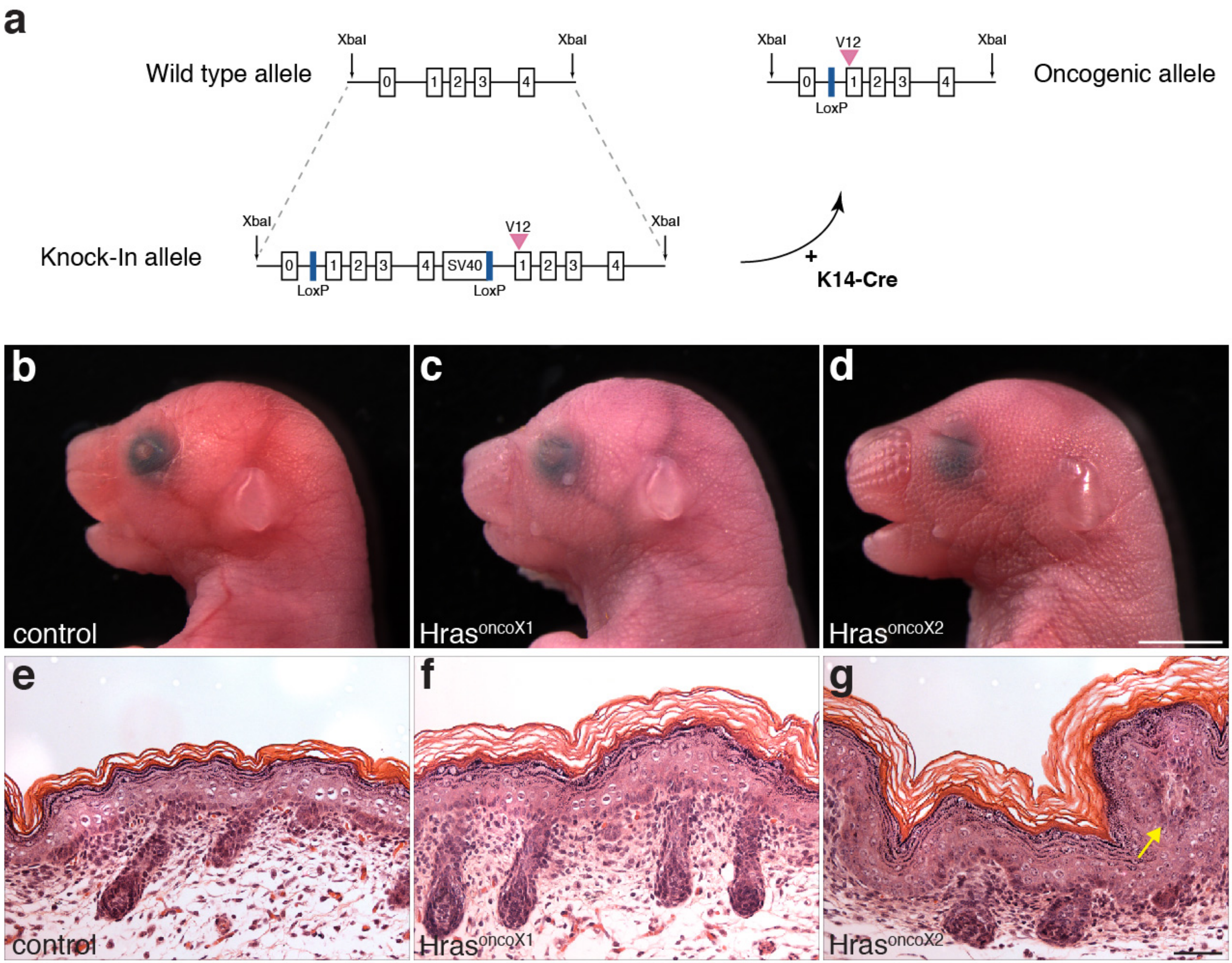
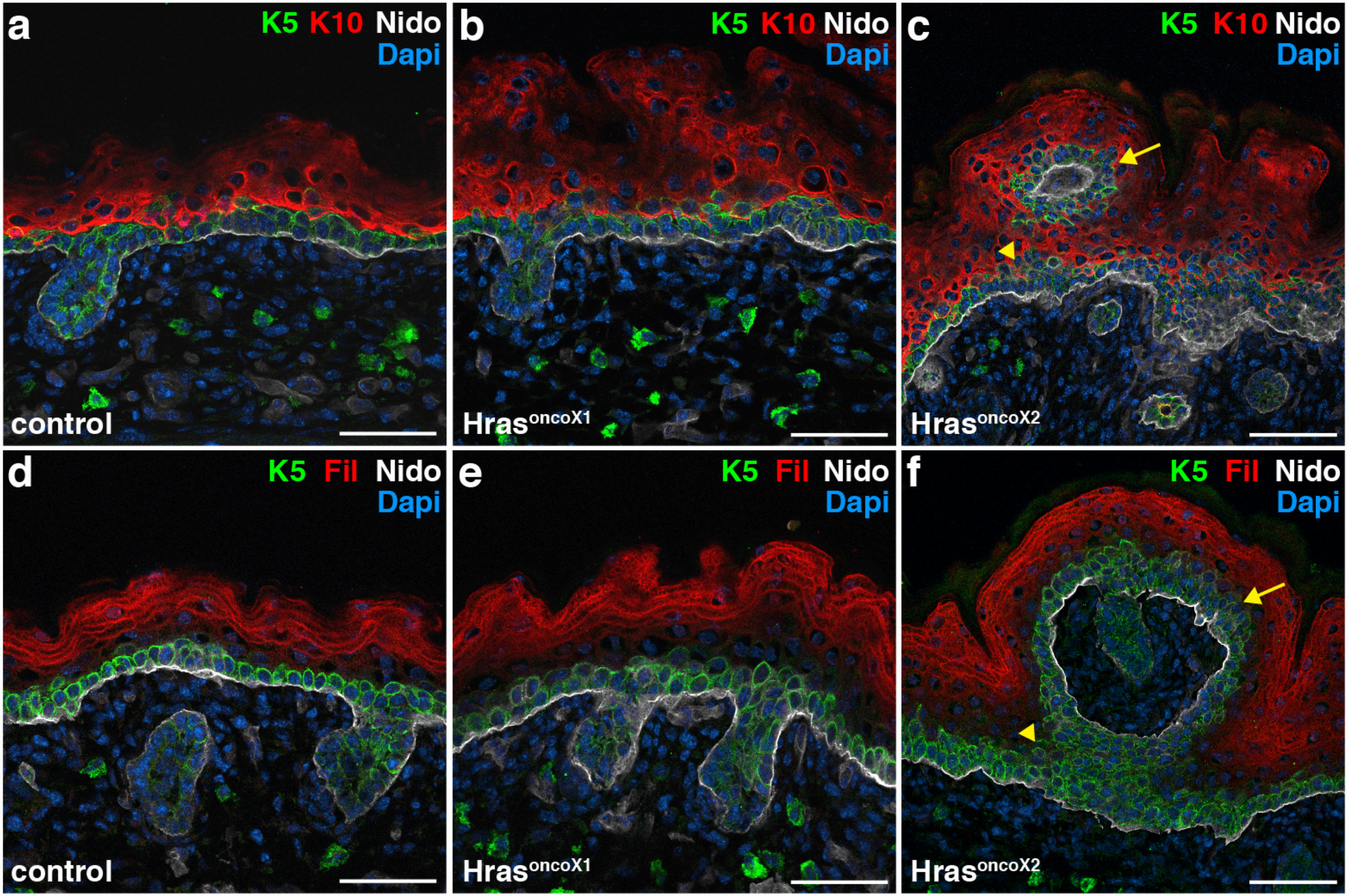
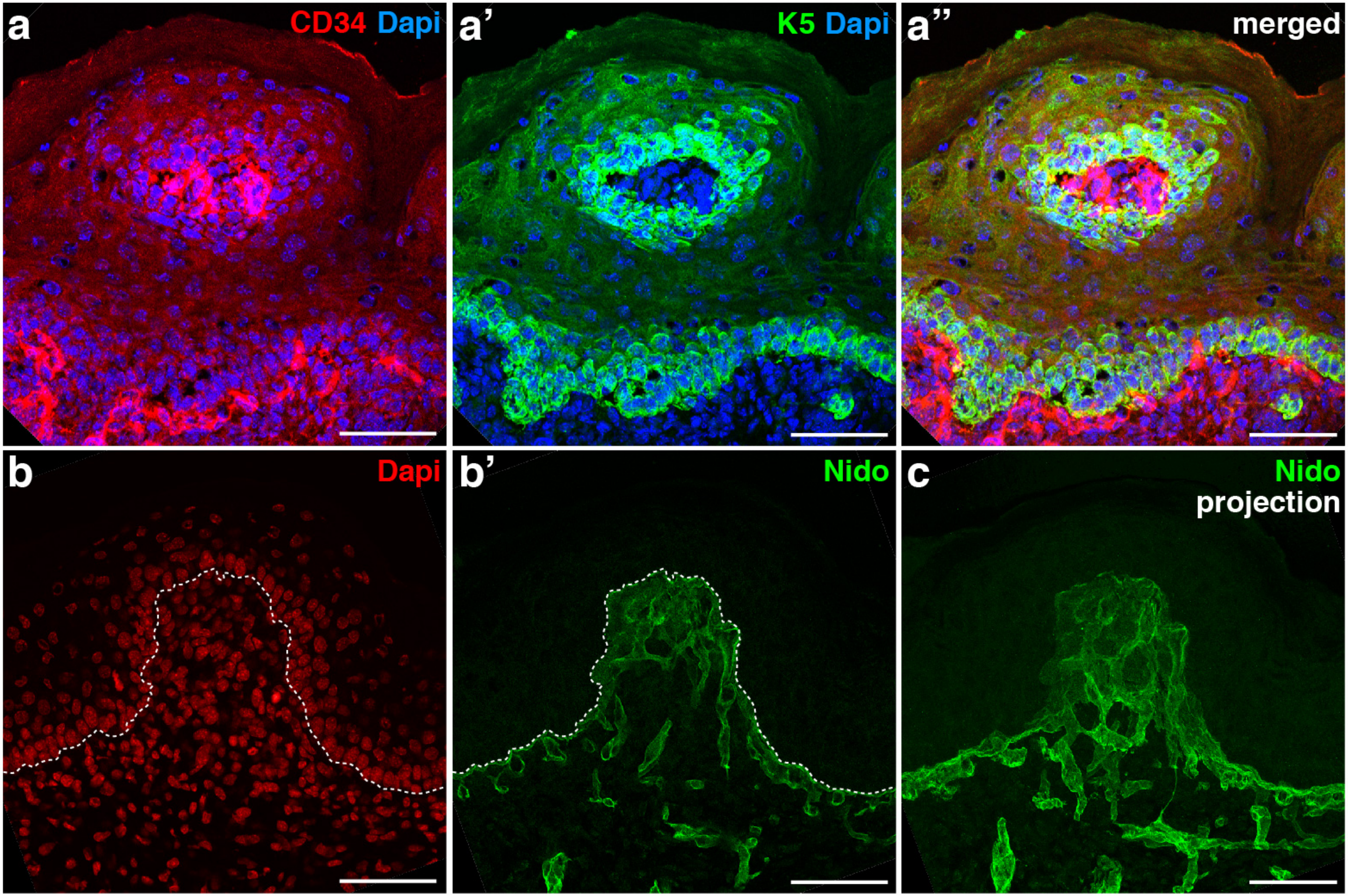


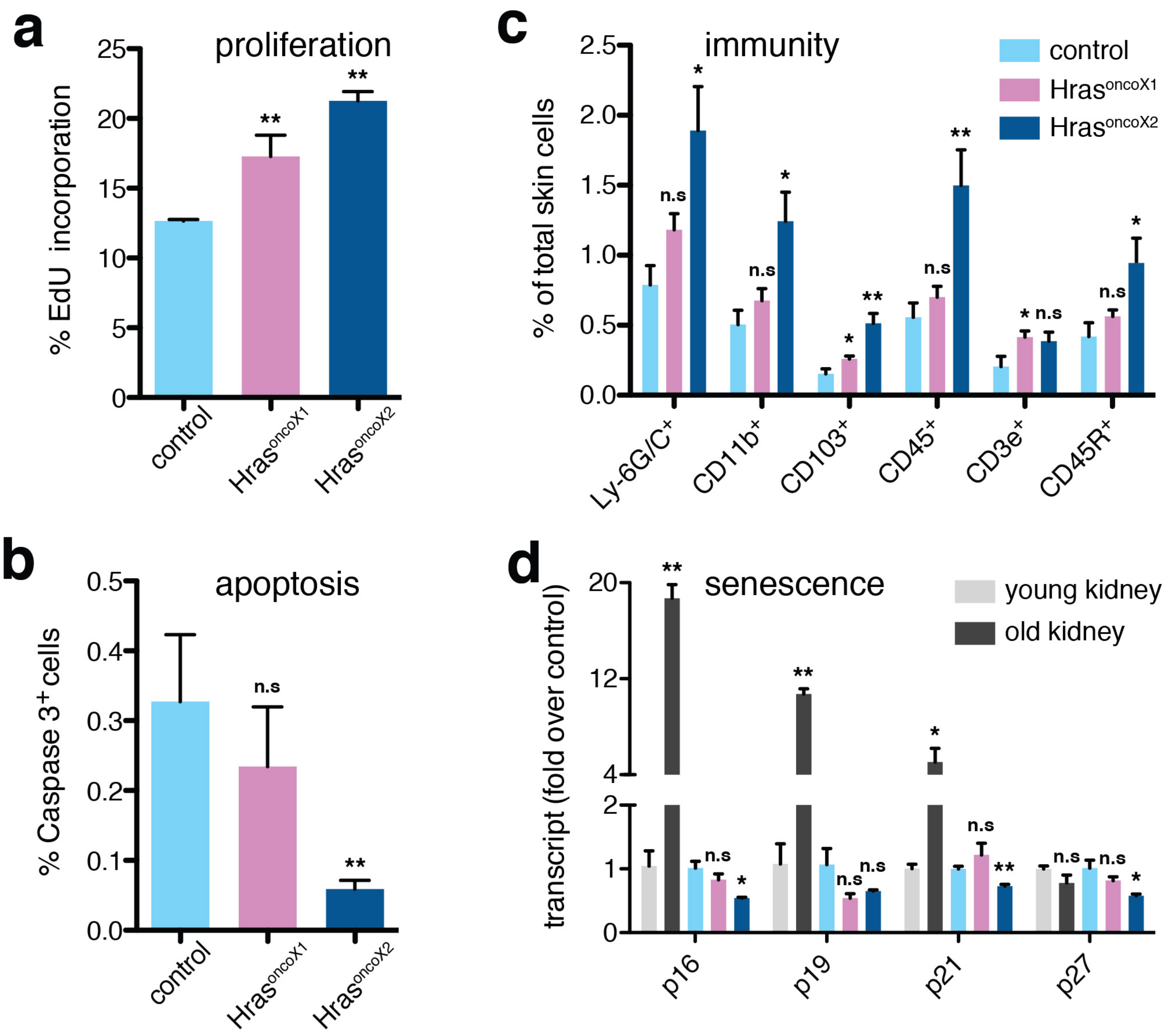
Supplementary Figure 1. Oncogenic Hras^{G12V}-dependent epidermal growth. a, Oncogene-dependent epidermal growth was modeled using a knock-in mouse where the endogenous *Hras1* locus was targeted with a cassette consisting of a loxP-flanked wild-type allele of *Hras1* followed by the oncogenic *Hras^{G12V}* allele. Epidermal co-expression of K14-Cre-recombinase resulted in expression of oncogenic Hras^{G12V} at endogenous levels. **b**-**d**, Embryos at E18.5. Epidermal expression of one (**c**, Hras^{oncoX1}) or two (**d**, Hras^{oncoX2}) copies of oncogenic Hras^{G12V} results in dose-dependent increases in tissue growth evidenced by changes in whisker-pad and eyelid morphology, and increased opaqueness of the tissue. (**e**-**g**), Sagittal sections of E18.5 skins are stained with hematoxylin and eosin. Note dose-dependent increases in epidermal thickness, and emergence of evaginations within the interfollicular epidermis of Hras^{oncoX2} (**g**, yellow arrow). Scale bars, (**b**-**d**) 3 mm, (**e**-**g**) 100 µm.



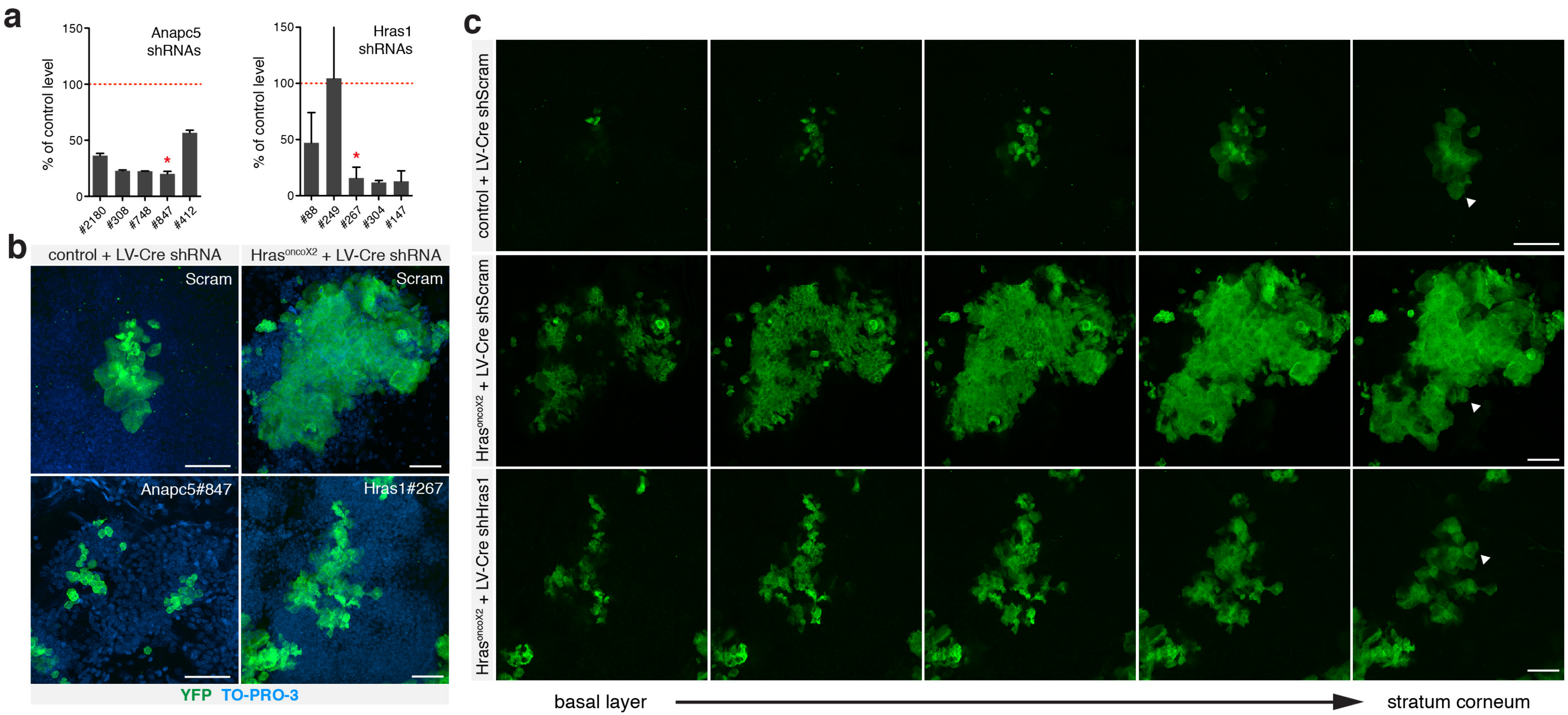
Supplementary Figure 2. Epidermal expression of oncogenic Hras^{G12V} during embryogenesis results in general hyperplasia and expansion of the progenitor cell layer. a-**c**, Expression of progenitor (basal cell) marker keratin 5 (K5), and early differentiation (spinous cell) marker keratin 10 (K10) in E18.5 embryonic epidermis. **d**-**f**, Expression of K5 and late stage differentiation (granular cell) marker Filaggrin (Fil) in E18.5 embryonic epidermis. Note expansion of the K5^{+} monolayer (yellow arrowhead) and formation of evaginations (yellow arrow) in Hras^{oncoX2} interfollicular epidermis (**c**,**f**). Nidogen (Nido) and Dapi mark the basement membrane and the nuclei, respectively. Scale bars, 50 µm.



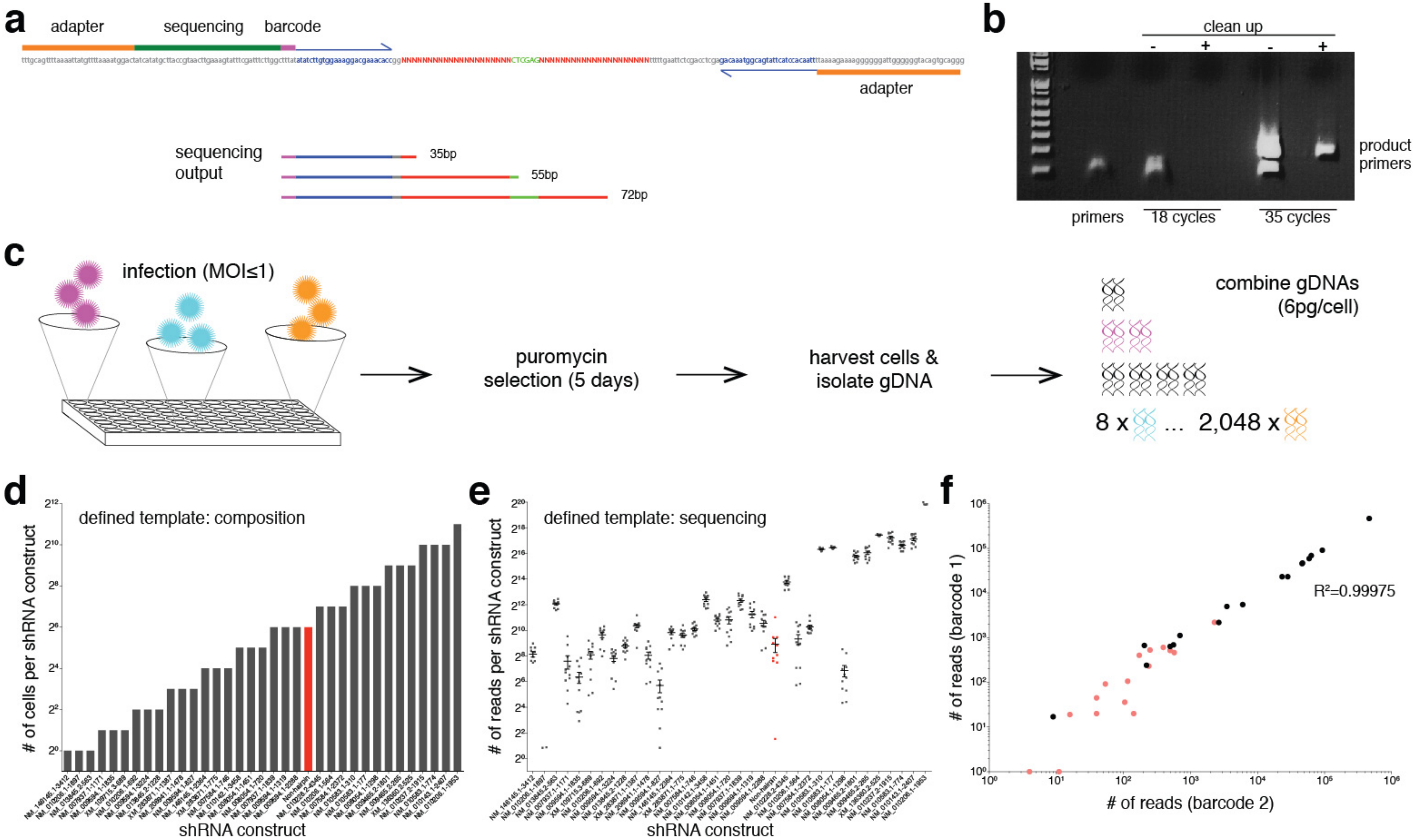
Supplementary Figure 3. Epidermal expression of oncogenic Hras^{G12V} during embryogenesis results in dermal extrusions into the overlying epidermis. a, Expression of dermal marker CD34 is detected in ectopic evaginations into the epidermis, which are surrounded by the progenitor cell marker keratin 5 (K5), in E18.5 embryonic epidermis. **b**, Larger dermal extrusions are also marked by the abundant network of blood vessels, marked by the expression of Nidogen (Nido). **c**, Maximum-projection of 10 µm z-stack shows extensive capillary network labeled with Nidogen. Dapi marks the nuclei. Dotted line (**b**) marks the epidemal-dermal boundary. Scale bars, 50 µm.



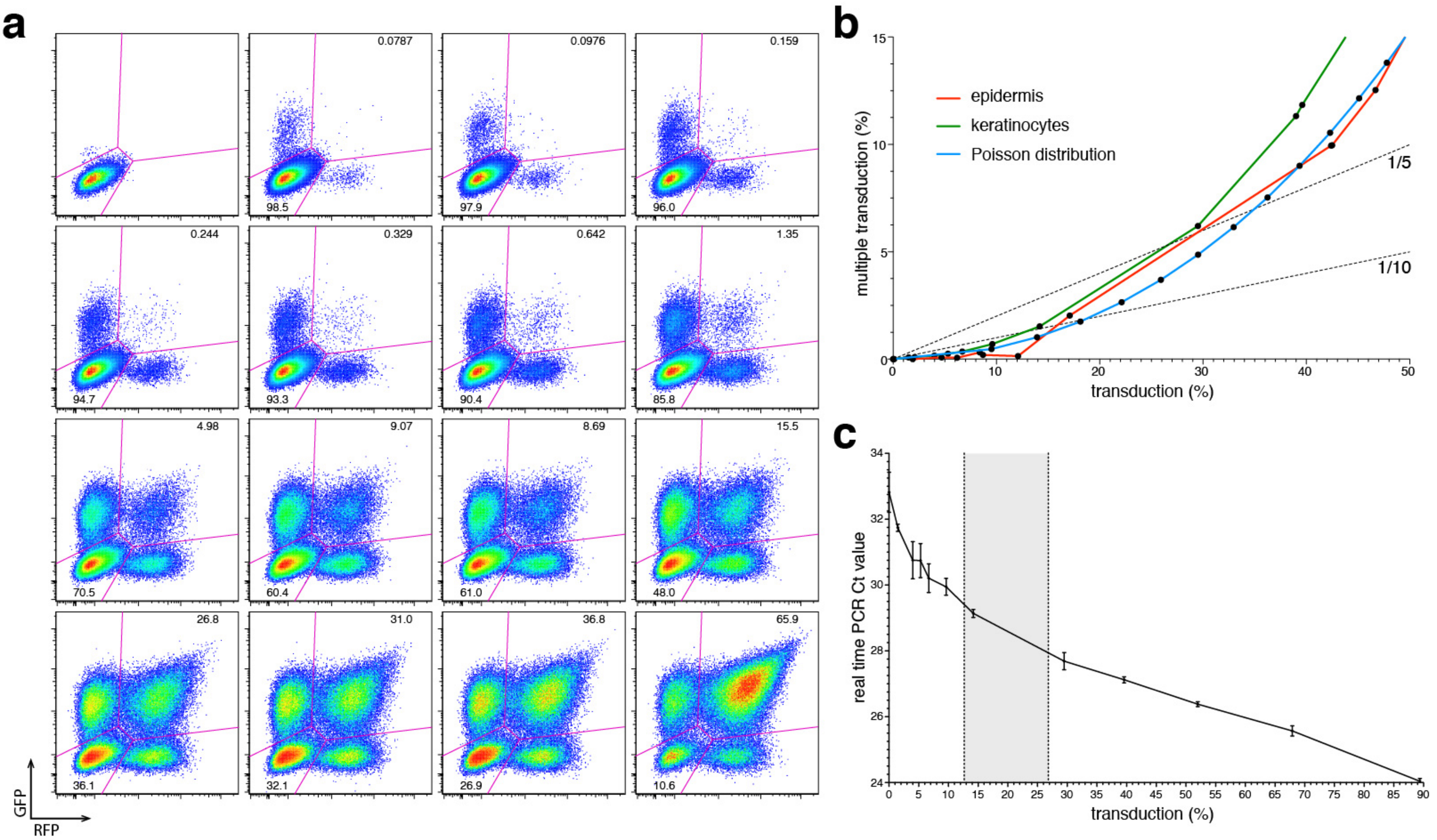
Supplementary Figure 4. Expression of oncogenic Hras^{G12V} during embryonic development results in increased proliferation, cell survival, and immune system activation. a-c, Flow cytometric analysis of proliferation, apoptosis, and immune system activation in back skin epidermis (**a**,**b**) or complete back skin (**c**) at E18.5. **a**, The numbers of epidermal cells incorporating EdU (S-phase, proliferative) following a 2 hour pulse are significantly increased with expression of one (*P*=0.0063) or two copies (*P*=0.0002) of Hras^{G12V}. Increasing dosage from Hras^{oncoX1} to Hras^{oncoX2} has a similar effect (*P*=0.0233). **b**, Numbers of apoptotic Caspase 3$^+$ epidermal cells are reduced in Hras^{oncoX2} animals compared to control (*P*=0.0085) and Hras^{oncoX1} (*P*=0.0355). **c**, Increased numbers of innate and adaptive immune cells (granulocytes: Ly-6G/C, macrophages: CD11b, dendritic epidermal cells: CD103, leukocytes: CD45, T cells: CD3ε, B lymphocytes: CD45R) in E18.5 back skin are detected with epidermal expression of Hras^{G12V}. **d**, Real-time PCR analysis of CDK inhibitor transcripts shows absence of senescence following epidermal Hras^{G12V} expression. Comparisons of transcript levels in young and old kidneys served as a positive control for senescence. Error bars (**a**-**c**) indicate s.e.m and (**d**) s.d. All data points represent individual embryos with *n*=3 (**a**,**b**), *n*=5 (**c**, control), or *n*=6 (**c**, Hras^{onco}). In real-time PCR experiment (**d**), data are shown for 3 embryos and two separate real-time reactions (*n*=6). n.s. (not significant, *P*>0.05), * (*P*≤0.05), and ** (*P*≤0.01) indicate statistical significance of comparison to control epidermis (**a**-**d**) and/or young kidney (**d**).



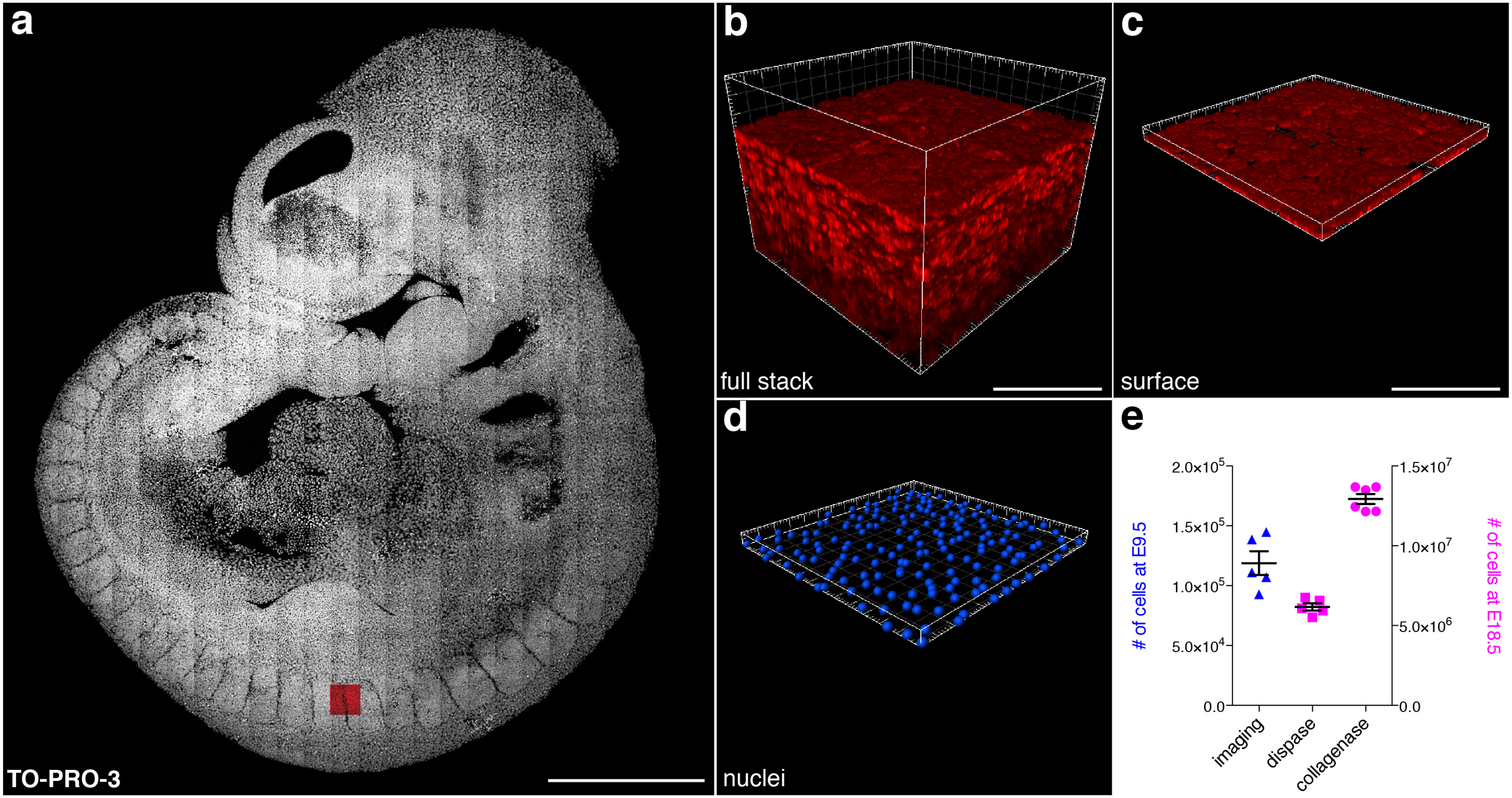
Supplementary Figure 5. RNAi affects normal and oncogene-dependent clonal expansion of a cell transduced at E9.5 with a single shRNA molecule. a, Real-time PCR analysis of *Anapc5* and *Hras1* transcript levels following shRNA-mediated knockdown. **b**, Transduced cell clones from E18.5 wild-type embryos infected at E9.5 with LV-Cre coexpressing scrambled or Anapc5#847 shRNAs, and Hras^{soncoX2} embryos infected at E9.5 with LV-Cre coexpressing scrambled or Hras1#267 shRNAs. Note a decrease in clone size when cells are transduced with an shRNA targeting *Anapc5* (control) or *Hras1* (Hras^{oncoX2}). **c**, Images from a z-series through epidermal clones at E18.5 (**b**) show normal cell morphology from the small cells in the deep-laying progenitor (basal) layer to the flattened superficial cells in the cornified envelope (stratum corneum). Transduced cells, YFP^{+}; TO-PRO-3, nuclei. Error bars (**a**) indicate s.d. In real-time PCR experiment (**a**) data are shown for 3 embryos and two separate real-time reactions (*n*=6). Red * (**a**) indicate strongest shRNAs used for gene knockdown (**b**,**c**). Scale bars, 50 µm.



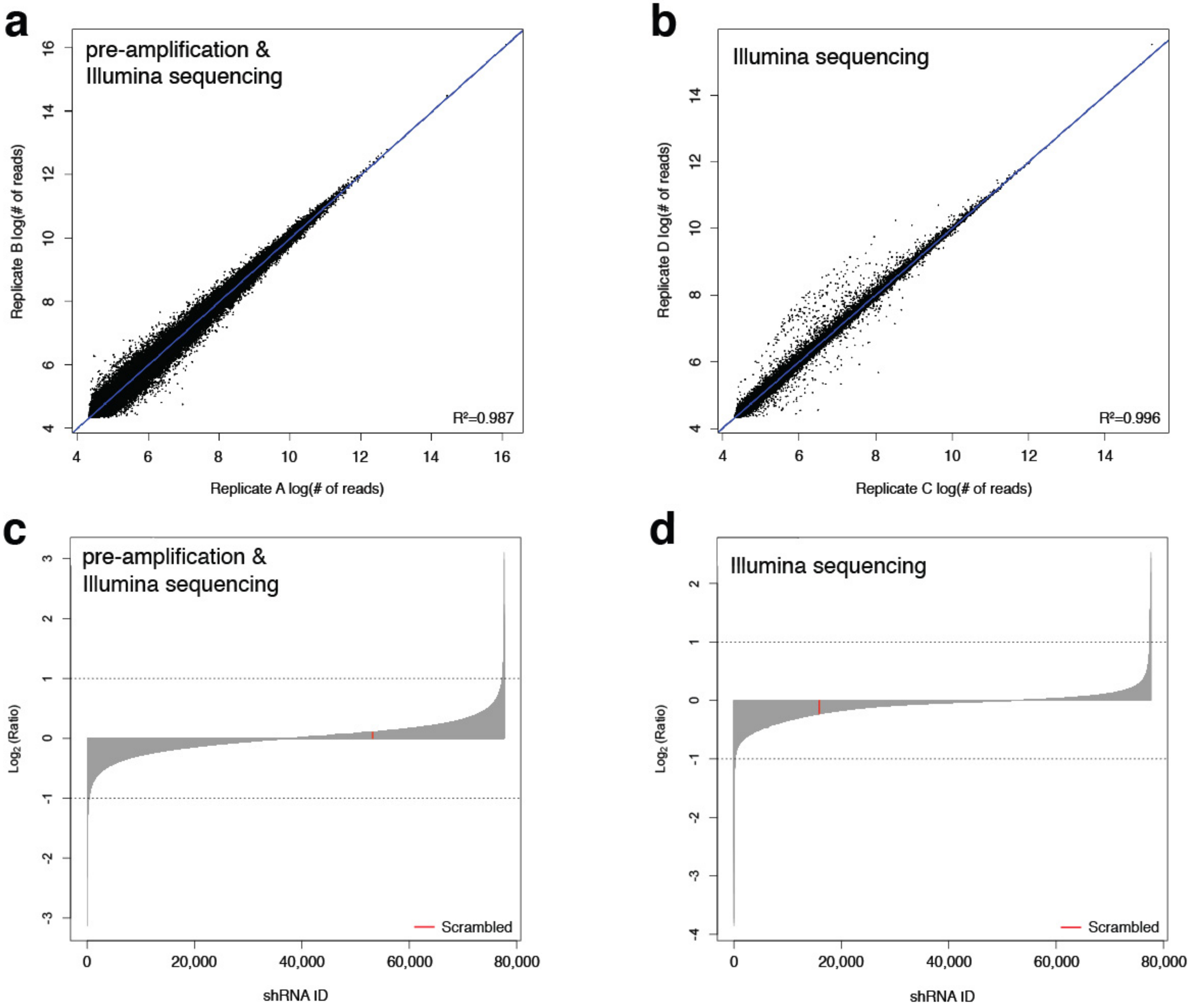
Supplementary Figure 6. shRNA identification using Illumina sequencing platform is quantitative, highly sensitive, and reproducible. a, To amplify the shRNA target sequence (red), custom oligonucleotides were designed that contain adapters (orange) and sequencing features (dark green) allowing for direct binding to the Illumina flow cell, and a 4nt barcode (pink) allowing for multiplex sequencing. **b**, Sequencing library preparation using fused-primer PCR reaction and dsDNA clean-up after 18 and 35 cycles produces a clean PCR product. **c**, To generate a defined gDNA template and test our sequencing approach, we infected cultured E18.5 mouse epidermal keratinocytes with individual shRNAs at MOI≤1 and selected for transduced cells after five days on media containing puromycin. Cells were used for isolation of gDNAs, which were combined in increasing amounts, representing a series from 1 to 2,048 cells. **d**, Composition of a defined gDNA template for test sequencing, expressed as cell numbers based on an estimate of 6 pg of gDNA per diploid cell. **e**, shRNA quantification by sequencing of the defined gDNA template from 11 independent runs. Red bar represents gDNA content (**d**) and sequencing count (**e**) of a non-hairpin target sequence. **f**, Pair-wise comparison of absolute shRNA counts from separate sequencing reaction confirms that Illumina based quantification of shRNAs stably integrated into the genome is reproducible (R^2=0.99975). Orange dots represent shRNAs present at ≤ 32 cells. [Note regarding data from **e**,**f**: The data from (**e**) demonstrate the sensitivity of our approach where even single copies of genome integrated shRNAs can be detected. The data from (**f**) show that any bias seen in quantification of genome integrated shRNA copy number seen in (**e**) is highly reproducible on independent Illumina sequencing runs. Since the biases are reproducible, they disappear in relative comparisons of Illumina sequencing quantifications.



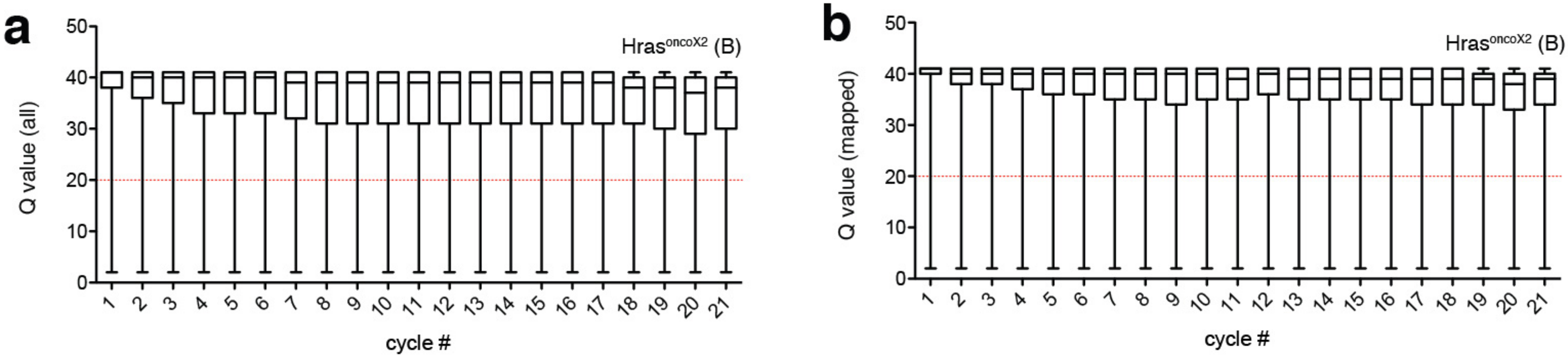
Supplementary Figure 7. Most cells are infected at MOI≤1 within the overall lentiviral transduction range of 15-25%. a, Flow cytometric analysis of fluorescent protein expression in keratinocytes infected with increasing amounts of LV-GFP and LV-RFP mixture shows that multiple transductions increase with higher viral titre. **b**, Percentage of embryonic epidermal cells (red) and keratinocytes in culture (green) infected at MOI>1 as a function of overall transduction. Note that the observed relationships of multiple to total transduction can be described by the Poisson distribution (blue). **c**, Real-time PCR with lentiviral vector-specific primers is used to measure transduction level in the absence of fluorescent protein expression, as with pooled shRNA library. Lines representing 1/10 and 1/5 fraction of infections at MOI>1 mark the range used in the screen.

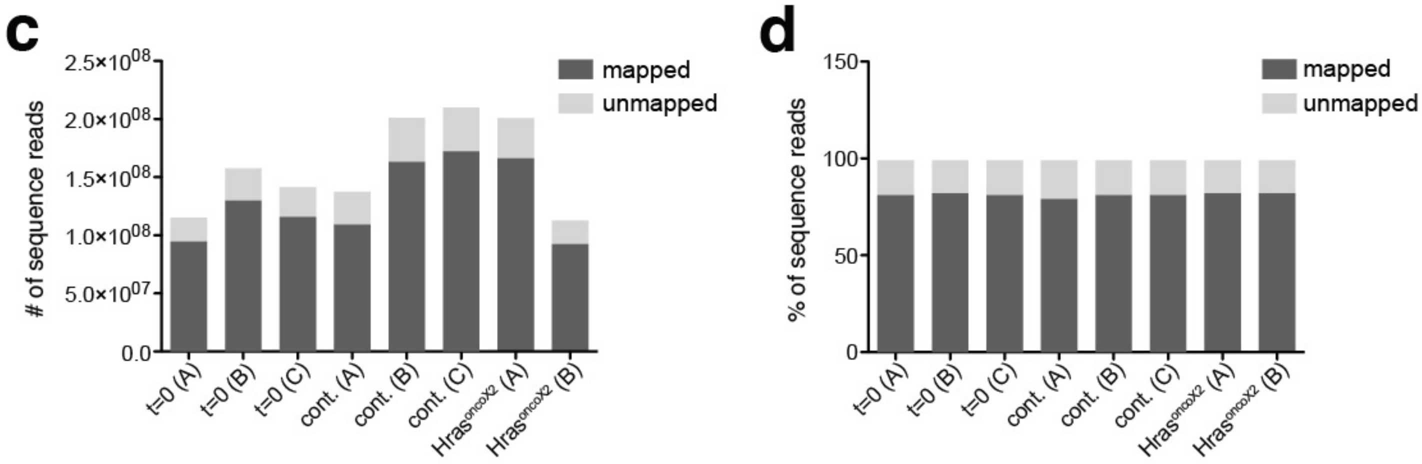


Supplementary Figure 8. Surface ectoderm at E9.5 contains at least 1.2X10^5 cells. a, Whole-mount image of an E9.5 embryo stained with nuclear marker TO-PRO-3, stitched from ~650 individual tiles. **b**, A single tile from **a** (red square), shown as a 3D volume projection of a 70 µm deep Z-stack. **c**, Top layer of cells, corresponding to surface ectoderm, from the Z-stack (**b**). **d**, Individual nuclei identified by segmentation of the surface layer (**c**). **e**, Counts of cells in the surface ectoderm at E9.5 from image analysis (blue), and cells in the interfollicular compartment (dispase/trypsin-treated epidermal fraction) or complete embryonic skin epithelium (collagenase-treated epithelial fraction ,i.e. epidermis+hair follicles) at E18.5 (pink). Error bars indicate s.e.m. All data points represent individual embryos with *n*=5 (imaging and dispase) or *n*=6 (collagenase). Scale bars, (**a**) 500 µm, (**b**,**c**) 50 µm.



Supplementary Figure 9. Pre-amplification and sequencing reactions are not a significant source of variability in the shRNA counts. a,**b**, Relative counts of shRNA reads generated from technical replicates of sequencing runs. **a**, The two replicates, A and B, were generated from the same gDNA template [t=0(B)] but were independently enriched for shRNA sequences by using our custom pre-amplification method. Samples were then subjected to independent Illumina sequencing runs. **b**, The two replicates, C and D, represent identical pre-amplified material that was sequenced by two independent Illumina runs. R^2 values (**a**,**b**) indicate high similarity between technical replicates. **c**,**d**, Analysis of relative shRNA abundance in technical replicate runs identified only 625 (**c**) and 384 (**d**) of 77,717 total shRNAs (input) that exhibited a 2-fold enrichment or depletion. Based on our screen selection criteria (gene is a hit if two shRNAs show the same effect, and no shRNAs show the opposite), 8 (**c**) and 3 (**d**) genes of ~16,000 total were identified as significantly altered, underscoring the exceedingly low rate of false positives obtained due to noise and/or bias of pre-amplification or Illumina sequencing reactions. Scrambled (red) denotes the control shRNA.

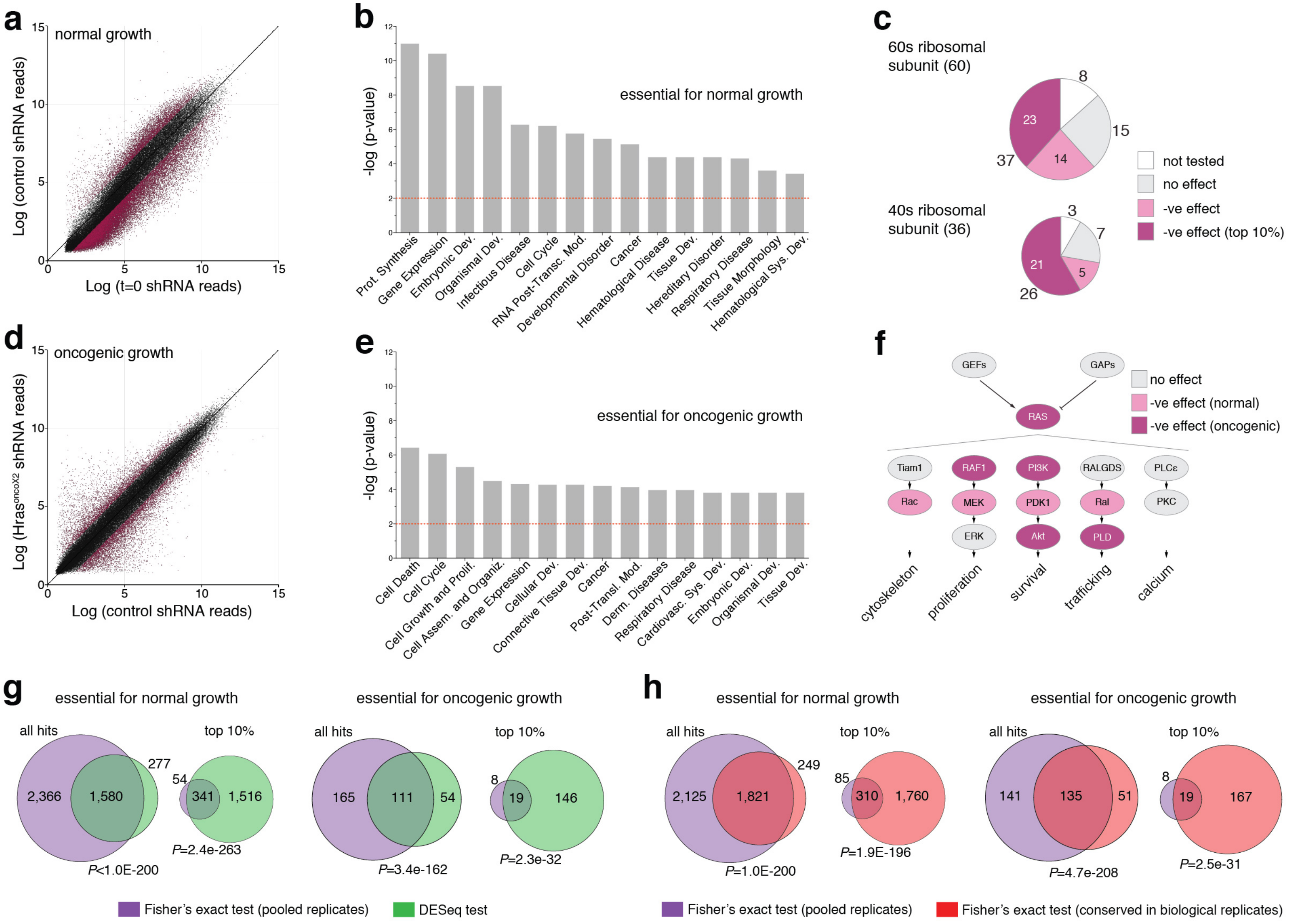




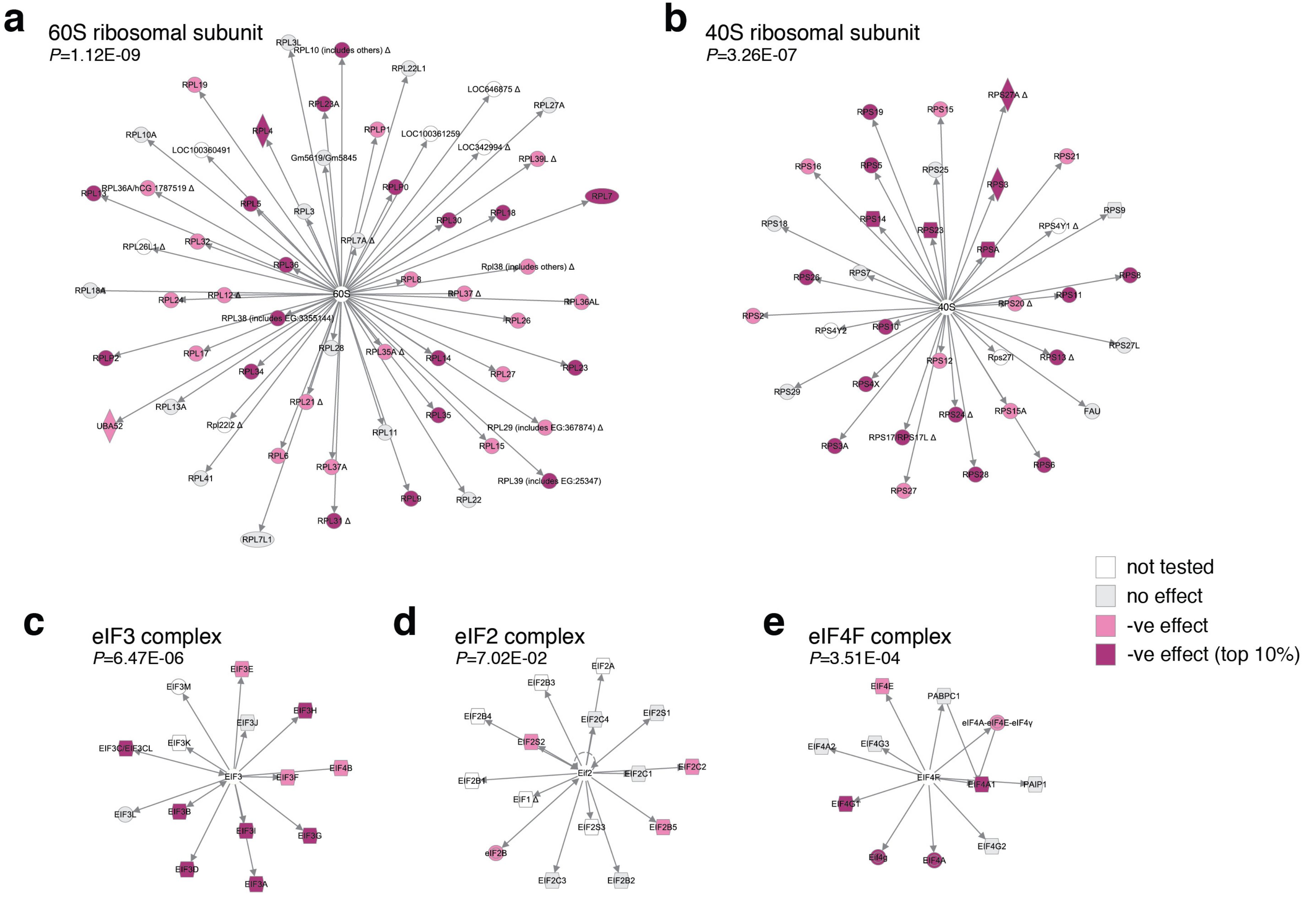
e

	# of shRNAs with ≤ :		
	0 reads	5 reads	10 reads
t=0	0	53	271
control	0	10	109
Hras^{oncoX2}	1	373	1,501

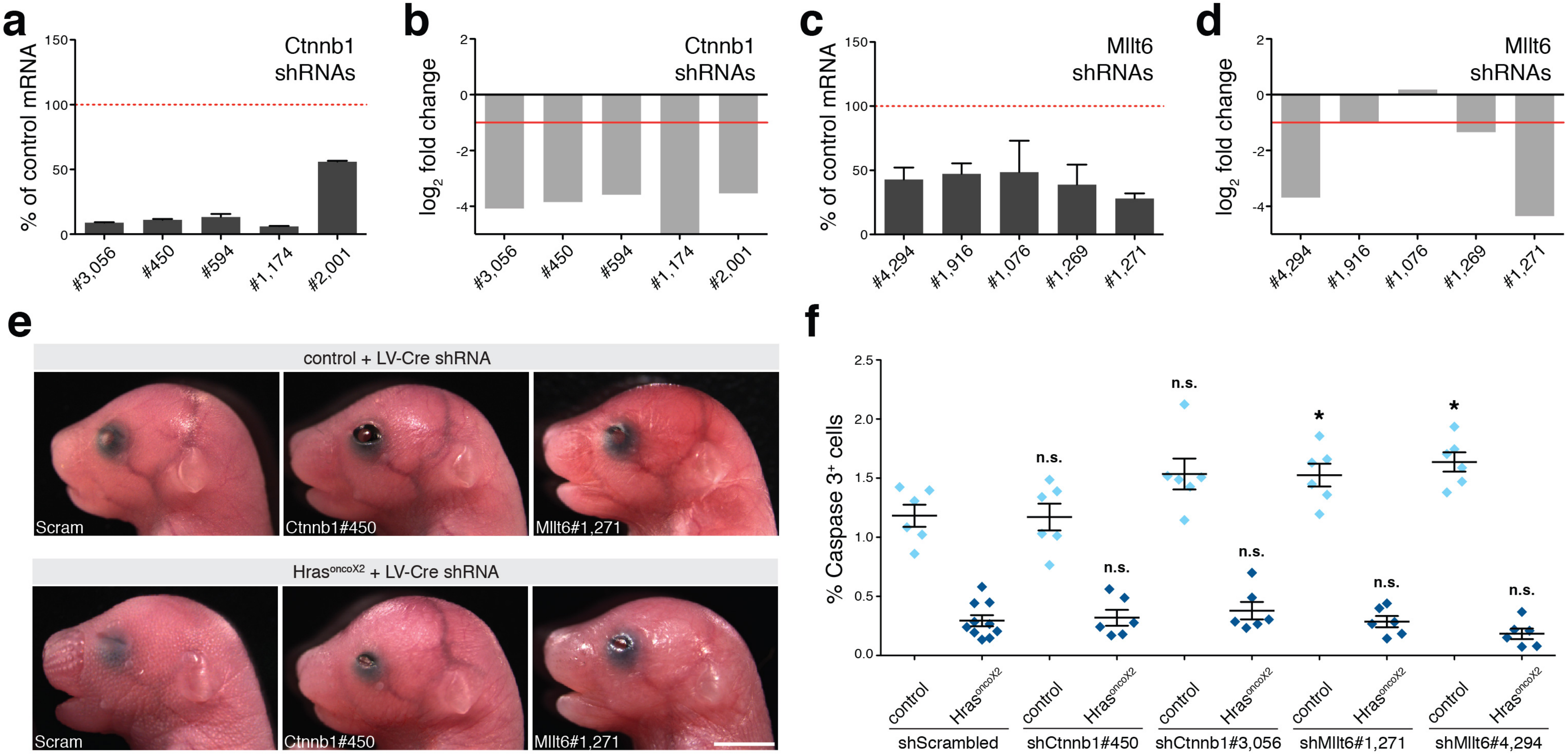
Supplementary Figure 10. shRNA quantification method yields sequences of high quality and achieves complete coverage of the lentiviral pool. **a**,**b**, Quality scores for a given base (Q-value) of the 21nt shRNA target sequence (cycle # corresponds to nt position) of the 1.12X10^8 sequence reads of Hras^{oncoX2} sample B (**a**), and the 9.24X10^7 sequencing reads that correctly mapped to the library of 77,717 shRNAs (**b**). Red line represents Q-value of 20, and a *P*=0.01 probability of an incorrect base call. **c**,**d**, Total number of sequencing reads across the samples ranged between 1.12-2.09X10^8 (**c**), with each sample having between 79-82% of correctly identified shRNAs (**d**). **e**, The screen achieved near complete coverage of the shRNA pool, with a single shRNA not identified in the Hras^{oncoX2} sample, and less than 2% identified with 10 reads or less. Data in **a**,**b** are represented with box-and-whisker plots.



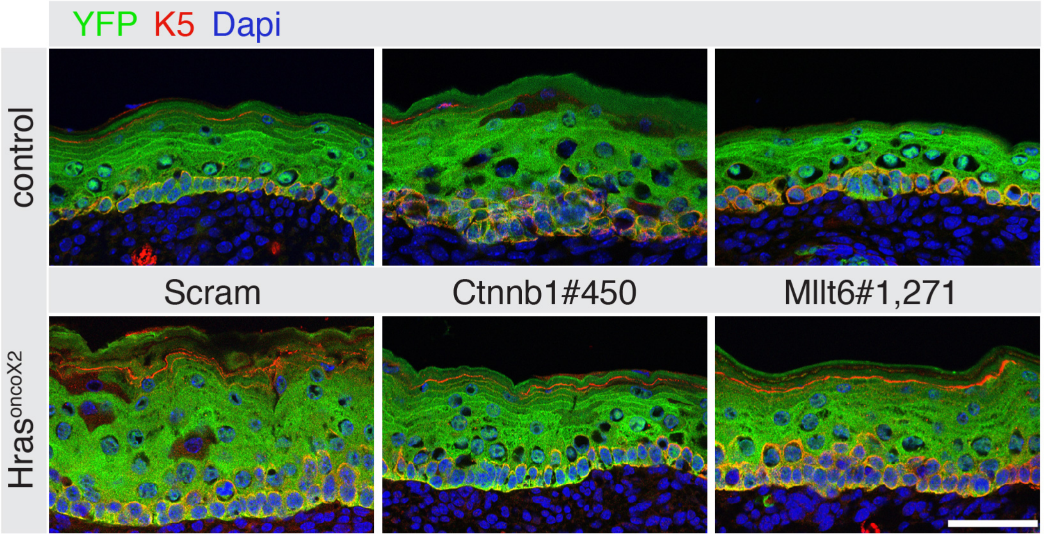
Supplementary Figure 11. Different statistical analyses identify conserved sets of putative growth regulators. a-f, Significantly enriched or depleted shRNAs identified using Fisher's exact test on pooled data sets. **a**, Dot plot of relative abundance of 77,717 shRNAs at t=0 and in E18.5 control epidermis. **b**, Putative normal growth regulators are significantly enriched (*P*≥0.01) for gene function categories that promote general cell viability and development. **c**, Genes scoring as essential for normal growth are enriched for ribosomal 60S and 40S subunits (*P*=1.12E-09 and *P*=3.26E-07), with many found in the top 10% of all hits (maroon). **d**, Dot plot of relative shRNA abundance at E18.5 in the control and Hras^{oncoX2} epidermis. shRNAs that are significantly enriched or depleted are shown in maroon (**a**,**d**). **e**, Putative oncogenic growth regulators are enriched (*P*≥0.01) in gene categories that promote cell viability and proliferation. **f**, Downstream effectors of Ras signaling score as essential for growth (pink), with many exhibiting an oncogene-specific requirement (maroon). **g**,**h** Analyses of the overlap between candidates identified as regulators of normal or Hras^{G12V}-dependent growth using Fisher's exact test on a pooled set of Illumina reads (purple) with: (**g**) candidates identified using DESeq test that directly accounts for variability among the biological replicates (green), or (**h**) candidates conserved in analysis of biological replicates using Fisher's exact test (salmon). Comparisons are shown for the full set of significant regulators (all hits), and the top 10% of significant regulators (top 10%). Probability that overlaps are due to chance is shown, suggesting significant conservation among identified regulators.



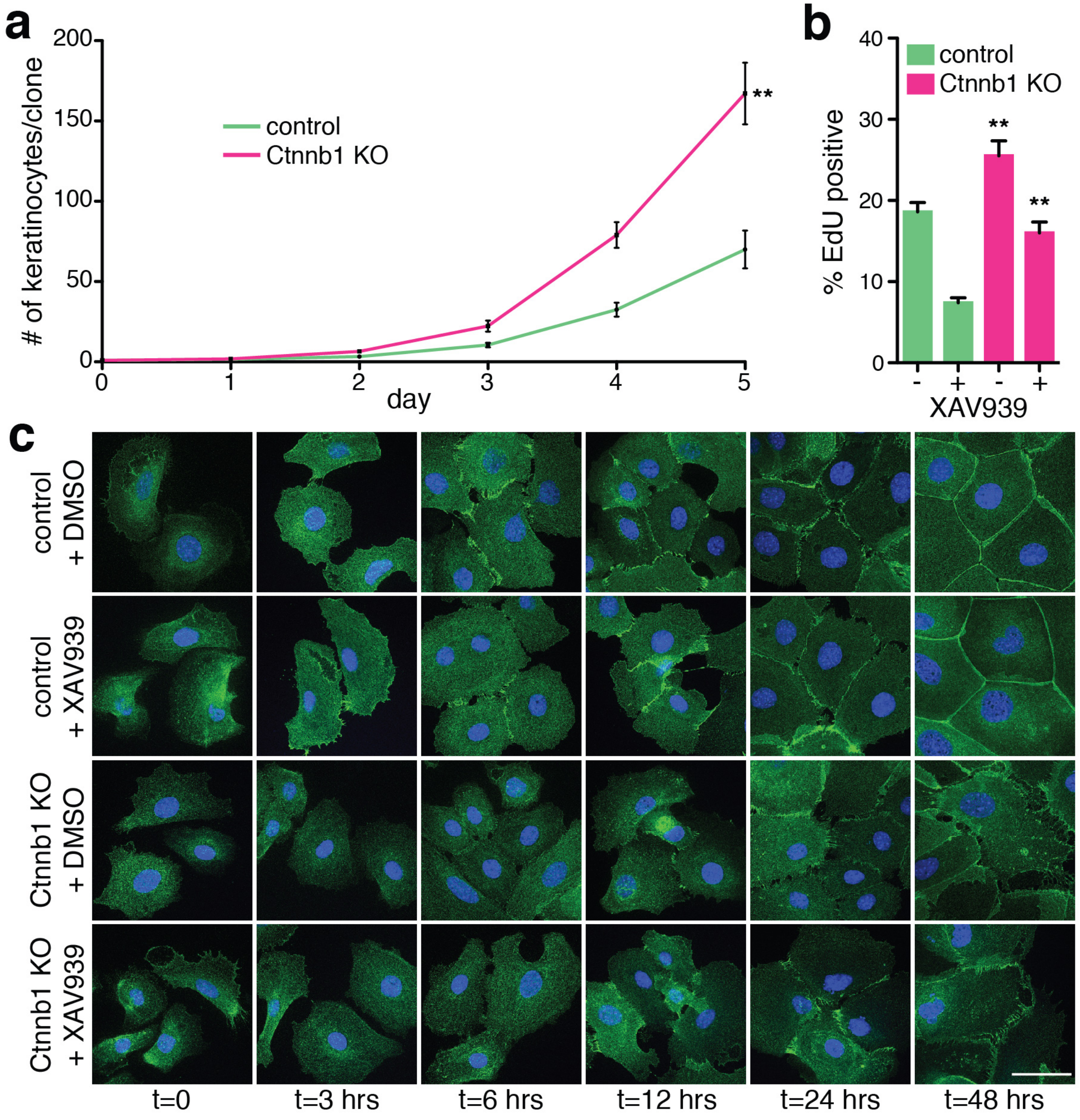
Supplementary Figure 12. Genes that function in basic cellular processes are overrepresented among the hits identified by the screen for normal growth regulators. a-e, Components of the translational machinery complexes including 60S (**a**) and 40S (**b**) ribosomal subunits, and eukaryotic initiation factor complexes eIF3 (**c**), and eIF4F (**e**) were significantly overrepresented among genes identified as essential for normal growth (*P*-value<0.05). Eukaryotic initiation factor 2 (eIF2, **d**) components were not significantly enriched. Color scheme identifies genes that were either: not targeted by the lentiviral shRNA pool (white); had no effect on growth (gray); significantly depleted during normal growth (pink); or significantly depleted and in the top 10% of all hits (maroon). –ve, negative.



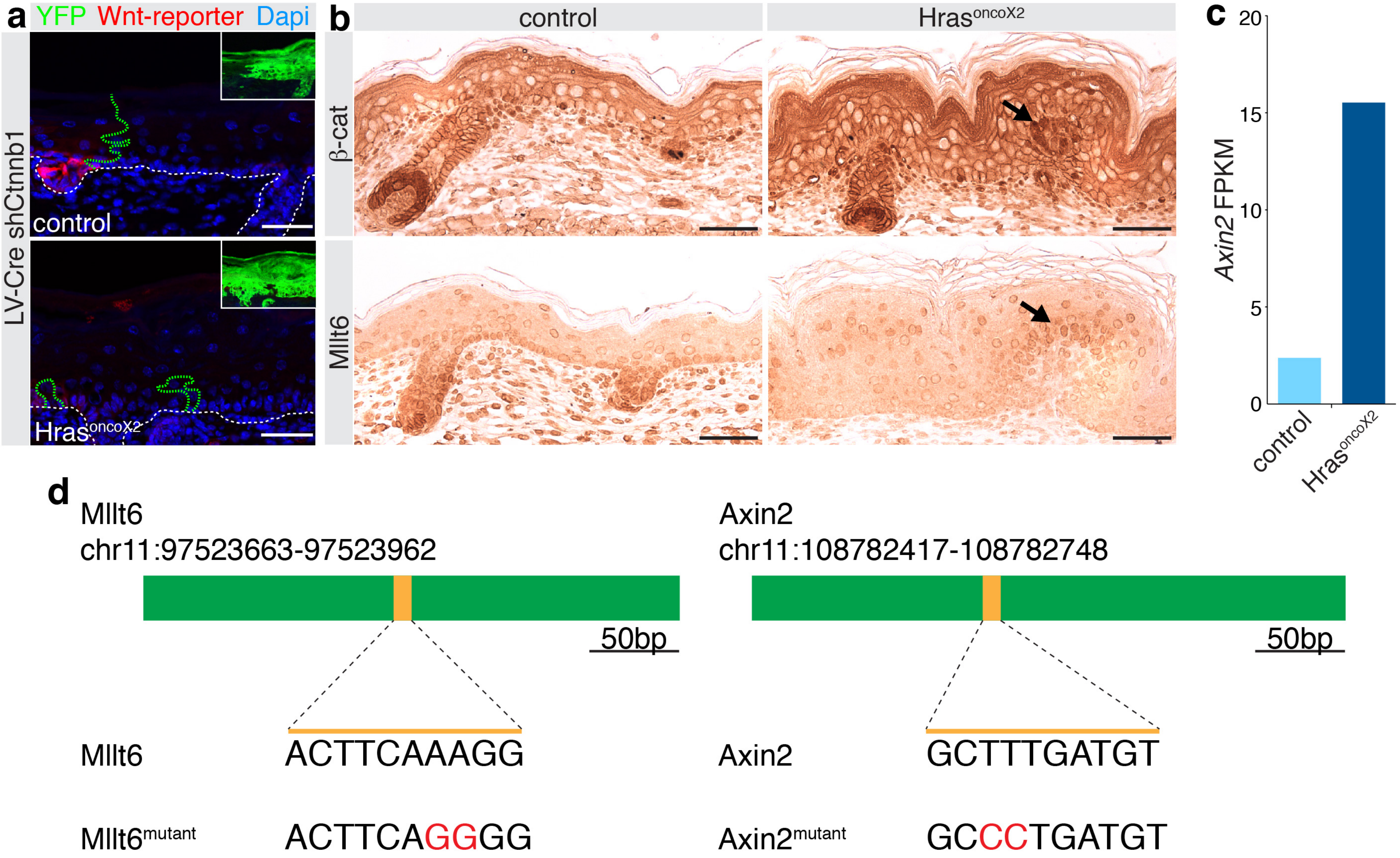
Supplementary Figure 13. β-Catenin and Mllt6 are essential regulators of Hras^{G12V}-dependent oncogenic growth. a-**d**, shRNA-mediated transcript depletion of *Ctnnb1* (β-catenin) and *Mllt6* is proportional to severity of oncogenic growth inhibition. **a**,**c**, Control *Ctnnb1* (**a**) and *Mllt6* (**c**) mRNA levels (red dashed line) are significantly depleted after shRNA-mediated gene knockdown. **b**,**d**, *Ctnnb1* (**b**) and *Mllt6* (**d**) knockdowns elicit selective growth inhibitory effects on Hras^{G12V} oncogenic relative to normal epidermis. Solid red line signifies a two-fold depletion. **e**, Representative control and Hras^{oncoX2} embryos transduced at E9.5 with LV-Cre expressing shRNAs against *Ctnnb1* and *Mllt6* and analyzed at E18.5. **f**, Analysis of the relative abundance of Caspase 3^+ cells in the basal layer of control and Hras^{oncoX2} epidermis transduced with LV-Cre expressing shRNAs. *Mllt6* depletion increases apoptosis in the control epidermis, while neither *Ctnnb1* nor *Mllt6* knockdown have an effect on cell death during oncogenic growth. Error bars indicate (**a**,**c**) s.d and (**f**) s.e.m. In real-time PCR experiment (**a**,**c**), data are shown for three independently transduced cell cultures, each analyzed in two independent reactions (*n*=6). Apoptosis data points (**f**) represent individual embryos with *n*=6 (all shCtnnb1 and shScram in control), *n*=7 (shMllt6#4,294 in control), *n*=8 (shMllt6#1.271), *n*=9 (shMllt6#4,294 in Hras^{G12V}), or *n*=10 (shScram in Hras^{G12V}), each scored through immunofluorescence analysis of ten 425.1 μm^2 images. **f**, n.s. (not significant, P>0.05) and * (P≤0.05) indicate statistical significance of comparison to LV-Cre + shScrambled transduced control and Hras^{oncoX2} epidermis. Scale bar, 3 mm.



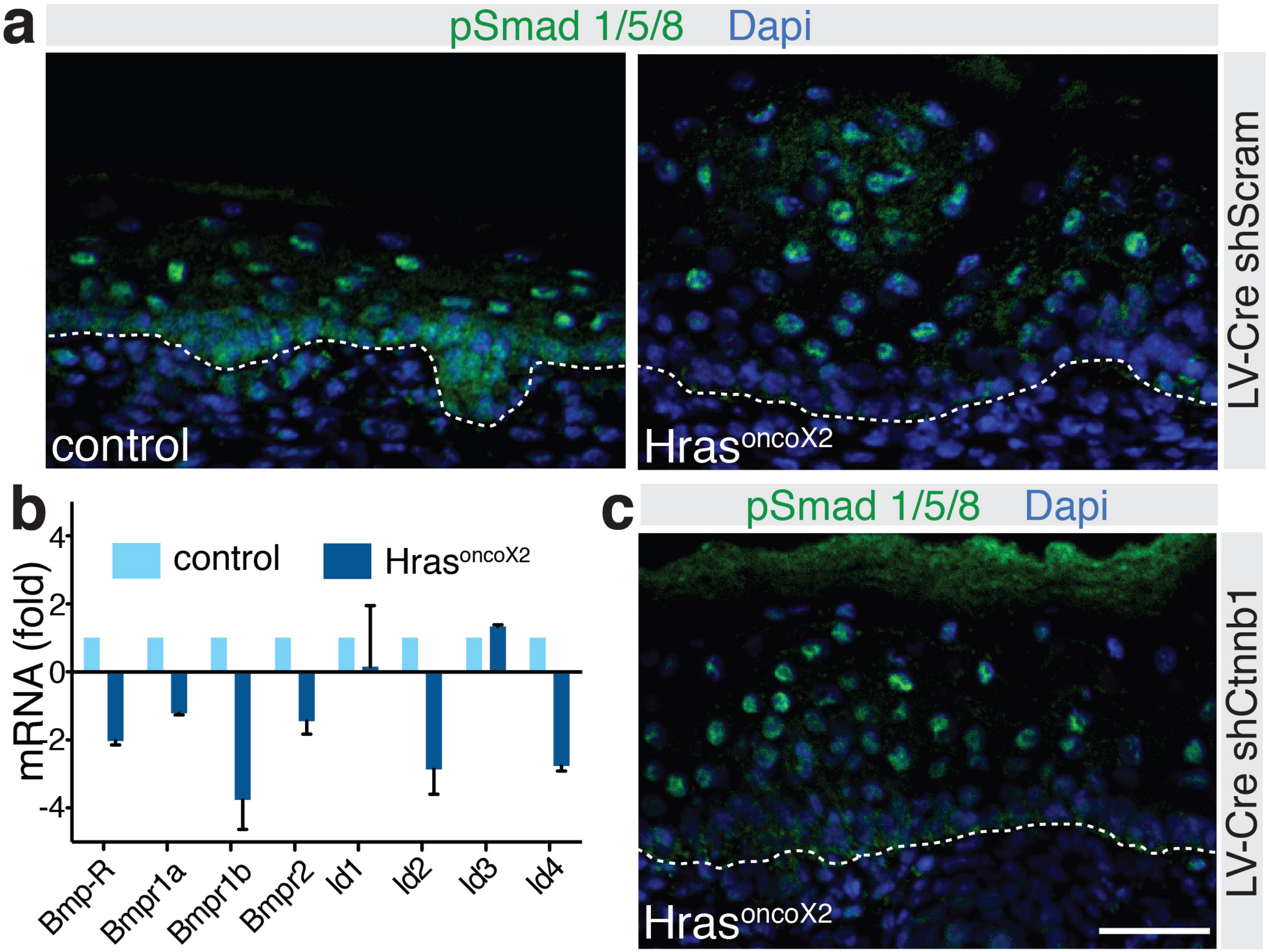
Supplementary Figure 14. Depletion of β-catenin and Mllt6 affects epidermal thickness in control and Hras^{oncoX2} animals. Thickness of epidermis of control and Hras^{oncoX2} animals transduced at E9.5 with shRNAs against *Ctnnb1* and *Mllt6* is strongly correlated with the rate of EdU incorporation (see Fig. 3e). YFP expression marks the transduced epidermis including the K5^{+} basal layer. Dapi labels the nuclei. Scale bar, 50 µm.



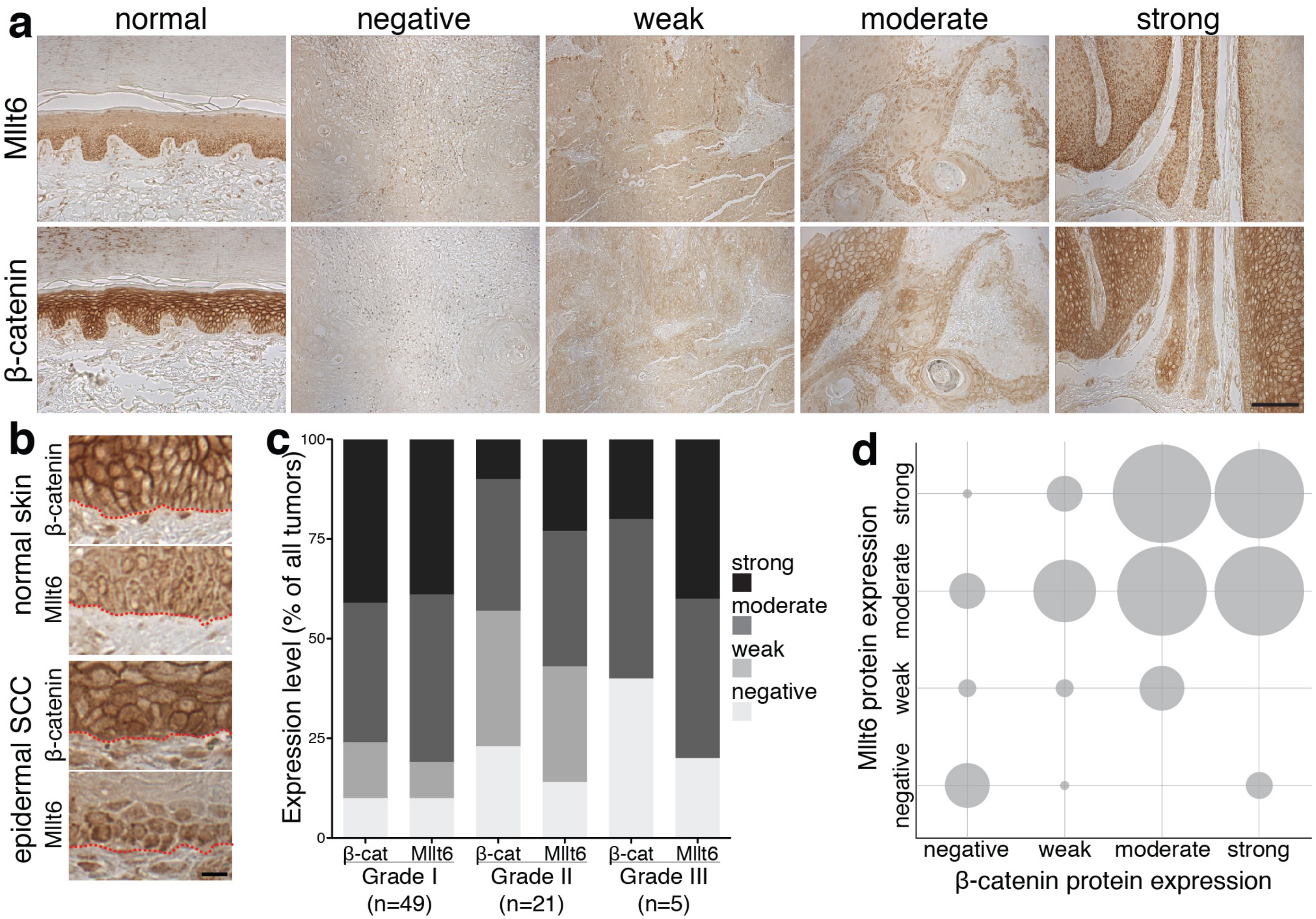
Supplementary Figure 15. Loss of β-catenin results in Wnt-independent hyperproliferation and loss of cell-cell adhesion. a,**b**, *Ctnnb1* knockout (Ctnnb1 KO) keratinocytes show significant increase in clonal expansion (**a**, *P*=0.0229) and EdU incorporation in culture (**b**, *P*=0.005). Treatment of control and *Ctnnb1* KO cells with a Wnt signaling inhibitor (XAV939) results in a marked reduction in EdU incorporation in both, yet the significant difference between control and *Ctnnb1* knockout cells is maintained (*P*=0.0005), consistent with it being due to Wnt-independent role of β-catenin. **c**, Establishment of cell-cell contacts following Ca^{2+} switch is impaired in *Ctnnb1* knockout keratinocytes, and is unaffected by disruption in Wnt-signaling. E-cadherin (green) marks the adherens junctions as they are being formed, and Dapi (blue) marks the nuclei. Error bars indicate s.e.m. (**a**) and s.d. (**b**). Data points represent (**a**) individual cell clones with n=12 (control) or n=16 (Ctnnb1 KO) or, (**b**) independent wells with n=3. n.s. (not significant, P>0.05), * (P≤0.05), and ** (P≤ 0.01) indicate statistical significance of comparison to control keratinocytes (**a**, **b**) or keratinocytes treated with a Wnt inhibitor (**b**). Scale bar, 50 µm.



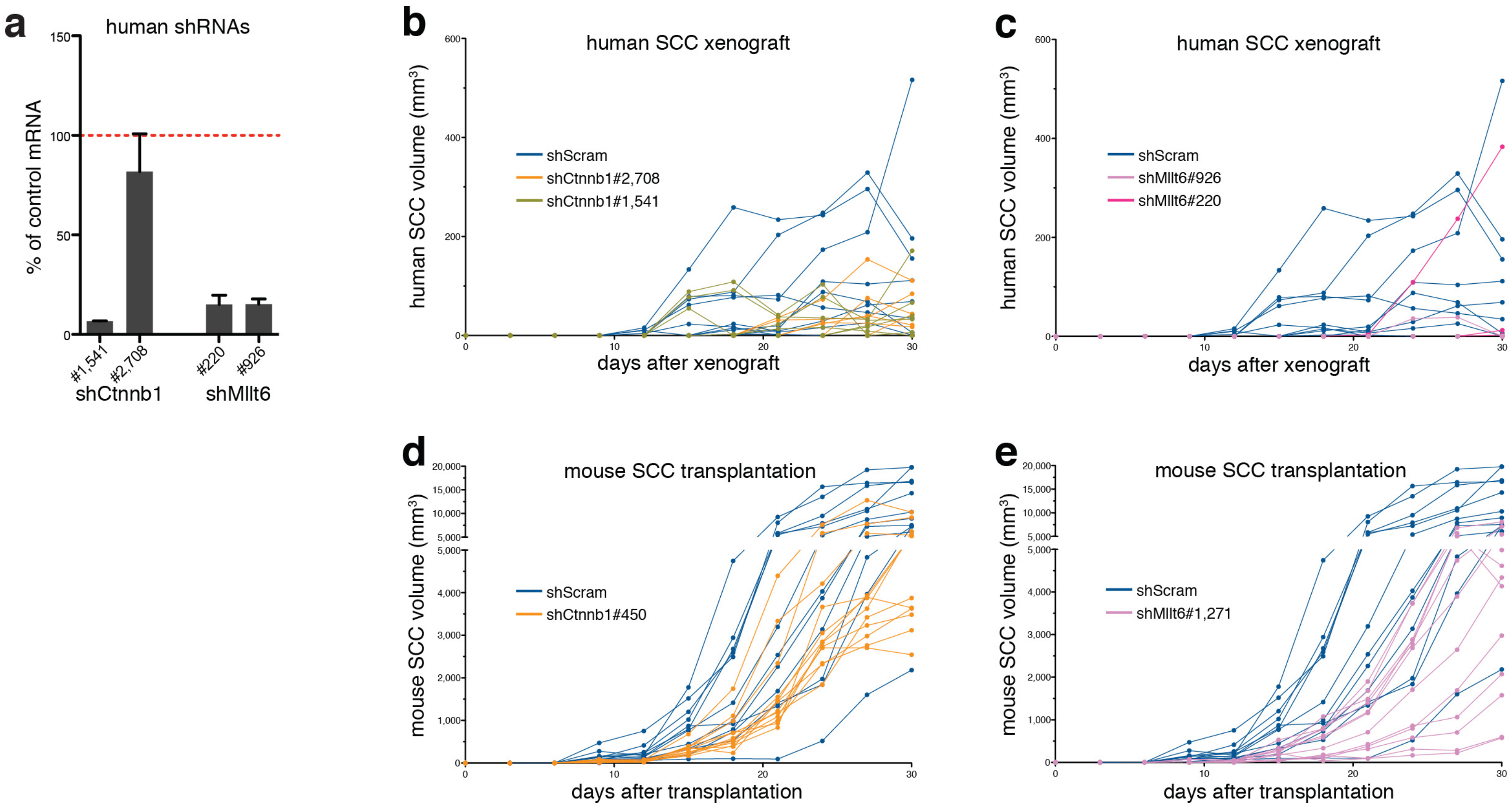
Supplementary Figure 16. Hras^{G12V} expression induces Wnt signaling in interfollicular epidermis. a, Wnt-reporter activity is suppressed by shRNA depletion of β-catenin in control (top) and Hras^{G12V} (bottom) animals. YFP (inset, in green) marks LV-Cre-transduced epidermis (to right of green dotted line in top; outside green-dotted lines in bottom). Dapi (blue) marks the nuclei. Dashed line demarcates epidermal-dermal interface. **b**, β-catenin and Mllt6 immunohistochemistry. Note nuclear β-catenin (top right) and Mllt6 accumulation (bottom right) in Hras^{oncoX2} epidermal evaginations (arrows). **c**, *Axin2* transcript levels (FPKM: Fragments Per Kilobase of transcript per Million mapped reads) are significantly upregulated in the epidermis of Hras^{G12V} animals. Values represent averages derived from RNA-Seq experiments, performed in duplicate. **d**, Genomic regions on Chromosome 11 where TCF3/4 binding sites upstream of *Mllt6* (left) and *Axin2* (right) were identified by CHIP-seq. Nucleotide substitutions (red) in the putative TCF3/4 binding motifs (yellow bar) of *Mllt6* and *Axin2* were generated to serve as negative controls (*Mllt6*^{mutant} and *Axin2*^{mutant}). Scale bars, 50 µm.



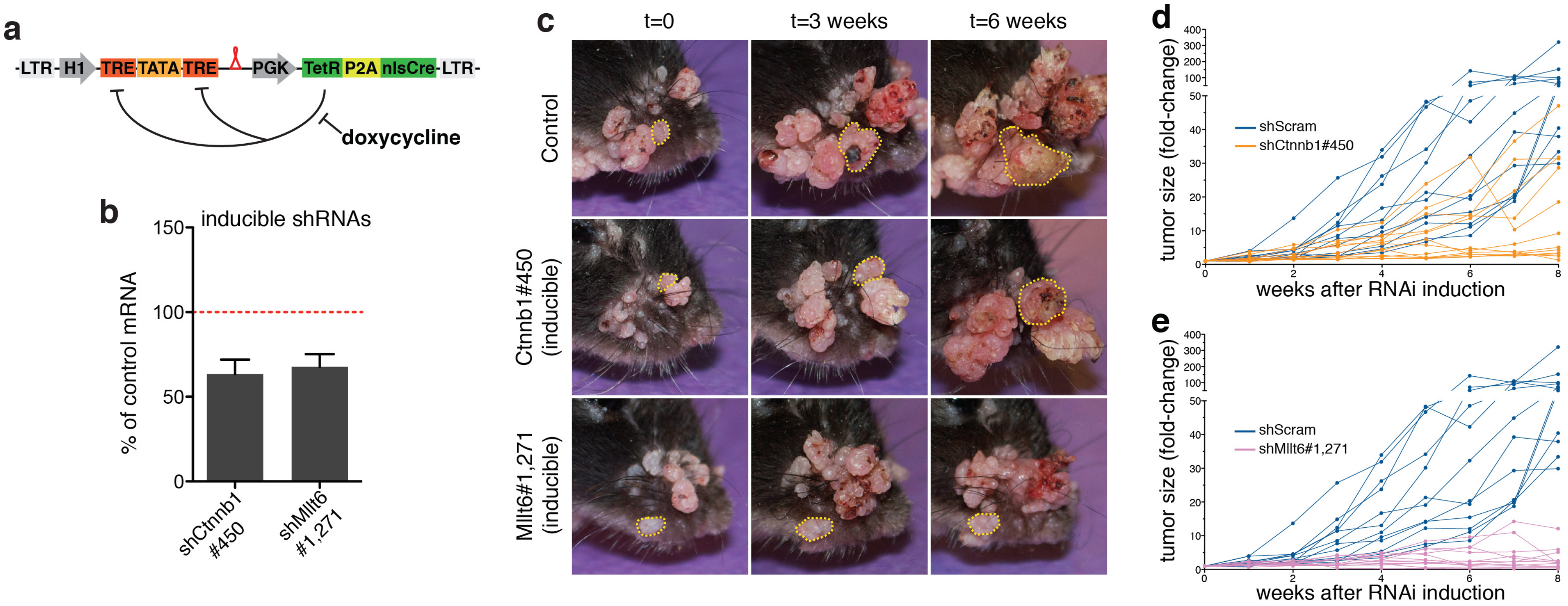
Supplementary Figure 17. BMP signaling is diminished during Hras^{G12V}-induced epidermal growth. a, Nuclear localization of pSmad1/5/8 in the basal progenitor layer (left) is diminished in Hras^{oncoX2} epidermis (right). **b**, mRNA levels of Bmp-reporter (Bmp-R) and downstream Bmp targets (Id2, Id4) are significantly reduced in Hras^{oncoX2} epidermal progenitors. **c**, Nuclear localization of pSmad1/5/8 in the progenitor layer is not rescued by shRNA-mediated depletion of β-catenin. White dotted line demarcates dermal-epidermal boundary. Dapi (blue) labels nuclei. In real-time PCR experiment (**b**), data are shown for 3 embryos analyzed in two separate real-time reactions (*n*=6), and error bars indicate s.e.m. Scale bar, 50 µm.



Supplementary Figure 18. β-catenin and Mllt6 expression in human epidermal SCC. a, A panel of human SCC samples was classified according to their expression of nuclear β-catenin and Mllt6, and included tumors where no signal was detected (negative), and where the signal was present at the levels <50% of the normal (weak), in the range of control expression (moderate), or at a level higher that in the control (strong). **b**, Nuclear localization of β-catenin and Mllt6 proteins is observed in epidermal cells that contact stroma in human SCC. Red dashed line marks the epidermal-dermal boundary. **c**,**d**, β-catenin and Mllt6 show parallel expression patterns in human SCCs (Spearman r=0.3018 and *P*=0.0085). The area of gray circles corresponds with the number of samples showing the trend. Scale bars, (**a**) 500 µm, (**b**) 50 µm.



Supplementary Figure 19. Depletion of β-catenin and Mllt6 results in significant SCC growth-retardation. **a**, shRNAs against human *Ctnnb1* and *Mllt6* transcripts are efficient at depleting their target levels relative to control (red dashed line). **b**,**c**, SCCs growing from 10^5 xenographed human SCC cells transduced with control (shScram) or two independent test shCtnnb1 (**b**) and shMllt6 (**c**) hairpins are sensitive to depletion of their targets. **d**,**e**, SCCs growing from 10^4 transplanted mouse cancer stem cells show a similar dependence on β-catenin and Mllt6 for growth. Data in **b-e** report tumor size as an absolute value over time, and represent individual transplants with n=12. Error bars indicate s.d. In real-time PCR experiment (**a**), data represent three independently transduced cell cultures and two real-time reactions (*n*=6).



Supplementary Figure 20. β-catenin and Mllt6 are essential for maintenance of Hras^{G12V}-dependent tumors. a, pLKO-Tet-On lentiviral construct allows for doxycycline regulated expression of shRNAs from an H1 promoter. In the absence of doxycycline, TetR, driven from a PGK promoter, represses shRNA expression by binding to the Tet responsive elements (TRE) flanking the TATA box. Addition of doxycycline removes the TetR-mediated repression and allows for shRNA expression and target knockdown. Note that TetR is linked to nlsCre through a self-cleaving P2A peptide, allowing for concomitant and constitutive expression of Cre-recombinase. **b**, Control *Ctnnb1* and *Mllt6* mRNA levels (red dashed line) are significantly depleted in tumors 8 weeks after doxycycline-mediated induction of shRNA knockdown. **c**, Examples of epidermal tumors induced by discrete Cre-mediated activation of Hras^{oncoX2} expression. Initial administration of doxycycline (t=0) was made 60 days after oncogene activation, and continued for 8 weeks through doxycycline diet. Tumors are also shown at 3 and 6 weeks of inducible knockdown of *Ctnnb1* and *Mllt6*. Representative papillomas are outlined (yellow dashed line). **d**,**e**, Spontaneous epidermal tumors arising from discrete Hras^{oncoX2} cells show reduction in growth rates following induction of shCtnnb1 (**d**) and shMllt6 (**e**) expression. Data in **d**,**e**, show tumor size over time as relative to their initial size (t=0), and represent individual tumors with n=12. Error bars indicate s.d. In real-time PCR experiment (**b**), data are shown for three tumors and two separate real-time reactions (*n*=6).

Supplementary Table 1. Putative regulators of normal growth identified by DESeq test of biological replicates.

Note: Candidates identified by both DESeq and Fisher's exact test are highlighted in purple.

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	67671	Rpl38	ribosomal protein L38	0	4	0	-4.339221
2	16785	Rpsa	ribosomal protein SA	0	4	0	-4.079998
3	20643	Snrpe	small nuclear ribonucleoprotein E	0	4	0	-3.810049
4	20088	Rps24	ribosomal protein S24	0	3	0	-3.68909
5	19946	Rpl30	ribosomal protein L30	0	4	0	-3.666467
6	53817	Bat1a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	0	3	0	-3.613878
7	268449	Rpl23a	ribosomal protein L23A	0	3	0	-3.609205
8	66373	Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	3	0	-3.41019
9	65019	Rpl23	ribosomal protein L23	0	3	0	-3.373683
10	60411	Cenpk	centromere protein K	0	3	0	-3.360687
11	75805	Nln	neurolysin (metallopeptidase M3 family)	0	3	0	-3.323194
12	113847	V1ra5	vomeronasal 1 receptor 43	0	3	0	-3.310562
13	68436	1100001I22Rik	ribosomal protein L34	0	4	0	-3.238885
14	75062	Sf3a3	splicing factor 3a, subunit 3	0	3	0	-3.148655
15	64436	Inpp5e	inositol polyphosphate-5-phosphatase E	0	3	0	-3.141052
16	69786	Tprkb	Tp53rk binding protein	0	3	0	-3.082626
17	110750	Cse1l	chromosome segregation 1-like (S. cerevisiae)	0	4	0	-3.068876
18	68052	Rps13	ribosomal protein S13	0	3	0	-3.063958
19	18249	Obp1a	odorant binding protein Ia	0	3	0	-3.030449
20	78070	Cpt1c	carnitine palmitoyltransferase 1c	0	3	0	-3.01639
21	81845	Bat4	G patch domain and ankyrin repeats 1	0	3	0	-2.996082
22	20091	Rps3a	ribosomal protein S3A	0	4	0	-2.978607
23	22627	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0	3	0	-2.963589
24	17463	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0	3	0	-2.949004
25	213469	Lgi3	leucine-rich repeat LGI family, member 3	0	3	0	-2.929412
26	12043	Bcl2	B cell leukemia/lymphoma 2	0	3	0	-2.898144
27	21372	Tbl1x	transducin (beta)-like 1 X-linked	0	3	0	-2.897752
28	20102	Rps4x	ribosomal protein S4, X-linked	0	5	0	-2.894
29	217692	Sipa1l1	signal-induced proliferation-associated 1 like 1	0	3	0	-2.878408
30	235184	BC024479	cDNA sequence BC024479	0	3	0	-2.875646

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
31	104831	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	0	3	0	-2.874595
32	27370	Rps26	ribosomal protein S26	0	4	0	-2.849476
33	20116	Rps8	ribosomal protein S8	0	4	0	-2.816489
34	57267	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	0	3	0	-2.802923
35	27207	Rps11	ribosomal protein S11	0	3	0	-2.783613
36	20103	Rps5	ribosomal protein S5	0	4	0	-2.78067
37	19899	Rpl18	ribosomal protein L18	0	3	0	-2.774511
38	71805	Nup93	nucleoporin 93	0	3	0	-2.773984
39	17096	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	0	3	0	-2.766454
40	19983	Rpl5	NA	0	4	0	-2.762295
41	17713	Grpel1	GrpE-like 1, mitochondrial	0	3	0	-2.758901
42	12468	Cct7	chaperonin containing Tcp1, subunit 7 (eta)	0	3	0	-2.74743
43	208634	Tspan10	tetraspanin 10	0	4	0	-2.740088
44	66055	0610009D07Rik	RIKEN cDNA 0610009D07 gene	0	3	0	-2.727277
45	66309	Tmem128	transmembrane protein 128	0	3	0	-2.7246
46	16341	Eif3s6	eukaryotic translation initiation factor 3, subunit E	0	3	0	-2.71133
47	17069	Ly6e	lymphocyte antigen 6 complex, locus E	0	3	0	-2.704518
48	233437	F830104D24Rik	vomeronasal 2, receptor 66	0	3	0	-2.695087
49	208643	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	0	3	0	-2.691456
50	50797	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	0	4	0	-2.686088
51	22700	Zfp40	zinc finger protein 40	0	3	0	-2.680161
52	66878	Riok3	RIO kinase 3 (yeast)	0	3	0	-2.668678
53	67097	Rps10	ribosomal protein S10	0	3	0	-2.665608
54	66537	2510048O06Rik	proteasome maturation protein	0	3	0	-2.659838
55	72843	Prdm4	PR domain containing 4	0	3	0	-2.652077
56	107999	Gtpbp6	GTP binding protein 6 (putative)	0	3	0	-2.645169
57	16401	Itga4	integrin alpha 4	0	3	0	-2.628811
58	27050	Rps3	ribosomal protein S3	0	5	0	-2.620946
59	66489	Rpl35	ribosomal protein L35	0	3	0	-2.612605
60	620654	UNK	NA	0	3	0	-2.606489
61	69354	Slc38a4	solute carrier family 38, member 4	0	3	0	-2.603837
62	20104	Rps6	ribosomal protein S6	0	4	0	-2.602653
63	66711	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	0	3	0	-2.590301
64	67115	Rpl14	ribosomal protein L14	0	4	0	-2.583297

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
65	109095	Rbm15b	RNA binding motif protein 15B	0	3	0	-2.577491
66	110954	Rpl10	ribosomal protein 10	0	3	0	-2.572107
67	12464	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	0	4	0	-2.563147
68	320106	9330158F14Rik	solute carrier family 38, member 11	0	3	0	-2.557726
69	15497	Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6	0	4	0	-2.552715
70	194456	UNK	NA	0	3	0	-2.551336
71	68365	Rab14	RAB14, member RAS oncogene family	0	4	0	-2.542897
72	22003	Tpm1	tropomyosin 1, alpha	0	3	0	-2.518739
73	17829	Muc1	mucin 1, transmembrane	0	3	0	-2.510883
74	320118	Fbxl13	F-box and leucine-rich repeat protein 13	0	3	0	-2.509783
75	20379	Sfrp4	secreted frizzled-related protein 4	0	3	0	-2.50256
76	76522	Lsm8	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	0	3	0	-2.490629
77	114641	Rpl31	ribosomal protein L31	0	3	0	-2.476485
78	66085	Eif3s5	eukaryotic translation initiation factor 3, subunit F	0	3	0	-2.475468
79	378435	Mafa	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian)	0	3	0	-2.467841
80	81898	Sf3b1	splicing factor 3b, subunit 1	0	4	0	-2.460782
81	19112	Prlpc1	prolactin family 8, subfamily a, member 6	0	3	0	-2.449631
82	246103	Atxn7	ataxin 7	0	3	0	-2.448723
83	70127	Dpf3	D4, zinc and double PHD fingers, family 3	0	3	0	-2.446845
84	16363	Irf2	interferon regulatory factor 2	0	3	0	-2.442872
85	270106	Rpl13	ribosomal protein L13	0	3	0	-2.442594
86	54127	Rps28	ribosomal protein S28	0	3	0	-2.435125
87	67186	Rplp2	ribosomal protein, large P2	0	3	0	-2.43432
88	214253	Etnk2	ethanolamine kinase 2	0	4	0	-2.425197
89	12015	Bad	BCL2-associated agonist of cell death	0	3	0	-2.424971
90	106582	Nrm	nurim (nuclear envelope membrane protein)	0	3	0	-2.420306
91	192986	Cyb5d2	cytochrome b5 domain containing 2	0	3	0	-2.416131
92	210126	Lpp	LIM domain containing preferred translocation partner in lipoma	0	4	0	-2.409133
93	433297	LOC433297	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle pseudogene	0	3	0	-2.40878
94	67332	Snrpd3	small nuclear ribonucleoprotein D3	0	3	0	-2.408524
95	17246	Mdm2	transformed mouse 3T3 cell double minute 2	0	3	0	-2.408074
96	72112	Ppp1r14d	protein phosphatase 1, regulatory (inhibitor) subunit 14D	0	3	0	-2.39796
97	18146	Npdc1	neural proliferation, differentiation and control gene 1	0	3	0	-2.393931
98	21346	Tagln2	transgelin 2	0	3	0	-2.391755

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
99	12466	Cct6a	chaperonin containing Tcp1, subunit 6a (zeta)	0	4	0	-2.389838
100	93670	Tac4	tachykinin 4	0	3	0	-2.385428
101	20068	Rps17	ribosomal protein S17	0	4	0	-2.379258
102	15013	H2-Q2	histocompatibility 2, Q region locus 2	0	4	0	-2.378056
103	57780	Fxyd7	FXYD domain-containing ion transport regulator 7	0	3	0	-2.374736
104	278097	Armcx6	armadillo repeat containing, X-linked 6	0	3	0	-2.374356
105	67168	P2ry5	lysophosphatidic acid receptor 6	0	3	0	-2.374344
106	21681	Thoc4	Aly/REF export factor	0	3	0	-2.372914
107	107767	Scamp1	secretory carrier membrane protein 1	0	3	0	-2.371455
108	21946	Pglyrp1	peptidoglycan recognition protein 1	0	3	0	-2.370492
109	113857	V1rb9	vomeronasal 1 receptor 41	0	3	0	-2.366996
110	171258	V1ri7	vomeronasal 1 receptor 202	0	3	0	-2.366009
111	433285	UNK	NA	0	3	0	-2.358734
112	53382	Txnl1	thioredoxin-like 1	0	3	0	-2.336602
113	20630	Snrp1c	U1 small nuclear ribonucleoprotein C	0	3	0	-2.336013
114	74589	4933428M03Rik	kelch repeat and BTB (POZ) domain containing 12	0	3	0	-2.3327
115	67143	Zfpn1a5	IKAROS family zinc finger 5	0	3	0	-2.321429
116	12753	Clock	circadian locomotor output cycles kaput	0	3	0	-2.31908
117	435766	Tnni3k	TNNI3 interacting kinase	0	3	0	-2.31581
118	114895	UNK	NA	0	3	0	-2.314364
119	19671	Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	0	3	0	-2.31051
120	67678	Lsm3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	4	0	-2.310446
121	76499	Clasp2	CLIP associating protein 2	0	3	0	-2.307653
122	241134	9430031J16Rik	RIKEN cDNA 9430031J16 gene	0	3	0	-2.306393
123	19989	Rpl7	ribosomal protein L7	0	4	0	-2.303568
124	20005	Rpl9	ribosomal protein L9	0	3	0	-2.30269
125	56194	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	0	4	0	-2.299517
126	104130	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0	3	0	-2.296626
127	245663	LOC245663	prohibitin pseudogene	0	4	0	-2.289553
128	66475	Rps23	ribosomal protein S23	0	4	0	-2.283045
129	245866	Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	0	3	0	-2.28257
130	12458	Ccr6	chemokine (C-C motif) receptor 6	0	3	0	-2.279072
131	11837	Arbp	ribosomal protein, large, P0	0	4	0	-2.275991
132	20637	Snrp70	small nuclear ribonucleoprotein 70 (U1)	0	3	0	-2.272878

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
133	15891	Ibsp	integrin binding sialoprotein	0	3	0	-2.271915
134	403200	4930504O13Rik	RIKEN cDNA 4930504O13 gene	0	3	0	-2.270211
135	22601	Yap1	yes-associated protein 1	0	4	0	-2.262612
136	432986	Kb16p	type II keratin Kb16P	0	4	0	-2.259583
137	78908	Igsf3	immunoglobulin superfamily, member 3	0	3	0	-2.258492
138	11787	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	0	3	0	-2.257702
139	98970	Fibcd1	fibrinogen C domain containing 1	0	5	0	-2.256076
140	12317	Calr	calreticulin	0	4	0	-2.255337
141	66882	Bzw1	basic leucine zipper and W2 domains 1	0	3	0	-2.245709
142	14113	Fbl	fibrillarin	0	3	0	-2.244987
143	68468	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	0	3	0	-2.23909
144	216616	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	0	3	0	-2.23812
145	68479	Phf5a	PHD finger protein 5A	0	3	0	-2.230631
146	54217	Rpl36	ribosomal protein L36	0	3	0	-2.229974
147	69787	Anxa13	annexin A13	0	4	0	-2.226859
148	67891	Rpl4	ribosomal protein L4	0	3	0	-2.226255
149	21689	Tekt1	tektin 1	0	3	0	-2.223372
150	15229	Foxd1	forkhead box D1	0	3	0	-2.222823
151	230103	Npr2	natriuretic peptide receptor 2	0	4	0	-2.220004
152	20085	Rps19	ribosomal protein S19	0	3	0	-2.208389
153	74653	4930444A02Rik	RIKEN cDNA 4930444A02 gene	0	3	0	-2.207932
154	68770	Phtf2	putative homeodomain transcription factor 2	0	3	0	-2.207409
155	18632	Pex11b	peroxisomal biogenesis factor 11 beta	0	3	0	-2.205925
156	56018	Stard10	START domain containing 10	0	4	0	-2.205127
157	209318	Gps1	G protein pathway suppressor 1	0	3	0	-2.203966
158	26445	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	0	4	0	-2.203463
159	27362	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	0	3	0	-2.19876
160	72308	Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	0	3	0	-2.192492
161	14651	Hagh	hydroxyacyl glutathione hydrolase	0	3	0	-2.191247
162	53319	Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	0	3	0	-2.18956
163	110809	Sfrs1	serine/arginine-rich splicing factor 1	0	3	0	-2.183404
164	109754	Cyb5r3	cytochrome b5 reductase 3	0	3	0	-2.175758
165	17749	Polr2k	polymerase (RNA) II (DNA directed) polypeptide K	0	3	0	-2.175589
166	14626	Gk2	glycerol kinase 2	0	3	0	-2.174739

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
167	268395	Mpg	N-methylpurine-DNA glycosylase	0	3	0	-2.170713
168	13226	Defcr-rs7	defensin, alpha, related sequence 7	0	3	0	-2.166744
169	71446	Wrb	tryptophan rich basic protein	0	3	0	-2.162425
170	13164	Dazl	deleted in azoospermia-like	0	3	0	-2.161805
171	14944	Gzmg	granzyme G	0	3	0	-2.16084
172	329302	UNK	NA	0	3	0	-2.159104
173	72780	Rspo3	R-spondin 3 homolog (Xenopus laevis)	0	3	0	-2.154918
174	16783	Lamp1	lysosomal-associated membrane protein 1	0	4	0	-2.152228
175	244144	Usp35	ubiquitin specific peptidase 35	0	3	0	-2.14748
176	66665	5730528L13Rik	RIKEN cDNA 5730528L13 gene	0	3	0	-2.146389
177	75627	Snapc1	small nuclear RNA activating complex, polypeptide 1	0	4	0	-2.146325
178	384361	UNK	NA	0	4	0	-2.145862
179	381511	Ppm2c	pyruvate dehyrogenase phosphatase catalytic subunit 1	0	3	0	-2.145784
180	67661	Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	0	3	0	-2.141744
181	20044	Rps14	ribosomal protein S14	0	3	0	-2.137683
182	20020	Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	0	3	0	-2.136608
183	22139	Ttr	transthyretin	0	3	0	-2.135728
184	67236	2810452K22Rik	cyclin-dependent kinase 2 interacting protein	0	3	0	-2.135489
185	60365	Rbm8a	RNA binding motif protein 8a	0	3	0	-2.134922
186	258904	Olfr1221	olfactory receptor 1221	0	3	0	-2.134388
187	78294	Rps27a	ribosomal protein S27A	0	4	0	-2.132393
188	73353	Actrt2	actin-related protein T2	0	4	0	-2.131837
189	83679	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	0	3	0	-2.128432
190	14394	Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	0	3	0	-2.124248
191	18740	Pitx1	paired-like homeodomain transcription factor 1	0	3	0	-2.124128
192	12425	Cckar	cholecystokinin A receptor	0	3	0	-2.1236
193	93691	Klf7	Kruppel-like factor 7 (ubiquitous)	0	3	0	-2.121214
194	12575	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	0	3	0	-2.116542
195	227683	Coq4	coenzyme Q4 homolog (yeast)	0	3	0	-2.116473
196	81879	Tcfcp2l1	transcription factor CP2-like 1	0	3	0	-2.11165
197	384639	LOC384639	tetraspanin 7 pseudogene	0	3	0	-2.11125
198	66492	Zmat2	zinc finger, matrin type 2	0	4	0	-2.101759
199	72085	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	0	3	0	-2.100954
200	109552	Sri	sorcin	0	3	0	-2.099236

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
201	14028	Evx1	even skipped homeotic gene 1 homolog	0	3	0	-2.098211
202	17975	Ncl	nucleolin	0	5	0	-2.094065
203	14705	Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	0	3	0	-2.090752
204	51960	Kctd18	potassium channel tetramerisation domain containing 18	0	3	0	-2.08915
205	19933	Rpl21	ribosomal protein L21	0	4	0	-2.089087
206	54713	Zfp312	Fez family zinc finger 2	0	3	0	-2.084881
207	319322	Sf3b2	splicing factor 3b, subunit 2	0	3	0	-2.083558
208	101023	Zfp513	zinc finger protein 513	0	3	0	-2.082396
209	14913	Guca1a	guanylate cyclase activator 1a (retina)	0	3	0	-2.076792
210	19951	Rpl32	ribosomal protein L32	0	3	0	-2.075773
211	20448	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltrans	0	4	0	-2.071198
212	83965	Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	0	3	0	-2.063434
213	15223	Foxj1	forkhead box J1	0	3	0	-2.05773
214	78304	Lsmd1	LSM domain containing 1	0	3	0	-2.054105
215	20899	Stra8	stimulated by retinoic acid gene 8	0	3	0	-2.047656
216	15039	H2-T22	histocompatibility 2, T region locus 22	0	3	0	-2.04332
217	19981	Rpl37a	ribosomal protein L37a	0	3	0	-2.039922
218	258927	Olfr481	olfactory receptor 481	0	3	0	-2.034612
219	13406	Dmp1	dentin matrix protein 1	0	4	0	-2.027262
220	18012	Neurod1	neurogenic differentiation 1	0	3	0	-2.008923
221	107508	Eprs	glutamyl-prolyl-tRNA synthetase	0	3	0	-2.002513
222	28077	D13Wsu50e	mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae)	0	3	0	-2.000825
223	20658	Son	Son DNA binding protein	0	3	0	-1.997952
224	240066	BC066107	zinc finger protein 870	0	3	0	-1.997125
225	64435	Fcamr	Fc receptor, IgA, IgM, high affinity	0	3	0	-1.995491
226	320435	5830482F20Rik	Ras and Rab interactor-like	0	3	0	-1.99443
227	66506	1810042K04Rik	proteasome (prosome, macropain) assembly chaperone 3	0	3	0	-1.993025
228	243382	Ppm1k	protein phosphatase 1K (PP2C domain containing)	0	4	0	-1.99278
229	73182	3110045G13Rik	platelet endothelial aggregation receptor 1	0	3	0	-1.991089
230	14148	Fdx1	ferredoxin 1	0	3	0	-1.990299
231	403183	4832428D23Rik	RIKEN cDNA 4832428D23 gene	0	3	0	-1.988978
232	19378	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	0	3	0	-1.987671
233	20319	Sfrp2	secreted frizzled-related protein 2	0	3	0	-1.982702
234	98363	Efhd1	EF hand domain containing 1	0	3	0	-1.979772

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
235	12396	Cbfa2t2h	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	0	3	0	-1.975358
236	67932	1700129C05Rik	RIKEN cDNA 1700129C05 gene	0	3	0	-1.97245
237	218100	Zfp322a	zinc finger protein 322A	0	3	0	-1.970895
238	103583	Fbxw11	F-box and WD-40 domain protein 11	0	3	0	-1.96888
239	12062	Bdkrb2	bradykinin receptor, beta 2	0	4	0	-1.968079
240	380601	C78212	FAST kinase domains 5	0	3	0	-1.960673
241	69032	Lyzl4	lysozyme-like 4	0	3	0	-1.953294
242	12346	Car1	carbonic anhydrase 1	0	3	0	-1.95096
243	319195	Rpl17	ribosomal protein L17	0	3	0	-1.950051
244	56447	Copz1	coatomer protein complex, subunit zeta 1	0	3	0	-1.94875
245	19356	Rad17	RAD17 homolog (S. pombe)	0	3	0	-1.947939
246	268294	Zbtb24	zinc finger and BTB domain containing 24	0	3	0	-1.94773
247	14787	Rhpn1	rhophilin, Rho GTPase binding protein 1	0	3	0	-1.944858
248	15504	Dnajb3	DnaJ (Hsp40) homolog, subfamily B, member 3	0	3	0	-1.935472
249	233489	Picalm	phosphatidylinositol binding clathrin assembly protein	0	4	0	-1.93358
250	74747	Ddit4	DNA-damage-inducible transcript 4	0	3	0	-1.932743
251	170736	Parvb	parvin, beta	0	3	0	-1.928655
252	50770	Atp11a	ATPase, class VI, type 11A	0	3	0	-1.92121
253	239151	Gm600	NA	0	3	0	-1.920541
254	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	0	3	0	-1.919689
255	12372	Casq1	calsequestrin 1	0	3	0	-1.915447
256	68221	1700049M11Rik	WAP four-disulfide core domain 15A	0	3	0	-1.912978
257	11606	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0	3	0	-1.912162
258	380839	Serpinb1c	serine (or cysteine) peptidase inhibitor, clade B, member 1c	0	3	0	-1.910636
259	230991	B930041F14Rik	RIKEN cDNA B930041F14 gene	0	3	0	-1.903894
260	70676	Gulp1	GULP, engulfment adaptor PTB domain containing 1	0	3	0	-1.903221
261	67126	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0	3	0	-1.902026
262	435287	UNK	NA	0	3	0	-1.901343
263	11568	Aebp1	AE binding protein 1	0	3	0	-1.899558
264	67344	Tctex1d1	Tctex1 domain containing 1	0	3	0	-1.892519
265	259011	Olfr389	olfactory receptor 389	0	4	0	-1.891594
266	140489	Bhlhb4	basic helix-loop-helix family, member e23	0	3	0	-1.891407
267	18103	Nme2	non-metastatic cells 2, protein (NM23B) expressed in	0	5	0	-1.888298
268	30853	Mlf2	myeloid leukemia factor 2	0	3	0	-1.887994

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
269	209225	Zfp710	zinc finger protein 710	0	3	0	-1.883288
270	103142	Rdh9	retinol dehydrogenase 9	0	3	0	-1.880657
271	320995	Rfxdc1	regulatory factor X, 6	0	3	0	-1.876787
272	93673	Cml2	camello-like 2	0	3	0	-1.87676
273	20054	Rps15	ribosomal protein S15	0	5	0	-1.875996
274	258468	Olfr1254	olfactory receptor 1254	0	3	0	-1.872929
275	13669	Eif3s10	eukaryotic translation initiation factor 3, subunit A	0	4	0	-1.871942
276	26961	Rpl8	ribosomal protein L8	0	4	0	-1.870848
277	68550	1110002N22Rik	RIKEN cDNA 1110002N22 gene	0	3	0	-1.869878
278	66922	Rras2	related RAS viral (r-ras) oncogene homolog 2	0	3	0	-1.86942
279	76932	Arfip2	ADP-ribosylation factor interacting protein 2	0	3	0	-1.868514
280	56717	Frap1	mechanistic target of rapamycin (serine/threonine kinase)	0	3	0	-1.867851
281	102680	Xtrp3s1	solute carrier family 6 (neurotransmitter transporter), member 20A	0	3	0	-1.867729
282	20807	Srf	serum response factor	0	3	0	-1.865409
283	319508	Syt15	synaptotagmin XV	0	3	0	-1.863561
284	12442	Ccnb2	cyclin B2	0	3	0	-1.862591
285	14199	Fhl1	four and a half LIM domains 1	0	3	0	-1.859711
286	22034	Traf6	TNF receptor-associated factor 6	0	3	0	-1.857557
287	66257	Nicn1	nicolin 1	0	3	0	-1.840389
288	69520	2310002A05Rik	late cornified envelope 3F	0	3	0	-1.839958
289	21461	Tcp10b	t-complex protein 10a	0	3	0	-1.837816
290	20196	S100a13	S100 calcium binding protein A13	0	3	0	-1.837202
291	68038	3110023E09Rik	chitinase domain containing 1	0	3	0	-1.83064
292	55944	Eif3s7	eukaryotic translation initiation factor 3, subunit D	0	3	0	-1.827583
293	18120	Mrpl49	mitochondrial ribosomal protein L49	0	3	0	-1.827508
294	641227	UNK	NA	0	3	0	-1.82386
295	18784	Pla2g5	phospholipase A2, group V	0	3	0	-1.82166
296	18715	Pim2	proviral integration site 2	0	3	0	-1.821351
297	66469	2810405K02Rik	RIKEN cDNA 2810405K02 gene	0	3	0	-1.821065
298	353234	Pcdha2	protocadherin alpha 2	0	3	0	-1.818826
299	67204	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	0	3	0	-1.817172
300	67395	4930403L05Rik	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 9	0	3	0	-1.810252
301	329278	Tnn	tenascin N	0	3	0	-1.806694
302	194162	BC035954	NA	0	3	0	-1.806535

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
303	233187	Lim2	lens intrinsic membrane protein 2	0	4	0	-1.797216
304	57808	Rpl35a	ribosomal protein L35A	0	3	0	-1.797049
305	103511	BB146404	family with sequence similarity 26, member E	0	3	0	-1.794471
306	12613	Cel	carboxyl ester lipase	0	3	0	-1.792809
307	17293	Mesp2	mesoderm posterior 2	0	3	0	-1.791005
308	71819	Kif23	kinesin family member 23	0	4	0	-1.78876
309	58205	Pdcd1lg2	programmed cell death 1 ligand 2	0	3	0	-1.784956
310	26386	Hsf4	heat shock transcription factor 4	0	3	0	-1.783701
311	100678	Psph	phosphoserine phosphatase	0	3	0	-1.783538
312	56031	Ppie	peptidylprolyl isomerase E (cyclophilin E)	0	4	0	-1.782773
313	20909	Stx4a	syntaxin 4A (placental)	0	3	0	-1.777408
314	21976	Top3b	topoisomerase (DNA) III beta	0	3	0	-1.771934
315	434390	UNK	NA	0	3	0	-1.768253
316	14427	Galr1	galanin receptor 1	0	3	0	-1.76503
317	56289	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	0	3	0	-1.755222
318	76025	Cant1	calcium activated nucleotidase 1	0	3	0	-1.754868
319	26946	Trpc7	transient receptor potential cation channel, subfamily C, member 7	0	3	0	-1.753607
320	84653	Hes7	hairy and enhancer of split 7 (Drosophila)	0	3	0	-1.752555
321	381971	UNK	NA	0	3	0	-1.747642
322	80284	BC003266	cDNA sequence BC003266	0	3	0	-1.747192
323	320484	A430107D22Rik	RAS protein activator like 3	0	3	0	-1.744776
324	16491	Kcna3	potassium voltage-gated channel, shaker-related subfamily, member 3	0	3	0	-1.7334
325	320795	Pkn1	protein kinase N1	0	3	0	-1.732132
326	67881	1810034K20Rik	magnesium-dependent phosphatase 1	0	4	0	-1.73029
327	26942	Spag1	sperm associated antigen 1	0	3	0	-1.725307
328	107503	Atf5	activating transcription factor 5	0	3	0	-1.723926
329	20861	Stfa1	stefin A1	0	3	0	-1.722652
330	219134	Tmem46	shisa homolog 2 (Xenopus laevis)	0	3	0	-1.719959
331	16476	Jun	Jun oncogene	0	3	0	-1.714142
332	69150	Snx4	sorting nexin 4	0	3	0	-1.710697
333	246049	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	0	3	0	-1.707702
334	381075	Gm936	NA	0	3	0	-1.706986
335	66887	1300002A08Rik	lon peptidase 2, peroxisomal	0	3	0	-1.706268
336	64660	Mrps24	mitochondrial ribosomal protein S24	0	3	0	-1.70547

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
337	67226	Tmem19	transmembrane protein 19	0	3	0	-1.699142
338	108096	Slco1a5	solute carrier organic anion transporter family, member 1a5	0	3	0	-1.697142
339	116810	Foxn4	forkhead box N4	0	3	0	-1.69015
340	13864	Nr2f6	nuclear receptor subfamily 2, group F, member 6	0	3	0	-1.687957
341	68394	0610037D15Rik	coiled-coil domain containing 163	0	4	0	-1.686642
342	20616	Snap91	synaptosomal-associated protein 91	0	3	0	-1.684893
343	68490	Zfp579	zinc finger protein 579	0	3	0	-1.683572
344	64085	Clstn2	calsyntenin 2	0	3	0	-1.678149
345	192650	Cabp7	calcium binding protein 7	0	3	0	-1.676291
346	70031	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	0	3	0	-1.674804
347	67220	Plekho1	pleckstrin homology domain containing, family O member 1	0	3	0	-1.665001
348	56459	Uble1a	SUMO1 activating enzyme subunit 1	0	3	0	-1.659287
349	71904	Paqr7	progestin and adipoQ receptor family member VII	0	3	0	-1.657571
350	240913	Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	0	3	0	-1.657095
351	22245	Uck1	uridine-cytidine kinase 1	0	3	0	-1.652274
352	17938	Naca	nascent polypeptide-associated complex alpha polypeptide	0	3	0	-1.649857
353	271424	Ihpk3	inositol hexaphosphate kinase 3	0	3	0	-1.649074
354	58859	Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	0	3	0	-1.643493
355	67334	1700054O13Rik	RIKEN cDNA 1700054O13 gene	0	3	0	-1.642705
356	23966	Odz4	odd Oz/ten-m homolog 4 (Drosophila)	0	3	0	-1.637421
357	56009	Refbp2	Aly/REF export factor 2	0	3	0	-1.637205
358	77976	Nuak1	NUAK family, SNF1-like kinase, 1	0	3	0	-1.631028
359	76894	Mett5d1	methyltransferase like 15	0	3	0	-1.627343
360	57330	Perq1	GRB10 interacting GYF protein 1	0	3	0	-1.626702
361	381680	BC055004	cDNA sequence BC055004	0	3	0	-1.62492
362	57294	Rps27	ribosomal protein S27	0	3	0	-1.622095
363	244672	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	0	3	0	-1.620563
364	72125	2600011E07Rik	family with sequence similarity 123, member A	0	3	0	-1.617317
365	16189	Il4	interleukin 4	0	3	0	-1.613697
366	232975	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	0	3	0	-1.605608
367	16841	Lect2	leukocyte cell-derived chemotaxin 2	0	3	0	-1.590037
368	16669	Krt1-19	keratin 19	0	3	0	-1.584136
369	68416	Sycn	syncollin	0	3	0	-1.583096
370	236193	Zfp709	zinc finger protein 709	0	3	0	-1.568911

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
371	21371	Tbca	tubulin cofactor A	0	3	0	-1.568531
372	20302	Ccl3	chemokine (C-C motif) ligand 3	0	3	0	-1.551862
373	105859	Csdc2	cold shock domain containing C2, RNA binding	0	3	0	-1.541976
374	541307	Ccl26l	chemokine (C-C motif) ligand 26	0	3	0	-1.539372
375	27274	Zfp354b	zinc finger protein 354B	0	3	0	-1.538782
376	12514	Cd68	CD68 antigen	0	3	0	-1.536279
377	226040	E030010A14Rik	RIKEN cDNA E030010A14 gene	0	3	0	-1.532274
378	19434	Rax	retina and anterior neural fold homeobox	0	3	0	-1.529605
379	67405	Nts	neurotensin	0	4	0	-1.528188
380	229658	Vangl1	vang-like 1 (van gogh, Drosophila)	0	3	0	-1.516711
381	99296	Hrh3	histamine receptor H3	0	3	0	-1.515707
382	171201	V1rc28	vomeronasal 1 receptor 21	0	3	0	-1.515048
383	66438	Hamp2	hepcidin antimicrobial peptide 2	0	3	0	-1.510203
384	56792	AI586015	signal transducing adaptor family member 1	0	3	0	-1.509529
385	69178	Snx5	sorting nexin 5	0	3	0	-1.504325
386	208967	Thnsl1	threonine synthase-like 1 (bacterial)	0	2	0	-4.955697
387	56347	Eif3s8	eukaryotic translation initiation factor 3, subunit C	0	2	0	-4.236063
388	241636	Tgm6	transglutaminase 6	0	2	0	-4.162727
389	75345	Slamf7	SLAM family member 7	0	2	0	-4.117643
390	232717	BC048599	protease, serine 58	0	2	0	-4.032783
391	353172	Gars	glycyl-tRNA synthetase	0	2	0	-3.954275
392	66880	Rsrc1	arginine/serine-rich coiled-coil 1	0	2	0	-3.942481
393	17164	Mapkapk2	MAP kinase-activated protein kinase 2	0	2	0	-3.868957
394	100727	Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	0	2	0	-3.83469
395	73547	1700094E07Rik	dual specificity phosphatase 21	0	2	0	-3.718188
396	94185	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	0	2	0	-3.713838
397	18208	Ntn1	netrin 1	0	2	0	-3.683826
398	101943	Sf3b3	splicing factor 3b, subunit 3	0	2	0	-3.647536
399	19335	Rab23	RAB23, member RAS oncogene family	0	2	0	-3.610032
400	50755	Fbxo18	F-box protein 18	0	2	0	-3.573242
401	171189	V1rc16	vomeronasal 1 receptor 17	0	2	0	-3.556701
402	53356	Eif3s4	eukaryotic translation initiation factor 3, subunit G	0	2	0	-3.542909
403	66480	Rpl15	ribosomal protein L15	0	2	0	-3.529384
404	12447	Ccne1	cyclin E1	0	2	0	-3.512436

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
405	93687	Csnk1a1	casein kinase 1, alpha 1	0	2	0	-3.502442
406	434683	UNK	NA	0	2	0	-3.491475
407	66616	Snx9	sorting nexin 9	0	2	0	-3.480285
408	21682	Tec	tec protein tyrosine kinase	0	2	0	-3.471379
409	227733	Pip5kl1	phosphatidylinositol-4-phosphate 5-kinase-like 1	0	2	0	-3.450262
410	170768	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0	2	0	-3.431403
411	12696	Cirbp	cold inducible RNA binding protein	0	2	0	-3.424378
412	56314	Zfp113	zinc finger protein 113	0	2	0	-3.422376
413	56224	Tspan5	tetraspanin 5	0	2	0	-3.419057
414	209824	V1rd15	vomeronasal 1 receptor 183	0	2	0	-3.401114
415	27979	Eif3s9	eukaryotic translation initiation factor 3, subunit B	0	2	0	-3.333096
416	380795	AI324046	Immunoglobulin heavy constant gamma 3	0	2	0	-3.313363
417	19113	Prlpe	prolactin family 7, subfamily a, member 1	0	2	0	-3.291908
418	493809	Taar3	trace amine-associated receptor 3	0	2	0	-3.277896
419	170786	Cd209a	CD209a antigen	0	2	0	-3.274969
420	19823	Rnf7	ring finger protein 7	0	2	0	-3.261129
421	19114	Prlpf	prolactin family 7, subfamily a, member 2	0	2	0	-3.251191
422	14625	Gykl1	glycerol kinase-like 1	0	2	0	-3.242027
423	70546	Zdhhc2	zinc finger, DHHC domain containing 2	0	2	0	-3.239931
424	18597	Pdha1	pyruvate dehydrogenase E1 alpha 1	0	2	0	-3.236328
425	258281	Olfr780	olfactory receptor 780	0	2	0	-3.235859
426	23983	Pcbp1	poly(rC) binding protein 1	0	2	0	-3.233275
427	16551	Kif11	kinesin family member 11	0	2	0	-3.227798
428	245026	E330026B02Rik	collagen, type VI, alpha 6	0	2	0	-3.218064
429	76789	2410129H14Rik	mitotic spindle organizing protein 1	0	2	0	-3.217067
430	57316	C1d	C1D nuclear receptor co-repressor	0	2	0	-3.200671
431	64658	Mrps25	mitochondrial ribosomal protein S25	0	2	0	-3.188544
432	15278	Tfb2m	transcription factor B2, mitochondrial	0	2	0	-3.166493
433	66298	2010016B13Rik	defensin, alpha, 21	0	2	0	-3.160064
434	171195	V1rc22	vomeronasal 1 receptor 30	0	2	0	-3.151747
435	503845	Ear12	eosinophil-associated, ribonuclease A family, member 12	0	2	0	-3.137255
436	66471	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0	2	0	-3.13376
437	215748	Cnksr3	Cnksr family member 3	0	2	0	-3.122159
438	241727	Snph	syntaphilin	0	2	0	-3.113755

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
439	67698	Tmem157	family with sequence similarity 174, member A	0	2	0	-3.11005
440	319210	4930518C23Rik	vomeronasal 2, receptor, pseudogene 11	0	2	0	-3.105013
441	21402	Skp1a	S-phase kinase-associated protein 1A	0	2	0	-3.097285
442	22094	Tshb	thyroid stimulating hormone, beta subunit	0	2	0	-3.096766
443	319740	Zfyve27	zinc finger, FYVE domain containing 27	0	2	0	-3.089759
444	24061	Smc1a	structural maintenance of chromosomes 1A	0	2	0	-3.085598
445	100066	Cyp2j11	cytochrome P450, family 2, subfamily j, polypeptide 11	0	2	0	-3.082458
446	214895	Lman2l	lectin, mannose-binding 2-like	0	2	0	-3.075993
447	14916	Guca2b	guanylate cyclase activator 2b (retina)	0	2	0	-3.075038
448	207350	Itih5l	NA	0	2	0	-3.067957
449	14068	F7	coagulation factor VII	0	2	0	-3.064701
450	331188	BC024063	zinc finger protein 781	0	2	0	-3.058862
451	435777	UNK	NA	0	2	0	-3.045952
452	71888	2310015J09Rik	keratin 33A	0	2	0	-3.027656
453	433238	LOC433238	predicted gene 5518	0	2	0	-3.021381
454	381493	S100a15	S100 calcium binding protein A7A	0	2	0	-3.021246
455	67710	Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	0	2	0	-3.021187
456	245000	Atr	ataxia telangiectasia and Rad3 related	0	2	0	-3.007175
457	244179	4922504M18Rik	ubiquilin-like	0	2	0	-3.00464
458	19024	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	0	2	0	-3.004281
459	12335	Capn3	calpain 3	0	2	0	-3.004172
460	78977	Popdc3	popeye domain containing 3	0	2	0	-2.996558
461	11736	Ankfy1	ankyrin repeat and FYVE domain containing 1	0	2	0	-2.994345
462	237436	Gas2l3	growth arrest-specific 2 like 3	0	2	0	-2.990316
463	17130	Smad6	MAD homolog 6 (Drosophila)	0	2	0	-2.989007
464	11632	Aip	aryl-hydrocarbon receptor-interacting protein	0	2	0	-2.987992
465	18438	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	0	2	0	-2.985434
466	59010	Sqrdl	sulfide quinone reductase-like (yeast)	0	2	0	-2.982504
467	23859	Dlgh2	discs, large homolog 2 (Drosophila)	0	2	0	-2.982256
468	218921	4930474N05Rik	RIKEN cDNA 4930474N05 gene	0	2	0	-2.976397
469	75820	4930511H01Rik	WD repeat domain 64	0	2	0	-2.969281
470	21881	Tkt	transketolase	0	2	0	-2.968311
471	170735	Arr3	arrestin 3, retinal	0	2	0	-2.965842
472	14805	Grik1	glutamate receptor, ionotropic, kainate 1	0	2	0	-2.950382

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
473	66943	Pqlc1	PQ loop repeat containing 1	0	2	0	-2.945745
474	16907	Lmnb2	lamin B2	0	2	0	-2.942817
475	252870	Usp7	ubiquitin specific peptidase 7	0	2	0	-2.937809
476	14469	Gbp2	guanylate binding protein 2	0	2	0	-2.936779
477	230598	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	0	2	0	-2.927941
478	53318	Pdlim3	PDZ and LIM domain 3	0	2	0	-2.926931
479	17149	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	0	2	0	-2.918912
480	12331	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	0	2	0	-2.91671
481	11905	Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	0	2	0	-2.916498
482	66656	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0	2	0	-2.909259
483	20500	Slc13a2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	0	2	0	-2.900488
484	14077	Fabp3	fatty acid binding protein 3, muscle and heart	0	2	0	-2.900245
485	68314	0610008F07Rik	RIKEN cDNA 0610008F07 gene	0	2	0	-2.896287
486	72821	Scn2b	sodium channel, voltage-gated, type II, beta	0	2	0	-2.892509
487	74996	Usp47	ubiquitin specific peptidase 47	0	2	0	-2.8857
488	56437	Rrad	Ras-related associated with diabetes	0	2	0	-2.883801
489	13525	Adam26a	a disintegrin and metallopeptidase domain 26A (testase 3)	0	2	0	-2.880389
490	14675	Gna14	guanine nucleotide binding protein, alpha 14	0	2	0	-2.880382
491	53880	Birc1g	NLR family, apoptosis inhibitory protein 7	0	2	0	-2.879332
492	67057	Yaf2	YY1 associated factor 2	0	2	0	-2.878444
493	75677	Cldn22	claudin 22	0	2	0	-2.876964
494	93726	Ear11	eosinophil-associated, ribonuclease A family, member 11	0	2	0	-2.876357
495	12500	Cd3d	CD3 antigen, delta polypeptide	0	2	0	-2.874563
496	215387	Brrn1	non-SMC condensin I complex, subunit H	0	2	0	-2.873647
497	233537	Gdpd4	glycerophosphodiester phosphodiesterase domain containing 4	0	2	0	-2.873322
498	29807	Tpk1	thiamine pyrophosphokinase	0	2	0	-2.872944
499	433926	Lrrc8b	leucine rich repeat containing 8 family, member B	0	2	0	-2.868734
500	17928	Myog	myogenin	0	2	0	-2.868159
501	19822	Rnf4	ring finger protein 4	0	2	0	-2.86409
502	110521	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	0	2	0	-2.860602
503	71954	2400003N08Rik	suppressor of defective silencing 3 homolog (S. cerevisiae)	0	2	0	-2.851562
504	67603	Dusp6	dual specificity phosphatase 6	0	2	0	-2.84917
505	71791	Cpa4	carboxypeptidase A4	0	2	0	-2.847032
506	20394	Scg5	secretogranin V	0	2	0	-2.843371

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
507	213827	Arcn1	archain 1	0	2	0	-2.842606
508	94187	Zfp423	zinc finger protein 423	0	2	0	-2.834448
509	217119	Xylt2	xylosyltransferase II	0	2	0	-2.832128
510	226043	Cbwd1	COBW domain containing 1	0	2	0	-2.823425
511	14811	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	0	2	0	-2.822842
512	217344	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	0	2	0	-2.819153
513	244199	Ovch2	ovochymase 2	0	2	0	-2.815039
514	67775	Rtp4	receptor transporter protein 4	0	2	0	-2.81502
515	67429	Nudcd1	NudC domain containing 1	0	2	0	-2.814584
516	214254	Nudt15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	0	2	0	-2.813464
517	67374	Jam2	junction adhesion molecule 2	0	2	0	-2.812572
518	14313	Fst	follistatin	0	2	0	-2.811331
519	26381	Esrrg	estrogen-related receptor gamma	0	2	0	-2.807749
520	80903	Fgf16	fibroblast growth factor 16	0	2	0	-2.804877
521	20400	Sh2d1a	SH2 domain protein 1A	0	2	0	-2.804368
522	56353	Rybp	RING1 and YY1 binding protein	0	2	0	-2.803474
523	67848	Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	0	2	0	-2.801523
524	16630	Klra12	killer cell lectin-like receptor subfamily A, member 12	0	2	0	-2.800171
525	28080	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0	2	0	-2.799423
526	20378	Frzb	frizzled-related protein	0	2	0	-2.798766
527	102193	Zdhhc7	zinc finger, DHHC domain containing 7	0	2	0	-2.79022
528	83701	Ars2	serrate RNA effector molecule homolog (Arabidopsis)	0	2	0	-2.789888
529	12455	Ccnt1	cyclin T1	0	2	0	-2.789021
530	22761	Zfpm1	zinc finger protein, multitype 1	0	2	0	-2.784271
531	70363	1700010C24Rik	family with sequence similarity 135, member B	0	2	0	-2.781068
532	77128	A930001N09Rik	RIKEN cDNA A930001N09 gene	0	2	0	-2.777195
533	80720	Pbx4	pre B cell leukemia homeobox 4	0	2	0	-2.775481
534	69481	1700029I08Rik	actin-like 9	0	2	0	-2.771111
535	386422	UNK	NA	0	2	0	-2.768877
536	18771	Pknox1	Pbx/knotted 1 homeobox	0	2	0	-2.767644
537	270135	BC038156	NA	0	2	0	-2.76554
538	433718	UNK	NA	0	2	0	-2.765443
539	214238	UNK	NA	0	2	0	-2.763873
540	13871	Ercc2	excision repair cross-complementing rodent repair deficiency, complementation group 2	0	2	0	-2.759652

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
541	56716	Gbl	MTOR associated protein, LST8 homolog (S. cerevisiae)	0	2	0	-2.758291
542	227622	BC029214	cDNA sequence BC029214	0	2	0	-2.757855
543	66970	Ssbp2	single-stranded DNA binding protein 2	0	2	0	-2.757219
544	433073	LOC433073	actin related protein 2/3 complex, subunit 2 pseudogene	0	2	0	-2.756187
545	270035	D030041N04Rik	leucine zipper-EF-hand containing transmembrane protein 2	0	2	0	-2.752613
546	76263	Gstk1	glutathione S-transferase kappa 1	0	2	0	-2.746811
547	267019	Rps15a	ribosomal protein S15A	0	2	0	-2.742636
548	85305	Kars	lysyl-tRNA synthetase	0	2	0	-2.736216
549	268470	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	0	2	0	-2.735038
550	20588	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	0	2	0	-2.730615
551	434203	Slc28a1	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	0	2	0	-2.729804
552	72486	2610206B13Rik	ring finger protein 219	0	2	0	-2.725686
553	103098	Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	0	2	0	-2.724254
554	69790	Thrap6	mediator complex subunit 30	0	2	0	-2.721611
555	383073	UNK	NA	0	2	0	-2.72064
556	11603	Agrn	agrin	0	2	0	-2.720337
557	93897	Fzd10	frizzled homolog 10 (Drosophila)	0	2	0	-2.720083
558	76897	0710005M24Rik	RALY RNA binding protein-like	0	2	0	-2.718516
559	110446	Acat1	acetyl-Coenzyme A acetyltransferase 1	0	2	0	-2.705567
560	382206	Ssx9	synovial sarcoma, X breakpoint 9	0	2	0	-2.705467
561	113852	V1rb1	vomeronasal 1 receptor 50	0	2	0	-2.704871
562	245841	Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	0	2	0	-2.704598
563	319229	Sctr	secretin receptor	0	2	0	-2.69939
564	71838	Phf7	PHD finger protein 7	0	2	0	-2.697445
565	103988	Gck	glucokinase	0	2	0	-2.697391
566	70616	Sf4	SURP and G patch domain containing 1	0	2	0	-2.69646
567	68801	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	0	2	0	-2.693582
568	56787	Ascl3	achaete-scute complex homolog 3 (Drosophila)	0	2	0	-2.690885
569	406186	Olfr142	olfactory receptor 142	0	2	0	-2.690674
570	353170	4932441K18Rik	taxilin gamma	0	2	0	-2.688114
571	75288	Slc35f4	solute carrier family 35, member F4	0	2	0	-2.686467
572	73016	Kremen2	kringle containing transmembrane protein 2	0	2	0	-2.684911
573	12939	Pcdha7	protocadherin alpha 7	0	2	0	-2.684721
574	384890	UNK	NA	0	2	0	-2.684117

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
575	68205	2900073H19Rik	ubiquitin related modifier 1 homolog (S. cerevisiae)	0	2	0	-2.68339
576	104303	Arl1	ADP-ribosylation factor-like 1	0	2	0	-2.67142
577	16198	Il9	interleukin 9	0	2	0	-2.66957
578	21343	Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	0	-2.664725
579	66586	Crls1	cardiolipin synthase 1	0	2	0	-2.66306
580	74412	Gle1l	GLE1 RNA export mediator (yeast)	0	2	0	-2.660233
581	272680	UNK	NA	0	2	0	-2.658779
582	212647	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	0	2	0	-2.652805
583	71986	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0	2	0	-2.651647
584	170733	Klra17	killer cell lectin-like receptor, subfamily A, member 17	0	2	0	-2.647379
585	270076	Gcdh	glutaryl-Coenzyme A dehydrogenase	0	2	0	-2.646232
586	13090	Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19	0	2	0	-2.645991
587	70673	Prdm16	PR domain containing 16	0	2	0	-2.641644
588	258450	Olfr1199	olfactory receptor 1199	0	2	0	-2.64036
589	113862	V1rc5	vomeronasal 1 receptor 13	0	2	0	-2.640302
590	226641	Atf6	activating transcription factor 6	0	2	0	-2.639768
591	213311	Fbxl21	F-box and leucine-rich repeat protein 21	0	2	0	-2.629896
592	67455	Klhl13	kelch-like 13 (Drosophila)	0	2	0	-2.629752
593	64294	Itm2c	integral membrane protein 2C	0	2	0	-2.629639
594	242109	Zfp697	zinc finger protein 697	0	2	0	-2.629135
595	54447	Asah2	N-acylsphingosine amidohydrolase 2	0	2	0	-2.626738
596	74616	Scrn3	secernin 3	0	2	0	-2.626103
597	18050	Klk1b3	kallikrein 1-related peptidase b3	0	2	0	-2.625593
598	15207	Hes3	hairy and enhancer of split 3 (Drosophila)	0	2	0	-2.625069
599	53311	Mybph	myosin binding protein H	0	2	0	-2.621833
600	29857	Mapk12	mitogen-activated protein kinase 12	0	2	0	-2.618559
601	67078	1700012G19Rik	phosphoglycolate phosphatase	0	2	0	-2.612566
602	17058	Klrb1b	NA	0	2	0	-2.61049
603	74102	Slc35a5	solute carrier family 35, member A5	0	2	0	-2.609134
604	13350	Dgat1	diacylglycerol O-acyltransferase 1	0	2	0	-2.607903
605	23988	Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	0	2	0	-2.605662
606	11479	Acvr1b	activin A receptor, type 1B	0	2	0	-2.605388
607	14712	Gnpat	glyceronephosphate O-acyltransferase	0	2	0	-2.60262
608	22333	Vdac1	voltage-dependent anion channel 1	0	2	0	-2.60065

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
609	192161	Pcdha9	protocadherin alpha 9	0	2	0	-2.599188
610	23908	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	0	2	0	-2.597429
611	16509	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	0	2	0	-2.597247
612	67248	Rpl39	ribosomal protein L39	0	2	0	-2.594541
613	67030	Fancl	Fanconi anemia, complementation group L	0	2	0	-2.594004
614	69906	Slc25a32	solute carrier family 25, member 32	0	2	0	-2.593505
615	67503	1700001G17Rik	RIKEN cDNA 1700001G17 gene	0	2	0	-2.592659
616	22598	Slc6a18	solute carrier family 6 (neurotransmitter transporter), member 18	0	2	0	-2.591104
617	233649	Cnga4	cyclic nucleotide gated channel alpha 4	0	2	0	-2.588184
618	231889	Bud31	BUD31 homolog (yeast)	0	2	0	-2.587539
619	15925	Ide	insulin degrading enzyme	0	2	0	-2.585972
620	432825	LOC432825	predicted gene 5458	0	2	0	-2.585296
621	319476	Lrtm1	leucine-rich repeats and transmembrane domains 1	0	2	0	-2.580502
622	71963	Cdca4	cell division cycle associated 4	0	2	0	-2.578791
623	19353	Rac1	RAS-related C3 botulinum substrate 1	0	2	0	-2.577521
624	22088	Tsg101	tumor susceptibility gene 101	0	2	0	-2.576704
625	16828	Ldha	lactate dehydrogenase A	0	2	0	-2.573499
626	19361	Rad51	RAD51 homolog (S. cerevisiae)	0	2	0	-2.571838
627	74204	Xpo6	exportin 6	0	2	0	-2.570558
628	57748	Jmy	junction-mediating and regulatory protein	0	2	0	-2.569681
629	384814	LOC384814	predicted gene 5347	0	2	0	-2.56546
630	73626	1810009J06Rik	RIKEN cDNA 1810009J06 gene	0	2	0	-2.565452
631	170750	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0	2	0	-2.563514
632	110391	Qdpr	quinoid dihydropteridine reductase	0	2	0	-2.560192
633	217169	Tns4	tensin 4	0	2	0	-2.558162
634	192164	Pcdha12	protocadherin alpha 12	0	2	0	-2.55658
635	242126	Slc22a15	solute carrier family 22 (organic anion/cation transporter), member 15	0	2	0	-2.555315
636	16675	Krt1-c29	keratin 27	0	2	0	-2.555285
637	74011	Slc25a27	solute carrier family 25, member 27	0	2	0	-2.550197
638	76654	Upp2	uridine phosphorylase 2	0	2	0	-2.550057
639	72181	Nsun4	NOL1/NOP2/Sun domain family, member 4	0	2	0	-2.543089
640	224640	Lemd2	LEM domain containing 2	0	2	0	-2.543074
641	67719	2310057J18Rik	RIKEN cDNA 2310057J18 gene	0	2	0	-2.542016
642	216285	Cart1	ALX homeobox 1	0	2	0	-2.542002

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
643	98878	Ehd4	EH-domain containing 4	0	2	0	-2.538045
644	67276	Thex1	exoribonuclease 1	0	2	0	-2.536523
645	171256	V1ri5	vomeronasal 1 receptor 218	0	2	0	-2.535598
646	269397	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	0	2	0	-2.534713
647	171194	V1rc21	vomeronasal 1 receptor 4	0	2	0	-2.53344
648	16518	Kcnj2	potassium inwardly-rectifying channel, subfamily J, member 2	0	2	0	-2.532688
649	268935	Scube3	signal peptide, CUB domain, EGF-like 3	0	2	0	-2.531408
650	17183	Matn4	matrilin 4	0	2	0	-2.530352
651	258348	Olfr1133	olfactory receptor 1133	0	2	0	-2.528554
652	108956	2210421G13Rik	apolipoprotein L 7c	0	2	0	-2.527866
653	243659	Styk1	serine/threonine/tyrosine kinase 1	0	2	0	-2.527673
654	231293	C130090K23Rik	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	0	2	0	-2.519173
655	75905	4930578C19Rik	RIKEN cDNA 4930578C19 gene	0	2	0	-2.51687
656	18805	Pld1	phospholipase D1	0	2	0	-2.516095
657	14380	G6pd2	glucose-6-phosphate dehydrogenase 2	0	2	0	-2.511757
658	71382	Pex1	peroxisomal biogenesis factor 1	0	2	0	-2.510611
659	22702	Zfp42	zinc finger protein 42	0	2	0	-2.508761
660	75212	Rnf121	ring finger protein 121	0	2	0	-2.505605
661	14462	Gata3	GATA binding protein 3	0	2	0	-2.50441
662	72124	Seh1l	SEH1-like (S. cerevisiae	0	2	0	-2.503087
663	12660	Chka	choline kinase alpha	0	2	0	-2.501303
664	17153	Mal	myelin and lymphocyte protein, T cell differentiation protein	0	2	0	-2.497152
665	14810	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	0	2	0	-2.497002
666	54709	Eif3s2	eukaryotic translation initiation factor 3, subunit I	0	2	0	-2.496609
667	258699	Olfr1446	olfactory receptor 1446	0	2	0	-2.495468
668	20307	Ccl8	chemokine (C-C motif) ligand 8	0	2	0	-2.491696
669	50773	Nt5c	5',3'-nucleotidase, cytosolic	0	2	0	-2.491248
670	215890	A330019N05Rik	clavesin 2	0	2	0	-2.49077
671	216618	Ccdc104	coiled-coil domain containing 104	0	2	0	-2.488224
672	11571	Crisp1	cysteine-rich secretory protein 1	0	2	0	-2.488132
673	19046	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	0	2	0	-2.48655
674	14719	Got2	glutamate oxaloacetate transaminase 2, mitochondrial	0	2	0	-2.485038
675	12045	Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1b	0	2	0	-2.484373
676	216019	Hkdc1	hexokinase domain containing 1	0	2	0	-2.483557

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
677	74042	4921501E09Rik	RIKEN cDNA 4921501E09 gene	0	2	0	-2.481985
678	74245	Ctbs	chitobiase, di-N-acetyl-	0	2	0	-2.479272
679	236790	6330505F04Rik	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	0	2	0	-2.478653
680	170729	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	0	2	0	-2.474228
681	268391	A830031A19Rik	RIKEN cDNA A830031A19 gene	0	2	0	-2.473295
682	54196	Pabpn1	poly(A) binding protein, nuclear 1	0	2	0	-2.472157
683	26414	Mapk10	mitogen-activated protein kinase 10	0	2	0	-2.471916
684	20361	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	0	2	0	-2.470606
685	93675	Clec2i	C-type lectin domain family 2, member i	0	2	0	-2.470402
686	20311	Cxcl5	chemokine (C-X-C motif) ligand 5	0	2	0	-2.463709
687	18548	Pcsk1	proprotein convertase subtilisin/kexin type 1	0	2	0	-2.459634
688	105148	Iars	isoleucine-tRNA synthetase	0	2	0	-2.455485
689	434071	UNK	NA	0	2	0	-2.454226
690	74318	Hod	HOP homeobox	0	2	0	-2.454117
691	80906	Kcnip2	Kv channel-interacting protein 2	0	2	0	-2.453441
692	20229	Sat1	spermidine/spermine N1-acetyl transferase 1	0	2	0	-2.45092
693	140579	Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	0	2	0	-2.450134
694	27411	Slc14a2	solute carrier family 14 (urea transporter), member 2	0	2	0	-2.449548
695	65079	Rtn4r	reticulon 4 receptor	0	2	0	-2.448655
696	22423	Wnt8b	wingless related MMTV integration site 8b	0	2	0	-2.448186
697	436244	UNK	NA	0	2	0	-2.442556
698	17535	Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	0	2	0	-2.441195
699	235324	UNK	NA	0	2	0	-2.439481
700	217116	Spata20	spermatogenesis associated 20	0	2	0	-2.435259
701	66380	Krtap3-3	keratin associated protein 3-3	0	2	0	-2.43453
702	15408	Hoxb13	homeobox B13	0	2	0	-2.433825
703	72654	Ccdc12	coiled-coil domain containing 12	0	2	0	-2.433116
704	69982	Spink2	serine peptidase inhibitor, Kazal type 2	0	2	0	-2.432134
705	11451	Acrv1	acrosomal vesicle protein 1	0	2	0	-2.428491
706	224045	Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	0	2	0	-2.425294
707	56357	Ivd	isovaleryl coenzyme A dehydrogenase	0	2	0	-2.424943
708	244555	UNK	NA	0	2	0	-2.424472
709	14950	H13	histocompatibility 13	0	2	0	-2.424175
710	67337	Cstf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	0	2	0	-2.422175

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
711	12476	Cd151	CD151 antigen	0	2	0	-2.4217
712	13115	Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	0	2	0	-2.421386
713	11836	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	0	2	0	-2.421363
714	11550	Adra1d	adrenergic receptor, alpha 1d	0	2	0	-2.420175
715	12803	Cntf	ciliary neurotrophic factor	0	2	0	-2.41682
716	19231	Ptma	prothymosin alpha	0	2	0	-2.416722
717	258682	Olfr1436	olfactory receptor 1436	0	2	0	-2.416352
718	18647	Pftk1	cyclin-dependent kinase 14	0	2	0	-2.416032
719	394436	Ugt1a1	UDP glucuronosyltransferase 1 family, polypeptide A1	0	2	0	-2.414542
720	23882	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	0	2	0	-2.413222
721	20322	Sord	sorbitol dehydrogenase	0	2	0	-2.412842
722	59056	Evc	Ellis van Creveld gene homolog (human)	0	2	0	-2.411098
723	232791	Cnot3	CCR4-NOT transcription complex, subunit 3	0	2	0	-2.408721
724	73720	Cst6	cystatin E/M	0	2	0	-2.406904
725	114584	Clic1	chloride intracellular channel 1	0	2	0	-2.404797
726	18706	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0	2	0	-2.404268
727	379043	Raet1e	retinoic acid early transcript 1E	0	2	0	-2.403622
728	73024	2900064A13Rik	RIKEN cDNA 2900064A13 gene	0	2	0	-2.403144
729	229877	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	0	2	0	-2.400739
730	170936	Zfp369	zinc finger protein 369	0	2	0	-2.398757
731	240215	Slc4a9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	0	2	0	-2.397298
732	238599	Gm269	NA	0	2	0	-2.396293
733	18952	39328	septin 4	0	2	0	-2.395833
734	17901	Myl1	myosin, light polypeptide 1	0	2	0	-2.395724
735	17156	Man1a2	mannosidase, alpha, class 1A, member 2	0	2	0	-2.395608
736	75764	Giyd2	SLX1 structure-specific endonuclease subunit homolog B (S. cerevisiae)	0	2	0	-2.39425
737	328752	UNK	NA	0	2	0	-2.39385
738	258755	Olfr672	olfactory receptor 672	0	2	0	-2.393758
739	102436	Lars2	leucyl-tRNA synthetase, mitochondrial	0	2	0	-2.393606
740	20259	Scin	scinderin	0	2	0	-2.393139
741	52563	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	0	2	0	-2.392604
742	20527	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	0	2	0	-2.388887
743	21953	Tnni2	troponin I, skeletal, fast 2	0	2	0	-2.388821
744	13733	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0	2	0	-2.387135

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
745	52009	D17Ertd441e	hematological and neurological expressed 1-like	0	2	0	-2.386317
746	15378	Hnf4a	hepatic nuclear factor 4, alpha	0	2	0	-2.38602
747	69511	Klk12	kallikrein related-peptidase 12	0	2	0	-2.385991
748	27078	Eppb9	B9 protein domain 1	0	2	0	-2.385513
749	258620	Olfr350	olfactory receptor 350	0	2	0	-2.384866
750	14291	Fpr-rs4	formyl peptide receptor, related sequence 4	0	2	0	-2.382198
751	13642	Efnb2	ephrin B2	0	2	0	-2.381481
752	224344	Rbm11	RNA binding motif protein 11	0	2	0	-2.379532
753	69537	Dnase1l1	deoxyribonuclease 1-like 1	0	2	0	-2.378549
754	66244	Sdccag1	nuclear export mediator factor	0	2	0	-2.378434
755	208158	Map6d1	MAP6 domain containing 1	0	2	0	-2.37834
756	52855	Lair1	leukocyte-associated Ig-like receptor 1	0	2	0	-2.378011
757	67427	Rps20	ribosomal protein S20	0	2	0	-2.375668
758	24099	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	0	2	0	-2.375329
759	212862	Chpt1	choline phosphotransferase 1	0	2	0	-2.374714
760	271639	Sacy	adenylate cyclase 10	0	2	0	-2.373421
761	74091	Npl	N-acetylneuraminate pyruvate lyase	0	2	0	-2.372327
762	80914	Uck2	uridine-cytidine kinase 2	0	2	0	-2.371503
763	227506	LOC227506	leukotriene A4 hydrolase pseudogene	0	2	0	-2.371148
764	243377	Svs1	seminal vesicle secretory protein 1	0	2	0	-2.367714
765	22031	Traf3	TNF receptor-associated factor 3	0	2	0	-2.36717
766	15519	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	0	2	0	-2.366468
767	387347	Tas2r118	taste receptor, type 2, member 118	0	2	0	-2.363026
768	258899	Olfr1214	olfactory receptor 1214	0	2	0	-2.362045
769	79555	BC005537	cDNA sequence BC005537	0	2	0	-2.361891
770	17843	Mup4	major urinary protein 4	0	2	0	-2.360882
771	237958	4933407P14Rik	RIKEN cDNA 4933407P14 gene	0	2	0	-2.36006
772	384401	LOC384401	tubulin, alpha 1A pseudogene	0	2	0	-2.359292
773	67684	3300001P08Rik	LUC7-like 3 (S. cerevisiae)	0	2	0	-2.358167
774	435267	UNK	NA	0	2	0	-2.357723
775	66708	Krtap3-2	keratin associated protein 3-2	0	2	0	-2.357227
776	54197	Rnf5	ring finger protein 5	0	2	0	-2.356814
777	77980	Sbf1	SET binding factor 1	0	2	0	-2.355598
778	210741	Kcnk12	potassium channel, subfamily K, member 12	0	2	0	-2.354032

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
779	19053	Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	0	2	0	-2.353782
780	240289	LOC240289	proteasome (prosome, macropain) subunit, beta type 3 pseudogene	0	2	0	-2.350961
781	15043	H2-T3	histocompatibility 2, T region locus 3	0	2	0	-2.350653
782	435233	UNK	NA	0	2	0	-2.348199
783	217431	Nol10	nucleolar protein 10	0	2	0	-2.347392
784	433822	UNK	NA	0	2	0	-2.346793
785	83561	Tdrd1	tudor domain containing 1	0	2	0	-2.346371
786	239857	Igsf4d	cell adhesion molecule 2	0	2	0	-2.346079
787	16367	Irs1	insulin receptor substrate 1	0	2	0	-2.344538
788	23879	Fxr2h	fragile X mental retardation, autosomal homolog 2	0	2	0	-2.343783
789	12966	Crygc	crystallin, gamma C	0	2	0	-2.343511
790	19344	Rab5b	RAB5B, member RAS oncogene family	0	2	0	-2.342516
791	11650	Akp5	alkaline phosphatase, placental-like 2	0	2	0	-2.341532
792	12927	Bcar1	breast cancer anti-estrogen resistance 1	0	2	0	-2.340023
793	19109	Prl	prolactin	0	2	0	-2.337981
794	11694	Alx3	aristaless-like homeobox 3	0	2	0	-2.337291
795	69836	Pla2g12b	phospholipase A2, group XIIB	0	2	0	-2.336572
796	26437	Psg17	pregnancy specific glycoprotein 17	0	2	0	-2.335388
797	17420	Mnat1	menage a trois 1	0	2	0	-2.333394
798	109225	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	0	2	0	-2.330549
799	75871	4930566A11Rik	zinc finger protein 821	0	2	0	-2.329258
800	21987	Tpd52l1	tumor protein D52-like 1	0	2	0	-2.328552
801	67383	2410127L17Rik	RIKEN cDNA 2410127L17 gene	0	2	0	-2.325926
802	67254	2900011O08Rik	RIKEN cDNA 2900011O08 gene	0	2	0	-2.325503
803	22696	Zfp37	zinc finger protein 37	0	2	0	-2.324266
804	16549	Khsrp	KH-type splicing regulatory protein	0	2	0	-2.322718
805	15415	Hoxb7	homeobox B7	0	2	0	-2.322453
806	73866	4930432H15Rik	family with sequence similarity 122, member C	0	2	0	-2.321276
807	140917	Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	0	2	0	-2.319514
808	66556	Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	0	2	0	-2.319097
809	59013	Hnrph1	heterogeneous nuclear ribonucleoprotein H1	0	2	0	-2.318142
810	228960	Stx16	syntaxin 16	0	2	0	-2.318077
811	93970	Klra18	killer cell lectin-like receptor, subfamily A, member 18	0	2	0	-2.317841
812	11793	Atg5	autophagy-related 5 (yeast)	0	2	0	-2.316339

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
813	68032	Tmem85	transmembrane protein 85	0	2	0	-2.315806
814	67425	Eps8l1	EPS8-like 1	0	2	0	-2.315405
815	81011	V1rd14	vomeronasal 1 receptor 148	0	2	0	-2.313612
816	17138	Magea2	melanoma antigen, family A, 2	0	2	0	-2.313606
817	99738	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	0	2	0	-2.312506
818	94043	Tm2d1	TM2 domain containing 1	0	2	0	-2.312299
819	20585	Smarca3	helicase-like transcription factor	0	2	0	-2.311629
820	383100	UNK	NA	0	2	0	-2.310594
821	53857	Tuba8	tubulin, alpha 8	0	2	0	-2.308704
822	18749	Prkacb	protein kinase, cAMP dependent, catalytic, beta	0	2	0	-2.306923
823	81701	Egfl8	EGF-like domain 8	0	2	0	-2.304198
824	13197	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	0	2	0	-2.30368
825	13684	Eif4e	eukaryotic translation initiation factor 4E	0	2	0	-2.301428
826	258351	Olfr633	olfactory receptor 633	0	2	0	-2.301121
827	18139	Zfml	zinc finger, matrin-like	0	2	0	-2.301072
828	258374	Olfr127	olfactory receptor 127	0	2	0	-2.299874
829	238323	Rps6kl1	ribosomal protein S6 kinase-like 1	0	2	0	-2.298469
830	78689	Mak10	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	0	2	0	-2.298138
831	22629	Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0	2	0	-2.297904
832	216440	4632413K17Rik	amplified in osteosarcoma	0	2	0	-2.294412
833	214580	Pstk	phosphoseryl-tRNA kinase	0	2	0	-2.294228
834	434655	UNK	NA	0	2	0	-2.293306
835	18033	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105	0	2	0	-2.292926
836	19170	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	0	2	0	-2.292674
837	219131	Phf11	PHD finger protein 11	0	2	0	-2.292534
838	71889	Epn3	epsin 3	0	2	0	-2.291717
839	19215	Ptgds	prostaglandin D2 synthase (brain)	0	2	0	-2.290846
840	237847	Rtn4rl1	reticulon 4 receptor-like 1	0	2	0	-2.289847
841	67054	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarb	0	2	0	-2.289807
842	215708	C030011O14Rik	family with sequence similarity 73, member A	0	2	0	-2.287955
843	26938	St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltrans	0	2	0	-2.286298
844	73287	1700040L02Rik	RIKEN cDNA 1700040L02 gene	0	2	0	-2.284588
845	101613	Nalp6	NLR family, pyrin domain containing 6	0	2	0	-2.284312
846	76804	Jmjd2c	lysine (K)-specific demethylase 4C	0	2	0	-2.284231

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
847	380660	8430416H19Rik	acyl-CoA synthetase short-chain family member 3	0	2	0	-2.28274
848	83453	Chrdl1	chordin-like 1	0	2	0	-2.280138
849	93877	Pcdhb6	protocadherin beta 6	0	2	0	-2.277842
850	12286	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0	2	0	-2.277242
851	67414	Mfn1	mitofusin 1	0	2	0	-2.276182
852	94186	Strn3	striatin, calmodulin binding protein 3	0	2	0	-2.275768
853	78444	C330024D12Rik	pyroglutamyl-peptidase I-like	0	2	0	-2.271903
854	12235	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	0	2	0	-2.271003
855	17089	Lyar	Ly1 antibody reactive clone	0	2	0	-2.269014
856	21835	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0	2	0	-2.267245
857	66437	Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	0	2	0	-2.264921
858	106200	Txndc11	thioredoxin domain containing 11	0	2	0	-2.264562
859	72047	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	0	2	0	-2.261701
860	170737	Znrf1	zinc and ring finger 1	0	2	0	-2.257283
861	16467	Atcay	ataxia, cerebellar, Cayman type homolog (human)	0	2	0	-2.257001
862	209815	Oatl1	TBC1 domain family, member 25	0	2	0	-2.256844
863	381038	Parl	presenilin associated, rhomboid-like	0	2	0	-2.255322
864	56642	Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	0	2	0	-2.254006
865	20737	Spn	sialophorin	0	2	0	-2.250974
866	258446	Olfr1231	olfactory receptor 1231	0	2	0	-2.249987
867	381530	MGC107671	major urinary protein 20	0	2	0	-2.248681
868	13615	Edn2	endothelin 2	0	2	0	-2.247674
869	12465	Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	0	2	0	-2.247398
870	68267	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	0	2	0	-2.246931
871	211924	Dsg1c	desmoglein 1 gamma	0	2	0	-2.244372
872	20623	Snrk	SNF related kinase	0	2	0	-2.244096
873	15426	Hoxc8	homeobox C8	0	2	0	-2.243623
874	68183	Bcas2	breast carcinoma amplified sequence 2	0	2	0	-2.243454
875	72978	Cnih3	cornichon homolog 3 (Drosophila)	0	2	0	-2.243291
876	24117	Wif1	Wnt inhibitory factor 1	0	2	0	-2.242546
877	106389	Eaf2	ELL associated factor 2	0	2	0	-2.241586
878	73656	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	0	2	0	-2.241445
879	53945	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	0	2	0	-2.241181
880	74121	Acoxl	acyl-Coenzyme A oxidase-like	0	2	0	-2.240866

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
881	67015	Ccdc91	coiled-coil domain containing 91	0	2	0	-2.239915
882	26374	Rfwd2	ring finger and WD repeat domain 2	0	2	0	-2.238602
883	17380	Mme	membrane metallo endopeptidase	0	2	0	-2.237272
884	269997	6430604K15Rik	zinc finger protein 747	0	2	0	-2.236938
885	225341	Lims2	LIM and senescent cell antigen like domains 2	0	2	0	-2.236916
886	114142	Foxp2	forkhead box P2	0	2	0	-2.23589
887	66433	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0	2	0	-2.235668
888	64450	Gpr85	G protein-coupled receptor 85	0	2	0	-2.234418
889	52683	D15Ertd785e	non-SMC condensin II complex, subunit H2	0	2	0	-2.233668
890	68135	Eif3s3	eukaryotic translation initiation factor 3, subunit H	0	2	0	-2.231757
891	97440	C76566	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9, pseudogene	0	2	0	-2.231713
892	113858	V1rc1	vomeronasal 1 receptor 10	0	2	0	-2.230897
893	14043	Ext2	exostoses (multiple) 2	0	2	0	-2.230674
894	66066	Gng11	guanine nucleotide binding protein (G protein), gamma 11	0	2	0	-2.230627
895	66401	Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	0	2	0	-2.230195
896	56040	Rplp1	ribosomal protein, large, P1	0	2	0	-2.229292
897	19921	Rpl19	ribosomal protein L19	0	2	0	-2.226051
898	78416	Rnase6	ribonuclease, RNase A family, 6	0	2	0	-2.225435
899	386042	LOC386042	NA	0	2	0	-2.223403
900	56189	Prodh2	proline dehydrogenase (oxidase) 2	0	2	0	-2.222513
901	12557	Cdh17	cadherin 17	0	2	0	-2.222262
902	245537	Nlgn3	neuroligin 3	0	2	0	-2.220427
903	268759	9930012K11Rik	RIKEN cDNA 9930012K11 gene	0	2	0	-2.218709
904	18109	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	0	2	0	-2.217686
905	258271	Olfr1311	olfactory receptor 1311	0	2	0	-2.216896
906	235028	Zfp426	zinc finger protein 426	0	2	0	-2.216892
907	104156	Etv5	ets variant gene 5	0	2	0	-2.216329
908	381937	LOC381937	predicted gene 5157	0	2	0	-2.215746
909	27369	Dguok	deoxyguanosine kinase	0	2	0	-2.215603
910	18557	Pctk3	cyclin-dependent kinase 18	0	2	0	-2.215542
911	238463	Tubal3	tubulin, alpha-like 3	0	2	0	-2.214013
912	246196	Zfp277	zinc finger protein 277	0	2	0	-2.213925
913	22186	Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	0	2	0	-2.210689
914	27756	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	2	0	-2.210293

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
915	280668	Adam1a	a disintegrin and metallopeptidase domain 1a	0	2	0	-2.209767
916	117005	Olfr74	olfactory receptor 74	0	2	0	-2.208155
917	214968	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	0	2	0	-2.206633
918	12741	Cldn5	claudin 5	0	2	0	-2.206526
919	235587	Parp3	poly (ADP-ribose) polymerase family, member 3	0	2	0	-2.203931
920	18174	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	0	2	0	-2.203916
921	385052	UNK	NA	0	2	0	-2.203531
922	56389	Stx5a	syntaxin 5A	0	2	0	-2.202198
923	259151	Olfr1037	olfactory receptor 1037	0	2	0	-2.201618
924	17169	Mark3	MAP/microtubule affinity-regulating kinase 3	0	2	0	-2.20098
925	545471	LOC545471	zinc finger protein 345	0	2	0	-2.194432
926	30055	Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	0	2	0	-2.193651
927	13681	Eif4a1	eukaryotic translation initiation factor 4A1	0	2	0	-2.193525
928	12070	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	0	2	0	-2.190452
929	73747	1110034G24Rik	RIKEN cDNA 1110034G24 gene	0	2	0	-2.190162
930	50540	Igbp1b	immunoglobulin (CD79A) binding protein 1b	0	2	0	-2.189684
931	67877	Nat5	N(alpha)-acetyltransferase 20, NatB catalytic subunit	0	2	0	-2.189037
932	99683	Sec24b	Sec24 related gene family, member B (S. cerevisiae)	0	2	0	-2.188108
933	58226	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	0	2	0	-2.187134
934	22698	Zfp39	zinc finger protein 39	0	2	0	-2.186879
935	329738	4921525H12Rik	AKNA domain containing 1	0	2	0	-2.18529
936	16165	Il13ra2	interleukin 13 receptor, alpha 2	0	2	0	-2.184841
937	278304	A930006D11Rik	zinc finger protein 385C	0	2	0	-2.183616
938	12929	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	0	2	0	-2.183544
939	228858	Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	0	2	0	-2.182494
940	14860	Gsta4	glutathione S-transferase, alpha 4	0	2	0	-2.181541
941	238384	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	0	2	0	-2.181178
942	75221	Dpp3	dipeptidylpeptidase 3	0	2	0	-2.180097
943	68401	G6pc3	glucose 6 phosphatase, catalytic, 3	0	2	0	-2.179637
944	231506	AI461788	lin-54 homolog (C. elegans)	0	2	0	-2.178226
945	16616	Klk1b21	kallikrein 1-related peptidase b21	0	2	0	-2.178121
946	245619	UNK	NA	0	2	0	-2.177817
947	105355	Slc17a3	solute carrier family 17 (sodium phosphate), member 3	0	2	0	-2.177138
948	67618	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0	2	0	-2.17709

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
949	66950	2310028N02Rik	transmembrane protein 206	0	2	0	-2.173511
950	17454	Mov10	Moloney leukemia virus 10	0	2	0	-2.172416
951	12461	Cct2	chaperonin containing Tcp1, subunit 2 (beta)	0	2	0	-2.171589
952	19089	Prkcsh	protein kinase C substrate 80K-H	0	2	0	-2.171243
953	12009	Azi1	5-azacytidine induced gene 1	0	2	0	-2.170181
954	68816	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0	2	0	-2.169011
955	70425	Csnk1g3	casein kinase 1, gamma 3	0	2	0	-2.168766
956	13018	Ctcf	CCCTC-binding factor	0	2	0	-2.168681
957	217653	C79407	MIS18 binding protein 1	0	2	0	-2.167571
958	109331	Rnf20	ring finger protein 20	0	2	0	-2.16646
959	383458	UNK	NA	0	2	0	-2.166346
960	319615	6330416L07Rik	zinc finger protein 944	0	2	0	-2.16449
961	230623	A630098G03Rik	selection and upkeep of intraepithelial T cells 11	0	2	0	-2.164381
962	19944	Rpl29	ribosomal protein L29	0	2	0	-2.164031
963	13909	LOC13909	carboxylesterase 3B	0	2	0	-2.163902
964	22164	Tnfsf4	tumor necrosis factor (ligand) superfamily, member 4	0	2	0	-2.163158
965	353328	Muc6	mucin 6, gastric	0	2	0	-2.162063
966	67623	Tm7sf3	transmembrane 7 superfamily member 3	0	2	0	-2.161288
967	19941	Rpl26	ribosomal protein L26	0	2	0	-2.161138
968	16173	Il18	interleukin 18	0	2	0	-2.160133
969	224661	Slc26a8	solute carrier family 26, member 8	0	2	0	-2.160131
970	104111	Adcy3	adenylate cyclase 3	0	2	0	-2.159585
971	20018	Rpo1-3	polymerase (RNA) I polypeptide D	0	2	0	-2.158531
972	26908	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	0	2	0	-2.157954
973	18148	Npm1	nucleophosmin 1	0	2	0	-2.157686
974	104112	Acly	ATP citrate lyase	0	2	0	-2.157008
975	100198	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0	2	0	-2.156452
976	73534	1700082M22Rik	RIKEN cDNA 1700082M22 gene	0	2	0	-2.155167
977	241175	C230078M14Rik	contactin associated protein-like 5B	0	2	0	-2.154611
978	69930	Zfp715	zinc finger protein 715	0	2	0	-2.154586
979	11491	Adam17	a disintegrin and metallopeptidase domain 17	0	2	0	-2.152957
980	259279	Tubgcp3	tubulin, gamma complex associated protein 3	0	2	0	-2.152885
981	71735	1200011O22Rik	leucine-rich repeats and WD repeat domain containing 1	0	2	0	-2.151369
982	14915	Guca2a	guanylate cyclase activator 2a (guanylin)	0	2	0	-2.150792

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
983	433839	LOC433839	NA	0	2	0	-2.149718
984	22143	Tuba2	tubulin, alpha 1B	0	2	0	-2.148613
985	545013	LOC545013	predicted gene 5797	0	2	0	-2.148397
986	12623	Ces1	carboxylesterase 1G	0	2	0	-2.147192
987	69731	Gemin7	gem (nuclear organelle) associated protein 7	0	2	0	-2.146735
988	17381	Mmp12	matrix metallopeptidase 12	0	2	0	-2.146188
989	21899	Tlr6	toll-like receptor 6	0	2	0	-2.145591
990	233877	Kctd13	potassium channel tetramerisation domain containing 13	0	2	0	-2.144626
991	223732	Ldoc1l	leucine zipper, down-regulated in cancer 1-like	0	2	0	-2.144086
992	100088	Rcc1	regulator of chromosome condensation 1	0	2	0	-2.143934
993	195434	Utp14b	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)	0	2	0	-2.143552
994	73473	Iws1	IWS1 homolog (S. cerevisiae)	0	2	0	-2.14284
995	14600	Ghr	growth hormone receptor	0	2	0	-2.142707
996	52377	Rcn3	reticulocalbin 3, EF-hand calcium binding domain	0	2	0	-2.142568
997	381806	LOC381806	murinoglobulin pseudogene	0	2	0	-2.14208
998	101314	6720456B07Rik	RIKEN cDNA 6720456B07 gene	0	2	0	-2.141999
999	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0	2	0	-2.141566
1000	26893	Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	0	2	0	-2.14039
1001	52163	Camk1	calcium/calmodulin-dependent protein kinase I	0	2	0	-2.140273
1002	93734	Mpv17l	Mpv17 transgene, kidney disease mutant-like	0	2	0	-2.139896
1003	213649	Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	0	2	0	-2.138212
1004	16582	Kifc3	kinesin family member C3	0	2	0	-2.137993
1005	93967	Klra20	killer cell lectin-like receptor subfamily A, member 20	0	2	0	-2.137399
1006	71355	Col24a1	collagen, type XXIV, alpha 1	0	2	0	-2.136645
1007	319513	A930025D01Rik	family with sequence similarity 113, member A	0	2	0	-2.136142
1008	112406	Egln2	EGL nine homolog 2 (C. elegans)	0	2	0	-2.13476
1009	12965	Crygb	crystallin, gamma B	0	2	0	-2.134094
1010	19711	Resp18	regulated endocrine-specific protein 18	0	2	0	-2.133614
1011	11517	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	0	2	0	-2.131955
1012	99982	Aof2	lysine (K)-specific demethylase 1A	0	2	0	-2.131911
1013	78330	1500032D16Rik	NADH dehydrogenase (ubiquinone) flavoprotein 3	0	2	0	-2.131318
1014	14538	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	0	2	0	-2.130684
1015	29873	Cspg5	chondroitin sulfate proteoglycan 5	0	2	0	-2.129585
1016	18195	Nsf	N-ethylmaleimide sensitive fusion protein	0	2	0	-2.129434

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1017	17936	Nab1	Ngfi-A binding protein 1	0	2	0	-2.129423
1018	77733	Rnf170	ring finger protein 170	0	2	0	-2.127657
1019	19111	Prlpb	prolactin family 6, subfamily a, member 1	0	2	0	-2.125664
1020	259095	Olfr568	olfactory receptor 568	0	2	0	-2.125493
1021	71448	Tmem80	transmembrane protein 80	0	2	0	-2.124662
1022	72088	Ush1c	Usher syndrome 1C homolog (human)	0	2	0	-2.12361
1023	53951	2310002B06Rik	coiled-coil domain containing 75	0	2	0	-2.122183
1024	12983	Csf2rb1	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0	2	0	-2.122143
1025	56455	Dynll1	dynein light chain LC8-type 1	0	2	0	-2.121814
1026	14687	Gnaz	guanine nucleotide binding protein, alpha z subunit	0	2	0	-2.119972
1027	432738	UNK	NA	0	2	0	-2.119302
1028	56505	Ruvbl1	RuvB-like protein 1	0	2	0	-2.117449
1029	19982	Rpl36a	ribosomal protein L36A	0	2	0	-2.117309
1030	12561	Cdh4	cadherin 4	0	2	0	-2.117036
1031	380785	BM948371	brain-enriched guanylate kinase-associated	0	2	0	-2.116738
1032	229541	Dennd4b	DENN/MADD domain containing 4B	0	2	0	-2.116543
1033	20589	Ighmbp2	immunoglobulin mu binding protein 2	0	2	0	-2.116542
1034	192653	BC021608	tetratricopeptide repeat domain 36	0	2	0	-2.115779
1035	56208	Becn1	beclin 1, autophagy related	0	2	0	-2.114863
1036	65086	Edg7	lysophosphatidic acid receptor 3	0	2	0	-2.114567
1037	232619	UNK	NA	0	2	0	-2.11361
1038	70481	Pnma1	paraneoplastic antigen MA1	0	2	0	-2.11237
1039	22632	Yy1	YY1 transcription factor	0	2	0	-2.11205
1040	14803	Grid1	glutamate receptor, ionotropic, delta 1	0	2	0	-2.110074
1041	21859	Timp3	tissue inhibitor of metalloproteinase 3	0	2	0	-2.108394
1042	68549	Sgol2	shugoshin-like 2 (S. pombe)	0	2	0	-2.10806
1043	69681	Cdk3	cyclin-dependent kinase 3, pseudogene	0	2	0	-2.106862
1044	225825	Cd226	CD226 antigen	0	2	0	-2.106415
1045	16912	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	0	2	0	-2.104628
1046	11546	Parp2	poly (ADP-ribose) polymerase family, member 2	0	2	0	-2.104248
1047	407823	Baz2b	bromodomain adjacent to zinc finger domain, 2B	0	2	0	-2.104126
1048	69732	2410018L13Rik	RIKEN cDNA 2410018L13 gene	0	2	0	-2.103947
1049	235047	BB114266	zinc finger protein 809	0	2	0	-2.101991
1050	67922	2510049I19Rik	family with sequence similarity 32, member A	0	2	0	-2.101964

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1051	243529	H1fx	H1 histone family, member X	0	2	0	-2.101841
1052	214931	Fbxl16	F-box and leucine-rich repeat protein 16	0	2	0	-2.101051
1053	109229	C030004A17Rik	family with sequence similarity 118, member B	0	2	0	-2.100936
1054	66827	Ttc1	tetratricopeptide repeat domain 1	0	2	0	-2.100631
1055	18798	Plcb4	phospholipase C, beta 4	0	2	0	-2.100562
1056	320558	4930518F03Rik	synaptonemal complex protein 2	0	2	0	-2.098941
1057	72723	Zfp74	zinc finger protein 74	0	2	0	-2.098907
1058	56188	Fxyd1	FXYD domain-containing ion transport regulator 1	0	2	0	-2.098807
1059	53324	Nptx2	neuronal pentraxin 2	0	2	0	-2.098508
1060	77432	9530002B09Rik	RIKEN cDNA 9530002B09 gene	0	2	0	-2.098321
1061	22092	Tsga2	radial spoke head 1 homolog (Chlamydomonas)	0	2	0	-2.097515
1062	232889	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	0	2	0	-2.097283
1063	66588	Cmpk	cytidine monophosphate (UMP-CMP) kinase 1	0	2	0	-2.097119
1064	328424	Kcnrg	potassium channel regulator	0	2	0	-2.097016
1065	258711	Olfr432	olfactory receptor 432	0	2	0	-2.096908
1066	57430	Sult3a1	sulfotransferase family 3A, member 1	0	2	0	-2.096762
1067	230558	C8a	complement component 8, alpha polypeptide	0	2	0	-2.096302
1068	66557	Bpil1	BPI fold containing family B, member 2	0	2	0	-2.096297
1069	66395	Ahnak	AHNAK nucleoprotein (desmoyokin)	0	2	0	-2.096141
1070	74133	1200011M11Rik	RIKEN cDNA 1200011M11 gene	0	2	0	-2.095887
1071	76701	Ctrc	chymotrypsin C (caldecrin)	0	2	0	-2.095321
1072	110310	Krt2-7	keratin 7	0	2	0	-2.094311
1073	71425	5430413K10Rik	BPI fold containing family B, member 9A	0	2	0	-2.094113
1074	109019	5830411E10Rik	oligonucleotide/oligosaccharide-binding fold containing 2A	0	2	0	-2.092413
1075	18014	Neurog1	neurogenin 1	0	2	0	-2.09194
1076	12661	Chl1	cell adhesion molecule with homology to L1CAM	0	2	0	-2.089517
1077	259053	Olfr362	olfactory receptor 362	0	2	0	-2.088626
1078	18369	Olfr68	olfactory receptor 68	0	2	0	-2.088145
1079	234384	BC051227	MPV17 mitochondrial membrane protein-like 2	0	2	0	-2.087634
1080	245074	UNK	NA	0	2	0	-2.087448
1081	73103	3110009E18Rik	RIKEN cDNA 3110009E18 gene	0	2	0	-2.086829
1082	74365	Lonrf3	LON peptidase N-terminal domain and ring finger 3	0	2	0	-2.086468
1083	54401	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	0	2	0	-2.08616
1084	80732	Mynn	myoneurin	0	2	0	-2.085848

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1085	56519	Defb4	defensin beta 4	0	2	0	-2.082637
1086	102626	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0	2	0	-2.081482
1087	20446	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltrans	0	2	0	-2.080429
1088	353283	Eras	ES cell-expressed Ras	0	2	0	-2.078156
1089	258456	Olfr1196	olfactory receptor 1196	0	2	0	-2.076367
1090	72508	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	0	2	0	-2.074139
1091	74463	4933417E01Rik	exocyst complex component 3-like 2	0	2	0	-2.074071
1092	107047	Tnfsf5ip1	proteasome (prosome, macropain) assembly chaperone 2	0	2	0	-2.073429
1093	19892	Rpe65	retinal pigment epithelium 65	0	2	0	-2.073036
1094	142681	Slc34a3	solute carrier family 34 (sodium phosphate), member 3	0	2	0	-2.071089
1095	56277	Tmem45a	transmembrane protein 45a	0	2	0	-2.070454
1096	22215	Ube3a	ubiquitin protein ligase E3A	0	2	0	-2.069656
1097	17350	Mlh1	mutL homolog 1 (E. coli)	0	2	0	-2.069625
1098	68231	1700113O17Rik	H2A histone family, member B1	0	2	0	-2.069031
1099	67241	Smc6	structural maintenance of chromosomes 6	0	2	0	-2.06824
1100	24064	Spry2	sprouty homolog 2 (Drosophila)	0	2	0	-2.067551
1101	67980	Gnpda2	glucosamine-6-phosphate deaminase 2	0	2	0	-2.067218
1102	434496	UNK	NA	0	2	0	-2.066759
1103	22230	Ufd1l	ubiquitin fusion degradation 1 like	0	2	0	-2.065463
1104	320640	9530098N22Rik	selection and upkeep of intraepithelial T cells 4	0	2	0	-2.06174
1105	27390	Mmel1	membrane metallo-endopeptidase-like 1	0	2	0	-2.061593
1106	268860	Abat	4-aminobutyrate aminotransferase	0	2	0	-2.059733
1107	70333	Cd3eap	CD3E antigen, epsilon polypeptide associated protein	0	2	0	-2.059133
1108	75705	Eif4b	eukaryotic translation initiation factor 4B	0	2	0	-2.056837
1109	280621	BC089491	cDNA sequence BC089491	0	2	0	-2.056758
1110	16159	Il12a	interleukin 12a	0	2	0	-2.056411
1111	241915	Phc3	polyhomeotic-like 3 (Drosophila)	0	2	0	-2.056061
1112	71950	Nanog	Nanog homeobox	0	2	0	-2.055992
1113	12048	Bcl2l1	BCL2-like 1	0	2	0	-2.055732
1114	56443	Arpc1a	actin related protein 2/3 complex, subunit 1A	0	2	0	-2.052426
1115	217262	Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	0	2	0	-2.051977
1116	240068	D10628	zinc finger protein 563	0	2	0	-2.050918
1117	17882	Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	0	2	0	-2.050549
1118	18712	Pim1	proviral integration site 1	0	2	0	-2.050511

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1119	171263	V1re10	vomeronasal 1 receptor 67	0	2	0	-2.049897
1120	12469	Cct8	chaperonin containing Tcp1, subunit 8 (theta)	0	2	0	-2.047305
1121	76299	Txndc4	endoplasmic reticulum protein 44	0	2	0	-2.045957
1122	17221	Cd46	CD46 antigen, complement regulatory protein	0	2	0	-2.045918
1123	14406	Gabrg2	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2	0	2	0	-2.044668
1124	404473	Olfr1082	olfactory receptor 1082	0	2	0	-2.042687
1125	20526	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	0	2	0	-2.040558
1126	223664	Lrrc14	leucine rich repeat containing 14	0	2	0	-2.039226
1127	279029	Gm711	predicted gene 711	0	2	0	-2.038253
1128	54483	Mefv	Mediterranean fever	0	2	0	-2.037355
1129	225875	Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	0	2	0	-2.036666
1130	13712	Elk1	ELK1, member of ETS oncogene family	0	2	0	-2.036492
1131	433995	UNK	NA	0	2	0	-2.034723
1132	68797	Pdgfrl	platelet-derived growth factor receptor-like	0	2	0	-2.034278
1133	93888	Pcdhb17	protocadherin beta 17	0	2	0	-2.033602
1134	64424	Polr1e	polymerase (RNA) I polypeptide E	0	2	0	-2.032484
1135	13804	Endog	endonuclease G	0	2	0	-2.031572
1136	84092	Usp8	ubiquitin specific peptidase 8	0	2	0	-2.029444
1137	269966	Nup98	nucleoporin 98	0	2	0	-2.028759
1138	28113	Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	0	2	0	-2.028085
1139	226866	Gm106	predicted gene 106	0	2	0	-2.026508
1140	83493	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	0	2	0	-2.025238
1141	17991	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	0	2	0	-2.023879
1142	20055	Rps16	ribosomal protein S16	0	2	0	-2.023575
1143	66138	Wbscr22	Williams Beuren syndrome chromosome region 22	0	2	0	-2.021787
1144	14588	Gfra4	glial cell line derived neurotrophic factor family receptor alpha 4	0	2	0	-2.021038
1145	18515	Pbx2	pre B cell leukemia homeobox 2	0	2	0	-2.020844
1146	15126	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	0	2	0	-2.020841
1147	12482	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	0	2	0	-2.020092
1148	56456	Actl6a	actin-like 6A	0	2	0	-2.018002
1149	64945	Cldn12	claudin 12	0	2	0	-2.01785
1150	245839	Gzmn	granzyme N	0	2	0	-2.017586
1151	19942	Rpl27	ribosomal protein L27	0	2	0	-2.016525
1152	329324	Syt14	synaptotagmin XIV	0	2	0	-2.016433

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1153	404285	V1rd11	vomeronasal 1 receptor 64	0	2	0	-2.01628
1154	224109	Lrrc33	leucine rich repeat containing 33	0	2	0	-2.014705
1155	12044	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a	0	2	0	-2.014644
1156	13819	Epas1	endothelial PAS domain protein 1	0	2	0	-2.014616
1157	69367	Glrx2	glutaredoxin 2 (thioltransferase)	0	2	0	-2.014483
1158	15260	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	0	2	0	-2.014087
1159	140792	Colec12	collectin sub-family member 12	0	2	0	-2.012174
1160	18673	Phb	prohibitin	0	2	0	-2.011141
1161	73845	Ankrd42	ankyrin repeat domain 42	0	2	0	-2.010996
1162	67701	Wfdc2	WAP four-disulfide core domain 2	0	2	0	-2.010696
1163	235293	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	0	2	0	-2.010677
1164	71988	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0	2	0	-2.010591
1165	11537	Cfd	complement factor D (adipsin)	0	2	0	-2.010515
1166	72585	Lypd1	Ly6/Plaur domain containing 1	0	2	0	-2.010403
1167	21789	Tfpi2	tissue factor pathway inhibitor 2	0	2	0	-2.008652
1168	279572	Tlr13	toll-like receptor 13	0	2	0	-2.008489
1169	58180	Hic2	hypermethylated in cancer 2	0	2	0	-2.00844
1170	270097	AI427515	vesicle amine transport protein 1 homolog-like (T. californica)	0	2	0	-2.006145
1171	14200	Fhl2	four and a half LIM domains 2	0	2	0	-2.005044
1172	12723	Clcn1	chloride channel 1	0	2	0	-2.002607
1173	14864	Gstm3	glutathione S-transferase, mu 3	0	2	0	-2.002506
1174	69232	2610028H07Rik	glutamine-rich 1	0	2	0	-2.002405
1175	20290	Ccl1	chemokine (C-C motif) ligand 1	0	2	0	-2.001963
1176	171196	V1rc23	vomeronasal 1 receptor 22	0	2	0	-2.000768
1177	11867	Arpc1b	actin related protein 2/3 complex, subunit 1B	0	2	0	-2.000145
1178	18570	Pdcd6	programmed cell death 6	0	2	0	-1.999335
1179	18096	Nkx6-1	NK6 homeobox 1	0	2	0	-1.999203
1180	109978	Art4	ADP-ribosyltransferase 4	0	2	0	-1.998903
1181	17768	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolas	0	2	0	-1.997968
1182	19277	Ptpro	protein tyrosine phosphatase, receptor type, O	0	2	0	-1.997269
1183	75717	Cul5	cullin 5	0	2	0	-1.997058
1184	66589	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	0	2	0	-1.996552
1185	52686	Mettl2	methyltransferase like 2	0	2	0	-1.995483
1186	58801	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	0	2	0	-1.995464

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1187	67150	Rnf141	ring finger protein 141	0	2	0	-1.995333
1188	258792	Olfr1499	olfactory receptor 1499	0	2	0	-1.995101
1189	14343	Fut1	fucosyltransferase 1	0	2	0	-1.99357
1190	109620	Dsp	desmoplakin	0	2	0	-1.990793
1191	382590	UNK	NA	0	2	0	-1.989443
1192	17979	Ncoa3	nuclear receptor coactivator 3	0	2	0	-1.989372
1193	18617	Rhox5	reproductive homeobox 5	0	2	0	-1.988742
1194	101869	Unc45a	unc-45 homolog A (C. elegans)	0	2	0	-1.988255
1195	194360	LOC194360	trypsinogen pseudogene	0	2	0	-1.98783
1196	244867	Arhgap20	Rho GTPase activating protein 20	0	2	0	-1.987706
1197	73690	Glipr1	GLI pathogenesis-related 1 (glioma)	0	2	0	-1.987464
1198	399549	H2-M10.6	histocompatibility 2, M region locus 10.6	0	2	0	-1.986839
1199	107993	Bfsp2	beaded filament structural protein 2, phakinin	0	2	0	-1.986788
1200	228576	Mall	mal, T cell differentiation protein-like	0	2	0	-1.986553
1201	12176	Bnip3	BCL2/adenovirus E1B interacting protein 3	0	2	0	-1.985861
1202	17898	Myl7	myosin, light polypeptide 7, regulatory	0	2	0	-1.98566
1203	258730	Olfr483	olfactory receptor 483	0	2	0	-1.984756
1204	50850	Spast	spastin	0	2	0	-1.98314
1205	227613	Tubb2c	tubulin, beta 4B class IVB	0	2	0	-1.982409
1206	74917	4930474M22Rik	RIKEN cDNA 4930474M22 gene	0	2	0	-1.980884
1207	17933	Myt1l	myelin transcription factor 1-like	0	2	0	-1.979926
1208	209378	Itih5	inter-alpha (globulin) inhibitor H5	0	2	0	-1.979926
1209	19225	Ptgs2	prostaglandin-endoperoxide synthase 2	0	2	0	-1.979858
1210	69352	Efcbp1	N-terminal EF-hand calcium binding protein 1	0	2	0	-1.979084
1211	66258	Mrps17	mitochondrial ribosomal protein S17	0	2	0	-1.97862
1212	64074	Smoc2	SPARC related modular calcium binding 2	0	2	0	-1.977843
1213	26572	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	0	2	0	-1.976763
1214	22044	Trh	thyrotropin releasing hormone	0	2	0	-1.976423
1215	76653	1700121K02Rik	chibby homolog 3 (Drosophila)	0	2	0	-1.975779
1216	13007	Csrp1	cysteine and glycine-rich protein 1	0	2	0	-1.974723
1217	16568	Kif3a	kinesin family member 3A	0	2	0	-1.974533
1218	84506	Hamp1	hepcidin antimicrobial peptide	0	2	0	-1.974111
1219	12638	Cftr	cystic fibrosis transmembrane conductance regulator homolog	0	2	0	-1.97407
1220	269261	Rpl12	ribosomal protein L12	0	2	0	-1.974032

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1221	209380	LOC209380	GTPase, very large interferon inducible 1 pseudogene	0	2	0	-1.973637
1222	435366	LOC435366	predicted gene 5665	0	2	0	-1.973112
1223	17207	Mcf2l	mcf.2 transforming sequence-like	0	2	0	-1.972564
1224	320407	Klri2	killer cell lectin-like receptor family I member 2	0	2	0	-1.972044
1225	29806	Limd1	LIM domains containing 1	0	2	0	-1.971063
1226	245877	Rprc1	microtubule-associated protein 7 domain containing 1	0	2	0	-1.970153
1227	69312	4930418G15Rik	protein phosphatase 1, regulatory subunit 42	0	2	0	-1.969964
1228	14969	H2-Eb1	histocompatibility 2, class II antigen E beta	0	2	0	-1.967628
1229	64339	Fndc4	fibronectin type III domain containing 4	0	2	0	-1.967404
1230	66317	Wdr61	WD repeat domain 61	0	2	0	-1.966719
1231	231002	Plekhn1	pleckstrin homology domain containing, family N member 1	0	2	0	-1.964969
1232	66957	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	0	2	0	-1.964968
1233	57438	39147	membrane-associated ring finger (C3HC4) 7	0	2	0	-1.964129
1234	328264	A030007L22	NA	0	2	0	-1.964094
1235	72195	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	0	2	0	-1.962981
1236	54611	Pde3a	phosphodiesterase 3A, cGMP inhibited	0	2	0	-1.962684
1237	380698	Obscn	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0	2	0	-1.961491
1238	338375	Atp6v1g3	ATPase, H+ transporting, lysosomal V1 subunit G3	0	2	0	-1.961081
1239	53619	Blcap	bladder cancer associated protein homolog (human)	0	2	0	-1.960476
1240	17168	Mare	nitrogen permease regulator-like 3 (S. cerevisiae)	0	2	0	-1.960415
1241	217845	1810023F06Rik	interferon, alpha-inducible protein 27 like 2B	0	2	0	-1.959955
1242	12362	Casp1	caspase 1	0	2	0	-1.959695
1243	101533	Klk9	kallikrein related-peptidase 9	0	2	0	-1.959304
1244	16671	Krt1-3	keratin 33B	0	2	0	-1.958643
1245	20587	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	0	2	0	-1.958635
1246	11625	Ahsg	alpha-2-HS-glycoprotein	0	2	0	-1.958222
1247	109093	Rarsl	arginyl-tRNA synthetase 2, mitochondrial	0	2	0	-1.957482
1248	69721	Nkiras1	NFKB inhibitor interacting Ras-like protein 1	0	2	0	-1.95741
1249	108800	Ston2	stonin 2	0	2	0	-1.956511
1250	74498	Gorasp1	golgi reassembly stacking protein 1	0	2	0	-1.955965
1251	26992	Brd7	bromodomain containing 7	0	2	0	-1.955832
1252	381815	UNK	NA	0	2	0	-1.955279
1253	56494	Gosr2	golgi SNAP receptor complex member 2	0	2	0	-1.955199
1254	18588	Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma	0	2	0	-1.954406

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1255	67554	Slc25a30	solute carrier family 25, member 30	0	2	0	-1.953507
1256	110312	Pmch	pro-melanin-concentrating hormone	0	2	0	-1.953024
1257	232023	AW146242	vesicular, overexpressed in cancer, prosurvival protein 1	0	2	0	-1.952729
1258	26446	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	0	2	0	-1.952084
1259	67399	Pdlim7	PDZ and LIM domain 7	0	2	0	-1.95191
1260	19732	Rgl2	ral guanine nucleotide dissociation stimulator-like 2	0	2	0	-1.951085
1261	103573	Xpo1	exportin 1, CRM1 homolog (yeast)	0	2	0	-1.949501
1262	319655	Podxl2	podocalyxin-like 2	0	2	0	-1.949081
1263	408190	Wfdc13	WAP four-disulfide core domain 13	0	2	0	-1.948172
1264	66840	Wdr45l	Wdr45 like	0	2	0	-1.947879
1265	433358	UNK	NA	0	2	0	-1.946687
1266	116940	Ncoa6ip	trimethylguanosine synthase homolog (S. cerevisiae)	0	2	0	-1.946405
1267	105787	Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	0	2	0	-1.945835
1268	12492	Scarb2	scavenger receptor class B, member 2	0	2	0	-1.944224
1269	217337	Srp68	signal recognition particle 68	0	2	0	-1.942732
1270	16949	Loxl1	lysyl oxidase-like 1	0	2	0	-1.942658
1271	210801	Unc5d	unc-5 homolog D (C. elegans)	0	2	0	-1.942291
1272	17203	Mc5r	melanocortin 5 receptor	0	2	0	-1.941739
1273	66916	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	0	2	0	-1.940393
1274	433642	UNK	NA	0	2	0	-1.939528
1275	13589	Mapre1	microtubule-associated protein, RP/EB family, member 1	0	2	0	-1.939387
1276	72727	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0	2	0	-1.939239
1277	17187	Max	Max protein	0	2	0	-1.938994
1278	22123	Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	0	2	0	-1.937946
1279	19268	Ptprf	protein tyrosine phosphatase, receptor type, F	0	2	0	-1.937758
1280	22642	Zbtb17	zinc finger and BTB domain containing 17	0	2	0	-1.93774
1281	64144	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	0	2	0	-1.935418
1282	71241	Dmrtc2	doublesex and mab-3 related transcription factor like family C2	0	2	0	-1.935113
1283	224598	BC021442	zinc finger protein 758	0	2	0	-1.934584
1284	108014	Sfrs9	serine/arginine-rich splicing factor 9	0	2	0	-1.934169
1285	78076	Lcn8	lipocalin 8	0	2	0	-1.93401
1286	208518	Cep78	centrosomal protein 78	0	2	0	-1.933688
1287	68420	Ankrd13a	ankyrin repeat domain 13a	0	2	0	-1.932999
1288	192897	Itgb4	integrin beta 4	0	2	0	-1.931715

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1289	67774	Loh12cr1	loss of heterozygosity, 12, chromosomal region 1 homolog (human)	0	2	0	-1.931373
1290	108098	Surb7	mediator complex subunit 21	0	2	0	-1.930908
1291	110902	Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	0	2	0	-1.930493
1292	78923	4833446K15Rik	chondroitin sulfate synthase 3	0	2	0	-1.930289
1293	171262	V1rl1	vomeronasal 1 receptor 70	0	2	0	-1.930245
1294	320183	Msrb3	methionine sulfoxide reductase B3	0	2	0	-1.930033
1295	108052	Slc14a1	solute carrier family 14 (urea transporter), member 1	0	2	0	-1.929198
1296	218171	UNK	NA	0	2	0	-1.929154
1297	11634	Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	0	2	0	-1.928426
1298	79044	Mrps34	mitochondrial ribosomal protein S34	0	2	0	-1.926718
1299	14972	H2-K1	histocompatibility 2, K1, K region	0	2	0	-1.926558
1300	18810	Plec1	plectin	0	2	0	-1.925425
1301	71810	Ranbp3	RAN binding protein 3	0	2	0	-1.925185
1302	110524	Dgkq	diacylglycerol kinase, theta	0	2	0	-1.925177
1303	258695	Olfr1453	olfactory receptor 1453	0	2	0	-1.924449
1304	20666	Sox11	SRY-box containing gene 11	0	2	0	-1.924396
1305	66481	Rps21	ribosomal protein S21	0	2	0	-1.923805
1306	258764	Olfr1099	olfactory receptor 1099	0	2	0	-1.923507
1307	11552	Adra2b	adrenergic receptor, alpha 2b	0	2	0	-1.923109
1308	279028	Adamts13	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13	0	2	0	-1.923046
1309	75425	2610036D13Rik	TELO2 interacting protein 1	0	2	0	-1.92044
1310	72194	Fbxl20	F-box and leucine-rich repeat protein 20	0	2	0	-1.919917
1311	70821	4921507P07Rik	RIKEN cDNA 4921507P07 gene	0	2	0	-1.919031
1312	108687	Edem2	ER degradation enhancer, mannosidase alpha-like 2	0	2	0	-1.91839
1313	19281	Ptprt	protein tyrosine phosphatase, receptor type, T	0	2	0	-1.91816
1314	14208	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	0	2	0	-1.917859
1315	209387	AI451617	tripartite motif-containing 30D	0	2	0	-1.917797
1316	110074	Dut	deoxyuridine triphosphatase	0	2	0	-1.916504
1317	21872	Tjp1	tight junction protein 1	0	2	0	-1.91608
1318	76156	6330503C03Rik	family with sequence similarity 131, member B	0	2	0	-1.915521
1319	19242	Ptn	pleiotrophin	0	2	0	-1.915274
1320	54126	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	0	2	0	-1.914991
1321	215472	E130012K09	predicted gene 4792	0	2	0	-1.913882
1322	14590	Ggh	gamma-glutamyl hydrolase	0	2	0	-1.913797

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1323	192194	Butr1	butyrophilin related 1	0	2	0	-1.913346
1324	11796	Birc3	baculoviral IAP repeat-containing 3	0	2	0	-1.912864
1325	68458	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	0	2	0	-1.912673
1326	229049	1700003N22Rik	NA	0	2	0	-1.912663
1327	80283	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	0	2	0	-1.911967
1328	140488	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	0	2	0	-1.911491
1329	11656	Alas2	aminolevulinic acid synthase 2, erythroid	0	2	0	-1.910539
1330	22074	Try4	trypsin 4	0	2	0	-1.909845
1331	68097	Dynll2	dynein light chain LC8-type 2	0	2	0	-1.908579
1332	192216	Tmem47	transmembrane protein 47	0	2	0	-1.904231
1333	72748	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3	0	2	0	-1.903683
1334	72345	2810002O09Rik	family with sequence similarity 123, member B	0	2	0	-1.903618
1335	76829	Dok5	docking protein 5	0	2	0	-1.903222
1336	227699	Nup188	nucleoporin 188	0	2	0	-1.901916
1337	226250	AU041783	actin filament associated protein 1-like 2	0	2	0	-1.900933
1338	66302	2410005O16Rik	family with sequence similarity 82, member B	0	2	0	-1.900083
1339	81907	Tmem108	transmembrane protein 108	0	2	0	-1.899979
1340	105245	Txndc5	thioredoxin domain containing 5	0	2	0	-1.898221
1341	12869	Cox8b	cytochrome c oxidase, subunit VIIIb	0	2	0	-1.897171
1342	17308	Mgat1	mannoside acetylglucosaminyltransferase 1	0	2	0	-1.896843
1343	19338	Rab33b	RAB33B, member of RAS oncogene family	0	2	0	-1.896576
1344	216134	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	0	2	0	-1.896156
1345	66629	Golph3	golgi phosphoprotein 3	0	2	0	-1.891824
1346	108148	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	0	2	0	-1.891282
1347	14027	Evpl	envoplakin	0	2	0	-1.890434
1348	18984	Por	P450 (cytochrome) oxidoreductase	0	2	0	-1.890411
1349	18725	Pira2	paired-Ig-like receptor A2	0	2	0	-1.889848
1350	67729	Mansc1	MANSC domain containing 1	0	2	0	-1.889574
1351	18145	Npc1	Niemann Pick type C1	0	2	0	-1.888654
1352	100163	Pafah2	platelet-activating factor acetylhydrolase 2	0	2	0	-1.888531
1353	194735	4930430D24Rik	RIKEN cDNA 4930430D24 gene	0	2	0	-1.888419
1354	18999	Pou5f1	POU domain, class 5, transcription factor 1	0	2	0	-1.888077
1355	70433	2610109H07Rik	RIKEN cDNA 2610109H07 gene	0	2	0	-1.887506
1356	117590	Asb10	ankyrin repeat and SOCS box-containing 10	0	2	0	-1.887496

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1357	67302	Zc3h13	zinc finger CCCH type containing 13	0	2	0	-1.886399
1358	66789	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	0	2	0	-1.884235
1359	73481	1700074P13Rik	RIKEN cDNA 1700074P13 gene	0	2	0	-1.884088
1360	381358	LOC381358	NA	0	2	0	-1.883324
1361	14311	Cidec	cell death-inducing DFFA-like effector c	0	2	0	-1.881448
1362	216343	Tph2	tryptophan hydroxylase 2	0	2	0	-1.881336
1363	18260	Ocln	occludin	0	2	0	-1.880621
1364	436121	UNK	NA	0	2	0	-1.88018
1365	238377	Gpr68	G protein-coupled receptor 68	0	2	0	-1.878268
1366	54711	Plagl2	pleiomorphic adenoma gene-like 2	0	2	0	-1.877895
1367	54616	Extl3	exostoses (multiple)-like 3	0	2	0	-1.876163
1368	13143	Dapk2	death-associated protein kinase 2	0	2	0	-1.876151
1369	59026	Huwe1	HECT, UBA and WWE domain containing 1	0	2	0	-1.875354
1370	23985	Slc26a4	solute carrier family 26, member 4	0	2	0	-1.875017
1371	16495	Kcna7	potassium voltage-gated channel, shaker-related subfamily, member 7	0	2	0	-1.874038
1372	58234	Shank3	SH3/ankyrin domain gene 3	0	2	0	-1.874014
1373	74477	4933427D14Rik	RIKEN cDNA 4933427D14 gene	0	2	0	-1.871768
1374	434423	Dppa5	developmental pluripotency associated 5A	0	2	0	-1.869811
1375	22017	Tpmt	thiopurine methyltransferase	0	2	0	-1.869269
1376	76784	Mtif2	mitochondrial translational initiation factor 2	0	2	0	-1.867693
1377	252966	Cables2	CDK5 and Abl enzyme substrate 2	0	2	0	-1.866611
1378	114332	Xlkd1	lymphatic vessel endothelial hyaluronan receptor 1	0	2	0	-1.865851
1379	331529	4930481M05	predicted gene 5128	0	2	0	-1.865428
1380	11542	Adora3	adenosine A3 receptor	0	2	0	-1.865262
1381	19120	Prm3	protamine 3	0	2	0	-1.86434
1382	224805	Aarsl	alanyl-tRNA synthetase 2, mitochondrial (putative)	0	2	0	-1.864172
1383	94254	Wbscr16	Williams-Beuren syndrome chromosome region 16 homolog (human)	0	2	0	-1.863468
1384	258564	Olfr1015	olfactory receptor 1015	0	2	0	-1.863186
1385	109113	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	0	2	0	-1.862896
1386	435839	UNK	NA	0	2	0	-1.86195
1387	277010	Marveld1	MARVEL (membrane-associating) domain containing 1	0	2	0	-1.861328
1388	16011	Igfbp5	insulin-like growth factor binding protein 5	0	2	0	-1.859247
1389	14263	Fmo5	flavin containing monooxygenase 5	0	2	0	-1.858035
1390	14055	Ezh1	enhancer of zeste homolog 1 (Drosophila)	0	2	0	-1.856571

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1391	93840	Ltap	vang-like 2 (van gogh, Drosophila)	0	2	0	-1.856476
1392	258850	Olfr295	olfactory receptor 295	0	2	0	-1.855094
1393	14167	Fgf12	fibroblast growth factor 12	0	2	0	-1.854526
1394	17691	Snf1lk	salt inducible kinase 1	0	2	0	-1.85418
1395	18582	Pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta	0	2	0	-1.854054
1396	26561	Mmp23	matrix metallopeptidase 23	0	2	0	-1.853964
1397	22361	Vnn1	vanin 1	0	2	0	-1.853226
1398	384894	UNK	NA	0	2	0	-1.851958
1399	224753	H2-M10.4	histocompatibility 2, M region locus 10.4	0	2	0	-1.851832
1400	228361	D030051N19Rik	autophagy/beclin 1 regulator 1	0	2	0	-1.851607
1401	69957	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	0	2	0	-1.851507
1402	329416	Nostrin	nitric oxide synthase trafficker	0	2	0	-1.851185
1403	320379	D630028G08Rik	RIKEN cDNA D630028G08 gene	0	2	0	-1.849663
1404	224836	Usp49	ubiquitin specific peptidase 49	0	2	0	-1.849534
1405	75721	4932414N04Rik	RIKEN cDNA 4932414N04 gene	0	2	0	-1.84828
1406	228769	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	0	2	0	-1.846653
1407	68566	Drd1ip	calcyon neuron-specific vesicular protein	0	2	0	-1.846009
1408	19387	Rangap1	RAN GTPase activating protein 1	0	2	0	-1.845893
1409	14797	Aes	amino-terminal enhancer of split	0	2	0	-1.843892
1410	68272	Rbm28	RNA binding motif protein 28	0	2	0	-1.843825
1411	16658	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	0	2	0	-1.843548
1412	80880	Ankrd47	KN motif and ankyrin repeat domains 3	0	2	0	-1.84215
1413	381101	BC048355	cDNA sequence BC048355	0	2	0	-1.841935
1414	76983	Scfd1	Sec1 family domain containing 1	0	2	0	-1.841525
1415	69282	1700001J03Rik	RIKEN cDNA 1700001J03 gene	0	2	0	-1.840344
1416	236537	Zfp352	zinc finger protein 352	0	2	0	-1.840062
1417	214597	Sidt2	SID1 transmembrane family, member 2	0	2	0	-1.839893
1418	74670	4930432O21Rik	zinc finger prtoein 943	0	2	0	-1.839418
1419	16331	Inpp5d	inositol polyphosphate-5-phosphatase D	0	2	0	-1.838783
1420	21406	Tcf12	transcription factor 12	0	2	0	-1.838102
1421	433292	Nms	neuromedin S	0	2	0	-1.836727
1422	383548	Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	0	2	0	-1.836424
1423	17222	Anapc1	anaphase promoting complex subunit 1	0	2	0	-1.835981
1424	106489	5630401J11Rik	SFT2 domain containing 1	0	2	0	-1.83426

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1425	11910	Atf3	activating transcription factor 3	0	2	0	-1.833105
1426	225896	D19Ertd721e	UBX domain protein 1	0	2	0	-1.832633
1427	380655	UNK	NA	0	2	0	-1.831805
1428	171190	V1rc17	vomeronasal 1 receptor 26	0	2	0	-1.830857
1429	435391	LOC435391	dual specificity phosphatase and pro isomerase domain containing 1	0	2	0	-1.830143
1430	435707	UNK	NA	0	2	0	-1.829142
1431	17220	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	0	2	0	-1.828448
1432	14679	Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3	0	2	0	-1.827418
1433	18997	Pou4f2	POU domain, class 4, transcription factor 2	0	2	0	-1.826732
1434	68705	Gtf2f2	general transcription factor IIF, polypeptide 2	0	2	0	-1.826049
1435	68239	2410039E07Rik	keratin 42	0	2	0	-1.825011
1436	170653	Krtap16-3	NA	0	2	0	-1.824052
1437	67996	Sfrs6	serine/arginine-rich splicing factor 6	0	2	0	-1.823302
1438	114716	Spred2	sprouty-related, EVH1 domain containing 2	0	2	0	-1.8229
1439	100087	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)	0	2	0	-1.821217
1440	22348	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	0	2	0	-1.819712
1441	226999	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	0	2	0	-1.81933
1442	72145	Wdfy3	WD repeat and FYVE domain containing 3	0	2	0	-1.818922
1443	68981	Snrpa1	small nuclear ribonucleoprotein polypeptide A'	0	2	0	-1.81828
1444	66626	5730403B10Rik	RIKEN cDNA 5730403B10 gene	0	2	0	-1.817745
1445	15413	Hoxb5	homeobox B5	0	2	0	-1.817551
1446	17433	Mobp	myelin-associated oligodendrocytic basic protein	0	2	0	-1.81669
1447	13170	Dbp	D site albumin promoter binding protein	0	2	0	-1.816627
1448	100710	Aprin	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	0	2	0	-1.815957
1449	192113	Atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	0	2	0	-1.815727
1450	68421	Lmbrd1	LMBR1 domain containing 1	0	2	0	-1.815718
1451	69269	Scnm1	sodium channel modifier 1	0	2	0	-1.815429
1452	74254	Xab1	GPN-loop GTPase 1	0	2	0	-1.812152
1453	20997	T	brachyury	0	2	0	-1.810497
1454	21422	Tcfcp2	transcription factor CP2	0	2	0	-1.809284
1455	14137	Fdft1	farnesyl diphosphate farnesyl transferase 1	0	2	0	-1.808125
1456	73666	Thoc3	THO complex 3	0	2	0	-1.807735
1457	22289	Utx	lysine (K)-specific demethylase 6A	0	2	0	-1.805932
1458	83430	Il23a	interleukin 23, alpha subunit p19	0	2	0	-1.803721

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1459	17480	Mpl	myeloproliferative leukemia virus oncogene	0	2	0	-1.80347
1460	109042	Prkcdbp	protein kinase C, delta binding protein	0	2	0	-1.802374
1461	74018	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	0	2	0	-1.80119
1462	56216	Stx1b2	syntaxin 1B	0	2	0	-1.800939
1463	17257	Mecp2	methyl CpG binding protein 2	0	2	0	-1.799611
1464	13839	Epha5	Eph receptor A5	0	2	0	-1.799421
1465	238379	UNK	NA	0	2	0	-1.799315
1466	20591	Jarid1c	lysine (K)-specific demethylase 5C	0	2	0	-1.798843
1467	94226	Edg8	sphingosine-1-phosphate receptor 5	0	2	0	-1.798543
1468	18534	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	0	2	0	-1.798033
1469	67205	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	0	2	0	-1.797947
1470	67320	Iqcf4	IQ motif containing F4	0	2	0	-1.797365
1471	21816	Tgm1	transglutaminase 1, K polypeptide	0	2	0	-1.797033
1472	12006	Axin2	axin2	0	2	0	-1.796107
1473	67252	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	0	2	0	-1.795388
1474	228602	4930402H24Rik	RIKEN cDNA 4930402H24 gene	0	2	0	-1.790336
1475	16825	Ldb1	LIM domain binding 1	0	2	0	-1.789335
1476	28078	Prlpl	prolactin family 5, subfamily a, member 1	0	2	0	-1.789052
1477	223527	Eny2	enhancer of yellow 2 homolog (Drosophila)	0	2	0	-1.78828
1478	11486	Ada	adenosine deaminase	0	2	0	-1.788224
1479	382588	UNK	NA	0	2	0	-1.787524
1480	246747	BC054059	adipogenin	0	2	0	-1.786737
1481	70831	4733401H21Rik	keratin associated protein 31-1	0	2	0	-1.784305
1482	19132	Prph1	peripherin	0	2	0	-1.783497
1483	67000	Prlpi	prolactin family 3, subfamily a, member 1	0	2	0	-1.782755
1484	21922	Clec3b	C-type lectin domain family 3, member b	0	2	0	-1.781601
1485	66421	2410004B18Rik	RIKEN cDNA 2410004B18 gene	0	2	0	-1.781188
1486	53333	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0	2	0	-1.780945
1487	12990	Csna	casein alpha s1	0	2	0	-1.780438
1488	235631	Tsp50	protease, serine, 50	0	2	0	-1.779486
1489	56484	Foxo3a	forkhead box O3	0	2	0	-1.77925
1490	14457	Gas7	growth arrest specific 7	0	2	0	-1.778204
1491	232408	Klrb1f	killer cell lectin-like receptor subfamily B member 1F	0	2	0	-1.776012
1492	245050	C730027P07Rik	family with sequence similarity 198, member A	0	2	0	-1.775663

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1493	75258	4930563M21Rik	RIKEN cDNA 4930563M21 gene	0	2	0	-1.774778
1494	20199	S100a5	S100 calcium binding protein A5	0	2	0	-1.77473
1495	434311	UNK	NA	0	2	0	-1.774459
1496	17533	Mrc1	mannose receptor, C type 1	0	2	0	-1.77431
1497	13427	Dync1i2	dynein cytoplasmic 1 intermediate chain 2	0	2	0	-1.773243
1498	24131	Ldb3	LIM domain binding 3	0	2	0	-1.773065
1499	21926	Tnf	tumor necrosis factor	0	2	0	-1.772966
1500	71710	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	0	2	0	-1.771731
1501	64378	Gpr88	G-protein coupled receptor 88	0	2	0	-1.771573
1502	74600	Mrpl47	mitochondrial ribosomal protein L47	0	2	0	-1.771512
1503	74734	Rhoh	ras homolog gene family, member H	0	2	0	-1.770165
1504	403395	Clec3a	C-type lectin domain family 3, member a	0	2	0	-1.769623
1505	271047	Serpina3b	serine (or cysteine) peptidase inhibitor, clade A, member 3B	0	2	0	-1.768843
1506	192976	BC046404	cDNA sequence BC046404	0	2	0	-1.767979
1507	56213	Htra1	HtrA serine peptidase 1	0	2	0	-1.767779
1508	76936	Hnrpm	heterogeneous nuclear ribonucleoprotein M	0	2	0	-1.767749
1509	140918	Slc7a12	solute carrier family 7 (cationic amino acid transporter, y+ system), member 12	0	2	0	-1.764149
1510	72729	Cdc42se2	CDC42 small effector 2	0	2	0	-1.763727
1511	72149	2610019A05Rik	STE20-related kinase adaptor alpha	0	2	0	-1.763264
1512	14408	Gabrr1	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1	0	2	0	-1.76317
1513	12556	Cdh16	cadherin 16	0	2	0	-1.762838
1514	26430	Parg	poly (ADP-ribose) glycohydrolase	0	2	0	-1.762708
1515	232044	UNK	NA	0	2	0	-1.762561
1516	18554	Pcsk7	proprotein convertase subtilisin/kexin type 7	0	2	0	-1.762031
1517	234582	Ccdc102a	coiled-coil domain containing 102A	0	2	0	-1.761133
1518	225845	Hrasls3	phospholipase A2, group XVI	0	2	0	-1.759492
1519	434174	LOC434174	high-mobility group (nonhistone chromosomal) protein 1-like 1	0	2	0	-1.758617
1520	56195	Ptbp2	polypyrimidine tract binding protein 2	0	2	0	-1.758004
1521	224674	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0	2	0	-1.757869
1522	74117	Actr3	ARP3 actin-related protein 3 homolog (yeast)	0	2	0	-1.757781
1523	269523	Vcp	valosin containing protein	0	2	0	-1.757325
1524	228880	Prkcbp1	zinc finger, MYND-type containing 8	0	2	0	-1.756994
1525	54353	Scap2	src family associated phosphoprotein 2	0	2	0	-1.756759
1526	11777	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	0	2	0	-1.75511

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1527	14866	Gstm5	glutathione S-transferase, mu 5	0	2	0	-1.754774
1528	67974	5730405I09Rik	cyclin Y	0	2	0	-1.754619
1529	240263	Fem1c	fem-1 homolog c (C.elegans)	0	2	0	-1.754619
1530	19051	Gsbs	protein phosphatase 1, regulatory subunit 17	0	2	0	-1.754326
1531	242939	Cpz	carboxypeptidase Z	0	2	0	-1.754212
1532	18209	Ntn2l	netrin 3	0	2	0	-1.752072
1533	13528	Dtnb	dystrobrevin, beta	0	2	0	-1.751853
1534	14262	Fmo3	flavin containing monooxygenase 3	0	2	0	-1.751669
1535	16971	Lrp1	low density lipoprotein receptor-related protein 1	0	2	0	-1.75166
1536	242317	LOC242317	NA	0	2	0	-1.751135
1537	83702	Akr1c6	aldo-keto reductase family 1, member C6	0	2	0	-1.750912
1538	14166	Fgf11	fibroblast growth factor 11	0	2	0	-1.750863
1539	66204	Acyp1	acylphosphatase 1, erythrocyte (common) type	0	2	0	-1.750541
1540	14765	Gpr50	G-protein-coupled receptor 50	0	2	0	-1.750432
1541	103765	Tmem17	transmembrane protein 17	0	2	0	-1.750278
1542	80509	Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	0	2	0	-1.748873
1543	434436	LOC434436	cDNA sequence BY080835	0	2	0	-1.748437
1544	320769	Prdx6-rs1	peroxiredoxin 6B	0	2	0	-1.748276
1545	94353	Hmgn3	high mobility group nucleosomal binding domain 3	0	2	0	-1.74803
1546	16797	Lat	linker for activation of T cells	0	2	0	-1.747886
1547	110886	Gabra5	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5	0	2	0	-1.747014
1548	66322	1700011A15Rik	RIKEN cDNA 1700011A15 gene	0	2	0	-1.746976
1549	56628	LOC56628	NA	0	2	0	-1.746845
1550	11651	Akt1	thymoma viral proto-oncogene 1	0	2	0	-1.746719
1551	432604	UNK	NA	0	2	0	-1.745445
1552	74481	Batf2	basic leucine zipper transcription factor, ATF-like 2	0	2	0	-1.744933
1553	56488	Nxt1	NTF2-related export protein 1	0	2	0	-1.744694
1554	436127	UNK	NA	0	2	0	-1.743723
1555	213541	Ythdf2	YTH domain family 2	0	2	0	-1.742989
1556	435489	LOC435489	carbonyl reductase 1 pseudogene	0	2	0	-1.742515
1557	18618	Pemt	phosphatidylethanolamine N-methyltransferase	0	2	0	-1.742252
1558	22264	Prap1	proline-rich acidic protein 1	0	2	0	-1.742193
1559	14708	Gng7	guanine nucleotide binding protein (G protein), gamma 7	0	2	0	-1.741837
1560	382038	AK122209	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	0	2	0	-1.741198

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1561	18426	Ovol1	OVO homolog-like 1 (Drosophila)	0	2	0	-1.740925
1562	217331	Zc3h5	unkempt homolog (Drosophila)	0	2	0	-1.740456
1563	83762	Otof	otoferlin	0	2	0	-1.740336
1564	12427	Ccna1	cyclin A1	0	2	0	-1.739995
1565	217306	Cd300e	CD300e antigen	0	2	0	-1.739333
1566	223776	1300018J18Rik	RIKEN cDNA 1300018J18 gene	0	2	0	-1.738922
1567	223917	BC031593	keratin 79	0	2	0	-1.738118
1568	192163	Pcdha3	protocadherin alpha 3	0	2	0	-1.736606
1569	56631	Trim17	tripartite motif-containing 17	0	2	0	-1.73647
1570	218038	Amph	amphiphysin	0	2	0	-1.736343
1571	230398	Ifna6T	predicted gene 13280	0	2	0	-1.735814
1572	16520	Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	0	2	0	-1.735593
1573	54128	Pmm2	phosphomannomutase 2	0	2	0	-1.7348
1574	381286	Serpinb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C	0	2	0	-1.733636
1575	171187	V1rc14	vomeronasal 1 receptor 33	0	2	0	-1.733431
1576	24075	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	0	-1.733331
1577	110355	Adrbk1	adrenergic receptor kinase, beta 1	0	2	0	-1.73333
1578	12234	Btrc	beta-transducin repeat containing protein	0	2	0	-1.73332
1579	69009	Thap7	THAP domain containing 7	0	2	0	-1.732352
1580	74335	Xrcc3	X-ray repair complementing defective repair in Chinese hamster cells 3	0	2	0	-1.731808
1581	101118	8430437G11Rik	transmembrane protein 168	0	2	0	-1.731694
1582	387512	Tas2r135	taste receptor, type 2, member 135	0	2	0	-1.730082
1583	66094	Lsm7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	2	0	-1.72837
1584	269437	Plch1	phospholipase C, eta 1	0	2	0	-1.727947
1585	15078	H3f3a	H3 histone, family 3A	0	2	0	-1.727842
1586	16560	Kif1a	kinesin family member 1A	0	2	0	-1.726675
1587	257938	Olfr1419	olfactory receptor 1419	0	2	0	-1.72606
1588	435219	UNK	NA	0	2	0	-1.724546
1589	14747	Cmklr1	chemokine-like receptor 1	0	2	0	-1.724132
1590	12515	Cd69	CD69 antigen	0	2	0	-1.724006
1591	243834	Zfp324	zinc finger protein 324	0	2	0	-1.723064
1592	21804	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	0	2	0	-1.722967
1593	209683	AI428795	tetratricopeptide repeat domain 28	0	2	0	-1.722315
1594	56418	Ykt6	YKT6 homolog (S. Cerevisiae)	0	2	0	-1.722001

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1595	11535	Adm	adrenomedullin	0	2	0	-1.721877
1596	319930	Ceacam19	carcinoembryonic antigen-related cell adhesion molecule 19	0	2	0	-1.721707
1597	17259	Mef2b	myocyte enhancer factor 2B	0	2	0	-1.721664
1598	17756	Mtap2	microtubule-associated protein 2	0	2	0	-1.721607
1599	66873	1200009O22Rik	TLR4 interactor with leucine-rich repeats	0	2	0	-1.721321
1600	269513	E130310K16Rik	Na+/K+ transporting ATPase interacting 3	0	2	0	-1.72071
1601	22297	V1ra2	vomeronasal 1 receptor 45	0	2	0	-1.720569
1602	269424	Phf17	PHD finger protein 17	0	2	0	-1.720081
1603	228136	Zdhhc5	zinc finger, DHHC domain containing 5	0	2	0	-1.719746
1604	56636	Fgf21	fibroblast growth factor 21	0	2	0	-1.718797
1605	56220	Zfp386	zinc finger protein 386 (Kruppel-like)	0	2	0	-1.716764
1606	14407	Gabrg3	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3	0	2	0	-1.716311
1607	18431	p	oculocutaneous albinism II	0	2	0	-1.716022
1608	19400	Rapsn	receptor-associated protein of the synapse	0	2	0	-1.715447
1609	12969	Crygf	crystallin, gamma F	0	2	0	-1.715428
1610	22371	Vwf	Von Willebrand factor homolog	0	2	0	-1.713978
1611	108078	Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	0	2	0	-1.713428
1612	67717	Lipf	lipase, gastric	0	2	0	-1.712205
1613	320858	D930040M24Rik	l(3)mbt-like 4 (Drosophila)	0	2	0	-1.710116
1614	56210	Rev1l	REV1 homolog (S. cerevisiae)	0	2	0	-1.709541
1615	16419	Itgb5	integrin beta 5	0	2	0	-1.709215
1616	64139	Ctsm	cathepsin M	0	2	0	-1.708294
1617	70061	Sdro	4short chain dehydrogenase/reductase family 9C, member 7	0	2	0	-1.707206
1618	14201	Fhl3	four and a half LIM domains 3	0	2	0	-1.706098
1619	23950	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	0	2	0	-1.70547
1620	22315	V2r9	NA	0	2	0	-1.705422
1621	76123	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0	2	0	-1.701867
1622	52513	Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	0	2	0	-1.701352
1623	83409	Mapbpip	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0	2	0	-1.701143
1624	56351	Ptges3	prostaglandin E synthase 3 (cytosolic)	0	2	0	-1.699995
1625	319535	Zfp182	zinc finger protein 182	0	2	0	-1.699202
1626	12014	Bach2	BTB and CNC homology 2	0	2	0	-1.698465
1627	66462	2810428I15Rik	RIKEN cDNA 2810428I15 gene	0	2	0	-1.695366
1628	66695	Aspn	asporin	0	2	0	-1.695335

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1629	22757	Zfp95	zinc finger with KRAB and SCAN domains 5	0	2	0	-1.695134
1630	20787	Srebf1	sterol regulatory element binding transcription factor 1	0	2	0	-1.69501
1631	235623	Scap	SREBF chaperone	0	2	0	-1.694243
1632	435499	LOC435499	kinesin family member 2C pseudogene	0	2	0	-1.694237
1633	18753	Prkcd	protein kinase C, delta	0	2	0	-1.693593
1634	74435	Lrrc44	leucine-rich repeats and IQ motif containing 3	0	2	0	-1.692568
1635	14168	Fgf13	fibroblast growth factor 13	0	2	0	-1.692364
1636	56534	Hspb3	heat shock protein 3	0	2	0	-1.692124
1637	13848	Ephb6	Eph receptor B6	0	2	0	-1.690671
1638	26909	Exo1	exonuclease 1	0	2	0	-1.689935
1639	58522	Trim54	tripartite motif-containing 54	0	2	0	-1.688745
1640	15495	Hsd3b4	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4	0	2	0	-1.688523
1641	12226	Btg1	B cell translocation gene 1, anti-proliferative	0	2	0	-1.688515
1642	258893	Olfr1225	olfactory receptor 1225	0	2	0	-1.688016
1643	18035	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha	0	2	0	-1.687829
1644	233824	Cog7	component of oligomeric golgi complex 7	0	2	0	-1.687553
1645	320011	Ugcgl1	UDP-glucose glycoprotein glucosyltransferase 1	0	2	0	-1.687378
1646	12724	Clcn2	chloride channel 2	0	2	0	-1.687282
1647	12715	Ckm	creatine kinase, muscle	0	2	0	-1.685367
1648	12564	Cdh8	cadherin 8	0	2	0	-1.685039
1649	70419	2810408A11Rik	RIKEN cDNA 2810408A11 gene	0	2	0	-1.684983
1650	57916	Tnfrsf13b	tumor necrosis factor receptor superfamily, member 13b	0	2	0	-1.683719
1651	76797	2410137M14Rik	RIKEN cDNA 2410137M14 gene	0	2	0	-1.683533
1652	213019	Pdlim2	PDZ and LIM domain 2	0	2	0	-1.683258
1653	20970	Sdc3	syndecan 3	0	2	0	-1.683153
1654	26406	Map3k3	mitogen-activated protein kinase kinase kinase 3	0	2	0	-1.681609
1655	13998	Fgd6	FYVE, RhoGEF and PH domain containing 6	0	2	0	-1.68096
1656	18000	39326	septin 2	0	2	0	-1.680706
1657	433641	UNK	NA	0	2	0	-1.680633
1658	21427	Vps72	vacuolar protein sorting 72 (yeast)	0	2	0	-1.680166
1659	94176	Dock2	dedicator of cyto-kinesis 2	0	2	0	-1.679529
1660	53375	Mtx2	metaxin 2	0	2	0	-1.677852
1661	109346	Ankrd39	ankyrin repeat domain 39	0	2	0	-1.676914
1662	237523	Ptprq	protein tyrosine phosphatase, receptor type, Q	0	2	0	-1.676638

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1663	209357	Gtf2h3	general transcription factor IIH, polypeptide 3	0	2	0	-1.676126
1664	68653	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	0	2	0	-1.675899
1665	116903	Calcb	calcitonin-related polypeptide, beta	0	2	0	-1.675185
1666	434656	UNK	NA	0	2	0	-1.674122
1667	12400	Cbfb	core binding factor beta	0	2	0	-1.673257
1668	69754	Fbxo7	F-box protein 7	0	2	0	-1.672923
1669	192156	Mvd	mevalonate (diphospho) decarboxylase	0	2	0	-1.672811
1670	12615	Cenpa	centromere protein A	0	2	0	-1.672604
1671	15267	Hist2h2aa1	histone cluster 2, H2aa1	0	2	0	-1.672547
1672	18053	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	0	2	0	-1.67139
1673	14657	Glra4	glycine receptor, alpha 4 subunit	0	2	0	-1.668352
1674	56335	Mettl3	methyltransferase like 3	0	2	0	-1.667339
1675	107305	Vps37c	vacuolar protein sorting 37C (yeast)	0	2	0	-1.666267
1676	56176	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	0	2	0	-1.665546
1677	242406	1110029E03Rik	RGP1 retrograde golgi transport homolog (S. cerevisiae)	0	2	0	-1.664589
1678	228061	Agps	alkylglycerone phosphate synthase	0	2	0	-1.664331
1679	56290	Prp15	NA	0	2	0	-1.663614
1680	19661	Rbp3	retinol binding protein 3, interstitial	0	2	0	-1.663176
1681	12269	C4bp	complement component 4 binding protein	0	2	0	-1.661882
1682	435625	UNK	NA	0	2	0	-1.661787
1683	15450	Lipc	lipase, hepatic	0	2	0	-1.660738
1684	13163	Daxx	Fas death domain-associated protein	0	2	0	-1.659635
1685	67017	2010011I20Rik	RIKEN cDNA 2010011I20 gene	0	2	0	-1.65724
1686	244216	G630024C07Rik	zinc finger protein 771	0	2	0	-1.656296
1687	15110	Hand1	heart and neural crest derivatives expressed transcript 1	0	2	0	-1.655618
1688	13168	Dbil5	diazepam binding inhibitor-like 5	0	2	0	-1.654467
1689	27062	Cadps	Ca2+-dependent secretion activator	0	2	0	-1.653611
1690	12539	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	0	2	0	-1.652867
1691	338365	Slc41a2	solute carrier family 41, member 2	0	2	0	-1.652571
1692	23853	Def6	differentially expressed in FDCP 6	0	2	0	-1.652245
1693	15424	Hoxc5	homeobox C5	0	2	0	-1.651908
1694	67648	4930542C12Rik	RIKEN cDNA 4930542C12 gene	0	2	0	-1.651773
1695	75406	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0	2	0	-1.651073
1696	436255	UNK	NA	0	2	0	-1.650309

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1697	15116	Has1	hyaluronan synthase1	0	2	0	-1.650065
1698	226977	Actr1b	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	0	2	0	-1.649153
1699	13649	Egfr	epidermal growth factor receptor	0	2	0	-1.649139
1700	59047	Pnkp	polynucleotide kinase 3'- phosphatase	0	2	0	-1.649094
1701	103149	Upb1	ureidopropionase, beta	0	2	0	-1.648996
1702	269328	Muc15	mucin 15	0	2	0	-1.6489
1703	67272	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5	0	2	0	-1.647601
1704	16569	Kif3b	kinesin family member 3B	0	2	0	-1.64725
1705	66461	Ptpmt1	protein tyrosine phosphatase, mitochondrial 1	0	2	0	-1.647023
1706	269604	Gpr157	G protein-coupled receptor 157	0	2	0	-1.644573
1707	70986	4931422A03Rik	RIKEN cDNA 4931422A03 gene	0	2	0	-1.644397
1708	14566	Gdf9	growth differentiation factor 9	0	2	0	-1.644079
1709	18231	Nxph1	neurexophilin 1	0	2	0	-1.643944
1710	257662	GA_x5J8B7W4T2P-8476	olfactory receptor 1290	0	2	0	-1.643773
1711	232685	AB041803	cDNA sequence AB041803	0	2	0	-1.640875
1712	80902	Zfp202	zinc finger protein 202	0	2	0	-1.638682
1713	268301	C820004L04Rik	sosondowah ankyrin repeat domain family member C	0	2	0	-1.637894
1714	13388	Dll1	delta-like 1 (Drosophila)	0	2	0	-1.637584
1715	11799	Birc5	baculoviral IAP repeat-containing 5	0	2	0	-1.637578
1716	117147	Acsm1	acyl-CoA synthetase medium-chain family member 1	0	2	0	-1.637509
1717	18633	Pex16	peroxisomal biogenesis factor 16	0	2	0	-1.637426
1718	23923	Aadat	aminoadipate aminotransferase	0	2	0	-1.636564
1719	93724	Pcdhga12	protocadherin gamma subfamily A, 12	0	2	0	-1.636333
1720	15381	Hnrpc	heterogeneous nuclear ribonucleoprotein C	0	2	0	-1.635894
1721	59024	Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	0	2	0	-1.635527
1722	13120	Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	0	2	0	-1.634753
1723	12728	Clcn5	chloride channel 5	0	2	0	-1.633534
1724	108686	A430106J12Rik	coiled coil domain containing 88A	0	2	0	-1.633054
1725	16981	Lrrn3	leucine rich repeat protein 3, neuronal	0	2	0	-1.632779
1726	66229	Rpl7l1	ribosomal protein L7-like 1	0	2	0	-1.632523
1727	66515	Cul7	cullin 7	0	2	0	-1.632335
1728	17986	Ndph	Norrie disease (pseudoglioma) (human)	0	2	0	-1.630666
1729	50781	Dkk3	dickkopf homolog 3 (Xenopus laevis)	0	2	0	-1.627104
1730	113865	V1rc8	vomeronasal 1 receptor 25	0	2	0	-1.624109

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1731	26444	Psma7	proteasome (prosome, macropain) subunit, alpha type 7	0	2	0	-1.623931
1732	107831	Bai1	brain-specific angiogenesis inhibitor 1	0	2	0	-1.620845
1733	56513	Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. elegans)	0	2	0	-1.620242
1734	330552	A230097C02	predicted gene 9801	0	2	0	-1.618867
1735	67579	Cpeb4	cytoplasmic polyadenylation element binding protein 4	0	2	0	-1.618402
1736	22115	Tssk2	testis-specific serine kinase 2	0	2	0	-1.61815
1737	57373	D930014E17Rik	RIKEN cDNA D930014E17 gene	0	2	0	-1.617722
1738	66154	Tmem14c	transmembrane protein 14C	0	2	0	-1.617709
1739	67979	Atad1	ATPase family, AAA domain containing 1	0	2	0	-1.617501
1740	11854	Rhod	ras homolog gene family, member D	0	2	0	-1.617147
1741	23795	Agr2	anterior gradient 2 (Xenopus laevis)	0	2	0	-1.616512
1742	75188	1700009J07Rik	RIKEN cDNA 1700009J07 gene	0	2	0	-1.61597
1743	68193	Rpl24	ribosomal protein L24	0	2	0	-1.615366
1744	16617	Klk1b24	kallikrein 1-related peptidase b24	0	2	0	-1.614413
1745	56844	Tssc4	tumor-suppressing subchromosomal transferable fragment 4	0	2	0	-1.614203
1746	235779	LOC235779	NLR family, pyrin domain containing 4G	0	2	0	-1.612368
1747	258955	Olfr531	olfactory receptor 531	0	2	0	-1.611926
1748	55946	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	0	2	0	-1.611692
1749	329333	B230218O03	NA	0	2	0	-1.610873
1750	320974	B430119L13Rik	leucine rich repeat neuronal 4	0	2	0	-1.61059
1751	20664	Sox1	SRY-box containing gene 1	0	2	0	-1.610434
1752	67310	Prlpc2	prolactin family8, subfamily a, member 9	0	2	0	-1.610022
1753	216144	AJ543404	vomeronasal 2, receptor 81	0	2	0	-1.609089
1754	258578	Olfr1517	NA	0	2	0	-1.605744
1755	15451	Hpn	hepsin	0	2	0	-1.605618
1756	93722	Pcdhga10	protocadherin gamma subfamily A, 10	0	2	0	-1.604115
1757	13877	Erh	enhancer of rudimentary homolog (Drosophila)	0	2	0	-1.602935
1758	11596	Ager	advanced glycosylation end product-specific receptor	0	2	0	-1.602568
1759	79263	Trim39	tripartite motif-containing 39	0	2	0	-1.602499
1760	72472	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0	2	0	-1.600115
1761	18020	Nfatc2ip	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 interacting protein	0	2	0	-1.599657
1762	386285	UNK	NA	0	2	0	-1.59838
1763	67943	Mesdc2	mesoderm development candidate 2	0	2	0	-1.597936
1764	232853	5730403M16Rik	zinc finger protein 954	0	2	0	-1.597119

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1765	171095	Il17rc	interleukin 17 receptor C	0	2	0	-1.596801
1766	50778	Rgs1	regulator of G-protein signaling 1	0	2	0	-1.596676
1767	15444	Hpca	hippocalcin	0	2	0	-1.595471
1768	57435	S3-12	perilipin 4	0	2	0	-1.594548
1769	14763	Gpr37	G protein-coupled receptor 37	0	2	0	-1.594522
1770	69046	Hbld2	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	0	2	0	-1.592788
1771	67759	5033414D02Rik	RIKEN cDNA 5033414D02 gene	0	2	0	-1.592581
1772	320040	9930039A11Rik	ring finger protein 222	0	2	0	-1.592407
1773	228770	Rspo4	R-spondin family, member 4	0	2	0	-1.59073
1774	19206	Ptch1	patched homolog 1	0	2	0	-1.590525
1775	243274	Tmem132d	transmembrane protein 132D	0	2	0	-1.589386
1776	12348	Car11	carbonic anhydrase 11	0	2	0	-1.589073
1777	218865	Chdh	choline dehydrogenase	0	2	0	-1.58815
1778	223870	Senp1	SUMO1/sentrin specific peptidase 1	0	2	0	-1.586278
1779	23892	Grem1	gremlin 1	0	2	0	-1.585858
1780	53621	Cnot4	CCR4-NOT transcription complex, subunit 4	0	2	0	-1.584597
1781	76441	Daam2	dishevelled associated activator of morphogenesis 2	0	2	0	-1.584403
1782	320209	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	0	2	0	-1.583721
1783	15463	Hrb	ArfGAP with FG repeats 1	0	2	0	-1.583237
1784	245666	Iqsec2	IQ motif and Sec7 domain 2	0	2	0	-1.582167
1785	54381	Pgcp	plasma glutamate carboxypeptidase	0	2	0	-1.580478
1786	72139	2610044O15Rik	RIKEN cDNA 2610044O15 gene	0	2	0	-1.577196
1787	105278	Ccrk	cyclin-dependent kinase 20	0	2	0	-1.576677
1788	227154	Als2cr2	STE20-related kinase adaptor beta	0	2	0	-1.575784
1789	140858	Wdr5	WD repeat domain 5	0	2	0	-1.575418
1790	27418	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	0	2	0	-1.574964
1791	12259	C1qa	complement component 1, q subcomponent, alpha polypeptide	0	2	0	-1.574791
1792	18088	Nkx2-2	NK2 transcription factor related, locus 2 (Drosophila)	0	2	0	-1.572989
1793	215632	Psd4	pleckstrin and Sec7 domain containing 4	0	2	0	-1.572606
1794	234362	AI449175	zinc finger protein 868	0	2	0	-1.572585
1795	208595	MTERF	predicted gene 9897	0	2	0	-1.571863
1796	26456	Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic doma	0	2	0	-1.570834
1797	17695	Msmb	beta-microseminoprotein	0	2	0	-1.570806
1798	102693	Phldb1	pleckstrin homology-like domain, family B, member 1	0	2	0	-1.569142

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1799	71960	Myh14	myosin, heavy polypeptide 14	0	2	0	-1.568063
1800	68323	Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	0	2	0	-1.567315
1801	20751	Spr	sepiapterin reductase	0	2	0	-1.566111
1802	216516	4930562D19Rik	coiled-coil domain containing 157	0	2	0	-1.564661
1803	14601	Ghrh	growth hormone releasing hormone	0	2	0	-1.561686
1804	210619	UNK	NA	0	2	0	-1.559366
1805	227800	Rabgap1	RAB GTPase activating protein 1	0	2	0	-1.558719
1806	208583	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	0	2	0	-1.558344
1807	17127	Smad3	MAD homolog 3 (Drosophila)	0	2	0	-1.557398
1808	66214	1190002H23Rik	RIKEN cDNA 1190002H23 gene	0	2	0	-1.557142
1809	231600	Chfr	checkpoint with forkhead and ring finger domains	0	2	0	-1.556132
1810	140742	Sesn1	sestrin 1	0	2	0	-1.555998
1811	19185	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	0	2	0	-1.554653
1812	17904	Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0	2	0	-1.55419
1813	170935	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	0	2	0	-1.553305
1814	237222	Ofd1	oral-facial-digital syndrome 1 gene homolog (human)	0	2	0	-1.552541
1815	67231	Tbc1d20	TBC1 domain family, member 20	0	2	0	-1.549264
1816	71111	Gpr39	G protein-coupled receptor 39	0	2	0	-1.548029
1817	12824	Col2a1	collagen, type II, alpha 1	0	2	0	-1.546316
1818	272661	UNK	NA	0	2	0	-1.545982
1819	17134	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	0	2	0	-1.54539
1820	12337	Capn5	calpain 5	0	2	0	-1.545197
1821	11513	Adcy7	adenylate cyclase 7	0	2	0	-1.544282
1822	68614	Letmd1	LETM1 domain containing 1	0	2	0	-1.541796
1823	99899	Ifi44	interferon-induced protein 44	0	2	0	-1.541503
1824	18566	Pdcd1	programmed cell death 1	0	2	0	-1.541412
1825	66618	2610209M04Rik	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0	2	0	-1.539962
1826	280121	LOC280121	ribosomal protein, large, P1, pseudogene 1	0	2	0	-1.538674
1827	109648	Npy	neuropeptide Y	0	2	0	-1.536349
1828	26438	Psg18	pregnancy specific glycoprotein 18	0	2	0	-1.535139
1829	241846	Lsm14b	LSM14 homolog B (SCD6, S. cerevisiae)	0	2	0	-1.530989
1830	107146	Glyat	glycine-N-acyltransferase	0	2	0	-1.530548
1831	56417	Adar	adenosine deaminase, RNA-specific	0	2	0	-1.528194
1832	76629	1700111I05Rik	Williams-Beuren syndrome chromosome region 28 (human)	0	2	0	-1.528067

Candidates for positive regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1833	17858	Mx2	myxovirus (influenza virus) resistance 2	0	2	0	-1.523541
1834	239652	Zfp641	zinc finger protein 641	0	2	0	-1.523288
1835	69694	Tatdn1	TatD DNase domain containing 1	0	2	0	-1.52259
1836	233081	Ffar1	free fatty acid receptor 1	0	2	0	-1.522564
1837	28071	Twistnb	TWIST neighbor	0	2	0	-1.520386
1838	259083	Olfr547	olfactory receptor 547	0	2	0	-1.519335
1839	170757	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	0	2	0	-1.519318
1840	93898	Lass1	LAG1 homolog, ceramide synthase 1	0	2	0	-1.518135
1841	15081	H3f3b	H3 histone, family 3B	0	2	0	-1.517545
1842	110648	Lmx1a	LIM homeobox transcription factor 1 alpha	0	2	0	-1.51385
1843	224024	Scarf2	scavenger receptor class F, member 2	0	2	0	-1.513785
1844	258663	Olfr739	olfactory receptor 739	0	2	0	-1.513486
1845	18821	Pln	phospholamban	0	2	0	-1.513449
1846	56371	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	0	2	0	-1.510983
1847	216166	6330514A18Rik	polo-like kinase 5 (Drosophila)	0	2	0	-1.51052
1848	13013	Cst9	cystatin 9	0	2	0	-1.510093
1849	75079	Zfp509	zinc finger and BTB domain containing 49	0	2	0	-1.50986
1850	53404	Atoh7	atonal homolog 7 (Drosophila)	0	2	0	-1.50932
1851	17764	Mtf1	metal response element binding transcription factor 1	0	2	0	-1.509176
1852	407243	AI840826	transmembrane protein 189	0	2	0	-1.50575
1853	224630	Bnip1	BCL2/adenovirus E1B interacting protein 1	0	2	0	-1.503173
1854	20907	Stx1a	syntaxin 1A (brain)	0	2	0	-1.50256

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	257635	Sdsl	serine dehydratase-like	2	0	0	5.73702
2	12387	Ctnnb1	catenin (cadherin associated protein), beta 1	4	0	0	4.974981
3	18155	Pnoc	prepronociceptin	2	0	0	4.543174
4	20667	Sox12	SRY-box containing gene 12	2	0	0	4.456768
5	22781	Zfpn1a4	IKAROS family zinc finger 4	2	0	0	4.335112
6	76980	3110006E14Rik	ubiquitin-conjugating enzyme E2Q family-like 1	2	0	0	4.33407
7	50708	Hist1h1c	histone cluster 1, H1c	2	0	0	4.068651
8	27423	Klra15	killer cell lectin-like receptor, subfamily A, member 15	2	0	0	3.952384
9	100689	Spon2	spondin 2, extracellular matrix protein	2	0	0	3.883759
10	66990	Tmem134	transmembrane protein 134	2	0	0	3.736325
11	232910	Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	2	0	0	3.732974
12	74195	Elp3	elongation protein 3 homolog (S. cerevisiae)	2	0	0	3.670223
13	26465	Zfp146	zinc finger protein 146	2	0	0	3.639934
14	27382	Tcl1b5	T cell leukemia/lymphoma 1B, 5	2	0	0	3.487731
15	68066	D11Ertd333e	solute carrier family 25, member 39	2	0	0	3.458957
16	109593	Lmo3	LIM domain only 3	2	0	0	3.453422
17	330721	Nek5	NIMA (never in mitosis gene a)-related expressed kinase 5	2	0	0	3.408763
18	21950	Tnfsf9	tumor necrosis factor (ligand) superfamily, member 9	2	0	0	3.394261
19	18073	Nid1	nidogen 1	2	0	0	3.37397
20	213012	Abhd10	abhydrolase domain containing 10	2	0	0	3.336467
21	26934	Racgap1	Rac GTPase-activating protein 1	2	0	0	3.260051
22	212167	A530088I07Rik	pigeon homolog (Drosophila)	2	0	0	3.212685
23	327900	9630054F20Rik	ubiquitin domain containing 2	2	0	0	3.149826
24	109280	9330176C04Rik	solute carrier family 22 (organic cation transporter), member 13b	2	0	0	3.120845
25	114663	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	2	0	0	3.100542
26	215351	Senp6	SUMO/sentrin specific peptidase 6	2	0	0	3.09762
27	382686	LOC382686	RIKEN cDNA 3110053B16 gene	3	0	0	3.094671
28	19156	Psap	prosaposin	3	0	0	3.059448
29	272790	Magee2	melanoma antigen, family E, 2	3	0	0	3.034066
30	224904	2410015M20Rik	RIKEN cDNA 2410015M20 gene	3	0	0	2.974453
31	73703	Dppa2	developmental pluripotency associated 2	2	0	0	2.970461
32	22592	Ercc5	excision repair cross-complementing rodent repair deficiency, complementation group 5	2	0	0	2.912217
33	16840	Lect1	leukocyte cell derived chemotaxin 1	2	0	0	2.877199
34	80987	Nckipsd	NCK interacting protein with SH3 domain	2	0	0	2.873466

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
35	74626	Tmem81	transmembrane protein 81	2	0	0	2.860366
36	214459	Fnbp1l	formin binding protein 1-like	3	0	0	2.854759
37	76858	Nalp14	NLR family, pyrin domain containing 14	2	0	0	2.833151
38	218194	Phactr1	phosphatase and actin regulator 1	2	0	0	2.78359
39	20024	Sub1	SUB1 homolog (S. cerevisiae)	2	0	0	2.77859
40	224833	AI661453	expressed sequence AI661453	2	0	0	2.731329
41	74666	4930432K21Rik	RIKEN cDNA 4930432K21 gene	2	0	0	2.728271
42	224454	Zdhhc14	zinc finger, DHHC domain containing 14	2	0	0	2.723168
43	238011	Enpp7	ectonucleotide pyrophosphatase/phosphodiesterase 7	2	0	0	2.722461
44	212974	Athl1	ATH1, acid trehalase-like 1 (yeast)	2	0	0	2.71732
45	66865	Pmpca	peptidase (mitochondrial processing) alpha	2	0	0	2.664393
46	17532	Mras	muscle and microspikes RAS	2	0	0	2.660672
47	26559	Hunk	hormonally upregulated Neu-associated kinase	2	0	0	2.654869
48	226646	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	2	0	0	2.647985
49	107932	Chd4	chromodomain helicase DNA binding protein 4	2	0	0	2.642334
50	272636	D9Ertd280e	extended synaptotagmin-like protein 3	2	0	0	2.639927
51	59025	Usp14	ubiquitin specific peptidase 14	2	0	0	2.637108
52	66598	3110001I22Rik	RIKEN cDNA 3110001I22 gene	2	0	0	2.633741
53	71907	Serpina9	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	2	0	0	2.633154
54	77794	Adamtsl2	ADAMTS-like 2	2	0	0	2.631688
55	20476	Six6	sine oculis-related homeobox 6 homolog (Drosophila)	2	0	0	2.630963
56	219151	Scara3	scavenger receptor class A, member 3	2	0	0	2.623779
57	18574	Pde1b	phosphodiesterase 1B, Ca2+-calmodulin dependent	2	0	0	2.617032
58	67811	Poldip2	polymerase (DNA-directed), delta interacting protein 2	2	0	0	2.614136
59	30060	Mfi2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	2	0	0	2.586174
60	107895	Mgat5	mannoside acetylglucosaminyltransferase 5	2	0	0	2.578212
61	21897	Tlr1	toll-like receptor 1	2	0	0	2.576724
62	228788	BC020535	cDNA sequence BC020535	2	0	0	2.574493
63	16648	Kpna3	karyopherin (importin) alpha 3	2	0	0	2.57353
64	213696	Duoxa1	dual oxidase maturation factor 1	2	0	0	2.552045
65	240817	5830403L16Rik	RIKEN cDNA 5830403L16 gene	2	0	0	2.552016
66	110157	Raf1	v-raf-leukemia viral oncogene 1	4	0	0	2.543896
67	20185	Ncor1	nuclear receptor co-repressor 1	2	0	0	2.540164
68	18722	Pira1	paired-Ig-like receptor A1	2	0	0	2.529442

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
69	69727	Usp46	ubiquitin specific peptidase 46	2	0	0	2.527837
70	11514	Adcy8	adenylate cyclase 8	2	0	0	2.52696
71	434437	Amt	aminomethyltransferase	2	0	0	2.518302
72	14417	Gad2	glutamic acid decarboxylase 2	2	0	0	2.505384
73	19059	Ppp3r2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)	2	0	0	2.505049
74	74413	Mtac2d1	tandem C2 domains, nuclear	3	0	0	2.503905
75	68166	Spire1	spire homolog 1 (Drosophila)	2	0	0	2.50085
76	66074	0610041E09Rik	transmembrane protein 167	2	0	0	2.492077
77	14065	F2rl3	coagulation factor II (thrombin) receptor-like 3	2	0	0	2.491837
78	20300	Ccl25	chemokine (C-C motif) ligand 25	2	0	0	2.483595
79	26894	Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana)	2	0	0	2.472832
80	212547	BC027231	cDNA sequence BC027231	2	0	0	2.471346
81	238328	Vash1	vasohibin 1	2	0	0	2.470853
82	232821	Ccdc106	coiled-coil domain containing 106	2	0	0	2.45819
83	12064	Bdnf	brain derived neurotrophic factor	3	0	0	2.448153
84	106298	Rrn3	RRN3 RNA polymerase I transcription factor homolog (yeast)	2	0	0	2.43853
85	20324	Sdpr	serum deprivation response	2	0	0	2.434226
86	19364	Rad51l3	RAD51-like 3 (S. cerevisiae)	2	0	0	2.42997
87	67857	Ppp6c	protein phosphatase 6, catalytic subunit	2	0	0	2.42692
88	13010	Cst3	cystatin C	2	0	0	2.425968
89	74192	Arpc5l	actin related protein 2/3 complex, subunit 5-like	2	0	0	2.413497
90	67838	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	2	0	0	2.413315
91	70257	2010107E04Rik	RIKEN cDNA 2010107E04 gene	2	0	0	2.406474
92	213027	B130050I23Rik	ecotropic viral integration site 5 like	2	0	0	2.405743
93	73730	1110008K04Rik	late cornified envelope 1L	2	0	0	2.400282
94	231327	Ppat	phosphoribosyl pyrophosphate amidotransferase	2	0	0	2.400077
95	23955	Nek4	NIMA (never in mitosis gene a)-related expressed kinase 4	2	0	0	2.400034
96	23874	Farslb	phenylalanyl-tRNA synthetase, beta subunit	2	0	0	2.397824
97	53814	Oaz3	ornithine decarboxylase antizyme 3	2	0	0	2.392405
98	54637	Praf2	PRA1 domain family 2	2	0	0	2.387377
99	224065	Uts2d	urotensin 2 domain containing	2	0	0	2.385893
100	225207	Zfp521	zinc finger protein 521	2	0	0	2.383188
101	68477	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	2	0	0	2.379593
102	72267	Lrrc8e	leucine rich repeat containing 8 family, member E	2	0	0	2.369083

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
103	276905	Armc7	armadillo repeat containing 7	2	0	0	2.365173
104	241128	A830043J08Rik	family with sequence similarity 124, member B	2	0	0	2.357856
105	54373	Prss16	protease, serine, 16 (thymus)	2	0	0	2.357606
106	16068	Il18bp	interleukin 18 binding protein	2	0	0	2.357197
107	76184	Abca6	ATP-binding cassette, sub-family A (ABC1), member 6	2	0	0	2.356596
108	11441	Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	2	0	0	2.355706
109	18782	Pla2g2d	phospholipase A2, group IID	3	0	0	2.354678
110	74071	4933403M22Rik	intermediate filament tail domain containing 1	2	0	0	2.353355
111	69192	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	2	0	0	2.352915
112	17251	Mds1	NA	2	0	0	2.352851
113	233810	Abca16	ATP-binding cassette, sub-family A (ABC1), member 16	2	0	0	2.349315
114	14121	Fbp1	fructose bisphosphatase 1	2	0	0	2.347284
115	80706	Olfr160	olfactory receptor 160	2	0	0	2.345659
116	74147	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	2	0	0	2.345472
117	12236	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	2	0	0	2.335329
118	74054	4931406B18Rik	RIKEN cDNA 4931406B18 gene	2	0	0	2.332611
119	14007	Cugbp2	CUGBP, Elav-like family member 2	2	0	0	2.330545
120	23887	Ggtla1	gamma-glutamyltransferase 5	2	0	0	2.328254
121	59001	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	2	0	0	2.326922
122	57869	Adck2	aarF domain containing kinase 2	3	0	0	2.321992
123	73873	4930430E16Rik	family with sequence similarity 161, member A	2	0	0	2.320126
124	18518	Igbp1	immunoglobulin (CD79A) binding protein 1	2	0	0	2.317395
125	70984	4931406C07Rik	RIKEN cDNA 4931406C07 gene	2	0	0	2.317035
126	17309	Mgat3	mannoside acetylglucosaminyltransferase 3	2	0	0	2.316903
127	238555	Btn2a2	butyrophilin, subfamily 2, member A2	2	0	0	2.316657
128	12405	Cbln2	cerebellin 2 precursor protein	2	0	0	2.312928
129	16600	Klf4	Kruppel-like factor 4 (gut)	2	0	0	2.301804
130	21379	Tbrg4	transforming growth factor beta regulated gene 4	2	0	0	2.30045
131	26401	Map3k1	mitogen-activated protein kinase kinase kinase 1	2	0	0	2.300124
132	73341	Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	2	0	0	2.29672
133	258463	Olfr1393	olfactory receptor 1393	2	0	0	2.295191
134	56399	Akap8	A kinase (PRKA) anchor protein 8	2	0	0	2.292302
135	54399	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	2	0	0	2.291691
136	18703	Pigr	polymeric immunoglobulin receptor	2	0	0	2.288426

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
137	27053	Asns	asparagine synthetase	2	0	0	2.288411
138	108950	1700049L16Rik	hematological and neurological expressed 1-like pseudogene	2	0	0	2.286619
139	19144	Klk6	kallikrein related-peptidase 6	2	0	0	2.278726
140	108946	Zzz3	zinc finger, ZZ domain containing 3	2	0	0	2.275646
141	15467	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	3	0	0	2.275387
142	67279	Med31	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)	2	0	0	2.274717
143	56338	Txnip	thioredoxin interacting protein	2	0	0	2.272533
144	387341	Tas2r106	taste receptor, type 2, member 106	3	0	0	2.269963
145	83559	Tex18	testis expressed gene 18	3	0	0	2.26889
146	68304	Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	2	0	0	2.266721
147	21819	Tgn	thyroglobulin	2	0	0	2.262876
148	231148	Ablim2	actin-binding LIM protein 2	2	0	0	2.261238
149	217353	Tmc6	transmembrane channel-like gene family 6	2	0	0	2.25885
150	83379	Klb	klotho beta	2	0	0	2.257068
151	258482	Olfr266	olfactory receptor 266	2	0	0	2.25703
152	230848	Zbtb40	zinc finger and BTB domain containing 40	2	0	0	2.251984
153	14359	Fxr1h	fragile X mental retardation gene 1, autosomal homolog	3	0	0	2.248053
154	230145	Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12	2	0	0	2.248025
155	394435	Ugt1a6b	UDP glucuronosyltransferase 1 family, polypeptide A6B	2	0	0	2.245422
156	239217	Kctd12	potassium channel tetramerisation domain containing 12	2	0	0	2.245041
157	72507	Dzip1l	DAZ interacting protein 1-like	3	0	0	2.239008
158	70315	Hdac8	histone deacetylase 8	2	0	0	2.238949
159	338368	C920005C14Rik	family with sequence similarity 109, member B	2	0	0	2.237702
160	14089	Fap	fibroblast activation protein	3	0	0	2.230605
161	67921	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	2	0	0	2.229074
162	78832	2700078E11Rik	RIKEN cDNA 2700078E11 gene	2	0	0	2.228656
163	17686	Msh3	mutS homolog 3 (E. coli)	2	0	0	2.223335
164	13990	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing D	2	0	0	2.220086
165	12823	Col19a1	collagen, type XIX, alpha 1	2	0	0	2.216205
166	381903	Alg8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	2	0	0	2.215534
167	67736	4930527D15Rik	coiled-coil domain containing 130	2	0	0	2.214901
168	210719	Mkx	mohawk homeobox	2	0	0	2.213374
169	18111	Nnat	neuronatin	2	0	0	2.210565
170	74571	Kcnk16	potassium channel, subfamily K, member 16	3	0	0	2.209352

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
171	70110	Ifi35	interferon-induced protein 35	2	0	0	2.208961
172	27206	Nrk	Nik related kinase	2	0	0	2.199358
173	234076	Tmco3	transmembrane and coiled-coil domains 3	2	0	0	2.198301
174	15370	Nr4a1	nuclear receptor subfamily 4, group A, member 1	2	0	0	2.19815
175	234967	Slc36a4	solute carrier family 36 (proton/amino acid symporter), member 4	3	0	0	2.197768
176	108151	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	3	0	0	2.196941
177	14456	Gas6	growth arrest specific 6	3	0	0	2.19417
178	259057	Olfr649	olfactory receptor 649	3	0	0	2.194165
179	110265	Msra	methionine sulfoxide reductase A	2	0	0	2.194159
180	224014	Fgd4	FYVE, RhoGEF and PH domain containing 4	2	0	0	2.18677
181	246728	Oas2	2'-5' oligoadenylate synthetase 2	3	0	0	2.184186
182	70208	Crsp3	mediator complex subunit 23	2	0	0	2.18108
183	408068	3830402I07Rik	zinc finger protein 738	2	0	0	2.178504
184	230661	Tesk2	testis-specific kinase 2	2	0	0	2.177426
185	258845	Olfr1161	olfactory receptor 1161	2	0	0	2.177115
186	233578	Olfr553	olfactory receptor 553	2	0	0	2.175703
187	74203	Eif4enif1	eukaryotic translation initiation factor 4E nuclear import factor 1	2	0	0	2.173799
188	11630	Aim1	absent in melanoma 1	2	0	0	2.170166
189	17977	Ncoa1	nuclear receptor coactivator 1	2	0	0	2.1686
190	258843	Olfr1087	olfactory receptor 1087	2	0	0	2.168345
191	20405	Sh3gl1	SH3-domain GRB2-like 1	2	0	0	2.167875
192	107751	Prrxl1	paired related homeobox protein-like 1	2	0	0	2.166369
193	58251	Ddc8	cDNA sequence BC100451	3	0	0	2.165269
194	72242	Psg21	pregnancy-specific glycoprotein 21	2	0	0	2.161856
195	72050	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	2	0	0	2.155147
196	330463	Zfp78	zinc finger protein 78	2	0	0	2.152578
197	18314	Olfr17	olfactory receptor 17	2	0	0	2.146221
198	22225	Usp5	ubiquitin specific peptidase 5 (isopeptidase T)	2	0	0	2.143757
199	223499	Wdsof1	DDB1 and CUL4 associated factor 13	2	0	0	2.14295
200	19733	Rgn	regucalcin	2	0	0	2.139777
201	235559	Topbp1	topoisomerase (DNA) II binding protein 1	2	0	0	2.135101
202	104086	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	2	0	0	2.133933
203	234407	Glt25d1	glycosyltransferase 25 domain containing 1	2	0	0	2.132207
204	54169	Myst4	MYST histone acetyltransferase monocytic leukemia 4	2	0	0	2.129097

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
205	66179	1110031I02Rik	RIKEN cDNA 1110031I02 gene	2	0	0	2.128312
206	27045	Nit1	nitrilase 1	2	0	0	2.126948
207	63857	Bcmo1	beta-carotene 15,15'-monooxygenase	2	0	0	2.123781
208	27380	Tcl1b4	T cell leukemia/lymphoma 1B, 4	2	0	0	2.120376
209	105522	Ankrd28	ankyrin repeat domain 28	2	0	0	2.116286
210	259037	Olfr711	olfactory receptor 711	2	0	0	2.114617
211	17289	Mertk	c-mer proto-oncogene tyrosine kinase	2	0	0	2.110693
212	12725	Clcn3	chloride channel 3	3	0	0	2.107907
213	52710	Gpr172b	G protein-coupled receptor 172B	2	0	0	2.107816
214	71934	Car13	carbonic anhydrase 13	2	0	0	2.107683
215	23837	Cfdp1	craniofacial development protein 1	3	0	0	2.106618
216	20980	Syt2	synaptotagmin II	2	0	0	2.102682
217	59287	Ncstn	nicastrin	3	0	0	2.099643
218	20650	Sntb2	syntrophin, basic 2	2	0	0	2.09811
219	73324	1700034F02Rik	RIKEN cDNA 1700034F02 gene	2	0	0	2.097888
220	104885	AI839735	transmembrane protein 179	2	0	0	2.096702
221	20845	Star	steroidogenic acute regulatory protein	2	0	0	2.095192
222	258487	Olfr722	olfactory receptor 722	2	0	0	2.094908
223	215413	A230074B11Rik	NA	2	0	0	2.094423
224	11784	Apba2	amyloid beta (A4) precursor protein-binding, family A, member 2	2	0	0	2.09171
225	20269	Scn3a	sodium channel, voltage-gated, type III, alpha	3	0	0	2.089114
226	75275	4930563P21Rik	transmembrane and coiled-coil domains 5B	3	0	0	2.086815
227	74016	Phf19	PHD finger protein 19	2	0	0	2.077359
228	237339	L3mbtl3	l(3)mbt-like 3 (Drosophila)	3	0	0	2.077281
229	276919	Gemin4	gem (nuclear organelle) associated protein 4	2	0	0	2.076963
230	230603	4922503N01Rik	tetratricopeptide repeat domain 39A	2	0	0	2.075884
231	67008	1600012F09Rik	RIKEN cDNA 1600012F09 gene	2	0	0	2.073094
232	14823	Grm8	glutamate receptor, metabotropic 8	2	0	0	2.071483
233	68015	Trap1	TNF receptor-associated protein 1	2	0	0	2.068175
234	213988	Tnrc6b	trinucleotide repeat containing 6b	2	0	0	2.06278
235	22325	Vav2	vav 2 oncogene	2	0	0	2.061175
236	14348	Fut9	fucosyltransferase 9	2	0	0	2.060971
237	433667	Ankrd13c	ankyrin repeat domain 13c	2	0	0	2.060821
238	236891	LOC236891	melanoma antigen family B, 17, pseudogene	2	0	0	2.059225

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
239	12663	Chml	choroideremia-like	2	0	0	2.057415
240	20192	Ryr3	ryanodine receptor 3	2	0	0	2.055629
241	54215	Cd160	CD160 antigen	2	0	0	2.054819
242	75812	Tasp1	taspase, threonine aspartase 1	2	0	0	2.054742
243	18102	Nme1	non-metastatic cells 1, protein (NM23A) expressed in	2	0	0	2.054721
244	21984	Tpbpa	trophoblast specific protein alpha	3	0	0	2.054181
245	21925	Tnnc2	troponin C2, fast	2	0	0	2.053546
246	18196	Nsg1	neuron specific gene family member 1	2	0	0	2.052153
247	230904	Fbxo2	F-box protein 2	2	0	0	2.051959
248	12028	Bax	BCL2-associated X protein	2	0	0	2.050745
249	384309	Trim56	tripartite motif-containing 56	2	0	0	2.047845
250	23972	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	2	0	0	2.043264
251	20905	Sts	steroid sulfatase	2	0	0	2.035747
252	259026	Olfr378	olfactory receptor 378	2	0	0	2.032803
253	231214	5730509K17Rik	coiled-coil and C2 domain containing 2A	2	0	0	2.03246
254	53870	Cntn6	contactin 6	2	0	0	2.032073
255	12338	Capn6	calpain 6	3	0	0	2.032042
256	56249	Actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)	2	0	0	2.026969
257	434648	UNK	NA	2	0	0	2.026518
258	14175	Fgf4	fibroblast growth factor 4	2	0	0	2.023041
259	56050	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	2	0	0	2.022599
260	106869	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	2	0	0	2.022015
261	100608	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	2	0	0	2.020604
262	218962	UNK	NA	2	0	0	2.019946
263	12279	C9	complement component 9	3	0	0	2.018071
264	218811	Sec24c	Sec24 related gene family, member C (S. cerevisiae)	2	0	0	2.017893
265	414801	BC063749	inositol 1,4,5-triphosphate receptor interacting protein	2	0	0	2.017578
266	72388	Ripk4	receptor-interacting serine-threonine kinase 4	2	0	0	2.017192
267	170731	Mfn2	mitofusin 2	2	0	0	2.013913
268	12483	Cd22	CD22 antigen	2	0	0	2.010959
269	320655	Perld1	post-GPI attachment to proteins 3	2	0	0	2.00701
270	20853	Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	2	0	0	2.001186
271	16204	Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	2	0	0	1.998351
272	269224	Pask	PAS domain containing serine/threonine kinase	2	0	0	1.995465

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
273	258603	Olfr972	olfactory receptor 972	2	0	0	1.99509
274	12380	Cast	calpastatin	2	0	0	1.994822
275	66422	2410015N17Rik	dCTP pyrophosphatase 1	2	0	0	1.993409
276	78593	Nrip3	nuclear receptor interacting protein 3	2	0	0	1.990946
277	216850	Jmjd3	KDM1 lysine (K)-specific demethylase 6B	3	0	0	1.989205
278	99526	Usp53	ubiquitin specific peptidase 53	2	0	0	1.98632
279	72584	Cul4b	cullin 4B	2	0	0	1.985538
280	20181	Rxra	retinoid X receptor alpha	3	0	0	1.985464
281	353148	Tas2r139	taste receptor, type 2, member 139	2	0	0	1.980944
282	66540	3110001A13Rik	family with sequence similarity 107, member B	2	0	0	1.980676
283	19045	Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	2	0	0	1.979237
284	104725	1110002B05Rik	RIKEN cDNA 1110002B05 gene	2	0	0	1.976265
285	13639	Efna4	ephrin A4	2	0	0	1.974096
286	259098	Olfr606	olfactory receptor 606	2	0	0	1.970863
287	380752	Tssc1	tumor suppressing subtransferable candidate 1	2	0	0	1.970774
288	215474	Sec22c	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	3	0	0	1.968414
289	11569	Aebp2	AE binding protein 2	2	0	0	1.966357
290	319757	Smo	smoothened homolog (Drosophila)	2	0	0	1.963685
291	229672	Gm566	BCLl2-like 15	2	0	0	1.96266
292	71743	Coasy	Coenzyme A synthase	2	0	0	1.961888
293	404338	Olfr1434	olfactory receptor 1434	2	0	0	1.960319
294	15510	Hspd1	heat shock protein 1 (chaperonin)	2	0	0	1.960235
295	72615	Anks3	ankyrin repeat and sterile alpha motif domain containing 3	2	0	0	1.960085
296	239719	Mkl2	MKL/myocardin-like 2	2	0	0	1.958162
297	20194	S100a10	S100 calcium binding protein A10 (calpactin)	2	0	0	1.951545
298	404341	Olfr1514	NA	3	0	0	1.948948
299	227325	Dner	delta/notch-like EGF-related receptor	3	0	0	1.947996
300	210198	Gprc6a	G protein-coupled receptor, family C, group 6, member A	2	0	0	1.94766
301	76131	Depdc1a	DEP domain containing 1a	2	0	0	1.947302
302	22414	Wnt2b	wingless related MMTV integration site 2b	2	0	0	1.94404
303	399548	Scn4b	sodium channel, type IV, beta	3	0	0	1.942195
304	16322	Inha	inhibin alpha	2	0	0	1.941226
305	50916	Irx4	Iroquois related homeobox 4 (Drosophila)	3	0	0	1.935417
306	258139	Olfr591	olfactory receptor 591	2	0	0	1.935336

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
307	331046	Tgm4	transglutaminase 4 (prostate)	2	0	0	1.93299
308	72205	Eml2	echinoderm microtubule associated protein like 2	2	0	0	1.930648
309	234728	BC025546	FtsJ methyltransferase domain containing 1	2	0	0	1.929748
310	404322	Olfr924	olfactory receptor 924	3	0	0	1.927076
311	319247	9530080O11Rik	RIKEN cDNA 9530080O11 gene	2	0	0	1.926047
312	17095	Lyl1	lymphoblastomic leukemia 1	2	0	0	1.925973
313	12568	Cdk5	cyclin-dependent kinase 5	4	0	0	1.92196
314	214763	E330016A19Rik	RIKEN cDNA E330016A19 gene	2	0	0	1.91965
315	22269	Upk2	uroplakin 2	2	0	0	1.916115
316	244310	Dlgap2	discs, large (Drosophila) homolog-associated protein 2	2	0	0	1.909478
317	71703	Armcx3	armadillo repeat containing, X-linked 3	2	0	0	1.898844
318	319196	Ankrd5	ankyrin repeat domain 5	2	0	0	1.897819
319	328365	Rai17	zinc finger, MIZ-type containing 1	2	0	0	1.896062
320	77574	3321401G04Rik	family with sequence similarity 115, member A	2	0	0	1.894275
321	83945	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	2	0	0	1.892725
322	16007	Cyr61	cysteine rich protein 61	3	0	0	1.892253
323	19106	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	2	0	0	1.89021
324	72542	Pgam5	phosphoglycerate mutase family member 5	2	0	0	1.89016
325	19888	Rp1h	retinitis pigmentosa 1 (human)	2	0	0	1.886849
326	17988	Ndrg1	N-myc downstream regulated gene 1	2	0	0	1.885664
327	68916	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	2	0	0	1.884032
328	329064	Pkd2l1	polycystic kidney disease 2-like 1	3	0	0	1.881854
329	241494	Zfp533	zinc finger protein 385B	2	0	0	1.880775
330	13101	Cyp2d10	cytochrome P450, family 2, subfamily d, polypeptide 10	2	0	0	1.880493
331	17868	Mybpc3	myosin binding protein C, cardiac	2	0	0	1.874855
332	106557	Ldhal6b	lactate dehydrogenase A-like 6B	2	0	0	1.87074
333	12523	Cd84	CD84 antigen	2	0	0	1.869449
334	242891	Gm443	chaperonin containing TCP1, subunit 8 (theta)-like 1	2	0	0	1.869271
335	209268	Igsf1	immunoglobulin superfamily, member 1	2	0	0	1.86787
336	209737	Kif15	kinesin family member 15	2	0	0	1.867814
337	12054	Bcl7b	B cell CLL/lymphoma 7B	2	0	0	1.867196
338	211401	Mtss1	metastasis suppressor 1	2	0	0	1.864779
339	19731	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	2	0	0	1.863894
340	24013	Grk1	G protein-coupled receptor kinase 1	2	0	0	1.861455

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
341	20452	St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	2	0	0	1.860944
342	223701	Mkl1	MKL (megakaryoblastic leukemia)/myocardin-like 1	2	0	0	1.858459
343	110893	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	2	0	0	1.857956
344	320938	Tnpo3	transportin 3	2	0	0	1.855597
345	26436	Psg16	pregnancy specific glycoprotein 16	2	0	0	1.854079
346	12524	Cd86	CD86 antigen	2	0	0	1.849849
347	27223	Trp53bp1	transformation related protein 53 binding protein 1	2	0	0	1.849193
348	12580	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	2	0	0	1.844808
349	19214	Ptgdr	prostaglandin D receptor	2	0	0	1.84432
350	74069	Serpina3a	serine (or cysteine) peptidase inhibitor, clade A, member 3A	4	0	0	1.842133
351	22137	Ttk	Ttk protein kinase	2	0	0	1.841712
352	23793	Adam25	a disintegrin and metallopeptidase domain 25 (testase 2)	2	0	0	1.84122
353	71724	Aox3	aldehyde oxidase 3	3	0	0	1.838829
354	67418	Ppil4	peptidylprolyl isomerase (cyclophilin)-like 4	2	0	0	1.83768
355	68291	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	2	0	0	1.837439
356	22418	Wnt5a	wingless-related MMTV integration site 5A	2	0	0	1.836806
357	60597	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	2	0	0	1.835851
358	68519	Eml1	echinoderm microtubule associated protein like 1	2	0	0	1.835261
359	12566	Cdk2	cyclin-dependent kinase 2	3	0	0	1.831932
360	117150	Pip5k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	2	0	0	1.830177
361	66349	2310004L02Rik	ATP5S-like	2	0	0	1.829718
362	56457	Clptm1	cleft lip and palate associated transmembrane protein 1	3	0	0	1.828487
363	18331	Olfr32	olfactory receptor 32	2	0	0	1.826338
364	194604	Gm46	predicted gene 46	3	0	0	1.826226
365	15042	H2-T24	histocompatibility 2, T region locus 24	3	0	0	1.825262
366	73937	1700029M20Rik	RIKEN cDNA 1700029M20 gene	2	0	0	1.824836
367	53611	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	2	0	0	1.82043
368	78266	Zfp687	zinc finger protein 687	2	0	0	1.814387
369	19157	Pscd1	cytohesin 1	2	0	0	1.814068
370	244653	Hydin	HYDIN, axonemal central pair apparatus protein	3	0	0	1.813401
371	239667	AI317237	DIP2 disco-interacting protein 2 homolog B (Drosophila)	2	0	0	1.809009
372	98985	AI462438	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	2	0	0	1.80868
373	17258	Mef2a	myocyte enhancer factor 2A	2	0	0	1.804071
374	22793	Zyx	zyxin	2	0	0	1.7908

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
375	67430	4921536K21Rik	RIKEN cDNA 4921536K21 gene	2	0	0	1.790425
376	278180	Vsig4	V-set and immunoglobulin domain containing 4	2	0	0	1.789486
377	171463	Il17rd	interleukin 17 receptor D	2	0	0	1.78786
378	13177	Dci	enoyl-Coenzyme A delta isomerase 1	2	0	0	1.787192
379	218503	Fcho2	FCH domain only 2	2	0	0	1.786667
380	71790	Anxa9	annexin A9	2	0	0	1.783681
381	105377	Ankrd32	ankyrin repeat domain 32	2	0	0	1.776161
382	545378	Sh2d1b2	SH2 domain protein 1B2	2	0	0	1.774629
383	13494	Drg1	developmentally regulated GTP binding protein 1	2	0	0	1.773803
384	14056	Ezh2	enhancer of zeste homolog 2 (Drosophila)	2	0	0	1.770795
385	64290	Foxb1	forkhead box B1	2	0	0	1.768052
386	66863	Lztr1	leucine-zipper-like transcriptional regulator, 1	2	0	0	1.766394
387	16709	Ktn1	kinectin 1	2	0	0	1.765867
388	76582	Ipo11	importin 11	2	0	0	1.765315
389	14616	Gja8	gap junction protein, alpha 8	2	0	0	1.764153
390	226407	Rab3gap1	RAB3 GTPase activating protein subunit 1	2	0	0	1.764126
391	210622	E430002G05Rik	peptidase domain containing associated with muscle regeneration 1	2	0	0	1.763119
392	20810	Srm	spermidine synthase	2	0	0	1.757193
393	18616	Peg3	paternally expressed 3	2	0	0	1.756688
394	19264	Ptprc	protein tyrosine phosphatase, receptor type, C	2	0	0	1.752664
395	50934	Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	2	0	0	1.752286
396	373864	Col27a1	collagen, type XXVII, alpha 1	3	0	0	1.751581
397	20274	Scn9a	sodium channel, voltage-gated, type IX, alpha	2	0	0	1.751421
398	27392	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	2	0	0	1.750665
399	436569	UNK	NA	2	0	0	1.750284
400	232679	Zc3hc1	zinc finger, C3HC type 1	2	0	0	1.750172
401	258868	Olfr894	olfactory receptor 894	3	0	0	1.749941
402	70902	4921521K07Rik	lysophosphatidylcholine acyltransferase 2B	2	0	0	1.748155
403	224860	Plcl2	phospholipase C-like 2	2	0	0	1.74367
404	13505	Dsc1	desmocollin 1	2	0	0	1.742365
405	17692	Msl31	male-specific lethal 3 homolog (Drosophila)	2	0	0	1.741908
406	20620	Plk2	polo-like kinase 2 (Drosophila)	3	0	0	1.741787
407	94332	Igsf4b	cell adhesion molecule 3	2	0	0	1.741696
408	244180	E030002O03Rik	RIKEN cDNA E030002O03 gene	2	0	0	1.741411

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
409	240168	Rasgrp3	RAS, guanyl releasing protein 3	2	0	0	1.741315
410	12672	Chrm4	cholinergic receptor, muscarinic 4	2	0	0	1.740378
411	74851	4930408F14Rik	predicted gene 14354	2	0	0	1.739837
412	228642	BC034902	cDNA sequence BC034902	2	0	0	1.739791
413	109672	Cyb5	cytochrome b-5	2	0	0	1.736374
414	109136	Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	2	0	0	1.73604
415	237005	UNK	NA	2	0	0	1.733428
416	26439	Psg19	pregnancy specific glycoprotein 19	2	0	0	1.732314
417	74430	4930452B06Rik	RIKEN cDNA 4930452B06 gene	2	0	0	1.730274
418	19126	Prom1	prominin 1	2	0	0	1.729118
419	626187	UNK	NA	2	0	0	1.727734
420	65257	Asb3	ankyrin repeat and SOCS box-containing 3	2	0	0	1.727614
421	29871	Scmh1	sex comb on midleg homolog 1	2	0	0	1.727188
422	67365	Hdhd1a	haloacid dehalogenase-like hydrolase domain containing 1A	2	0	0	1.726246
423	12915	Crebl1	activating transcription factor 6 beta	2	0	0	1.725324
424	18584	Pde8a	phosphodiesterase 8A	2	0	0	1.725114
425	384283	Gm1389	NA	2	0	0	1.724176
426	74066	4933404G15Rik	RIKEN cDNA 4933404G15 gene	2	0	0	1.721535
427	101320	Dyrk4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	2	0	0	1.720536
428	20917	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	2	0	0	1.718238
429	234515	Inpp4b	inositol polyphosphate-4-phosphatase, type II	2	0	0	1.713499
430	403088	Eapa2	family with sequence similarity 115, member E	2	0	0	1.71136
431	69482	Nup35	nucleoporin 35	2	0	0	1.710306
432	241568	Lrrc4c	leucine rich repeat containing 4C	2	0	0	1.710135
433	22035	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	2	0	0	1.710069
434	246256	Fcgr3a	Fc receptor, IgG, low affinity IV	2	0	0	1.709692
435	18751	Prkcb1	protein kinase C, beta	2	0	0	1.709579
436	23797	Akt3	thymoma viral proto-oncogene 3	2	0	0	1.70887
437	28254	Slco1a6	solute carrier organic anion transporter family, member 1a6	2	0	0	1.706697
438	232946	Bloc1s3	biogenesis of lysosome-related organelles complex-1, subunit 3	2	0	0	1.706337
439	66482	Exoc2	exocyst complex component 2	3	0	0	1.705295
440	235628	Tessp2	protease, serine, 42	3	0	0	1.70248
441	209773	Dennd2a	DENN/MADD domain containing 2A	2	0	0	1.702369
442	77040	Atg16l1	autophagy-related 16-like 1 (yeast)	3	0	0	1.699784

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
443	94215	Ugt2a1	UDP glucuronosyltransferase 2 family, polypeptide A1	2	0	0	1.693049
444	27402	Pdhx	pyruvate dehydrogenase complex, component X	2	0	0	1.692339
445	320683	Zfp629	zinc finger protein 629	2	0	0	1.6922
446	68195	Rnaset2	ribonuclease T2B	2	0	0	1.691798
447	16769	Dsg4	desmoglein 4	3	0	0	1.688046
448	68278	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	2	0	0	1.687817
449	26874	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	2	0	0	1.686939
450	270893	Tmem132e	transmembrane protein 132E	2	0	0	1.684773
451	13595	Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	2	0	0	1.682808
452	54678	Zfp108	zinc finger protein 108	2	0	0	1.682443
453	22258	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	2	0	0	1.682021
454	12916	Crem	cAMP responsive element modulator	3	0	0	1.680637
455	18844	Plxna1	plexin A1	3	0	0	1.680592
456	545047	MGC118309	predicted gene 5800	2	0	0	1.677681
457	18663	Pgk2	phosphoglycerate kinase 2	2	0	0	1.676287
458	20411	Sorbs1	sorbin and SH3 domain containing 1	2	0	0	1.673918
459	21857	Timp1	tissue inhibitor of metalloproteinase 1	2	0	0	1.672744
460	102060	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	2	0	0	1.671874
461	19141	Lgmn	legumain	2	0	0	1.66694
462	228019	Mettl8	methyltransferase like 8	2	0	0	1.662049
463	211548	Nomo1	nodal modulator 1	2	0	0	1.659142
464	109820	Pgc	progastricsin (pepsinogen C)	2	0	0	1.657534
465	227377	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	2	0	0	1.6573
466	19385	Ranbp1	RAN binding protein 1	2	0	0	1.656777
467	209324	Stfna3l1	predicted gene 4758	4	0	0	1.653126
468	19743	Rhag	Rhesus blood group-associated A glycoprotein	2	0	0	1.646375
469	83925	Trps1	trichorhinophalangeal syndrome I (human)	2	0	0	1.640717
470	80285	Parp9	poly (ADP-ribose) polymerase family, member 9	2	0	0	1.636157
471	94047	Cecr6	cat eye syndrome chromosome region, candidate 6 homolog (human)	2	0	0	1.633798
472	269252	Gtf3c4	general transcription factor IIIC, polypeptide 4	2	0	0	1.630269
473	72199	Mms19l	MMS19 (MET18 S. cerevisiae)	2	0	0	1.625135
474	20916	Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	2	0	0	1.621663
475	72400	2610028A01Rik	PIN2/TERF1 interacting, telomerase inhibitor 1	2	0	0	1.616748
476	52250	Reep1	receptor accessory protein 1	2	0	0	1.616634

Candidates for negative regulators of normal growth (DESeq)

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477	232409	Clec2e	C-type lectin domain family 2, member e	2	0	0	1.61472
478	11677	Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	2	0	0	1.614617
479	15288	Hmbs	hydroxymethylbilane synthase	2	0	0	1.612163
480	233876	Hirip3	HIRA interacting protein 3	2	0	0	1.611381
481	226245	9930023K05Rik	RIKEN cDNA 9930023K05 gene	2	0	0	1.608284
482	76365	Tbx18	T-box18	2	0	0	1.608102
483	11839	Areg	amphiregulin	2	0	0	1.606908
484	383133	UNK	NA	2	0	0	1.606148
485	237029	4932411N23Rik	RIKEN cDNA 4932411N23 gene	2	0	0	1.604769
486	68083	Pak1ip1	PAK1 interacting protein 1	2	0	0	1.602799
487	22202	Ube1y1	ubiquitin-activating enzyme E1, Chr Y 1	2	0	0	1.602372
488	66449	Magmas	presequence translocase-asssociated motor 16 homolog (S. cerevisiae)	2	0	0	1.600658
489	16528	Kcnk4	potassium channel, subfamily K, member 4	2	0	0	1.599341
490	11600	Angpt1	angiopoietin 1	2	0	0	1.598571
491	80294	Pofut2	protein O-fucosyltransferase 2	2	0	0	1.597918
492	12267	C3ar1	complement component 3a receptor 1	2	0	0	1.597268
493	57743	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	2	0	0	1.595019
494	13114	Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	3	0	0	1.594904
495	75528	1700018L24Rik	RIKEN cDNA 1700018L24 gene	2	0	0	1.593652
496	234678	D230025D16Rik	RIKEN cDNA D230025D16 gene	2	0	0	1.588997
497	65114	Vps35	vacuolar protein sorting 35	2	0	0	1.587887
498	320022	4930532D21Rik	coiled-coil domain containing 79	2	0	0	1.587847
499	12864	Cox6c	cytochrome c oxidase, subunit VIc	2	0	0	1.58773
500	386655	Cri2	EP300 interacting inhibitor of differentiation 2	2	0	0	1.586717
501	106947	Slc39a3	solute carrier family 39 (zinc transporter), member 3	2	0	0	1.583463
502	258866	Olfr1008	olfactory receptor 1008	2	0	0	1.58133
503	76899	Golga1	golgi autoantigen, golgin subfamily a, 1	2	0	0	1.57765
504	73010	Gpr22	G protein-coupled receptor 22	2	0	0	1.575501
505	387356	Tas2r131	taste receptor, type 2, member 131	2	0	0	1.571658
506	109575	Tbx10	T-box 10	2	0	0	1.571207
507	12023	Barx2	BarH-like homeobox 2	3	0	0	1.57084
508	211430	4930533C12Rik	fer-1-like 5 (C. elegans)	3	0	0	1.570024
509	209203	UNK	NA	2	0	0	1.568678
510	67282	Ccdc53	coiled-coil domain containing 53	2	0	0	1.566525

Candidates for negative regulators of normal growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
511	65246	Xpo7	exportin 7	2	0	0	1.565255
512	216225	Slc5a8	solute carrier family 5 (iodide transporter), member 8	2	0	0	1.561888
513	12350	Car3	carbonic anhydrase 3	2	0	0	1.559522
514	66067	Gtpbp8	GTP-binding protein 8 (putative)	2	0	0	1.556504
515	212670	Catsper2	cation channel, sperm associated 2	2	0	0	1.556443
516	234988	Mbd3l2	methyl-CpG binding domain protein 3-like 2	2	0	0	1.556292
517	217365	Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	2	0	0	1.554039
518	27273	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	2	0	0	1.549834
519	232210	8430410A17Rik	RIKEN cDNA 8430410A17 gene	2	0	0	1.547106
520	67164	2610209A20Rik	lipoyl(octanoyl) transferase 2 (putative)	2	0	0	1.545511
521	76820	D12Ertd553e	family with sequence similarity 49, member A	2	0	0	1.542757
522	12946	Crry	complement component (3b/4b) receptor 1-like	2	0	0	1.534408
523	404312	Olfr250	olfactory receptor 250	2	0	0	1.531132
524	68904	Abhd13	abhydrolase domain containing 13	2	0	0	1.527763
525	258639	Olfr1158	olfactory receptor 1158	2	0	0	1.525582
526	239611	Muc19	mucin 19	2	0	0	1.524904
527	71468	Obox1	oocyte specific homeobox 1	2	0	0	1.524111
528	15958	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	2	0	0	1.523304
529	22750	Zfp9	zinc finger protein 9	2	0	0	1.520118
530	258464	Olfr1384	olfactory receptor 1384	2	0	0	1.51843
531	71877	Efhc1	EF-hand domain (C-terminal) containing 1	2	0	0	1.517156
532	68059	Tm9sf2	transmembrane 9 superfamily member 2	2	0	0	1.513544
533	83671	Sytl2	synaptotagmin-like 2	3	0	0	1.510559
534	20466	Sin3a	transcriptional regulator, SIN3A (yeast)	2	0	0	1.508565
535	246727	Oas3	2'-5' oligoadenylate synthetase 3	2	0	0	1.507793
536	29817	Igfbp7	insulin-like growth factor binding protein 7	2	0	0	1.507274
537	27967	Cherp	calcium homeostasis endoplasmic reticulum protein	2	0	0	1.505072
538	71729	Rgs12	regulator of G-protein signaling 12	2	0	0	1.50489
539	170460	Stard5	StAR-related lipid transfer (START) domain containing 5	2	0	0	1.502445

Supplementary Table 2. Putative regulators of normal growth identified by Fisher's exact test of pooled samples.

Note: Candidates identified by both DESeq and Fisher's exact test are highlighted in green.

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	16785	Rpsa	ribosomal protein SA	0	4	1	-3.73851
2	20643	Snrpe	small nuclear ribonucleoprotein E	0	4	1	-3.57433
3	67671	Rpl38	ribosomal protein L38	0	5	0	-3.50838
4	19946	Rpl30	ribosomal protein L30	0	5	0	-3.1928
5	53817	Bat1a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	0	4	1	-3.11671
6	20102	Rps4x	ribosomal protein S4, X-linked	0	5	0	-3.11064
7	208967	Thnsl1	threonine synthase-like 1 (bacterial)	0	4	1	-3.1023
8	27370	Rps26	ribosomal protein S26	0	4	1	-3.09298
9	20088	Rps24	ribosomal protein S24	0	4	1	-3.06523
10	110750	Cse1l	chromosome segregation 1-like (S. cerevisiae)	0	4	1	-3.06462
11	113847	V1ra5	vomeronasal 1 receptor 43	0	3	2	-3.06325
12	81845	Bat4	G patch domain and ankyrin repeats 1	0	3	2	-3.05406
13	66373	Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	3	2	-3.04212
14	69786	Tprkb	Tp53rk binding protein	0	3	1	-3.02671
15	213469	Lgi3	leucine-rich repeat LGI family, member 3	0	3	1	-2.97588
16	75062	Sf3a3	splicing factor 3a, subunit 3	0	3	1	-2.96977
17	268449	Rpl23a	ribosomal protein L23A	0	4	1	-2.96016
18	20116	Rps8	ribosomal protein S8	0	4	1	-2.95521
19	20091	Rps3a	ribosomal protein S3A	0	4	1	-2.95033
20	20104	Rps6	ribosomal protein S6	0	4	1	-2.93698
21	27050	Rps3	ribosomal protein S3	0	5	0	-2.90537
22	65019	Rpl23	ribosomal protein L23	0	4	1	-2.90331
23	208634	Tspan10	tetraspanin 10	0	4	1	-2.90191
24	66878	Riok3	RIO kinase 3 (yeast)	0	3	2	-2.86003
25	93687	Csnk1a1	casein kinase 1, alpha 1	0	3	2	-2.83069
26	18249	Obp1a	odorant binding protein Ia	0	3	2	-2.79845
27	20103	Rps5	ribosomal protein S5	0	5	0	-2.79677
28	12043	Bcl2	B cell leukemia/lymphoma 2	0	3	1	-2.76514
29	16391	Isgf3g	interferon regulatory factor 9	0	3	2	-2.75037
30	67097	Rps10	ribosomal protein S10	0	4	1	-2.7329
31	19983	Rpl5	NA	0	4	1	-2.72904
32	434683	UNK	NA	0	3	2	-2.71542
33	170768	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0	3	2	-2.71376

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
34	60411	Cenpk	centromere protein K	0	4	1	-2.71062
35	21372	Tbl1x	transducin (beta)-like 1 X-linked	0	3	2	-2.70554
36	21682	Tec	tec protein tyrosine kinase	0	3	2	-2.68084
37	270106	Rpl13	ribosomal protein L13	0	3	2	-2.66367
38	171195	V1rc22	vomeronasal 1 receptor 30	0	3	2	-2.65768
39	109754	Cyb5r3	cytochrome b5 reductase 3	0	3	2	-2.65401
40	106582	Nrm	nurim (nuclear envelope membrane protein)	0	3	1	-2.65215
41	268935	Scube3	signal peptide, CUB domain, EGF-like 3	0	3	2	-2.64676
42	101943	Sf3b3	splicing factor 3b, subunit 3	0	3	2	-2.64643
43	66616	Snx9	sorting nexin 9	0	3	2	-2.62609
44	114641	Rpl31	ribosomal protein L31	0	3	2	-2.61387
45	17463	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0	3	2	-2.61284
46	12464	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	0	4	1	-2.61257
47	94185	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	0	3	2	-2.59893
48	12391	Cav3	caveolin 3	0	3	2	-2.59791
49	11837	Arbp	ribosomal protein, large, P0	0	4	1	-2.58876
50	67115	Rpl14	ribosomal protein L14	0	5	0	-2.58114
51	217692	Sipa1l1	signal-induced proliferation-associated 1 like 1	0	3	2	-2.56815
52	16363	Irf2	interferon regulatory factor 2	0	3	2	-2.56386
53	383042	UNK	NA	0	3	2	-2.56245
54	17096	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	0	3	2	-2.55424
55	22003	Tpm1	tropomyosin 1, alpha	0	3	2	-2.55011
56	14913	Guca1a	guanylate cyclase activator 1a (retina)	0	3	2	-2.54672
57	12696	Cirbp	cold inducible RNA binding protein	0	3	1	-2.52649
58	17829	Muc1	mucin 1, transmembrane	0	3	2	-2.52512
59	66475	Rps23	ribosomal protein S23	0	4	1	-2.52035
60	50797	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	0	4	1	-2.51143
61	81898	Sf3b1	splicing factor 3b, subunit 1	0	4	1	-2.51126
62	14916	Guca2b	guanylate cyclase activator 2b (retina)	0	3	2	-2.50751
63	19822	Rnf4	ring finger protein 4	0	3	2	-2.50697
64	67603	Dusp6	dual specificity phosphatase 6	0	3	2	-2.49794
65	26381	Esrrg	estrogen-related receptor gamma	0	3	2	-2.47821
66	20379	Sfrp4	secreted frizzled-related protein 4	0	3	2	-2.47261
67	76789	2410129H14Rik	mitotic spindle organizing protein 1	0	3	1	-2.47259
68	13488	Drd1a	dopamine receptor D1A	0	3	2	-2.47239
69	16341	Eif3s6	eukaryotic translation initiation factor 3, subunit E	0	3	2	-2.47048
70	56347	Eif3s8	eukaryotic translation initiation factor 3, subunit C	0	5	0	-2.4668

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
71	71954	2400003N08Rik	suppressor of defective silencing 3 homolog (S. cerevisiae)	0	3	2	-2.46338
72	56353	Rybp	RING1 and YY1 binding protein	0	3	2	-2.45901
73	72308	Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	0	3	2	-2.45429
74	17219	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	0	3	2	-2.45243
75	214253	Etnk2	ethanolamine kinase 2	0	4	1	-2.44912
76	76499	Clasp2	CLIP associating protein 2	0	3	2	-2.43604
77	14469	Gbp2	guanylate binding protein 2	0	3	2	-2.43039
78	53356	Eif3s4	eukaryotic translation initiation factor 3, subunit G	0	4	0	-2.42344
79	68314	0610008F07Rik	RIKEN cDNA 0610008F07 gene	0	3	1	-2.42185
80	245026	E330026B02Rik	collagen, type VI, alpha 6	0	3	2	-2.4188
81	72821	Scn2b	sodium channel, voltage-gated, type II, beta	0	3	2	-2.41674
82	93670	Tac4	tachykinin 4	0	3	2	-2.4163
83	17246	Mdm2	transformed mouse 3T3 cell double minute 2	0	4	1	-2.41225
84	19899	Rpl18	ribosomal protein L18	0	5	0	-2.40962
85	104831	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	0	4	1	-2.40478
86	14694	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	0	6	4	-2.40441
87	18438	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	0	3	2	-2.40093
88	406186	Olfr142	olfactory receptor 142	0	3	2	-2.39986
89	192170	Ddx48	eukaryotic translation initiation factor 4A3	0	3	2	-2.39519
90	66711	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	0	3	2	-2.39422
91	66085	Eif3s5	eukaryotic translation initiation factor 3, subunit F	0	3	1	-2.39358
92	14113	Fbl	fibrillarin	0	3	2	-2.39186
93	233437	F830104D24Rik	vomeronasal 2, receptor 66	0	3	2	-2.39086
94	235184	BC024479	cDNA sequence BC024479	0	4	1	-2.38992
95	14028	Evx1	even skipped homeotic gene 1 homolog	0	3	2	-2.38922
96	16898	Rps2	ribosomal protein S2	0	3	2	-2.38715
97	66970	Ssbp2	single-stranded DNA binding protein 2	0	3	2	-2.38529
98	72843	Prdm4	PR domain containing 4	0	3	2	-2.38294
99	75805	Nln	neurolysin (metallopeptidase M3 family)	0	5	0	-2.3826
100	93726	Ear11	eosinophil-associated, ribonuclease A family, member 11	0	3	2	-2.38183
101	22700	Zfp40	zinc finger protein 40	0	3	2	-2.38035
102	102436	Lars2	leucyl-tRNA synthetase, mitochondrial	0	3	2	-2.38022
103	387343	Tas2r109	taste receptor, type 2, member 109	0	3	1	-2.37994
104	81879	Tcfcp2l1	transcription factor CP2-like 1	0	3	2	-2.37852
105	210126	Lpp	LIM domain containing preferred translocation partner in lipoma	0	4	1	-2.37477
106	83453	Chrdl1	chordin-like 1	0	3	1	-2.37236
107	66433	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0	3	1	-2.36488

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
108	68436	1100001I22Rik	ribosomal protein L34	0	7	3	-2.36449
109	194456	UNK	NA	0	3	2	-2.36422
110	320118	Fbxl13	F-box and leucine-rich repeat protein 13	0	3	2	-2.35879
111	67848	Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	0	3	2	-2.3586
112	20400	Sh2d1a	SH2 domain protein 1A	0	3	2	-2.35639
113	109095	Rbm15b	RNA binding motif protein 15B	0	4	1	-2.35399
114	12466	Cct6a	chaperonin containing Tcp1, subunit 6a (zeta)	0	4	1	-2.35346
115	66480	Rpl15	ribosomal protein L15	0	3	2	-2.35048
116	68052	Rps13	ribosomal protein S13	0	5	0	-2.34452
117	19112	Prlpc1	prolactin family 8, subfamily a, member 6	0	4	1	-2.34412
118	107999	Gtpbp6	GTP binding protein 6 (putative)	0	4	0	-2.34102
119	27367	Rpl3	ribosomal protein L3	0	4	1	-2.33917
120	433926	Lrrc8b	leucine rich repeat containing 8 family, member B	0	3	2	-2.33635
121	217119	Xylt2	xylosyltransferase II	0	3	2	-2.33533
122	75985	Rab30	RAB30, member RAS oncogene family	0	3	2	-2.33527
123	53382	Txnl1	thioredoxin-like 1	0	4	0	-2.33337
124	20448	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltran	0	4	1	-2.33168
125	27207	Rps11	ribosomal protein S11	0	5	0	-2.32864
126	66489	Rpl35	ribosomal protein L35	0	4	1	-2.32661
127	403200	4930504O13Rik	RIKEN cDNA 4930504O13 gene	0	3	2	-2.32624
128	22348	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	0	3	2	-2.32328
129	380795	AI324046	Immunoglobulin heavy constant gamma 3	0	4	1	-2.32193
130	20637	Snrp70	small nuclear ribonucleoprotein 70 (U1)	0	3	2	-2.32129
131	76522	Lsm8	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	0	4	1	-2.32085
132	22186	Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	0	3	2	-2.32043
133	68770	Phtf2	putative homeodomain transcription factor 2	0	3	2	-2.31846
134	353172	Gars	glycyl-tRNA synthetase	0	4	1	-2.3174
135	16509	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	0	3	2	-2.31518
136	15497	Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6	0	4	1	-2.31431
137	11787	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	0	4	1	-2.30689
138	17975	Ncl	nucleolin	0	5	0	-2.30159
139	11905	Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	0	3	2	-2.29983
140	227733	Pip5kl1	phosphatidylinositol-4-phosphate 5-kinase-like 1	0	3	2	-2.29908
141	68048	Isg20l1	apoptosis enhancing nuclease	0	3	2	-2.29785
142	15425	Hoxc6	homeobox C6	0	3	2	-2.29738
143	110809	Sfrs1	serine/arginine-rich splicing factor 1	0	3	2	-2.29634
144	11632	Aip	aryl-hydrocarbon receptor-interacting protein	0	3	2	-2.29492

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
145	67678	Lsm3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	4	1	-2.29339
146	11571	Crisp1	cysteine-rich secretory protein 1	0	3	2	-2.2923
147	110521	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	0	3	2	-2.29145
148	67332	Snrpd3	small nuclear ribonucleoprotein D3	0	5	0	-2.29063
149	64436	Inpp5e	inositol polyphosphate-5-phosphatase E	0	5	0	-2.28828
150	20923	Supt4h2	NA	0	3	2	-2.28676
151	73182	3110045G13Rik	platelet endothelial aggregation receptor 1	0	3	2	-2.28516
152	21881	Tkt	transketolase	0	3	2	-2.28385
153	75434	1700001C02Rik	RIKEN cDNA 1700001C02 gene	0	3	2	-2.28033
154	100066	Cyp2j11	cytochrome P450, family 2, subfamily j, polypeptide 11	0	3	2	-2.28032
155	53318	Pdlim3	PDZ and LIM domain 3	0	3	2	-2.2778
156	21346	Tagln2	transgelin 2	0	3	2	-2.27641
157	56529	Sec11l1	SEC11 homolog A (S. cerevisiae)	0	3	2	-2.27513
158	68365	Rab14	RAB14, member RAS oncogene family	0	4	1	-2.2751
159	433297	LOC433297	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle pseudogene	0	3	2	-2.27385
160	245663	LOC245663	prohibitin pseudogene	0	4	1	-2.27195
161	215748	Cnksr3	Cnksr family member 3	0	4	1	-2.27095
162	233081	Ffar1	free fatty acid receptor 1	0	3	2	-2.27066
163	16001	Igf1r	insulin-like growth factor I receptor	0	3	2	-2.26617
164	68032	Tmem85	transmembrane protein 85	0	3	1	-2.26435
165	83679	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	0	3	2	-2.26243
166	56437	Rrad	Ras-related associated with diabetes	0	3	2	-2.25982
167	110954	Rpl10	ribosomal protein 10	0	5	0	-2.25727
168	258804	Olfr1240	olfactory receptor 1240	0	3	2	-2.25718
169	56642	Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	0	3	2	-2.25582
170	12468	Cct7	chaperonin containing Tcp1, subunit 7 (eta)	0	4	1	-2.2548
171	435766	Tnni3k	TNNI3 interacting kinase	0	3	7	-2.25416
172	70127	Dpf3	D4, zinc and double PHD fingers, family 3	0	3	2	-2.25361
173	14068	F7	coagulation factor VII	0	4	1	-2.25238
174	98878	Ehd4	EH-domain containing 4	0	3	2	-2.25213
175	22094	Tshb	thyroid stimulating hormone, beta subunit	0	3	2	-2.24992
176	93715	Pcdhga7	protocadherin gamma subfamily A, 7	0	3	2	-2.24958
177	26961	Rpl8	ribosomal protein L8	0	4	1	-2.24506
178	67684	3300001P08Rik	LUC7-like 3 (S. cerevisiae)	0	3	2	-2.24215
179	93877	Pcdhb6	protocadherin beta 6	0	3	2	-2.24183
180	268395	Mpg	N-methylpurine-DNA glycosylase	0	3	2	-2.23964
181	20068	Rps17	ribosomal protein S17	0	5	0	-2.23708

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
182	233115	Dpy19l3	dpy-19-like 3 (C. elegans)	0	3	2	-2.23695
183	12009	Azi1	5-azacytidine induced gene 1	0	3	1	-2.23637
184	433238	LOC433238	predicted gene 5518	0	3	2	-2.23486
185	384401	LOC384401	tubulin, alpha 1A pseudogene	0	3	2	-2.23441
186	240672	Dusp5	dual specificity phosphatase 5	0	3	2	-2.23371
187	71994	Cnn3	calponin 3, acidic	0	3	2	-2.23263
188	11736	Ankfy1	ankyrin repeat and FYVE domain containing 1	0	3	2	-2.23134
189	170936	Zfp369	zinc finger protein 369	0	3	2	-2.22976
190	23983	Pcbp1	poly(rC) binding protein 1	0	3	2	-2.22919
191	12346	Car1	carbonic anhydrase 1	0	3	2	-2.22881
192	104112	Acly	ATP citrate lyase	0	3	2	-2.22845
193	16630	Klra12	killer cell lectin-like receptor subfamily A, member 12	0	4	1	-2.22823
194	67135	2310021H06Rik	BPI fold containing family A, member 5	0	3	2	-2.22568
195	270076	Gcdh	glutaryl-Coenzyme A dehydrogenase	0	3	2	-2.22481
196	67168	P2ry5	lysophosphatidic acid receptor 6	0	3	2	-2.22426
197	14380	G6pd2	glucose-6-phosphate dehydrogenase 2	0	3	2	-2.2239
198	503845	Ear12	eosinophil-associated, ribonuclease A family, member 12	0	3	1	-2.22145
199	77592	4931406H21Rik	RIKEN cDNA 4931406H21 gene	0	3	1	-2.21992
200	71854	Dpep3	dipeptidase 3	0	3	2	-2.21833
201	12939	Pcdha7	protocadherin alpha 7	0	3	2	-2.21821
202	20394	Scg5	secretogranin V	0	3	2	-2.21777
203	109226	A930002I21Rik	RIKEN cDNA A930002I21 gene	0	3	1	-2.21702
204	20322	Sord	sorbitol dehydrogenase	0	3	2	-2.21419
205	53880	Birc1g	NLR family, apoptosis inhibitory protein 7	0	3	2	-2.21252
206	24061	Smc1a	structural maintenance of chromosomes 1A	0	4	1	-2.21197
207	18673	Phb	prohibitin	0	3	2	-2.21035
208	57780	Fxyd7	FXYD domain-containing ion transport regulator 7	0	3	2	-2.20974
209	19981	Rpl37a	ribosomal protein L37a	0	4	1	-2.20966
210	107508	Eprs	glutamyl-prolyl-tRNA synthetase	0	3	1	-2.2095
211	226641	Atf6	activating transcription factor 6	0	3	2	-2.20708
212	227622	BC029214	cDNA sequence BC029214	0	3	1	-2.20667
213	56459	Uble1a	SUMO1 activating enzyme subunit 1	0	3	2	-2.20549
214	71448	Tmem80	transmembrane protein 80	0	3	2	-2.20399
215	59010	Sqrdl	sulfide quinone reductase-like (yeast)	0	3	2	-2.20388
216	19823	Rnf7	ring finger protein 7	0	3	1	-2.20359
217	18208	Ntn1	netrin 1	0	3	2	-2.2035
218	107047	Tnfsf5ip1	proteasome (prosome, macropain) assembly chaperone 2	0	4	0	-2.19982

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
219	16907	Lmnb2	lamin B2	0	3	2	-2.19976
220	113862	V1rc5	vomeronasal 1 receptor 13	0	4	1	-2.19869
221	20429	Shox2	short stature homeobox 2	0	3	2	-2.19701
222	216440	4632413K17Rik	amplified in osteosarcoma	0	3	1	-2.1952
223	73353	Actrt2	actin-related protein T2	0	4	1	-2.19503
224	113857	V1rb9	vomeronasal 1 receptor 41	0	3	2	-2.19473
225	67226	Tmem19	transmembrane protein 19	0	3	2	-2.19442
226	225896	D19Ertd721e	UBX domain protein 1	0	3	2	-2.19378
227	98970	Fibcd1	fibrinogen C domain containing 1	0	5	0	-2.19337
228	71805	Nup93	nucleoporin 93	0	5	0	-2.19332
229	74589	4933428M03Rik	kelch repeat and BTB (POZ) domain containing 12	0	3	2	-2.19252
230	28080	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0	3	2	-2.19207
231	320183	Msrb3	methionine sulfoxide reductase B3	0	3	2	-2.1918
232	258271	Olfr1311	olfactory receptor 1311	0	3	1	-2.19055
233	240215	Slc4a9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	0	3	2	-2.18943
234	12500	Cd3d	CD3 antigen, delta polypeptide	0	3	2	-2.18723
235	11517	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	0	3	2	-2.18703
236	240066	BC066107	zinc finger protein 870	0	3	2	-2.18635
237	17928	Myog	myogenin	0	3	2	-2.18583
238	215387	Brrn1	non-SMC condensin I complex, subunit H	0	3	2	-2.18361
239	258927	Olfr481	olfactory receptor 481	0	4	1	-2.18338
240	74245	Ctbs	chitobiase, di-N-acetyl-	0	3	1	-2.18336
241	68479	Phf5a	PHD finger protein 5A	0	4	1	-2.1833
242	74441	Slco6c1	solute carrier organic anion transporter family, member 6c1	0	3	2	-2.18113
243	69520	2310002A05Rik	late cornified envelope 3F	0	3	1	-2.18058
244	170735	Arr3	arrestin 3, retinal	0	3	1	-2.18029
245	19277	Ptpro	protein tyrosine phosphatase, receptor type, O	0	3	2	-2.1769
246	217344	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	0	3	2	-2.17643
247	69790	Thrap6	mediator complex subunit 30	0	3	2	-2.17596
248	22627	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0	5	0	-2.17446
249	244141	Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	0	3	2	-2.17316
250	15013	H2-Q2	histocompatibility 2, Q region locus 2	0	4	1	-2.17308
251	13038	Ctsk	cathepsin K	0	3	7	-2.17041
252	12335	Capn3	calpain 3	0	3	2	-2.17022
253	319229	Sctr	secretin receptor	0	3	2	-2.17005
254	66055	0610009D07Rik	RIKEN cDNA 0610009D07 gene	0	4	1	-2.16984
255	75905	4930578C19Rik	RIKEN cDNA 4930578C19 gene	0	3	1	-2.16804

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
256	103583	Fbxw11	F-box and WD-40 domain protein 11	0	3	2	-2.16775
257	56443	Arpc1a	actin related protein 2/3 complex, subunit 1A	0	3	2	-2.1671
258	57438	39147	membrane-associated ring finger (C3HC4) 7	0	3	2	-2.16671
259	72723	Zfp74	zinc finger protein 74	0	3	2	-2.16579
260	13350	Dgat1	diacylglycerol O-acyltransferase 1	0	3	2	-2.1649
261	192986	Cyb5d2	cytochrome b5 domain containing 2	0	3	2	-2.16273
262	53319	Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	0	3	2	-2.16218
263	20909	Stx4a	syntaxin 4A (placental)	0	3	2	-2.16087
264	114674	Gtf2ird2	GTF2I repeat domain containing 2	0	3	2	-2.15998
265	12455	Ccnt1	cyclin T1	0	3	2	-2.15825
266	11606	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0	3	2	-2.15682
267	245000	Atr	ataxia telangiectasia and Rad3 related	0	4	1	-2.15637
268	267019	Rps15a	ribosomal protein S15A	0	4	1	-2.15488
269	66380	Krtap3-3	keratin associated protein 3-3	0	3	1	-2.1534
270	23879	Fxr2h	fragile X mental retardation, autosomal homolog 2	0	3	1	-2.15269
271	18033	Nfkb1	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105	0	3	2	-2.15266
272	21343	Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	3	2	-2.15157
273	77128	A930001N09Rik	RIKEN cDNA A930001N09 gene	0	3	2	-2.14935
274	104303	Arl1	ADP-ribosylation factor-like 1	0	3	2	-2.14604
275	19989	Rpl7	ribosomal protein L7	0	4	1	-2.14401
276	269997	6430604K15Rik	zinc finger protein 747	0	3	2	-2.14252
277	22761	Zfpm1	zinc finger protein, multitype 1	0	3	2	-2.14243
278	433336	UNK	NA	0	3	2	-2.14149
279	66537	2510048O06Rik	proteasome maturation protein	0	4	1	-2.13865
280	258468	Olfr1254	olfactory receptor 1254	0	3	2	-2.13842
281	14708	Gng7	guanine nucleotide binding protein (G protein), gamma 7	0	4	0	-2.13462
282	380855	Rsl1	regulator of sex limited protein 1	0	3	2	-2.13393
283	224045	Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	0	3	2	-2.13386
284	17156	Man1a2	mannosidase, alpha, class 1A, member 2	0	3	2	-2.13379
285	233877	Kctd13	potassium channel tetramerisation domain containing 13	0	3	2	-2.13314
286	20913	Stxbp4	syntaxin binding protein 4	0	3	2	-2.13185
287	19231	Ptma	prothymosin alpha	0	3	2	-2.13139
288	66747	4933400A11Rik	capping protein (actin filament) muscle Z-line, alpha 1 pseudogene	0	3	2	-2.12953
289	64450	Gpr85	G protein-coupled receptor 85	0	3	2	-2.12718
290	12425	Cckar	cholecystokinin A receptor	0	3	1	-2.12683
291	69982	Spink2	serine peptidase inhibitor, Kazal type 2	0	3	2	-2.12618
292	27362	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	0	3	2	-2.12601

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
293	208643	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	0	4	1	-2.12567
294	66845	Mrpl33	mitochondrial ribosomal protein L33	0	3	2	-2.12462
295	278097	Armcx6	armadillo repeat containing, X-linked 6	0	3	2	-2.12214
296	17713	Grpel1	GrpE-like 1, mitochondrial	0	4	1	-2.1214
297	102193	Zdhhc7	zinc finger, DHHC domain containing 7	0	3	2	-2.11942
298	381511	Ppm2c	pyruvate dehyrogenase phosphatase catalytic subunit 1	0	3	2	-2.11936
299	74653	4930444A02Rik	RIKEN cDNA 4930444A02 gene	0	3	2	-2.11917
300	67186	Rplp2	ribosomal protein, large P2	0	5	0	-2.11818
301	240289	LOC240289	proteasome (prosome, macropain) subunit, beta type 3 pseudogene	0	3	2	-2.11811
302	432986	Kb16p	type II keratin Kb16P	0	4	1	-2.11805
303	170729	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	0	4	1	-2.1178
304	93765	Ube2n	ubiquitin-conjugating enzyme E2N	0	3	2	-2.11712
305	319210	4930518C23Rik	vomeronasal 2, receptor, pseudogene 11	0	4	1	-2.11639
306	20044	Rps14	ribosomal protein S14	0	5	0	-2.11479
307	20826	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0	4	1	-2.11314
308	12442	Ccnb2	cyclin B2	0	3	2	-2.11248
309	20020	Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	0	3	2	-2.11212
310	17130	Smad6	MAD homolog 6 (Drosophila)	0	4	1	-2.11156
311	15260	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	0	4	1	-2.11152
312	54127	Rps28	ribosomal protein S28	0	4	1	-2.10713
313	57808	Rpl35a	ribosomal protein L35A	0	3	1	-2.10587
314	93691	Klf7	Kruppel-like factor 7 (ubiquitous)	0	3	2	-2.10586
315	12545	Cdc7	cell division cycle 7 (S. cerevisiae)	0	3	2	-2.10448
316	171258	V1ri7	vomeronasal 1 receptor 202	0	4	1	-2.10387
317	319195	Rpl17	ribosomal protein L17	0	3	2	-2.10383
318	14787	Rhpn1	rhophilin, Rho GTPase binding protein 1	0	3	2	-2.10363
319	21681	Thoc4	Aly/REF export factor	0	4	0	-2.10285
320	493809	Taar3	trace amine-associated receptor 3	0	4	1	-2.10055
321	20479	Vps4b	vacuolar protein sorting 4b (yeast)	0	3	2	-2.1004
322	69836	Pla2g12b	phospholipase A2, group XIIB	0	3	2	-2.09955
323	433285	UNK	NA	0	3	2	-2.0995
324	54711	Plagl2	pleiomorphic adenoma gene-like 2	0	3	2	-2.09809
325	230676	BC059842	seizure threshold 2	0	3	1	-2.09757
326	386042	LOC386042	NA	0	3	2	-2.09751
327	238384	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	0	3	2	-2.09713
328	223732	Ldoc1l	leucine zipper, down-regulated in cancer 1-like	0	3	1	-2.09609
329	381806	LOC381806	murinoglobulin pseudogene	0	3	2	-2.09556

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
330	20005	Rpl9	ribosomal protein L9	0	4	1	-2.09094
331	18771	Pknox1	Pbx/knotted 1 homeobox	0	4	1	-2.09049
332	14738	Gpr12	G-protein coupled receptor 12	0	3	7	-2.09006
333	11595	Agc1	aggrecan	0	3	2	-2.08825
334	227699	Nup188	nucleoporin 188	0	3	1	-2.08514
335	52563	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	0	3	2	-2.08474
336	620654	UNK	NA	0	4	1	-2.08377
337	26445	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	0	5	0	-2.08213
338	76897	0710005M24Rik	RALY RNA binding protein-like	0	3	2	-2.08114
339	278304	A930006D11Rik	zinc finger protein 385C	0	3	2	-2.0809
340	22629	Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	0	3	2	-2.07963
341	21689	Tekt1	tektin 1	0	4	1	-2.07948
342	16783	Lamp1	lysosomal-associated membrane protein 1	0	4	1	-2.07824
343	69077	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0	3	2	-2.07794
344	71889	Epn3	epsin 3	0	3	2	-2.07792
345	238323	Rps6kl1	ribosomal protein S6 kinase-like 1	0	3	2	-2.0778
346	216760	Mfap3	microfibrillar-associated protein 3	0	4	1	-2.07721
347	241134	9430031J16Rik	RIKEN cDNA 9430031J16 gene	0	4	1	-2.07305
348	208666	Diras1	DIRAS family, GTP-binding RAS-like 1	0	4	1	-2.07182
349	57748	Jmy	junction-mediating and regulatory protein	0	3	1	-2.07013
350	11546	Parp2	poly (ADP-ribose) polymerase family, member 2	0	3	2	-2.06954
351	15891	Ibsp	integrin binding sialoprotein	0	3	2	-2.06754
352	269397	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	0	3	2	-2.06742
353	20201	S100a8	S100 calcium binding protein A8 (calgranulin A)	0	3	2	-2.06682
354	192164	Pcdha12	protocadherin alpha 12	0	3	2	-2.06645
355	106200	Txndc11	thioredoxin domain containing 11	0	3	2	-2.06617
356	384639	LOC384639	tetraspanin 7 pseudogene	0	4	1	-2.06557
357	19941	Rpl26	ribosomal protein L26	0	3	2	-2.06472
358	209318	Gps1	G protein pathway suppressor 1	0	4	1	-2.06467
359	231889	Bud31	BUD31 homolog (yeast)	0	3	2	-2.06248
360	67701	Wfdc2	WAP four-disulfide core domain 2	0	3	2	-2.06217
361	545013	LOC545013	predicted gene 5797	0	3	2	-2.06182
362	78908	Igsf3	immunoglobulin superfamily, member 3	0	4	1	-2.06155
363	56417	Adar	adenosine deaminase, RNA-specific	0	3	2	-2.05765
364	71838	Phf7	PHD finger protein 7	0	3	2	-2.05689
365	18548	Pcsk1	proprotein convertase subtilisin/kexin type 1	0	4	1	-2.05677
366	384361	UNK	NA	0	4	0	-2.05643

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
367	109331	Rnf20	ring finger protein 20	0	3	2	-2.0547
368	207350	Itih5l	NA	0	4	1	-2.05427
369	56018	Stard10	START domain containing 10	0	4	1	-2.05422
370	56388	Cyp3a25	cytochrome P450, family 3, subfamily a, polypeptide 25	0	3	2	-2.05392
371	56455	Dynll1	dynein light chain LC8-type 1	0	3	2	-2.05363
372	64435	Fcamr	Fc receptor, IgA, IgM, high affinity	0	3	2	-2.05359
373	71382	Pex1	peroxisomal biogenesis factor 1	0	3	2	-2.05236
374	67661	Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	0	4	1	-2.05137
375	12396	Cbfa2t2h	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	0	3	2	-2.05117
376	75764	Giyd2	SLX1 structure-specific endonuclease subunit homolog B (S. cerevisiae)	0	4	1	-2.05113
377	59125	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	0	3	2	-2.05059
378	14719	Got2	glutamate oxaloacetate transaminase 2, mitochondrial	0	3	2	-2.04876
379	67220	Plekho1	pleckstrin homology domain containing, family O member 1	0	4	1	-2.04774
380	243659	Styk1	serine/threonine/tyrosine kinase 1	0	3	2	-2.04729
381	270035	D030041N04Rik	leucine zipper-EF-hand containing transmembrane protein 2	0	4	1	-2.04633
382	20807	Srf	serum response factor	0	3	2	-2.04543
383	64136	Sdf2l1	stromal cell-derived factor 2-like 1	0	3	2	-2.04478
384	22139	Ttr	transthyretin	0	4	1	-2.04427
385	18999	Pou5f1	POU domain, class 5, transcription factor 1	0	3	2	-2.04226
386	17069	Ly6e	lymphocyte antigen 6 complex, locus E	0	3	2	-2.03793
387	218921	4930474N05Rik	RIKEN cDNA 4930474N05 gene	0	3	2	-2.03682
388	246103	Atxn7	ataxin 7	0	4	1	-2.03654
389	18632	Pex11b	peroxisomal biogenesis factor 11 beta	0	3	2	-2.03555
390	16159	Il12a	interleukin 12a	0	3	2	-2.03441
391	104130	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	0	3	2	-2.03401
392	66257	Nicn1	nicolin 1	0	3	1	-2.03386
393	241915	Phc3	polyhomeotic-like 3 (Drosophila)	0	3	2	-2.03301
394	541307	Ccl26l	chemokine (C-C motif) ligand 26	0	3	2	-2.03292
395	19726	Rfx3	regulatory factor X, 3 (influences HLA class II expression)	0	3	2	-2.03097
396	97440	C76566	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9, pseudogene	0	4	1	-2.03084
397	12461	Cct2	chaperonin containing Tcp1, subunit 2 (beta)	0	3	2	-2.02905
398	16401	Itga4	integrin alpha 4	0	5	0	-2.02885
399	69354	Slc38a4	solute carrier family 38, member 4	0	4	1	-2.02735
400	192194	Butr1	butyrophilin related 1	0	3	1	-2.02709
401	216136	Ilvbl	ilvB (bacterial acetolactate synthase)-like	0	3	2	-2.02688
402	435391	LOC435391	dual specificity phosphatase and pro isomerase domain containing 1	0	3	2	-2.02688
403	71819	Kif23	kinesin family member 23	0	4	1	-2.02588

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
404	13716	Ell	elongation factor RNA polymerase II	0	3	2	-2.02491
405	14609	Gja1	gap junction protein, alpha 1	0	4	1	-2.02476
406	67774	Loh12cr1	loss of heterozygosity, 12, chromosomal region 1 homolog (human)	0	3	2	-2.02448
407	78070	Cpt1c	carnitine palmitoyltransferase 1c	0	5	0	-2.0221
408	54624	Paf1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	0	4	1	-2.02172
409	170736	Parvb	parvin, beta	0	3	2	-2.02136
410	252870	Usp7	ubiquitin specific peptidase 7	0	4	1	-2.02041
411	21813	Tgfbr2	transforming growth factor, beta receptor II	0	4	1	-2.01874
412	170737	Znrf1	zinc and ring finger 1	0	3	2	-2.01857
413	67698	Tmem157	family with sequence similarity 174, member A	0	4	1	-2.01761
414	319513	A930025D01Rik	family with sequence similarity 113, member A	0	3	1	-2.01755
415	24131	Ldb3	LIM domain binding 3	0	3	2	-2.0146
416	383101	UNK	NA	0	5	0	-2.01428
417	78294	Rps27a	ribosomal protein S27A	0	4	1	-2.01403
418	108687	Edem2	ER degradation enhancer, mannosidase alpha-like 2	0	3	2	-2.01397
419	214931	Fbxl16	F-box and leucine-rich repeat protein 16	0	3	2	-2.01341
420	66492	Zmat2	zinc finger, matrin type 2	0	4	1	-2.01258
421	68816	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0	3	2	-2.01223
422	353283	Eras	ES cell-expressed Ras	0	3	2	-2.01099
423	67344	Tctex1d1	Tctex1 domain containing 1	0	3	1	-2.01092
424	83701	Ars2	serrate RNA effector molecule homolog (Arabidopsis)	0	4	1	-2.01071
425	213311	Fbxl21	F-box and leucine-rich repeat protein 21	0	3	2	-2.01067
426	243382	Ppm1k	protein phosphatase 1K (PP2C domain containing)	0	4	1	-2.00921
427	18012	Neurod1	neurogenic differentiation 1	0	3	2	-2.00836
428	171189	V1rc16	vomeronasal 1 receptor 17	0	5	0	-2.00833
429	268470	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	0	3	2	-2.00825
430	14705	Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	0	4	1	-2.00661
431	22598	Slc6a18	solute carrier family 6 (neurotransmitter transporter), member 18	0	4	1	-2.00638
432	27979	Eif3s9	eukaryotic translation initiation factor 3, subunit B	0	4	1	-2.00532
433	227506	LOC227506	leukotriene A4 hydrolase pseudogene	0	3	2	-2.00524
434	117005	Olfr74	olfactory receptor 74	0	3	1	-2.00518
435	19671	Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	0	4	1	-2.00482
436	100678	Psph	phosphoserine phosphatase	0	3	2	-2.00354
437	109161	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	0	3	2	-2.00235
438	20623	Snrk	SNF related kinase	0	3	2	-2.00234
439	20378	Frzb	frizzled-related protein	0	3	2	-2.0021
440	19353	Rac1	RAS-related C3 botulinum substrate 1	0	4	1	-2.00204

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
441	66421	2410004B18Rik	RIKEN cDNA 2410004B18 gene	0	3	1	-2.00199
442	72194	Fbxl20	F-box and leucine-rich repeat protein 20	0	3	2	-2.00144
443	66887	1300002A08Rik	lon peptidase 2, peroxisomal	0	3	2	-2.00084
444	329333	B230218O03	NA	0	3	2	-2.00034
445	67877	Nat5	N(alpha)-acetyltransferase 20, NatB catalytic subunit	0	3	2	-1.99948
446	319322	Sf3b2	splicing factor 3b, subunit 2	0	5	0	-1.99925
447	13684	Eif4e	eukaryotic translation initiation factor 4E	0	3	2	-1.99922
448	67236	2810452K22Rik	cyclin-dependent kinase 2 interacting protein	0	4	1	-1.99887
449	56429	Dpt	dermatopontin	0	3	2	-1.99847
450	24099	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	0	3	2	-1.9979
451	94254	Wbscr16	Williams-Beuren syndrome chromosome region 16 homolog (human)	0	3	2	-1.99775
452	26893	Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	0	3	2	-1.99656
453	66665	5730528L13Rik	RIKEN cDNA 5730528L13 gene	0	4	1	-1.99611
454	73407	1700055M20Rik	testis, prostate and placenta expressed	0	3	1	-1.99569
455	14784	Grb2	growth factor receptor bound protein 2	0	3	2	-1.99546
456	353234	Pcdha2	protocadherin alpha 2	0	3	2	-1.99326
457	71963	Cdca4	cell division cycle associated 4	0	3	1	-1.99274
458	108800	Ston2	stonin 2	0	3	2	-1.99267
459	101023	Zfp513	zinc finger protein 513	0	5	0	-1.99226
460	64424	Polr1e	polymerase (RNA) I polypeptide E	0	3	2	-1.99174
461	13669	Eif3s10	eukaryotic translation initiation factor 3, subunit A	0	5	0	-1.99088
462	54217	Rpl36	ribosomal protein L36	0	4	1	-1.98968
463	59013	Hnrph1	heterogeneous nuclear ribonucleoprotein H1	0	3	2	-1.98964
464	12048	Bcl2l1	BCL2-like 1	0	3	2	-1.98887
465	14457	Gas7	growth arrest specific 7	0	3	2	-1.98808
466	70575	Gfod2	glucose-fructose oxidoreductase domain containing 2	0	4	1	-1.9875
467	14038	Expi	extracellular proteinase inhibitor	0	3	2	-1.98667
468	258366	Olfr434	olfactory receptor 434	0	3	2	-1.98505
469	13733	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	0	3	2	-1.98472
470	94043	Tm2d1	TM2 domain containing 1	0	3	2	-1.98354
471	170733	Klra17	killer cell lectin-like receptor, subfamily A, member 17	0	3	2	-1.9826
472	66395	Ahnak	AHNAK nucleoprotein (desmoyokin)	0	3	2	-1.98258
473	20499	Slc12a7	solute carrier family 12, member 7	0	3	2	-1.98204
474	73626	1810009J06Rik	RIKEN cDNA 1810009J06 gene	0	3	2	-1.98192
475	233187	Lim2	lens intrinsic membrane protein 2	0	4	1	-1.98095
476	68468	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	0	3	1	-1.98026
477	245866	Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	0	5	0	-1.98011

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
478	104156	Etv5	ets variant gene 5	0	3	2	-1.97886
479	75288	Slc35f4	solute carrier family 35, member F4	0	3	2	-1.97806
480	109552	Sri	sorcin	0	4	1	-1.97795
481	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	0	4	1	-1.97735
482	214254	Nudt15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	0	3	1	-1.97713
483	245074	UNK	NA	0	3	2	-1.97706
484	21762	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	0	3	2	-1.9769
485	50755	Fbxo18	F-box protein 18	0	4	1	-1.97664
486	71446	Wrb	tryptophan rich basic protein	0	4	1	-1.97652
487	11861	Arl4a	ADP-ribosylation factor-like 4A	0	3	2	-1.97626
488	66469	2810405K02Rik	RIKEN cDNA 2810405K02 gene	0	4	1	-1.97569
489	74365	Lonrf3	LON peptidase N-terminal domain and ring finger 3	0	3	2	-1.97499
490	114895	UNK	NA	0	4	1	-1.97388
491	17454	Mov10	Moloney leukemia virus 10	0	3	2	-1.97266
492	329302	UNK	NA	0	4	1	-1.97062
493	435946	LOC435946	predicted gene 5726	0	3	2	-1.9702
494	277010	Marveld1	MARVEL (membrane-associating) domain containing 1	0	3	2	-1.96922
495	259279	Tubgcp3	tubulin, gamma complex associated protein 3	0	3	2	-1.96853
496	233489	Picalm	phosphatidylinositol binding clathrin assembly protein	0	3	2	-1.96836
497	101613	Nalp6	NLR family, pyrin domain containing 6	0	3	1	-1.96654
498	19933	Rpl21	ribosomal protein L21	0	5	0	-1.96531
499	71735	1200011O22Rik	leucine-rich repeats and WD repeat domain containing 1	0	4	1	-1.96512
500	229658	Vangl1	vang-like 1 (van gogh, Drosophila)	0	4	1	-1.96473
501	67731	Fbxo32	F-box protein 32	0	4	1	-1.96465
502	77963	Hook1	hook homolog 1 (Drosophila)	0	3	2	-1.9641
503	27274	Zfp354b	zinc finger protein 354B	0	3	2	-1.96383
504	20630	Snrp1c	U1 small nuclear ribonucleoprotein C	0	4	1	-1.96285
505	107767	Scamp1	secretory carrier membrane protein 1	0	4	1	-1.96096
506	20055	Rps16	ribosomal protein S16	0	3	2	-1.96068
507	434390	UNK	NA	0	3	2	-1.96064
508	12927	Bcar1	breast cancer anti-estrogen resistance 1	0	3	2	-1.96022
509	57267	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	0	5	0	-1.96014
510	229543	Ints3	integrator complex subunit 3	0	4	1	-1.95878
511	66309	Tmem128	transmembrane protein 128	0	5	0	-1.95817
512	75425	2610036D13Rik	TELO2 interacting protein 1	0	3	2	-1.95816
513	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0	3	2	-1.95781
514	258385	Olfr1323	olfactory receptor 1323	0	4	0	-1.95761

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
515	67143	Zfpn1a5	IKAROS family zinc finger 5	0	4	1	-1.95707
516	17533	Mrc1	mannose receptor, C type 1	0	3	2	-1.95706
517	74091	Npl	N-acetylneuraminate pyruvate lyase	0	3	2	-1.95552
518	380660	8430416H19Rik	acyl-CoA synthetase short-chain family member 3	0	3	2	-1.95501
519	233490	Zf	CREB/ATF bZIP transcription factor	0	3	2	-1.95497
520	15378	Hnf4a	hepatic nuclear factor 4, alpha	0	3	2	-1.9548
521	69481	1700029I08Rik	actin-like 9	0	3	2	-1.9544
522	19179	Psmc1	protease (prosome, macropain) 26S subunit, ATPase 1	0	4	1	-1.95331
523	54709	Eif3s2	eukaryotic translation initiation factor 3, subunit I	0	4	1	-1.95324
524	26437	Psg17	pregnancy specific glycoprotein 17	0	3	2	-1.95283
525	18534	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	0	4	1	-1.9526
526	103511	BB146404	family with sequence similarity 26, member E	0	3	2	-1.95214
527	320825	E130306M17Rik	sterile alpha motif domain containing 5	0	3	1	-1.95214
528	64454	Slc5a4b	solute carrier family 5 (neutral amino acid transporters, system A), member 4b	0	3	2	-1.95146
529	12062	Bdkrb2	bradykinin receptor, beta 2	0	4	1	-1.95145
530	11827	Aqp2	aquaporin 2	0	3	2	-1.95132
531	217262	Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	0	3	2	-1.95091
532	13848	Ephb6	Eph receptor B6	0	3	2	-1.95022
533	237436	Gas2l3	growth arrest-specific 2 like 3	0	4	1	-1.94982
534	74424	Tmc5	transmembrane channel-like gene family 5	0	3	2	-1.9498
535	67254	2900011O08Rik	RIKEN cDNA 2900011O08 gene	0	3	2	-1.94908
536	18103	Nme2	non-metastatic cells 2, protein (NM23B) expressed in	0	7	3	-1.94884
537	18174	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	0	3	2	-1.94878
538	78304	Lsmd1	LSM domain containing 1	0	4	1	-1.94864
539	22088	Tsg101	tumor susceptibility gene 101	0	4	1	-1.94828
540	18997	Pou4f2	POU domain, class 4, transcription factor 2	0	3	2	-1.94611
541	66317	Wdr61	WD repeat domain 61	0	4	1	-1.94603
542	100226	Stx12	syntaxin 12	0	3	2	-1.9459
543	18805	Pld1	phospholipase D1	0	3	2	-1.94544
544	27078	Eppb9	B9 protein domain 1	0	5	0	-1.94479
545	93675	Clec2i	C-type lectin domain family 2, member i	0	3	2	-1.94368
546	225264	LOC225264	pyruvate kinase, muscle pseudogene	0	3	2	-1.94306
547	12458	Ccr6	chemokine (C-C motif) receptor 6	0	4	1	-1.94214
548	403183	4832428D23Rik	RIKEN cDNA 4832428D23 gene	0	3	1	-1.94193
549	15408	Hoxb13	homeobox B13	0	3	2	-1.94132
550	72544	Exosc6	exosome component 6	0	3	1	-1.94079
551	230103	Npr2	natriuretic peptide receptor 2	0	5	5	-1.9403

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
552	78444	C330024D12Rik	pyroglutamyl-peptidase I-like	0	3	2	-1.93918
553	67126	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0	3	2	-1.93905
554	319476	Lrtm1	leucine-rich repeats and transmembrane domains 1	0	4	1	-1.93843
555	13681	Eif4a1	eukaryotic translation initiation factor 4A1	0	5	0	-1.9378
556	67710	Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	0	3	2	-1.93766
557	52855	Lair1	leukocyte-associated Ig-like receptor 1	0	3	1	-1.93763
558	18476	Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	0	3	2	-1.93664
559	18740	Pitx1	paired-like homeodomain transcription factor 1	0	4	1	-1.9364
560	56787	Ascl3	achaete-scute complex homolog 3 (Drosophila)	0	4	1	-1.93627
561	30838	Fbxw4	F-box and WD-40 domain protein 4	0	3	1	-1.93605
562	68394	0610037D15Rik	coiled-coil domain containing 163	0	5	0	-1.93533
563	13909	LOC13909	carboxylesterase 3B	0	3	2	-1.935
564	320435	5830482F20Rik	Ras and Rab interactor-like	0	4	1	-1.93497
565	64085	Clstn2	calsyntenin 2	0	3	2	-1.93417
566	20609	Sstr5	somatostatin receptor 5	0	3	2	-1.93344
567	214580	Pstk	phosphoseryl-tRNA kinase	0	3	2	-1.93242
568	16582	Kifc3	kinesin family member C3	0	3	2	-1.93239
569	20813	Srp14	signal recognition particle 14	0	3	2	-1.93199
570	20517	Slc22a1	solute carrier family 22 (organic cation transporter), member 1	0	3	2	-1.93159
571	30853	Mlf2	myeloid leukemia factor 2	0	4	1	-1.93056
572	71966	Nkiras2	NFKB inhibitor interacting Ras-like protein 2	0	3	2	-1.93018
573	239151	Gm600	NA	0	3	2	-1.92923
574	100465	Mobkl2c	MOB kinase activator 3C	0	3	2	-1.92889
575	12613	Cel	carboxyl ester lipase	0	3	2	-1.92809
576	12824	Col2a1	collagen, type II, alpha 1	0	3	2	-1.9279
577	60365	Rbm8a	RNA binding motif protein 8a	0	5	0	-1.92651
578	212647	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	0	4	1	-1.92639
579	11733	Ank1	ankyrin 1, erythroid	0	4	1	-1.92594
580	216285	Cart1	ALX homeobox 1	0	4	1	-1.92505
581	20229	Sat1	spermidine/spermine N1-acetyl transferase 1	0	3	2	-1.9236
582	12475	Cd14	CD14 antigen	0	3	2	-1.92356
583	74763	1200013P24Rik	N-acetyltransferase 15 (GCN5-related, putative)	0	3	2	-1.92312
584	23908	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	0	3	2	-1.92276
585	12804	Cntfr	ciliary neurotrophic factor receptor	0	3	2	-1.92226
586	19046	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	0	3	2	-1.92207
587	53324	Nptx2	neuronal pentraxin 2	0	3	2	-1.92197
588	15115	Hars	histidyl-tRNA synthetase	0	3	2	-1.92145

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
589	12235	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	0	3	2	-1.92133
590	433718	UNK	NA	0	4	1	-1.92012
591	379043	Raet1e	retinoic acid early transcript 1E	0	3	2	-1.91975
592	18976	Pomc1	pro-opiomelanocortin-alpha	0	3	2	-1.91934
593	19089	Prkcsh	protein kinase C substrate 80K-H	0	3	2	-1.91885
594	108052	Slc14a1	solute carrier family 14 (urea transporter), member 1	0	3	2	-1.91821
595	227800	Rabgap1	RAB GTPase activating protein 1	0	3	1	-1.91761
596	381968	UNK	NA	0	3	2	-1.91717
597	11479	Acvr1b	activin A receptor, type 1B	0	4	1	-1.91702
598	435287	UNK	NA	0	4	1	-1.91616
599	23853	Def6	differentially expressed in FDCP 6	0	3	2	-1.91608
600	72552	Hsdl1	hydroxysteroid dehydrogenase like 1	0	3	2	-1.91506
601	16367	Irs1	insulin receptor substrate 1	0	3	2	-1.91464
602	80284	BC003266	cDNA sequence BC003266	0	3	2	-1.91438
603	70359	Gtpbp3	GTP binding protein 3	0	3	2	-1.91416
604	105148	Iars	isoleucine-tRNA synthetase	0	4	1	-1.91386
605	14293	Fpr1	formyl peptide receptor 1	0	3	2	-1.91314
606	26936	AA536749	myosin phosphatase Rho interacting protein	0	3	2	-1.91214
607	17749	Polr2k	polymerase (RNA) II (DNA directed) polypeptide K	0	4	1	-1.91149
608	24075	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	4	6	-1.91072
609	70481	Pnma1	paraneoplastic antigen MA1	0	3	2	-1.91055
610	360214	Defb39	defensin beta 39	0	3	2	-1.91008
611	546631	Gm300	NA	0	3	2	-1.90905
612	226866	Gm106	predicted gene 106	0	3	2	-1.9074
613	109032	5830484A20Rik	Sp110 nuclear body protein	0	3	2	-1.90736
614	15223	Foxj1	forkhead box J1	0	4	1	-1.90732
615	71986	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	0	4	1	-1.90651
616	56194	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	0	5	0	-1.90572
617	54401	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	0	4	1	-1.90556
618	72112	Ppp1r14d	protein phosphatase 1, regulatory (inhibitor) subunit 14D	0	4	1	-1.90551
619	110524	Dgkq	diacylglycerol kinase, theta	0	4	1	-1.90465
620	434496	UNK	NA	0	4	1	-1.90451
621	68135	Eif3s3	eukaryotic translation initiation factor 3, subunit H	0	4	1	-1.90331
622	73677	Psma8	proteasome (prosome, macropain) subunit, alpha type, 8	0	4	1	-1.90322
623	13164	Dazl	deleted in azoospermia-like	0	3	2	-1.90307
624	108911	Rcc2	regulator of chromosome condensation 2	0	3	2	-1.90298
625	381286	Serpinb3c	serine (or cysteine) peptidase inhibitor, clade B, member 3C	0	3	2	-1.90284

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
626	67943	Mesdc2	mesoderm development candidate 2	0	4	0	-1.90192
627	243274	Tmem132d	transmembrane protein 132D	0	3	1	-1.90154
628	380601	C78212	FAST kinase domains 5	0	3	2	-1.90123
629	14208	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	0	3	2	-1.9006
630	66882	Bzw1	basic leucine zipper and W2 domains 1	0	3	2	-1.90029
631	58206	Zbtb32	zinc finger and BTB domain containing 32	0	3	2	-1.90024
632	75721	4932414N04Rik	RIKEN cDNA 4932414N04 gene	0	3	2	-1.89971
633	11807	Apoa2	apolipoprotein A-II	0	3	2	-1.89951
634	245619	UNK	NA	0	3	2	-1.89724
635	11782	Ap4s1	adaptor-related protein complex AP-4, sigma 1	0	4	1	-1.89716
636	320795	Pkn1	protein kinase N1	0	4	0	-1.89628
637	209225	Zfp710	zinc finger protein 710	0	3	2	-1.89624
638	66885	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	0	4	1	-1.89596
639	15504	Dnajb3	DnaJ (Hsp40) homolog, subfamily B, member 3	0	3	2	-1.89573
640	258904	Olfr1221	olfactory receptor 1221	0	4	1	-1.89532
641	18784	Pla2g5	phospholipase A2, group V	0	3	2	-1.89498
642	12715	Ckm	creatine kinase, muscle	0	3	2	-1.89456
643	13406	Dmp1	dentin matrix protein 1	0	4	1	-1.89452
644	71904	Paqr7	progestin and adipoQ receptor family member VII	0	5	0	-1.89412
645	74133	1200011M11Rik	RIKEN cDNA 1200011M11 gene	0	4	1	-1.89191
646	381813	Prmt8	protein arginine N-methyltransferase 8	0	3	2	-1.89131
647	56717	Frap1	mechanistic target of rapamycin (serine/threonine kinase)	0	4	6	-1.89038
648	328752	UNK	NA	0	3	2	-1.89009
649	67030	Fancl	Fanconi anemia, complementation group L	0	4	1	-1.88983
650	15463	Hrb	ArfGAP with FG repeats 1	0	3	2	-1.88948
651	18120	Mrpl49	mitochondrial ribosomal protein L49	0	3	2	-1.88939
652	98363	Efhd1	EF hand domain containing 1	0	4	1	-1.88927
653	216616	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	0	3	2	-1.8892
654	110532	Adarb1	adenosine deaminase, RNA-specific, B1	0	3	1	-1.88919
655	19735	Rgs2	regulator of G-protein signaling 2	0	3	7	-1.88904
656	12015	Bad	BCL2-associated agonist of cell death	0	3	2	-1.88782
657	56336	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	0	3	2	-1.88779
658	216019	Hkdc1	hexokinase domain containing 1	0	5	0	-1.88732
659	433995	UNK	NA	0	3	2	-1.88719
660	14171	Fgf17	fibroblast growth factor 17	0	4	0	-1.88717
661	171194	V1rc21	vomeronasal 1 receptor 4	0	3	2	-1.88685
662	56040	Rplp1	ribosomal protein, large, P1	0	3	2	-1.88674

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
663	19268	Ptprf	protein tyrosine phosphatase, receptor type, F	0	4	1	-1.88565
664	75185	4930542N07Rik	RIKEN cDNA 4930542N07 gene	0	3	1	-1.88539
665	243377	Svs1	seminal vesicle secretory protein 1	0	4	1	-1.88507
666	209131	Snx30	sorting nexin family member 30	0	3	2	-1.88481
667	11568	Aebp1	AE binding protein 1	0	4	6	-1.8843
668	258450	Olfr1199	olfactory receptor 1199	0	3	2	-1.88421
669	54197	Rnf5	ring finger protein 5	0	4	1	-1.88412
670	76804	Jmjd2c	lysine (K)-specific demethylase 4C	0	3	2	-1.88391
671	215890	A330019N05Rik	clavesin 2	0	3	2	-1.88371
672	320640	9530098N22Rik	selection and upkeep of intraepithelial T cells 4	0	3	1	-1.88335
673	15557	Htr1f	5-hydroxytryptamine (serotonin) receptor 1F	0	3	2	-1.88315
674	19062	RP23-136K12.4	inositol polyphosphate 5-phosphatase K	0	3	2	-1.88184
675	11982	Atp10a	ATPase, class V, type 10A	0	3	2	-1.88118
676	14651	Hagh	hydroxyacyl glutathione hydrolase	0	4	1	-1.8809
677	18096	Nkx6-1	NK6 homeobox 1	0	3	2	-1.88052
678	14394	Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	0	4	0	-1.88037
679	66089	Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	0	3	2	-1.88002
680	67445	C1qtnf4	C1q and tumor necrosis factor related protein 4	0	3	2	-1.87958
681	171095	Il17rc	interleukin 17 receptor C	0	3	2	-1.87947
682	21976	Top3b	topoisomerase (DNA) III beta	0	3	2	-1.87936
683	69282	1700001J03Rik	RIKEN cDNA 1700001J03 gene	0	3	2	-1.87896
684	381971	UNK	NA	0	3	2	-1.87889
685	73534	1700082M22Rik	RIKEN cDNA 1700082M22 gene	0	3	2	-1.87804
686	20167	Rtn2	reticulon 2 (Z-band associated protein)	0	3	2	-1.87755
687	66622	5730410I19Rik	ubiquitin protein ligase E3 component n-recognin 7 (putative)	0	4	0	-1.87738
688	21872	Tjp1	tight junction protein 1	0	3	2	-1.87538
689	53951	2310002B06Rik	coiled-coil domain containing 75	0	3	2	-1.87515
690	13007	Csrp1	cysteine and glycine-rich protein 1	0	3	2	-1.87472
691	78249	Gpr115	G protein-coupled receptor 115	0	3	2	-1.87316
692	242109	Zfp697	zinc finger protein 697	0	4	1	-1.87208
693	69787	Anxa13	annexin A13	0	5	0	-1.87164
694	69537	Dnase1l1	deoxyribonuclease 1-like 1	0	3	2	-1.87101
695	66244	Sdccag1	nuclear export mediator factor	0	3	2	-1.87003
696	20588	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	0	4	1	-1.86982
697	17768	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrola	0	3	2	-1.86903
698	11499	Adam5	a disintegrin and metallopeptidase domain 5	0	3	2	-1.86898
699	213649	Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	0	3	2	-1.86754

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
700	227683	Coq4	coenzyme Q4 homolog (yeast)	0	4	1	-1.86726
701	73103	3110009E18Rik	RIKEN cDNA 3110009E18 gene	0	3	1	-1.86722
702	18041	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	0	4	1	-1.86722
703	13492	Drd5	dopamine receptor D5	0	3	2	-1.86672
704	72947	2900006B13Rik	alanine-glyoxylate aminotransferase 2-like 2	0	3	2	-1.86649
705	383100	UNK	NA	0	3	2	-1.86636
706	12070	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	0	3	2	-1.86618
707	102626	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0	3	7	-1.86546
708	258374	Olfr127	olfactory receptor 127	0	3	1	-1.86537
709	69876	Thap3	THAP domain containing, apoptosis associated protein 3	0	3	1	-1.86475
710	103142	Rdh9	retinol dehydrogenase 9	0	4	1	-1.86428
711	28113	Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	0	3	2	-1.86384
712	16511	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0	4	1	-1.86335
713	383458	UNK	NA	0	3	2	-1.86257
714	11836	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	0	4	6	-1.86252
715	328547	A830008O07Rik	NA	0	3	2	-1.86233
716	72978	Cnih3	cornichon homolog 3 (Drosophila)	0	3	2	-1.86192
717	103844	AI842396	inhibitor of CDK, cyclin A1 interacting protein 1	0	3	2	-1.86034
718	67334	1700054O13Rik	RIKEN cDNA 1700054O13 gene	0	4	1	-1.86023
719	259083	Olfr547	olfactory receptor 547	0	3	1	-1.86009
720	74781	Wipi2	WD repeat domain, phosphoinositide interacting 2	0	3	1	-1.85955
721	15039	H2-T22	histocompatibility 2, T region locus 22	0	4	1	-1.85939
722	67204	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	0	3	2	-1.85873
723	75627	Snapc1	small nuclear RNA activating complex, polypeptide 1	0	5	0	-1.85789
724	18706	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0	3	2	-1.85785
725	258456	Olfr1196	olfactory receptor 1196	0	3	2	-1.85694
726	14600	Ghr	growth hormone receptor	0	3	2	-1.85638
727	434777	UNK	NA	0	4	1	-1.8561
728	64652	Nisch	nischarin	0	3	2	-1.85593
729	55944	Eif3s7	eukaryotic translation initiation factor 3, subunit D	0	4	0	-1.85477
730	70375	Ica1l	islet cell autoantigen 1-like	0	3	2	-1.85435
731	382741	UNK	NA	0	3	2	-1.85412
732	209380	LOC209380	GTPase, very large interferon inducible 1 pseudogene	0	3	1	-1.85385
733	77579	Myh10	myosin, heavy polypeptide 10, non-muscle	0	3	2	-1.85374
734	52683	D15Ertd785e	non-SMC condensin II complex, subunit H2	0	3	2	-1.85311
735	384814	LOC384814	predicted gene 5347	0	4	1	-1.85305
736	74025	Nphp3	nephronophthisis 3 (adolescent)	0	3	2	-1.85262

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
737	12671	Chrm3	cholinergic receptor, muscarinic 3, cardiac	0	4	1	-1.85183
738	22601	Yap1	yes-associated protein 1	0	5	0	-1.85117
739	21859	Timp3	tissue inhibitor of metalloproteinase 3	0	3	2	-1.85086
740	72345	2810002O09Rik	family with sequence similarity 123, member B	0	4	1	-1.85078
741	20602	Ncor2	nuclear receptor co-repressor 2	0	3	2	-1.84995
742	77432	9530002B09Rik	RIKEN cDNA 9530002B09 gene	0	3	2	-1.84943
743	19892	Rpe65	retinal pigment epithelium 65	0	3	2	-1.84897
744	53896	Slc7a10	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10	0	3	2	-1.84897
745	71900	Tmem106b	transmembrane protein 106B	0	3	2	-1.84889
746	258601	Olfr984	olfactory receptor 984	0	3	2	-1.84854
747	66557	Bpil1	BPI fold containing family B, member 2	0	4	1	-1.84829
748	245841	Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	0	4	1	-1.84813
749	215632	Psd4	pleckstrin and Sec7 domain containing 4	0	3	2	-1.8481
750	258991	Olfr1496	olfactory receptor 1496	0	3	2	-1.8474
751	244672	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	0	3	2	-1.84649
752	76653	1700121K02Rik	chibby homolog 3 (Drosophila)	0	3	2	-1.84567
753	17882	Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	0	3	2	-1.84495
754	320558	4930518F03Rik	synaptonemal complex protein 2	0	3	1	-1.84429
755	102857	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0	3	2	-1.84338
756	103172	Ndg2	coiled-coil-helix-coiled-coil-helix domain containing 10	0	3	1	-1.8432
757	18952	39328	septin 4	0	3	2	-1.84281
758	67015	Ccdc91	coiled-coil domain containing 91	0	3	2	-1.84273
759	23882	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	0	4	1	-1.84255
760	238463	Tubal3	tubulin, alpha-like 3	0	3	2	-1.84231
761	109093	Rarsl	arginyl-tRNA synthetase 2, mitochondrial	0	4	1	-1.84203
762	56513	Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. elegans)	0	3	2	-1.8419
763	384894	UNK	NA	0	3	2	-1.84177
764	11910	Atf3	activating transcription factor 3	0	3	2	-1.84148
765	14944	Gzmg	granzyme G	0	4	1	-1.84112
766	17183	Matn4	matrilin 4	0	3	2	-1.8404
767	78689	Mak10	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	0	3	1	-1.8403
768	67302	Zc3h13	zinc finger CCCH type containing 13	0	3	2	-1.84027
769	72125	2600011E07Rik	family with sequence similarity 123, member A	0	3	1	-1.83901
770	67248	Rpl39	ribosomal protein L39	0	4	1	-1.83896
771	27356	Insl6	insulin-like 6	0	3	2	-1.8389
772	56210	Rev1l	REV1 homolog (S. cerevisiae)	0	3	2	-1.8384
773	20591	Jarid1c	lysine (K)-specific demethylase 5C	0	3	2	-1.83803

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
774	208583	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	0	3	2	-1.83798
775	52392	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	0	3	2	-1.8371
776	16825	Ldb1	LIM domain binding 1	0	3	2	-1.83638
777	19340	Rab3d	RAB3D, member RAS oncogene family	0	3	2	-1.83508
778	258657	Olfr733	olfactory receptor 733	0	3	2	-1.83481
779	79560	Ublcp1	ubiquitin-like domain containing CTD phosphatase 1	0	3	2	-1.83447
780	67383	2410127L17Rik	RIKEN cDNA 2410127L17 gene	0	3	2	-1.83403
781	60504	Il21r	interleukin 21 receptor	0	3	2	-1.83351
782	83434	Rshl1	radial spoke head 6 homolog A (Chlamydomonas)	0	3	1	-1.83349
783	81907	Tmem108	transmembrane protein 108	0	3	2	-1.83328
784	15932	Idua	iduronidase, alpha-L-	0	4	0	-1.83309
785	75188	1700009J07Rik	RIKEN cDNA 1700009J07 gene	0	3	2	-1.83304
786	382075	Odf3l1	outer dense fiber of sperm tails 3-like 1	0	3	1	-1.83279
787	109978	Art4	ADP-ribosyltransferase 4	0	3	2	-1.83201
788	69305	Dcps	decapping enzyme, scavenger	0	3	1	-1.83192
789	66589	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	0	3	2	-1.83191
790	22642	Zbtb17	zinc finger and BTB domain containing 17	0	4	1	-1.83145
791	17843	Mup4	major urinary protein 4	0	4	1	-1.83107
792	77683	Ehmt1	euchromatic histone methyltransferase 1	0	3	2	-1.83065
793	102680	Xtrp3s1	solute carrier family 6 (neurotransmitter transporter), member 20A	0	3	2	-1.83054
794	216161	Stno	strawberry notch homolog 2 (Drosophila)	0	3	2	-1.83029
795	66629	Golph3	golgi phosphoprotein 3	0	3	2	-1.83007
796	109115	Supt3h	suppressor of Ty 3 homolog (S. cerevisiae)	0	3	2	-1.82888
797	67320	Iqcf4	IQ motif containing F4	0	3	2	-1.82882
798	435477	UNK	NA	0	4	1	-1.82847
799	69207	Sfrs11	serine/arginine-rich splicing factor 11	0	4	1	-1.82823
800	16912	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	0	3	2	-1.82772
801	13819	Epas1	endothelial PAS domain protein 1	0	3	2	-1.82763
802	627468	UNK	NA	0	3	2	-1.82565
803	22698	Zfp39	zinc finger protein 39	0	3	2	-1.82504
804	20196	S100a13	S100 calcium binding protein A13	0	4	1	-1.82481
805	73481	1700074P13Rik	RIKEN cDNA 1700074P13 gene	0	3	2	-1.82424
806	381815	UNK	NA	0	4	0	-1.82421
807	70031	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	0	4	1	-1.82401
808	26414	Mapk10	mitogen-activated protein kinase 10	0	3	2	-1.82355
809	57294	Rps27	ribosomal protein S27	0	4	1	-1.82314
810	12044	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a	0	3	2	-1.82299

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
811	11625	Ahsg	alpha-2-HS-glycoprotein	0	3	2	-1.82257
812	14862	Gstm1	glutathione S-transferase, mu 1	0	3	2	-1.82214
813	19921	Rpl19	ribosomal protein L19	0	5	0	-1.82193
814	13649	Egfr	epidermal growth factor receptor	0	3	7	-1.82167
815	67980	Gnpda2	glucosamine-6-phosphate deaminase 2	0	3	2	-1.82154
816	16580	Kifc1	kinesin family member C5B	0	3	7	-1.82137
817	72195	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	0	3	1	-1.82111
818	54126	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	0	3	2	-1.82072
819	15116	Has1	hyaluronan synthase1	0	3	2	-1.82066
820	258351	Olfr633	olfactory receptor 633	0	3	1	-1.82006
821	78076	Lcn8	lipocalin 8	0	3	2	-1.81976
822	11670	Aldh3a1	aldehyde dehydrogenase family 3, subfamily A1	0	3	2	-1.81939
823	64945	Cldn12	claudin 12	0	3	2	-1.81908
824	73016	Kremen2	kringle containing transmembrane protein 2	0	3	2	-1.81858
825	16994	Ltb	lymphotoxin B	0	3	2	-1.81807
826	56357	Ivd	isovaleryl coenzyme A dehydrogenase	0	3	2	-1.81752
827	20527	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	0	4	1	-1.81656
828	15078	H3f3a	H3 histone, family 3A	0	5	0	-1.8163
829	240913	Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	0	4	1	-1.81571
830	59056	Evc	Ellis van Creveld gene homolog (human)	0	4	1	-1.81523
831	435267	UNK	NA	0	3	2	-1.81449
832	107686	Snrpd2	small nuclear ribonucleoprotein D2	0	3	2	-1.81424
833	11444	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	0	4	1	-1.8142
834	13067	Cyct	cytochrome c, testis	0	3	2	-1.8128
835	244448	BC050188	tripartite motif family-like 1	0	3	2	-1.81208
836	11852	Rhob	ras homolog gene family, member B	0	3	2	-1.81154
837	15228	Foxg1	forkhead box G1	0	3	2	-1.81141
838	328424	Kcnrg	potassium channel regulator	0	4	1	-1.81139
839	99296	Hrh3	histamine receptor H3	0	3	2	-1.8111
840	16447	Ivl	involucrin	0	3	2	-1.81092
841	268301	C820004L04Rik	sosondowah ankyrin repeat domain family member C	0	5	0	-1.81031
842	26427	Creb3l1	cAMP responsive element binding protein 3-like 1	0	3	2	-1.80939
843	74412	Gle1l	GLE1 RNA export mediator (yeast)	0	4	1	-1.80752
844	20587	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	0	3	2	-1.80697
845	66066	Gng11	guanine nucleotide binding protein (G protein), gamma 11	0	3	2	-1.80696
846	18712	Pim1	proviral integration site 1	0	3	2	-1.80687
847	27369	Dguok	deoxyguanosine kinase	0	3	2	-1.80642

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
848	64294	Itm2c	integral membrane protein 2C	0	4	1	-1.80584
849	14263	Fmo5	flavin containing monooxygenase 5	0	3	2	-1.8058
850	12660	Chka	choline kinase alpha	0	4	1	-1.80543
851	243834	Zfp324	zinc finger protein 324	0	3	2	-1.80534
852	17381	Mmp12	matrix metallopeptidase 12	0	4	5	-1.80503
853	21892	Tll1	tolloid-like	0	4	1	-1.80468
854	66513	Map3k7ip1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	0	3	2	-1.80453
855	100647	Upk3b	uroplakin 3B	0	3	2	-1.80443
856	75291	Zbtb3	zinc finger and BTB domain containing 3	0	3	2	-1.80373
857	320869	4732415M23Rik	RIKEN cDNA 4732415M23 gene	0	4	0	-1.80357
858	67974	5730405I09Rik	cyclin Y	0	4	1	-1.80332
859	217012	Unc45b	unc-45 homolog B (C. elegans)	0	3	2	-1.80303
860	26938	St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltran	0	3	2	-1.80274
861	269966	Nup98	nucleoporin 98	0	4	0	-1.80258
862	142681	Slc34a3	solute carrier family 34 (sodium phosphate), member 3	0	3	2	-1.80212
863	269261	Rpl12	ribosomal protein L12	0	5	0	-1.80186
864	19361	Rad51	RAD51 homolog (S. cerevisiae)	0	5	0	-1.80057
865	53945	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	0	3	2	-1.79991
866	213019	Pdlim2	PDZ and LIM domain 2	0	3	2	-1.79958
867	56290	Prp15	NA	0	3	2	-1.79914
868	53415	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	0	5	0	-1.79859
869	17695	Msmb	beta-microseminoprotein	0	4	0	-1.79847
870	14972	H2-K1	histocompatibility 2, K1, K region	0	3	2	-1.79847
871	70676	Gulp1	GULP, engulfment adaptor PTB domain containing 1	0	3	2	-1.79708
872	54483	Mefv	Mediterranean fever	0	3	2	-1.79605
873	50721	Sirt6	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	0	3	2	-1.79479
874	26444	Psma7	proteasome (prosome, macropain) subunit, alpha type 7	0	3	2	-1.79433
875	19886	Ros1	Ros1 proto-oncogene	0	3	7	-1.79425
876	17691	Snf1lk	salt inducible kinase 1	0	4	1	-1.79404
877	238393	Serpina3f	serine (or cysteine) peptidase inhibitor, clade A, member 3F	0	4	1	-1.79371
878	18781	Pla2g2c	phospholipase A2, group IIC	0	3	2	-1.79345
879	18606	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0	3	2	-1.79314
880	319655	Podxl2	podocalyxin-like 2	0	3	2	-1.79218
881	77976	Nuak1	NUAK family, SNF1-like kinase, 1	0	4	1	-1.79213
882	28077	D13Wsu50e	mediator of RNA polymerase II transcription, subunit 10 homolog (NUT2, S. cerevisiae)	0	5	0	-1.79008
883	434655	UNK	NA	0	3	1	-1.78974
884	12372	Casq1	calsequestrin 1	0	3	2	-1.78957

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
885	229309	UNK	NA	0	3	2	-1.78913
886	26946	Trpc7	transient receptor potential cation channel, subfamily C, member 7	0	3	2	-1.78901
887	22361	Vnn1	vanin 1	0	3	2	-1.78847
888	22282	Usf2	upstream transcription factor 2	0	3	2	-1.78796
889	26992	Brd7	bromodomain containing 7	0	3	2	-1.78756
890	58859	Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	0	3	2	-1.78712
891	319520	Dusp4	dual specificity phosphatase 4	0	4	1	-1.78695
892	116810	Foxn4	forkhead box N4	0	4	1	-1.78666
893	383507	UNK	NA	0	3	2	-1.78596
894	21678	Tead3	TEA domain family member 3	0	3	2	-1.78449
895	329278	Tnn	tenascin N	0	3	2	-1.78425
896	21946	Pglyrp1	peptidoglycan recognition protein 1	0	4	1	-1.78414
897	18570	Pdcd6	programmed cell death 6	0	3	2	-1.78373
898	235587	Parp3	poly (ADP-ribose) polymerase family, member 3	0	3	2	-1.78341
899	65086	Edg7	lysophosphatidic acid receptor 3	0	3	2	-1.78329
900	74335	Xrcc3	X-ray repair complementing defective repair in Chinese hamster cells 3	0	3	2	-1.78325
901	217030	Ap1gbp1	synergin, gamma	0	3	2	-1.78316
902	67891	Rpl4	ribosomal protein L4	0	5	0	-1.78292
903	100088	Rcc1	regulator of chromosome condensation 1	0	3	2	-1.78283
904	14120	Fbp2	fructose bisphosphatase 2	0	3	2	-1.78279
905	20863	Stfa3	stefin A3	0	3	2	-1.78158
906	76943	2310020A21Rik	prosaposin-like 1	0	3	2	-1.78156
907	12623	Ces1	carboxylesterase 1G	0	3	2	-1.78058
908	106759	Ticam1	toll-like receptor adaptor molecule 1	0	3	2	-1.78054
909	214968	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	0	3	2	-1.78029
910	65079	Rtn4r	reticulon 4 receptor	0	4	1	-1.78019
911	380839	Serpinb1c	serine (or cysteine) peptidase inhibitor, clade B, member 1c	0	3	2	-1.7798
912	22034	Traf6	TNF receptor-associated factor 6	0	3	2	-1.77968
913	16011	Igfbp5	insulin-like growth factor binding protein 5	0	3	2	-1.77822
914	194597	Tmprss11a	transmembrane protease, serine 11a	0	3	2	-1.77812
915	17152	Mak	male germ cell-associated kinase	0	3	1	-1.77733
916	20302	Ccl3	chemokine (C-C motif) ligand 3	0	3	2	-1.77679
917	109229	C030004A17Rik	family with sequence similarity 118, member B	0	3	2	-1.7767
918	12983	Csf2rb1	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0	4	1	-1.77639
919	17535	Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	0	4	1	-1.77639
920	13498	Atn1	atrophin 1	0	3	2	-1.77604
921	26386	Hsf4	heat shock transcription factor 4	0	5	0	-1.77597

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
922	18317	Olfr2	olfactory receptor 2	0	3	2	-1.77557
923	74277	Chic2	cysteine-rich hydrophobic domain 2	0	4	1	-1.77555
924	217337	Srp68	signal recognition particle 68	0	4	1	-1.77521
925	114584	Clic1	chloride intracellular channel 1	0	3	2	-1.77494
926	15229	Foxd1	forkhead box D1	0	4	0	-1.77471
927	214531	Tmprss13	transmembrane protease, serine 13	0	3	2	-1.77454
928	13842	Epha8	Eph receptor A8	0	3	2	-1.77417
929	56418	Ykt6	YKT6 homolog (S. Cerevisiae)	0	3	2	-1.77399
930	216516	4930562D19Rik	coiled-coil domain containing 157	0	3	1	-1.77381
931	209378	Itih5	inter-alpha (globulin) inhibitor H5	0	3	2	-1.77341
932	17261	Mef2d	myocyte enhancer factor 2D	0	3	2	-1.77198
933	226040	E030010A14Rik	RIKEN cDNA E030010A14 gene	0	3	2	-1.77141
934	68401	G6pc3	glucose 6 phosphatase, catalytic, 3	0	3	2	-1.77108
935	68777	Tmem53	transmembrane protein 53	0	3	1	-1.77096
936	71988	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0	3	2	-1.77091
937	26942	Spag1	sperm associated antigen 1	0	3	2	-1.76982
938	320995	Rfxdc1	regulatory factor X, 6	0	3	2	-1.76912
939	18148	Npm1	nucleophosmin 1	0	3	2	-1.76877
940	59024	Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	0	4	1	-1.76845
941	76646	1700123D08Rik	WD repeat domain 38	0	3	1	-1.76746
942	16797	Lat	linker for activation of T cells	0	3	2	-1.7661
943	381113	Cdkl4	cyclin-dependent kinase-like 4	0	4	1	-1.76553
944	320581	4833405L16Rik	isopentenyl-diphosphate delta isomerase 2	0	3	2	-1.76452
945	21784	Tff1	trefoil factor 1	0	3	2	-1.76447
946	108097	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0	3	2	-1.76329
947	56856	Insm2	insulinoma-associated 2	0	3	2	-1.76235
948	17826	Mtvr2	family with sequence similarity 89, member B	0	3	2	-1.76213
949	52513	Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	0	3	2	-1.762
950	99045	Mrps26	mitochondrial ribosomal protein S26	0	4	1	-1.76157
951	14148	Fdx1	ferredoxin 1	0	4	1	-1.76147
952	19982	Rpl36a	ribosomal protein L36A	0	3	2	-1.76136
953	380768	Gm1568	predicted gene 1568	0	3	1	-1.76113
954	78891	Scyl1	SCY1-like 1 (S. cerevisiae)	0	3	1	-1.76099
955	71111	Gpr39	G protein-coupled receptor 39	0	4	1	-1.76096
956	217995	Heatr1	HEAT repeat containing 1	0	4	0	-1.76036
957	108147	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	0	4	1	-1.75988
958	20818	Srprb	signal recognition particle receptor, B subunit	0	3	2	-1.75987

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
959	70616	Sf4	SURP and G patch domain containing 1	0	5	0	-1.75914
960	73804	Kif2c	kinesin family member 2C	0	3	2	-1.75911
961	13134	Dach1	dachshund 1 (Drosophila)	0	4	1	-1.75896
962	78634	1700094C09Rik	sperm acrosome associated 7	0	3	2	-1.75763
963	194952	Jmjd4	jumonji domain containing 4	0	3	2	-1.75755
964	17191	Mbd2	methyl-CpG binding domain protein 2	0	3	2	-1.75685
965	140887	Lnx2	ligand of numb-protein X 2	0	3	2	-1.75656
966	11435	Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	0	3	2	-1.75642
967	12181	Bop1	block of proliferation 1	0	5	0	-1.75547
968	264895	BC018371	acyl-CoA synthetase family member 2	0	3	2	-1.7543
969	13615	Edn2	endothelin 2	0	3	2	-1.75413
970	51801	Ramp1	receptor (calcitonin) activity modifying protein 1	0	3	2	-1.75367
971	268294	Zbtb24	zinc finger and BTB domain containing 24	0	3	2	-1.75312
972	20054	Rps15	ribosomal protein S15	0	5	0	-1.75298
973	56289	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	0	5	0	-1.7522
974	13393	Dlx3	distal-less homeobox 3	0	5	0	-1.75207
975	70839	P2ry12	purinergic receptor P2Y, G-protein coupled 12	0	3	2	-1.75186
976	26440	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	0	3	2	-1.75098
977	64660	Mrps24	mitochondrial ribosomal protein S24	0	4	1	-1.75091
978	21846	Tie1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	0	3	2	-1.74924
979	18599	Padi1	peptidyl arginine deiminase, type I	0	3	2	-1.74891
980	19344	Rab5b	RAB5B, member RAS oncogene family	0	4	1	-1.74854
981	243529	H1fx	H1 histone family, member X	0	3	2	-1.74751
982	211924	Dsg1c	desmoglein 1 gamma	0	3	2	-1.74731
983	68272	Rbm28	RNA binding motif protein 28	0	3	2	-1.74716
984	404473	Olfr1082	olfactory receptor 1082	0	3	1	-1.74697
985	23966	Odz4	odd Oz/ten-m homolog 4 (Drosophila)	0	3	2	-1.74673
986	17979	Ncoa3	nuclear receptor coactivator 3	0	4	1	-1.74585
987	56188	Fxyd1	FXYD domain-containing ion transport regulator 1	0	3	2	-1.74542
988	234582	Ccdc102a	coiled-coil domain containing 102A	0	3	2	-1.74532
989	228787	Xkr7	X Kell blood group precursor related family member 7 homolog	0	3	2	-1.74518
990	14585	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	0	3	2	-1.74504
991	231002	Plekhn1	pleckstrin homology domain containing, family N member 1	0	3	2	-1.74503
992	17938	Naca	nascent polypeptide-associated complex alpha polypeptide	0	4	1	-1.74487
993	66258	Mrps17	mitochondrial ribosomal protein S17	0	3	2	-1.74357
994	21885	Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	0	5	0	-1.7434
995	385356	LOC385356	actin, gamma, cytoplasmic 1 pseudogene	0	3	2	-1.74297

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
996	68038	3110023E09Rik	chitinase domain containing 1	0	3	1	-1.74149
997	18821	Pln	phospholamban	0	4	1	-1.74108
998	381075	Gm936	NA	0	3	2	-1.74103
999	11603	Agrn	agrin	0	4	1	-1.74095
1000	104479	BC018601	coiled-coil domain containing 117	0	3	1	-1.74013
1001	327956	Vmo1	vitelline membrane outer layer 1 homolog (chicken)	0	3	2	-1.73947
1002	231863	Fbxl18	F-box and leucine-rich repeat protein 18	0	3	2	-1.73907
1003	19378	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	0	4	0	-1.73799
1004	75497	1700008G05Rik	fatty acid binding protein 12	0	3	2	-1.73781
1005	12467	Cct6b	chaperonin containing Tcp1, subunit 6b (zeta)	0	3	2	-1.73778
1006	227715	Exosc2	exosome component 2	0	4	1	-1.73716
1007	93898	Lass1	LAG1 homolog, ceramide synthase 1	0	3	2	-1.73707
1008	224836	Usp49	ubiquitin specific peptidase 49	0	4	1	-1.73683
1009	68183	Bcas2	breast carcinoma amplified sequence 2	0	3	2	-1.73675
1010	69833	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	0	3	2	-1.7366
1011	13046	Cugbp1	CUGBP, Elav-like family member 1	0	3	2	-1.73653
1012	380676	Gm1872	NA	0	4	1	-1.73641
1013	75212	Rnf121	ring finger protein 121	0	3	2	-1.73566
1014	11642	Akap3	A kinase (PRKA) anchor protein 3	0	3	2	-1.73565
1015	110648	Lmx1a	LIM homeobox transcription factor 1 alpha	0	4	1	-1.73547
1016	17222	Anapc1	anaphase promoting complex subunit 1	0	4	1	-1.73532
1017	208372	Asb18	ankyrin repeat and SOCS box-containing 18	0	3	2	-1.73506
1018	237958	4933407P14Rik	RIKEN cDNA 4933407P14 gene	0	4	1	-1.73506
1019	170759	Atp13a1	ATPase type 13A1	0	3	2	-1.73489
1020	16419	Itgb5	integrin beta 5	0	4	1	-1.73471
1021	75608	Chmp4b	charged multivesicular body protein 4B	0	3	2	-1.73467
1022	103149	Upb1	ureidopropionase, beta	0	3	2	-1.73441
1023	11475	Acta2	actin, alpha 2, smooth muscle, aorta	0	3	2	-1.7343
1024	21958	Tnp1	transition protein 1	0	3	2	-1.73412
1025	18974	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	0	3	2	-1.73405
1026	70425	Csnk1g3	casein kinase 1, gamma 3	0	3	2	-1.73334
1027	106877	AI173486	actin filament associated protein 1-like 1	0	4	1	-1.73282
1028	435625	UNK	NA	0	4	1	-1.73229
1029	66585	Wdr57	small nuclear ribonucleoprotein 40 (U5)	0	3	2	-1.73209
1030	22215	Ube3a	ubiquitin protein ligase E3A	0	3	2	-1.73127
1031	170738	Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	0	3	2	-1.73099
1032	20878	Aurka	aurora kinase A	0	3	2	-1.7309

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1033	74074	4933405I11Rik	NA	0	3	2	-1.73072
1034	67425	Eps8l1	EPS8-like 1	0	3	2	-1.73048
1035	113855	V1rb7	vomeronasal 1 receptor 40	0	3	2	-1.73009
1036	13388	Dll1	delta-like 1 (Drosophila)	0	3	2	-1.72959
1037	73390	1700060H10Rik	male-specific lethal 3-like 2 (Drosophila)	0	3	2	-1.72913
1038	381937	LOC381937	predicted gene 5157	0	3	2	-1.72913
1039	243764	Chrm2	cholinergic receptor, muscarinic 2, cardiac	0	4	1	-1.729
1040	64074	Smoc2	SPARC related modular calcium binding 2	0	3	2	-1.72868
1041	20907	Stx1a	syntaxin 1A (brain)	0	3	2	-1.72867
1042	18710	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	0	3	2	-1.72744
1043	17180	Matn1	matrilin 1, cartilage matrix protein	0	3	2	-1.72743
1044	13821	Epb4.1l1	erythrocyte protein band 4.1-like 1	0	3	2	-1.72715
1045	66322	1700011A15Rik	RIKEN cDNA 1700011A15 gene	0	3	2	-1.72692
1046	237934	4732494G06Rik	keratin 39	0	3	2	-1.72681
1047	19894	Rph3a	rabphilin 3A	0	3	2	-1.72618
1048	22123	Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	0	3	2	-1.72567
1049	72155	2610510J17Rik	centromere protein N	0	3	1	-1.7256
1050	22401	Wig1	zinc finger matrin type 3	0	3	2	-1.7251
1051	12994	Csnk	casein kappa	0	3	1	-1.72477
1052	14735	Gpc4	glypican 4	0	3	2	-1.72415
1053	13801	Enam	enamelin	0	3	2	-1.72403
1054	105348	Golph2	golgi membrane protein 1	0	3	2	-1.72358
1055	13476	Reep5	receptor accessory protein 5	0	3	2	-1.72356
1056	17347	Mknk2	MAP kinase-interacting serine/threonine kinase 2	0	3	2	-1.7232
1057	433406	LOC433406	predicted gene 13363	0	4	1	-1.72291
1058	52440	Tax1bp1	Tax1 (human T cell leukemia virus type I) binding protein 1	0	3	2	-1.72283
1059	22230	Ufd1l	ubiquitin fusion degradation 1 like	0	3	2	-1.72276
1060	12683	Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	0	3	1	-1.72262
1061	14427	Galr1	galanin receptor 1	0	3	2	-1.72244
1062	229049	1700003N22Rik	NA	0	4	1	-1.72172
1063	20526	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	0	3	2	-1.72164
1064	224630	Bnip1	BCL2/adenovirus E1B interacting protein 1	0	3	2	-1.72153
1065	66071	Ethe1	ethylmalonic encephalopathy 1	0	3	2	-1.72093
1066	72440	5930416I19Rik	RIKEN cDNA 5930416I19 gene	0	3	2	-1.7204
1067	67405	Nts	neurotensin	0	3	2	-1.72008
1068	14043	Ext2	exostoses (multiple) 2	0	3	2	-1.72007
1069	72508	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	0	3	2	-1.7199

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1070	432889	UNK	NA	0	3	2	-1.71957
1071	71911	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	0	3	2	-1.71936
1072	217845	1810023F06Rik	interferon, alpha-inducible protein 27 like 2B	0	3	2	-1.71836
1073	20264	Scn10a	sodium channel, voltage-gated, type X, alpha	0	3	2	-1.71787
1074	11513	Adcy7	adenylate cyclase 7	0	3	2	-1.71745
1075	18431	p	oculocutaneous albinism II	0	4	1	-1.71725
1076	380655	UNK	NA	0	4	1	-1.71715
1077	66713	Actr2	ARP2 actin-related protein 2 homolog (yeast)	0	4	1	-1.71686
1078	19275	Ptprn	protein tyrosine phosphatase, receptor type, N	0	4	1	-1.71648
1079	170828	Vgll1	vestigial like 1 homolog (Drosophila)	0	3	2	-1.71646
1080	67623	Tm7sf3	transmembrane 7 superfamily member 3	0	3	2	-1.71606
1081	16658	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	0	4	1	-1.71515
1082	381680	BC055004	cDNA sequence BC055004	0	4	1	-1.71383
1083	65107	Lrp10	low-density lipoprotein receptor-related protein 10	0	3	2	-1.71325
1084	18636	Cfp	complement factor properdin	0	3	1	-1.7131
1085	232969	2410005H09Rik	zinc finger protein 428	0	3	1	-1.71285
1086	16518	Kcnj2	potassium inwardly-rectifying channel, subfamily J, member 2	0	4	1	-1.71225
1087	258718	Olfr513	olfactory receptor 513	0	3	1	-1.71119
1088	269254	Als4	senataxin	0	3	2	-1.71102
1089	16323	Inhba	inhibin beta-A	0	3	2	-1.7105
1090	320407	Klri2	killer cell lectin-like receptor family I member 2	0	3	2	-1.71044
1091	15191	Hdgf	hepatoma-derived growth factor	0	3	2	-1.71023
1092	259300	Ehd2	EH-domain containing 2	0	3	2	-1.7091
1093	229228	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0	3	2	-1.7091
1094	330731	LOC330731	trimethylguanosine synthase homolog pseudogene	0	3	2	-1.70866
1095	16498	Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0	3	2	-1.70777
1096	432738	UNK	NA	0	3	2	-1.70738
1097	73473	Iws1	IWS1 homolog (S. cerevisiae)	0	4	1	-1.70718
1098	74340	4631427C17Rik	S-adenosylhomocysteine hydrolase-like 2	0	3	2	-1.70663
1099	317717	Sec22a	SEC22 vesicle trafficking protein homologe A (S. cerevisiae)	0	3	2	-1.70639
1100	56420	Ppp4c	protein phosphatase 4, catalytic subunit	0	3	2	-1.70636
1101	67205	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	0	3	2	-1.70634
1102	68572	Ict1	immature colon carcinoma transcript 1	0	3	1	-1.70615
1103	83383	Tcfap4	transcription factor AP4	0	3	2	-1.70585
1104	70427	Mier2	mesoderm induction early response 1, family member 2	0	3	2	-1.70571
1105	219134	Tmem46	shisa homolog 2 (Xenopus laevis)	0	3	2	-1.70481
1106	54672	Gpr97	G protein-coupled receptor 97	0	3	2	-1.70471

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1107	226982	Eif5b	eukaryotic translation initiation factor 5B	0	4	0	-1.70451
1108	257662	GA-x5J8B7W4T2P-84764	olfactory receptor 1290	0	3	2	-1.70448
1109	84092	Usp8	ubiquitin specific peptidase 8	0	3	2	-1.70441
1110	67016	Tbc1d2b	TBC1 domain family, member 2B	0	3	2	-1.70414
1111	69577	2310010B21Rik	FAST kinase domains 3	0	3	1	-1.7038
1112	110596	Rgnef	Rho-guanine nucleotide exchange factor	0	4	1	-1.70277
1113	76932	Arfip2	ADP-ribosylation factor interacting protein 2	0	4	1	-1.70276
1114	21922	Clec3b	C-type lectin domain family 3, member b	0	4	1	-1.70209
1115	14055	Ezh1	enhancer of zeste homolog 1 (Drosophila)	0	3	2	-1.70205
1116	22352	Vim	vimentin	0	3	2	-1.70191
1117	11703	Amd2	NA	0	3	2	-1.70134
1118	68416	Sycn	syncollin	0	4	1	-1.70073
1119	235345	4833427G06Rik	RIKEN cDNA 4833427G06 gene	0	3	2	-1.7007
1120	223978	C530044N13Rik	calcineurin-like phosphoesterase domain containing 1	0	3	2	-1.70062
1121	116849	Iltifb	interleukin 10-related T cell-derived inducible factor beta	0	4	1	-1.69984
1122	258939	Olfr63	olfactory receptor 63	0	3	1	-1.69983
1123	23795	Agr2	anterior gradient 2 (Xenopus laevis)	0	3	2	-1.69977
1124	72119	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	0	5	0	-1.69937
1125	69150	Snx4	sorting nexin 4	0	4	1	-1.69874
1126	237016	LOC237016	pyruvate kinase, muscle pseudogene	0	3	2	-1.69852
1127	12661	Chl1	cell adhesion molecule with homology to L1CAM	0	4	1	-1.69814
1128	215472	E130012K09	predicted gene 4792	0	4	0	-1.69796
1129	17936	Nab1	Ngfi-A binding protein 1	0	3	2	-1.69785
1130	22044	Trh	thyrotropin releasing hormone	0	4	1	-1.69756
1131	66438	Hamp2	hepcidin antimicrobial peptide 2	0	4	1	-1.69727
1132	19072	Prep	prolyl endopeptidase	0	4	1	-1.69718
1133	14201	Fhl3	four and a half LIM domains 3	0	3	2	-1.69718
1134	68614	Letmd1	LETM1 domain containing 1	0	3	2	-1.69627
1135	66090	Ypel3	yippee-like 3 (Drosophila)	0	3	1	-1.69611
1136	56427	Tubd1	tubulin, delta 1	0	3	2	-1.69527
1137	192653	BC021608	tetratricopeptide repeat domain 36	0	3	2	-1.69522
1138	15139	Hc	hemolytic complement	0	3	2	-1.69514
1139	17972	Ncf4	neutrophil cytosolic factor 4	0	3	2	-1.69478
1140	66922	Rras2	related RAS viral (r-ras) oncogene homolog 2	0	4	1	-1.69478
1141	19226	Pth	parathyroid hormone	0	3	2	-1.69462
1142	231474	Paqr3	progestin and adipoQ receptor family member III	0	3	2	-1.69444
1143	101314	6720456B07Rik	RIKEN cDNA 6720456B07 gene	0	3	2	-1.69421

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1144	56395	Tmem115	transmembrane protein 115	0	3	2	-1.69401
1145	11542	Adora3	adenosine A3 receptor	0	3	2	-1.69391
1146	67866	Wfdc1	WAP four-disulfide core domain 1	0	3	2	-1.69351
1147	245050	C730027P07Rik	family with sequence similarity 198, member A	0	4	0	-1.69328
1148	333669	LOC333669	predicted gene 5134	0	3	2	-1.69311
1149	107449	Unc5b	unc-5 homolog B (C. elegans)	0	3	2	-1.69248
1150	268759	9930012K11Rik	RIKEN cDNA 9930012K11 gene	0	3	2	-1.69226
1151	13644	Efs	embryonal Fyn-associated substrate	0	3	2	-1.6921
1152	226122	Ubtd1	ubiquitin domain containing 1	0	3	1	-1.692
1153	16173	Il18	interleukin 18	0	3	2	-1.69195
1154	17898	Myl7	myosin, light polypeptide 7, regulatory	0	3	2	-1.69189
1155	545471	LOC545471	zinc finger protein 345	0	3	1	-1.69036
1156	14969	H2-Eb1	histocompatibility 2, class II antigen E beta	0	3	2	-1.6903
1157	213550	AV340375	DIS3 mitotic control homolog (S. cerevisiae)-like	0	3	1	-1.68951
1158	13629	Eef2	eukaryotic translation elongation factor 2	0	3	2	-1.68945
1159	18972	Pold2	polymerase (DNA directed), delta 2, regulatory subunit	0	3	2	-1.68942
1160	71950	Nanog	Nanog homeobox	0	3	2	-1.68865
1161	258503	Olfr98	olfactory receptor 98	0	3	2	-1.68819
1162	56636	Fgf21	fibroblast growth factor 21	0	4	1	-1.68815
1163	18511	Pax9	paired box gene 9	0	3	2	-1.68812
1164	12514	Cd68	CD68 antigen	0	3	7	-1.68805
1165	20085	Rps19	ribosomal protein S19	0	4	1	-1.68721
1166	67618	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0	3	2	-1.68718
1167	70835	Prss22	protease, serine, 22	0	3	1	-1.6871
1168	26364	Cd97	CD97 antigen	0	3	2	-1.68692
1169	243813	Leng9	leukocyte receptor cluster (LRC) member 9	0	3	2	-1.68652
1170	75586	2310040M23Rik	keratin associated protein 9-3	0	3	1	-1.68619
1171	73716	Krtap21-1	NA	0	3	1	-1.68601
1172	72727	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0	3	2	-1.68569
1173	13386	Dlk1	delta-like 1 homolog (Drosophila)	0	3	2	-1.6852
1174	21415	Tcf3	transcription factor 7 like 1 (T cell specific, HMG box)	0	3	2	-1.68505
1175	74387	4932438H23Rik	RIKEN cDNA 4932438H23 gene	0	3	1	-1.685
1176	72560	Naalad2	N-acetylated alpha-linked acidic dipeptidase 2	0	3	2	-1.68439
1177	19206	Ptch1	patched homolog 1	0	3	2	-1.68404
1178	17221	Cd46	CD46 antigen, complement regulatory protein	0	3	2	-1.6838
1179	74481	Batf2	basic leucine zipper transcription factor, ATF-like 2	0	5	0	-1.68324
1180	76123	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0	3	2	-1.68251

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1181	68323	Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	0	3	1	-1.68249
1182	16491	Kcna3	potassium voltage-gated channel, shaker-related subfamily, member 3	0	4	1	-1.6823
1183	55932	Gbp4	guanylate binding protein 3	0	3	2	-1.68212
1184	58180	Hic2	hypermethylated in cancer 2	0	4	1	-1.68155
1185	12227	Btg2	B cell translocation gene 2, anti-proliferative	0	4	1	-1.68106
1186	80281	Cttnbp2nl	CTTNBP2 N-terminal like	0	3	1	-1.68087
1187	330941	AI593442	expressed sequence AI593442	0	4	0	-1.68056
1188	21371	Tbca	tubulin cofactor A	0	3	2	-1.68054
1189	13589	Mapre1	microtubule-associated protein, RP/EB family, member 1	0	3	2	-1.68047
1190	16467	Atcay	ataxia, cerebellar, Cayman type homolog (human)	0	3	1	-1.68041
1191	14199	Fhl1	four and a half LIM domains 1	0	5	0	-1.68032
1192	21877	Tk1	thymidine kinase 1	0	4	1	-1.68014
1193	225631	Onecut2	one cut domain, family member 2	0	3	2	-1.68009
1194	269695	Tmem118	ring finger protein, transmembrane 2	0	4	1	-1.68009
1195	75258	4930563M21Rik	RIKEN cDNA 4930563M21 gene	0	3	2	-1.6798
1196	268420	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	0	3	2	-1.67976
1197	59026	Huwe1	HECT, UBA and WWE domain containing 1	0	3	2	-1.67976
1198	20747	Spop	speckle-type POZ protein	0	3	2	-1.6797
1199	241175	C230078M14Rik	contactin associated protein-like 5B	0	4	1	-1.67917
1200	16617	Klk1b24	kallikrein 1-related peptidase b24	0	3	2	-1.67916
1201	20666	Sox11	SRY-box containing gene 11	0	3	2	-1.67914
1202	20658	Son	Son DNA binding protein	0	4	1	-1.67895
1203	22115	Tssk2	testis-specific serine kinase 2	0	3	2	-1.67892
1204	14765	Gpr50	G-protein-coupled receptor 50	0	3	2	-1.67884
1205	113863	V1rc6	vomeronasal 1 receptor 15	0	3	2	-1.67843
1206	67932	1700129C05Rik	RIKEN cDNA 1700129C05 gene	0	3	2	-1.6782
1207	18569	Pdcd4	programmed cell death 4	0	3	2	-1.67803
1208	16909	Lmo2	LIM domain only 2	0	3	2	-1.67727
1209	232975	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	0	3	2	-1.67701
1210	93840	Ltap	vang-like 2 (van gogh, Drosophila)	0	3	2	-1.67659
1211	12575	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	0	5	5	-1.67632
1212	218100	Zfp322a	zinc finger protein 322A	0	4	1	-1.67601
1213	69454	Clic3	chloride intracellular channel 3	0	4	1	-1.67576
1214	219105	9830124H08Rik	zinc finger, MYM-type 5	0	3	2	-1.67576
1215	69009	Thap7	THAP domain containing 7	0	4	0	-1.67542
1216	17279	Melk	maternal embryonic leucine zipper kinase	0	3	2	-1.67499
1217	319642	Rab9b	RAB9B, member RAS oncogene family	0	3	2	-1.67482

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1218	619298	G930045G22Rik	RIKEN cDNA G930045G22 gene	0	3	2	-1.67467
1219	19185	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	0	4	1	-1.67457
1220	333715	H2-M10.2	histocompatibility 2, M region locus 10.2	0	4	1	-1.67446
1221	332713	BC051628	cDNA sequence BC051628	0	4	1	-1.67438
1222	57330	Perq1	GRB10 interacting GYF protein 1	0	4	0	-1.67436
1223	76964	2610028H24Rik	RIKEN cDNA 2610028H24 gene	0	3	2	-1.67399
1224	30800	Mmp20	matrix metallopeptidase 20 (enamelysin)	0	3	2	-1.67393
1225	18573	Pde1a	phosphodiesterase 1A, calmodulin-dependent	0	3	2	-1.67386
1226	231293	C130090K23Rik	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	0	4	1	-1.67367
1227	11477	Acvr1	activin A receptor, type 1	0	3	2	-1.67361
1228	271424	Ihpk3	inositol hexaphosphate kinase 3	0	3	2	-1.67345
1229	22217	Usp12	ubiquitin specific peptidase 12	0	3	2	-1.67331
1230	66314	Tpd52l2	tumor protein D52-like 2	0	3	2	-1.67287
1231	75512	Gpx6	glutathione peroxidase 6	0	4	1	-1.67268
1232	11549	Adra1a	adrenergic receptor, alpha 1a	0	3	1	-1.6726
1233	15247	Hiat1	hippocampus abundant gene transcript 1	0	3	2	-1.67251
1234	11936	Fxyd2	FXYD domain-containing ion transport regulator 2	0	3	2	-1.67189
1235	67141	Fbxo5	F-box protein 5	0	3	2	-1.67153
1236	435723	UNK	NA	0	3	2	-1.67145
1237	68981	Snrpa1	small nuclear ribonucleoprotein polypeptide A'	0	3	2	-1.67141
1238	17187	Max	Max protein	0	4	1	-1.67047
1239	22286	Utf1	undifferentiated embryonic cell transcription factor 1	0	3	2	-1.66995
1240	70986	4931422A03Rik	RIKEN cDNA 4931422A03 gene	0	3	1	-1.66884
1241	19210	Ptdss1	phosphatidylserine synthase 1	0	3	2	-1.66853
1242	269513	E130310K16Rik	Na+/K+ transporting ATPase interacting 3	0	4	1	-1.66822
1243	73747	1110034G24Rik	RIKEN cDNA 1110034G24 gene	0	3	2	-1.66799
1244	259011	Olfr389	olfactory receptor 389	0	4	1	-1.66797
1245	433470	AA467197	expressed sequence AA467197	0	3	2	-1.66795
1246	246049	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	0	4	1	-1.66747
1247	110829	Lims1	LIM and senescent cell antigen-like domains 1	0	3	2	-1.66721
1248	18655	Pgk1	phosphoglycerate kinase 1	0	3	7	-1.66706
1249	107522	Ece2	endothelin converting enzyme 2	0	3	2	-1.6668
1250	18550	Furin	furin (paired basic amino acid cleaving enzyme)	0	4	1	-1.66674
1251	20787	Srebf1	sterol regulatory element binding transcription factor 1	0	3	2	-1.66668
1252	433861	UNK	NA	0	3	2	-1.66503
1253	14415	Gad1	glutamic acid decarboxylase 1	0	3	2	-1.66493
1254	74318	Hod	HOP homeobox	0	3	2	-1.66418

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1255	432929	LOC432929	NA	0	3	6	-1.66416
1256	239833	Lmln	leishmanolysin-like (metallopeptidase M8 family)	0	4	1	-1.66409
1257	16997	Ltbp2	latent transforming growth factor beta binding protein 2	0	3	2	-1.66392
1258	116847	Prelp	proline arginine-rich end leucine-rich repeat	0	3	2	-1.66331
1259	18567	Pdcd2	programmed cell death 2	0	4	1	-1.6633
1260	71960	Myh14	myosin, heavy polypeptide 14	0	3	2	-1.66325
1261	246703	Apoa1bp	apolipoprotein A-I binding protein	0	3	1	-1.66295
1262	68458	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	0	4	1	-1.66292
1263	227290	Aamp	angio-associated migratory protein	0	4	1	-1.66283
1264	59069	Tpm3	tropomyosin 3, gamma	0	3	2	-1.66222
1265	56546	Sec1	secretory blood group 1	0	3	2	-1.66219
1266	29859	Sult4a1	sulfotransferase family 4A, member 1	0	3	2	-1.66216
1267	14149	Fdxr	ferredoxin reductase	0	4	1	-1.66208
1268	93673	Cml2	camello-like 2	0	3	2	-1.66189
1269	29806	Limd1	LIM domains containing 1	0	3	2	-1.66135
1270	75221	Dpp3	dipeptidylpeptidase 3	0	3	2	-1.66123
1271	209512	Taar2	trace amine-associated receptor 2	0	3	2	-1.66123
1272	11799	Birc5	baculoviral IAP repeat-containing 5	0	3	2	-1.66105
1273	58522	Trim54	tripartite motif-containing 54	0	4	1	-1.66105
1274	73690	Glipr1	GLI pathogenesis-related 1 (glioma)	0	4	1	-1.66037
1275	192654	Lypla3	phospholipase A2, group XV	0	3	2	-1.66037
1276	223690	C730048E16Rik	ankyrin repeat domain 54	0	3	2	-1.66032
1277	319508	Syt15	synaptotagmin XV	0	4	1	-1.66019
1278	386392	LOC386392	NA	0	3	2	-1.66019
1279	70843	4733401L19Rik	keratin 28	0	3	2	-1.65879
1280	20319	Sfrp2	secreted frizzled-related protein 2	0	4	1	-1.65832
1281	14626	Gk2	glycerol kinase 2	0	5	0	-1.65777
1282	71832	Csl	citrate synthase like	0	3	2	-1.65771
1283	77733	Rnf170	ring finger protein 170	0	3	2	-1.65765
1284	240186	Zfp438	zinc finger protein 438	0	3	2	-1.65749
1285	16852	Lgals1	lectin, galactose binding, soluble 1	0	3	2	-1.6574
1286	56196	Ttrap	tyrosyl-DNA phosphodiesterase 2	0	3	1	-1.65714
1287	54123	Irf7	interferon regulatory factor 7	0	3	2	-1.65703
1288	19942	Rpl27	ribosomal protein L27	0	4	1	-1.65678
1289	67171	Tmem77	DNA-damage regulated autophagy modulator 2	0	3	1	-1.65598
1290	210172	Zfp526	zinc finger protein 526	0	4	1	-1.65596
1291	214895	Lman2l	lectin, mannose-binding 2-like	0	4	1	-1.65555

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1292	72472	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0	4	1	-1.65539
1293	15551	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	0	3	2	-1.65481
1294	258378	Olfr593	olfactory receptor 593	0	3	1	-1.65329
1295	245537	Nlgn3	neuroligin 3	0	4	1	-1.65324
1296	19246	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	0	3	2	-1.65312
1297	12482	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	0	5	0	-1.65252
1298	216749	Nmur2	neuromedin U receptor 2	0	3	2	-1.6519
1299	18979	Pon1	paraoxonase 1	0	3	2	-1.65159
1300	21907	Nr2e1	nuclear receptor subfamily 2, group E, member 1	0	3	2	-1.65151
1301	14709	Gng8	guanine nucleotide binding protein (G protein), gamma 8	0	3	2	-1.65129
1302	17064	Cd93	CD93 antigen	0	3	2	-1.65085
1303	385052	UNK	NA	0	4	1	-1.64914
1304	16841	Lect2	leukocyte cell-derived chemotaxin 2	0	4	1	-1.64904
1305	16660	Krt1-1	keratin 31	0	3	2	-1.64874
1306	14343	Fut1	fucosyltransferase 1	0	4	1	-1.64846
1307	64144	Mllt1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	0	3	2	-1.64831
1308	243369	Sspo	SCO-spondin	0	3	2	-1.6477
1309	52857	Gramd1a	GRAM domain containing 1A	0	3	2	-1.64767
1310	68550	1110002N22Rik	RIKEN cDNA 1110002N22 gene	0	3	2	-1.64736
1311	11651	Akt1	thymoma viral proto-oncogene 1	0	6	4	-1.64683
1312	394252	Serpinb3d	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3D	0	3	2	-1.64638
1313	270135	BC038156	NA	0	3	1	-1.64551
1314	13864	Nr2f6	nuclear receptor subfamily 2, group F, member 6	0	4	1	-1.64462
1315	70227	3000002G13Rik	zinc finger protein 619	0	3	2	-1.64381
1316	217214	Nags	N-acetylglutamate synthase	0	4	1	-1.64379
1317	16434	Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	0	3	2	-1.64377
1318	80985	Trim44	tripartite motif-containing 44	0	3	2	-1.64375
1319	280121	LOC280121	ribosomal protein, large, P1, pseudogene 1	0	3	2	-1.64349
1320	18845	Plxna2	plexin A2	0	4	1	-1.64293
1321	20616	Snap91	synaptosomal-associated protein 91	0	4	1	-1.64259
1322	433670	UNK	NA	0	3	2	-1.64206
1323	68221	1700049M11Rik	WAP four-disulfide core domain 15A	0	4	1	-1.64093
1324	69551	2310022B05Rik	RIKEN cDNA 2310022B05 gene	0	3	2	-1.64088
1325	14747	Cmklr1	chemokine-like receptor 1	0	3	2	-1.64076
1326	69957	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	0	3	2	-1.64068
1327	22174	Tyro3	TYRO3 protein tyrosine kinase 3	0	4	1	-1.6406
1328	57440	Ehd3	EH-domain containing 3	0	3	2	-1.64056

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1329	15937	Ier3	immediate early response 3	0	3	1	-1.64046
1330	269344	Ell3	elongation factor RNA polymerase II-like 3	0	4	1	-1.64043
1331	19272	Ptprk	protein tyrosine phosphatase, receptor type, K	0	3	2	-1.63995
1332	12226	Btg1	B cell translocation gene 1, anti-proliferative	0	3	2	-1.63974
1333	15126	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	0	3	2	-1.63957
1334	107477	Guca1b	guanylate cyclase activator 1B	0	4	1	-1.63927
1335	22260	Nr1h2	nuclear receptor subfamily 1, group H, member 2	0	3	2	-1.63791
1336	58245	Gpr180	G protein-coupled receptor 180	0	3	2	-1.63785
1337	268739	E130112L23Rik	Rho guanine nucleotide exchange factor (GEF) 40	0	3	2	-1.63769
1338	50784	Ppap2c	phosphatidic acid phosphatase type 2C	0	4	1	-1.63754
1339	69367	Glrx2	glutaredoxin 2 (thioltransferase)	0	4	1	-1.63754
1340	102693	Phldb1	pleckstrin homology-like domain, family B, member 1	0	3	2	-1.63678
1341	52040	Ppp1r10	protein phosphatase 1, regulatory subunit 10	0	3	2	-1.6363
1342	20861	Stfa1	stefin A1	0	3	2	-1.63629
1343	15424	Hoxc5	homeobox C5	0	3	2	-1.636
1344	140858	Wdr5	WD repeat domain 5	0	3	2	-1.63543
1345	71990	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	0	3	2	-1.63522
1346	227613	Tubb2c	tubulin, beta 4B class IVB	0	3	2	-1.63516
1347	67881	1810034K20Rik	magnesium-dependent phosphatase 1	0	5	0	-1.63511
1348	14533	Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1	0	3	2	-1.63476
1349	52187	Rragd	Ras-related GTP binding D	0	4	1	-1.63451
1350	12234	Btrc	beta-transducin repeat containing protein	0	5	0	-1.63446
1351	210801	Unc5d	unc-5 homolog D (C. elegans)	0	3	2	-1.63443
1352	14788	Gpr162	G protein-coupled receptor 162	0	3	2	-1.63442
1353	216343	Tph2	tryptophan hydroxylase 2	0	3	2	-1.63432
1354	22264	Prap1	proline-rich acidic protein 1	0	3	2	-1.63373
1355	66053	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	0	3	2	-1.63331
1356	333088	Crim2	kielin/chordin-like protein	0	3	2	-1.63285
1357	28199	Wdr23	DDB1 and CUL4 associated factor 11	0	3	1	-1.63275
1358	11431	Acp1	acid phosphatase 1, soluble	0	3	1	-1.63244
1359	54394	Crlf3	cytokine receptor-like factor 3	0	4	1	-1.63243
1360	50883	Chek2	checkpoint kinase 2	0	3	2	-1.63234
1361	67755	Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	0	3	2	-1.63201
1362	67217	2810055F11Rik	RIKEN cDNA 2810055F11 gene	0	3	2	-1.6317
1363	24110	Usp18	ubiquitin specific peptidase 18	0	4	1	-1.63161
1364	14181	Fgfbp1	fibroblast growth factor binding protein 1	0	3	2	-1.63143
1365	17904	Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0	4	1	-1.63136

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1366	116903	Calcb	calcitonin-related polypeptide, beta	0	3	2	-1.63094
1367	433839	LOC433839	NA	0	4	1	-1.63022
1368	29810	Bag3	BCL2-associated athanogene 3	0	3	2	-1.62979
1369	16476	Jun	Jun oncogene	0	4	6	-1.62964
1370	228228	Olfr1102	olfactory receptor 1102	0	3	2	-1.62926
1371	24082	Gtlf3a	predicted gene, Gm16516	0	3	1	-1.62918
1372	320858	D930040M24Rik	l(3)mbt-like 4 (Drosophila)	0	4	1	-1.62916
1373	17168	Mare	nitrogen permease regulator-like 3 (S. cerevisiae)	0	3	2	-1.62907
1374	230979	Tnfrsf14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0	3	2	-1.62892
1375	66653	Brf2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	0	3	2	-1.62865
1376	14166	Fgf11	fibroblast growth factor 11	0	4	1	-1.6286
1377	13180	Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (	0	4	1	-1.62833
1378	333473	Zfp36l3	zinc finger protein 36, C3H type-like 3	0	3	1	-1.6283
1379	18035	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha	0	4	1	-1.62824
1380	14228	Fkbp4	FK506 binding protein 4	0	3	2	-1.62802
1381	66264	Ccdc28b	coiled coil domain containing 28B	0	4	1	-1.6279
1382	67642	4930515G01Rik	RIKEN cDNA 4930515G01 gene	0	3	2	-1.62771
1383	19356	Rad17	RAD17 homolog (S. pombe)	0	4	1	-1.62741
1384	56421	Pfkp	phosphofructokinase, platelet	0	3	2	-1.62735
1385	338375	Atp6v1g3	ATPase, H+ transporting, lysosomal V1 subunit G3	0	4	1	-1.6265
1386	107747	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	0	3	2	-1.62576
1387	12269	C4bp	complement component 4 binding protein	0	3	2	-1.62542
1388	22423	Wnt8b	wingless related MMTV integration site 8b	0	5	0	-1.62537
1389	70069	H1fnt	H1 histone family, member N, testis-specific	0	4	1	-1.62447
1390	223864	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	0	3	2	-1.6239
1391	70980	4931431F19Rik	RIKEN cDNA 4931431F19 gene	0	4	1	-1.62383
1392	12561	Cdh4	cadherin 4	0	4	1	-1.62376
1393	399549	H2-M10.6	histocompatibility 2, M region locus 10.6	0	3	2	-1.6233
1394	22297	V1ra2	vomeronasal 1 receptor 45	0	3	2	-1.62245
1395	16416	Itgb3	integrin beta 3	0	3	2	-1.62226
1396	12966	Crygc	crystallin, gamma C	0	4	1	-1.62168
1397	16157	Il11ra1	interleukin 11 receptor, alpha chain 1	0	3	2	-1.62127
1398	12741	Cldn5	claudin 5	0	4	1	-1.62118
1399	215332	Slc36a3	solute carrier family 36 (proton/amino acid symporter), member 3	0	3	2	-1.62009
1400	110074	Dut	deoxyuridine triphosphatase	0	4	1	-1.62008
1401	258730	Olfr483	olfactory receptor 483	0	3	1	-1.6198
1402	19951	Rpl32	ribosomal protein L32	0	5	0	-1.61974

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1403	69955	Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	0	3	2	-1.61966
1404	217837	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	0	3	2	-1.61933
1405	18003	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	0	3	2	-1.61895
1406	378430	Nanos2	nanos homolog 2 (Drosophila)	0	3	2	-1.61891
1407	70419	2810408A11Rik	RIKEN cDNA 2810408A11 gene	0	3	2	-1.61887
1408	14693	Gnb2	guanine nucleotide binding protein (G protein), beta 2	0	4	1	-1.61871
1409	19727	Rfxank	regulatory factor X-associated ankyrin-containing protein	0	4	1	-1.61828
1410	20660	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	0	3	1	-1.61799
1411	259095	Olfr568	olfactory receptor 568	0	4	0	-1.61799
1412	258898	Olfr1203	olfactory receptor 1205	0	3	2	-1.61795
1413	69312	4930418G15Rik	protein phosphatase 1, regulatory subunit 42	0	4	1	-1.61739
1414	18037	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	0	3	2	-1.61706
1415	66467	Gtf2h5	general transcription factor IIH, polypeptide 5	0	4	1	-1.61686
1416	434071	UNK	NA	0	3	2	-1.6168
1417	12053	Bcl6	B cell leukemia/lymphoma 6	0	3	2	-1.6165
1418	17420	Mnat1	menage a trois 1	0	4	1	-1.61628
1419	18369	Olfr68	olfactory receptor 68	0	3	2	-1.61582
1420	27276	Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1	0	3	2	-1.61579
1421	20364	Sepw1	selenoprotein W, muscle 1	0	3	1	-1.6154
1422	57430	Sult3a1	sulfotransferase family 3A, member 1	0	3	2	-1.61535
1423	108078	Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	0	3	2	-1.61513
1424	14961	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	0	4	6	-1.61496
1425	11656	Alas2	aminolevulinic acid synthase 2, erythroid	0	3	2	-1.61452
1426	232664	4921511K06Rik	coiled-coil domain containing 136	0	3	2	-1.61426
1427	79263	Trim39	tripartite motif-containing 39	0	3	2	-1.61362
1428	194360	LOC194360	trypsinogen pseudogene	0	7	3	-1.61359
1429	66401	Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	0	3	2	-1.61302
1430	27426	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	0	3	2	-1.61281
1431	66834	Them2	acyl-CoA thioesterase 13	0	3	1	-1.6128
1432	70432	Rufy2	RUN and FYVE domain-containing 2	0	3	2	-1.61199
1433	227696	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1	0	4	4	-1.61186
1434	228880	Prkcbp1	zinc finger, MYND-type containing 8	0	3	2	-1.61182
1435	12969	Crygf	crystallin, gamma F	0	4	1	-1.61179
1436	66656	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0	4	1	-1.61164
1437	236537	Zfp352	zinc finger protein 352	0	3	2	-1.61127
1438	11854	Rhod	ras homolog gene family, member D	0	3	2	-1.61067
1439	52033	Pbk	PDZ binding kinase	0	4	1	-1.60985

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1440	78428	Wibg	within bgcn homolog (Drosophila)	0	3	1	-1.60983
1441	17259	Mef2b	myocyte enhancer factor 2B	0	3	2	-1.60981
1442	380714	Rph3al	rabphilin 3A-like (without C2 domains)	0	3	2	-1.60932
1443	17701	Msx1	homeobox, msh-like 1	0	3	2	-1.60867
1444	212114	8030451K01Rik	NHL repeat containing 3	0	3	1	-1.60859
1445	18160	Npr1	natriuretic peptide receptor 1	0	4	1	-1.60845
1446	110385	Pde4c	phosphodiesterase 4C, cAMP specific	0	3	2	-1.60807
1447	22757	Zfp95	zinc finger with KRAB and SCAN domains 5	0	3	2	-1.60657
1448	231798	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	0	3	2	-1.6064
1449	21422	Tcfcp2	transcription factor CP2	0	3	2	-1.60561
1450	19290	Pura	purine rich element binding protein A	0	3	2	-1.6056
1451	18223	Numbl	numb-like	0	3	2	-1.60482
1452	214897	Csnk1g1	casein kinase 1, gamma 1	0	4	1	-1.60475
1453	50880	Scly	selenocysteine lyase	0	3	2	-1.60459
1454	76295	Atp11b	ATPase, class VI, type 11B	0	3	2	-1.60441
1455	72536	Tagap	T cell activation Rho GTPase activating protein	0	5	0	-1.60363
1456	217705	9830169C18Rik	family with sequence similarity 161, member B	0	3	2	-1.60326
1457	94179	Krt1-23	keratin 23	0	4	1	-1.60306
1458	68024	Hist1h2bc	histone cluster 1, H2bc	0	4	0	-1.60271
1459	21873	Tjp2	tight junction protein 2	0	3	2	-1.6026
1460	16687	Krt2-6a	keratin 6A	0	3	2	-1.60214
1461	235527	Plscr4	phospholipid scramblase 4	0	3	2	-1.60201
1462	16682	Krt2-4	keratin 4	0	3	2	-1.6016
1463	69698	2310046K01Rik	RIKEN cDNA 2310046K01 gene	0	3	2	-1.6008
1464	98741	Kcnb2	potassium voltage gated channel, Shab-related subfamily, member 2	0	3	2	-1.60058
1465	22648	Zfp11	zinc finger protein 11	0	3	2	-1.60029
1466	67905	Ppm1m	protein phosphatase 1M	0	3	2	-1.59988
1467	76199	Thrap2	mediator complex subunit 13-like	0	3	2	-1.59982
1468	73666	Thoc3	THO complex 3	0	3	2	-1.5992
1469	18322	Olfr24	olfactory receptor 24	0	3	2	-1.59906
1470	18984	Por	P450 (cytochrome) oxidoreductase	0	3	2	-1.59904
1471	26561	Mmp23	matrix metallopeptidase 23	0	3	2	-1.59873
1472	14284	Fosl2	fos-like antigen 2	0	3	2	-1.59775
1473	243963	Zfp473	zinc finger protein 473	0	3	2	-1.59758
1474	50764	Fbxo15	F-box protein 15	0	3	2	-1.59736
1475	210933	Bai3	brain-specific angiogenesis inhibitor 3	0	3	2	-1.59715
1476	113846	V1ra4	vomeronasal 1 receptor 47	0	3	2	-1.59715

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1477	11496	Adam22	a disintegrin and metallopeptidase domain 22	0	3	2	-1.59698
1478	16796	Lasp1	LIM and SH3 protein 1	0	3	2	-1.59688
1479	16563	Kif2a	kinesin family member 2A	0	3	2	-1.59675
1480	17067	Ly6c	lymphocyte antigen 6 complex, locus C1	0	4	1	-1.59658
1481	258850	Olfr295	olfactory receptor 295	0	4	0	-1.59637
1482	73656	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	0	3	1	-1.59616
1483	67528	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	0	3	2	-1.59608
1484	107373	4632417K18Rik	family with sequence similarity 111, member A	0	3	1	-1.59476
1485	65099	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	0	3	2	-1.59461
1486	18285	Odf1	outer dense fiber of sperm tails 1	0	3	2	-1.59415
1487	11690	Alox5ap	arachidonate 5-lipoxygenase activating protein	0	3	2	-1.59409
1488	60534	Fancg	Fanconi anemia, complementation group G	0	3	2	-1.59405
1489	235631	Tsp50	protease, serine, 50	0	4	1	-1.59348
1490	217011	Nle1	notchless homolog 1 (Drosophila)	0	3	2	-1.59258
1491	22245	Uck1	uridine-cytidine kinase 1	0	4	1	-1.59248
1492	226182	Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	3	2	-1.59234
1493	258871	Olfr898	olfactory receptor 898	0	3	1	-1.591
1494	641227	UNK	NA	0	4	1	-1.59068
1495	16524	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	0	3	2	-1.59007
1496	12398	Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0	3	2	-1.58978
1497	19656	Rbmxrt	RNA binding motif protein, X linked-like-1	0	3	2	-1.58845
1498	72088	Ush1c	Usher syndrome 1C homolog (human)	0	3	2	-1.58843
1499	11576	Afp	alpha fetoprotein	0	3	2	-1.58829
1500	15405	Hoxa9	homeobox A9	0	3	2	-1.58816
1501	626662	UNK	NA	0	3	2	-1.5881
1502	258695	Olfr1453	olfactory receptor 1453	0	4	1	-1.58801
1503	72014	1500005I02Rik	BTB (POZ) domain containing 17	0	3	2	-1.58777
1504	14187	Akr1b8	aldo-keto reductase family 1, member B8	0	3	2	-1.58686
1505	14173	Fgf2	fibroblast growth factor 2	0	3	2	-1.58574
1506	14608	Gpr83	G protein-coupled receptor 83	0	3	1	-1.58568
1507	14200	Fhl2	four and a half LIM domains 2	0	3	2	-1.58564
1508	20899	Stra8	stimulated by retinoic acid gene 8	0	5	0	-1.58517
1509	258578	Olfr1517	NA	0	3	2	-1.5846
1510	21687	Tek	endothelial-specific receptor tyrosine kinase	0	3	2	-1.58357
1511	105298	Epdr2	ependymin related protein 1 (zebrafish)	0	3	2	-1.58283
1512	223337	Ugt3a2	UDP glycosyltransferases 3 family, polypeptide A2	0	3	2	-1.58279
1513	16616	Klk1b21	kallikrein 1-related peptidase b21	0	5	0	-1.58251

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1514	266692	Cpne1	copine I	0	3	2	-1.58232
1515	320001	E230015B07Rik	RIKEN cDNA E230015B07 gene	0	3	2	-1.58226
1516	209357	Gtf2h3	general transcription factor IIH, polypeptide 3	0	3	2	-1.58214
1517	193403	LOC193403	serine (or cysteine) peptidase inhibitor, clade B pseudogene	0	3	2	-1.58096
1518	234959	Crsp6	mediator complex subunit 17	0	3	2	-1.57913
1519	14682	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	0	3	2	-1.5791
1520	233058	B230312I18Rik	zinc finger protein 420	0	4	1	-1.5789
1521	20420	Shd	src homology 2 domain-containing transforming protein D	0	3	1	-1.57879
1522	14866	Gstm5	glutathione S-transferase, mu 5	0	3	2	-1.57861
1523	15407	Hoxb1	homeobox B1	0	3	2	-1.57858
1524	69216	Ccdc23	coiled-coil domain containing 23	0	3	2	-1.57851
1525	16189	Il4	interleukin 4	0	3	2	-1.57802
1526	217980	Larp5	La ribonucleoprotein domain family, member 4B	0	4	0	-1.5777
1527	258517	Olfr855	olfactory receptor 855	0	3	2	-1.5777
1528	215160	Rhbdd2	rhomboid domain containing 2	0	3	2	-1.57738
1529	103551	E130012A19Rik	RIKEN cDNA E130012A19 gene	0	3	2	-1.57736
1530	226517	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0	3	1	-1.5768
1531	17991	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	0	3	2	-1.57671
1532	13544	Dvl3	dishevelled 3, dsh homolog (Drosophila)	0	3	2	-1.57657
1533	69681	Cdk3	cyclin-dependent kinase 3, pseudogene	0	3	2	-1.57644
1534	234779	Plcg2	phospholipase C, gamma 2	0	3	2	-1.57634
1535	15450	Lipc	lipase, hepatic	0	4	1	-1.57613
1536	107448	Unc5a	unc-5 homolog A (C. elegans)	0	3	2	-1.57603
1537	13531	Dub1	deubiquitinating enzyme 1	0	3	2	-1.57572
1538	269338	Vps39	vacuolar protein sorting 39 (yeast)	0	3	2	-1.57562
1539	77031	Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0	3	2	-1.57557
1540	18117	Cox4nb	COX4 neighbor	0	4	0	-1.57526
1541	245877	Rprc1	microtubule-associated protein 7 domain containing 1	0	4	1	-1.57487
1542	18164	Nptx1	neuronal pentraxin 1	0	3	1	-1.57483
1543	18140	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	0	3	2	-1.57459
1544	67150	Rnf141	ring finger protein 141	0	4	1	-1.57439
1545	26456	Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic doma	0	3	2	-1.57412
1546	109075	Exosc4	exosome component 4	0	3	2	-1.57407
1547	19895	Rpia	ribose 5-phosphate isomerase A	0	4	0	-1.5735
1548	64378	Gpr88	G-protein coupled receptor 88	0	3	2	-1.57317
1549	20276	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	0	4	1	-1.57309
1550	93967	Klra20	killer cell lectin-like receptor subfamily A, member 20	0	3	2	-1.57277

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1551	67272	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5	0	3	2	-1.57185
1552	218865	Chdh	choline dehydrogenase	0	3	2	-1.57123
1553	56496	Tspan6	tetraspanin 6	0	4	1	-1.57115
1554	21855	Timm17b	translocase of inner mitochondrial membrane 17b	0	3	2	-1.57079
1555	65100	Zic5	zinc finger protein of the cerebellum 5	0	3	2	-1.57064
1556	258453	Olfr1209	olfactory receptor 1209	0	3	2	-1.5705
1557	67395	4930403L05Rik	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 9	0	5	0	-1.56996
1558	15959	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	0	3	2	-1.56954
1559	594844	Tceal3	transcription elongation factor A (SII)-like 3	0	3	1	-1.56907
1560	235316	UNK	NA	0	3	2	-1.56899
1561	67778	Zfp639	zinc finger protein 639	0	3	2	-1.56889
1562	497106	Rnase12	ribonuclease, RNase A family, 12 (non-active)	0	3	2	-1.56871
1563	19132	Prph1	peripherin	0	4	1	-1.56869
1564	67106	Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	0	3	2	-1.56867
1565	20471	Six1	sine oculis-related homeobox 1 homolog (Drosophila)	0	3	2	-1.56839
1566	20851	Stat5b	signal transducer and activator of transcription 5B	0	3	2	-1.56798
1567	26396	Map2k2	mitogen-activated protein kinase kinase 2	0	5	5	-1.56773
1568	216781	Trim58	tripartite motif-containing 58	0	3	2	-1.56714
1569	381574	UNK	NA	0	3	2	-1.56645
1570	381358	LOC381358	NA	0	4	6	-1.56602
1571	12549	Cdgap	Rho GTPase activating protein 31	0	3	2	-1.56597
1572	14601	Ghrh	growth hormone releasing hormone	0	3	2	-1.56564
1573	75717	Cul5	cullin 5	0	3	2	-1.56542
1574	170935	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	0	3	2	-1.56527
1575	66506	1810042K04Rik	proteasome (prosome, macropain) assembly chaperone 3	0	5	0	-1.56526
1576	240095	D130003B22Rik	histocompatibility 2, M region locus 5	0	3	2	-1.56479
1577	213484	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	0	4	1	-1.56473
1578	12345	Capzb	capping protein (actin filament) muscle Z-line, beta	0	3	1	-1.56459
1579	11520	Adfp	perilipin 2	0	3	2	-1.56414
1580	22165	Txk	TXK tyrosine kinase	0	3	2	-1.56401
1581	235293	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	0	3	2	-1.564
1582	101502	Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0	3	2	-1.56391
1583	67145	Tomm34	translocase of outer mitochondrial membrane 34	0	4	1	-1.56352
1584	56031	Ppie	peptidylprolyl isomerase E (cyclophilin E)	0	4	1	-1.56346
1585	18146	Npdc1	neural proliferation, differentiation and control gene 1	0	4	1	-1.56286
1586	27373	Csnk1e	casein kinase 1, epsilon	0	3	1	-1.5624
1587	17293	Mesp2	mesoderm posterior 2	0	5	0	-1.56211

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1588	244144	Usp35	ubiquitin specific peptidase 35	0	4	1	-1.56179
1589	75083	Usp50	ubiquitin specific peptidase 50	0	4	1	-1.56172
1590	16149	Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	0	3	2	-1.56119
1591	436380	UNK	NA	0	3	2	-1.56097
1592	69601	Dab2ip	disabled homolog 2 (Drosophila) interacting protein	0	3	2	-1.5605
1593	338367	Myo1d	myosin ID	0	3	2	-1.56018
1594	12427	Ccna1	cyclin A1	0	4	1	-1.55952
1595	11486	Ada	adenosine deaminase	0	3	2	-1.55933
1596	433259	LOC433259	NA	0	3	2	-1.55912
1597	19883	Rora	RAR-related orphan receptor alpha	0	4	6	-1.5577
1598	218772	Rarb	retinoic acid receptor, beta	0	3	2	-1.55724
1599	382590	UNK	NA	0	3	2	-1.55714
1600	317757	Gimap5	GTPase, IMAP family member 5	0	3	2	-1.55661
1601	16480	Jup	junction plakoglobin	0	3	2	-1.55661
1602	67862	2310033P09Rik	RIKEN cDNA 2310033P09 gene	0	3	2	-1.55527
1603	434656	UNK	NA	0	4	1	-1.55498
1604	14251	Flot1	flotillin 1	0	3	2	-1.55495
1605	66839	0610009O20Rik	RIKEN cDNA 0610009O20 gene	0	3	2	-1.55478
1606	57278	Bcam	basal cell adhesion molecule	0	3	2	-1.55476
1607	110355	Adrbk1	adrenergic receptor kinase, beta 1	0	3	2	-1.55467
1608	385234	LOC385234	predicted gene 5376	0	3	2	-1.55452
1609	433182	LOC433182	predicted gene 5506	0	4	1	-1.55395
1610	192976	BC046404	cDNA sequence BC046404	0	4	1	-1.55362
1611	30954	Siva	SIVA1, apoptosis-inducing factor	0	3	2	-1.55299
1612	69159	Rhebl1	Ras homolog enriched in brain like 1	0	4	1	-1.55284
1613	17769	Mthfr	5,10-methylenetetrahydrofolate reductase	0	3	2	-1.55284
1614	72482	Acbd6	acyl-Coenzyme A binding domain containing 6	0	3	2	-1.55279
1615	106707	Rpusd1	RNA pseudouridylate synthase domain containing 1	0	3	2	-1.55248
1616	53378	Sdcbp	syndecan binding protein	0	3	2	-1.5519
1617	56009	Refbp2	Aly/REF export factor 2	0	3	2	-1.55187
1618	22275	Urod	uroporphyrinogen decarboxylase	0	3	2	-1.55139
1619	58187	Cldn10	claudin 10	0	3	2	-1.55125
1620	108927	Lhfp	lipoma HMGIC fusion partner	0	3	2	-1.55037
1621	12176	Bnip3	BCL2/adenovirus E1B interacting protein 3	0	4	1	-1.5501
1622	434436	LOC434436	cDNA sequence BY080835	0	3	2	-1.5501
1623	11418	Accn1	amiloride-sensitive cation channel 1, neuronal (degenerin)	0	3	2	-1.55007
1624	75553	Zc3h14	zinc finger CCCH type containing 14	0	4	1	-1.54948

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1625	54128	Pmm2	phosphomannomutase 2	0	3	2	-1.54944
1626	12808	Cobl	cordon-bleu	0	3	2	-1.54936
1627	11853	Rhoc	ras homolog gene family, member C	0	3	2	-1.54919
1628	70560	Wars2	tryptophanyl tRNA synthetase 2 (mitochondrial)	0	3	2	-1.549
1629	231842	6530401C20Rik	archaelysin family metallopeptidase 1	0	4	1	-1.54897
1630	18830	Pltp	phospholipid transfer protein	0	3	1	-1.54873
1631	57740	Stk32c	serine/threonine kinase 32C	0	5	0	-1.54848
1632	76501	Commd9	COMM domain containing 9	0	3	1	-1.54815
1633	69094	Tmem160	transmembrane protein 160	0	3	2	-1.54805
1634	76894	Mett5d1	methyltransferase like 15	0	4	1	-1.54765
1635	77891	Ube2s	ubiquitin-conjugating enzyme E2S	0	4	6	-1.54743
1636	243755	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	0	4	1	-1.54724
1637	18789	Papola	poly (A) polymerase alpha	0	3	1	-1.54723
1638	12896	Cpt2	carnitine palmitoyltransferase 2	0	3	2	-1.54712
1639	107375	AW491445	solute carrier family 25, member 45	0	3	2	-1.54626
1640	20850	Stat5a	signal transducer and activator of transcription 5A	0	3	2	-1.54601
1641	50774	Krtap5-1	keratin associated protein 5-1	0	3	2	-1.54589
1642	103742	1810046J19Rik	RIKEN cDNA 1810046J19 gene	0	3	1	-1.54563
1643	75572	Acyp2	acylphosphatase 2, muscle type	0	4	1	-1.54551
1644	66664	Tmem41a	transmembrane protein 41a	0	3	2	-1.54536
1645	56442	Serinc1	serine incorporator 1	0	3	2	-1.54534
1646	258584	Olfr1101	olfactory receptor 1101	0	3	1	-1.54513
1647	68146	Arl13b	ADP-ribosylation factor-like 13B	0	3	2	-1.54504
1648	53328	Pgrmc1	progesterone receptor membrane component 1	0	3	2	-1.54474
1649	228543	Rhov	ras homolog gene family, member V	0	4	1	-1.54444
1650	21854	Timm17a	translocase of inner mitochondrial membrane 17a	0	3	2	-1.54417
1651	69806	Slc39a11	solute carrier family 39 (metal ion transporter), member 11	0	3	2	-1.54406
1652	70239	Gtf3c5	general transcription factor IIIC, polypeptide 5	0	3	2	-1.54329
1653	230396	Ifna13	interferon alpha 13	0	3	2	-1.54285
1654	21991	Tpi1	triosephosphate isomerase 1	0	3	2	-1.54239
1655	15451	Hpn	hepsin	0	4	6	-1.54225
1656	69816	2010001M09Rik	RIKEN cDNA 2010001M09 gene	0	3	2	-1.54218
1657	57435	S3-12	perilipin 4	0	3	2	-1.54182
1658	75660	1810054G18Rik	lin-37 homolog (C. elegans)	0	3	1	-1.5417
1659	20168	Rtn3	reticulon 3	0	3	2	-1.54096
1660	225929	AV312086	protein associated with topoisomerase II homolog 1 (yeast)	0	3	2	-1.54056
1661	113856	V1rb8	vomeronasal 1 receptor 46	0	3	2	-1.54053

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1662	319184	Hist1h2bk	histone cluster 1, H2bk	0	3	2	-1.54044
1663	106326	Osbpl11	oxysterol binding protein-like 11	0	4	1	-1.53971
1664	329248	UNK	NA	0	3	2	-1.53961
1665	14582	Gfi1b	growth factor independent 1B	0	3	2	-1.53935
1666	432604	UNK	NA	0	4	1	-1.53927
1667	105245	Txndc5	thioredoxin domain containing 5	0	4	1	-1.53907
1668	231329	Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	0	3	2	-1.53885
1669	16881	Lig1	ligase I, DNA, ATP-dependent	0	4	1	-1.53878
1670	27390	Mmel1	membrane metallo-endopeptidase-like 1	0	4	1	-1.53851
1671	18628	Per3	period homolog 3 (Drosophila)	0	4	1	-1.5385
1672	16210	Impact	imprinted and ancient	0	3	1	-1.53839
1673	64697	Keg1	kidney expressed gene 1	0	3	2	-1.53807
1674	258372	Olfr918	olfactory receptor 918	0	3	1	-1.53806
1675	67979	Atad1	ATPase family, AAA domain containing 1	0	4	1	-1.53772
1676	56644	Clec7a	C-type lectin domain family 7, member a	0	3	2	-1.53741
1677	258390	Olfr1276	olfactory receptor 1276	0	3	2	-1.53728
1678	216178	UNK	NA	0	3	2	-1.5353
1679	94089	Trim7	tripartite motif-containing 7	0	3	2	-1.53494
1680	215415	Gm555	NA	0	3	2	-1.53476
1681	20931	Surf2	surfeit gene 2	0	4	1	-1.5347
1682	18000	39326	septin 2	0	4	1	-1.53443
1683	16008	Igfbp2	insulin-like growth factor binding protein 2	0	4	1	-1.53442
1684	226421	5430435G22Rik	RIKEN cDNA 5430435G22 gene	0	3	2	-1.53431
1685	13548	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	0	3	2	-1.5339
1686	18566	Pdcd1	programmed cell death 1	0	4	1	-1.53342
1687	16971	Lrp1	low density lipoprotein receptor-related protein 1	0	3	2	-1.53338
1688	18162	Npr3	natriuretic peptide receptor 3	0	4	6	-1.5333
1689	17229	Mcpt6	tryptase beta 2	0	3	2	-1.53313
1690	50772	Mapk6	mitogen-activated protein kinase 6	0	3	2	-1.53219
1691	17207	Mcf2l	mcf.2 transforming sequence-like	0	4	1	-1.53205
1692	385499	LOC385499	predicted pseudogene 5401	0	5	0	-1.53176
1693	258353	Olfr521	olfactory receptor 521	0	3	1	-1.53176
1694	53895	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	0	3	2	-1.53167
1695	15977	Ifnb1	interferon beta 1, fibroblast	0	3	2	-1.53167
1696	18088	Nkx2-2	NK2 transcription factor related, locus 2 (Drosophila)	0	3	2	-1.53099
1697	240754	Lax1	lymphocyte transmembrane adaptor 1	0	3	1	-1.5308
1698	27219	Sgk2	serum/glucocorticoid regulated kinase 2	0	3	2	-1.53076

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1699	13481	Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	0	3	2	-1.53041
1700	22778	Zfpn1a1	IKAROS family zinc finger 1	0	3	2	-1.53031
1701	214855	Arid5a	AT rich interactive domain 5A (MRF1-like)	0	3	1	-1.52976
1702	107568	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0	4	1	-1.52965
1703	50780	Rgs3	regulator of G-protein signaling 3	0	4	1	-1.52936
1704	19111	Prlpb	prolactin family 6, subfamily a, member 1	0	5	0	-1.52932
1705	11833	Aqp8	aquaporin 8	0	3	2	-1.52805
1706	13226	Defcr-rs7	defensin, alpha, related sequence 7	0	4	1	-1.528
1707	12122	Bid	BH3 interacting domain death agonist	0	3	2	-1.52774
1708	69269	Scnm1	sodium channel modifier 1	0	4	1	-1.5277
1709	76025	Cant1	calcium activated nucleotidase 1	0	3	2	-1.52731
1710	58205	Pdcd1lg2	programmed cell death 1 ligand 2	0	5	0	-1.5272
1711	83430	Il23a	interleukin 23, alpha subunit p19	0	4	1	-1.52701
1712	212919	Kctd7	potassium channel tetramerisation domain containing 7	0	3	2	-1.52699
1713	21432	Tcl1	T cell lymphoma breakpoint 1	0	4	1	-1.52649
1714	20277	Scnn1b	sodium channel, nonvoltage-gated 1 beta	0	3	2	-1.52636
1715	233824	Cog7	component of oligomeric golgi complex 7	0	3	2	-1.52606
1716	56869	Zfp109	zinc finger protein 109	0	3	2	-1.5258
1717	66898	Baiap2l1	BAI1-associated protein 2-like 1	0	4	1	-1.5257
1718	442804	A130066N16Rik	RIKEN cDNA A130066N16 gene	0	3	2	-1.52505
1719	93674	Cml3	camello-like 3	0	3	2	-1.52399
1720	214639	4930486L24Rik	RIKEN cDNA 4930486L24 gene	0	4	1	-1.52384
1721	67759	5033414D02Rik	RIKEN cDNA 5033414D02 gene	0	3	2	-1.52373
1722	435499	LOC435499	kinesin family member 2C pseudogene	0	4	1	-1.52367
1723	76580	Mib2	mindbomb homolog 2 (Drosophila)	0	4	1	-1.52345
1724	75870	Tcam1	testicular cell adhesion molecule 1	0	3	2	-1.52305
1725	19659	Rbp1	retinol binding protein 1, cellular	0	4	1	-1.52301
1726	15433	Hoxd13	homeobox D13	0	3	2	-1.52252
1727	230775	Bai2	brain-specific angiogenesis inhibitor 2	0	3	2	-1.52217
1728	14168	Fgf13	fibroblast growth factor 13	0	3	2	-1.52154
1729	109246	Tspan9	tetraspanin 9	0	3	2	-1.52087
1730	406220	4732484G22Rik	keratin 77	0	3	1	-1.52085
1731	385236	UNK	NA	0	3	2	-1.52074
1732	12351	Car4	carbonic anhydrase 4	0	3	2	-1.5205
1733	76560	Prss8	protease, serine, 8 (prostasin)	0	3	2	-1.52005
1734	12954	Cryaa	crystallin, alpha A	0	3	2	-1.51923
1735	20388	Sftpb	surfactant associated protein B	0	3	2	-1.51922

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1736	69654	Dctn2	dynactin 2	0	4	1	-1.51907
1737	15402	Hoxa5	homeobox A5	0	3	2	-1.51825
1738	20084	Rps18	ribosomal protein S18	0	3	2	-1.51817
1739	14874	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	0	3	2	-1.51718
1740	67868	Ela3	chymotrypsin-like elastase family, member 3B	0	3	2	-1.51652
1741	234964	Ccdc67	coiled-coil domain containing 67	0	3	1	-1.51635
1742	229395	UNK	NA	0	3	2	-1.51616
1743	20595	Smn1	survival motor neuron 1	0	3	2	-1.51564
1744	192163	Pcdha3	protocadherin alpha 3	0	3	2	-1.51559
1745	107029	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	0	3	2	-1.51544
1746	74309	Osbp2	oxysterol binding protein 2	0	3	2	-1.51539
1747	234395	Ushbp1	Usher syndrome 1C binding protein 1	0	3	2	-1.51524
1748	66464	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	3	2	-1.51491
1749	13549	Dyrk1b	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	0	3	2	-1.51449
1750	26385	Gprk6	G protein-coupled receptor kinase 6	0	3	2	-1.51434
1751	27416	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	0	4	1	-1.51432
1752	18226	Nup62	nucleoporin 62	0	4	1	-1.51279
1753	15464	Hrc	histidine rich calcium binding protein	0	5	0	-1.51244
1754	19293	Pvalb	parvalbumin	0	3	2	-1.5124
1755	226652	Arhgap30	Rho GTPase activating protein 30	0	3	2	-1.51203
1756	433680	UNK	NA	0	3	2	-1.51137
1757	20512	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	0	3	2	-1.51108
1758	109042	Prkcdbp	protein kinase C, delta binding protein	0	3	2	-1.51079
1759	226778	Mark1	MAP/microtubule affinity-regulating kinase 1	0	3	2	-1.51054
1760	19824	Trim10	tripartite motif-containing 10	0	3	2	-1.51047
1761	20135	Rrm2	ribonucleotide reductase M2	0	4	6	-1.51033
1762	432734	UNK	NA	0	3	2	-1.51007
1763	57260	Ltb4r2	leukotriene B4 receptor 2	0	3	2	-1.50971
1764	100087	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)	0	3	2	-1.50948
1765	76367	Trp53rk	transformation related protein 53 regulating kinase	0	3	2	-1.50935
1766	83493	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	0	3	2	-1.50909
1767	20908	Stx3	syntaxin 3	0	3	2	-1.50876
1768	17299	Mettl1	methyltransferase like 1	0	3	2	-1.50821
1769	26412	Map4k2	mitogen-activated protein kinase kinase kinase kinase 2	0	3	2	-1.50808
1770	53859	Map3k14	mitogen-activated protein kinase kinase kinase 14	0	3	2	-1.50788
1771	224923	UNK	NA	0	3	2	-1.50782
1772	54698	Crtam	cytotoxic and regulatory T cell molecule	0	3	2	-1.50761

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1773	66483	Rpl36al	ribosomal protein L36A-like	0	3	2	-1.50756
1774	27424	Klra16	killer cell lectin-like receptor, subfamily A, member 16	0	4	1	-1.50741
1775	228361	D030051N19Rik	autophagy/beclin 1 regulator 1	0	4	1	-1.50736
1776	14008	Etv2	ets variant gene 2	0	3	2	-1.50734
1777	12837	Col8a1	collagen, type VIII, alpha 1	0	3	2	-1.50719
1778	215085	Slc35f1	solute carrier family 35, member F1	0	3	2	-1.50685
1779	94232	Ubqln4	ubiquilin 4	0	3	2	-1.50643
1780	19703	Renbp	renin binding protein	0	3	2	-1.50625
1781	11634	Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	0	3	2	-1.50612
1782	13656	Egr4	early growth response 4	0	3	2	-1.50612
1783	76072	Rnf183	ring finger protein 183	0	3	1	-1.50575
1784	12968	Cryge	crystallin, gamma E	0	3	2	-1.50571
1785	16520	Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	0	3	2	-1.50556
1786	231836	LOC231836	predicted gene 4869	0	3	2	-1.50524
1787	12035	Bcat1	branched chain aminotransferase 1, cytosolic	0	3	2	-1.50472
1788	15421	Hoxc12	homeobox C12	0	4	1	-1.50409
1789	64685	Nmi	N-myc (and STAT) interactor	0	3	2	-1.50402
1790	12406	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	0	3	2	-1.50343
1791	433641	UNK	NA	0	3	2	-1.50248
1792	11657	Alb1	albumin	0	3	2	-1.50242
1793	74747	Ddit4	DNA-damage-inducible transcript 4	0	3	2	-1.50214
1794	224132	Dirc2	disrupted in renal carcinoma 2 (human)	0	3	2	-1.50192
1795	218630	Ung2	cyclin O	0	3	2	-1.50179
1796	15495	Hsd3b4	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4	0	4	1	-1.50143
1797	80905	Polh	polymerase (DNA directed), eta (RAD 30 related)	0	3	2	-1.50143
1798	76784	Mtif2	mitochondrial translational initiation factor 2	0	3	2	-1.5012
1799	214230	Pak6	p21 protein (Cdc42/Rac)-activated kinase 6	0	3	2	-1.50099
1800	242711	LOC242711	predicted gene 13011	0	3	2	-1.50063
1801	74477	4933427D14Rik	RIKEN cDNA 4933427D14 gene	0	3	1	-1.50057
1802	232717	BC048599	protease, serine 58	0	2	3	-3.86343
1803	241636	Tgm6	transglutaminase 6	0	2	3	-3.82875
1804	75345	Slamf7	SLAM family member 7	0	2	3	-3.82336
1805	73547	1700094E07Rik	dual specificity phosphatase 21	0	2	3	-3.59464
1806	100727	Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	0	2	3	-3.55165
1807	56224	Tspan5	tetraspanin 5	0	2	3	-3.4842
1808	19335	Rab23	RAB23, member RAS oncogene family	0	2	3	-3.34766
1809	66880	Rsrc1	arginine/serine-rich coiled-coil 1	0	2	3	-3.28096

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1810	50529	Mrps7	mitchondrial ribosomal protein S7	0	2	3	-3.20724
1811	258946	Olfr348	olfactory receptor 348	0	2	3	-3.20691
1812	19113	Prlpe	prolactin family 7, subfamily a, member 1	0	2	2	-3.14179
1813	226043	Cbwd1	COBW domain containing 1	0	2	3	-3.09471
1814	70546	Zdhhc2	zinc finger, DHHC domain containing 2	0	2	3	-3.08453
1815	15492	Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	0	2	3	-3.0783
1816	319740	Zfyve27	zinc finger, FYVE domain containing 27	0	2	2	-3.05664
1817	85305	Kars	lysyl-tRNA synthetase	0	2	3	-3.05455
1818	56314	Zfp113	zinc finger protein 113	0	2	3	-3.04627
1819	94187	Zfp423	zinc finger protein 423	0	2	3	-3.03109
1820	209824	V1rd15	vomeronasal 1 receptor 183	0	2	3	-3.02531
1821	258654	Olfr1135	olfactory receptor 1135	0	2	2	-3.02066
1822	66298	2010016B13Rik	defensin, alpha, 21	0	2	3	-3.01744
1823	20500	Slc13a2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	0	2	3	-3.01576
1824	16551	Kif11	kinesin family member 11	0	2	3	-2.99227
1825	108907	Nusap1	nucleolar and spindle associated protein 1	0	2	2	-2.98891
1826	64658	Mrps25	mitochondrial ribosomal protein S25	0	2	3	-2.97908
1827	107702	Rnh1	ribonuclease/angiogenin inhibitor 1	0	2	2	-2.95873
1828	241727	Snph	syntaphilin	0	2	3	-2.95662
1829	21402	Skp1a	S-phase kinase-associated protein 1A	0	2	3	-2.95501
1830	15278	Tfb2m	transcription factor B2, mitochondrial	0	2	3	-2.95034
1831	14625	Gykl1	glycerol kinase-like 1	0	2	3	-2.94475
1832	170786	Cd209a	CD209a antigen	0	2	3	-2.93982
1833	216445	Arhgap9	Rho GTPase activating protein 9	0	2	3	-2.93643
1834	66943	Pqlc1	PQ loop repeat containing 1	0	2	3	-2.91477
1835	19114	Prlpf	prolactin family 7, subfamily a, member 2	0	2	3	-2.90076
1836	57316	C1d	C1D nuclear receptor co-repressor	0	2	3	-2.88865
1837	321020	Fpr-rs6	formyl peptide receptor, related sequence 6	0	2	3	-2.8753
1838	216618	Ccdc104	coiled-coil domain containing 104	0	2	2	-2.87334
1839	66471	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0	2	3	-2.86886
1840	14810	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	0	2	3	-2.86533
1841	58193	Extl2	exostoses (multiple)-like 2	0	2	3	-2.82381
1842	71791	Cpa4	carboxypeptidase A4	0	2	3	-2.8107
1843	331188	BC024063	zinc finger protein 781	0	2	3	-2.79716
1844	75677	Cldn22	claudin 22	0	2	3	-2.79527
1845	18245	Oaz1	ornithine decarboxylase antizyme 1	0	2	2	-2.79338
1846	383073	UNK	NA	0	2	3	-2.79167

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1847	17164	Mapkapk2	MAP kinase-activated protein kinase 2	0	2	3	-2.79051
1848	16870	Lhx2	LIM homeobox protein 2	0	2	3	-2.78464
1849	103988	Gck	glucokinase	0	2	3	-2.78102
1850	52009	D17Ertd441e	hematological and neurological expressed 1-like	0	2	3	-2.77799
1851	14313	Fst	follistatin	0	2	3	-2.77597
1852	72486	2610206B13Rik	ring finger protein 219	0	2	3	-2.77452
1853	15043	H2-T3	histocompatibility 2, T region locus 3	0	2	3	-2.77197
1854	207227	Stxbp5l	syntaxin binding protein 5-like	0	2	3	-2.76255
1855	244179	4922504M18Rik	ubiquilin-like	0	2	3	-2.76175
1856	238599	Gm269	NA	0	2	3	-2.75177
1857	72654	Ccdc12	coiled-coil domain containing 12	0	2	3	-2.75154
1858	226049	Dmrt2	doublesex and mab-3 related transcription factor 2	0	2	3	-2.74901
1859	237847	Rtn4rl1	reticulon 4 receptor-like 1	0	2	3	-2.74846
1860	13871	Ercc2	excision repair cross-complementing rodent repair deficiency, complementation group 2	0	2	3	-2.74839
1861	17920	Myo6	myosin VI	0	2	3	-2.74388
1862	19271	Ptprj	protein tyrosine phosphatase, receptor type, J	0	2	3	-2.74175
1863	27411	Slc14a2	solute carrier family 14 (urea transporter), member 2	0	2	3	-2.7339
1864	105355	Slc17a3	solute carrier family 17 (sodium phosphate), member 3	0	2	3	-2.72188
1865	15519	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	0	2	3	-2.71712
1866	78977	Popdc3	popeye domain containing 3	0	2	3	-2.71416
1867	74996	Usp47	ubiquitin specific peptidase 47	0	2	3	-2.71274
1868	14915	Guca2a	guanylate cyclase activator 2a (guanylin)	0	2	3	-2.70569
1869	14805	Grik1	glutamate receptor, ionotropic, kainate 1	0	2	3	-2.7051
1870	230598	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	0	2	3	-2.7026
1871	14675	Gna14	guanine nucleotide binding protein, alpha 14	0	2	3	-2.70119
1872	432825	LOC432825	predicted gene 5458	0	2	3	-2.69808
1873	436244	UNK	NA	0	2	3	-2.69314
1874	99470	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	0	2	3	-2.6916
1875	242126	Slc22a15	solute carrier family 22 (organic anion/cation transporter), member 15	0	2	3	-2.68483
1876	232791	Cnot3	CCR4-NOT transcription complex, subunit 3	0	2	3	-2.68393
1877	18508	Pax6	paired box gene 6	0	2	3	-2.67987
1878	83561	Tdrd1	tudor domain containing 1	0	2	2	-2.67342
1879	12958	Cryba2	crystallin, beta A2	0	2	3	-2.655
1880	353170	4932441K18Rik	taxilin gamma	0	2	3	-2.64958
1881	11451	Acrv1	acrosomal vesicle protein 1	0	2	2	-2.64752
1882	236574	Gm1847	sperm motility kinase 2B	0	2	3	-2.64098
1883	78783	Brpf1	bromodomain and PHD finger containing, 1	0	2	2	-2.63932

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1884	23859	Dlgh2	discs, large homolog 2 (Drosophila)	0	2	3	-2.6369
1885	17149	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	0	2	3	-2.63581
1886	14077	Fabp3	fatty acid binding protein 3, muscle and heart	0	2	3	-2.63203
1887	272680	UNK	NA	0	2	3	-2.63105
1888	114713	Rasa2	RAS p21 protein activator 2	0	2	3	-2.63082
1889	233537	Gdpd4	glycerophosphodiester phosphodiesterase domain containing 4	0	2	3	-2.63049
1890	258348	Olfr1133	olfactory receptor 1133	0	2	3	-2.63048
1891	19170	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	0	2	3	-2.62613
1892	384890	UNK	NA	0	2	3	-2.62594
1893	79555	BC005537	cDNA sequence BC005537	0	2	3	-2.62541
1894	329738	4921525H12Rik	AKNA domain containing 1	0	2	3	-2.62541
1895	74616	Scrn3	secernin 3	0	2	3	-2.61872
1896	103098	Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	0	2	3	-2.61853
1897	56811	Dkk2	dickkopf homolog 2 (Xenopus laevis)	0	2	3	-2.61406
1898	12331	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	0	2	3	-2.61394
1899	113852	V1rb1	vomeronasal 1 receptor 50	0	2	3	-2.61316
1900	72124	Seh1l	SEH1-like (S. cerevisiae	0	2	3	-2.60744
1901	12476	Cd151	CD151 antigen	0	2	3	-2.58461
1902	11650	Akp5	alkaline phosphatase, placental-like 2	0	2	3	-2.58456
1903	12045	Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1b	0	2	3	-2.58432
1904	18597	Pdha1	pyruvate dehydrogenase E1 alpha 1	0	2	2	-2.58405
1905	67455	Klhl13	kelch-like 13 (Drosophila)	0	2	3	-2.56943
1906	258095	Olfr119	olfactory receptor 119	0	2	3	-2.56935
1907	77980	Sbf1	SET binding factor 1	0	2	3	-2.56572
1908	217127	Myst2	MYST histone acetyltransferase 2	0	2	3	-2.56495
1909	80906	Kcnip2	Kv channel-interacting protein 2	0	2	3	-2.56335
1910	18050	Klk1b3	kallikrein 1-related peptidase b3	0	2	3	-2.56277
1911	56771	Trfp	mediator complex subunit 20	0	2	3	-2.5624
1912	114142	Foxp2	forkhead box P2	0	2	3	-2.55862
1913	67775	Rtp4	receptor transporter protein 4	0	2	3	-2.55699
1914	12832	Col5a2	collagen, type V, alpha 2	0	2	3	-2.55455
1915	22702	Zfp42	zinc finger protein 42	0	2	3	-2.55192
1916	209815	Oatl1	TBC1 domain family, member 25	0	2	3	-2.54844
1917	56447	Copz1	coatomer protein complex, subunit zeta 1	0	2	3	-2.54408
1918	214238	UNK	NA	0	2	3	-2.54083
1919	75820	4930511H01Rik	WD repeat domain 64	0	2	3	-2.53974
1920	70673	Prdm16	PR domain containing 16	0	2	3	-2.53473

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1921	66131	Tipin	timeless interacting protein	0	2	3	-2.53349
1922	244199	Ovch2	ovochymase 2	0	2	3	-2.53307
1923	18191	Nrxn3	neurexin III	0	2	3	-2.53138
1924	68267	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	0	2	3	-2.53113
1925	29857	Mapk12	mitogen-activated protein kinase 12	0	2	3	-2.53108
1926	22632	Yy1	YY1 transcription factor	0	2	3	-2.5282
1927	74204	Xpo6	exportin 6	0	2	3	-2.52731
1928	56716	Gbl	MTOR associated protein, LST8 homolog (S. cerevisiae)	0	2	3	-2.52729
1929	435233	UNK	NA	0	2	3	-2.52707
1930	383525	Gm1295	NA	0	2	3	-2.52292
1931	213827	Arcn1	archain 1	0	2	3	-2.52243
1932	381038	Parl	presenilin associated, rhomboid-like	0	2	3	-2.51829
1933	71785	Pdgfd	platelet-derived growth factor, D polypeptide	0	2	3	-2.51404
1934	67028	2610002M06Rik	RIKEN cDNA 2610002M06 gene	0	2	3	-2.51357
1935	140579	Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	0	2	3	-2.51261
1936	15207	Hes3	hairy and enhancer of split 3 (Drosophila)	0	2	3	-2.51241
1937	228136	Zdhhc5	zinc finger, DHHC domain containing 5	0	2	3	-2.51116
1938	170750	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0	2	3	-2.50857
1939	329244	Il19	interleukin 19	0	2	3	-2.50816
1940	239857	Igsf4d	cell adhesion molecule 2	0	2	3	-2.50662
1941	54447	Asah2	N-acylsphingosine amidohydrolase 2	0	2	3	-2.50332
1942	258699	Olfr1446	olfactory receptor 1446	0	2	3	-2.50065
1943	19024	Ppfibp2	PTPRF interacting protein, binding protein 2 (liprin beta 2)	0	2	3	-2.50034
1944	110446	Acat1	acetyl-Coenzyme A acetyltransferase 1	0	2	3	-2.49926
1945	108978	4930555G01Rik	RIKEN cDNA 4930555G01 gene	0	2	3	-2.49865
1946	14191	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	0	2	3	-2.4962
1947	268860	Abat	4-aminobutyrate aminotransferase	0	2	3	-2.49543
1948	66556	Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	0	2	3	-2.49101
1949	223809	Smgc	submandibular gland protein C	0	2	2	-2.48992
1950	19242	Ptn	pleiotrophin	0	2	3	-2.48712
1951	235028	Zfp426	zinc finger protein 426	0	2	3	-2.48652
1952	67429	Nudcd1	NudC domain containing 1	0	2	2	-2.48627
1953	18810	Plec1	plectin	0	2	3	-2.48371
1954	93790	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	0	2	3	-2.48115
1955	57781	Cd200r1	CD200 receptor 1	0	2	3	-2.4809
1956	381530	MGC107671	major urinary protein 20	0	2	3	-2.47674
1957	67427	Rps20	ribosomal protein S20	0	2	3	-2.47402

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1958	13018	Ctcf	CCCTC-binding factor	0	2	3	-2.47295
1959	229877	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	0	2	3	-2.47259
1960	56868	Psg23	pregnancy-specific glycoprotein 23	0	2	3	-2.47112
1961	13525	Adam26a	a disintegrin and metallopeptidase domain 26A (testase 3)	0	2	3	-2.4705
1962	67465	Sf3a1	splicing factor 3a, subunit 1	0	2	3	-2.46804
1963	68801	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	0	2	3	-2.46781
1964	114249	Npnt	nephronectin	0	2	3	-2.4675
1965	381599	UNK	NA	0	2	3	-2.46749
1966	81701	Egfl8	EGF-like domain 8	0	2	2	-2.46669
1967	93725	Ear10	eosinophil-associated, ribonuclease A family, member 10	0	2	3	-2.46377
1968	19715	Rex2	NA	0	2	3	-2.46158
1969	18760	Prkcm	protein kinase D1	0	2	3	-2.45965
1970	170459	Stard4	StAR-related lipid transfer (START) domain containing 4	0	2	3	-2.45728
1971	11793	Atg5	autophagy-related 5 (yeast)	0	2	3	-2.45652
1972	73024	2900064A13Rik	RIKEN cDNA 2900064A13 gene	0	2	2	-2.4541
1973	57436	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	0	2	3	-2.45271
1974	382006	LOC382006	NA	0	2	3	-2.4452
1975	216456	Gls2	glutaminase 2 (liver, mitochondrial)	0	2	2	-2.44481
1976	13853	Epm2a	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	0	2	3	-2.44152
1977	192113	Atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	0	2	3	-2.4413
1978	71375	Ches1	forkhead box N3	0	2	3	-2.44057
1979	20290	Ccl1	chemokine (C-C motif) ligand 1	0	2	3	-2.43565
1980	50773	Nt5c	5',3'-nucleotidase, cytosolic	0	2	2	-2.43132
1981	271639	Sacy	adenylate cyclase 10	0	2	3	-2.43121
1982	21420	Tcfap2c	transcription factor AP-2, gamma	0	2	3	-2.43082
1983	73866	4930432H15Rik	family with sequence similarity 122, member C	0	2	2	-2.42933
1984	258281	Olfr780	olfactory receptor 780	0	2	2	-2.42668
1985	16469	Jrk	jerky	0	2	2	-2.42505
1986	14776	Gpx2	glutathione peroxidase 2	0	2	3	-2.42449
1987	78789	Vsig1	V-set and immunoglobulin domain containing 1	0	2	3	-2.42439
1988	76282	Gpt1	glutamic pyruvic transaminase, soluble	0	2	3	-2.42403
1989	76877	Rab36	RAB36, member RAS oncogene family	0	2	3	-2.423
1990	14712	Gnpat	glyceronephosphate O-acyltransferase	0	2	2	-2.42186
1991	26374	Rfwd2	ring finger and WD repeat domain 2	0	2	3	-2.42178
1992	66411	Ckap1	tubulin folding cofactor B	0	2	3	-2.42102
1993	258755	Olfr672	olfactory receptor 672	0	2	3	-2.42085
1994	223631	BC025446	cDNA sequence BC025446	0	2	3	-2.41828

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1995	12615	Cenpa	centromere protein A	0	2	3	-2.41777
1996	208084	AI449441	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0	2	3	-2.41689
1997	433501	LOC433501	NA	0	2	3	-2.41578
1998	18607	Pdpk1	3-phosphoinositide dependent protein kinase 1	0	2	3	-2.41538
1999	53857	Tuba8	tubulin, alpha 8	0	2	3	-2.41509
2000	27756	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	2	3	-2.41503
2001	22301	V2r10	vomeronasal 2, receptor 89	0	2	3	-2.415
2002	20911	Stxbp2	syntaxin binding protein 2	0	2	3	-2.41407
2003	74121	Acoxl	acyl-Coenzyme A oxidase-like	0	2	3	-2.41345
2004	16842	Lef1	lymphoid enhancer binding factor 1	0	2	3	-2.41076
2005	11556	Adrb3	adrenergic receptor, beta 3	0	2	3	-2.40989
2006	14538	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	0	2	3	-2.40903
2007	93897	Fzd10	frizzled homolog 10 (Drosophila)	0	2	2	-2.40798
2008	18343	Olfr44	olfactory receptor 44	0	2	2	-2.40777
2009	21975	Top3a	topoisomerase (DNA) III alpha	0	2	3	-2.40723
2010	18014	Neurog1	neurogenin 1	0	2	2	-2.4024
2011	53311	Mybph	myosin binding protein H	0	2	2	-2.4016
2012	16198	Il9	interleukin 9	0	2	3	-2.40114
2013	382206	Ssx9	synovial sarcoma, X breakpoint 9	0	2	2	-2.40075
2014	69511	Klk12	kallikrein related-peptidase 12	0	2	3	-2.39939
2015	16675	Krt1-c29	keratin 27	0	2	3	-2.39845
2016	386422	UNK	NA	0	2	3	-2.39831
2017	17884	Myh4	myosin, heavy polypeptide 4, skeletal muscle	0	2	3	-2.39819
2018	12965	Crygb	crystallin, gamma B	0	2	3	-2.39764
2019	11501	Adam8	a disintegrin and metallopeptidase domain 8	0	2	3	-2.39655
2020	83429	Ctns	cystinosis, nephropathic	0	2	3	-2.39635
2021	14400	Gabrb1	gamma-aminobutyric acid (GABA) A receptor, subunit beta 1	0	2	3	-2.39483
2022	72780	Rspo3	R-spondin 3 homolog (Xenopus laevis)	0	2	3	-2.39015
2023	433073	LOC433073	actin related protein 2/3 complex, subunit 2 pseudogene	0	2	3	-2.39013
2024	14080	Fabp1	fatty acid binding protein 1, liver	0	2	3	-2.38966
2025	236790	6330505F04Rik	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	0	2	3	-2.38906
2026	17138	Magea2	melanoma antigen, family A, 2	0	2	3	-2.38472
2027	109660	Ctrl	chymotrypsin-like	0	2	3	-2.38241
2028	16549	Khsrp	KH-type splicing regulatory protein	0	2	3	-2.37718
2029	54390	Sit1	suppression inducing transmembrane adaptor 1	0	2	3	-2.37685
2030	56298	Arl6ip2	atlastin GTPase 2	0	2	2	-2.37389
2031	66827	Ttc1	tetratricopeptide repeat domain 1	0	2	3	-2.37312

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2032	171207	Arhgap4	Rho GTPase activating protein 4	0	2	3	-2.37282
2033	66736	4921531G14Rik	tetratricopeptide repeat domain 35	0	2	3	-2.37277
2034	329919	A430070M19	selection and upkeep of intraepithelial T cells 2	0	2	2	-2.37139
2035	100604	Lrrc8c	leucine rich repeat containing 8 family, member C	0	2	2	-2.37007
2036	18749	Prkacb	protein kinase, cAMP dependent, catalytic, beta	0	2	3	-2.36768
2037	117229	Stk33	serine/threonine kinase 33	0	2	3	-2.36383
2038	72181	Nsun4	NOL1/NOP2/Sun domain family, member 4	0	2	3	-2.36172
2039	14811	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	0	2	3	-2.36033
2040	246196	Zfp277	zinc finger protein 277	0	2	3	-2.3561
2041	224705	Vps52	vacuolar protein sorting 52 (yeast)	0	2	3	-2.35534
2042	235324	UNK	NA	0	2	3	-2.35495
2043	258704	Olfr411	olfactory receptor 411	0	2	3	-2.35355
2044	216443	Mars	methionine-tRNA synthetase	0	2	3	-2.3529
2045	58234	Shank3	SH3/ankyrin domain gene 3	0	2	3	-2.35232
2046	104111	Adcy3	adenylate cyclase 3	0	2	3	-2.35218
2047	353325	Tas2r115	taste receptor, type 2, member 115	0	2	3	-2.35212
2048	21953	Tnni2	troponin I, skeletal, fast 2	0	2	2	-2.35203
2049	68420	Ankrd13a	ankyrin repeat domain 13a	0	2	2	-2.3515
2050	433180	LOC433180	serine peptidase inhibitor, Kazal type 6	0	2	3	-2.34999
2051	12649	Chek1	checkpoint kinase 1	0	2	3	-2.34758
2052	17144	Magea8	melanoma antigen, family A, 8	0	2	3	-2.34748
2053	30956	Aass	aminoadipate-semialdehyde synthase	0	2	3	-2.34499
2054	67154	Mtdh	metadherin	0	2	3	-2.34464
2055	13489	Drd2	dopamine receptor D2	0	2	3	-2.34426
2056	17901	Myl1	myosin, light polypeptide 1	0	2	3	-2.34153
2057	16923	Lnk	SH2B adaptor protein 3	0	2	3	-2.33855
2058	67276	Thex1	exoribonuclease 1	0	2	3	-2.33764
2059	67719	2310057J18Rik	RIKEN cDNA 2310057J18 gene	0	2	2	-2.33676
2060	66586	Crls1	cardiolipin synthase 1	0	2	3	-2.3367
2061	216395	Tmem5	transmembrane protein 5	0	2	3	-2.33627
2062	20973	Syngr2	synaptogyrin 2	0	2	3	-2.3296
2063	66302	2410005O16Rik	family with sequence similarity 82, member B	0	2	2	-2.32892
2064	214779	9630041N07Rik	zinc figer protein 879	0	2	3	-2.32727
2065	67281	Rpl37	ribosomal protein L37	0	2	3	-2.32439
2066	14803	Grid1	glutamate receptor, ionotropic, delta 1	0	2	3	-2.32428
2067	66889	Rnf128	ring finger protein 128	0	2	3	-2.32395
2068	69032	Lyzl4	lysozyme-like 4	0	2	3	-2.32253

Candidates for positive regulators of normal growth (Fisher's)

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2069	101533	Klk9	kallikrein related-peptidase 9	0	2	2	-2.31849
2070	224805	Aarsl	alanyl-tRNA synthetase 2, mitochondrial (putative)	0	2	3	-2.31686
2071	66601	Tmigd	transmembrane and immunoglobulin domain containing 1	0	2	3	-2.31633
2072	230991	B930041F14Rik	RIKEN cDNA B930041F14 gene	0	2	3	-2.31228
2073	13839	Epha5	Eph receptor A5	0	2	3	-2.31061
2074	52163	Camk1	calcium/calmodulin-dependent protein kinase I	0	2	3	-2.31007
2075	217431	Nol10	nucleolar protein 10	0	2	2	-2.30815
2076	171283	Havcr1	hepatitis A virus cellular receptor 1	0	2	3	-2.30674
2077	72149	2610019A05Rik	STE20-related kinase adaptor alpha	0	2	3	-2.30285
2078	229541	Dennd4b	DENN/MADD domain containing 4B	0	2	3	-2.30217
2079	280621	BC089491	cDNA sequence BC089491	0	2	2	-2.30154
2080	433642	UNK	NA	0	2	3	-2.30123
2081	207958	Alg11	asparagine-linked glycosylation 11 homolog (yeast, alpha-1,2-mannosyltransferase)	0	2	3	-2.29927
2082	108014	Sfrs9	serine/arginine-rich splicing factor 9	0	2	2	-2.29906
2083	321021	Fpr-rs7	formyl peptide receptor, related sequence 7	0	2	3	-2.29836
2084	232044	UNK	NA	0	2	3	-2.29774
2085	30932	Zfp330	zinc finger protein 330	0	2	3	-2.29738
2086	18399	Slc22a6	solute carrier family 22 (organic anion transporter), member 6	0	2	3	-2.29626
2087	259108	Olfr550	olfactory receptor 550	0	2	3	-2.29612
2088	93888	Pcdhb17	protocadherin beta 17	0	2	3	-2.29522
2089	69352	Efcbp1	N-terminal EF-hand calcium binding protein 1	0	2	3	-2.29485
2090	18947	Pnliprp2	pancreatic lipase-related protein 2	0	2	3	-2.29425
2091	75871	4930566A11Rik	zinc finger protein 821	0	2	3	-2.29283
2092	11287	Pzp	pregnancy zone protein	0	2	3	-2.2925
2093	14262	Fmo3	flavin containing monooxygenase 3	0	2	3	-2.29226
2094	13090	Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19	0	2	3	-2.29222
2095	80903	Fgf16	fibroblast growth factor 16	0	2	3	-2.29018
2096	214597	Sidt2	SID1 transmembrane family, member 2	0	2	3	-2.288
2097	258697	Olfr1444	olfactory receptor 1444	0	2	3	-2.2867
2098	72391	Cdkn3	cyclin-dependent kinase inhibitor 3	0	2	3	-2.28419
2099	71355	Col24a1	collagen, type XXIV, alpha 1	0	2	3	-2.28058
2100	435777	UNK	NA	0	2	3	-2.2782
2101	19400	Rapsn	receptor-associated protein of the synapse	0	2	3	-2.27528
2102	71804	2610016C23Rik	family with sequence similarity 54, member A	0	2	3	-2.27492
2103	69732	2410018L13Rik	RIKEN cDNA 2410018L13 gene	0	2	3	-2.27487
2104	258075	Olfr832	olfactory receptor 832	0	2	3	-2.27402
2105	107513	Ssr1	signal sequence receptor, alpha	0	2	3	-2.27358

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2106	217116	Spata20	spermatogenesis associated 20	0	2	3	-2.27348
2107	207728	Pde2a	phosphodiesterase 2A, cGMP-stimulated	0	2	3	-2.27248
2108	258711	Olfr432	olfactory receptor 432	0	2	3	-2.27204
2109	67054	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarb	0	2	3	-2.27191
2110	68231	1700113O17Rik	H2A histone family, member B1	0	2	3	-2.27114
2111	258630	Olfr1141	olfactory receptor 1141	0	2	2	-2.27076
2112	67065	Polr3d	polymerase (RNA) III (DNA directed) polypeptide D	0	2	3	-2.27005
2113	93700	Pcdhgb2	protocadherin gamma subfamily B, 2	0	2	3	-2.2683
2114	268391	A830031A19Rik	RIKEN cDNA A830031A19 gene	0	2	3	-2.26748
2115	12371	Casp9	caspase 9	0	2	3	-2.2674
2116	67239	Bxdc1	ribosome production factor 2 homolog (S. cerevisiae)	0	2	2	-2.26723
2117	13664	Eif1a	eukaryotic translation initiation factor 1A	0	2	3	-2.26676
2118	26560	Krtap15	keratin associated protein 15	0	2	3	-2.26562
2119	244555	UNK	NA	0	2	3	-2.26466
2120	55934	Rp9h	retinitis pigmentosa 9 (human)	0	2	3	-2.26305
2121	20307	Ccl8	chemokine (C-C motif) ligand 8	0	2	2	-2.26113
2122	192161	Pcdha9	protocadherin alpha 9	0	2	3	-2.2607
2123	270097	AI427515	vesicle amine transport protein 1 homolog-like (T. californica)	0	2	3	-2.26034
2124	20739	Spna1	spectrin alpha 1	0	2	3	-2.25946
2125	17350	Mlh1	mutL homolog 1 (E. coli)	0	2	3	-2.25872
2126	12369	Casp7	caspase 7	0	2	3	-2.25799
2127	19087	Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	0	2	3	-2.25797
2128	20446	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltran	0	2	3	-2.25792
2129	23988	Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	0	2	3	-2.25665
2130	269523	Vcp	valosin containing protein	0	2	3	-2.25412
2131	17256	Mea1	male enhanced antigen 1	0	2	3	-2.2535
2132	224344	Rbm11	RNA binding motif protein 11	0	2	2	-2.2531
2133	20315	Cxcl12	chemokine (C-X-C motif) ligand 12	0	2	3	-2.25236
2134	17169	Mark3	MAP/microtubule affinity-regulating kinase 3	0	2	3	-2.25079
2135	18798	Plcb4	phospholipase C, beta 4	0	2	3	-2.25026
2136	66716	4921510H08Rik	RIKEN cDNA 4921510H08 gene	0	2	2	-2.25014
2137	68988	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	0	2	3	-2.24749
2138	171256	V1ri5	vomeronasal 1 receptor 218	0	2	3	-2.24734
2139	12286	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0	2	3	-2.24726
2140	80720	Pbx4	pre B cell leukemia homeobox 4	0	2	3	-2.2469
2141	231986	AI591476	JAZF zinc finger 1	0	2	3	-2.24603
2142	69726	Smyd3	SET and MYND domain containing 3	0	2	3	-2.24468

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2143	74409	4932701A20Rik	hyaluronoglucosaminidase 6	0	2	3	-2.24351
2144	24117	Wif1	Wnt inhibitory factor 1	0	2	3	-2.24291
2145	18647	Pftk1	cyclin-dependent kinase 14	0	2	3	-2.24262
2146	14860	Gsta4	glutathione S-transferase, alpha 4	0	2	3	-2.23851
2147	70361	Lman1	lectin, mannose-binding, 1	0	2	3	-2.23729
2148	230596	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	0	2	3	-2.2372
2149	15953	Ifi47	interferon gamma inducible protein 47	0	2	3	-2.23607
2150	407823	Baz2b	bromodomain adjacent to zinc finger domain, 2B	0	2	3	-2.2353
2151	80914	Uck2	uridine-cytidine kinase 2	0	2	3	-2.2349
2152	70363	1700010C24Rik	family with sequence similarity 135, member B	0	2	2	-2.23441
2153	18515	Pbx2	pre B cell leukemia homeobox 2	0	2	3	-2.23317
2154	226849	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	0	2	3	-2.23302
2155	69930	Zfp715	zinc finger protein 715	0	2	3	-2.23295
2156	70797	Ankib1	ankyrin repeat and IBR domain containing 1	0	2	2	-2.23249
2157	11363	Acadl	acyl-Coenzyme A dehydrogenase, long-chain	0	2	3	-2.23068
2158	19732	Rgl2	ral guanine nucleotide dissociation stimulator-like 2	0	2	3	-2.2281
2159	66722	Spag16	sperm associated antigen 16	0	2	2	-2.22721
2160	258620	Olfr350	olfactory receptor 350	0	2	2	-2.22677
2161	11694	Alx3	aristaless-like homeobox 3	0	2	3	-2.22547
2162	66901	Proz	protein Z, vitamin K-dependent plasma glycoprotein	0	2	3	-2.22231
2163	74153	Ube1l	ubiquitin-like modifier activating enzyme 7	0	2	3	-2.22204
2164	13972	Gnb1l	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	0	2	3	-2.22166
2165	17474	Clec4d	C-type lectin domain family 4, member d	0	2	3	-2.22007
2166	15415	Hoxb7	homeobox B7	0	2	3	-2.21891
2167	329260	BC042698	DENN/MADD domain containing 1B	0	2	3	-2.21871
2168	219131	Phf11	PHD finger protein 11	0	2	3	-2.21856
2169	74011	Slc25a27	solute carrier family 25, member 27	0	2	3	-2.21853
2170	67117	Dynlt3	dynein light chain Tctex-type 3	0	2	3	-2.21773
2171	208518	Cep78	centrosomal protein 78	0	2	3	-2.21628
2172	101739	Psip1	PC4 and SFRS1 interacting protein 1	0	2	3	-2.21574
2173	67211	2810037C14Rik	armadillo repeat containing 10	0	2	3	-2.21552
2174	59042	Cope	coatomer protein complex, subunit epsilon	0	2	3	-2.2148
2175	73720	Cst6	cystatin E/M	0	2	3	-2.21363
2176	394436	Ugt1a1	UDP glucuronosyltransferase 1 family, polypeptide A1	0	2	3	-2.21303
2177	234396	Ankrd41	ankyrin repeat and LEM domain containing 1	0	2	2	-2.21283
2178	76889	Adck4	aarF domain containing kinase 4	0	2	3	-2.21173
2179	15382	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	0	2	3	-2.21159

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2180	435230	UNK	NA	0	2	3	-2.21092
2181	93970	Klra18	killer cell lectin-like receptor, subfamily A, member 18	0	2	3	-2.21016
2182	69962	2810422O20Rik	RIKEN cDNA 2810422O20 gene	0	2	2	-2.20854
2183	78330	1500032D16Rik	NADH dehydrogenase (ubiquinone) flavoprotein 3	0	2	3	-2.20699
2184	24064	Spry2	sprouty homolog 2 (Drosophila)	0	2	3	-2.20546
2185	22262	Uox	urate oxidase	0	2	3	-2.20507
2186	69536	Hemk1	HemK methyltransferase family member 1	0	2	8	-2.20301
2187	217169	Tns4	tensin 4	0	2	2	-2.20301
2188	14017	Evi2a	ecotropic viral integration site 2a	0	2	3	-2.203
2189	20737	Spn	sialophorin	0	2	3	-2.20266
2190	12400	Cbfb	core binding factor beta	0	2	3	-2.20263
2191	50911	Exosc9	exosome component 9	0	2	3	-2.20233
2192	12465	Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	0	2	3	-2.20212
2193	72082	Cyp2c55	cytochrome P450, family 2, subfamily c, polypeptide 55	0	2	2	-2.20207
2194	73379	Dcbld2	discoidin, CUB and LCCL domain containing 2	0	2	3	-2.20031
2195	71952	2410016O06Rik	RIKEN cDNA 2410016O06 gene	0	2	2	-2.19639
2196	18516	Pbx3	pre B cell leukemia homeobox 3	0	2	3	-2.19626
2197	83602	Gtf2a1	general transcription factor II A, 1	0	2	3	-2.19527
2198	76701	Ctrc	chymotrypsin C (caldecrin)	0	2	3	-2.19526
2199	72459	Htatsf1	HIV TAT specific factor 1	0	2	3	-2.19479
2200	382588	UNK	NA	0	2	3	-2.19135
2201	56456	Actl6a	actin-like 6A	0	2	2	-2.19074
2202	54611	Pde3a	phosphodiesterase 3A, cGMP inhibited	0	2	3	-2.18852
2203	14679	Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3	0	2	3	-2.1869
2204	53867	Col5a3	collagen, type V, alpha 3	0	2	3	-2.18591
2205	18600	Padi2	peptidyl arginine deiminase, type II	0	2	3	-2.18544
2206	116701	Fgfrl1	fibroblast growth factor receptor-like 1	0	2	3	-2.18533
2207	11552	Adra2b	adrenergic receptor, alpha 2b	0	2	3	-2.18516
2208	15372	Hmx2	H6 homeobox 2	0	2	3	-2.1839
2209	106052	Fbxo4	F-box protein 4	0	2	3	-2.18244
2210	56615	Mgst1	microsomal glutathione S-transferase 1	0	2	3	-2.18197
2211	103963	Rpn1	ribophorin I	0	2	3	-2.1815
2212	74185	Gbe1	glucan (1,4-alpha-), branching enzyme 1	0	2	3	-2.18139
2213	20259	Scin	scinderin	0	2	3	-2.17864
2214	384313	UNK	NA	0	2	2	-2.1783
2215	242317	LOC242317	NA	0	2	3	-2.17755
2216	99683	Sec24b	Sec24 related gene family, member B (S. cerevisiae)	0	2	3	-2.1775

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2217	11550	Adra1d	adrenergic receptor, alpha 1d	0	2	3	-2.1766
2218	76654	Upp2	uridine phosphorylase 2	0	2	2	-2.17539
2219	22210	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	0	2	3	-2.17529
2220	17153	Mal	myelin and lymphocyte protein, T cell differentiation protein	0	2	3	-2.17383
2221	338467	Morc3	microrchidia 3	0	2	3	-2.17346
2222	353188	Adam32	a disintegrin and metallopeptidase domain 32	0	2	3	-2.17277
2223	195434	Utp14b	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)	0	2	3	-2.17112
2224	20997	T	brachyury	0	2	3	-2.1706
2225	17756	Mtap2	microtubule-associated protein 2	0	2	3	-2.17032
2226	104444	Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	0	2	3	-2.16895
2227	13048	Cutl2	cut-like homeobox 2	0	2	3	-2.16895
2228	209776	Gpr139	G protein-coupled receptor 139	0	2	2	-2.16859
2229	14950	H13	histocompatibility 13	0	2	3	-2.16849
2230	230779	Serinc2	serine incorporator 2	0	2	3	-2.16607
2231	18139	Zfml	zinc finger, matrin-like	0	2	2	-2.16593
2232	243862	BC050099	pregnancy-specific glycoprotein 22	0	2	3	-2.1651
2233	214944	Mobkl2b	MOB kinase activator 3B	0	2	3	-2.16496
2234	12803	Cntf	ciliary neurotrophic factor	0	2	3	-2.16464
2235	333182	Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	0	2	3	-2.16402
2236	387347	Tas2r118	taste receptor, type 2, member 118	0	2	2	-2.16379
2237	140917	Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	0	2	2	-2.16136
2238	258815	Olfr1218	olfactory receptor 1218	0	2	3	-2.16014
2239	73287	1700040L02Rik	RIKEN cDNA 1700040L02 gene	0	2	2	-2.15988
2240	21753	Tes	testis derived transcript	0	2	3	-2.15923
2241	21345	Tagln	transgelin	0	2	1	-2.15597
2242	399673	Tdpoz2	TD and POZ domain containing 2	0	2	3	-2.15463
2243	72047	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	0	2	3	-2.15345
2244	329626	A930011G24	predicted gene 12541	0	2	3	-2.15196
2245	19076	Prim2	DNA primase, p58 subunit	0	2	3	-2.14676
2246	24000	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	0	2	3	-2.14421
2247	226251	Ablim1	actin-binding LIM protein 1	0	2	3	-2.14373
2248	223917	BC031593	keratin 79	0	2	3	-2.14299
2249	258858	Olfr371	olfactory receptor 371	0	2	3	-2.1428
2250	330157	F830003B07	NA	0	2	2	-2.14272
2251	75219	Dusp18	dual specificity phosphatase 18	0	2	3	-2.14267
2252	22092	Tsga2	radial spoke head 1 homolog (Chlamydomonas)	0	2	3	-2.14096
2253	19305	Pex5	peroxisomal biogenesis factor 5	0	2	3	-2.14076

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2254	223870	Senp1	SUMO1/sentrin specific peptidase 1	0	2	3	-2.14055
2255	70061	Sdro	4short chain dehydrogenase/reductase family 9C, member 7	0	2	3	-2.14028
2256	17703	Msx3	homeobox, msh-like 3	0	2	3	-2.13788
2257	106389	Eaf2	ELL associated factor 2	0	2	2	-2.13738
2258	109225	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	0	2	2	-2.13726
2259	21940	Tnfrsf7	CD27 antigen	0	2	3	-2.13685
2260	232078	BC051244	threonine synthase-like 2 (bacterial)	0	2	3	-2.13519
2261	78416	Rnase6	ribonuclease, RNase A family, 6	0	2	3	-2.13479
2262	56321	Aatf	apoptosis antagonizing transcription factor	0	2	3	-2.13479
2263	17237	Mgrn1	mahogunin, ring finger 1	0	2	3	-2.1347
2264	74039	Nfam1	Nfat activating molecule with ITAM motif 1	0	2	3	-2.13375
2265	18119	Nodal	nodal	0	2	3	-2.13345
2266	353169	Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	0	2	3	-2.13278
2267	16164	Il13ra1	interleukin 13 receptor, alpha 1	0	2	3	-2.13259
2268	17089	Lyar	Ly1 antibody reactive clone	0	2	3	-2.13101
2269	110542	Amhr2	anti-Mullerian hormone type 2 receptor	0	2	3	-2.13079
2270	72322	Xpo5	exportin 5	0	2	2	-2.13075
2271	66204	Acyp1	acylphosphatase 1, erythrocyte (common) type	0	2	2	-2.12846
2272	330552	A230097C02	predicted gene 9801	0	2	2	-2.12743
2273	243372	C130032F08Rik	zinc finger protein 775	0	2	3	-2.1264
2274	13828	Epb4.2	erythrocyte protein band 4.2	0	2	3	-2.12625
2275	208158	Map6d1	MAP6 domain containing 1	0	2	2	-2.12574
2276	74469	Taf7l	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	3	-2.12389
2277	20648	Snta1	syntrophin, acidic 1	0	2	3	-2.12227
2278	21648	Dynlt1	dynein light chain Tctex-type 1D	0	2	3	-2.12217
2279	75991	5033405K12Rik	SLAIN motif family, member 2	0	2	2	-2.12186
2280	76263	Gstk1	glutathione S-transferase kappa 1	0	2	3	-2.12184
2281	433890	UNK	NA	0	2	3	-2.1205
2282	241877	Slc10a5	solute carrier family 10 (sodium/bile acid cotransporter family), member 5	0	2	3	-2.11967
2283	244867	Arhgap20	Rho GTPase activating protein 20	0	2	3	-2.11877
2284	75705	Eif4b	eukaryotic translation initiation factor 4B	0	2	2	-2.1185
2285	67578	4930424G05Rik	protein associated with topoisomerase II homolog 2 (yeast)	0	2	3	-2.11815
2286	280668	Adam1a	a disintegrin and metallopeptidase domain 1a	0	2	3	-2.11802
2287	235623	Scap	SREBF chaperone	0	2	2	-2.11653
2288	72180	Zfp661	zinc finger protein 661	0	2	3	-2.11646
2289	114644	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	0	2	3	-2.11515
2290	13836	Epha2	Eph receptor A2	0	2	3	-2.1149

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2291	13642	Efnb2	ephrin B2	0	2	3	-2.11476
2292	26572	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	0	2	3	-2.11426
2293	101869	Unc45a	unc-45 homolog A (C. elegans)	0	2	3	-2.1129
2294	435219	UNK	NA	0	2	3	-2.11206
2295	328110	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	0	2	3	-2.11184
2296	18987	Pou2f2	POU domain, class 2, transcription factor 2	0	2	3	-2.11047
2297	93880	Pcdhb9	protocadherin beta 9	0	2	3	-2.11021
2298	51885	D2Ertd435e	tubulin, gamma complex associated protein 4	0	2	3	-2.11013
2299	19711	Resp18	regulated endocrine-specific protein 18	0	2	3	-2.11003
2300	258113	Olfr748	olfactory receptor 748	0	2	3	-2.10991
2301	20312	Cx3cl1	chemokine (C-X3-C motif) ligand 1	0	2	3	-2.10973
2302	14158	Fert2	fer (fms/fps related) protein kinase, testis specific 2	0	2	3	-2.10763
2303	109006	Ciapin1	cytokine induced apoptosis inhibitor 1	0	2	2	-2.10731
2304	17308	Mgat1	mannoside acetylglucosaminyltransferase 1	0	2	3	-2.10662
2305	432447	LOC432447	phosphatidylethanolamine-binding protein pseudogene	0	2	3	-2.10623
2306	11867	Arpc1b	actin related protein 2/3 complex, subunit 1B	0	2	3	-2.10609
2307	76484	Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1	0	2	3	-2.10595
2308	14066	F3	coagulation factor III	0	2	3	-2.10591
2309	72972	Gcap14	granule cell antiserum positive 14	0	2	2	-2.10542
2310	258764	Olfr1099	olfactory receptor 1099	0	2	2	-2.10479
2311	68691	1110028C15Rik	RIKEN cDNA 1110028C15 gene	0	2	3	-2.10477
2312	12558	Cdh2	cadherin 2	0	2	3	-2.10433
2313	15193	Hdgfrp2	hepatoma-derived growth factor, related protein 2	0	2	3	-2.10268
2314	20361	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	0	2	3	-2.10137
2315	93734	Mpv17l	Mpv17 transgene, kidney disease mutant-like	0	2	3	-2.10124
2316	378460	Pram1	PML-RAR alpha-regulated adaptor molecule 1	0	2	3	-2.10061
2317	330998	B230218L05Rik	ankyrin repeat domain 34C	0	2	3	-2.09972
2318	277343	Wfdc8	WAP four-disulfide core domain 8	0	2	3	-2.09938
2319	14536	Nr6a1	nuclear receptor subfamily 6, group A, member 1	0	2	3	-2.09795
2320	110391	Qdpr	quinoid dihydropteridine reductase	0	2	3	-2.09777
2321	435839	UNK	NA	0	2	3	-2.09689
2322	224753	H2-M10.4	histocompatibility 2, M region locus 10.4	0	2	3	-2.09641
2323	12977	Csf1	colony stimulating factor 1 (macrophage)	0	2	3	-2.0959
2324	110310	Krt2-7	keratin 7	0	2	3	-2.09535
2325	243043	Kctd8	potassium channel tetramerisation domain containing 8	0	2	3	-2.09503
2326	109620	Dsp	desmoplakin	0	2	3	-2.09431
2327	66708	Krtap3-2	keratin associated protein 3-2	0	2	2	-2.09266

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2328	21815	Tgif	TGFB-induced factor homeobox 1	0	2	3	-2.09232
2329	18472	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, subunit 1	0	2	3	-2.0912
2330	20354	Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic doma	0	2	3	-2.09097
2331	269951	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0	2	3	-2.09069
2332	56505	Ruvbl1	RuvB-like protein 1	0	2	2	-2.08972
2333	103655	Sec14l4	SEC14-like 4 (S. cerevisiae)	0	2	3	-2.08944
2334	258788	Olfr1246	olfactory receptor 1246	0	2	3	-2.08805
2335	435406	UNK	NA	0	2	3	-2.08709
2336	77629	4930544G21Rik	SPHK1 interactor, AKAP domain containing	0	2	3	-2.08657
2337	67037	Pmf1	polyamine-modulated factor 1	0	2	3	-2.08656
2338	16331	Inpp5d	inositol polyphosphate-5-phosphatase D	0	2	2	-2.08648
2339	15110	Hand1	heart and neural crest derivatives expressed transcript 1	0	2	3	-2.08644
2340	76411	1700019E19Rik	RIKEN cDNA 1700019E19 gene	0	2	2	-2.08629
2341	66043	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0	2	3	-2.08595
2342	214601	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0	2	3	-2.08568
2343	22164	Tnfsf4	tumor necrosis factor (ligand) superfamily, member 4	0	2	3	-2.08431
2344	224109	Lrrc33	leucine rich repeat containing 33	0	2	2	-2.0828
2345	74200	2810403A07Rik	RIKEN cDNA 2810403A07 gene	0	2	2	-2.08213
2346	218038	Amph	amphiphysin	0	2	3	-2.08013
2347	268756	Gulo	gulonolactone (L-) oxidase	0	2	2	-2.08008
2348	241118	Accn4	amiloride-sensitive cation channel 4, pituitary	0	2	2	-2.07765
2349	17380	Mme	membrane metallo endopeptidase	0	2	3	-2.07721
2350	14027	Evpl	envoplakin	0	2	3	-2.07607
2351	26908	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	0	2	3	-2.07503
2352	80886	Senp3	SUMO/sentrin specific peptidase 3	0	2	3	-2.07396
2353	64075	Smoc1	SPARC related modular calcium binding 1	0	2	3	-2.07339
2354	57913	Lrdd	leucine-rich and death domain containing	0	2	3	-2.07303
2355	17700	Gdf8	myostatin	0	2	3	-2.07247
2356	383548	Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	0	2	3	-2.07173
2357	215708	C030011O14Rik	family with sequence similarity 73, member A	0	2	3	-2.07123
2358	97165	Hmgb2	high mobility group box 2	0	2	3	-2.07091
2359	70333	Cd3eap	CD3E antigen, epsilon polypeptide associated protein	0	2	3	-2.0693
2360	15218	Foxn1	forkhead box N1	0	2	3	-2.06926
2361	108148	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	0	2	3	-2.06773
2362	170757	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	0	2	3	-2.06686
2363	18195	Nsf	N-ethylmaleimide sensitive fusion protein	0	2	3	-2.06546
2364	12450	Ccng1	cyclin G1	0	2	3	-2.06544

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2365	13115	Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	0	2	3	-2.06514
2366	14762	Gpr33	G protein-coupled receptor 33	0	2	3	-2.06371
2367	232685	AB041803	cDNA sequence AB041803	0	2	3	-2.06301
2368	229595	Adamtsl4	ADAMTS-like 4	0	2	3	-2.06169
2369	66515	Cul7	cullin 7	0	2	3	-2.06143
2370	50770	Atp11a	ATPase, class VI, type 11A	0	2	3	-2.06094
2371	259042	Olfr1351	olfactory receptor 1351	0	2	2	-2.0583
2372	16568	Kif3a	kinesin family member 3A	0	2	3	-2.05798
2373	231201	AF366264	cDNA sequence AF366264	0	2	3	-2.05757
2374	224613	Flywch1	FLYWCH-type zinc finger 1	0	2	2	-2.05741
2375	79044	Mrps34	mitochondrial ribosomal protein S34	0	2	3	-2.05736
2376	22371	Vwf	Von Willebrand factor homolog	0	2	3	-2.05722
2377	212862	Chpt1	choline phosphotransferase 1	0	2	3	-2.05568
2378	23934	Ly6h	lymphocyte antigen 6 complex, locus H	0	2	2	-2.05562
2379	20710	Serpinb9e	serine (or cysteine) peptidase inhibitor, clade B, member 9e	0	2	3	-2.05537
2380	14990	H2-M2	histocompatibility 2, M region locus 2	0	2	2	-2.05423
2381	15925	Ide	insulin degrading enzyme	0	2	3	-2.05314
2382	69257	Elf2	E74-like factor 2	0	2	3	-2.05187
2383	70231	Gorasp2	golgi reassembly stacking protein 2	0	2	3	-2.05107
2384	50918	Myadm	myeloid-associated differentiation marker	0	2	3	-2.05036
2385	69171	1810031K17Rik	RIKEN cDNA 1810031K17 gene	0	2	3	-2.04999
2386	80283	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	0	2	3	-2.0499
2387	27281	Hrasls	HRAS-like suppressor	0	2	3	-2.04975
2388	74254	Xab1	GPN-loop GTPase 1	0	2	3	-2.04964
2389	228960	Stx16	syntaxin 16	0	2	3	-2.04914
2390	18391	Oprs1	sigma non-opioid intracellular receptor 1	0	2	3	-2.04624
2391	66138	Wbscr22	Williams Beuren syndrome chromosome region 22	0	2	3	-2.04594
2392	69129	Pex11c	peroxisomal biogenesis factor 11 gamma	0	2	3	-2.04565
2393	107798	V1rb5	NA	0	2	3	-2.0456
2394	12014	Bach2	BTB and CNC homology 2	0	2	3	-2.04445
2395	15445	Hpd	4-hydroxyphenylpyruvic acid dioxygenase	0	2	3	-2.04415
2396	71609	Tradd	TNFRSF1A-associated via death domain	0	2	2	-2.04319
2397	108083	Pip5k2b	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	0	2	3	-2.04113
2398	207596	Thsd4	thrombospondin, type I, domain containing 4	0	2	3	-2.03965
2399	208266	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	0	2	3	-2.03827
2400	67554	Slc25a30	solute carrier family 25, member 30	0	2	2	-2.03792
2401	50540	Igbp1b	immunoglobulin (CD79A) binding protein 1b	0	2	3	-2.03779

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2402	14702	Gng2	guanine nucleotide binding protein (G protein), gamma 2	0	2	3	-2.03746
2403	328789	Tmhs	lipoma HMGIC fusion partner-like 5	0	2	3	-2.03717
2404	18521	Pcbp2	poly(rC) binding protein 2	0	2	3	-2.0368
2405	64339	Fndc4	fibronectin type III domain containing 4	0	2	3	-2.03574
2406	16801	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	0	2	3	-2.03397
2407	75273	Pelp1	proline, glutamic acid and leucine rich protein 1	0	2	2	-2.03347
2408	22163	Tnfrsf4	tumor necrosis factor receptor superfamily, member 4	0	2	3	-2.03268
2409	237831	Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	0	2	3	-2.03208
2410	227522	Rpp38	ribonuclease P/MRP 38 subunit (human)	0	2	3	-2.03191
2411	74215	1700007N14Rik	NA	0	2	3	-2.03047
2412	12757	Clta	clathrin, light polypeptide (Lca)	0	2	3	-2.02928
2413	24074	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	3	-2.02826
2414	279572	Tlr13	toll-like receptor 13	0	2	3	-2.02824
2415	66437	Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	0	2	3	-2.02775
2416	14560	Gdf10	growth differentiation factor 10	0	2	3	-2.02769
2417	12457	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0	2	3	-2.02718
2418	11699	Ambp	alpha 1 microglobulin/bikunin	0	2	3	-2.02495
2419	213389	Prdm9	PR domain containing 9	0	2	3	-2.02448
2420	110304	Glra3	glycine receptor, alpha 3 subunit	0	2	3	-2.02389
2421	230737	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	0	2	3	-2.0236
2422	319803	A430090L17Rik	RIKEN cDNA A430090L17 gene	0	2	2	-2.02337
2423	432637	LOC432637	predicted gene 5433	0	2	3	-2.023
2424	231506	AI461788	lin-54 homolog (C. elegans)	0	2	3	-2.02228
2425	20585	Smarca3	helicase-like transcription factor	0	2	3	-2.01919
2426	53600	Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	0	2	3	-2.01844
2427	240063	BC052046	zinc finger protein 811	0	2	3	-2.0184
2428	433649	UNK	NA	0	2	3	-2.01828
2429	22031	Traf3	TNF receptor-associated factor 3	0	2	3	-2.01788
2430	80297	Spnb4	spectrin beta 4	0	2	2	-2.01779
2431	237979	Sdk2	sidekick homolog 2 (chicken)	0	2	3	-2.01744
2432	13427	Dync1i2	dynein cytoplasmic 1 intermediate chain 2	0	2	3	-2.01734
2433	14528	Gch1	GTP cyclohydrolase 1	0	2	3	-2.01725
2434	328967	4933429F08Rik	Rho guanine nucleotide exchange factor (GEF) 37	0	2	3	-2.01717
2435	70988	4931428L18Rik	RIKEN cDNA 4931428L18 gene	0	2	3	-2.01588
2436	21987	Tpd52l1	tumor protein D52-like 1	0	2	3	-2.01582
2437	108705	Pttg1ip	pituitary tumor-transforming 1 interacting protein	0	2	3	-2.01557
2438	18679	Phka1	phosphorylase kinase alpha 1	0	2	3	-2.01552

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2439	73046	Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	0	2	3	-2.01526
2440	67996	Sfrs6	serine/arginine-rich splicing factor 6	0	2	3	-2.01511
2441	14254	Flt1	FMS-like tyrosine kinase 1	0	2	3	-2.01437
2442	11798	Birc4	X-linked inhibitor of apoptosis	0	2	3	-2.01387
2443	434423	Dppa5	developmental pluripotency associated 5A	0	2	3	-2.01366
2444	170653	Krtap16-3	NA	0	2	2	-2.01363
2445	75710	Rbm12	RNA binding motif protein 12	0	2	3	-2.01354
2446	140488	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	0	2	3	-2.01343
2447	80732	Mynn	myoneurin	0	2	3	-2.01291
2448	18109	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	0	2	3	-2.01281
2449	23954	Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	0	2	3	-2.0127
2450	116940	Ncoa6ip	trimethylguanosine synthase homolog (S. cerevisiae)	0	2	3	-2.01157
2451	238395	LOC238395	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3J	0	2	3	-2.01121
2452	70831	4733401H21Rik	keratin associated protein 31-1	0	2	3	-2.01112
2453	56458	Foxo1	forkhead box O1	0	2	3	-2.0103
2454	108043	Chrnb3	cholinergic receptor, nicotinic, beta polypeptide 3	0	2	3	-2.00992
2455	27404	Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	0	2	3	-2.00734
2456	19303	Pxn	paxillin	0	2	3	-2.00703
2457	21804	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	0	2	3	-2.00659
2458	258726	Olfr599	olfactory receptor 599	0	2	2	-2.00514
2459	223527	Eny2	enhancer of yellow 2 homolog (Drosophila)	0	2	2	-2.00452
2460	194162	BC035954	NA	0	2	3	-2.00431
2461	22628	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	0	2	3	-2.00388
2462	20305	Ccl6	chemokine (C-C motif) ligand 6	0	2	3	-2.00315
2463	14294	Fprl1	formyl peptide receptor 3	0	2	3	-2.00266
2464	68239	2410039E07Rik	keratin 42	0	2	3	-2.0022
2465	108105	B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	0	2	3	-2.00207
2466	56419	Diap3	diaphanous homolog 3 (Drosophila)	0	2	3	-2.00136
2467	209488	Hsh2d	hematopoietic SH2 domain containing	0	2	3	-2.00133
2468	16330	Inpp5b	inositol polyphosphate-5-phosphatase B	0	2	3	-2.00114
2469	29807	Tpk1	thiamine pyrophosphokinase	0	2	3	-2.00073
2470	56066	Cxcl11	chemokine (C-X-C motif) ligand 11	0	2	3	-2.00073
2471	108812	Als2cr12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human)	0	2	2	-2.00028
2472	20523	Slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14	0	2	3	-1.99967
2473	65973	Asph	aspartate-beta-hydroxylase	0	2	3	-1.99868
2474	19122	Prnp	prion protein	0	2	3	-1.99868
2475	53605	Nap1l1	nucleosome assembly protein 1-like 1	0	2	3	-1.99835

Candidates for positive regulators of normal growth (Fisher's)

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2476	241452	Dhrs9	dehydrogenase/reductase (SDR family) member 9	0	2	3	-1.9981
2477	381936	LOC381936	NA	0	2	3	-1.99795
2478	67605	Akt1s1	AKT1 substrate 1 (proline-rich)	0	2	2	-1.9978
2479	23963	Odz1	odd Oz/ten-m homolog 1 (Drosophila)	0	2	3	-1.99717
2480	381203	Slc22a20	solute carrier family 22 (organic anion transporter), member 20	0	2	3	-1.99704
2481	17999	Nedd4	neural precursor cell expressed, developmentally down-regulated 4	0	2	3	-1.99694
2482	22402	Wisp1	WNT1 inducible signaling pathway protein 1	0	2	3	-1.9956
2483	14588	Gfra4	glial cell line derived neurotrophic factor family receptor alpha 4	0	2	3	-1.99494
2484	171278	V1rh21	vomeronasal 1 receptor 197	0	2	3	-1.99474
2485	383341	LOC383341	ubiquitin A-52 residue ribosomal protein fusion product 1 pseudogene	0	2	3	-1.99383
2486	54616	Extl3	exostoses (multiple)-like 3	0	2	2	-1.99344
2487	78779	2610039E05Rik	spermatogenesis associated 2-like	0	2	3	-1.99283
2488	192216	Tmem47	transmembrane protein 47	0	2	3	-1.99235
2489	66541	Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0	2	3	-1.99165
2490	109019	5830411E10Rik	oligonucleotide/oligosaccharide-binding fold containing 2A	0	2	3	-1.99143
2491	71241	Dmrtc2	doublesex and mab-3 related transcription factor like family C2	0	2	3	-1.99136
2492	18554	Pcsk7	proprotein convertase subtilisin/kexin type 7	0	2	2	-1.99097
2493	20348	Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	0	2	3	-1.99092
2494	56534	Hspb3	heat shock protein 3	0	2	2	-1.99005
2495	114671	4930444G20Rik	RIKEN cDNA 4930444G20 gene	0	2	3	-1.98865
2496	13380	Dkk1	dickkopf homolog 1 (Xenopus laevis)	0	2	3	-1.98863
2497	209517	Taar7b	trace amine-associated receptor 7B	0	2	2	-1.98842
2498	74568	Mlkl	mixed lineage kinase domain-like	0	2	3	-1.98838
2499	109314	A030004J04Rik	proline rich 9	0	2	3	-1.98662
2500	15209	Hesx1	homeobox gene expressed in ES cells	0	2	3	-1.98652
2501	77697	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	0	2	3	-1.98564
2502	242517	LOC242517	predicted gene 12597	0	2	3	-1.98392
2503	80287	Apobec3	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	0	2	2	-1.98379
2504	14751	Gpi1	glucose phosphate isomerase 1	0	2	3	-1.98232
2505	18792	Plau	plasminogen activator, urokinase	0	2	3	-1.98136
2506	66593	Diablo	diablo homolog (Drosophila)	0	2	3	-1.98084
2507	75533	Nme5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	0	2	3	-1.9803
2508	20612	Siglec1	sialic acid binding Ig-like lectin 1, sialoadhesin	0	2	3	-1.97999
2509	228413	Prrg4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	0	2	3	-1.97956
2510	217653	C79407	MIS18 binding protein 1	0	2	3	-1.97933
2511	16495	Kcna7	potassium voltage-gated channel, shaker-related subfamily, member 7	0	2	3	-1.97894
2512	67922	2510049I19Rik	family with sequence similarity 32, member A	0	2	3	-1.97836

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2513	231050	Galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	0	2	3	-1.97802
2514	20018	Rpo1-3	polymerase (RNA) I polypeptide D	0	2	3	-1.97773
2515	105833	Ccdc65	coiled-coil domain containing 65	0	2	2	-1.9773
2516	211586	Tfdp2	transcription factor Dp 2	0	2	3	-1.97718
2517	330914	Grit	Rho GTPase activating protein 32	0	2	3	-1.97686
2518	216961	Coro6	coronin 6	0	2	3	-1.97679
2519	21959	Tnp2	transition protein 2	0	2	3	-1.97612
2520	74100	Arpp21	cyclic AMP-regulated phosphoprotein, 21	0	2	7	-1.97585
2521	72739	Zfp306	zinc finger with KRAB and SCAN domains 3	0	2	3	-1.97524
2522	57376	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	0	2	3	-1.97432
2523	238673	Zfp367	zinc finger protein 367	0	2	3	-1.97402
2524	18316	Olfr19	olfactory receptor 19	0	2	3	-1.97389
2525	21908	Tlx1	T cell leukemia, homeobox 1	0	2	3	-1.97339
2526	68797	Pdgfrl	platelet-derived growth factor receptor-like	0	2	3	-1.96999
2527	226744	9630058J23Rik	consortin, connexin sorting protein	0	2	2	-1.96973
2528	14462	Gata3	GATA binding protein 3	0	2	3	-1.96886
2529	623215	LOC623215	predicted gene 10339	0	2	3	-1.96836
2530	56791	Ube2l6	ubiquitin-conjugating enzyme E2L 6	0	2	3	-1.96731
2531	67739	4930570C03Rik	solute carrier family 48 (heme transporter), member 1	0	2	3	-1.96729
2532	13496	Arid3a	AT rich interactive domain 3A (BRIGHT-like)	0	2	3	-1.96704
2533	229776	Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	0	2	3	-1.96677
2534	70433	2610109H07Rik	RIKEN cDNA 2610109H07 gene	0	2	3	-1.96663
2535	56473	Fads2	fatty acid desaturase 2	0	2	2	-1.96648
2536	246317	Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	0	2	2	-1.96567
2537	239408	Tmem74	transmembrane protein 74	0	2	2	-1.96553
2538	259151	Olfr1037	olfactory receptor 1037	0	2	3	-1.96523
2539	93874	Pcdhb3	protocadherin beta 3	0	2	3	-1.96401
2540	19225	Ptgs2	prostaglandin-endoperoxide synthase 2	0	2	3	-1.96365
2541	432552	RP23-273O7.4	family with sequence similarity 71, member B	0	2	2	-1.96349
2542	98710	Rabif	RAB interacting factor	0	2	3	-1.96346
2543	223332	C130037N17Rik	RAN binding protein 3-like	0	2	3	-1.96277
2544	14687	Gnaz	guanine nucleotide binding protein, alpha z subunit	0	2	3	-1.96214
2545	24001	Tiam2	T cell lymphoma invasion and metastasis 2	0	2	3	-1.96119
2546	69721	Nkiras1	NFKB inhibitor interacting Ras-like protein 1	0	2	2	-1.96049
2547	171196	V1rc23	vomeronasal 1 receptor 22	0	2	3	-1.95835
2548	67673	Tceb2	transcription elongation factor B (SIII), polypeptide 2	0	2	2	-1.95828
2549	11909	Atf2	activating transcription factor 2	0	2	3	-1.95747

Candidates for positive regulators of normal growth (Fisher's)

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2550	259053	Olfr362	olfactory receptor 362	0	2	2	-1.95743
2551	67507	1700019N19Rik	RIKEN cDNA 1700019N19 gene	0	2	2	-1.95567
2552	252966	Cables2	CDK5 and Abl enzyme substrate 2	0	2	2	-1.95509
2553	338403	Cndp1	carnosine dipeptidase 1 (metallopeptidase M20 family)	0	2	3	-1.95504
2554	382407	Gad1-ps	glutamic acid decarboxylase 1, pseudogene	0	2	2	-1.95459
2555	234788	Gm587	solute carrier family 38, member 8	0	2	3	-1.95432
2556	386445	Trav7d-3	NA	0	2	3	-1.95262
2557	11537	Cfd	complement factor D (adipsin)	0	2	3	-1.95231
2558	56809	Gmeb1	glucocorticoid modulatory element binding protein 1	0	2	3	-1.95081
2559	268749	Rnf31	ring finger protein 31	0	2	3	-1.94993
2560	109624	Cald1	caldesmon 1	0	2	3	-1.94932
2561	245839	Gzmn	granzyme N	0	2	3	-1.9492
2562	71810	Ranbp3	RAN binding protein 3	0	2	2	-1.94913
2563	387340	Tas2r104	taste receptor, type 2, member 104	0	2	3	-1.94623
2564	109857	Cbr3	carbonyl reductase 3	0	2	3	-1.94621
2565	99982	Aof2	lysine (K)-specific demethylase 1A	0	2	3	-1.94598
2566	72145	Wdfy3	WD repeat and FYVE domain containing 3	0	2	3	-1.94574
2567	14864	Gstm3	glutathione S-transferase, mu 3	0	2	3	-1.94399
2568	14943	Gzmf	granzyme F	0	2	3	-1.94398
2569	16181	Il1rn	interleukin 1 receptor antagonist	0	2	3	-1.94389
2570	21427	Vps72	vacuolar protein sorting 72 (yeast)	0	2	3	-1.94299
2571	276770	Eif5a	eukaryotic translation initiation factor 5A	0	2	3	-1.94274
2572	13163	Daxx	Fas death domain-associated protein	0	2	3	-1.94145
2573	116873	Stim2	stromal interaction molecule 2	0	2	3	-1.94104
2574	225875	Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	0	2	2	-1.94078
2575	56390	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	0	2	2	-1.94072
2576	12492	Scarb2	scavenger receptor class B, member 2	0	2	3	-1.9407
2577	13831	Epc1	enhancer of polycomb homolog 1 (Drosophila)	0	2	2	-1.94033
2578	71099	Tssk4	testis-specific serine kinase 4	0	2	3	-1.94032
2579	383619	Gm1313	absent in melanoma 2	0	2	3	-1.94029
2580	23985	Slc26a4	solute carrier family 26, member 4	0	2	3	-1.94028
2581	22068	Trpc6	transient receptor potential cation channel, subfamily C, member 6	0	2	3	-1.93937
2582	12627	Cfc1	cripto, FRL-1, cryptic family 1	0	2	3	-1.93932
2583	258475	Olfr889	olfactory receptor 889	0	2	2	-1.93931
2584	241197	Serpinb10	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10, pseudogene	0	2	3	-1.9386
2585	12424	Cck	cholecystokinin	0	2	3	-1.93853
2586	19885	Rorc	RAR-related orphan receptor gamma	0	2	3	-1.93839

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2587	380698	Obscn	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0	2	3	-1.93821
2588	242585	Slc35d1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member	0	2	3	-1.93797
2589	68556	Uckl1	uridine-cytidine kinase 1-like 1	0	2	3	-1.93783
2590	450219	Gsdm3	gasdermin A3	0	2	3	-1.9375
2591	218171	UNK	NA	0	2	3	-1.93749
2592	18213	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	0	2	3	-1.93628
2593	215257	Il1f9	interleukin 1 family, member 9	0	2	3	-1.93599
2594	244234	5830411N06Rik	RIKEN cDNA 5830411N06 gene	0	2	3	-1.93545
2595	18753	Prkcd	protein kinase C, delta	0	2	3	-1.93521
2596	54409	Ramp2	receptor (calcitonin) activity modifying protein 2	0	2	3	-1.93432
2597	67439	Xab2	XPA binding protein 2	0	2	3	-1.9343
2598	21968	Tom1	target of myb1 homolog (chicken)	0	2	3	-1.93418
2599	19281	Ptprt	protein tyrosine phosphatase, receptor type, T	0	2	3	-1.93401
2600	68473	Mobkl1a	MOB kinase activator 1B	0	2	3	-1.93342
2601	68421	Lmbrd1	LMBR1 domain containing 1	0	2	3	-1.93302
2602	213945	Col28a1	collagen, type XXVIII, alpha 1	0	2	3	-1.93295
2603	56696	Gpr132	G protein-coupled receptor 132	0	2	3	-1.93277
2604	19280	Ptprs	protein tyrosine phosphatase, receptor type, S	0	2	3	-1.93275
2605	66840	Wdr45l	Wdr45 like	0	2	2	-1.93264
2606	16211	Kpnb1	karyopherin (importin) beta 1	0	2	3	-1.93185
2607	192193	Edem1	ER degradation enhancer, mannosidase alpha-like 1	0	2	3	-1.93182
2608	217830	9030617O03Rik	RIKEN cDNA 9030617O03 gene	0	2	3	-1.93169
2609	239126	C1qtnf9	C1q and tumor necrosis factor related protein 9	0	2	3	-1.93145
2610	435386	UNK	NA	0	2	3	-1.93087
2611	15245	Hhip	Hedgehog-interacting protein	0	2	3	-1.93005
2612	67133	Gp2	glycoprotein 2 (zymogen granule membrane)	0	2	3	-1.9298
2613	20450	St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	0	2	3	-1.92864
2614	19064	Ppy	pancreatic polypeptide	0	2	3	-1.92844
2615	17346	Mknk1	MAP kinase-interacting serine/threonine kinase 1	0	2	3	-1.92814
2616	65961	Crlz1	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	0	2	3	-1.92801
2617	12801	Cnr1	cannabinoid receptor 1 (brain)	0	2	3	-1.92713
2618	240216	E230025N22	Riken cDNA E230025N22 gene	0	2	3	-1.92712
2619	69024	Snx15	sorting nexin 15	0	2	2	-1.92674
2620	19221	Ptgfrn	prostaglandin F2 receptor negative regulator	0	2	3	-1.92594
2621	277898	9830102E05Rik	solute carrier family 15, member 5	0	2	3	-1.92546
2622	12515	Cd69	CD69 antigen	0	2	3	-1.92468
2623	66532	2210417D09Rik	RAB15 effector protein	0	2	2	-1.92454

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2624	11536	Admr	G protein-coupled receptor 182	0	2	3	-1.92434
2625	107652	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	0	2	3	-1.92388
2626	66916	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	0	2	3	-1.92382
2627	73708	Dppa3	developmental pluripotency-associated 3	0	2	2	-1.9213
2628	71835	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	0	2	2	-1.92128
2629	74917	4930474M22Rik	RIKEN cDNA 4930474M22 gene	0	2	2	-1.92125
2630	20700	Serpina1a	serine (or cysteine) peptidase inhibitor, clade A, member 1A	0	2	3	-1.92068
2631	244646	Pkd1l3	polycystic kidney disease 1 like 3	0	2	3	-1.92057
2632	12723	Clcn1	chloride channel 1	0	2	3	-1.91961
2633	20174	Ruvbl2	RuvB-like protein 2	0	2	3	-1.91912
2634	72759	Tmem135	transmembrane protein 135	0	2	2	-1.91909
2635	24071	Synj2bp	synaptojanin 2 binding protein	0	2	3	-1.91901
2636	171243	V1rg8	vomeronasal 1 receptor 83	0	2	2	-1.91836
2637	18506	Pax4	paired box gene 4	0	2	3	-1.91796
2638	17433	Mobp	myelin-associated oligodendrocytic basic protein	0	2	2	-1.91788
2639	14161	Fga	fibrinogen alpha chain	0	2	3	-1.9175
2640	225825	Cd226	CD226 antigen	0	2	3	-1.91608
2641	105787	Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	0	2	3	-1.91536
2642	70821	4921507P07Rik	RIKEN cDNA 4921507P07 gene	0	2	2	-1.91525
2643	270160	Rab39	RAB39, member RAS oncogene family	0	2	3	-1.9148
2644	67936	Wdr55	WD repeat domain 55	0	2	3	-1.91232
2645	258499	Olfr945	olfactory receptor 945	0	2	3	-1.91186
2646	69234	Zfp688	zinc finger protein 688	0	2	3	-1.91186
2647	170813	Ms4a3	membrane-spanning 4-domains, subfamily A, member 3	0	2	2	-1.91173
2648	110902	Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	0	2	3	-1.91148
2649	16508	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	0	2	3	-1.91122
2650	75901	Dcp1a	DCP1 decapping enzyme homolog A (S. cerevisiae)	0	2	3	-1.91122
2651	20449	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	0	2	3	-1.91044
2652	231997	Fkbp14	FK506 binding protein 14	0	2	3	-1.90996
2653	109077	Ints5	integrator complex subunit 5	0	2	3	-1.90988
2654	72962	Ecgf1	thymidine phosphorylase	0	2	3	-1.90977
2655	18750	Prkca	protein kinase C, alpha	0	2	3	-1.90914
2656	216144	AJ543404	vomeronasal 2, receptor 81	0	2	3	-1.90906
2657	234852	Pcoln3	charged multivesicular body protein 1A	0	2	3	-1.90788
2658	78521	B230219D22Rik	RIKEN cDNA B230219D22 gene	0	2	2	-1.90755
2659	258930	Olfr808	olfactory receptor 808	0	2	2	-1.90754
2660	67389	C1qdc2	family with sequence similarity 132, member A	0	2	3	-1.90753

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2661	403395	Clec3a	C-type lectin domain family 3, member a	0	2	3	-1.90733
2662	54196	Pabpn1	poly(A) binding protein, nuclear 1	0	2	3	-1.90727
2663	14704	Gng3	guanine nucleotide binding protein (G protein), gamma 3	0	2	3	-1.90606
2664	208595	MTERF	predicted gene 9897	0	2	3	-1.90572
2665	14581	Gfi1	growth factor independent 1	0	2	3	-1.90563
2666	258677	Olfr76	olfactory receptor 76	0	2	3	-1.90498
2667	433358	UNK	NA	0	2	3	-1.90443
2668	407972	Gapdh	NA	0	2	3	-1.90414
2669	13168	Dbil5	diazepam binding inhibitor-like 5	0	2	3	-1.90413
2670	228602	4930402H24Rik	RIKEN cDNA 4930402H24 gene	0	2	2	-1.90379
2671	20352	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic doma	0	2	3	-1.90374
2672	234847	Spg7	spastic paraplegia 7 homolog (human)	0	2	3	-1.90305
2673	399642	Ptprh	NA	0	2	3	-1.90251
2674	110312	Pmch	pro-melanin-concentrating hormone	0	2	2	-1.9025
2675	171263	V1re10	vomeronasal 1 receptor 67	0	2	2	-1.90243
2676	94176	Dock2	dedicator of cyto-kinesis 2	0	2	3	-1.9024
2677	233079	Ffar2	free fatty acid receptor 2	0	2	3	-1.90206
2678	56189	Prodh2	proline dehydrogenase (oxidase) 2	0	2	3	-1.90198
2679	12469	Cct8	chaperonin containing Tcp1, subunit 8 (theta)	0	2	3	-1.90194
2680	22057	Tob1	transducer of ErbB-2.1	0	2	3	-1.90193
2681	30935	Tor3a	torsin family 3, member A	0	2	3	-1.90066
2682	89867	Lztr2	SEC16 homolog B (S. cerevisiae)	0	2	2	-1.90003
2683	113858	V1rc1	vomeronasal 1 receptor 10	0	2	3	-1.89985
2684	23938	Map2k5	mitogen-activated protein kinase kinase 5	0	2	3	-1.89918
2685	68095	Ociad1	OCIA domain containing 1	0	2	3	-1.89916
2686	269152	BC056349	kinesin family member 26B	0	2	3	-1.89872
2687	386467	UNK	NA	0	2	3	-1.89851
2688	56389	Stx5a	syntaxin 5A	0	2	3	-1.89824
2689	66306	2810012G03Rik	family with sequence similarity 53, member C	0	2	3	-1.89796
2690	16581	Kifc2	kinesin family member C2	0	2	3	-1.89722
2691	213438	A630033H20Rik	RIKEN cDNA A630033H20 gene	0	2	3	-1.89706
2692	23892	Grem1	gremlin 1	0	2	3	-1.89683
2693	66078	Tsen34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	0	2	3	-1.89635
2694	108101	BC032204	fermitin family homolog 3 (Drosophila)	0	2	3	-1.89625
2695	28109	D10Wsu102e	DNA segment, Chr 10, Wayne State University 102, expressed	0	2	2	-1.89598
2696	19108	Prkx	protein kinase, X-linked	0	2	3	-1.89496
2697	21949	Tnfsf8	tumor necrosis factor (ligand) superfamily, member 8	0	2	3	-1.89456

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2698	258404	Olfr1080	olfactory receptor 1080	0	2	2	-1.89417
2699	53414	Bysl	bystin-like	0	2	3	-1.89395
2700	319615	6330416L07Rik	zinc finger protein 944	0	2	3	-1.89345
2701	15968	Ifna5	interferon alpha 5	0	2	3	-1.89344
2702	94186	Strn3	striatin, calmodulin binding protein 3	0	2	3	-1.89197
2703	382814	UNK	NA	0	2	3	-1.89189
2704	107951	Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	0	2	3	-1.8918
2705	16560	Kif1a	kinesin family member 1A	0	2	3	-1.89093
2706	18198	Musk	muscle, skeletal, receptor tyrosine kinase	0	2	3	-1.89024
2707	21406	Tcf12	transcription factor 12	0	2	3	-1.89021
2708	270198	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0	2	3	-1.88984
2709	244484	Wdr17	WD repeat domain 17	0	2	3	-1.88853
2710	52690	Setd3	SET domain containing 3	0	2	2	-1.88812
2711	76425	2310003C23Rik	RIKEN cDNA 2310003C23 gene	0	2	3	-1.88787
2712	270328	9930109F21Rik	gasdermin C3	0	2	3	-1.88743
2713	56208	Becn1	beclin 1, autophagy related	0	2	3	-1.88676
2714	13074	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	0	2	3	-1.88651
2715	55981	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	0	2	3	-1.88632
2716	66180	1110036O03Rik	leprecan-like 4	0	2	3	-1.8863
2717	107605	Rdh1	retinol dehydrogenase 1 (all trans)	0	2	3	-1.88628
2718	69700	Col22a1	collagen, type XXII, alpha 1	0	2	3	-1.88495
2719	320209	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	0	2	3	-1.88486
2720	55925	Syt8	synaptotagmin VIII	0	2	3	-1.8847
2721	55983	Pdzrn3	PDZ domain containing RING finger 3	0	2	3	-1.88469
2722	17919	Myo5b	myosin VB	0	2	3	-1.88466
2723	73178	Wasl	Wiskott-Aldrich syndrome-like (human)	0	2	3	-1.88391
2724	21672	Prdx2	peroxiredoxin 2	0	2	2	-1.88322
2725	258994	Olfr204	olfactory receptor 204	0	2	3	-1.88311
2726	67414	Mfn1	mitofusin 1	0	2	3	-1.88242
2727	18504	Pax2	paired box gene 2	0	2	3	-1.88215
2728	17110	Lzp-s	lysozyme 1	0	2	3	-1.88192
2729	75320	Etnk1	ethanolamine kinase 1	0	2	3	-1.88165
2730	30877	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)	0	2	3	-1.8811
2731	110794	Cebpe	CCAAT/enhancer binding protein (C/EBP), epsilon	0	2	3	-1.88109
2732	107993	Bfsp2	beaded filament structural protein 2, phakinin	0	2	3	-1.88101
2733	68172	4930517K11Rik	ribosomal protein L39-like	0	2	3	-1.8804
2734	17250	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0	2	3	-1.87898

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2735	57439	1300007B12Rik	transmembrane protein 183A	0	2	2	-1.87892
2736	18028	Nfib	nuclear factor I/B	0	2	3	-1.87871
2737	320379	D630028G08Rik	RIKEN cDNA D630028G08 gene	0	2	3	-1.87871
2738	503844	Ang5	angiogenin, ribonuclease A family, member 5	0	2	3	-1.87858
2739	271127	Adamts16	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16	0	2	3	-1.87841
2740	18181	Nrf1	nuclear respiratory factor 1	0	2	3	-1.87841
2741	432981	Gm5474	predicted gene 5474	0	2	3	-1.8767
2742	16569	Kif3b	kinesin family member 3B	0	2	3	-1.87657
2743	217310	C630004H02Rik	RIKEN cDNA C630004H02 gene	0	2	3	-1.87641
2744	216527	Ccm2	cerebral cavernous malformation 2 homolog (human)	0	2	3	-1.87636
2745	19207	Ptch2	patched homolog 2	0	2	3	-1.87608
2746	107885	Mthfs	5, 10-methenyltetrahydrofolate synthetase	0	2	3	-1.87608
2747	19023	Ppef2	protein phosphatase, EF hand calcium-binding domain 2	0	2	3	-1.87602
2748	19354	Rac2	RAS-related C3 botulinum substrate 2	0	2	3	-1.87589
2749	435791	LOC435791	predicted gene 13271	0	2	3	-1.8745
2750	22194	Ube2e1	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	0	2	3	-1.87428
2751	69504	2310001H12Rik	zinc finger protein 932	0	2	3	-1.87377
2752	12918	Crh	corticotropin releasing hormone	0	2	1	-1.87351
2753	109905	Rap1a	RAS-related protein-1a	0	2	3	-1.87325
2754	71756	Cpn2	carboxypeptidase N, polypeptide 2	0	2	3	-1.8732
2755	228356	1110051M20Rik	RIKEN cDNA 1110051M20 gene	0	2	2	-1.87236
2756	232408	Klrb1f	killer cell lectin-like receptor subfamily B member 1F	0	2	3	-1.87164
2757	76477	Pcolce2	procollagen C-endopeptidase enhancer 2	0	2	3	-1.87145
2758	69034	4930579G22Rik	RIKEN cDNA 4930579G22 gene	0	2	2	-1.87117
2759	20924	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	0	2	3	-1.87095
2760	19051	Gsbs	protein phosphatase 1, regulatory subunit 17	0	2	3	-1.8706
2761	66083	0610039J04Rik	SET domain containing 6	0	2	3	-1.87059
2762	66763	4933425L06Rik	RIKEN cDNA 4933425L06 gene	0	2	3	-1.87049
2763	99899	Ifi44	interferon-induced protein 44	0	2	3	-1.87042
2764	16069	Igj	immunoglobulin joining chain	0	2	3	-1.86974
2765	21337	Tacr2	tachykinin receptor 2	0	2	3	-1.86909
2766	223664	Lrrc14	leucine rich repeat containing 14	0	2	3	-1.86893
2767	56494	Gosr2	golgi SNAP receptor complex member 2	0	2	3	-1.8688
2768	57252	Tas2r105	taste receptor, type 2, member 105	0	2	3	-1.86847
2769	75578	2310009E04Rik	FGGY carbohydrate kinase domain containing	0	2	3	-1.86842
2770	381751	UNK	NA	0	2	3	-1.86809
2771	78912	Sp2	Sp2 transcription factor	0	2	3	-1.86768

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2772	13495	Drg2	developmentally regulated GTP binding protein 2	0	2	3	-1.86707
2773	66902	Mtap	methylthioadenosine phosphorylase	0	2	3	-1.86665
2774	94353	Hmgn3	high mobility group nucleosomal binding domain 3	0	2	3	-1.86639
2775	15398	Hoxa13	homeobox A13	0	2	3	-1.86608
2776	66789	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	0	2	3	-1.86603
2777	113861	V1rc4	vomeronasal 1 receptor, pseudogene 8	0	2	3	-1.86572
2778	226830	Smyd2	SET and MYND domain containing 2	0	2	3	-1.86552
2779	70661	BC033915	SIK family kinase 3	0	2	3	-1.86547
2780	259114	Olfr570	olfactory receptor 570	0	2	2	-1.86547
2781	110948	Hlcs	holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	0	2	3	-1.8652
2782	24012	Rgs7	regulator of G protein signaling 7	0	2	3	-1.86484
2783	228769	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	0	2	3	-1.86453
2784	235047	BB114266	zinc finger protein 809	0	2	2	-1.86428
2785	26371	Wdr39	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	0	2	3	-1.86336
2786	211914	Ddef2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	0	2	3	-1.86318
2787	16451	Jak1	Janus kinase 1	0	2	3	-1.86308
2788	114716	Spred2	sprouty-related, EVH1 domain containing 2	0	2	3	-1.86298
2789	11614	Nr0b1	nuclear receptor subfamily 0, group B, member 1	0	2	3	-1.86243
2790	56844	Tssc4	tumor-suppressing subchromosomal transferable fragment 4	0	2	3	-1.86204
2791	433915	UNK	NA	0	2	2	-1.8616
2792	68260	Trmt12	tRNA methyltranferase 12 homolog (S. cerevisiae)	0	2	3	-1.8614
2793	71393	Kctd6	potassium channel tetramerisation domain containing 6	0	2	3	-1.86126
2794	13714	Elk4	ELK4, member of ETS oncogene family	0	2	3	-1.86091
2795	13712	Elk1	ELK1, member of ETS oncogene family	0	2	3	-1.86076
2796	232889	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	0	2	3	-1.8607
2797	66155	Ufc1	ubiquitin-fold modifier conjugating enzyme 1	0	2	2	-1.8596
2798	99738	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	0	2	3	-1.85942
2799	66841	Etfdh	electron transferring flavoprotein, dehydrogenase	0	2	3	-1.85935
2800	74760	Rab3il1	RAB3A interacting protein (rabin3)-like 1	0	2	3	-1.85897
2801	385528	UNK	NA	0	2	3	-1.85892
2802	27056	Irf5	interferon regulatory factor 5	0	2	3	-1.85828
2803	69357	1700003E24Rik	cDNA sequence BC061195	0	2	2	-1.85809
2804	242574	C130073F10Rik	RIKEN cDNA C130073F10 gene	0	2	2	-1.85806
2805	78558	Htra3	HtrA serine peptidase 3	0	2	3	-1.85711
2806	76829	Dok5	docking protein 5	0	2	2	-1.85689
2807	211347	Pank3	pantothenate kinase 3	0	2	3	-1.85649
2808	58238	A830059I20Rik	family with sequence similarity 181, member B	0	2	2	-1.85633

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2809	18260	Ocln	occludin	0	2	3	-1.85598
2810	22654	Zfp13	zinc finger protein 13	0	2	3	-1.85565
2811	140792	Colec12	collectin sub-family member 12	0	2	3	-1.85529
2812	432545	UNK	NA	0	2	3	-1.8547
2813	94062	Mrpl3	mitochondrial ribosomal protein L3	0	2	3	-1.85358
2814	333452	LOC333452	predicted gene 5132	0	2	3	-1.85206
2815	66642	Ctnnbl1	catenin, beta like 1	0	2	3	-1.85026
2816	171190	V1rc17	vomeronasal 1 receptor 26	0	2	3	-1.85023
2817	268783	Mtmr12	myotubularin related protein 12	0	2	3	-1.85016
2818	66454	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	0	2	3	-1.84996
2819	83395	Sp6	trans-acting transcription factor 6	0	2	3	-1.8491
2820	21898	Tlr4	toll-like receptor 4	0	2	3	-1.84895
2821	50909	C1r	complement component 1, r subcomponent A	0	2	3	-1.84884
2822	67000	Prlpi	prolactin family 3, subfamily a, member 1	0	2	3	-1.84882
2823	22644	Rnf103	ring finger protein 103	0	2	2	-1.84724
2824	14309	Fshr	follicle stimulating hormone receptor	0	2	3	-1.84722
2825	21769	Zfand3	zinc finger, AN1-type domain 3	0	2	3	-1.84716
2826	235505	Cd109	CD109 antigen	0	2	3	-1.84699
2827	408190	Wfdc13	WAP four-disulfide core domain 13	0	2	2	-1.84692
2828	66881	Pcyox1	prenylcysteine oxidase 1	0	2	3	-1.84675
2829	20422	Shfm1	split hand/foot malformation (ectrodactyly) type 1	0	2	2	-1.84673
2830	14381	G6pdx	glucose-6-phosphate dehydrogenase X-linked	0	2	3	-1.8464
2831	68549	Sgol2	shugoshin-like 2 (S. pombe)	0	2	3	-1.84614
2832	234911	Mmp27	matrix metallopeptidase 27	0	2	3	-1.8439
2833	68705	Gtf2f2	general transcription factor IIF, polypeptide 2	0	2	3	-1.84356
2834	11876	Artn	artemin	0	2	3	-1.84249
2835	98267	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	0	2	3	-1.84184
2836	21934	Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	0	2	3	-1.84181
2837	258592	Olfr697	olfactory receptor 697	0	2	3	-1.84179
2838	22323	Vasp	vasodilator-stimulated phosphoprotein	0	2	3	-1.84103
2839	238803	Zfp366	zinc finger protein 366	0	2	2	-1.84058
2840	26400	Map2k7	mitogen-activated protein kinase kinase 7	0	2	3	-1.84007
2841	68603	Pmvk	phosphomevalonate kinase	0	2	3	-1.84006
2842	19120	Prm3	protamine 3	0	2	3	-1.83973
2843	93882	Pcdhb11	protocadherin beta 11	0	2	3	-1.83915
2844	384009	Glipr2	GLI pathogenesis-related 2	0	2	3	-1.83893
2845	381413	Gpr176	G protein-coupled receptor 176	0	2	3	-1.83868

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2846	14311	Cidec	cell death-inducing DFFA-like effector c	0	2	2	-1.83834
2847	108899	2700081O15Rik	RIKEN cDNA 2700081O15 gene	0	2	2	-1.83769
2848	117590	Asb10	ankyrin repeat and SOCS box-containing 10	0	2	3	-1.83658
2849	30959	Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	0	2	3	-1.83637
2850	224674	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0	2	3	-1.83625
2851	12308	Calb2	calbindin 2	0	2	3	-1.83594
2852	74018	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	0	2	3	-1.83574
2853	19200	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	0	2	3	-1.83545
2854	67229	Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	0	2	3	-1.83521
2855	16848	Lfng	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0	2	3	-1.83513
2856	76383	1700012L04Rik	RIKEN cDNA 1700012L04 gene	0	2	1	-1.83513
2857	207495	Baiap2l2	BAI1-associated protein 2-like 2	0	2	2	-1.83466
2858	238257	Tmem30b	transmembrane protein 30B	0	2	3	-1.83306
2859	71869	Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	0	2	3	-1.83285
2860	83961	Nrg4	neuregulin 4	0	2	3	-1.83225
2861	11803	Aplp1	amyloid beta (A4) precursor-like protein 1	0	2	3	-1.83147
2862	17220	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	0	2	3	-1.83059
2863	71833	Wdr68	DDB1 and CUL4 associated factor 7	0	2	3	-1.8304
2864	67333	Stk35	serine/threonine kinase 35	0	2	3	-1.83025
2865	243277	Gpr133	G protein-coupled receptor 133	0	2	2	-1.82971
2866	54683	Prdx5	peroxiredoxin 5	0	2	3	-1.82961
2867	71425	5430413K10Rik	BPI fold containing family B, member 9A	0	2	3	-1.82898
2868	102093	Phkb	phosphorylase kinase beta	0	2	3	-1.82876
2869	436127	UNK	NA	0	2	3	-1.82873
2870	53333	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0	2	2	-1.82843
2871	14797	Aes	amino-terminal enhancer of split	0	2	3	-1.82841
2872	245109	Gm397	zinc finger and SCAN domain containing 4C	0	2	3	-1.82837
2873	110279	Bcr	breakpoint cluster region	0	2	3	-1.82812
2874	228858	Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	0	2	2	-1.82708
2875	20355	Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	0	2	2	-1.82692
2876	19172	Psmb4	proteasome (prosome, macropain) subunit, beta type 4	0	2	3	-1.82666
2877	67338	Rffl	ring finger and FYVE like domain containing protein	0	2	3	-1.82642
2878	50905	Il17rb	interleukin 17 receptor B	0	2	3	-1.8264
2879	207278	Fchsd2	FCH and double SH3 domains 2	0	2	2	-1.8262
2880	60345	Nrip2	nuclear receptor interacting protein 2	0	2	3	-1.82584
2881	20589	Ighmbp2	immunoglobulin mu binding protein 2	0	2	3	-1.82583
2882	328264	A030007L22	NA	0	2	3	-1.82563

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2883	66194	Pycrl	pyrroline-5-carboxylate reductase-like	0	2	3	-1.82539
2884	76797	2410137M14Rik	RIKEN cDNA 2410137M14 gene	0	2	3	-1.82512
2885	101142	Itfg2	integrin alpha FG-GAP repeat containing 2	0	2	3	-1.82487
2886	72284	Oraov1	oral cancer overexpressed 1	0	2	2	-1.82452
2887	26950	Vsnl1	visinin-like 1	0	2	3	-1.82354
2888	67503	1700001G17Rik	RIKEN cDNA 1700001G17 gene	0	2	2	-1.82197
2889	74648	S100pbp	S100P binding protein	0	2	2	-1.82054
2890	23950	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	0	2	3	-1.82046
2891	226419	Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	0	2	3	-1.82031
2892	97387	Strn4	striatin, calmodulin binding protein 4	0	2	3	-1.82005
2893	27388	Ptdss2	phosphatidylserine synthase 2	0	2	3	-1.8192
2894	79233	Zfp319	zinc finger protein 319	0	2	3	-1.8187
2895	19338	Rab33b	RAB33B, member of RAS oncogene family	0	2	3	-1.81835
2896	259105	Olfr549	olfactory receptor 549	0	2	3	-1.81822
2897	73608	Marveld3	MARVEL (membrane-associating) domain containing 3	0	2	3	-1.81814
2898	18478	Pah	phenylalanine hydroxylase	0	2	3	-1.81708
2899	404285	V1rd11	vomeronasal 1 receptor 64	0	2	2	-1.8169
2900	74776	Ppa2	pyrophosphatase (inorganic) 2	0	2	3	-1.8164
2901	18046	Nfyc	nuclear transcription factor-Y gamma	0	2	3	-1.81572
2902	209513	Taar4	trace amine-associated receptor 4	0	2	3	-1.81566
2903	68673	1110033F04Rik	keratin associated protein 4-2	0	2	3	-1.81508
2904	407243	AI840826	transmembrane protein 189	0	2	3	-1.81456
2905	320981	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	0	2	3	-1.81415
2906	225888	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	0	2	3	-1.81392
2907	68653	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	0	2	3	-1.81359
2908	13616	Edn3	endothelin 3	0	2	3	-1.81349
2909	11512	Adcy6	adenylate cyclase 6	0	2	3	-1.81311
2910	22248	Unc119	unc-119 homolog (C. elegans)	0	2	2	-1.81288
2911	245576	LOC245576	phosphoribosyl pyrophosphate synthetase-associated protein 2 pseudogene	0	2	3	-1.81276
2912	69888	Cyp2c66	cytochrome P450, family 2, subfamily c, polypeptide 66	0	2	2	-1.8126
2913	27418	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	0	2	3	-1.81234
2914	22341	Vegfc	vascular endothelial growth factor C	0	2	3	-1.81234
2915	12686	Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	0	2	2	-1.81176
2916	66588	Cmpk	cytidine monophosphate (UMP-CMP) kinase 1	0	2	3	-1.81171
2917	13877	Erh	enhancer of rudimentary homolog (Drosophila)	0	2	3	-1.81136
2918	76971	2810007J24Rik	RIKEN cDNA 2810007J24 gene	0	2	3	-1.81134
2919	21916	Tmod1	tropomodulin 1	0	2	3	-1.81098

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2920	26926	Pdcd8	apoptosis-inducing factor, mitochondrion-associated 1	0	2	3	-1.81096
2921	27062	Cadps	Ca2+-dependent secretion activator	0	2	3	-1.81071
2922	380997	9030605E09Rik	cytochrome P450, family 2, subfamily d, polypeptide 12	0	2	2	-1.8107
2923	20965	Syn2	synapsin II	0	2	3	-1.81056
2924	217721	BC011209	major facilitator superfamily domain containing 7C	0	2	3	-1.81015
2925	20598	Smpd2	sphingomyelin phosphodiesterase 2, neutral	0	2	3	-1.80994
2926	381372	Gm1890	NA	0	2	2	-1.80964
2927	27999	D6Wsu176e	family with sequence similarity 3, member C	0	2	3	-1.8092
2928	13602	Sparcl1	SPARC-like 1	0	2	3	-1.80893
2929	69623	2310012P17Rik	zinc finger protein 33B	0	2	3	-1.80887
2930	258134	Olfr426	olfactory receptor 426	0	2	3	-1.80852
2931	76629	1700111I05Rik	Williams-Beuren syndrome chromosome region 28 (human)	0	2	3	-1.80827
2932	246746	Cd300lf	CD300 antigen like family member F	0	2	2	-1.8079
2933	436444	UNK	NA	0	2	3	-1.80757
2934	23827	Bpnt1	bisphosphate 3'-nucleotidase 1	0	2	3	-1.80734
2935	20638	Snrpb	small nuclear ribonucleoprotein B	0	2	3	-1.80729
2936	68460	Dhrs7c	dehydrogenase/reductase (SDR family) member 7C	0	2	2	-1.80711
2937	71733	Susd2	sushi domain containing 2	0	2	3	-1.80674
2938	228012	Tlk1	tousled-like kinase 1	0	2	3	-1.80643
2939	329416	Nostrin	nitric oxide synthase trafficker	0	2	3	-1.80595
2940	16770	Lalba	lactalbumin, alpha	0	2	2	-1.80582
2941	240638	Slc16a12	solute carrier family 16 (monocarboxylic acid transporters), member 12	0	2	3	-1.80527
2942	434518	UNK	NA	0	2	3	-1.8052
2943	109648	Npy	neuropeptide Y	0	2	3	-1.80512
2944	227723	5830434P21Rik	proline-rich coiled-coil 2B	0	2	3	-1.80489
2945	382761	UNK	NA	0	2	3	-1.80481
2946	230558	C8a	complement component 8, alpha polypeptide	0	2	3	-1.80414
2947	13349	Darc	Duffy blood group, chemokine receptor	0	2	3	-1.8041
2948	22646	Zfp105	zinc finger protein 105	0	2	3	-1.80363
2949	243300	6430598A04Rik	RIKEN cDNA 6430598A04 gene	0	2	3	-1.80333
2950	114714	Rad51c	RAD51 homolog c (S. cerevisiae)	0	2	3	-1.8033
2951	233987	BC003267	zinc finger protein 958	0	2	3	-1.80284
2952	56174	Nagk	N-acetylglucosamine kinase	0	2	3	-1.80215
2953	213895	Bms1l	BMS1 homolog, ribosome assembly protein (yeast)	0	2	3	-1.80087
2954	20815	Srpk1	serine/arginine-rich protein specific kinase 1	0	2	3	-1.80017
2955	235050	BC005471	zinc finger protein 810	0	2	3	-1.79966
2956	442835	9230002F21Rik	defensin beta 22	0	2	3	-1.79906

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
2957	208795	Tmem63a	transmembrane protein 63a	0	2	3	-1.79887
2958	67337	Cstf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	0	2	3	-1.79808
2959	114889	Vsx1	visual system homeobox 1 homolog (zebrafish)	0	2	3	-1.79796
2960	75732	Iqcd	IQ motif containing D	0	2	2	-1.79763
2961	67800	Dgat2	diacylglycerol O-acyltransferase 2	0	2	3	-1.79755
2962	52653	Nudcd2	NudC domain containing 2	0	2	2	-1.79743
2963	106572	Rab31	RAB31, member RAS oncogene family	0	2	3	-1.79723
2964	319468	Ppm1h	protein phosphatase 1H (PP2C domain containing)	0	2	2	-1.7968
2965	14991	H2-M3	histocompatibility 2, M region locus 3	0	2	3	-1.79648
2966	54151	Cyhr1	cysteine and histidine rich 1	0	2	3	-1.79594
2967	18426	Ovol1	OVO homolog-like 1 (Drosophila)	0	2	3	-1.79551
2968	16878	Lif	leukemia inhibitory factor	0	2	3	-1.79516
2969	29819	Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	0	2	3	-1.79444
2970	72585	Lypd1	Ly6/Plaur domain containing 1	0	2	3	-1.7941
2971	22032	Traf4	TNF receptor associated factor 4	0	2	3	-1.79386
2972	20416	Shc1	src homology 2 domain-containing transforming protein C1	0	2	3	-1.79318
2973	76983	Scfd1	Sec1 family domain containing 1	0	2	3	-1.79292
2974	21429	Ubtf	upstream binding transcription factor, RNA polymerase I	0	2	3	-1.79279
2975	22315	V2r9	NA	0	2	3	-1.7926
2976	57358	Cmar	NA	0	2	3	-1.79252
2977	11735	Ank3	ankyrin 3, epithelial	0	2	3	-1.7925
2978	21835	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0	2	3	-1.79185
2979	22184	U2af1-rs2	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	0	2	3	-1.79136
2980	69754	Fbxo7	F-box protein 7	0	2	3	-1.79119
2981	21389	Tbx6	T-box 6	0	2	3	-1.79068
2982	68240	Rpa3	replication protein A3	0	2	3	-1.79026
2983	258216	Olfr1034	olfactory receptor 1034	0	2	2	-1.79015
2984	69387	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	0	2	3	-1.78929
2985	319930	Ceacam19	carcinoembryonic antigen-related cell adhesion molecule 19	0	2	2	-1.78904
2986	223776	1300018J18Rik	RIKEN cDNA 1300018J18 gene	0	2	2	-1.78865
2987	20887	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	0	2	3	-1.78864
2988	83762	Otof	otoferlin	0	2	3	-1.78856
2989	20779	Src	Rous sarcoma oncogene	0	2	3	-1.78832
2990	72772	Rint1	RAD50 interactor 1	0	2	2	-1.78789
2991	21899	Tlr6	toll-like receptor 6	0	2	3	-1.78708
2992	71726	Smug1	single-strand selective monofunctional uracil DNA glycosylase	0	2	2	-1.78639
2993	237758	Zfp454	zinc finger protein 454	0	2	3	-1.78613

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2994	83408	Gimap3	GTPase, IMAP family member 3	0	2	3	-1.78509
2995	17123	Madcam1	mucosal vascular addressin cell adhesion molecule 1	0	2	3	-1.78501
2996	18557	Pctk3	cyclin-dependent kinase 18	0	2	3	-1.78451
2997	14407	Gabrg3	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3	0	2	3	-1.78449
2998	58230	Rnf8	ring finger protein 8	0	2	3	-1.78441
2999	56086	Set	SET nuclear oncogene	0	2	3	-1.784
3000	239436	Slc30a8	solute carrier family 30 (zinc transporter), member 8	0	2	3	-1.78264
3001	257898	Olfr867	olfactory receptor 867	0	2	2	-1.7826
3002	20725	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8	0	2	3	-1.78205
3003	241794	LOC241794	potassium voltage-gated channel, subfamily G, member 1	0	2	3	-1.78204
3004	140580	Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	0	2	3	-1.78181
3005	78240	Cst11	cystatin 11	0	2	3	-1.78155
3006	381556	UNK	NA	0	2	3	-1.78143
3007	74264	1700045I19Rik	ring finger protein 138 pseudogene	0	2	3	-1.78137
3008	21750	Terf2	telomeric repeat binding factor 2	0	2	3	-1.78129
3009	18725	Pira2	paired-Ig-like receptor A2	0	2	3	-1.78115
3010	69731	Gemin7	gem (nuclear organelle) associated protein 7	0	2	3	-1.78018
3011	243900	4930432E11Rik	RIKEN cDNA 4930432E11 gene	0	2	3	-1.78003
3012	69668	Ccdc115	coiled-coil domain containing 115	0	2	3	-1.77978
3013	22359	Vldlr	very low density lipoprotein receptor	0	2	3	-1.77925
3014	69635	Dapk1	death associated protein kinase 1	0	2	3	-1.779
3015	18400	Slc22a18	solute carrier family 22 (organic cation transporter), member 18	0	2	3	-1.77888
3016	73503	Mbd3l1	methyl-CpG binding domain protein 3-like 1	0	2	3	-1.77825
3017	16949	Loxl1	lysyl oxidase-like 1	0	2	3	-1.77794
3018	69046	Hbld2	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	0	2	2	-1.77745
3019	68755	Cgrrf1	cell growth regulator with ring finger domain 1	0	2	3	-1.77724
3020	212442	Lactb2	lactamase, beta 2	0	2	2	-1.77683
3021	18587	Pde6b	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide	0	2	2	-1.77546
3022	11740	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	0	2	3	-1.77542
3023	18459	Pabpc2	poly(A) binding protein, cytoplasmic 2	0	2	3	-1.7753
3024	243308	A430033K04Rik	RIKEN cDNA A430033K04 gene	0	2	3	-1.77515
3025	77397	9530003J23Rik	RIKEN cDNA 9530003J23 gene	0	2	3	-1.77434
3026	52530	Nola2	NHP2 ribonucleoprotein homolog (yeast)	0	2	3	-1.77409
3027	434371	LOC434371	NA	0	2	3	-1.77367
3028	240068	D10628	zinc finger protein 563	0	2	3	-1.77346
3029	56041	Vdp	USO1 homolog, vesicle docking protein (yeast)	0	2	3	-1.77321
3030	13857	Epor	erythropoietin receptor	0	2	3	-1.77294

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3031	71755	Dhdh	dihydrodiol dehydrogenase (dimeric)	0	2	2	-1.77285
3032	68080	Atpbd1c	GPN-loop GTPase 3	0	2	3	-1.77253
3033	14760	Gpr19	G protein-coupled receptor 19	0	2	3	-1.77212
3034	12592	Cdx4	caudal type homeobox 4	0	2	3	-1.77182
3035	230726	9130416B15	rhomboid, veinlet-like 2 (Drosophila)	0	2	3	-1.77157
3036	258955	Olfr531	olfactory receptor 531	0	2	2	-1.77139
3037	14623	Gjb6	gap junction protein, beta 6	0	2	3	-1.77135
3038	434175	LOC434175	predicted gene 5593	0	2	3	-1.77116
3039	207425	Brwd2	WD repeat domain 11	0	2	2	-1.77104
3040	20219	Apcs	serum amyloid P-component	0	2	3	-1.77102
3041	72297	B3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	0	2	3	-1.77011
3042	66606	Lrrc57	leucine rich repeat containing 57	0	2	2	-1.76964
3043	52686	Mettl2	methyltransferase like 2	0	2	3	-1.76931
3044	230674	Jmjd2a	lysine (K)-specific demethylase 4A	0	2	3	-1.76915
3045	22427	Wrn	Werner syndrome homolog (human)	0	2	3	-1.76891
3046	436196	LOC436196	predicted pseudogene 5755	0	2	3	-1.76835
3047	108098	Surb7	mediator complex subunit 21	0	2	3	-1.76811
3048	59091	Jph2	junctophilin 2	0	2	3	-1.76764
3049	83555	Tex13	testis expressed gene 13	0	2	2	-1.76748
3050	69479	1700029J07Rik	RIKEN cDNA 1700029J07 gene	0	2	3	-1.76748
3051	67729	Mansc1	MANSC domain containing 1	0	2	3	-1.76726
3052	58176	Rhbg	Rhesus blood group-associated B glycoprotein	0	2	3	-1.76693
3053	22017	Tpmt	thiopurine methyltransferase	0	2	3	-1.76691
3054	26889	Cln8	ceroid-lipofuscinosis, neuronal 8	0	2	3	-1.76679
3055	54132	Pdlim1	PDZ and LIM domain 1 (elfin)	0	2	3	-1.76671
3056	142682	Zcchc14	zinc finger, CCHC domain containing 14	0	2	3	-1.76638
3057	214239	A430105I19Rik	RIKEN cDNA A430105I19 gene	0	2	3	-1.76634
3058	18617	Rhox5	reproductive homeobox 5	0	2	3	-1.76628
3059	66864	Clec14a	C-type lectin domain family 14, member a	0	2	3	-1.76614
3060	67382	Brd3	bromodomain containing 3	0	2	3	-1.76593
3061	236733	Usp11	ubiquitin specific peptidase 11	0	2	3	-1.76575
3062	67466	Pdcl	phosducin-like	0	2	3	-1.76541
3063	54152	Dnalc4	dynein, axonemal, light chain 4	0	2	3	-1.76487
3064	54192	Pbsn	probasin	0	2	3	-1.76484
3065	18372	Olfr8	olfactory receptor 8	0	2	2	-1.76483
3066	107305	Vps37c	vacuolar protein sorting 37C (yeast)	0	2	3	-1.76456
3067	56519	Defb4	defensin beta 4	0	2	3	-1.76444

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3068	73316	Calr3	calreticulin 3	0	2	2	-1.76432
3069	230279	6330416G13Rik	RIKEN cDNA 6330416G13 gene	0	2	2	-1.76428
3070	20733	Spint2	serine protease inhibitor, Kunitz type 2	0	2	3	-1.76413
3071	16885	Limk1	LIM-domain containing, protein kinase	0	2	3	-1.76399
3072	23992	Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	0	2	3	-1.76354
3073	259123	Olfr632	olfactory receptor 632	0	2	2	-1.76334
3074	67201	2700085E05Rik	glyoxalase domain containing 4	0	2	3	-1.76324
3075	22041	Trf	transferrin	0	2	3	-1.76295
3076	18216	Ntsr1	neurotensin receptor 1	0	2	3	-1.76237
3077	14387	Gaa	glucosidase, alpha, acid	0	2	3	-1.76231
3078	226541	Klhl20	kelch-like 20 (Drosophila)	0	2	3	-1.76195
3079	259064	Olfr124	olfactory receptor 124	0	2	3	-1.76181
3080	15135	Hbb-y	hemoglobin Y, beta-like embryonic chain	0	2	3	-1.76173
3081	170571	Cntnap4	contactin associated protein-like 4	0	2	2	-1.76161
3082	217684	4933426M11Rik	RIKEN cDNA 4933426M11 gene	0	2	3	-1.7612
3083	93724	Pcdhga12	protocadherin gamma subfamily A, 12	0	2	3	-1.76106
3084	11974	Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E	0	2	3	-1.76047
3085	54451	Cpsf3	cleavage and polyadenylation specificity factor 3	0	2	3	-1.76046
3086	17763	Mtcp1	mature T cell proliferation 1	0	2	3	-1.76006
3087	51792	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	0	2	3	-1.75962
3088	258564	Olfr1015	olfactory receptor 1015	0	2	3	-1.75953
3089	102570	Slc22a13	solute carrier family 22 (organic cation transporter), member 13	0	2	3	-1.75933
3090	223267	BC006662	AIG2-like domain 1	0	2	3	-1.75905
3091	19146	Prss7	transmembrane protease, serine 15	0	2	3	-1.75868
3092	270120	Fat3	FAT tumor suppressor homolog 3 (Drosophila)	0	2	3	-1.75849
3093	50758	Fbxl17	F-box and leucine-rich repeat protein 17	0	2	3	-1.75825
3094	20937	Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0	2	3	-1.75808
3095	76793	Snip1	Smad nuclear interacting protein 1	0	2	3	-1.75742
3096	77809	Lrrc42	leucine rich repeat containing 42	0	2	2	-1.75727
3097	216164	Dos	NA	0	2	2	-1.75718
3098	241230	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	0	2	3	-1.75702
3099	70202	2310051M13Rik	cathepsin L-like 3	0	2	3	-1.7569
3100	270672	Map3k15	mitogen-activated protein kinase kinase kinase 15	0	2	3	-1.75662
3101	18294	Ogg1	8-oxoguanine DNA-glycosylase 1	0	2	3	-1.75634
3102	170823	Glmn	glomulin, FKBP associated protein	0	2	3	-1.75629
3103	20340	Glg1	golgi apparatus protein 1	0	2	3	-1.75603
3104	18457	Pldn	pallidin	0	2	3	-1.75583

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3105	269437	Plch1	phospholipase C, eta 1	0	2	3	-1.75573
3106	70207	Ccdc44	translational activator of mitochondrially encoded cytochrome c oxidase I	0	2	2	-1.7554
3107	54402	Stk19	serine/threonine kinase 19	0	2	3	-1.75514
3108	56631	Trim17	tripartite motif-containing 17	0	2	3	-1.75382
3109	70211	2810407A14Rik	NA	0	2	3	-1.75325
3110	225608	Sh3tc2	SH3 domain and tetratricopeptide repeats 2	0	2	2	-1.75284
3111	84682	Cox4i2	cytochrome c oxidase subunit IV isoform 2	0	2	3	-1.75241
3112	15469	Prmt1	protein arginine N-methyltransferase 1	0	2	2	-1.75208
3113	210741	Kcnk12	potassium channel, subfamily K, member 12	0	2	3	-1.75182
3114	20443	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	0	2	3	-1.75179
3115	19152	Prtn3	proteinase 3	0	2	3	-1.75172
3116	71710	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	0	2	3	-1.75094
3117	213541	Ythdf2	YTH domain family 2	0	2	2	-1.74871
3118	50850	Spast	spastin	0	2	2	-1.74856
3119	53325	Banp	BTG3 associated nuclear protein	0	2	3	-1.7482
3120	171382	Trpm8	transient receptor potential cation channel, subfamily M, member 8	0	2	3	-1.74799
3121	52466	D11Ertd18e	solute carrier family 46, member 1	0	2	3	-1.74799
3122	56371	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	0	2	3	-1.74698
3123	104080	Nxph4	neurexophilin 4	0	2	3	-1.74693
3124	14767	Nmur1	neuromedin U receptor 1	0	2	3	-1.74682
3125	434197	LOC434197	family with sequence similarity 169, member B	0	2	3	-1.74622
3126	53375	Mtx2	metaxin 2	0	2	3	-1.74542
3127	19697	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	0	2	2	-1.74501
3128	70956	4921530G04Rik	testis expressed gene 19.2	0	2	2	-1.74497
3129	104252	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	0	2	2	-1.74483
3130	102580	Alg9	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase)	0	2	3	-1.74481
3131	242691	Gpatc3	G patch domain containing 3	0	2	3	-1.74458
3132	22353	Vip	vasoactive intestinal polypeptide	0	2	3	-1.74381
3133	22074	Try4	trypsin 4	0	2	3	-1.74341
3134	347710	Pramel5	preferentially expressed antigen in melanoma like 4	0	2	2	-1.74306
3135	171506	H1foo	H1 histone family, member O, oocyte-specific	0	2	3	-1.74303
3136	17761	Mtap7	microtubule-associated protein 7	0	2	3	-1.74302
3137	80902	Zfp202	zinc finger protein 202	0	2	3	-1.74274
3138	75645	1700011F14Rik	RIKEN cDNA 1700011F14 gene	0	2	3	-1.7427
3139	268741	5730589K01Rik	TOX high mobility group box family member 4	0	2	3	-1.74253
3140	272661	UNK	NA	0	2	3	-1.74239
3141	66525	Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	0	2	3	-1.74177

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3142	16866	Lhb	luteinizing hormone beta	0	2	3	-1.74171
3143	14432	Gap43	growth associated protein 43	0	2	3	-1.74142
3144	258792	Olfr1499	olfactory receptor 1499	0	2	3	-1.741
3145	228770	Rspo4	R-spondin family, member 4	0	2	3	-1.74063
3146	71885	2310003H01Rik	RIKEN cDNA 2310003H01 gene	0	2	2	-1.74043
3147	11545	Parp1	poly (ADP-ribose) polymerase family, member 1	0	2	3	-1.7403
3148	15285	Hlxb9	motor neuron and pancreas homeobox 1	0	2	3	-1.74019
3149	216134	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	0	2	3	-1.74014
3150	22116	Stk22s1	testis-specific serine kinase substrate	0	2	3	-1.73913
3151	56193	Plek	pleckstrin	0	2	3	-1.73909
3152	272381	Lrrc4b	leucine rich repeat containing 4B	0	2	3	-1.73831
3153	404222	Olfr244	olfactory receptor 231	0	2	3	-1.73826
3154	320040	9930039A11Rik	ring finger protein 222	0	2	3	-1.73791
3155	76688	Arfrp1	ADP-ribosylation factor related protein 1	0	2	3	-1.73721
3156	68259	Ift80	intraflagellar transport 80 homolog (Chlamydomonas)	0	2	3	-1.73701
3157	17173	Ascl2	achaete-scute complex homolog 2 (Drosophila)	0	2	3	-1.73682
3158	56222	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	0	2	3	-1.73667
3159	12724	Clcn2	chloride channel 2	0	2	3	-1.73643
3160	228662	Btbd3	BTB (POZ) domain containing 3	0	2	3	-1.73629
3161	98752	Fcrla	Fc receptor-like A	0	2	3	-1.73624
3162	21816	Tgm1	transglutaminase 1, K polypeptide	0	2	3	-1.73576
3163	14732	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	0	2	3	-1.73571
3164	83702	Akr1c6	aldo-keto reductase family 1, member C6	0	2	3	-1.73563
3165	114660	Etos1	ectopic ossification 1	0	2	2	-1.7355
3166	53861	Zranb2	zinc finger, RAN-binding domain containing 2	0	2	3	-1.73546
3167	209387	AI451617	tripartite motif-containing 30D	0	2	3	-1.7354
3168	20751	Spr	sepiapterin reductase	0	2	3	-1.73518
3169	80888	Hspb8	heat shock protein 8	0	2	3	-1.73512
3170	329470	2610203E10Rik	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	0	2	3	-1.73487
3171	228576	Mall	mal, T cell differentiation protein-like	0	2	3	-1.73452
3172	14829	Grpr	gastrin releasing peptide receptor	0	2	3	-1.73452
3173	240832	Tor1aip2	torsin A interacting protein 2	0	2	2	-1.73399
3174	16184	Il2ra	interleukin 2 receptor, alpha chain	0	2	3	-1.73384
3175	103573	Xpo1	exportin 1, CRM1 homolog (yeast)	0	2	3	-1.73363
3176	216151	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	0	2	3	-1.733
3177	231549	Lrrc8d	leucine rich repeat containing 8D	0	2	2	-1.73277
3178	246316	Lgi2	leucine-rich repeat LGI family, member 2	0	2	3	-1.73238

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3179	15461	Hras1	Harvey rat sarcoma virus oncogene 1	0	2	3	-1.73228
3180	11428	Aco1	aconitase 1	0	2	3	-1.73205
3181	11801	Cd5l	CD5 antigen-like	0	2	3	-1.73171
3182	64010	Sav1	salvador homolog 1 (Drosophila)	0	2	3	-1.73145
3183	258534	Olfr1361	olfactory receptor 1361	0	2	3	-1.73139
3184	108670	Epsti1	epithelial stromal interaction 1 (breast)	0	2	2	-1.7313
3185	12794	Cnih2	cornichon homolog 2 (Drosophila)	0	2	3	-1.7307
3186	72381	2210409E12Rik	transcription elongation factor B (SIII), polypeptide 2 pseudogene	0	2	2	-1.73058
3187	73293	Ccdc103	coiled-coil domain containing 103	0	2	3	-1.73047
3188	101240	9530020G05Rik	WD repeat domain 91	0	2	2	-1.73024
3189	12006	Axin2	axin2	0	2	3	-1.73015
3190	17921	Myo7a	myosin VIIA	0	2	3	-1.73004
3191	319178	Hist1h2bb	histone cluster 1, H2bb	0	2	3	-1.73003
3192	20617	Snca	synuclein, alpha	0	2	3	-1.72943
3193	237880	1700071K01Rik	RIKEN cDNA 1700071K01 gene	0	2	3	-1.72924
3194	14159	Fes	feline sarcoma oncogene	0	2	3	-1.72893
3195	66277	Klf15	Kruppel-like factor 15	0	2	3	-1.72857
3196	19204	Ptafr	platelet-activating factor receptor	0	2	3	-1.72734
3197	233726	Ipo7	importin 7	0	2	3	-1.7271
3198	15267	Hist2h2aa1	histone cluster 2, H2aa1	0	2	3	-1.72699
3199	54673	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	0	2	3	-1.72693
3200	66175	Mustn1	musculoskeletal, embryonic nuclear protein 1	0	2	3	-1.72678
3201	230866	C230096C10Rik	RIKEN cDNA C230096C10 gene	0	2	2	-1.72667
3202	21954	Tnni3	troponin I, cardiac 3	0	2	2	-1.72615
3203	57895	6330407D12Rik	coiled-coil domain containing 126	0	2	3	-1.72615
3204	66932	Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	0	2	3	-1.72613
3205	18973	Pole	polymerase (DNA directed), epsilon	0	2	3	-1.72607
3206	320734	C920008G01Rik	RIKEN cDNA C920008G01 gene	0	2	3	-1.72553
3207	229699	Slc16a4	solute carrier family 16 (monocarboxylic acid transporters), member 4	0	2	3	-1.72538
3208	12348	Car11	carbonic anhydrase 11	0	2	3	-1.72502
3209	435667	UNK	NA	0	2	3	-1.7248
3210	71412	Dhrs2	dehydrogenase/reductase member 2	0	2	3	-1.7239
3211	70454	Cenpl	centromere protein L	0	2	2	-1.72338
3212	11481	Acvr2b	activin receptor IIB	0	2	3	-1.7233
3213	381406	2810408M09Rik	RIKEN cDNA 2810408M09 gene	0	2	3	-1.7229
3214	66047	Mrpl54	mitochondrial ribosomal protein L54	0	2	2	-1.72267
3215	51795	Srpx	sushi-repeat-containing protein	0	2	2	-1.72246

Candidates for positive regulators of normal growth (Fisher's)

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3216	19058	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	0	2	3	-1.72245
3217	320974	B430119L13Rik	leucine rich repeat neuronal 4	0	2	3	-1.7223
3218	84506	Hamp1	hepcidin antimicrobial peptide	0	2	3	-1.72175
3219	74123	Foxp4	forkhead box P4	0	2	3	-1.72159
3220	53404	Atoh7	atonal homolog 7 (Drosophila)	0	2	3	-1.72156
3221	380713	Scarf1	scavenger receptor class F, member 1	0	2	3	-1.72126
3222	66462	2810428I15Rik	RIKEN cDNA 2810428I15 gene	0	2	3	-1.72113
3223	22722	Zfp64	zinc finger protein 64	0	2	3	-1.72073
3224	73635	1700113I22Rik	RIKEN cDNA 1700113I22 gene	0	2	3	-1.72058
3225	18302	Oit3	oncoprotein induced transcript 3	0	2	3	-1.72052
3226	75671	Tex22	testis expressed gene 22	0	2	3	-1.72033
3227	246747	BC054059	adipogenin	0	2	3	-1.71975
3228	15168	Hcn3	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	0	2	3	-1.71914
3229	109676	Ank2	ankyrin 2, brain	0	2	3	-1.71898
3230	12638	Cftr	cystic fibrosis transmembrane conductance regulator homolog	0	2	3	-1.71888
3231	22145	Tuba4	tubulin, alpha 4A	0	2	3	-1.71841
3232	245622	BC031748	family with sequence similarity 199, X-linked	0	2	2	-1.71835
3233	83984	Tssk6	testis-specific serine kinase 6	0	2	3	-1.71728
3234	19650	Rbl1	retinoblastoma-like 1 (p107)	0	2	3	-1.71597
3235	433822	UNK	NA	0	2	2	-1.71576
3236	68193	Rpl24	ribosomal protein L24	0	2	3	-1.71504
3237	234734	Aars	alanyl-tRNA synthetase	0	2	3	-1.71325
3238	24047	Ccl19	chemokine (C-C motif) ligand 19	0	2	3	-1.7131
3239	231287	Atp10d	ATPase, class V, type 10D	0	2	3	-1.7119
3240	381101	BC048355	cDNA sequence BC048355	0	2	3	-1.71149
3241	14590	Ggh	gamma-glutamyl hydrolase	0	2	3	-1.71061
3242	19348	Kif20a	kinesin family member 20A	0	2	3	-1.71031
3243	67675	Cuta	cutA divalent cation tolerance homolog (E. coli)	0	2	3	-1.71019
3244	19142	Prss12	protease, serine, 12 neurotrypsin (motopsin)	0	2	3	-1.71008
3245	22608	Ybx1	Y box protein 1	0	2	3	-1.71
3246	20927	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	0	2	3	-1.70955
3247	107141	Cyp2c50	cytochrome P450, family 2, subfamily c, polypeptide 50	0	2	3	-1.70955
3248	50498	Ebi3	Epstein-Barr virus induced gene 3	0	2	3	-1.70929
3249	14170	Fgf15	fibroblast growth factor 15	0	2	3	-1.70924
3250	83703	Dbr1	debranching enzyme homolog 1 (S. cerevisiae)	0	2	3	-1.70902
3251	328280	Rslcan24	predicted gene 10037	0	2	3	-1.7082
3252	218977	Dlg7	discs, large (Drosophila) homolog-associated protein 5	0	2	3	-1.7079

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Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3253	18772	Pkp1	plakophilin 1	0	2	3	-1.70769
3254	14198	Fhit	fragile histidine triad gene	0	2	3	-1.70733
3255	74342	Lrrtm1	leucine rich repeat transmembrane neuronal 1	0	2	3	-1.70727
3256	57916	Tnfrsf13b	tumor necrosis factor receptor superfamily, member 13b	0	2	3	-1.70723
3257	73660	Cabp4	calcium binding protein 4	0	2	3	-1.70705
3258	434349	UNK	NA	0	2	3	-1.70692
3259	231332	AY487415	phosphoprotein enriched in astrocytes 15B	0	2	2	-1.70688
3260	13429	Dnm1	dynamin 1	0	2	3	-1.7066
3261	231600	Chfr	checkpoint with forkhead and ring finger domains	0	2	3	-1.7065
3262	22526	Xmr	predicted gene 4836	0	2	3	-1.70635
3263	70026	Bzrpl1	translocator protein 2	0	2	3	-1.70567
3264	11777	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	0	2	3	-1.70532
3265	12909	Crcp	calcitonin gene-related peptide-receptor component protein	0	2	2	-1.70514
3266	319185	Hist1h2bl	histone cluster 1, H2bl	0	2	3	-1.70452
3267	228869	Ncoa5	nuclear receptor coactivator 5	0	2	3	-1.7045
3268	68044	2510006C20Rik	ChaC, cation transport regulator homolog 2 (E. coli)	0	2	3	-1.7044
3269	382264	UNK	NA	0	2	3	-1.70427
3270	56335	Mettl3	methyltransferase like 3	0	2	3	-1.70372
3271	330723	Htra4	HtrA serine peptidase 4	0	2	3	-1.70371
3272	394433	Ugt1a5	UDP glucuronosyltransferase 1 family, polypeptide A5	0	2	3	-1.70347
3273	22223	Uchl1	ubiquitin carboxy-terminal hydrolase L1	0	2	3	-1.70297
3274	14376	Ganab	alpha glucosidase 2 alpha neutral subunit	0	2	3	-1.70256
3275	21341	Taf1c	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	0	2	3	-1.70241
3276	20384	Sfrs5	serine/arginine-rich splicing factor 5	0	2	3	-1.70202
3277	69019	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	0	2	3	-1.70144
3278	74048	4632428N05Rik	RIKEN cDNA 4632428N05 gene	0	2	3	-1.70111
3279	23831	Car14	carbonic anhydrase 14	0	2	3	-1.70103
3280	93876	Pcdhb5	protocadherin beta 5	0	2	3	-1.70068
3281	20516	Slc20a2	solute carrier family 20, member 2	0	2	3	-1.70055
3282	68449	Tbc1d10b	TBC1 domain family, member 10b	0	2	3	-1.7002
3283	20692	Sparc	secreted acidic cysteine rich glycoprotein	0	2	2	-1.69985
3284	51811	Clec4f	C-type lectin domain family 4, member f	0	2	3	-1.69912
3285	11500	Adam7	a disintegrin and metallopeptidase domain 7	0	2	3	-1.6989
3286	67888	Tmem100	transmembrane protein 100	0	2	2	-1.69852
3287	12978	Csf1r	colony stimulating factor 1 receptor	0	2	3	-1.69814
3288	258964	Olfr541	olfactory receptor 541	0	2	2	-1.6979
3289	434259	UNK	NA	0	2	3	-1.69764

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3290	75604	Tm4sf5	transmembrane 4 superfamily member 5	0	2	2	-1.69711
3291	27494	Amot	angiomotin	0	2	3	-1.69694
3292	75770	Brsk2	BR serine/threonine kinase 2	0	2	3	-1.69689
3293	68126	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	0	2	3	-1.69683
3294	14063	F2rl1	coagulation factor II (thrombin) receptor-like 1	0	2	3	-1.69625
3295	99237	Tm9sf4	transmembrane 9 superfamily protein member 4	0	2	2	-1.69612
3296	65972	Ifi30	interferon gamma inducible protein 30	0	2	3	-1.69608
3297	17203	Mc5r	melanocortin 5 receptor	0	2	3	-1.69588
3298	320878	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2	0	2	3	-1.69584
3299	328457	UNK	NA	0	2	3	-1.69542
3300	12337	Capn5	calpain 5	0	2	3	-1.69531
3301	212225	4930509O22	sperm motility kinase W	0	2	3	-1.69515
3302	15565	Htr6	5-hydroxytryptamine (serotonin) receptor 6	0	2	3	-1.69511
3303	12352	Car5a	carbonic anhydrase 5a, mitochondrial	0	2	3	-1.69483
3304	74435	Lrrc44	leucine-rich repeats and IQ motif containing 3	0	2	3	-1.69444
3305	18365	Olfr64	olfactory receptor 65	0	2	2	-1.69439
3306	236643	Sytl5	synaptotagmin-like 5	0	2	3	-1.69398
3307	217069	Trim25	tripartite motif-containing 25	0	2	3	-1.69241
3308	269604	Gpr157	G protein-coupled receptor 157	0	2	3	-1.69211
3309	75747	Sesn3	sestrin 3	0	2	3	-1.69166
3310	258446	Olfr1231	olfactory receptor 1231	0	2	3	-1.69145
3311	333329	Cngb1b	cyclic nucleotide gated channel beta 1	0	2	3	-1.69142
3312	66271	Tmem126a	transmembrane protein 126A	0	2	3	-1.69134
3313	16163	Il13	interleukin 13	0	2	3	-1.69116
3314	20742	Spnb2	spectrin beta 2	0	2	3	-1.69115
3315	241201	Cdh7	cadherin 7, type 2	0	2	3	-1.68989
3316	13508	Dscam	Down syndrome cell adhesion molecule	0	2	3	-1.68982
3317	108903	Tbcd	tubulin-specific chaperone d	0	2	3	-1.68955
3318	269587	Epb4.1	erythrocyte protein band 4.1	0	2	3	-1.68903
3319	382571	Kcnf1	potassium voltage-gated channel, subfamily F, member 1	0	2	3	-1.68903
3320	76441	Daam2	dishevelled associated activator of morphogenesis 2	0	2	3	-1.68893
3321	13522	Adam28	a disintegrin and metallopeptidase domain 28	0	2	3	-1.68832
3322	66044	Hars2	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	0	2	3	-1.68829
3323	60595	Actn4	actinin alpha 4	0	2	3	-1.68796
3324	108100	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	0	2	3	-1.68766
3325	19725	Rfx2	regulatory factor X, 2 (influences HLA class II expression)	0	2	3	-1.68743
3326	13360	Dhcr7	7-dehydrocholesterol reductase	0	2	3	-1.68739

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3327	228875	Slc35c2	solute carrier family 35, member C2	0	2	3	-1.68687
3328	54199	Ccrl2	chemokine (C-C motif) receptor-like 2	0	2	3	-1.68635
3329	67487	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	0	2	3	-1.68598
3330	66070	0610040D20Rik	CWC15 homolog (S. cerevisiae)	0	2	3	-1.68402
3331	17058	Klrb1b	NA	0	2	3	-1.68376
3332	18715	Pim2	proviral integration site 2	0	2	3	-1.68355
3333	67313	5730559C18Rik	RIKEN cDNA 5730559C18 gene	0	2	3	-1.68348
3334	56213	Htra1	HtrA serine peptidase 1	0	2	3	-1.68305
3335	64176	Sv2b	synaptic vesicle glycoprotein 2 b	0	2	3	-1.68111
3336	83554	Fstl3	follistatin-like 3	0	2	2	-1.68025
3337	12869	Cox8b	cytochrome c oxidase, subunit VIIIb	0	2	3	-1.68013
3338	258689	Olfr1466	olfactory receptor 1466	0	2	2	-1.67967
3339	93716	Pcdhga8	protocadherin gamma subfamily A, 8	0	2	3	-1.67937
3340	70369	Bag5	BCL2-associated athanogene 5	0	2	3	-1.67931
3341	71591	Zfp251	zinc finger protein 251	0	2	2	-1.67864
3342	21756	Tesp2	protease, serine, 40	0	2	3	-1.67827
3343	66587	Fastk	Fas-activated serine/threonine kinase	0	2	3	-1.67811
3344	26446	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	0	2	3	-1.67797
3345	213539	Bag2	BCL2-associated athanogene 2	0	2	3	-1.6774
3346	546214	LOC546214	NA	0	2	3	-1.67727
3347	76478	2410004L22Rik	4HAUS augmin-like complex, subunit 8	0	2	2	-1.67656
3348	14598	Ggt1	gamma-glutamyltransferase 1	0	2	3	-1.6758
3349	56835	Ctsr	cathepsin R	0	2	3	-1.67547
3350	14466	Gba	glucosidase, beta, acid	0	2	2	-1.67542
3351	30943	Tmprss8	protease, serine, 30	0	2	3	-1.67463
3352	17858	Mx2	myxovirus (influenza virus) resistance 2	0	2	3	-1.67453
3353	69085	Zcchc9	zinc finger, CCHC domain containing 9	0	2	3	-1.67446
3354	15976	Ifnar2	interferon (alpha and beta) receptor 2	0	2	3	-1.67431
3355	50930	Tnfsf14	tumor necrosis factor (ligand) superfamily, member 14	0	2	3	-1.6739
3356	19131	Prh1	proline rich protein HaeIII subfamily 1	0	2	2	-1.67359
3357	14248	Fliih	flightless I homolog (Drosophila)	0	2	3	-1.67344
3358	246694	Hps5	Hermansky-Pudlak syndrome 5 homolog (human)	0	2	2	-1.67334
3359	17933	Myt1l	myelin transcription factor 1-like	0	2	3	-1.6732
3360	98365	Slamf9	SLAM family member 9	0	2	3	-1.6731
3361	72562	Pcbd2	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (	0	2	3	-1.67302
3362	384444	UNK	NA	0	2	3	-1.67215
3363	11816	Apoe	apolipoprotein E	0	2	3	-1.67183

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3364	171191	V1rc18	vomeronasal 1 receptor 24	0	2	3	-1.67176
3365	20717	Serpina3m	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0	2	3	-1.67128
3366	67477	1300007F04Rik	abhydrolase domain containing 15	0	2	2	-1.67116
3367	24068	Sra1	steroid receptor RNA activator 1	0	2	1	-1.67057
3368	52245	Commd2	COMM domain containing 2	0	2	3	-1.67054
3369	64139	Ctsm	cathepsin M	0	2	3	-1.67009
3370	11534	Adk	adenosine kinase	0	2	2	-1.66984
3371	13998	Fgd6	FYVE, RhoGEF and PH domain containing 6	0	2	3	-1.66976
3372	258756	Olfr414	olfactory receptor 414	0	2	2	-1.66917
3373	433752	AA415398	expressed sequence AA415398	0	2	3	-1.66866
3374	107971	Frs3	fibroblast growth factor receptor substrate 3	0	2	3	-1.66851
3375	433545	UNK	NA	0	2	3	-1.66825
3376	59050	5730427N09Rik	NSA2 ribosome biogenesis homolog (S. cerevisiae)	0	2	3	-1.66762
3377	12531	Cdc25b	cell division cycle 25 homolog B (S. pombe)	0	2	3	-1.66726
3378	66979	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	0	2	3	-1.66692
3379	20298	Ccl21a	NA	0	2	3	-1.66644
3380	434405	LOC434405	NA	0	2	3	-1.66643
3381	12642	Ch25h	cholesterol 25-hydroxylase	0	2	3	-1.66639
3382	66385	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	0	2	3	-1.66629
3383	331392	LOC331392	nucleolar and coiled-body phosphoprotein 1 pseudogene	0	2	3	-1.6661
3384	102334	Ankrd10	ankyrin repeat domain 10	0	2	3	-1.6659
3385	279766	Rhbdd3	rhomboid domain containing 3	0	2	3	-1.66569
3386	18114	Nnp1	ribosomal RNA processing 1 homolog (S. cerevisiae)	0	2	3	-1.66528
3387	259125	Olfr644	olfactory receptor 644	0	2	2	-1.66474
3388	338374	Il28	interleukin 28B	0	2	3	-1.66441
3389	433292	Nms	neuromedin S	0	2	3	-1.66425
3390	50701	Ela2	elastase, neutrophil expressed	0	2	3	-1.66424
3391	12321	Calu	calumenin	0	2	3	-1.66411
3392	93722	Pcdhga10	protocadherin gamma subfamily A, 10	0	2	3	-1.66368
3393	26914	H2afy	H2A histone family, member Y	0	2	3	-1.6636
3394	30055	Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	0	2	2	-1.66355
3395	114566	Krt2-20	keratin 82	0	2	3	-1.66259
3396	17202	Mc4r	melanocortin 4 receptor	0	2	3	-1.66211
3397	20674	Sox2	SRY-box containing gene 2	0	2	3	-1.66154
3398	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain	0	2	3	-1.6615
3399	106393	Srl	sarcalumenin	0	2	3	-1.66139
3400	14163	Fgd1	FYVE, RhoGEF and PH domain containing 1	0	2	3	-1.65967

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3401	54519	Apbb1ip	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	0	2	3	-1.65919
3402	54326	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	0	2	3	-1.65913
3403	69008	Cab39l	calcium binding protein 39-like	0	2	3	-1.65912
3404	14421	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	0	2	3	-1.65899
3405	12477	Ctla4	cytotoxic T-lymphocyte-associated protein 4	0	2	3	-1.65898
3406	319188	Hist1h2bp	histone cluster 1, H2bp	0	2	3	-1.65848
3407	18453	P4hb	prolyl 4-hydroxylase, beta polypeptide	0	2	3	-1.65845
3408	69639	Exosc8	exosome component 8	0	2	3	-1.658
3409	65116	Prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	0	2	3	-1.65584
3410	66307	Isoc1	isochorismatase domain containing 1	0	2	3	-1.65567
3411	78242	9230117E20Rik	serine peptidase inhibitor, Kazal type 11	0	2	3	-1.65558
3412	22019	Tpp2	tripeptidyl peptidase II	0	2	3	-1.65551
3413	12539	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	0	2	3	-1.6553
3414	14252	Flot2	flotillin 2	0	2	3	-1.65419
3415	12728	Clcn5	chloride channel 5	0	2	3	-1.654
3416	406219	Krt2-25	keratin 83	0	2	3	-1.65395
3417	56792	AI586015	signal transducing adaptor family member 1	0	2	3	-1.65394
3418	19038	Ppic	peptidylprolyl isomerase C	0	2	3	-1.65332
3419	23857	Dmtf1	cyclin D binding myb-like transcription factor 1	0	2	3	-1.65329
3420	22171	Tyms	thymidylate synthase	0	2	3	-1.65327
3421	19769	Rit1	Ras-like without CAAX 1	0	2	3	-1.65312
3422	381993	UNK	NA	0	2	3	-1.65285
3423	15483	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	0	2	3	-1.65282
3424	22367	Vrk1	vaccinia related kinase 1	0	2	3	-1.6526
3425	71601	Ceacam20	carcinoembryonic antigen-related cell adhesion molecule 20	0	2	2	-1.65227
3426	18145	Npc1	Niemann Pick type C1	0	2	3	-1.65153
3427	83409	Mapbpip	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	0	2	2	-1.65148
3428	12982	Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0	2	3	-1.65132
3429	70584	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	0	2	3	-1.65065
3430	14183	Fgfr2	fibroblast growth factor receptor 2	0	2	3	-1.65056
3431	436255	UNK	NA	0	2	3	-1.64994
3432	14167	Fgf12	fibroblast growth factor 12	0	2	3	-1.64982
3433	21673	Dntt	deoxynucleotidyltransferase, terminal	0	2	3	-1.64981
3434	71481	Alpk1	alpha-kinase 1	0	2	3	-1.64883
3435	67963	Npc2	Niemann Pick type C2	0	2	3	-1.64866
3436	20402	Zfp106	zinc finger protein 106	0	2	3	-1.64831
3437	67619	Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	0	2	3	-1.64804

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3438	235312	C1qtnf5	C1q and tumor necrosis factor related protein 5	0	2	3	-1.64769
3439	107684	Coro2a	coronin, actin binding protein 2A	0	2	3	-1.64742
3440	64818	Krt2-19	keratin 81	0	2	3	-1.64736
3441	399591	4930488E11Rik	thymosin beta 15b like	0	2	2	-1.64734
3442	78797	Ndor1	NADPH dependent diflavin oxidoreductase 1	0	2	2	-1.64732
3443	19124	Procr	protein C receptor, endothelial	0	2	3	-1.64722
3444	74600	Mrpl47	mitochondrial ribosomal protein L47	0	2	3	-1.64708
3445	13723	Emb	embigin	0	2	3	-1.64689
3446	19729	Rag1ap1	solute carrier family 50 (sugar transporter), member 1	0	2	3	-1.6468
3447	67489	Ap4b1	adaptor-related protein complex AP-4, beta 1	0	2	3	-1.64616
3448	67579	Cpeb4	cytoplasmic polyadenylation element binding protein 4	0	2	3	-1.64613
3449	218271	B4galt7	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	0	2	3	-1.64597
3450	213053	Slc39a14	solute carrier family 39 (zinc transporter), member 14	0	2	3	-1.6455
3451	76183	Brunol6	CUGBP, Elav-like family member 6	0	2	3	-1.64534
3452	70385	Ccdc99	coiled-coil domain containing 99	0	2	3	-1.64525
3453	20843	Stag2	stromal antigen 2	0	2	3	-1.6452
3454	18575	Pde1c	phosphodiesterase 1C	0	2	3	-1.64517
3455	242773	Slc45a1	solute carrier family 45, member 1	0	2	3	-1.64507
3456	382038	AK122209	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	0	2	3	-1.64464
3457	106039	Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	0	2	3	-1.64456
3458	80752	BC004044	family with sequence similarity 20, member C	0	2	3	-1.64442
3459	434008	LOC434008	predicted gene 5567	0	2	2	-1.64348
3460	55946	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	0	2	3	-1.64298
3461	229949	Ak5	adenylate kinase 5	0	2	3	-1.64273
3462	14569	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	0	2	3	-1.64221
3463	26910	Figla	folliculogenesis specific basic helix-loop-helix	0	2	3	-1.64183
3464	236223	UNK	NA	0	2	3	-1.64158
3465	93747	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0	2	3	-1.64157
3466	98711	Rdh10	retinol dehydrogenase 10 (all-trans)	0	2	3	-1.64148
3467	227059	Slc39a10	solute carrier family 39 (zinc transporter), member 10	0	2	3	-1.64147
3468	97848	Serpinb6c	serine (or cysteine) peptidase inhibitor, clade B, member 6c	0	2	3	-1.64102
3469	66226	Trappc2	trafficking protein particle complex 2	0	2	3	-1.64086
3470	19294	Pvrl2	poliovirus receptor-related 2	0	2	3	-1.6406
3471	320508	Cachd1	cache domain containing 1	0	2	2	-1.64054
3472	13846	Ephb4	Eph receptor B4	0	2	3	-1.63974
3473	107586	Ovol2	ovo-like 2 (Drosophila)	0	2	3	-1.63945
3474	216453	Rdhs	retinol dehydrogenase 19	0	2	3	-1.63929

Candidates for positive regulators of normal growth (Fisher's)

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3475	54140	Avpr1a	arginine vasopressin receptor 1A	0	2	3	-1.63858
3476	66147	Necap2	NECAP endocytosis associated 2	0	2	3	-1.63857
3477	229958	UNK	NA	0	2	3	-1.63849
3478	14726	Pdpn	podoplanin	0	2	2	-1.63813
3479	435262	UNK	NA	0	2	3	-1.63786
3480	27217	Mixl1	Mix1 homeobox-like 1 (Xenopus laevis)	0	2	3	-1.63744
3481	54631	Nphs1	nephrosis 1 homolog, nephrin (human)	0	2	3	-1.63665
3482	67707	Mrpl24	mitochondrial ribosomal protein L24	0	2	3	-1.63658
3483	59047	Pnkp	polynucleotide kinase 3'- phosphatase	0	2	3	-1.63613
3484	14205	Figf	c-fos induced growth factor	0	2	3	-1.63583
3485	22637	Zap70	zeta-chain (TCR) associated protein kinase	0	2	3	-1.63565
3486	225471	Ticam2	toll-like receptor adaptor molecule 2	0	2	3	-1.63477
3487	20729	Spin	spindlin 1	0	2	3	-1.6345
3488	78369	Icam4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	0	2	3	-1.63424
3489	331623	AK122525	BEN domain containing 3	0	2	3	-1.63418
3490	13367	Diap1	diaphanous homolog 1 (Drosophila)	0	2	3	-1.63343
3491	57751	Rnf25	ring finger protein 25	0	2	2	-1.63239
3492	14842	Gsh1	GS homeobox 1	0	2	2	-1.63202
3493	19349	Rab7	RAB7, member RAS oncogene family	0	2	3	-1.63168
3494	18100	Mrpl40	mitochondrial ribosomal protein L40	0	2	2	-1.63078
3495	74890	4930438O03Rik	MORN repeat containing 3	0	2	3	-1.6306
3496	74450	Pank2	pantothenate kinase 2	0	2	3	-1.63009
3497	70439	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	3	-1.62996
3498	226977	Actr1b	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	0	2	3	-1.62951
3499	78906	9130017N09Rik	RIKEN cDNA 9130017N09 gene	0	2	3	-1.62939
3500	20508	Slc18a3	solute carrier family 18 (vesicular monoamine), member 3	0	2	3	-1.62932
3501	72185	Dbndd1	dysbindin (dystrobrevin binding protein 1) domain containing 1	0	2	3	-1.62922
3502	11843	Arf4	ADP-ribosylation factor 4	0	2	3	-1.62877
3503	67717	Lipf	lipase, gastric	0	2	2	-1.62837
3504	382039	UNK	NA	0	2	3	-1.62806
3505	258663	Olfr739	olfactory receptor 739	0	2	2	-1.62795
3506	225341	Lims2	LIM and senescent cell antigen like domains 2	0	2	3	-1.62781
3507	74356	4931428F04Rik	RIKEN cDNA 4931428F04 gene	0	2	2	-1.62774
3508	21809	Tgfb3	transforming growth factor, beta 3	0	2	3	-1.62761
3509	103694	Tmed4	transmembrane emp24 protein transport domain containing 4	0	2	3	-1.62759
3510	320707	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	0	2	3	-1.62725
3511	26359	Anxa10	annexin A10	0	2	3	-1.62721

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3512	57271	Olfr1509	olfactory receptor 1509	0	2	3	-1.62694
3513	214899	Jarid1a	lysine (K)-specific demethylase 5A	0	2	3	-1.62674
3514	319163	Hist1h2aa	histone cluster 1, H2aa	0	2	3	-1.62617
3515	217057	Ptrh2	peptidyl-tRNA hydrolase 2	0	2	3	-1.62612
3516	225865	Catsper1	cation channel, sperm associated 1	0	2	3	-1.62591
3517	541610	Trcg1	taste receptor cell gene 1	0	2	2	-1.62587
3518	21453	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	0	2	3	-1.62576
3519	17127	Smad3	MAD homolog 3 (Drosophila)	0	2	3	-1.62439
3520	16597	Klf12	Kruppel-like factor 12	0	2	3	-1.62429
3521	14172	Fgf18	fibroblast growth factor 18	0	2	3	-1.6241
3522	67738	Ppid	peptidylprolyl isomerase D (cyclophilin D)	0	2	3	-1.62385
3523	69834	1810048P08Rik	RAB43, member RAS oncogene family	0	2	3	-1.62355
3524	12310	Calca	calcitonin/calcitonin-related polypeptide, alpha	0	2	2	-1.6231
3525	319180	Hist1h2bf	histone cluster 1, H2bf	0	2	3	-1.62252
3526	12972	Cryz	crystallin, zeta	0	2	3	-1.62178
3527	13445	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	0	2	3	-1.62164
3528	213068	Tmem71	transmembrane protein 71	0	2	2	-1.62154
3529	67859	2310002J15Rik	RIKEN cDNA 2310002J15 gene	0	2	2	-1.62139
3530	69232	2610028H07Rik	glutamine-rich 1	0	2	3	-1.62091
3531	434767	UNK	NA	0	2	3	-1.62048
3532	17993	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	0	2	3	-1.61953
3533	104349	Zfp119	zinc finger protein 119a	0	2	3	-1.61869
3534	50501	Prok2	prokineticin 2	0	2	3	-1.61838
3535	208258	Ankrd33	ankyrin repeat domain 33	0	2	3	-1.61818
3536	278672	1110051B16Rik	double homeobox B-like	0	2	3	-1.61752
3537	69217	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	0	2	3	-1.61732
3538	17385	Mmp11	matrix metallopeptidase 11	0	2	2	-1.61729
3539	94226	Edg8	sphingosine-1-phosphate receptor 5	0	2	1	-1.61679
3540	12785	Cnbp	cellular nucleic acid binding protein	0	2	3	-1.61555
3541	66603	Sip1	survival of motor neuron protein interacting protein 1	0	2	3	-1.61538
3542	435997	UNK	NA	0	2	3	-1.61499
3543	77318	C030011J08Rik	ankyrin repeat domain 55	0	2	3	-1.61489
3544	215512	5730593F17Rik	family with sequence similarity 117, member A	0	2	3	-1.61479
3545	94279	Sfxn2	sideroflexin 2	0	2	3	-1.61395
3546	28253	Slco1b2	solute carrier organic anion transporter family, member 1b2	0	2	3	-1.61382
3547	66866	Nhlrc2	NHL repeat containing 2	0	2	2	-1.6135
3548	258583	Olfr1085	olfactory receptor 1085	0	2	3	-1.61337

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3549	68342	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	0	2	3	-1.61321
3550	21647	Tcte3	t-complex-associated testis expressed 3	0	2	3	-1.61289
3551	12721	Coro1a	coronin, actin binding protein 1A	0	2	3	-1.61204
3552	17540	Mrvi1	MRV integration site 1	0	2	3	-1.61196
3553	100710	Aprin	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	0	2	2	-1.61176
3554	105670	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	0	2	3	-1.61157
3555	12314	Calm2	calmodulin 2	0	2	2	-1.61146
3556	16800	Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	0	2	3	-1.61131
3557	66154	Tmem14c	transmembrane protein 14C	0	2	3	-1.61114
3558	140559	Igsf8	immunoglobulin superfamily, member 8	0	2	3	-1.61106
3559	225845	Hrasls3	phospholipase A2, group XVI	0	2	3	-1.61081
3560	14395	Gabra2	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2	0	2	3	-1.61054
3561	16485	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	0	2	3	-1.61018
3562	258426	Olfr995	olfactory receptor 995	0	2	3	-1.60998
3563	20248	Serpinb3a	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A	0	2	3	-1.60993
3564	17179	Matk	megakaryocyte-associated tyrosine kinase	0	2	3	-1.60984
3565	12643	Chad	chondroadherin	0	2	3	-1.6091
3566	16768	Lag3	lymphocyte-activation gene 3	0	2	3	-1.60881
3567	234736	Rfwd3	ring finger and WD repeat domain 3	0	2	3	-1.60848
3568	14685	Gnat1	guanine nucleotide binding protein, alpha transducing 1	0	2	3	-1.60838
3569	268591	Serpina5	serine (or cysteine) peptidase inhibitor, clade A, member 5	0	2	3	-1.60818
3570	70357	Kcnip1	Kv channel-interacting protein 1	0	2	3	-1.60814
3571	381724	BC061212	cDNA sequence BC061212	0	2	2	-1.60782
3572	72018	Fundc1	FUN14 domain containing 1	0	2	3	-1.60747
3573	66282	1810029B16Rik	RIKEN cDNA 1810029B16 gene	0	2	2	-1.60727
3574	75406	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0	2	3	-1.60717
3575	237859	Ccdc55	coiled-coil domain containing 55	0	2	3	-1.60705
3576	27395	Mrpl15	mitochondrial ribosomal protein L15	0	2	3	-1.60691
3577	16407	Itgae	integrin alpha E, epithelial-associated	0	2	3	-1.60661
3578	436441	UNK	NA	0	2	3	-1.60654
3579	58222	Rab37	RAB37, member of RAS oncogene family	0	2	3	-1.60648
3580	76376	Slc24a2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	0	2	3	-1.6061
3581	224022	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	0	2	3	-1.60603
3582	74596	Cds1	CDP-diacylglycerol synthase 1	0	2	3	-1.60558
3583	20618	Sncg	synuclein, gamma	0	2	2	-1.60453
3584	11796	Birc3	baculoviral IAP repeat-containing 3	0	2	3	-1.60266
3585	13191	Dctn1	dynactin 1	0	2	3	-1.60263

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3586	338346	Gpr21	G protein-coupled receptor 21	0	2	3	-1.60263
3587	12921	Crhr1	corticotropin releasing hormone receptor 1	0	2	3	-1.60226
3588	18676	Phf2	PHD finger protein 2	0	2	3	-1.60155
3589	18390	Oprm1	opioid receptor, mu 1	0	2	3	-1.60149
3590	14460	Gata1	GATA binding protein 1	0	2	3	-1.60148
3591	18143	Npas2	neuronal PAS domain protein 2	0	2	3	-1.60066
3592	73739	Pgea1	chibby homolog 1 (Drosophila)	0	2	3	-1.60016
3593	16421	Itgb7	integrin beta 7	0	2	3	-1.59978
3594	208884	Zdhhc9	zinc finger, DHHC domain containing 9	0	2	3	-1.59941
3595	19182	Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	0	2	3	-1.59936
3596	216190	Dip3b	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0	2	3	-1.59932
3597	81018	Zfp313	ring finger protein 114	0	2	3	-1.59876
3598	17313	Mgp	matrix Gla protein	0	2	3	-1.59865
3599	21754	Tesk1	testis specific protein kinase 1	0	2	3	-1.59771
3600	67070	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	0	2	3	-1.59754
3601	56485	Slc2a5	solute carrier family 2 (facilitated glucose transporter), member 5	0	2	2	-1.59734
3602	107868	Usp9y	ubiquitin specific peptidase 9, Y chromosome	0	2	3	-1.59678
3603	435231	UNK	NA	0	2	2	-1.59673
3604	212483	BC021381	family with sequence similarity 193, member B	0	2	2	-1.59635
3605	432436	LOC432436	predicted gene 5420	0	2	3	-1.59577
3606	224624	Rab40c	Rab40c, member RAS oncogene family	0	2	3	-1.59564
3607	16553	Kif13a	kinesin family member 13A	0	2	3	-1.59553
3608	329986	BC080695	cDNA sequence BC080695	0	2	3	-1.59536
3609	14800	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	0	2	3	-1.59506
3610	69299	Asb9	ankyrin repeat and SOCS box-containing 9	0	2	2	-1.59491
3611	17257	Mecp2	methyl CpG binding protein 2	0	2	3	-1.59468
3612	12401	Serpina6	serine (or cysteine) peptidase inhibitor, clade A, member 6	0	2	3	-1.59463
3613	70113	2010001J22Rik	outer dense fiber of sperm tails 3B	0	2	2	-1.59357
3614	58170	Accn5	amiloride-sensitive cation channel 5, intestinal	0	2	3	-1.59325
3615	66308	2810021B07Rik	RIKEN cDNA 2810021B07 gene	0	2	3	-1.59324
3616	13796	Emx1	empty spiracles homolog 1 (Drosophila)	0	2	2	-1.59307
3617	71820	Wdr34	WD repeat domain 34	0	2	3	-1.59297
3618	12259	C1qa	complement component 1, q subcomponent, alpha polypeptide	0	2	3	-1.59293
3619	69444	Lyzl6	lysozyme-like 6	0	2	2	-1.5929
3620	66873	1200009O22Rik	TLR4 interactor with leucine-rich repeats	0	2	3	-1.59288
3621	258717	Olfr429	olfactory receptor 429	0	2	2	-1.59286
3622	66240	Kcne1l	potassium voltage-gated channel, Isk-related family, member 1-like, pseudogene	0	2	3	-1.59224

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3623	435655	UNK	NA	0	2	3	-1.59119
3624	14368	Fzd6	frizzled homolog 6 (Drosophila)	0	2	3	-1.59093
3625	57272	Olfr140	olfactory receptor 140	0	2	3	-1.59087
3626	244701	Mtnr1b	melatonin receptor 1B	0	2	3	-1.59087
3627	12307	Calb1	calbindin 1	0	2	3	-1.59007
3628	69048	Slc30a5	solute carrier family 30 (zinc transporter), member 5	0	2	3	-1.5894
3629	436002	Olfr627	olfactory receptor 243	0	2	3	-1.58936
3630	29862	Ninj2	ninjurin 2	0	2	2	-1.58891
3631	71690	Esm1	endothelial cell-specific molecule 1	0	2	2	-1.58874
3632	18095	Nkx3-1	NK-3 transcription factor, locus 1 (Drosophila)	0	2	3	-1.5886
3633	19139	Prps1	phosphoribosyl pyrophosphate synthetase 1	0	2	3	-1.58852
3634	14373	G0s2	G0/G1 switch gene 2	0	2	3	-1.58785
3635	230809	Pdik1l	PDLIM1 interacting kinase 1 like	0	2	3	-1.58704
3636	68338	Golt1a	golgi transport 1 homolog A (S. cerevisiae)	0	2	2	-1.58626
3637	56209	Mir16	glycerophosphodiester phosphodiesterase 1	0	2	3	-1.58613
3638	66402	Sln	sarcolipin	0	2	3	-1.586
3639	69773	1810026J23Rik	RIKEN cDNA 1810026J23 gene	0	2	3	-1.5842
3640	73242	2610110G12Rik	alpha tubulin acetyltransferase 1	0	2	2	-1.58395
3641	171210	Acot2	acyl-CoA thioesterase 2	0	2	3	-1.58385
3642	109113	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	0	2	3	-1.58384
3643	436015	LOC436015	RIKEN cDNA B130016D09 cDNA	0	2	3	-1.58362
3644	11732	Ank	progressive ankylosis	0	2	3	-1.5834
3645	17083	Tmed1	transmembrane emp24 domain containing 1	0	2	3	-1.58336
3646	27360	Add3	adducin 3 (gamma)	0	2	3	-1.5833
3647	17217	Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	0	2	3	-1.58323
3648	381337	BC050210	family with sequence similarity 178, member B	0	2	2	-1.58273
3649	399510	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	0	2	3	-1.58258
3650	319317	A930034L06Rik	small nucleolar RNA host gene 11	0	2	3	-1.58253
3651	74670	4930432O21Rik	zinc finger prtoein 943	0	2	3	-1.58192
3652	21951	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	0	2	2	-1.58186
3653	56722	Litaf	LPS-induced TN factor	0	2	3	-1.58145
3654	64103	Tnmd	tenomodulin	0	2	3	-1.5811
3655	68566	Drd1ip	calcyon neuron-specific vesicular protein	0	2	3	-1.5806
3656	238831	Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	0	2	2	-1.58036
3657	140475	Bsnd	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	0	2	2	-1.57963
3658	73680	2410081M15Rik	zinc finger and BTB domain containing 8a	0	2	3	-1.57937
3659	18214	Ddr2	discoidin domain receptor family, member 2	0	2	3	-1.57937

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3660	20317	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	0	2	3	-1.57918
3661	258493	Olfr319	olfactory receptor 319	0	2	3	-1.57917
3662	57321	Terf2ip	telomeric repeat binding factor 2, interacting protein	0	2	3	-1.57914
3663	69080	Gmppa	GDP-mannose pyrophosphorylase A	0	2	3	-1.57899
3664	102220	E330037G11Rik	RIKEN cDNA E330037G11 gene	0	2	3	-1.57889
3665	106581	Itfg3	integrin alpha FG-GAP repeat containing 3	0	2	2	-1.57864
3666	68947	Chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	0	2	3	-1.5779
3667	232157	Mobk1b	MOB kinase activator 1A	0	2	3	-1.57786
3668	435820	UNK	NA	0	2	2	-1.57731
3669	258913	Olfr1377	olfactory receptor 1377	0	2	2	-1.57727
3670	239528	Eif2c2	eukaryotic translation initiation factor 2C, 2	0	2	3	-1.57701
3671	67052	Kntc2	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0	2	3	-1.57675
3672	258472	Olfr899	olfactory receptor 899	0	2	3	-1.57658
3673	69309	Slc16a13	solute carrier family 16 (monocarboxylic acid transporters), member 13	0	2	3	-1.5759
3674	12990	Csna	casein alpha s1	0	2	3	-1.57578
3675	243362	Stard13	StAR-related lipid transfer (START) domain containing 13	0	2	3	-1.57565
3676	67103	Ltb4dh	prostaglandin reductase 1	0	2	3	-1.57547
3677	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0	2	3	-1.57541
3678	14867	Gstm6	glutathione S-transferase, mu 6	0	2	3	-1.57536
3679	102032	AI316807	expressed sequence AI316807	0	2	2	-1.57531
3680	72324	Plxdc1	plexin domain containing 1	0	2	3	-1.57501
3681	326619	Hist1h4a	histone cluster 1, H4a	0	2	3	-1.57489
3682	224093	BC022623	family with sequence similarity 43, member A	0	2	3	-1.57448
3683	104886	Rab15	RAB15, member RAS oncogene family	0	2	3	-1.57394
3684	237759	Col23a1	collagen, type XXIII, alpha 1	0	2	3	-1.57375
3685	69123	1810022C23Rik	enoyl-Coenzyme A delta isomerase 3	0	2	3	-1.57285
3686	171262	V1rl1	vomeronasal 1 receptor 70	0	2	2	-1.57272
3687	67864	Yipf4	Yip1 domain family, member 4	0	2	3	-1.57263
3688	268465	Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0	2	2	-1.57164
3689	16815	Lbx2	ladybird homeobox homolog 2 (Drosophila)	0	2	3	-1.57154
3690	18389	Oprl1	opioid receptor-like 1	0	2	3	-1.57139
3691	74325	Cltb	clathrin, light polypeptide (Lcb)	0	2	2	-1.57118
3692	14109	Fau	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	0	2	3	-1.57095
3693	50500	Ttpa	tocopherol (alpha) transfer protein	0	2	3	-1.57085
3694	76652	Arpm1	actin related protein M1	0	2	3	-1.57049
3695	319955	Ercc6	excision repair cross-complementing rodent repair deficiency, complementation group 6	0	2	2	-1.57037
3696	319301	A730027B03Rik	NA	0	2	3	-1.57021

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3697	320898	A430107P09Rik	T cell receptor alpha variable 3-3	0	2	3	-1.56971
3698	218490	Btf3	basic transcription factor 3	0	2	3	-1.56942
3699	20505	Slc34a1	solute carrier family 34 (sodium phosphate), member 1	0	2	3	-1.56891
3700	104002	Ctsq	cathepsin Q	0	2	3	-1.56862
3701	66958	Txndc14	thioredoxin-related transmembrane protein 2	0	2	3	-1.56852
3702	436019	UNK	NA	0	2	3	-1.5685
3703	72061	2010111I01Rik	RIKEN cDNA 2010111I01 gene	0	2	3	-1.56812
3704	386546	UNK	NA	0	2	3	-1.5681
3705	58200	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	0	2	3	-1.56792
3706	14526	Gcg	glucagon	0	2	3	-1.56776
3707	76938	Rbm17	RNA binding motif protein 17	0	2	3	-1.56765
3708	234290	BC030500	cDNA sequence BC030500	0	2	3	-1.5674
3709	107351	Ankrd15	KN motif and ankyrin repeat domains 1	0	2	3	-1.56725
3710	333667	UNK	NA	0	2	3	-1.56698
3711	22113	Phlda2	pleckstrin homology-like domain, family A, member 2	0	2	3	-1.56652
3712	17885	Myh8	myosin, heavy polypeptide 8, skeletal muscle, perinatal	0	2	3	-1.56624
3713	22379	Fmnl3	formin-like 3	0	2	2	-1.56607
3714	56742	Psrc1	proline/serine-rich coiled-coil 1	0	2	3	-1.56581
3715	68097	Dynll2	dynein light chain LC8-type 2	0	2	2	-1.56544
3716	109889	Mzf1	myeloid zinc finger 1	0	2	3	-1.56531
3717	21814	Tgfbr3	transforming growth factor, beta receptor III	0	2	3	-1.56371
3718	14260	Fmn1	formin 1	0	2	3	-1.56363
3719	215031	Vgll2	vestigial like 2 homolog (Drosophila)	0	2	3	-1.56354
3720	258649	Olfr441	olfactory receptor 441	0	2	2	-1.56313
3721	97287	1110061O04Rik	myotubularin related protein 14	0	2	3	-1.56295
3722	12034	Phb2	prohibitin 2	0	2	3	-1.56215
3723	232333	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	0	2	3	-1.56162
3724	76568	1500035H01Rik	intraflagellar transport 46 homolog (Chlamydomonas)	0	2	3	-1.5616
3725	66326	Dnajc5b	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	0	2	3	-1.56153
3726	22324	Vav1	vav 1 oncogene	0	2	3	-1.56141
3727	30795	Fkbp3	FK506 binding protein 3	0	2	3	-1.56137
3728	93836	Rnf111	ring finger 111	0	2	3	-1.56114
3729	19158	Pscd2	cytohesin 2	0	2	3	-1.56109
3730	75292	Prkcn	protein kinase D3	0	2	3	-1.56095
3731	80978	Mrgprh	MAS-related GPR, member H	0	2	3	-1.56095
3732	20762	Sprr2h	small proline-rich protein 2H	0	2	2	-1.56072
3733	12967	Crygd	crystallin, gamma D	0	2	3	-1.56066

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3734	234814	Mthfsd	methenyltetrahydrofolate synthetase domain containing	0	2	2	-1.56065
3735	53598	Dctn3	dynactin 3	0	2	3	-1.56028
3736	113848	V1ra6	vomeronasal 1 receptor 42	0	2	3	-1.55988
3737	17354	Mllt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	0	2	3	-1.55985
3738	12739	Cldn3	claudin 3	0	2	3	-1.55984
3739	73724	Mcee	methylmalonyl CoA epimerase	0	2	2	-1.55976
3740	18559	Pctp	phosphatidylcholine transfer protein	0	2	3	-1.55924
3741	109346	Ankrd39	ankyrin repeat domain 39	0	2	3	-1.55868
3742	16886	Limk2	LIM motif-containing protein kinase 2	0	2	3	-1.55858
3743	16326	Inhbe	inhibin beta E	0	2	3	-1.55838
3744	21410	Tcf2	HNF1 homeobox B	0	2	3	-1.55774
3745	208188	Ghsr	growth hormone secretagogue receptor	0	2	3	-1.55767
3746	258731	Olfr491	olfactory receptor 491	0	2	2	-1.55766
3747	70853	4921511C04Rik	von Willebrand factor A domain containing 3B	0	2	2	-1.55759
3748	238021	Fscn2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	0	2	3	-1.55728
3749	117592	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	0	2	3	-1.55728
3750	83796	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	0	2	3	-1.55705
3751	73062	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	0	2	3	-1.55702
3752	228061	Agps	alkylglycerone phosphate synthase	0	2	3	-1.55698
3753	216874	Camta2	calmodulin binding transcription activator 2	0	2	2	-1.55656
3754	258561	Olfr1012	olfactory receptor 1012	0	2	2	-1.55641
3755	258330	Olfr1274	olfactory receptor 1274, pseudogene	0	2	3	-1.55633
3756	14426	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	0	2	3	-1.55628
3757	435974	UNK	NA	0	2	3	-1.55612
3758	68828	Sync	syncoilin	0	2	3	-1.55572
3759	320736	E130203B14Rik	RIKEN cDNA E130203B14 gene	0	2	2	-1.55508
3760	100986	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	0	2	3	-1.55508
3761	442816	F830005K03Rik	RIKEN cDNA F830005K03 gene	0	2	3	-1.55495
3762	268396	G431001E03Rik	SH3 and PX domains 2B	0	2	3	-1.55471
3763	66073	Txndc12	thioredoxin domain containing 12 (endoplasmic reticulum)	0	2	3	-1.55414
3764	19267	Ptpre	protein tyrosine phosphatase, receptor type, E	0	2	3	-1.55411
3765	449000	BC018101	zinc finger protein 960	0	2	3	-1.55403
3766	54124	Cks1b	CDC28 protein kinase 1b	0	2	3	-1.55402
3767	72826	2810485I05Rik	family with sequence similarity 76, member B	0	2	3	-1.55392
3768	18419	Otog	otogelin	0	2	3	-1.55382
3769	15434	Hoxd3	homeobox D3	0	2	3	-1.55359
3770	17762	Mapt	microtubule-associated protein tau	0	2	3	-1.55331

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3771	104099	Itga9	integrin alpha 9	0	2	3	-1.5533
3772	22355	Vipr2	vasoactive intestinal peptide receptor 2	0	2	3	-1.55323
3773	107526	Gimap4	GTPase, IMAP family member 4	0	2	3	-1.55321
3774	67073	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	0	2	3	-1.55318
3775	58239	Dexi	dexamethasone-induced transcript	0	2	3	-1.55296
3776	20524	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	0	2	2	-1.55255
3777	58996	Arhgap23	Rho GTPase activating protein 23	0	2	3	-1.5525
3778	268780	AU040377	EGF-like, fibronectin type III and laminin G domains	0	2	3	-1.55235
3779	239157	Pnma2	paraneoplastic antigen MA2	0	2	3	-1.55221
3780	193286	BC049762	cDNA sequence BC049762	0	2	3	-1.55159
3781	57442	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	0	2	3	-1.55148
3782	19773	Rln1	relaxin 1	0	2	2	-1.55098
3783	60363	Cldn15	claudin 15	0	2	3	-1.54998
3784	171275	V1rh18	vomeronasal 1 receptor 212	0	2	2	-1.54978
3785	74080	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	0	2	3	-1.54906
3786	239835	UNK	NA	0	2	3	-1.54883
3787	20671	Sox17	SRY-box containing gene 17	0	2	3	-1.54842
3788	14870	Gstp1	glutathione S-transferase, pi 1	0	2	3	-1.54744
3789	66234	Sc4mol	sterol-C4-methyl oxidase-like	0	2	3	-1.54663
3790	243197	Mfsd7	major facilitator superfamily domain containing 7A	0	2	3	-1.54638
3791	11540	Adora2a	adenosine A2a receptor	0	2	3	-1.54603
3792	11767	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	0	2	3	-1.54596
3793	12818	Col14a1	collagen, type XIV, alpha 1	0	2	3	-1.5455
3794	12182	Bst1	bone marrow stromal cell antigen 1	0	2	3	-1.54516
3795	71761	Amdhd1	amidohydrolase domain containing 1	0	2	3	-1.54508
3796	399599	Ccdc87	coiled-coil domain containing 87	0	2	2	-1.54503
3797	74513	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	0	2	3	-1.54478
3798	240067	BC057593	zinc finger protein 952	0	2	3	-1.54463
3799	11567	Avil	advillin	0	2	2	-1.54446
3800	13169	Dbnl	drebrin-like	0	2	3	-1.54412
3801	14237	Foxd4	forkhead box D4	0	2	3	-1.5441
3802	17878	Myf6	myogenic factor 6	0	2	3	-1.54406
3803	13497	Drp2	dystrophin related protein 2	0	2	2	-1.54386
3804	216166	6330514A18Rik	polo-like kinase 5 (Drosophila)	0	2	3	-1.54368
3805	12151	Bmi1	Bmi1 polycomb ring finger oncogene	0	2	3	-1.5432
3806	18846	Plxna3	plexin A3	0	2	3	-1.54301
3807	56492	Cldn18	claudin 18	0	2	3	-1.54285

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3808	70420	2610034B18Rik	RIKEN cDNA 2610034B18 gene	0	2	3	-1.5428
3809	66890	Lman2	lectin, mannose-binding 2	0	2	3	-1.54271
3810	15975	Ifnar1	interferon (alpha and beta) receptor 1	0	2	3	-1.54268
3811	74376	Myo18b	myosin XVIIIb	0	2	3	-1.54223
3812	233900	Rnf40	ring finger protein 40	0	2	3	-1.54216
3813	229534	Pbxip1	pre B cell leukemia transcription factor interacting protein 1	0	2	3	-1.54209
3814	381149	Nrg2	NA	0	2	3	-1.54163
3815	268980	Strn	striatin, calmodulin binding protein	0	2	2	-1.54144
3816	258443	Olfr164	olfactory receptor 164	0	2	3	-1.54131
3817	85030	Tnfrsf25	tumor necrosis factor receptor superfamily, member 25	0	2	3	-1.54104
3818	76413	1700016D06Rik	RIKEN cDNA 1700016D06 gene	0	2	3	-1.54069
3819	242466	Zfp462	zinc finger protein 462	0	2	3	-1.54057
3820	14661	Glud1	glutamate dehydrogenase 1	0	2	3	-1.5403
3821	14580	Gfap	glial fibrillary acidic protein	0	2	3	-1.54007
3822	80796	Calm4	calmodulin 4	0	2	3	-1.53921
3823	64337	Gng13	guanine nucleotide binding protein (G protein), gamma 13	0	2	3	-1.53898
3824	215814	Ccdc28a	coiled-coil domain containing 28A	0	2	2	-1.53883
3825	15184	Hdac5	histone deacetylase 5	0	2	3	-1.53865
3826	78798	Eml4	echinoderm microtubule associated protein like 4	0	2	3	-1.53856
3827	22289	Utx	lysine (K)-specific demethylase 6A	0	2	3	-1.53836
3828	242406	1110029E03Rik	RGP1 retrograde golgi transport homolog (S. cerevisiae)	0	2	2	-1.53757
3829	218241	Gm270	NA	0	2	3	-1.53739
3830	66151	Prr13	proline rich 13	0	2	3	-1.53717
3831	13209	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	0	2	3	-1.53688
3832	13346	Des	desmin	0	2	3	-1.53655
3833	19362	Rad51ap1	RAD51 associated protein 1	0	2	2	-1.53608
3834	72599	Pdia5	protein disulfide isomerase associated 5	0	2	3	-1.53544
3835	50762	Fbxo6b	F-box protein 6	0	2	3	-1.53527
3836	18133	Nov	nephroblastoma overexpressed gene	0	2	3	-1.53508
3837	14299	Freq	neuronal calcium sensor 1	0	2	3	-1.53472
3838	67125	Tspan31	tetraspanin 31	0	2	2	-1.53457
3839	16716	Ky	kyphoscoliosis peptidase	0	2	3	-1.53446
3840	385509	UNK	NA	0	2	3	-1.53446
3841	17194	Mbl1	mannose-binding lectin (protein A) 1	0	2	3	-1.5344
3842	381181	UNK	NA	0	2	3	-1.53422
3843	384957	LOC384957	predicted gene 5367	0	2	3	-1.53394
3844	268417	Zfp496	zinc finger with KRAB and SCAN domains 17	0	2	3	-1.53383

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3845	107656	Krt1-9	keratin 9	0	2	3	-1.53349
3846	67797	6530403A03Rik	small nuclear ribonucleoprotein 48 (U11/U12)	0	2	3	-1.5329
3847	16627	Klra1	killer cell lectin-like receptor, subfamily A, member 1	0	2	3	-1.53225
3848	233890	BC026432	zinc finger protein 768	0	2	3	-1.53221
3849	77220	C030003D03Rik	transmembrane protein 200A	0	2	3	-1.53132
3850	384244	LOC384244	predicted gene 5294	0	2	2	-1.53101
3851	80733	Car15	carbonic anhydrase 15	0	2	3	-1.53052
3852	67664	Rnf125	ring finger protein 125	0	2	3	-1.53043
3853	621071	UNK	NA	0	2	3	-1.53035
3854	21926	Tnf	tumor necrosis factor	0	2	2	-1.53026
3855	17201	Mc3r	melanocortin 3 receptor	0	2	3	-1.52963
3856	70097	Sash1	SAM and SH3 domain containing 1	0	2	3	-1.52952
3857	170779	Cd209d	CD209d antigen	0	2	3	-1.52942
3858	50781	Dkk3	dickkopf homolog 3 (Xenopus laevis)	0	2	3	-1.52935
3859	74682	Wdr35	WD repeat domain 35	0	2	3	-1.5292
3860	252866	Adam34	a disintegrin and metallopeptidase domain 34	0	2	3	-1.52914
3861	215445	Rab11fip3	RAB11 family interacting protein 3 (class II)	0	2	2	-1.52869
3862	12142	Prdm1	PR domain containing 1, with ZNF domain	0	2	3	-1.52869
3863	69585	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	0	2	3	-1.52824
3864	12572	Cdk7	cyclin-dependent kinase 7	0	2	3	-1.52761
3865	258773	Olfr818	olfactory receptor 818	0	2	2	-1.52713
3866	64707	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0	2	3	-1.52694
3867	73274	Gpbp1	GC-rich promoter binding protein 1	0	2	3	-1.52671
3868	75462	1700001C19Rik	RIKEN cDNA 1700001C19 gene	0	2	3	-1.52642
3869	381802	Tsen2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	0	2	2	-1.52628
3870	320590	9430071P14Rik	SV2 related protein homolog (rat)-like	0	2	3	-1.52608
3871	435707	UNK	NA	0	2	3	-1.52607
3872	213498	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	0	2	3	-1.52575
3873	67144	Lrrc40	leucine rich repeat containing 40	0	2	3	-1.52567
3874	16633	Klra2	killer cell lectin-like receptor, subfamily A, member 2	0	2	3	-1.52551
3875	232370	Clstn3	calsyntenin 3	0	2	3	-1.52434
3876	68938	Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	0	2	2	-1.52427
3877	67067	2010100O12Rik	reactive oxygen species modulator 1	0	2	3	-1.5242
3878	264134	Ttc26	tetratricopeptide repeat domain 26	0	2	2	-1.52388
3879	75646	Rai14	retinoic acid induced 14	0	2	3	-1.52333
3880	67854	Slco6b1	solute carrier organic anion transporter family, member 6b1	0	2	3	-1.52332
3881	353235	Pcdha8	protocadherin alpha 8	0	2	3	-1.52318

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3882	14317	Ftcd	formiminotransferase cyclodeaminase	0	2	3	-1.52299
3883	12445	Ccnd3	cyclin D3	0	2	6	-1.52184
3884	22157	Tulp1	tubby like protein 1	0	2	3	-1.52176
3885	14297	Fxn	frataxin	0	2	3	-1.52176
3886	435897	UNK	NA	0	2	3	-1.52159
3887	66161	Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	0	2	3	-1.5213
3888	240690	St18	suppression of tumorigenicity 18	0	2	3	-1.52105
3889	81906	Cyp4x1	cytochrome P450, family 4, subfamily x, polypeptide 1	0	2	3	-1.52027
3890	22147	Tuba7	tubulin, alpha 3B	0	2	3	-1.51981
3891	66125	Sf3b5	splicing factor 3b, subunit 5	0	2	3	-1.51907
3892	330305	A630038D02	predicted gene 5111	0	2	2	-1.51845
3893	68134	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	0	2	3	-1.51842
3894	75302	Asxl2	additional sex combs like 2 (Drosophila)	0	2	3	-1.5177
3895	75607	Wnk2	WNK lysine deficient protein kinase 2	0	2	3	-1.51746
3896	258466	Olfr1261	olfactory receptor 1261	0	2	3	-1.51695
3897	215378	B830045N13Rik	family with sequence similarity 5, member C	0	2	3	-1.51672
3898	233328	Lrrk1	leucine-rich repeat kinase 1	0	2	3	-1.5163
3899	18105	Nqo2	NAD(P)H dehydrogenase, quinone 2	0	2	3	-1.51552
3900	258292	Olfr446	olfactory receptor 446	0	2	3	-1.5149
3901	18624	Pepd	peptidase D	0	2	3	-1.51418
3902	217379	Ubxd4	UBX domain protein 2A	0	2	3	-1.51402
3903	20707	Serpinb9c	serine (or cysteine) peptidase inhibitor, clade B, member 9c	0	2	3	-1.51335
3904	433391	UNK	NA	0	2	3	-1.51313
3905	258807	Olfr910	olfactory receptor 910	0	2	2	-1.51253
3906	14632	Gli1	GLI-Kruppel family member GLI1	0	2	3	-1.51208
3907	20363	Sepp1	selenoprotein P, plasma, 1	0	2	3	-1.51094
3908	56190	Rnpc1	RNA binding motif protein 38	0	2	3	-1.51074
3909	20362	39332	septin 8	0	2	3	-1.51003
3910	435253	UNK	NA	0	2	3	-1.51002
3911	18514	Pbx1	pre B cell leukemia homeobox 1	0	2	3	-1.50983
3912	234542	Rtbdn	retbindin	0	2	3	-1.50979
3913	30945	Rnf19	ring finger protein 19A	0	2	3	-1.50919
3914	74205	Acsl3	acyl-CoA synthetase long-chain family member 3	0	2	3	-1.50913
3915	20849	Stat4	signal transducer and activator of transcription 4	0	2	3	-1.50855
3916	56484	Foxo3a	forkhead box O3	0	2	3	-1.50815
3917	329251	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	0	2	3	-1.50776
3918	329541	A630008I04	NA	0	2	2	-1.50769

Candidates for positive regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
3919	24111	Uts2	urotensin 2	0	2	3	-1.50727
3920	56214	Scamp4	secretory carrier membrane protein 4	0	2	3	-1.5069
3921	20472	Six2	sine oculis-related homeobox 2 homolog (Drosophila)	0	2	3	-1.50678
3922	56044	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	0	2	3	-1.50671
3923	15561	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	0	2	3	-1.5065
3924	228866	F730014I05Rik	PDX1 C-terminal inhibiting factor 1	0	2	3	-1.50625
3925	72269	Cda	cytidine deaminase	0	2	2	-1.50567
3926	319181	Hist1h2bg	histone cluster 1, H2bg	0	2	3	-1.50542
3927	69185	Dtwd1	DTW domain containing 1	0	2	3	-1.50539
3928	12981	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	0	2	3	-1.50499
3929	76483	2400010G15Rik	lipase maturation factor 1	0	2	2	-1.50425
3930	20928	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0	2	3	-1.50391
3931	245666	Iqsec2	IQ motif and Sec7 domain 2	0	2	3	-1.50387
3932	11535	Adm	adrenomedullin	0	2	3	-1.50371
3933	80744	BC003993	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	0	2	3	-1.50363
3934	12479	Cd1d1	CD1d1 antigen	0	2	3	-1.50345
3935	214105	Sox30	SRY-box containing gene 30	0	2	3	-1.50334
3936	73681	2410075D05Rik	tRNA methyltransferase 11 homolog (S. cerevisiae)	0	2	2	-1.50238
3937	77057	4921524J06Rik	stonin 1	0	2	3	-1.50211
3938	19359	Rad23b	RAD23b homolog (S. cerevisiae)	0	2	3	-1.50172
3939	16369	Irs3	insulin receptor substrate 3	0	2	3	-1.50168
3940	26951	Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	0	2	3	-1.50127
3941	19325	Rab10	RAB10, member RAS oncogene family	0	2	3	-1.5012
3942	100163	Pafah2	platelet-activating factor acetylhydrolase 2	0	2	3	-1.50119
3943	76872	4930432J16Rik	coiled-coil domain containing 116	0	2	2	-1.50101
3944	258709	Olfr415	olfactory receptor 248	0	2	2	-1.50055
3945	14729	Gp5	glycoprotein 5 (platelet)	0	2	3	-1.50039
3946	71775	1300017J02Rik	RIKEN cDNA 1300017J02 gene	0	2	3	-1.50023

Candidates for negative regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	12387	Ctnnb1	catenin (cadherin associated protein), beta 1	4	0	1	4.173271
2	108151	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	3	0	2	1.973799
3	224904	2410015M20Rik	RIKEN cDNA 2410015M20 gene	3	0	2	1.951938
4	74413	Mtac2d1	tandem C2 domains, nuclear	3	0	2	1.910865
5	387341	Tas2r106	taste receptor, type 2, member 106	4	0	1	1.881055
6	83559	Tex18	testis expressed gene 18	3	0	2	1.871645
7	57869	Adck2	aarF domain containing kinase 2	3	0	2	1.867268
8	14089	Fap	fibroblast activation protein	3	0	1	1.815643
9	214459	Fnbp1l	formin binding protein 1-like	3	0	1	1.808063
10	72507	Dzip1l	DAZ interacting protein 1-like	3	0	2	1.777676
11	234967	Slc36a4	solute carrier family 36 (proton/amino acid symporter), member 4	3	0	2	1.656406
12	21984	Tpbpa	trophoblast specific protein alpha	3	0	1	1.642226
13	209324	Stfna3l1	predicted gene 4758	3	0	2	1.618576
14	104836	Cbll1	Casitas B-lineage lymphoma-like 1	3	0	2	1.611628
15	69192	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	4	0	1	1.609671
16	59287	Ncstn	nicastrin	3	0	2	1.593427
17	71724	Aox3	aldehyde oxidase 3	3	0	2	1.570283
18	20620	Plk2	polo-like kinase 2 (Drosophila)	3	0	2	1.56609
19	12725	Clcn3	chloride channel 3	3	0	2	1.561527
20	75275	4930563P21Rik	transmembrane and coiled-coil domains 5B	3	0	2	1.552259
21	69727	Usp46	ubiquitin specific peptidase 46	3	0	2	1.543912
22	50916	Irx4	Iroquois related homeobox 4 (Drosophila)	3	0	2	1.538668
23	224014	Fgd4	FYVE, RhoGEF and PH domain containing 4	4	0	1	1.538243
24	216850	Jmjd3	KDM1 lysine (K)-specific demethylase 6B	3	0	2	1.537687
25	19059	Ppp3r2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)	3	0	2	1.524451
26	15467	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	3	0	2	1.479682
27	258882	Olfr874	olfactory receptor 874	3	0	1	1.475258
28	13114	Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	3	0	2	1.468151
29	117198	Ivns1abp	influenza virus NS1A binding protein	3	0	1	1.451487
30	224860	Plcl2	phospholipase C-like 2	3	0	2	1.441496
31	67008	1600012F09Rik	RIKEN cDNA 1600012F09 gene	3	0	2	1.427374
32	70556	5730438N18Rik	solute carrier family 25, member 33	3	0	2	1.420766
33	331046	Tgm4	transglutaminase 4 (prostate)	3	0	2	1.417887
34	12279	C9	complement component 9	3	0	2	1.417132
35	383133	UNK	NA	3	0	2	1.395556
36	381622	5031410I06Rik	RIKEN cDNA 5031410I06 gene	3	0	2	1.394361
37	280662	Afm	afamin	3	0	2	1.360315

Candidates for negative regulators of normal growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
38	16769	Dsg4	desmoglein 4	3	0	2	1.339893
39	63857	Bcmo1	beta-carotene 15,15'-monooxygenase	3	0	2	1.329378
40	211430	4930533C12Rik	fer-1-like 5 (C. elegans)	3	0	2	1.309693
41	18844	Plxna1	plexin A1	3	0	2	1.305834
42	387356	Tas2r131	taste receptor, type 2, member 131	3	0	2	1.269943
43	225348	Wdr36	WD repeat domain 36	3	0	1	1.250725
44	68519	Eml1	echinoderm microtubule associated protein like 1	3	0	1	1.245585
45	50490	Nox4	NADPH oxidase 4	3	0	2	1.24293
46	105513	Chmp7	charged multivesicular body protein 7	3	0	2	1.213845
47	53599	Cd164	CD164 antigen	3	0	2	1.161322
48	330502	Zfp82	zinc finger protein 82	3	0	1	1.158448
49	215474	Sec22c	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	3	0	2	1.143149
50	67269	Agtpbp1	ATP/GTP binding protein 1	3	0	2	1.142271
51	58251	Ddc8	cDNA sequence BC100451	3	0	2	1.123179
52	373864	Col27a1	collagen, type XXVII, alpha 1	4	0	1	1.090804

Supplementary Table 3. Putative regulators of oncogenic growth identified by DESeq test of biological replicates.

Note: Candidates identified by both DESeq and Fisher's exact test are highlighted in purple.

Candidates for positive regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	12387	Ctnnb1	catenin (cadherin associated protein), beta 1	0	5	0	-4.176623
2	68836	Mrpl52	mitochondrial ribosomal protein L52	0	3	0	-4.805133
3	268449	Rpl23a	ribosomal protein L23A	0	3	0	-3.449678
4	381979	Brsk1	BR serine/threonine kinase 1	0	3	0	-3.279939
5	110157	Raf1	v-raf-leukemia viral oncogene 1	0	3	0	-3.119321
6	13002	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	0	3	0	-2.978181
7	51813	Ccnc	cyclin C	0	3	0	-2.923364
8	77116	Mtmr2	myotubularin related protein 2	0	3	0	-2.680317
9	98386	Lbr	lamin B receptor	0	3	0	-2.294465
10	15461	Hras1	Harvey rat sarcoma virus oncogene 1	0	3	0	-1.861432
11	319186	Hist1h2bm	histone cluster 1, H2bm	0	2	0	-6.309125
12	18131	Notch3	Notch gene homolog 3 (Drosophila)	0	2	0	-5.310052
13	50708	Hist1h1c	histone cluster 1, H1c	0	2	0	-5.263624
14	319151	Hist1h3e	histone cluster 1, H3e	0	2	0	-4.892688
15	105148	Iars	isoleucine-tRNA synthetase	0	2	0	-4.501878
16	72113	Adck1	aarF domain containing kinase 1	0	2	0	-4.434846
17	192212	Prom2	prominin 2	0	2	0	-4.329995
18	76846	Rps9	ribosomal protein S9	0	2	0	-4.186061
19	26465	Zfp146	zinc finger protein 146	0	2	0	-4.140398
20	103710	Slc35e4	solute carrier family 35, member E4	0	2	0	-4.019999
21	74195	Elp3	elongation protein 3 homolog (S. cerevisiae)	0	2	0	-3.971798
22	20667	Sox12	SRY-box containing gene 12	0	2	0	-3.957874
23	213696	Duoxa1	dual oxidase maturation factor 1	0	2	0	-3.894298
24	57266	Cxcl14	chemokine (C-X-C motif) ligand 14	0	2	0	-3.867642
25	66548	Adamtsl5	ADAMTS-like 5	0	2	0	-3.808016
26	107932	Chd4	chromodomain helicase DNA binding protein 4	0	2	0	-3.764744
27	66497	2610528E23Rik	RIKEN cDNA 2610528E23 gene	0	2	0	-3.754096
28	66489	Rpl35	ribosomal protein L35	0	2	0	-3.720453
29	246198	Mllt6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	0	2	0	-3.712614
30	234967	Slc36a4	solute carrier family 36 (proton/amino acid symporter), member 4	0	2	0	-3.498919

Candidates for positive regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
31	66078	Tsen34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	0	2	0	-3.489445
32	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0	2	0	-3.375817
33	64929	Scel	sciellin	0	2	0	-3.372655
34	69786	Tprkb	Tp53rk binding protein	0	2	0	-3.301148
35	58249	Fibp	fibroblast growth factor (acidic) intracellular binding protein	0	2	0	-3.263401
36	20971	Sdc4	syndecan 4	0	2	0	-3.247902
37	68055	Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	0	2	0	-3.184875
38	20103	Rps5	ribosomal protein S5	0	2	0	-3.177766
39	17904	Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0	2	0	-3.170266
40	11461	Actb	actin, beta	0	2	0	-3.140525
41	67205	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	0	2	0	-3.083366
42	83679	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	0	2	0	-3.069466
43	19946	Rpl30	ribosomal protein L30	0	2	0	-3.064526
44	16175	Il1a	interleukin 1 alpha	0	2	0	-3.044574
45	12370	Casp8	caspase 8	0	2	0	-3.030518
46	54637	Praf2	PRA1 domain family 2	0	2	0	-3.021195
47	22032	Traf4	TNF receptor associated factor 4	0	2	0	-3.013076
48	20024	Sub1	SUB1 homolog (S. cerevisiae)	0	2	0	-2.98058
49	71881	2310001A20Rik	RIKEN cDNA 2310001A20 gene	0	2	0	-2.94657
50	78308	Gpr108	G protein-coupled receptor 108	0	2	0	-2.945147
51	15929	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	0	2	0	-2.940022
52	107767	Scamp1	secretory carrier membrane protein 1	0	2	0	-2.916582
53	94181	Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	0	2	0	-2.916317
54	20409	Ostf1	osteoclast stimulating factor 1	0	2	0	-2.914364
55	15587	Hyal2	hyaluronoglucosaminidase 2	0	2	0	-2.863063
56	11983	Atpif1	ATPase inhibitory factor 1	0	2	0	-2.85331
57	22154	Tubb5	tubulin, beta 5 class I	0	2	0	-2.85207
58	68134	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	0	2	0	-2.848585
59	19951	Rpl32	ribosomal protein L32	0	2	0	-2.836481
60	19336	Rab24	RAB24, member RAS oncogene family	0	2	0	-2.835622
61	55981	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	0	2	0	-2.834769
62	72133	Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	0	2	0	-2.826572
63	107568	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0	2	0	-2.779715
64	208518	Cep78	centrosomal protein 78	0	2	0	-2.731514

Candidates for positive regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
65	226043	Cbwd1	COBW domain containing 1	0	2	0	-2.72242
66	228410	Cstf3	cleavage stimulation factor, 3' pre-RNA, subunit 3	0	2	0	-2.712224
67	14156	Fen1	flap structure specific endonuclease 1	0	2	0	-2.710883
68	67281	Rpl37	ribosomal protein L37	0	2	0	-2.692699
69	23938	Map2k5	mitogen-activated protein kinase kinase 5	0	2	0	-2.680126
70	29870	Gtse1	G two S phase expressed protein 1	0	2	0	-2.679875
71	14137	Fdft1	farnesyl diphosphate farnesyl transferase 1	0	2	0	-2.653879
72	14694	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	0	2	0	-2.636517
73	114774	Pawr	PRKC, apoptosis, WT1, regulator	0	2	0	-2.615131
74	68755	Cgrrf1	cell growth regulator with ring finger domain 1	0	2	0	-2.610989
75	219103	Cenpj	centromere protein J	0	2	0	-2.578647
76	224045	Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	0	2	0	-2.57717
77	78816	Gmip	Gem-interacting protein	0	2	0	-2.567097
78	13135	Dad1	defender against cell death 1	0	2	0	-2.546705
79	15525	Hspa4	heat shock protein 4	0	2	0	-2.543569
80	60406	Sap30	sin3 associated polypeptide	0	2	0	-2.541804
81	19384	Ran	RAN, member RAS oncogene family	0	2	0	-2.540966
82	12579	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0	2	0	-2.530074
83	107686	Snrpd2	small nuclear ribonucleoprotein D2	0	2	0	-2.522211
84	67689	Aldh3b1	aldehyde dehydrogenase 3 family, member B1	0	2	0	-2.517537
85	20022	Polr2j	polymerase (RNA) II (DNA directed) polypeptide J	0	2	0	-2.492666
86	27207	Rps11	ribosomal protein S11	0	2	0	-2.480417
87	19822	Rnf4	ring finger protein 4	0	2	0	-2.464901
88	17448	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	0	2	0	-2.450353
89	13730	Emp1	epithelial membrane protein 1	0	2	0	-2.44541
90	105675	Ppif	peptidylprolyl isomerase F (cyclophilin F)	0	2	0	-2.439222
91	228545	Vps18	vacuolar protein sorting 18 (yeast)	0	2	0	-2.429264
92	15932	Idua	iduronidase, alpha-L-	0	2	0	-2.409139
93	13033	Ctsd	cathepsin D	0	2	0	-2.398762
94	70101	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	0	2	0	-2.379271
95	56417	Adar	adenosine deaminase, RNA-specific	0	2	0	-2.373014
96	15980	Ifngr2	interferon gamma receptor 2	0	2	0	-2.367999
97	23950	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	0	2	0	-2.363662
98	11844	Arf5	ADP-ribosylation factor 5	0	2	0	-2.363108

Candidates for positive regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
99	75735	Pank1	pantothenate kinase 1	0	2	0	-2.361488
100	67338	Rffl	ring finger and FYVE like domain containing protein	0	2	0	-2.324452
101	74202	Fblim1	filamin binding LIM protein 1	0	2	0	-2.321249
102	20437	Siah1a	seven in absentia 1A	0	2	0	-2.307286
103	72198	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	0	2	0	-2.296714
104	22388	Wdr1	WD repeat domain 1	0	2	0	-2.285061
105	12406	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	0	2	0	-2.280153
106	81898	Sf3b1	splicing factor 3b, subunit 1	0	2	0	-2.271514
107	24075	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0	2	0	-2.269374
108	70584	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	0	2	0	-2.261308
109	67439	Xab2	XPA binding protein 2	0	2	0	-2.249503
110	53885	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	0	2	0	-2.235107
111	16451	Jak1	Janus kinase 1	0	2	0	-2.232868
112	68365	Rab14	RAB14, member RAS oncogene family	0	2	0	-2.20973
113	13506	Dsc2	desmocollin 2	0	2	0	-2.20773
114	27061	Bcap31	B cell receptor associated protein 31	0	2	0	-2.175508
115	114663	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	0	2	0	-2.15429
116	12527	Cd9	CD9 antigen	0	2	0	-2.144156
117	20133	Rrm1	ribonucleotide reductase M1	0	2	0	-2.143485
118	494124	Calm5	calmodulin 5	0	2	0	-2.103088
119	14897	Trip12	thyroid hormone receptor interactor 12	0	2	0	-2.096929
120	16443	Itsn1	intersectin 1 (SH3 domain protein 1A)	0	2	0	-2.096191
121	12466	Cct6a	chaperonin containing Tcp1, subunit 6a (zeta)	0	2	0	-2.085344
122	218820	Zfp503	zinc finger protein 503	0	2	0	-2.083018
123	17756	Mtap2	microtubule-associated protein 2	0	2	0	-2.068454
124	69540	Klk10	kallikrein related-peptidase 10	0	2	0	-2.065693
125	66993	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	0	2	0	-2.057363
126	66860	Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0	2	0	-2.054888
127	20815	Srpk1	serine/arginine-rich protein specific kinase 1	0	2	0	-2.045431
128	13663	Ei24	etoposide induced 2.4 mRNA	0	2	0	-2.042968
129	329908	Usp24	ubiquitin specific peptidase 24	0	2	0	-2.036511
130	232201	Arhgap25	Rho GTPase activating protein 25	0	2	0	-2.03199
131	27362	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	0	2	0	-2.02858
132	67217	2810055F11Rik	RIKEN cDNA 2810055F11 gene	0	2	0	-2.012176

Candidates for positive regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
133	11793	Atg5	autophagy-related 5 (yeast)	0	2	0	-2.00712
134	112405	Egln1	EGL nine homolog 1 (C. elegans)	0	2	0	-1.991391
135	17865	Mybl2	myeloblastosis oncogene-like 2	0	2	0	-1.982642
136	21888	Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	0	2	0	-1.955746
137	70052	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	0	2	0	-1.950804
138	21354	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0	2	0	-1.94664
139	214505	Gnptg	N-acetylglucosamine-1-phosphotransferase, gamma subunit	0	2	0	-1.934422
140	73046	Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	0	2	0	-1.921989
141	15183	Hdac3	histone deacetylase 3	0	2	0	-1.921237
142	21374	Tbp	TATA box binding protein	0	2	0	-1.920274
143	14859	Gsta3	glutathione S-transferase, alpha 3	0	2	0	-1.88372
144	67500	Ccar1	cell division cycle and apoptosis regulator 1	0	2	0	-1.873752
145	227746	Rabepk	Rab9 effector protein with kelch motifs	0	2	0	-1.864275
146	57810	Cdon	cell adhesion molecule-related/down-regulated by oncogenes	0	2	0	-1.832443
147	67728	Dph2	DPH2 homolog (S. cerevisiae)	0	2	0	-1.818795
148	69953	2810025M15Rik	RIKEN cDNA 2810025M15 gene	0	2	0	-1.801606
149	11857	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	0	2	0	-1.779759
150	114565	Zfp295	zinc finger protein 295	0	2	0	-1.728715
151	16832	Ldhb	lactate dehydrogenase B	0	2	0	-1.728576
152	18195	Nsf	N-ethylmaleimide sensitive fusion protein	0	2	0	-1.725145
153	54198	Snx3	sorting nexin 3	0	2	0	-1.698583
154	19300	Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	0	2	0	-1.690722
155	71393	Kctd6	potassium channel tetramerisation domain containing 6	0	2	0	-1.690584
156	53621	Cnot4	CCR4-NOT transcription complex, subunit 4	0	2	0	-1.679797
157	14634	Gli3	GLI-Kruppel family member GLI3	0	2	0	-1.608601
158	70349	Copb1	coatomer protein complex, subunit beta 1	0	2	0	-1.606087
159	26886	Cenph	centromere protein H	0	2	0	-1.526953
160	23797	Akt3	thymoma viral proto-oncogene 3	0	2	0	-1.440133
161	16204	Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	0	2	0	-1.422833
162	66701	Spryd4	SPRY domain containing 4	0	2	0	-1.415484
163	74585	Sppl3	signal peptide peptidase 3	0	2	0	-1.03727

Candidates for negative regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	56462	Mtch1	mitochondrial carrier homolog 1 (C. elegans)	2	0	0	5.150296
2	14609	Gja1	gap junction protein, alpha 1	2	0	0	4.937435
3	14381	G6pdx	glucose-6-phosphate dehydrogenase X-linked	2	0	0	4.63813
4	56289	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	2	0	0	4.262562
5	14957	Hist1h1d	histone cluster 1, H1d	2	0	0	4.148987
6	64136	Sdf2l1	stromal cell-derived factor 2-like 1	2	0	0	3.817014
7	11758	Prdx6	peroxiredoxin 6	3	0	0	3.670943
8	140721	Caskin2	CASK-interacting protein 2	2	0	0	3.548683
9	18117	Cox4nb	COX4 neighbor	2	0	0	3.512259
10	19240	Tmsb10	thymosin, beta 10	3	0	0	3.463588
11	22333	Vdac1	voltage-dependent anion channel 1	2	0	0	3.348978
12	20912	Stxbp3a	syntaxin binding protein 3A	2	0	0	3.310092
13	12514	Cd68	CD68 antigen	2	0	0	2.926897
14	23808	Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	2	0	0	2.912088
15	53328	Pgrmc1	progesterone receptor membrane component 1	2	0	0	2.905557
16	170750	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	2	0	0	2.836124
17	24071	Synj2bp	synaptojanin 2 binding protein	2	0	0	2.765778
18	11804	Aplp2	amyloid beta (A4) precursor-like protein 2	2	0	0	2.748337
19	69029	1500032L24Rik	RIKEN cDNA 1500032L24 gene	2	0	0	2.656156
20	23856	Dido1	death inducer-obliterator 1	2	0	0	2.655234
21	21838	Thy1	thymus cell antigen 1, theta	2	0	0	2.646249
22	14199	Fhl1	four and a half LIM domains 1	2	0	0	2.624509
23	215748	Cnksr3	Cnksr family member 3	2	0	0	2.577662
24	229445	Ctso	cathepsin O	2	0	0	2.561291
25	240672	Dusp5	dual specificity phosphatase 5	2	0	0	2.532042
26	66177	Ubl5	ubiquitin-like 5	2	0	0	2.519894
27	23991	Cib1	calcium and integrin binding 1 (calmyrin)	2	0	0	2.491497
28	66665	5730528L13Rik	RIKEN cDNA 5730528L13 gene	2	0	0	2.485449
29	214601	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	3	0	0	2.356519
30	22612	Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	2	0	0	2.343623
31	56419	Diap3	diaphanous homolog 3 (Drosophila)	2	0	0	2.337557
32	22627	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2	0	0	2.333405
33	72349	Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	2	0	0	2.322377
34	227800	Rabgap1	RAB GTPase activating protein 1	2	0	0	2.321058

Candidates for negative regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
35	73720	Cst6	cystatin E/M	2	0	0	2.309278
36	68185	Chchd8	coiled-coil-helix-coiled-coil-helix domain containing 8	2	0	0	2.299877
37	12497	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	2	0	0	2.271208
38	18203	Ntan1	N-terminal Asn amidase	2	0	0	2.263622
39	330361	AW146020	expressed sequence AW146020	2	0	0	2.225839
40	71446	Wrb	tryptophan rich basic protein	2	0	0	2.188306
41	106393	Srl	sarcalumenin	2	0	0	2.149767
42	17423	Ndst2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	2	0	0	2.120654
43	65079	Rtn4r	reticulon 4 receptor	3	0	0	2.102539
44	21419	Tcfap2b	transcription factor AP-2 beta	2	0	0	2.088474
45	71780	Isyna1	myo-inositol 1-phosphate synthase A1	2	0	0	2.042152
46	15902	Id2	inhibitor of DNA binding 2	2	0	0	2.019157
47	11477	Acvr1	activin A receptor, type 1	2	0	0	1.946922
48	76608	Hectd3	HECT domain containing 3	2	0	0	1.940368
49	11479	Acvr1b	activin A receptor, type 1B	2	0	0	1.93593
50	71069	Stox2	storkhead box 2	2	0	0	1.913461
51	72085	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	3	0	0	1.890805
52	71745	Cul2	cullin 2	2	0	0	1.843776
53	68219	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	2	0	0	1.814787
54	66839	0610009O20Rik	RIKEN cDNA 0610009O20 gene	2	0	0	1.803024
55	72141	Adpgk	ADP-dependent glucokinase	2	0	0	1.802917
56	79044	Mrps34	mitochondrial ribosomal protein S34	2	0	0	1.801459
57	12042	Bcl10	B cell leukemia/lymphoma 10	2	0	0	1.778075
58	19084	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	2	0	0	1.712054
59	15159	Hccs	holocytochrome c synthetase	2	0	0	1.705887
60	11828	Aqp3	aquaporin 3	2	0	0	1.699845
61	56440	Snx1	sorting nexin 1	2	0	0	1.668303
62	26951	Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	2	0	0	1.658931
63	11465	Actg1	actin, gamma, cytoplasmic 1	2	0	0	1.65531
64	67145	Tomm34	translocase of outer mitochondrial membrane 34	3	0	0	1.591692
65	268564	Zbtb1	zinc finger and BTB domain containing 1	2	0	0	1.56918
66	20688	Sp4	trans-acting transcription factor 4	2	0	0	1.566193
67	12816	Col12a1	collagen, type XII, alpha 1	2	0	0	1.563503
68	66826	Taz	tafazzin	2	0	0	1.562961

Candidates for negative regulators of oncogenic growth (DESeq)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
69	70454	Cenpl	centromere protein L	2	0	0	1.544397
70	19691	Recql	RecQ protein-like	2	0	0	1.543099
71	338367	Myo1d	myosin ID	2	0	0	1.523257
72	66943	Pqlc1	PQ loop repeat containing 1	2	0	0	1.448255
73	230661	Tesk2	testis-specific kinase 2	2	0	0	1.447342
74	67778	Zfp639	zinc finger protein 639	2	0	0	1.440194
75	66079	Tmem42	transmembrane protein 42	2	0	0	1.377148
76	232314	Ppp4r2	protein phosphatase 4, regulatory subunit 2	2	0	0	1.373663
77	18521	Pcbp2	poly(rC) binding protein 2	2	0	0	1.365813
78	67095	Trak1	trafficking protein, kinesin binding 1	2	0	0	1.312791
79	215615	Rnpep	arginyl aminopeptidase (aminopeptidase B)	2	0	0	1.311754
80	11431	Acp1	acid phosphatase 1, soluble	2	0	0	1.187072
81	15161	Hcfc1	host cell factor C1	2	0	0	1.10549

Supplementary Table 4. Putative regulators of oncogenic growth identified by Fisher's exact test of pooled samples.

Note: Candidates identified by both DESeq and Fisher's exact test are highlighted in green.

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	12387	Ctnnb1	catenin (cadherin-associated protein), beta 1, 88kDa	0	5	0	-3.60994
2	23797	Akt3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	0	4	6	-1.48674
3	68836	Mrpl52	mitochondrial ribosomal protein L52	0	3	1	-2.99207
4	268449	Rpl23a	ribosomal protein L23A	0	3	2	-2.87292
5	110157	Raf1	v-raf-1 murine leukemia viral oncogene homolog 1	0	3	7	-2.3608
6	77116	Mtmr2	myotubularin related protein 2	0	3	2	-2.23639
7	246198	Mllt6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	0	3	2	-2.17635
8	114774	Pawr	PRKC, apoptosis, WT1, regulator	0	3	2	-2.17517
9	93890	Pcdhb19	protocadherin beta 11	0	3	2	-2.14404
10	51813	Ccnc	cyclin C	0	3	2	-2.13849
11	20971	Sdc4	syndecan 4	0	3	2	-2.13573
12	13730	Emp1	epithelial membrane protein 1	0	3	2	-2.09697
13	98386	Lbr	lamin B receptor	0	3	2	-2.06861
14	69656	Pir	pirin (iron-binding nuclear protein)	0	3	2	-1.96175
15	22388	Wdr1	WD repeat domain 1	0	3	1	-1.95957
16	28000	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	0	3	2	-1.89974
17	74202	Fblim1	filamin binding LIM protein 1	0	3	2	-1.85599
18	16176	Il1b	interleukin 1, beta	0	3	2	-1.84088
19	101197	Zfp956 (AI894139)	zinc finger protein 956	0	3	2	-1.83174
20	320100	Relt (Tnfrsf19l)	RELT tumor necrosis factor receptor	0	3	2	-1.81627
21	22154	Tubb5	tubulin, beta class I	0	3	2	-1.80672
22	81898	Sf3b1	splicing factor 3b, subunit 1, 155kDa	0	3	2	-1.80285
23	19336	Rab24	RAB24, member RAS oncogene family	0	3	2	-1.77865
24	12544	Cdc45 (Cdc45l)	cell division cycle 45 homolog (S. cerevisiae)	0	3	2	-1.75888
25	55981	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	0	3	2	-1.75676
26	18195	Nsf	N-ethylmaleimide-sensitive factor	0	3	2	-1.7189
27	15183	Hdac3	histone deacetylase 3	0	3	2	-1.66183
28	14859	Gsta3	glutathione S-transferase alpha 3	0	3	2	-1.63366
29	18628	Per3	period homolog 3 (Drosophila)	0	3	2	-1.62419
30	16443	Itsn1	intersectin 1 (SH3 domain protein)	0	3	7	-1.59483
31	19364	Rad51l3	RAD51 homolog D (S. cerevisiae)	0	3	1	-1.59235
32	27362	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	0	3	2	-1.4556
33	15461	Hras1	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0	3	2	-1.41727

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
34	72193	Scaf11 (Sfrs2ip)	SR-related CTD-associated factor 11	0	3	2	-1.40599
35	56417	Adar	adenosine deaminase, RNA-specific	0	3	2	-1.39486
36	12014	Bach2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	0	3	2	-1.38942
37	105675	Ppif	peptidylprolyl isomerase F	0	3	2	-1.37636
38	108837	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	0	3	2	-1.37515
39	16885	Limk1	LIM domain kinase 1	0	3	2	-1.31093
40	71710	Lrrcc1	leucine rich repeat and coiled-coil centrosomal protein 1	0	3	2	-1.30101
41	20103	Rps5	ribosomal protein S5	0	3	2	-1.29185
42	17218	Mcm5	minichromosome maintenance complex component 5	0	3	2	-1.28398
43	68052	Rps13	ribosomal protein S13	0	3	2	-1.28174
44	20403	Itsn2	intersectin 2	0	3	2	-1.28122
45	225929	Patl1 (AV312086)	protein associated with topoisomerase II homolog 1 (yeast)	0	3	2	-1.2267
46	16330	Inpp5b	inositol polyphosphate-5-phosphatase, 75kDa	0	3	2	-1.22204
47	76281	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3	0	3	2	-1.2138
48	26441	Psma4	proteasome (prosome, macropain) subunit, alpha type, 4	0	3	2	-1.20741
49	69019	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	0	3	2	-1.20063
50	13640	Efna5	ephrin-A5	0	3	2	-1.20051
51	12561	Cdh4	cadherin 4, type 1, R-cadherin (retinal)	0	3	2	-1.18912
52	21849	Trim28	tripartite motif containing 28	0	3	2	-1.16675
53	11911	Atf4	activating transcription factor 4 (tax-responsive enhancer element B67)	0	3	2	-1.16652
54	170753	Zfp704	zinc finger protein 704	0	3	2	-1.13704
55	18131	Notch3	notch 3	0	2	3	-3.84783
56	74195	Elp3	elongation protein 3 homolog (S. cerevisiae)	0	2	3	-3.79323
57	105148	Iars	isoleucyl-tRNA synthetase	0	2	3	-3.47262
58	107932	Chd4	chromodomain helicase DNA binding protein 4	0	2	3	-3.39842
59	192212	Prom2	prominin 2	0	2	3	-3.35551
60	213696	Duoxa1	dual oxidase maturation factor 1	0	2	3	-3.33641
61	26465	Zfp146	zinc finger protein 146	0	2	3	-3.29408
62	76846	Rps9	ribosomal protein S9	0	2	3	-3.26828
63	64929	Scel	sciellin	0	2	3	-3.17614
64	93887	Pcdhb16	protocadherin beta 8	0	2	3	-3.17598
65	72113	Adck1	aarF domain containing kinase 1	0	2	2	-3.16383
66	234967	Slc36a4	solute carrier family 36 (proton/amino acid symporter), member 4	0	2	3	-3.15241
67	327900	Ubtd2 (9630054F20Rik)	ubiquitin domain containing 2	0	2	2	-3.03834
68	171168	Asah3	alkaline ceramidase 1	0	2	3	-3.00099
69	20227	Sart1	squamous cell carcinoma antigen recognized by T cells	0	2	3	-2.97283
70	69786	Tprkb	TP53RK binding protein	0	2	2	-2.89594

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
71	19763	Ring1	ring finger protein 1	0	2	3	-2.82123
72	244954	Prss35	protease, serine, 35	0	2	3	-2.68395
73	259302	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	0	2	3	-2.67071
74	16175	Il1a	interleukin 1, alpha	0	2	3	-2.6705
75	12370	Casp8	caspase 8, apoptosis-related cysteine peptidase	0	2	3	-2.61828
76	15929	Idh3g	isocitrate dehydrogenase 3 (NAD+) gamma	0	2	3	-2.6169
77	14137	Fdft1	farnesyl-diphosphate farnesyltransferase 1	0	2	2	-2.61194
78	233315	Mtmr10 (BB128963)	myotubularin related protein 10	0	2	3	-2.57568
79	59001	Pole3	polymerase (DNA directed), epsilon 3, accessory subunit	0	2	3	-2.55437
80	276770	Eif5a	eukaryotic translation initiation factor 5A	0	2	3	-2.53231
81	20667	Sox12	SRY (sex determining region Y)-box 12	0	2	3	-2.51997
82	107767	Scamp1	secretory carrier membrane protein 1	0	2	3	-2.49334
83	66497	2610528E23Rik	RIKEN cDNA 2610528E23 gene	0	2	3	-2.49141
84	381979	Brsk1	BR serine/threonine kinase 1	0	2	3	-2.4846
85	15587	Hyal2	hyaluronoglucosaminidase 2	0	2	3	-2.48121
86	20024	Sub1	SUB1 homolog (S. cerevisiae)	0	2	3	-2.44011
87	71881	Apmap	adipocyte plasma membrane associated protein	0	2	3	-2.438
88	29870	Gtse1	G-2 and S-phase expressed 1	0	2	3	-2.43331
89	67383	2410127L17Rik	RIKEN cDNA 2410127L17 gene	0	2	3	-2.42349
90	19057	Ppp3cc	protein phosphatase 3, catalytic subunit, gamma isozyme	0	2	3	-2.39495
91	228410	Cstf3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	0	2	3	-2.38464
92	54637	Praf2	PRA1 domain family, member 2	0	2	3	-2.37865
93	74268	Aven	apoptosis, caspase activation inhibitor	0	2	3	-2.3651
94	107568	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0	2	3	-2.35058
95	64008	Aqp9	aquaporin 9	0	2	3	-2.34226
96	224045	Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	0	2	3	-2.33475
97	226043	Cbwd1	COBW domain containing 1	0	2	3	-2.30643
98	54402	Stk19	serine/threonine kinase 19	0	2	3	-2.30597
99	381668	Fbrsl1 (2410025L10Rik)	fibrosin-like 1	0	2	3	-2.29641
100	12447	Ccne1	cyclin E1	0	2	3	-2.2214
101	19946	Rpl30	ribosomal protein L30	0	2	3	-2.19914
102	11848	Rhoa	ras homolog family member A	0	2	3	-2.19805
103	20194	S100a10	S100 calcium binding protein A10	0	2	3	-2.18906
104	68365	Rab14	RAB14, member RAS oncogene family	0	2	3	-2.17753
105	16168	Il15	interleukin 15	0	2	3	-2.17056
106	75735	Pank1	pantothenate kinase 1	0	2	3	-2.15541
107	71586	Ifih1	interferon induced with helicase C domain 1	0	2	3	-2.15253

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
108	72198	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	0	2	3	-2.1517
109	237052	Tceal1	transcription elongation factor A (SII)-like 1	0	2	3	-2.13964
110	60406	Sap30	Sin3A-associated protein, 30kDa	0	2	3	-2.12794
111	232941	Ppm1n	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)	0	2	3	-2.11787
112	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0	2	3	-2.10859
113	21888	Tle4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	0	2	3	-2.09726
114	12466	Cct6a	chaperonin containing TCP1, subunit 6A (zeta 1)	0	2	3	-2.09575
115	21374	Tbp	TATA box binding protein	0	2	3	-2.093
116	18585	Pde9a	phosphodiesterase 9A	0	2	3	-2.09013
117	27207	Rps11	ribosomal protein S11	0	2	3	-2.08786
118	74637	Shpk (Carkl)	sedoheptulokinase	0	2	3	-2.06099
119	23938	Map2k5	mitogen-activated protein kinase kinase 5	0	2	3	-2.05812
120	16565	Kif21b	kinesin family member 21B	0	2	3	-2.04985
121	66548	Adamtsl5	ADAMTS-like 5	0	2	3	-2.04603
122	69534	Avpi1	arginine vasopressin-induced 1	0	2	3	-2.01909
123	19128	Pros1	protein S (alpha)	0	2	3	-2.0067
124	24116	Whsc2	Wolf-Hirschhorn syndrome candidate 2	0	2	3	-2.00475
125	15525	Hspa4	heat shock 70kDa protein 4	0	2	3	-2.00259
126	14694	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	0	2	8	-2.00088
127	13135	Dad1	defender against cell death 1	0	2	3	-1.99999
128	19822	Rnf4	ring finger protein 4	0	2	3	-1.99638
129	12858	Cox5a	cytochrome c oxidase subunit Va	0	2	3	-1.99175
130	11793	Atg5	autophagy related 5	0	2	3	-1.98001
131	56305	Pitpnb	phosphatidylinositol transfer protein, beta	0	2	3	-1.9789
132	56878	Rbms1	RNA binding motif, single stranded interacting protein 1	0	2	3	-1.97732
133	76559	Atg2b	autophagy related 2B	0	2	2	-1.96633
134	226982	Eif5b	eukaryotic translation initiation factor 5B	0	2	2	-1.96255
135	16206	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	0	2	3	-1.95958
136	13506	Dsc2	desmocollin 2	0	2	3	-1.95958
137	270106	Rpl13	ribosomal protein L13	0	2	3	-1.95676
138	12527	Cd9	CD9 molecule	0	2	3	-1.95446
139	18706	Pik3ca	phosphoinositide-3-kinase, catalytic, alpha polypeptide	0	2	3	-1.95349
140	57266	Cxcl14	chemokine (C-X-C motif) ligand 14	0	2	3	-1.9513
141	11983	Atpif1	ATPase inhibitory factor 1	0	2	2	-1.94855
142	209737	Kif15	kinesin family member 15	0	2	3	-1.94846
143	14634	Gli3	GLI family zinc finger 3	0	2	3	-1.94737
144	17765	Mtf2	metal response element binding transcription factor 2	0	2	3	-1.94574

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
145	66617	Ntmt1	N-terminal Xaa-Pro-Lys N-methyltransferase 1	0	2	3	-1.93763
146	22032	Traf4	TNF receptor-associated factor 4	0	2	3	-1.93125
147	30805	Slc22a4	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	0	2	3	-1.92825
148	212569	Zfp273	zinc finger protein 273	0	2	3	-1.9184
149	50708	Hist1h1c	histone cluster 1, H1c	0	2	3	-1.91458
150	231326	Aasdh	aminoadipate-semialdehyde dehydrogenase	0	2	2	-1.91322
151	14869	Gstp2	glutathione S-transferase pi 1	0	2	3	-1.90012
152	13663	Ei24	etoposide induced 2.4 mRNA	0	2	3	-1.89958
153	11641	Akap2	A kinase (PRKA) anchor protein 2	0	2	3	-1.89687
154	231872	Jtv1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	0	2	3	-1.87636
155	26406	Map3k3	mitogen-activated protein kinase kinase kinase 3	0	2	3	-1.87365
156	14897	Trip12	thyroid hormone receptor interactor 12	0	2	3	-1.87173
157	68134	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	0	2	3	-1.8682
158	12465	Cct5	chaperonin containing TCP1, subunit 5 (epsilon)	0	2	3	-1.86606
159	70101	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	0	2	3	-1.86172
160	67689	Aldh3b1	aldehyde dehydrogenase 3 family, member B1	0	2	2	-1.83987
161	26450	Rbbp9	retinoblastoma binding protein 9	0	2	3	-1.83789
162	67500	Ccar1	cell division cycle and apoptosis regulator 1	0	2	3	-1.83474
163	14456	Gas6	growth arrest-specific 6	0	2	3	-1.82776
164	12579	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0	2	3	-1.81898
165	20963	Syk	spleen tyrosine kinase	0	2	3	-1.81838
166	329506	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	0	2	3	-1.81567
167	11303	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	0	2	3	-1.81191
168	67949	Mki67ip	MKI67 (FHA domain) interacting nucleolar phosphoprotein	0	2	3	-1.8071
169	20102	Rps4x	ribosomal protein S4, Y-linked 1	0	2	3	-1.8001
170	17448	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	0	2	3	-1.79758
171	70052	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	0	2	3	-1.79528
172	20409	Ostf1	osteoclast stimulating factor 1	0	2	3	-1.79427
173	66815	Ccdc109b	coiled-coil domain containing 109B	0	2	2	-1.79293
174	11441	Chrna7	cholinergic receptor, nicotinic, alpha 7 (neuronal)	0	2	3	-1.78492
175	18705	Pik3c2g	phosphoinositide-3-kinase, class 2, gamma polypeptide	0	2	3	-1.78423
176	27061	Bcap31	B-cell receptor-associated protein 31	0	2	3	-1.78275
177	269397	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	0	2	3	-1.78221
178	380601	Fastkd5	FAST kinase domains 5	0	2	3	-1.77588
179	11777	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	0	2	3	-1.77164
180	19359	Rad23b	RAD23 homolog B (S. cerevisiae)	0	2	3	-1.76992
181	229644	Trim45	tripartite motif containing 45	0	2	3	-1.76911

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
182	11857	Arhgdib	Rho GDP dissociation inhibitor (GDI) beta	0	2	3	-1.75342
183	20861	Stfa1	stefin A1	0	2	3	-1.75013
184	78816	Gmip	GEM interacting protein	0	2	3	-1.74257
185	110012	Gm16517	tubulin polyglutamylase complex subunit 1	0	2	3	-1.7419
186	17865	Mybl2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0	2	3	-1.74027
187	19266	Ptprd	protein tyrosine phosphatase, receptor type, D	0	2	2	-1.73819
188	66596	Gtf3a	general transcription factor IIIA	0	2	3	-1.73735
189	107250	Kazald1	Kazal-type serine peptidase inhibitor domain 1	0	2	3	-1.73672
190	17311	Kitl	KIT ligand	0	2	3	-1.73086
191	66993	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	0	2	3	-1.7308
192	70584	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	0	2	3	-1.72723
193	70510	Rnf167	ring finger protein 167	0	2	3	-1.72553
194	22123	Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	0	2	3	-1.72473
195	56368	Cyb561d2	cytochrome b-561 domain containing 2	0	2	3	-1.72007
196	14156	Fen1	flap structure-specific endonuclease 1	0	2	3	-1.70703
197	14423	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	0	2	2	-1.70416
198	20437	Siah1a	siah E3 ubiquitin protein ligase 1	0	2	3	-1.70266
199	214505	Gnptg	N-acetylglucosamine-1-phosphate transferase, gamma subunit	0	2	3	-1.69906
200	16666	Krt1-16	keratin 16	0	2	3	-1.69536
201	20643	Snrpe	small nuclear ribonucleoprotein polypeptide E	0	2	3	-1.69534
202	19719	Rfng	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	0	2	3	-1.69361
203	18475	Pafah1b2	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	0	2	3	-1.69309
204	16450	Jag2	jagged 2	0	2	3	-1.67738
205	229681	St7l	suppression of tumorigenicity 7 like	0	2	3	-1.67653
206	20815	Srpk1	SRSF protein kinase 1	0	2	3	-1.67631
207	329015	Atg2a	autophagy related 2A	0	2	2	-1.67343
208	102626	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0	2	8	-1.6691
209	53890	Sart3	squamous cell carcinoma antigen recognized by T cells 3	0	2	3	-1.6668
210	75578	Fggy (2310009E04Rik)	FGGY carbohydrate kinase domain containing	0	2	3	-1.66382
211	65019	Rpl23	ribosomal protein L23	0	2	3	-1.66326
212	210808	Lacc1	laccase (multicopper oxidoreductase) domain containing 1	0	2	2	-1.66035
213	16918	Mycl1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	0	2	2	-1.65618
214	14365	Fzd3	frizzled family receptor 3	0	2	3	-1.65606
215	22652	Mkrn3	makorin ring finger protein 3	0	2	2	-1.65574
216	27984	Efhd2	EF-hand domain family, member D2	0	2	3	-1.65465
217	494448	Cbx6	chromobox homolog 6	0	2	3	-1.65429
218	28295	D10Jhu81e	chromosome 21 open reading frame 33	0	2	2	-1.65199

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
219	56457	Clptm1	cleft lip and palate associated transmembrane protein 1	0	2	3	-1.64579
220	23950	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	0	2	3	-1.6401
221	74349	Fam160a2	family with sequence similarity 160, member A2	0	2	3	-1.639
222	19300	Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	0	2	3	-1.63591
223	268510	Mgat5b	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	0	2	3	-1.63379
224	67027	Mkrn2	makorin ring finger protein 2	0	2	3	-1.63375
225	114663	Impa2	inositol(myo)-1(or 4)-monophosphatase 2	0	2	3	-1.63288
226	53621	Cnot4	CCR4-NOT transcription complex, subunit 4	0	2	3	-1.62787
227	74342	Lrrtm1	leucine rich repeat transmembrane neuronal 1	0	2	3	-1.62638
228	214137	Arhgap29	Rho GTPase activating protein 29	0	2	3	-1.62485
229	17084	Ly86	lymphocyte antigen 86	0	2	3	-1.62295
230	18805	Pld1	phospholipase D1, phosphatidylcholine-specific	0	2	3	-1.62225
231	11739	Slc25a4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	0	2	3	-1.61845
232	75607	Wnk2	WNK lysine deficient protein kinase 2	0	2	3	-1.61833
233	70405	Calml3	calmodulin-like 3	0	2	3	-1.61756
234	16832	Ldhb	lactate dehydrogenase B	0	2	3	-1.61594
235	29875	Iqgap1	IQ motif containing GTPase activating protein 1	0	2	3	-1.61395
236	224836	Usp49	ubiquitin specific peptidase 49	0	2	3	-1.61114
237	26886	Cenph	centromere protein H	0	2	3	-1.60844
238	215351	Senp6	SUMO1/sentrin specific peptidase 6	0	2	3	-1.60587
239	52679	E2f7	E2F transcription factor 7	0	2	3	-1.6023
240	78308	Gpr108	G protein-coupled receptor 108	0	2	3	-1.6022
241	15932	Idua	iduronidase, alpha-L-	0	2	2	-1.60174
242	97848	Serpinb6c	serine (or cysteine) peptidase inhibitor, clade B, member 6c	0	2	3	-1.59578
243	208518	Cep78	centrosomal protein 78kDa	0	2	3	-1.59235
244	20620	Plk2	polo-like kinase 2	0	2	3	-1.59206
245	12295	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	0	2	3	-1.59082
246	83429	Ctns	cystinosin, lysosomal cystine transporter	0	2	3	-1.58833
247	20713	Serpini1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	0	2	3	-1.58546
248	50874	Tmod4	tropomodulin 4 (muscle)	0	2	3	-1.58294
249	84004	Mcam	melanoma cell adhesion molecule	0	2	3	-1.57188
250	55984	Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	0	2	3	-1.57043
251	58231	Stk4	serine/threonine kinase 4	0	2	3	-1.56927
252	106707	Rpusd1	RNA pseudouridylate synthase domain containing 1	0	2	3	-1.56634
253	26394	Lypla2	lysophospholipase II	0	2	3	-1.56217
254	68953	Chmp2a	charged multivesicular body protein 2A	0	2	3	-1.56178
255	110750	Cse1l	CSE1 chromosome segregation 1-like (yeast)	0	2	3	-1.56114

Candidates for positive regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
256	230157	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	0	2	3	-1.55631
257	66860	Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0	2	2	-1.54853
258	214897	Csnk1g1	casein kinase 1, gamma 1	0	2	3	-1.53484
259	103172	Ndg2	coiled-coil-helix-coiled-coil-helix domain containing 10	0	2	2	-1.53065
260	20068	Rps17	ribosomal protein S17	0	2	3	-1.52827
261	21354	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0	2	3	-1.5282
262	218699	Pxk	PX domain containing serine/threonine kinase	0	2	3	-1.52544
263	16204	Fabp6	fatty acid binding protein 6, ileal	0	2	3	-1.52452
264	93707	Pcdhgc4	protocadherin gamma subfamily C, 4	0	2	3	-1.5236
265	12416	Cbx2	chromobox homolog 2	0	2	3	-1.52191
266	210925	Ints9	integrator complex subunit 9	0	2	2	-1.51936
267	18605	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	0	2	3	-1.51847
268	74103	Nebl	nebulette	0	2	3	-1.51689
269	140483	Hnmt	histamine N-methyltransferase	0	2	3	-1.50997
270	240066	Zfp870 (BC066107)	zinc finger protein 870	0	2	3	-1.50668
271	212998	BC016579	cDNA sequence BC016579	0	2	2	-1.50569
272	228545	Vps18	vacuolar protein sorting 18 homolog (S. cerevisiae)	0	2	3	-1.50406
273	259279	Tubgcp3	tubulin, gamma complex associated protein 3	0	2	3	-1.50375
274	19982	Rpl36a	ribosomal protein L36a	0	2	3	-1.5012
275	26894	Cops7a	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	0	2	2	-1.50039
276	72935	Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	0	2	3	-1.50006

Candidates for negative regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
1	17760	Mtap6	microtubule-associated protein 6	4	0	1	1.504101
2	99650	4933434E20Rik	RIKEN cDNA 4933434E20 gene	4	0	1	1.335483
3	19240	Tmsb10	thymosin beta 4, X-linked	3	0	1	2.997635
4	20912	Stxbp3a	syntaxin binding protein 3	3	0	2	2.393958
5	214601	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	3	0	2	2.352889
6	216440	Os9 (4632413K17Rik)	osteosarcoma amplified 9, endoplasmic reticulum lectin	3	0	1	2.186796
7	12583	Cdo1	cysteine dioxygenase, type I	3	0	2	2.18178
8	242285	Sdr16c5 (Rdhe2)	short chain dehydrogenase/reductase family 16C, member 5	3	0	2	2.167538
9	18103	Nme2	NME/NM23 nucleoside diphosphate kinase 2	3	0	7	2.034861
10	21838	Thy1	Thy-1 cell surface antigen	3	0	2	1.928814
11	21956	Tnnt2	troponin T type 2 (cardiac)	3	0	2	1.815209
12	215748	Cnksr3	CNKSR family member 3	3	0	2	1.752163
13	242819	Rundc3b (Gm440)	RUN domain containing 3B	3	0	2	1.701845
14	17966	Nbr1	neighbor of BRCA1 gene 1	3	0	2	1.602133
15	67145	Tomm34	translocase of outer mitochondrial membrane 34	3	0	2	1.467991
16	12946	Cr1l (Crry)	complement component (3b/4b) receptor 1-like	3	0	2	1.354341
17	13688	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	3	0	2	1.340723
18	70396	Asnsd1	asparagine synthetase domain containing 1	3	0	2	1.324157
19	72141	Adpgk	ADP-dependent glucokinase	3	0	2	1.29385
20	13618	Ednrb	endothelin receptor type B	3	0	2	1.246541
21	56462	Mtch1	mitochondrial carrier 1	2	0	3	4.115456
22	14609	Gja1	gap junction protein, alpha 1, 43kDa	2	0	3	4.031505
23	14381	G6pdx	glucose-6-phosphate dehydrogenase	2	0	3	3.517335
24	57358	Cmar (Spg7)	spastic paraplegia 7 (pure and complicated autosomal recessive)	2	0	3	3.404294
25	109077	Ints5	integrator complex subunit 5	2	0	3	3.328553
26	109815	H47	VCP-interacting membrane protein	2	0	2	3.182336
27	17342	Mitf	microphthalmia-associated transcription factor	2	0	3	3.084003
28	53328	Pgrmc1	progesterone receptor membrane component 1	2	0	3	3.03049
29	12830	Col4a5	collagen, type IV, alpha 5	2	0	3	2.961371
30	66320	Tmem208 (Hspc171)	transmembrane protein 208	2	0	3	2.957803
31	20850	Stat5a	signal transducer and activator of transcription 5A	2	0	3	2.946551
32	18117	Emc8	ER membrane protein complex subunit 8	2	0	2	2.894288
33	193813	Mcfd2	multiple coagulation factor deficiency 2	2	0	2	2.888546
34	22333	Vdac1	voltage-dependent anion channel 1	2	0	3	2.848489
35	64136	Sdf2l1	stromal cell-derived factor 2-like 1	2	0	3	2.828783
36	21754	Tesk1	testis-specific kinase 1	2	0	3	2.787309
37	24071	Synj2bp	synaptojanin 2 binding protein	2	0	3	2.786967

Candidates for negative regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
38	78088	Sowahb	sosondowah ankyrin repeat domain family member B	2	0	3	2.736565
39	23808	Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	2	0	3	2.640771
40	56289	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	2	0	3	2.622498
41	14957	Hist1h1d	histone cluster 1, H1d	2	0	3	2.578884
42	227800	Rabgap1	RAB GTPase activating protein 1	2	0	2	2.471741
43	107652	Uap1	UDP-N-acteylglucosamine pyrophosphorylase 1	2	0	3	2.449981
44	22627	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2	0	3	2.383973
45	114301	Palmd	palmdelphin	2	0	3	2.374722
46	69029	1500032L24Rik	RIKEN cDNA 1500032L24 gene	2	0	3	2.348735
47	12497	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)	2	0	3	2.320445
48	11854	Rhod	ras homolog family member D	2	0	3	2.280416
49	23856	Dido1	death inducer-obliterator 1	2	0	2	2.274753
50	233890	Zfp768 (BC026432)	zinc finger protein 768	2	0	3	2.267083
51	11546	Parp2	poly (ADP-ribose) polymerase 2	2	0	3	2.242664
52	56419	Diap3	diaphanous homolog 3 (Drosophila)	2	0	3	2.232301
53	69253	Hspb2	heat shock 27kDa protein 2	2	0	3	2.230754
54	17423	Ndst2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	2	0	3	2.212722
55	74133	1200011M11Rik	smg-8 homolog, nonsense mediated mRNA decay factor (C. elegans)	2	0	3	2.191855
56	16211	Kpnb1	karyopherin (importin) beta 1	2	0	3	2.187491
57	229445	Ctso	cathepsin O	2	0	3	2.151808
58	68219	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	2	0	3	2.121114
59	65079	Rtn4r	reticulon 4 receptor	2	0	3	2.089179
60	170750	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	2	0	3	2.084535
61	76608	Hectd3	HECT domain containing E3 ubiquitin protein ligase 3	2	0	3	2.076412
62	27756	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	2	0	3	2.071125
63	23959	Nt5e	5'-nucleotidase, ecto (CD73)	2	0	3	2.034553
64	11477	Acvr1	activin A receptor, type I	2	0	3	1.998632
65	16157	Il11ra1	interleukin 11 receptor, alpha	2	0	3	1.941139
66	66665	5730528L13Rik	Myb/SANT-like DNA-binding domain containing 3	2	0	3	1.939924
67	269338	Vps39	vacuolar protein sorting 39 homolog (S. cerevisiae)	2	0	3	1.92889
68	71446	Wrb	tryptophan rich basic protein	2	0	3	1.91818
69	330361	AW146020	GC-rich sequence DNA-binding factor 2	2	0	3	1.913966
70	23991	Cib1	calcium and integrin binding 1 (calmyrin)	2	0	3	1.91351
71	20660	Sorl1	sortilin-related receptor, L(DLR class) A repeats containing	2	0	2	1.903269
72	17714	Grpel2	GrpE-like 2, mitochondrial (E. coli)	2	0	2	1.901428
73	11828	Aqp3	aquaporin 3 (Gill blood group)	2	0	3	1.878379
74	21930	Tnfaip6	tumor necrosis factor, alpha-induced protein 6	2	0	3	1.875452

Candidates for negative regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
75	100737	Dcun1d4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	2	0	2	1.866643
76	15159	Hccs	holocytochrome c synthase	2	0	3	1.856507
77	53608	Map3k6	mitogen-activated protein kinase kinase kinase 6	2	0	3	1.845115
78	71745	Cul2	cullin 2	2	0	3	1.843076
79	66871	Cpne8	copine VIII	2	0	3	1.835332
80	26951	Zw10	ZW10, kinetochore associated, homolog (Drosophila)	2	0	3	1.816004
81	70351	Ppp4r1	protein phosphatase 4, regulatory subunit 1	2	0	3	1.801579
82	68185	Chchd8	coiled-coil-helix-coiled-coil-helix domain containing 8	2	0	3	1.800265
83	16372	Irx2	iroquois homeobox 2	2	0	3	1.797388
84	26885	Casp8ap2	caspase 8 associated protein 2	2	0	3	1.791817
85	56440	Snx1	sorting nexin 1	2	0	3	1.785254
86	72349	Dusp3	dual specificity phosphatase 3	2	0	3	1.78234
87	19335	Rab23	RAB23, member RAS oncogene family	2	0	3	1.77411
88	225849	Ppp2r5b	protein phosphatase 2, regulatory subunit B', beta	2	0	3	1.770982
89	26891	Cops4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	2	0	3	1.767117
90	237500	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	2	0	2	1.766351
91	228866	Pcif1 (F730014I05Rik)	PDX1 C-terminal inhibiting factor 1	2	0	3	1.743279
92	68239	Krt42 (2410039E07Rik)	keratin 42	2	0	3	1.734422
93	108927	Lhfp	lipoma HMGIC fusion partner	2	0	3	1.715071
94	12816	Col12a1	collagen, type XII, alpha 1	2	0	3	1.713318
95	65246	Xpo7	exportin 7	2	0	3	1.711696
96	19210	Ptdss1	phosphatidylserine synthase 1	2	0	3	1.709867
97	15902	Id2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	2	0	3	1.706014
98	269328	Muc15	mucin 15, cell surface associated	2	0	2	1.70209
99	216119	Ybey (A130042E20Rik)	ybeY metallopeptidase (putative)	2	0	2	1.694963
100	69612	Kansl2	KAT8 regulatory NSL complex subunit 2	2	0	2	1.690599
101	66184	Rps4y2 (1110033J19Rik)	ribosomal protein S4, Y-linked 2	2	0	3	1.674935
102	18203	Ntan1	N-terminal asparagine amidase	2	0	3	1.668233
103	268564	Zbtb1	zinc finger and BTB domain containing 1	2	0	3	1.64775
104	216453	Rdh19	retinol dehydrogenase 1 (all trans)	2	0	3	1.646191
105	75782	Lca5 (4930431B11Rik)	Leber congenital amaurosis 5	2	0	3	1.645394
106	26914	H2afy	H2A histone family, member Y	2	0	3	1.637421
107	67619	Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	2	0	3	1.637211
108	66839	0610009O20Rik	RIKEN cDNA 0610009O20 gene	2	0	3	1.633545
109	319178	Hist1h2bb	histone cluster 1, H2bb	2	0	3	1.631491
110	80838	Hist1h1a	histone cluster 1, H1a	2	0	3	1.624471
111	68449	Tbc1d10b	TBC1 domain family, member 10B	2	0	3	1.622633

Candidates for negative regulators of oncogenic growth (Fisher's)

Rank	entrez#	Gene Symbol	Gene name	enriched shRNAs	depleted shRNAs	no change shRNAs	average Fold Change
112	380785	Begain (BM948371)	brain-enriched guanylate kinase-associated homolog (rat)	2	0	3	1.618538
113	330657	Prss53 (BC039632)	protease, serine, 53	2	0	3	1.618312
114	20688	Sp4	Sp4 transcription factor	2	0	3	1.617765
115	106393	Srl	sarcalumenin	2	0	3	1.614678
116	17913	Myo1c	myosin IC	2	0	3	1.614225
117	52840	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	2	0	2	1.598134
118	67103	Ptgr1 (Ltb4dh)	prostaglandin reductase 1	2	0	3	1.573039
119	228361	Ambra1 (D030051N19Rik	autophagy/beclin-1 regulator 1	2	0	3	1.568679
120	70454	Cenpl	centromere protein L	2	0	2	1.566376
121	232314	Ppp4r2	protein phosphatase 4, regulatory subunit 2	2	0	3	1.561153
122	71908	Cldn23	claudin 23	2	0	2	1.555402
123	19691	Recql	RecQ protein-like (DNA helicase Q1-like)	2	0	3	1.547136
124	228136	Zdhhc5	zinc finger, DHHC-type containing 5	2	0	3	1.542208
125	67938	Myl12b (Mylc2b)	myosin, light chain 12B, regulatory	2	0	3	1.539765
126	12176	Bnip3	BCL2/adenovirus E1B 19kDa interacting protein 3	2	0	3	1.538725
127	67006	Cisd2 (1500009M05Rik)	CDGSH iron sulfur domain 2	2	0	3	1.512992
128	71306	Mfap3l	microfibrillar-associated protein 3-like	2	0	3	1.503454

Supplementary Table 5. Sequence of shRNA constructs used in the study

Gene symbol	shRNA name	cloneId	shRNA target sequence
Anapc5	shAnapc5#2180	TRCN0000088403	GCCAAGAACTACTTTGCACAA
Anapc5	shAnapc5#308	TRCN0000088404	GCCCAGATATTACACTGTCAA
Anapc5	shAnapc5#748	TRCN0000088405	GCCGCTTTGTTGAAGAATGAT
Anapc5	shAnapc5#847	TRCN0000088406	GCTCATTACCTCAGCTACTTA
Anapc5	shAnapc5#412	TRCN0000088407	CTGAAGGATATGGAACAATTT
Hras1	shHras1#88	TRCN0000034379	GACGAGTATGATCCCACTATA
Hras1	shHras1#249	TRCN0000034380	CATCAACAACACCAAGTCCTT
Hras1	shHras1#267	TRCN0000034381	CTTCGAGGACATCCATCAGTA
Hras1	shHras1#304	TRCN0000034382	CGGGTGAAAGATTCAGATGAT
Hras1	shHras1#147	TRCN0000034383	GACATGTCTACTGGACTACTT
Mllt6	shMllt6#4294	TRCN0000126604	CCTGTCTGTCTATCTGTCATT
Mllt6	shMllt6#1916	TRCN0000126605	GCAGGCATCTATACCAGTAAT
Mllt6	shMllt6#1076	TRCN0000126606	CGAAAGGACAAAGAACGCCTT
Mllt6	shMllt6#1269	TRCN0000126607	GCCTGAGTCATAAGGACAAGA
Mllt6	shMllt6#1271	TRCN0000126608	CTGAGTCATAAGGACAAGAAA
Ctnnb1	shCtnnb1#3056	TRCN0000012688	GCGTTATCAAACCCTAGCCTT
Ctnnb1	shCtnnb1#2001	TRCN0000012689	CCATTGTTTGTGCAGTTGCTT
Ctnnb1	shCtnnb1#450	TRCN0000012690	GCTGATATTGACGGGCAGTAT
Ctnnb1	shCtnnb1#594	TRCN0000012691	CCATCACAGATGTTGAAACAT
Ctnnb1	shCtnnb1#1174	TRCN0000012692	CCCAAGCCTTAGTAAACATAA
Mllt6 (human)	shMllt6#926	custom generated	AGCCATAGCCTGAGTCATAAA
Mllt6 (human)	shMllt6#220	custom generated	GCATTGAAGAGGACTGATAAT
Ctnnb1 (human)	shCtnnb1#2708	custom generated	GGGAGTGGTTTAGGCTATTTG
Ctnnb1 (human)	shCtnnb1#1541	custom generated	TCTAACCTCACTTGCAATAAT