A Multiomic Analysis Reveals How Breast Cancers Disseminated to the Bone Marrow Acquire Aggressive Phenotypes through Tumor-Stroma Tunnels

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Running title

GIV borrowed through nanotubes drives aggressive disease in ER+ breast cancer

Key Words

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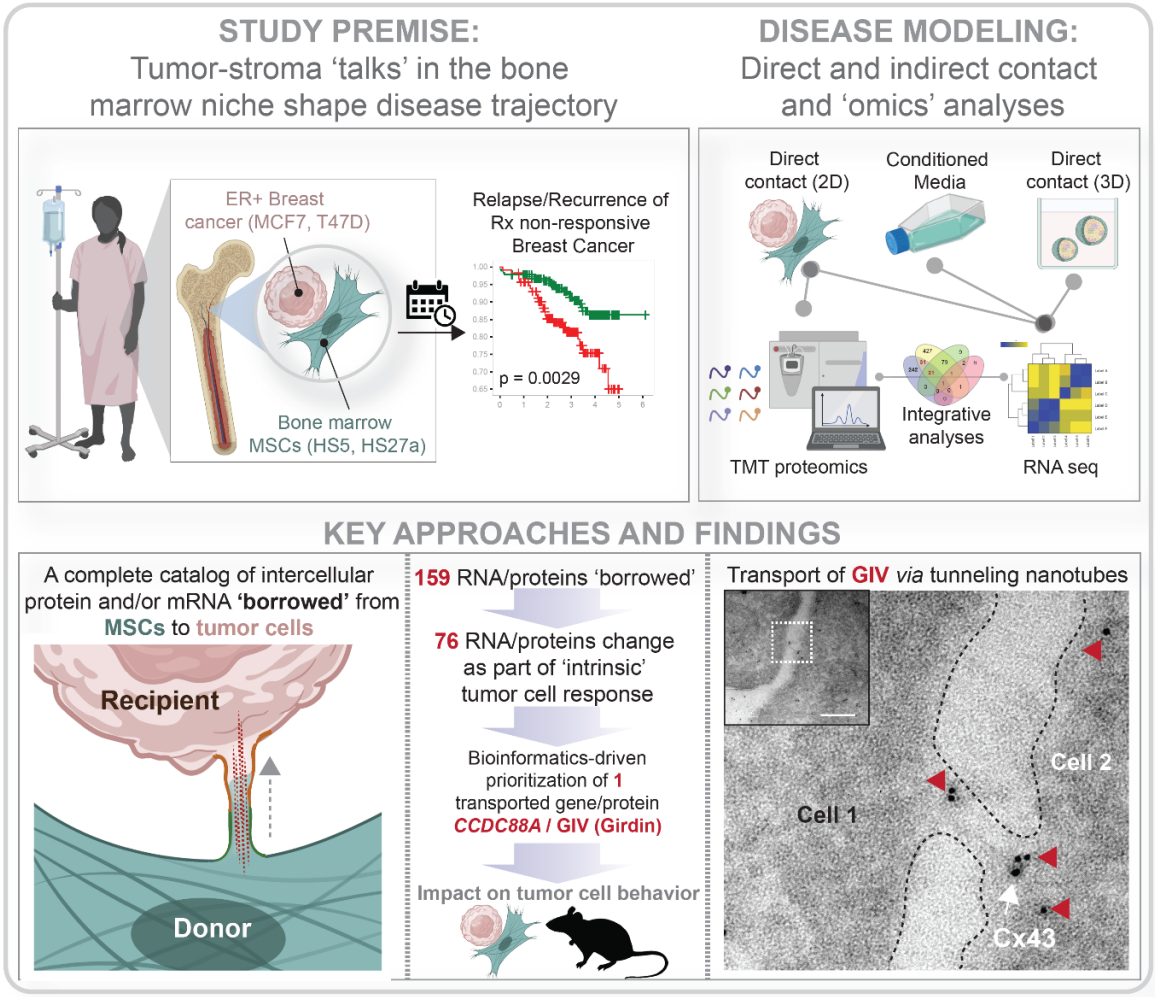
Abstract

Estrogen receptor-positive (ER+) breast cancer commonly disseminates to bone marrow, where interactions with mesenchymal stromal cells (MSCs) shape disease trajectory. We modeled these interactions with tumor-MSC co-cultures and used an integrated transcriptome-proteome-network-analyses workflow to identify a comprehensive catalog of contact-induced changes. Induced genes and proteins in cancer cells, some borrowed and others tumor-intrinsic, were not recapitulated merely by conditioned media from MSCs. Protein-protein interaction networks revealed the rich connectome between 'borrowed' and 'intrinsic' components. Bioinformatic approaches prioritized one of the 'borrowed' components, *CCDC88A*/GIV, a multi-modular metastasis-related protein which has recently been implicated in driving one of the hallmarks of cancers, i.e., growth signaling autonomy. MSCs transferred GIV protein to ER+ breast cancer cells (that lack GIV) through tunnelling nanotubes via connexin (Cx)43-facilitated intercellular transport. Reinstating GIV alone in GIV-negative breast cancer cells reproduced ~20% of both the 'borrowed' and the 'intrinsic' gene induction patterns from contact co-cultures; conferred resistance to anti-estrogen drugs; and enhanced tumor dissemination. Findings provide a multiomic insight into MSC→tumor cell intercellular transport and validate how transport of one such candidate, GIV, from the haves (MSCs) to have-nots (ER+ breast cancer) orchestrates aggressive disease states.

GRAPHIC ABSTRACT



Introduction

Estrogen receptor-positive (ER+) breast cancer, the most common subtype, preferentially disseminates to bone and bone marrow(1, 2). Bone metastases are incurable, and cause debilitating symptoms, e.g., pain, fractures, and life-threatening hypercalcemia(3). The bone marrow, on the other hand, harbors disseminated tumor cells (DTCs) in breast cancer; DTCs may persist in a clinically occult state for decades before they may ultimately proliferate and potentially travel to other organs to produce delayed recurrences that occur in ~40% of patients with ER+ breast cancer(4). Recurrent disease is more aggressive, relatively resistant to treatment, and currently incurable. Little progress has been made in treating breast cancer that has already disseminated to bone(5), largely because we lack a comprehensive understanding of the molecular mechanisms that make ER+ breast cancer cells more aggressive in the bone marrow niche(6).

What is widely believed is that interactions with stromal cells in the bone marrow environment shape key functions of breast cancer cells that ultimately determine disease progression and outcomes(7). Mesenchymal stem cells (MSCs), a multipotent cell type that contributes to formation of bone, fat, and cartilage tissues, are a major stromal cell type driving aggressive phenotypes of disseminated ER+ breast cancer cells in bone marrow. MSCs regulate ER+ breast cancer cells through mechanisms such as secreted cytokines and direct intercellular interactions(8). Work by us and others have established that direct interactions with MSCs, rather than soluble molecules, drive changes in gene expression and metabolism that promote cancer stem-like cell states, resistance to anti-estrogen drugs, and metastasis in ER+ breast cancer(9-11). Breast cancer cells and MSCs are known to establish channels of intercellular communication that transport molecules and organelles. The two major structures for such intercellular communication include: Gap junctions and tunneling nanotubes (TNTs), both of which share connexin 43 (Cx43) as an essential molecular player. Gap junctions are intercellular channels comprised of various subsets of connexin proteins(12). Gap junctions and Cx43 are upregulated in lymph node and systemic metastases in breast cancer and other malignancies, suggesting these structures contribute to essential steps in the metastatic cascade(13). TNTs are actin-rich long, thin tubes that may form between cells of the same or different types, thereby allowing long-range communication via the exchange of materials. A broad range of intracellular contents, including microRNAs, proteins, and organelles, exchange between cells via TNTs. TNTs increase drug resistance of cancer cells; regulate proliferation; and promote metastasis.

Despite these insights, a limited number of molecules transferred from MSCs via gap junctions or TNTs have been implicated in aggressive phenotypes of breast cancer cells, whereas the identity of most remains unknown. Here we tackle this knowledge gap by performing a comprehensive multiomic network analysis to identify molecules and biologic processes regulated by direct contact between bone marrow MSCs and ER+ breast cancer cells. We identified genes and proteins that cancer cells acquire from MSCs through direct transfer ("borrowed" components) and additional molecules they induce because of such transfer ("intrinsic components"). We use bioinformatic

approaches to explore the implications of these gene expression changes on patient outcome and subsequently prioritized one 'borrowed' gene/protein (*CCDC88A/*GIV) to explore further and validate through a series of *in vitro* and *in vivo* studies. Our findings establish a comprehensive resource for changes induced in ER+ breast cancer cells by contact with bone marrow MSCs and pinpoint GIV as a promising target to overcome aggressive phenotypes that breast cancer cells acquire in a bone marrow environment.

Results

Multiomic analysis of the impact of close contact between ER+ breast cancer cells and MSCs

DTCs in the bone marrow displace hematopoietic stem cells from supportive niches(14), where they establish direct contact with various subsets of MSCs and eventually gain aggressiveness. To identify how MSCs may impact ER+ breast cancer cells through direct contact, we used a 2D co-culture model combining MCF7 or T47D human ER+ breast cancer cells with human HS5 or HS27a MSCs in a 1:9 ratio (**Fig 1A**). After 3 days of co-culture in medium with low serum and physiologic concentrations of glucose, we recovered the tumor cells using EpCAM immunomagnetic beads, capitalizing on the fact that EpCAM is expressed exclusively on tumor cells of epithelial origin. We previously showed that such EpCAM-based immunoisolation is relatively devoid of MSC contamination(15). To control for the effects of soluble molecules produced by MSCs, we cultured MCF7 or T47D cells for 3 days in conditioned medium from MSCs (**Fig 1A**). Monocultures of MSCs and tumor cells were used as additional comparator groups. All samples were analyzed by bulk RNA sequencing; mono- and contact cultured MCF7 cells were also analyzed by TMT proteomics.

Exposure of MCF7 cells to contact culture (CC) but not conditioned media (CMed), was associated with a significant lowering of tumor dormancy score (**Fig 1B**); low scores were previously shown to confer a ~2-fold increase in the risk of recurrence in 4 independent cohorts of patients with ER+ breast cancers(16). These findings suggest that our co-culture model captures key transcriptomic changes in ER+ breast cancer cells of translational relevance that correlate with more aggressive disease in patients.

We carried out a combinatorial multiomics analyses to determine what proteins or transcripts may be expressed highly in MSCs that are 'borrowed' by MCF7 cells. To this end, we first created a catalog of genes that are differentially expressed (DEGs; upregulated) in MSCs, but not in MCF7 cells (MCF7 vs HS5; n = 1471; **Fig 1C**). This catalog served as a denominator for all likely candidate genes that a tumor cell may lack originally but acquire from MSCs via intercellular communication. Next, we performed pair-wise DEG analysis on the other MCF7 samples that were subjected to different co-culture conditions. Many genes (n = 482) and proteins (n = 295) were induced due to direct contact culture (CC-induced genes; **Fig 1C**). Few genes were induced because of exposure to conditioned media (CMed-induced genes, n = 13; **Fig 1C**). An overlay of these showed the following: (i) Exposure to conditioned media alone induced only a single unique proteins/transcripts in MCF7 cells, implying soluble mediators or exosomes as potential modes of communication; (ii) By contrast, contact culture could account for 487 unique proteins/transcripts, implying direct contact as the major mode of tumor-MSC communication, accounting for the largest share of the uniquely induced genes; (iii) 242 unique proteins/transcripts (39 transcripts and 203 proteins, with no proteome-transcriptome overlap) were upregulated in MCF7 cells as a consequence of contact culture. These transcripts/proteins were not highly expressed in HS5 cells. This last category was presumed to be tumor cell-intrinsic response to

139 contact culture, unlikely to be transferred directly from MSCs to breast cancer cells. It is noteworthy
140 that neither the experimental design, nor the analytical steps can conclude with certainty if transport
141 of a given target occurred as a protein or as mRNA because unknown factors (transcript/protein half-
142 life) are expected to confound such conclusions. Similarly, while we infer that 487 unique
143 RNAs/proteins could be transferred during contact culture, i.e., "borrowed" directly by cancer cells
144 from the MSCs, we cannot exclude some cancer cell-intrinsic contributions to the overall levels. We
145 did observe, however, that the 'borrowed' RNA/proteins were enriched for biological processes that
146 govern tube morphogenesis, organization of extracellular encapsulated structures, and movement of
147 anatomic structures in the context of multicellular systems (**Fig 1D**). Enrichment of these processes
148 further suggests the potential for direct transfer of RNA/protein from MSCs to cancer cells through
149 structures such as tunneling nanotubes. Reactome and gene ontology analyses of the genes induced
150 by conditioned media, contact culture and intrinsic response present a comprehensive picture of
151 distinct modes by which MSCs shape behavior and function of cancer cells (**Supplementary Fig 2**).
152 A similar analysis for the transcripts and proteins that were downregulated during contact culture and
153 when exposed to conditioned media was notable for genes/proteins that reduce the dependence on
154 ER signaling (**Supplemental Fig 1**). A full catalog of all the genes/proteins that are upregulated
155 (**Supplemental information 1**) and downregulated (**Supplemental information 2**) during contact
156 culture are provided.
157
158 **A gene signature of contact culture is prognostic and predictive in ER+ breast cancers.**
159 We noted that 39 unique genes were upregulated, identified by both RNA seq and TMT proteomics,
160 in MCF7 cells during contact co-cultures (**Fig 1C**). Almost all of them (n=38; **Fig 1E**) were uniquely
161 upregulated during contact culture, whereas 1 (*KYNU*) was upregulated in conditioned media. A
162 heatmap analysis showed that these 39 genes are poorly expressed in monocultured MCF7 cells
163 (MC; **Fig 1E**) but highly expressed in HS5 cells (lane 2; **Fig 1E**). The gene expression patterns in
164 MCF7 cells that were subjected to culture in direct contact with HS5 cells (CC; **Fig 1E**) looked more
165 like that in HS5 cells. By contrast, MCF7 cells subjected to culture in conditioned medium looked
166 virtually indistinguishable from monocultured MCF7 cells (compare MC and CMed; **Fig 1E**). A
167 composite score of the levels of expression of these 39 genes confirmed their statistically significant
168 increase in contact, but not conditioned media cultures (**Fig 1F**). This pattern of gene induction was
169 reproducibly observed when we swapped HS5 in the co-cultures with another MSC line (HS27a; **Fig**
170 **1G**) or swapped the MCF7 tumor cell line with another ER+ breast cancer line (T47D; **Fig 1H**). These
171 findings demonstrate that the 39-gene signature represents a conserved feature of how MSCs impact
172 the properties or behavior of ER+ breast cancer.
173 The 39 genes showed an enrichment of processes that related to growth factor, PI3K/Akt and
174 an *IL4/IL13 and IL10*-centric tolerogenic cytokine signaling (**Fig 2A**), suggesting that the tumor cell's

175 acquisition of these 39 genes from MSCs may impact these aspects of tumor cell biology and/or
176 behavior, including those that concern its interactions with and its ability to evade the immune system.
177 To test its translational relevance, we applied this 39-gene signature to a publicly available
178 dataset that prospectively tracked the outcomes of ER+ breast cancers following neoadjuvant taxane-
179 anthracycline chemotherapy(17) (**Fig 2B-E**). Kaplan-Meier curves revealed that high levels of the
180 contact culture signature correlated with significantly worse distant relapse-free survival in patients
181 with ER+ (**Fig 2B**), but not ER- breast cancers (**Fig 2C**). High levels of the close contact signature
182 also predicted worse outcomes in patients with treatment resistant, but not treatment sensitive,
183 disease (**Fig 2D-E**). Taken together, these findings establish that the 39 genes presumed to be
184 borrowed by ER+ breast cancer cells via direct contact with MSCs carry translationally relevant
185 information; they identify patients at greater risk for death from recurrent breast cancer.
186
187 **The connectome of genes either 'borrowed' or induced as intrinsic response during contact**
188 **culture**
189 To discover how contact culture with MSCs reprograms signaling networks in ER+ breast cancer
190 cells, we used the 39-proteins as 'seeds' to build a protein-protein interaction (PPI) network (**Fig 3A**).
191 The resultant network (comprised of 2743 proteins) was overlayed with 'borrowed' (n=487) and
192 'intrinsic' (n=242) gene sets (see **Fig 1B**); this allowed construction of a more focused network using
193 159 genes that the ER+ breast cancer cells borrow from MSCs and 76 genes in the cancer cell
194 intrinsic response group. We visualized this network as a multilayer network connecting borrowed
195 (pink; **Fig 3C**) and intrinsic response (green; **Fig 3C**) genes. Within the resultant PPI network, 1482
196 nodes/proteins interacted within 'borrowed' layer and 835 nodes/proteins interacted within the intrinsic
197 layer. The two layers shared 567 common nodes/proteins, indicative of meaningful connectivity
198 between the two layers (*p* value of 0.00096, determined by hypergeometric test). The edge and node
199 list of the entire PPI network, along with its various subnetworks are presented in **Supplemental**
200 **Information 3**. Findings also suggest functional integration between the two components such that
201 the induction of one (the intrinsic tumor genes) may either enable the functions of and/or reflect the
202 consequences of the other (the borrowed genes).
203 The borrowed response interactome was notable for Akt, growth factors and/or their receptors
204 (*EGFR, VEGFA, WNT5A*) and integrins (**Fig 3C**), as noted earlier (**Fig 2A**). Also found in the borrowed
205 network was the gap junction protein, *GJA1*/CX43, which has been implicated in establishment of
206 tunneling nanotubes(18). The intrinsic interactome was notable for VEGFR2-mediated cell
207 proliferation, activation of RHO GTPases and cytokine signaling (**Fig 3D**).
208
209 ***CCDC88A*/GIV as a key gene borrowed by cancer cells amidst robust intercellular transport**
210 With an intent to validate and/or characterize key components of the borrowed
211 proteome/transcriptome, we further refined the list of borrowed genes derived in our 2D contact

212 culture model (**Fig 1A**) leveraging a previously published 3D contact culture of MCF7 or T47D cells
213 with HS5 (**Fig 3E**)(19). Such a refinement was carried out with a two-fold intention: (i) to enhance the
214 physiological context and translational relevance because TNTs have been shown to be formed in
215 3D culture systems(20); and (ii) to provide a continuity between 2D and 3D TNT biology, which has
216 been a difficult task to achieve in a field that is still in its infancy(21). Refinement gave a handful genes
217 (n=19) that are induced also during 3D close contact culture in both MCF7 and T47D cells (**Fig 3F**).
218 Gene ontology (GO) analysis of these 19 genes revealed that one gene, *CCDC88A* [which encodes
219 the protein Gα-Interacting, Vesicle-associated (GIV, a.k.a, Girdin)] is commonly shared among all key
220 processes upregulated in ER+ breast cells by contact with MSCs (**Fig 3G**). Compared to
221 monocultured *CCDC88A* transcript was significantly upregulated in our 2D direct contact but not the
222 conditioned medium cultured MCF7 cells (**Fig 3H**). A focused analysis of the *CCDC88A/GIV*-
223 subnetwork from the multi-layer interactome (in **Fig 3C**) revealed that the interactome of GIV could
224 support numerous pathways and processes involved in cell projections and membrane domains (**Fig**
225 **3I**), suggesting that *CCDC88A* associates with direct intercellular contacts.
226 We confirmed by interferometry microscopy that 'borrowing' of *CCDC88A* in our 2D contact
227 culture system (**Fig 3H**) was associated with the presence of numerous TNTs connecting MCF7 and
228 HS5 cells (**Fig 3J**, **Supplementary Figure 3**). TNT formation in contact cultures was associated also
229 with the elevated expression of two proteins previously implicated as central factors for TNT formation:
230 (i) the gap junction protein *GJA1* (18)(connexin 43, CX43; **Fig 3K**) and the TNT marker, *TNFAIP2*
231 (22)(M-Sec; **Fig 3L**). To investigate if gap-junction or TNT-facilitated intercellular communication is
232 functional (i.e., allowed intercellular communication) we carried out the well-established calcein-AM
233 transfer assay(23, 24). When MCF7 cells that stably expressed mCherry (recipients) were cocultured
234 with calcein-labeled HS5 MSCs (donors) or Calcein-labeled MCF7 cells, we detected the successful
235 transfer of calcein into mCherry-labeled MCF7 cells (**Supplementary Figure 4**). While both donor
236 cells (HS5 and MCF7 cells) transferred calcein to the recipient MCF7 cells, transfer was markedly
237 more from HS5 cells (**Supplementary Figure 4**). These results confirm that our 2D contact cultures
238 were permissive to intercellular transport.
239 Together these findings suggest that TNTs in contact cultures could serve as a route for breast
240 cancer cells to borrow from MSCs certain RNAs and proteins, among which, *CCDC88A*/GIV may be
241 a central player.
242
243 **GIV(*CCDC88A*) is transported from MSCs to ER+ breast cancer cells**
244 Although GIV was prioritized through computational rationale (**Fig 3E-I**), we prioritized its candidacy
245 for further validation as opposed to any of the other 18/19 candidate genes (**Fig 3F**) because of three
246 key reasons: *First*, as a large multi-modular protein shown to integrate signals initiated by diverse
247 classes of receptors and those transduced through diverse signaling pathways, GIV has been
248 implicated in tumor cell aggressiveness (stemness(25), survival after DNA damage(26),

249 invasiveness(26), chemoresistance(27) and acquisition of metastatic potential(28)) by diverse groups
250 in a multitude of cancers, including breast(29) and is considered to be a metastasis-related
251 protein(30). *Second*, unlike stromal cells(31, 32) and triple negative breast cancers, which express
252 high levels of GIV, ER+ breast cancer cells, such as MCF7 and T47D, have been shown to be GIV-
253 deficient(33) due to an alternative splicing event [intron 19 retention], which leads to the loss of the
254 resultant transcript to non-sense mediated decay. The concept of haves (MSCs) lending GIV to have
255 nots (ER+ tumor cells) for a potential gain in metastatic potential by the latter appeared interesting.
256 Consistent with this concept, prior studies had in fact demonstrated that patients with ER+ breast
257 cancers do express GIV, and such expression correlates with more metastasis and poorer
258 survival(34, 35). *Third*, GIV has recently been shown to be a key orchestrator of secretion-coupled
259 autonomy(36), wherein cancer cells may secrete and sense their own growth factors to survive.
260 Proteomic studies confirmed that GIV enabled autocrine growth factor signaling autonomy specifically
261 within the EGF/EGFR system(36). It is noteworthy that EGFR is one of the initially identified list of 39
262 'borrowed' RNAs and proteins in contact culture (**Fig 1E**). EGFR remained on the list even after the
263 3D contact culture refinement (**Fig 3E**) as one of the 19 "borrowed" genes, alongside *CCDC88A* (**Fig**
264 **3F**).
265 GIV protein was virtually undetectable in the lysates from monocultures of 3 different ER+
266 breast cancer cells but detected as a full-length protein (~250 kDa) in cells recovered with EpCAM-
267 based immunocapture and lysis following 3 days in contact cultures with HS5 cells (**Fig 4B**). GIV
268 protein was detected by immunoblotting in MCF7 cells that were lysed immediately after separation
269 from HS5 cells but not in those after 24 to 96 h of additional culture post separation (**Fig 4C**). These
270 findings indicate that once acquired, GIV is rapidly lost upon returning tumor cells to monoculture,
271 and ongoing close contact with MSCs is essential to maintain the levels of GIV in tumor cells.
272 To confirm if GIV in MCF7 cells was indeed acquired from HS5 cells and determine if transport
273 occurred as transcripts or proteins, we stably expressed short hairpin (sh) RNA targeting GIV in either
274 MCF7 or HS5 cells and put them in contact culture with each other in various combinations (see **Fig**
275 **4D**). Batch populations of cells showed ~80% depletion of GIV in HS5 cells (**Fig 4E-***right*). Contact
276 cultures of control MCF7 and HS5 cells showed expected upregulation of both full-length GIV in MCF7
277 cells (**Fig 4E-***left*; lane 3). Contact cultures of MCF7-shGIV cells and HS5 still showed increased
278 amounts of GIV protein, indicating that shRNA against *CCDC88A* did not reduce GIV transfer (**Fig**
279 **4E-***left*; lane 4). However, MCF7 cells co-cultured with HS5-shGIV cells did not result in GIV protein
280 transfer (**Fig 4E-***left*; lane 5). Because MCF7 cells expressing shGIV continued to express GIV
281 protein, findings indicate that the observed upregulation of GIV in MCF7 cells that were subjected to
282 contact culture with HS5 relies predominantly on transfer of GIV as a protein. Some transfer of GIV
283 as mRNA cannot be ruled out.
284
285 **Cx43 and GIV interact and are co-transported through intercellular communication sites**

286 Because gap junctions are known to serve as sites for TNT formation and/or attachment(20, 37) and
287 CX43 is a shared molecular entity for them both, we assessed CX43 expression in MCF7 cells that
288 were either in monocultures or recovered from contact cultures with HS5 cells. Co-culture with HS5
289 cells increased CX43 in MCF7 cells, while monocultures of MCF7 cells showed undetectable levels
290 of this protein (**Fig 5A**). Next we used two perturbagens to modulate intercellular communication via
291 gap junctions: (i) Carbenoxolone, a widely used chemical inhibitor of GJIC; and (ii) Fulvestrant, which
292 inhibits the transcriptional functions of ER, and by that token, inhibits various ER targets, including
293 the transcription of CX43(38, 39). Both perturbagens virtually eliminated the upregulation of GIV and
294 CX43 in MCF7 cells co-cultured with HS5 cells (**Fig 5B**), while these compounds had minimal effects
295 on amounts of CX43 in HS5 cells alone (**Supplementary Figure 5**). These results show that direct,
296 CX43-mediated intercellular communication is necessary for MCF7 cells to borrow GIV protein from
297 HS5 cells.
298 To resolve the nature of these CX43-dependent compartments that facilitate intercellular
299 communication, we carried out an ultrastructural analysis by immunogold electron microscopy. CX43
300 and GIV were found to co-localize either near gap junctions (**Fig 5C**-*top left*),at/near more elaborate
301 and less defined contact sites (**Fig 5C**-*bottom left*), or within tube like passages connecting cells (**Fig**
302 **5C**-*right*).
303 Co-localization of CX43 and GIV suggested that these proteins may interact; we asked if they
304 do. Using CX43-GFP expressed in Cos7 cells and purified GST fusions of N-terminal or C-terminal
305 part of GIV in pull down assays, we confirmed that the N-terminus, but not the C-terminus of GIV
306 binds directly to CX43 (**Fig 5D-F**). This finding is consistent with a prior work demonstrating the
307 importance of GIV-NT in junctional localization(40).
308 Together, these findings suggest that CX43 and GIV interact and co-migrate from MSCs to
309 ER+ breast cancer cells during CX43-mediated intercellular transport.
310
311 **Adding GIV to ER+ breast cancer cells recapitulates key functions gained during contact**
312 **culture**
313 Next, we asked what proportion of the functions gained during contact culture with MSCs may be
314 accounted for or recapitulated by GIV alone. To this end, we created MCF7 cells that stably expressed
315 GIV using a piggyBac transposase system (**Fig 6A**) and analyzed them by RNA Seq (**Fig 6B**).
316 Approximately ~20% of the genes in the 'borrowed' (n = 32 genes) and 'intrinsic' response (n = 17
317 genes) components of contact culture were able to perfectly classify the MCF7 cells with or without
318 GIV (**Fig 6C**). A complete catalog of these genes is presented in **Supplemental Information 4**. Heat
319 maps display the differential expression of these genes (**Fig 6E, F**). Of the tumor intrinsic gene
320 response, we previously discovered that co-culture with MSCs upregulated *LCN2,* an iron
321 sequestering protein, and *CD44,* a marker of stem-like cells, in breast cancer cells (15). Pathway
322 analysis of the 32-gene borrowed signature recapitulated by stable expression of GIV alone showed

323 enrichment for numerous processes related to response to external stimuli, while the 17-gene
324 signature included vesicular transport and exocytosis (**Supplemental Figure 6**). These data reinforce
325 our focus on GIV within the list of genes that are transferred from MSCs to breast cancer cells in the
326 bone marrow environment to enhance aggressive traits and facilitate disease progression.

327 To investigate effects of GIV on drug resistance, we focused on anti-estrogen drugs tamoxifen
328 (a selective estrogen receptor modulator)(41) and fulvestrant (a selective estrogen receptor
329 degrader)(42). We also tested combination therapy with fulvestrant and palbociclib, an inhibitor of
330 CDK4/6 used with anti-estrogen therapy for patients with metastatic ER+ breast cancer. Following
331 three days of treatment in low serum, physiologic glucose medium, we quantified relative numbers of
332 viable cells at various concentrations of tamoxifen, fulvestrant, or fulvestrant plus a fixed concentration
333 of palbociclib. MCF7-GIV cells showed resistance to each of these treatment regimens, particularly
334 for fulvestrant (**Fig 6G-I**). These data establish that GIV confers resistance to clinically used drugs for
335 ER+ breast cancer and suggest that upregulation of GIV in cancer cells in close contact with MSCs
336 may permit disseminated ER+ breast cancer cells to survive therapy in the bone marrow environment.

337 Because GIV coordinates intracellular signaling pathways enabling growth-factor autonomous
338 survival and proliferation of circulating tumor cells(36, 43), we investigated the effects of GIV on
339 hematogenous dissemination of ER+ breast cancer cells. We injected MCF7 and MCF7-GIV cells into
340 the left cardiac ventricle of female immunodeficient NOD.Cg-Prkdc scid (NSG) mice and tracked
341 cancer cells using bioluminescence (**Fig 6J**). Viable MCF7 cells dropped significantly and steadily
342 from day 1 through day 10, while the drop was insignificant in mice injected with MCF7-GIV. From
343 days 0-1, signal from control MCF7 cells decreased by approximately 70%, while MCF7-GIV cells
344 diminished by only approximately 10%. From days 1-3, losses of viable cells were approximately 20%
345 and <10% for MCF7 and MCF7-GIV cells, respectively. The rapid drop in MCF7 cells is not
346 unexpected because we did not supplement mice with estrogen, which typically is required for MCF7
347 cells to thrive and proliferate in vivo. Intriguingly, we noted that the differences between groups
348 diminished over time from days 10-24 and became virtually indistinguishable thereafter. These results
349 reveal that GIV facilitates survival during the early stages in dissemination of ER+ breast cancer cells.
350 Because contact culture studies in vitro take ~3 days to transfer GIV, it is possible that MCF7 cells
351 borrowed GIV from stromal cells that have abundant amounts of the same.
352

353 **Tumor cells may acquire *CCDC88A* and other 'borrowed' genes also from fibroblasts**

354 Studies have documented that disseminated tumor cells and metastases in one organ can seed
355 metastatic disease in a second site, emphasizing the need to understand how the bone marrow
356 environment promotes aggressive phenotypes in breast cancer(44). We asked if the usefulness of
357 the catalog of 'borrowed' genes we describe here maintained relevance beyond MSCs and perhaps
358 extend to resident tissue fibroblasts; the latter also are well known to establish TNTs with cancer
359 cells(45). To this end, we leveraged the only publicly available, previously published study that

360 compared monocultures of MCF7 with contact cultures of MCF7 cells and BJ fibroblasts by RNA
361 seq(46). As a third comparator group, they cultured the MCF7 cells in extracellular matrix (ECM) that
362 was derived by concentrating conditioned media from the BJ fibroblasts (CMed) (**Fig 7A**). Contact
363 culture, but not ECM-treated grow conditions induced each of the 3 borrowed gene signatures we
364 described earlier (**Fig 7D-F**). Most importantly, *CCDC88A* was among the "borrowed" gene signature
365 induced during contact culture with fibroblasts. These results suggest that ER+ tumor cells may
366 acquire GIV via intercellular transport from diverse stromal cells, which are known to express GIV at
367 high levels.

Discussion

The major problem we address here is the widely recognized, but poorly understood, means by which the bone marrow environment harbors disseminated tumor cells in ER+ breast cancer, permitting long-term survival of these cells despite hormone targeted therapy(47). Persistence of disseminated tumor cells poses a documented, progressively increasing risk of delayed recurrence that most often occurs in bone (48-50) (~50%) for patients with ER+ breast cancer. MSCs have been implicated as key enablers of tumor cells in the bone marrow niche(51) (52)However, mechanisms that support disseminated tumor cells in bone marrow and potentiate potential recurrence remain unclear. The compendium of TNT tumor-stromal transport we reveal here provides a wealth of potentially actionable targets to disrupt MSC niches for cancer cells and end the current impasse in treating bone metastases. There are potentially three major ways in which this work advances the field of cancer biology.

A catalog of MCS-to-tumor gene transfer

First, we provide here a comprehensive catalog of genes transferred from the MSCs to ER+ breast cancer cells during direct contact culture. The catalog is likely to be physiologically relevant and reproducible because the multiomic rigor we employed went beyond our own datasets generated using all 4 possible combinations of two ER+ breast cancer cell lines and two MSCs. We further refined using datasets from independent laboratories that span both 2D and 3D models. This catalog not only provides a prioritized list of genes for the scientific community to pursue but also provides new knowledge of molecular mechanisms that reprogram breast cancer cells in the bone marrow. For example, while MSCs are known to regulate breast cancer cells through soluble mediators such as cytokines(53), work done by others and us had revealed that key functional changes in ER+ breast cancer cells required direct close contact with MSCs(54). The present catalog provides a new multiomic resource to begin to dissect how MSCs shape disease phenotypes in ER+ breast cancer and to what extent effects rely upon intercellular transfer of key molecules ('borrowed'). We show that the borrowed components integrate seamlessly with a second set of gene expression changes that reflect the cancer cell 'intrinsic' responses; together, they establish a robust connectome. The key borrowed components belong to the growth factor and prosurvival PI3K-Akt signaling pathways. The key intrinsic response is augmentation within the VEGF signaling pathway, which supports proliferation and angiogenesis. The key process suppressed is dependance on estrogen signaling, consistent with environmentally-mediated resistance to hormone targeted therapies(55). The 'borrowed' gene signature showed demonstrable translational relevance in that it prognosticated and predicted outcome in patients with ER+ breast cancers, especially in those who had treatment-resistant disease. We conclude that the catalog of genes may represent high value targets for preventing MSCs from empowering tumor cells that lie in the bone marrow niche. Several key genes

405 from this list also were reproducibly upregulated during tumor-fibroblasts contact culture, implying that
406 findings may have broader relevance in the context of tumor cells in other tissue niches.
407
408 *Gene transfer occurs through a nanotube-based connectivity grid*
409 Second, the catalog of genes provides valuable clues into the predominant mode of intercellular
410 communication between MSCs and tumor cells. Intercellular protein transfer encompasses several
411 different biologic processes and cellular structures that establish dynamic communication networks
412 among cells in direct contact or proximity: Gap junctions, TNTs, extracellular vesicles, trogocytosis,
413 and direct cell fusion are among such processes(56). Gene ontology analyses of our catalog of
414 borrowed genes hinted at the formation of extracellular tube-like structures, such as TNTs, as a likely
415 mode of transport. This is consistent with prior reports of MSCs establishing TNTs with multiple types
416 of cancer cells, including MCF7 and other breast cancer cell lines(57). Discovered originally in
417 2004(58), and critiqued initially by some as artifacts of 2D culture(59), TNTs are now increasingly
418 recognized as conduits for cell-cell communication in both physiology and disease(20, 37, 60, 61).
419 They are F-actin rich structures with junctional proteins at one end(62, 63); TNTs couple with adjacent
420 cells through gap junctions(64-67) and both share CX43 as common molecular component. We
421 observed the formation of abundant TNTs connecting MCF7 cells with MSCs and demonstrated that
422 they are functional using pharmacologic inhibitors, implicating gap junctions and CX43 as facilitators
423 of transport in our cultures. The presence of EGFR on the list of 'borrowed' genes is intriguing. While
424 we did not investigate transfer of this receptor as RNA or protein, transmembrane and membrane
425 bound proteins have previously been reported to be transferred via TNTs(68). Most of the borrowed
426 genes, however, represent cytoplasmic proteins and/or organelle- or cytoskeleton-associated
427 proteins, which are known to use TNTs as a route for intercellular protein transfer(20, 37, 61). That
428 the 483 borrowed genes carried an overwhelming message of intercellular transport structures (tube
429 morphogenesis and development) suggests that these genes are selected for their ability to facilitate
430 or support TNT formation, stabilization, and transport. Integration of the borrowed and intrinsic genes
431 through PPI networks indicates that the nature of the exchange is meaningful and advantageous to
432 tumor cells (and potentially also to the MSCs). In doing so, the TNT-dependent tumor-MSC
433 communication we reveal here is resembles the nanotubes(69, 70) and pili-dependent communication
434 in pathogenic biofilm-producing microbes (which are responsible for ~80% of chronic infectious
435 diseases)(71). Unicellular pathogens deploy these strucutures to communicate with each other, or
436 diverse host cells or other pathogens, to ultimately produce a network of extracellular grid to adopt a
437 'multicellular lifestyle'(72, 73). Such adaptation promotes drug resistance, survival, transfer of
438 resistance genes, metabolic dormancy, in effect, making bacteria difficult to eradicate than when
439 present as unicellular organisms (reviewed in)(74, 75).
440
441 *Acquisition of GIV exemplifies how nanotube-dependent gene transfer benefits cancers*

Our bioinformatic analyses pipeline helped prioritize one borrowed gene, *CCDC88A*/GIV, from a list of several interesting candidates. We rationalized it because of its known protumorigenic properties (outlined earlier in *Results*) and because we found it intriguing that the ER+ breast cancer cells typically silence this gene through alternative splicing(33), only to 'borrow' it back from MSCs later in the bone marrow niche (this work). We show that GIV is transferred primarily as protein (not RNA). Because protein transfer is not driven by gradients, and instead relies upon mechanisms of sorting and selective exchange, what governs such selectivity of the borrowed genes remains unclear. In the case of GIV, we show that it binds and co-localizes with CX43 near gap junctions and within TNTs and that the two proteins are co-transferred from MSCs to tumor cells in ways that require functional gap junctions. Discovered originally as an actin binding/remodeling protein in breast cancers(32, 33), and found later to directly bind microtubules and localize to cell junctions under bioenergetic stress(40), both actin and microtubule filaments may serve as highways for transport of GIV between MSCs and tumor cells, as described previously for motor proteins(76) within TNTs. Alternatively, because GIV associates with and regulates the functions and/or the localization of diverse cellular organelles (ERGIC-Golgi vesicles(77), exocytic vesicles(78), endosomes(78, 79), autophagosomes(80)) and of cell surface receptors (e.g., EGFR, integrins, TLR4 etc.)(81), co-transport with such organelles or membrane proteins is also possible. While we did not resolve which of these mechanisms of transfer are at play, we assessed the impact of GIV transfer.

By stably expressing GIV alone (among the list of borrowed candidates) in an ER+ breast cancer cell line we recapitulated ~20% of the gene expression patterns within the borrowed and intrinsic response components. Expression of GIV in ER+ breast cancer cells conferred resistance to clinical anti-estrogen drugs and promoted early survival and dissemination of circulating breast cancer cells. *CCDC88A*/GIV is also induced when ER+ tumor cells were placed in contact cultures with fibroblasts, which is in keeping with prior work demonstrating the role of GIV in cancer-associated fibroblasts in the dissemination of cancer(82). Considering the recent revelations that GIV scaffolds a circuit for secretion coupled cellular autonomy (or growth signaling autonomy) in multicellular eukaryotic cells, it is possible that sharing of GIV between haves (stromal cells) and have nots (tumors that are originally GIV-negative) as 'ready-to-use' protein reflects a core biological phenomenon of sharing of resources during an urgent need for survival in growth factor restrictive environments. Transfer as protein bypasses the need for energy expenditure for protein translation and yet achieve higher levels of protein than possible through mRNA transfer; the latter is estimated to be never more than >1% of levels in donor cells(83). Although we found that GIV protein that was acquired during 3 days in contact culture was rapidly lost when tumor cells were returned to monoculture, prolonged contact cultures (for months and years, as happens in patients) may allow transferred GIV to initiate the GIV↔STAT3 feedforward loop shown to enhance its own transcription(84). We conclude that intercellular protein transport is a major way for cells to exchange GIV as an essential commodity within a heterotypic population of haves and have nots.

479

480 *Study limitations*

481 A detailed characterization of all that is transported was not pursued. Some genes are likely to be
482 transported from the tumor cells to MSCs; this was not evaluated here. Tolerant immunogenic signals
483 were induced in tumor cells during contact culture; how these signals impact the cancer cell's ability
484 to evade the immune system and/or immune checkpoint blockade therapies will require further studies
485 in humanized mice. TNT-mediated tumor- CAF exchanges are also known to shape tumor cell
486 behaviors(45, 85); dedicated studies are required to further investigate the shared and distinct patters
487 between these (and potentially others, e.g., tumor-myeloid cell) forms of cell-cell communication.

488

489 In conclusion, this work opens new horizons as to how close contact interactions and
490 intercellular communication networks through RNA/protein transfer between ER+ breast cancer cells
491 and MSCs reprograms tumor cells to more aggressive states. Based on the omics-based revelations
492 and experimental evidence (this work) and phenotypic characterization of MSC-tumor contact culture
493 we published earlier(47), we conclude that the TNT-based cell-cell communication in the bone marrow
494 niche (or tumor-stromal or tumor-immune cell communication in any other tissue) may provide the
495 same to tumor cells that nanotube-based communication provides to the bacteria within biofilms; a
496 nutrition- and metabolic stress-free haven to promote sustained survival in new environments.
497 Blocking or redirecting these communication networks, or components transferred through these
498 networks, offers novel opportunities to prevent or cure breast cancer metastasis to bone.

499 ## Materials and Methods
500
501 **Cell culture**
502 We purchased MCF7 (HTB-22) and T47D (HTB-133) human ER+ breast cancer cell lines, Cos7 cells,
503 and HS5 (CRL-11882) and HS27a (CRL-2496) human bone marrow MSC line from the American
504 Type Culture Collection (ATCC, Manassas, VA, USA). We thank Dr. James Rae (University of
505 Michigan, Ann Arbor, MI, USA) for providing human HCC1428 ER+ breast cancer cells. We cultured
506 HS5, MCF7, T47D, and Cos7 cells in DMEM (#11995, Gibco, Thermo Fisher, Grand Island, NY, USA)
507 with 10% fetal bovine serum (FBS) (HyClone, ThermoScientific, Waltham, MA, USA), 1% GlutaMAX
508 (#35050, Gibco), and 1% Penicillin-Streptomycin (P/S, #15140, Gibco). We cultured HCC1428 and
509 HS27a cells in RPMI (#11875, Gibco) with 10% FBS, 1% P/S, 1% Sodium Pyruvate (#11360070,
510 Gibco), 1% HEPES (#15630080, Gibco), and 2500 mg/L glucose (#A24940, Gibco). We added
511 50mg/L Plasmocin™ prophylactic (Invivogen, San Diego, CA, USA) to both DMEM and RPMI media.
512 We maintained cells as previously described (47). We performed mycoplasma testing and
513 authenticated cell lines with short tandem repeats analysis upon initial passaging. We removed cell
514 lines from culture after three months and replaced them with new cells from previously frozen stocks.
515
516 **Vectors and stable cell lines**
517 We previously described MCF7 cells stably transduced with click beetle green luciferase (MCF7-
518 CBG)(86). For stable RNA interference against GIV, we transduced MCF7 and HS5 cells with shRNA
519 against CCDC88A (clone TRCN0000129915, Millipore Sigma, Burlington, MA, USA), preparing
520 lentiviruses as described previously (87). We used puromycin to select stably transduced cells and
521 performed experiments with batch populations. To stably express full-length GIV in MCF7-CBG cells,
522 we used a PiggyBac transposon with a CAG promoter driving co-expression of GIV and hygromycin
523 linked by a P2A site (VectorBuilder, Chicago, IL, USA). We transfected cells with a 3:1 ratio of GIV
524 transposon to Super PiggyBac Transposase (Systems Biosciences, Palo Alto, CA, USA) using
525 Fugene-HD transfection reagent (Promega, Madison, WI, USA) according to the manufacturer's
526 protocol. Two days after transfection, we selected cells with 150 µg/ml hygromycin B (ThermoFisher,
527 Waltham, MA, USA). After two weeks of culture with hygromycin B, we returned surviving cells to
528 normal growth medium. We transduced MCF7-CBG cells with a lentiviral vector expressing mCherry
529 with a nuclear localization sequence as we reported previously(88).
530
531 **Co-cultures of breast cancer cells and MSCs**
532 For co-culture assays, we seeded 12,000 total cells per cm^2 in 35 mm dishes with a ratio of 1:9 ER+
533 breast cancer cells to MSCs. One day after seeding, we washed cells once with phosphate buffered
534 saline (PBS) and then changed medium to phenol-red free DMEM (#A14430-01, Gibco),
535 supplemented with 1% FBS, 1% P/S, 1% Glutamax, 1% sodium pyruvate, 10 nM β-estradiol (#E2758,

536 Sigma-Aldrich, Millipore Sigma, Saint Louis, MO, USA), and 5 mM glucose(89). We cultured cells in
537 low serum (1%), low glucose (4 mM), and 10 nM estrogen (LG/LF) medium for 3 days before
538 analyzing experimental endpoints. We performed assays with conditioned medium as described
539 previously (90).
540
541 **RNA sequencing and differentially expressed gene (DEG) analysis**
542
543 We separated cancer cells from stromal cells with human EpCAM (CD326) immunomagnetic beads
544 (#130-061-101, Miltenyi, Auburn, California, USA) for RNA sequencing as described previously(15).
545 We deposited RNA sequencing data to GEO under accession number GSE224322. Differentially
546 expressed genes from the pairs of experimental conditions are identified using DESeq2 program in
547 R. Genes with log fold change >=2 and a p adjusted value < 0.05 were identified and rank ordered
548 as differentially expressed genes (DEGs) (**Supplemental Information 5**).
549
550 **Hierarchical clustering of RNA seq readouts**
551 Expression patterns of the identified 100 genes that are highly expressed in MCF7 cells post coculture
552 with HS5 cells, are unbiasedly clustered based on their z normalized expression in all the samples
553 using the seaborn clustermap package (v 0.12) in python.
554
555 **Tandem Mass Tag™ (TMT) proteomics and analyses**
556 MCF7 monoculture and post coculture with HS5 cells were subsequently processed for TMT
557 proteomics using LUMOS Orbitrap-Fusion analyzer. Samples were processed at the UC San Diego
558 Biomolecular and Proteomics Mass Spectrometry Core Facility (https://bpmsf.ucsd.edu/). Peptides
559 are identified and mapped using Peaks X Pro pipeline. Intensity ratio of each identified proteins in
560 MCF7 monoculture and post coculture with HS5 cells has been identified and selected if the
561 significance score >20. The mass spectrometry proteomics data have been deposited to the
562 ProteomeXchange Consortium via the PRIDE(91) partner repository with the dataset identifier
563 (**PXD039860**). A list of differentially expressed proteins is provided in **Supplemental Information 6**.
564
565 **StepMiner analysis**
566 StepMiner is an algorithm that identifies step-wise transitions using step function in a time-series
567 data(92). StepMiner undergoes an adaptive regression scheme to verify the best possible up and
568 down steps based on sum-of-square errors. The steps are placed between time points at the sharpest
569 change between expression levels, which gives us the information about timing of the gene
570 expression-switching event. To fit a step function, the algorithm evaluates all possible steps for each
571 position and computes the average of the values on both sides of a step for the constant segments.

572 An adaptive regression scheme is used that chooses the step positions that minimize the square error
573 with the fitted data. Finally, a regression test statistic is computed as follows:

574 $$F\ stat = \frac{\sum_{i=1}^{n}(\widehat{X_i} - \bar{X})^2/(m-1)}{\sum_{i=1}^{n}(X_i - \widehat{X_i})^2/(n-m)}$$

575 Where X_i for $i = 1$ to n are the values, $\widehat{X_i}$ for $i = 1$ to n are fitted values. m is the degrees of freedom
576 used for the adaptive regression analysis. $\bar{X}$ is the average of all the values: $\bar{X} = \frac{1}{n} * \sum_{j=1}^{n} X_j$. For a
577 step position at k, the fitted values $\widehat{X_l}$ are computed by using $\frac{1}{k} * \sum_{j=1}^{n} X_j$ for $i = 1$ to k and $\frac{1}{(n-k)} *$
578 $\sum_{j=k+1}^{n} X_j$ for $i = k + 1$ to n.
579

580 **Composite gene signature analysis using Boolean Network Explorer (BoNE)**

581 Boolean network explorer (BoNE)(93) provides an integrated platform for the construction,
582 visualization and querying of a gene expression signature underlying a disease or a biological process
583 in three steps: First, the expression levels of all genes in these datasets were converted to binary
584 values (high or low) using the StepMiner algorithm. Second, Gene expression values were normalized
585 according to a modified Z-score approach centered around *StepMiner* threshold (formula = (expr -
586 SThr)/3*stddev). Third, the normalized expression values for every genes were added together to
587 create the final score for the gene signature. The samples were ordered based on the final signature
588 score. Classification of sample categories using this ordering is measured by ROC-AUC (Receiver
589 Operating Characteristics Area Under The Curve) values. Welch's Two Sample t-test (unpaired,
590 unequal variance (equal_var=False), and unequal sample size) parameters were used to compare
591 the differential signature score in different sample categories. Violin, Swarm and Bubble plots are
592 created using python seaborn package version 0.10.1. Pathway enrichment analyses for genes were
593 carried out via the reactome database (https://reactome.org/) and algorithm(94). Violin plots are
594 created using python seaborn package version 0.10.1.
595

596 **Survival outcome analyses**

597 Kaplan-Meier (KM) analyses were done for gene signature identified from transcriptome and
598 proteome overlap. The high and low groups were separated based on *StepMiner* threshold on the
599 composite score of the gene expression values. The statistical significance of KM plots was assessed
600 by log rank test. Kaplan-Meier analyses were performed using lifelines python package version
601 0.14.6.
602

603 **Flow cytometry for intercellular transfer of calcein, AM**

604 To measure transfer of dye between cells by intercellular connections, we incubated MCF7 or HS5
605 cells with 10 μM calcein, AM (C3099, Thermo Fisher Scientific) in LG/LF medium for one hour. We
606 then washed cells three times with PBS and seeded labeled MCF7 or HS5 cells with MCF7-mCherry

607 cells at a 9:1 ratio in 10 cm dishes using the cell density described above for co-culture assays. After
608 three days in co-culture, we analyzed amounts of calcein, AM dye in MCF7-mCherry cells by flow
609 cytometry presented as histogram plots.
610
611 **Immunogold electron microscopy**
612 We plated MCF7 monocultures or co-cultures of MCF7 and HS5 cells in 10 cm dishes at densities
613 described above for electron microscopy. After culturing cells for three days in LG/LF medium, we
614 washed cells twice with PBS and then fixed cells with 2% paraformaldehyde and 0.2% glutaraldehyde
615 (#15700 and #16200, respectively, Electron Microscopy Services, Hatfield, PA, USA) for one hour at
616 4°C. We then replaced the solution with ice-cold 4% paraformaldehyde with 0.1% Probumin® BSA in
617 200 mM HEPES and scraped the cells with a soft Teflon scraper (07-200-366, Thermo Fisher). The
618 frozen sample blocks were cryosectioned (60-70 nm thick section 10 µm apart) on EM grid. For
619 immunolabelling, grids were washed with 2% gelatin (cat# ES-006-B; Sigma-Aldrich) in phosphate
620 buffer at 30-37 °C for 15-20 min followed by 10-20 mM (~0.15%) glycine for 5 min and 1% BSA/PBS
621 for 2 min. Grids were incubated with 1:1 anti CX43 antibody (mouse mAb, epitope aa 247-382;
622 BioLegend Cat#850001) and 1:10 anti GIV antibody (Cat#ABT80; Millipore) in 1% BSA/PBS for 1
623 hour at room temperature. For gold labelling the grids were incubated with Goat Anti-Mouse IgG
624 tagged with 12 nm Colloidal Gold (Jackson Immuno research lab cat#115-205-068) and Goat Anti-
625 Rabbit IgG tagged with 6 nm Colloidal Gold (Jackson Immuno research lab cat#111-195-144) diluted
626 in 1:1 in 1% BSA for 1 h at room temperature followed by washing with PBS for 4 times. Then the
627 grids were incubated with 1% Glutaraldehyde in PBS for 5 min. Then the grids were rinsed with
628 distilled water 6 times. For contrast enhancement, the grids were incubated with 2% uranyl acetate
629 at pH 7 for 5 min and in uranyl acetate (4%) (cat# 21447-25; polysciences) and methylcellulose (2%)
630 (cat# 9004-67-5; sigma aldrich) mixture for 5 min. Then the grids were dried in a wire loop at room
631 temperature for 15 min. After that, the grids were mounted in Jeol 1400 plus Transmission Electron
632 Microscope for visualization.
633
634 **Immunoblotting**
635 For immunoblotting in combination with GST pull-down assays (see below), we transfected Cos7 cells
636 with Cx43-GFP (gift from David Spray (Addgene plasmid #69007;
637 http://n2t.net/addgene:69007;RRID:Addgene_69007) (95)) using polyethylenimine (PEI) following the
638 manufacturer's protocol as described in prior work(96, 97). Whole-cell lysates were prepared after
639 washing cells with cold PBS before re-suspending and boiling them in sample buffer. For
640 immunoblotting, protein samples were separated by SDS-PAGE and transferred to polyvinylidene
641 fluoride membranes (Millipore Sigma, MO, USA). The membrane was stained with Ponceau S to
642 visualize proteins Membranes were blocked with PBS supplemented with 5% nonfat milk before
643 incubation with primary antibodies. Infrared imaging with dual-color detection and quantification were

644 performed using a Li-Cor Odyssey imaging system. The anti-CX43 (Biogened, CA, 247-382) antibody
645 was used at 1:1000 v/v dilution. Figures were assembled for presentation using the Photoshop
646 (Adobe, San Jose, CA, USA) and Illustrator (Adobe, San Jose, CA, USA). For co-culture experiments,
647 we separated cancer cells from HS5 cells using EpCAM immunomagnetic beads as described above.
648 We made whole-cell lysates using RIPA lysis buffer and quantified amounts of protein per sample by
649 BCA assay (23235, Thermo Fisher Scientific). We used primary antibodies against GIV (H-6, Santa
650 Cruz Biotechnology, Dallas, TX, USA), CX43 (#3512, Cell Signaling Technology, Danvers, MA, USA),
651 or β-Actin (#4970, Cell Signaling Technology) and detected primary antibodies with appropriate anti-
652 mouse or anti-rabbit secondary antibodies (ThermoFisher) conjugated to horseradish peroxidase. We
653 developed blots with ECL plus reagent (ThermoFisher) and quantified bands using ImageJ.
654
655 **GST pull-down assays**
656 Recombinant GST proteins were expressed in E. coli stain BL21 (DE3) and purified as previously
657 described. Briefly, cultures were induced using 1mM IPTG overnight at 25°C. Cells were then pelleted
658 and resuspended in either GST lysis buffer (25 mM Tris-HCl, pH 7.5, 20 mM NaCl, 1 mM EDTA, 20%
659 (vol/vol) glycerol, 1% (vol/vol) Triton X-100, 2×protease inhibitor cocktail). Recombinant GST alone
660 (control) or GST-tagged GIV proteins, GST-GIV-NT (1-166 aa) and GST-GIV-CT (1660-1870 aa) from
661 *E. coli* were immobilized onto glutathione-Sepharose beads and incubated with binding buffer (50 mM
662 Tris-HCl pH 7.4, 100 mM NaCl, 0.4% (v:v) Nonidet P-40, 10 mM MgCl2, 5 mM EDTA, 2 mM DTT, 1X
663 Complete protease inhibitor) overnight at 4oC temperature. For binding with cell lysates, cells were
664 lysed in cell lysis buffer (20 mM HEPES pH 7.2, 5 mM Mg-acetate, 125 mM K-acetate, 0.4% Triton
665 X-100, 1 mM DTT, 500 μM sodium orthovanadate, phosphatase inhibitor cocktail (Sigma-Aldrich, MO,
666 USA) and protease inhibitor cocktail (Roche Life Science) using a 28G syringe, followed by
667 centrifugation at 10,000Xg for 20 min. Cleared supernatant was then used in binding reaction with
668 immobilized GST-proteins for 4 h at 4°C. After binding, bound complexes were washed four times
669 with 1 ml phosphate wash buffer (4.3 mM Na2HPO4, 1.4 mM KH2PO4, pH 7.4, 137 mM NaCl, 2.7
670 mM KCl, 0.1% (v:v) Tween 20, 10 mM MgCl2, 5 mM EDTA, 2 mM DTT, 0.5 mM sodium
671 orthovanadate). Bound proteins were then eluted through boiling at 100°C in Laemmli sample buffer
672 (BIORAD, CA, USA). The bound proteins were eluted at 37ºC for 10 min.
673
674 **Cell viability assays**
675 For viability assays, we seeded MCF7-CBG or MCF7-CBG-GIV cells at 10,000 cells per well in black
676 wall 96 well plates. We washed cells once PBS and then added various concentrations of tamoxifen,
677 fulvestrant, or fulvestrant with 100 nM palbociclib (all from Cayman Chemical, Ann Arbor, MI, USA) in
678 LG/LF medium with 4 wells per condition. Control wells received vehicle only. After three days in
679 culture, we quantified relative numbers of viable cells by bioluminescence imaging using an IVIS

680 Lumina system with Living Image 4.3.1 software (Perkin Elmer, Waltham, MA, USA) as described
681 previously(47). We plotted data fraction change from vehicle only wells, which we defined as 1.
682
683 **Animal studies**
684 The University of Michigan Institutional Animal Care and Use Committee approved all experiments.
685 We seeded MCF7-CBG or MCF7-CBG-GIV cells in T175 flasks. The following day, we changed
686 medium to LG/LF medium without added estrogen and cultured cells overnight before harvesting cells
687 with cell dissociation buffer (Gibco, ThermoFisher Scientific). We resuspended cells at 1 x 10^5 cells
688 per 100 µl sterile 0.9% NaCl for intracardiac injection. Prior to injection, we verified equal numbers of
689 viable cells based on bioluminescence imaging of aliquots of each cell type. To generate systemic
690 metastases, we injected 1 x 10^5 MCF7-CBG or MCF7-CBG-GIV cells into the left ventricle of 7–10-
691 week-old female NSG mice (7-8 mice per group) (The Jackson Lab, Bar Harbor, ME, USA) as
692 described previously by our lab (89).
693 We performed bioluminescence imaging (IVIS Spectrum, Perkin Elmer) on mice at days
694 indicated in the figure legend. At the end of the study, we measured metastases in defined organs by
695 ex vivo bioluminescence imaging as we reported previously(89). We quantified total bioluminescence
696 signal above background using Living Image software.
697
698 **Study Approval**
699 The University of Michigan IACUC approved all animal procedures under protocol number
700 PRO00010534.
701
702 **Statistics**
703 We performed all cell-based experiments at least three times and presented results as either a
704 representative experiment or average of experiments ± SEM. For statistical analyses, we used
705 python, R, GraphPad Prism software (San Diego, CA, USA) or MATLAB (Mathworks, Natick, MA,
706 USA). $P<0.05$ defined statistical significance for methods listed in figure legends. We assessed
707 statistical significance of Kaplan-Meier plots by log rank test. Kaplan-Meier analyses were performed
708 using lifelines python package version 0.14.6.
709

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AUTHOR CONTRIBUTIONS:

S.S, supervised by P.G, carried out and analyzed all electron microscopy, RNA seq, TMT proteomics and computational analyses showcased in this work. Su.R. carried out protein purification and GST pulldown assays. B.W.C, A.P.F., S.C., Sh.R., and J.M.B performed mouse experiments and cell-based assays. K.E.L. provided new reagents. B.W.C. S.S, P.G. and G.D.L. assembled the figures. K.E.L., Su.R., S.S., P.G., and G.D.L. helped write methods and edit the manuscript. G.D.L. and P.G conceptualized, designed, supervised, and analyzed the experiments. K.E.L, S.S. P.G and G.D.L wrote the manuscript. All authors and approved the manuscript prior to submission.

CONFLICT OF INTEREST DISCLOSURE STATEMENT

G.D.L. has received research materials from Spexis. All other authors declare no competing interests.

DATA AVAILABILITY

Data are available via ProteomeXchange with identifier PXD039860 and Gene Expression Omnibus with id GSE224322. The computational analyses can be found at https://github.com/sinha7290/cx43

FIGURE AND LEGENDS

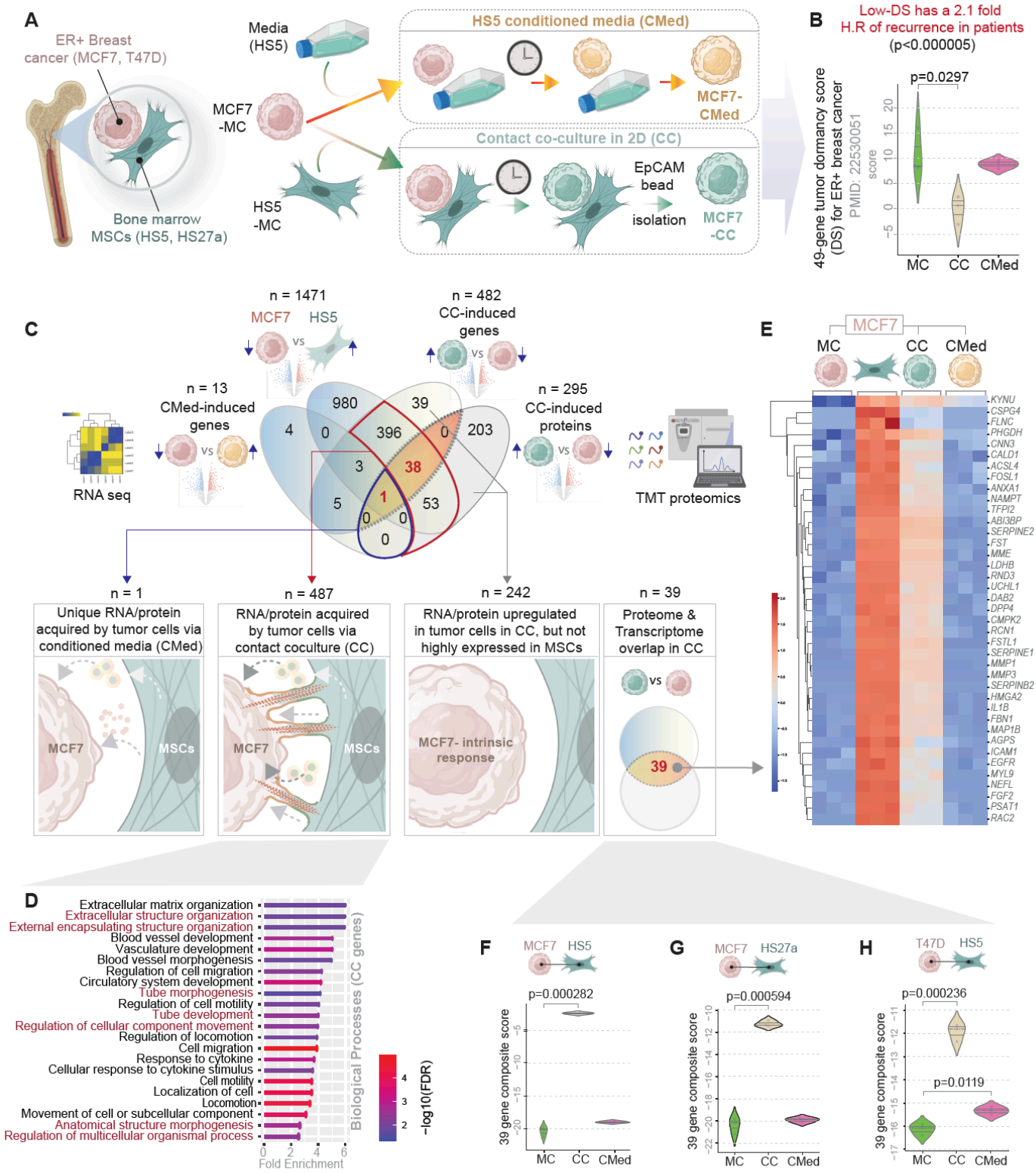

Figure 1. Multiomic analysis reveals RNA/protein acquired by ER+ breast cancer cells from MSCs in contact coculture.

A. Schematic of the general experimental set up for recapitulating disseminated ER+ breast tumor cells in the bone marrow amidst mesenchymal stem cells (MSCs). Two different types of coculture models were used, one with conditioned media (CMed; *top*) and one that involves direct contact co-culture (CC; *bottom*). MC, monoculture.

B. Violin plots display the composite score of a 49-gene tumor dormancy score (DS), which was determined as specific for ER+ breast cancers and previously validated in 4 independent cohorts to be predictive of tumor recurrence. Statistical significance was assessed by Welch's t-test (n = 3 in each comparator group). Only significant p values are displayed.

C. *Top*: Venn diagram depicts the outcome of multiple DEG analyses between different indicated comparator groups that catalogs the number of suppressed genes or proteins in contact co-culture (CC) or conditioned media (CMed) and the overall differential gene expression between the two cell types (MCF7 cells vs the HS5 bone marrow MSCs; bottom). *Bottom*: Genes/proteins that are induced in MCF7 tumor cells in coculture with HS5 MSCs are binned into 3 categories (connected by arrows) based on the likely mechanisms for such induction. Red = 39 uniquely upregulated transcripts in tumor cells in contact co-culture that were also identified by proteomics. See also **Supplementary Figure 1** for suppression of genes and proteins upon coculture.

D. Results of a gene ontology analysis (GO Biological processes) on the transcripts and/or proteins that are acquired by MCF7 cells from MSCs during contact coculture. See also **Supplementary Figure 2** for Reactome pathway and GO enrichment analyses on the genes within each category in C.

E. Heatmap displays the findings of hierarchical unsupervised clustering of samples using the 39 genes identified in C.

F-H. Violin plots display the composite score of the 39 genes in E in various tumor cell-MSC co-culture models, e.g., MCF7↔HS5 (F), MCF7↔HS27a (G) and T47D↔HS5 (H). Statistical significance was assessed by Welch's t-test (n = 3 in each comparator group). Only significant p values are displayed.

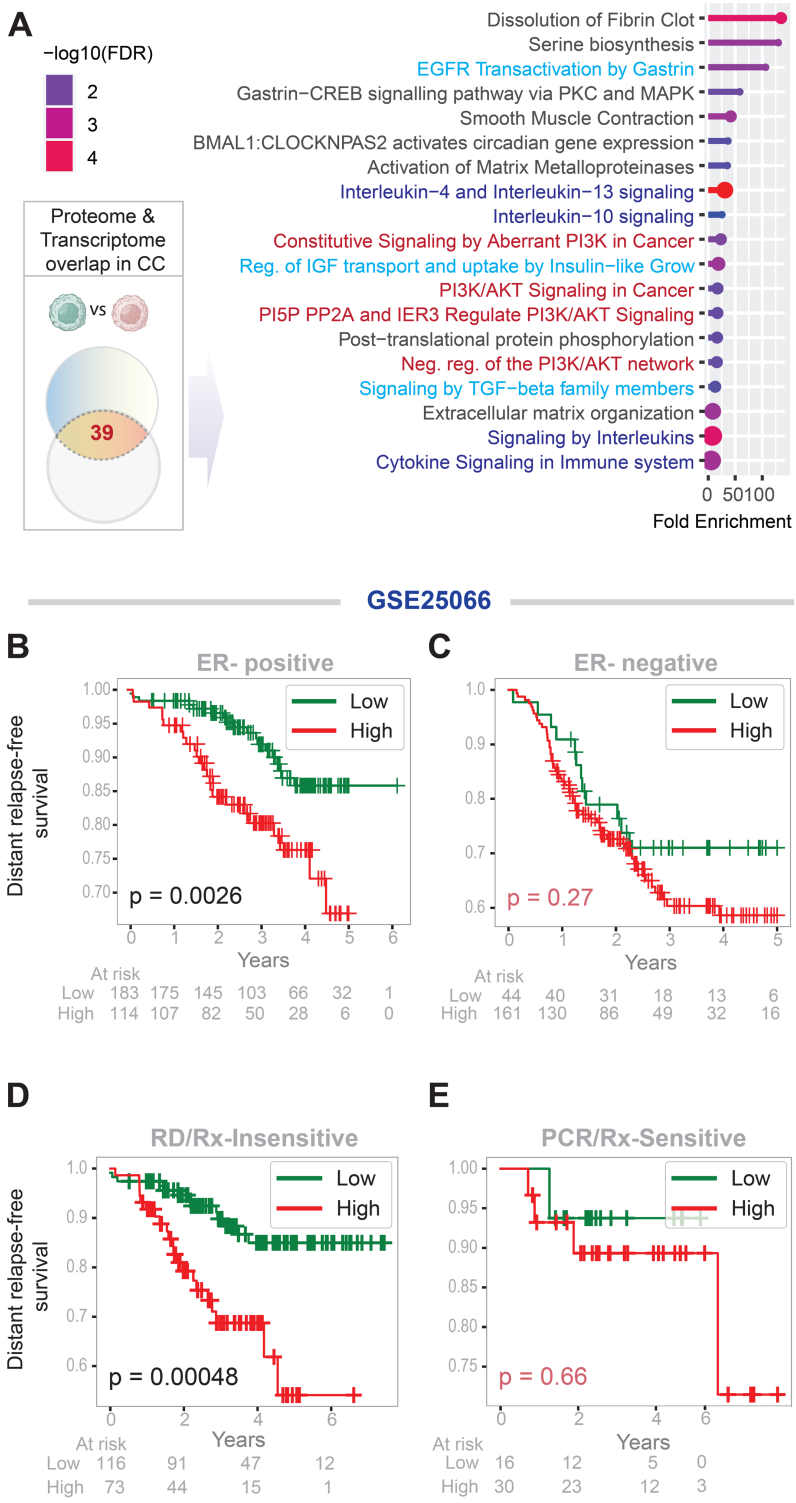

Figure 2. A contact culture signature derived from proteome-transcriptome overlap carries prognostic and predictive value in ER-positive breast cancer.

A. Reactome pathways enriched in the 39 genes identified in **Figure 1C**. The PI3K-Akt signaling pathway (red), growth factor signaling pathways (teal blue) and the tolerogenic cytokine pathways (navy blue) are highlighted.

B-E. Kaplan Meier survival plots on a cohort of breast cancer patients with known outcome over time (relapse/metastasis-free survival), stratified as high vs low expression of the 39-gene signature. Statistical significance was assessed by Log Rank analyses.

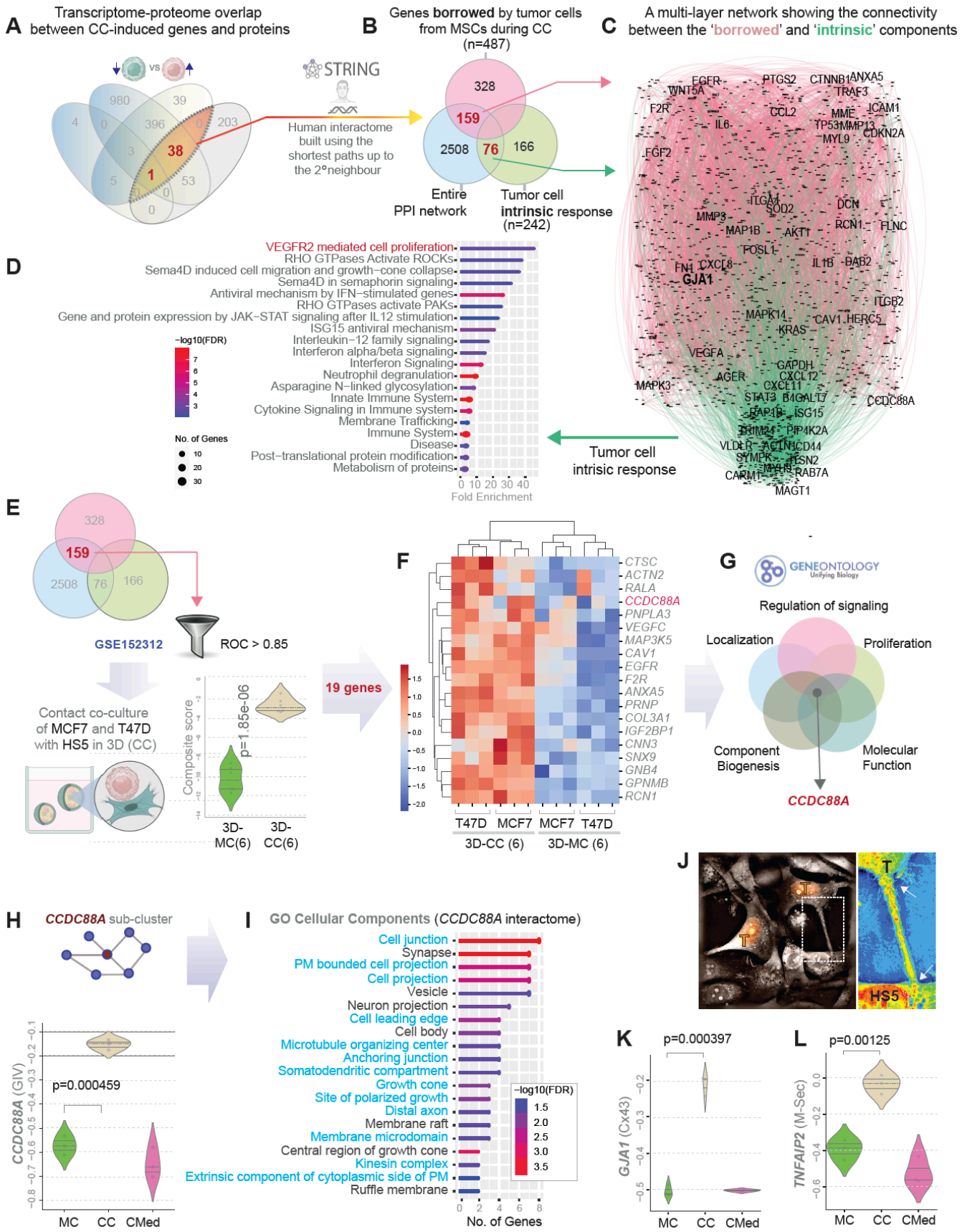

Figure 3. Network analysis pinpoints GIV as a central orchestrator of the co-culture borrowed gene signature.

783 **A**. Schematic shows the workflow for protein-protein interaction (PPI) network analysis. The 39
784 gene signature from Figure 1E is used as 'seeds' to build a PPI network using the STRING
785 database (see *Methods*).

786 **B**. Venn diagram showing the overlaps between the resultant PPI network and the candidate
787 genes/proteins that were identified in **Figure 1C** as either likely to be 'borrowed' from MSCs or
788 upregulated as part of tumor cell's 'intrinsic' response during contact co-cultures.

789 **C**. A multi-layer PPI network shows connectivity between 'borrowed' (n = 159) and 'intrinsic' (n = 76)
790 proteins. Key nodes in the network are labeled.

791 **D**. Reactome pathways enriched in the 76 proteins that constitute intrinsic responses of breast cancer
792 cells to contact co-culture.

793 **E**. The 158 'borrowed' genes identified in our 2D co-culture models were further filtered using a
794 publicly available dataset generated from 3D co-culture models wherein MCF7 and T47D cells were
795 grown with HS5 MSCs. A threshold of ROC AUC > 0.85 led to the identification of 19 genes. A violin
796 plot shows the composite score of the expression of 19 genes in the 3D mono (MC) vs contact (CC)
797 cultures. Statistical significance was assessed by Welch's t-test.

798 **F**. A heatmap of z-score normalized expression of the 19 genes. MC, monoculture; CC, contact
799 culture.

800 **G**. Venn diagram summarizes findings of gene ontology (GO) analyses, identifying *CCDC88A* as an
801 invariant player across diverse biological processes enriched within the 19 genes.

802 **H-I**. Violin plot (H) shows the patterns of induction of *CCDC88A* in MCF7 cells when subjected to
803 contact coculture (CC) but not when grown in conditioned media (CMed). Statistical significance was
804 assessed by Welch's t-test. Only significant p values are displayed. Graph (I) displays the GO cellular
805 components enriched within the *CCDC88A*/GIV-subcluster within the PPI network in C. Components
806 highlighted in blue indicate processes that are required for enabling long-range intercellular transport
807 via tunneling nanotubes.

808 **J**. Images obtained by inferometry microscopy of MCF7 cells (red nuclei; "T") in contact coculture with
809 MSCs (HS5) with nanotube connecting the cells. Boxed area on left is magnified on the right. Arrows
810 mark the two ends of the nanotube. See also **Supplementary Figure 3** for a montage of images of
811 MCF7 cells in mono- (MC) or contact coculture (CC) with HS5 MSCs.

812 **K-L**. Violin plots show the patterns of induction of *GJA1* (K) and *TNFAIP2* (L) in MCF7 cells when
813 subjected to contact coculture (CC) but not when grown in conditioned media (CMed). Statistical
814 significance was assessed by Welch's t-test. Only significant p values are displayed.

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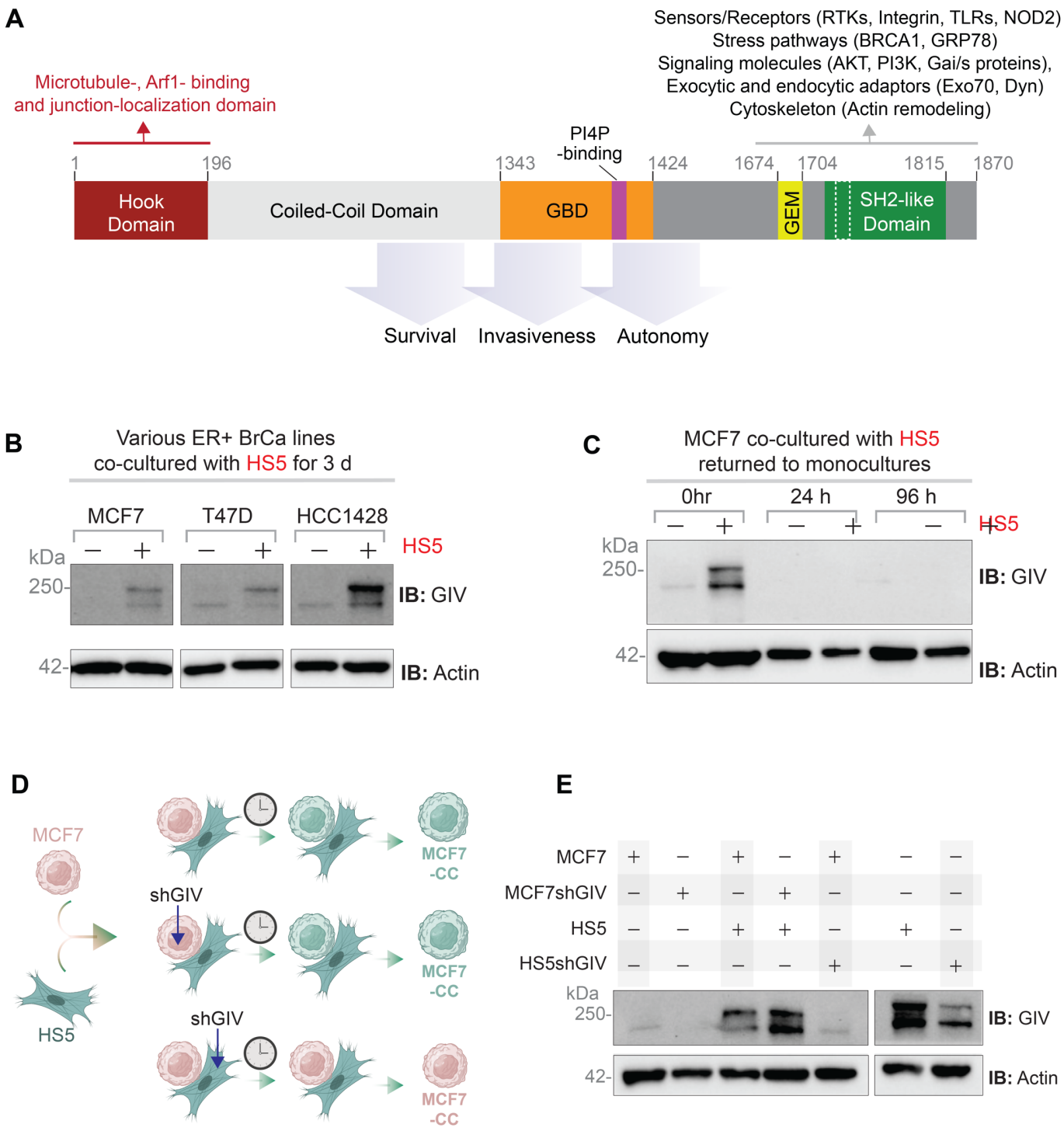

Figure 4. GIV transport from MSCs to ER+ breast cancer cells requires ongoing interactions. **A**. Schematic illustrates key functional domains of GIV. The C-terminus contains multiple short linear motifs that enable diverse tumor-promoting interactions (receptors, signaling molecules within diverse pathways, and components of membrane trafficking). GBD, G protein binding domain; GEM, guanine nucleotide exchange modulator; SH2, Src-like homology domain.

829 **B**. Equal aliquots of lysates of 3 ER+ breast cancer cells (MCF7, T47D or HCC1428) in monoculture
830 or recovered after co-culture with HS5 cells were analyzed for GIV and actin (as a loading control) by
831 immunoblotting (IB).
832 **C**. Equal aliquots of lysates of MCF7 cells prepared either immediately after recovery from co-cultures
833 with HS5 cells (0 h) or after an additional 24 or 96 h of culture after removal from HS5 contact were
834 analyzed for GIV and actin (as a loading control) by immunoblotting (IB).
835 **D-E**. Schematic (D) outlines the key manipulations (i.e., treatment with shRNA for GIV) done to either
836 MCF7 or HS5 cells in contact co-cultures. Equal aliquots of MCF7 cells recovered from the co-cultures
837 (left) or HS5 cells in monocultures were analyzed for GIV and action (loading control) by
838 immunoblotting (IB).

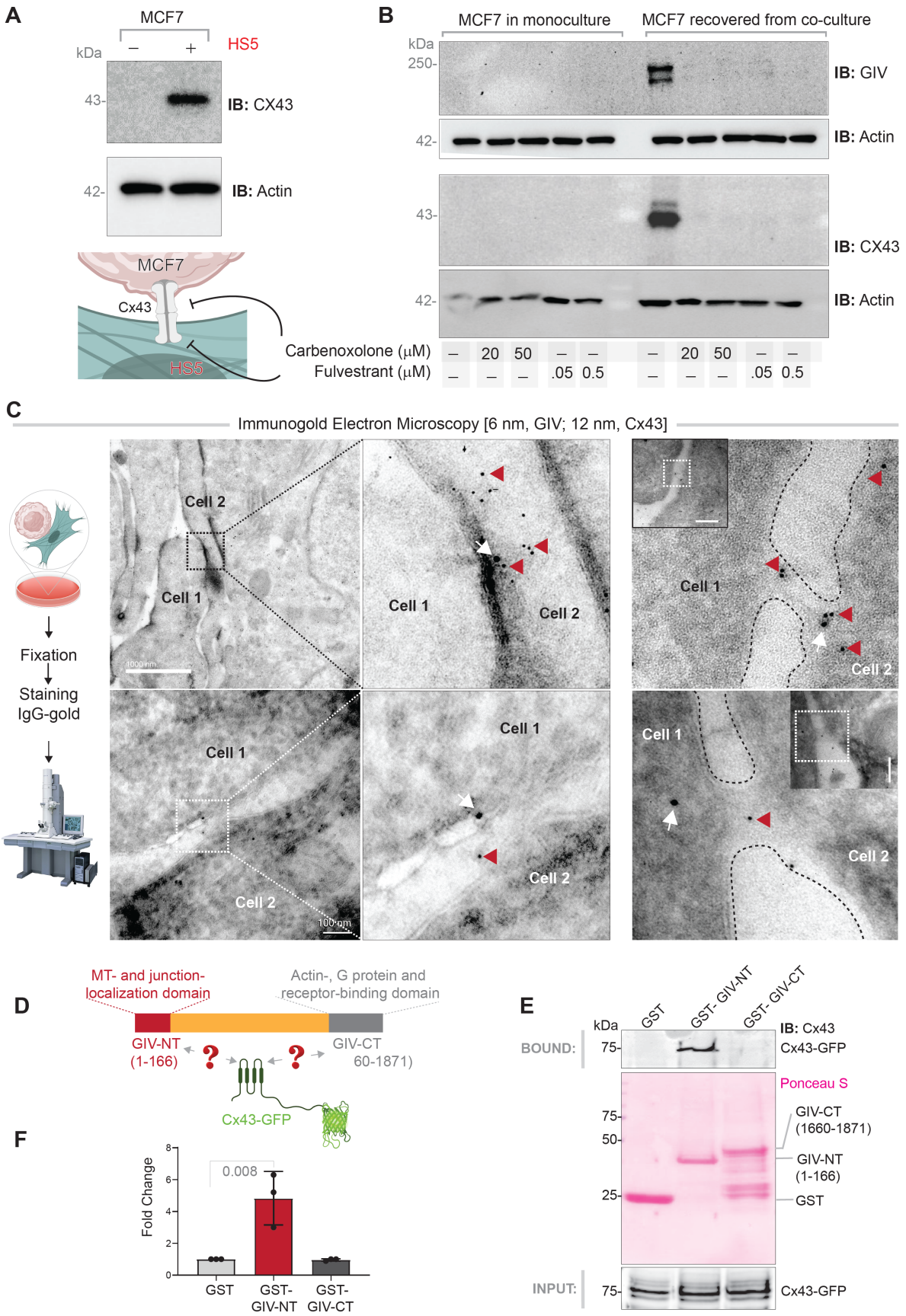

Figure 5. Cx43 and GIV interact and are co-transported through intercellular communication sites.

842 **A**. Equal aliquots of lysates of MCF7 cells in monoculture or recovered after co-culture with HS5 cells
843 were analyzed for Cx43 and actin (as a loading control) by immunoblotting (IB).
844 **B**. MCF7 cells in monoculture or in co-culture with HS5 cells were treated with the indicated
845 concentrations of Carbenoxolone or Fulvestrant prior to lysis. Equal aliquots of lysates were analyzed
846 for GIV, Cx43 or actin (the latter as a loading control) by immunoblotting (IB). See **Supplementary**
847 **Figure 5** for similar studies on HS5 monocultures.
848 **C**. Electron micrographs of immunogold stained MCF7↔HS5 contact co-cultures. Red arrowhead
849 denotes 6 nm gold particles (GIV); White arrow denotes 12 nm gold particles (Cx43). Scale bar = 100
850 μm.
851 **D-F**. Schematic of constructs (D) used in pull-down assays using recombinant GST-tagged GIV N- or
852 C-term fragments or GST alone (Neg control) proteins immobilized on glutathione beads and lysates
853 of Cos7 cells transiently expressing GFP-Cx43. Bound Cx43 was visualized by immunoblotting (E-
854 top). Equal loading of GST proteins was confirmed by Ponceau S staining (C-bottom). Bar graphs (F)
855 display the relative binding of Cx43 to various GST proteins. Data are represented as mean ± SEM
856 (n = 3); $**p=<0.01$ determined by one-way ANOVA.

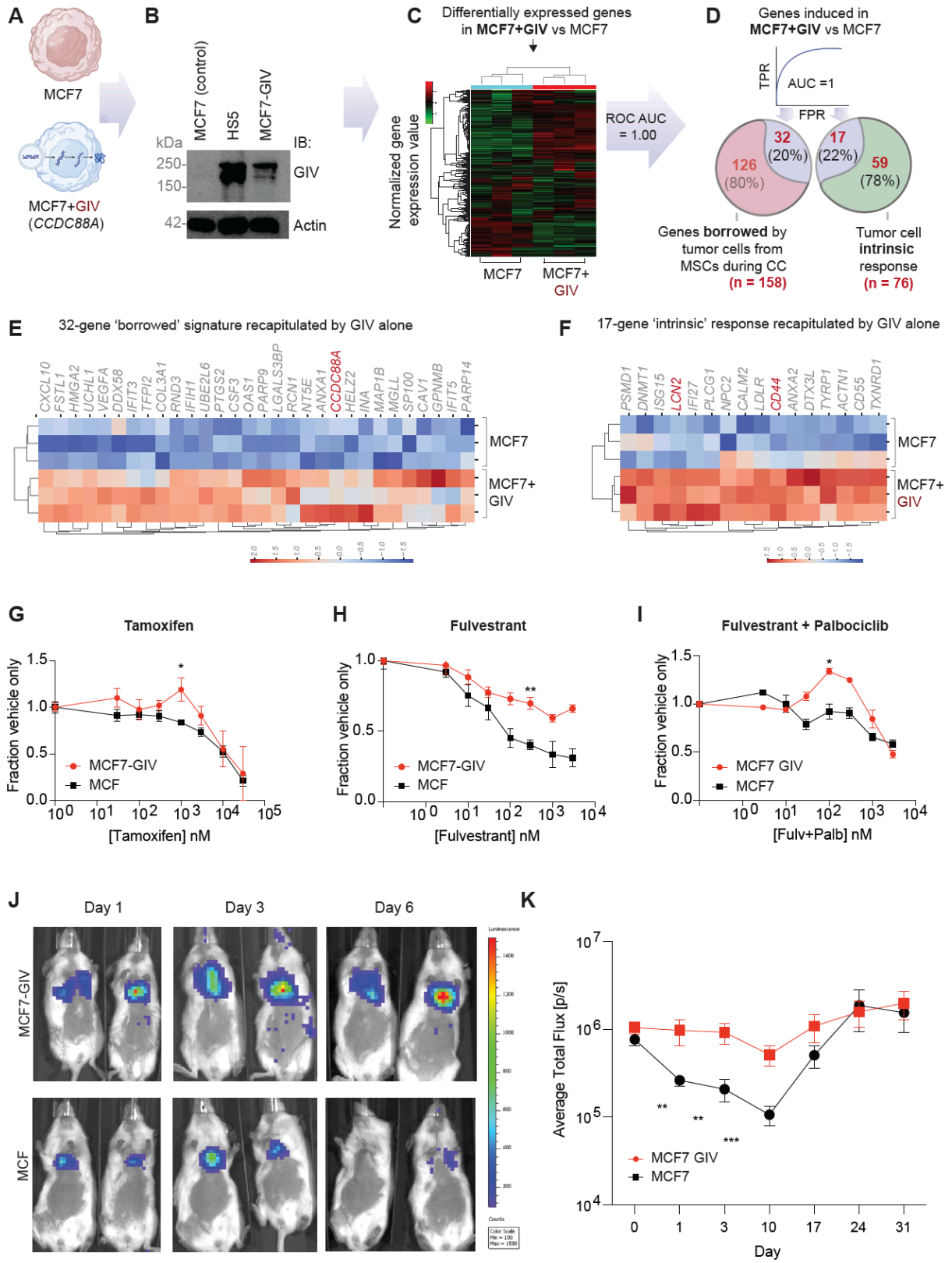

Figure 6. Expression of GIV recapitulates the MSC close contact signature;confers resistance to ER-targeted therapies; and promotes early dissemination and survival of ER+ breast cancer cells.

862 **A**. Schematic shows creation of a stable MCF7 cell population with expression of exogenous GIV
863 (CCDC88A) by a piggyBac transposase vector.
864 **B**. Immunoblots of equal aliquots of whole cell lysates of cells in A, confirming the expression of full-
865 length GIV.
866 **C-D**. Workflow (C) of RNA seq and normalized gene expression analysis of the cells in B, analyzed
867 for the ability of the 'borrowed' (n=158) and 'intrinsic' (n=76) genes to perfectly classify the cells with
868 GIV (MCF7-GIV) from those without (MCF7) (ROC-AUC 1.00). Venn diagram (D) shows the genes
869 induced with GIV alone, as % of the total 'borrowed' and 'intrinsic' signatures.
870 **E-F**: Heatmaps display the hierarchical unsupervised clustering of MCF7 and MCF7-GIV cells by z-
871 score normalized gene expression patterns for the subset of genes that are induced among the
872 borrowed (E) and intrinsic (F) signatures. See also **Supplementary Figure 6** for reactome pathway
873 analysis of these genes.
874 **G-I**. Graphs display cell viability as determined by bioluminescence when MCF7-GIV and control
875 MCF7 cells were exposed to increasing concentrations of tamoxifen (G), fulvestrant (H), or fulvestrant
876 and 100 nM palpociclib (I). Data are displayed after normalization to viable cells treated with vehicle
877 only. Graphs show mean values ± SEM. *, $p < 0.05$ and **, $p < 0.01$ by AUC analysis.
878 **J-K**. Equal number (1×10^5) of MCF7-GIV or control MCF7 cells were injected into the left cardiac
879 ventricle of 7-10-wk-old female NSG mice (n=8 per group). Representative bioluminescence images
880 (J) of mice at day 1-, 3-, and 6-days post injection are shown. Images are displayed on a constant
881 pseudocolor scale for photon flux with red and blue depicting high and low values, respectively.
882 Graphs (K) show mean values ± SEM for photon flux for mice with MCF7-GIV and MCF7 cells at
883 listed times after intracardiac injection. *, $p < 0.05$, **, $p < 0.01$, and ***, $p < 0.005$ at selected
884 concentrations by Mann-Whitney U test.

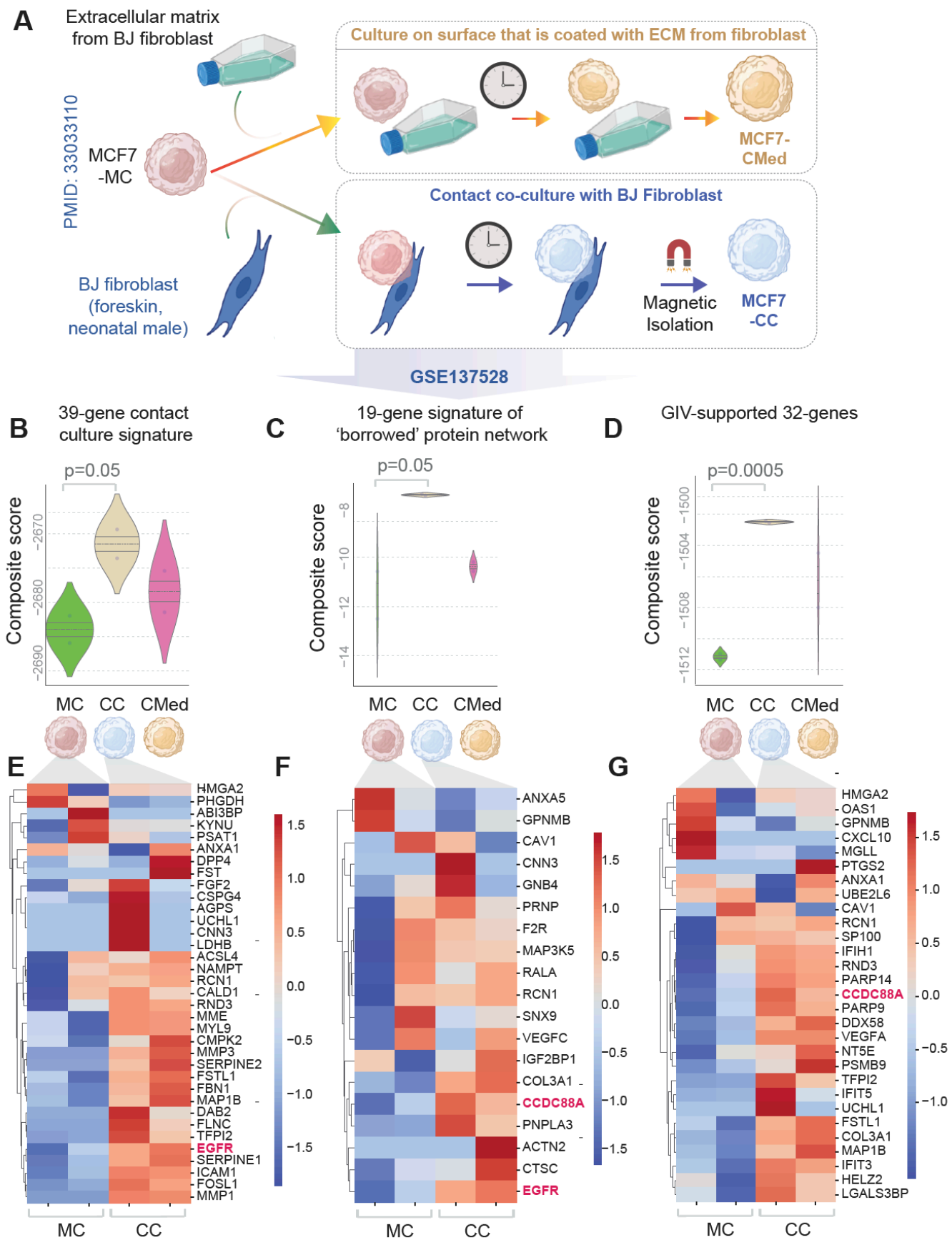

Figure 7. MCF7 cells borrow *CCDC88A* and other key genes during contact culture with fibroblasts

A. Schematic of the general experimental setup in which MCF7 cells were grown either as monoculture (MC), or in direct contact cultures with BJ fibroblasts (CC) or cultured on ECM produced by the BJ fibroblasts (CMed).

B-D. Violin plots show the degrees of induction of 39-gene 2D contact culture signature (**B**), the 19-gene signature of network of 'borrowed' proteins/transcripts that survived refinement through 3D contact cultures (**C**), and GIV-supported 'borrowed' transcriptional program of 32 genes (as in **Fig 5D**). p-values are calculated using a two-tailed t-test.

E-G. Heatmaps show the induction pattern of each gene within the signatures described in B-D. Color key denotes z-score normalized counts per million (cpm).

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