

**Supplementary Figure 1. LS-iPSC formation. a**, Schematic representation of iPSC generation. **b**, Typical image of a TRA-1-81 positive colony growing in the plate three weeks after infection.

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HES2 **BJ-iPSB5** L1-iPS1 L2-iPS6 46,XX 46,XY 46,XX 46,XY EMB BMD 100 25 71 Х ) ]c K 71 1003 t and 38 11 21 21 81 55 31 11 11 11 11 Iζ 11 12 11 28 76 28 38 88 38 ĺĆ 38 0-off 0-off 31 11 â Â ц× 8.8 28 Å1 88 តិ និ őă 8.6 66 88 66 śś ы 6 н à é âź đđ 36 8< 38 ð í 85 88 1 8.5 8,8 4.4 ε¢. 2.3 .... 3.5 \*\* ā, d 1 3 38 88 8 8 6 8 ş

Supplementary Figure 2. LS–iPSC lines are derived from their parental fibroblasts and maintain normal karyotypes. a, We PCR amplified across three discrete genomic loci containing highly variable numbers of tandem repeats with different primer sets (D10S1214, D17S1290, and D21S2055). The resulting amplification patterns confirmed that each iPSC line is derived from its indicated parental fibroblast. **b**, G-banding of HES2 cell line, wild-type iPS clone BJ-iPSB5, and LS-iPSC lines (one clone of each patient) demonstrates normal diploid chromosomal contents.



Supplementary Figure 3. *PTPN11* T468M mutation analysis in LS-iPSC and fibroblasts. a, The T468M point mutation in exon 12 of one allele of *PTPN11* gene was verified by DNA sequencing. b, We amplified by RT-PCR a 1.2 Kb region containing the mutation sequence and the DNA was digested with BsmFI, an enzyme which cuts the 5'-GGGAC(N)<sub>10</sub>-3' sequence contained in wt allele but not in the mutant. In all the LS samples an undigested 1.2 Kb band was observed.



**Supplementary Figure 4. Retroviral transgenes integration in iPSC. a,** Transgenespecific primers were used to amplify *OCT4*, *SOX2*, *KLF4* and *c-MYC*. Three LSderived iPSC lines from each patient were analyzed, and HES2 cells and parental fibroblasts were used as negative controls. **b**, Southern blot analyses of BgI-II digested gDNA extracted from HES2 cells, parental fibroblasts and iPSC, using DIG-labeled DNA probes against *OCT4*, *SOX2*, *KLF4* and *c-MYC*. Retrovirally-inserted transgenic copies of these genes are indicated by asterisks and the number of detected bands is shown at the bottom. The parental fibroblasts and HES2 cells share bands in common with all the iPSC lines (arrowheads), which reflect the endogenous loci (including potential pseudogenes).



Supplementary Figure 5. Retroviral transgenes silencing in iPSC lines. a, Transgene-specific primers were used to determine *OCT4*, *SOX2*, *KLF4* and *c-MYC* expression. b, qPCR analysis of retroviral transgene (Tg) expression. Results were normalized against  $\beta$ -*ACTIN* and plotted relative to the expression levels in transfected GP2 cells.



**Supplementary Figure 6. LS-iPSC expressed markers common to pluripotent cells. a**, SSEA4 expression was determined by flow cytometry in two iPSC lines derived from two LEOPARD syndrome (LS) patients (L1-iPS1, L1-iPS13, L2-iPS6 and L2-iPS16), and a wt-iPSC line derived from BJ fibroblasts (BJ-iPSB5). HES2 cell line was used as positive control. **b**, HES2 and iPSC were grown on MEFs, and the day of the immunocytochemistry cells were fixed and stained for the pluripotency markers, alkaline phosphatase (AP), TRA-1-81, TRA-1-60, NANOG and OCT4. Nuclei were stained with DAPI.



Supplementary Figure 7. Gene expression analysis. a, qPCR was used to evaluate the expression of hGDF3, hDPPA4, hREX1 and hTERT in two LS-iPSC lines from each patient and compared to their parental fibroblasts. HES2 cells were used as positive control of pluripotency gene expression. PCR reactions were normalized against  $\beta$ -ACTIN and represented relative to the expression in HES2 cells. b, Two sample comparison plots of log 2 expression values with the line Y=X as a basis for comparison along with Y = X + - 1 or 2 lines, representing 2-fold and 4-fold expression changes, respectively. In each scatter-plot the position of SOX2, LIN28 and OCT4 transcription factors is indicated.



**Supplementary Figure 8.** *In vitro* differentiation of iPSC lines. **a**, Day 8 EBs of HES2, BJ-iPSB5, L1-iPS13 and L2-iPS6 cells. **b**, After 16 days of differentiation, cells were stained with SMA, GFAP and Vimentin antibodies. Scale bar, 100 µm.





Supplementary Figure 9. LS-iPSC differentiate into hematopoietic cells. a, Red EBs, an indication of erythrocyte development, can be observed in L1-iPSC plates 14 days after differentiation. Scale bar, 100  $\mu$ m. b, CD41, CD45, CD11b, CD71 and CD235a hematopoietic markers were analyzed by flow cytometry in EBs derived from HES2 and L1-iPSC, 18 days after induction of hematopoietic differentiation.

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Supplementary Figure 10. Characterization of wt S3-iPS4 and L2-iPSC. a, The iPSC have the four transgenes integrated in their genome. b, Tg silencing analysis. c, Fingerprinting analysis of the iPSC lines using their parental fibroblasts and HES2 cells as controls.



**Supplementary Figure 11. Pluripotency of S3-iPS4 and L2-iPSC. a-b,** S3-iPS4, L2-iPS10 and L2-iPS20 expressed pluripotency markers. **c**, The iPSC differentiated into derivatives of the three germ layers.



Supplementary Figure 12. Disruption of MAPK activation upon bFGF stimulation in LS-iPSC. a, FGF receptors expression analysis by RT-gPCR in LS-iPSC and fibroblasts compared to HES2. b, L1-iPS1, L1-iPS6 and HES2 cells were serum- and bFGF-starved overnight. The following day, the cells were treated with bFGF for 10 minutes (+) or not (-). Total ERK1/2 and p-ERK1/2 expression was analyzed by immunobloting of total lysates. c, Basal p-ERK1/2 was guantified in each sample and compared to HES2C (top left panel). The relative increase of p-ERK1/2 level upon stimulation was quantified in each sample (top right and lower panels). All the p-ERK1/2 values were normalized to their corresponding total ERK1/2 values.

## Table 1. Primer sets for PCR reactions.

Percention     Sequences (5 to 3)       D195125     F     ACAGAACCAATAGGCTATCTATC       R     TACAGTAAATCACTTGGTAGGAGA       D1951214     F     ATTGCCCCAAAAACTTITTTG       R     TTGAAGACCAACTTGTGGGAGA       D1751290     F     GCAAACAGCAGTCGGGAAG       QPCR for endogenous pluripotent genes     GGAAACAGTTTAAATGGCCAA       GENE     Accesion     Position       1293-1316     R     GGAACAGGTTGAGCAGGAGAG       NM_002701     1194-1217     123     F       ACCTGGAGGTTGAGAGGAGAGGAGAGGA     R     IGGAACTCACCTCCCCCCAACCA       NANOG     NM_024865     1120-1141     190     F     CCTGAAGAGCAGTGTAGAGGAGAGAGA       DPPA4     N18189     1128-1148     223     F     AGTCCTGTGCTTGCTTGCACCA       MD018189     1128-1148     223     F     AGTCACTGAGAGTAGAGATCACAGAGTGGAGAGA       NESRB     NM 004452     1400-1423     18     F     GTACATCCAGGAGTATAGAGGCTGT       NSOX2     NM 004452     1400-1423     150     F     AGAGAGGCAAACGGAAGAGAAGAGAGAGA       NGDF3     NM 020634	DCD for fingerminting					
D2132003     PACAGRACONTING       D1051214     F     ACAGIAAATCACTTGGTAGGAGA       D1051214     F     ATTGCCCCAAAACTITTIG       D1751290     F     GCCAACAGAGCACGACTGTCG       D1751290     F     GCCAACAGAGCACAACTGTC       QPCR for endogenous pluripotent genes     GGENE     Accresion     Position       GENE     Accession     Position     Size     Sequences (5'to 3')       hOC74     NM_002701     1198-1316     R     TGAACTTCACCTTCCCTCCACACCA       hNANOG     NM_024865     1122-1141     190     F     CCTGAAGACGTGTGAAGATGAGG       hDPPA4     NM_018189     1128-1148     223     F     AGCGCTGTAGAGATGAGGAGGAGGA       hESRB     NM 004452     1400-1423     181     F     GTACATCGAGGAGAAGAAAGAGGAGGAGA       hSX2     NM_003106     108-132     150     F     AGAAGAGGAGAAACACGAGAGAAAAGAAGGGAGAGA       hREX1     NM_174900     1026-1047     267     F     AAGAGCATCACACCTAAGAAGAAGAGAGAGAGA       hGDF3     NM_020634     829-850     231     F     CACGGTCAACGCAAGAGAAGAGAGAGAGAGA </td <td colspan="4"></td> <td></td> <td></td>						
D1051214     F     ATTGCCCCAAACTITITTG       ITTGARGACCATT     R     TTGARGACCAAACTITITTG       ITTGARGACCAGTCTGGGAAG     F     GCCAACAGGCAGGCAAGCATGGCAA       ITTGARGACCAGTTAAATGGCCAA     R     GGAAACAGTTAAATGGCCAA       GENE     Accesion     Position     Size     Sequences (5'to 3')       hOC74     NM_002701     1194-1217     123     F     AACCTGGAGTTGACACAGATGGCAA       hOC74     NM_024865     1120-1141     190     F     CCTGAAGAGGTGTGAAGATGAG       hNANOG     NM_024865     1128-1148     223     F     AGCTGCAGGATTAGAGGTGCAACAGATGAG       hDPPA4     NM_018189     1128-1148     223     F     AGGTGCTGTTGCTTGTGGAGT       hDPPA4     NM_01452     1400-1423     181     F     GTACATCGAGAGTGCAACAGGAGTGGAGT       hSDX2     NM_004452     1400-1423     181     F     GACAGGAGAGAAGAGAAAGGAAGGAGAGA       hSDX2     NM_004452     1400-1423     181     F     GAGAGAGGAGAGAAAAGGAAAGGAAGGAGAGA       hCDF3     NM_004352     1400-1423     181     F     GAGAGAGGAGAAAACTGAAAGGGAGAGA </td <td colspan="4"></td> <td></td> <td></td>						
DIOSIZITY     Initial Construction       DITS1290     F     R     CRACAGCAGCAGCTGTGGGAAG       DITS1290     F     GCCAACGAGCAAGCAGCGTG       R     GGAAACAGTAAATGGCCAA       gPCR for endogenous pluripotent genes     GGAAACAGTTAAATGGCCAGGGTTT       GENE     Accesion     Position     Size     Sequences (5'to 3')       hOC74     NM_002701     1194-1217     123     F     AACCTGGAGGTGGAAGGGGGGGGAGGGGGGGGGGGGGGG	D1061014					
D1751290     F     CCCAACAGACAGACTGTC       gPCR for endogenous pluripotent genes     GGAAACAGTTAAATGGCCAA       GENE     Accesion     Position     Size     Sequences (5'to 3')       hOC714     NM_002701     1194-1217     123     F     AACCTGGAGTTGGCCAGCGGTT       hOC74     NM_027465     1120-1141     190     F     CCTGAAGAGCTGCACCACCA       hNANOG     NM_024865     1120-1141     190     F     CCTGAAGAGCTGCACCACCACACA       hDPPA4     NM 018189     1288-1309     R     GGCGATTAGAGGCTCAACCATAC       hDPPA4     NM 018189     1330-1350     R     TGCACTGAAGCTGAGAGTGGAGC       hESRRB     NM 004452     1400-1423     181     F     GACACGAGAGAGAAGAAAGGAAAGGAAGGAAGA       hSOX2     NM 004452     1400-1423     181     F     GACACGAGAGAGAGAGAAAGGAAAGGAAGGAAGA       hESRRB     NM 004452     1400-1423     181     F     GACACGAGGAGAGAGAAAGAAAGGAAGGAAAG       hESX2     NM 0174900     1026-1047     267     F     AAAGCATTCACTGAGATTCATGAGGATCACAA       hREX1     NM 174900     1026-1047	01031214					
D1/151230     I     GGAAACAGREGACAGREGCAA       qPCR for endogenous pluripotent genes     GGAAACAGRETTAAATGGCCAA       GENE     Accesion     Position     Size     Sequences (5'to 3')       NOC74     NM_002701     1194-1217     123     F     AACCTGCAGTTGCCCAGCGGGTTT       1293-1316     R     TGAACTTCACCTTCCCCTCCAACCA     AAGTGCAAGAGAGGGGGGGGGAAGAGGGGGGGGGGGGGG	D1761200					
IR     Convector       gPCR for endogenous pluripotent genes     Genu       GENE     Accession     Position     Size     Sequences (5'to 3)       NOC74     NM_002701     1194-1217     123     F     AACCTGAGAGTTTGTGCCAGAGGTTT       NANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTGTGAAAGTGGG       NANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTTGCACACCATAC       hDPPA4     NM 018189     1128-1148     223     F     AGTGCTTGAGGTTGAAGGTGCCACCATAC       hESRRB     NM 004452     1400-1423     181     F     GTGACTGAGAGAGAGAGAGAGGCAGT       hSOX2     NM 003106     108-132     150     F     AGAGAGGAGAGAAGGGCAGAC       hSOX2     NM 003106     108-132     150     F     AGAGCAGCAGAGAGAGAGGCAGACA       hREX7     NM 174900     1026-1047     287     F     AAGGCATCCAAGGAAGGGAGACA       hRDF3     NM 020634     829-850     231     F     CACCGTCACCAGGAATGGAACG       hTFR7     NM 198253     31998-3220     115     F	D1731290					
gPCR for endogenous pluripotent genes     Size     Sequences (5 to 3')       GENE     Accession     Position     Size     F     AACCTGGAGTTTGTGCCAGGGTTT       h0C74     NM_002701     1194-1217     123     F     AACCTGGAGTTTGTGCCAGGGTTT       1293-1316     R     TGAACTTCACCTTCCCTCCAACCA     NM_0024865     1120-1141     190     F     CCTGAAGACGTGTGAAGATGAG       hDPPA4     NM 018189     1128-1148     223     F     AGTGCCTGTGTGTTGTGTGGAGAT       hDPPA4     NM 018189     1128-1148     223     F     AGTGCAGAGAGAGAGAGAGGAGGAGAGA       hESR7B     NM 004452     1400-1423     181     F     GTGCATGAAGGGAGAGAGAGAGAGAGAGAGAGAGA       hSDX2     NM 003106     108-132     150     F     AGAAGAGGAGAGAGAGAGAGAGAGAGAGAGA       hREX1     NM_174900     1028-1047     267     F     AAGAGAGGCAAACTGGAATGGAATGAGAC       hREX1     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       hGDF3     NM 020634     829-850     231     F     CAAGGCATGAAAGGGAGAGA       hFERT     NM_19						GGAAACAGTTAAATGGCCAA
GENE     Accesion     Position     Size     Sequences (5 to 3)       h0C74     NM_002701     1194-1217     123     F     AACCTGGAGTTTGTGCCAGGGTTT       1293-1316     R     TGAACTTCACCTTCCCTCCAACCA     1293-1316     R     TGAACTTCAACGTGTGAAGATGAG       hNANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTGTGAAGATGCC       hDPPA4     NM_018189     1128-1148     223     F     AGTGCCTGTTGTGAGAGT       hDPPA4     NM_01452     1400-1423     181     F     GTACATCGAGGATCTAGAGTGCAC       hESRRB     NM_003106     108-132     150     F     AGAGAGGGAAACTGAAACTGGAACAGGACAAA       hSOX2     NM_003106     108-132     150     F     AAAGCATCCACACAGGAAACTGAGAAGAAGAGGAAAA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTCATCATCATGGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGGAAACGAAACGAAC       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCATGGAATGGAAC       hF_GACTIN     NM_001101     1332-1353 <td>qPCR for en</td> <td>dogenous pluripo</td> <td>tent genes</td> <td></td> <td></td> <td></td>	qPCR for en	dogenous pluripo	tent genes			
h0C74     NM_002701     1194-1217     123     F     AACCTGGAGTTTGTGCCAGGGTTT       hNANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTGGAAGATGAG       hNANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTGCAACCATAC       hDPPA4     NM_018189     1128-1148     223     F     AGTGCCTGTTGCTTGTGAGATTGCAC       hESRRB     NM_004452     1400-1423     181     F     GTACATGAAGAGAAGAAGAGAGAAGAGAGAGAAGGAGAGAAGAA	GENE	Accesion	Position	Size		Sequences (5'to 3')
Image     1293-1316     R     TGAACTTCACCTTCCCTCCAACCA       hNANOG     NM_024865     1120-1141     190     F     CCTGAAGACGTGTGAAGATGAG       hDPPA4     NM 018189     1128-1148     223     F     AGTGCCTGTGCTTGTGGTT       hDPPA4     NM 018189     1128-1148     223     F     AGTGCCTGTGCTTTGTGAGT       hESRRB     NM 004452     1400-1423     181     F     GTACATCGAGGATTGCAC       hESRRB     NM 003106     108-132     150     F     AGAAGGGCAAACTGAGAAAGGGAGGAGA       hREX1     NM 174900     1026-1047     267     F     AAGCATCTCCTCATTCATGGAT       hGDF3     NM_020634     829-850     231     F     CAGGCTTAGAGAAACGGAAGAGAGAGAGA       hTERT     NM_198253     3198-3220     115     F     TGAAGCAGAAGACAGACGGGAATG       h.p.A.CTIN     NM_020101     1332-1353     169     F     TTTTTGGCTTGACTCAGGATT       hAGR for retroviral silencing     Size     Sequences (5'to 3')     GCCCTCAAAGTAGACGGAAACC       qPCR.Tg-pMX     F     CCCTCAAAGTAGACGGAAAACTGGACAGC     GCAGAGAGACAACACTGAGACGGACAC	hOCT4	NM_002701	1194-1217	123	F	AACCTGGAGTTTGTGCCAGGGTTT
hNANOG     NM_024865     1120-1141     190     F     CCTGAAGAGCGTGTGAAGAGTGAG       hDPPA4     NM_018189     1128-1148     223     F     AGTGCTGATGGGCTCCAACCATAC       hDPPA4     NM_018189     1128-1148     223     F     AGTGCCTGTTGCTTGTGAGT       hESRRB     NM_004452     1400-1423     181     F     GTACATCGAGATTGCAC       hESRRB     NM_003106     108-132     150     R     CAGTTTGACGCTATAGAAGGGCAG       hSOx2     NM_003106     108-132     150     F     AGAGAGGAGAGAGAGAGAGAAAAGAGAGAGAA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCAGGTTATTGAGATCAGGATCAAA       hAEX1     NM_020634     829-850     231     F     CACCGTCACCAGCAACTGAACAC       hTERT     NM_198253     3198-3220     115     T GAAGCACAACGCAGGAGAC     T       hFEACTIN     NM_001101     1332-1353     169     F     TTTTGCTTGACTTGAGCAGGAATG       hFA-ACTIN     NM_001101     1332-1353     169     F     CCTCAAAGCAAACGCAGGCAACAC       qPCR-Tg-hDX     F     CCCTCAAA			1293-1316		R	TGAACTTCACCTTCCCTCCAACCA
1288-1309     R     GCTGATTAGGCTCCAACCATAC       hDPPA4     NM_018189     1128-1148     223     F     AGTGCCTGTGTTCTTTGTGACT       hESRRB     NM_004452     1400-1423     181     F     GTACATCGAGGATTGCAC       hESRRB     NM_004452     1400-1423     181     F     GTACATCGAGGATTAGAAGTGCTG       hSOX2     NM_003106     108-132     150     F     AGAAGAGGAAAACTGAAAGGAAAGGAAGAA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCCCTCATCAGGTATTGAAGGTACAAA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCCCCAGCTATTCAAGGTATTGAGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCATATGAAA       h7ERT     NM_198253     3198-3220     115     F     TGAAAGCCAACCACAGAACCCAGGGAATG       h-β-ACT/IN     NM_001101     1332-1353     169     F     TTTTGGCATGAACAGCAAACGCAGAATG       qPCR for retroviral silencing     Size     Sequences (5'to 3')     GCCAGAGAGGCAAAATTGCACAC       qPCR.Tg-hOC74     F     R     GCGAGAAGGGCAAAAATGGAGCAGA     GCGAGAAGGGCAA	hNANOG	NM_024865	1120-1141	190	F	CCTGAAGACGTGTGAAGATGAG
hDPPA4     NM_018189     1128-1148     223     F     AGTGCCTGTTGCTTTGTGAGT       hESRRB     NM_004452     1400-1423     181     F     GTACATGAGATTGCAC       hESRRB     NM_004452     1400-1423     181     F     GTACATCGAGGATCTAGAGGCTGT       hSOX2     NM_003106     108-132     150     F     AGAGAGGGAAAGAAGAAGGGAAAGAAGGGAGAA       hREX1     NM_174900     1026-1047     267     F     AAACCATCTCCTCATTCATGGT       hGDF3     NM_020634     829-850     231     F     CACGTACAGAGAACGAGAACG       hGDF3     NM_020634     829-850     231     F     CACGCGTACCAGGAATCGAAATGGGAGC       hTERT     NM_198253     3198-3220     115     F     TGCAGGTAGCTAGGCAGAGAACGCAGGGAATG       h-g-ACTIN     NM_001101     1332-1355     169     F     TTTTGGCAGTCAGCTGAGCAGGAATG       h-g-RCTg-pMX     F     CCCTCAAAGTAGACGGAATG     F     CCCTCAAAGTAGACGGAATG       qPCR-Tg-h0C74     1479-1500     R     GCAAGGGAAAGGCAAAATCTGAA     GPCR-Tg-h0C74       qPCR-Tg-h0C74     1479-1500     R     GCCAG			1288-1309		R	GCTGATTAGGCTCCAACCATAC
Image: https://www.conversion.org/limits/c	hDPPA4	NM 018189	1128-1148	223	F	AGTGCCTGTTGCTTTGTGAGT
hESRRB     NM_004452     1400-1423     181     F     GTACATCGAGGATCTAGAGGCTGT       hSOX2     NM_003106     108-132     150     F     AGAAGAGGAGAGAAAAGGGAAAGGAAAGGAAAG       hSOX2     NM_003106     108-132     150     F     AGAAGAGGAGAGACAAAGGGAAAGGAAAGGAAAG       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTCATTCATGGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCAAATGGAAATGGAGAC       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCATTATA       hGDF3     NM_020634     829-850     231     F     TGACACCAGCAAATGGAAATGGAGAC       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGACAGCAGGAATG       h-β-ACT/N     NM_001101     1332-1353     169     F     TITTGGCTTGACCTGAGCAGGAATG       h-β-ACT/N     NM_001101     1332-1353     169     F     CCTCAAAGTAGACGCATC       qPCR-Tg-pMX     F     CCCTCAAAGTAGACGGCATC     G     GCAAGGGACAAATCTGAA       qPCR-Tg-hOCT4     157     R <td< td=""><td></td><td>_</td><td>1330-1350</td><td></td><td>R</td><td>TGCACTGAACTGAGATTGCAC</td></td<>		_	1330-1350		R	TGCACTGAACTGAGATTGCAC
Instruction     Instruction     R     CAGTTTGACGCTATAGAAGTGCTG       hSOX2     NM_003106     108-132     150     F     AGAAGAGAGAGAGAAAAGGGAGAGA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTCATTCATGGT       hREX1     NM_020634     829-850     231     F     CACGGTATTCAGGTATTTGACT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGGAAATGGGAGAC       hTERT     NM_198253     3198-3220     115     F     TGAAGCCAGGAAATGGGAGAC       h7ERT     NM_001101     1332-1353     169     F     TTTTTGGCTTGACTCAGCAGAGACGCAGAC       h-β-ACTIN     NM_001101     1332-1353     169     F     TTTTTGGCTTGACTAGCAGGAATG       h-β-ACTIN     NM_001101     1332-1353     169     F     CCCTCAAAGTAGAGCGCAATC       qPCR-Tg-pMX     F     CCCTCAAAGTAGACGGCAATT     CCCTGAAGCGCAAACC     GCAGGGAAAATCTGAA       qPCR-Tg-hOC74     157     R     GCGAGGGAAAATCTGAA     GPCR-Tg-hCAAG       qPCR-Tg-hSOX2     146     R     TTCAGCTCCTCATCAT     GCCTGGAAGAGCAAAATCTGAA <td>hESRRB</td> <td>NM 004452</td> <td>1400-1423</td> <td>181</td> <td>F</td> <td>GTACATCGAGGATCTAGAGGCTGT</td>	hESRRB	NM 004452	1400-1423	181	F	GTACATCGAGGATCTAGAGGCTGT
hSOX2     NM_003106     108-132     150     F     AGAAGAGGAGAGAGAAAGAAAGGAAAGGAGAGA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTATTCATGGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       hTERT     NM_198253     3198-3220     115     F     TGAAGCATGGAAATGGGAAGAC       h7ERT     NM_001101     1332-1353     169     F     TTTTTGGCTTGACCAGGAATG       h-β-ACTIN     NM_001101     1332-1353     169     F     CCCTCAAAGTAACAGC       qPCR for retroviral silencing     Size     Sequences (5'to 3')     GCAGGGAAACCTGGAAACCAC       qPCR-Tg-hOC74     157     R     GCGAGAAAGCAGAGAGCAAA     GCAGAGAGCAAAACCTGAA       qPCR-Tg-hcC74     157     R     GCGAGAAAGCAGGAAGGCAAA     GCAGGGACAG       qPCR-Tg-hC74     157     R     GCGAGGAAAGGCAAAATCTGAA     GPCR-Tg-hCAA       qPCR-Tg-hC74     291     R     AGGCTGCTGTCACATCAT     GCTTGCAAACCTACAGGGAGA			1557-1580		R	CAGTTTGACGCTATAGAAGTGCTG
NM_174900     233-257     R     GAGAGAGGCAAACTGGAATCAGGATCAAAA       hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTCATTGAGGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGGTATTGACT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGGCATTCATTA       1038-1059     R     GTAGAGCATGGAAATGGGAGAC     T     T     T       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGGAACGCAGGAATG       h.fEACT/N     NM_001101     1332-1353     169     F     TTTTGGCTTGACTCAGGATTACAAC       qPCR-Tg-pMX     R     GCAAGGGACTTCCTGTAACAAC     C     GCAAGGGACTTCCTGTAACAAC       qPCR-Tg-hOC74     1479-1500     R     GCCAGGAAGGCAAAATCTGAA     GCCCCTCAAAGTAGACGGCATC       qPCR-Tg-hOC74     157     R     GCGGAGAAGGCAAAATCTGAA     GCCCCCAGGACGCAGG       qPCR-Tg-hSOX2     146     R     TTCAGCTCCCTCAATCAT     GCGGAGAAGGCAGG       qPCR-Tg-hC/T4     168     R     GTGGACAACCTACAGGGAGGCAG     GCTGGCACCCAGGAACGACGGCAG       qPCR	hSOX2	NM 003106	108-132	150	F	AGAAGAGGAGAGAGAAAGAAAGGGAGAGA
hREX1     NM_174900     1026-1047     267     F     AAAGCATCTCCTCATTCATGGT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       1038-1059     R     GTAGAGCATGGAAATGGGAGAC     TATAA       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGAACGCAGGGAATG       h- <i>β</i> -ACT/N     NM_001101     1332-1353     169     F     TITTTGGCTTGACTCAGGATTT       h- <i>β</i> -ACT/N     NM_001101     1332-1353     169     F     TTTTTGGCTTGACTCAGGATTT       h- <i>β</i> -ACT/N     NM_001101     1332-1353     169     F     CCCTCAAAGTAGCAGCAGCAGCACC       qPCR-Tg-pMX     R     GCAAGGGACATTCCTGACTAGGATT     GCAAGGGACATC     GCCCTCAAGTAGACGGCATC       qPCR-Tg-hX     F     CCCTCAAAGTAGACGGCAACAC     GCCCTCCAAACTGCACACAC     GPCR-Tg-hX/F4     168     R     GTGGAGAAGACGGGCAAACATGAGAGGGCAGG       qPCR-Tg-hX/LF4     168     R     GTGGAGAAAGATGGGAGCAG     GCTTGCCAAACCTACAGGTG     F     CCCCCAGGGCCCCATAAT			233-257		R	GAGAGAGGCAAACTGGAATCAGGATCAAA
hGDF3     NM_020634     829-850     231     F     TGGGCTTTCAGGTTATTGACT       hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       1038-1059     R     GTGGAGCATGGAAATGGGAGAC     F     TAGAAGCCAGGAATGGGAGAC       hTERT     NM_198253     3198-3220     115     F     TGGAGCCAGGAAATGGGAGGGAGG       h-β-ACT/N     NM_001101     1332-1353     169     F     TTTTTGGCTTGACTCAGGATTT       m     1479-1500     R     GCAAGGGACTTCCTGTAACAAC     GCACGGCAAATCGGAAAT       qPCR-Tg-pMX     F     CCCTCAAAGTAGACGGCAAAT     GCAAGGGAAAATCTGAA       qPCR-Tg-h0C74     157     R     GCGAGAAGGCAAAATCTGAA       qPCR-Tg-hXZ     146     R     TTCAGCTCCGTCCCATCAT       qPCR-Tg-hSOX2     146     R     TTCAGCTCGGAGGAGAG       qPCR-Tg-hC/H     157     R     GCGAGAAGAAGATGGGAGCAG       qPCR-Tg-hSOX2     146     R     TTCAGCTCCCTCATCAT       qPCR-Tg-hC/H     252     F     CCCCCAGGGCCCCATT       PCR for retroviral integration     Size     Sequences (5'to 3')	hREX1	NM 174900	1026-1047	267	F	AAAGCATCTCCTCATTCATGGT
hGDF3     NM_020634     829-850     231     F     CACCGTCACCAGCTATTCATTA       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGAAACGCAGGAATG       hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGAACGCAGGAATG       h-β-ACTIN     NM_001101     1332-1353     169     F     TITTIGGCTTGACTCAGCAGGAATG       h-β-ACTIN     NM_001101     1332-1353     169     F     TITTIGGCTTGACTCAGCAGGAATG       h-β-ACTIN     NM_001101     1332-1353     169     F     TITTIGGCTTGACTCAGCAGGAATG       qPCR-for retroviral silencing     Size     Sequences (5'to 3')     F     CCCTCAAAGTAGACGGCATC       qPCR-Tg-h/OC74     157     R     GCGAGAAGGCAAAATCTGAA     GPCR-Tg-h/OC74     168     R     TTGGCTCGCTCCATCAT       qPCR-Tg-h/KLF4     168     R     GTGGAGAAAGATGGGAGCAG     GPCR-Tg-h/CLAT     PCR-Tg-h/CLAT     Sequences (5'to 3')       PCR-Tg-h/KLF4     168     R     GTGGCCCAAACCTACAGGTG     GCTGCCCAAACCTACAGGTG       PCR-Tg-h/KLF4     168     R     GCTGCCCCAAACCTACAGGTG     GCTTGCCCAAACCTACAGGTG			1271-1292		R	TGGGCTTTCAGGTTATTTGACT
hTERT1038-1059RGTAGAGCATGGAAATGGGAGAChTERTNM_1982533198-3220115FTGAAAGCCAAGAACGCAGGGATG3288-3312RTGTCGAGTCAGCTTGACCAGGAGGATGh-β-ACT/NNM_0011011332-1353169FTTTTTGGCTTGACTCAGGATTT1479-1500RGCAAGGGACTTCCTGTAACAACqPCR for retroviral silencingSizeSequences (5'to 3')qPCR-Tg-pMXFCCCTCAAAGTAGACGGCATCqPCR-Tg-hOC74157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hOZ74157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hC74168RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-hOC74252FCCCCAGGGCCCCATTTGGACCPCR-Tg-hOC74252FCCCCAGGGCCCCATTTGGTACCPCR-Tg-hOC74252FCCCCAGGGCCCCATTTGGTACCPCR-Tg-hOC74252FCCCCAGGGCCCCATTTGGTACCPCR-Tg-hC74252FCCCCAGGGCCCCATGCTTGGCTCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-Tg-hC74424FACGATCGTGGCCCGGAAAAGGACCPCR-	hGDF3	NM 020634	829-850	231	F	CACCGTCACCAGCTATTCATTA
hTERT     NM_198253     3198-3220     115     F     TGAAAGCCAAGAACGCAGGGATG       h-β-ACTIN     NM_001101     1332-1353     169     F     TITTTGGCTTGACTCAGGATTT       h-β-ACTIN     NM_001101     1332-1353     169     F     TITTTGGCTTGACTCAGGATTT       qPCR for retroviral silencing     R     GCAAGGGACTTCCTGTAACAAC     R     GCAAGGGACTTCCTGTAACAAC       qPCR-Tg-pMX     F     CCCTCAAAGTAGACGGCATC     R     GCAGGGAAGGCAAAATCTGAA       qPCR-Tg-hOCT4     157     R     GCGAGGAAAGGCGAAAATCTGAA     R       qPCR-Tg-hKLF4     168     R     TTCAGCTCCGTCTCCATCAT     R       qPCR-Tg-hc-MYC     291     R     AGGCTGCTGGTTTTCCACTA       PCR for retroviral integration     Size     Sequences (5'to 3')       PCR-Tg-hX     R     GCTTGCCAAACCTACAGGTG       PCR-Tg-hX     R     GCACCCCTGGCATGGCTCTTGGCTC			1038-1059		R	GTAGAGCATGGAAATGGGAGAC
$h\beta$ -ACTINNM_0011011332-1353169FTTTTTGGCTGACTCAGCAGGAATG $h\beta$ -ACTINNM_0011011332-1353169FTTTTTGGCTTGACTCAGGATTT $1479-1500$ RGCAAGGGACTTCCTGTAACAAC <b>qPCR for retroviral silencing</b> SizeSequences (5'to 3') $qPCR-Tg-pMX$ FCCCTCAAAGTAGACGGCATC $qPCR-Tg-hCT4$ 157R $qPCR-Tg-hSOX2$ 146R $qPCR-Tg-hKLF4$ 168R $qPCR-Tg-hc-MYC$ 291RAGGCTGCTGGCTTTCCATAPCR-Tg-hCT4 $PCR-Tg-hOCT4$ 252F $PCR-Tg-hOCT4$ 252F $QCC-Tg-hSOX2$ 389F $GCCAGGGCCCCATTTGGTACC$ PCR-Tg-hSOX2 $PCR-Tg-hNLF4$ 424F $PCR-Tg-hNYC$ 417F $CACAGCGCAAAATGCACCAGCCCCAGGCCCCCAGGCCCCCC$	h <i>TERT</i>	NM 198253	3198-3220	115	F	TGAAAGCCAAGAACGCAGGGATG
h-β-ACT/INNM_0011011332-1353169FTTTTTGGCTTGACTCAGGATTTqPCR for retroviral silencing1479-1500RGCAAGGGACTTCCTGTAACAACqPCR-Tg-pMXFCCCTCAAAGTAGACGGCATCqPCR-Tg-hOCT4157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hSOX2146RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-hOC74252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hOC74252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hCMYC417FCAACAACCGAAAATGCACCAGCCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')PCR for polymorphism detectionSizeSequences (5'to 3')			3288-3312		R	TGTCGAGTCAGCTTGAGCAGGAATG
Image: constraint of the systemImage: constrai	h-β-ACTIN	NM_001101	1332-1353	169	F	TTTTTGGCTTGACTCAGGATTT
qPCR for retroviral silencingSizeSequences (5'to 3')qPCR-Tg- pMXFCCCTCAAAGTAGACGGCATCqPCR-Tg-hOCT4157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hSOX2146RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOCT4252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hCT4252FCCCCAGGGCCCCATGGCTCTTGGCTCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hCMYC417FCAACAACCGAAAATGCACCAGGCCCAGGPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGDACTCCCTTAATTCCATTACC			1479-1500		R	GCAAGGGACTTCCTGTAACAAC
qPCR for retroviral shericingSizeSequences (5 to 3 )qPCR-Tg-pMXFCCCTCAAAGTAGACGGCATCqPCR-Tg-hOCT4157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hSOX2146RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5 to 3')PCR-Tg-hOCT4252FCCCCAGGGCCCCATTTGGTACCPCR-Tg-hOCT4252FCCCCAGGGCCCCATTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAAGGACCPCR-Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGG	PCD for retractivel allowed as			Sime		
Image: transformationImage: transformationPCR-Tg-hSOX2146RTTCAGCTCCGTCTCCATCATImage: transformation168RGTGGAGAAAGATGGGAGCAGImage: transformation291RAGGCTGCTGGTTTTCCACTAPCR-Tg-hC-MYC291RAGGCTGCTGGTTTTCCACTAPCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOCT4252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAAGGACCPCR-Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCCAGPCR-Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')Image: transformationImage: transformationImage: transformationACTCCCCTAGCGTCATGCGTGTTAGG1194FTATGGCGTCATGCGTGTTAGGImage: transformationImage: transformationIma				Size	┝┍	
qPCR-1g-hOC14157RGCGAGAAGGCAAAATCTGAAqPCR-Tg-hSOX2146RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOC74252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAAGGACCPCR -Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGIntegrationIntegrationSizeSequences (5'to 3')IntegrationSizeSequences (5'to 3')IntegrationSizeSequences (5'to 3')IntegrationPCR-Tg-hC74PCR-Tg-hC74PCR-Tg-hC74PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76PCR-Tg-hC76 <tr< td=""><td colspan="3"></td><td></td><td></td><td></td></tr<>						
qPCR-1g-hSOX2146RTTCAGCTCCGTCTCCATCATqPCR-Tg-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOC74252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hCMYC417FACGATCGTGGCCCCGGAAAAGGACCPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGPCR1194FTATGGCGTCATGCGTGTTAGG				157	R	GCGAGAAGGCAAAATCTGAA
qPCR-1g-hKLF4168RGTGGAGAAAGATGGGAGCAGqPCR-Tg-hc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOCT4252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAGGACCPCR-Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGPC1194FTATGGCGTCATGCGTGTTAGG				146	<u>R</u>	
qPCR-1g-nc-MYC291RAGGCTGCTGGTTTTCCACTAPCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOCT4252FCCCCAGGGCCCCATTTTGGTACCPCR-Tg-hSOX2389FGGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAAGGACCPCR -Tg-hc-MYC417FCAACAACCGAAAATGCACCAGCCCAGPCR for polymorphism detectionSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGPCRPACTCCCTTAATTCTCATTCCCC	qPUK-1g-nKLF4   16			168	R	GIGGAGAAAGAIGGGAGCAG
PCR for retroviral integrationSizeSequences (5'to 3')PCR-Tg-pMXRGCTTGCCAAACCTACAGGTGPCR-Tg-hOCT4252FPCR-Tg-hSOX2389FGCACCCCTGGCATGGCTCTTGGCTCPCR-Tg-hKLF4424FACGATCGTGGCCCCGGAAAAGGACCPCR -Tg-hc-MYC417FCR for polymorphism detectionSizeSizeSequences (5'to 3')1194FTATGGCGTCATGCGTGTTAGGDACTCCCTTAATTCTCATTCCCC	qPCR-Ig-nc-MYC			291	R	
PCR-Tg-pMX   R   GCTTGCCAAACCTACAGGTG     PCR-Tg-hOC74   252   F   CCCCAGGGCCCCATTTTGGTACC     PCR-Tg-hSOX2   389   F   GGCACCCCTGGCATGGCTCTTGGCTC     PCR-Tg-hKLF4   424   F   ACGATCGTGGCCCCGGAAAAGGACC     PCR-Tg-hc-MYC   417   F   CAACAACCGAAAATGCACCAGCCCAG     PCR for polymorphism detection   Size   Sequences (5'to 3')     1194   F   TATGGCGTCATGCGTGTTAGG	PCR for retroviral integration			Size		Sequences (5´to 3´)
PCR-Tg-hOCT4   252   F   CCCCAGGGCCCCATTTTGGTACC     PCR-Tg-hSOX2   389   F   GGCACCCCTGGCATGGCTCTTGGCTC     PCR-Tg-hKLF4   424   F   ACGATCGTGGCCCCGGAAAAGGACC     PCR-Tg-hc-MYC   417   F   CAACAACCGAAAATGCACCAGCCCAG     PCR for polymorphism detection   Size   Sequences (5'to 3')     1194   F   TATGGCGTCATGCGTGTTAGG	PCR-Tg-pMX				R	GCTTGCCAAACCTACAGGTG
PCR -Tg-hSOX2 389 F GGCACCCCTGGCATGGCTCTTGGCTC   PCR-Tg-hKLF4 424 F ACGATCGTGGCCCCGGAAAAGGACC   PCR -Tg-hc-MYC 417 F CAACAACCGAAAATGCACCAGCCCAG   PCR for polymorphism detection Size Sequences (5'to 3')   1194 F TATGGCGTCATGCGTGTTAGG	PCR-Tg-hOCT4 252			252	F	CCCCAGGGCCCCATTTTGGTACC
PCR-Tg-hKLF4   424   F   ACGATCGTGGCCCCGGAAAAGGACC     PCR -Tg-hc-MYC   417   F   CAACAACCGAAAATGCACCAGCCCCAG     PCR for polymorphism detection   Size   Sequences (5'to 3')     1194   F   TATGGCGTCATGCGTGTTAGG	PCR -Tg-hSOX2 389			389	F	GGCACCCCTGGCATGGCTCTTGGCTC
PCR -Tg-hc-MYC   417   F   CAACAACCGAAAATGCACCAGCCCCAG     PCR for polymorphism detection   Size   Sequences (5'to 3')     1194   F   TATGGCGTCATGCGTGTTAGG     PCR for polymorphism detection   D   ACTCCCTTAATTCTCATTCCCCC	PCR-Tg-h <i>KLF4</i> 424				F	ACGATCGTGGCCCCGGAAAAGGACC
PCR for polymorphism detection Size Sequences (5 'to 3')   1194 F TATGGCGTCATGCGTGTTAGG	PCR -Tg-hc-MYC 417				F	CAACAACCGAAAATGCACCAGCCCCAG
1194 F TATGGCGTCATGCGTGTTAGG	PCR for polymorphism detection			Size		Sequences (5'to 3')
				1194	F	TATGGCGTCATGCGTGTTAGG
					R	ACTGGCTTAATTCTCATTTGGCC

F: Forward, R: Reverse