for chemotherapy (bottom row), cancer (middle row), and the combination of cancer (*Apc*^{Pirc/+}) and chemotherapy (OX) (top row). Gene sets are grouped into functionally related cohorts. Gene sets not reaching statistical significance indicated by (X). d, Chord diagram shows enriched pathways (Database for Annotation, Visualization, and

Integrated Discovery; DAVID) on the right, and genes contributing to enrichment are shown on the left. Squares on left indicate genes differentially expressed in $Apc^{WT}+OX$, $Apc^{Pirc/+}+control$, or $Apc^{Pirc/+}+OX$ groups compared to control (see the key for gene differential expression). Statistical significance determined by permutation testing with normalized enrichment score (NES) and Benjamini–Hochberg false discovery rate (FDR) < 0.25. DEG, differentially expressed genes; ROS, reactive oxygen species; ECM, extracellular matrix.

Summary

Taken together, our analyses indicate significant dysregulation of genes and proteins mediating core cellular processes of $Apc^{Pirc/+}+OX$ sensory neurons. Our integrated transcriptomics and protein level findings confirmed that cancer and chemotherapy effect common processes (Ahles and Saykin 2007; Reuter, Gupta *et al.* 2010; Argyriou, Bruna *et al.* 2017). Moreover, our findings support our central hypothesis that clinically relevant neuropathy depends on systemic interaction between cancer and chemotherapy by showing for the first time that cancer-chemotherapy codependence exacerbates neuropathy and revealing it operates through distinct mechanistic pathways, unpredicted from cancer or chemotherapy alone.

Aim 2: Test the hypothesis that cancer-chemotherapy codependent genetic dysregulation is conserved at a protein level.

Introduction

Because inflammatory pathways play multiple roles in regulating neuron function (Vezzani and Viviani 2015), we focused attention on their significant response to codependent neuropathy. We selected the most dysregulated gene in the inflammatory

pathways, *Il6*, for the first molecular validation by assessing gene—protein correspondence.

Aim Specific Methods

Tissue Collection

At the conclusion of in vivo experiments, rats were overdosed with isoflurane inhalation (5%) then immediately transcardially perfused with cold vascular rinse (0.01 M PBS pH 7.4) followed by room temperature fixative (2% paraformaldehyde in 0.1 M PBS, pH 7.4). Muscles and dorsal root ganglia were quickly dissected and post-fixed for one hour in the same fixative. After a brief wash in a 0.1 M PBS, tissues were incubated in 0.1 M PBS containing 20% sucrose at 4°C overnight. After DRG removal, colonic tumors from *Apc^{Pirc/+}* rats were dissected and counted prior to post fixation for immunohistochemical analysis.

Immunohistochemistry

Details of our immunohistochemistry procedures have been previously described (Carrasco, Vincent *et al.* 2017). Briefly, 50- μ m thick sections of skeletal muscles, DRGs, and tumors were cut using a Cryostat (Leica). Tissues sections from all treatment groups were processed simultaneously. All tissue sections were incubated overnight in primary antibodies diluted in blocking buffer (5% normal goat serum, 0.3% Triton100 in PBS). The primary antibodies used were as follow: rabbit polyclonal anti-NaV1.6 (ASC-009, Alomone Laboratories, 1:200), rabbit polyclonal anti-NaV1.1 (ASC-001, Alomone Laboratories, 1:300), rabbit polyclonal anti-NaV1.7 (ASC-008, Alomone Laboratories, 1:100), rabbit polyclonal anti-Kv3.3 (APC-102, Alomone Laboratories, 1:300), mouse monoclonal anti-Kv1.1 (K36/, NeuroMab, University of California Davis, 1:300), guinea pig polyclonal anti-VGLUT1 (135-

104 Synaptic Systems, 1:300), chicken polyclonal anti-neurofilament protein (NF-H, Aves Laboratories, 1:200), mouse monoclonal anti-ASIC2, (E-20, Santa Cruz Biotechnologies, 1:200), mouse monoclonal anti-EGRF (SC-120, Santa Cruz Biotechnolgy, 1:100), mouse monoclonal anti-KI67 (SC-23900, Santa Cruz Biotechnology, 1:100), mouse monoclonal anti-IL6 (SC-57315, Santa Cruz Biotechnology, 1:100). After washing with PBS, tissue sections were incubated with appropriate fluorescent-conjugated secondary antibodies (Jackson ImmunoResearch Laboratories) diluted in blocking buffer, for 1 hr. at room temperature. Following washes with PBS, slides were mounted using Vectashield containing DAPI (Vector Laboratories) in order to label cell nuclei.

3D Digital Reconstructions and Anatomical Quantifications

Z-axis stacks of images of muscle spindles receptor endings, DRGs and tumors were constructed by sequentially imaging using a confocal microscope (LSM 700A, Zeiss). Muscle spindles terminals z-stacks (1 μ m steps) were captured with a 40X oil immersion objective (N.A 0.6) at 0.6 digital zoom. DRG and tumors z-stacks (1 μ m steps) were captured with a 20X objective (N.A 0.4) at 0.6 digital zoom. Stacks of images were processed and analyzed using Amaris (Bitplane) or imageJ (NIH) imaging software. Figures present images as flat maximal projections of the sum of the z-axis optical slices. Analysis of neuron receptor endings (spindles) and soma (DRG) were performed by an investigator blinded to treatment group. Immunoreactivity in nerve terminals and DRG was determined by measuring the mean pixel intensity of on each en-face portions of the terminal (visualized by the VGLUT1 staining) observed on every 1 μ m single image or on the medium and large size cell somas observed on the flat maximal projections of the z-stacks images respectively.

Results

Dysregulation is conserved at protein level

Sensory neurons in dorsal root ganglia were immunolabeled with monoclonal antibodies targeting IL6 (Figure 8c). As predicted from the transcriptional profiling (Figure 8d), the IL6 protein was constitutively expressed in *Apc*^{WT}+control rats at lower levels than in *Apc*^{Pirc/+} control animals or *Apc*^{WT}+OX animals, and at significantly higher levels in *Apc*^{Pirc/+}+OX neurons (Figure 8e), demonstrating that codependent neuropathy was conserved in protein expression (Figure 8e and Figure 11). Previous studies implicate IL6's capacity to mediate hyperexcitability and morphological changes associated with neuron death (Nelson, Ur *et al.* 2002). However, these studies restricted investigation to acute neurotoxicity, which limits generalizability to symptoms that persist long after treatment. Our data present the first evidence that *Il6* (IL6) expression levels remain elevated long after treatment cessation without observable morphological changes. We show that codependent neuropathy significantly increases *Il6* (IL6) when compared to chemotherapy or cancer alone. In light of IL6's capacity to decrease excitability following chronic exposure (Nelson, Ur *et al.* 2002), our data suggest that neuronal dysfunction (see below) as a result of codependent neuropathy may be expressed as hypo-excitability, in contrast with previous work (Sisignano, Baron *et al.* 2014).

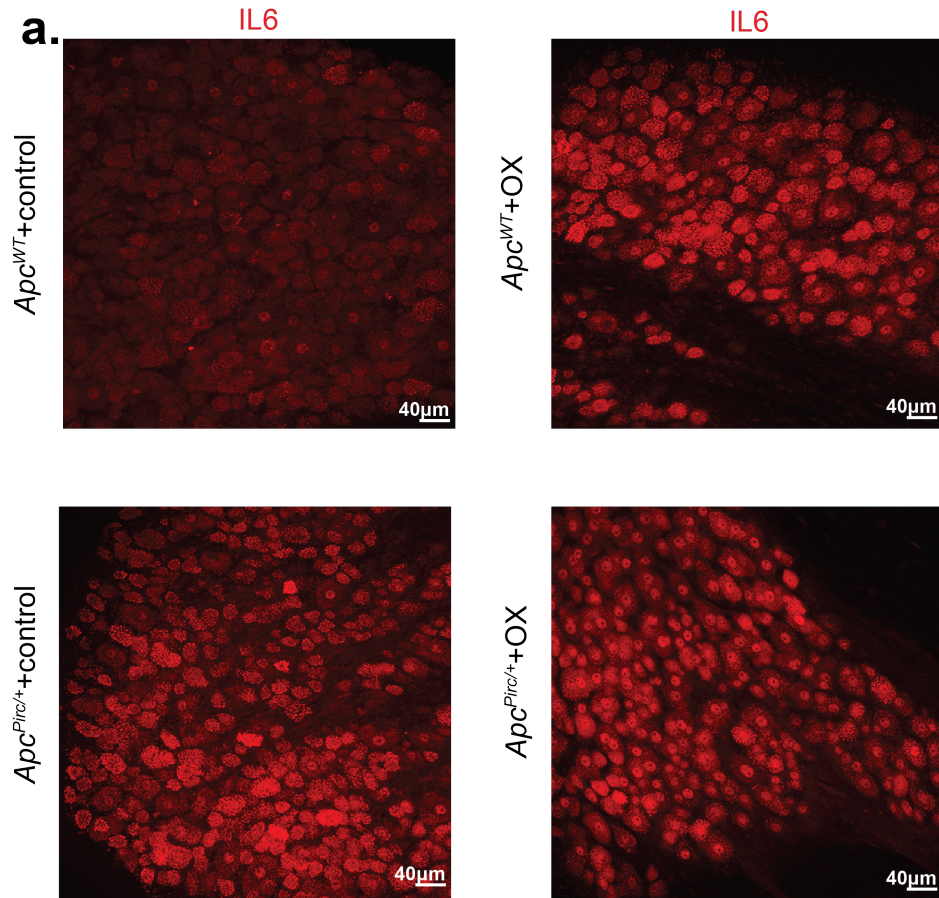


Figure 11.

Immunostaining of sensory neurons in dorsal root ganglia. Whole-mount staining and confocal axial projections of DRG neurons highlight expression of IL6 (a) in $Apc^{WT}+control$, $Apc^{WT}+OX$, $Apc^{Pirc/+}+control$, and $Apc^{Pirc/+}+OX$ rats

Novel voltage-gated ion channel dysfunction

Sensory deficits, e.g. somatosensory and hearing loss, are commonly reported by patients long after cessation of chemotherapy, but knowledge of the combined effects of cancer and chemotherapy is missing. Mechanosensory systems, e.g. cochlear hair cells, and various somatosensory neurons in skin and muscle are responsible for encoding this information and exhibit deficits following chemotherapy (Avan, Postma *et al.* 2015).

We therefore next focused on identifying the combined effects of cancer and chemotherapy on a representative member of mechanosensory neurons, called muscle spindles. Muscle spindles share many of the molecular mechanisms (Bewick and Banks 2015) underlying mechanotransduction and encoding found in this broad class of sensory neurons (e.g. hair cells (Chalfie 2009), Merkel (Maksimovic, Nakatani *et al.* 2014)). Further, signaling by these neurons encodes sensory features of muscle mechanics necessary for perceiving (proprioception) and coordinating body position and movement, functions which, when impaired, have the potential to explain persistent disorders in patients (Proske and Gandevia 2009). We performed targeted analyses of our transcriptome database by querying differentially expressed genes identified in *Apc^{Pirc/+}*+OX rats compared to all other groups against genes encoding proteins known to be constitutively expressed in mechanosensory neurons that mediate unique contributions to neuronal signaling (Figure 12) (Bewick and Banks 2015; Woo, Lukacs *et al.* 2015; Carrasco, Vincent *et al.* 2017). We found no evidence for independent nor combinatorial effects of cancer or chemotherapy at the genetic level (Figure 16a and Extended Data) for channels mediating mechanotransduction (e.g. *Asic2*, *Piezo2*, *ENaCs*), signal amplification, and spike encoding (e.g. *Scn1a* (Nav1.1), *Scn8a* (Nav1.6), *Scn9a* (Nav1.7), *Cacna1s,-c,-d,-f* (Cav1.1-4), *Kcnn2* (SK2), *Kcna1* (Kv1.1) which was subsequently confirmed in downstream immunohistochemical analyses (Figure 13, Figure 14, Figure 15).

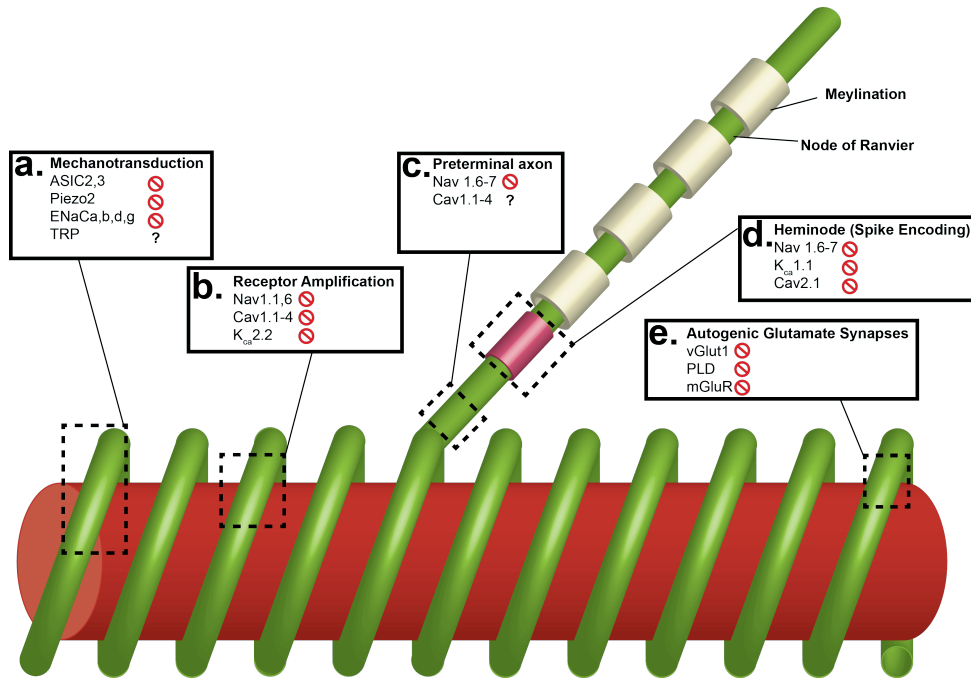


Figure 12.

Model of molecular determinants of neuronal signalling of sensory neurons. Model of mechanically-, voltage- and ligand-gated ion channels and their distribution in muscle spindle Ia primary ending. The intrafusal muscle fiber (red) is wrapped by an annulospiral ending (green) and a preterminal axon that extends unmyelinated from the terminal to the heminode (pink) followed by a myelinated axon. Dotted-boxes represent specific regional distributions believed to underlie specific functional characteristics of neuronal signaling e.g. mechanotransduction, receptor potential amplification, spike encoding, and autogenic feedback. Red circles with slashes indicate no gene and protein level evidential support for involvement in mediating cancer-chemotherapy codependent neuronal dysfunction. Bold question marks (?) indicate protein as a possible candidate due to evidential support from transcriptome, yet protein level confirmation is unavailable. a, Deformation of the receptor ending opens mechanotransduction channels that initiate excitatory currents mediated by ASIC2/3 (Simon et al 2010), Piezo2 (Woo et al 2015), ENaCa,b,d,g and to some extent TRP channels (Bewick and Banks 2015). Various Nav (Carrasco et al 2017) and Cav (Bewick and Banks 2015) channels are believed to amplify receptor potentials (b) and assist transmission toward encoding in the preterminal axons (c). d, Recent discovery of specific distribution of Nav channels in the heminodes (Carrasco et al 2017) are believed to underlie encoding of action potential similar to axon initial segments in other systems (Foust et al 2010). e, three components known to regulate auto-genic glutamatergic synapses in proprioceptors critical for signalling.

Next, we performed cell-specific immunohistochemical analyses to test gene–protein correspondence. We found no evidence to suggest dysregulated protein expression nor did evidence emerge to suggest altered protein distributions for most proteins, including those mediating mechanotransduction (ASIC2) (Figure 13), signal amplification (Nav1.1, Nav1.6 shown in Figure 14, and Nav1.7), spike encoding (Kv1.1), and mechanosensory sensitivity (VGLUT1) (Figure 15). These findings demonstrate that many of the molecular mechanisms responsible for mechanotransduction and determining excitability of mechanosensory neurons were preserved in the *Apc^{Pirc/+}+OX* rats. These findings narrow the field of candidate mechanisms for which treatment might reasonably restore normal function.

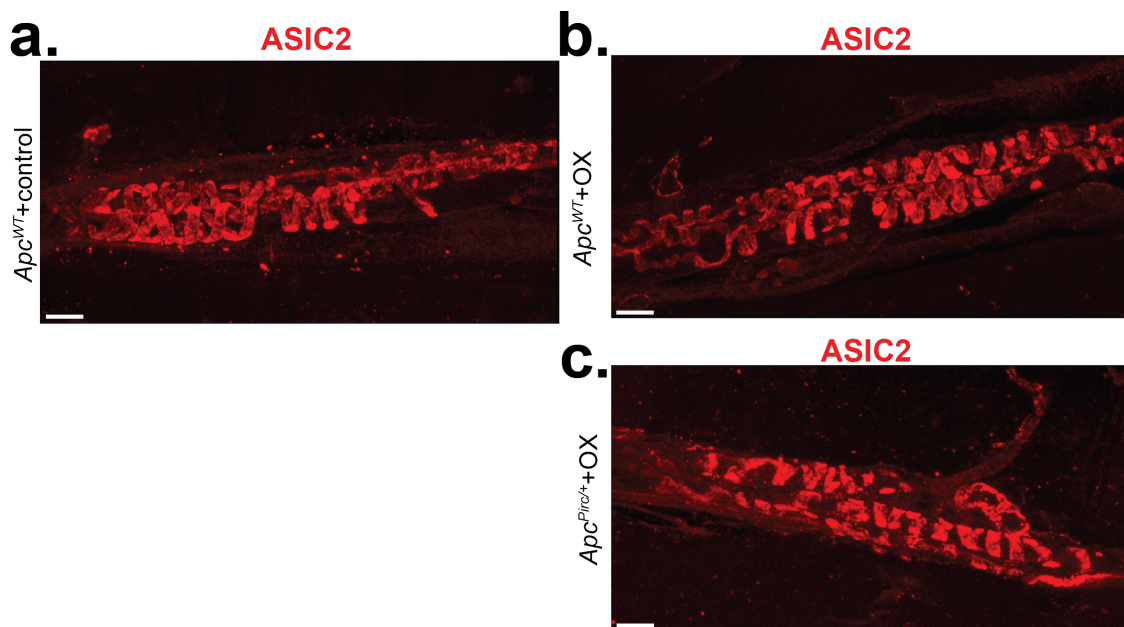


Figure 13.

ASIC2 immunostaining of proprioceptive sensory neurons receptor endings. Whole-mount staining and confocal axial projection of the preterminal axons and annulospiral receptor endings of proprioceptive sensory neurons showing single channel images of ASIC2 (red) from: a, *Apc^{WT}+control* rat; b, *Apc^{Pirc/+}+control*; c, *Apc^{WT}+OX*; d, and *Apc^{Pirc/+}+OX* rats.

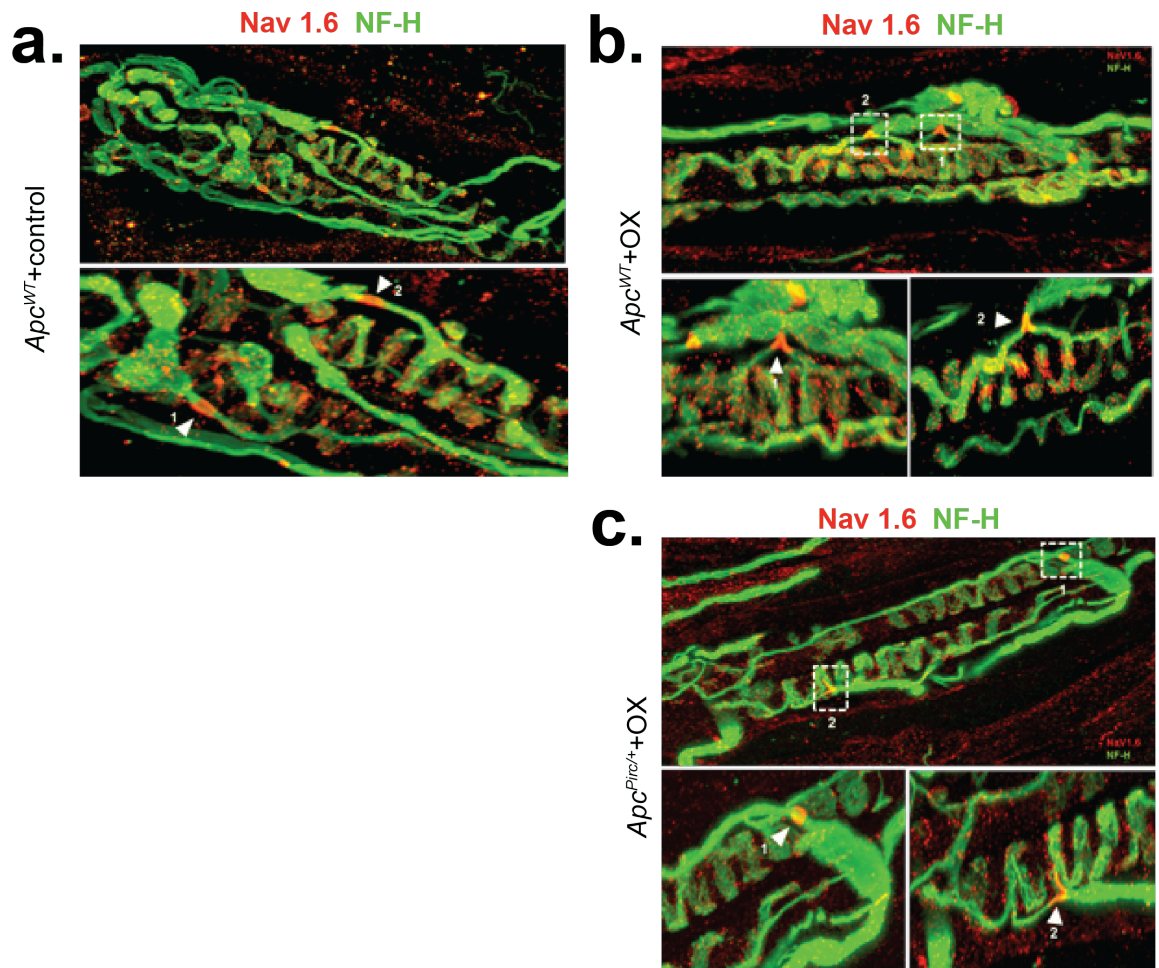


Figure 14.

Nav1.6 immunostaining of proprioceptive sensory neurons receptor endings. Whole-mount staining and confocal axial projection of the preterminal axons and annulospiral receptor endings of proprioceptive sensory neurons showing single channel images of Nav1.6 (red) and NF-H (green) in top row from: a, $Apc^{WT}+control$ rat; b, c, $Apc^{WT}+OX$; d, and $Apc^{Pirc/+}+OX$ rats. Bottom rows show Nav1.6 distribution in heminodes where spike encoding is initiated.

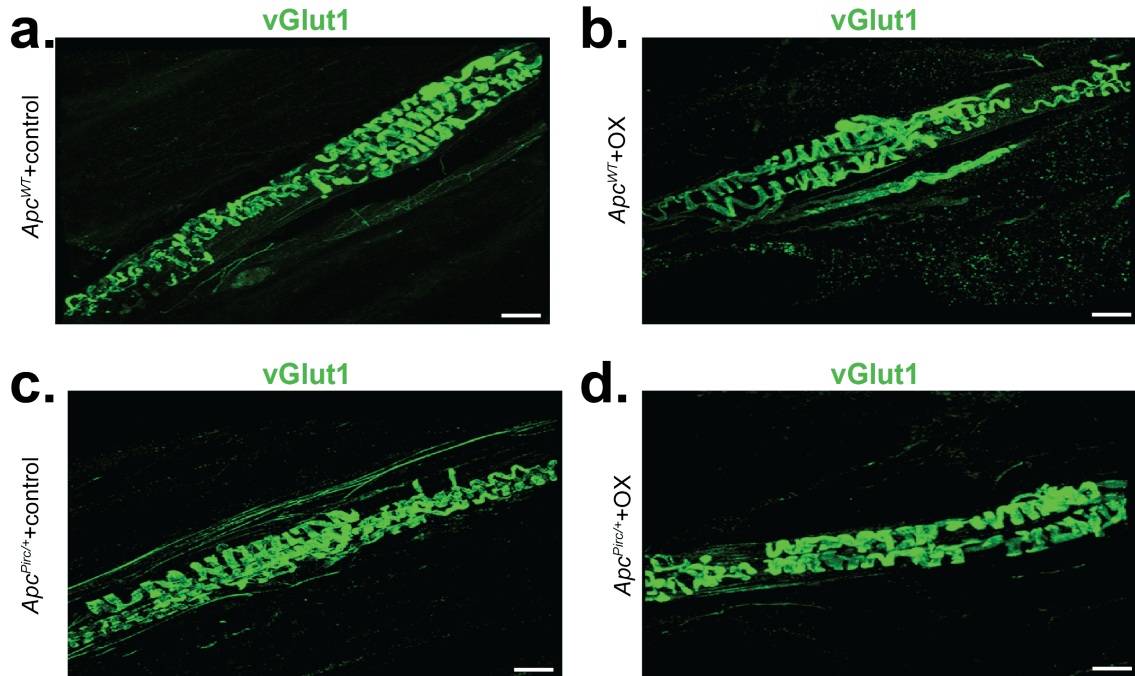


Figure 15.

vGlut1 immunostaining of proprioceptive sensory neurons receptor endings. Whole-mount staining and confocal axial projection of the preterminal axons and annulospiral receptor endings of proprioceptive sensory neurons showing single channel images of vGlut1 (green) from: a, Apc^{WT} +control rat; b, $Apc^{Pirc/+}$ +control; c, Apc^{WT} +OX; d, and $Apc^{Pirc/+}$ +OX rats.

Having exhausted examination of proteins known to be expressed in mechanosensory neurons, we extended our search to include ion channels yet to be identified, but known to regulate neuronal signaling in other classes of neurons (Rudy, Chow *et al.* 1999; Akemann and Knöpfel 2006; Espinosa, Torres-Vega *et al.* 2008; Waxman and Zamponi 2014). As one of the most dysregulated voltage-gated ion channels, *Kcnc3* (encoding protein Kv3.3) emerged as a novel candidate (Figure 16a, b, Figure 17). Pharmacologic and genetic perturbation of Kv3.3 (*Kcnc3*) impairs neuronal signaling (Akemann and Knöpfel 2006; Espinosa, Torres-Vega *et al.* 2008) and is causally linked to ataxias

(Figuroa, Minassian *et al.* 2010) that are consistent with functional deficits observed in patients with cancer long after cessation of chemotherapy. We then immunolabeled sensory cell bodies in dorsal root ganglia and their receptor endings taken from Apc^{WT} +control with monoclonal antibodies targeting Kv3.3, which revealed the first evidence of this ion channel in all large diameter cell bodies in the dorsal root ganglia that supply mechanosensors (Figure 16c and Figure 18) and endings (Figure 16e). Results of comparison across experimental groups indicate that Kv3.3 expression was significantly lower in $Apc^{Pirc/+}$ +OX compared with Apc^{WT} +control (Figure 16d), $Apc^{Pirc/+}$ +control, or Apc^{WT} +OX (Figure 18), demonstrating that codependent dysfunction is conserved in cell-type specific protein expression. Notably, while we discovered correspondence between protein and gene dysregulation, genetic dysregulation appeared larger. This finding may represent the expression of a faulty epigenetic regulatory process that is incompletely compensated at the protein level. Moreover, conserved Kv3.3 expression in neuromuscular junctions suggests that Kv3.3 dysfunction was constrained to sensory neurons (Figure 19).

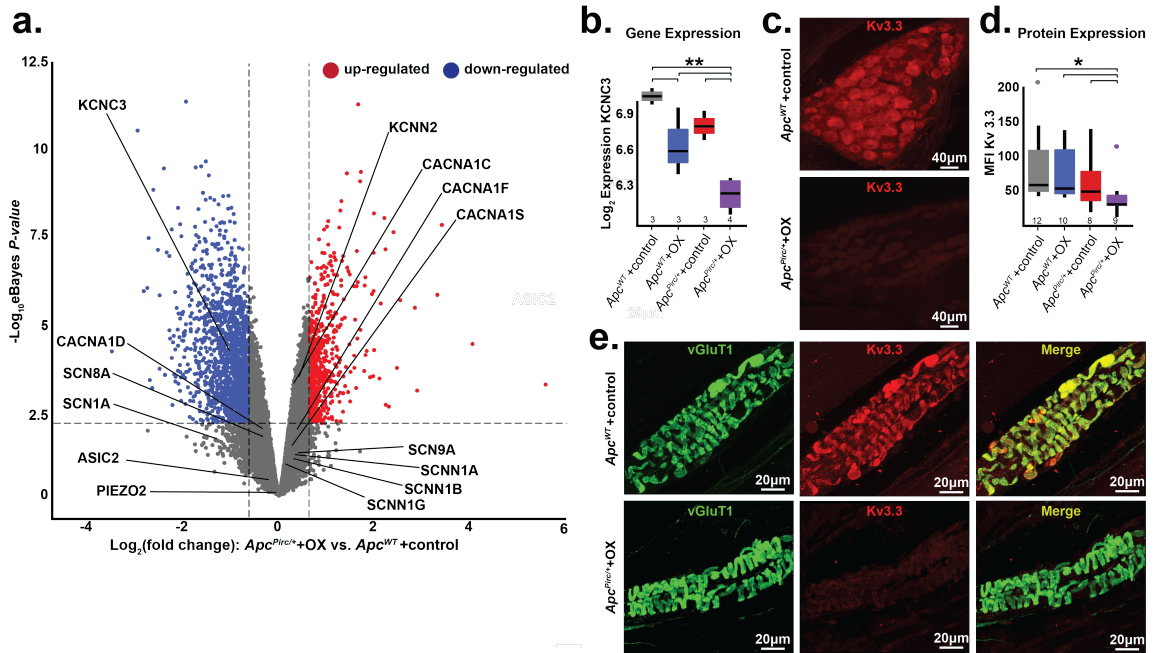


Figure 16.

Targeted transcriptional analysis reveals mechanisms for cancer-chemotherapy interaction. a, Volcano plot comparing up- and downregulated genes in *Apc^{Pirc/+}+OX* and *Apc^{WT}+control* sensory neuron transcriptomes. Annotation of genes involved in mechanotransduction, signal amplification, action potential generation and maintenance is shown. Significance was determined as Benjamini–Hochberg FDR < 0.01 and log2fold change ≥ 1. **b,** Gene expression of *Kcnc3* encoding Kv3.3, as determined through transcriptional profiling (*Kcnc3*: 1369133_a_at). **c,** Confocal images of dorsal root ganglia immunolabeled against Kv3.3 illustrates expression of *Apc^{Pirc/+}+OX* relative to *Apc^{WT}+control* neurons. **d,** Quantification of receptor protein expression (mean fluorescence intensity (MFI)) of Kv3.3 determined through averaging over all annulospiral endings (617 from 12 *Apc^{WT}+control* neurons, 434 from 10 *Apc^{WT}+OX* neurons, 459 from 8 *Apc^{Pirc/+}+control* neurons, and 362 from 9 *Apc^{Pirc/+}+OX* neurons) for each neuron per experimental group. **e,** Confocal images of mechanosensory nerve terminals in muscle spindles immunolabeled against vGluT1 (green), Kv3.3 (red), and merged (yellow) illustrates protein expression levels and distribution in *Apc^{Pirc/+}+OX* relative to *Apc^{WT}+control*. * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (*stan_glm*). ** indicates $P_{eBayesAdj} < 0.005$ and fold-change (FC) > 1.5 using a Bayesian moderated linear fixed effects model. Data presented as mean ± s.e.m

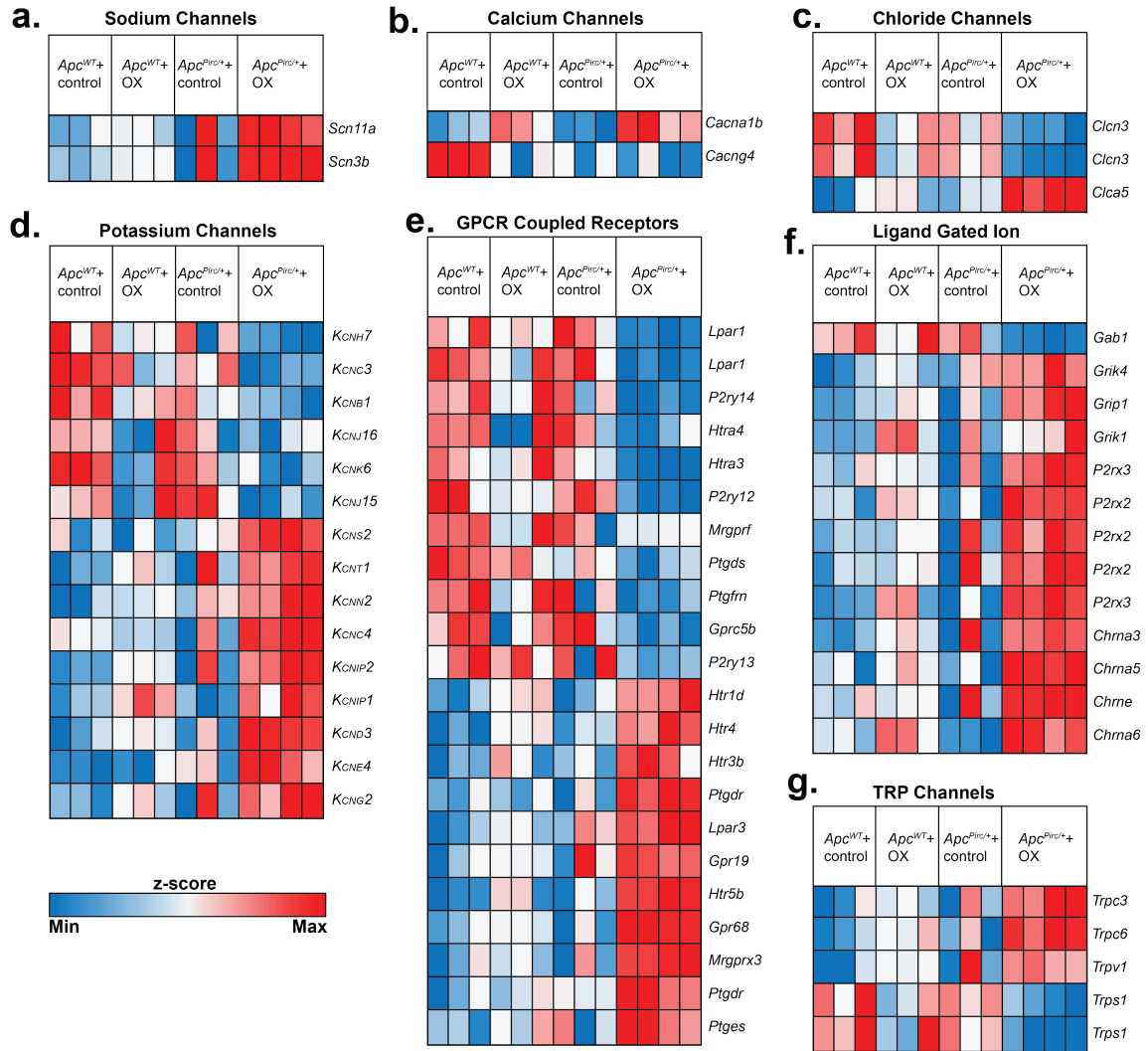


Figure 17.

Heat-map distribution of significantly differentially expressed genes specific to neuron neuronal excitability. Major voltage-gated, mechanically gated, TRP channels and ligand-gated and G-protein coupled receptors across experimental groups. Expression patterns of different sub-types channels and receptors were identified by empirical Bayesian moderated linear fixed effects models (columns are individual samples, heat-maps). (a) Sodium channel levels, (b) calcium channel levels, (c) chloride channel levels (d) potassium channel levels, (e) G-protein coupled receptors (GPCRs) levels, (f) ligand-gated channel levels, and (g) transient receptor potential (TRP) channel levels are plotted as heat-maps. Data row standardized (mean centered and s.d. normalized) to specific genes.

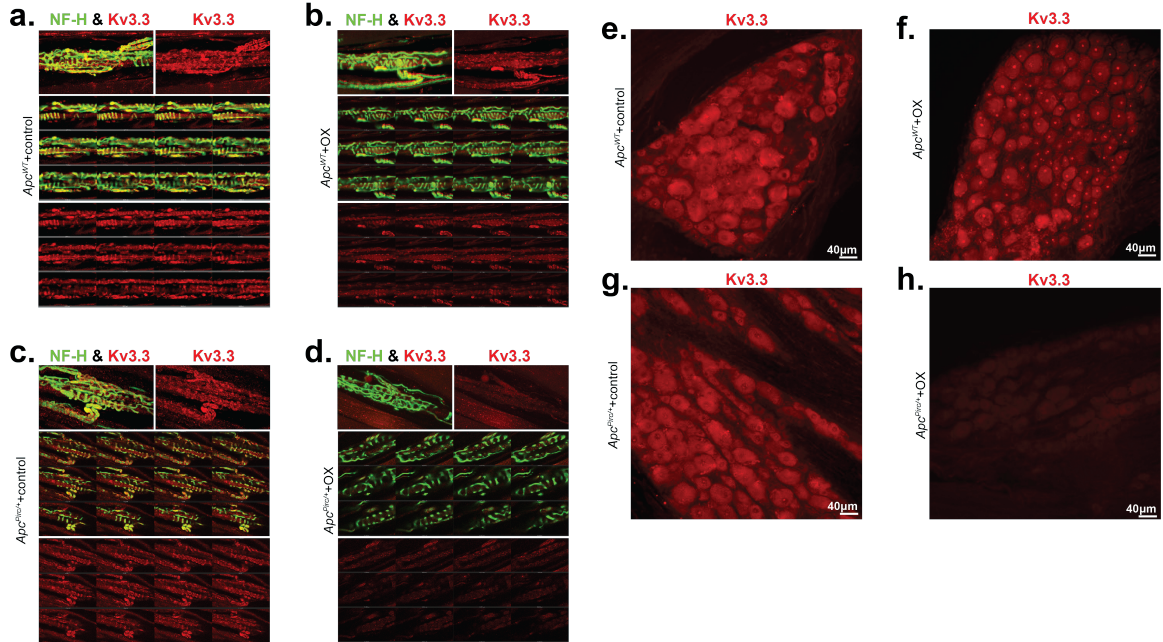


Figure 18.

Kv3.3 immunostaining of proprioceptive sensory neurons receptor endings and cell bodies. a-d, Whole-mount staining and confocal axial projection of the preterminal axons and annulospiral receptor endings of proprioceptive sensory neurons showing merged and single channel images of Kv3.3 (red) and NF-H (green) in top row from: **a**, *Apc^{WT}+control* rat; **b**, *Apc^{Pirc/+}+control*; **c**, *Apc^{WT}+OX*; **d**, and *Apc^{Pirc/+}+OX* rats. Individual optical planes (from z-stack projection) of axial projection highlight fine three-dimensional structural distribution of merged and single channel images of Kv3.3 (bottom). Whole-mount staining and confocal axial projections of DRG neurons highlight expression of Kv3.3 in **e**, *Apc^{WT}+control* rat; **f**, *Apc^{Pirc/+}+control*; **g**, *Apc^{WT}+OX*; **h**, and *Apc^{Pirc/+}+OX* rats.

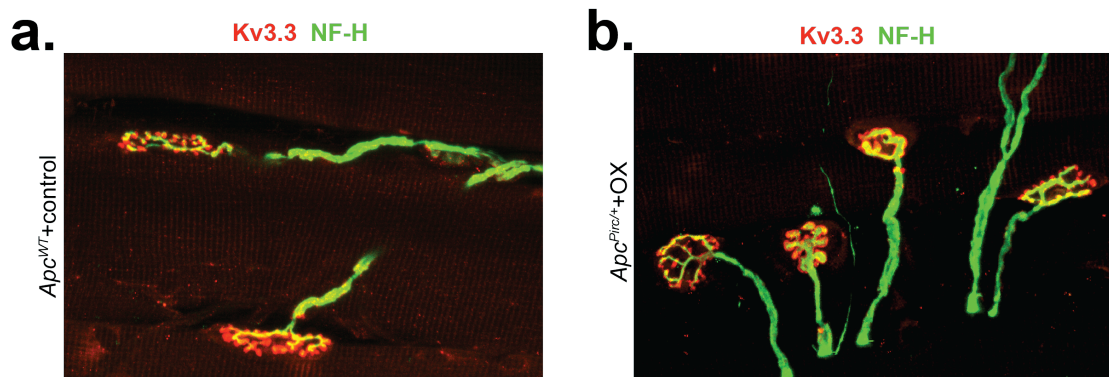


Figure 19.

Kv3.3 Immunostaining of neuromuscular junction. Whole-mount staining and confocal axial projection of the neuromuscular junction showing merged images of Kv3.3 (red) and NF-H (green) from: **a**, $Apc^{WT}+control$ and **b**, $Apc^{Pirc/+}+OX$ rats.

Summary

This is the first evidence implicating Kv3.3 in the development of neuropathy and the first data, to our knowledge, demonstrating a channelopathy that persists long after treatment cessation. The capacity of Kv3.3 to drive fast spiking and to enhance transmitter release – processes that are required for mechanotransduction and spike encoding– suggests that this ion channel might provide both a potential novel mechanism for the dysfunction of mechanosensory neurons and a potential target for therapy.

Aim 3: Test the hypothesis that neuronal dysfunction depends on cancer-chemotherapy interaction.

Introduction

To test whether interaction we discovered at gene and protein levels was conserved at a functional neuron level in living animals, we tested whether *APC^{Pirc/+}* mutants treated with OX express neuronal signaling dysfunction *in vivo* by examining the capacity of single proprioceptive neurons to respond to physiologically-relevant stimuli (Figure 21).

Aim Specific Methods

In vivo Intracellular Recording

Dorsal rootlets positioned in continuity on bipolar recording electrodes were selected for sampling sensory neurons when they produced robust action potential activity in response to stretch of triceps surae muscles. Individual axons penetrated in these rootlets by glass micropipettes (~30 MΩ filled with 2 M K⁺ acetate) were selected for study when electrical stimulation of triceps surae nerves produced orthodromic action potentials that were readily resolvable and had conduction delay of <2ms. Continuous intracellular recordings from sensory neurons were acquired with Spike2 software (version 8.02). Sensory neurons were classified as Ia by their perfect entrainment to 1-s bouts of high-frequency, small-amplitude vibration (100Hz, 80 μm), pause in firing during rising twitch force response (muscle shortening), and by responding with an initial burst of high-frequency firing (>100 pulses per second (pps)) at the onset of muscle stretch (Vincent, Gabriel *et al.* 2017). Two stretch paradigms were used to characterize the firing responses of afferents to physiologically relevant mechanical stimuli. In both paradigms, triceps surae muscles were stretched by 3 mm from L₀ (7% strain). Ramp-hold-release stretches tested afferent encoding of both fast dynamic (20mm/s, 47% strain rate) and

static stimuli; successive triplets of triangular stretch tested slow (4mm/s, 9% strain rate) dynamic and activity-dependent encoding in dynamic stretch known to be influenced by recent signaling history (Vincent, Gabriel *et al.* 2017). Strains and strain-rates fall within values expected for animals engaged in normal activities e.g. locomotion, and have been previously used in our lab (Vincent, Gabriel *et al.* 2017).

Intracellular Recording Pre-Processing

Intra-axonal recordings of action potentials together with records of muscle length and force were digitized (20 kHz) and were monitored online and stored on computer for later analysis with Spike2 and custom-written MATLAB scripts. From raw intracellular data of both paradigms, we extracted 31 measured and derived features (Figure 20) that provide a comprehensive quantification of neuronal signaling characteristics. We then categorized features into four broad clusters that represent functional features encoded by these neurons, containing sensitivity (Thr), dynamic (Dyn), static (Stat), and history-dependent (Hx) signaling information. Figure 20 identifies and describes the measured and computed features and functional clustering used for inference.

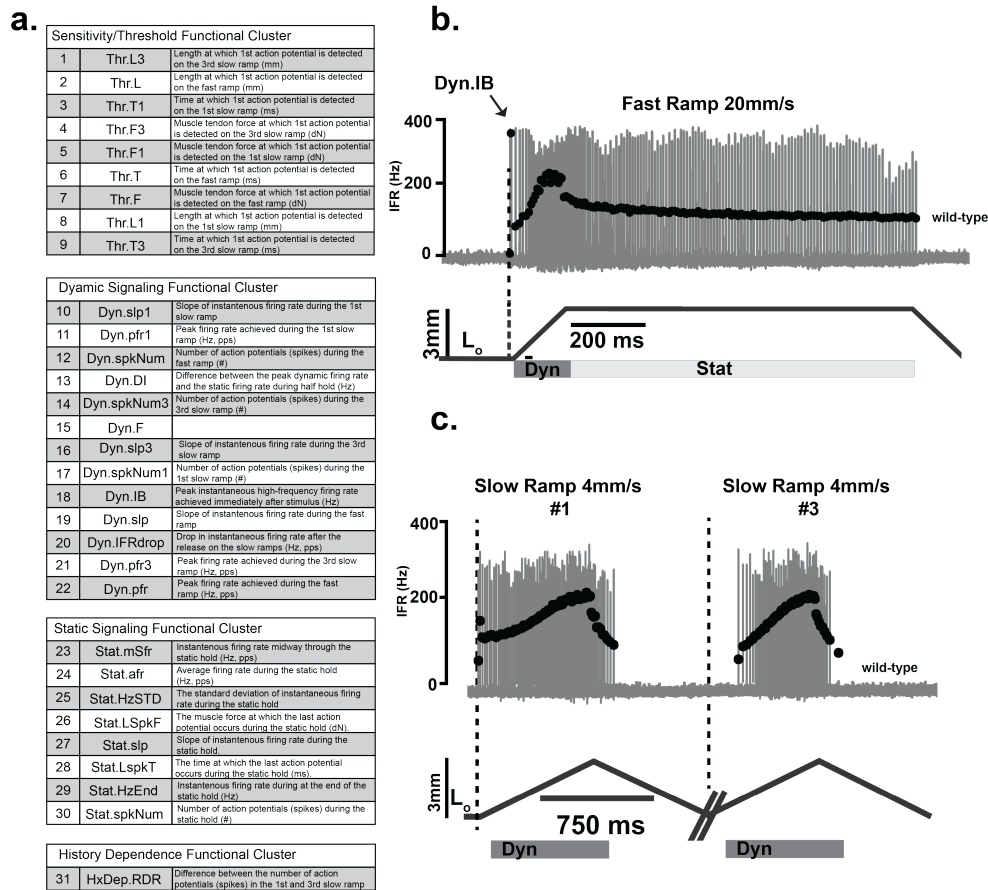


Figure 20.

List of Parameters used for Neurophysiological Analyses, related to Figures 2, 3 and Extended Data Figure 12. **a**, Measured and derived parameters were computed offline using custom written MATLAB scripts. Letters in the left column indicate the specific parameters included in analyses for each functional feature cluster. Thr: threshold (9 parameters); Dyn: dynamic (11 parameters); Stat: static (8 parameters); HxDep: history-dependent (1 parameter). For detailed experimental recording paradigms see Online Methods. **b**, Representative fast ramp-hold-release (3 mm at 20mm/s) trial from a proprioceptive neuron recorded from dorsal roots in *in vivo* electrophysiological experiments of a wild-type rat. **c**, Representative slow repeated ramp (3 mm at 4mm/s) trial from a proprioceptive neuron recorded from dorsal roots in *in vivo* electrophysiological experiments of a wild-type rat. Corresponding action potential trains and overlaid black circles indicate individual action potentials (spikes) and instantaneous firing rates (IFRs) of the responses. Dashed line marks the point of muscle stretch from background length (L_0) and indicates the starting point for threshold/sensitivity measurements. Boxes indicate dynamic (dark grey, 150 ms duration after stretch command onset) and static phases for analysis (light grey, 1 s duration after the dynamic phase)

Statistical Analysis of Intracellular Recordings

Linear discriminant analysis (LDA) provided supervised dimensionality reduction for the multiple features of neuron signaling, in an attempt to find a linear combination of features that separated and characterized independent and combinatorial treatment effects. Data were first de-meant, normalized to unit standard deviation, and tested by Bayesian one-way ANOVA (*stan_glm*) (Gabry and Goodrich 2018). The derived covariance matrix was then normalized by within-group, pooled covariance. The eigenvectors of that modified covariance matrix defined three canonical variables that characterized and separated the four treatment groups identified *a priori* as $Apc^{WT}+\text{control}$, $Apc^{WT}+\text{OX}$, $Apc^{Pirc/+}+\text{control}$, and $Apc^{Pirc/+}+\text{OX}$. LDA and 10-fold cross validation of model performance (repeated holdout method) was performed with the MASS (7.3-51.1) (Venables and Ripley 2002) library in the R environment (3.5.0) (Team 2018). Individual features characterizing the firing responses of neurons sampled from multiple rats were tested for statistically significant differences with Bayesian one-way ANOVA (*stan_glm*). Descriptions of the general approach and detailed model construction and validation is below.

Results

Neuronal signaling is impaired

Applying electrophysiological methods to rats in vivo, we recorded spiking activity from single mechanosensory neurons responding to naturalistic mechanical stimuli (Figure 23). From these spiking responses, we collected 31 measured and derived parameters (average of four trials; $n = 11 Apc^{WT}+\text{control}$, $n=19 Apc^{WT}+\text{OX}$, $n=20 Apc^{Pirc/+}+\text{control}$, $n = 10 Apc^{Pirc/+}+\text{OX}$; Figure 20) from which we extract four functional features encoded by these neurons, sensitivity, dynamic, static, and history-dependent signaling information (Figure 20). In $Apc^{WT}+\text{control}$ rats, we found that muscle stretch elicited the spiking

expected from sensory neurons in normal animals (Vincent, Gabriel *et al.* 2017) and humans (Burke, Hagbarth *et al.* 1978), specifically high frequency initial bursting at stimulus onset, increasing dynamic firing during increasing stimulus, sustained static firing with slow accommodation during the hold phase of stretch (Figure 23b), and history-dependent reduction in spike number (Figure 22 and Figure 27h).

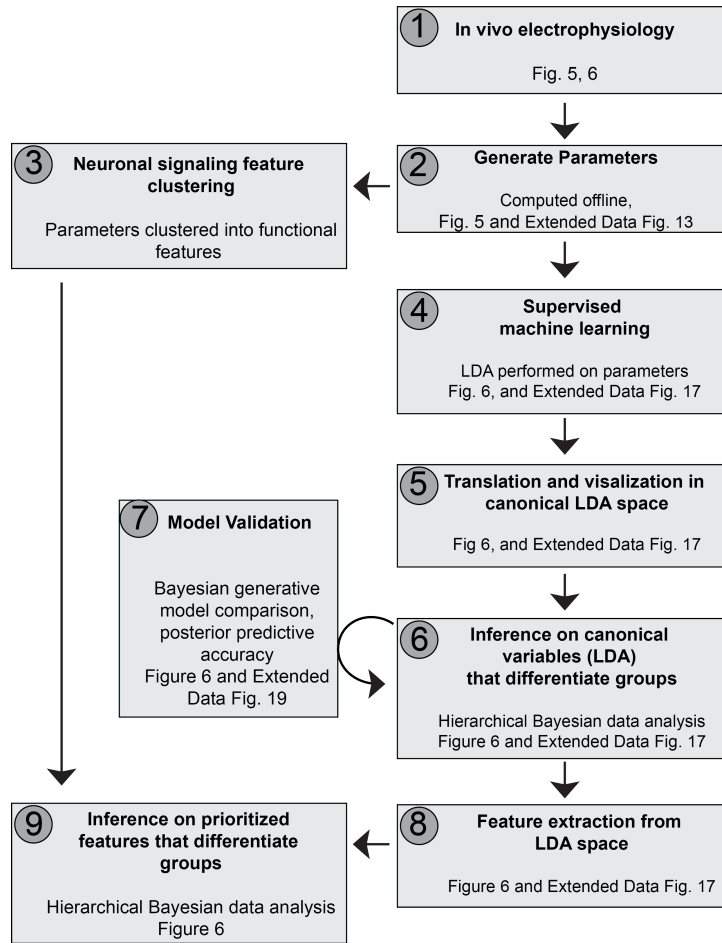


Figure 21.

Steps of In Vivo Electrophysiology Analysis. Data analysis flowchart depicts the multi-step approach applied for single neuron physiological analyses, inferences and downstream model validation. A detailed description of each step is available in the **Methods Sections**. Linear discriminant analysis, LDA.

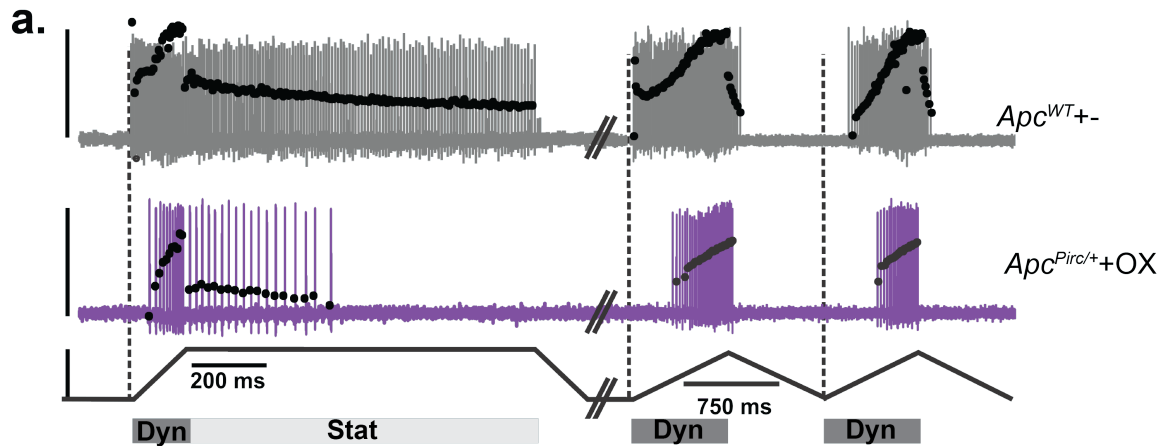


Figure 22.

Neuronal signaling responses to slow and fast naturalistic stimulus. related to Figures 5, 6. **a**, Representative fast ramp-hold-release (left, 3 mm at 20mm/s) and slow repeated ramp (right, 3 mm at 4mm/s) trial from a proprioceptive neuron recorded from dorsal roots in *in vivo* electrophysiological experiments of an Apc^{WT+} control (grey) and $Apc^{Pirc/+OX}$ rat (purple). Corresponding action potential trains and overlaid black circles indicate individual action potentials (spikes) and IFRs (instantaneous firing rates) of the responses. Dashed line marks the point of muscle stretch from background length (L_0) and indicates the starting point for threshold/sensitivity measurements. Boxes indicate dynamic (dark grey, 150 ms duration after stretch command onset) and static phases for analysis (light grey, 1 s duration after the dynamic phase).

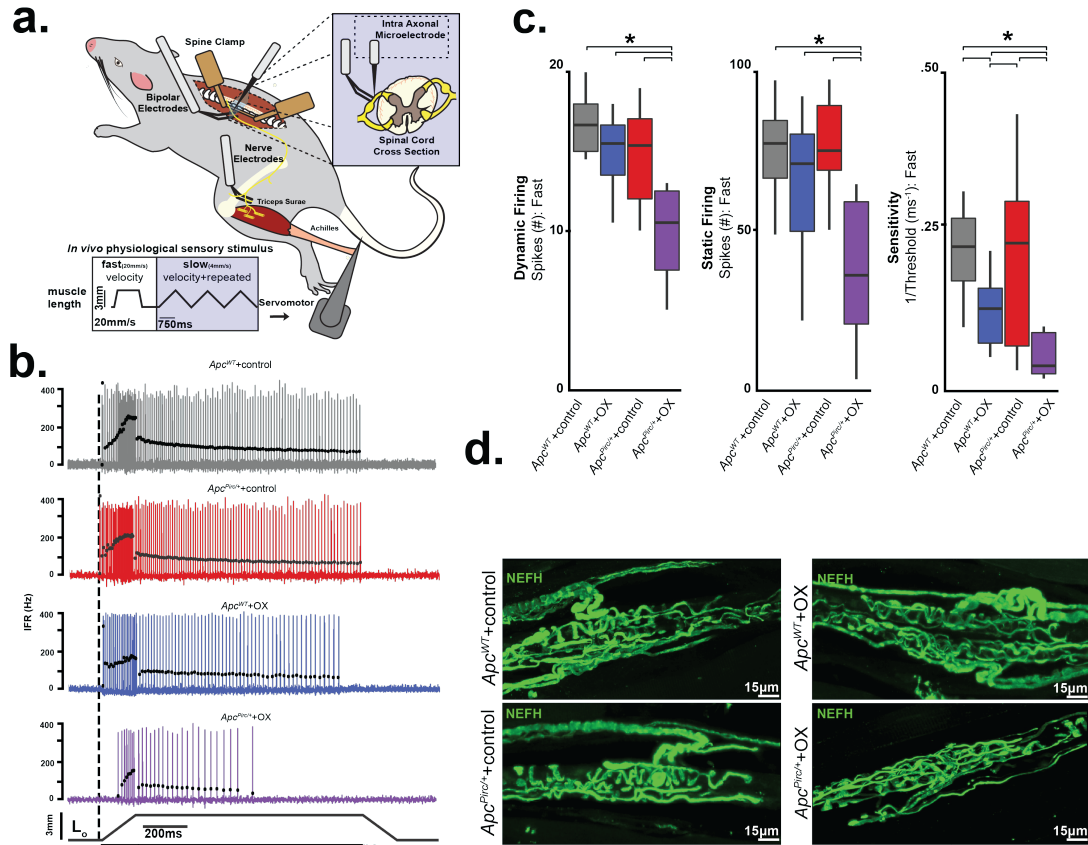


Figure 23.

Mechanosensory signal degradation exacerbated by the cancer-chemotherapy interaction.

a, Schematic of experimental approach for in vivo recordings centrally from intact mechanosensory neurons firing action potentials in response to fast (20mm/s) and slow (4mm/s) naturalistic mechanical stimuli delivered in the periphery. b, Representative cases of spiking activity in *Apc*^{WT}+control, *Apc*^{WT}+OX, *Apc*^{Pirc/+}+control, and *Apc*^{Pirc/+}+OX as a measure of sensory encoding. Black circles plot instantaneous firing rates (pps) of corresponding spike (action potential) intervals. Dashed vertical line marks onset of muscle stretch (3mm from resting length (Lo)) shown in bottom trace divided into dynamic and static phases by dark grey (150 ms duration after stretch command onset) and light grey (1 s duration after the dynamic phase) bars. c, Neuronal spiking parameters (n=31 averaged from four trials in each neuron, four shown from fast ramp stimulus) representing different features of sensory stimulus (*Apc*^{WT}+control (n = 11), *Apc*^{WT}+OX (n = 19), *Apc*^{Pirc/+}+control (n = 20) and *Apc*^{Pirc/+}+OX (n = 10)): mean initial burst frequency (pps) signaling stretch onset; the number of spikes during dynamic sensory stimulation (shown as a dark grey bar in b); the number of spikes during static sensory stimulation (shown as a light grey bar in b); sensitivity assessed as the inverse of latency to stimulus detection (ms⁻¹), i.e. lower sensitivity corresponds to longer latency and higher

threshold. d, Confocal image of a neurofilament heavy-chain (NEFH, in green) with immunolabeling of the terminal axon and receptor structure in $Apc^{WT}+control$, $Apc^{WT}+OX$, $Apc^{Pirc/+}+control$, and $Apc^{Pirc/+}+OX$ rats. Scale bar, 15 μ m. * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (stan_glm): 95% highest density intervals do not overlap between groupwise contrasts. Data presented as mean \pm s.e.m.

We next tested whether $Apc^{Pirc/+}$ or OX treatment alone induce signaling dysfunction. Although we find transcriptional dysregulation in $Apc^{Pirc/+}+control$ (Figure 6c and Figure 9a), we found a remarkable degree of concordance with signaling in $Apc^{WT}+control$ (Figure 23b). $Apc^{Pirc/+}+control$ neuronal signaling displayed comparable sensitivity to stimuli and showed similar static behavior across all neurons ($n = 20$; Figure 23b,c) as the $Apc^{WT}+control$. We then found that OX treatment of Apc^{WT} rats induced mild signaling deficits that were less pronounced, occurred in a small proportion of neurons (5/19), and were primarily restricted to sensitivity functional clusters (Figure 23b,c and Figure 24d), validating our previous findings of restricted deficits (to single signaling parameters) observed in a different strain of healthy rats treated with OX alone (Vincent, Wieczorzak *et al.* 2016).

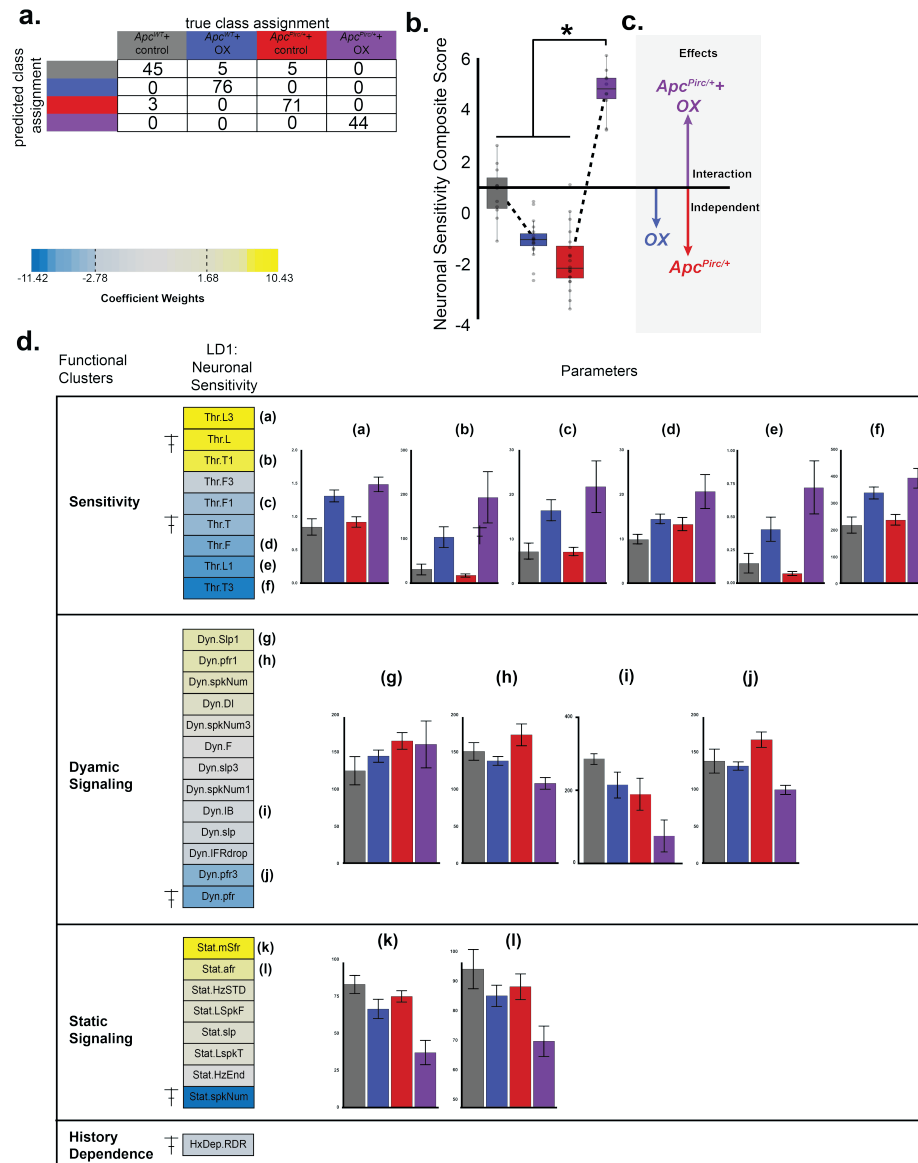


Figure 24.

LD1 analysis of all neuronal parameters. **a**, Confusion matrix illustrates the results of 10-fold cross validation of LDA model performance (repeated holdout method) that achieved overall 94.7% classification accuracy (posterior prediction check). Table values represent the sum of out-of-sample cross validation predictions (row) against true class assignment (column) **b**, Histogram plot, mean values of LD1 scores (Figure 27) for each group were compared with hierarchical Bayesian ANOVA model. Asterisk indicates statistically significant differences between experimental groups in hierarchical Bayesian ANOVA, (*) indicates 95% highest density intervals (HDI) do not overlap between groupwise contrasts. **c**, Vectors represent the magnitude and direction of the independent and combinatorial effects of cancer and/or chemotherapy. **d**, Parameters ($n = 31$, middle) and respective discriminant coefficients weights with the

interaction-specific LD1, were regrouped into functional feature clusters (left). Histogram plots report mean values for individual parameters (right, a-l) with significant contribution to LD1 loading. Cross symbol indicate parameters are included in Figure 23 and Figure 27. Analyzed from Apc^{WT} +control (n = 11), Apc^{WT} +OX (n = 19), $Apc^{Pirc/+}$ +control (n = 20) and $Apc^{Pirc/+}$ +OX (n = 10) neurons.

In contrast to the observations in Apc^{WT} +control, Apc^{WT} +OX, or $Apc^{Pirc/+}$ +control rats, we found drastically impaired neuronal signaling in $Apc^{Pirc/+}$ +OX rats (Figure 23b). High frequency initial bursting was attenuated four-fold and sensitivity to stimuli was reduced by three-fold at both high (Figure 24d) and low velocity stretch (Figure 22, Figure 24d). During dynamic stimuli, we found marked reduction in the number of spikes over both stretch conditions (Figure 23c). Neurons in $Apc^{Pirc/+}$ +OX rats also failed to sustain firing (Figure 23b). In addition, we observed fewer spikes (Figure 23c) during rapid accommodation immediately preceding signal deletion, despite constant stimulus (Figure 23b). We then simulated naturalistic compensation by subjecting $Apc^{Pirc/+}$ +OX neurons to repeated trials at 1, 2, and 3x background stimulus (L_o strain) intensity, which failed to completely rescue signaling back to Apc^{WT} +control levels (Figure 25b, c, d). These data are the first to directly demonstrate a damaging functional interaction between the systemic effects of cancer and chemotherapy in sensory neurons in a living animal. While validating our previous findings of signaling deficits in chemotherapy alone (Vincent, Wiczerzak *et al.* 2016), these data indicate that restrictive signaling deficits induced by chemotherapy or cancer alone were insufficient to reproduce the magnitude, direction and number of dysfunctional parameters induced by codependent neuropathy.

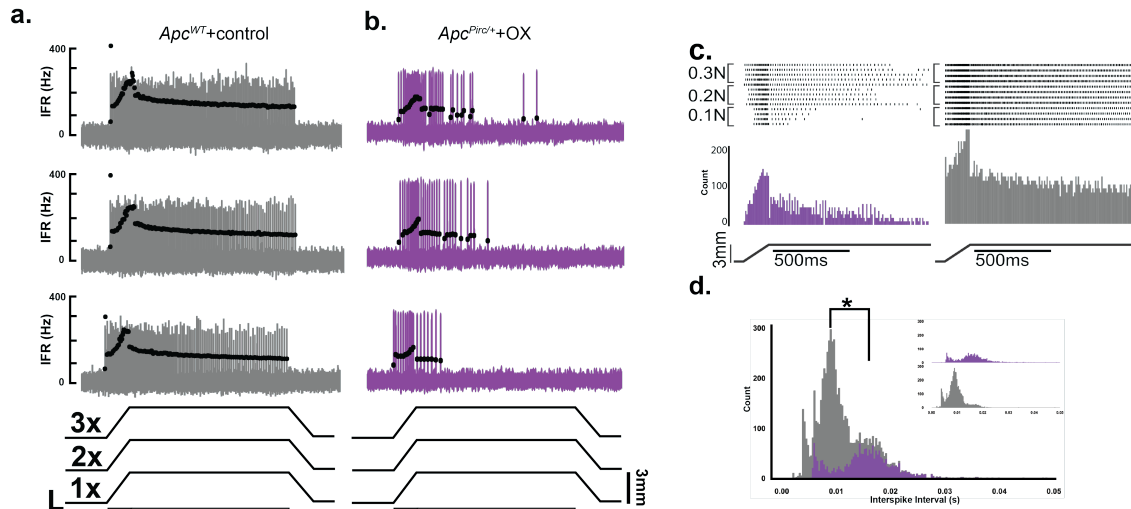


Figure 25.

Effects of physiologic compensation. **a, b**, Representative fast ramp-hold-release (left, 3 mm at 20mm/s) trial from a proprioceptive neuron recorded from dorsal roots in *in vivo* electrophysiological experiments of a *Apc^{WT}+control* (grey **a**) and *Apc^{Pirc/+}+OX* rat (purple **b**). Corresponding action potential trains and overlaid black circles indicate individual action potentials (spikes) and IFRs (instantaneous firing rates) of the responses. Dashed line marks the point of muscle stretch from background length (L_0) and indicates the starting point for threshold/sensitivity measurements. Boxes indicate dynamic (dark grey, 150 ms duration after stretch command onset) and static phases for analysis (light grey, 1 s duration after the dynamic phase). Stretch evoked (3mm) responses recorded from replicate trials at 1, 2, and 3x L_0 for *Apc^{WT}+control* (**a**) and *Apc^{Pirc/+}+OX* (**b**). **c**, Raster plots of stretch evoked (3mm) responses from representative neurons in control (right) and *Apc^{Pirc/+}+OX* (left) neurons recorded from repeated trials (4 trials) at 1, 2, and 3x background stimulus (L_0 strain) intensity. Frequency histograms show cumulative distributions across 4 trials. **d**, Overlaid interval histogram (four trials per neuron at each of three stimulus intensities shows population shift. Inset show non-overlaid interval histograms for clarity. * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (*stan_glm*): 95% highest density intervals do not overlap between groupwise contrasts.

Dysfunction does not depend on degeneration

We next tested whether the impaired neuronal signaling of $Apc^{Pirc/+}$ +OX neurons might be explained by dying-back degeneration of sensory nerve terminals. While the underlying mechanisms for chemotherapy induced neuropathy are not understood, current opinion identifies 'dying-back' axon degeneration as a major pathology in this disorder (Park, Goldstein *et al.* 2013; Fukuda, Li *et al.* 2017). Blinded reviewers assessed the structural integrity of sensory afferents and receptor endings immunolabeled against neurofilament protein (NEFH) (Carrasco, Vincent *et al.* 2017). We then tested for functional evidence of degeneration by comparing differences in conduction delays, a physical measure of nerve degeneration that is used clinically (Burakgazi, Messersmith *et al.* 2011). Neither histological observation of sensory afferents and receptors (Figure 23d) nor axon conduction tests (Figure 26) revealed evidence of dying-back degeneration of sensory nerve terminals ($Apc^{Pirc/+}$ +OX: 1.41 ± 0.13 ms, n=10. Apc^{WT} +control: 1.52 ± 0.14 ms, n=11, Figure 26). Our findings demonstrate that transcriptional changes we observed for some markers of nerve degeneration (Figure 10) were insufficient to yield nerve degeneration. While our results indicate selective resistance of mechanosensory neurons in $Apc^{Pirc/+}$ +OX rats, they are in line with the inconsistency of physical evidence for nerve degeneration reported in clinical studies (Burakgazi, Messersmith *et al.* 2011). Furthermore, the ability of muscle vibration to entrain firing of these neurons in all treatment groups as they do in Apc^{WT} +control rats further refutes the existence of degeneration's necessity in signaling disorders (Figure 26). Overall, our findings suggest that the structure and core ability of mechanosensory neurons to produce action potentials remain unimpaired by codependent neuropathy and does not depend on dying-back degeneration.

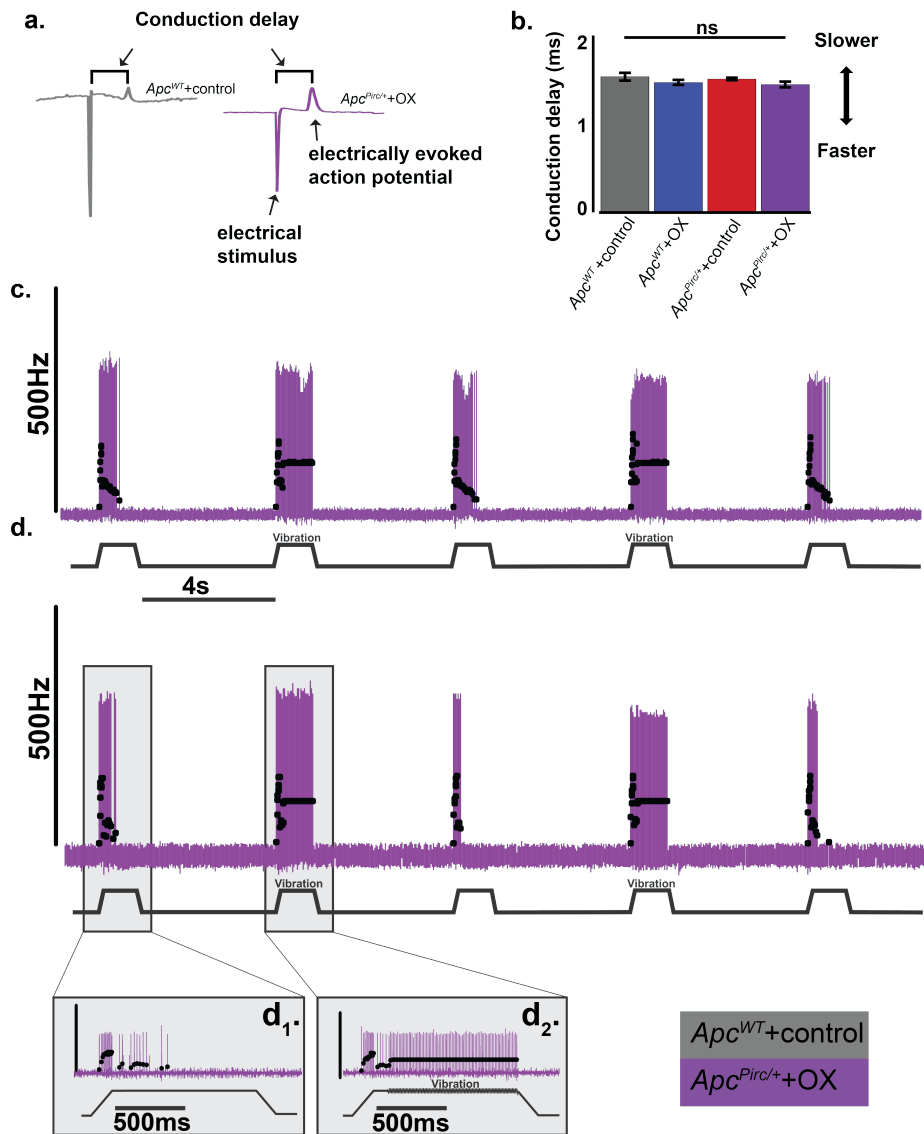


Figure 26.

Cancer and chemotherapy interaction does not lead to electrophysiological evidence of degeneration. **a**, raw intracellular record from control and $Apc^{Pirc/+}+OX$ neurons shows derivation of conduction delay (ms). Conduction delay is calculated by subtracting the time from electrical stimulus to electrically evoked action potential. **b**, Mean conduction delay (ms) computed for all neurons as a measure of axonal demyelination were analyzed from $Apc^{WT}+control$ ($n = 11$), $Apc^{WT}+OX$ ($n = 19$), $Apc^{Pirc/+}+control$ ($n = 20$) and $Apc^{Pirc/+}+OX$ ($n = 10$) neurons with hierarchical Bayesian ANOVA model. ns, no significant difference. **c & d**, Two representative stretch evoked responses of two sensory neurons ($Apc^{Pirc/+}+OX$) recorded from dorsal roots in *in vivo* electrophysiological experiments with corresponding action potential trains. Overlaid black circles are IFRs of the responses. Insets show expanded view from **(d)** in a trial without (**d**₁) and with (**d**₂) superimposed vibration stimulus.

Neuronal dysfunction depends on cancer-chemotherapy interaction

Data presented in Figure 23 suggests damaging cancer-chemotherapy interactions are conserved *in vivo* and have consequences in sensory function. In order to assess the extent of interaction quantitatively, we took an unbiased statistical approach by subjecting all neurons (n=60, 240 total trials) from all experimental groups to a machine learning algorithm (linear discriminant (LD) analysis). Our approach reduced complex feature space into canonical variables giving us a high-level understanding of where interaction emerges, without biased feature selection *a priori*. Our analysis yielded three canonical variables (Figure 27a) that achieved overall 94.7% classification accuracy (Figure 24a). We then visualized neuronal signaling in the new 3D composite space created by LD1-3 (Figure 27a). By projecting high dimensional parameter and feature data onto a simplified 3D canonical space, statistically significant non-linear interaction between cancer and chemotherapy clearly emerged in the first dimension (LD1; 54.23% proportion of variance; Figure 27a and Figure 24b). Notably, dysfunction in LD1 induced by the cancer—chemotherapy interaction occurred in the opposite direction to that predicted by independent effects, and its magnitude was amplified greater than their sum (Figure 27a and Figure 24b, c). To test the statistical significance of the cancer—chemotherapy interaction, we conducted Bayesian model comparison with full factorial and all restricted models using leave-one-out cross validation. We then quantified and validated each model's predictive performance by computing the expected log predictive densities (ELPD; measure of a model's out-of-sample predictive accuracy in Figure 27b-e) (Vehtari, Gelman *et al.* 2017). We found decisive evidence in favor of a model including a cancer—chemotherapy interaction predictor (ELPD diff ≥ 48 SE < 8.1 ; Figure 27e). Moreover, our data and generative modeling conclude that codependent

interaction (Figure 27b-d) is necessary to accurately and reliability reproduce clinically relevant neuronal signaling deficits observed in $Apc^{Pirc/+}$ +OX rats (Figure 27e).

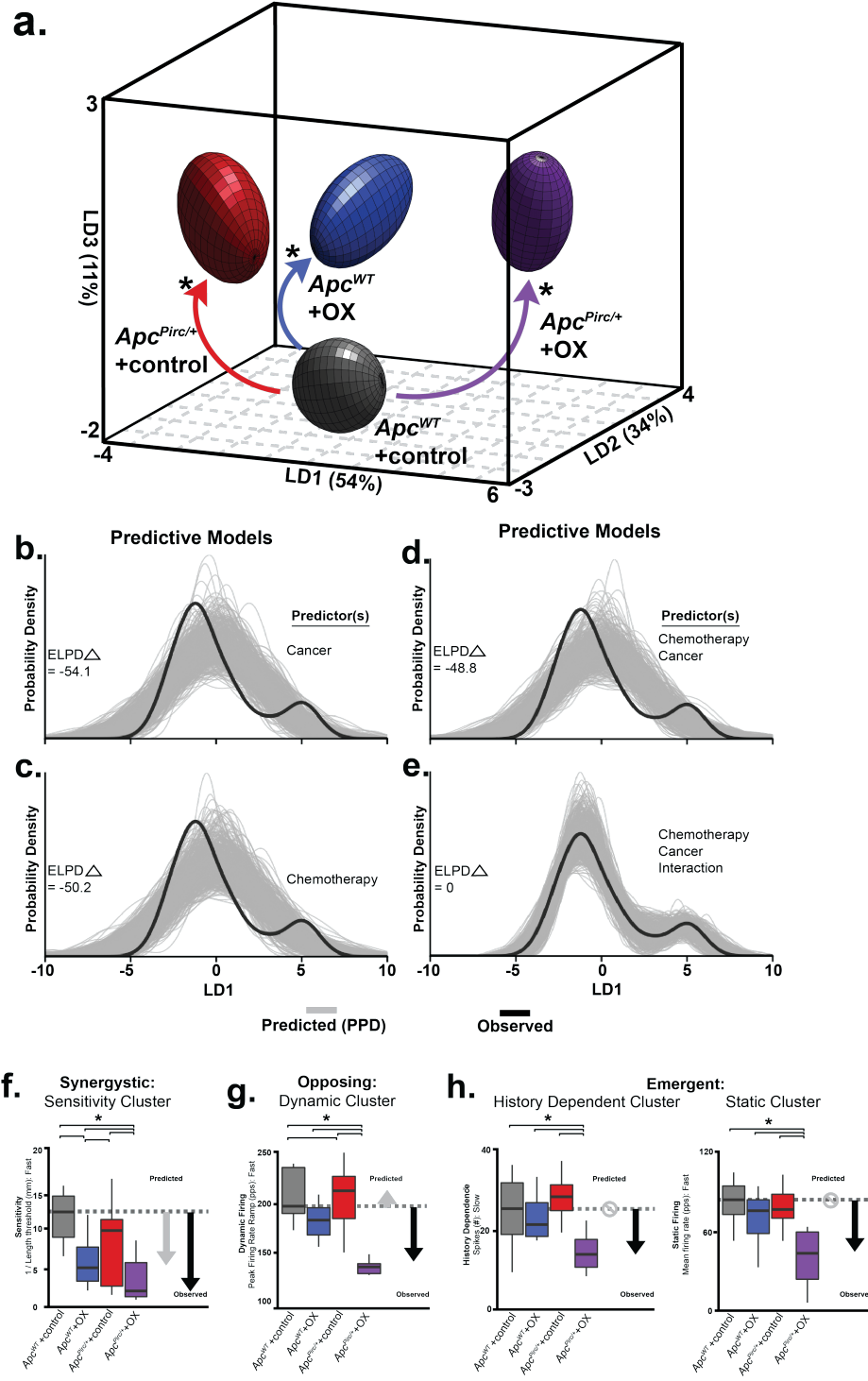


Figure 27.

Cancer-chemotherapy codependence exacerbates sensory dysfunction beyond that predicted by cancer or chemotherapy alone. a, Neuronal spiking parameters (n=31, averaged from four trials, from each neuron (n=60)) representing different features of sensory stimuli were subjected to linear discriminant

(LD) analysis. Neuronal signaling was visualized in the new 3D composite space created by LD1-3. 3D ellipsoids enclosing 68% of data were computed with least-squares elliptical fitting to emphasize differences between control and $Apc^{Pirc/+}$ +OX neurons. Effects of independent (OX or $Apc^{Pirc/+}$) and combinatorial

($Apc^{Pirc/+}$ +OX) treatment are indicated by curved arrows. b-e, The hierarchical Bayesian model used to test for significant group differences in LD1 scores reconfigured to operate in a predictive fashion. Predictors

included in each model are listed to the right of each plot. Generative models in (b-d) utilizing one (b,c) or both independent (d) predictor(s), i.e. cancer ($Apc^{Pirc/+}$) or chemotherapy (OX) for posterior prediction. The generative model in (e) utilizes both independent predictors and an interaction term for posterior prediction.

Grey lines in b-e represent 500 novel (generative) samples drawn from the posterior distributions. Black lines illustrate experimentally observed mean LD1 score. Predictive accuracy was measured by calculating expected log predictive density (ELPD) for each model and benchmarked off of the highest performing model. Delta ELPD (triangular symbol) indicates difference from optimal model. Negative models represent worse predictive performance. f, Sensitivity assessed as the inverse of latency to stimulus detection (mm-1),

i.e. lower sensitivity corresponds to longer latency and higher threshold. g, Peak firing rate (pps) achieved during the dynamic sensory stimulus (shown as dark grey bar in Figure 23b). h, change in dynamic spike number in successive, slow stretch dynamic sensory stimulus (see Methods and Figure 20) and mean firing rate (pps) achieved during the static sensory stimulus (shown as light grey bar in Figure 23b). Recordings

were analyzed from Apc^{WT} +control (n = 11), Apc^{WT} +OX (n = 19), $Apc^{Pirc/+}$ +control (n = 20) and $Apc^{Pirc/+}$ +OX (n = 10) in b-g, * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (stan_glm). Grey arrows in f-h indicate direction and significant differences from Apc^{WT} +control predicted from the linear sum of the independent effects of Apc^{WT} +OX and $Apc^{Pirc/+}$ +control groups. Black arrows indicate experimentally observed effects of their combination. Circles

with slashes indicated no difference predicted for Apc^{WT} +OX group and $Apc^{Pirc/+}$ +control groups. Data presented as mean \pm s.e.m.

Having determined the significance of an interactive effect, we then asked which functional clusters are highly enriched in LD1. By examining the discriminant function

coefficients, we found that static signaling and sensitivity functional clusters represent a large portion of the explained variance in LD1. These findings suggest the sensitivity and static signaling clusters are most susceptible to codependent neuropathy (Figure 24d).

While dynamic signaling provided relatively modest contributions to LD1 (lower coefficient weights in Figure 24d), examining the parameter level data allowed us to discover the expression of distinct classes of interactions. Independently, OX and $Apc^{Pirc/+}$ induce highly conserved (87.5%) opposing effects exclusively within the dynamic functional cluster. We consistently found that $Apc^{Pirc/+}$ mutation increased and OX treatment decreased dynamic firing (Figure 27g). This led us to predict that their combination would nullify dysfunction and approximate Apc^{WT} +control signaling. Instead, we observed opposing interactions that resulted in drastic reduction in dynamic firing properties. By contrast, for history-dependent functional clusters, we found that cancer-chemotherapy interaction emerged exclusively in $Apc^{Pirc/+}$ +OX neurons, since neither Apc^{WT} +OX nor $Apc^{Pirc/+}$ +control neurons were disrupted (Figure 27h).

Summary

Taken together, we found that 58% of the neuronal signaling parameters in $Apc^{Pirc/+}$ +OX rats showed high-confidence interaction effects, in that those deficits were greater than those observed in either Apc^{WT} +OX nor $Apc^{Pirc/+}$ +control rats. Our findings demonstrate that complex systemic perturbations of chemotherapy and cancer result in synergistic interactions for sensitivity signaling characteristics, i.e. where cancer and chemotherapy impart influence in the same direction. (Figure 27f), opposing interactions for peak firing rate during dynamic signaling, i.e. where cancer and chemotherapy impart influence in the opposite directions. (Figure 27g), and emergent interactions for history dependent and static signaling characteristics, i.e. where cancer and chemotherapy independently impart no influence but their combination has effects (Figure 27h). In summary,

$Apc^{Pirc/+}$ +OX rats express widespread neuronal signaling dysfunction that targets all functional clusters, was independent of structural or physiologically detected degeneration and were not fully accounted for by a global decrease in sensitivity.

Aim 4: Test the hypothesis that down regulated Kv3.3 expression is sufficient to reproduce neuronal dysfunction observed following chronic chemotherapy treatment of cancer.

Introduction

To test the sufficiency of down-regulated Kv3.3 receptor (annulospinal) currents to reproduce $Apc^{Pirc/+}$ +OX neuronal dysfunction, we developed a novel biophysical model of rat muscle-spindle based on the known region-specific channel composition of rat muscle spindles (Bewick and Banks 2015; Woo, Lukacs *et al.* 2015; Carrasco, Vincent *et al.* 2017) and newly discovered Kv3.3 channel.

Aim Specific Methods

Biophysical modeling of muscle spindle firing

In the NEURON 7.6 simulation environment, we developed a novel biophysical model of rat muscle-spindle based on the known region-specific channel composition of rat muscle spindles (Bewick and Banks 2015; Woo, Lukacs *et al.* 2015; Carrasco, Vincent *et al.* 2017) and newly discovered Kv3.3 channel. The model was designed to simulate the behavior of muscle spindles from Apc^{WT} +control animals as they respond to identical stimulations to those presented *in vivo*.

We modeled a single branch of the Ia fiber system with terminal, preterminal axon, heminode (first node), and subsequent four myelin and node segments. Figure 28 shows channels distributions for different compartments based on available information. When

channels are found in more than one location, their densities are higher on the nodes and paranodes than elsewhere. We also included an activating Ca channel that is built into the modeled SK channels. The mechano-sensitive channel is activated by tension in the receptor area and also has a slow tension-dependent inactivation.

We modelled mechanotransduction by dividing the spindle into a polar (intrafusal muscle) and non-polar region (sensory terminal). The non-polar region is purely elastic whereas the tension developed in the polar regions shows a non-linear relation between tension and muscle length and velocity analogous to extrafusal muscle as described by (Hasan 1983). We derived the following equation relating sensory terminal length (m) to muscle length (x) and velocity as described by Hasan 1983 with the exception of not directly translating this function into spindle firing rate as originally described. Instead we model the transformation of stretch-evoked mechanical stimuli to conductance depending on the length of the sensory region, e.g. proportional to m and $\frac{dm}{dt}$:

$$\frac{dm}{dt} = \frac{dx}{dt} a \left(\frac{bm - x - c}{x - c - m} \right)^3$$

where a (0.0003 (mm/ms)), b (250) and c (-15 (mm)) are constants. Constant a is inversely related to the strength of the velocity effect, b reflects the relative compliance of the two regions and c represents the slack length of the polar regions (Hasan 1983). Additionally, we model the max conductance (gbar) of the mechanotransduction region (gbar=0.01 (MΩt/cm²)), the slope of Boltzman equation specifying sensory length (Lslp) to conductance (Lslp = 0.05 (mm)), half activation point (Lhalf = 0.1 (mm)), and membrane time constant (taum = 5 (ms)). Along with the modeled mechanotransduction process we modeled gbar for each channel in each specific region as documented in the following table.

Table 1.

Conductances Parameters for Biophysical Modeling. Breakdown of maximum conductances for each of the four modelled regions for both Apc^{WT} +control and $Apc^{Pirc/+}$ +OX animals. Parameters labelled in red indicate experimentally altered values in $Apc^{Pirc/+}$ +OX.

Terminal	Apc^{WT} +control	$Apc^{Pirc/+}$ +OX
	gbar	gbar
Na1.6	200pS/ μm^2	200pS/ μm^2
Nav1.7	200pS/ μm^2	200pS/ μm^2
Nav1.8	0.001M Ω t/cm ²	0.001M Ω t/cm ²
Na1.1	200pS/ μm^2	200pS/ μm^2
KCNQ	0.004M Ω t/cm ²	0.006M Ω t/cm ²
Kv3.3	0.008S/cm ²	0.000S/cm ²
Kv1.1	0.008S/cm ²	0.008S/cm ²
SK(mAHP)	0.0005 S/cm ²	0.0005 S/cm ²
Ca2+lowThr	5e-5 S/cm ²	5e-5 S/cm ²

Na1.6	200pS/ μm^2	200pS/ μm^2
Nav1.7	200pS/ μm^2	200pS/ μm^2
Na1.1	200pS/ μm^2	200pS/ μm^2
KCNQ	0.004M Ω t/cm ²	0.006M Ω t/cm ²
Kv1.1	0.008S/cm ²	0.008S/cm ²
SK(mAHP)	0.0005 S/cm ²	0.0005 S/cm ²
Ca2+lowThr	5e-5 S/cm ²	5e-5 S/cm ²

Paranode	Apc^{WT} +control	$Apc^{Pirc/+}$ +OX
	gbar	gbar
Nav1.8	0.001M Ω t/cm ²	0.001M Ω t/cm ²
Kv3.3	0.008S/cm ²	0.000S/cm ²
Kv1.1	0.008S/cm ²	0.008S/cm ²

Nodes	Apc^{WT} +control	$Apc^{Pirc/+}$ +OX
	gbar	gbar
Na1.6	200pS/ μm^2	200pS/ μm^2
Nav1.7	200pS/ μm^2	200pS/ μm^2
KCNQ	0.004M Ω t/cm ²	0.006M Ω t/cm ²

Pre-Terminal	Apc^{WT} +control	$Apc^{Pirc/+}$ +OX
	gbar	gbar

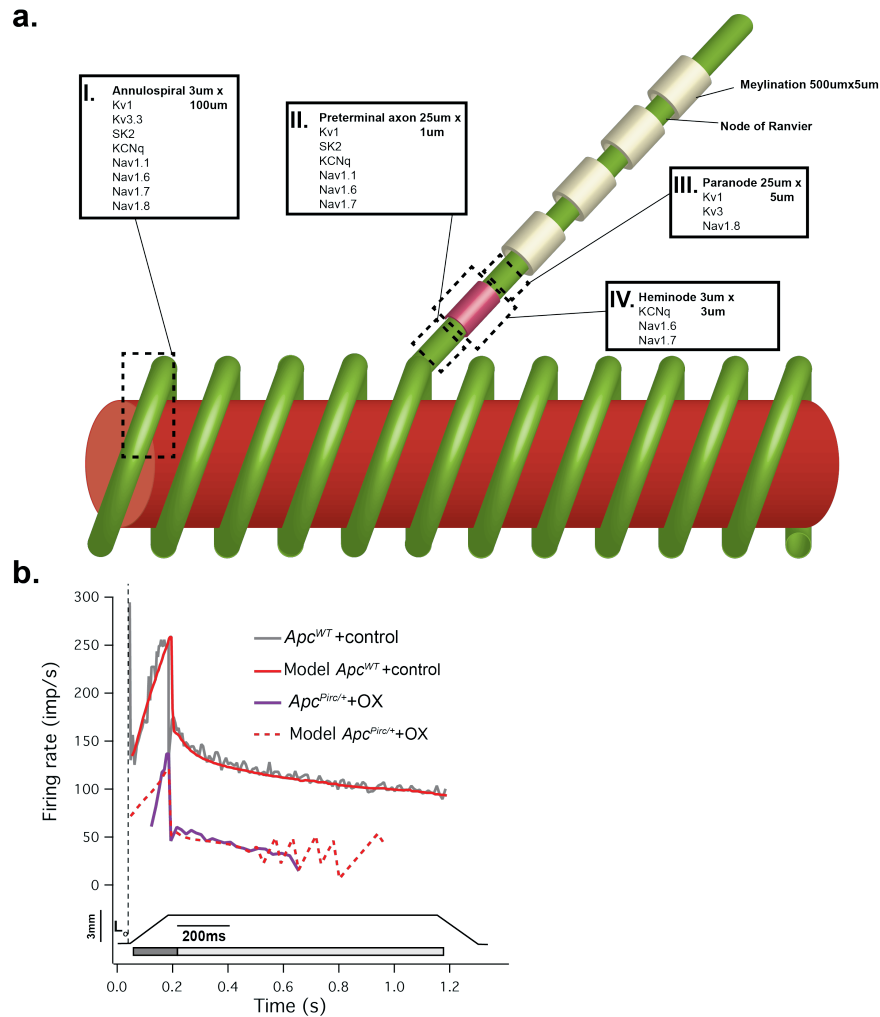


Figure 28.

Anatomical distribution of ion channel constituents of biophysical computational model of muscle spindle. a, Model of one branch of the Ia fiber system with terminal, preterminal axon, first node (heminode), and subsequent node-myelin pairs. Model identifies the spatial distribution of ion channels in muscle spindle Ia primary ending. The intrafusal muscle fiber (red) is wrapped by an annulospiral ending (green) and a preterminal axon that extends unmyelinated from the terminal to the heminode (pink) followed by a myelinated axon. Dotted-boxes represent specific regional distributions believed to underlie specific functional characteristics of neuronal signaling e.g. mechanotransduction, signal amplification, encoding, and autogenic feedback. b, Example of $Apc^{WT}+control$ and $Apc^{Pirc/+}+OX$ response from the biophysical spindle model (red) overlaying experimental $Apc^{WT}+control$ and $Apc^{Pirc/+}+OX$ data. Figure shows the mean instantaneous firing rates. Dashed vertical line marks onset of muscle stretch (3mm) from resting length (L_0). Dynamic and static phases of naturalistic stimuli indicated by dark grey (150ms duration after stretch command onset) and light grey (1s duration after the dynamic phase) bars.

Results

Biophysical model of muscle spindle reproduces canonical firing behavior

The model was developed and implemented in NEURON 7.6 to simulate the behavior of muscle spindles from Apc^{WT} +control animals and those treated with $Apc^{Pirc/+}$ +OX as they respond to identical stimulations to those presented *in vivo* (Methods). The Apc^{WT} +control simulation (Figure 28b) reproduced experimental firing behaviors over dynamic and static simulated length change stimuli i.e., linearly increasing firing rates as length changes over constant velocity and slow firing rate accommodate (decay) as length stimuli is held at a constant length.

Down regulating Kv3.3 is sufficient to explain key features of firing dysfunction

We then modelled $Apc^{Pirc/+}$ +OX muscle spindles by systematically eliminating Kv3.3 expression on the receptor as was seen in the above immunohistochemical analyses (section 1.3.2.2). $Apc^{Pirc/+}$ +OX simulation (Figure 28b) reproduced certain features of *in vivo* data and not others. Notably, through this targeted ionic perturbation we eliminated static firing throughout the hold phase and blunted the dynamic firing rates whereas no change in threshold was observed.

Summary

Collectively, the results of computer simulations indicate that a reduction in Kv3.3 expression, as observed experimentally, is sufficient to reproduce many of the firing defects in mechanosensory neurons and suggest this as one candidate biophysical mechanism that may be directly or indirectly targeted by the cancer-chemotherapy interaction. Moreover, the failure of simulated Kv3.3 down-regulation to reproduce defects in threshold provides strong evidence that additional biophysical mechanisms are present. For example, up-regulated gene KCNN2 that encodes SK2 (Figure 17) recently discovered in mammalian muscle spindle receptors may provide the additional

Ca²⁺ gated K⁺ current to increase threshold. Alternatively, and increased Kv1.1 or KCNQ could lead to a comparable change in threshold. Because both Kv1.1 and KCNQ channels have low voltage thresholds, small increases in expression, that could be masked by our bulk transcriptional profiling, of either channel could increase spindle threshold.

Aim 5: Test the hypothesis that cancer exacerbates sensorimotor dysfunction after chronic chemotherapy treatment in an awake behaving animal.

Introduction

To test the behavioral consequences of the cancer-chemotherapy interaction, we evaluated *Apc*^{Pirc1+} OX rats' performance in horizontal random rung ladder walking. This precise walking task overbalances performance on proprioceptive function (Metz and Whishaw 2002; Metz and Whishaw 2009) since rats move forward with vision directed forward. Under these experimental conditions, success relies on proprioceptive function that assists with foot placement on rungs that pass out of sight.

Aim Specific Methods

Behavioral analysis

We used the ladder rung walking task as a validated outcome to detect and describe sensorimotor deficits (Metz and Whishaw 2002; Metz and Whishaw 2009). The ladder rung apparatus was built as previously described (Metz and Whishaw 2002). Secure hind foot placement was assessed using the seven-category scale scoring system introduced by (Metz and Whishaw 2002; Metz and Whishaw 2009) with modifications as to not distinguish whether or not an error was associated with a deep fall. The total

number of errors in forelimb (e.g. Figure 29d) and hindlimb (e.g. Figure 29e) placement was calculated and the mean error/step ratio was calculated per animal and represented as percent of error where an increase in the number of errors/steps corresponds to a decrease in secure foot placement of the hind and/or fore foot.

Results

Behavioral dysfunction exacerbated by cancer-chemotherapy interaction

Apc^{WT}+control and *Apc*^{Pirc1+}+control rats achieved a high incidence of rear and fore foot placement, when walking on the rungs of a uneven horizontal ladder, with a foot-drop error rate of only 2.4% ($\pm 2.7\%$ SD, 6 animals; Figure 29a and Movie S1) and 2.5% respectively ($\pm 2.9\%$ SD, 4 animals; Figure 29a and Movie S1). In contrast, *Apc*^{Pirc1+}+ OX exhibited a 19.2% foot-drop error rate ($\pm 5.6\%$ SD, 7 animals; hierarchical Bayesian model (stan_glm) vs. *Apc*^{WT}+control and *Apc*^{Pirc1+}+control; Figure 29a and Movie S2). *Apc*^{Pirc1+}+ OX error rates significantly exceeded our previous findings following OX treatment alone (*Wistar*+OX) of 8.4% ($\pm 3.1\%$ SD, 7 animals; hierarchical Bayesian model (stan_glm) vs *Apc*^{Pirc1+}+ OX; Figure 29). Independent analysis of fore- (Figure 29b) and hind-foot (Figure 29c) error rates revealed that skilled motor behavior degradation was significantly exacerbated by the emergence of fore-limb errors ($10.4\% \pm 3.9\text{SD}$) not present in *Apc*^{WT}+control (0%), *Apc*^{Pirc1+}+control ($2.3\% \pm 2.8\text{SD}$), or *Wistar*+OX (0%; hierarchical Bayesian model (stan_glm)).

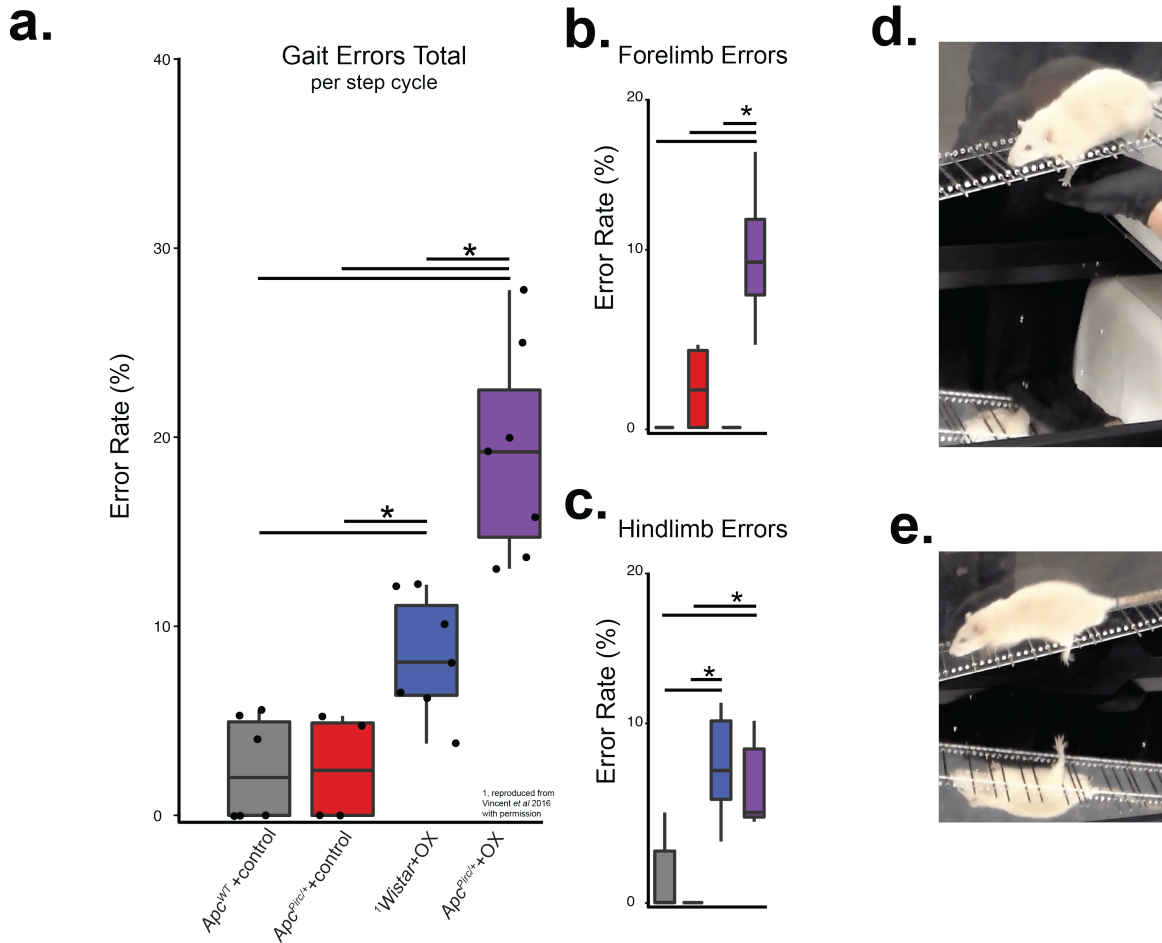


Figure 29.

Behavioral dysfunction exacerbated by cancer-chemotherapy interaction. a, Total gait errors as measured by secure fore- and hindfoot placement was scored by errors/step cycle during ladder rung walking. Recordings were analyzed from *Apc^{WT}+control* (n = 6), *Wistar+OX* (n = 7), *Apc^{Pirc/+}+control* (n = 4) and *Apc^{Pirc/+}+OX* (n = 7) animals. b-c, indicate the contributions of fore- (b) and hindlimb (c) errors to total error rates. d, Photograph shows left forelimb slip in double image (simultaneous side and underneath views) of *Apc^{Pirc/+}+OX* rat walking on ladder rungs. e, Photograph shows left hind limb slip in double image (simultaneous side and underneath views) of *Apc^{Pirc/+}+OX* rat walking on ladder rungs (representative cases of entire ladder rung walking trials can be viewed at Movie S1 and Movie S2 for *Apc^{WT}+control* and *Apc^{Pirc/+}+OX* rats respectively). * indicates statistically significant differences between experimental groups as empirically derived from hierarchical Bayesian model (stan_glm): 95% highest density intervals do not overlap between group contrasts. ¹*Wistar+OX* data reproduced from Vincent et al 2016 with permission.

Summary

Our data reveal that proprioceptive sensory input from muscle spindles ensures limb placement accuracy in a skilled motor behavioral task. Moreover, discovering that cancer-chemotherapy interaction results in the emergence of novel forelimb deficits (Figure 29b, d) typically not observed in this challenge to hindlimb capacities (Figure 29c, e) provides further evidence that exacerbation effects are unpredicted from studying chemotherapy alone.

Project 1: Discussion

Here we present original evidence that cancer transforms the nature and magnitude of neuropathy induced by chemotherapy alone. Our preclinical study of rats is the first to compare the neuropathic effects of chemotherapy and cancer, both independently and in combination, currently impractical in human study. These comparisons for global transcriptional analysis of sensory neurons in dorsal root ganglia revealed dysregulation of genes uniquely induced, amplified or suppressed by the combination of cancer and chemotherapy. Codependence was conserved as impaired spike encoding of mechanosensory stimuli and novel ion channelopathy.

Our transcription analyses expose two potential targets for treating sensorimotor disorders among the debilitating patient symptoms that persist following treatment of various cancers with platinum-based compounds and other antineoplastic agents, e.g. taxanes. Patients display deficits in the spatiotemporal parameters (speed and stride) of walking gait, in control of posture, and in balance relying on proprioception (Marshall, Zipp *et al.* 2017; Monfort, Pan *et al.* 2019). Acknowledging that these disabilities may

arise from a variety of lesions in the nervous system, the deficits we observe here at the receptor origin of detection and encoding of muscle mechanics would necessarily impair movements and postures and cannot be fully compensated by other senses, e.g. vision. Furthermore, signaling by mechanosensory neurons in rats closely resembles that in human (Burke, Hagbarth *et al.* 1978). For these reasons, we assign special attention to depressed signaling by muscle spindles and to the associated decrease in expression of the voltage-gated ion channel Kv3.3 and its gene *Kcnc3*. Kv3 channels play important role in attaining and maintaining high neuronal firing rates. Unique biophysical properties, e.g. high activation threshold, rapid activation, and deactivation kinetics, allow neurons that express Kv3 channels to quickly repolarize without compromising the inward current or Nav channels reactivation (Rudy and McBain 2001; Kaczmarek and Zhang 2017; Gu, Servello *et al.* 2018). Reports that *Kcnc3* gene knock out impairs firing responses of neurons (Akemann and Knöpfel 2006; Espinosa, Torres-Vega *et al.* 2008) and results in ataxia (Figueroa, Minassian *et al.* 2010) promote this gene and its ion channel as potential contributors to signaling deficits observed in the present study.

While our biophysical modelling provides evidence that Kv3.3 is sufficient to explain certain neuronal signaling deficit, we are uncertain about the necessity of Kv3.3 channelopathy to explain the full suite of deficient mechanosensory signaling in cancer treated by chemotherapy. Uncertainty arises in part, because comprehensive understanding of the molecular mechanisms underlying the function of these sensory neurons is lacking, although advanced by our discovery of Kv3.3 in mechanoreceptors of healthy animals. Another candidate target for treating sensorimotor disorders is the inflammatory signaling molecule IL6, shown here to express large increases in both gene and protein expression. As a result of its effect in suppressing neuronal firing behavior (Nelson, Ur *et al.* 2002) IL6 has the potential to explain decreased signaling by

mechanosensory neurons. We identify both Kv3.3 and IL6, therefore, as targets worthy of testing for their potential value in treating movement disorders. Additional points of interaction likely exist, which remain either undiscussed (e.g. FosB) or potentially masked due to transcriptional profiling of DRG's that may result in variable differential expression across heterogenous cell types.

Muscle proprioceptors (Group Ia) provide invaluable sensory feedback to control movement (Prochazka and Ellaway 2012; Proske and Gandevia 2012), make rapid adjustments to unexpected perturbations (Nichols, Cope *et al.* 1999; Shemmell, Krutky *et al.* 2010), and preserve an internal representation of the body's interaction with the environment (Ivanenko, Dominici *et al.* 2011). It seems to reason then that disruption in sensory encoding is a plausible model to explain the severely compromised ability to carry out precision ladder walking (Abelew, Miller *et al.* 2000; Sghirlanzoni, Pareyson *et al.* 2005). We observed abnormal sensorimotor behavior characterized as difficulty with achieving proper limb placement in *Apc^{Pirc/+}*+OX rats. Deficits were significantly greater than those previously observed in our lab from animals treated with OX alone. This observation further supports a link to altered proprioceptor signaling while also suggesting that the magnitude of signaling deficits might contribute to the magnitude of sensorimotor deficits, as evidenced by the emergence of forelimb errors that coincide with additional exacerbated signaling deficits. Data obtained in *Apc^{Pirc/+}*+ OX rats were in agreement with previous results observed in animals without functional spindles (*Egr3* mutants) (Akay, Tourtellotte *et al.* 2014), indicating that the loss of sensory feedback from muscle spindles following cancer treatment may be sufficient to explain sensorimotor deficits experienced by cancer survivors.

The emergence of forelimb errors might be explained by greater signaling impairment, i.e. lost sensitivity to stimuli and reduced dynamic response, in addition to the previously

described impaired static responsiveness. This necessarily results in larger information loss that may not be able to be compensated by vision or the CNS learning a new representation of the corrupt information. Stated another way, while the forelimbs are in the line of site for this task (ladder rung walking), the extent of sensory information loss may result in such decompensated (e.g. fragile) motor performance that even tasks that can rely on another feedback source, e.g. vision, can suffer. In addition, shifting dependence of feedback away from proprioceptive signals, that can operate on the scale of 10s of milliseconds, onto visual systems that operate on the scale of 100s of milliseconds imparts additional feedback delay that can accentuate errors that occur during the rapid movements required to complete the ladder rung walking task.

Another contributor to the emergence of forelimb errors when cancer and chemotherapy interact might be differences in spinal circuitry and their interaction with corrupt sensory feedback. It is well documented that forelimbs and hindlimbs are controlled by functionally and anatomically distinct spinal circuits (Ballion, Morin *et al.* 2001; Juvin, Simmers *et al.* 2005; Frigon 2017). Various experimental preparations showing the forelimbs and hindlimbs can be physically and/or functionally uncoupled suggests that their responses to perturbations, e.g. chemotherapy alone or cancer and chemotherapy, might also be uncoupled (Ballion, Morin *et al.* 2001; Juvin, Simmers *et al.* 2005). This latter suggestion highlights the possibility that the signaling deficits identified in our previous reports (Vincent, Wiczerzak *et al.* 2016) could have been restricted to the hindlimb alone and it is not until the extent of the systemic perturbation was large enough, e.g. due to the addition of cancer that forelimb sensorimotor control faltered.

Our study, being restricted to a single time point following chemotherapy, does not assess the stability of potential treatment targets that emerge from codependent neuropathy. It is reasonable to expect, however, that the codependence undergoes

dynamic change. Cancer, presumably also its associated systemic effects, undergoes complex progression as subpopulations of cancer cells differentially resist, adapt, or succumb to chemotherapy. Moreover, biological systems themselves initiate dynamic responses to perturbations. In the nervous system, homeostatic regulation initiates compensatory mechanisms to offset perturbations in neuronal excitability (Waxman and Zamponi 2014). It is thought provoking in this regard to consider the possibility that the chronic hypoexcitability which follows the acute hyperexcitability (Cavaletti and Marmioli 2010; Park, Goldstein *et al.* 2013) that develops during chemotherapy reflects the actions of a dysregulated compensatory mechanism. Understanding these non-linear interactions processes and their effects on potential treatment are both challenging and necessary for developing effective cancer treatment.

CHAPTER 4. PROJECT 2

Project 2 is based on a single manuscript:

1. Housley, S. N., Nardelli, P, and Cope, T. C. (2019). Mechanosensory encoding and neural decoding of musculoskeletal dynamics impaired following cancer treatment. (in preparation)

Introduction

Chemotherapy induced neuropathy (CIN) comprises a constellation of debilitating neurological disorders including sensorimotor impairments severe enough to persist long into disease free survival (Quasthoff and Hartung 2002; Cavaletti and Marmiroli 2010; Alcindor and Beauger 2011; Seretny, Currie *et al.* 2014; Sisignano, Baron *et al.* 2014; Stone and DeAngelis 2016). CIN reduces quality of life for many patients and can limit antineoplastic treatment, complicating its utility (Cavaletti and Marmiroli 2010; Alcindor and Beauger 2011; Stone and DeAngelis 2016). Despite intense pursuit, clinical trials founded on preclinical studies in animals without cancer (Currie, Angel-Scott *et al.* 2018), have largely failed to deliver effective treatment for and/or prevention of CIN (Hershman, Lacchetti *et al.* 2014).

This fundamental gap in understanding of CIN pathophysiology led us to test, in **Project 1**, whether clinically relevant CIN depends on codependence between cancer and chemotherapy (Housley, Nardelli *et al.* 2019). Through multiscale study of a class of sensory neurons in animals with cancer treated by chemotherapy, we discovered the first evidence that CIN cannot be explained by the effects of chemotherapy alone but depend instead on complex interactions with cancer-related processes. Among the observed changes across genetic, protein and whole cell neurologic function, neurons

failed to encode natural movement stimuli in their spiking activity with dysfunction depending on both cancer and chemotherapy.

A key question that remains relates to whether the cancer—chemotherapy codependence that causes dysfunction in neuronal encoding is conserved across diverse classes of mechanosensory neurons. Mechanosensory neurons are necessary for generating the information content (population code) needed for proprioception. For example, Golgi tendon organs (Ib) and group Ia and II muscle spindle afferents encode unique static and time-varying information, e.g. length, velocity, and inertial loads of body position as movements result in physical interactions with the environment. If deficits are conserved across the population, conflicting sensory signals or deletions of critical pieces of information would prove detrimental for a unified representation of body position under static and dynamic conditions, e.g. proprioception. Deficits in this population code may explain the lasting perceptual and functional deficits documented in patients treated with chemotherapy. Alternatively, the central nervous system (CNS) may compensate for the loss of information by learning a new representation of the population code to partially or fully compensate for information loss, thus preserving proprioception performance. Therefore, developing a detailed understanding of dysfunction across the population is necessary for developing mechanistic understanding, for predicting functional deficits or for understanding how the CNS may compensate for profound information loss.

The present study was designed to test the hypothesis that cancer's exacerbation of chemotherapy induced neuronal signaling deficits is conserved across the population of mechanosensory neurons in muscle. We recorded intracellular spiking activity from four classes of physiologically identified mechanosensory neurons responding to naturalistic mechanical stimuli *in vivo*. Results support our hypothesis in finding significant deficits in spike encoding across multiple measures used to

parameterize responses to naturalistic stimuli in all neuron classes. Analyses reveal co-suppression of specific signaling parameters across all neuronal classes, suggesting the existence of a global co-regulatory process that governs the balance of information content from multiple neuron classes flowing to the central nervous system. To understand the consequences of corrupt population spiking activity, we employed deep-learning algorithms to test how decoding of spatiotemporal features of movement are altered after chemotherapy treatment of cancer. Results indicate that spiking activity from the population of neurons in animals with cancer, treated by chemotherapy contain significantly less information about key features of movement including: timing, magnitudes, and velocity. We then modeled the CNS's capacity to compensate for this information loss by retraining the networks on corrupt population codes which revealed the CNS would not be able to fully compensate (learn) a new representation that restores predictive abilities. Intracellular recordings of synaptic potentials in a CNS neuron provided biological validation of modeling results confirming upstream neurons ability to accurately predict stimuli remain impaired. Collectively, our results show global deficiency in the population code of mechanosensory neuron population and resulting corrupt spatiotemporal decoding of movement features necessarily results in upstream neurons or networks to unpredictable inferences about the bodies interaction with the external environment and may contribute to lasting behavioral deficits documented in patients treated with chemotherapy.

Aim 6: Test the hypothesis that cancer's exacerbation of chemotherapy induced neuronal signaling deficits is conserved across the population of mechanosensory neurons in muscle.

Aim Specific Methods

Neuronal Classification

Dorsal rootlets positioned in continuity on bipolar recording electrodes were selected for sampling sensory neurons when they produced robust population activity (extracellular responses from many sensory neurons) in response to both electrical stimulation of triceps surae nerves and stretch of triceps surae muscles. Individual axons penetrated in these rootlets by glass micropipettes (~30 M Ω filled with 2 M K⁺ acetate) were selected for study when electrical stimulation of triceps surae nerves produced orthodromic action potentials that were readily resolvable and had conduction delay of <3 ms. We classified muscle afferents on the basis of their responses to specific stimuli, e.g., muscle twitch contraction and vibration on basis of binary scoring of three criteria (Vincent, Gabriel *et al.* 2017). Afferents that fired during the rising phase of isometric twitch force (evoked by nerve stimulation with electrical pulses 0.04-ms duration at 1 pps) were designated group Ib tendon organ afferents, while those that did not were labeled muscle spindle afferents. Muscle spindle afferents designated Ia were distinguished from group II by firing with virtually perfect entrainment to 1-s bouts of high-frequency, small-amplitude vibration (100 –333 Hz, 80 μ m) and by responding with an initial burst of high-frequency firing (>100 pulses per second (pps)) at the onset of muscle stretch. These same criteria distinguish analogous afferent groups in the cat (Matthews 1972).

Population code construction

Intracellular recordings from physiologically identified sensory neurons of all four classes were used to construct population codes (ensembles of neuronal firing). Since identical natural stimulation patterns were used for all neuronal recordings, the stimulation profiles were used to precisely time synchronized independently recorded neurons. This allowed us to model population codes of physiologically identified neurons of precisely known locations from Apc^{WT} +control and $Apc^{Pirc/+}$ +OX animals, not possible in previous studies (Stein, Weber *et al.* 2004; Weber, Stein *et al.* 2007).

Results

Encoding deficits conserved across diverse classes of mechanosensory neurons

Applying electrophysiological methods to rats in vivo, we recorded spiking activity from single mechanosensory neurons responding to naturalistic mechanical stimuli (Figure 30). We sampled group Ia, unclassified spindle, group Ib, and group II totaling 225 neurons from Apc^{WT} +control, Apc^{WT} +OX, $Apc^{Pirc/+}$ +control, and $Apc^{Pirc/+}$ +OX experimental groups (Figure 30 and see Table 2 for complete description). For simplicity raw data and canonical analyses of group Ia neurons are not reproduced from **Project 1**.

Table 2.

Distribution of decoding data. Breakdown of data from 225 neurons acquired from 20 animals. Neuronal classes in top row and experimental group left most column.

	Ia (n=60)	Unclassified (n=57)	II (n=57)	Ib (n=51)
Apc^{WT} +control (n=6)	11	19	17	14
Apc^{WT} +OX (n=3)	19	14	9	5
$Apc^{Pirc/+}$ +control (n=4)	20	19	17	18
$Apc^{Pirc/+}$ +OX (n=7)	10	5	14	14

From these spiking responses, we collected 31 measured and derived parameters (average of four trials: (Figure 20 and Table 3). In Apc^{WT} +control rats, we found that muscle stretch elicited the expected spike encoding behavior from multiple classes of sensory neurons in normal animals (Vincent, Gabriel *et al.* 2017) and humans (Burke, Hagbarth *et al.* 1978) (grey traces Figure 30). We next asked whether $Apc^{Pirc/+}$ or OX treatment alone induce signaling dysfunction. In agreement analyses of group Ia neurons presented in Aim 3, we found a remarkable degree of concordance with signaling in Apc^{WT} +control (Figure 30). $Apc^{Pirc/+}$ +control neuronal signaling displayed comparable sensitivity to stimuli and showed similar static behavior across all neuronal classes (red traces in Figure 30) as the Apc^{WT} +control with the exception of group II neurons that spiked longer Apc^{WT} +control. As was true for group Ia neurons, OX treatment of Apc^{WT} rats induced mild signaling deficits. Deficits were primarily restricted to sustained firing (blue traces in Figure 30), validating our previous findings of restricted deficits observed in a different strain of healthy rats treated with OX alone (Vincent, Wiczerzak *et al.* 2016).

Table 3.

Summary Statistics of Neuronal Signaling. Breakdown of summary statistics of each neuronal class and their respective signaling parameters.

Group II	Apc^{WT} +control	N=17	Apc^{WT} +OX	N=9	$Apc^{Pirc/+}$ +control	N=17	$Apc^{Pirc/+}$ +OX	N=14
Variables	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
Dyn.DI	61.28	4.68	48.33	5.74	60.96	8.22	38.34	5.73
Dyn.F	156.71	18.43	172.44	25.23	188.05	25.04	186.48	16.02
Dyn.IFRdrop	29.61	6.3	18.86	4.35	30.88	8.7	51.41	19.87
Dyn.pfr	127.93	5.35	103.8	15.02	118.42	11.73	72.08	9.81
Dyn.pfr1	102.29	8.13	89.95	17.29	94.2	8.75	64.59	6.45
Dyn.pfr3	96	8.93	80.27	15.38	87.38	8.27	54.44	7.25

Table 3 continued

Dyn.RDR	17.47	1.7	12.33	2.39	12.76	1.44	5.79	1.71
Dyn.slp	700.22	71.12	628.37	62.21	1114.62	154.25	777.86	140.92
Dyn.slp1	87.3	8.96	111.97	18.06	131.08	14.4	139.41	27.93
Dyn.slp3	147.04	18.81	138.17	21.61	181.14	22.34	135.78	27.54
Dyn.spkNum	11.54	0.54	10.19	1.31	8.65	0.88	5.23	0.74
Dyn.spkNum1	48.18	4.07	38.11	8.31	37.06	3.93	17.43	3.05
Dyn.spkNum3	30.94	3	25.78	6.26	24.29	2.78	11.64	1.73
Stat.afr	73.19	4.76	64.44	10.39	66.15	6.37	38.54	5.7
Stat.HzEnd	56.87	5.22	52.77	8.73	50.02	5.45	23.44	5.45
Stat.HzSTD	19.03	1.37	26.19	9.28	21.35	3.42	14.78	2.07
Stat.LSpkF	110.75	9.87	107.43	4.92	112.21	10.11	105.39	4.79
Stat.LSpkT	994.73	1.18	964.82	27.9	991.11	2.05	906.6	68.3
Stat.mSfr	66.65	4.84	55.91	10.3	57.46	5.71	32.91	5.59
Stat.slp	-44.31	2.51	-38.18	5.19	-45.92	5.5	-31.41	3.66
Stat.spkNum	67.99	5	57.82	10.33	59.56	6.52	33.39	5.63
Thr.F	11.03	0.84	13.64	1.1	22.9	4.01	31.6	8.04
Thr.F1	8.15	1.37	24.85	8.71	20.84	4.33	41.64	10.85
Thr.F3	17.65	2.99	35.48	10.46	31.58	5.28	47.45	10
Thr.L	0.16	0.03	0.2	0.03	0.55	0.11	0.89	0.22
Thr.L1	0.18	0.06	0.57	0.23	0.55	0.14	1.08	0.22
Thr.L3	0.76	0.1	1.07	0.24	1.16	0.12	1.44	0.15
Thr.T	8.84	1.35	9.52	1.63	26.77	5.36	45.32	10.69
Thr.T1	43.64	14.28	145.93	58.69	136.98	33.67	267.06	55.02
Thr.T3	200.45	24.32	272.67	61.1	295.37	29.82	367.2	38.11

Table 3 continued

Group Ib	<i>Apc</i>^{WT}+control	N=14	<i>Apc</i>^{WT}+OX	N=5	<i>Apc</i>^{Pirc/+}+control	N=18	<i>Apc</i>^{Pirc/+}+OX	N=14
variable	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
Dyn.DI	68.41	7.14	72.24	6.36	41.95	5.34	26.99	8.49
Dyn.F	286.55	13.76	214.62	35.18	226.12	24.98	265.07	24.01
Dyn.IFRdrop	23.91	4.38	35.98	15.08	22.46	5.68	60	16.89
Dyn.pfr	145.78	13.51	102.36	4.3	95.11	8.41	40.78	11.74
Dyn.pfr1	149.61	11.69	98.32	7.22	101.84	11.1	53.72	9.36
Dyn.pfr3	136.6	11.08	92.55	6.99	93.02	10.82	41.59	9.97
Dyn.RDR	7.64	0.89	8.2	3.34	10.94	1.22	2.5	0.57
Dyn.slp	2144.72	323.56	1708.74	735.8	1146.52	260.42	336.44	137.58
Dyn.slp1	259.76	54.67	297.86	91.14	160.45	22.37	267.74	61.51
Dyn.slp3	377.86	31.98	381.65	81.26	189.87	32.28	202.51	49.17
Dyn.spkNum	7.98	0.84	7	1.7	6.35	0.68	2	0.46
Dyn.spkNum1	33.93	4.02	23.4	5.21	32.39	3.62	7.21	1.86
Dyn.spkNum3	26.29	3.66	15.2	2.63	21.44	2.94	4.79	1.38
Stat.afr	87.79	8.26	58.71	3.88	57.98	4.52	42.3	8.81
Stat.HzEnd	62.88	9.55	6.56	6.34	44.42	4.72	9.96	5.56
Stat.HzSTD	26.67	2.44	20.11	2.15	14.29	1.32	14.28	3.7
Stat.LSpkF	166.04	15.23	121.93	16.86	121.61	13.73	149.08	11.96
Stat.LSpkT	990.38	4.08	752.28	63.25	990.31	2.55	316.84	113.42
Stat.mSfr	75.54	8.42	39.67	4.67	52.33	4.27	13.06	6.54
Stat.slp	-61.81	5.23	-90.77	16.72	-36.71	3.25	-51.03	24.47
Stat.spkNum	79.95	8.56	28.75	5.14	53.57	4.44	14.13	6.7
Thr.F	47.86	10.39	47.16	22.01	37.04	10.22	96.39	19.51
Thr.F1	66.42	9.93	82.25	30.21	37.61	10.41	121.7	20.69
Thr.F3	83.46	9.32	102.23	26.18	55.65	10.5	126.48	24.76
Thr.L	1.01	0.18	0.86	0.44	0.78	0.17	1.86	0.28
Thr.L1	1.37	0.17	1.42	0.47	0.77	0.17	2.2	0.2

Table 3 continued

Thr.L3	1.78	0.1	1.99	0.25	1.55	0.12	2.13	0.26
Thr.T	50.71	9.18	53.76	24.54	37.47	8.4	96.96	14.29
Thr.T1	324.18	49.42	360.65	119.97	177.2	42.28	562.46	35.74
Thr.T3	457.52	24.25	512.72	64.6	388.79	28.7	605.41	37.43

Group unclassified	<i>Apc^{WT}</i>+control	N=19	<i>Apc^{WT}</i>+OX	N=14	<i>Apc^{Pirc/+}</i>+control	N=19	<i>Apc^{Pirc/+}</i>+OX	N=5
variable	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
Dyn.DI	106.72	7.95	120.52	11.13	129.67	7.12	84.38	13.96
Dyn.F	248.81	21.74	159.98	12.59	233.98	24.84	143.33	11.79
Dyn.IFRdrop	72.86	8.77	92.57	9.06	114.26	8.42	65.1	15.26
Dyn.pfr	173.79	7.42	168.61	11.11	185.4	8.79	103.32	13.77
Dyn.pfr1	131.93	4.55	112.07	8.44	134.35	8.23	73.43	13.06
Dyn.pfr3	134.16	6.99	104.16	8.3	132.48	8.46	61.9	18.76
Dyn.RDR	20.68	1.02	13.43	2.18	19.11	1.64	7	0.63
Dyn.slp	1459.37	140.71	2001.68	220.49	1677.63	93.59	1641.3	358.14
Dyn.slp1	142.08	7.59	168.86	10.62	175.21	11.23	189.73	33.6
Dyn.slp3	213.73	12.52	246.02	19.92	274.11	19.28	225.45	69.6
Dyn.spkNum	13.12	0.6	10.32	0.8	11.87	0.75	4.65	0.52
Dyn.spkNum1	60.63	2.99	38.64	4.26	52.37	4.15	15.6	2.8
Dyn.spkNum3	39.42	2.65	25.21	2.67	33.26	3.51	8.6	2.93
Stat.afr	73.84	3.97	68.92	4.23	68.11	3.65	46.48	6.27
Stat.HzEnd	49.15	5.95	40.71	5.13	44.91	3.78	12.3	7.56
Stat.HzSTD	27.23	2.22	35.2	4.22	35.11	2	31.25	5.71
Stat.LSpkF	116.26	8.71	109.91	7.57	121.45	9.06	110.13	9.71
Stat.LSpkT	985.25	5.95	899.9	45.2	992.09	1.45	497.85	128.72
Stat.mSfr	65.26	5.23	53.62	3.84	55.73	3.83	19.93	7.92

Table 3 continued

Stat.slp	-58.45	5.52	-69.11	6.88	-71.93	4.44	-195.39	34.99
Stat.spkNum	64.39	4.49	50.84	4.53	56.68	3.76	16.53	6.52
Thr.F	17.59	1.59	31.18	3.61	22.34	3.57	41.44	10.09
Thr.F1	11.96	2.24	29.91	4.19	15.81	2.13	49.01	6.85
Thr.F3	31.06	2.7	46.32	6.19	39.18	3.97	78.01	18.59
Thr.L	0.51	0.08	0.89	0.12	0.54	0.08	1.38	0.33
Thr.L1	0.21	0.05	0.75	0.12	0.37	0.07	1.69	0.16
Thr.L3	1.01	0.09	1.4	0.14	1.29	0.07	2.33	0.19
Thr.T	25.02	3.87	45.12	6.23	25.56	4	112.06	50.34
Thr.T1	53.35	14.85	214.73	41.31	91.38	16.68	419.77	39.16
Thr.T3	271.17	18.46	371.08	38.44	328.78	16.81	585.55	47.13

Group Ia	<i>Apc^{WT}</i>+control	N=11	<i>Apc^{WT}</i>+OX	N=19	<i>Apc^{Pirc/+}</i>+control	N=20	<i>Apc^{Pirc/+}</i>+OX	N=10
variable	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
Dyn.DI	120.23	12.93	116.75	6.16	149.53	7.78	108.85	11.9
Dyn.F	185.55	25.91	160.02	12.99	251.45	28.39	150.63	7.95
Dyn.IB	282.63	14.33	205.66	36.76	175.31	48.52	76.12	51.18
Dyn.IFRdrop	86.41	10.38	111.06	6.46	87.5	8.93	82.52	8.41
Dyn.pfr	203.16	15.79	186.39	5.71	224.28	10.06	134.27	4.21
Dyn.pfr1	150.52	11.87	137.87	5.8	172.9	14.55	107.62	7.79
Dyn.pfr3	137.51	16.15	130.91	5.5	166.29	10.42	99.15	6.12
Dyn.RDR	24.64	2.63	23.05	1.29	28	1.8	14.1	1.47
Dyn.slp	929.94	137.19	1103.86	110.65	1243.56	104.05	1373.12	177.08
Dyn.slp1	124.51	18.98	144.3	7.99	164.65	11.12	160.04	31.58
Dyn.slp3	206.58	31.49	226.11	9.04	271.66	17.3	250.56	34.01
Dyn.spkNum	18.77	1.41	16.04	0.82	17	1.27	9.9	0.9

Table 3 continued

Dyn.spkNum1	72.73	7.75	61.53	4.31	79	6.09	35.6	3.77
Dyn.spkNum3	48.09	5.45	38.47	3.81	51	4.5	21.5	2.5
Stat.afr	93.98	6.64	84.97	3.61	88.05	4.34	67.6	4.88
Stat.HzEnd	73.47	6.47	50.72	7.09	62.75	4	24.02	8.41
Stat.HzSTD	29.85	3.15	29.26	2.1	37.23	2.21	35.69	3.71
Stat.LSpkF	122.5	11.3	113.24	10.12	115.67	8.63	120.71	7.15
Stat.LSpkT	991.44	6.28	877.94	52.03	994.86	1.85	723.29	115.62
Stat.mSfr	82.93	6.28	66.23	6.58	74.75	3.8	34.78	7.4
Stat.slp	-59.42	7.87	-153.24	73.55	-75.47	4.55	-289.61	145.17
Stat.spkNum	85.64	6.57	66.88	6.27	76.8	4.25	36.8	7.36
Thr.F	9.86	1.07	14.41	1.09	13.25	1.47	20.62	3.84
Thr.F1	7.14	1.8	16.37	2.37	7.08	0.92	21.71	5.84
Thr.F3	19.44	3.3	36.32	3.36	29.64	3.46	37.72	4.66
Thr.L	0.09	0.01	0.24	0.03	0.2	0.05	0.65	0.16
Thr.L1	0.15	0.07	0.4	0.09	0.07	0.01	0.72	0.2
Thr.L3	0.84	0.12	1.31	0.09	0.91	0.08	1.48	0.11
Thr.T	6.18	1.36	13.09	2.01	9.68	2.3	33.01	7.74
Thr.T1	29.89	12.06	102.97	23.37	16.16	3.61	192.75	58.1
Thr.T3	217.57	30.48	338.68	22.71	236.96	19.58	393.54	36.69

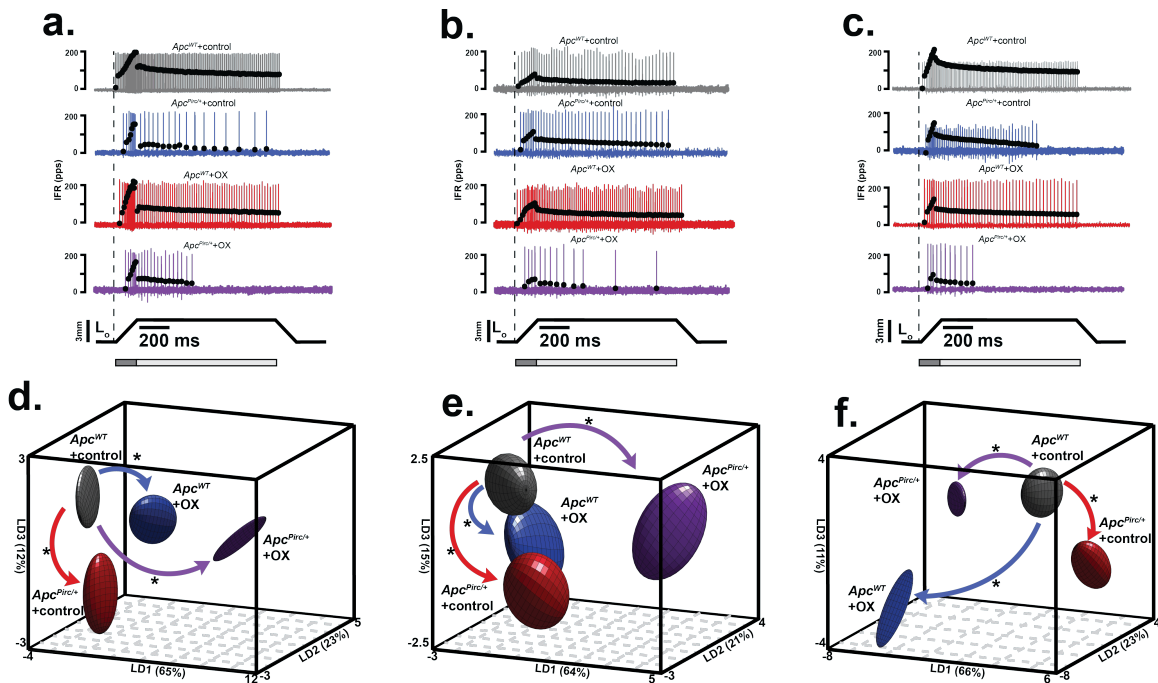


Figure 30.

Impaired Mechanosensory Neuron Population Code After Cancer Treatment. a-c. Representative cases of spiking activity in $Apc^{WT}+control$ (grey), $Apc^{WT}+OX$ (blue), $Apc^{Pirc/+}+control$ (red) and $Apc^{Pirc/+}+OX$ (purple) as a measure of sensory encoding in unclassified spindle (a), group II (b), and group Ib (c). Black circles plot instantaneous firing rates (pps) of corresponding spike (action potential) intervals. Dashed vertical line marks onset of muscle stretch (3mm from resting length (L_0)) shown in bottom trace divided into dynamic and static phases by dark grey (150ms duration after stretch command onset) and light grey (1s duration after the dynamic phase) bars. d-f. Neuronal spiking parameters (n=31, averaged from four trials, from each neuron in each of the neuronal classes, unclassified spindle (d), group Ib (e), and group II (f)). Features represent different features of sensory stimuli and were subjected to linear discriminant (LD) analysis. Neuronal signaling was visualized in the new 3D composite space created by LD1-3. 3D ellipsoids enclosing 68% of data were computed with least-squares elliptical fitting. Effects of independent (OX or $Apc^{Pirc/+}$) and combinatorial ($Apc^{Pirc/+}+OX$) treatment are indicated by colored curved arrows.

Purple traces in Figure 30 illustrate representative firing profiles for each neuron class in $Apc^{Pirc/+}+OX$ rats. We found drastically impaired neuronal signaling across all classes.

Sensitivity to stimuli was reduced at both high and low velocity stretch (data not shown). During dynamic stimuli, we found marked reduction in the number of spikes over both stretch conditions. Neurons also failed to sustain firing. In addition, we observed fewer spikes during rapid accommodation immediately preceding signal deletion, despite constant stimulus. These data confirm that a damaging functional interaction between the systemic effects of cancer and chemotherapy is conserved across multiple classes of sensory neurons in living animals.

To quantify inferences drawn from raw data, we took an unbiased statistical approach by subjecting all signaling parameters from all neurons, classes and experimental groups to a LD analysis. This reduced complex feature space into canonical variables giving us a high-level understanding of where interaction emerges, without biased parameter selection *a priori*. Our analysis yielded three canonical variables (Figure 30d-f) that achieved overall 98.7% classification accuracy. We then visualized neuronal signaling in the new 3D composite space created by LD1-3 (Figure 30d-f) revealing a first dimension (LD1) that accounted for a large fraction of the explained variance for each class of neurons, ranging from 64-66% (Figure 30 d-f). Coincidentally, LD1 also represented the non-linear interaction between cancer and chemotherapy, that can be visualized by the 3D separation of the purple spheroid in LD1 (as was the case for group Ia).

By examining the discriminant function coefficients, we found that fast and slow threshold levels, static firing average (and number of spikes), and dynamic firing rates represent the dominant portion of the explained variance in LD1. This suggests that these parameters are most susceptible to codependent interaction and justify further quantification and validation. Line graphs in (Figure 31) show the hierarchal Bayesian modeling results for the selected parameters as well as the experimentally measured data used to power the generative models. Across all parameters and neurons classes

the codependent interaction significantly exacerbated signaling deficits. Interestingly, the balance of parameter values between neuronal classes, e.g. the relative thresholds between group Ia and Ib, appear to be conserved, which suggest a global co-regulatory process may be present. In other words, a process that governs the balance of information content from multiples neuron classes flowing to the central nervous system. Collectively, our data indicate that all muscle proprioceptors are vulnerable to neurotoxic hypo-excitability induced by chronic cancer treatment.

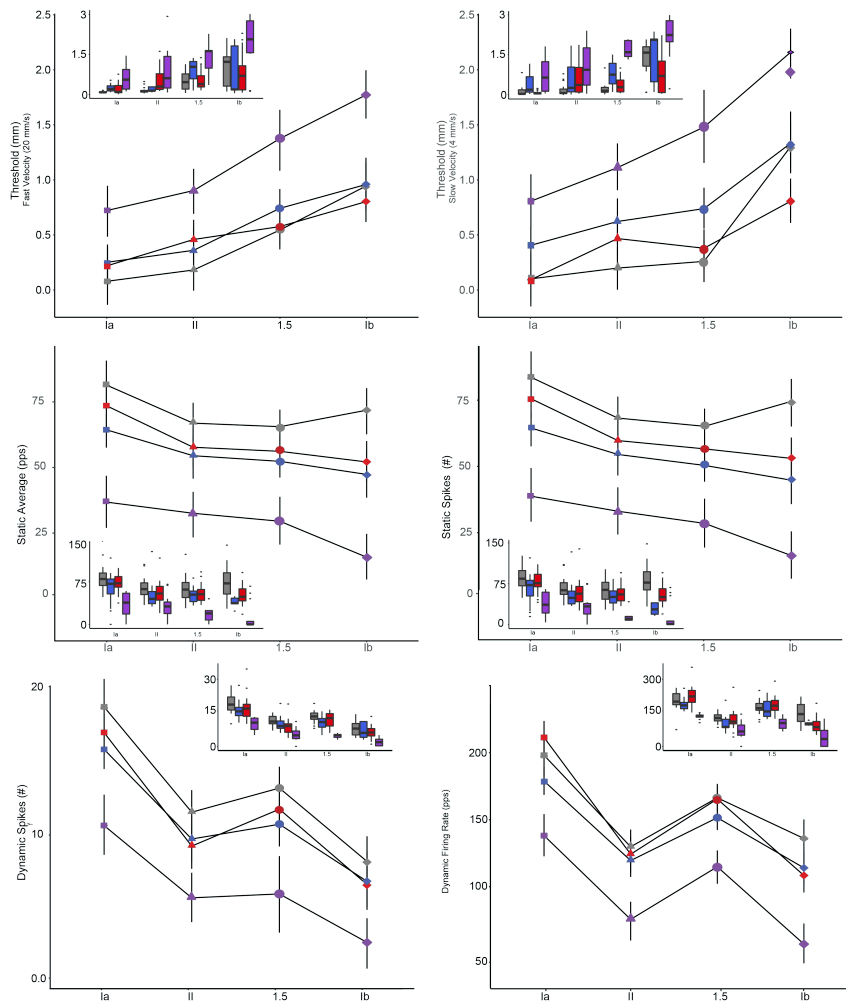


Figure 31.

Co-Suppression of Key Mechanosensory Features. Hierarchical Bayesian modeling results used to test for significant group differences of neuronal spiking parameters (six shown). Colored and shape coded points represented the empirically derived mean posterior predictive density and 95% highest density intervals (vertical lines). Statistical significance is determined when vertical lines do not overlap between parameters, i.e. 95% highest density intervals are exclusive. Insets in each model output display boxplots of experimentally measured data used in hierarchical models.

Latent Mechanosensory Features Similarly Impaired

We leveraged an unsupervised analytical approach, principal component analysis (PCA), to validate the supervised analyses performed above. PCA was simultaneously

applied to 31 parameters of mechanosensory encoding measured in response to natural stimuli for all classes and experimental groups. PCA confirmed fast and slow threshold levels, static firing average and number of spikes, and dynamic firing rates represent the parameters most indicative of groupwise separation (vectors in (Figure 32a). Neurons were then visualized in the new latent feature space created by PC1–3 where individual points represent individual neurons. Failure to adequately separate groups by either class (Figure 32b, unclassified spindle: green, group Ib: blue, group II: purple, and group Ia: yellow) or treatment group (Figure 32c, Apc^{WT} +control: grey, Apc^{WT} +OX: blue, $Apc^{Pirc/+}$ +control: red and $Apc^{Pirc/+}$ + OX: purple) indicates substantial class by treatment interaction. To overcome this, neurons were co-labeled based on class and treatment. Mean centroids were calculated and visualized in 2D projections (Figure 32d and expanded view of dotted box in Figure 32d) created from PC1-2. Vectors were calculated to show the magnitude and direction of independent (OX or $Apc^{Pirc/+}$) and combinatorial ($Apc^{Pirc/+}$ +OX) treatment effects across each class in the latent feature space. $Apc^{Pirc/+}$ consistently influenced PC2, whereas OX effects consistently acted on PC1. While $Apc^{Pirc/+}$ +OX similarly acted on PC1, the magnitude was significantly greater than that observed from OX. Interestingly, linear summation of OX and $Apc^{Pirc/+}$ effects does not accurately predict the location of $Apc^{Pirc/+}$ +OX. Collectively, our results confirm that using cancer or chemotherapy as independent predictor fails to accurately predict their combination. Further, our analyses indicate that despite unique encoding properties and firing profiles, the combinatorial effects of cancer and chemotherapy influence neuronal firing in a similar manner. This becomes evident when high dimensional parameter spaces, that accurately described neuronal firing, are simplified to low-dimensional latent variables.

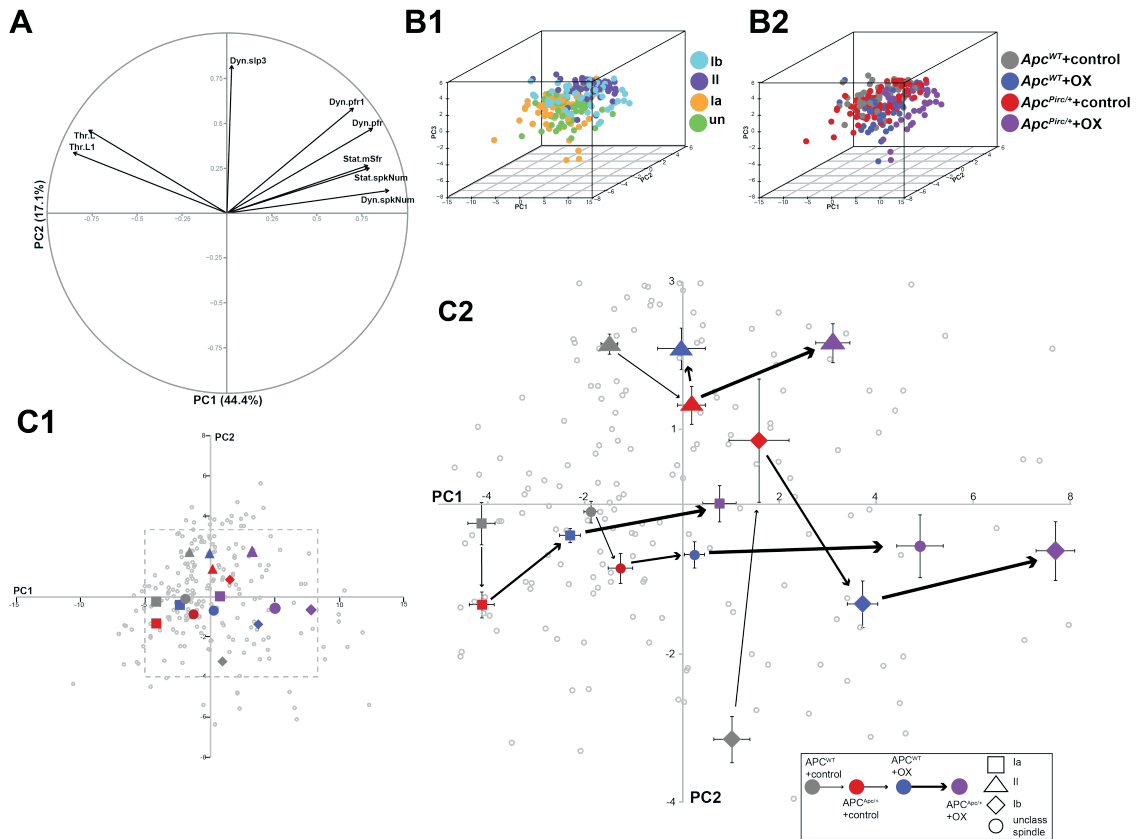


Figure 32.

Latent Mechanosensory Features Similarly Impaired Across Diverse Mechanosensory Neuron

Classes. Principal component (PC) analysis was applied to 31 parameters of mechanosensory encoding

measured in response to natural stimuli. a, vectors represent the magnitude and direction of correlation

between individual parameters and the two latent features capturing the most variance (PC1-2). b-c,

Neurons visualized in the new latent feature space created by PC1–3. Points represent individual neurons

highlighted by specific mechanosensory class (b, unclassified spindle: green, group Ib: blue, group II: purple,

and group Ia: yellow) or treatment group (c, *Apc*^{WT}+control: grey, *Apc*^{WT}+OX: blue, *Apc*^{Pirc/+}+control: red and

Apc^{Pirc/+}+ OX: purple). Neurons were co-labeled based on class and treatment and mean centroids were

calculated and visualized in the 2D projections (d) created from PC1-2. e, expanded view of dotted box in d.

Magnitude and direction of arrows demonstrates the independent (OX or *Apc*^{Pirc/+}) and combinatorial

(*Apc*^{Pirc/+}+OX) treatment effects across the latent feature space.

Population level deficits do not reflect hypoexcitable scaling

Having established codependent interactions are conserved across multiple sensory neuron classes, we aimed to understand the consequences of those deficits when the information is convolved in a population code as it is at a sensorium level. Intracellular recordings from physiologically identified sensory neurons of all four classes were used to construct population codes (ensembles of neuronal firing). We precisely time synchronized independently recorded neurons by aligning identical stimulation patterns. This allowed us to model population codes of physiologically identified neurons of precisely known locations from Apc^{WT} +control and $Apc^{Pirc/+}$ + OX animals, not possible in previous studies (Stein, Weber *et al.* 2004; Weber, Stein *et al.* 2007). Figure 33 presents the population code of 40 neurons recorded each from both Apc^{WT} +control rats (grey) and $Apc^{Pirc/+}$ + OX rats (purple). Visual inspection of the Apc^{WT} +control population reveals that while variable firing responses exist (top panel), likely reflecting the diverse encoding properties of multiple neuron classes, the average firing rate (bottom panel) closely mirrored the stimuli (bottom traces), both in onset and shape. By contrast, the sparse $Apc^{Pirc/+}$ + OX population (top panel) displayed delayed onset and reduced correlation to stimuli.

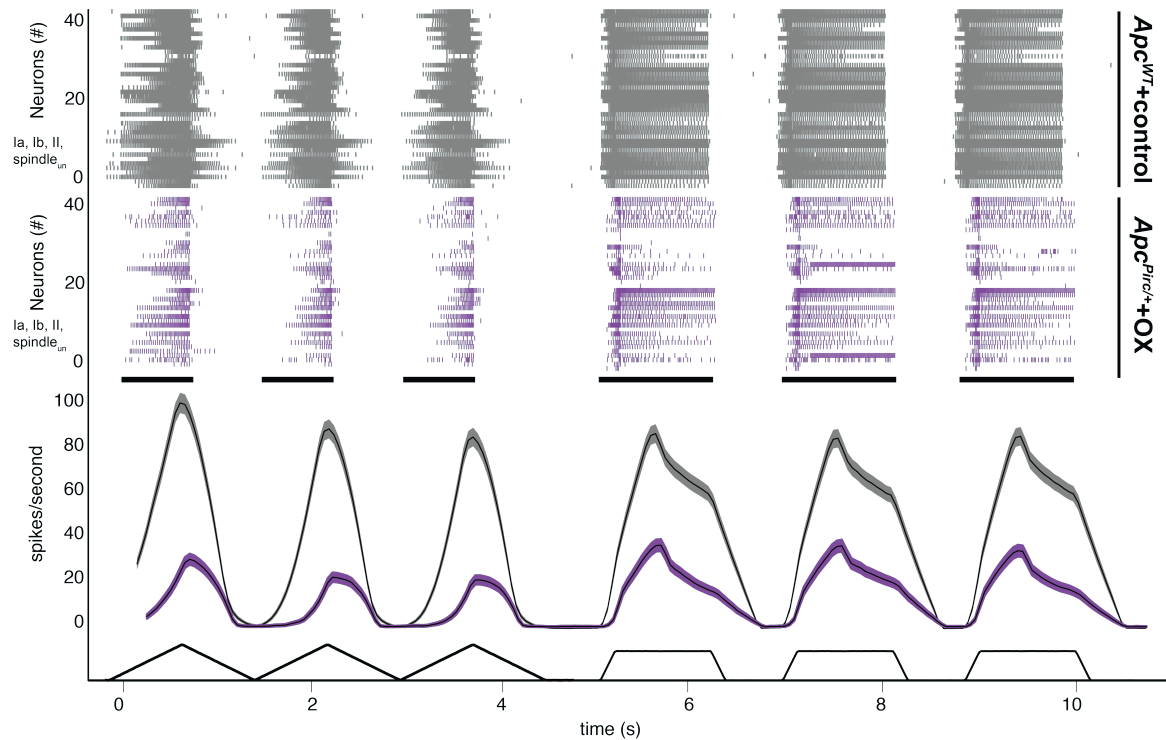


Figure 33.

Blunted Population Code. Population code of 40 neurons recorded each from both Apc^{WT} +control rats (grey) and $Apc^{Pirc/+}$ +OX rats (purple). Vertical lines in raster plot (top panel) indicate the presence of individual spiking events during a representative 10s recording as three slow (4mm/s) ramp-release followed by three, fast (20mm/s) ramp-hold-release mechanical stimuli initiate neuronal activity. Bottom panel illustrates the average firing rate (black line) and standard error (shaded region) computed from the same recording epoch as above. Both population codes were constructed from the same distribution of neuronal classes, 10 group Ia, 5 unclassified spindle, 14 group Ib, and 11 group II.

Summary

Collectively, results confirm the expected blunted population code while also providing the first evidence that the codependent interactions does not result in a simple hypoexcitable scaling, as evidence by substantial temporal dispersion.

Aim 7: Test the hypothesis that decoding of spatiotemporal features of movement from a population code of mechanosensory neurons is attenuated after chemotherapy treatment of cancer.

Aim Specific Methods

General deep learning methods

We leverage deep, recurrent artificial neural networks to discover structure in high dimensional inputs (binned ensemble neuronal firing rates). These methods are inspired by biologically plausible models of neural circuits, particularly the spinal sensory-motor circuits studied here, that learn a hierarchical representation or transformation of the input data that make prediction easier (Rumelhart, Hinton *et al.* 1988; Goodfellow, Bengio *et al.* 2016). The deep neural network utilized here, consists of a layer of computational units called neurons or nodes. The deepness refers to the number of layers between the input and output. We selected a single hidden layer that represents the LV/VI interneuronal populations that is fully connected to the output layer.

Biologically these interneuronal populations receive a vast synaptic connections from the mechanosensory neurons (input data) studied here (Vincent, Gabriel *et al.* 2017) and reside directly upstream of the motor pools (analogous to our output layer). By tuning the connection weights, the network can learn to approximate a function used for prediction, i.e. how a motor pool receiving this synaptic input could draw inferences about its previous activity. In this work we are interested in training a deep neural network to decode (extract) relevant musculoskeletal features of the rat hindlimb from activity recorded from ensembles of healthy mechanosensory neurons activity and how that ensemble of neuronal activity is altered following cancer treatment (Figure 33). This

approach allows predictions to be made of specific sensory-motor deficits not possible from analyzing spike trains alone. Because both the full structural and functional connectivity remain unknown throughout the segmental spinal circuits we chose a fully connected schema throughout as a rational starting point.

Model architecture.

The model architecture was constructed using the Keras library for Python (Chollet 2018), using TensorFlow backend (Abadi, Agarwal *et al.* 2016). The architecture relates the multidimensional input (binned neuronal firing rates) to output (musculoskeletal parameter) space, as described in Figure 34. The model considered not only the current time bin but the six-time bins that preceded and followed it to better inform its decisions about the musculoskeletal parameters. The network comprised a single layer of long-short-term memory units (LSTMs), a modification on the basic recurrent structure that minimized the impact of numerical instability during back-propagation and further improve the capture of long-term dependencies (Hochreiter and Schmidhuber 1997). The LSTM units were fully connected to an output layer with three units (length, force, stiffness) using RMSprop (Tieleman and Hinton 2012) as the optimization routine. Models were run with GPU parallelization using NVIDIA's cuDNN package (v 7.6). To combat the tendency to overfit unconstrained predictors, particularly on smaller data sets, we utilized an effective method to curb overfitting. We used a technique called dropout to prevent complex co-adaptations, or paired relationships between units in the network by allowing connections between individual units to be removed with some specified probability, range from 0-1, during training (Srivastava, Hinton *et al.* 2014; Gal and Ghahramani 2016). The specific dropout probability was set as a hyperparameter prior to training during each fold. This and other hyperparameters, e.g number LSTM units, is discussed below.

Preprocessing

Input data (neuronal activity) was z-score normalized. Output data (musculoskeletal parameter) was zero-centered. Data for training/validation/testing were preprocessed using identical approaches.

Predictive Performance

Predictive performance of models was measured as the fraction of variance accounted defined as $R^2 = 1 - \frac{\sum_i (y_i - \hat{y}_i)^2}{\sum_i (y_i - \bar{y}_i)^2}$ where \hat{y}_i are the predicted values, y_i are the true values, and \bar{y}_i is the mean value. R^2 values are reported for each musculoskeletal parameter: length, force, and stiffness. R^2 values in the range [0, 1] are interpreted in the same way as the Coefficient of Determination. Negative R^2 values are interpreted as the model injecting more variance into the process than there exists in the data set.

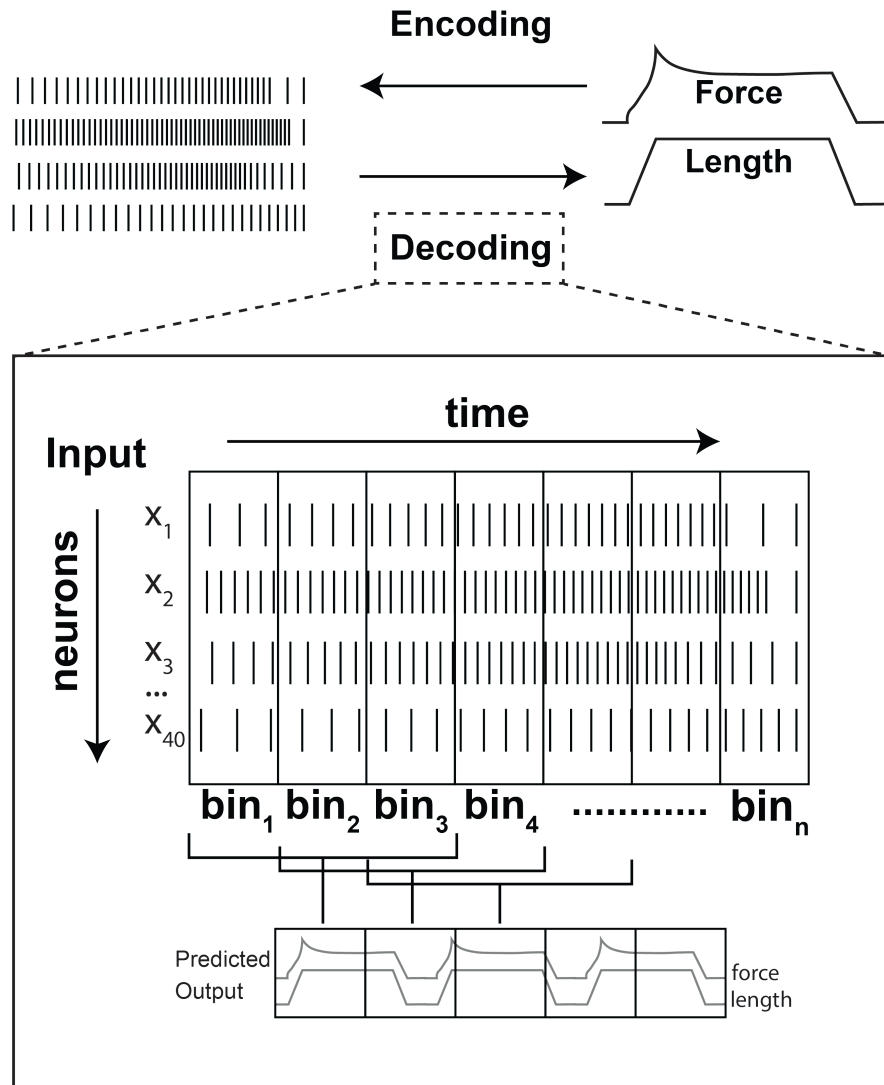


Figure 34.

Conceptual schematic of encoding and decoding processes. Encoding is the process by which static and dynamic musculoskeletal parameters (top right) is translated into ensembles of spiking neurons. Decoding is the process by which information, e.g. about the musculoskeletal parameters, is extracted from spiking activity. Bottom inset illustrates the decoding methodology via artificial neural network. To decode (predict or extract information from spikes) the output in a given time bin, the firing rates of all neurons ($N=40$) in time bins (bins=3), In this schematic, one bin preceding the output, one concurrent bin, and one following bin). Here, we show two outputs being predicted for simplicity but we report three outputs; muscle length, force, and stiffness.

Cross-validation

Models were assessed using a 10-fold cross-validation approach by splitting the data into a training, validation and testing sets (Stone 1974; Browne 2000). For each fold, a separate model was constructed, leaving that fold out for use as test data and using eight of the remaining folds as training data. The test data fold was used to compare the performance across different model forms. The one remaining fold was used as a validation data set: model performance with respect to this data set was used to select some independently optimize hyperparameters (described below) before evaluating the model for comparison with other model forms using the test data thereby eliminating any bias introduced by selecting hyperparameters on the basis of the test performance (Bishop 1996). For each fold, models were trained to minimize the mean squared error between the predicted and true musculoskeletal parameter of the training data.

Hyperparameter optimization

In addition to parameters that link the neural activity to the output variables, e.g. weights on connections in network, the model also has hyperparameters, which relate to the design of the network itself that needs to be identified prior to training. Unbiased hyperparameters (number of hidden units in the layers, amount of dropout (Srivastava, Hinton *et al.* 2014), and number of training epochs) selection was performed on each cross-validation fold. Optimization was directed to identify hyperparameters that led to the highest R^2 on the validation set using Bayesian optimization (hyperopt Python package) (Bergstra, Yamins *et al.* 2013). This algorithm uses a Bayesian-based optimization algorithm called the Tree-structured Parzen Estimator to explore a hyperparameter space across multiple epochs. Briefly, this optimization approach samples hyperparameter values from pre-defined prior distributions, uses a loss function to evaluate the current hyperparameters, and then repeats these steps using knowledge

gained from the evaluations it has already performed. After a desired number of epochs, the hyperparameter set associated with the minimal loss value across all epochs is chosen as the optimal hyperparameter set. Those hyperparameters were used to calculate the R^2 value on the testing set.

In Vivo Validation of Decoding Deficits

Biological validation of decoding results was obtained by recording synaptic potentials in triceps surae motoneurons in response mechanical stretch of the triceps surae muscles. The triceps surae muscles were stretched by 3mm at a constant velocity (20 mm/s) over 150ms rise during ramp-hold-release stretch, the muscles were held at that length for 1s, and then released to resting length at constant velocity over 150ms. Stretches were repeated for 15-20 trials at 4-s intervals then averaged.

Results

High fidelity feature extraction by healthy nervous system

Since the $Apc^{Pirc/+}$ OX population code was not a downscaled Apc^{WT} +control sensorium, the potential for information loss encouraged us to test the consequences of the $Apc^{Pirc/+}$ OX population. We employed a deep-learning algorithm (long-short-term memory network: LSTM) to test how decoding of spatiotemporal features of movement are altered after chemotherapy treatment of cancer. The process of decoding allows neurons and networks of neurons upstream of the sensorium to extract features of the spiking activity in order to draw inferences on that information, e.g. current body position or inertial loads on limbs as movements result in physical interactions with the environment. First, we aimed to understand LSTM performance when decoding the Apc^{WT} +control sensorium. Figure 35 (left) summarizes average decoding performance quantified across all 10-fold cross validation runs for LSTM trained on Apc^{WT} +control data. Results indicate highly accurate decoding of all parameters but muscle force was

consistently decoded more significantly more accurate than length or stiffness. Figure 35 (right) shows representative raw traces of three ground truths and three model predictions generated after training.

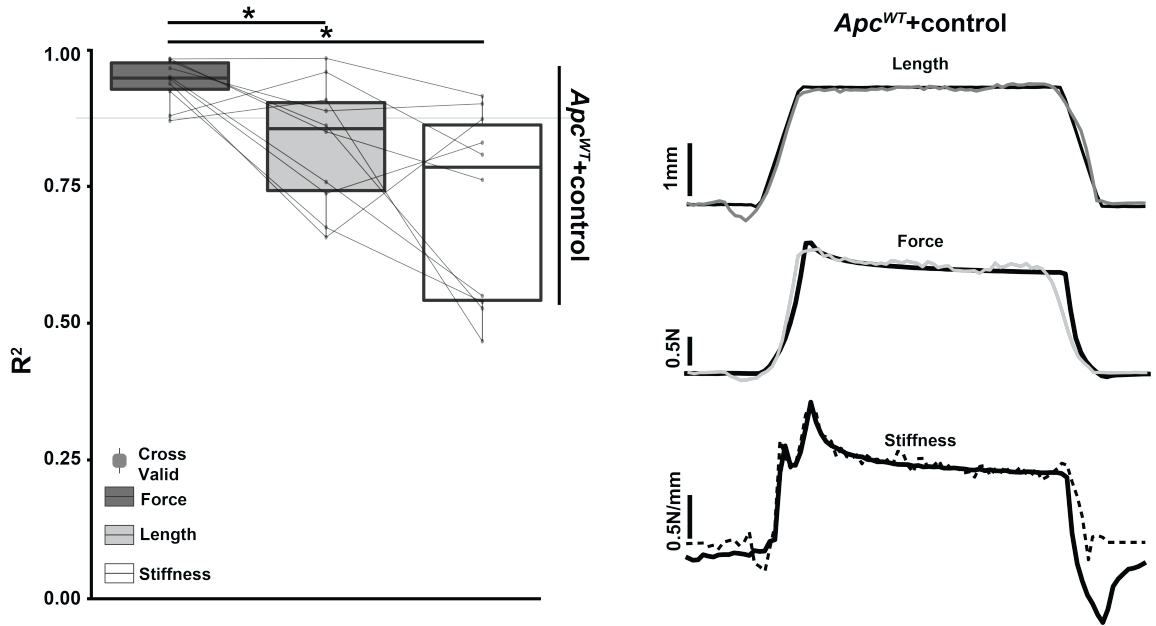


Figure 35.

High fidelity feature extraction by healthy nervous system. **a**, Average decoding performance across all 10-fold cross validation runs for model trained on Ap^{WT}+control data. Boxes represent the three outputs (mechanical stimuli) being predicted by model force, length, stiffness. **b**, Raw traces of three ground truths (black lines) and three model predictions generated after training (color coded after a). Model contained $\sim 7.5 \times 10^5$ parameters. * indicates statistically significant differences as empirically derived from hierarchical Bayesian model (stan_glm): 95% highest density intervals do not overlap.

Cancer treatment degrades accurate decoding

We then computed the LSTM model performance when tested on the Ap^{Pirc/+}+ OX population. Figure 36 illustrates the three musculoskeletal parameters with superimposed LSTM predictions for two types of stimuli, fast ramp-hold-release (a) and slow ramp-release (b). Figure 36c summarizes average decoding performance

quantified across all 10-fold cross validation runs when compared to Apc^{WT} +control model performance. Significant degradation in predictive accuracy was observed with muscle force experiencing the greatest reduction in accuracy ($R^2=-0.03\%$) while length and stiffness conserved the greatest accuracy ($R^2=20\%$ and 30.2%).

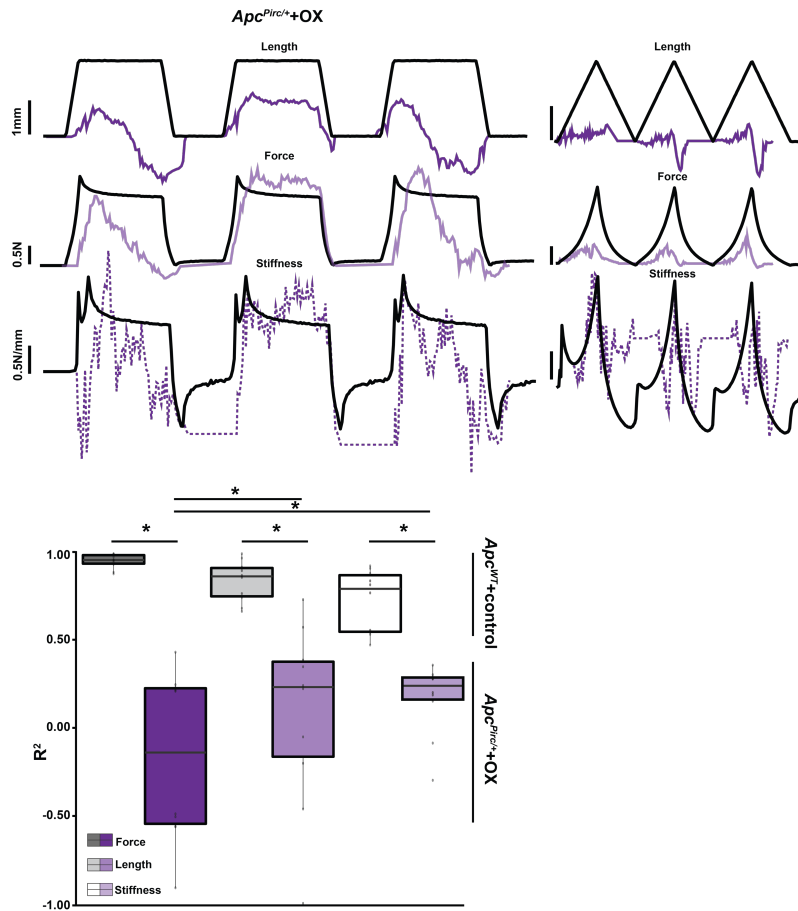


Figure 36.

Cancer treatment degrades accurate decoding. a-b, Long-short-term memory (LSTM) model predictions of mechanical stimuli for $Apc^{Pirc/+}$ + OX neuronal population (Purple) and ground truth (Black) for each of the three outputs. Model trained on Apc^{WT} +control data and tested on same number and proportion (classes) of $Apc^{Pirc/+}$ + OX neurons for various stimuli, e.g. fast ramp- hold-release (a) and slow velocity ramp-release stretches (b). b. Average decoding performance across all 10-fold cross validation runs for $Apc^{Pirc/+}$ + OX neurons when compared to Apc^{WT} +control performance. * indicates statistically significant differences as empirically derived from hierarchical Bayesian model (stan_glm): 95% highest density intervals do not overlap.

Functional consequences

We then focused on specific features of the LSTM predictions to gain insight into where functional consequences may manifest during animal (human included) movement.

Analyses quantified the features as defined in Figure 37a. We find significant errors were made for the background force and stiffness whereas background lengths were largely conserved (Figure 37b), significant lag in discriminating the onset of stimuli (Figure 37c), significantly impaired detection of sustained lengths, forces, and stiffnesses, as well as inconsistent predictions of peak forces and length changes.

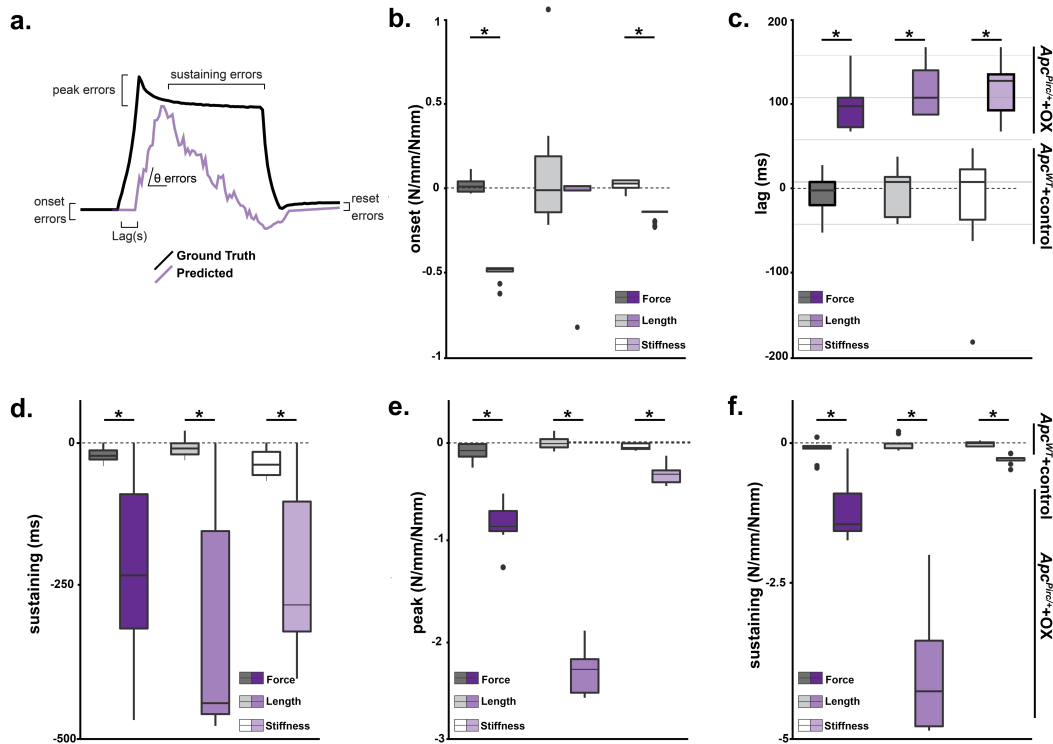


Figure 37.

Functional consequences. **a.** Analytic schematic for measuring functional errors. **b-f.** Average errors for various parameters across the three outputs (length, force, stiffness) predicted by both $Apc^{WT}+control$ and $Apc^{Pirc/+}+OX$ neuronal models. Boxes indicate average errors from ground truth, e.g. 0 is perfect prediction.

* indicates statistically significant differences as empirically derived from hierarchical Bayesian model (stan_glm): 95% highest density intervals do not overlap.

Aim 8: Test the hypothesis that learning can compensate for a corrupt population code after chemotherapy treatment of cancer.

Aim Specific Methods

Reparametrizing Decoding Model

To model how the CNS may compensate for a corrupt sensory population, restore predictive power and improve the accuracy of feature extraction, we trained a LSTM network, *de novo*, on the $\text{Apc}^{\text{Pirc/+}}$ +OX population hereafter designated LSTM_{OX}. During training, this affords the LSTM_{OX} access to ground truth. This affords iterative updating of the relationship between input data and predictive outputs and is a biologically plausible process by which the representations and transformations of neuronal input could update a unified representation of body position under static and dynamic conditions, e.g. learning or compensating. The LSTM_{OX} was trained, tested and validated, under identical conditions as described above for the LSTM.

Results

CNS cannot fully compensate

Figure 38 illustrates the three musculoskeletal parameters with superimposed LSTM_{OX} predictions. LSTM_{OX} performance was substantially improved as compared to the predictions (Figure 36a, b), yet fell significantly short of Apc^{WT} +control model performance (Figure 35). This suggested that the CNS would not be able to fully compensate for and learn a new representation of the corrupt population code that restores predictive abilities.

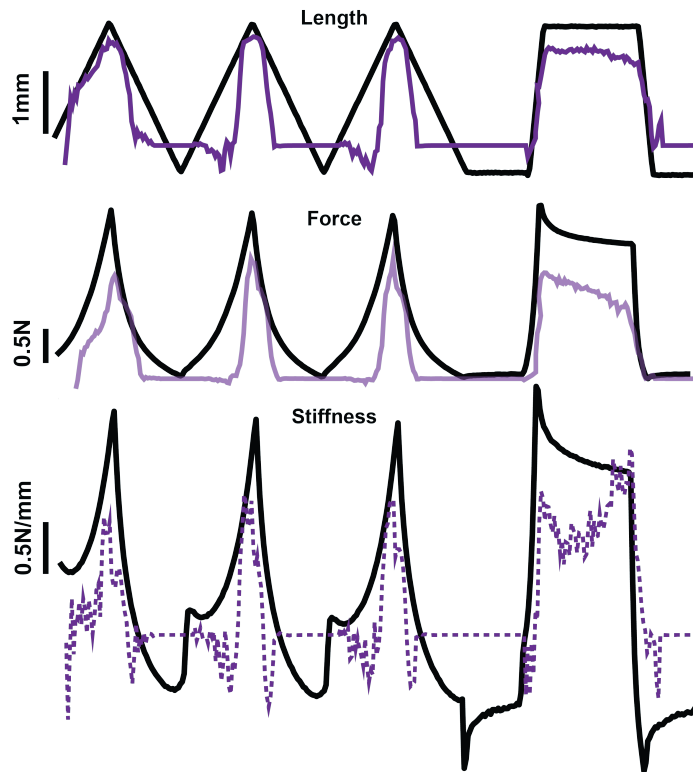


Figure 38.

CNS cannot fully compensate. Long-short-term memory (LSTM_{ox}) model predictions of mechanical stimuli for *Apc^{Pirc/+}* OX neuronal population (purple) and ground truth (black) for each of the three outputs. Model trained, tested and validated *Apc^{Pirc/+}* OX data for various stimuli, e.g. fast ramp- hold-release (right) and slow velocity ramp-release stretches (left).

Project 2: Discussion

Here we present original evidence that encoding deficits induced by chemotherapy, exacerbated by cancer are conserved across diverse classes of mechanosensory neurons. Our results show global deficiency in the population code of mechanosensory neuron population and resulting corrupt spatiotemporal decoding of movement features. Since these neurons are responsible for encoding the foundational spiking activity to generate a unified representation of body position under static and dynamic conditions,

their impairment necessarily results in upstream neurons or networks to unpredictable inferences about the bodies interaction with the external environment. By modeling the compensatory or learning processes, our results further suggest that the CNS would not have the capacity to fully compensated through learning. This inability may help to explain the lasting behavioral deficits documented in patients treated with chemotherapy.

Redundancy as a Compensatory Mechanism

Multiple classes of mechanosensory neurons combine their signals in a population code that is decoded by the CNS to regulate and perceive body movements and postures. A large portion of that population code is uniquely provided by the neurons studied here, namely Golgi tendon organs (Ib) and group Ia and II muscle spindle afferents.

Mechanosensory neurons are classically understood to encode unique time varying features of muscle mechanics. Dynamic muscle parameters are thought to be represented by group Ia afferents, static muscle parameters by group II afferents, and higher stretch threshold by group Ib afferents. Despite these unique capabilities, we have previously documented that this diverse population of neurons encode parameters that are distributed in a continuum with substantial overlap, e.g. robust Ib response to passive muscle stretch in the physiological range (Vincent, Gabriel *et al.* 2017). From this, we infer that the mechanosensory population code, is to some degree, redundant. While other have suggested that redundant codes may be unnecessary to decode information about movement (Stein, Weber *et al.* 2004), redundancy reduction can be problematic since codes maybe sensitive to noise and require careful processing when attempting to encoded and extract information (Schneidman, Bialek *et al.* 2003). In fact, the existence of redundancy may actually indicate the prevalence of a stimulus, a critical factor in developing representation and performing analysis via probabilistic computations (Barlow 2001). Outside of probabilistic encoding or decoding processes,

specific behavioral success has been attributed to sensory feedback that emerges from both distinct and redundant mechanosensory sources (Akay, Tourtellotte *et al.* 2014). Sensory feedback from muscle spindles appears to selectively influence the pattern of flexor muscles activations during locomotion, whereas the joint responses of muscle spindles and Ib afferents determine the pattern of extensor muscle firing (Akay, Tourtellotte *et al.* 2014). Taken together, redundant mechanosensory population code may protect or compensate for losses in specific classes of neurons or encoded parameters in *Apc^{Pirc/+}* OX rats or cancer survivors that have undergone chemotherapy treatment. Alternatively, dysfunctional encoding might overwhelm redundancies resulting in decompensated sensorimotor performance. Dysfunction might similarly arise during certain behaviors or phases of movement that depend on selective mechanosensory information. Population statistics, canonical analyses, and computational modeling provided rigorous tests of these hypotheses. In all cases, we find that the redundancy in the mechanosensory population code is insufficient to compensate for distributed information loss across each neuron class. This finding strengthens the evidential support that mechanosensory deficits play a prominent role in behavioral deficits observed in clinical cancer settings. These findings may also explain why *Apc^{Pirc/+}* OX rat task performance is worse than our previous observations in animals treated with OX alone, in that selective dysfunction of muscle spindles static responsiveness was compensated, by redundant signals from Ib and II neurons.

Clinical and Functional Significance

While we have yet to establish a causal relationship, impaired sensory feedback has real potential to contribute to decompensated sensorimotor performance observed in our precision behavioral tasks in awake behaving animals (Aim 5) and is likely involved in instability and ataxia's seen in cancer survivors (Burakgazi, Messersmith *et al.* 2011;

Toftagen, Overcash *et al.* 2012; Kneis, Wehrle *et al.* 2016; Marshall, Zipp *et al.* 2017; Taleb, Bouzobra *et al.* 2017). This is due to the fact that these neurons provide the CNS with its only means of detecting mechanical perturbation in the muscular system.

As we have previously documented, reasonable predictions about the consequences of corrupt signaling can be drawn from evaluating spike trains (neuronal signaling).

However, the extent to which you can draw direct comparisons between neuronal signaling and their behavioral consequences is less certain given the precise nature and features of the transformation from external stimuli to action potentials remains unknown. This makes understanding objective consequences and making real-world predictions of compromised neuronal signals challenging.

We took the first steps to overcome this limitation by using a deep-learning neuronal decoding algorithm in a novel way. Neural decoding typically uses population level data recorded from the nervous system to make predictions about variables in the outside world, e.g. arm position, that can be used to control devices (e.g., robotic limbs). In this way, neuronal decoding algorithms model the processes by which information is extracted by the CNS. We extended this analytic method to understand and quantify prediction errors that could be made when exposed to compromised neuronal signals. This allowed us to, for the first time, make quantifiable measures about what movement limitations would emerge from neuronal signaling deficit. Our analyses revealed several unexpected predictions including: both over and underestimation of applied forces, severe delays in detection of applied perturbation (in some cases adding 100s of milliseconds of delay, e.g. Figure 38), and drift in perceived length changes despite constant stimuli. These unique insights should inform the focus of future clinical evaluations and direct resources toward specific rehabilitative interventions.

CNS Implications

The CNS has a vast capacity to reorganize or develop a new representation following insult (Chen, Cohen *et al.* 2002; Anderson, Spencer-Smith *et al.* 2011; Ionta, Villiger *et al.* 2016). To investigate this role, we also took the first steps toward understanding the CNS's capacity to compensate for signaling losses by modeling the maximum decoding potential when our deep-learning neural decoding was given access to ground truth during optimization. This advantage improved the accuracy of decoding external states yet revealed that substantial errors persist. Moreover, these data further support our hypothesis that sensory encoding deficits contribute to functional limitations and that despite the impressive capacity for reorganization, the CNS would not be able to fully compensate.

It remains to be seen how deficits in primary afferent signaling propagate to higher network level dysfunction, e.g. perception, body schema despite its suspected dominant role in on-line representations (Shenton, Schwoebel *et al.* 2004). Our modeling was limited by the fact that we estimated errors that the CNS may make if it were only exposed to mechanosensory neuron populations. In this way, our modeling approximates spinal neurons populations, e.g. motoneurons, pre-motoneurons, dorsal spinocerebellar tract (DSCT) neurons, etc. best. These neuron populations have limited access to other forms of sensory information that may augment losses. While no compensation can be made for absent/corrupt primary afferent information, its precise contribution to errors in global phenomena, e.g. body schema remains to be determined since they likely emerge from the convergence of primary afferent information with a vast array of other sensory information, e.g. vestibular or visual (Driver and Spence 1998; Shimojo and Shams 2001; Stein 2012).

CHAPTER 5. CONCLUSIONS

Our overall objective was designed to correct the limitations of previous preclinical studies to gain understanding of clinically relevant *chronic* CIPN. Our unbiased integrative genomics and protein level studies revealed that clinically relevant chemotherapy induced neurotoxicity is codependent and exacerbated by cancer itself. Further, we confirm codependence is conserved in the living adult nervous system and is expressed as profound neuronal signaling dysfunction. Corrupted signaling necessarily impairs the central nervous system of information about body position, sensorimotor coordination, and error detection that likely contributes to significant errors we discovered in validated measures of sensorimotor behavior in awake behaving animals similar to those described by patients. Further, *in silico* biophysical modeling of sensory encoding deficits helped test the sufficiency of our newly identified molecular mechanisms of codependent interaction that may act as a novel clinical treatment strategy, while deep-learning decoding algorithms afforded the first insights into the extent to which sensory encoding errors might compromise information processes by the central nervous system. Collectively, our results confirm cancer as a critical feature in understanding mechanisms that contribute to neuronal dysfunction caused by chemotherapy and have the potential to explain the abject failure of current treatments for neuronal dysfunction in cancer treatment.

While the present report is limited to rats, extensive conservation of core molecular and cellular processes across mammalian species (Breschi, Gingeras *et al.* 2017) leads reasonable expectation that cancer-chemotherapy codependency, whether different in detail, extends to humans. All considered, we conclude that inattention to co-dependencies necessarily prevents the development of mechanism-based treatments

for sensory neuropathy, which remains unexplained and unabated in patients receiving chemotherapy for cancer.

Role of the Mechanical Environment in Sensory Encoding Deficits

While this work focused on developing a deeper understanding and testing specific hypotheses surrounding the role of cancer in chronic chemotherapy-induced sensory neuropathy, the sensory nervous system's (and more specifically the mechanosensory system studied in this work) inextricable link to the mechanical environment their housed in, i.e. muscular system, necessitates discussion of its potential role in our findings.

Mechanosensory function depends on the transduction of mechanical stimuli, e.g. kinetics or kinematics, by receptor endings into trains of action potentials (encoding). Any alteration to active or passive properties of muscular system or motor physiology has the potential to contribute to encoding deficits. This possibility is plausible since both chemotherapy (Sakai, Sagara *et al.* 2014; Sorensen, Petersen *et al.* 2017) and cancer (Dodson, Baracos *et al.* 2011; Aoyagi, Terracina *et al.* 2015; VanderVeen, Hardee *et al.* 2017; Schmidt, Rohm *et al.* 2018) are known to influence muscle homeostasis.

Cachexia is a well-documented adverse effect of cancer that primarily targets skeletal muscle, as opposed to anorexia or starvation which typically affects adipose tissue (Porporato 2016). It is associated with severe muscle wasting, reduced physical function, reduced tolerance to anticancer therapy, and reduced survival in a variety of clinical populations (Tisdale 2002; Fearon, Strasser *et al.* 2011). Preclinical studies have begun to identified specific mechanisms not entirely explained by the muscle atrophy (Roberts, Frye *et al.* 2013) such as: decreased tetanic force, and specific tension, along with slowed contraction rates and increases in muscle fatigability (VanderVeen, Hardee *et al.* 2017); Roberts, Frye *et al.* 2013). These findings are consistent with observations of *ex vivo* muscle preparations extracted from cancer patients, e.g. decreases in

stiffness (relative stiffness– pCa^{2+} relationship) and maximal force production per cross-sectional area, and a right-shift in Ca^{2+} activation sensitivity across both MyHC type I and IIa (Ochala and Larsson 2008). While we did not observe overt alteration in peak muscle contraction force or rate of rise during electrically evoked twitch contractions or changes to the force-length relationships during physiologic stimuli, all of the above have the potential to contribute to alterations in mechanotransduction that we may not be able to detect from our whole muscle measures.

Chemotherapy also has the potential to influence certain aspects of muscle homeostasis (Sakai, Sagara *et al.* 2014; Sorensen, Petersen *et al.* 2017). Following oxaliplatin treatment histological analysis of pretibial flexors revealed significant leftward shift in the fiber size distribution, i.e. smaller cross-sectional area, whereas whole quadriceps muscle atrophy could be detected in as little as 5 days of cisplatin treatment (Sakai, Sagara *et al.* 2014). In addition, chemotherapy induces changes consistent with myopathy including accumulation of both Ca^{2+} and lipids along with higher levels of collagen deposition present another challenge to canonical muscular architecture that could contribute to altered mechanotransduction.

While the previous discussion, centers on the independent effects of cancer and chemotherapy, the present work underscores the potential for combinatorial effects on different systems including motor physiology. This becomes credible since some effects of chemotherapy overlap those seen in cancer cachexia (Sakai, Sagara *et al.* 2014; Sorensen, Petersen *et al.* 2017). As an example, recent gene expression data suggest that changes in skeletal muscle induced by oxaliplatin may activate similar pathways to those activated during cancer cachexia (Feather, Lees *et al.* 2018). Recent preclinical data suggest even more explicit evidence of suspected interaction at a muscular systems level (Damrauer, Stadler *et al.* 2018) which is in agreement with our gross level

measure of muscle homeostasis (body weight as an analogue of muscle mass in Figure 39) that may help clarify some unexplained problems in clinical populations (Vichaya, Chiu *et al.* 2015; Vardy, Dhillon *et al.* 2016) and paucity of treatment approaches. Collectively, these results suggest that both cancer and chemotherapy treatment induced pathological changes to the muscular system may contribute to corrupt sensory encoding. Notably changes to the mechanical environment may help explain the as yet unknown cause of decreases in sensitivity (increases in threshold) for all mechanosensitive neurons studied (Aims 3, 4, and 6).

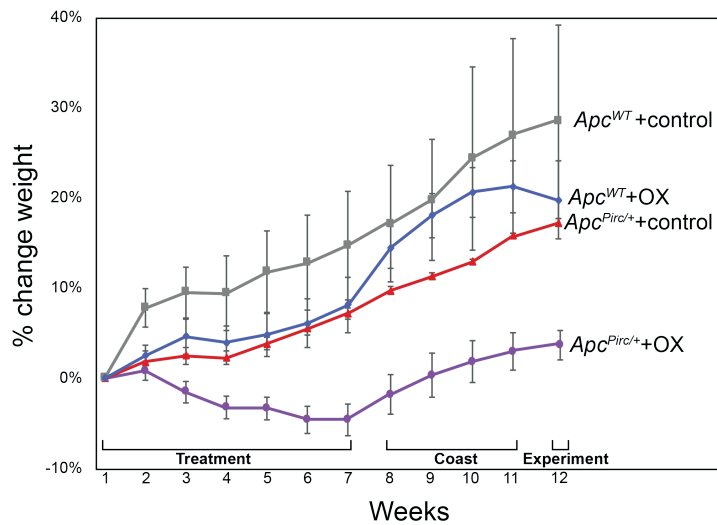


Figure 39.

Longitudinal change in animal weight. Longitudinal study of animal weights reveals systemic non-linear interaction of cancer and chemotherapy. a, Weekly weight measures tracking systemic effects of cancer and/or chemotherapy. Rats included were used for transcriptional, protein, and physiologic studies. Data are mean±s.d. from 15 *Apc*^{WT}+control, 10 *Apc*^{WT}+OX, 6 *Apc*^{Pirc/+}+control, and 8 *Apc*^{Pirc/+}+OX rats.

Role of the Motoneurons in Decompensated Task Performance

Despite having strong reason to suspect sensory encoding defects (Aim 3) are prominent players in preclinical (Aim 5) and clinical measures of decompensated task

performance and patient complaints (see Introduction), we have not established a causal link. This leaves the possibility of additional contributors. One prominent candidate is the motoneuron, the efferent component of sensorimotor behaviors. We recently identified the first evidence that chemotherapy chronically impairs firing behavior of spinal motoneurons (Housley, Nardelli *et al.* 2020 in revision). Data indicate that unstable and unpredictable repetitive firing originates in the motoneurons central integrative components, possibly as a result of imbalance in the subthreshold currents that regulate firing.

Their erratic firing necessarily disturbs steady muscle contraction, motor performance and might lead to the development of movement disorders experienced by patients following chemotherapy (Bennett, Park *et al.* 2012; Tofthagen, Donovan *et al.* 2013). Specifically, effects on motoneurons could degrade task performance at two levels. Motoneurons may act directly via altered neuromuscular control and/or indirectly by influencing sensory neuron encoding by altering the mechanical environment that sensory neurons operate in (discussed above). Direct influence of altered active neuromuscular control would be in addition to the potential corruption of intrinsic muscle homeostasis (discussed above). While previous reports have observed deficits consistent with motoneuron involvement, these studies utilized either indirect measures or focused on acute hyper-excitability which in both instances do not necessarily provide insight into the lasting signs and symptoms experienced by cancer survivors (Burakgazi, Messersmith *et al.* 2011; Tofthagen, Overcash *et al.* 2012; Kneis, Wehrle *et al.* 2016; Taleb, Bouzobra *et al.* 2017). In any event, motoneuron involvement would work to compound any effects induced independently from corrupt sensory encoding.

Evidence for Codependency.

For many studies, particularly those at the clinical level, decoupling chemotherapy-induced effects and those induced by cancer is difficult. As we have identified, no preclinical study has investigated the synergistic effect of the disease and chemotherapy for CIPN (Currie, Angel-Scott *et al.* 2018) with most opting to investigate each in isolation. Outside of CIPN, one preclinical study did examine fatigue-related behaviors in mice with Lewis Lung Carcinoma cell tumors (Wood, Nail *et al.* 2006) that received Etoposide a topoisomerase II inhibitor and member of the broadly family of alkaloid agents. Etoposide significantly reduced voluntary wheel running activity, an index of fatigue (Novak, Burghardt *et al.* 2012), above control with further reductions in activity noted in animals with tumors. Human studies only allow us to infer exacerbation of symptoms by chemotherapy on existing fatigue in cancer patients. For example, reduced muscle strength and function was observed in individuals with acute lymphoblastic leukemia diagnosis prior to treatment (Ness, Kaste *et al.* 2015). Symptoms worsened following chemotherapy treatment, which suggests a significant role of chemotherapy in the development of these symptoms. A recent large-scale observational study found increased fatigue in a cohort of individuals diagnosed with colorectal cancer that underwent chemotherapy treatment, as opposed to those that did not (Vardy, Dhillon *et al.* 2016). These few reports highlight the fact that little work has been done to investigate and test for the explicit role of interaction effects between cancer and chemotherapy in any side-effect of treatment or disease. Coupled with the abject failure of current treatment approaches for *chronic* CIPN, the above discussion underscores the importance of our findings and necessitate further study of these non-linear interactions and their effects on potential treatments.

Mechanisms of Codependency

We have now firmly established that codependent effects of chemotherapy and cancer exist at multiple levels of biological control, e.g. gene and protein expression, control neuron excitability, and behavioral performance, and that their interactions significantly exacerbate deficits at each level. We must now move to determine the underlying mechanisms (sites) of this interaction. More importantly, with the recognition that neither process is stationary with respect to time, e.g. development of cancer, accumulation of chemotherapy, and subsequent suppression of cancer, we must uncouple the temporal pattern by which these two systemic perturbations work together to influence pathophysiology of chronic CIPN (and likely other side effect that remain recalcitrant to treatment). Filling this gap in knowledge is needed to expose the most effective treatment targets or cures for chronic CIPN (Hershman, Lacchetti *et al.* 2014). Barriers to obtaining this information are formidable, given the overwhelming abundance and complexity of possible pathways identified by our multiscale approach. However, given the magnitude and multiple scales of dysregulation we observed leads us to suspect that codependent interactions may be mediated by high-levels of biological control. Such candidates include DNA methylation and hydroxymethylation, histone modification, e.g. acetylation and deacetylation and non-coding RNA regulation, e.g. miRNAs, all of which comprise global regulatory processes known as epigenetic phenomena. While it is clear that perturbation to epigenetic control may lead to alterations in gene expression which results in cellular transformation and ultimately cancer development (Lund and van Lohuizen 2004; Esteller 2008); it is less clear whether cancer itself can cause alterations to epigenetic control either directly or indirectly via systemic signaling pathways (inflammatory). Identifying the existence of such reciprocal relationships may be crucial to determine where feedback loops intersect with the known influences of chemotherapy

on epigenetic control in the nervous system of animals in preclinical study, e.g. increase H3 acetylation and decreased histone deacetylase activity (Briones and Woods 2011; Wang, Walitt *et al.* 2015). While the evidence is far from conclusive, we hypothesize that the administration of chemotherapy agents in the presence of systemic influence of cancer initiates a cascade of biological changes, with transient alterations in low levels of biological control, e.g. hyperexcitability: a positive acute effect observed throughout the nervous system and changes in inflammatory milieu that ultimately converge on high level epigenetic alterations that persist long after treatment cessation and disease free survival. These epigenetic changes would then lead to gene expression changes, altering metabolic activity and neuronal alterations that are responsible for generating clinically relevant *chronic* CIPN. Effects of epigenetic alterations may also help explain heterogeneity in patient populations. A recent study indicated a strong association between the strength of persistent methylation changes and developed persistent neuropsychological symptoms, whereas patients with preserved methylation status were protected from chronic symptoms (Lyon, Elmore *et al.* 2014).

Alternatively, lower levels of biologic control might be the center of codependent interactions between cancer and chemotherapy that ultimately result in exacerbated *chronic* neurologic deficits. Fortunately, our unbiased transcriptional analyses afforded some insight into this possibility. Our data point to changes in oxidative, inflammatory, and metabolic pathways as likely culprits. While previous studies suggest changes to systemic inflammatory milieu are transient (Wang, Walitt *et al.* 2015), our data point to both genetic (Aim 1) and protein (Aim 2) level pathway disruption that persists after treatment cessation. Differences may be attributable to divergence in experimental targets. Our preclinical studies afforded unique tissue specific focus on the sensory nervous system, while prior work was limited to experimental targets accessible in

clinical populations namely minimally invasive sampling from blood. Moreover, the expression of persistent changes in low levels of biologic control simply rules in their potential role and does not rule out the possibility that they emerge from high-level epigenetic alterations that this work cannot currently disentangle.

In summary, innumerable pathways and/or loci exist that could house interaction. It is tempting then to speculate where and when interactions are taking place; however, despite definitive evidence that clinically relevant sensory neuropathy is codependent on cancer and chemotherapy, it is futile to attempt to constrain possibilities at this time because we simply don't have adequate spatiotemporal resolution across the relevant tissue specific domains. That being said, we are hopeful that the trends in big data and powerful computational modeling, some of which we developed in this project, will coincide with the acquisition of the requisite data to answer this most fundamental question.

Supplemental Tables

Supplemental Table 1.

Supplemental Table 1. Members of cluster C1a: n=350.

1389043_at	1371781_at	1383860_at	1371785_at	1382059_at
1369772_at	1390519_at	1387558_at	1384260_at	1377187_at
1382074_at	1388812_at	1369885_at	1367973_at	1384147_at
1367499_at	1371550_at	1373225_at	1377340_at	1387606_at
1378552_at	1387153_at	1370023_at	1393550_at	1385180_at
1389675_at	1369352_at	1374468_at	1378925_at	1376645_at
1374806_at	1367825_at	1377210_at	1379935_at	1377387_a_at
1367715_at	1390535_at	1373984_at	1372520_at	1377019_at
1392107_at	1387132_at	1368353_at	1372729_at	1368473_at
1369814_at	1378005_at	1372691_at	1380229_at	1393553_at
1370928_at	1371019_at	1367712_at	1397437_at	1375041_at
1374228_at	1391543_at	1385869_at	1377103_at	1374137_at
1397916_s_at	1375866_at	1369191_at	1391643_at	1369035_a_at
1376737_at	1369012_at	1393456_at	1379311_at	1376425_at
1371529_at	1378126_at	1388944_at	1380772_at	1377380_at
1384389_at	1391095_at	1393730_at	1372211_at	1383661_at
1371697_at	1392267_at	1384294_at	1371194_at	1377310_at
1385627_at	1374626_at	1388722_at	1388587_at	1392640_at
1369778_at	1372579_at	1388924_at	1387343_at	1388666_at
1373219_at	1368489_at	1373224_at	1382351_at	1375901_at
1368370_at	1367721_at	1378800_at	1391042_at	1384993_at
1380414_at	1371237_a_at	1376151_a_at	1382379_at	1394953_at
1390571_at	1388271_at	1392818_at	1396217_at	1382275_at

Supplemental Table 1 continued

1388528_at	1379910_at	1369871_at	1378440_at	1384381_at
1368585_at	1398482_at	1370051_at	1393563_at	1369738_s_at
1374857_at	1371644_at	1368487_at	1393316_at	1382404_at
1367938_at	1370257_at	1373623_at	1372414_at	1374422_at
1375714_at	1393728_at	1376775_at	1373554_at	1368947_at
1380972_at	1376100_at	1376144_at	1387610_at	1386181_at
1371792_at	1367741_at	1380110_at	1383935_at	1368856_at
1382527_at	1383486_at	1368224_at	1369550_at	1368527_at
1369055_at	1370080_at	1372236_at	1377768_at	1370141_at
1371824_at	1374474_at	1377049_at	1388170_at	1373035_at
1387319_at	1378420_at	1381775_at	1383354_a_at	1371079_at
1388858_at	1382154_at	1376891_at	1391582_at	1384507_at
1374570_at	1368266_at	1373975_at	1376628_at	1373062_at
1383993_at	1387090_a_at	1387050_s_at	1369391_at	1397848_at
1373499_at	1372599_at	1373286_at	1374911_at	1374113_at
1382950_at	1372752_at	1391026_at	1373730_at	1388672_at
1372750_at	1374758_at	1386552_at	1390391_at	1371988_at
1373421_at	1392502_at	1398706_at	1386611_at	1387995_a_at
1368420_at	1389742_at	1383574_at	1384063_at	1388482_at
1387868_at	1385568_at	1373989_at	1377221_at	1371974_at
1387037_at	1387769_a_at	1397304_at	1376204_at	1377761_at
1367940_at	1371713_at	1384968_at	1376125_at	1387959_at
1390969_at	1368645_at	1368332_at	1398455_at	1388054_a_at
1387202_at	1386888_at	1368014_at	1389569_at	1371040_at
1389754_at	1378196_at	1368361_a_at	1377688_at	1389295_at
1369737_at	1382315_at	1374473_at	1387453_at	1373310_at

Supplemental Table 1 continued

1376102_at	1376648_at	1373590_at	1383489_at	1370650_s_at
1388149_at	1369619_at	1381923_at	1370047_at	1369496_at
1382919_at	1368892_at	1369766_at	1386870_at	1388686_at
1396163_at	1376976_at	1390943_at	1386660_at	1376867_at
1376481_at	1385450_at	1387389_at	1393331_at	1367795_at
1394160_at	1373403_at	1368921_a_at	1382533_at	1378074_at
1392881_at	1394047_at	1393825_at	1368924_at	1397527_at
1387759_s_at	1393516_at	1370773_a_at	1368853_at	1385753_at
1370177_at	1380318_at	1369845_at	1387824_at	1387585_at
1395765_at	1369973_at	1370406_a_at	1369781_at	1390801_at
1392946_at	1370445_at	1385857_at	1393480_at	1380054_at
1371450_at	1370595_a_at	1395789_at	1383180_at	1369222_at
1370452_at	1370606_at	1398273_at	1385217_at	1390262_a_at
1385827_at	1379312_at	1370781_a_at	1368980_at	1380611_at
1388485_at	1391808_at	1395620_at	1384950_at	1369577_at
1383655_at	1368931_at	1395840_at	1378261_at	1385808_at
1368015_at	1379500_at	1368864_at	1368941_at	1368758_a_at
1393477_at	1387952_a_at	1382199_at	1395696_at	1368962_at
1383949_at	1393105_at	1386106_at	1369421_at	1370757_at
1368254_a_at	1383551_at	1381611_at	1369069_at	1369428_a_at
1389380_at	1370624_at	1371166_at	1388233_at	

Supplemental Table 2.

Supplemental Table 2. Members of cluster C2b: n=632.

1395359_at	1383849_at	1379412_at	1381958_at	1367728_at
1377617_at	1376865_at	1398217_at	1384133_at	1375396_at
1385422_at	1394079_at	1378003_at	1390983_at	1369628_at
1379338_at	1385393_at	1370260_at	1388167_at	1380062_at
1393813_at	1370932_at	1379578_at	1370432_at	1379555_at
1368939_a_at	1395154_at	1373566_at	1387146_a_at	1382118_at
1396803_at	1381115_at	1384182_at	1368080_at	1382265_at
1380144_at	1394243_at	1376967_at	1389214_at	1392840_at
1393596_at	1388000_at	1371003_at	1377923_at	1397700_x_at
1382312_at	1383066_at	1381021_at	1367860_a_at	1398716_at
1391689_at	1391305_at	1380172_at	1373432_at	1396141_at
1383334_at	1395714_at	1394347_at	1394574_at	1379715_at
1390486_at	1368858_at	1375523_at	1388101_at	1369044_a_at
1394972_at	1376194_at	1369742_at	1372668_at	1391758_at
1392738_at	1383811_at	1382064_at	1392166_at	1368411_a_at
1380475_at	1385431_at	1380371_at	1395535_at	1380730_at
1377906_at	1368825_at	1394746_at	1386089_at	1369678_a_at
1395100_at	1370114_a_at	1376725_at	1370948_a_at	1391838_at
1390706_at	1375542_at	1390813_at	1393702_at	1397201_at
1395923_at	1384648_at	1383053_x_at	1379485_at	1384355_at
1396207_at	1384812_at	1383455_at	1382620_at	1380063_at
1383786_at	1374780_at	1370935_at	1384573_at	1397241_at
1379615_at	1391598_at	1392249_at	1376299_at	1395358_at
1397335_at	1382812_at	1391170_at	1387964_a_at	1382565_at
1381394_at	1382171_at	1374803_at	1378775_at	1394699_at

Supplemental Table 2 continued

1396676_at	1391906_at	1374708_at	1390136_at	1375640_at
1384728_at	1382658_at	1374144_at	1383240_at	1395201_at
1387406_at	1393418_at	1376170_at	1393368_at	1374448_at
1397505_at	1370955_at	1385887_at	1391139_at	1368514_at
1393866_at	1397851_at	1387854_at	1368993_at	1395794_at
1397573_at	1392566_at	1367563_at	1393576_at	1373676_at
1392269_at	1376770_at	1389546_at	1390423_at	1398387_at
1382286_at	1376733_at	1373648_at	1370831_at	1371518_at
1380195_at	1394985_at	1390404_at	1392799_at	1398354_at
1389894_at	1396612_at	1372758_at	1372480_at	1392935_at
1389986_at	1385087_at	1375138_at	1379755_at	1372101_at
1395092_at	1376208_at	1387024_at	1383827_at	1373151_at
1381967_at	1369093_at	1393663_at	1385243_at	1389003_at
1369159_at	1395105_at	1387767_a_at	1386979_at	1388592_at
1390277_at	1371361_at	1372440_at	1390480_at	1391556_at
1392730_at	1368087_a_at	1390429_at	1388742_at	1390411_at
1390340_a_at	1370946_at	1388392_at	1370907_at	1387040_at
1375739_at	1377753_at	1388618_at	1371430_at	1398258_at
1391285_at	1376313_at	1387897_at	1373521_at	1389157_at
1380696_at	1383013_at	1375862_at	1370302_at	1373122_at
1397666_at	1389441_at	1377821_at	1387112_at	1373130_at
1369810_at	1390728_at	1391848_at	1374216_at	1382108_at
1390655_at	1367968_at	1390569_at	1375726_at	1392597_at
1398125_at	1375857_at	1389306_at	1389711_at	1382732_at
1382920_at	1385779_at	1374535_at	1376700_at	1387313_at
1394392_at	1383222_at	1384792_at	1379444_at	1370956_at
1381644_at	1374241_at	1370950_at	1398362_at	1370895_at

Supplemental Table 2 continued

1375266_at	1372643_at	1384386_at	1382524_at	1374974_at
1368202_a_at	1379345_at	1382561_at	1374283_at	1385202_at
1391448_at	1369955_at	1396255_at	1378544_at	1374546_at
1388557_at	1370951_at	1395251_at	1388157_at	1389562_at
1368671_at	1368989_at	1396154_at	1375444_at	1374171_at
1380133_at	1395590_at	1380363_at	1373759_at	1373658_at
1371847_at	1368388_at	1384639_at	1387260_at	1375030_at
1373538_at	1372926_at	1393606_at	1397884_at	1385367_at
1391012_at	1393933_at	1371173_a_at	1386935_at	1372479_at
1375709_at	1395157_at	1373358_at	1368453_at	1387094_at
1389553_at	1385191_at	1369172_at	1379803_at	1390159_at
1384707_at	1385493_at	1397525_at	1371104_at	1390300_at
1371394_x_at	1379822_at	1397164_at	1387793_at	1379568_at
1385527_at	1392178_at	1377445_at	1375214_at	1392157_at
1367971_at	1371186_at	1369248_a_at	1375531_at	1368542_at
1390738_at	1393558_at	1385364_at	1393433_at	1382914_at
1367517_at	1385825_at	1375721_at	1393860_at	1389763_at
1393808_at	1370693_a_at	1393198_at	1385641_at	1391167_at
1382691_at	1379516_at	1379397_at	1398591_at	1372069_at
1372110_at	1370032_at	1395799_at	1398256_at	1392785_at
1386943_at	1386041_a_at	1369323_at	1368290_at	1387454_at
1368090_at	1395721_at	1382478_at	1375043_at	1384841_at
1371310_s_at	1388034_at	1378666_at	1372389_at	1392587_at
1373911_at	1387367_at	1393910_at	1386995_at	1386026_at
1370155_at	1397983_at	1387563_at	1368321_at	1382134_at
1388422_at	1371069_at	1387998_at	1373401_at	1382535_at
1368861_a_at	1387760_a_at	1368589_at	1387060_at	1368728_at

Supplemental Table 2 continued

1382599_at	1377781_at	1380825_at	1394837_at	1398020_at
1384617_at	1384513_at	1378548_at	1384890_at	1382068_at
1389235_at	1376129_at	1378628_at	1396450_at	1393594_at
1373544_at	1390351_at	1398130_at	1391523_at	1395030_at
1386947_at	1377651_at	1385156_at	1394416_at	1397453_at
1392929_at	1375538_at	1384692_at	1375468_at	1375782_at
1381449_s_at	1379506_at	1376388_at	1382847_at	1393674_at
1382454_at	1394834_at	1380701_at	1368242_at	1395264_at
1368146_at	1381817_at	1393995_at	1377151_at	1381121_at
1387450_at	1391552_at	1390302_at	1396952_at	1397690_at
1386811_at	1380685_at	1392311_at	1376742_at	1373972_at
1376569_at	1385889_at	1395436_at	1391863_at	1389104_s_at
1389974_at	1390942_at	1397120_at	1390733_at	1394467_at
1376463_at	1390077_at	1395130_at	1371776_at	1380693_at
1395744_at	1394727_at	1396773_at	1390100_s_at	1397999_at
1394891_at	1379511_at	1378486_at	1396502_at	1378062_at
1379763_at	1398528_at	1379722_at	1380738_at	1391304_at
1377629_at	1381402_at	1392650_at	1377589_at	1375577_at
1386064_at	1392182_at	1377305_at	1396066_at	1395365_at
1386707_at	1380777_at	1382951_at	1380882_at	1397786_at
1379058_at	1378745_at	1377212_at	1392055_at	1395205_at
1381175_at	1376531_at	1397608_at	1393548_at	1376938_at
1382413_at	1390743_at	1378682_at	1378161_at	1378814_at
1390723_at	1396894_at	1382911_at	1371771_at	1398225_at
1392555_at	1395521_at	1397422_at	1383214_at	1396775_at
1389996_at	1382020_at	1396877_at	1379089_at	1396135_at
1398445_at	1394330_at	1396957_at	1390345_at	1381253_at

Supplemental Table 2 continued

1368841_at	1384969_at	1380154_at	1385164_at	1379150_at
1395460_at	1380168_at	1381668_at	1381133_at	1377377_at
1392026_at	1368320_at	1379815_at	1383479_at	1380087_at
1376667_at	1383982_at	1370991_at	1394848_at	1374263_at
1376917_at	1394714_at	1391975_at	1376524_at	1392368_at
1394778_at	1391701_at	1386102_at	1393029_at	1395335_at
1387350_at	1397673_at	1378099_at	1385091_at	1390320_at
1389908_at	1375449_at	1395249_at	1397004_at	1396965_at
1380541_at	1384380_at	1393879_at	1379594_at	1397624_at
1376138_at	1382749_at	1381125_at	1375689_at	1382982_at
1376096_a_at	1391160_at	1391841_at	1392846_at	1392017_at
1376750_at	1388604_at	1397692_at	1396252_at	1390671_at
1382229_at	1377045_at	1381646_at	1396850_at	1391579_at
1379779_at	1393662_at	1395772_at	1385177_at	1375217_at
1381489_at	1384146_at	1397153_at	1378604_at	1377208_at
1385453_at	1392704_at	1396254_at	1373534_at	1391196_at
1381985_at	1393692_at	1374786_at	1378038_at	1394729_at
1372911_at	1380097_at	1378367_at	1395728_at	1380940_at
1375767_at	1368887_at	1377919_at	1394283_at	
1391209_at	1379753_at	1381472_at	1397217_at	
1379936_at	1398131_at	1396791_at	1381210_at	

Supplemental Table 3.

Supplemental Table 3. Members of cluster C2a: n=636.

1396348_at	1380050_at	1382027_at	1385608_at	1368154_at
1385668_at	1374572_at	1384724_at	1374565_at	1370097_a_at
1389172_at	1377169_at	1373661_a_at	1389232_at	1387093_at
1379971_at	1386881_at	1389244_x_at	1378252_at	1370333_a_at
1397317_at	1392234_at	1390406_at	1383218_at	1392569_at
1384996_at	1380267_at	1376285_at	1384971_at	1388469_at
1381732_at	1395204_at	1384515_at	1382252_at	1374016_at
1374043_at	1388725_at	1389720_at	1373374_at	1373725_at
1380941_at	1393641_at	1385432_at	1375654_at	1373288_at
1386059_at	1392722_at	1392521_at	1376368_at	1370048_at
1367902_at	1389697_at	1389918_at	1398360_at	1377353_a_at
1389734_x_at	1383008_at	1374615_at	1388425_at	1372042_at
1389413_at	1393552_x_at	1380312_at	1375905_at	1371942_at
1391637_at	1381902_at	1377792_at	1371150_at	1368344_at
1382173_at	1387571_at	1383453_at	1382072_at	1376688_a_at
1373740_at	1382296_at	1393806_at	1385200_at	1368474_at
1398732_at	1376036_at	1379075_at	1393398_at	1388426_at
1397610_at	1385252_at	1384420_at	1398661_at	1377637_at
1373748_at	1378094_at	1376263_at	1393012_at	1393336_at
1385275_at	1379688_at	1384864_at	1379281_at	1382613_at
1379766_at	1384392_at	1382096_at	1373210_at	1367922_at
1383020_at	1397808_at	1371643_at	1392971_at	1377156_at
1389034_at	1390148_a_at	1372966_at	1391911_at	1377946_at
1379253_at	1370391_at	1398578_at	1373017_at	1395819_at
1395439_at	1384869_at	1374871_at	1393460_at	1396833_at

Supplemental Table 3 continued

1392972_at	1393228_at	1384535_at	1383058_at	1370414_at
1390436_at	1375622_at	1377632_at	1380387_at	1370531_a_at
1389586_at	1391447_at	1372125_at	1388569_at	1397511_at
1392943_at	1374652_at	1396383_at	1376344_at	1385051_at
1394761_at	1381190_at	1395472_at	1389617_at	1398250_at
1396009_at	1388745_at	1395644_at	1384310_at	1392118_at
1376082_at	1389648_at	1373659_at	1379200_at	1385692_at
1389305_at	1373270_at	1368919_at	1394033_at	1388385_at
1389229_at	1384211_at	1393876_at	1393691_at	1367887_at
1374874_at	1374746_at	1389612_at	1390881_at	1382525_at
1372294_at	1388949_at	1383414_at	1371015_at	1372672_at
1376105_at	1373410_at	1378397_at	1388298_at	1372213_at
1382630_at	1376575_at	1392928_at	1388211_s_at	1383743_at
1378645_at	1376674_at	1380822_at	1368930_at	1377392_at
1376868_at	1378049_at	1390037_at	1391383_at	1399019_at
1383840_at	1393345_at	1384699_at	1368381_at	1384505_at
1384940_at	1393226_at	1380810_at	1396316_at	1381574_at
1380091_at	1382458_at	1381208_at	1370024_at	1373903_at
1385798_at	1391904_at	1392170_at	1379374_at	1370235_at
1375984_at	1393575_at	1373484_at	1390964_at	1374908_at
1382084_at	1395410_at	1383439_at	1374475_at	1389221_at
1375001_at	1376785_at	1371530_at	1396001_at	1386718_at
1379347_at	1381131_at	1394678_at	1378324_at	1398255_at
1370420_at	1381591_at	1383920_at	1370823_at	1377375_at
1389705_at	1383197_at	1384081_at	1389622_at	1393028_at
1377342_s_at	1382882_x_at	1395126_at	1371052_at	1368674_at
1367989_at	1367659_s_at	1374403_at	1368587_at	1377455_at

Supplemental Table 3 continued

1388876_at	1378601_at	1376028_at	1384709_at	1384178_at
1392215_at	1379614_at	1379948_at	1395000_at	1382558_at
1368554_at	1397343_at	1375369_at	1390459_at	1394497_at
1383546_at	1379669_at	1372775_at	1397246_at	1368703_at
1382358_at	1379824_at	1382976_at	1371363_at	1380471_at
1377878_at	1378480_at	1379300_at	1380459_at	1380045_at
1397652_at	1374104_at	1380027_at	1377064_at	1371429_at
1383225_at	1375990_a_at	1391117_at	1376045_at	1385912_at
1390283_at	1370657_at	1389132_at	1378878_at	1374558_at
1370157_at	1375983_at	1390940_at	1382190_at	1378164_at
1374762_at	1380577_at	1395353_at	1370845_at	1376878_at
1373908_at	1368008_at	1370833_at	1380563_at	1375658_at
1370310_at	1372587_at	1378155_at	1390518_at	1380228_at
1389161_at	1369133_a_at	1375305_at	1369944_at	1375231_a_at
1370068_at	1382276_at	1397194_at	1388939_at	1392595_at
1374496_at	1377914_at	1394964_at	1385333_at	1378048_at
1390138_at	1376779_at	1385981_at	1368005_at	1387111_at
1373696_at	1389999_at	1378409_at	1368322_at	1369751_at
1378320_at	1392932_at	1370307_at	1367562_at	1385876_at
1370530_a_at	1393491_at	1398251_a_at	1380142_at	1389324_at
1367811_at	1377908_at	1391803_at	1369135_at	1371045_at
1383086_at	1389995_at	1382510_at	1380248_at	1368339_at
1376084_a_at	1379469_at	1376771_at	1388116_at	1376998_a_at
1398453_at	1367844_at	1379370_at	1368612_at	1376240_at
1384273_at	1376516_at	1383284_at	1379997_at	1374200_at
1383721_at	1398351_at	1385006_at	1386833_at	1378802_at
1373818_at	1376355_at	1392915_at	1394375_x_at	1370106_at

Supplemental Table 3 continued

1391618_at	1368555_at	1387470_at	1386261_x_at	1395184_at
1373161_at	1380088_at	1393356_at	1389404_at	1373065_at
1393974_at	1380616_at	1385248_a_at	1374530_at	1372585_at
1377840_at	1384127_at	1383263_at	1367700_at	1373596_at
1371352_at	1373881_at	1393210_at	1370960_at	1377452_at
1380175_at	1375247_at	1367631_at	1376398_at	1367939_at
1376063_at	1387789_at	1372615_at	1382905_at	1373000_at
1368295_at	1368563_at	1392510_at	1383852_at	1397548_at
1379677_at	1393259_at	1372647_at	1388920_at	1371475_at
1380405_at	1389490_at	1373175_at	1387348_at	1393330_at
1387164_at	1389059_at	1368380_at	1389662_at	1389873_at
1375660_at	1387323_at	1369633_at	1386901_at	1372297_at
1374257_at	1368047_at	1372818_at	1370816_at	1377239_at
1373642_at	1371595_at	1374273_at	1379057_at	1374544_at
1370334_at	1387655_at	1375638_at	1374444_at	1372870_at
1377943_at	1382278_at	1384770_at	1375856_at	1386128_at
1388511_at	1381498_at	1383946_at	1382050_at	1368558_s_at
1389475_at	1392741_at	1388176_at	1396150_at	1390914_at
1370959_at	1396152_s_at	1376708_at	1370019_at	1367850_at
1371924_at	1388201_at	1376937_at	1372273_at	1372305_at
1386899_at	1381179_at	1368533_at	1368170_at	1373032_at
1392672_at	1370166_at	1388880_at	1372111_at	1374527_at
1394451_at	1370131_at	1379379_at	1386911_at	1393227_at
1373240_at	1393281_at	1382078_at	1371815_at	1389649_at
1372070_at	1389905_at	1377642_at	1373348_at	1382825_at
1387886_at	1389423_at	1375962_at	1376394_at	1368270_at
1395003_at	1369181_at	1390800_a_at	1370982_at	1383189_at

Supplemental Table 3 continued

1373523_at	1393249_at	1367679_at	1379344_at	1374247_at
1368482_at	1379760_at	1370882_at	1385047_x_at	1382184_at
1370987_at	1397958_at	1392074_at	1393109_at	1384298_at
1384837_at	1387113_at	1382531_at	1376047_at	1393038_at
1368463_at	1370516_at	1379295_at	1373829_at	1369725_at
1385213_at	1381311_at	1390798_at	1388784_at	1373785_at
1392515_at	1370382_at	1367912_at	1382692_at	1392813_at
1389696_at	1385465_at	1397736_at	1376457_at	1383658_at
1398467_at	1389123_at	1385572_at	1388730_at	1390849_at
1393387_at	1398304_at	1383708_at	1370449_at	1384195_at
1394766_at	1372299_at	1389783_s_at	1370301_at	1392965_a_at
1388164_at	1387029_at	1393688_at	1391812_at	1374730_at
1391067_at	1370883_at	1372200_at	1387022_at	1385682_at
1379404_at	1370383_s_at	1398246_s_at	1370864_at	1391630_at
1398407_at	1389006_at	1370202_at	1387922_at	1390510_at
1392655_at	1373575_at	1367791_at	1386912_at	1371913_at
1377835_at	1371033_at	1391977_at	1389403_at	1381145_at
1385832_s_at	1368006_at	1372029_at	1391341_at	1368395_at
1373490_at	1370822_at	1368027_at	1378720_at	
1378193_at	1390420_at	1380894_at	1390348_at	
1374778_at	1387947_at	1367749_at	1385978_at	
1373164_at	1370154_at	1373932_at	1392265_s_at	

Supplemental Table 4

Supplemental Table 4. Members of cluster C2c: n=570.

1370949_at	1391719_at	1378595_at	1382308_at	1381229_at
1384394_at	1379664_at	1391794_at	1395836_at	1393454_at
1382307_at	1393564_at	1392854_at	1377232_at	1384509_s_at
1391625_at	1391416_at	1398846_at	1377427_at	1384766_a_at
1379571_at	1397535_at	1392054_at	1395064_at	1381410_a_at
1393836_at	1387199_a_at	1390704_at	1394935_at	1381821_at
1397362_at	1383063_a_at	1379232_at	1378303_at	1376843_at
1383825_at	1370607_a_at	1394784_at	1376996_at	1381075_at
1371093_at	1374463_at	1377816_at	1376256_at	1395762_at
1390398_at	1383044_at	1377105_at	1391852_at	1395136_at
1379101_at	1382775_at	1379130_at	1384809_at	1393613_at
1373347_at	1380069_at	1380314_at	1384240_at	1383194_a_at
1368725_at	1376562_at	1376739_at	1390463_at	1374350_at
1381850_at	1394961_at	1395616_at	1384335_at	1385163_at
1375459_at	1372542_at	1385041_at	1385102_at	1375486_at
1391430_at	1382130_at	1381809_at	1385101_a_at	1397889_at
1378965_at	1367652_at	1385931_at	1394474_at	1381515_at
1393795_at	1396036_at	1384293_at	1376490_at	1383829_at
1384376_at	1394504_at	1380981_at	1393735_at	1375532_at
1377457_a_at	1383075_at	1386525_at	1395336_at	1385923_at
1390710_x_at	1392523_at	1398483_at	1384484_at	1380744_at
1383054_at	1374593_at	1389868_at	1389972_at	1391222_at
1368401_at	1379409_at	1392902_at	1388015_at	1393189_at
1369679_a_at	1390426_at	1368867_at	1377556_at	1398595_at
1375174_at	1382952_at	1393881_at	1382262_at	1395222_at

Supplemental Table 4 continued

1391128_at	1391979_at	1392231_at	1380783_at	1378962_at
1370387_at	1395333_at	1377090_at	1397373_at	1380325_at
1396437_at	1375358_at	1374320_at	1368255_at	1384311_at
1383266_at	1375011_at	1374779_at	1381063_at	1377172_at
1385157_at	1370072_at	1380600_at	1369681_at	1392144_at
1380446_at	1370465_at	1385525_at	1395395_at	1385017_at
1377774_at	1382211_at	1387154_at	1391549_at	1393804_at
1389554_at	1374676_at	1379387_at	1385773_at	1379077_at
1388999_at	1393811_at	1384180_at	1385974_at	1375582_at
1383127_at	1393777_at	1379055_x_at	1390797_at	1372000_at
1396550_at	1375350_at	1377051_at	1376836_at	1384542_at
1379912_at	1398500_at	1383932_at	1370090_at	1398582_at
1385638_at	1370145_at	1389601_at	1383064_at	1378493_at
1378389_at	1373666_at	1383644_at	1391711_at	1382614_at
1373463_at	1376610_a_at	1371483_at	1394401_at	1391474_at
1368770_at	1391428_at	1377308_a_at	1392040_at	1383145_at
1383527_at	1390687_at	1377266_at	1395076_at	1397779_at
1376755_at	1370205_at	1372002_at	1390777_at	1380699_at
1370678_s_at	1368221_at	1383353_at	1393901_at	1377974_at
1383199_at	1377640_at	1393589_at	1370043_at	1390866_at
1393672_at	1390782_at	1387349_at	1385215_at	1382913_at
1382452_at	1371951_at	1377857_at	1384181_at	1384048_at
1392842_at	1369156_at	1382301_at	1378509_at	1392717_at
1372814_at	1389632_at	1385972_at	1391935_at	1370570_at
1382776_at	1368691_at	1396696_at	1379062_at	1369215_a_at
1379724_at	1398727_at	1383343_at	1382705_at	1378282_at
1384250_a_at	1377934_at	1383795_at	1380523_at	1392051_at

Supplemental Table 4 continued

1375785_at	1397531_at	1394425_at	1380824_at	1384857_at
1387204_at	1379872_at	1379416_at	1370085_at	1382368_at
1384610_at	1393622_at	1376933_at	1384587_at	1394436_at
1393505_x_at	1398440_at	1385227_at	1390592_at	1385108_at
1383219_at	1393582_at	1377072_at	1389998_at	1394010_at
1394483_at	1392864_at	1392660_at	1394849_at	1380545_at
1391524_at	1378624_at	1395986_at	1380547_at	1379645_at
1375469_at	1376627_at	1380937_at	1392453_at	1375552_at
1380763_at	1382489_at	1379286_at	1391089_at	1379544_at
1383615_a_at	1376685_at	1385519_at	1373494_at	1370035_at
1379221_at	1390858_at	1389989_at	1389116_at	1367884_at
1394578_at	1391757_at	1371679_at	1368824_at	1375524_at
1382960_at	1397630_at	1370830_at	1379733_at	1391438_at
1373773_at	1383726_at	1377029_at	1395075_at	1390048_at
1396225_at	1377345_at	1397676_at	1391297_at	1370176_at
1394654_at	1390757_at	1382268_at	1392653_at	1379509_at
1392245_at	1392806_at	1378457_at	1370267_at	1374066_at
1376744_at	1374246_at	1384125_at	1387165_at	1370262_at
1391594_at	1395015_at	1390266_at	1368842_at	1392180_at
1389444_at	1375763_at	1398420_at	1377070_at	1384759_at
1385350_at	1383253_at	1391439_at	1368958_at	1381048_at
1382584_at	1392715_at	1397179_at	1390184_at	1376080_at
1379866_at	1393643_at	1392764_at	1391743_at	1377526_at
1382898_at	1385953_at	1383112_at	1376419_at	1379941_at
1384164_at	1392592_at	1390506_at	1375723_at	1383069_at
1376619_at	1392198_at	1374909_at	1383052_a_at	1375545_at
1381296_at	1384115_at	1393981_at	1390871_at	1379313_at

Supplemental Table 4 continued

1384948_at	1378325_at	1378740_at	1391687_at	1394493_at
1375278_at	1398544_at	1395021_at	1382939_at	1395318_at
1382303_at	1370052_at	1379886_at	1378413_at	1380525_at
1377111_at	1389957_at	1385044_at	1375426_a_at	1384804_at
1379140_at	1379398_at	1389442_at	1390443_at	1394576_at
1375119_at	1391576_at	1386063_at	1375303_at	1383833_at
1369735_at	1390923_a_at	1368933_at	1397286_at	1397959_at
1397632_at	1382226_at	1382551_at	1378255_at	1394422_at
1380503_at	1375699_at	1376654_at	1384609_a_at	1391405_at
1379804_at	1375259_at	1391770_at	1396403_at	1379603_at
1397552_at	1392666_at	1394756_at	1375215_x_at	1383632_at
1375453_at	1380143_at	1381471_at	1384339_s_at	1376523_at
1379461_at	1382654_at	1381753_at	1367958_at	1388108_at
1391600_at	1377881_at	1392675_at	1382382_at	1385552_at
1375378_at	1382953_at	1382313_at	1391075_at	1377513_at
1395711_at	1379423_at	1385903_at	1381100_at	1388866_at
1396470_at	1382778_at	1382258_at	1385240_at	1388710_at
1379103_at	1385888_at	1385925_at	1387233_at	1391436_at
1368871_at	1375612_at	1379107_at	1376853_at	1379719_at
1375212_at	1379535_at	1376226_at	1375703_at	1377686_at
1376533_at	1390467_at	1379112_at	1376436_at	1375343_at
1370063_at	1382291_at	1389840_at	1376644_at	1380552_at
1370512_at	1390347_at	1391968_at	1383296_a_at	1378269_at
1392441_at	1370221_at	1370810_at	1378581_at	1370089_at
1372812_at	1378453_at	1371005_at	1378368_at	1384478_at
1389836_a_at	1373497_at	1391855_at	1380406_at	1393585_at
1371202_a_at	1393752_at	1375724_at	1389761_at	1371024_at

Supplemental Table 4 continued

1392044_at	1369404_a_at	1376848_at	1369957_at	1371034_at
1394626_at	1379126_at	1384168_at	1376623_at	1395255_at
1369654_at	1398739_at	1381167_at	1371541_at	1371281_at
1378610_at	1369499_at	1394824_at	1393167_at	1392295_a_at
1396256_at	1391569_at	1395361_at	1398649_at	1392607_at
1383552_at	1391187_at	1369756_a_at	1385354_at	1390097_at
1393661_at	1377508_at	1379492_at	1371472_at	1392582_at
1398202_at	1395546_at	1388527_at	1377675_at	1378904_at

Supplemental Table 5

Supplemental Table 5. Members of cluster C1b: n=313.

1376872_at	1393283_at	1368720_at	1389500_at	1378539_at
1384393_at	1393547_at	1383879_at	1387951_at	1387179_at
1382682_at	1383846_at	1368311_at	1391707_at	1387269_s_at
1375999_at	1368059_at	1377453_at	1371162_at	1396206_at
1393952_at	1370361_at	1383853_at	1378498_at	1389177_at
1372004_at	1387766_a_at	1368400_at	1370139_a_at	1394710_at
1393157_at	1390912_at	1371536_at	1392531_at	1384034_at
1385559_at	1390707_at	1368622_at	1390828_at	1368789_at
1389507_at	1370450_at	1388663_at	1380460_at	1383797_a_at
1378120_at	1388802_at	1368085_at	1371243_at	1387369_at
1368358_a_at	1384921_at	1383692_at	1376829_at	1377168_at
1385099_at	1373085_at	1381276_at	1397850_at	1388077_a_at
1393111_at	1385587_at	1374146_at	1381626_at	1367925_at
1373267_at	1369590_a_at	1387032_at	1383742_at	1373559_at
1392206_at	1369179_a_at	1393124_at	1377517_at	1391106_at
1372423_at	1368238_at	1368846_at	1376579_at	1368359_a_at
1379814_at	1378855_a_at	1380346_at	1381064_at	1394908_at
1379757_at	1374649_at	1394070_at	1368313_a_at	1396387_at
1392999_at	1396199_at	1367754_s_at	1369474_a_at	1379363_at
1381770_at	1370944_at	1368559_at	1369019_at	1393729_at
1395456_at	1373606_at	1369755_at	1389092_at	1368916_at
1374367_at	1376174_at	1372832_at	1390607_at	1393706_at
1368545_at	1393747_at	1371134_at	1368927_at	1372590_at
1387660_at	1370936_at	1369204_at	1396176_at	1369664_at

Supplemental Table 5 continued

1392948_at	1379022_at	1376893_at	1376098_a_at	1368692_a_at
1387523_at	1389007_at	1391879_at	1376215_at	1376988_at
1378400_at	1368412_a_at	1396687_at	1380457_at	1370694_at
1373783_at	1368355_at	1392425_x_at	1384564_at	1370336_at
1394855_at	1374672_at	1381173_at	1388544_at	1389054_at
1378315_at	1372844_at	1372885_at	1386321_s_at	1367774_at
1374948_at	1369050_at	1393147_at	1367767_at	1379486_at
1398431_at	1384667_x_at	1379425_at	1379907_at	1383304_at
1374787_at	1398623_at	1378274_at	1377739_at	1381341_at
1389350_at	1371883_at	1393047_at	1390042_at	1387221_at
1388187_at	1372755_at	1392274_at	1373120_at	1387818_at
1368300_at	1377885_at	1375051_at	1376754_at	1371259_at
1378470_at	1395673_at	1374632_at	1378586_at	1368187_at
1393081_at	1387543_at	1372808_at	1367834_at	1374330_at
1393307_at	1368194_at	1376076_at	1379401_a_at	1393441_at
1375925_at	1385176_at	1393057_at	1379477_at	1368072_at
1369717_at	1390999_at	1384522_at	1385464_at	1367624_at
1388219_at	1384683_at	1382739_at	1387645_at	1391121_at
1388968_at	1368197_at	1373632_at	1378536_at	1374819_at
1378557_at	1378818_at	1389573_at	1390114_at	1378605_at
1372989_at	1395536_at	1375052_at	1387201_at	1370695_s_at
1377034_at	1384526_at	1376195_at	1382319_at	1388261_at
1395655_at	1377867_at	1388919_at	1394297_at	1372013_at
1385434_at	1384165_at	1384488_at	1388659_at	1368443_at
1371801_at	1378111_at	1379493_at	1372851_at	1384444_at
1374117_at	1381080_at	1398840_at	1370902_at	1392082_a_at
1369752_a_at	1381233_at	1372642_at	1385325_at	1368708_a_at

Supplemental Table 5 continued

1367762_at	1383220_at	1373987_at	1382002_at	1391586_at
1369137_at	1393957_at	1387065_at	1370805_at	1394522_at
1391074_at	1393190_at	1369475_x_at	1387063_at	1385229_at
1383887_at	1392077_at	1387578_a_at	1370922_at	1367888_at
1382541_at	1369165_at	1388891_at	1378479_at	1370850_at
1386679_at	1376417_at	1369632_a_at	1374724_at	1368667_at
1384863_at	1390473_at	1368595_at	1387360_at	1393163_at
1387208_at	1374095_at	1377176_at	1379545_at	1391656_at
1376410_at	1387799_at	1373782_a_at	1380016_at	1376345_at
1368037_at	1371049_at	1388099_a_at	1389461_at	1370964_at
1387395_at	1374818_at	1377056_at	1382975_at	
1376788_at	1375868_at	1371908_at	1376443_at	

Appendix

Data availability

Microarray datasets supporting the conclusions of this article are available in the Gene Expression Omnibus (GEO) repository under accession code: GSE126773. Other datasets supporting the conclusions of this article are included within the article and its Supplementary Files or have been deposited in the public repository

<https://github.com/nickh89/Stephen-N.-Housley-Public-Repository-for-Publication-Code-and-Data>.

Code

All code and models used can be accessed in the public repository

<https://github.com/nickh89/Stephen-N.-Housley-Public-Repository-for-Publication-Code-and-Data>

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