Olmeda et al. Extended Data. Table S2

Gene symbols	**451LU vs WM164**	**SK-Mel-103 vs WM164**	**SK-Mel-28 vs WM164**
MDK	5.34	3.91	2.37
PRRT2	4.11	7.36	10.35
PROCR	4.10	5.49	5.32
RPL12	3.75	3.20	3.34
RPL28	3.40	1.93	1.66
AGRN	3.38	2.24	3.45
CD9	3.24	1.70	1.77
SDC1	3.12	5.50	3.83
TMSB10	2.81	3.38	3.19
IGF2BP3	2.61	4.54	3.86
IGF2BP1	2.53	3.26	2.75
CTSZ	2.35	2.30	1.75
RNPEP	2.28	2.91	1.96
CALU	2.19	1.26	2.30
ILF2	2.09	5.76	4.29
HNRNPK	2.05	2.42	2.36
RPS15A	2.05	3.81	1.08
TUBB4A	1.94	1.52	1.67
DBN1	1.86	1.30	1.44
SRP14	1.84	9.13	7.88
CAPNS1	1.74	1.66	1.19
ITGB5	1.72	2.61	2.46
RBM3	1.61	5.83	4.60
PLAUR	1.60	3.98	3.18
RHOB	1.58	1.99	1.62
ALCAM	1.53	5.14	3.89
FLG2	1.52	4.02	5.16
CBR1	1.45	0.82	0.77
RPL31	1.45	1.12	1.05
RPS3A	1.43	1.62	1.44
LGALS1	1.39	1.34	1.67
RPS23	1.37	1.13	0.92
TUBB3	1.29	1.15	0.74
RPLP0	1.14	1.48	0.70
RPS3	1.14	1.33	0.72
RUVBL1	1.11	1.28	1.04
HSD17B12	1.07	1.42	2.31
PSMD14	1.01	0.97	1.14
RPLP2	1.00	1.96	1.57
TUBA1C	0.96	1.60	1.28
TAOK3	0.91	2.01	2.40
MARCKSL1	-0.98	-1.43	-1.12
IGF1R	-2.21	-2.75	-1.12
DAAM2	-2.49	-2.14	-2.12
FXYD3	-4.99	-2.05	-1.56

Table S2. Pro-metastatic factors identified by proteomic analyses of the secretome of the indicated cell lines. Shown are differential ratios of protein expression (Log2 scale) estimated with respect to basal levels in the non-lymphangiogenic cell line WM164. Additional filters were applied to remove factors present in the non-metastatic WM35, which does not activate distant lymphangiogenesis.