Cancer associated talin point mutations disorganise cell adhesion and migration

Latifeh Azizi[1], Alana R. Cowell[2], Vasyl V. Mykuliak[1], Benjamin T. Goult[2*], Paula Turkki[1,3*], Vesa P. Hytönen[1,3*]
[1]BioMediTech, Faculty of Medicine and Health Technology, Tampere University
[2]School of Biosciences, University of Kent, Canterbury, Kent, CT2 7NJ, UK.
[3]Fimlab Laboratories, Tampere, Finland

**Corresponding authors: Benjamin T. Goult: B.T.Goult@kent.ac.uk, Paula Turkki: paula.turkki@tuni.fi, Vesa P. Hytönen: vesa.hytonen@tuni.fi*

Abstract

Talin–1 is a key component of the multiprotein adhesion complexes which mediate cell migration, adhesion and integrin signalling and has been linked to cancer in several studies. We analysed talin–1 mutations reported in the Catalogue of Somatic Mutations in Cancer and developed a bioinformatics pipeline to predict the severity of the mutations. These predictions were then assessed using molecular dynamic simulations, biochemistry and cell biology experiments. With this approach we were able to identify several talin–1 mutations affecting integrin activity, actin recruitment and Deleted in Liver Cancer 1 localization. We explored potential changes in talin-1 signalling responses by assessing impact on migration, invasion and proliferation. Altogether, this study describes a pipeline approach of experiments for crude characterization of talin–1 mutants in order to evaluate their functional effects and potential pathogenicity. Our findings suggest that cancer related point mutations in talin–1 can drastically affect cell behaviour and so may contribute to cancer progression.

Keywords: talin, COSMIC, somatic mutations, cancer, migration, invasion, focal adhesion

Introduction

For cells to maintain homeostasis and co–operate within tissues, they need to dynamically interact with the extracellular matrix (ECM). In recent years the role of the microenvironment has become increasingly recognised [1] and disturbances between cell–ECM interactions, intracellular signalling events, and signals derived from the ECM have been shown to contribute to cancer progression (Fig.1A). Talin is a major component of focal adhesions (FAs), responsible for mediating the link between the ECM via integrins and the actin cytoskeleton. Talin is a large ~250 kDa mechanosensitive protein consisting of an N–terminal FERM head domain (F0, F1, F2, F3; residues 1–405) followed by a linker (~80aa) and ~2000aa rod region comprised of 13 domains (R1 to R13) ending in a C–terminal dimerisation domain (DD) [2] (Fig.1B). The FERM domain interacts with the membrane–proximal NPxY motif of beta integrin tail and the negatively charged plasma membrane [3, 4]. The rod domain contains two F–actin binding sites (ABS2 and ABS3) [5-7], 11 vinculin binding sites (VBS) [8] and binding sites for regulatory proteins such as RIAM, KANK [9, 10] and the tumour suppressor DLC–1 [11, 12] (Fig.1B). Studies have shown that ABS3 is essential for FA assembly [13], whereas ABS1 and ABS2 have a reinforcing role [14, 15].

Talin is the main scaffold protein in focal adhesions which form at the leading edge of a polarised cell. Talin links the intracellular tails of integrins to the actin cytoskeleton and mechanical forces exerted on talin can disrupt and reveal binding sites leading to formation of mature multiprotein FA complexes [16-18]. These are dynamic processes regulated by a complex signalling network, gathering information from intracellular and extracellular events. The mechanical properties of the ECM are reflected by intracellular changes via the FAs and actomyosin network, having a direct effect on cell behaviour, such as cell shape, migration and proliferation [19, 20] (Fig.1A).

Talin–1 overexpression has been shown to correlate with increased invasion and decreased survival with oral squamous cell carcinoma [21] as well as migration, invasion and anoikis resistance in prostate cancer cells [22]. Loss of talin–1 leads to diminished *in vivo* metastasis of prostate cancer cells via FAK–Src complexes and AKT kinase signalling [22]. Conversely, downregulation of talin–1 has also been shown to promote hepatocellular carcinoma progression [23].

The COSMIC (Catalogue Of Somatic Mutations In Cancer) database [24] contains exon sequencing data of human cancers and provides a vast resource of somatic mutation information. In light of talins integral role in regulating cell behaviour, integrin adhesion signalling and its connection to cancer

progression, we sought to explore how cancer–associated talin mutations may alter talin function and the behaviour of cells.

Here we provide a pipeline approach in order to evaluate the effect of talin–1 mutations. First, we applied a suite of bioinformatic prediction tools in order to rank each mutation based on its location and predicted effects on protein structure. We used the scoring function to select mutations with the potential to disrupt talin function and/or affect its interactions with known binding partners for further characterisation. Next we assessed the mutations effects via computational methods, and biochemical and cell biological analysis was performed to determine the mutations effects on known interactions. Lastly, we studied the effects of mutations on essential cellular behaviours, such as cell migration, invasion and proliferation. This pipeline would be amenable to other proteins and so provides a way to convert the COSMIC information into biological insights.

Results

Screening of *TLN–1* mutations from COSMIC database

To investigate functional consequences of talin–1 point mutations, 368 talin–1 mutations in COSMIC database (accessed January 2017) were evaluated, and 258 missense mutations were further screened using bioinformatic tools (Fig.1C). We investigated each of the 258 point mutations individually and determined the position of the mutation within the talin structure (Fig.1B). The pathogenicity of the amino acid substitutions were predicted using the PON–P2–algorithm [25]. We used a BLOSUM62 substitution matrix [26] and CBSM60 matrix [27] to obtain a numeric penalty for each amino acid deviation and to predict the protein structure/function, respectively. Next we investigated if the mutations cause changes in amino acid polarity as the stability of talin domains are strongly dependent on hydrophobic effect [28, 29]. The degree of evolutionary conservation of the amino acids in the talin sequence was investigated using ConSurf [30]. Finally, we evaluated if the mutation is close to known ligand–binding sites. All these factors were used to build a scoring coefficient and the weight for each variable was obtained using the manual iteration process described in the Supplementary material.

Based on this analysis, eleven mutations were selected for further investigation with the E1770Q mutation also included despite a lower score due to its location in the previously defined talin autoinhibition site [31, 32] (Table1; Fig.1B).

Table 1. The list of talin–1 point mutations selected from the COSMIC database. In each column a normalised value close to 1 predicts defects in protein function. BH=mutation located between helices and DD=dimerisation domain. CBSM60= conformation–specific amino acid substitution matrix. BLOSUM62=BLOcks SUbstitution Matrix. The recurrence value has been updated 27.06.2020.

Talin–1 mutant	Recurrence	Primary tissue	Histology	Domain	Location	PON–P2 probability of pathogenicity	Normalised BLOSUM 62–matrix score	Normalised CBSM60 matrix score	Normalised ConSurf score	Final score
P229L	2	Skin	Carcinoma	F2	BH/buried	0.94	1	1	1	8.20
I392N	1	Pancreas	Carcinoma	F3	Buried	0.86	1	0.83	1	8.95
V577D	1	Liver	Carcinoma	R1	Buried	0.94	1	1	0.60	8.39
A893E	3	Central nervous system/pituitary	Glioma/Cranio pharyngioma	R3	BH/buried	0.95	0.75	0.33	0.60	7.63
R1368W	2	Hematopoietic and lymphoid tissue /large intestine	Lymphoid neoplasm /carcinoma	R7	Surface	0.98	1	1	1	7.75
Y1389C	2	Liver	Carcinoma/car cinoma	R7	Buried	0.90	0.87	0.67	1	8.58
L1539P	1	Liver	Carcinoma	R8	Buried	0.98	1	1	0.60	8.45
S1750F	1	Skin	Malignant melanoma	R9	Buried	0.89	0.87	0.5	0.60	7.55
E1770Q	1	Breast	Carcinoma	R9	Surface	0.81	0.37	– 0.33	1	6.01
D2086V	1	Breast	Carcinoma	R11	Surface	0.96	1	1	1	7.71
L2509P	1	Large intestine	Carcinoma	DD	DD /Surface	0.96	1	1	0.64	7.46

We next evaluated the selected COSMIC mutations against the 1000 Genomes Project database, which is a large database of human genetic variant data [33]. None of the selected mutations were found in the 1000 Genomes (although six were referenced as being in the COSMIC database), indicating that these mutations have not been found in healthy individuals.

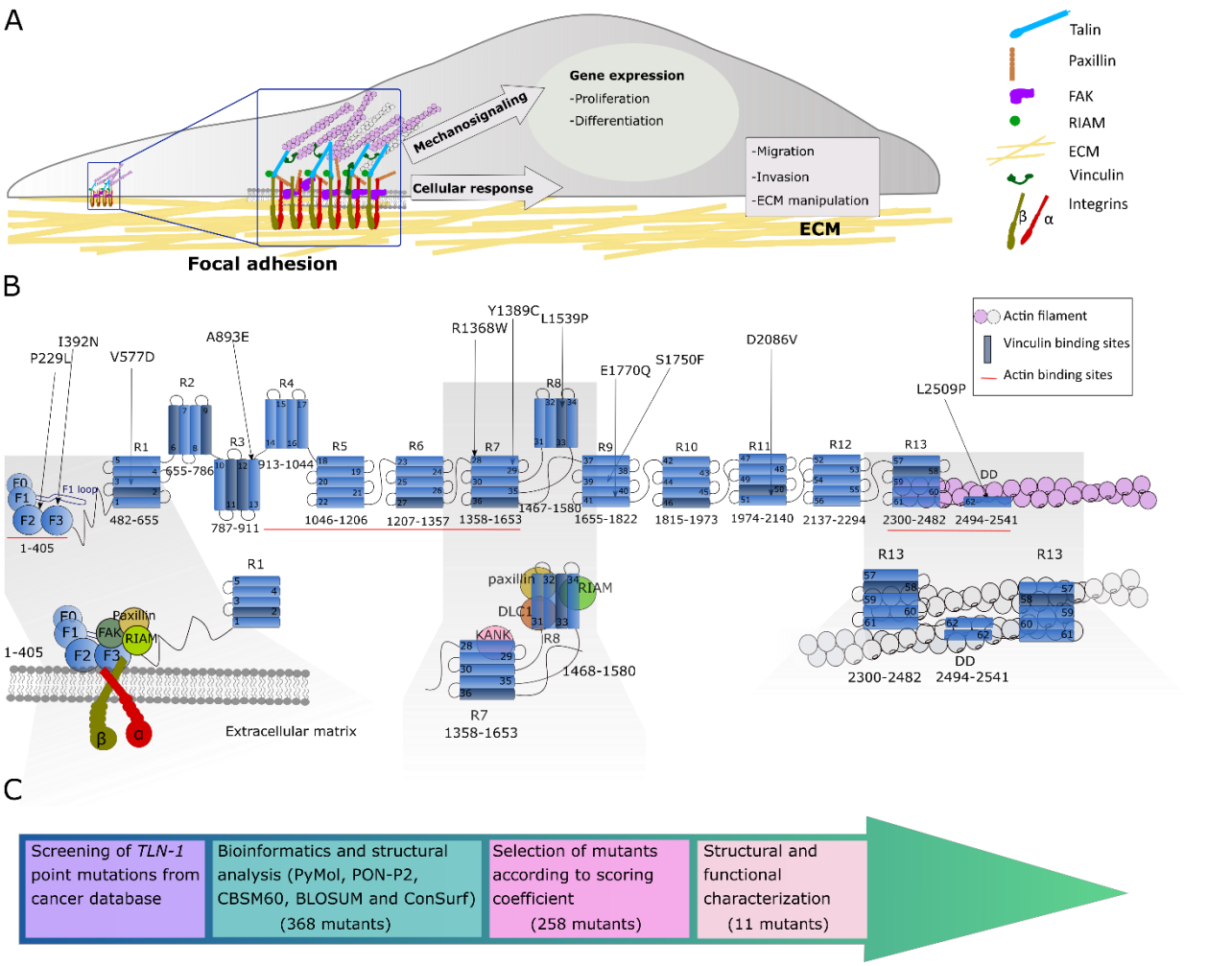

Figure 1: Analysis of talin–1 mutations found in the COSMIC database. A) Schematic representation of focal adhesion role on cell function. B) Schematic representation of talin–1 and the positions of the selected missense mutations. Bottom: cartoon of the talin head complexes that form with integrin, FAK, paxillin and RIAM (left), talin R7–R8 complexes with KANK, DLC–1, RIAM and paxillin (middle) and the R13–DD actin cytoskeletal linkage (right). C) Flowchart showing the study pipeline to investigate TLN–1 mutations from COSMIC database.

Molecular Dynamics simulations suggest that mutations destabilise the talin–1 domains

To investigate how mutations affect talin–1 subdomain stability, we employed Molecular Dynamics (MD) simulations for each mutant, including non–equilibrium simulations of free energy changes in subdomain stability upon mutation (Fig.S1A,B). Most of the selected mutations showed high free energy changes with especially high values of 20 kJ/mol or above with I392N (38.28±1.27 kJ/mol), V577D (52.15±13.71 kJ/mol) and Y1389C (20.60±4.09 kJ/mol) indicating strong destabilisation of the corresponding subdomains. For more detailed characterisation, we selected mutations closest to sites with known interaction partners: P229L, I392N were selected due to their proximity to the integrin binding site in F3; R1368W, Y1389C, and L1539P within the R7–R8 fragment which is

known to interact with paxillin, RIAM, KANK and DLC–1, and L2509P which is situated within the dimerisation domain (DD) and the C–terminal actin binding site, ABS3 [7] (Fig. 1C).

Mutation of Isoleucine–392, which is located inside the hydrophobic core of the F3 subdomain, to Asparagine (I392N) leads to replacement of the hydrophobic isoleucine side chain with a hydrophilic side chain. A snapshot of the MD simulation demonstrates instability caused by introduction of the mutation and can be visualised with the water molecule penetrating into the F3 fold (Fig.2A). MD simulations carried out for R7–R8 WT and mutants suggest that the R7 and R8 subdomains interact over the course of 100 ns MD (Fig.S1A). Analysis of the R7–R8 binding energy using the Molecular Mechanics Poisson–Boltzmann Surface area (MM–PBSA) method further suggested that the R1368W mutation may enhance an interaction between R7 and R8 (Fig.2B, Fig.S1C). Analysis of free energy changes upon mutation showed strong destabilization of R7 subdomain by 20.60±4.09 kJ/mol upon Y1389C mutation (Fig.2C, Fig.S1B). MD simulations revealed that the L1539P mutation effectively breaks the structure of helix three (H3) in the R8 subdomain (Fig.2D), and secondary structure analysis using Dictionary of Secondary Structure of Proteins algorithm (DSSP) indicated clear disruption of H3 in the L1539P–mutated R8 when compared to wildtype (Fig.S1D). Finally, MD simulations revealed high flexibility of the mutated helix, L2509P, in the dimerisation domain, with the proline in the mutant form breaking the helical structure (Fig.2E).

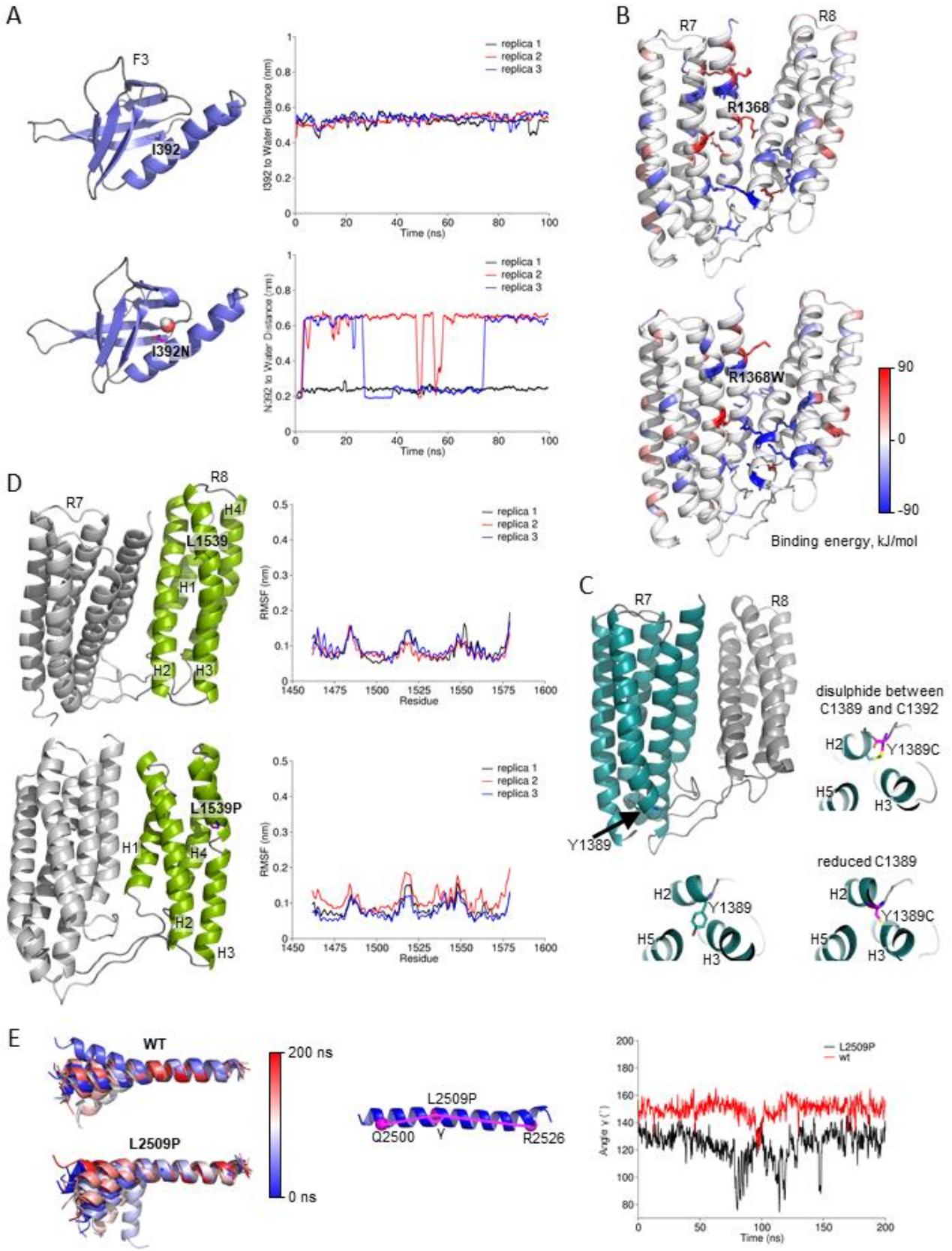

Figure 2: MD simulation analysis of the effects of cancer–associated mutations on talin domains. A) Structure snapshots of the F3 subdomain for WT and I392N mutant. Residue 392 and a water molecule inside the F3 domain in the I392N mutant simulation are shown. The distance between the residue 392 side chain and closest water molecule as function of the MD simulation time in WT and I392N mutant. Three 100 ns replicas are shown. The distance of ~0.6 nm

in the WT indicates that the closest water molecule is located at the F3 surface, while in the I392N mutant the distance ~0.2 nm indicates that the nearest water molecule has penetrated the F3 fold. B) R7–R8 inter–domain binding energy distribution for WT and R1368W predicted using MM–PBSA. Residue R1368W and other that have contribution to the inter–domain binding energy lower than –50 kJ/mol and higher than 50 kJ/mol are shown as sticks. Snapshots captured before MD were used for visualisation. Snapshots captured after 100 ns MD are shown in Fig.S1A. C) Visualisation of Y1389C mutation in R7–R8 structure. D) R7–R8 structure snapshots captured at 100 ns of MD for WT and L1539P (in R8); the R7–R8 was used in the simulations, but the Root Mean Square Fluctuation (RMSF) analysis was performed for R8 only. Proline breaks the secondary structure and increase the flexibility of the domain, which reflects RMSF. R7 is shown in grey and R8 in green. E) MD simulation of DD helix showing increased flexibility of the helix caused by L2509P compared to the WT. Superposition was performed using C–alpha atoms of residues 2510 to 2529. The angle (γ) in L2509P mutant and WT in a single helix measured as a function of time.

Biochemical characterisation indicates that Y1389C decreases R7–R8 domain stability and L2509P leads to loss of dimerisation

We next sought to characterise the effects of these mutations on talin structure and to validate the MD simulation data. We used Nuclear Magnetic Resonance (NMR) and Circular Dichroism (CD) to provide biophysical insight into the structural effects of each mutation. Comparison of the ^{15}N–HSQC spectra of the R7–R8 wildtype and R1368W mutant revealed similar peak dispersion in both spectra, with only minor shifts in peak positions that occur as a result of the altered sidechain suggesting that R1368W does not significantly affect talin R7–R8 structure (Fig.3A). In support of this, CD analysis of the R7–R8 WT and R1368W proteins yielded similar spectra confirming similar secondary structure, and no change in thermal stability which supports the NMR analysis (Fig.3B,C).

In contrast, the Y1389C mutation caused a striking 6.5°C reduction in the thermostability of R7–R8 (45.5°C compared with 52°C for the wildtype) assessed using CD (Fig.3C). Mutation to cysteine introduces the possibility of a potential to form a disulphide bond. To test whether the effects seen are due to disulphide bond formation with the adjacent cysteine (C1392), we performed this analysis in the presence and absence of dithiothreitol and saw no difference between the spectra.

Finally, L2509P, located in the talin dimerisation domain, was predicted to disrupt talins ability to dimerise and thus alter actin binding as shown in previous research [7]. Size exclusion chromatography with Multi–Angle Light Scattering (SEC–MALS) showed that wildtype R13–DD (residues 2300–2541) is a constitutive dimer, consistent with our previous study [7]. In contrast the L2509P mutant of the R13–DD runs as a monomer, confirming that the proline is disrupting talin dimerisation (Fig.3D).

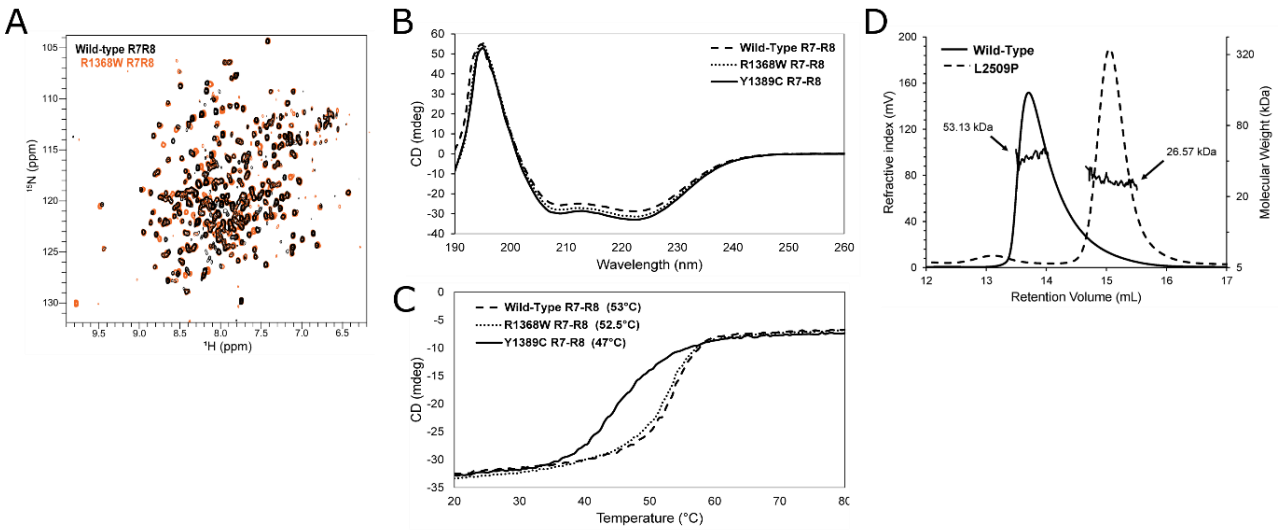

Figure 3. Influence of point mutations on biophysical properties of talin. A) NMR spectra of R7–R8 WT (black) and R1368W (orange). B–C) CD analysis of R7–R8 WT, R1368W and Y1389C. (B) CD spectra of each mutant. (C) Melting temperature curves; the melting temperature of each protein is shown. D) SEC–MALS analysis of R13–DD WT and L2509P showing that the R13–DD L2509P is monomeric. The molecular weight obtained from MALS is shown for each peak.

Most of the talin mutations have only minor effects on cell morphology, except for the L2509P mutation

We transiently transfected talin double knock–out (TLN1$^{-/-}$TLN2$^{-/-}$) mouse kidney fibroblasts (MKF) [34] with talin–1 constructs containing the mutations shown in Table 1 using equal quantities of plasmid. Western blot analysis ensured translation of full–length proteins (Fig.S2A,E). The expression levels showed decreased expression for I392N and slightly increased expression for S1750F and D2086V but otherwise the expression levels were constant (Fig.S2A,E). The adhesion size and abundance were analysed from the cell periphery and did not reveal significant changes in either the adhesion area or adhesion number with the various talin mutations (Fig.S3A,B).

To evaluate the effect the mutations have on cell morphology, we visualised talin and vinculin in transfected cells (Fig.4A) and quantified the effect of the mutations on cell area and circularity (Fig.S3C,D). The mutations caused little variance on cell morphology when compared to WT, except for cells carrying the dimerisation domain (DD) mutation L2509P, which were significantly smaller than the WT expressing cells and showed a more circular cell phenotype (Fig.S3C,D), indicating a loss in cell polarisation.

In order to study the L2509P in more detail, we engineered a series of truncated talin–1 constructs with deletions in the c–terminus as follows: WT (residues 1–2541), ΔDD (residues 1–2493), ΔR13–

DD (residues 1–2299) and ΔR1–DD (residues 1–481) (Fig.4B). Immunofluorescence analysis of the cells transfected with L2509P, ΔDD, ΔR13–DD and ΔR1–DD showed the same cell morphology as for the L2509P (Fig.S3E,F), in addition to loss of; i) maturation of adhesion, ii) localisation of the FA components paxillin and vinculin, and iii) filamentous actin into the adhesion sites, indicating that the point mutation L2509P disrupts dimerisation and interaction with actin to the same extent as deletion of the entire domain. Furthermore, all of the constructs led to anisotropic cell spreading (Fig.4C, FigS3G) as observed earlier for cells expressing talin head alone [35].

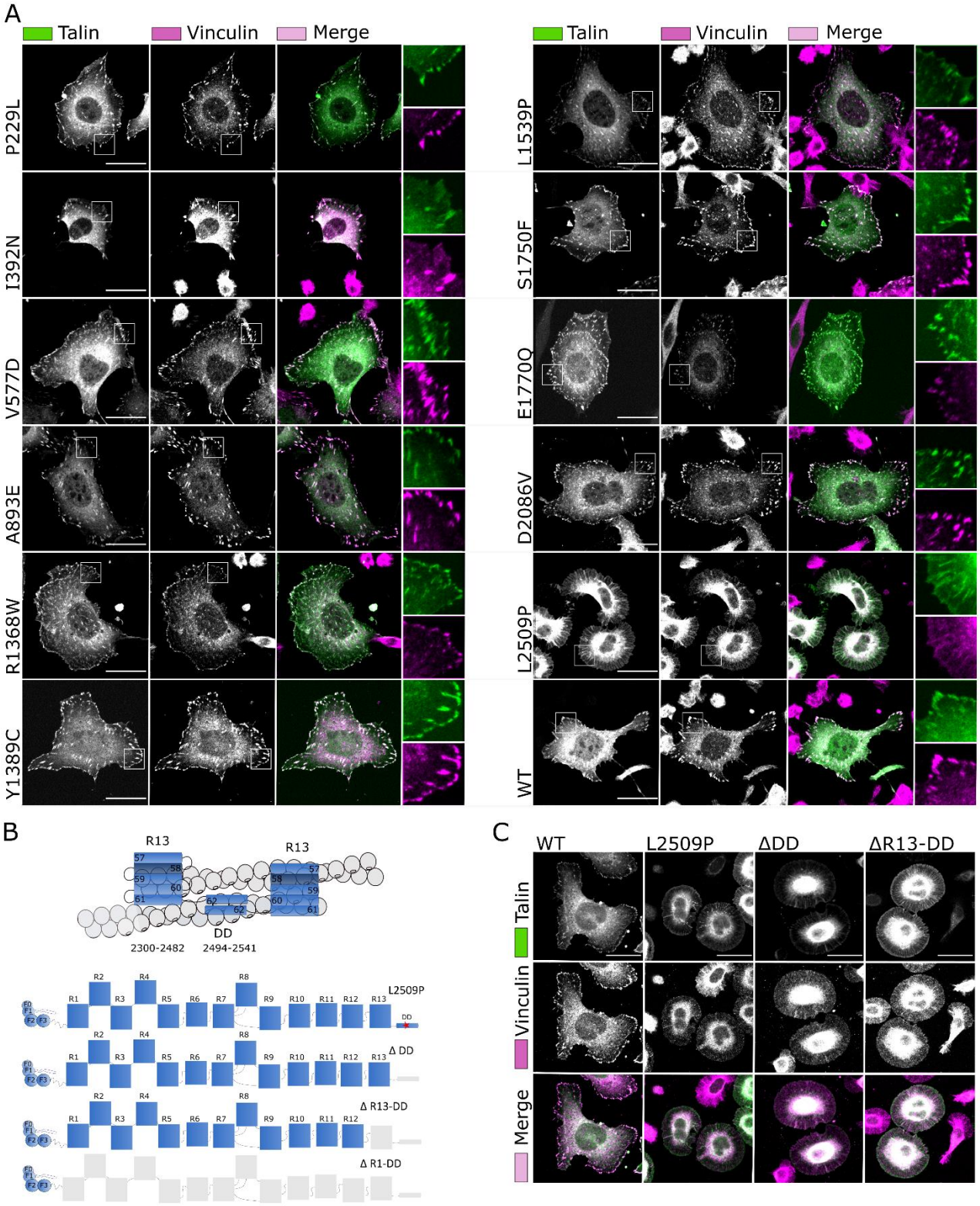

Figure 4. Talin dimerisation domain mutants show a loss of co–localisation with FA markers. A) SUM projections of z–stacks of cells expressing GFP–tagged talin–1 forms and immunolabeled for vinculin. Scale bars are 25 µm, zoom–in square size is 12.5 µm x 12.5 µm. B) Cartoon of the R13–DD dimerisation domain bound to actin and schematic representation of the point mutation L2509P in full–length talin and the truncations; ΔDD, ΔR13–DD and ΔR1–DD. C) SUM projections of z–stacks of cells expressing WT, L2509P, ΔDD, ΔR13–DD talin and immunolabeled against vinculin. No clear localisation of vinculin or other FA components (Fig.S3G) was evident with any of the mutants. Scale bars are 25 µm.

Predicting the effect of mutations on talin interactions with other adhesion proteins through cellular and biochemical analysis

We next assessed the levels of vinculin, and paxillin within the talin–1 rich adhesion sites with the aid of immunofluorescence labelling and confocal imaging (Fig.5A,B) and the total level of phosphorylated FAK in the cells via WB (Fig.5C,Fig.S2F). FAK phosphorylated at tyrosine 397 (FAKpTyr397) is a marker for adhesion maturation and corresponds with mechanical activation of talin. As FAKpTyr397 is present only at low level in non–transfected talin double knock–out MKF cells [35] to enabled us to monitor the relative levels of FAK phosphorylation with western blotting. As indicated by the anisotropic spreading of cells carrying the L2509P mutation, FAKpTyr397 levels were decreased when compared to WT talin expressing cells but this also reflected a decrease in total FAK levels (Fig.S2B,G). Interestingly, several mutants showed decreased levels of vinculin and paxillin within the adhesion sites compared to cells expressing WT talin–1, with the mutants R1368W, L1539P and E1770Q showing significantly less recruitment (Fig.5A,B). We noticed that total vinculin expression level was not majorly influenced by the expression of the talin–1 mutants. In contrast, expression of the talin mutants, P229L, V577D, A893E, L1539P and D2086V led to lower levels of paxillin expression when compared to WT–talin expressing cells (Fig.S2C,D).

Two of the vinculin binding sites of talin are located in the R7–R8 region, and their exposure is regulated by stability of the α–helical bundles in response to mechanical load [36-38]. To determine whether vinculin Vd1 domain (residues 1–258) binding to talin was affected by the R1368W and Y1389C mutations we used a size exclusion chromatography assay as previously described [36]. Our previous study showed that despite containing two VBS, only one of them is accessible to vinculin [36], and here we found that R7–R8 WT and R1368W both only bind one vinculin Vd1 molecule (Fig.5D). In contrast, the Y1389C mutation, which is in the core of the R7 domain, can bind two Vd1 molecules (Fig.5D), indicating that this mutation enhances the accessibility of the R7 vinculin binding site and alters the stoichiometry of the R7–R8–vinculin interaction. On its own the Y1389C mutation runs as a monomer, eluting at the same position as the R7–R8 WT. So, the 2:1 vinculin stoichiometry is due to the R7 domain being destabilised rather than the protein being denatured.

A Fluorescence Polarisation (FP) assay was used to determine the impact of these mutations on KANK1 and RIAM binding to R7 and R8. Neither KANK1 binding to R7 nor RIAM binding to R8 had significant differences in binding affinity with the R1368W and Y1389C mutants as compared to WT (Fig.5E). The talin–KANK1 interaction is important for coordinating the targeting of

microtubules to adhesion sites [9]. Consistent with the negligible impact on the talin–KANK1 interaction no apparent changes in tubulin organisation between WT, R1368W, Y1389C, and L1539P R7–R8 were observed (Fig.5G; Fig.S4A).

Since L1539P is located near to the DLC–1 binding site we also assessed the mutations effect on DLC–1 recruitment to the adhesions. For this we quantified the amount of DLC–1 within the adhesions and found that L1539P leads to ~42% decrease in DLC–1 amount within the adhesion as compared to the WT (Fig.5F). As I392N is in close proximity to the integrin binding site in F3, (PDB:2H7D) [39], we assessed whether the mutation can affect the talin–mediated integrin activation. For this, we quantified the amount of activated integrins within adhesions. Expression of I392N lead to ~53% decrease in the amount of activated integrin when compared to WT talin (Fig.5H).

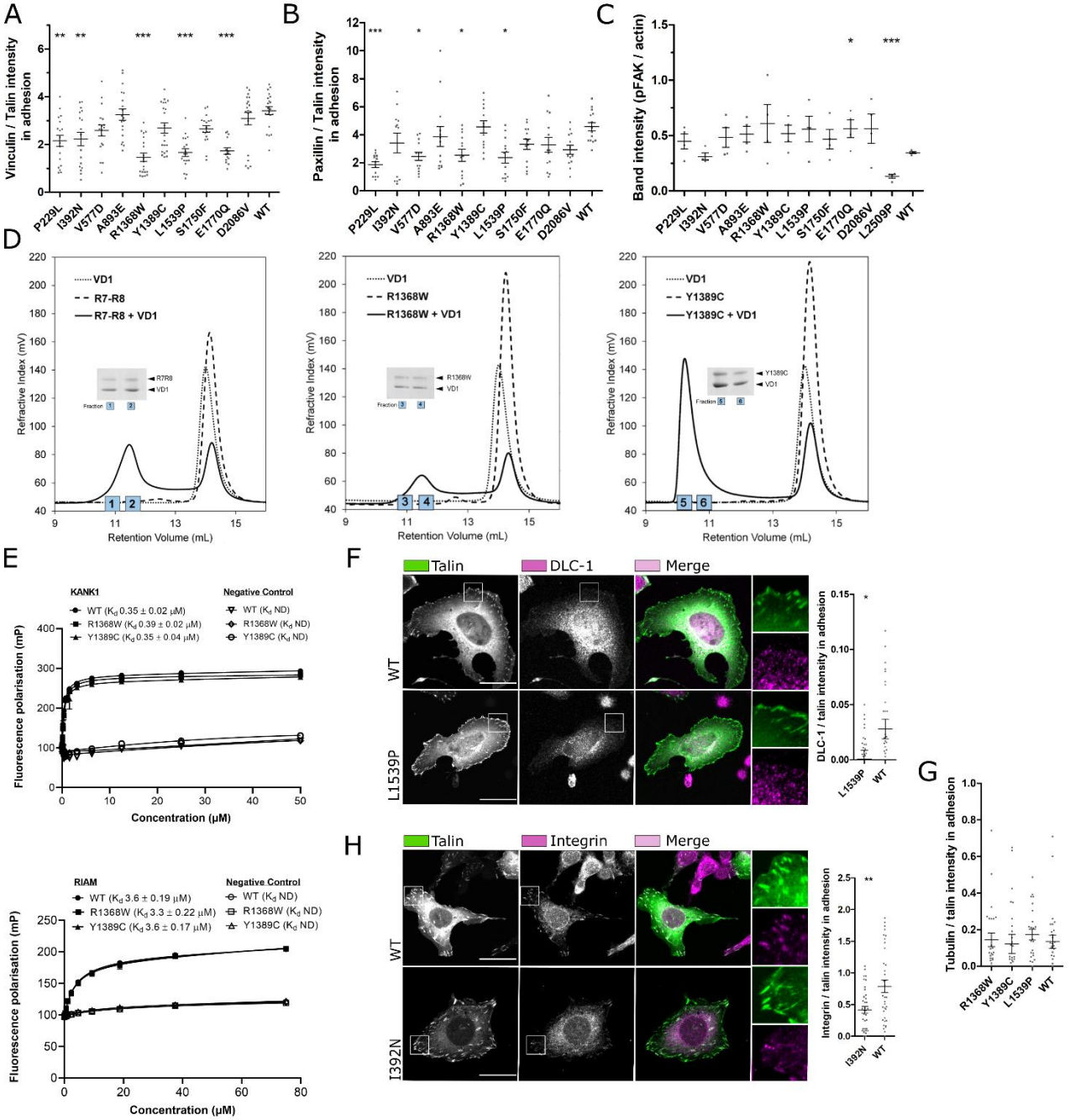

Figure 5: Mutations alter the interaction/colocalisation of talin with vinculin, paxillin, pFAK, DLC–1 and β1–integrin. A, B) Analysis of vinculin (A) and paxillin (B) colocalisation with talin in adhesions; n~20 cells per mutation from two separate experiments. C) FAKpTyr397 expression levels quantified from four western blots. The statistical analysis was calculated by unpaired t–test. D) Vinculin Vd1 binding analysed by size exclusion chromatography for R7–R8 WT (left), R1368W (centre) and Y1389C (right). The SDS–PAGE gel of the elution fractions is shown. E) Fluorescence Polarisation (FP) assay for R7–R8 binding to KANK (top) and RIAM (bottom) peptides. R1368W and Y1389C showed no significant changes in the interaction with KANK and RIAM compared with WT. Fluorescence polarisation assays were performed using protein serially diluted from a starting concentration of 60 μM with target KANK1 (30–68) peptide at 1 μM and 75 μM with target RIAM (4–30) peptide concentration at 1 μM. Measurements were taken using a CLARIOstar plate reader (BMGLabTech) at 20°C. GraphPad Prism 7 software was used for data analysis with one–site total binding equation used to generate a K_d. F) Representative confocal immunofluorescence images of the co–localisation of DLC–1 organisation in the cells with talin WT and L1539P. G) Data obtained from the colocalisation of tubulin in adhesion sites. H) Representative confocal immunofluorescence images of the co–localisation of active integrin CD29 organisation in the cells with talin WT and I392N. Sum projections of z–stacks of cells expressing GFP–tagged talin–1 (WT and/or point mutated) and immunolabeled against integrin CD29 or DLC–1, and ~30 cells per

label have been analysed. The statistical significance of all results was analysed by one–way ANOVA and Bonferroni test: *P<0.05, **P<0.01, ***P<0.001. Scale bars are 25 µm, zoom–in square size is 12.5 µm x 12.5 µm.

Cancer–derived talin–1 point mutations affect cell migration, invasion and proliferation

To study the functional characteristics of the talin mutants, we measured random cell migration speed on cells cultured on fibronectin–coated coverslips (Fig.6A,B). WT–transfected cells had an average migration speed of 0.65 µm/min. I392N was the only mutant that caused increased migration speed (0.82 µm/min). In contrast, R1368W caused a slight decrease and L2509P caused a marked decrease in cell migration with average speeds of 0.54 and 0.37 µm/min respectively, with the migration speed of L2509P close to that of non–transfected cells (0.35 µm/min) (Fig.S4B).

Since many cell types express both, talin–1 and talin–2, we were curious to see whether the L2509P mutation in talin–1 would show a phenotype when expressed together with talin–2. Indeed, we found that the mutation caused significant decrease in migration speed in cells co–transfected with talin–2 when compared to cells expressing both WT talins (Fig.6C).

Based on the migration assay, we selected I392N, R1368W, Y1389C, L1539P and L2509P for invasion assays and further analysis. We characterised how these five mutants affected the ability of cells to invade through a 3D Matrigel matrix (Fig.6D). I392N and R1368W showed the highest invasion rates, whereas Y1389C and L1539P did not significantly differ from WT. Further, the mutant L2509P, which showed a poorly polarised cell phenotype (Fig.4C) and significantly reduced migration speed on 2D culture (Fig.6A,B), was only able to promote limited cell invasion in 3D (Fig.6D). The impact on cell migration and invasion, was the same for the L2509P and the truncated mutants whether we removed the entire rod, R13–DD, DD or applied the point mutation L2509P (Fig.6B,E).

In full–serum conditions the mutants and the mock–transfected cells (Fig.S4C) showed equally efficient cell proliferation rate when compared to WT talin–1 expressing cells (Fig.6F). However, during serum depletion, I392N, Y1389C, L2509P and mock–transfected cells showed significant decrease (~53%, ~53%, ~91% and ~45%, respectively) and the P229L showed ~30% increase in cell division as compared to the cells transfected with WT talin–1 (Fig.6F,Fig.S4C), suggesting that talin–1 mediated changes can affect cell proliferation.

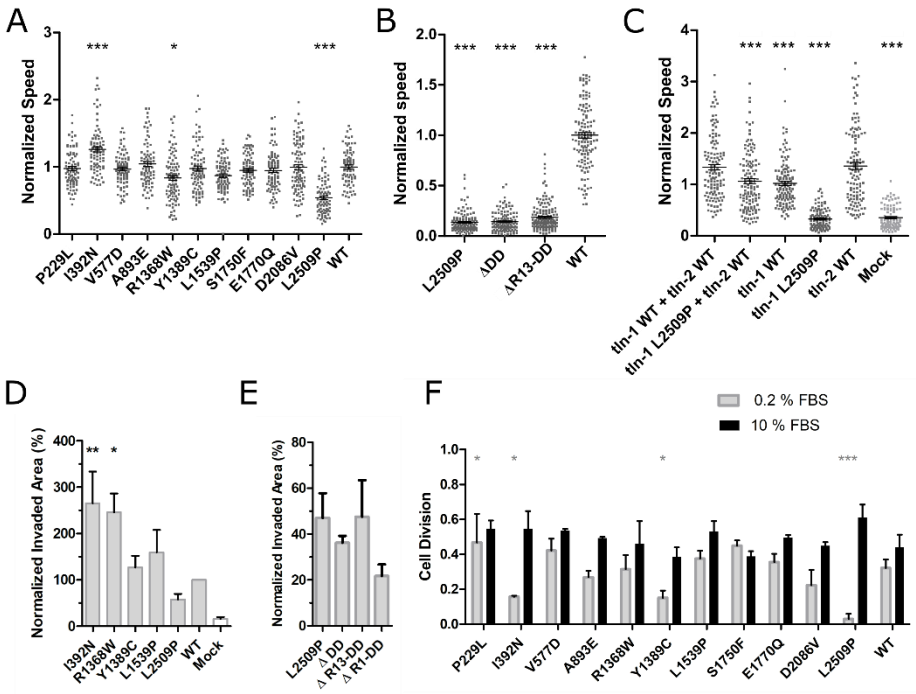

Figure 6: Talin mutations affect cell migration and proliferation. A) Random migration speed (µm/min) determined from time–lapse images of talin expressing cells. B) Migration speed on 2D surface showing reduced migration speed in all mutated/truncated constructs in comparison to WT. C) Migration assay on 2D surface showing reduced migration speed in cells co–transfected with talin–1 L2509P and full–length WT talin–2. The statistical significance of all results analysed in comparison to talin–1 WT + talin–2 WT by one–way ANOVA and Bonferroni test: *P<0.05, **P<0.01, ***P<0.001. The results are normalised with talin–1 WT. D) Invasion assay through Matrigel matrix towards 10% FBS containing medium. Control cells were mock–transfected with GFP–expressing plasmid. The values are normalised to WT and statistical significance measured in comparison to WT. Data are mean +/–SEM. The statistical significance was analysed by one–way ANOVA and Bonferroni test: *P<0.05, **P<0.01, ***P<0.001. E) Cell invasion through Matrigel in 3D environment showing the invasiveness potential of the L2509P and truncated talin constructs. Invasion assay was repeated at least three times in triplicate chamber for each construct on separate days. F) Cell proliferation analysis in the presence of 10% FBS and 0.2% FBS, showing the number of times the cells divide in 12 h; n~80 cells per mutation from four separate experiments. The statistical analysis was calculated by t–test, non–parametric test of Mann–Whitney: *P<0.05, **P<0.01, ***P<0.001 compared to WT for each condition.

Table 2. Summary table of the analysis of talin–1 mutations. Migration speed for the WT–talin was 0.65 ±0.18 µm/min.

Mutation	Free energy changes ΔΔG (kJ/mol)	Structural changes (MD)	Structural analysis (biochemical)	Cell morphology	Interactions (protein–protein* or within adhesions)			Proliferation 0.2% FBS	Proliferation 10% FBS	Migration speed (µm/min)	Invasion	Bioinformatic score
P229L	–	n.s.	–	↔	vinculin↓	paxillin↓	pFAK↔	↑	↔	0.64 ±0.19	–	8.20
I392N	38.28 ±1.27	severe destabilisation	could not be produced	↔	vinculin↓ β1 active↓	paxillin↔	pFAK↔	↓	↔	0.82 ±0.24	↑	8.95
V577D	52.15 ±13.71	severe destabilisation	–	↔	vinculin↔	paxillin↓	pFAK↔	↔	↔	0.63 ±0.16	–	8.39
A893E	10.5 ±1.91	significant destabilisation	–	↔	vinculin↔	paxillin↔	pFAK↔	↔	↔	0.68 ±0.22	–	7.63
R1368W	12.63 0.27	significant destabilisation (enhances R7–R8 interaction)	NMR ↔ CD ↔	↔	vinculin↓ Vd1↔ tubulin↔	paxillin↓ KANK1↔	pFAK↔ RIAM↔	↔	↔	0.54 ±0.23	↑	7.75
Y1389C	20.6 ±4.09	strong destabilisation	– CD↓	↔	vinculin↓ Vd1↑ tubulin↔	paxillin↓ KANK1↔	pFAK↔ RIAM↔	↓	↔	0.64 ±0.21	↔	8.58
L1539P	–	disruption of H3 of R8	could not be produced	↔	vinculin↔ Vd1↔	paxillin↔ DLC–1↓	pFAK↔ tubulin↔	↔	↔	0.57 ±0.15	↔	8.45
S1750F	2.28 ±2.33	n.s.	–	↔	vinculin↔	paxillin↔	pFAK↔	↔	↔	0.62 ±0.16	–	7.55
E1770Q	–4.17 ±0.35	mild stabilisation	–	↔	vinculin↓	paxillin↔	pFAK↑	↔	↔	0.61 ±0.19	–	6.01
D2086V	12.96 ±0.82	significant destabilisation	–	↔	vinculin↔	paxillin↔	pFAK↔	‘↔	↔	0.64 ±0.24	–	7.71
L2509P	–	severe destabilisation (helix breaks)	SEC (monomer)	non–polarised	vinculin↔	paxillin↔	pFAK↓	↓	↔	0.37 ±0.20	↔	7.46

↔ indicating no change when compared to WT talin–1
↑ indicating an increase when compared to WT talin-1
↓ indicating a decrease when compared to WT talin-1
– indicating not tested
n.s. indicating as not significant
* Vinculin Vd1, KANK1, RIAM were assessed via protein–protein interaction.

Discussion

Talin is a central regulator of cell adhesion to the ECM and is critical for integrin activation and FA formation. It provides mechanical linkage between ECM and actin cytoskeleton, and is an essential scaffold for the organisation of the FA multi–protein complex [40]. Loss of anchorage–dependent growth, changes in ECM remodelling, and cytoskeletal changes are necessary for cancer progression [41].

There are two isoforms of talin, talin–1 and talin–2, which show different expression patterns [42, 43]. While talin–1 is expressed in all tissues, talin–2 has more variability and generally lower expression levels. Overall expression levels, derived from GEPIA (gene expression profiling interactive analysis) server [44], indicate that talin–1 expression levels are more variable between different cancers and their counterpart healthy tissues than those of talin–2 (Fig.S5) with several cancer types showing significant changes in talin–1 expression level. The highest overexpression is associated with Glioblastomas (GBM; >300%), Brain Gliomas (LGG; >300%) and Pancreatic adenocarcinomas (PAAD; >300%). In contrast, the most drastic talin–1 downregulation is seen in uveal melanoma (UCS; –25%) and endometrial carcinoma of the uterine (UCEC; –25%).

Here we emphasized the bioinformatic classification method to explore the large quantity of talin–1 mutations and predict the impact of the mutations on the stability of protein structure. With the aid of molecular modelling, biochemical analyses and functional cell biology assays, we found that mutations in talin–1 affect cellular processes linked with cancer progression, such as migration, invasion and proliferation (Table 2). We have shown previously that the mechanical stability of the talin rod alpha–helix bundles can be drastically influenced by point mutations and these small changes can further lead into changes in traction forces and cellular response [2, 45, 46].

Talin is a known integrin adapter, providing a link between integrins and the actin cytoskeleton. A previous study by Isenberg et al. [29] proposed the amino acids 385–406 of F3 helix as a potential membrane–anchoring domain. I392 was identified as one of the residues that inserts into the lipid bilayer [29] and mediates integrin activation [47]. Out of the eleven mutants studied here, I392N, originally found from pancreatic carcinoma, had the most pronounced effect in terms of activating migration and invasion. The mutation is in close proximity to the integrin binding site in F3, (PDB:2H7D) [39] and localization analysis of active β1 integrin showed clear decrease in the amount of active integrin in talin–rich adhesions, when compared to WT (Fig.5H). Integrins have been

associated in nearly all steps of cancer progression and dysregulated integrin–mediated mechanotransduction can initiate the pathogenesis of different diseases, including cancer [48]. The observed decrease in active integrins could be due to increase in FA turnover as this was accompanied with increased migration and invasion. The exact mechanism whereby I392N causes these effects should be studied in more detail. Our biochemical experiments with this mutant were hampered by proteolytic truncation of the mutated talin head, indicating folding defect in the C–terminal part of the protein. However, a significant amount of full–length I392N talin was expressed (Fig.S2A,E), suggesting that the mutated form has partial functionality and can support most major cellular functions. The mutated helix in F3 experiences mechanical tension applied on talin [49], which results in increased dissociation of the destabilised mutated helix from the rest of the F3 under applied load, influencing integrin association and thereby contributing to the adhesion turnover/dynamics.

The R7–R8 domains have cooperative function, with R8 sitting outside the force transduction pathway, and protected from mechanical stress by R7 [38]. In addition, there are binding sites for multiple molecules such as KANK1, DLC–1, RIAM, paxillin and vinculin in both domains. MD simulation suggested that the R1368W mutant might enhance interactions between R7 and R8 domains (Fig.2B), which might perturb the localisation of the FA markers within adhesions (Fig.5A,B), affecting cell behaviour. However, binding affinity for KANK1 and protein stability remained consistent with WT, suggesting that the cellular effects of this mutation could be due to an, as of yet, unidentified R7 function perturbed in this mutant.

The VBS in R7 is one of the hardest to expose [36] but can be stretch activated [38], interestingly, the Y1389C mutation significantly enhanced the VBS accessibility. Gel filtration analysis of vinculin Vd1 binding to Y1389C revealed that while R7–R8 WT and the R1368W mutant only bind a single Vd1 molecule, the R7–R8 Y1389C was able to bind two Vd1 (Fig.5D). This suggests that introduction of the mutation destabilises the R7 helical bundle, allowing vinculin binding more readily in the absence of force. Furthermore, reduced R7 stability will likely have a knock–on effect on R8 stability which may indirectly lead to signalling defects by perturbing R8 [12]. The additional actin recruitment via vinculin could have a direct effect on FA dynamics by facilitating formation of talin–vinculin pre–complexes, necessary to enable efficient adhesion maturation [46]. This could also affect actomyosin contractility and Rho/ROCK signalling, which have been shown to regulate cell proliferation [50].

DLC–1 is a tumour suppressor [51] and contains an LD–like motif, which is required for the full tumour suppressor activity of DLC–1 via interaction with talin [47]. DLC–1 residue D470 makes direct contact with the positively charged side chain of K1530 and K1544 in R8 [11]. In cells transfected with L1539P mutant, the colocalisation between talin and DLC–1 was significantly decreased (Fig.5F), indicating that this mutation interferes with DLC–1 binding.

The linkage between the C–terminal actin–binding site, ABS3 and actin is required for polarisation of cells [35] and this linkage depends on talin dimerisation. Mutation in the dimerization domain, L2509P, resulted in an unpolarised and non–migratory cell phenotype lacking mature FAs and actin contacts on the cell surface. This mutation sits in the talin dimerisation domain, a single helix which forms an antiparallel dimer [7, 52]. The same phenotype was observed with complete removal of the dimerisation domain helix (ΔDD) as with L2509P point mutation. Our biochemical results showed that the L2509P mutant resulted in complete loss of dimerisation compared to the R13–DD WT which is a constitutive dimer in solution (Fig.3D). We found previously that cell polarization in cells expressing talin without ABS3 can be rescued by overexpression of vinculin [35]. In line with this, overexpression of vinculin in L2509P transfected cells led to the polarisation of cells (data not shown).

Focal adhesion dynamics affect cell proliferation by regulating YAP activation and Hippo pathway [53]. Hippo pathway is balanced between negative signals such as contact inhibition and promoting mitogenic signalling such as growth factors and hormones. Also cell shape and mechanotransduction are known to regulate YAP activity, as stretched cells on stiff ECM positively regulate YAP nuclear localisation [53]. This regulation is believed to be independent of the canonical Hippo–pathway or cell–cell junctions but mediated by Rho–ROCK signalling and actin dynamics [54]. However, cell adhesion to fibronectin, but not poly–D–lysine or laminin, can promote YAP translocation via the canonical Hippo pathway, suggesting that adhesion–mediated integrin activation can mimic mitogen–caused activation, without the presence of soluble mitogenic growth factors [55]. This possibly explains the rescue of cell proliferation of mock–transfected cells in serum–free conditions by talin expression (Fig. 6F, FigS4C).

In this study, we systematically explored hundreds of talin–associated mutations and the pipeline described here enabled us to rapidly and robustly screen this huge number and narrow it down to an experimentally tractable subset for detailed analysis. Using this approach, we selected 11 mutants for thorough analysis. Out of those, two mutants promoted cell invasion, one mutant significantly

accelerated cell migration in 2D and four mutants significantly diminished cell proliferation in low–serum conditions. Investigation of the contribution of talin to cancer progression is timely. During this study ~600 more cancer–associated talin mutations have been added to the COSMIC database and there are recent studies discussing the connection between talin and cancer [56, 57]. The work we present here demonstrates how single point mutations in talin can drastically alter cell behaviour, potentially contributing to cancer metastasis.

Materials and methods

Cell lines and talin constructs

Theodosiou et al. [34] previously described the TLN1$^{-/-}$TLN2$^{-/-}$ mouse kidney fibroblast (MKF) cell line. Cells were maintained in a humidified 37°C, 5% CO_2 incubator. High glucose Dulbecco´s modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS) was used in all experiments except in the starvation conditions where 0.2% serum was used. The cell line was regularly tested for mycoplasma contamination. Talin variants were subcloned into a modified pEGFP–C1 vector backbone (Clontech). Cells were transfected with 6 µg plasmid DNA per 10^6 cells using Neon transfection system (Thermo Fisher Scientific) using parameters 1400 V, 30 ms, one pulse. The expression constructs for cell culture experiments with the c–terminal EGFP–tag are as follows: wild–type talin–1 1–2541; ΔR13–DD (1–2299); ΔDD (1–2493); ΔR1–DD (1–481) and the point mutants in the full–length talin–1 P229L, I392N, V557D, A893E, R1368W, Y1389C, L1539P, S1750F, E1770Q, D2086V, L2509P.

Migration and Matrigel invasion analysis

Transfected cells were incubated for 24 h, trypsinised and plated on well–plates coated with 10 µg/ml fibronectin. Cells were allowed to attach for 90 minutes, after which the media was changed. The time–lapse images captured with EVOS FL auto microscope (Thermo Fisher Scientific) were analysed manually using ImageJ (Fiji) and MTrackJ plugin [58, 59].

Corning BioCoat Matrigel Invasion Chamber containing an 8–micron pore size PET membrane with a thin layer of Matrigel basement membrane matrix were used for the invasion assay. Transfected TLN1$^{-/-}$TLN2$^{-/-}$ MKF cells were cultured overnight, followed by cultivation in starvation medium containing 0.2% FBS for 40–45 h. Number of transfected cells was measured by Luna–FL dual Fluorescence Cell Counter (BioCat GmbH) Chambers prepared according to the manufacturer. DMEM medium containing 10% FBS was used as chemoattractant in the lower level of chamber. The chamber plate was incubated at humidified 37°C and 5% CO_2 incubator for 24 h, after which the

cells were fixed with 100% methanol. Cells were stained with 0.2% crystal blue for 10 minutes following by rinsing the excess stain. The non–invaded cells were removed from the upper membrane surface using cotton tipped swab. The inserts were allowed to air dry overnight. The membrane was removed using scalpel and placed bottom side down on a microscope objective slide on which a small drop of immersion oil. The membranes were scanned using PRIOR OpenStand microscope using 20x objective and Jilab SlideStrider software (1.2.0). The invaded cell area was calculated using ImageJ (Fiji). Invasion assay was repeated at least three times in triplicate chamber for each selected construct.

Immunostaining and confocal imaging

After 24 h transfection, cells were trypsinised and plated on coverslips coated with 10 µg/ml fibronectin and incubated for 24 h. Cells were fixed with 4% paraformaldehyde, permeabilised and immunostained using standard protocol. Antibodies are listed in Table S1.

Immunostained samples were imaged with Zeiss Cell ObserverZ1 inverted microscope and LSM 780 confocal unit (Zeiss, Oberkochen, Germany) using 63x/1.4, WD 0.19 mm oil immersion objective. Images were taken using Zeiss Zen Black software and analysed by ImageJ as described previously [35]. Within each experiment, the imaging parameters were kept constant to allow quantitative image analysis. Detailed image analysis is described in Supplementary material.

Western blotting

Transfected cells were grown for 24 h, lysed with RIPA buffer supplemented with protease inhibitor cocktail (Sigma–Aldrich lot#126M4016V). After centrifugation, cell lysates were applied on an SDS–PAGE to separate protein. A wet blot system was used to transfer the separated protein from gel onto a polyvinylidene fluoride (PVDF) membrane. Blots were quantified using ImageJ. Antibodies are listed in Table S1.

Constructs for protein expression in *E. coli*

The talin–1 fragments, generated using full–length talin–1 as a template, were introduced into a modified pHis vector to create N–terminal His6–tag constructs. The His6–tag is separated from talin fragment by an eleven–residue linker: SSSGPSASGTG. Mutagenesis was performed using QuikChange II Site–Directed Mutagenesis kit. Talin constructs were expressed in BL21(DE3) *E. coli*

cells and induced with 0.1 mM IPTG at 18°C for overnight. Clarified lysates were loaded onto an affinity column (HisTrap HP 5 ml; GE Healthcare). Eluted protein was further purified using anion exchange column (HiTrap Q HP 5 ml; GE Healthcare) before buffer exchange into PBS and storage at –20°C.

NMR Spectroscopy and Fluorescence Polarisation Assay

Talin constructs were grown in 2M9 minimal media with ^{15}N–labeled NH_4Cl. Protein was purified as above and buffer exchanged into 20 mM Na–phosphate pH 6.5, 50 mM NaCl, 2 mM DTT, 5% (v/v) D_2O. NMR spectra were obtained at 298 K on a Bruker AVANCE III 600 MHz spectrometer equipped with CryoProbe. All R7–R8 ^{1}H,^{15}N-HSQC spectra were obtained at a concentration of 160 µM. For fluorescence polarisation (FP) experiments, peptides were synthesised by GLBiochem (China) and coupled with either BODIPY or Fluorescein dye via a C–terminal cysteine residue.

Size Exclusion Chromatography with Multi–Angle Light Scattering

Talin R13–DD wild–type and L2509P were analysed by SEC–MALS at a concentration of 100 µM at room temperature with a Superdex 75 column (GE Healthcare Life Sciences). Eluted proteins were analysed with Viscotek SEC–MALS 9 and Viscotek RI detector VE3580 (Malvern Panalytical). Molecular mass was determined using OmniSEC software. For analysis of Vd1 binding to talin, proteins were incubated at a 2:1 ratio at a concentration of 100 µM and analysed at room temperature.

MD Simulations

RCSB PDB structures were used as starting conformations for MD: 3IVF for F2–F3 (residues 208 to 398) [60], 2H7E for F3 [39], 2X0C for R7–R8 [36] and 2QDQ for DD domain [7]. The R7–R8 binding energy was calculated using MM–PBSA [61]. Structural analysis was performed using PyMOL. The secondary structure analysis was based on the Dictionary of Secondary Structure of Proteins (DSSP) algorithm [62]. MD simulations were performed using Gromacs [63] at the Sisu and Puhti supercomputers, CSC, Finland. The CHARMM27 force field [64] and explicit TIP3P water model [65] in 0.15 M KCl solution were used. The energy minimisation of the system was performed in 10000 steps. The system was equilibrated in three phases using harmonic position restraints on all heavy atoms of the protein. Integration time step of 2 fs was used in all the simulations. NPT ensemble was maintained at 310 K using the V–rescale algorithm [66], and 1 atm using Berendsen algorithm [67]. Alchemical free energy calculations were prepared using PMX [68]. The simulations were performed using Amber99SB*-

ILDN force field [69] and TIP3P water model in 0.15 M NaCl solution, following standard procedure. The whole calculation was repeated three times and average free energy value was obtained.

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Competing interests

The authors declare no competing or financial interests.

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