Supplementary Figure 1 Human caldesmon gene and transcript variants.
Caldesmon (CALD1) gene structure on chromosome 7q33, showing exon
(numbered boxes) and intron (lines) regions , transcript length in base pairs,
and translation length (number of amino acids in the protein). CALD1 gene has
24 transcripts or splice variants (201–224) as described in Ensembl. Red
transcripts (203-206, 208, 209, 211, 212, 214 and 222) are protein coding; as per
either the Ensembl automatic annotation pipeline or manual curation by the
VEGA/Havana project. A gold transcript (201 and 202) is identical between
Ensembl automated annotation and VEGA/Havana manual curation protein
coding. This transcript can be thought of as stable (unlikely to change). A blue
transcript is non-coding (transcript 207, 210, 213, 215-219, 220, 221, 223, 224)
(nonsense mediated decay, a process which detects nonsense mutations and
prevents the expression of truncated or erroneous proteins; processed
transcript: does not contain an open reading frame). Transcripts 202–206 and
222 can generate Fibro-type and HeLa-type l-caldesmon, transcript 205 (Fibro
l-caldesmonI, 563aa), transcript 202 and transcript 204 (Fibro L-caldesmonII,
538aa), transcript 222 and transcript 203 (HeLa l-caldesmonI (557–558aa), and

transcript 206 (HeLa L-caldesmonII 532aa). Sources: https://asia.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000122786;r=7:134744252-134970729;t=ENST00000393118. Accessed on 14 March 2022 11:38 PM. Editable at BioRender.