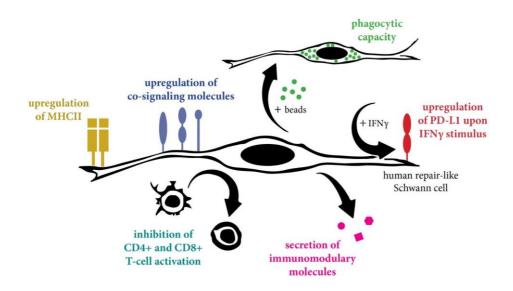
1	Human repair-related Schwann cells adopt functions of antigen-presenting cells in vitro
2	
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- 38 cells.
- **39** HrSCs up-regulate PD-L1 upon pro-inflammatory IFNγ stimulation.
- 40 HrSCs hamper CD4+ and CD8+ T-cell activation.
- 41
- 42 Graphical abstract
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#### immunoregulatory features of human repair-related Schwann cells



44

# 45 Abstract

The plastic potential of Schwann cells (SCs) is increasingly recognized to play a role after nerve
injury and in diseases of the peripheral nervous system. In addition, reports on the interaction
between SCs and immune cells indicate their involvement in inflammatory processes. However,
data about the immunocompetence of human SCs are primarily derived from neuropathies and
it is currently unknown whether SCs directly regulate an adaptive immune response after nerve
injury.

52 Here, we performed a comprehensive analysis of the immunomodulatory capacities of human repair-related SCs (hrSCs), which recapitulate SC response to nerve injury in vitro. We used our 53 previously established protocol for the culture of primary hrSCs from human peripheral nerves 54 55 and analyzed the transcriptome, secretome, and cell surface proteins for signatures and 56 markers relevant in innate and adaptive immunity, performed phagocytosis assays, and 57 monitored T-cell subset activation in co-cultures with autologous human T-cells. 58 Our findings show that hrSCs are highly phagocytic, which is in line with high MHCII expression. 59 In addition, hrSCs express co-regulatory molecules, such as CD40, CD80, B7H3, CD58, CD86, 60 HVEM, release a plethora of chemoattractants, matrix remodelling proteins and pro- as well as

anti-inflammatory cytokines, and upregulate the T-cell inhibiting PD-L1 molecule upon pro inflammatory stimulation with IFNγ. Furthermore, hrSC contact reduced the number and
 activation status of allogenic CD4+ and CD8+ T-cells.

64 This study demonstrates that hrSCs possess features and functions typical for professional
65 antigen presenting cells *in vitro*, and suggest a new role of these cells as negative regulators of
66 T-cell immunity during nerve regeneration.

# 67 Introduction

68 Schwann cells (SCs) are glial cells of the peripheral nervous system and possess capacities that go far beyond the preservation of axon integrity. Upon nerve injury, SCs undergo extensive 69 70 morphological and expression changes and acquire distinct repair features in a process referred 71 to as 'adaptive cellular reprogramming' (Jessen & Mirsky, 2016). In this dedicated repair cell 72 state, SCs re-enter the cell cycle and execute specialized functions to coordinate the multi-step 73 process of nerve regeneration, such as the recruitment of immune cells, the breakdown of 74 myelin debris, remodeling of the extracellular matrix, and the expression of neurotrophic and 75 neuritogenic factors for axon survival, regrowth, and guidance (Gomez-Sanchez et al., 2015; 76 Jang et al., 2016; Jessen & Mirsky, 2016; Nocera & Jacob, 2020; Tofaris, Patterson, Jessen, & 77 Mirsky, 2002; Weiss et al., 2016). Moreover, numerous studies support that the highly adaptive 78 cellular state of SCs plays a role in pathological conditions such as neuropathies and tumor development (Azam & Pecot, 2016; Bunimovich, Keskinov, Shurin, & Shurin, 2017; Direder et 79 80 al., 2021; Weiss et al., 2021). We have recently shown that tumor-associated SCs in neuroblastic tumors adopt a similar phenotype as upon nerve injury and exert anti-proliferative 81 82 and pro-differentiating effects through the release of until then unknown neurotrophins, such 83 as EGFL8 (Ambros et al., 1996; Crawford et al., 2001; Direder et al., 2021). As knowledge on the 84 involvement of SCs during regeneration and pathologies is continuously expanding, their 85 immunomodulatory potential gains increasing interest (Armati, Pollard, & Gatenby, 1990; Hörste, Hu, Hartung, Lehmann, & Kieseier, 2008; Zhang et al., 2020). SCs have been 86 87 demonstrated as immune competent cells that contribute to inflammatory and hereditary neuropathies (Ydens et al., 2013). However, less is known about the impact of human SCs on 88 89 the inflammatory processes during peripheral nerve regeneration (Bergsteinsdottir, Kingston, 90 Mirsky, & Jessen, 1991; Rutkowski et al., 1999; Toews, Barrett, & Morell, 1998; Weiss et al., 91 2016).

92 Similar to any injury site in the body, injured nerves experience an early pro-inflammatory 93 response by the influx of immune cells that is followed by termination of the immune response 94 to allow tissue regeneration. Previous studies showed that SCs secrete a variety of cytokines 95 and chemokines which attract monocytes and neutrophils to the site of nerve injury 96 (Bergsteinsdottir et al., 1991; Rutkowski et al., 1999; Tofaris et al., 2002). Their expression could 97 be partially mediated by axon derived molecules recognized by SCs via toll-like receptors (TLRs)

98 (Goethals, Ydens, Timmerman, & Janssens, 2010; Kaisho & Akira, 2000; Karanth, Yang, Yeh, & 99 Richardson, 2006; Lee et al., 2006; Meyer Zu Horste et al., 2010; Meyer zu Hörste, Hu, Hartung, Lehmann, & Kieseier, 2008). Within injured nerves, recruited and/or tissue resident 100 101 macrophages adapt a specialized regenerative phenotype with neuroprotective capacities and 102 express proteins associated with an anti-inflammatory profile (Gaudet, Popovich, & Ramer, 103 2011; La Fleur, Underwood, Rappolee, & Werb, 1996; Ydens et al., 2012). Of note, SCs might 104 be involved in polarizing macrophages towards a regenerative phenotype, but so far, the 105 underlying factors remain unknown (Stratton & Shah, 2016; Stratton et al., 2016).

106 SCs can also interact with T-cells by expressing major histocompatibility complex class II (MHCII) 107 receptors and co-signaling molecules (Armati et al., 1990; Hörste et al., 2008; Murata & 108 Dalakas, 2000). However, upregulation of MHCII on SCs was primarily reported in neuropathies 109 (Mancardi et al., 1988; Meyer Zu Horste et al., 2010; Van Rhijn, Van den Berg, Bosboom, Otten, 110 & Logtenberg, 2000) and upon treatment with IFNy (Armati et al., 1990; Lilje & Armati, 1997; 111 Samuel, Mirsky, Grange, & Jessen, 1987), which is a potent inducer of MHCII expression in 112 antigen presenting cells (APCs). In contrast, our previous research showed that human repair-113 related SCs highly upregulate MHCII in culture and within nerve explants independent of IFNy 114 (Weiss et al., 2016). Furthermore, these repair-related SCs expressed genes of co-signaling 115 molecules, MHCII transcriptional co-activator CIITA, and other molecules involved in the 116 antigen processing and presentation machinery (Weiss et al., 2016), suggesting a biological 117 relevance of MHCII expressing SCs in response to injury.

118 APCs function as local modulators of T-cell response upon inflammatory stimulation. The 119 outcome of this modulation is dependent on the expression of sets of co-stimulatory or co-120 inhibitory surface molecules recognized by T-cells together with MHCII. Indeed, rodent SCs 121 could be induced to activate T-cells by presenting endogenous as well as exogenous antigens 122 (Duan et al., 2007; Kingston et al., 1989; Spierings, De Boer, Zulianello, & Ottenhoff, 2000; 123 Steinhoff & Kaufmann, 1988; Wekerle, Schwab, Linington, & Meyermann, 1986). Moreover, T-124 cell activation through MHCII expressing SCs has been associated with post-traumatic 125 inflammation and neuropathic pain in diseased peripheral nerves of rodents (Hartlehnert et al., 126 2017). Hence, the SC function as non-professional APC has mainly focused on the promotion 127 of T-cell activation resulting in (auto-) inflammatory or infectious neuropathies, rather than 128 suppression of activated T-cells. The latter is executed by APCs to restore immune homeostasis 129 and prevent auto-immunity to self-proteins. In line with a potential T-cell inhibiting function of SCs, our previous transcriptomic analyses have indicated that primary human SCs express
genes associated with T-cell suppression such as *PD-L1* and *DC-HIL* (Weiss et al., 2016).

Based on the increasing body of studies supporting the immunocompetence of SCs and their recognized role in nerve injury and disease (Meyer zu Hörste et al., 2008; Weiss et al., 2021; Zhang et al., 2020), we here set out to investigate immunoregulatory features of human SCs in an injury condition. To this end, we cultured primary human SCs and performed phagocytosis assays, analyzed the secretion of immunomodulatory mediators, and profiled their repertoire of co-signaling molecules as well as upon TLR and inflammatory stimulation. We further assessed the ability of SCs to modulate T-cell activation and polarization *in vitro*.

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- 140

# 141 Methods

#### 142 Human material

143 The collection and research use of human peripheral nerve tissues and human tumor specimen 144 was conducted according to the guidelines of the Council for International Organizations of 145 Medical Sciences and World Health Organisation and has been approved by the local ethics 146 committees of the Medical University of Vienna (EK2281/2016 and 1216/2018). Informed 147 consent has been obtained from all patients participating in this study.

148 Neuroblastoma cell lines and primary cultures are available upon request. Primary Schwann149 cell cultures and tumor tissues are limited materials and therefore cannot be provided.

150

## 151 Isolation of primary human Schwann cells

SCs were isolated, cultured and enriched as previously described (Weiss, Taschner-Mandl, 152 153 Ambros, & Ambros, 2018). Briefly, peripheral nerves were cut into 2-3 cm pieces and nerve 154 fascicles were pulled out of the surrounding epineural tissue. The isolated fascicles were cut 155 into ~0.5 cm pieces and incubated in a digestion solution containing  $\alpha$ MEM GlutaMAX<sup>TM</sup> 156 (Gibco), 10% FCS (PAA), 1% Pen/strep (Pan Biotech), 1 mM sodium pyruvate (Pan Biotech), 25 157 mM HEPES (Pan Biotech), 0.125% collagenase Type IV (Gibco), 1.25 U/mL Dispase II (Sigma-Aldrich) and 3 mM CaCl (Sigma-Aldrich) at 37 °C, for 20 h. The digested tissue was pelleted and 158 159 resuspended in SC expansion medium (SCEM) containing MEMα, 1% Pen/Strep, 1 mM sodium 160 pyruvate, 25 mM HEPES, 10 ng/mL hu FGF basic (PeproTech), 10 ng/mL hu Heregulin-β1 (PeproTech), 5 ng/mL hu PDGF-AA (PeproTech), 0.5% N2 supplement (Gibco), 2 μM forskolin
(Sigma-Aldrich) and 2% FCS. Cells were seeded in 0.01% Poly-L-lysine (PLL, Sigma-Aldrich) and
4 μg/ml laminin (Sigma-Aldrich) coated culture dishes. Half of the medium was changed twice
a week. As passage 0 (p0) cultures consisted of SCs and fibroblast-like cells, SCs were enriched
before experimentation, by exploiting their differential adhesion potential to plastic, described
in (Weiss et al., 2018). As previously shown, human SCs adopt a repair-related phenotype in
culture (Weiss et al., 2016) and SCs are referred to as human repair-related SCs (hrSC).

168

## 169 Neuroblastoma cell lines

The used neuroblastoma cell lines (NB cells) are derived from biopsies or surgical resection of 170 171 aggressively behaving, high-risk neuroblastomas. In-house established, low passage NB cell 172 lines STA-NB-6, 7, -10 and -15 as well as the cell lines, SH-SY5Y, IMR5 and CLB-Ma (kindly 173 provided by Dr Valerie Combaret, Centre Leon Berard, France) (I M Ambros et al., 1997; Biedler, 174 Helson, & Spengler, 1973; Biedler, Roffler-Tarlov, Schachner, & Freedman, 1978; Combaret et 175 al., 1995; Fischer & Berthold, 2003; Momoi, Kennett, & Glick, 1980; Stock et al., 2008) were used for experimentation and cultured in MEMα GlutaMAX<sup>TM</sup>, 1% Pen/Strep, 1 mM sodium 176 pyruvate, 25 mM HEPES and 10% FCS. NB cells are used in this study as model to reflect 177 178 neuronal cells.

179

## 180 Primary human T-cells

181 For the T-cell isolation, a buffy coat was obtained from the Austrian Red Cross and diluted 1:4 182 in 1x PBS. Density gradient centrifugation was performed by transferring the blood onto 20 mL 183 Lymphoprep solution (StemCell Technologies) and centrifugation for 30 min at 400g at room 184 temperature (RT) without breaks. Mononuclear cells were carefully removed from the 185 interphase layer and transferred into 50 mL 1x PBS and centrifuged at 300g for 10 min. Then, 186 the medium was removed and T-cells were isolated with the Pan T-cell Isolation Kit (Miltenyi 187 Biotec) according to the manufacturer's protocol using magnetic activated cell sorting (MACS). 188 Briefly, cells were counted and resuspended in 40 µL of MACS buffer (PBS, pH 7.2, 0.5% bovine serum albumin (BSA), 2 mM EDTA) per 10<sup>7</sup> cells. For each 40 μL, 10 μL of PAN T-Cell Biotin 189 190 Antibody Cocktail (Miltenyi Biotec) was added and incubated for 5 minutes at 4°C. Then 30 µL 191 of MACS buffer and 20 µL of Pan T-Cell Microbead Cocktail was added per each 50 µL solution 192 and incubated for additional 10 min at 4°C. For the magentic separation, MACS LS columns

(Miltenyi Biotec) were placed in the magnetic field of a MACS separator (Miltenyi Biotech) and
the column was rinsed with 3 mL MACS buffer. The cell suspension was added and the flowthrough containing the unlabelled, CD3 positive T-cells, was collected. Cells were frozen in
Cryostor freezing medium (Biolife Solutions) and stored in liquid nitrogen until the day of the
experiments.

198

## 199 RNA Sequencing and data analysis

200 RNA-sequencing datasets have been previously published and are available at the Gene 201 expression omnibus (GEO) repository under the identifiers GSE94035 (MNC, n=5), GSE90711 (SC, n=5), GSE90711 (NB primary cultures, n=5 over 3 patient cultures STA-NB-6, STA-NB-7 and 202 203 STA-NB-15). RNA isolation, library preparation and sequencing on a Illumna Hiseq 2000 204 platform were performed as previously described (Weiss et al., 2016, 2021). Short read 205 sequencing data quality checked using FASTQC was 206 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc) and QoRTs (Hartley & Mullikin, 207 2015) and then aligned to the human genome hs37d5 (ftp://ftp.1000genomes.ebi.ac.uk/) using 208 the STAR aligner (Dobin et al., 2013) yielding a minimum of 11.6 million aligned reads in each sample. Further analysis was performed in R statistical environment using Bioconductor 209 210 packages (Gentleman et al., 2004). Count statistics for Ensembl (GRCh37.75) genes were 211 obtained by the "featureCounts" function (package "Rsubread") and differential expression 212 analysis was performed by edgeR and voom (Law, Chen, Shi, & Smyth, 2014; Ritchie et al., 213 2015). For differential gene expression analysis only genes passing a cpm (counts per gene per 214 million reads in library) cut-off of 1 in more than two samples were included. All p-values were 215 corrected for multiple testing by the Benjamini-Hochberg method. Genes with an adjusted q-216 value <0.05 and a log2 fold change > 1 ( $|\log_{2}FC|$ >1) were referred to as 'significantly regulated' and used for functional annotation analysis via gene set enrichment analysis (GSEA) using 217 218 MSigDB according to Subramanian, Tamayo, et al. (Subramanian et al., 2005) and Mootha, 219 Lindgren, et al. (Mootha et al., 2003)

220

## 221 Phagocytosis assay

5x10<sup>4</sup> enriched p1 hrSCs were seeded per well of an 8-well chamber slide (Ibidi) coated with
 PLL/laminin and cultured in SCEM. After 48 h, half of the medium was replaced with fresh SCEM
 containing 1 μm big carboxylate-modified polystyrene, fluorescent yellow-green latex beads

225 (SIGMA-Aldrich) at a concentration of  $8 \times 10^6$  beads/well (~100 beads/cell) for 15 h at 37°C.

226 Thereafter, cells were washed three times with 1x PBS and fixed with Roti-Histofix (Roth) for 10

227 min at RT. Cells were stored at 4°C in 1x PBS until multi-color immunofluorescence staining was228 performed.

229

#### 230 Immunofluorescence stainings

All antibody details, dilutions and incubation times are listed in **Supplementary Table 1**. If not 231 232 stated otherwise, the staining procedure was performed on RT and a washing step (3 times with 1x PBS for 5 min) was performed after each antibody incubation step, except after 233 permeabilization. For extracellular staining, grown cells were blocked with 1x PBS containing 234 235 3% goat serum (DAKO) for 30 min at RT, followed by incubation with antibodies against extracellular targets diluted in 1x PBS containing 1% BSA (Sigma-Aldrich) and 1% goat serum. 236 237 Cells were then incubated with secondary antibodies diluted in 1x PBS containing 1% BSA and 238 1% goat serum. For permeabilization, cells were exposed to 1x PBS containing 1% BSA, 0.3% 239 Triton-X (Sigma-Aldrich) and 3% goat serum for 10 min. Thereafter, cells were incubated with 240 primary antibodies against intracellular targets diluted in 1x PBS containing 1% BSA, 0.1% Triton-X and 1% goat serum, followed by incubation with secondary antibodies diluted in 1X 241 242 PBS containing 1% BSA, 0.1% Triton-X and 1% goat serum. Afterwards, 2 µg/mL 4',6-Diamidin-2-phenylindol (DAPI, Sigma-Aldrich) in 1X PBS was added for 2 min followed by a final washing 243 step. Cells were embedded in Fluoromount-G<sup>™</sup> mounting medium (Southern Biotech) and 244 stored at 4°C. Images were taken with a confocal laser scanning microscope (Leica 245 246 Microsystems, TCS SP8X) using Leica application suite X version 1.8.1.13759 or LAS AF Lite 247 software. Confocal images are depicted as maximum projection of total z-stacks and brightness 248 and contrast were adjusted in a homogenous manner using the Leica LAS AF software.

249

## 250 FACS characterization of hrSCs

All antibodies used for flow cytometry stainings are listed in Supplementary Table 1. If not stated
otherwise, the staining procedure was performed on 4°C. For all phenotyping experiments,
cells were cultured in duplicates in each condition. HrSCs were cultured in the presence of IFNγ
(10<sup>3</sup> U/mL, Bio-Techne Ltd.), LPS (10 ng/mL, Sigma-Aldrich,), Poly:IC (2 µg/mL, Bio-Techne Ltd.)
cross-linked CD40L (500 ng/mL, Bio-Techne Ltd.) and IL-1β (10<sup>4</sup> U/mL Bio-Techne Ltd.) for 24 h.
Cells were harvested with Accutase (Sigma-Aldrich) and transferred into FACS tubes containing

257 200 µL FACS buffer (0.1% BSA and 0.05% natrium acides in 1x PBS). Cells were washed once with FACS buffer at 1200rpm for 5 min, resuspended in 50 µL FACS buffer and incubated with 258 50 µL of an antibody master mix in FACS buffer for 30 min in the dark. Then, cells were washed 259 260 with FACS buffer and resuspended in 100 µL of Cytofix/Cytoperm solution (BD Biosciences), incubated for 20 min, and again washed with BD 1x perm buffer (BD Biosciences). Next, cells 261 262 were resuspended in 100  $\mu$ L 1x perm buffer containing the S100 antibody and incubated for 30 263 min in the dark. Cells were then washed in 1x perm buffer and resuspended in 100  $\mu$ L 1x perm 264 buffer with the secondary antibody for 20 min. After a washing step in 1x perm buffer, cells 265 were washed with FACS buffer and resuspended in 100 µL FACS buffer. All samples were 266 measured with a FACSFortessa flow cytometer equipped with 5 lasers (355, 405, 488, 561 and 267 640 nm) and the FACSDiva software version 8.0 (BD Biosciences) was used.

268

## 269 T-cell proliferation assay

270 For all T-cell experiments, hrSCs and freshly thawed human CD3<sup>+</sup> T-cells were used in various 271 conditions. For IFNy stimulation, hrSCs were cultured in the presence of 10<sup>3</sup> U/mL IFNy for 24 272 h prior to the T-cell co-culture experiments. For co-culture, p1 hrSCs were harvested, counted and seeded at  $4x10^4$  cells per 96 well plates in duplicates. T-cells were thawed, washed once 273 274 with 1XPBS and centrifuged at 300g for 7 min at RT. Cells were counted and labelled with CFSE 275 (Thermo Fisher) at  $1 \mu L/10^7$  cells for 10 min at 37°C. Thereafter, 1 mL FCS buffer was added for 276 2 min at RT and then washed with  $\alpha$ MEM at 300g for 7 min. Then, cells were FACS sorted for 277 intact cells using a FSC vs SSC gate using the FACS Aria instrument (BD Bioscience). The obtained cells were washed with  $\alpha$ MEM at 300g for 7 min, counted and 1x10<sup>5</sup> cells were seeded to the 278 279 hrSCs (co-culture) or cultured alone (controls) in 96 well plates. For the T-cell stimulation, 0.25 280 µL of anti-CD3/CD28 beads (Gibco) were added. Culture medium containing CD3/CD28 beads was thoroughly replenished every 3 days by one half. 281

Cells were analysed via flow cytometry at different time points, i.e. at day 2, 4 and 10.
Therefore, cells were harvested with Accutase and washed once with FACS buffer. All
antibodies used for flow cytometry stainings are listed in Supplementary Table 1. Extracellular
staining was performed with 50 μL of antibody mix containing all extracellular antibodies (CD3FITC, CD4-PerCP, CD8APC-Cy7, CD25-PE-Cy7) in 50 μL of FACS buffer for 30 min at 4°C. Cells
were washed and incubated in Fix/Perm solution (Thermo Fisher) at 4°C for 30 min. For the
permeabilization, 1x perm buffer (Thermo Fisher) was added and cells were centrifuged at 300g

289 for 7 min. Then, the supernatant was discarded and the S100 antibody for intracellular staining was added in 100 µL 1x perm buffer and incubated for 20 min at RT in the dark. After this, cells 290 291 were washed once with 1x perm buffer, once with FACS buffer and resuspended in 100  $\mu$ L FACS 292 buffer. For exact quantification of absolute cell numbers, 10 µL AccuCheck Counting Beads (LifeTechnologies) were added to each sample prior to FACS analysis at a FACSFortessa flow 293 294 cytometer. For data analysis, FACSDiva software version 8.0 was used. Gating for CD4<sup>+</sup> Th 295 subsets was performed in accordance to Mahnke et al. 2013 (Mahnke, Beddall, & Roederer, 296 2013).

297

#### 298 **Protein array**

299 The RayBio G-Series Human Cytokine Antibody Array 4000 Kit (RayBiotech Inc.) was used to 300 assay secretomes of cell supernatants pooled from 2 independent experiments each from hrSC 301 (n=5), hrSCs co-cultured with 5 different NB cell cultures (n=5) or NB cell cultures alone (n=5). 302 A total of 274 factors were evaluated (for a complete list of factors, refer to 303 https://www.raybiotech.com/human-cytokine-array-g4000-4/). Arrays were processed 304 according to the manufacturer's instructions. Briefly, protein array membranes were blocked 305 with Blocking Buffer (RayBiotech Inc.) for 30 min at RT. Membranes were then incubated with 306 100  $\mu$ L of undiluted sample for 2 h. After extensive washing with Wash Buffer I and II 307 (RayBiotech Inc.) to remove unbound materials, the membranes were incubated with biotin-308 conjugated antibodies for 2 h at RT. The membranes were then washed and incubated with 309 streptavidin-fluorescin, again for 2 hours at RT, followed by final washing steps. Finally, 310 fluorescence signals were obtained with the GenePix 4000 array scanner (Molecular Devices) 311 using the green channel (Cy3) at an excitation frequency of 532 nm and 700 PMT. The image 312 files generated in this way were aligned to respective .gal files (RayBiotech) and Gene Pix Pro 7 313 (Molecular Devices) was used to create .gpr files. Each spot was manually inspected on the .gpr 314 file images to ensure accuracy. After background correction and normalization to the internal control, the mean fluorescence intensity (MFI) values were combined for all cell lines and 315 316 proteins that were differentially expressed (q < 0.05) between hrSCs and hrSCs in co-cultures, compared to neuronal cells as controls, were selected for visualization using the Qlucore Omics 317 Explorer V3.1 software. 318

319

#### 320 Quantification and statistical analysis

If not mentioned otherwise, statistical analysis was performed with R version 3.4.2 within the R studio interface including publicly available packages CRAN, GGPLOT2, GGBEESWARM and RESHAPE. For pair-wise comparison paired t-tests were used, for multiple comparisons twoway ANOVA using a post-hoc Holm p value correction was used. P values of less than 0.05 were considered significant and displayed as \*, p values of less than 0.01 were displayed as \*\*, p values of less than 0.001 were displayed as \*\*\*.

327

## 328 Data and code availability

No original code has been generated in this study. Original/source data for all figures and
supplementary figures are available upon request. RNA-sequencing data are available at the
Gene Expression Omnibus (GEO) repository (<u>Home - GEO - NCBI (nih.gov</u>) under the identifier
GSE94A035, GSE90711 and GSE90711.

333

# 334 **Results**

## 335 Human repair-related Schwann cells show a phagocytic capacity

336 APCs are characterized by their phagocytic ability of exogenous material to process and present 337 antigens via MHCII. To evaluate whether human SCs can take-up material different from myelin, we applied our previously established protocol for the culture of primary SCs from human 338 339 peripheral nerves (Weiss et al., 2018). As human SCs possess a repair-like phenotype and 340 perform repair-associated functions in culture (Weiss et al., 2016), they are referred to as 341 human repair-related SCs (hrSCs) in the following. The cultured hrSCs showed the typical 342 spindle-shaped morphology with a swirled parallel alignment (Fig. 1A) and were characterized 343 by immunostainings for the SC marker NGFR (also known as TNR16 or p75<sup>NTR</sup>) (Fig. 1B). The co-344 staining for vimentin, an intermediate filament expressed by SCs and fibroblasts, visualized a 345 straight filament network within the long hrSC processes and a more branched appearance in fibroblasts (Fig. 1B). To obtain information about their phagocytic capacity, we challenged the 346 347 hrSCs with green fluorescent latex beads (1 µm diameter) for 15 hours and stained the cultures for NGFR and vimentin. 3D confocal image analysis demonstrated that hrSCs were able to 348 349 phagocytose the beads and to accumulate them within the cell body (Fig. 1C).

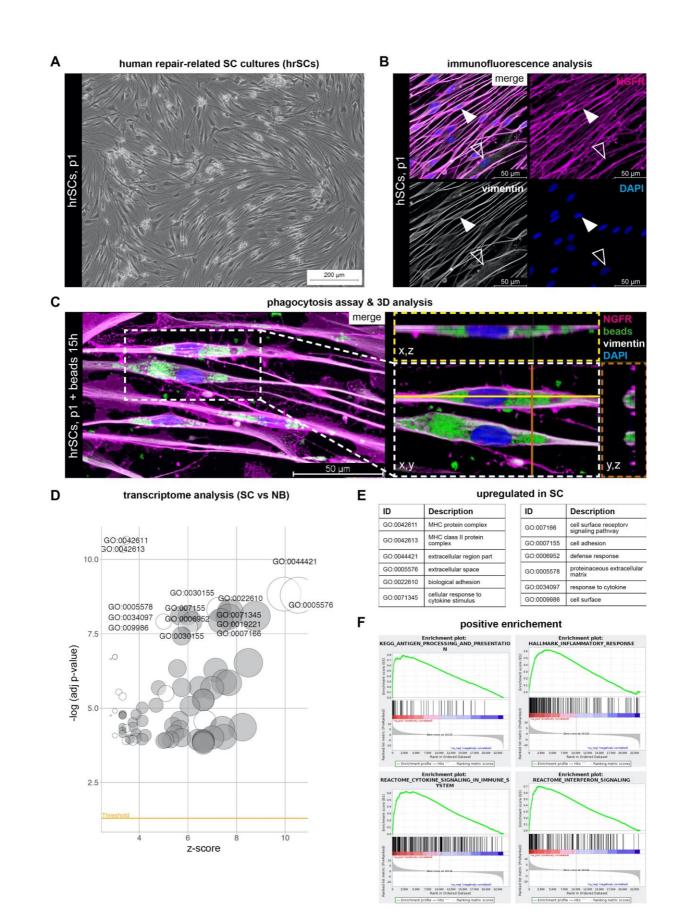


Figure 1 | Phagocytosis potential and inflammatory response of hrSCs. (A) Phase contrast image of a
representative passage 1 (p1) hrSC culture. (B) Immunostaining of p1 hrSCs for SC marker NGFR
(magenta), intermediate filament vimentin (grey) and nuclear stain DAPI (blue); arrowheads indicate a

353 NGFR negative and vimentin positive fibroblast. (C) 3D confocal image analysis of hrSCs exposed to 1 354 µm in diameter green fluorescent latex beads for 15 hours. Cross sections show internalized beads 355 within the SC cytoplasm. (D) Gene ontology (GO) analysis of differentially expressed genes by RNA-seq 356 between hrSCs (n=5) and NB cultures (n=5 independent biological replicates of 3 donors), -log10 of the 357 enrichment p values (cut-off <0.05) for filtered GO categories are plotted relative to Z-scores of average 358 ratios in each category. Circle size represents the fraction of regulated genes per GO term. (E) Top 12 359 GO terms among genes upregulated in hrSCs vs NB cultures. (F) Gene set enrichment analysis (GSEA) 360 plots of hrSCs compared to NB cultures. Source data are provided in Suppl. Tables 2-4.

361

# 362 Transcriptome profiling of human repair-related Schwann cells363 revealed immunomodulatory gene signatures

364 The phagocytic capacity of hrSCs towards cell-extrinsic material prompted us to evaluate whether pathways associated with inflammation and antigen presentation were active in 365 366 hrSCs. To this end, we interrogated the transcriptome data generated by deep RNA-sequencing (RNA-seq) of hrSC cultures (n=5) and of neuroblastic tumor cells (NB cells) (n=5), which serve 367 368 as models for neuronal cells. Comparison of the transcriptomes of hrSCs and NB cells revealed 5822 differentially expressed genes (q-value<0.01, log2FC>1), of which 3057 were 369 upregulated and 2754 were down-regulated in hrSCs (Suppl. Table 2). Subsequent functional 370 371 annotation analysis of genes unique to hrSCs demonstrated gene ontology (GO) terms 372 prominent in MHC class I and class II protein complexes, cellular response to cytokine stimulus, 373 and cytokine mediated signaling pathways (Fig. 1D, Suppl. Table 3). These results were further 374 supported by a gene set enrichment analysis (GSEA), which confirmed the enrichment of genes 375 associated with antigen processing and presentation alongside with cytokine signaling and an 376 inflammatory response in hrSCs (Fig. 1E, Suppl. Table 4). Taken together, transcriptome profiling 377 of hrSCs provides further evidence of cytokine signaling and upregulation of MHCII in response 378 to nerve damage.

# Human repair-related SCs express MHCII and the co-signaling molecules CD40, CD80, CD86, CD58, HVEM and B7-H3

381 As the primary function of APCs is to modulate T-cell activation through MHCII and the 382 expression of co-signalling molecules, we further investigated whether the latter can be found 383 on hrSCs. Therefore, we cultured hrSCs from eight different donor nerves and used flow 384 cytometry to profile the expression of MHCII and selected co-signalling molecules. As the 385 interaction of SCs with immune cells has been described as a dynamic process (Gold, Zielasek, 386 Kiefer, Toyka, & Hartung, 1996), the analysis was performed at two time points, in passage one 387 and passage two hrSC cultures. SC identity was determined by S100 expression, a well-388 established SC marker, and showed that mean purity of hrSCs cultures was 82% in passage one 389 (p1) and 70% in passage 2 (p2) (Fig. 2A). The S100 negative cells, presumably nerve-associated 390 fibroblasts, were excluded from further analysis (Fig. 2A). In the S100 positive hrSCs, we 391 quantified the surface expression of MHCII and co-signalling molecules CD40, CD80, CD86, B7-392 H3, HVEM, PD-L1, PD-L2 and CD58. About 76% and 87% of hrSCs were positive for MHCII in p1 393 and p2, respectively (Fig. 2B), which is in line with our previously published observation that 394 MHCII expression increased with prolonged culture time (Weiss et al., 2016). Further, p1 as well as p2 hrSCs demonstrated expression of CD40, CD80, B7-H3, CD58, and HVEM (Fig. 2C-G). 395 396 In contrast, neither PD-L1 nor PD-L2 were detected in p1 or p2 hrSC (Fig. 2H-I). Interestingly, 397 most of p1 hrSCs were negative for CD86, while it was significantly upregulated in p2 cells (Fig. 398 2J). Hence, hSCs indeed express - next to MHCII - several canonical co-signalling molecules that 399 are required for T-cell activation and inhibition.

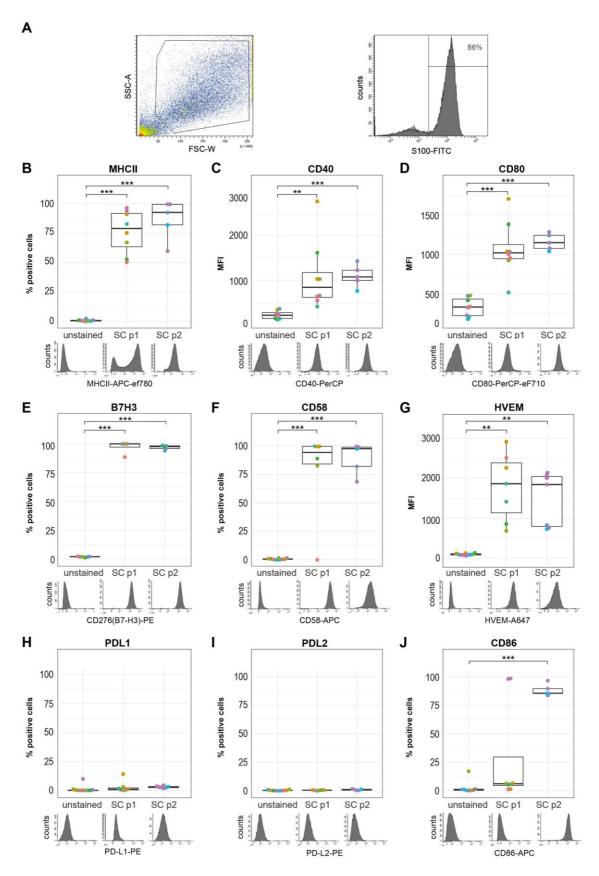




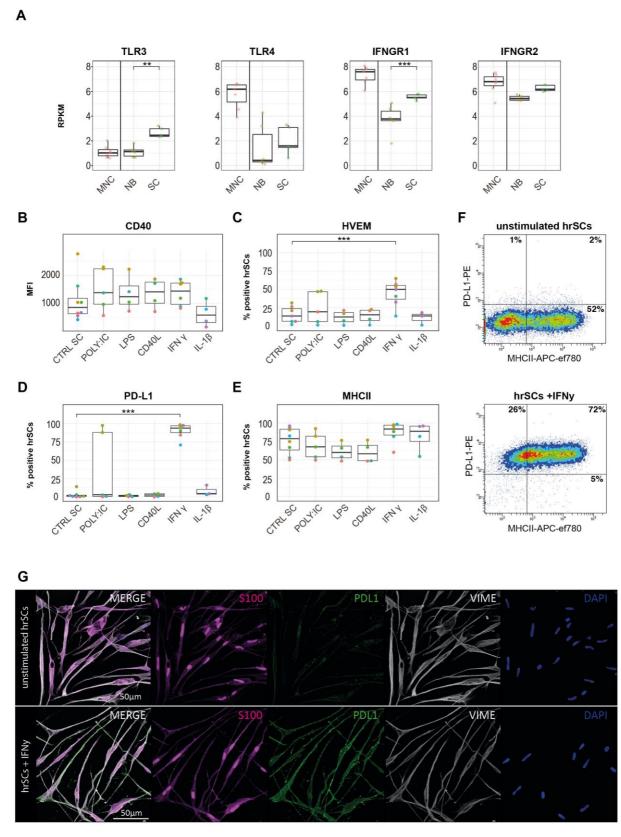
Figure 2 | Flow cytometry phenotyping of MHCII and co-signaling molecules present on human repair related Schwann cells. (A) Gating strategy for the identification of S100 positive hrSCs illustrated for one
 representative experiment. Intact cells are gated in the FSC vs SSC blot and S100 positive cells were

404 selected for further analysis. (B-J) Box plots show the expression status of MHCII and co-signaling 405 molecules CD40, CD80, B7H3, CD58, HVEM, PD-L1, PD-L2 and CD86 of S100 positive hrSCs in passage 1 406 (p1) and p2; technical replicates (same color); biological replicates (different color). The histograms 407 underneath depict one representative experiment. Each biological replicate is conducted with hrSCs 408 isolated from a different donor nerve. (B, E, F, H, J) Box plots represent the percentage of positive cells 409 based on gates set in relation to unstained controls as displayed in the histograms. (C, D, G, I) Boxplots 410 represent the mean fluorescence intensity (MFI). Boxes contain 50% of data and whiskers the upper 411 and lower 25%; means are displayed as black horizontal lines. A two-way ANOVA using a post-hoc Holm 412 p value correction was performed. \*  $p \le 0.05$ ; \*\*  $p \le 0.01$ ; \*\*\*  $p \le 0.001$ 

413

# The stimulation of TLR3 and TLR4 had no effect on the expression of co-signaling molecules in human repair-related Schwann cells

416 Professional as well as non-professional APCs can upregulate the expression of co-signaling 417 molecules upon toll-like receptor (TLR) ligation (Chen & Flies, 2013; Fitzgerald & Kagan, 2020; 418 Mehrfeld, Zenner, Kornek, & Lukacs-Kornek, 2018). Our RNA-seq data of hrSCs showed 419 enrichment in TLR signaling in comparison to neuronal cells (Suppl. Table 4), which motivated 420 us to explore the expression of co-signaling molecules in response to inflammatory stimulation. 421 First, we investigated which TLRs are expressed by hrSCs, to choose the corresponding ligands 422 for further analysis. We found elevated expression levels of TLR1, TLR3, TLR4 and TLR6 mRNA 423 (Fig. 3A, Suppl. Fig. 1). As TLR1 and TLR6 mainly function as heterodimers with TLR2, which was 424 not expressed, we focused on TLR3 and TLR4. We thus stimulated p1 hrSC with the TLR4 agonist 425 LPS and TLR3 agonist POLY:IC for 24 hours and subsequently analysed the expression status of 426 co-signalling molecules (Fig. 3A, Suppl. Fig. 1). Interestingly, neither the addition of LPS nor 427 POLY:IC caused a significant expression change of the analyzed co-signaling molecules in hrSCs 428 (Fig. 3B-E), which might be due to the low expression levels of TLR3 and TLR4 (Fig.3A). Upon 429 stimulation with POLY:IC a trend towards upregulation of CD40 and HVEM was seen, but 430 substantial donor variance was observed (Fig. 3B-E). CD40 is not only a co-stimulatory molecule, 431 but also a molecule that facilitates the activation of APCs upon binding of CD40-ligand (Chen & 432 Flies, 2013). CD40-ligand did, however, not affect the expression of CD40 or any other co-433 signaling molecules tested (Fig. 3B). Together these data show that TLR and CD40 ligation do not affect the expression of co-signaling molecules. 434



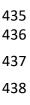


Figure 3 | Immunophenotyping of human repair-related Schwann cells upon toll-like receptor and cytokine stimulation. (A) Enrichment of toll-like receptor (TLR)-related pathways. GSEA of RNA-seq data sets of hrSCs compared to NB cultures. Box plots show the mRNA expression in reads per kilobase million 439 (RPKM) of TLR3, IFNGR1 and IFNGR2 by RNA-seq in NB cultures (NB, n=5) and hrSCs (SC, n=5). Bone 440 marrow mononuclear cells (MNC, n=5) are shown as reference. (B-E) FACS analysis of p1 cultures of 441 hrSCs stimulated with POLY:IC, LPS, CD40L, IFNy and IL-1β for 24 h. Box plots show the MFI of CD40 (B), 442 percentage of HVEM (C), PD-L1 (D) and MHCII (E) positive hrSCs in p1 cultures stimulated with POLY:IC, 443 LPS, CD40L, IFNy and IL-1B. Each biological replicate is conducted with hrSCs isolated from a different 444 donor nerve. Boxes contain 50% of data and whiskers the upper and lower 25%. Means are displayed 445 as black horizontal lines. All experiments were performed in at least 4 independent biological replicates. 446 A two-way ANOVA using a post-hoc Holm p value correction was performed; \*  $p \le 0.05$ ; \*\*  $p \le 0.01$ ; 447 \*\*\*  $p \le 0.001$ . (F) Representative FACS plots showing PD-L1 vs. MHCII expression of p1 hrSCs either 448 unstimulated (upper plot) and after IFNy stimulation. (G) Immunofluorescence image of p1 hrSCs at day 449 2 after purification without (upper panels) or with (lower panels) IFNy stimulation. HrSC cultures are 450 stained for S100 (magenta), PD-L1 (green), vimentin (grey) and DAPI (blue).

451

# Human repair-related Schwann cells upregulate HVEM and PD-L1 upon stimulation with IFNγ

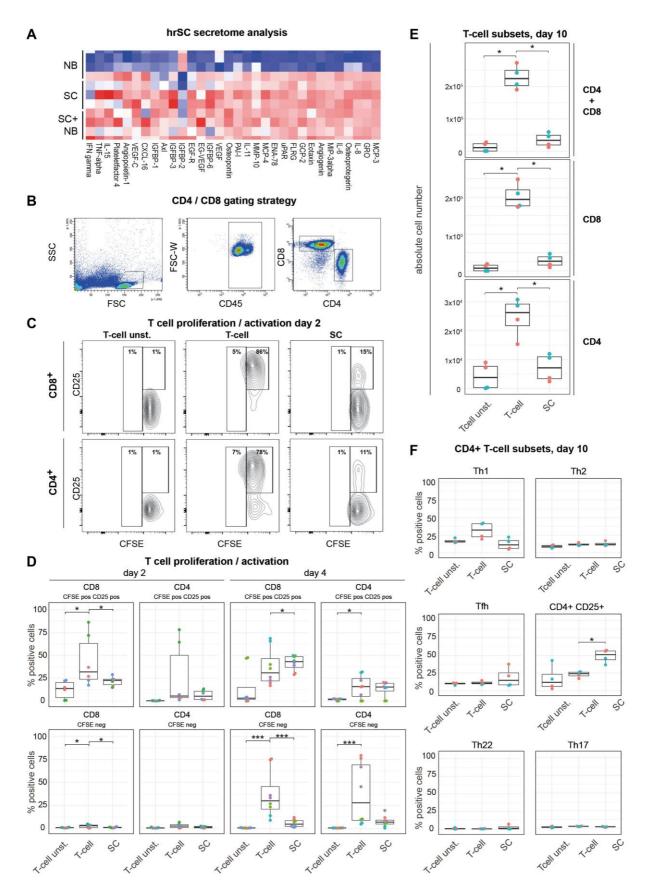
454 Inflammatory processes in peripheral nerve tissues as well as upon injury responses involve the 455 release of pro-inflammatory mediators such as IFNy and IL-1 $\beta$  by macrophages (Chiu, Von 456 Hehn, & Woolf, 2012; Yao, Graham, Akahata, Oh, & Jacobson, 2010). Notably, we found that the expression of both IFNy genes, IFNGR1 and IFNGR2, was also upregulated in hrSC in 457 458 comparison to neuronal cells (Fig. 3A). We further investigated the response of hrSCs to IFNy 459 as well as IL-1 $\beta$ . While IL-1 $\beta$  did not alter the expression of MHCII and any of the co-stimulatory molecules tested, IFNy led to a significant increase in HVEM expression (Fig. 3C). In addition, 460 IFNy stimulation induced a profound upregulation of PD-L1 (Fig. 3D). PD-L1 expression in 461 462 response to IFNy was further validated on stimulated hrSC using multicolor 463 immunofluorescence stainings for S100, PD-L1 and vimentin (Fig. 3G). Concordant with our flow 464 cytometry data, unstimulated p1 hrSC did not show a notable PD-L1 staining, whereas IFNy 465 stimulation strongly induced PD-L1 protein expression (Fig. 3G). These findings show that hrSCs 466 can respond to IFNy, but not to IL-1 $\beta$ , by a significant up-regulation of the co-stimulatory 467 molecule HVEM and the immune check-point molecule PD-L1.

468

# 469 Secretome analysis of human repair-related Schwann cells reveals a 470 broad spectrum of immunoactive mediators

471 As the inducible expression of co-signalling molecules by hrSCs together with their well-472 described function to recruit macrophages and neutrophils (Stratton et al., 2016; Tzekova,

473 Heinen, & Küry, 2014) points towards their active involvement in shaping a local immune 474 response upon nerve injury, we further investigated a panel of immunoregulatory molecules 475 secreted by hrSC. In order to model the *in vivo* situation following nerve injury, supernatants of 476 hrSCs cultured in the absence or presence of neuronal cells and neuronal cell control cultures 477 were analysed. Secretome analysis was performed using a protein array able to detect 274 478 different secreted factors. A total of 84 secreted molecules were unique to hrSCs and one was 479 only secreted by NB cells (q < 0.05). None of the 84 proteins was differentially secreted in the 480 SC-NB co-culture model as compared to SCs alone. We therefore considered these secreted proteins to be derived from hrSCs and further compared those to secreted proteins obtained 481 482 from NB cultures (Suppl. Table 5). HrSC secreted factors included interleukins IL-6, IL-11, IL-15, 483 TNFα, IFNγ, molecules involved in phagocyte attraction and activation such as MCP-3, MCP-4 484 or CXCL-16, molecules for neutrophil attraction and activation such as GRO, MIP3-alpha, IL-8 485 (CXCL-8) or ENA-78 (Fig. 4A). Many of these molecules also directly acting on lymphocytes (Fig. 486 4A), for example IL-6 that is stimulating the proliferation of antibody producing B-lymphocytes 487 or IL-15 stimualting T-and NK- cell proliferation. Interestingly, hrSCs secreted osteopontin, a 488 molecule involved in multiple processes including the induction of IFNγ through NF-κB 489 activation (Icer & Gezmen-Karadag, 2018). These findings demonstrate the plethora of 490 immunoactive mediators secreted by hrSCs and suggests autocrine activity as well as paracrine 491 modulation of myeloid cells and lymphocytes.





493 Figure 4 | HrSCs secrete immunoactive mediators and inhibit allogenic T-cell activation. (A) Secretome
494 analysis by antibody array. Heatmap displays the top 32 differentially secreted proteins (q < 0.05,</li>
495 |log2FC>0.3|) of hrSCs (n=5) and SC-NB co-cultures (n=5) vs. NB cultures (as neuronal cell model) (n=5).

496 (B-F) Allogeneic CD3<sup>+</sup>T-cells were cultured for 2, 4 or 10 days in the absence (Tcell) or presence of hrSCs 497 (SC) and stimulated with anti-CD3/CD28 beads and analysed by flow cytometry. As control unstimulated 498 T-cells (Tcell unst.) were cultured. (B) Representative FACS plots show the gating strategy for CD4<sup>+</sup> and 499 CD8<sup>+</sup> T-cells. (C) Representative FACS plots showing CD25 expression against CFSE of T-cells at day 2 of 500 co-cultivation and in control cultures. (D) Boxplots show the absolute number of CFSE<sup>+</sup>/CD25<sup>+</sup> and CFSE<sup>-</sup> 501 CD4<sup>+</sup> and CD8<sup>+</sup> T-cells at day 2 and day 4 based on gates set as illustrated in (B-C). (E) Boxplots show the 502 absolute number of alive CD4<sup>+</sup>, CD8<sup>+</sup> or combined CD4<sup>+</sup> and CD8<sup>+</sup> cells and **(F)** percentage of CD4<sup>+</sup> subsets 503 evaluated via flow cytometry at day 10 based on gates set as published by (Mahnke et al., 2013). (D-F) 504 Boxes contain 50% of data and whiskers the upper and lower 25% Means are displayed as black 505 horizontal lines. All experiments were performed in at least 3 independent biological replicates. A two-506 way ANOVA using a post-hoc Holm p value correction was performed; \*  $p \le 0.05$ ; \*\*  $p \le 0.01$ ; \*\*\*  $p \le 0.01$ ; 507 0.001.

508

# 509 Human repair-related Schwann cells reduce proliferation of allogeneic510 T-cells

Based on the overlapping features of hrSCs and APCs, i.e. phagocytosis, expression of MHCII, 511 512 co-signaling and immune checkpoint molecules, and their inducible upregulation and secretion 513 of T-cell modulatory molecules, we next asked whether hrSCs might affect T-cell activation and 514 fate in the nerve injury context. Thus, we performed co-culture assays of hrSCs and allogenic 515 T-cells. More specifically, we used T-cells from healthy donors stimulated with anti-CD3/CD28 516 beads to simulate an inflammatory environment similarly to peripheral nerve injury. We then 517 evaluated the impact of co-culture assessing the total number of activated (CFSE<sup>+</sup>CD25<sup>+</sup>) and proliferated (CFSE<sup>-/dim</sup>) CD4<sup>+</sup> and CD8<sup>+</sup> T-cells (Fig. 4B-C). At day 2 stimulated T-cells showed a 518 519 significant increase in CFSE<sup>+</sup>CD25<sup>+</sup> and to a minor extend proliferated (CFSE<sup>-/dim</sup>) CD8<sup>+</sup> T-cells whereas the presence of hrSCs in co-culture significantly reduced this effect (Fig. 4D). At day 4, 520 stimulation of T-cells resulted in an increase of both, CD8<sup>+</sup> and CD4<sup>+</sup>, CFSE<sup>+</sup>CD25<sup>+</sup> as well as 521 522 proliferated (CFSE<sup>-/dim</sup>) fraction. While proliferation was significantly reduced in CD8<sup>+</sup> T-cells by 523 the presence of hrSCs in co-culture, CFSE<sup>+</sup>CD25<sup>+</sup> cells slightly increased (Fig. 4D). A similar trend 524 was observed in the  $CD4^+$  population (Fig. 4D). This effect became even more apparent at day 10, when the total number of CD8<sup>+</sup> as well as CD4<sup>+</sup> T-cells was reduced to numbers comparable 525 526 with those of unstimulated T-cells. (Fig. 4E). Further, we interrogated the CD4<sup>+</sup> T-cell population 527 for a potential shift among T-helper subpopulations, i.e. Th1, Th2, Tfh, Th17 and Th22, using a 528 13-plex flow cytometry panels as previously published by Mahnke et al (Mahnke et al., 2013).

Notably, there was no clear trend towards a specific CD4<sup>+</sup> Th subset, yet a significantly higher
percentage of CD4<sup>+</sup>CD25<sup>+</sup> cells was detected (Fig. 4F). In summary, hrSCs delayed proliferation
of CD8<sup>+</sup> and CD4<sup>+</sup> T-cells, while promoting the long-term survival or potential switch towards a
CD4<sup>+</sup>CD25<sup>+</sup> phenotype.

533

# 534 Discussion

Building on our previous characterization of the transcriptome and proteome of human repair-535 536 type SCs (Weiss et al., 2016) and studies on SCs and nerve inflammation in rodents (Hartlehnert 537 et al., 2017; Meyer zu Hörste et al., 2010), we aimed to provide novel insight into the 538 immunocompetence of human SCs in an injury condition. Using primary human repair-related 539 SCs, hrSCs, as a unique model to study their immunophenotype and associated functional 540 aspects, our study presents several layers of evidence that hrSCs possess features and functions 541 of APCs and are capable of mediating T-cell dependent immunity. We demonstrate that hrSCs can express CD40, CD80, B7H3, CD58, CD86, HVEM and PD-L1 in addition to MHCII, secrete 542 543 numerous immunomodulatory molecules, and inhibit allogeneic T-cell activation. It is well 544 accepted that many functions of professional APCs, including the presentation of antigen via 545 MHCII, the expression of co-signalling molecules and the secretion of anti- and pro-546 inflammatory molecules, are also carried out by non-professional APCs such as mast cells, 547 eosinophils, and non-hematopoietic cells like epithelial cells (Kambayashi & Laufer, 2014; 548 Schuijs, Hammad, & Lambrecht, 2019). With this study, we add compelling evidence that hrSCs 549 could also act as non-professional APCs that may modulate the inflammatory processes within 550 injured nerves. Studying the interaction of primary hrSCs and T-cells allowed the development 551 of a broadly applicable functional *in vitro* model that contributes to the ongoing research in the 552 field of neuroinflammatory disorders, regenerative medicine and immune oncology.

553

## 554 Human repair-related SCs possess features of antigen presenting cells

In line with our previous studies we show that hrSCs actively perform phagocytosis and express
MHCII on their surface (Weiss et al., 2016). It has been recently described that rodent SCs have
the ability to regulate MHCII dependent immunity, as the deletion of MHCII lead to a decreased
infiltration of CD4+ cells to the site of nerve injury (Hartlehnert et al., 2017). This suggests a

functional necessity of MHCII expression in nerve repair. The ability of SCs to present ingested
molecules via MHCII and shape an immune response has been suggested before (Baetas-daCruz et al., 2009; Meyer Zu Horste et al., 2010; Steinhoff & Kaufmann, 1988; Van Rhijn et al.,
2000), yet more detailed studies were needed to understand the role of SCs in phagocytosis,
antigen presentation and immune cell modulation in human SCs.

564 It is well-established that not only classical APCs but also non-professional APCs, like mast cells 565 or epithelial cells, are capable of phagocytosis and antigen presentation via MHC II to CD4+ T-566 cells (Kambayashi & Laufer, 2014; Schuijs et al., 2019). As non-professional APCs of non-567 hematopoietic origin do not primarily migrate to lymph nodes, their role in priming naïve T-568 cells may be less relevant, but their modulation of a local T-cell responses is widely accepted (Kambayashi & Laufer, 2014). Thus, the expression of co-signalling molecules alongside with 569 570 MHCII and the secretion of other immunomodulatory molecules defines the effect of non-571 professional APCs in different tissues and conditions. In this study, we show that hrSC are able 572 to express the co-signaling molecules CD58, CD80, and CD86 in addition to MHCII. These 573 molecules are associated with an activation of T-cells (Chen & Flies, 2013; Greenwald, Freeman, 574 & Sharpe, 2004).

575 Interestingly, a study comparing nerve biopsies of healthy patients and patients with chronic 576 inflammatory demyelinating polyneuropathy (CIDP) identified that CD58 expressing SCs were only found in the latter (Van Rhijn et al., 2000). This could be due to a similarity in the role of 577 578 SCs after nerve injury and during the interaction with immune cells in autoimmune diseases. 579 However, Van Rhijn et al. did not observe CD86 or CD80 expressing SCs in healthy or CIDP 580 patients, which indicates that the expression of co-signaling molecules detected in our in vitro 581 model reflects a unique feature of hrSCs. Of note, our primary human SCs were isolated from 582 peripheral nerves obtained after amputational surgeries and knowledge on pre-existing 583 conditions such as non-diagnosed neuropathies and medication are limited. However, we observed consistent and reproducible effects throughout our molecular, phenotypic and 584 585 functional characterization of hrSCs. Future studies should combine the knowledge derived 586 from human nerve biopsies and isolated human SCs to validate the immunomodulatory 587 capacities of this unique cell type in nerve injury and different diseases.

In addition to surface expression of co-signalling molecules, we found that hrSC secrete a
variety of immunomodulators. This is in line with previous studies on human SCs that
demonstrated the secretion of IL-6, IL-8, IL-15 and MCP-1 (Ozaki, Nagai, Lee, Myong, & Kim,

591 2008; Rutkowski et al., 1999). Our study enriches the repertoire of secreted hrSC molecules by 592 cytokines like IL-11 and chemoattractants like MCP-3, MCP-4, CXCL-16, GRO and MIP3 $\alpha$ 593 suggesting an unexpected functional diversity. In contrast to Rutkowski et al., 1999, we did not 594 detect the expression of IL-1 $\beta$  in our assay (Rutkowski et al., 1999). Taken together, these 595 findings demonstrate that hrSCs express the co-signalling molecules CD58, CD80 and CD86 596 together with MHCII and provide novel insight into the repertoire of hrSC secreted molecules, 597 beyond neurotrophins, with immunoregulatory functions.

598

# Inhibition of allogeneic T-cell activation - evidence for an immuno-regulatory function of human repair SCs

601 Furthermore, we show that the exposure to hrSCs causes a delayed or even abrogated CD4<sup>+</sup>T-602 cell proliferation and activation. In line with this finding, we demonstrate that SCs express co-603 inhibitory molecules such as B7-H3, HVEM and provide the first report that hrSC upregulate 604 PD-L1 after stimulation with IFNy. As not only the activation, but also the termination and 605 resolution of inflammation through surface expression of inhibitory molecules is a hallmark of 606 APCs, the presence of these molecules in hrSCs is remarkable. The source for IFNy release in 607 inflammatory tissues are mainly NK, CD4<sup>+</sup> and CD8<sup>+</sup> T-cells as well as macrophages. HrSCs may 608 even trigger the release of IFNy via secreted osteopontin that has been shown to induce IFNy 609 production in T-cells (Icer & Gezmen-Karadag, 2018). In this study we show that hrSCs are also 610 capable of IFNy secretion. Whether the autocrine production of IFNy by hrSCs or the paracrine 611 IFNy released by other cell types present at the site of nerve injury induces the surface 612 expression of PD-L1 on hrSCs remains to be determined.

We further observed that delayed T-cell activation was not accompanied by a shift towards any 613 614 particular T helper subset, but rather resulted in CD4+ T-cells with high CD25 expression, which may represent a regulatory or exhausted phenotype. The hypothesis of regulatory/exhausted 615 616 T-cells is supported by previous observations in rodent models (Meyer zu Horste et al., 2014; 617 Meyer zu Hörste et al., 2010; F.-J. Wang, Cui, & Qian, 2018; X. Wang et al., 2014). Similarly, it 618 has been shown that non-professional APCs like type II alveolar epithelial cells can prime 619 antigen specific CD4+ T-cells towards regulatory T-cells (Kambayashi & Laufer, 2014). This 620 suggests that hrSCs in their activated state might, despite high MHCII, CD40, CD80 and CD58 621 expression and secretion of pro-inflammatory cytokines IL-6, IL-8, TNF $\alpha$  and IFN $\gamma$ , adopt an 622 antigen presenting cell phenotype similar to M2 macrophages, which tightly control and terminate T-cell responses via B7-H3 and the PD-L1/PD-1 axis. Thus, a balance between the
initiation and termination of an immune response may be essentially controlled through repair
SCs during the multistep process of nerve regeneration.

626 The expression of PD-L1 by hrSCs after stimulation with IFNy supports the idea of a time and 627 situation dependent role of repair SCs. It is tempting to speculate that repair SCs initiate the 628 termination of the inflammatory response they helped to induce as first responders to nerve 629 injury. Our data suggest that repair SCs might possess an immunoregulatory function that could 630 prevent unnecessary damage to the neuronal environment by terminating an exceeding 631 immune response, in which large amounts of IFNy are produced by immune cells recruited to 632 the site of injury. To address this possibility, deeper phenotypic and functional characterization of especially CD4+CD25+ T-cells in vitro/ex vivo will be required in the future. Furthermore, 633 634 manipulating the balance of pro- and anti-inflammatory profile of repair SCs might represent a 635 novel therapeutic target in regenerative and pathological processes.

636

# 637 Implications for the field of neuro-inflammatory disorders,638 regenerative medicine and immune oncology

639 As the interaction between SCs and immune cells is of importance not only after nerve injury 640 but also regarding infectious, inflammatory and autoimmune disease of the peripheral nervous 641 system, a comprehensive understanding of this interaction is crucial. It has recently been 642 suggested that the activation of T-helper cells via MHCII by SC promotes neuropathic pain and 643 axonal loss after nerve injury in mice (Hartlehnert et al., 2017). In this regard the presented 644 panel of co-signaling molecules provides additional pharmaceutical targets to tackle this 645 interaction. In addition, it has been shown that rats with experimental autoimmune neuritis, a 646 common model for Guillain-Barrè syndrome, showed a clinical improvement, reduced neuronal 647 lymphocyte infiltration and a shift towards regulatory T-cells in the peripheral blood after 648 administration of PD-L1 (Ding et al., 2016).

649 Importantly, it could be shown that SCs play a fundamental role in certain immune-oncological 650 processes. SCs with a repair-related phenotype (including MHCII expression) are attracted by 651 favorable forms of peripheral neuroblastic tumors, neuroblastomas, of a genetic subtype and 652 trigger tumor cell maturation/differentiation and apoptosis, a phenomenon which could also 653 be recapitulated in *in vitro* experiments (Weiss et al., 2021). These tumors, in comparison to 654 their malignant counterpart, frequently show prominent MHCII+ and CD3+ immune cell infiltrates (Ambros et al., 1996; Weiss et al., 2021). It will be interesting to study the
composition of these infiltrates and whether and how SCs contribute to their recruitment and
modulation.

658

In summary, we here provide *in vitro* evidence that human SCs in an injury condition adopt functions of APCs, i.e, phagocytosis, up-regulation of MHCII and co-signaling molecules, secretion of an array of immunoregulatory molecules, and repression of T-cell activation. Our data suggest that repair SCs can participate in the termination of the inflammatory response to prevent excessive tissue damage and allow nerve regeneration. The molecules expressed and secreted by hrSC presented in this study will help to understand their complex interplay with immune cells after injury and in disease.

666

# 667 Author contributions

S.T.-M. conceptualized the project; J.B., T.W. and S.T.-M. planned experiments, performed
research, analyzed and interpreted data and wrote the manuscript; H.S. and F.R. performed
research and analyzed data; M.K. developed bioinformatics tools and analyzed data; A.D. and
P.S. provided essential reagents, planned experiments and interpreted data; R.W. provided
essential material; P.F.A. and I.M.A interpreted data; all authors reviewed the manuscript.

673

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680

# 681 Conflict of Interest Statement

682 The authors declare no conflict of interest.

#### 683

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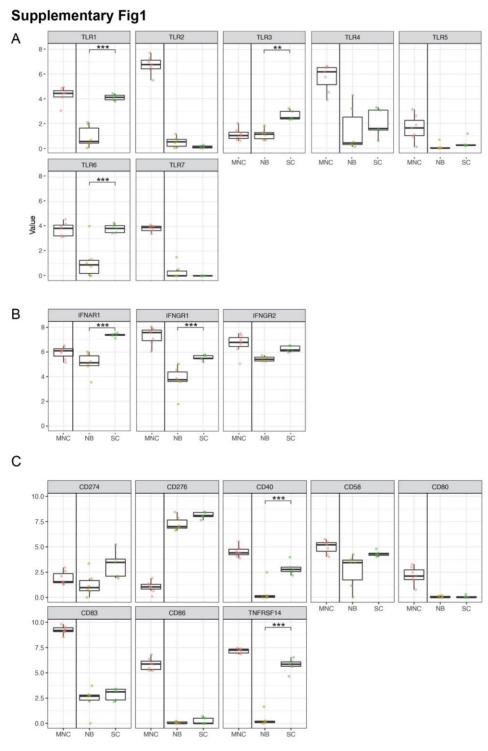
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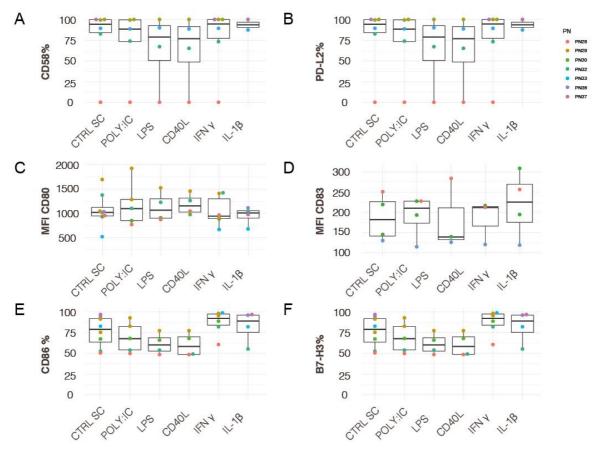
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# 953 Supplementary Figures



954

Supplementary Figure 1 | mRNA expression of Toll-like receptors, interferon receptors and co-signaling
 molecules. Boxplots show mRNA levels (RPKM) in hrSCs (n=5) versus NB cells (n=5). MNCs are shown as
 reference. (A) Toll-like receptors (B) interferon receptors and (C) co-stimulatory and –inhibitory
 molecules. Boxes contain 50% of data and whiskers the upper and lower 25% means are displayed as
 black horizontal lines.



#### Supplementary Figure 2 Berner, Weiss et al, 2021

960

961 Supplementary Figure 2 | Flow cytometry-based phenotyping of MHCII and co-signaling molecules upon 962 inflammatory stimulation. Box plots show the expression status of CD58 (A), PDL2 (B), CD80 (C), CD83 963 (D), CD86 (E) and B7H3 (F) of S100 positive hrSCs after stimulation with POLY:IC, LPS, CD40L, IFNy and 964 IL-1β; n=9; technical replicates (same color); biological replicates (different color). Each biological 965 replicate is conducted with hrSCs isolated from a different donor nerve. (A, B, E, F) Boxplots represent 966 the percentage of positive cells based on gates set in relation to unstained controls. (C, D) Boxplots 967 represent the mean fluorescence intensity (MFI). Boxes contain 50% of data and whiskers the upper 968 and lower 25%; means are displayed as black horizontal lines. A two-way ANOVA using a post-hoc Holm 969 p value correction was performed; \*  $p \le 0.05$ ; \*\*  $p \le 0.01$ ; \*\*\*  $p \le 0.001$ .

# 970 Supplementary Tables

#### 971

1 <sup>st</sup> antibodies				Application	
Antigen	Species	catalog No	company	dilution	comment
S100	rabbit	#Z0311	DAKO	1:200	1 hr, RT, perm
vimentin	chicken	#AB5733	Merck Millipore	1:200	1 hr, RT, perm
NGFR	rabbit	#8238S	CellSignaling	1:300	o.n. <i>,</i> 4°C
PD-L1	Mouse	#4274539	eBioscience	1:50	o.n. 4°C
HLA-DR-α1	mouse	#M0746	DAKO	1:50	o.n., 4°C

2 <sup>nd</sup> antibodies				Application	
Antigen	Species	catalog No	company	dilution	comment
α rb FITC	swine	#F0205	DAKO	1:50	1 hr, RT
α ch AF647	goat	#SA5-10073	LifeTech.	1:300	1 hr, RT
α ms AF594	goat	#A11032	LifeTech.	1:300	1 hr, RT

directly labelled antibodies				Application	
Antigen	Species	catalog No	company	dilution	comment
S100B-FITC*	rabbit	#Z0311	DAKO	1:50	20 min, 4°C, perm
CD80-PerCP-eF710	mouse	46-0809-42	eBioscience	1:25	
CD276(B7-H3)-PE	mouse	565829	BD Bioscience	1:50	
CD40-PerCP	mouse	Ab91282	Abcam	1:5	
MHCII-APC-ef780	mouse	47-9956-42	eBioscience	1:50	
PD-L1-PE	mouse	557924	BD Bioscience	1:5	
HVEM-A647	mouse	564411	BD Bioscience	1:25	
CD86-APC	mouse	555660	BD Bioscience	1:25	
CD273- PE	mouse	565829	BD Bioscience	1:25	
CD58-APC	mouse	17-0578-41	eBioscience	1:25	

972

973 Supplementary Table 1 | List of antibodies.

974 perm = permeabilization necessary, RT = room temperature.

975

976 Supplementary Table 2 | RNA-sequencing. Differential gene expression analysis of hrSCs compared to

977 NB cell lines.

- 978 Supplementary Table 3 | RNA-sequencing. GO functional annotation of top 250 genes upregulated in
- 979 hrSCs versus NB cell lines.
- 980
- 981 Supplementary Table 4 | RNA-sequencing. Gene set enrichment analysis (GSEA) in hrSC versus NB cell
- 982 lines.
- 983
- 984 Supplementary Table 5 | Protein array. Differential protein secretion of hrSCs versus NB cell lines.