

Additional file 2: Supplementary Table S1. List of sgRNA sequences used in this study.

sgRNA	targeted sequence (5' - 3')	Reference
VEGFA	GATGTCTGCAGGCCAGATGA	15
PRNP	GCAGTGGTGGGGGGCCTTGG	15
HEK3	GTCAACCAGTATCCCGGTGC	15
HEK4	GGCACTGCGGCTGGAGGTGG	15
RNF2	GTCATCTTAGTCATTACCTG	15
TRAC	AGAGTCTCTCAGCTGGTACA	15
EMX1	GAGTCCGAGCAGAAGAAGAA	15
RUNX1	GCATTTTCAGGAGGAAGCGA	15
BCR	TATCCGAGGCACGTTAAGGG	10
ABL1	AGCCGCTCGTTGGA ACTCCA	21
DNMT1	GATTCCTGGTGCCAGAAACA	15
ERG1	GTATTTGTTGCATGAGCTCC	14
TMPRSS2	GGGCTGACCTCCTAGGCCAT	14
TOP3B	GGTCTCTCCTACCTCTAGAG	14
TNRC6C	AGTTCCAGAAGATGCCGCTT	14
EML4	GACCTGAACAGCAAGTTTGT	6
ALK	GGCCTTGCTGAAACTTCCTT	6
chr11 16.8MB Knock out-HBB	CACGTTACCTTGCCCCACA	7
chr11 16.8MB Knock out-FANCH	GGGGTCCCAGGTGCTGACGT	7
VEGFA-misaligned sgRNA	ATGTACAGAGAGCCCAGGGC	15
PRNP-misaligned sgRNA	GCATGTTTTACGATAGTAA	15
chr3 imaging sgRNA	TGATATCACAG	23
chr13 imaging sgRNA	ACCATTCTTC	23
SPACA7	GGATGTAGGAGTCAGTCCAG	This study
PPP1R2	GTTAGCTGACTTGAAGAAAA	This study
chr11-HBB-pegRNA-l-secl insertion	CACGTTACCTTGCCCCACAGT TTTAGAGCTAGAAATAGCAAGTT AAAATAAGGCTAGTCCGTTATCAA CTTGAAAAAGTGGCACCGAGTCG GTGCATTACCCTGTTATCCCTAGGG GCAAGGTGAAC	7
chr11-FANCH-pegRNA-l-secl insertion	GGAATCCCTTCTGCAGCACCGTTTT AGAGCTAGAAATAGCAAGTTAAAT AAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCTAGGG ATAACAGGGTAATGCTGCAGAAGGGAT	7

Additional file 2: Supplementary Table S2. List of primer sequence used in this study.

Primer name	Sequence (5' - 3')
BCR/ABL1-BCR-F	GGGCTGGTTGCTTCACAAAG
BCR/ABL1-ABL1-R	CATTCCCCATTGTGATTATAGCCTAAGACC
ABL1/BCR-BCR-F	CCAAACTAAGAGATGGGCAGAACTG
ABL1/BCR-ABL1-R	CCCTTCAGCGGCCAGTAGCA
VEGFA/PRNP-VEGFA-F	AGGAACAAGGGCCTCTGTCT
VEGFA/PRNP-PRNP-R	TTGTGATATTGACGCAGTCGTGC
HEK3/HEK4-HEK3-F	ACGCCTGTGATGGGCTAATTG
HEK3/HEK4-HEK4-R	TTCAACCCGAACGGAGACAC
RNF2/TRAC-RNF2-F	TGCAGACAAACGGAACCTCAAC
RNF2/TRAC-TRAC-R	AAGGAAACAGCCTGCGAAGG
Chr11 KO-HBB-F	CACGTTGCCCAGGAGCTGTG
Chr11 KO-FANCF-R	GCAGAGAGTCGCCGTCTCCA
HEK3/RUNX1-HEK3-F	ACGCCTGTGATGGGCTAATTG
HEK3/RUNX1-RUNX1-R	ATCACCAACCCACAGCCAAG
HEK4/TRAC-HEK4-F	CCAGTGGTTCAATGGTCATCCCA
HEK4/TRAC-TRAC-R	AAGGAAACAGCCTGCGAAGG
RUNX1/TRAC-RUNX1-F	GACAAAGTTCTCACGCACCGAC
RUNX1/TRAC-TRAC-R	AATGGATAAGGCCGAGACCAC
HEK4/RUNX1-HEK4-F	CCAGTGGTTCAATGGTCATCCCA
HEK4/RUNX1-RUNX1-R	GAATGCAAACCACAGGGTTTCG
EMX1/DNMT1-EMX1-F	GGGGCCCCTAACCTATGTA
EMX1/DNMT1-DNMT1-R	GGGACCGTTTGAGGAGTGTT
ERG/TMPRSS2-ERG-F	GGCAGCTTGAGACACTGGT
ERG/TMPRSS2-TMPRSS2-R	GCAGTATGACATGGCCAGAGT
TOP3B/TNRC6C-TOP3B-F	CCTGTAACACATAAACGACCGTG
TOP3B/TNRC6C-TNRC6C-R	CTCCAAGCATGGCCACTCT
EML4/ALK-EML4-F	AGCTCTGAACCTTTCCATCATACT
EML4/ALK-ALK-R	GTGTCCTCCCTCTCGTGGTAA
VEGFA/PRNP-primer insertion-VEGFA-F	AGGAACAAGGGCCTCTGTCT
VEGFA/PRNP-primer insertion-primerV1	CTCTGACAATGTGCCATCTGGAG
RNF2/TRAC-primer insertion-primerT1	CCCACAGATATCCAGAACCCTG
RNF2/TRAC-primer insertion-TRAC-R	AAGGAAACAGCCTGCGAAGG
VEGFA-misaligned donor-VEGFA-F	GTCTGGGCTTGGGCTGATAGAA
VEGFA-misaligned donor-PRNP-R	TCATCTTAACGTCGGTCTCGGT

Additional file 2: Supplementary Table S3. Representative homologous arm sequence.

Homologous arm name	Homologous arm sequence
BCR/ABL1 Translocation	TGACGGGGCTTCGCCCATCTGGCATCTTTCTTTCT GCATCAAGGACTGCAAACCCGTTGGGCAGTGCCA GGGGATACCGAGGTGGATGTCCAGGCTTGGAGTG CCCAACTGATCAGCAGCATCTGCCCCAGGAATGG CAGGGGCAGGGGCAAAGCACAGGCATCTATCATC CTGCCTTAGCCACCATCAAGCCACCTCCCAGTTCC AACGAGCGGCTTCACTCAGACCCTGAGGCTCAAA GTCAGATGCTACTGGCCGCTGAAGGGCTTCTGGA AGAGAAAGGGGGGAACAGAAAAAAGAAAAAGGAA GAGAAAATTGGGAGAAAAAATTAGTTTTATTCTCAG AAGCAAAAATATTTGTGTTTCCAACATTACACATTCT TATTTTCATTTCTTAACATC
ABL1/BCR Translocation	GCTGCTCCTTTAACGAGCAAAGGGTGGTAGGTCA AACCGCAATTCCCAGATTTCTATCTCCTGCAACCAC CACTAGCTGCCCACAACCCTTTTACCTTTAGTTATG CTTAGAGTGTTATCTCCACTGGCCACAAAATCATAC AGTGCAACGAAAAGGTTGGGGTCATTTTCACTGG GTCCAGCGAGAAGGTTTTCTTGTTAACGTGCCT CGGATAGAAAGCTCTGAGTGAAGGGGTGCTGGTC AGACTCACGGTGACTTTTCTAGAGTCATTAGTCCT CCACCTTGCTTTGCAGCTAAGGCACCCAGGTGAC CCCTCCTCAATGAGCAAGTGCCCCCTCCACCAGGG CGAGGTCCTGGGGAGGATGCAGATCCAGGCCCT GCCTTTGTGAAGCAACCA
VEGFA/PRNP Translocation (I-SceI insertion)	ACAGTGCATACGTGGGCTCCAACAGGTCCTCTTCC CTCCCACTACTGACTAACCCCGGAACCACACAG CTTCCCGTTCTCAGCTCCACAACTTGGTGCCAAA TTCTTCTCCCCTGGGAAGCATCCCTGGACACTTCC CAAAGGACCCCACTACTCCAGCCTGTTGGCTGC CGCTCACTTTGATGTCTGCAGGCCAGAAATTACCT GTTATCCCTATGGCGGCTACATGCTGGGAAGTGCC ATGAGCAGGCCCATCATACATTTGGCAGTGACTA TGAGGACCGTTACTATCGTGAAAACATGCACCGTT ACCCAACCAAGTGACTACAGGCCCATGGATGAG TACAGCAACCAGAACAACTTTGTGCACGACTGCGT CAATATCACAATCAAGCAGCACACGGTCACCACAA

RNF2/TRAC Translocation (I-SceI insertion)	CTTCATTGAGATTAGATTTCAACGTAGGAATTTTGG TGGGACACATACATTAGACCATAGCACTTCCCTT CCAAATACTAAAATTGTTTTCTCTCTTTATTTTC CAGCAATGTCTCAGGCTGTGCAGACAAACGGAAC TCAACCATTAAGCAAAACATGGGAACTCAGTTTATA TGAGTTACAACGAACACCTCAGATTACCCTGTTATC CCTAACCAAGCTGAGAGACTCTAAATCCAGTGACAA GTCTGTCTGCCTATTCACCGATTTTGATTCTCAAAC AAATGTGTCACAAAGTAAGGATTCTGATGTGTATAT CACAGACAAAACGTGTGCTAGACATGAGGTCTATGG ACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAA CAAATCTGACTTTGCATGTGCAAACGCC
HEK3/HEK4 Translocation (I-SceI insertion)	GCAATTAGTCTATTTCTGCTGCAAGTAAGCATGCAT TTGTAGGCTTGATGCTTTTTTCTGCTTCTCCAGCC CTGGCCTGGGTCAATCCTTGGGGCCAGACTGAG CACGTGATGGCAGAGGAAAGGAAGCCCTGCTTCC TCCAGAGGGCGTCGCAGGACAGCTTTTCCTAGAC AGGGGCTAGTATGTGCAGCTCCTGCAATTACCCTG TTATCCCTATGGGGGTTAAAGCGGAGACTCTGGTG CTGTGTGACTACAGTGGGGGCCCTGCCCTCTCTG AGCCCCGCCTCCAGGCCTGTGTGTGTGTCTCCG TTCGGGTTGAAAGGAGCCCGGGAAAAAGGCCCA GAAGGAGTCTGGTTTTGGACGTCTGACCCACCC CTCCCGCTTAGGGCTTCTGATCCCCAGGGTGATT TCA
VEGFA/PRNP Translocation (VEGFA primer insertion)	ACAGTGCATACGTGGGCTCCAACAGGTCCTCTTCC CTCCAGTCACTGACTAACCCCGGAACCACACAG CTTCCCGTTCTCAGCTCCACAACTTGGTGCCAAA TTCTTCTCCCCTGGGAAGCATCCCTGGACACTTCC CAAAGGACCCAGTCACTCCAGCCTGTTGGCTGC CGCTCACTTTGATGTCTGCAGGCCAGACTCCAGAT GGCACATTGTCAGAGTGGCGGCTACATGCTGGGA AGTGCCATGAGCAGGCCCATCATACATTTCGGCAG TGACTATGAGGACCGTTACTATCGTGAAAACATGC ACCGTTACCCCAACCAAGTGTAAGGAGGCCCATG GATGAGTACAGCAACCAGAACAACCTTGTGCACGA CTGCGTCAATATCACAATCAAGCAGCACACGGTCA CCACAA
RNF2/TRAC Translocation (TRAC primer insertion)	CTTCATTGAGATTAGATTTCAACGTAGGAATTTTGG TGGGACACATACATTAGACCATAGCACTTCCCTT CCAAATACTAAAATTGTTTTCTCTCTTTATTTTC CAGCAATGTCTCAGGCTGTGCAGACAAACGGAAC TCAACCATTAAGCAAAACATGGGAACTCAGTTTATA

	TGAGTTACAACGAACACCTCAGCCCACAGATATCC AGAACCCTGACCAGCTGAGAGACTCTAAATCCAGT GACAAGTCTGTCTGCCTATTCACCGATTTTGATTCT CAAACAAATGTGTCACAAAGTAAGGATTCTGATGT GTATATCACAGACAAAACCTGTGCTAGACATGAGGT CTATGGACTTCAAGAGCAACAGTGCTGTGGCCTG GAGCAACAAATCTGACTTTGCATGTGCAAACGCC
Chr11 HBB/FANCF 16.8MB Knock out	GGTCCAAGGGTAGACCACCAGCAGCCTAAGGGTG GGAAAATAGACCAATAGGCAGAGAGAGTCAAGTGC CTATCAGAAACCCAAGAGTCTTCTCTGTCTCCACA TGCCCAGTTTCTATTGGTCTCCTTAAACCTGTCTTG TAACCTTGATACCAACCTGCCAGGGCCTCACCAC CAACTTCATCCACGTTACCTTGCCCCGCTGCAGA AGGGATTCCATGAGGTGCGCGAAGGCCCTACTTC CGCTTTCACCTTGGAGACGGCGACTCTCTGCGTA CTGATTGGAACATCCGCGAAATGATACGCCTCTCT GCAATGCTATTGGTCGAAATGCATGTCAATCTCCCA GCGTCTTTATCCGTGTTCTTGAAGTCTGGGCAACT TAAAGCCCTAATACTTT
VEGFA/PRNP Translocation (I-SceI insertion) HA-misaligned 50bp	AGGGCCTCTGTCTGCCAGCTGCCTCCCCCTTTG GGTTTTGCCAGACTCCACAGTGCATACGTGGGCT CCAACAGGTCCTCTTCCCTCCCAGTCACTGACTAA CCCCGGAACCACACAGCTTCCCGTTCTCAGCTCC ACAACTTGGTGCCAAATCTTCTCCCCCTGGGAAG CATCCCTGGACACTTCCCAAAGGACCCCATTACCC TGTATCCCTAGCAGTGAAGTATGAGGACCGTTACTA TCGTGAAAACATGCACCGTTACCCCAACCAAGTGT ACTACAGGCCCATGGATGAGTACAGCAACCAGAAC AACTTTGTGCACGACTGCGTCAATATCACAATCAA GCAGCACACGGTCACCACAACCACCAAGGGGGA GAACTTCACCGAGACCGACGTTAAGATGATGGAG CGCGT
VEGFA/PRNP Translocation (I-SceI insertion) HA-misaligned 100bp	CTGGCCTCAGTTCCTGGCAACATCTGGGGTTGG GGGGGCAGCAGGAACAAGGGCCTCTGTCTGCCC AGCTGCCTCCCCCTTTGGGTTTTGCCAGACTCCA CAGTGCATACGTGGGCTCCAACAGGTCCTTTCC CTCCAGTCACTGACTAACCCCGGAACCACACAG CTTCCCGTTCTCAGCTCCACAACTTGGTGCTTA CCCTGTTATCCCTAAACCAAGTGTACTACAGGCC ATGGATGAGTACAGCAACCAGAACAACTTTGTGCA CGACTGCGTCAATATCACAATCAAGCAGCACACGG TCACCACAACCACCAAGGGGGAGAACTTCACCGA

	GACCGACGTTAAGATGATGGAGCGCGTGGTTGAG CAGATGTGTATCACCCAGTACGAGAGGGAATCTCA GGCCTAGTACC
VEGFA/PRNP Translocation (I-Scel insertion) HA-misaligned 200bp	GTGGGAGCTCTGGGCAGCTGGCCTACAGACGTTG CTTAGTGCTGGCGGGTAGGTTTGAATCATCACGCA GGCCCTGGCCTCCACCCGCCCCCACCAGCCCCC TGGCCTCAGTTCCCTGGCAACATCTGGGGTTGGG GGGGCAGCAGGAACAAGGGCCTCTGTCTGCCCA GCTGCCTCCCCCTTTGGGTTTTGCCAGACTCCATT ACCCTGTTATCCCTACCACCAAGGGGGAGAACTTC ACCGAGACCGACGTTAAGATGATGGAGCGCGTGG TTGAGCAGATGTGTATCACCCAGTACGAGAGGGAA TCTCAGGCCTATTACCAGAGAGGATCGAGCATGGT CCTCTTCTCCTCTCCACCTGTGATCCTCCTGATCT CTTTCCTCATCTTCCTGATAGTGGGATGAGGAAGG TCTTCC