Title: Mapping transmembrane binding partners for E-cadherin ectodomains.

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Abstract:

We combine proximity labeling and single molecule binding assays, to discover novel transmembrane protein interactions in cells. We first screen for proximal membrane proteins by tagging the extracellular and cytoplasmic regions of the protein of interest with TurboID biotin ligase, and then test direct binding interactions using single molecule Atomic Force Microscopy. Using this approach, we identify previously unknown direct interactions between membrane proteins and the extracellular regions of cadherin adhesion proteins in epithelial cells.

Transmembrane proteins play essential roles in coupling cells and in sensing mechanical and biochemical signals from the environment. However, it is extremely challenging to identify membrane protein interactions using traditional methods like affinity pulldown, because of the hydrophobicity of membrane spanning regions, harsh extraction conditions that disrupt protein interactions, and the inability of these methods to discriminate between cytoplasmic and extracellular protein interactions. Consequently, membrane protein interactomes have been mapped using several proximity-tagging systems such as BioID [1], APEX [2],and PUP-IT [3], where a protein of interest is genetically fused to a proximity-based labeling enzyme which activates a substrate like biotin or Pup, and then releases substrate to label proximal proteins. Recently, a micro-mapping platform using a photocatalytic induced carbene was also introduced for proximity labeling of membrane bound proteins [4]. While enormously powerful, these assays merely report on protein proximity; testing direct interactions between the proximate proteins require these techniques to be integrated with a complementary biophysical method.

Here we integrate the most widely used proximity-tagging scheme, BioID, with single molecule Atomic Force Microscope (AFM) binding assays to identify transmembrane proteins that bind to the extracellular regions of E-cadherin (Ecad), a ubiquitous cell-cell adhesion protein. While over 170 proteins, including signaling molecules, scaffolding proteins and cytoskeletal regulators, have been reported to associate directly or indirectly with the Ecad cytoplasmic tail [5], Ecad ectodomains are primarily believed to interact with identical Ecad ectodomains from opposing cells. Although cell-free binding studies and microscopy suggest interactions between Ecad ectodomains and other adhesion proteins and cell-surface receptors [6-8], heterophilic Ecad binding partners have not been systematically catalogued.

Unfortunately, the number of proximate proteins reported in a typical BioID screen are enormous (hundreds of candidate proteins), which limits the number of binding interactions that can be directly tested. We reasoned that transmembrane proteins that directly interact with Ecad

would be positioned in close proximity to both the Ecad ectodomain and cytoplasmic regions. Consequently, if BioID was fused to both the Ecad extracellular and cytoplasmic regions, identifying transmembrane proteins that are biotinylated in both regions would enable us to narrow down the list of possible Ecad binding partners for subsequent AFM binding measurements. However, the BioID method has only been utilized to identify intracellular binding partners [9], including to the cytoplasmic region of cadherins [10-12] and other junctional proteins [13]; it is unclear if BioID can successfully be used to screen for extracellular binding partners of transmembrane proteins.

In our experiments, we fused the biotin ligase TurboID [14] to the ectodomain (EC-BioID) and cytoplasmic region (C-BioID) of Ecad and expressed these fusion constructs in epithelial Madin-Darby Canine Kidney (MDCK) cells. Due to post translational cleavage of the N-terminal signal- and pro-peptide, inserting BioID at the Ecad N-terminus was not feasible. Furthermore, since the Ecad homophilic binding site is located on the proteins N-terminal domain, modifications in this region abolish Ecad adhesion. We therefore generated the EC-BioID, by inserting TurboID at amino acid 152 from N-terminal sequence (Fig.1a); this location was previously used to insert a GFP without affecting Ecad function [15]. C-BioID was generated by fusing TurboID to the C-terminus of Ecad (Fig. 1b). Both these constructs included a GFP at C-terminus (Fig. 1a, b, S1 a, c). Because of high levels of endogenous Ecad in parental MDCK cells, we rescued Ecad knockout MDCK cells with EC-BioID and C-BioID and generated stable cell lines. Both EC-BioID and C-BioID localized to intercellular junctions, verifying that the insertion of TurboID, did not disrupt the incorporation of Ecad into intercellular junctions (Fig. 1c, 1d, top row). Next, to demonstrate that the TurboID was functional, we incubated the cells with free biotin, and tagged the resulting biotinylated proteins with fluorescently labeled streptavidin (Fig. 1c, 1d, middle row). In the absence of exogenous biotin, we observed very little fluorescent streptavidin signal. Western blots (Fig. S1 b, d) also confirmed that the TurboID required an external source of biotin

to efficiently label proteins. Merging GFP and streptavidin images (Fig. 1c, 1d, bottom row) showed that most of the biotinylated proteins were localized to intercellular junctions.

To identify Ecad-proximate proteins, we captured the biotinylated proteins from EC-BioID and C-BioID cell lysates using streptavidin coated beads. Trypsin digestion of the beads released protein fragments that were analyzed using Mass Spectrometry (MS). The proteomics analysis reported 300 proximate proteins in EC-BioID cells and 946 proximate proteins in C-BioID cells (MS data attached in SI), similar to previous published cytoplasmic interactomes of Ecad [10, 12]. However, since our primary focus was to identify extracellular binding partners, we selected transmembrane proteins found in all replicates with more than 4.8% peptide coverage (ratio between detected peptides and predicted peptides from trypsin digestion). This resulted in 19 proteins that were found in the EC-BioID (Fig. 1 e, table S1) and 16 that were found in C-BioID (Fig. 1e, table S2). Of these 'hits', 7 proteins in addition to Ecad were common to both samples and consequently are possible binding partners for Ecad (Fig. 1e). These proteins (along with their gene IDs) are: Desmoglein-2 (DSG2), Desmocollin-3 (DSC3), Integrin alpha 2 (ITGA2), Integrin beta 1 (ITGB1), Ephrin-B1 (EFNB1), Coxsackie and adenovirus receptor (CXADR; CAR), and P-cadherin (CDH3; Pcad). Only few of these proteins were detected at a significant level in the absence of biotin (table S1, S2). It is important to note that our BioID experiments cannot distinguish if these proteins bound to Ecad in *trans* (from opposing cells) or *cis* (from the same cell) orientations since *trans* interacting proteins could still be in close *cis* proximity to Ecad.

Since BioID merely screens for protein proximity, we next probed the direct binding of ectodomains of 5 of the 7 candidate protein hits (Dsc3, Intα2-Intβ1 heterodimers, EfnB1, and CAR) with Ecad ectodomains, using single molecule AFM binding assays. We have already shown, using single molecule and cellular structure-function experiments, that the ectodomain of Dsg2 (the sixth protein hit in the BioID experiments) directly interacts with Ecad ectodomains [6]. Consequently, only Pcad-Ecad interactions remain untested. In our AFM experiments, we used

the complete extracellular region of all the target proteins expressed and purified from mammalian cells. The C-terminus of the proteins were either tagged with human Fc-dimer fragments (EfnB1 and CAR), biotin (Dsc3 and Ecad) or human c-Jun and c-Fos (Intα2β1 heterodimer). The biotin, c-Jun and Fc tags were used to immobilize the proteins on AFM tips and glass coverslips (Fig. 2a, 2c, 2e, 2g, 2i; Methods). We measured the homophilic interaction of every candidate protein, the heterophilic interaction of every candidate protein with Ecad, and nonspecific interactions under each measurement condition. Nonspecific interactions were determined using both an Ecad functionalized AFM cantilever and a coverslip lacking the candidate protein and also using an AFM cantilever lacking Ecad and a coverslip functionalized with the candidate proteins. For ease of comparison, all binding probabilities measured with a candidate protein were normalized by the corresponding Ca^{2+}-dependent homophilic binding rates. We confirmed that the Ecad is functional by measuring its homophilic binding properties (Fig. 2b). Since Ecad is a Ca^{2+} dependent adhesion protein, we confirmed that its homophilic binding probability was reduced in the presence of EGTA, a Ca^{2+} chelating agent (Fig. 2b, table S3).

One of the most abundant proteins found in both EC-BioID and C-BioID were different isoforms of the desmosome associated proteins, Dsc and Dsg, which mediate robust cell-cell adhesion in tissues like the epidermis and heart that are exposed to significant levels of mechanical stress. While Dsg2 and Dsc3 were identified in both EC-BioID and C-BioID, Dsc2 and Dsg1 were identified in C-BioID. As predicted by previous biophysical studies [16], our AFM measurements showed that Dsc3 interacts homophilically in a Ca^{2+} dependent fashion (Fig. 2d, table S3). Surprisingly, Dsc3 ectodomains also interacted heterophillically with Ecad ectodomains in a Ca^{2+} independent fashion (Fig. 2d, table S3). It is important to point out that we have previously shown that Dsg2 [6], our top BioID candidate, also interacts with Ecad in a similar Ca^{2+} independent heterophilic manner and plays an essential role in facilitating desmosome assembly. The interaction of Dsg2 and Dsc3 with Ecad provide a molecular explanation for previous studies

showing that blocking Ecad adhesion with antibodies or knocking down Ecad, delay desmosome formation in cells [17, 18], and that classical cadherin deficient mice show defective desmosome assembly [19].

Interestingly, both EC-BioID and C-BioID showed that the integrin focal adhesion proteins, Intα2 and Intβ1, were proximate to Ecad ectodomain. Since integrins are composed of non-covalently associated αβ heterodimers and Intα2 forms a heterodimer exclusively with Intβ1, we used Intα2β1 in our AFM binding measurements. Similar to Intα3β1 that interacts homophilically in a cation dependent manner [20], our AFM measurements demonstrated homophilic Ca^{2+} dependent Intα2β1 adhesion (Fig. 2f, table S3). Furthermore, as anticipated from the BioID results, we measured heterophilic adhesion between Ecad ectodomains and Intα2β1 ectodomains in Ca^{2+} (Fig. 2f, table S3). In support of this finding, previous immunofluorescence studies have shown that Intα2β1 localizes to cell-cell contacts in keratinocyte cells [21] and with Ecad and N-cadherin in melanoma cells [22]. Furthermore, cell-spreading assays show that interaction between cells and an Ecad coated surface is abolished by monoclonal antibodies that target Intα2β1 [23]. Our demonstration of homophilic binding and heterotypic adhesion with Ecad suggest that Intα2β1 could play a functional role in cell-cell adhesion and in collective cell migration.

Next, we measured the homophilic and heterophilic binding of EfnB1, a ligand for Eph, the largest subfamily of receptor tyrosine kinases. In agreement with previous structural reports [24], our measurements showed that EfnB1 also dimerizes homophilically (Fig. 2h, table S3). Interestingly, the heterophilic binding between Ecad monomers and EfnB1-Fc dimers was almost 3 fold higher than EfnB1 homophilic binding (Fig. 2h, table S3). While EfnB1 is known to interact with the tight junction protein claudin [25], direct binding of EfnB1 and Ecad has not been previously reported.

The last candidate protein we tested using AFM force measurements were Fc-dimers of CAR, a transmembrane virus receptor that localizes to tight junctions. In agreement with structural and sedimentation analysis [26], our AFM data also showed homophilic CAR interactions (Fig. 2j, table S3). However, the heterophilic binding probability of CAR and Ecad was only ~30% greater than nonspecific binding (Fig. 2j, table S3). This suggests that CAR ectodomains either do not interact with Ecad or bind to Ecad with a low probability. Previous studies show that while Ecad and CAR are not co-localized in stable cell-cell junctions, CAR localization is observed with internalized Ecad in vesicles [27]. This suggests that CAR can be biotinylated in internalized vesicles with both EC-BioID and C-BioID, even though it might not directly interact with Ecad on the cell surface. Another possible explanation for the low Ecad-CAR heterophilic binding measured in our AFM experiments is that CAR and Ecad interactions are primarily mediated by their respective cytoplasmic domains which would still result in detection in EC-BioID and C-BioID screens, but not in the single molecule AFM binding assay that only tests for ectodomain interactions. Nonetheless, the results we obtain with CAR clearly demonstrate the advantage of integrating a direct assay for protein interaction with proximity screening assays.

Our data demonstrates that BioID proximity tagging can be used to map ectodomain interactomes and that performing tandem BioID experiments on the extracellular and cytoplasmic region, targets transmembrane binding partners. Furthermore, we show that integrating BioID screens with single molecule AFM force measurements is an extremely powerful approach to discover transmembrane protein interactions. The results of our integrated assay demonstrate that Ecad ectodomains do not merely engage in homophilic binding, but instead, like the Ecad cytoplasmic region, also bind to a range of junctional proteins. We anticipate that integrated BioID-AFM experiments can be similarly applied to identify heterophilic binding partners for other transmembrane proteins.

Methods:

Molecular cloning of EC2-BioID and C-BioID: We inserted TurboID in Ecad at a site where GFP had previously been inserted in mouse N-cadherin using *in vitro* transposition [15]. We identified, from sequence alignment, a similar sequence at position 309 (amino acid 152 from N-terminal sequence) in canine Ecad sequence and inserted TurboID with a peptide linker on both ends; the linker was composed of the same amino acids (***AYSILT***- LSLIHIWRA- **V5**-**TurboID**-GRARADVYKRQ- ***QDPLLP***; canine Ecad sequence is in bold italicized font while linker sequence is in normal font) used previously [15].

We PCR amplified Ecad using pEGFP-N1-Ecad plasmid [28] and V5-TurboID using mutant BirA R118S (TurboID) (Addgene [14]) using PCR primers (table S4). The PCR products were inserted between EcoRV and BglII using gibson assembly (New England Biolabs) in pEGFP-N1-Ecad vector. We PCR amplified the EC-BioID sequence and inserted it into the PiggyBac-GFP vector using NheI site (PB533A, System Biosciences, Mountain View, CA). For C-BioID, we PCR amplified the complete Ecad using pEGFP-N1-Ecad plasmid using PCR primers (table S4). The PCR products were inserted at BamHI site in a PiggyBac vector.

The PiggyBac EC-BioID-GFP and C-BioID-EGFP plasmids were transfected into Ecad-KO cells [29] using Lipofectamine2000 (Invitrogen) along with PiggyBac Transposase expression plasmid (System Biosciences) and selected with 500 µg/ml G418 (Invitrogen). G418-resistant cells were sub-cloned and selected by confocal microscopy and western blotting to obtain homogeneous cell populations.

Immuno-fluorescence: EC-BioID and C-BioID expressing MDCK cells were grown to confluency and switched to serum free DMEM cell culture media and supplemented with 50 µM biotin overnight. To selectively detect the extracellular biotinylation, AlexaFluor-568-conjugated

streptavidin (Invitrogen) was added for 30 minutes before cell fixation and permeabilization. Cells were fixed using 3% paraformaldehyde and 0.3% Triton X-100 in PBS for 10 minutes and blocked with 1% BSA and 0.3% Triton X-100 in PBS for 30 minutes. Anti-GFP (rabbit polyclonal, Invitrogen) antibody and AlexaFluor-488-conjugated anti-rabbit antibody were used to detect GFP-tagged proteins. For C-BioID expressing cells, biotinylated proteins were detected by incubating the fixed cells for 30 mins with AlexaFluor-568-conjugated streptavidin. Cells were imaged using a Zeiss AxioObserver equipped with a Yokogawa CSU-10 spinning disk confocal system, 40× objective, 488- and 561-nm solid-state lasers, a Photometrics CoolSNAP HQ2 camera, and Slidebook software (Intelligent Imaging Innovations). Images were reconstructed using ImageJ.

Purification of biotinylated proteins for MS analysis: Cells expressing EC-BioID and C-BioID were seeded on p150 dishes and cultured to 70%-90% confluency in Dulbecco's Modified Eagle's Medium (DMEM) (Invitrogen) supplemented with 10% fetal bovine serum (Gibco), penicillin (Invitrogen), streptomycin (Invitrogen) and 200 µg/ml G418 (Invitrogen). Cells were then incubated overnight with serum free media supplemented with 50 µM biotin. After three PBS washes, cells were scraped and centrifuged. Pelleted cells were re-suspended in lysis buffer [30, 31] (50 mM Tris pH 7.5, 150 mM NaCl, 0.4 % SDS, 1 % IGEPAL CA-630, 1.5 mM $MgCl_2$, 1 mM EGTA) with 2 µL/ml of protease inhibitor cocktail (Sigma-Aldrich), and 1 µL/ml Benzonase (250 U/µL) (EMD-Millipore). Cell lysate was incubated for 30 min at 4 °C and then sonicated at 10%-30% duty ratio for 1 min, and centrifuged at 13000 rpm for 30 min at 4 °C. The supernatant was collected, and their concentrations were measured with a RC/DC protein assay kit (Bio-Rad). Supernatant (1 ml at ~4-5 mg/ml) was incubated with 50 µl of superparamagnetic Dynabeads Streptavidin C1 (Invitrogen) and rotated overnight at 4 °C. First, beads were washed with the lysis buffer and transferred to new tubes. The beads were washed again with the 2% SDS in 50 mM

Tris HCl pH 7.4, then washed twice with lysis buffer. Next, the beads were washed three times with 100mM ammonium bicarbonate (NH_4HCO_3) and re-suspended in 30uL of digestion buffer containing 1 µg/µL of trypsin gold in 50 mM NH_4HCO_3 for overnight digestion at 37 °C. To stop the digestion, the reaction mixture was acidified with 1% trifluoroacetic acid (TFA). The resulting peptides were recovered from the beads using a magnet and then acidified with 0.5% TFA final concentration. The eluted tryptic peptides were dried in a vacuum centrifuge and re-constituted in 0.1% formic acid. Tryptic peptides were analyzed using nano-scale liquid chromatographic tandem mass spectrometry (nLC-MS/MS).

Nano-scale liquid chromatography: Nano-scale liquid chromatography (nLC) was performed on an ultra-high pressure nano-flow Easy nLC system (Bruker Baltonics). Liquid chromatography was performed at 40 °C with a constant flow rate of 400 nL/min on an in-house packed reversed-phase column (25 cm x 75 µm i.d.) with a pulled emitter tip, packed with 1.9 µm C18-coated porous silica beads (Dr. Maisch, Ammerbuch-Entringen, Germany). Mobile phases A and B were water with 0.1% formic acid (v/v) and 80/20/0.1% ACN/water/formic acid (v/v/v), respectively. Peptides were separated using a 33 min gradient from 5% to 38% B within 25 min, followed by an increase to 95% B within 1 min, a 1 min washing step at 95% B, ending with 8 min of re-equilibration at 5% B.

Mass Spectrometry: Mass Spectrometry (MS) was performed on a hybrid trapped ion mobility spectrometry-quadrupole time of flight mass spectrometer (timsTOF Pro, Bruker Daltonics, Bremen, Germany) with a modified nano-electrospray ion source (CaptiveSpray, Bruker Daltonics). In the experiments described here, the mass spectrometer was operated in PASEF mode. All experiments were acquired with a 100 ms ramp and 10 PASEF MS/MS scans per topN

acquisition cycle. Low-abundance precursors with an intensity below a ‘target value’ were repeatedly scheduled for PASEF-MS/MS scans until the summed ion counts reached a target value of 20,000 a.u. MS and MS/MS spectra were recorded from m/z 100 to 1700. A polygon filter was applied to the m/z and ion mobility plane to select features most likely representing peptide precursors rather than singly charged background ions. The quadrupole isolation width was set to 2 Th for m/z under 700 and 3 Th for m/z larger than 700, and the collision energy was ramped stepwise as a function of increasing ion mobility: 52 eV for 0%–19% of the ramp time; 47 eV from 19%–38%; 42 eV from 38%–57%; 37 eV from 57%–76%; and 32 eV for the remainder.

MS Data Analysis: Mass spectrometry raw files were processed with MsFragger [32]. For all searches, a protein sequence database of reviewed canine proteins (accessed 11/27/2019 from UniProt; 1886 entries including decoys and 115 common contaminant sequences) was used. Decoy sequences were generated and appended to the original database for MsFragger. A maximum of two missing cleavages were allowed, the required minimum peptide sequence length was 7 amino acids, and the peptide mass was limited to a maximum of 5000 Da. Carbamidomethylation of cysteine residues was set as a fixed modification, and methionine oxidation and acetylation of protein N termini as variable modifications. The initial maximum mass tolerances were 50 ppm for precursor and fragment ions. A reversed sequence library was generated/used to control the false discovery rate (FDR) at less than 1% for peptide spectrum matches and protein group identifications. Decoy database hits, proteins identified as potential contaminants, and proteins identified exclusively by one site modification were excluded from further analysis. Label-free protein quantification was performed with the IonQuant algorithm [32]. All other MsFragger parameters were kept at their default values.

Cloning, purification and biotinylation of Ecad and Dsc3 monomers for single molecule AFM experiments: The extracellular region of the Dsc3 was PCR amplified from full length human Dsc3 purchased from DNASU plasmid repository (clone ID: HsCD00821324). For Dsc3, the following PCR primers were used: 5'-tgtggtggaattctgcagatatcATGGCTGCCGCTGGCCCC (forward) and gcaagctttcgctagcCTTTCCCAGAATCACGCCTGTGCTTCTG (reverse). Avi-tag-Tev-6x His (ATH) sequence was amplified using pcDNA3.1(+) Ecad-pATH [33] using forward primer 5'-aaaggctagcGAAAGCTTGCTTGGTGGC and reverse primer 5'-gttcgaagggccctctagactcgagGATTAGTGATGATGGTGATGG. The Dsc3 extracellular region and ATH fragments were cloned into pcDNA3.1(+) Ecad-pATH between EcoRV and XhoI sites.

Cloning of Ecad-ATH plasmids has been described elsewhere [34]. The Ecad and Dsc3 plasmids were transiently transfected into HEK 293T cells using Polyethylenimine (PEI) (Polysciences, Inc.). Four days post transfection, the conditioned media was collected for protein purification. As described previously [6], protein was purified using the NGC Chromatography Systems (BioRad). In 4 ºC, media containing cadherin was flowed through Ni-NTA agarose beads (Qiagen) packed on 1 ml Empty Bio-Scale Mini Cartridges (Biorad #7324660). The column was then washed with buffer at pH 7.5 (25mM HEPES, 5mM NaCl, 1mM $CaCl_2$, pH 7.5). We directly biotinylated the proteins bound to Ni-NTA by incubating the beads with BirA enzyme (BirA500 kit; Avidity) for 1hr in 30 °C followed by an overnight incubation at 4 °C. Next, the column was washed with 25 mM HEPES, 500mM NaCl, 1mM $CaCl_2$ with 20mM Imidazole at pH 7.5 and then eluted with the same buffer containing 250 mM imidazole. Following purification, the protein was exchanged to a Tris 10mM, NaCl 100mM, KCl 10mM, $CaCl_2$ 2.5mM, buffer at pH 7.5.

Single molecule AFM force measurements: Biotinylated monomeric Ecad & Dsc3, and dimeric Intα2β1-c-Jun/c-Fos, EfnB1-Fc & CAR-Fc were immobilized on coverslips (CS) and AFM cantilevers (Olympus, model TR400PSA) using previously described method [33]. Briefly, the CS

and cantilevers were cleaned with 25% H_2O_2:75% H_2SO_4 and washed with DI water. Then the CS was cleaned with 1 M KOH and washed with DI water. Both the CS and cantilevers were washed with acetone and functionalized using 2% (v/v) 3-aminopropyltriethoxysilane (Sigma) dissolved in acetone. Next, N-hydroxysuccinimide ester functionalized PEG spacers (MW 5000, Lysan Bio) were covalently attached to the silanized AFM tip and coverslip; 7% of the PEG spacers were decorated with biotin groups. Prior to a measurement, the functionalized AFM cantilever and coverslip were incubated overnight with BSA (1 mg/ml) to further reduce non-specific binding. The tip and surface were then incubated with 0.1 mg/ml streptavidin for 30 minutes and biotinylated cadherins were attached to the streptavidin. Recombinant rat EfnB1-FC (R&D catalog no: 1596-B1) and recombinant human CAR-FC (R&D catalog no: 3336-CX) were linked to streptavidin using biotinylated protein G as previously shown [34]. Human Integrin α2β1 heterodimer with human c-Jun and human c-Fos (R&D catalog no: 5698-A2) was linked to biotinylated protein G by c-Jun antibody (R&D catalog no: MAB2670). Finally, the surfaces were incubated with 0.02 mg/ml biotin for 10 minutes to block the free biotin binding sites on streptavidin.

Force measurements were performed using an Agilent 5500 AFM with a closed loop scanner. The spring constants of the cantilevers were measured using the thermal fluctuation method [35]. All the experiments were performed in a pH 7.5 buffer containing 10 mM Tris-HCl, 100 mM NaCl and 10 mM KCl with either 2.5 mM Ca^{2+} or 2 mM EGTA. For each experiment 960-1800 force curves were collected. Force curves with non-linear polymer stretching greater than the contour length of a single PEG molecule, was counted as an interaction.

Acknowledgements: Research in SS lab was supported in part by the National Institute of General Medical Sciences of the National Institutes of Health (R01GM121885). SY's research was supported in part by NIH R03 EB021636 and NSF 1562095. We thank Dr. Gabriela

Grigorean for performing LC-MS/MS and data analysis in Proteomics Core Facility of the Genome Center at University of California, Davis.

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Figure Legends:

Figure 1: Characterizing the Ecad BioID constructs. TurboID was fused at **(a)** EC2 domain of Ecad (EC-BioID) and **(b)** C-terminal of Ecad (C-BioID). Proteomic analysis of both constructs identified ephrin-B1 (EfnB1), coxsackie and adenovirus receptor (CAR), P-cadherin (Pcad), desmocollin-3 (Dsc3), desmoglein-2 (Dsg2), Integrin β1 (Intβ1) and Integrin α2 (Intα2) as proteins that were proximal to Ecad. Proteins are depicted using deposited PDB structures or predicted from homology modelling using Modeller. The following PDB-IDs were used in generating the images: EfnB1: 6P7Y, CAR: 3J6N, TurboID: 4WF2, GFP: 1GFL, Ecad and Pcad: 3Q2V, Dsc3: 5IRY, Dsg2: 5ERD, Intα2: 3K6S, Intβ1: 3IJE, and membrane: POPE. Images were reconstructed using PyMOL. All cytoplasmic domains are schematic representations. GFP localized to intercellular junction in **(c)** EC-BioID and **(d)** C-BioID confirming that Ecad is functional.

Fluorescent streptavidin (Sta) staining showed that while BioID biotinylated proteins in the presence (+) of exogenous biotin, low levels of biotinylation was observed in the absence (-) of exogenous biotin. Merged images of GFP and Sta shows most of the biotinylation occur near the junction. **(e)** Venn diagram showing Ecad proximal transmembrane proteins identified from MS analysis of EC-BioID (green) and C-BioID (pink). Transmembrane candidate proteins observed in both BioID screens are listed in the overlapping region. Scale bar: 10 µm.

Figure 2: Single molecule AFM force measurements confirm novel binding partners for Ecad. (a) Schematic of single molecule AFM force measurement experiment. The AFM tip and substrate were functionalized with PEG linkers, some of which were decorated with streptavidins (Sta). Biotinylated Ecad was directly attached to Sta. **(b)** Ecad showed Ca^{2+} dependent homophilic interactions. **(c)** Homophilic binding probability was determined with biotinylated Dsc3 immobilized on both AFM tip and substrate. Heterophilic measurements were performed with Ecad on AFM tip and biotinylated Dsc3 on substrate. **(d)** Dsc3 showed Ca^{2+} dependent homophilic interactions and Ca^{2+} independent interactions with Ecad. **(e)** Intα2β1 heterodimer tagged with c-Jun was immobilized using c-Jun antibody and biotinylated protein G (Pro-G) **(f)** Intα2β1 formed Ca^{2+} dependent homophilic complexes and also formed heterophilic complexes with Ecad. **(g)** Fc-tagged EfnB1 was attached to Sta using biotinylated Pro-G **(h)** EfnB1 interacted homophilically and also bound heterophilic to Ecad. **(i)** CAR-Fc was immobilized using biotinylated Pro-G. **(j)** CAR showed low probability of heterophilic interactions with Ecad. Error bars are s.e. calculated using bootstrap with replacement.

Figure 1

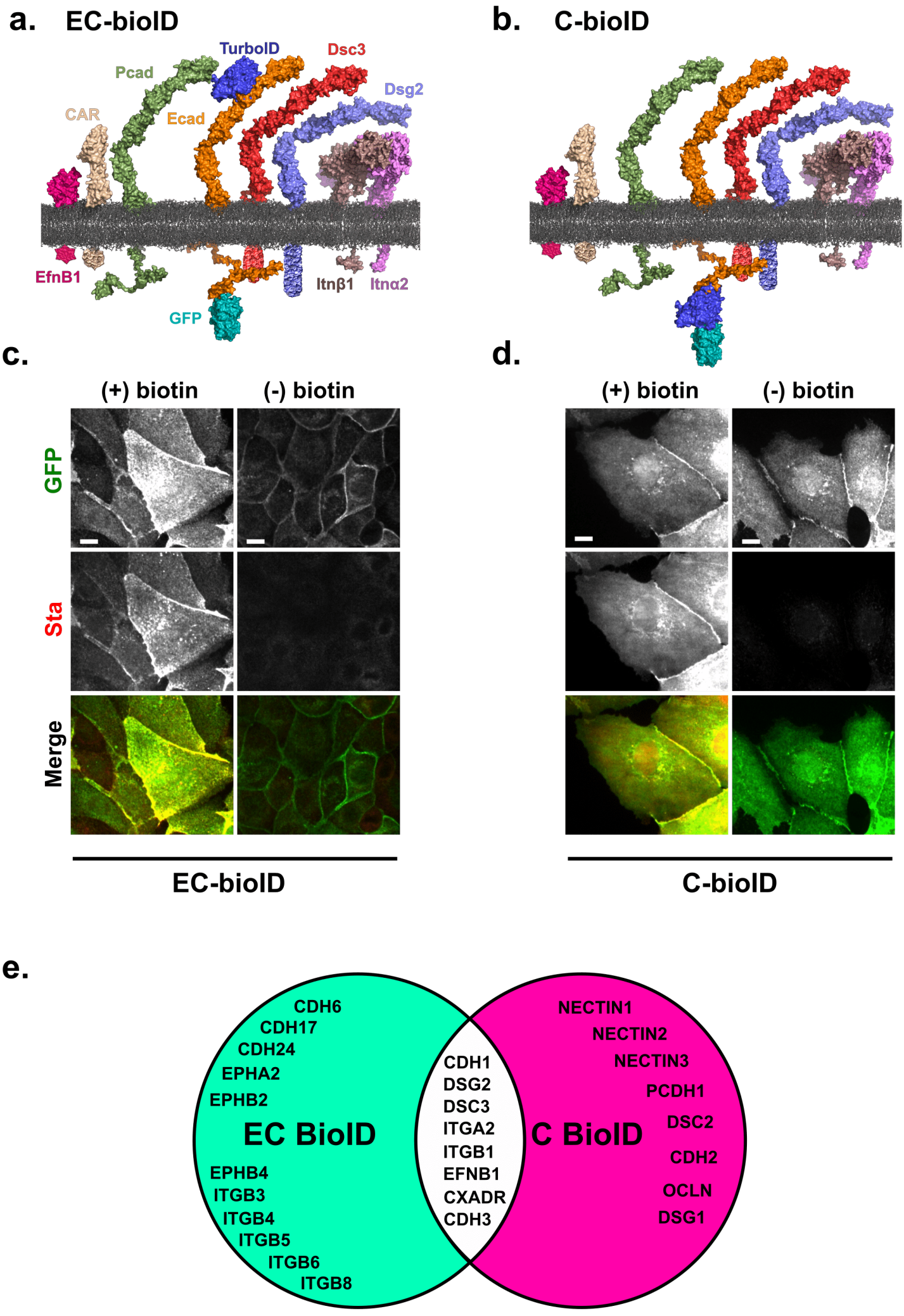
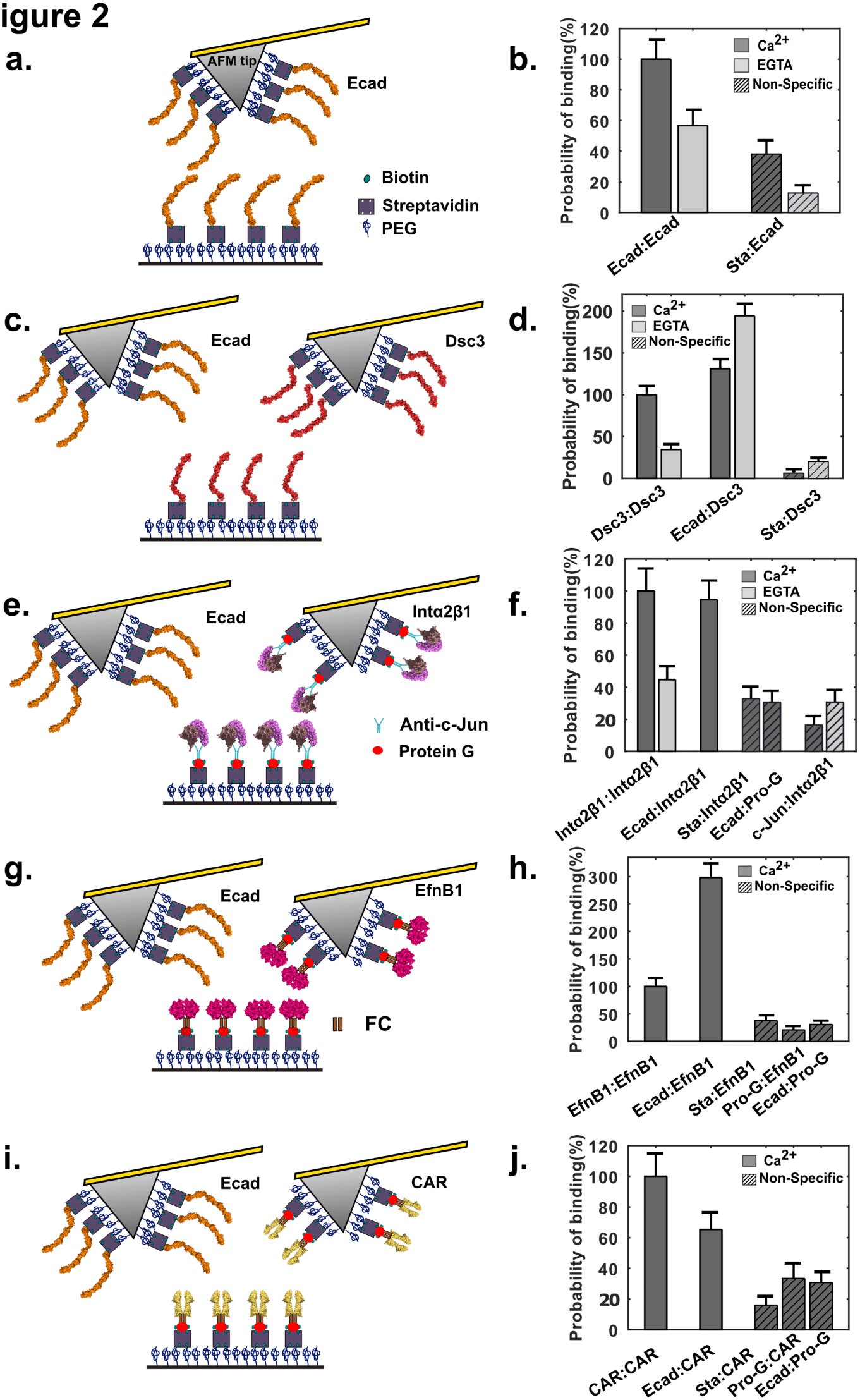

a.
EC-bioID
TurboID
Dsc3
Pcad
Dsg2
CAR
Ecad
EfnB1
Itnβ1
Itnα2
GFP
b.
C-bioID
c.
(+) biotin
(-) biotin
GFP
Sta
Merge
EC-bioID
d.
(+) biotin
(-) biotin
C-bioID
e.
CDH6
CDH17
CDH24
EPHA2
EPHB2
EC BioID
EPHB4
ITGB3
ITGB4
ITGB5
ITGB6
ITGB8
CDH1
DSG2
DSC3
ITGA2
ITGB1
EFNB1
CXADR
CDH3
NECTIN1
NECTIN2
NECTIN3
PCDH1
DSC2
C BioID
CDH2
OCLN
DSG1

Figure 2


a.
AFM tip
Ecad
Biotin
Streptavidin
PEG
b.
Probability of binding(%)
Ca2+
EGTA
Non-Specific
Ecad:Ecad
Sta:Ecad
c.
Ecad
Dsc3
d.
Probability of binding(%)
Ca2+
EGTA
Non-Specific
Dsc3:Dsc3
Ecad:Dsc3
Sta:Dsc3
e.
Ecad
Intα2β1
Anti-c-Jun
Protein G
f.
Probability of binding(%)
Ca2+
EGTA
Non-Specific
Intα2β1:Intα2β1
Ecad:Intα2β1
Sta:Intα2β1
Ecad:Pro-G
c-Jun:Intα2β1
g.
Ecad
EfnB1
FC
h.
Probability of binding(%)
Ca2+
Non-Specific
EfnB1:EfnB1
Ecad:EfnB1
Sta:EfnB1
Pro-G:EfnB1
Ecad:Pro-G
i.
Ecad
CAR
j.
Probability of binding(%)
Ca2+
Non-Specific
CAR:CAR
Ecad:CAR
Sta:CAR
Pro-G:CAR
Ecad:Pro-G