

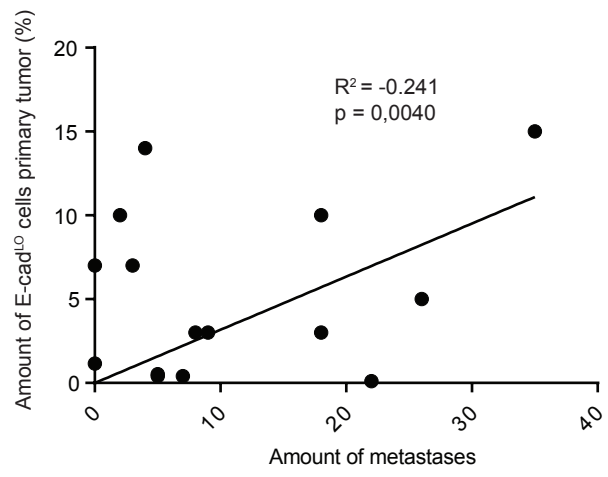
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## Supplemental Information

### ***Fsp1*-Mediated Lineage Tracing Fails to Detect the Majority of Disseminating Cells Undergoing EMT**

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**Figure S1:** Mesenchymal E-cad<sup>LO</sup> population in the primary tumor is proportional to amount of metastases. Related to Figures 1 and 2.

(A) The percentage of E-cad<sup>LO</sup> cells in the primary tumor relates to the amount of metastases.  
( $p=0,0040$ )

Mouse	Donor tumor	time of tumor growth wks	Macro Metastases			FACS analysis	Primary tumor					CTCs						
			>99.9 RFP <sup>+</sup>	>99.9 GFP <sup>+</sup>	total		RFP <sup>+</sup>	RFP <sup>+</sup> GFP <sup>+</sup>	GFP <sup>+</sup>	Ecad <sup>Hi</sup>	Ecad <sup>Lo</sup>	blood (ul)	total amount of CTCs	RFP <sup>+</sup>	RFP <sup>+</sup> GFP <sup>+</sup>	GFP <sup>+</sup>	Ecad <sup>Hi</sup>	Ecad <sup>Lo</sup>
1	1	8,4	26	0	26	YES	99,68	0,19	0,13	94	5	950	501	99,6	0,2	0,2	92,8	7,2
2	1	7,4	8	1	9	YES	99,92	0,06	0,02	96	3	500	0	0	0	0	0	0
3	1	9,4	9	0	9	YES	99,46	0,25	0,29	96	3	850	9	100	0	0	55,6	44,4
4	1	8,1	18	0	18	YES	99,56	0,32	0,12	89	10	350	3	100	0	0	66,7	33,3
5	1	6,4	0	0	0	YES	99,86	0,08	0,06	92	7	850	2	100	0	0	50	50
6	1	6,0	3	0	3	NO												
7	1	4,3	0	0	0	NO												
8	1	6,0	35	0	35	YES	99,79	0,05	0,16	84	15	650	0	0	0	0	0	0
9	1	4,0	5	0	5	NO												
10	1	6,3	0	0	0	NO												
11	2	7,1	3	0	3	YES	95,00	2,27	2,67	92	7	1100	0	0	0	0	0	0
12	2	7,3	2	0	2	NO												
13	2	8,1	0	0	0	NO												
14	2	9,1	2	0	2	YES	98,96	0,42	0,61	89	10	1050	0	0	0	0	0	0
15	2	7,1	8	0	8	NO												
16	2	6,1	8	0	8	YES	98,68	0,20	1,13	97	3	900	0	0	0	0	0	0
17	3	7,1	18	0	18	YES	99,5	0,45	0,05	97	3	700	0	0	0	0	0	0
18	3	8,0	5	0	5	YES	99,90	0,08	0,02	99,6	0,4	850	1	100	0	0	100	0
19	3	7,9	7	0	7	YES	99,8	0,16	0,04	99,6	0,4	350	8	100	0	0	87,5	12,5
20	3	7,9	0	0	0	YES	99,90	0,09	0,01	98,85	1,15	750	17	100	0	0	70,6	29,4
21	3	7,1	22	0	22	YES	99,7	0,29	0,01	99,9	0,1	550	3	100	0	0	66,7	33,3
22	3	7,7	4	0	4	YES	99,50	0,45	0,05	86	14	650	46	100	0	0	78,3	21,7
23	3	7,0	5	0	5	YES	99,7	0,17	0,13	99,6	0,52	700	0	0	0	0	0	0
Average			8,2	0,0	8,2		99,3	0,3	0,3	94,3	5,2		36,9		0,0	0,0	74,2	25,8

**Table S1:** Experimental summary of recipient mice. Related to Figure 1 and 2.

Oligonucleotides			
name	sequence	Source	Identifier
GAPDH fwr	5'-GGT CCT CAG TGT AGC CCA AG-3'	Beerling <i>et al.</i> , 2016	N/A
GAPDH rev	5'-AAT GTG TCCGTC GTG GAT CT-3'	Beerling <i>et al.</i> , 2016	N/A
E-cad fwr	5'-GCT TCA GTT CCG AGG TCT AC-3'	Beerling <i>et al.</i> , 2016	N/A
E-cad rev	5'-GCC AGT GCA TCC TTC AAA TC-3'	Beerling <i>et al.</i> , 2016	N/A
Vim fwr	5'-GAG GAG ATG CTC CAG AGA GA-3'	Beerling <i>et al.</i> , 2016	N/A
Vim rev	5'-TCC TGC AAG GAT TCC ACT TT-3'	Beerling <i>et al.</i> , 2016	N/A
FN fwr	5'-GGT GTC CGA TAC CAG TGT TAC-3'	Beerling <i>et al.</i> , 2016	N/A
FN rev	5'-TCT CCG TGA TAA TTA CTT GGA CAG-3'	Beerling <i>et al.</i> , 2016	N/A
Zeb1 fwr	5'-TGG CAA GAC AAC GTG AAA GA-3'	Beerling <i>et al.</i> , 2016	N/A
Zeb1 rev	5'-AAC TGG GAA AAT GCA TCT GG-3'	Beerling <i>et al.</i> , 2016	N/A
N-cad fwr	5'-GTG GAG GCT TCT GGT GAA AT-3'	Beerling <i>et al.</i> , 2016	N/A
N-cad rev	5'-GGC TCG CTG CTT TCA TAC T-3'	Beerling <i>et al.</i> , 2016	N/A
Slug fwr	5'-TGA TGC CCA GTC TAG GAA AT-3'	Beerling <i>et al.</i> , 2016	N/A
Slug rev	5'-AGT GAG GGC AAG AGA AAG G-3'	Beerling <i>et al.</i> , 2016	N/A

**Tabel S2:** Oligonucleotides used in this study. Related to Figure 1 D.