Table S1. Primer sequences and PCR product sizes for gene expression validation by qPCR.

Gene name	Forward primer/reverse primer (PCR product size in bp)
ACTA2	5’- CTATGAGGGCTATGCCTTGCC -3’/5’- GCTCAGCAGTAGTAACGAAGGA -3’ (122)
ALDH1A1	5’- CTGCTGGCGACAATGGAGT -3’/5’- CGCAATGTTTTGATGCAGCCT -3’ (89)
ARHGAP5	5’- CCTTGCCCAAGAACTAGCAAA -3’/5’- GGCAGTCCATAACTGACTCAAAA -3’ (139)
AXL	5’- ATCAGCTTCGGCTAGGCAG -3’/5’- TCCGCGTAGCACTAATGTTCT -3’ (159)
BDKRB1	5’- ACTGAACGTGGCAGAAATCTAC -3’/5’- GCTCCGAAAGGCCAGTTAAAC -3’ (117)
CCND3	5’- TACCCGCCATCCATGATCG -3’/5’- AGGCAGTCCACTTCAGTGC -3’ (128)
CD44	5’- CTGCCGCTTTGCAGGTGTA -3’/5’- CATTGTGGGCAAGGTGCTATT -3’ (109)
CEACAM5	5’- AAGAAATGACGCAAGAGCCTATG -3’/5’- CCCGAAAGGTAAGACGAGTCTG -3’ (138)
CEACAM6	5’- TCAATGGGACGTTCCAGCAAT -3’/5’- CACTCCAATCGTGATGCCGA -3’ (194)
CYR61	5’- GGTCAAAGTTACCGGGCAGT -3’/5’- GGAGGCATCGAATCCCAGC -3’ (115)
DKK1	5’- ATAGCACCTTGGATGGGTATTCC -3’/5’- CTGATGACCGGAGACAAACAG -3’ (96)
EEF1B2	5’- GGGAAGAACGTCTTGCACAAT -3’/5’- CGCACTCCTCTAATTTCGCCA -3’ (129)
ETV6	5’- ATCAACCTCTCTCATCGGGAA -3’/5’- CAGTCTGCTATTCTCCCAATGG -3’ (104)
FSIP1	5’- AAAGGCTGGTTGAGCTTTTGA -3’/5’- CATCACGGTCAGGTTTCTGATTA -3’ (237)
GAPDH	5’- GGTGGTCTCCTCTGACTTCAACA -3’/5’- GTTGCTGTAGCCAAATTCGTTGT -3’ (126)
GAS6	5’- CTCGTGCAGCCTATAAACCCT -3’/5’- TCCTCGTGTTCACTTTCACCG -3’ (106)
GJA1	5’- TGGTAAGGTGAAAATGCGAGG -3’/5’- GCACTCAAGCTGAATCCATAGAT -3’ (123)
IGFBP3	5’- AGACACACTGAATCACCTGAAGT -3’/5’- AGGGCGACACTGCTTTTTCTT -3’ (106)
LBH	5’- GCCCCGACTATCTGAGATCG -3’/5’- GCGGTCAAAATCTGACGGGT -3’ (134)
LTBP1	5’- GCTTCCGTCCAGATACATCAG -3’/5’- CTTGGTACGAGACTTGGGATTG -3’ (97)
MDM2	5’- GGCAGGGGAGAGTGATACAGA -3’/5’- GAAGCCAATTCTCACGAAGGG -3’ (146)
MFAP5	5’- AGTCGGAAGTAATTGGAGCGA -3’/5’- TAACCAAGAGGAATGCGGTCA -3’ (84)
NDUFS1	5’- TGCCCTGTAGGTGCCCTAA -3’/5’- CCAACCGCATCCATTACATCAAT -3’ (98)
PAICS	5’- GCAGGGTTGTAGTGTTGATGG -3’/5’- GCCACTGCCACAAATACAGTAG -3’ (190)
PLEC	5’- CTCCGCAGCGAGTTTGAGAG -3’/5’- CTGCACGTCGTTGAAGAGCA -3’ (222)
S100A8	5’- ATGCCGTCTACAGGGATGAC -3’/5’- ACTGAGGACACTCGGTCTCTA -3’ (54)
SEMA3C	5’- TAACCAAGAGGAATGCGGTCA -3’/5’- TGCTCCTGTTATTGTCAGTCAGT -3’ (159)
SHC1	5’- GCCAAAGACCCTGTGAATCAG -3’/5’- GTATTGTTTGAAGCGCAACTCG -3’ (114)
SLC40A1	5’- CCACAATACGAAGGATTGACCA -3’/5’- ACTGGGGAGCCAAATGTCATA -3’ (82)
TACSTD2	5’- CATCAAGGGCGAGTCTCTATTC -3’/5’- CCCGACTTTCTCCGGTTGG -3’ (225)
TSPAN8	5’- CGCCACAGGGGAAAGTGAAA -3’/5’- CAGCTCCATTGACCAAACCG -3’ (89)
VGF	5’- CCTTCCCGAAACCCACAAGTT -3’/5’- GCCTTGGTACGCCTTGGAC -3’ (94)
WIF1	5’- GCCCACAACCCTGTCGAAAT -3’/5’- CTCCCTGGTAACCTTTGGAAC -3’ (75)

Table S2. Validation by qPCR of differentially expressed genes identified by RNA-Seq analysis between KLF5-expressing DU 145 xenograft tumors and the PLHCX vector control or between K369R-expressing tumors and PLHCX.

Gene name	Fold change	
	qPCR	RNA-Seq (*p* value, FDR)
KLF5 vs PLHCX		
KLF5	9.49	12.89(<0.01, <0.05)
EEF1B2[a]	1.12	-∞(<0.01, <0.05)
NDUFS1[a]	1.55	-∞(<0.01, <0.05)
PAICS[a]	1.16	-∞(<0.01, <0.05)
FSIP1[a]	-1.02	-29.69(<0.01, <0.05)
PLEC[a]	1.23	∞(<0.01, <0.05)
MDM2[b]	1.28	1.52(0.02, 1)
CEACAM6	2.02	2.35(<0.01, <0.05)
CEACAM5	2.37	2.63(<0.01, <0.05)
S100A8	-3.04	-3.34(0.03, 1)
ETV6[c]	1.04	-2.71(0.01, 1)
K369R vs. PLHCX		
KLF5	8.24	12.57(<0.01, <0.05)
ARHGAP5[a]	39.20	-∞(<0.01, <0.05)
MFAP5[a]	25.90	39.16(<0.01, <0.05)
BDKRB1[a]	1.34	59.48(<0.01, <0.05)
SHC1[a]	-1.34	∞(<0.01, <0.05)
CD44[b]	1.76	1.91(<0.01, <0.05)
CEACAM5	-5.46	-3.96(<0.01, 0.21)
S100A8	-3.64	-3.37(0.03, 1)
ALDH1A1	12.08	-13.7(0.01, 0.51)
GJA1	-2.03	-3.16(0.04, 1)
LTBP1	-4.41	-3.36(0.01, 0.55)
SEMA3C	2.07	2.15(<0.01, 0.09)
SLC40A1	-4.12	-3.97(0.04, 1)
VGF	10.10	18.32(<0.01, 0.16)
WIF1	-19.92	-18.13(<0.01, 0.19)
AXL	4.07	3.09(<0.01, <0.05)
CCND3	-3.98	-2.76(<0.01, <0.05)
DKK1	-3.69	-2.44(<0.01, <0.05)
GAS6	2.93	4.16(<0.01, <0.05)
IGFBP3	-3.72	-2.52(<0.01, <0.05)

LBH	-9.01	-7.55(<0.01, <0.05)
TACSTD2	13.00	14.15(<0.01, <0.05)
TSPAN8	-9.26	-6.97(<0.01, <0.05)
FSIP1	-3.04	-9.16(<0.01, <0.05)
CYR61	1.44	2.66(<0.01, <0.05)
ETV6[c]	-1.06	7.6(<0.01, <0.05)
ACTA2[c]	1.08	2.94(0.03, 0.89)

Notes: A minus sign "-" indicates downregulation for a gene.

[a] Genes that showed >20 fold of changes in RNA-Seq analysis but could not be validated by qPCR. This group of genes were thus removed from the list of differentially expressed genes.

[b] Genes that had 1.5-2 fold of change in RNA-Seq analysis and were validated by qPCR. This group of genes were included in the list of differentially expressed genes.

[c] Genes that had 1.5-20 fold of change and p values < 0.05 in RNA-Seq analysis but could not be validated by qPCR. Three of the 29 (10.3%) genes belong to this group.

Table S3. Differentially expressed genes between KLF5-expressing DU 145 xenograft tumors and the PLHCX vector control as identified by RNA-Seq analysis.

Gene name	**FPKM**		**Fold change**	***p* value**
	KLF5	**PLHCX**		
Upregulated by KLF5				
KLF5	114.215	8.862	12.888	0.000
HMSD	15.990	1.266	12.625	0.001
AK3	8.615	1.225	7.032	0.035
AC004854.4	8.357	1.224	6.825	0.035
ALG13-AS1	12.484	1.928	6.474	0.004
PPAN-P2RY11	8.616	1.459	5.907	0.035
FNTA	16.607	2.977	5.578	0.001
AL158147.2	21.318	3.959	5.384	0.000
COPZ2	28.759	6.220	4.624	0.000
RNU4ATAC	33.010	7.956	4.149	0.000
FXYD3	31.482	8.052	3.910	0.000
DKFZP547B0914	19.644	5.511	3.565	0.005
AL353354.1	723.097	219.787	3.290	0.000
RN7SL1	5579.920	1860.130	3.000	0.000
ETV6	23.555	8.400	2.804	0.008
CGA	45.846	16.687	2.747	0.000
CEACAM5	57.793	21.962	2.632	0.000
AL591806.1	29.296	11.273	2.599	0.005
PRR11	30.649	11.851	2.586	0.003
AC138393.1	17.516	6.808	2.573	0.027
AC008914.1	118.405	47.828	2.476	0.000
CEACAM6	157.550	66.940	2.354	0.000
EMP2	34.066	16.716	2.038	0.008
CMTM1	27.038	13.347	2.026	0.030
RP11-552F3.13	47.964	23.826	2.013	0.003
ARRB1	35.160	17.986	1.955	0.010
CRABP2	50.292	27.180	1.850	0.007
RP11-27M24.1	44.919	24.336	1.846	0.012
AC007193.8	47.986	27.028	1.775	0.016
MT-ND5	3616.840	2081.760	1.737	0.000
EXOC6	32.049	18.600	1.723	0.038
MT-ND6	4429.100	2600.980	1.703	0.000
APOC1	49.624	29.776	1.667	0.018

CTD-2562J17.9	66.424	39.891	1.665	0.005
PFKFB3	40.620	24.799	1.638	0.036
PTCHD3P1	60.013	36.814	1.630	0.011
CTD-2562J17.7	46.326	29.122	1.591	0.040
MDK	49.252	31.558	1.561	0.035
TMEM64	57.061	37.546	1.520	0.032
MDM2	64.070	42.200	1.518	0.021
Downregulated by KLF5				
RP11-612B6.2	5.340	30.278	0.176	0.000
UBE3D	2.056	11.599	0.177	0.036
RP3-410C9.1	27.469	104.813	0.262	0.000
GDPD3	3.348	12.115	0.276	0.050
SNORD3B-1	4.469	16.111	0.277	0.017
SNORD3A	10.244	34.498	0.297	0.001
S100A8	3.954	13.194	0.300	0.031
AC007216.2	10.512	31.451	0.334	0.002
AP003068.12	9.924	25.094	0.395	0.012
S100A9	56.525	130.623	0.433	0.000
A2M	12.228	28.233	0.433	0.021
SIPA1L3	10.865	24.503	0.443	0.030
BPIFA1	17.494	38.146	0.459	0.011
FXYD2	13.501	28.970	0.466	0.033
CCDC57	16.486	35.029	0.471	0.019
RP3-406A7.7	14.582	29.020	0.502	0.037
AL669831.1	18.380	35.753	0.514	0.042
FAM95B1	27.955	51.488	0.543	0.014
AKR1B1	484.003	841.481	0.575	0.000
RP11-329L6.1	248.555	415.521	0.598	0.000
VEGFA	82.999	136.701	0.607	0.001
HSPA1A	54.166	85.962	0.630	0.018
SPTSSA	204.517	323.318	0.633	0.000
NAPSA	71.080	110.663	0.642	0.010
EDIL3	69.116	105.562	0.655	0.016
HLA-F	58.507	88.187	0.663	0.032

Notes:

1. FPKM, fragment per kilobase of exon model per million mapped reads.
2. Genes are listed according to their fold changes from high to low for those with upregulation and from high to low for those with downregulation.

Table S4. Differentially expressed genes between K369R-expressing DU 145 xenograft tumors and the PLHCX vector control as identified by RNA-Seq analysis.

Genes name	**FPKM**		**Fold change**	***p* value**
	K369R	**PLHCX**		
Upregulated by K369R				
VGF	10.472	0.572	18.322	0.003
ANXA8	38.314	2.289	16.738	0.000
MYH4	8.619	0.546	15.792	0.010
CKM	14.846	0.943	15.749	0.000
ANXA8L1	37.419	2.576	14.525	0.000
TACSTD2	21.149	1.495	14.149	0.000
MYH2	9.706	0.687	14.126	0.005
BNC1	11.444	0.811	14.113	0.001
TNNC2	27.393	1.969	13.914	0.000
MYH1	11.073	0.800	13.848	0.001
SERPINE1	8.237	0.616	13.375	0.010
PYGM	6.405	0.491	13.047	0.035
KLF5	111.432	8.862	12.574	0.000
F13A1	10.268	0.848	12.104	0.003
ANXA8L2	37.092	3.136	11.827	0.000
MYLPF	7.310	0.650	11.247	0.019
SLCO1B3	11.608	1.053	11.028	0.006
DES	13.296	1.217	10.923	0.002
TNNI2	14.065	1.340	10.496	0.001
KCNMA1	8.945	0.885	10.107	0.010
ACTA1	66.008	6.546	10.084	0.000
KRT6C	6.509	0.806	8.080	0.035
NEB	7.483	0.968	7.733	0.019
ETV6	63.839	8.400	7.600	0.000
CRYAB	39.218	5.245	7.478	0.000
SLC35F3	6.808	0.953	7.141	0.035
PLEKHG4	114.833	16.761	6.851	0.000
LINC00511	13.360	2.117	6.311	0.006
SFTA1P	9.321	1.501	6.211	0.020
ATP2A1	34.006	5.539	6.139	0.000
PLK2	36.228	6.373	5.685	0.000
RP11-789C17.5	8.578	1.509	5.683	0.034
MET	29.258	5.150	5.681	0.000

FNTA	16.825	2.977	5.651	0.001
CTD-2195B23.3	15.892	2.857	5.563	0.002
SEMA7A	12.831	2.385	5.380	0.011
AFAP1L2	9.675	1.883	5.138	0.020
RP1-261D10.2	10.764	2.203	4.886	0.031
RNF128	11.007	2.312	4.760	0.019
ALG13-AS1	8.922	1.928	4.627	0.034
CASP4	28.529	6.177	4.619	0.000
SMYD3	49.881	10.992	4.538	0.000
EFEMP1	77.112	17.111	4.507	0.000
COL4A2	55.443	13.236	4.189	0.000
GAS6	90.968	21.846	4.164	0.000
CPA4	49.977	12.151	4.113	0.000
ECM1	20.393	5.081	4.013	0.003
AMIGO2	21.374	5.430	3.937	0.002
TPM2	42.633	11.012	3.872	0.000
FBXO32	15.758	4.071	3.871	0.015
FRMD6	13.058	3.489	3.742	0.017
RN7SL1	6757.030	1860.130	3.633	0.000
TPM1	294.597	82.849	3.556	0.000
AP001048.4	10.627	2.989	3.555	0.031
RPPH1	25.804	7.403	3.486	0.002
IL32	84.076	24.580	3.421	0.000
NABP1	35.559	10.469	3.397	0.000
CD68	50.729	15.609	3.250	0.000
RHPN1-AS1	11.136	3.436	3.241	0.045
SLC22A3	11.591	3.582	3.236	0.045
SERPINA1	44.575	13.793	3.232	0.000
FHOD3	26.207	8.193	3.199	0.002
CCDC80	14.828	4.700	3.155	0.024
ERAP2	70.465	22.747	3.098	0.000
AXL	91.550	29.672	3.085	0.000
RAMP1	42.660	13.871	3.076	0.000
TNC	21.568	7.040	3.064	0.009
RP11-373D23.3	16.442	5.413	3.037	0.020
SIPA1L1	30.307	10.025	3.023	0.002
MICB	31.818	10.631	2.993	0.001
RP11-331F9.10	179.772	60.100	2.991	0.000
COTL1	133.256	45.172	2.950	0.000

ACTA2	17.792	6.060	2.936	0.026
DCBLD2	191.382	66.149	2.893	0.000
S100A2	38.861	13.495	2.880	0.000
ARHGAP23	14.966	5.200	2.878	0.048
CD70	50.632	17.622	2.873	0.000
AC037459.4	15.097	5.275	2.862	0.031
KRTAP5-2	13.748	4.825	2.849	0.038
ARNTL2	20.025	7.042	2.844	0.014
RP11-661A12.4	32.747	11.583	2.827	0.001
COL4A1	14.229	5.067	2.808	0.048
MATN2	16.235	5.832	2.784	0.020
HSPG2	40.513	14.577	2.779	0.000
CDA	70.743	25.958	2.725	0.000
DGKA	27.095	10.032	2.701	0.006
FHL2	55.330	20.616	2.684	0.000
C6orf141	16.951	6.334	2.676	0.040
BMP1	92.915	34.788	2.671	0.000
EPB41L2	47.870	18.019	2.657	0.000
CYR61	54.856	20.655	2.656	0.000
CAV1	105.312	40.444	2.604	0.000
RP11-793A3.1	14.433	5.645	2.557	0.048
CFB	16.586	6.505	2.550	0.040
SYTL2	18.699	7.431	2.516	0.033
RP11-265D17.2	38.372	15.314	2.506	0.001
TNS4	49.861	20.037	2.488	0.000
RBPMS	77.551	31.248	2.482	0.000
FSTL3	54.778	22.122	2.476	0.000
LETM2	17.679	7.160	2.469	0.048
S100A6	3972.900	1621.310	2.450	0.000
ANXA3	219.748	90.953	2.416	0.000
ST5	16.466	6.846	2.405	0.040
MFI2	81.037	33.840	2.395	0.000
PSORS1C1	20.938	8.769	2.388	0.027
C19orf33	275.022	117.436	2.342	0.000
IFI27	95.279	40.687	2.342	0.000
PHLDA3	52.757	22.581	2.336	0.000
MOK	66.670	28.558	2.335	0.000
MYO1B	78.375	33.645	2.329	0.000
MAP1B	46.126	20.019	2.304	0.001

AC008914.1	110.002	47.828	2.300	0.000
LAMC2	36.581	16.042	2.280	0.004
RRAD	79.468	34.893	2.277	0.000
AHR	26.064	11.638	2.240	0.015
RP11-244F12.2	64.131	28.814	2.226	0.000
IL15RA	22.213	9.987	2.224	0.022
CAV2	90.549	40.866	2.216	0.000
UPP1	60.420	27.270	2.216	0.000
PMEPA1	74.450	33.633	2.214	0.000
JUN	59.330	26.824	2.212	0.000
DST	143.819	65.251	2.204	0.000
DSG2	121.809	55.298	2.203	0.000
C3	65.667	29.823	2.202	0.000
TNFSF9	39.101	17.814	2.195	0.002
GFPT2	30.617	13.963	2.193	0.007
LGALS1	883.293	403.738	2.188	0.000
PDLIM1	142.798	65.329	2.186	0.000
PERP	209.049	95.720	2.184	0.000
AC034220.3	27.476	12.745	2.156	0.018
SEMA3C	45.203	20.977	2.155	0.001
DNAJB4	117.186	54.494	2.150	0.000
IL18	42.657	19.848	2.149	0.002
GADD45A	31.320	14.577	2.149	0.008
RHOD	85.417	39.978	2.137	0.000
UAP1	87.608	41.020	2.136	0.000
PRKCDBP	21.061	9.912	2.125	0.032
ZFP36L1	170.658	80.614	2.117	0.000
RP11-124N14.3	411.790	195.589	2.105	0.000
PRR11	24.930	11.851	2.104	0.031
VIM	810.275	387.418	2.091	0.000
S100A16	410.386	196.574	2.088	0.000
P4HA2	61.141	29.334	2.084	0.000
C19orf21	26.650	12.879	2.069	0.026
CHI3L2	44.060	21.299	2.069	0.003
FLNC	49.438	24.001	2.060	0.002
TUBA4A	153.675	74.727	2.056	0.000
KLF6	38.874	19.104	2.035	0.009
MAN2A1	28.508	14.211	2.006	0.024
PEA15	77.424	38.872	1.992	0.000

ESYT1	77.718	39.029	1.991	0.000
AC002472.1	27.525	13.940	1.974	0.021
RALB	41.912	21.251	1.972	0.008
DOCK9	23.172	11.760	1.970	0.044
HERPUD1	174.294	89.202	1.954	0.000
EHD2	58.498	29.994	1.950	0.001
PTPRF	109.501	56.156	1.950	0.000
TNFAIP2	135.051	69.668	1.939	0.000
RP11-79P5.2	43.974	22.701	1.937	0.007
RAB32	33.686	17.399	1.936	0.018
DDIT3	36.701	19.172	1.914	0.017
CD44	205.617	107.557	1.912	0.000
HSPB1	544.691	285.448	1.908	0.000
CLIC4	139.391	73.083	1.907	0.000
TGM2	373.898	196.512	1.903	0.000
ZNF395	30.213	15.902	1.900	0.020
AP1S1	95.129	50.215	1.894	0.000
TINAGL1	34.950	18.493	1.890	0.020
SMS	58.105	30.860	1.883	0.001
CYBRD1	67.271	35.733	1.883	0.001
TRNP1	121.897	65.146	1.871	0.000
FGFR1	40.718	21.773	1.870	0.011
ATP2B4	49.132	26.290	1.869	0.006
NTAN1	29.602	15.988	1.852	0.027
RP5-977B1.11	179.003	96.970	1.846	0.000
CHST3	36.918	20.021	1.844	0.025
SAT1	420.157	228.447	1.839	0.000
LAMA3	30.493	16.593	1.838	0.030
FHOD1	39.486	21.523	1.835	0.015
KRT19	434.863	237.147	1.834	0.000
AHNAK2	76.019	41.480	1.833	0.001
LOXL2	85.583	47.042	1.819	0.000
BMI1	101.806	56.228	1.811	0.000
EPN2	38.010	21.042	1.806	0.021
SH3BGRL3	129.933	72.133	1.801	0.000
S100A11	866.858	486.623	1.781	0.000
SLC25A37	79.600	44.839	1.775	0.001
OCIAD1-AS1	32.064	18.132	1.768	0.037
ASAP1	55.978	31.663	1.768	0.005

ITGB4	50.391	28.695	1.756	0.010
TPST2	26.163	14.916	1.754	0.046
ADAM9	231.257	132.213	1.749	0.000
RHOC	171.312	98.020	1.748	0.000
HSPH1	91.161	52.275	1.744	0.000
ANKRD13A	121.072	69.742	1.736	0.000
RP11-218E20.5	63.748	36.784	1.733	0.004
PINK1	34.054	19.654	1.733	0.031
DYNC1H1	62.950	36.366	1.731	0.005
OPTN	56.207	32.486	1.730	0.006
MICAL3	99.017	57.595	1.719	0.000
HMOX2	37.408	21.764	1.719	0.028
MMP24	40.169	23.420	1.715	0.025
RP5-956O18.3	80.550	47.007	1.714	0.001
SCAMP1	35.230	20.623	1.708	0.034
CTB-151G24.1	35.071	20.536	1.708	0.034
PTCHD3P1	62.758	36.814	1.705	0.005
GALNT2	82.508	48.564	1.699	0.001
CHORDC1	48.406	28.518	1.697	0.017
RIPK2	33.032	19.623	1.683	0.041
DNAJB2	44.147	26.300	1.679	0.024
CHST15	33.534	19.982	1.678	0.041
PTRF	178.177	106.867	1.667	0.000
AL358113.1	128.441	77.311	1.661	0.000
CDV3	96.284	58.153	1.656	0.001
PYGL	175.046	106.138	1.649	0.000
GPX1	196.375	119.217	1.647	0.000
MYH9	187.199	113.668	1.647	0.000
MYL9	74.791	45.453	1.645	0.005
PITX1	63.756	38.790	1.644	0.008
PDLIM2	39.760	24.213	1.642	0.047
TJP2	35.282	21.534	1.638	0.048
TES	56.987	34.892	1.633	0.012
BAIAP2	38.412	23.572	1.630	0.043
CLDN1	60.981	37.454	1.628	0.012
ARPC1B	286.184	175.931	1.627	0.000
SBDS	82.571	50.821	1.625	0.002
CDH3	175.831	108.260	1.624	0.000
THBS1	40.581	25.013	1.622	0.050

NCOR2	69.656	42.975	1.621	0.006
RP11-1017G21.4	87.567	54.044	1.620	0.002
TGFBI	546.654	339.453	1.610	0.000
DPYSL2	97.789	60.905	1.606	0.001
CCDC85B	40.056	25.044	1.599	0.050
WNK1	92.452	57.828	1.599	0.002
PMAIP1	60.071	37.648	1.596	0.012
PTPN12	85.915	53.887	1.594	0.003
CLIC1	207.221	130.329	1.590	0.000
SLC39A14	111.841	70.431	1.588	0.001
TIMP2	178.979	112.751	1.587	0.000
PHLDA2	49.015	31.043	1.579	0.027
DTX2	47.167	29.881	1.578	0.031
ETS2	92.458	58.710	1.575	0.003
GNG12	65.095	41.453	1.570	0.012
CORO1C	116.816	74.439	1.569	0.001
GPN1	49.023	31.248	1.569	0.027
LAMB3	192.053	122.476	1.568	0.000
RP11-323N12.5	317.930	203.000	1.566	0.000
SDC1	184.947	118.214	1.565	0.000
KIF1C	50.033	32.061	1.561	0.029
ELAC2	61.977	39.788	1.558	0.017
PRNP	68.656	44.109	1.557	0.015
ZYX	115.491	74.316	1.554	0.001
PXN	126.043	81.228	1.552	0.001
GRAMD1B	51.559	33.301	1.548	0.031
GNAI2	109.923	71.064	1.547	0.002
ITGB1BP1	99.034	64.081	1.545	0.002
TPBG	48.001	31.062	1.545	0.035
OCLN	48.522	31.470	1.542	0.035
HPCAL1	92.186	59.824	1.541	0.003
PSAP	1038.670	677.639	1.533	0.000
AGAP3	54.712	35.818	1.527	0.028
PKM	903.983	591.887	1.527	0.000
CRIM1	83.614	54.820	1.525	0.006
UBE2F	66.323	43.525	1.524	0.017
RP4-816N1.7	86.716	57.003	1.521	0.008
BCAP29	60.719	40.020	1.517	0.029
ALDH2	59.704	39.409	1.515	0.027

ARMC10	51.978	34.329	1.514	0.042
CLTB	61.345	40.520	1.514	0.023
MYO1C	95.893	63.529	1.509	0.005
PABPC1	1284.340	851.297	1.509	0.000
MT-ND6	3916.780	2600.980	1.506	0.000
TSPO	126.345	84.035	1.503	0.001
PPP1R14B	114.594	76.300	1.502	0.002
DPP9	100.989	67.257	1.502	0.004
SPARC	127.393	84.847	1.501	0.001

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WIF1	0.647	11.735	0.055	0.004
ALDH1A1	0.684	9.367	0.073	0.012
C8orf4	5.543	72.601	0.076	0.000
NELL2	2.282	24.138	0.095	0.000
COL14A1	3.684	37.427	0.098	0.000
CRISPLD1	2.569	26.027	0.099	0.000
NPNT	0.969	9.178	0.106	0.012
FSIP1	3.543	32.451	0.109	0.000
A2M	3.447	28.233	0.122	0.000
NDNF	1.842	14.025	0.131	0.002
LBH	5.751	43.416	0.132	0.000
SFTPB	18.007	135.699	0.133	0.000
DEFB1	7.233	54.110	0.134	0.000
EHF	1.653	12.356	0.134	0.008
CLDN2	5.762	42.917	0.134	0.000
SPINK1	7.674	55.199	0.139	0.000
TSPAN8	4.187	29.167	0.144	0.000
RSPO3	2.216	15.124	0.147	0.005
C5	6.989	46.339	0.151	0.000
CXCL17	7.094	46.001	0.154	0.000
TMTC2	2.609	16.792	0.155	0.003
AQP3	46.725	300.097	0.156	0.000
CGA	2.615	16.687	0.157	0.003
UBE3D	1.878	11.599	0.162	0.013
RGCC	6.741	40.895	0.165	0.000
CTD-2269F5.1	2.787	16.338	0.171	0.003
NPR3	2.908	16.285	0.179	0.003
CRLF1	2.314	12.786	0.181	0.022

PER1	3.689	19.843	0.186	0.002
BCOR	1.756	9.373	0.187	0.039
PAG1	2.691	13.603	0.198	0.013
AGR2	3.506	17.541	0.200	0.005
SAMD11	2.813	13.922	0.202	0.013
PRR5L	2.356	11.314	0.208	0.036
RP11-4K16.2	8.444	40.344	0.209	0.000
SLC7A2	4.849	22.805	0.213	0.001
SUSD2	7.252	33.912	0.214	0.000
GGT5	2.779	12.665	0.219	0.022
RP11-160E2.6	2.451	11.163	0.220	0.036
GPCPD1	6.089	27.694	0.220	0.001
LPAR1	19.769	89.065	0.222	0.000
NR4A1	31.531	141.570	0.223	0.000
NAPSA	24.679	110.663	0.223	0.000
IGFBP2	18.905	84.316	0.224	0.000
RP11-1100L3.8	26.887	118.409	0.227	0.000
DIRAS3	3.372	14.830	0.227	0.020
FAM107B	27.121	117.482	0.231	0.000
RASD1	5.775	24.971	0.231	0.001
RP3-410C9.1	24.913	104.813	0.238	0.000
CRIP1	6.834	28.667	0.238	0.000
CTD-3193O13.8	3.359	14.055	0.239	0.020
RP11-806O11.1	4.113	17.154	0.240	0.011
CISH	3.375	13.924	0.242	0.032
SYNE1	10.605	43.667	0.243	0.000
SLC40A1	2.942	11.694	0.252	0.036
CEACAM5	5.547	21.962	0.253	0.004
ECH1	5.910	22.828	0.259	0.003
DAPK1	6.570	25.231	0.260	0.001
EDIL3	27.967	105.562	0.265	0.000
ITPR1	5.323	20.057	0.265	0.006
GDF15	16.248	60.971	0.266	0.000
SNORD3B-2	4.320	15.945	0.271	0.028
GALNT11	37.995	139.150	0.273	0.000
NR4A3	5.657	20.679	0.274	0.006
SNORD3A	9.456	34.498	0.274	0.000
ASS1	19.596	70.904	0.276	0.000
RP11-262H14.4	5.424	19.618	0.276	0.010

SNORD3C	3.970	14.223	0.279	0.020
ABCA8	5.723	19.914	0.287	0.010
RP11-499O7.7	10.257	35.645	0.288	0.001
SLC45A4	12.221	41.484	0.295	0.000
S100A8	3.910	13.194	0.296	0.032
LTBP1	6.097	20.507	0.297	0.013
FGL1	4.736	15.835	0.299	0.028
PDK4	19.506	65.045	0.300	0.000
SELENBP1	3.974	13.149	0.302	0.032
RP5-981O7.2	8.057	26.625	0.303	0.004
AL161784.1	94.556	312.302	0.303	0.000
CFI	6.503	21.411	0.304	0.009
FAM95B1	15.717	51.488	0.305	0.000
DNAJC12	42.262	138.151	0.306	0.000
RP11-612B6.2	9.426	30.278	0.311	0.002
AKR1C2	233.297	738.971	0.316	0.000
GJA1	5.096	16.084	0.317	0.036
SPTSSA	103.778	323.318	0.321	0.000
PEG10	22.727	70.765	0.321	0.000
F3	56.690	173.884	0.326	0.000
ZNF275	5.888	17.886	0.329	0.024
CEA	5.647	17.032	0.332	0.024
CEACAM6	22.678	66.940	0.339	0.000
SNORD3B-1	5.571	16.111	0.346	0.036
BPIFA1	13.653	38.146	0.358	0.001
TFPI2	24.744	69.085	0.358	0.000
AKR1C4	8.071	22.325	0.362	0.021
CCND3	26.170	72.238	0.362	0.000
STAMBPL1	15.706	43.198	0.364	0.001
DUSP4	24.131	65.123	0.371	0.000
CD46	295.889	796.779	0.371	0.000
PITPNC1	9.119	24.406	0.374	0.018
RP11-304L19.5	87.330	232.893	0.375	0.000
NBEAL2	32.145	84.872	0.379	0.000
CTD-2562J17.7	11.044	29.122	0.379	0.013
GULP1	14.946	39.215	0.381	0.002
CORO6	16.327	42.591	0.383	0.002
RP11-329L6.1	159.378	415.521	0.384	0.000
FKBP10	11.586	30.160	0.384	0.009

CPM	87.969	228.460	0.385	0.000
ZNF189	7.936	20.497	0.387	0.025
EGFL7	10.181	26.132	0.390	0.015
KLF2	9.603	24.538	0.391	0.018
LPGAT1	62.104	158.610	0.392	0.000
SNTB1	8.005	20.294	0.394	0.045
IGFBP3	112.198	282.378	0.397	0.000
SEP11	49.940	125.179	0.399	0.000
GYLTL1B	7.973	19.903	0.401	0.037
SNHG10	14.570	36.333	0.401	0.005
NAB2	10.969	27.252	0.403	0.010
SLC26A2	17.314	42.755	0.405	0.003
EMC10	88.397	218.070	0.405	0.000
AKR1C1	124.369	305.135	0.408	0.000
DKK1	43.967	107.067	0.411	0.000
SLC27A2	25.079	60.808	0.412	0.001
STOM	25.135	60.813	0.413	0.001
PCSK6	11.796	28.094	0.420	0.013
CTD-2292P10.2	11.182	26.557	0.421	0.025
SIPA1L3	10.400	24.503	0.424	0.031
RHOBTB2	31.149	73.202	0.426	0.000
APOE	15.420	36.132	0.427	0.008
FGA	132.994	309.543	0.430	0.000
AGPAT2	52.204	120.501	0.433	0.000
IRX3	19.344	44.558	0.434	0.004
CADM1	17.329	39.885	0.434	0.008
XBP1	110.761	252.458	0.439	0.000
SLPI	79.611	181.303	0.439	0.000
LPIN2	13.024	29.564	0.441	0.034
SLC46A3	22.034	49.932	0.441	0.003
RGS3	10.398	23.473	0.443	0.043
ADM	12.255	27.610	0.444	0.041
RP13-582O9.5	13.270	29.685	0.447	0.034
MEGF9	62.134	138.216	0.450	0.000
AC007216.2	14.178	31.451	0.451	0.028
IMPA2	73.605	161.903	0.455	0.000
EGLN3	11.660	25.506	0.457	0.036
MAPK4	16.892	36.862	0.458	0.014
JUP	65.017	140.981	0.461	0.000

CTSL1	49.462	107.132	0.462	0.000
ERRFI1	92.874	201.124	0.462	0.000
AKR1C3	89.255	190.895	0.468	0.000
AHCYL2	18.057	38.125	0.474	0.017
GPX2	149.142	313.295	0.476	0.000
OLFM2	15.330	32.127	0.477	0.031
FGG	245.031	512.632	0.478	0.000
DPP7	28.479	59.546	0.478	0.003
TRMT11	18.452	38.560	0.479	0.017
HILPDA	14.534	30.335	0.479	0.038
FXYD2	13.887	28.970	0.479	0.046
EPB41L5	11.930	24.854	0.480	0.050
LIF	21.958	45.212	0.486	0.007
SFTA3	20.505	42.218	0.486	0.012
ANXA4	92.587	189.726	0.488	0.000
IDH2	38.598	79.055	0.488	0.000
RDH10	34.193	69.718	0.490	0.002
GLRX	25.037	50.721	0.494	0.009
ABCA2	17.830	36.083	0.494	0.021
CMTM8	19.561	39.567	0.494	0.020
PLAGL1	18.526	37.210	0.498	0.024
TP53INP2	28.309	56.548	0.501	0.007
PPP2R1B	19.648	38.965	0.504	0.026
TMEM205	44.369	87.696	0.506	0.001
FBXW2	40.619	80.010	0.508	0.001
ATP11A	18.818	37.011	0.508	0.024
BTG1	55.059	107.335	0.513	0.000
IQCJ-SCHIP1	22.400	43.570	0.514	0.020
CCDC64	22.176	43.024	0.515	0.020
PDE4D	37.305	72.374	0.515	0.002
IFI30	24.162	46.735	0.517	0.018
PON3	18.510	35.771	0.517	0.042
CRLS1	32.763	62.844	0.521	0.006
CYBA	46.944	89.902	0.522	0.001
SEMA4B	61.826	118.285	0.523	0.000
ZNF580	18.611	35.507	0.524	0.042
CMPK1	77.824	146.820	0.530	0.000
PRPS2	21.377	40.230	0.531	0.032
TM4SF1	227.583	426.879	0.533	0.000

CTD-3149D2.4	19.714	36.914	0.534	0.046
WDR34	34.900	65.299	0.534	0.005
RP11-638I2.6	33.471	62.506	0.535	0.008
NOL6	31.210	58.006	0.538	0.011
LIMCH1	51.693	95.418	0.542	0.001
SGPP1	33.575	61.607	0.545	0.010
ANKRD18B	35.485	64.527	0.550	0.009
CD320	35.655	64.215	0.555	0.009
CEBPD	30.012	53.372	0.562	0.029
EPAS1	80.919	143.774	0.563	0.000
CYB561A3	37.246	65.924	0.565	0.014
P2RY6	25.836	45.655	0.566	0.034
FBLN1	104.137	183.571	0.567	0.000
TXNIP	27.967	49.177	0.569	0.024
SLC39A7	59.108	103.489	0.571	0.002
RP11-498C9.13	46.294	81.019	0.571	0.006
DPM3	72.793	127.051	0.573	0.000
BASP1	102.075	177.309	0.576	0.000
WSB1	128.679	222.285	0.579	0.000
SLC6A6	95.011	164.003	0.579	0.000
ICA1	27.956	48.245	0.579	0.031
SNHG9	52.354	90.266	0.580	0.004
TSPAN13	83.266	143.461	0.580	0.000
CHEK2	25.681	44.229	0.581	0.044
TROAP	31.955	54.956	0.581	0.031
SLC25A29	26.907	46.236	0.582	0.037
PHF19	39.831	68.294	0.583	0.013
EPCAM	144.405	247.049	0.585	0.000
FURIN	26.514	45.268	0.586	0.047
EPDR1	61.710	105.274	0.586	0.003
NUB1	53.099	90.327	0.588	0.006
HMGB3	158.178	267.781	0.591	0.000
MALL	28.477	48.161	0.591	0.042
ZFP36	41.932	70.832	0.592	0.014
SCD5	37.838	63.812	0.593	0.022
PCBP1-AS1	30.565	51.479	0.594	0.047
TOP2A	58.290	97.885	0.595	0.005
FADS1	54.396	91.200	0.596	0.006
GSTT1	117.928	195.902	0.602	0.000

G6PC3	53.144	88.227	0.602	0.009
LAPTM4B	156.309	259.263	0.603	0.000
MAGEF1	38.060	63.085	0.603	0.030
FUS	55.526	91.377	0.608	0.008
VEGFA	83.119	136.701	0.608	0.002
VAMP2	33.950	55.800	0.608	0.045
ATP6V1G1	112.074	183.491	0.611	0.000
NDRG1	78.796	128.642	0.613	0.002
NME4	60.980	99.075	0.615	0.006
HEATR5A	68.859	111.241	0.619	0.005
AC002117.1	48.634	78.560	0.619	0.021
GAA	38.875	62.072	0.626	0.037
TOB1	161.842	258.256	0.627	0.000
TMEM9	65.116	103.792	0.627	0.011
KIAA0101	47.782	76.146	0.628	0.025
PGD	88.971	141.607	0.628	0.002
UGDH	139.882	222.615	0.628	0.000
LMO3	94.916	150.887	0.629	0.002
CTD-2033A16.1	135.294	215.063	0.629	0.000
TXN	296.597	471.437	0.629	0.000
IGFBP4	228.631	363.118	0.630	0.000
ECT2	48.138	76.395	0.630	0.032
SETD5-AS1	57.912	91.676	0.632	0.014
LACTB2	72.307	113.463	0.637	0.008
ICAM1	96.112	150.019	0.641	0.003
NEAT1	170.520	265.718	0.642	0.000
MT-ND3	4841.790	7535.040	0.643	0.000
AHCYL1	46.894	72.446	0.647	0.036
MBTPS1	52.258	80.623	0.648	0.038
PTP4A1	905.159	1395.760	0.649	0.000
NFKBIA	88.283	136.083	0.649	0.005
SMIM14	65.640	101.008	0.650	0.016
TMED3	85.079	130.909	0.650	0.008
CHMP1B	72.406	111.213	0.651	0.012
PYCR1	57.615	88.068	0.654	0.026
STMN1	144.843	219.421	0.660	0.001
PHPT1	54.573	82.414	0.662	0.041
RP11-78A19.3	230.881	348.665	0.662	0.000
CPSF6	60.239	90.803	0.663	0.035

RP11-126K1.8	68.514	103.045	0.665	0.022
SMIM4	65.855	98.894	0.666	0.029
MT-ATP8	51538.400	77076.700	0.669	0.000

Note:

1. FPKM, fragment per kilobase of exon model per million mapped reads.
2. Genes are listed according to their fold changes from high to low for those with upregulation and from high to low for those with downregulation.

Table S5. Differentially expressed genes between KLF5- and K369R-expressing DU 145 xenograft tumors as identified by RNA-Seq analysis.

Gene name	**FPKM**		**Fold change**	***p* value**
	K369R	**KLF5**		
Upregulated by K369R				
MFAP5	43.501	2.243	19.397	0.000
TNNT3	23.101	1.689	13.676	0.000
ANXA8L2	37.092	2.840	13.061	0.000
ANXA8	38.314	3.050	12.561	0.000
F13A1	10.268	0.841	12.216	0.003
SERPINE1	8.237	0.680	12.118	0.011
VGF	10.472	0.867	12.084	0.003
ANXA8L1	37.419	3.196	11.708	0.000
NEB	7.483	0.651	11.499	0.021
PLEKHG4	114.833	10.000	11.484	0.000
BNC1	11.444	1.124	10.178	0.007
TNNC2	27.393	2.802	9.777	0.000
TACSTD2	21.149	2.180	9.700	0.000
MYH2	9.706	1.064	9.122	0.022
KRT6C	6.509	0.716	9.093	0.038
CKM	14.846	1.648	9.006	0.001
MYH4	8.619	0.959	8.985	0.011
ACTA1	66.008	8.080	8.169	0.000
RNF128	11.007	1.356	8.117	0.007
MYLPF	7.310	0.953	7.674	0.021
DES	13.296	1.867	7.121	0.002
SLCO1B3	11.608	1.636	7.097	0.007
MYH1	11.073	1.563	7.084	0.007
PYGM	6.405	0.918	6.976	0.038
CRYAB	39.218	5.886	6.663	0.000
RP11-793A3.1	14.433	2.553	5.653	0.004
SLC22A3	11.591	2.087	5.554	0.021
COL4A2	55.443	10.356	5.354	0.000
RP11-338N10.3	12.202	2.296	5.314	0.012
ATP2A1	34.006	6.455	5.268	0.000
GDPD3	17.125	3.348	5.115	0.002
TNNI2	14.065	2.752	5.111	0.004
SEMA7A	12.831	2.593	4.948	0.012

(*Table S5 continued*)

S100A3	8.655	1.802	4.803	0.038
LINC00511	13.360	2.866	4.662	0.007
RP11-227H15.5	8.195	1.777	4.612	0.038
BX470102.3	14.131	3.068	4.606	0.011
CPA4	49.977	10.910	4.581	0.000
PLK2	36.228	8.085	4.481	0.000
FBXO32	15.758	3.566	4.419	0.007
RP1-261D10.2	10.764	2.474	4.351	0.034
SMYD3	49.881	11.856	4.207	0.000
RAMP1	42.660	10.695	3.989	0.000
CTD-2195B23.3	15.892	4.138	3.841	0.016
MET	29.258	7.644	3.828	0.000
CASP4	28.529	7.533	3.787	0.000
NABP1	35.559	9.523	3.734	0.000
TPM2	42.633	11.571	3.684	0.000
GAS6	90.968	25.255	3.602	0.000
TPM1	294.597	81.844	3.599	0.000
CD70	50.632	14.217	3.561	0.000
AMIGO2	21.374	6.181	3.458	0.005
IL32	84.076	24.330	3.456	0.000
EFEMP1	77.112	22.337	3.452	0.000
AP003068.12	34.059	9.924	3.432	0.000
SIPA1L1	30.307	8.915	3.400	0.000
ENC1	12.390	3.687	3.360	0.030
ECM1	20.393	6.099	3.343	0.008
CLTCL1	18.287	5.634	3.246	0.009
TNC	21.568	6.844	3.151	0.005
FHOD3	26.207	8.319	3.150	0.002
CCDC80	14.828	4.737	3.130	0.026
CDA	70.743	22.910	3.088	0.000
COL4A1	14.229	4.622	3.079	0.026
C6orf141	16.951	5.599	3.027	0.022
CYR61	54.856	18.863	2.908	0.000
CD68	50.729	17.820	2.847	0.000
LGALS1	883.293	310.563	2.844	0.000
S100A2	38.861	13.790	2.818	0.001
CHI3L2	44.060	15.927	2.766	0.000
KRTAP5-2	13.748	4.993	2.753	0.041
COTL1	133.256	48.723	2.735	0.000

(*Table S5 continued*)

GADD45A	31.320	11.505	2.722	0.002
ETV6	63.839	23.555	2.710	0.000
BMP1	92.915	34.369	2.703	0.000
DDIT3	36.701	13.607	2.697	0.001
S100A6	3972.900	1480.500	2.683	0.000
AC037459.4	15.097	5.724	2.637	0.034
IFI27	95.279	36.226	2.630	0.000
AXL	91.550	34.895	2.624	0.000
SERPINA1	44.575	17.069	2.611	0.001
RP11-331F9.10	179.772	68.998	2.605	0.000
UPP1	60.420	23.224	2.602	0.000
DCBLD2	191.382	73.818	2.593	0.000
RPPH1	25.804	9.962	2.590	0.007
LINC00842	18.371	7.094	2.590	0.035
MYO1B	78.375	31.026	2.526	0.000
RP11-124N14.3	411.790	163.088	2.525	0.000
PHLDA3	52.757	20.985	2.514	0.000
EPB41L2	47.870	19.275	2.483	0.001
RP11-265D17.2	38.372	15.459	2.482	0.002
TANC2	20.232	8.206	2.465	0.029
RBPMS	77.551	32.326	2.399	0.000
MOK	66.670	27.894	2.390	0.000
VIM	810.275	341.912	2.370	0.000
ANXA3	219.748	92.816	2.368	0.000
RP11-79P5.2	43.974	18.881	2.329	0.001
AC002472.1	27.525	11.872	2.318	0.011
MFI2	81.037	34.997	2.316	0.000
HSPB1	544.691	238.354	2.285	0.000
HSPG2	40.513	17.803	2.276	0.003
PERP	209.049	92.275	2.266	0.000
TUBA4A	153.675	67.878	2.264	0.000
TAP2	22.471	9.972	2.253	0.024
RRAD	79.468	35.275	2.253	0.000
PSORS1C1	20.938	9.321	2.246	0.049
LAMC2	36.581	16.313	2.242	0.006
PRKCDBP	21.061	9.423	2.235	0.034
HES1	19.466	8.743	2.226	0.042
TNFSF9	39.101	17.586	2.223	0.004
CLDN1	60.981	27.685	2.203	0.000

(*Table S5 continued*)

FHL2	55.330	25.160	2.199	0.001
PMAIP1	60.071	27.318	2.199	0.000
PDLIM1	142.798	65.267	2.188	0.000
CD44	205.617	94.735	2.170	0.000
FLNC	49.438	22.796	2.169	0.001
MAP1B	46.126	21.522	2.143	0.002
RP11-127L20.5	30.268	14.124	2.143	0.018
LOXL2	85.583	39.946	2.142	0.000
JUN	59.330	27.697	2.142	0.001
P4HA2	61.141	28.630	2.136	0.000
SAT1	420.157	197.308	2.129	0.000
TSPAN1	21.142	9.946	2.126	0.034
SEBOX	44.792	21.087	2.124	0.005
ARNTL2	20.025	9.434	2.123	0.049
IL15RA	22.213	10.488	2.118	0.040
C19orf33	275.022	130.053	2.115	0.000
DST	143.819	68.028	2.114	0.000
TNS4	49.861	23.629	2.110	0.002
ERAP2	70.465	33.634	2.095	0.000
UAP1	87.608	41.968	2.088	0.000
IL11	25.090	12.067	2.079	0.038
RP5-977B1.11	179.003	86.594	2.067	0.000
DSG2	121.809	59.413	2.050	0.000
DGKA	27.095	13.225	2.049	0.031
TGFBI	546.654	268.946	2.033	0.000
MAN2A1	28.508	14.042	2.030	0.035
DNAJB4	117.186	57.921	2.023	0.000
AAMDC	23.085	11.431	2.019	0.046
S100A16	410.386	203.915	2.013	0.000
CCDC57	33.071	16.486	2.006	0.017
RAB32	33.686	16.809	2.004	0.017
PMEPA1	74.450	37.164	2.003	0.000
ESYT1	77.718	38.888	1.998	0.000
S100A11	866.858	434.760	1.994	0.000
ANKRD13A	121.072	61.043	1.983	0.000
PEA15	77.424	39.163	1.977	0.000
GFPT2	30.617	15.593	1.964	0.029
ADAM9	231.257	117.807	1.963	0.000
SMS	58.105	29.650	1.960	0.002

(*Table S5 continued*)

AP1S1	95.129	48.553	1.959	0.000
HSPH1	91.161	46.661	1.954	0.000
ITGB4	50.391	25.812	1.952	0.004
HMOX2	37.408	19.165	1.952	0.018
RP11-244F12.2	64.131	32.921	1.948	0.001
EMP3	205.783	106.235	1.937	0.000
SH3BGRL3	129.933	67.298	1.931	0.000
FADS3	92.806	48.080	1.930	0.000
FUT8	33.549	17.409	1.927	0.026
IL18	42.657	22.139	1.927	0.014
HERPUD1	174.294	90.963	1.916	0.000
CTD-2012K14.3	34.721	18.133	1.915	0.029
FHOD1	39.486	20.679	1.910	0.015
CAV1	105.312	55.163	1.909	0.000
BMI1	101.806	53.473	1.904	0.000
RHOC	171.312	90.299	1.897	0.000
LAMA3	30.493	16.095	1.895	0.044
TNFAIP2	135.051	71.580	1.887	0.000
CLIC4	139.391	74.451	1.872	0.000
MICB	31.818	17.001	1.872	0.048
HSPA1A	101.049	54.166	1.866	0.000
ZFP36L1	170.658	91.588	1.863	0.000
TINAGL1	34.950	18.786	1.860	0.029
XAGE1B	27.754	14.994	1.851	0.048
AHNAK2	76.019	41.082	1.850	0.001
HSPA1B	141.724	76.971	1.841	0.000
MYL9	74.791	40.663	1.839	0.002
ELOVL1	66.603	36.247	1.837	0.003
CDH3	175.831	95.703	1.837	0.000
CTB-151G24.1	35.071	19.164	1.830	0.032
FGFR1	40.718	22.300	1.826	0.024
TRNP1	121.897	66.831	1.824	0.000
MMP24	40.169	22.033	1.823	0.024
CLIC1	207.221	113.955	1.818	0.000
RHOD	85.417	46.978	1.818	0.001
TSPAN15	91.961	50.614	1.817	0.001
PTPRF	109.501	60.494	1.810	0.000
RP5-1050D4.3	57.994	32.065	1.809	0.009
PRNP	68.656	38.434	1.786	0.004

(*Table S5 continued*)

PINK1	34.054	19.119	1.781	0.043
CAV2	90.549	50.883	1.780	0.001
PITX1	63.756	35.879	1.777	0.005
TGM2	373.898	210.836	1.773	0.000
SLC25A37	79.600	44.922	1.772	0.002
UBE2F	66.323	37.819	1.754	0.004
ATP2B4	49.132	28.016	1.754	0.018
PHLDA2	49.015	27.981	1.752	0.012
FSTL3	54.778	31.334	1.748	0.013
KRT19	434.863	248.959	1.747	0.000
PYGL	175.046	100.376	1.744	0.000
LAMB3	192.053	110.278	1.742	0.000
RALB	41.912	24.080	1.741	0.038
RP11-343N15.5	40.913	23.674	1.728	0.035
MXRA7	308.021	178.621	1.724	0.000
EHD2	58.498	34.007	1.720	0.013
ROMO1	236.641	138.083	1.714	0.000
CORO1C	116.816	68.222	1.712	0.000
GPX1	196.375	115.481	1.700	0.000
SEMA3C	45.203	26.600	1.699	0.026
MICAL3	99.017	58.320	1.698	0.001
ACTN1	93.505	55.098	1.697	0.002
ITGB1BP1	99.034	58.498	1.693	0.001
DSE	40.937	24.217	1.690	0.049
CHRNB1	35.437	20.997	1.688	0.047
ADI1	94.106	55.901	1.683	0.001
OPTN	56.207	33.445	1.681	0.016
ASAP1	55.978	33.348	1.679	0.020
TPBG	48.001	28.632	1.676	0.023
LIMA1	44.038	26.445	1.665	0.034
PLOD2	494.157	297.940	1.659	0.000
PRR13	286.297	172.656	1.658	0.000
PLAU	222.969	134.475	1.658	0.000
SPARC	127.393	77.257	1.649	0.000
PPP1R14B	114.594	69.809	1.642	0.001
FLII	114.020	69.468	1.641	0.001
GALNT2	82.508	50.441	1.636	0.006
PKM	903.983	552.652	1.636	0.000
ARPC1B	286.184	175.348	1.632	0.000

(*Table S5 continued*)

XPO6	68.905	42.363	1.627	0.014
PDLIM7	61.917	38.132	1.624	0.022
RP11-354M1.2	62.607	38.600	1.622	0.017
SBDS	82.571	50.963	1.620	0.006
HGS	144.122	89.153	1.617	0.000
TIMP2	178.979	110.796	1.615	0.000
AC092964.1	52.256	32.432	1.611	0.031
AL358113.1	128.441	79.931	1.607	0.001
EIF6	153.850	95.748	1.607	0.000
CARHSP1	48.950	30.531	1.603	0.044
RP5-956O18.3	80.550	50.319	1.601	0.009
PHF10	45.924	28.691	1.601	0.050
DTX2	47.167	29.501	1.599	0.041
PLAUR	45.586	28.581	1.595	0.050
OCIAD2	115.822	72.687	1.593	0.002
ETS2	92.458	58.176	1.589	0.006
MYH9	187.199	117.940	1.587	0.000
RP11-323N12.5	317.930	200.326	1.587	0.000
CDV3	96.284	60.879	1.582	0.004
SLC39A14	111.841	70.774	1.580	0.002
ZNF706	105.314	66.795	1.577	0.003
COPS6	148.858	95.217	1.563	0.001
CSRP1	195.688	125.515	1.559	0.000
CNN3	265.998	170.872	1.557	0.000
DNAJB1	187.326	120.338	1.557	0.000
PTPN12	85.915	55.208	1.556	0.012
S100A9	87.929	56.525	1.556	0.010
CYBRD1	67.271	43.289	1.554	0.023
AKR1B1	749.742	484.003	1.549	0.000
PXN	126.043	81.914	1.539	0.002
MAP1LC3B	63.958	41.586	1.538	0.032
LYN	56.635	36.956	1.533	0.039
WDR45	58.596	38.242	1.532	0.043
SLC25A39	206.522	135.213	1.527	0.000
ATP6V1D	125.369	82.194	1.525	0.003
CMTM3	71.918	47.295	1.521	0.028
PTRF	178.177	117.178	1.521	0.000
RP11-218E20.5	63.748	41.924	1.521	0.032
DYNC1H1	62.950	41.429	1.519	0.040

(*Table S5 continued*)

CLDN12	55.861	36.774	1.519	0.049
CACYBP	220.431	145.167	1.518	0.000
TMEM2	108.870	71.910	1.514	0.006
PABPC1	1284.340	849.276	1.512	0.000
KRT7	735.862	487.333	1.510	0.000
GLUD1	64.077	42.522	1.507	0.034
ALDH2	59.704	39.749	1.502	0.045
ZYX	115.491	76.965	1.501	0.005

Downregulated by K369R

HMSD	0.857	15.990	0.054	0.000
HOPX	0.395	7.214	0.055	0.039
CGA	2.615	45.846	0.057	0.000
ALDH1A1	0.684	10.680	0.064	0.006
NELL2	2.282	26.797	0.085	0.000
C8orf4	5.543	60.564	0.092	0.000
CEACAM5	5.547	57.793	0.096	0.000
CRISPLD1	2.569	25.087	0.102	0.000
SFTPB	18.007	155.329	0.116	0.000
RGCC	6.741	55.501	0.121	0.000
LBH	5.751	46.696	0.123	0.000
COL14A1	3.684	25.753	0.143	0.000
CEACAM6	22.678	157.550	0.144	0.000
SCNN1G	1.394	9.426	0.148	0.039
CRLF1	2.314	14.966	0.155	0.008
BCOR	1.756	10.964	0.160	0.022
C5	6.989	42.775	0.163	0.000
SPINK1	7.674	46.675	0.164	0.000
PER1	3.689	22.431	0.164	0.000
AGR2	3.506	21.156	0.166	0.001
SLC40A1	2.942	17.547	0.168	0.001
DIRAS3	3.372	19.316	0.175	0.002
NDNF	1.842	10.501	0.175	0.022
FXYD3	5.623	31.482	0.179	0.000
CRIP1	6.834	37.793	0.181	0.000
PAG1	2.691	14.391	0.187	0.008
DEFB1	7.233	38.120	0.190	0.000
CXCL17	7.094	36.759	0.193	0.000
RSPO3	2.216	11.202	0.198	0.035

(*Table S5 continued*)

PRR5L	2.356	11.644	0.202	0.035
LRRN4	2.271	11.093	0.205	0.035
CTD-3193O13.8	3.359	16.219	0.207	0.007
TMTC2	2.609	12.572	0.208	0.021
COPZ2	5.995	28.759	0.208	0.000
AQP3	46.725	220.837	0.212	0.000
GGT5	2.779	13.066	0.213	0.013
TSPAN8	4.187	19.527	0.214	0.004
LPAR1	19.769	91.580	0.216	0.000
CLDN2	5.762	26.035	0.221	0.000
SYNE1	10.605	47.493	0.223	0.000
SUSD2	7.252	32.082	0.226	0.000
IGFBP2	18.905	82.734	0.228	0.000
SLC7A2	4.849	20.945	0.232	0.003
CEA	5.647	24.087	0.234	0.001
SFTPD	2.749	11.720	0.235	0.035
NR4A1	31.531	132.936	0.237	0.000
RP11-1100L3.8	26.887	113.032	0.238	0.000
CTD-2562J17.7	11.044	46.326	0.238	0.000
DAPK1	6.570	26.883	0.244	0.001
GDF15	16.248	65.246	0.249	0.000
LTBP1	6.097	24.315	0.251	0.002
NR4A3	5.657	22.510	0.251	0.002
ABCA8	5.723	22.212	0.258	0.002
RASD1	5.775	22.380	0.258	0.002
GPCPD1	6.089	22.847	0.266	0.005
TFPI2	24.744	92.689	0.267	0.000
RP11-4K16.2	8.444	31.537	0.268	0.000
RCN3	2.991	11.114	0.269	0.035
FAM107B	27.121	100.358	0.270	0.000
AL161784.1	94.556	348.118	0.272	0.000
RP11-499O7.7	10.257	37.631	0.273	0.000
RP11-806O11.1	4.113	14.915	0.276	0.041
A2M	3.447	12.228	0.282	0.049
CFI	6.503	22.925	0.284	0.005
RNU4ATAC	9.632	33.010	0.292	0.000
ARRB1	10.261	35.160	0.292	0.000
PEG10	22.727	76.641	0.297	0.000
ITPR1	5.323	17.635	0.302	0.023

(*Table S5 continued*)

LPGAT1	62.104	199.617	0.311	0.000
SLC45A4	12.221	38.934	0.314	0.000
ZNF275	5.888	18.544	0.318	0.015
FGL1	4.736	14.871	0.318	0.041
SLC6A16	6.873	20.658	0.333	0.013
AL353354.1	246.164	723.097	0.340	0.000
CPM	87.969	258.231	0.341	0.000
GSTA4	6.561	19.153	0.343	0.019
NAPSA	24.679	71.080	0.347	0.000
APOC1	17.350	49.624	0.350	0.000
FAM69B	7.505	21.403	0.351	0.016
PDK4	19.506	55.597	0.351	0.000
CNTN1	5.809	16.389	0.354	0.035
ASS1	19.596	54.839	0.357	0.000
GALNT11	37.995	106.067	0.358	0.000
CTD-2562J17.9	24.206	66.424	0.364	0.000
ZNF189	7.936	21.621	0.367	0.016
CCND3	26.170	70.215	0.373	0.000
FOS	7.952	21.252	0.374	0.016
FKBP10	11.586	30.606	0.379	0.005
APOE	15.420	40.500	0.381	0.001
RHOBTB2	31.149	81.775	0.381	0.000
CTXN1	9.717	25.394	0.383	0.011
STAMBPL1	15.706	41.038	0.383	0.001
AKR1C2	233.297	606.520	0.385	0.000
DUSP4	24.131	60.938	0.396	0.000
Sep11	49.940	125.765	0.397	0.000
ENDOD1	10.731	26.761	0.401	0.014
EDIL3	27.967	69.116	0.405	0.000
LAMA1	7.708	19.036	0.405	0.036
MEGF9	62.134	153.112	0.406	0.000
OLFM2	15.330	37.692	0.407	0.004
MAPK4	16.892	41.430	0.408	0.002
GPX2	149.142	365.662	0.408	0.000
CD46	295.889	724.847	0.408	0.000
NAB2	10.969	26.816	0.409	0.014
RP11-304L19.5	87.330	208.535	0.419	0.000
NBEAL2	32.145	76.735	0.419	0.000
EMP2	14.283	34.066	0.419	0.007

(*Table S5 continued*)

XBP1	110.761	263.476	0.420	0.000
DKK1	43.967	102.387	0.429	0.000
GULP1	14.946	34.654	0.431	0.007
EGFL7	10.181	23.595	0.432	0.041
RP11-27M24.1	19.403	44.919	0.432	0.003
F3	56.690	130.804	0.433	0.000
STOM	25.135	57.792	0.435	0.001
AKR1C1	124.369	285.455	0.436	0.000
JUP	65.017	148.466	0.438	0.000
AGPAT2	52.204	118.962	0.439	0.000
DNAJC12	42.262	94.179	0.449	0.000
IRX3	19.344	43.011	0.450	0.004
AL591806.1	13.187	29.296	0.450	0.023
MDM2	28.941	64.070	0.452	0.000
CRIP2	13.388	29.577	0.453	0.023
CTD-3149D2.4	19.714	43.333	0.455	0.004
EPB41L5	11.930	26.184	0.456	0.024
PCSK6	11.796	25.877	0.456	0.034
CADM1	17.329	37.302	0.465	0.010
LPIN2	13.024	27.739	0.470	0.044
GNG11	23.251	49.492	0.470	0.003
RDH10	34.193	72.723	0.470	0.000
PDE4D	37.305	79.240	0.471	0.000
DPP7	28.479	58.734	0.485	0.002
IQCJ-SCHIP1	22.400	46.025	0.487	0.006
IMPA2	73.605	149.225	0.493	0.000
TEAD2	13.572	27.286	0.497	0.044
ERRFI1	92.874	186.249	0.499	0.000
EMC10	88.397	176.966	0.500	0.000
AKR1C3	89.255	177.248	0.504	0.000
SFTA3	20.505	40.426	0.507	0.015
SPTSSA	103.778	204.517	0.507	0.000
FGG	245.031	481.888	0.508	0.000
PLEKHG2	35.492	69.675	0.509	0.001
MDK	25.246	49.252	0.513	0.008
ISYNA1	17.318	33.625	0.515	0.037
FGA	132.994	257.660	0.516	0.000
PRPS2	21.377	41.301	0.518	0.017
KITLG	15.921	30.738	0.518	0.040

(*Table S5 continued*)

PFKFB3	21.095	40.620	0.519	0.023
SEMA4B	61.826	119.012	0.519	0.000
FBXW2	40.619	78.095	0.520	0.001
IFI30	24.162	46.281	0.522	0.013
TM4SF1	227.583	435.876	0.522	0.000
WDR34	34.900	66.227	0.527	0.002
RBM47	14.973	28.403	0.527	0.049
AKAP12	24.426	46.303	0.528	0.013
SLC9A3R1	21.400	40.386	0.530	0.023
IGFBP3	112.198	210.966	0.532	0.000
SLC26A2	17.314	32.488	0.533	0.049
LIMCH1	51.693	96.180	0.537	0.000
CTSL1	49.462	90.812	0.545	0.001
INO80C	21.667	39.715	0.546	0.030
ATP11A	18.818	34.202	0.550	0.040
MALL	28.477	51.684	0.551	0.014
RP11-638I2.6	33.471	60.583	0.552	0.007
CTC-273B12.8	27.066	48.783	0.555	0.022
SLC25A29	26.907	48.148	0.559	0.016
SGPP1	33.575	59.995	0.560	0.010
TP53INP2	28.309	50.421	0.561	0.018
HEATR5A	68.859	122.476	0.562	0.000
BTG1	55.059	97.920	0.562	0.001
SCD5	37.838	67.263	0.563	0.005
IDH2	38.598	68.599	0.563	0.005
HMGB3	158.178	277.969	0.569	0.000
FURIN	26.514	46.307	0.573	0.027
CRLS1	32.763	57.024	0.575	0.012
INO80E	32.124	55.760	0.576	0.019
ALDH3B1	38.755	67.195	0.577	0.007
PRRC2B	41.436	71.522	0.579	0.006
LAPTM4B	156.309	268.598	0.582	0.000
EDEM1	29.828	51.217	0.582	0.020
EPDR1	61.710	105.920	0.583	0.001
EPAS1	80.919	138.268	0.585	0.000
CD320	35.655	60.907	0.585	0.014
UGDH	139.882	238.134	0.587	0.000
CEBPD	30.012	50.888	0.590	0.035
P2RY6	25.836	43.714	0.591	0.042

(*Table S5 continued*)

CITED2	69.423	116.995	0.593	0.001
ANXA4	92.587	155.869	0.594	0.000
NOL6	31.210	52.424	0.595	0.030
HDGFRP2	29.748	49.436	0.602	0.033
B4GALNT1	30.800	51.046	0.603	0.028
TXNIP	27.967	45.530	0.614	0.048
ITGB5	46.821	75.826	0.617	0.011
SMARCA1	31.641	51.137	0.619	0.038
SMIM4	65.855	106.242	0.620	0.002
NDRG1	78.796	126.427	0.623	0.001
BSCL2	33.964	54.487	0.623	0.034
NME4	60.980	97.743	0.624	0.004
NT5DC2	48.612	77.676	0.626	0.013
GPR107	38.222	60.957	0.627	0.035
ICAM1	96.112	153.157	0.628	0.000
MUC1	53.793	85.607	0.628	0.009
RP11-78A19.3	230.881	367.308	0.629	0.000
TMEM64	36.086	57.061	0.632	0.040
BCAM	37.332	59.019	0.633	0.034
STARD10	42.079	66.432	0.633	0.028
CRABP2	31.946	50.292	0.635	0.048
ECT2	48.138	75.419	0.638	0.020
EPCAM	144.405	225.627	0.640	0.000
RP11-329L6.1	159.378	248.555	0.641	0.000
ATP6V1G1	112.074	174.143	0.644	0.000
SLC39A7	59.108	91.571	0.645	0.012
TXN	296.597	458.994	0.646	0.000
SLC6A6	95.011	146.778	0.647	0.002
CSGALNACT1	38.432	59.336	0.648	0.044
CRNDE	90.021	138.968	0.648	0.002
CMPK1	77.824	119.735	0.650	0.004
GAA	38.875	59.777	0.650	0.044
CYBA	46.944	71.981	0.652	0.028
SLPI	79.611	121.496	0.655	0.004
SLC25A36	46.278	70.593	0.656	0.034
AC002117.1	48.634	74.115	0.656	0.025
MBTPS1	52.258	79.592	0.657	0.024
RABL6	41.800	63.182	0.662	0.041
FADS1	54.396	82.028	0.663	0.021

(*Table S5 continued*)

WSB1	128.679	193.424	0.665	0.000
PGD	88.971	133.357	0.667	0.004

Note:

1. FPKM, fragment per kilobase of exon model per million mapped reads.

2. Genes are listed according to their fold changes from high to low for those with upregulation and from high to low for those with downregulation.

Table S6. Enriched process networks, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from KLF5-expressing DU 145 xenograft tumors and the PLHCX vector control. Different processes with the same function are bracketed together, ranked based on *p* value (from low to high). Genes contributing to a process are listed alphabetically.

Function	**Process**	***p* value**	**Genes**	**Number**
Protein folding	Response to unfolded proteins	1.512e-3	HSP70, HSPA1A, HSPA1B	3
	Folding in normal condition	7.077e-3	HSP70, HSPA1A, HSPA1B	3
	Protein folding nucleus	1.596e-2	HSP70, HSPA1B	2
Signal transduction	Leptin signaling	5.131e-3	A2M, T-A2MG, VEGF-A	3
Reproduction	FSH-beta signaling pathway	1.582e-2	Beta-arrestin1, CGalpha, VEGF-A	3
Proliferation	Positive regulation cell proliferation	3.668e-2	Beta-arrestin1, MDM2, VEGF-A	3
Development	Blood vessel morphogenesis	3.968e-2	F263, KLF5, VEGF-A	3
Immune response	Th17-derived cytokines	4.231e-2	Calgranulin A, Calgranulin B	2
	Phagosome in antigen presentation	4.653e-2	A2M, HSP70, SEC15L	3

Table S7. Enriched process networks, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from K369R-expressing DU 145 xenograft tumors and the PLHCX vector control. Different processes with the same function are bracketed together, ranked based on *p* value (from low to high). Genes contributing to a process are listed alphabetically.

Function	**Process**	***p* value**	**Genes**	**Number**
Development	Skeletal muscle development	1.498e-8	ACTA1, ACTA2, Alpha crystallin B, Collagen IV, Desmin, Filamin C, G-protein alpha-i2, MAP-1B, MRLC, MYH4, MYRL2, Nebulin, Smooth muscle myosin, Tropomyosin, Tropomyosin-1, Troponin C, skeletal muscle, Troponin I, fast skeletal muscle, VEGF-A	20
	EMT_ Regulation of epithelial-to-mesenchymal transition	2.172e-2	ACTA2, Actin, c-Jun, Claudin-1, Claudin-2, Desmin, FGFR1,G-protein alpha-i family, HGF receptor (Met), I-kB, LOXL2, Occludin, PAI1, Tropomyosin-1, Vimentin	15
Cell adhesion	Cell-matrix interactions	3.863e-7	ADAM9, BETA-IG-H3, CD44, COL4A1, COL4A2, Collagen XIV, Connexin 43, ECM1, Fibulin-1, Fibulin-3, Galectin-1, ITGB4, LAMA3 (Epiligrin), LAMB3, LAMC2, MMP-24, Perlecan, Tenascin-C, Thrombospondin 1, TIMP2	20
	Integrin-mediated	1.889e-5	Actin, c-Jun, Caveolin-1, Caveolin-2, Collagen IV,	21

	cell-matrix adhesion		Collagen XIV, Cyr61, Filamin C, Galectin-1, ITGB4, LAMA4, Laminin 5, MRLC, MyHC, Osteonectin, Paxillin, Tenascin-C, Tetraspanin-8, TGM2, Tubulin alpha, Zyxin	
	Cell junctions	2.503e-3	Actin, BPAG1, Caveolin-1, Claudin-1, Claudin-2, Connexin 43, Desmoglein 2, Keratin 6A, M-cadherin, Occludin, Paxillin, Plakoglobin, Tubulin alpha, Vimentin, ZO-2	15
	Platelet-endothelium-leucocyte interactions	1.168e-2	CD44, CD68, Collagen IV, Cyr61, HGF receptor (Met), I-kB, ICAM1, IL-18, Occludin, PAI1, TFPI-2, Thrombospondin 1, VEGF-A	13
Inflammation _	Innate inflammatory response	1.084e-6	Beta-defensin 1, c-Jun, C3, C5, C5 convertase (C3bBb), Factor I, G-protein alpha-i family, I-kB, IL-18, IP3 receptor, NFKBIA, PLUNC, RIPK2, SP-A, SP-B, Tissue factor	16
	Complement system	6.492e-6	C3, C5, C5 convertase (C3bBb), Factor B, Factor I, iC3b, MCP	7
	Kallikrein-kinin system	6.152e-5	A2M, Alpha 1-antitrypsin, AP-1, C3, C5, Carboxypeptidase M, Coagulation factor XIII, Fibrinogen alpha, Fibrinogen gamma, G-protein alpha-i family, G-protein gamma, I-kB,	17

			IP3 receptor, NFKBIA, PAI1, T-A2MG, Tissue factor	
	Amphoterin signaling	8.662e-3	Actin, c-Jun, Calgranulin A, I-kB, ICAM1, MRLC, MyHC, NFKBIA, PAI1	9
	IL-6 signaling	9.208e-3	A2M, Alpha 1-antitrypsin, c-Jun, C/EBP, C3, Fibrinogen alpha, Fibrinogen gamma, I-kB, TATI	9
	Protein C signaling	3.221e-2	Actin, c-Jun, G-protein alpha-i family, Galpha(i)-specific EDG GPCRs, I-kB, IP3 receptor, NFKBIA, PAI1, Tissue factor	9
Muscle contraction		1.848e-6	ACTA1, ACTA2, Alpha crystallin B, Ca-ATPase1, Connexin 43, Desmin, G-protein alpha-i family, MaxiK alpha subunit, MRLC, MYH4, MYRL2, Smooth muscle myosin, Syntrophin B, Thrombospondin 1, Tropomyosin, Tropomyosin-1, Troponin C, cardiac, Troponin C, skeletal muscle, Troponin I, fast skeletal muscle	22
	Nitric oxide signaling in the cardiovascular system	3.163e-2	c-Jun, Ca-ATPase1, Caveolin-1, EPAS1, ETS2, G-protein alpha-i family, IP3 receptor, KLF2, VEGF-A	9
Cytoskeleton	Actin filaments	2.474e-6	ACTA1, ARPC1, Band 4.1-like protein 2, BPAG1, Brush border myosin I, CD44, Filamin C, MRLC, MYH4, MYH9, Myosin I,	18

			Nebulin, Paxillin, Tropomyosin, Tropomyosin-1, Troponin I, fast skeletal muscle, Zyxin	
	Regulation of cytoskeleton rearrangement	5.267e-5	ACTA1, ARPC1, Band 4.1-like protein 2, BPAG1, CD44, Desmin, ECT2, Filamin C, G-protein alpha-i family, MRLC, MYH4, Nebulin, Paxillin, Tubulin alpha, Vimentin, Zyxin	16
	Intermediate filaments	5.560e-3	Actin, BPAG1, Desmin, Keratin 19, Keratin 6A, Nesprin 1, Tubulin alpha, Vimentin	8
Blood coagulation		1.047e-4	A2M, Alpha 1-antitrypsin, Annexin IV, Caveolin-1, Coagulation factor XIII A, Collagen IV, Fibrinogen alpha, Fibrinogen gamma, Galpha(q)-specific nucleotide-like GPCRs, PAI1, TFPI-2, Thrombospondin 1, Tissue factor	13
Proteolysis	ECM remodeling	1.579e-4	Alpha 1-antitrypsin, Antileukoproteinase 1,Collagen IV, Collagen XIV, Laminin 5, MMP-24, Osteonectin, PACE4, PAI1, Tenascin-C, TIMP2, TFPI-2	12
	Connective tissue degradation	3.303e-3	ADAM9, Alpha 1-antitrypsin, Antileukoproteinase 1, Collagen IV, Furin, Laminin 5, MMP-24, PACE4, PAI1, Tenascin-C, TFPI-2, TIMP2	12

Reproduction	FSH-beta signaling pathway	2.216e-3	BTG1, c-Jun, CG alpha, Cyclin D, FSRP, G-protein alpha-i family, IBP, IBP3, IP3 receptor, NFKBIA, PP2A structural, PP2A structural, Tob1, VEGF-A	14
	Feeding and Neurohormone signaling	2.585e-2	ADAM9,AKR1C1, Antileukoproteinase 1, c-Jun, CD44, Cyclin D3, G-protein alpha-i family, HSP27, IBP3, PAI1, Paxillin, PP2A structural, PSG2, Stathmin, VGF	15
Apoptosis	Endoplasmic reticulum stress pathway	8.839e-3	c-Jun, C/EBP zeta, HERP, I-kB, IP3R1, NOXA, NUR77, S1P, XBP1	9
Immune response	Phagocytosis	9.278e-3	Actin, APOE, c-Jun, C/EBP, C3, I-kB, iC3b, IL-15RA, IP3 receptor, MRLC, MyHC, Myosin I, NFKBIA, p22-phox, Paxillin	15
Response to hypoxia and oxidative stress		1.585e-2	AHR, AP-1, Chk2, Gamma-glutamyltranspeptidase, Glutaredoxin, GPX1, GPX2, GSTT1, HIF-prolyl hydroxylase, Oxidized thioredoxin, SP-A	11
Proliferation	Positive regulation cell proliferation	3.689e-2	Basonuclin, c-Jun, Dexras1, FGFR1, G-protein alpha-i family, HGF receptor (Met), LIF, LMO1, MRLC, TACSTD2 (TROP2), Tob1, VEGF-A	13

Table S8. Enriched process networks, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from xenografts expressing K369R and KLF5. Different processes with the same function are bracketed together, ranked based on *p* value (from low to high). Genes contributing to a process are listed alphabetically. Process highlighted by bold font means the same process enriched by comparing K369R and PLHCX.

Function	Process	*p* value	Genes	Number
Cytoskeleton	**Actin filaments**	7.134e-10	ACTA1, Alpha-actinin, ARPC1, Band 4.1-like protein 2, Beta TnTF, BPAG1, Brush border myosin I, CD44, Filamin C, MRLC, MYH4, MYH9, MyHC, Myosin I, Nebulin, Paxillin, Tropomyosin, Tropomyosin-1, Tropomyosin-2, Troponin I, fast skeletal muscle, Troponin T, cardiac, Zyxin	24
	Regulation of cytoskeleton rearrangement	8.066e-6	ACTA1, Alpha-actinin,ARPC1, Band 4.1-like protein 2, BPAG1, CD44, Desmin, ECT2, Filamin C, MRLC, MYH4, MyHC, Nebulin, Paxillin, Tubulin alpha, Vimentin, Zyxin	17
	Intermediate filaments	6.336e-5	Actin, Alpha-actinin, BPAG1, Desmin, Keratin 19, Keratin 6A, Keratin 6C, Keratin 7 ,Nesprin 1, Tubulin alpha, Vimentin	11
Cell adhesion	**Cell-matrix interactions**	4.010e-8	ADAM9, BCAM, BETA-IG-H3, CD44, COL4A1, COL4A2, Collagen XIV, ECM1, Fibulin-3, Galectin-1, ITGB4, ITGB5, LAMA1, LAMA3 (Epiligrin), LAMB3, Laminin 5 MMP-24, Perlecan, SP-D, Tenascin-C, TIMP2	21

	Integrin-mediated cell-matrix adhesion	2.084e-7	Actin, Alpha-actinin,c-Jun, Caveolin-1, Caveolin-2, Collagen IV, Collagen XIV, Cyr61, Filamin C, Galectin-1, ITGB4, ITGB5, LAMA4, Laminin 5, MRLC, MyHC, Osteonectin, Paxillin, Tenascin-C, Tetraspanin-8, TGM2, Tubulin alpha, Zyxin	23
	Cell junctions	4.284e-3	Actin, Alpha-actinin, BPAG1, Caveolin-1, Claudin-1, Claudin-2, Desmoglein 2, Keratin 6A, M-cadherin, Paxillin, Plakoglobin, Tubulin alpha, Vimentin	13
	Cadherins	4.902e-2	Actin, Alpha-actinin, BPAG1, Desmoglein 2, DKK1, FHL2, HGF receptor (Met), M-cadherin, P-cadherin, Plakoglobin, PTPRF (LAR)	11
Development	**Skeletal muscle development**	3.141e-8	ACTA1, Alpha crystallin B, Beta TnTF, Collagen IV, Desmin, Filamin C, HGF receptor (Met), MAP-1B, MRLC, MYH4, MyHC, MYRL2, Nebulin, Smooth muscle myosin, Tropomyosin, Tropomyosin-1, Tropomyosin-2, Troponin C, skeletal muscle troponin I, fast skeletal muscle troponin T	20
	EMT_ Regulation of epithelial-to-mesenchymal transition	2.993e-2	Actin, c-Jun, c-Fos,Claudin-1, Claudin-2, Desmin, FGFR1, HGF receptor (Met), LOXL2, MUC1, PAI1, Tropomyosin-1,	13

			Vimentin	
Muscle contraction		2.120e-7	ACTA1, Alpha crystallin B, Alpha-actinin, Beta TnTF, Ca-ATPase1, Calponin-3, Desmin, MRLC, MYH4, MyHC, MYRL2, nAChR beta, Smooth muscle myosin, Tropomyosin, Tropomyosin-1, Troponin C, skeletal muscle troponin I, fast skeletal muscle troponin T	18
Proteolysis	**ECM remodeling**	7.937e-7	Alpha 1-antitrypsin, Antileukoproteinase 1, Collagen IV, Collagen XIV, Laminin 5, MMP-24, MTCBP-1, Osteonectin, PACE4, PAI1, PLAU (UPA), PLAUR (uPAR),Tenascin-C, TIMP2, TFPI-2	15
	Connective tissue degradation	3.164e-6	ADAM9, Alpha 1-antitrypsin, Antileukoproteinase 1, Collagen IV, EDEM, Furin, ITGB5, Laminin 5, MMP-24, MTCBP-1, PACE4, PAI1, PLAU (UPA), PLAUR (uPAR),Tenascin-C, TFPI-2, TIMP2	17
Inflammation	**Kallikrein-kinin system**	1.024e-4	A2M, Alpha 1-antitrypsin, AP-1, c-Fos, C5, Carboxypeptidase M, Coagulation factor XIII, Fibrinogen alpha, Fibrinogen gamma, G-protein gamma, IP3 receptor, PAI1, PLAU (UPA), PLAUR (uPAR),T-A2MG, Tissue factor	16
	IL-6 signaling	1.767e-2	A2M, Alpha 1-antitrypsin,	8

			c-Fos, c-Jun, C/EBP, Fibrinogen alpha, Fibrinogen gamma, TATI	
	Amphoterin signaling	1.674e-2	Actin, c-Jun, Calgranulin B, ICAM1, MRLC, MyHC, PAI1	7
	Protein C signaling	2.496e-2	Actin, Alpha-actinin, c-Jun, Galpha(i)-specific EDG GPCRs, IP3 receptor, PAI1, PLAU (UPA),Tissue factor	8
	Innate inflammatory response	2.466e-2	Beta-defensin 1, c-Jun, C5, Factor I, HSPA1A, I-kB, IL-18, IP3 receptor, SP-B, SP-D, Tissue factor	11
Blood coagulation		1.461e-5	A2M, Alpha 1-antitrypsin, Annexin IV, Caveolin-1, Coagulation factor XIII A, Collagen IV, Fibrinogen alpha, Fibrinogen gamma, Galpha(q)-specific nucleotide-like GPCRs, PAI1, PLAU (UPA), PLAUR (uPAR), TFPI-2, Tissue factor	14
Apoptosis	**Endoplasmic reticulum stress pathway**	1.975e-3	c-Jun, C/EBP zeta, EDEM, HERP, IP3R1, NOXA, NUR77, S1P, XBP1	9
Reproduction	**Feeding and Neurohormone signaling**	1.461e-3	ADAM9, AKR1C1, Antileukoproteinase 1, c-Fos, c-Jun, CD44, Cyclin D3, HSP27, HSP70, IBP3, IL-11, Lyn, MGF, MUC1, PAI1, Paxillin, PSG2, VGF	18
	FSH-beta signaling pathway	2.247e-2	Beta-arrestin1, BTG1, c-Fos, c-Jun, CG alpha, Cyclin D, FSRP, IBP, IBP3, IP3 receptor, TGM2	11
	Gonadotropin regulation	2.364e-2	AKR1C3, AP-1, Beta-arrestin1, c-Fos, c-Jun, CG alpha, Ionotropic glutamate	12

			receptor, IP3 receptor, MAP-1B, MKP-2, NUR77, PER1	
Protein folding	Response to unfolded proteins	1.349e-3	EDEM, HERP, HSP105, HSP27, HSP40, HSP70, XBP1	7
Immune response	**Phagocytosis**	1.310e-2	Actin, Alpha-actinin,APOE, c-Fos, c-Jun, C/EBP, IL-15RA, IP3 receptor, Lyn, MRLC, MyHC, Myosin I, p22-phox, Paxillin	14

Table S9. Significant pathway maps, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from xenografts expressing KLF5 and PLHCX. All maps with *p* value less than 0.01 are shown, and ranked by *p* value from low to high.

Maps	***p* value**	**Genes**	**Number**
Role of ZNF202 in regulation of expression of genes involved in atherosclerosis	6.887E-04	VEGF-A, CRABP2	2
Development_Angiotensin signaling via beta-Arrestin	9.795E-04	MDM2, Beta-arrestin 1	2
Transcription_Role of Akt in hypoxia induced HIF1 activation	1.143E-03	VEGF-A, HSP70	2
Transcription_Role of AP-1 in regulation of cellular metabolism	2.262E-03	FXYD2, CG alpha	2
Transcription_P53 signaling pathway	2.382E-03	VEGF-A, MDM2	2
Tissue Factor signaling in cancer via PAR1 and PAR2	3.739E-03	VEGF-A, Beta-arrestin 1	2
IL-6 signaling in multiple myeloma	4.045E-03	VEGF-A, MDM2	2
PGE2 pathways in cancer	4.690E-03	VEGF-A, Beta-arrestin 1	2
Neuroprotective action of lithium	6.114E-03	VEGF-A, HSP70	2
Fructose metabolism	8.136E-03	F263, ALDR	2

Table S10. Significant pathway maps, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from K369R-expressing DU 145 xenograft tumors and the PLHCX vector control. All maps with *p* value less than 0.01 are shown, and ranked by *p* value from low to high.

Maps	***p* value**	**Genes**	**Number**
Immune response_Alternative complement pathway	1.102E-14	C5, C3, C5 convertase (C3bBb), Factor I, MCP, iC3b, Factor B	7
Immune response_Lectin induced complement pathway	2.794E-08	C5, C3, Factor I, MCP, iC3b	5
Immune response_Classical complement pathway	5.416E-08	C5, C3, Factor I, MCP, iC3b	5
Cell adhesion_Chemokines and adhesion	1.316E-06	CD44, Caveolin-2, Thrombospondin 1, VEGF-A, Actin, LAMA4, PAI1, G-protein alpha-i family, Zyxin, Paxillin, c-Jun, Caveolin-1, Collagen IV	13
Stimulation of TGF-beta signaling in lung cancer	2.671E-06	Furin, I-kB, ACTA2, Vimentin, VEGF-A, Tropomyosin-1, Keratin 19, PAI1, Tropomyosin-2	9
Development_Regulation of epithelial-to-mesenchymal transition (EMT)	3.080E-05	Occludin, HGF receptor (Met), ACTA2, Vimentin, Claudin-1, Tropomyosin-1, PAI1, FGFR1, c-Jun	9
Muscle contraction_Regulation of eNOS activity in endothelial cells	3.497E-05	EPAS1, ETS2, VEGF-A, G-protein alpha-i family, KLF2, c-Jun, IP3 receptor, Caveolin-1	8
Cell adhesion_Cadherin-mediated cell adhesion	3.790E-05	PTPRF (LAR), HGF receptor (Met), M-cadherin, Actin, P-cadherin, Plakoglobin	6
Cell adhesion_Endothelial cell contacts by junctional mechanisms	3.790E-05	Occludin, Vimentin, Claudin-1, Connexin 43, Plakoglobin, ZO-2	6
Cell adhesion_ECM remodeling	4.411E-05	IBP4, CD44, TIMP2,	8

		Laminin 5, Osteonectin, LAMA4, PAI1, Collagen IV	
Blood coagulation_Blood coagulation	4.798E-05	Tissue factor, Alpha 1-antitrypsin, A2M, Coagulation factor XIII A, Fibrinogen gamma, PAI1, Fibrinogen alpha	7
Immune response_HMGB1/RAGE signaling pathway	5.083E-05	Tissue factor, ICAM1, I-kB, Chromogranin A, PAI1, Paxillin, c-Jun	7
Immune response_CCL2 signaling	5.838E-05	ICAM1, Occludin, VEGF-A, G-protein alpha-i family, c-Jun, ZO-2, Caveolin-1	7
Cell adhesion_Gap junctions	8.977E-05	Occludin, Actin, Tubulin alpha, Connexin 43, ZO-2, Caveolin-1	6
Development_TGF-beta-dependent induction of EMT via RhoA, PI3K and ILK.	1.436E-04	Occludin, I-kB, ACTA2, Vimentin, Claudin-1, Actin, Tropomyosin-1	7
Role of Tissue factor-induced Thrombin signaling in cancerogenesis	2.480E-04	Tissue factor, VEGF-A, G-protein alpha-i family, MRLC, Paxillin, c-Jun, IP3 receptor, Fibrinogen alpha	8
Cytoskeleton remodeling_Keratin filaments	2.592E-04	Vimentin, Keratin 6A, BPAG1, Keratin 19, Tubulin alpha	5
Cell adhesion_Tight junctions	2.592E-04	Claudin-2, Occludin, Claudin-1, Actin, ZO-2, Caveolin-1	6
Cell adhesion_Cell-matrix glycoconjugates	3.522E-04	CD44, TIMP2, CEACAM5, Tenascin-C, ECM1, Fibulin-1	6
Development_WNT signaling pathway. Part 2	3.555E-04	CD44, Vimentin, VEGF-A, Claudin-1, WIF1, c-Jun, DKK1	7
Apoptosis and survival_Endoplasmic reticulum stress response pathway	4.484E-04	IP3R1, I-kB, XBP1, S1P, C/EBP zeta, c-Jun, HERP	7
Regulation of Tissue factor signaling	6.996E-04	Tissue factor, EPAS1,	4

in cancer		VEGF-A, c-Jun	
Immune response_IL-1 signaling pathway	7.932E-04	Tissue factor, I-kB, PAI1, c-Jun	4
Immune response_MIF-induced cell adhesion, migration and angiogenesis	1.009E-03	ICAM1, CD44, VEGF-A, G-protein alpha-i family, c-Jun	5
Cytoskeleton remodeling_Cytoskeleton remodeling	1.112E-03	MyHC, VEGF-A, PAI1, Zyxin, MRLC, Paxillin, c-Jun, Caveolin-1, Collagen IV	9
Development_TGF-beta-dependent induction of EMT via MAPK	1.132E-03	Occludin, Vimentin, Claudin-1, PAI1, c-Jun	5
Immune response_Histamine H1 receptor signaling in immune response	1.267E-03	Tissue factor, ICAM1, I-kB, c-Jun, IP3 receptor	5
Cytoskeleton remodeling_Role of Activin A in cytoskeleton remodeling	1.428E-03	ACTA2, FTase-alpha, Paxillin, c-Jun	4
Oxidative stress_Role of ASK1 under oxidative stress	1.546E-03	Oxidized thioredoxin, Thioredoxin, Glutaredoxin, Stathmin, GPX1	5
Immune response_C5a signaling	1.573E-03	I-kB, PAI1, G-protein alpha-i family, C5a, c-Jun	5
Cytoskeleton remodeling_TGF, WNT and cytoskeletal remodeling	2.014E-03	VEGF-A, WIF1, Actin, PAI1, MRLC, Paxillin, c-Jun, Caveolin-1, Collagen IV	9
Expression targets of Tissue factor signaling in cancer	2.072E-03	Tissue factor, GFPT2, PAI1, Cyr61	4
Immune response_MIF-mediated glucocorticoid regulation	2.072E-03	ICAM1, I-kB, c-Jun	3
Reproduction_GnRH signaling	2.261E-03	MKP-2,PER1, CG alpha, c-Jun, IP3 receptor, NUR77	6
Transcription_Role of AP-1 in regulation of cellular metabolism	2.568E-03	ITGB4, FXYD2, CG alpha, c-Jun	4
Cytoskeleton remodeling_Neurofilaments	3.376E-03	Desmin, Vimentin, BPAG1, Tubulin alpha	4
Development_Cross-talk between VEGF and Angiopoietin 1 signaling pathways	3.911E-03	ICAM1, I-kB, VEGF-A, IP3 receptor	4

Muscle contraction_Delta-type opioid receptor in smooth muscle contraction	3.911E-03	G-protein alpha-i family, MRLC, MYRL2, IP3 receptor	4
Apoptosis and survival_Inhibition of ROS-induced apoptosis by 17beta-estradiol	4.913E-03	Oxidized thioredoxin, Thioredoxin, p22-phox, I-kB, GPX1	5
Role of alpha-6/beta-4 integrins in carcinoma progression	5.415E-03	ITGB4, HGF receptor (Met), Laminin 5, VEGF-A, IP3 receptor	5
Development_Role of IL-8 in angiogenesis	5.968E-03	I-kB, VEGF-A, S1P, G-protein alpha-i family, Paxillin, Caveolin-1	6
Development_Transcription factors in segregation of hepatocytic lineage	6.624E-03	Alpha 1-antitrypsin, HGF receptor (Met), A2M, Keratin 19	4
Muscle contraction_Relaxin signaling pathway	7.137E-03	I-kB, VEGF-A, G-protein alpha-i family, PDE4D	4
Cell adhesion_Integrin-mediated cell adhesion and migration	7.137E-03	MyHC, Zyxin, MRLC, Paxillin, Collagen IV	5
Cytoskeleton remodeling_Reverse signaling by ephrin B	7.456E-03	RGS3, G-protein alpha-i family, Tubulin alpha, Paxillin	4
DNA damage_ATM/ATR regulation of G1/S checkpoint	8.355E-03	GADD45 alpha, Chk2, I-kB, Cyclin D	4
Multiple myeloma (general schema)	9.965E-03	VEGF-A, Cyclin D3, DKK1	3

Table S11. Significant pathway maps, as analyzed by MetaCore with differentially expressed genes identified in RNA-Seq from K369R- and KLF5-expressing DU 145 xenograft tumors. All maps with *p* value less than 0.01 are shown, and ranked by *p* value from low to high.

Maps	***p* Value**	**Genes**	**Number**
Cell adhesion_Chemokines and adhesion	7.236E-08	CD44, Caveolin-2, PLAUR (uPAR), Actin, Alpha-actinin, LAMA4, PAI1, Zyxin, PLAU (UPA), Paxillin, c-Jun, Alpha-actinin 1, Caveolin-1, Collagen IV	14
Blood coagulation_Blood coagulation	2.606E-06	Tissue factor, Alpha 1-antitrypsin, A2M, Coagulation factor XIII A, Fibrinogen gamma, PAI1, PLAU (UPA), Fibrinogen alpha	8
Cell adhesion_ECM remodeling	2.738E-06	CD44, TIMP2, Laminin 5, PLAUR (uPAR), Osteonectin, LAMA4, PAI1, PLAU (UPA), Collagen IV	9
Cytoskeleton remodeling_Cytoskeleton remodeling	4.209E-06	PLAUR (uPAR), MyHC, Alpha-actinin, PAI1, Zyxin, PLAU (UPA), MRLC, Paxillin, c-Jun, Alpha-actinin 1, Caveolin-1, Collagen IV	12
Expression targets of Tissue factor signaling in cancer	8.367E-06	Tissue factor, GFPT2, PLAUR (uPAR), PAI1, PLAU (UPA), Cyr61	6
Cytoskeleton remodeling_TGF, WNT and cytoskeletal remodeling	1.021E-05	PLAUR (uPAR), Actin, Alpha-actinin, PAI1, PLAU (UPA), MRLC, Paxillin, c-Jun, Alpha-actinin 1, MDM2, Caveolin-1, Collagen IV	12
Cytoskeleton remodeling_Keratin filaments	1.636E-05	Vimentin, Keratin 6C, Keratin 7, BPAG1, Keratin 19, Tubulin alpha	6
Transcription_Role of AP-1 in regulation of cellular	2.377E-05	ITGB4, PLAUR (uPAR), c-Jun, c-Fos, CG alpha,	6

metabolism		AP-1	
Cell adhesion_Cadherin-mediated cell adhesion	2.387E-05	PTPRF (LAR), HGF receptor (Met), M-cadherin, Actin, P-cadherin, Plakoglobin	6
Apoptosis and survival_Endoplasmic reticulum stress response pathway	3.738E-05	IP3R1, c-Jun/c-Fos, XBP1, S1P, C/EBP zeta, EDEM, HERP	7
Reproduction_GnRH signaling	4.224E-05	MKP-2, c-Jun, PER1, CG alpha, IP3 receptor, NUR77, c-Fos	7
Development_TGF-beta-dependent induction of EMT via MAPK	9.908E-05	Vimentin, Claudin-1, PAI1, c-Jun, c-Fos	5
Cell adhesion_Cell-matrix glycoconjugates	2.264E-04	CD44, TIMP2, CEACAM5, Tenascin-C, ECM1, MUC1	6
Immune response_Human NKG2D signaling	2.264E-04	MICB, c-Jun, IP3 receptor, c-Fos	4
Development_Transcription factors in segregation of hepatocytic lineage	5.932E-04	Alpha 1-antitrypsin, HGF receptor (Met), A2M, Keratin 7, Keratin 19	5
Immune response_MIF-induced cell adhesion, migration and angiogenesis	6.576E-04	ICAM1, CD44, c-Jun, c-Fos	4
Development_Regulation of epithelial-to-mesenchymal transition (EMT)	6.993E-04	HGF receptor (Met), Vimentin, Claudin-1, Tropomyosin-1, PAI1, FGFR1, c-Jun	7
Stimulation of TGF-beta signaling in lung cancer	8.287E-04	Furin, Vimentin, Tropomyosin-1, Keratin 19, PAI1, Tropomyosin-2	6
Immune response_Histamine H1 receptor signaling in immune response	8.287E-04	Tissue factor, ICAM1, c-Jun, IP3 receptor, c-Fos	5
Cell adhesion_Integrin-mediated cell adhesion and migration	8.287E-04	MyHC, Alpha-actinin, Zyxin, MRLC, Paxillin, Collagen IV	6
Immune response_C5a signaling	1.032E-03	PAI1, C5a, c-Jun, c-Fos	4
Development_WNT signaling pathway. Part 2	1.407E-03	CD44, Vimentin, Claudin-1, ENC1, c-Jun,	6

		DKK1	
Immune response_HMGB1/RAGE signaling pathway	1.407E-03	Tissue factor, ICAM1, Chromogranin A, PAI1, Paxillin, c-Jun	6
Immune response_CCL2 signaling	1.553E-03	ICAM1, c-Jun, c-Fos, Caveolin-1	4
Immune response_Alternative complement pathway	2.020E-03	C5, Factor I, MCP	3
CFTR folding and maturation (normal and CF)	2.148E-03	HSP70, HSP40, HSP105, EDEM	4
Cytoskeleton remodeling_Neurofilaments	2.511E-03	Desmin, Vimentin, BPAG1, Tubulin alpha	4
Immune response_IL-18 signaling	2.680E-03	IL-18, ICAM1, c-Jun, c-Fos	4
Immune response_Murine NKG2D signaling	2.821E-03	c-Jun, IP3 receptor, c-Fos	3
Cell cycle_Regulation of G1/S transition (part 2)	2.913E-03	Cyclin D3, c-Jun, Cyclin D, c-Fos	4
Cell adhesion_Endothelial cell contacts by junctional mechanisms	2.913E-03	Vimentin, Claudin-1, Alpha-actinin, Plakoglobin	4
Regulation of Tissue factor signaling in cancer	3.132E-03	Tissue factor, EPAS1, c-Jun	3
Development_VEGF signaling via VEGFR2 - generic cascades	3.441E-03	PLAUR (uPAR), c-Jun/c-Fos, HSP27, PLAU (UPA), Paxillin, c-Jun, IP3 receptor	7
Immune response_IL-1 signaling pathway	3.468E-03	Tissue factor, PAI1, c-Jun, c-Fos	4
Development_Ligand-dependent activation of the ESR1/AP-1 pathway	3.806E-03	c-Jun, c-Fos	2
Development_EPO-induced MAPK pathway	3.828E-03	MGF, Lyn, c-Jun, IP3 receptor, c-Fos	5
Muscle contraction_Regulation of eNOS activity in endothelial cells	4.015E-03	EPAS1, ETS2, c-Jun, IP3 receptor, Caveolin-1	5
Immune response_IL-5 signalling	4.215E-03	ICAM1, Lyn, Cyclin D3, c-Jun, c-Fos	5
Role of Tissue factor-induced Thrombin signaling in cancerogenesis	4.332E-03	Tissue factor, MRLC, Paxillin, c-Jun, IP3 receptor, Fibrinogen alpha	6
Immune response_Lectin	5.541E-03	C5, Factor I, MCP	3

induced complement pathway			
Immune response_ETV3 affect on CSF1-promoted macrophage differentiation	5.598E-03	ETS2, PLAU (UPA), c-Jun, c-Fos	4
Inhibition of neutrophil migration by proresolving lipid mediators in COPD	5.788E-03	ICAM1, c-Fos, Alpha-actinin, C5a, c-Jun, IP3 receptor	6
Immune response_Classical complement pathway	7.139E-03	C5, Factor I, MCP	3
Oxidative stress_Role of ASK1 under oxidative stress	7.813E-03	Oxidized thioredoxin, HSP70, Thioredoxin, GPX1	4
Development_Role of proteases in hematopoietic stem cell mobilization	7.964E-03	CD44, MGF, Carboxypeptidase M	3
Immune response_HSP60 and HSP70/ TLR signaling pathway	8.366E-03	ICAM1, HSP70, c-Fos, c-Jun	4
Androstenedione and testosterone biosynthesis and metabolism p.2	8.662E-03	AKR1C2, AKR1C1, AKR1C3, AKR1C4	4
Cell adhesion_Plasmin signaling	8.662E-03	TFPI-2, PLAU (UPA), FGFR1, Collagen IV	4
HBV signaling via protein kinases leading to HCC	9.570E-03	c-Jun, c-Fos	2
Androstenedione and testosterone biosynthesis and metabolism p.2/ Rodent version	9.570E-03	AKR1C2, AKR1C1, AKR1C3, AKR1C4	4

Table S12. Molecular networks and related biological processes identified by MetaCore's network analysis algorithm with differentially expressed genes between KLF5 and the PLHCX vector control. Networks are ranked by their *p* values. Total nodes refer to all nodes in a network, and seed nodes refer to differentially expressed genes between the two groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	Calgranulin A, HSPA1A, A2M, KLF5, AML1 (RUNX1)	response to organic substance (88.0%; 8.309e-15), positive regulation of progesterone secretion (20.0%; 1.238e-14), positive regulation of myeloid cell differentiation (36.0%; 1.873e-14), regulation of hair follicle cell proliferation (20.0%; 4.331e-14), regulation of progesterone secretion (20.0%; 4.331e-14)	50	9	0	1.080E-18	49.7	49.7
2	HLA-F, FTase-alpha, CEACAM5, HSPA1B, AK3	gamma-aminobutyric acid signaling pathway (35.4%; 2.434e-32), synaptic transmission, GABAergic (29.2%; 6.390e-29), chloride transport (35.4%; 1.835e-26), inorganic anion transport (35.4%; 1.469e-24), innervation (25.0%; 6.699e-23)	50	7	0	6.670E-15	36.53	36.53
3	ALDR, Calgranulin B, KLF5, CRABP2, Calgranulin A	response to organic substance (78.8%; 5.645e-15), regulation of mismatch repair (15.2%; 9.228e-15), canonical Wnt receptor signaling pathway (27.3%; 1.981e-13), regulation of signal transduction (66.7%; 2.518e-12), cellular response to stimulus (93.9%; 3.777e-12)	50	6	0	3.180E-13	35.68	35.68
4	microRNA 663, FXYD2, VEGF-A, Beta-arrestin1, PKC-delta	positive regulation of cellular metabolic process (83.0%; 4.347e-27), regulation of immune system process (70.2%; 8.627e-27), Fc-epsilon receptor signaling pathway (42.6%; 2.405e-26), positive regulation of metabolic process (83.0%; 4.610e-26), Fc receptor signaling pathway (44.7%; 9.352e-26)	50	4	0	6.560E-08	20.37	20.37

Table S13. Molecular networks and related biological processes identified by MetaCore's network analysis algorithm with differentially expressed genes between K369R and the PLHCX vector control. Networks are ranked by their *p* values. Total nodes refer to all nodes in a network, and seed nodes refer to differentially expressed genes between the two groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	Factor B, NFKBIA, p22-phox, TC1, ST5	superoxide anion generation (17.4%; 3.232e-17), smooth muscle hypertrophy (13.0%; 1.101e-16), negative regulation of renal output by angiotensin (13.0%; 1.101e-16), negative regulation of glomerular filtration by angiotensin (13.0%; 1.101e-16), hydrogen peroxide biosynthetic process (15.2%; 3.766e-16)	50	20	2	1.050E-25	28.12	30.62
2	c-Jun, EDIL3, PHLDA3, Brush border myosin I, CD70(TNFSF7)	G-protein coupled purinergic receptor signaling pathway (20.5%; 1.632e-18), G-protein coupled purinergic nucleotide receptor signaling pathway (18.2%; 3.760e-18), purinergic receptor signaling pathway (20.5%; 2.705e-17), purinergic nucleotide receptor signaling pathway (18.2%; 2.121e-16), phospholipase C-activating G-protein coupled receptor signaling pathway (25.0%; 3.898e-16)	50	17	1	1.220E-21	24.36	25.61
3	Trp53inp2, CHMP1B, RNF141, FAM62A, C4orf34	cAMP metabolic process (21.7%; 1.198e-17), cyclic nucleotide metabolic process (21.7%; 3.799e-15), cAMP catabolic process (15.2%; 1.681e-14), cyclic nucleotide catabolic process (15.2%; 3.686e-14), purine ribonucleotide metabolic process (37.0%; 2.561e-13)	50	13	0	2.400E-16	19.45	19.45
4	tRNA, NAB2, BPAG1, LAMB3, UBE2F	MAPK cascade (20.7%; 2.427e-06), intracellular protein kinase cascade (24.1%; 7.769e-06), SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (10.3%; 8.951e-06), regulation of appetite (10.3%; 9.974e-06), phospholipase D-activating G-protein coupled receptor signaling pathway (6.9%; 1.233e-05)	50	13	0	6.020E-16	20	20
5	MYRL2, RRAD, Tob1, BAIAP2, NAB2	regulation of system process (38.0%; 4.629e-14), regulation of multicellular organismal process (60.0%; 6.531e-14), cell surface receptor signaling pathway (68.0%; 8.898e-14), smooth muscle contraction (18.0%; 5.432e-13), phospholipase C-activating G-protein coupled acetylcholine receptor signaling pathway (10.0%; 1.723e-12)	50	12	0	1.310E-14	17.71	17.71
6	AP1S1A, Tmem205, ABCA2, WSB1, LETM2	regulation of defense response to virus by virus (19.6%; 4.442e-16), intracellular protein transport (37.0%; 4.670e-13), regulation of response to biotic stimulus (21.7%; 1.177e-12), regulation of defense response to virus (19.6%; 1.787e-12), post-Golgi vesicle-mediated transport (19.6%; 2.327e-12)	50	12	0	4.770E-13	16.18	16.18
7	Slc35f3, SLC25A37, CAT-3, CENTG3, Clathrin light chain B	glucose transport (22.4%; 8.759e-17), hexose transport (22.4%; 1.006e-16), monosaccharide transport (22.4%; 1.321e-16), mitotic nuclear envelope disassembly (18.4%; 6.532e-16), nuclear envelope disassembly (18.4%; 1.035e-15)	50	11	0	6.070E-13	16	16
8	CHP1, RNMT, DTX2, PHP14, ARPC1B	proton transport (40.0%; 4.025e-33), hydrogen transport (40.0%; 5.983e-33), mitochondrial ATP synthesis coupled proton transport (22.0%; 1.305e-24), energy coupled proton transport, down electrochemical gradient (24.0%; 2.117e-24), ATP synthesis coupled proton transport (24.0%; 2.117e-24)	50	10	0	7.860E-12	15.16	15.16
9	CORO6, FMNL3, ST4S6, RhoD, OLFM2	energy coupled proton transport, down electrochemical gradient (18.8%; 2.462e-17), ATP synthesis coupled proton transport (18.8%; 2.462e-17), mitochondrial ATP synthesis coupled proton transport (16.7%; 7.768e-17), ATP biosynthetic process (18.8%; 8.851e-15), synaptic transmission (39.6%; 1.743e-14)	50	10	0	7.860E-12	15.16	15.16
10	SLC22A3, EGFL7, PYGL, CD68, S1P	regulation of protein complex assembly (38.2%; 4.918e-16), regulation of actin filament polymerization (26.5%; 4.591e-13), immune response-regulating cell surface receptor signaling pathway involved in phagocytosis (26.5%; 8.172e-13), Fc-gamma receptor signaling pathway involved in phagocytosis (26.5%; 8.172e-13), Fc-gamma receptor signaling pathway (26.5%; 8.760e-13)	55	10	3	1.240E-11	14.81	18.56
11	PABPC1, LOXL3, RhoC, FTase-alpha, NPR3	cyclic nucleotide catabolic process (20.4%; 1.984e-21), cAMP catabolic process (18.4%; 2.561e-19), cAMP metabolic process (18.4%; 2.971e-15), cyclic nucleotide metabolic process (20.4%; 7.580e-15), cGMP catabolic process (12.2%; 1.373e-14)	50	11	0	1.240E-11	14.81	14.81

12	MYO1E, UAP1, FKBP10, Band 4.1-like protein 2, ATP11A	cellular response to glucagon stimulus (38.8%; 4.129e-36), response to glucagon stimulus (38.8%; 4.095e-34), energy reserve metabolic process (44.9%; 1.383e-30), energy derivation by oxidation of organic compounds (44.9%; 2.200e-24), generation of precursor metabolites and energy (44.9%; 1.385e-22)	50	10	0	1.240E-11	14.81	14.81
13	GALNT2, IMPA2, NPM3, MA2A1, DNAJC12	viral transcription (28.6%; 3.180e-22), translational termination (28.6%; 7.132e-22), viral gene expression (28.6%; 2.051e-21), protein targeting to membrane (32.7%; 2.483e-21), nuclear-transcribed mRNA catabolic process (32.7%; 1.526e-20)	50	10	0	1.550E-11	14.65	14.65
14	MICB, NDPK D (mitochondrial), AKR1C1, FACVL1, Calgizzarin	viral transcription (18.2%; 7.346e-09), translational termination (18.2%; 1.019e-08), viral gene expression (18.2%; 1.567e-08), symbiosis, encompassing mutualism through parasitism (36.4%; 1.570e-08), interspecies interaction between organisms (36.4%; 1.570e-08)	50	9	0	1.980E-10	13.74	13.74
15	ICA69, NTPBP, PREI4, Zizimin 1, SBDS	signal peptide processing (14.3%; 1.286e-14), regulation of secretion (35.7%; 1.069e-11), regulation of cellular localization (40.5%; 2.785e-11), regulation of hormone secretion (26.2%; 4.860e-11), single-organism transport (61.9%; 5.705e-11)	50	9	0	2.990E-10	13.42	13.42
16	BNaC1 (ASIC2), CLF-1, Stomatin, HERP, 6PGD	muscle contraction (30.2%; 1.984e-14), muscle organ development (32.6%; 4.546e-14), muscle filament sliding (18.6%; 1.024e-13), actin-myosin filament sliding (18.6%; 1.217e-13), actin filament-based movement (20.9%; 1.563e-13)	50	9	0	2.990E-10	13.42	13.42
17	FUS, PMCA4, M-cadherin, GRAIL, Rab-32	cell-cell signaling (43.5%; 7.407e-13), signaling (82.6%; 1.067e-12), single organism signaling (82.6%; 1.067e-12), regulation of signaling (60.9%; 2.157e-12), cell communication (82.6%; 2.611e-12)	50	10	0	2.990E-10	13.42	13.42
18	PHI-1, TSSC3, H41, SAHH2, PLEKHG4	cell-cell recognition (14.6%; 2.942e-10), canonical Wnt receptor signaling pathway (16.7%; 3.297e-10), binding of sperm to zona pellucida (12.5%; 1.640e-09), cell recognition (16.7%; 1.757e-09), cell-cell signaling (35.4%; 1.834e-09)	50	9	0	4.440E-10	13.12	13.12
19	KPR2, ZIP7 (SLC39A7), TMED3, TRL1, NOL6	SRP-dependent cotranslational protein targeting to membrane (36.4%; 2.640e-25), cotranslational protein targeting to membrane (36.4%; 3.519e-25),viral transcription (34.1%; 4.241e-25), protein targeting to ER (36.4%; 4.666e-25), establishment of protein localization to endoplasmic reticulum (36.4%; 5.363e-25)	50	8	0	9.440E-09	11.72	11.72
20	IP-30, Zyxin, CLIC4, TIMP2, HIG 2	cell-cell signaling (53.1%; 4.716e-19), cell surface receptor signaling pathway (75.5%; 2.677e-17), protein kinase C-activating G-protein coupled receptor signaling pathway (20.4%; 5.659e-17), positive regulation of protein transport (28.6%; 1.170e-15), phospholipase C-activating G-protein coupled receptor signaling pathway (22.4%; 1.449e-15)	50	9	2	1.120E-08	11.59	14.09
21	HIF-prolyl hydroxylase, TOP2, LTBP1, VAMP2, PAG	phosphatidylinositol-mediated signaling (27.3%; 9.287e-12), inositol lipid-mediated signaling (27.3%; 9.771e-12), epidermal growth factor receptor signaling pathway (27.3%; 1.049e-10), ERBB signaling pathway (27.3%; 1.090e-10), fibroblast growth factor receptor signaling pathway (24.2%; 1.114e-09)	50	7	0	6.810E-08	11.11	11.11
22	Factor I, MCP, C3b, Clathrin light chain, BCoR	response to growth factor stimulus (54.8%; 6.250e-22), cellular response to growth factor stimulus (52.4%; 5.175e-21), response to organic substance (81.0%; 6.843e-20), cellular response to organic substance (71.4%; 1.405e-19), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (35.7%; 2.497e-19)	50	7	0	2.110E-07	10.17	10.17
23	Paxillin, VEGF-A, c-Jun, FGFR1, IP3 receptor	enzyme linked receptor protein signaling pathway (72.9%; 1.189e-35), Fc*receptor signaling pathway* (54.2%; 1.604e-34), regulation of immune system process (79.2%; 4.938e-34), response to growth factor stimulus (66.7%; 5.379e-34), cellular response to growth factor stimulus (64.6%; 4.245e-33)	57	7	10	5.530E-07	9.42	21.92
24	MYO1C, FHOD1, DIPA, CREB1, APOA4	regulation of translational initiation in response to stress (17.1%; 1.596e-15), negative regulation of translational initiation in response to stress (14.3%; 7.563e-14), regulation of translation in response to stress (17.1%; 9.439e-14), translational initiation (28.6%; 1.340e-13), regulation of translational initiation (22.9%; 1.281e-12)	50	6	0	1.340E-06	9.57	9.57
25	Slc39a14 (Zip14), SLC46A3, LBH, ZNF189, ATP6V1G1	divalent metal ion transport (34.0%; 2.831e-18), divalent inorganic cation transport (34.0%; 3.928e-18), calcium ion transmembrane transport (27.7%; 1.208e-17), calcium ion transport (31.9%; 2.928e-17), metal ion transport (40.4%; 3.016e-16)	50	7	0	2.080E-06	9.19	9.19

26	ERK4, FBXW2, DNAJB2, MTCH1, G-protein alpha-i family	energy reserve metabolic process (29.2%; 1.020e-16), cellular response to glucagon stimulus (20.8%; 3.439e-16), response to glucagon stimulus (20.8%; 3.187e-15), calcium ion transmembrane transport (22.9%; 4.146e-14), energy derivation by oxidation of organic compounds (29.2%; 6.793e-13)	52	5	2	5.260E-05	7.26	9.76
27	WIF1, Semaphorin 7A, PMEPA1, RGC32, CREB1	serotonin receptor signaling pathway (22.4%; 1.018e-24), cell-cell signaling (59.2%; 6.148e-23), synaptic transmission (51.0%; 5.144e-22), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (34.7%; 1.697e-21), adenylate cyclase-modulating G-protein coupled receptor signaling pathway (32.7%; 6.601e-21)	50	5	0	7.160E-05	6.99	6.99
28	Tropomyosin, Troponin I, fast skeletal muscle, SCAMP1, FADS1, CREB1	synaptic transmission, cholinergic (24.4%; 8.748e-21), behavioral response to nicotine (17.8%; 1.549e-17), muscle contraction (33.3%; 3.473e-17), muscle system process (33.3%; 6.302e-16), synaptic transmission (42.2%; 4.144e-15)	50	4	0	5.080E-04	6	6
29	G-protein alpha-i family, DKK1, CEACAM5, WIF1, c-Myc	Wnt receptor signaling pathway (37.5%; 4.339e-21), canonical Wnt receptor signaling pathway (29.2%; 9.792e-21), viral transcription (27.1%; 2.339e-20), translational termination (27.1%; 4.927e-20), viral gene expression (27.1%; 1.305e-19)	50	4	34	9.900E-04	5.39	47.89

Table S14. Molecular networks and related biological processes identified by MetaCore's network analysis algorithm with differentially expressed genes between K369R and KLF5. Networks are ranked by their *p* values. Total nodes refer to all nodes in a network, and seed nodes refer to differentially expressed genes between the two groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	Keratin 7, 6PGD, PLOD2, MIG6, TANC2	regulation of translational initiation in response to stress (12.2%; 1.373e-14), negative regulation of translational initiation in response to stress (10.2%; 4.440e-13), regulation of translation in response to stress (12.2%; 8.087e-13), translational initiation (20.4%; 5.448e-12), negative regulation of translation in response to stress (10.2%; 9.273e-12)	50	28	2	1.450E-45	43.27	45.77
2	FXYD3, Fibrinogen gamma, AKR1C3, Tropomyosin-2, TM4SF1 (TAAL6)	muscle contraction (21.4%; 6.505e-09), muscle system process (21.4%; 3.497e-08), muscle filament sliding (11.9%; 5.890e-08), actin-myosin filament sliding (11.9%; 6.534e-08), regeneration (19.0%; 7.006e-08)	50	26	0	3.390E-42	41.44	41.44
3	PGD2R, Basonuclin, ITGB5, CEACAM6, TFPI-2	single-multicellular organism process (88.4%; 1.269e-11), developmental process (79.1%; 3.659e-11), multicellular organismal process (88.4%; 4.817e-11), multicellular organismal development (74.4%; 1.296e-10), cellular response to chemical stimulus (55.8%; 1.393e-10)	52	24	5	5.150E-37	37	43.25
4	AP1S1A, LOXL3, Tmem64, FADS1, MALL	regulation of dopamine metabolic process (18.0%; 2.412e-18), regulation of catecholamine metabolic process (18.0%; 3.761e-18), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (26.0%; 7.375e-15), fear response (18.0%; 1.561e-14), behavioral fear response (16.0%; 5.264e-13)	50	23	0	1.870E-33	34.59	34.59
5	IL-18, CG alpha, Hrs, Pitx1, ACTA1	anatomical structure development (77.1%; 4.041e-13), peptide hormone processing (14.6%; 4.428e-12), regulation of hormone levels (25.0%; 1.073e-11), developmental process (77.1%; 1.941e-11), single-organism developmental process (68.8%; 2.311e-11)	50	21	0	3.040E-29	31.05	31.05
6	Slc39a14 (Zip14), TSSC3, H41, UAP1, LRCH4	glutamate receptor signaling pathway (14.0%; 7.667e-11), ionotropic glutamate receptor signaling pathway (12.0%; 1.059e-10), regulation of synaptic transmission, glutamatergic (14.0%; 2.581e-10), positive regulation of synaptic transmission, GABAergic (10.0%; 9.329e-10), positive regulation of synaptic transmission, glutamatergic (10.0%; 1.576e-08)	50	19	0	1.950E-25	27.88	27.88
7	AKR1C1, ETV6(TEL1), Midkine, ICAP-1, BMP1	cell-substrate adhesion (25.8%; 4.673e-10), cell-substrate junction assembly (19.4%; 5.006e-10), cell junction assembly (25.8%; 6.192e-10), cell junction organization (25.8%; 2.277e-09), cellular response to organic substance (54.8%; 5.253e-09)	50	14	0	6.600E-20	24.29	24.29
8	HGF receptor (Met), Lyn, MGF, ETS, CD44 (ICD)	positive regulation of intracellular protein kinase cascade (47.8%; 3.079e-20), response to cytokine stimulus (47.8%; 1.253e-18), regulation of intracellular protein kinase cascade (50.0%; 3.972e-18), cellular response to chemical stimulus (69.6%; 1.099e-17), positive regulation of signal transduction (52.2%; 1.357e-17)	50	14	10	1.970E-18	21.78	34.28
9	MYRL2, OATP8, Ca-ATPase1, TAP2 (PSF2), EPLIN	muscle system process (36.7%; 9.466e-20), actin filament-based movement (22.4%; 1.154e-16), regulation of system process (40.8%; 1.901e-15), muscle filament sliding (18.4%; 2.971e-15), actin-myosin filament sliding (18.4%; 3.617e-15)	50	14	0	2.740E-18	21.54	21.54
10	FAM69B, CHC22, RhoD, RNMT, CAT-3	regulation of very-low-density lipoprotein particle remodeling (26.2%; 3.146e-25), high-density lipoprotein particle clearance (26.2%; 2.217e-24), positive regulation of cholesterol esterification (26.2%; 1.896e-23), phospholipid efflux (26.2%; 4.810e-23), regulation of cholesterol esterification (26.2%; 4.810e-23)	50	14	0	2.960E-18	22.83	22.83
11	PHI-1, Tropomyosin, MAP1LC3B, ES1, LBH	adenylate cyclase-modulating G-protein coupled receptor signaling pathway (24.5%; 2.810e-14), phospholipase C-activating G-protein coupled receptor signaling pathway (20.4%; 8.407e-14), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (24.5%; 1.813e-13), G-protein coupled receptor signaling pathway (49.0%; 3.254e-13), muscle contraction (24.5%; 3.344e-12)	50	14	0	3.780E-18	21.32	21.32

12	Tenascin-C, HGF receptor (Met), IDH2, Cyclin D, TIMP2	cellular response to chemical stimulus (72.7%; 1.287e-18), regulation of multicellular organismal development (61.4%; 6.207e-18), response to organic substance (75.0%; 1.615e-17), cellular response to organic substance (65.9%; 1.822e-17), positive regulation of biological process (81.8%; 1.491e-15)	53	14	43	7.020E-18	20.88	74.63
13	PERP, PLCB, GPX1, PHLDA3, Brush border myosin I	G-protein coupled purinergic receptor signaling pathway (16.1%; 4.247e-10), peptidyl-proline hydroxylation to 4-hydroxy-L-proline (12.9%; 6.087e-10), peptidyl-proline hydroxylation (12.9%; 1.591e-09), purinergic receptor signaling pathway (16.1%; 1.781e-09), relaxation of vascular smooth muscle (12.9%; 3.439e-09)	50	13	0	3.830E-17	22.29	22.29
14	nAChR beta-1, DTX2, Band 4.1-like protein 2, PREI4, Reticulocalbin-3	synaptic transmission (46.8%; 1.752e-18), transmission of nerve impulse (46.8%; 3.771e-17), multicellular organismal signaling (46.8%; 6.922e-17), cell-cell signaling (46.8%; 7.734e-15), synaptic transmission, cholinergic (17.0%; 5.840e-14)	50	13	0	4.380E-15	18.58	18.58
15	SNF2L1, FHOD1, PLEKHG4, IP-30, LAPTM4B	behavioral response to nicotine (21.7%; 6.714e-23), synaptic transmission involved in micturition (15.2%; 1.771e-18), response to nicotine (23.9%; 1.064e-17), micturition (17.4%; 8.672e-17), synaptic transmission, cholinergic (19.6%; 3.518e-16)	50	12	0	5.760E-15	18.38	18.38
16	tRNA, Rbm47, ATP6M, CCDC57, SART2	transferrin transport (37.0%; 2.194e-34), ferric iron transport (37.0%; 7.605e-34), trivalent inorganic cation transport (37.0%; 7.605e-34), phagosome maturation (37.0%; 3.751e-32), ATP hydrolysis coupled proton transport (34.8%; 7.689e-32)	50	11	0	1.050E-13	17.37	17.37
17	PACE4, Paxillin, DDEF1, PABPC1, Semaphorin 4B	adenylate cyclase-modulating G-protein coupled receptor signaling pathway (31.2%; 2.443e-19), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (31.2%; 2.608e-18), adenylate cyclase-activating G-protein coupled receptor signaling pathway (22.9%; 4.100e-16), response to organic substance (66.7%; 1.221e-14), receptor-mediated endocytosis (22.9%; 7.506e-14)	50	12	0	1.760E-13	16.98	16.98
18	NOL6, KPR2, MA2A1, TRL1, Melanotransferrin	protein targeting to membrane (36.0%; 5.792e-13), establishment of protein localization to membrane (36.0%; 4.397e-12), translational elongation (32.0%; 1.054e-11), protein localization to membrane (36.0%; 9.017e-11), protein targeting (36.0%; 3.456e-09)	50	11	0	2.670E-13	17.94	17.94
19	Collagen IV, CLIM1, Tubulin alpha, COPS6, GRAIL	protein polymerization (34.0%; 1.260e-30), 'de novo' posttranslational protein folding (28.0%; 7.801e-24), 'de novo' protein folding (28.0%; 1.853e-23), cellular protein complex assembly (36.0%; 1.250e-20), GTP catabolic process (34.0%; 3.744e-19)	50	11	4	2.860E-13	16.61	21.61
20	ZIP7 (SLC39A7), IP3 receptor, Perlecan, FSRP, MCP	symbiosis, encompassing mutualism through parasitism (30.3%; 1.756e-06), interspecies interaction between organisms (30.3%; 1.756e-06), mitotic spindle organization in nucleus (6.1%; 2.678e-06), regeneration (18.2%; 4.274e-06), urate biosynthetic process (6.1%; 8.026e-06)	50	10	0	1.910E-12	16.32	16.32
21	AKR1C4, CRABP2, Alpha crystallin B, P-cadherin, Cyclin D3	response to hormone stimulus (52.4%; 2.554e-08), response to stimulus (100.0%; 9.497e-08), response to oxygen-containing compound (57.1%; 9.813e-08), response to endogenous stimulus (57.1%; 1.112e-07), response to chemical stimulus (81.0%; 1.361e-07)	50	9	0	1.930E-12	17.72	17.72
22	SLC25A37, Troponin I, fast skeletal muscle, FKBP10, Trp53inp2, CAT-2	cellular response to glucagon stimulus (40.8%; 1.409e-38), response to glucagon stimulus (40.8%; 1.865e-36), nucleobase-containing compound catabolic process (65.3%; 8.341e-31), cellular nitrogen compound catabolic process (65.3%; 4.559e-30), heterocycle catabolic process (65.3%; 5.176e-30)	50	10	0	6.280E-12	15.38	15.38
23	ASSY, EMP2, RRAD, PAG, PMCA4	positive regulation of T cell mediated cytotoxicity (38.0%; 1.073e-36), regulation of T cell mediated cytotoxicity (38.0%; 1.315e-35), antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway (28.0%; 3.747e-35), antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-dependent (28.0%; 3.747e-35), antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (30.0%; 1.294e-34)	50	10	0	9.720E-12	15.04	15.04
24	CD68, ZNF189, Optineurin, EPLIN, Filamin C	regulation of locomotion (41.0%; 1.153e-13), regulation of cell migration (38.5%; 3.578e-13), regulation of cell motility (38.5%; 7.789e-13), locomotion (48.7%; 1.241e-12), regulation of cellular component movement (38.5%; 3.735e-12)	50	9	0	4.370E-11	15.01	15.01

25	Paxillin, PAI1, Actin, PLAU (UPA), Alpha-actinin 1	cellular component movement (78.7%; 9.012e-33), anatomical structure morphogenesis (85.1%; 1.326e-29), cell projection organization (68.1%; 4.658e-29), locomotion (70.2%; 3.565e-28), coagulation (57.4%; 4.603e-28)	54	9	10	4.230E-10	13.19	25.69
26	CRIP2, eIF6 (ITGB4BP), Beta TnTF, EGFL7, GRAIL	phosphatidylethanolamine acyl-chain remodeling (27.8%; 5.052e-22), phosphatidylcholine acyl-chain remodeling (27.8%; 1.898e-21), phosphatidylcholine metabolic process (33.3%; 1.940e-20), glycerolipid metabolic process (47.2%; 4.160e-20), ethanolamine-containing compound metabolic process (33.3%; 4.007e-19)	50	9	0	1.470E-09	13.27	13.27
27	BNaC1 (ASIC2), Stomatin, LTBP1, BPAG1, PMEPA1	signaling (85.1%; 3.614e-14), single organism signaling (85.1%; 3.614e-14), cell surface receptor signaling pathway (70.2%; 4.864e-14), cell communication (85.1%; 9.423e-14), signal transduction (80.9%; 1.520e-13)	50	8	0	7.720E-09	11.9	11.9
28	CCDC95, UBE2F, GALGT, CREB1, MYO1E	phospholipase C-activating G-protein coupled receptor signaling pathway (38.0%; 3.200e-31), G-protein coupled receptor signaling pathway (74.0%; 8.579e-29), G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (38.0%; 8.528e-25), cell surface receptor signaling pathway (86.0%; 4.039e-24), serotonin receptor signaling pathway (20.0%; 7.107e-22)	50	7	0	1.770E-07	10.34	10.34

Table S15. Key transcription factors significantly associated with differentially expressed genes between KLF5 and the PLHCX vector control, as defined by MetaCore's interactome analysis for transcription factors. Related biological processes are also shown. The ranking is based on *p* values. Total nodes refer to all nodes in a transcription factor network, while seed nodes refer to the genes differentially expressed between the experimental groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	CREB1	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (28.6%; 5.830e-07), negative regulation of cysteine-type endopeptidase activity (28.6%; 6.825e-07), regulation of hydrolase activity (50.0%; 1.133e-05), negative regulation of endopeptidase activity (28.6%; 1.469e-05), positive regulation of deacetylase activity (14.3%; 2.070e-05)	15	14	0	7.410E-45	138.35	138.35
2	HIF1A	regulation of cysteine-type endopeptidase activity involved in apoptotic process (50.0%; 3.577e-09), regulation of cysteine-type endopeptidase activity (50.0%; 4.824e-09), regulation of endopeptidase activity (50.0%; 5.447e-08), regulation of peptidase activity (50.0%; 1.783e-07), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (33.3%; 2.905e-07)	13	12	0	2.650E-38	127.38	127.38
3	GCR-alpha	hormone metabolic process (36.4%; 4.003e-06), regulation of hormone levels (36.4%; 2.022e-05), cellular hormone metabolic process (27.3%; 4.980e-05), regulation of biological quality (72.7%; 1.508e-04), single-multicellular organism process (90.9%; 4.832e-04)	11	10	0	8.180E-32	115.39	115.39
4	c-Myc	positive regulation of cell proliferation (60.0%; 3.463e-06), regulation of cell proliferation (70.0%; 4.038e-06), regulation of cysteine-type endopeptidase activity involved in apoptotic process (40.0%; 5.167e-06), regulation of cysteine-type endopeptidase activity (40.0%; 6.297e-06), positive regulation of deacetylase activity (20.0%; 1.025e-05)	11	10	0	8.180E-32	115.39	115.39
5	SP1	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (44.4%; 7.481e-08), negative regulation of cysteine-type endopeptidase activity (44.4%; 8.766e-08), negative regulation of inclusion body assembly (22.2%; 1.825e-06), negative regulation of endopeptidase activity (44.4%; 1.934e-06), regulation of cysteine-type endopeptidase activity involved in apoptotic process (44.4%; 3.132e-06)	10	9	0	1.360E-28	108.92	108.92
6	p53	regulation of cysteine-type endopeptidase activity involved in apoptotic process (50.0%; 7.872e-08), regulation of cysteine-type endopeptidase activity (50.0%; 1.010e-07), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (40.0%; 1.242e-07), negative regulation of cysteine-type endopeptidase activity (40.0%; 1.455e-07), regulation of endopeptidase activity (50.0%; 7.593e-07)	10	9	0	1.360E-28	108.92	108.92
7	Oct-3/4	response to carbon dioxide (12.5%; 4.029e-04), ectodermal cell fate commitment (12.5%; 4.029e-04), regulation of complement activation, lectin pathway (12.5%; 8.056e-04), ITP metabolic process (12.5%; 8.056e-04), negative regulation of gene silencing by RNA (12.5%; 8.056e-04)	8	7	0	3.370E-22	94.71	94.71
8	STAT3	regulation of endopeptidase activity (75.0%; 1.768e-09), regulation of peptidase activity (75.0%; 5.880e-09), response to ethanol (62.5%; 1.650e-08), regulation of cysteine-type endopeptidase activity involved in apoptotic process (62.5%; 1.787e-08), regulation of cysteine-type endopeptidase activity (62.5%; 2.294e-08)	8	7	0	3.370E-22	94.71	94.71
9	C/EBPbeta	neutrophil aggregation (33.3%; 2.282e-07), sequestering of zinc ion (33.3%; 1.141e-06), granulocyte chemotaxis (50.0%; 1.156e-06), regulation of endopeptidase activity (66.7%; 2.380e-06), chemokine production (33.3%; 2.736e-06)	7	6	0	4.990E-19	86.78	86.78
10	c-Jun	negative regulation of neuron death (57.1%; 7.439e-07), regulation of neuron death (57.1%; 2.371e-06), negative regulation of cell death (71.4%; 9.622e-06), positive regulation of cellular metabolic process (85.7%; 3.289e-05), negative regulation of neuron apoptotic process (42.9%; 4.301e-05)	7	6	0	4.990E-19	86.78	86.78

11	E2F1	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (50.0%; 2.451e-06), negative regulation of cysteine-type endopeptidase activity (50.0%; 2.759e-06), cellular response to hypoxia (50.0%; 8.647e-06), cellular response to decreased oxygen levels (50.0%; 8.647e-06), cellular response to oxygen levels (50.0%; 1.047e-05)	7	6	0	4.990E-19	86.78	86.78
12	SMAD3	regulation of cysteine-type endopeptidase activity involved in apoptotic process (80.0%; 1.294e-07), regulation of cysteine-type endopeptidase activity (80.0%; 1.581e-07), regulation of endopeptidase activity (80.0%; 8.062e-07), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (60.0%; 1.230e-06), negative regulation of cysteine-type endopeptidase activity (60.0%; 1.385e-06)	7	6	0	4.990E-19	86.78	86.78
13	RelA (p65 NF-kB subunit)	regulation of cysteine-type endopeptidase activity involved in apoptotic process (66.7%; 3.843e-07), regulation of cysteine-type endopeptidase activity (66.7%; 4.693e-07), regulation of endopeptidase activity (66.7%; 2.380e-06), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (50.0%; 2.451e-06), negative regulation of cysteine-type endopeptidase activity (50.0%; 2.759e-06)	6	5	0	7.050E-16	78.11	78.11
14	EGR1	rhythmic process (66.7%; 1.481e-06), positive regulation of receptor internalization (33.3%; 1.298e-05), ovulation cycle (50.0%; 1.365e-05), positive regulation of nucleobase-containing compound metabolic process (83.3%; 2.266e-05), regulation of receptor internalization (33.3%; 2.275e-05)	6	5	0	7.050E-16	78.11	78.11
15	NANOG	gonad development (60.0%; 3.789e-05), development of primary sexual characteristics (60.0%; 4.979e-05), sex differentiation (60.0%; 7.300e-05), reproductive structure development (60.0%; 8.049e-05), reproductive system development (60.0%; 8.349e-05)	5	4	0	9.450E-13	68.45	68.45
16	AP-1	positive regulation of smooth muscle cell proliferation (60.0%; 1.268e-06), regulation of smooth muscle cell proliferation (60.0%; 4.885e-06), negative regulation of neuron death (60.0%; 1.777e-05), monocyte differentiation (40.0%; 2.836e-05), positive regulation of cell proliferation (80.0%; 3.517e-05)	5	4	0	9.450E-13	68.45	68.45
17	Androgen receptor	mammary gland lobule development (50.0%; 1.233e-05), mammary gland alveolus development (50.0%; 1.233e-05), regulation of morphogenesis of a branching structure (50.0%; 1.055e-04), basophil chemotaxis (25.0%; 2.014e-04), activation of prostate induction by androgen receptor signaling pathway (25.0%; 2.014e-04)	5	4	0	9.450E-13	68.45	68.45
18	ESR1 (nuclear)	positive regulation of cell proliferation (100.0%; 3.811e-07), regulation of cell proliferation (100.0%; 5.471e-06), hormone metabolic process (60.0%; 1.198e-05), regulation of hormone levels (60.0%; 4.085e-05), cellular response to endogenous stimulus (80.0%; 7.805e-05)	5	4	0	9.450E-13	68.45	68.45
19	c-Fos	response to cold (40.0%; 1.048e-04), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (40.0%; 2.486e-04), basophil chemotaxis (20.0%; 2.518e-04), cellular response to UV-C (20.0%; 2.518e-04), cellular response to vitamin B1 (20.0%; 2.518e-04)	5	4	0	9.450E-13	68.45	68.45
20	PPAR-gamma	regulation of cysteine-type endopeptidase activity involved in apoptotic process (80.0%; 1.294e-07), regulation of cysteine-type endopeptidase activity (80.0%; 1.581e-07), regulation of endopeptidase activity (80.0%; 8.062e-07), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (60.0%; 1.230e-06), negative regulation of cysteine-type endopeptidase activity (60.0%; 1.385e-06)	5	4	0	9.450E-13	68.45	68.45
21	p63	negative regulation of inclusion body assembly (40.0%; 5.070e-07), negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (60.0%; 1.230e-06), negative regulation of cysteine-type endopeptidase activity (60.0%; 1.385e-06), regulation of inclusion body assembly (40.0%; 2.787e-06), response to radiation (80.0%; 4.590e-06)	5	4	0	9.450E-13	68.45	68.45

Table S16. Key transcription factors significantly associated with differentially expressed genes between K369R and the PLHCX vector control, as defined by MetaCore's interactome analysis for transcription factors. Related biological processes are also shown. The ranking is based on *p* values. Total nodes refer to all nodes in a transcription factor network, while seed nodes refer to the genes differentially expressed between the experimental groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	CREB1	biological regulation (83.3%; 1.851e-10), negative regulation of cellular process (40.0%; 5.215e-10), regulation of cellular component organization (25.0%; 1.295e-09), negative regulation of biological process (41.1%; 5.112e-09), regulation of cellular process (76.1%; 5.181e-09)	188	187	0	0.000E+00	151.16	151.16
2	c-Myc	response to organic cyclic compound (30.1%; 8.398e-17), response to organic substance (44.4%; 4.011e-14), response to endogenous stimulus (33.8%; 4.702e-14), positive regulation of biological process (54.1%; 1.366e-13), organ development (43.6%; 4.736e-13)	137	136	0	3.400E-291	128.73	128.73
3	GCR-alpha	response to endogenous stimulus (36.8%; 5.969e-15), negative regulation of biological process (53.0%; 1.864e-13), response to organic cyclic compound (28.2%; 3.177e-13), response to lipid (27.4%; 8.745e-13), response to oxidative stress (17.1%; 2.303e-12)	118	117	0	2.600E-249	119.31	119.31
4	SP1	response to endogenous stimulus (44.0%; 1.554e-21), response to organic substance (50.9%; 1.447e-17), developmental process (68.1%; 2.015e-17), response to hormone stimulus (32.8%; 8.076e-17), single-multicellular organism process (75.9%; 1.654e-16)	117	116	0	4.060E-247	118.79	118.79
5	Androgen receptor	tissue development (31.7%; 1.866e-10), negative regulation of cellular process (47.1%; 4.310e-10), negative regulation of biological process (49.0%; 9.632e-10), developmental process (58.7%; 1.029e-09), positive regulation of cellular metabolic process (36.5%; 1.470e-09)	108	107	0	2.010E-227	114.04	114.04
6	ESR1 (nuclear)	positive regulation of biological process (55.7%; 4.506e-12), negative regulation of biological process (51.9%; 1.277e-11), regulation of cell death (32.1%; 1.744e-11), developmental process (61.3%; 1.937e-11), response to organic cyclic compound (27.4%; 1.970e-11)	108	107	0	2.010E-227	114.04	114.04
7	p53	positive regulation of cellular process (64.0%; 6.160e-20), positive regulation of biological process (65.0%; 7.615e-18), developmental process (70.0%; 1.382e-16), regulation of cell death (36.0%; 8.506e-14), regulation of programmed cell death (35.0%; 1.388e-13)	101	100	0	3.650E-212	110.21	110.21
8	RelA (p65 NF-kB subunit)	response to endogenous stimulus (42.4%; 3.886e-16), response to organic cyclic compound (33.7%; 7.338e-15), response to oxygen-containing compound (40.2%; 1.175e-14), positive regulation of biological process (60.9%; 9.260e-14), positive regulation of cellular process (56.5%; 2.673e-13)	93	92	0	8.710E-195	105.66	105.66
9	Oct-3/4	cell differentiation (51.1%; 1.839e-12), response to organic substance (48.9%; 2.016e-12), developmental process (65.9%; 3.077e-12), negative regulation of biological process (55.7%; 5.585e-12), regulation of gene expression (56.8%; 5.765e-12)	91	90	0	1.880E-190	104.49	104.49
10	c-Jun	response to endogenous stimulus (46.9%; 1.391e-17), response to inorganic substance (29.6%; 7.218e-16), response to organic cyclic compound (37.0%; 1.030e-15), response to organic substance (55.6%; 1.300e-15), positive regulation of cellular process (61.7%; 5.953e-15)	81	81	0	6.540E-173	99.68	99.68
11	HIF1A	response to organic cyclic compound (36.2%; 5.993e-15), developmental process (71.2%; 2.653e-14), single-organism developmental process (62.5%; 5.451e-14), system development (62.5%; 8.317e-14), response to endogenous stimulus (41.2%; 1.839e-13)	83	82	0	3.710E-173	99.67	99.67

12	NANOG	regulation of transcription from RNA polymerase II promoter (38.0%; 1.601e-12), regulation of gene expression (58.2%; 1.246e-11), organ development (49.4%; 3.059e-11), developmental process (65.8%; 4.383e-11), single-organism developmental process (57.0%; 9.070e-11)	79	78	0	1.560E-164	97.18	97.18
13	STAT3	response to inorganic substance (32.4%; 6.990e-17), response to endogenous stimulus (45.9%; 1.552e-15), developmental process (73.0%; 2.467e-14), response to organic substance (55.4%; 2.699e-14), response to external stimulus (41.9%; 3.469e-14)	76	75	0	4.460E-158	95.27	95.27
14	SP3	response to endogenous stimulus (43.1%; 2.449e-13), organ development (54.2%; 6.839e-13), developmental process (70.8%; 8.809e-13), response to hormone stimulus (34.7%; 3.490e-12), regulation of transcription from RNA polymerase II promoter (38.9%; 4.467e-12)	72	71	0	1.750E-149	92.65	92.65
15	C/EBPbeta	response to endogenous stimulus (48.6%; 1.836e-16), response to oxygen-containing compound (44.3%; 7.070e-14), response to organic cyclic compound (37.1%; 7.738e-14), response to organic substance (55.7%; 8.983e-14), tissue development (42.9%; 1.721e-13)	71	70	0	2.460E-147	91.99	91.99
16	E2F1	regulation of transcription from RNA polymerase II promoter (42.6%; 1.099e-13), cellular response to stress (38.2%; 3.150e-12), positive regulation of cellular metabolic process (47.1%; 1.229e-11), positive regulation of macromolecule metabolic process (45.6%; 4.749e-11), single-organism developmental process (60.3%; 5.247e-11)	71	70	0	2.460E-147	91.99	91.99
17	p63	regulation of transcription from RNA polymerase II promoter (39.7%; 6.014e-12), positive regulation of cellular process (55.9%; 6.661e-10), developmental process (66.2%; 6.808e-10), negative regulation of biological process (55.9%; 1.149e-09), positive regulation of biological process (58.8%; 1.338e-09)	69	68	0	4.780E-143	90.64	90.64
18	EGR1	regulation of transcription from RNA polymerase II promoter (47.1%; 1.744e-16), positive regulation of cellular process (67.6%; 4.108e-16), positive regulation of biological process (70.6%; 1.068e-15), developmental process (76.5%; 2.771e-15), single-organism developmental process (66.2%; 4.650e-14)	68	67	0	6.650E-141	89.96	89.96
19	NF-kB1 (p50)	response to endogenous stimulus (42.4%; 5.430e-12), regulation of gene expression (62.1%; 8.760e-12), response to organic cyclic compound (34.8%; 9.906e-12), response to inorganic substance (27.3%; 1.461e-11), regulation of transcription from RNA polymerase II promoter (39.4%; 1.830e-11)	67	66	0	9.220E-139	89.28	89.28
20	YY1	regulation of transcription from RNA polymerase II promoter (40.3%; 2.433e-11), circulatory system development (29.0%; 1.067e-09), cardiovascular system development (29.0%; 1.067e-09), organ development (50.0%; 2.143e-09), regulation of gene expression (58.1%; 2.332e-09)	65	64	0	1.760E-134	87.89	87.89
21	NF-kB	regulation of transcription from RNA polymerase II promoter (42.9%; 6.706e-13), negative regulation of biological process (61.9%; 9.080e-12), response to endogenous stimulus (42.9%; 9.714e-12), developmental process (71.4%; 1.217e-11), response to organic cyclic compound (34.9%; 2.663e-11)	63	62	0	3.340E-130	86.49	86.49

Table S17. Key transcription factors significantly associated with differentially expressed genes between K369R and KLF5, as defined by MetaCore's interactome analysis for transcription factors. Related biological processes are also shown. The ranking is based on *p* values. Total nodes refer to all nodes in a transcription factor network, while seed nodes refer to the genes differentially expressed between the experimental groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p* value	zScore	gScore
1	CREB1	biological regulation (84.4%; 9.568e-11), blood vessel development (13.2%; 9.668e-09), negative regulation of cellular process (38.9%; 1.276e-08), blood vessel morphogenesis (12.0%; 1.567e-08), response to external stimulus (23.4%; 1.789e-08)	175	174	0	0.000E+00	150.68	150.68
2	c-Myc	response to organic cyclic compound (29.4%; 1.509e-14), response to inorganic substance (21.0%; 1.019e-12), response to organic substance (43.7%; 2.627e-12), regeneration (13.4%; 4.790e-12), regulation of cell death (31.1%; 6.458e-12)	124	123	0	1.670E-266	126.49	126.49
3	SP1	developmental process (71.8%; 1.256e-19), single-multicellular organism process (80.0%; 3.537e-19), multicellular organismal process (80.9%; 9.725e-19), multicellular organismal development (66.4%; 7.402e-18), single-organism developmental process (60.9%; 2.036e-17)	113	112	0	5.880E-242	120.64	120.64
4	GCR-alpha	anatomical structure development (59.1%; 6.634e-13), tissue development (33.6%; 2.075e-12), system development (53.6%; 5.817e-12), negative regulation of biological process (51.8%; 5.841e-12), vasculature development (20.0%; 7.462e-12)	111	110	0	1.650E-237	119.55	119.55
5	ESR1 (nuclear)	regulation of cell death (35.9%; 4.168e-14), regulation of programmed cell death (34.0%; 3.794e-13), regulation of apoptotic process (33.0%; 1.643e-12), developmental process (61.2%; 4.603e-11), response to endogenous stimulus (33.0%; 1.237e-10)	103	102	0	9.230E-220	115.07	115.07
6	Androgen receptor	tissue development (34.0%; 2.254e-11), positive regulation of cellular metabolic process (40.2%; 3.128e-11), positive regulation of metabolic process (41.2%; 4.795e-11), regulation of multicellular organismal process (41.2%; 5.014e-11), positive regulation of biological process (54.6%; 1.390e-10)	102	101	0	1.510E-217	114.5	114.5
7	p53	regulation of programmed cell death (42.2%; 7.964e-18), positive regulation of cellular process (63.3%; 1.347e-17), positive regulation of biological process (66.7%; 2.243e-17), regulation of cell death (42.2%; 3.391e-17), regulation of apoptotic process (41.1%; 4.684e-17)	90	89	0	4.490E-191	107.4	107.4
8	RelA (p65 NF-kB subunit)	regulation of cell death (39.8%; 5.492e-15), regulation of programmed cell death (38.6%; 1.048e-14), positive regulation of cellular process (59.1%; 2.231e-14), positive regulation of biological process (62.5%; 3.092e-14), regulation of apoptotic process (37.5%; 5.511e-14)	88	87	0	1.120E-186	106.17	106.17
9	Oct-3/4	regulation of signal transduction (47.1%; 5.460e-14), anatomical structure development (64.7%; 1.941e-13), single-organism developmental process (60.0%; 3.131e-13), developmental process (68.2%; 3.196e-13), tissue development (38.8%; 3.206e-13)	88	87	0	1.120E-186	106.17	106.17
10	HIF1A	response to endogenous stimulus (45.0%; 5.226e-16), response to organic cyclic compound (37.5%; 6.909e-16), response to external stimulus (42.5%; 1.185e-15), system development (65.0%; 2.433e-15), response to lipid (36.2%; 2.940e-15)	82	81	0	1.630E-173	102.4	102.4
11	STAT3	response to external stimulus (45.7%; 6.203e-16), developmental process (74.3%; 2.198e-14), single-organism developmental process (65.7%; 3.612e-14), anatomical structure development (70.0%; 3.953e-14), positive regulation of biological process (67.1%; 4.313e-14)	71	70	0	1.750E-149	95.09	95.09
12	c-Jun	positive regulation of cellular process (66.7%; 9.752e-16), response to inorganic substance (31.9%; 2.074e-15), response to endogenous stimulus (46.4%; 7.554e-15), positive regulation of biological process (68.1%; 1.855e-14), positive regulation of gene expression (40.6%; 4.214e-14)	69	69	0	3.800E-149	95.09	95.09

13	p63	positive regulation of cellular process (62.1%; 1.211e-12), positive regulation of biological process (65.2%; 2.492e-12), regulation of cell death (40.9%; 3.151e-12), system development (63.6%; 3.361e-12), regulation of apoptotic process (39.4%; 6.857e12)	66	65	0	1.330E-138	91.58	91.58
14	NANOG	circulatory system development (33.8%; 4.595e-13), cardiovascular system development (33.8%; 4.595e-13), blood vessel development (27.7%; 6.179e-13), vasculature development (27.7%; 1.702e-12), blood vessel morphogenesis (24.6%; 7.501e-12)	66	65	0	1.330E-138	91.58	91.58
15	E2F1	cellular response to extracellular stimulus (17.7%; 1.144e-10), blood vessel development (24.2%; 4.319e-10), positive regulation of gene expression (35.5%; 4.908e-10), positive regulation of metabolic process (46.8%; 6.043e-10), positive regulation of cellular metabolic process (45.2%; 7.719e-10)	63	62	0	4.350E-132	89.4	89.4
16	C/EBPbeta	response to endogenous stimulus (50.8%; 7.641e-16), response to external stimulus (45.9%; 3.586e-14), tissue development (45.9%; 1.340e-13), response to lipid (37.7%; 8.285e-13), organ development (57.4%; 1.067e-12)	61	60	0	9.460E-128	87.92	87.92
17	KLF4	anatomical structure development (76.7%; 7.857e-16), tissue development (48.3%; 8.940e-15), developmental process (78.3%; 1.188e-14), system development (70.0%; 2.312e-14), organ development (60.0%; 7.546e-14)	60	59	0	1.390E-125	87.18	87.18
18	SP3	tissue development (46.6%; 2.388e-13), response to external stimulus (43.1%; 4.812e-12), regeneration (20.7%; 1.231e-11), blood vessel development (27.6%; 1.281e-11), anatomical structure development (69.0%; 1.844e-11)	58	57	0	2.980E-121	85.66	85.66
19	YY1	circulatory system development (40.0%; 8.031e-15), cardiovascular system development (40.0%; 8.031e-15), tissue development (49.1%; 4.607e-14), blood vessel development (30.9%; 3.668e-13), vasculature development (30.9%; 9.659e-13)	58	57	0	2.980E-121	85.66	85.66
20	STAT1	regulation of cell death (47.4%; 4.005e-14), positive regulation of cellular process (68.4%; 4.031e-14), positive regulation of biological process (71.9%; 4.667e-14), regulation of programmed cell death (45.6%; 1.325e-13), regulation of apoptotic process (43.9%; 9.634e-13)	57	56	0	4.350E-119	84.89	84.89
21	NF-kB1 (p50)	response to external stimulus (50.0%; 2.228e-15), regulation of cell death (50.0%; 2.294e-15), response to oxidative stress (30.4%; 4.240e-15), regulation of apoptotic process (48.2%; 6.424e-15), regulation of programmed cell death (48.2%; 7.989e-15)	57	56	0	4.350E-119	84.89	84.89