

<b>Supplement Table S1. Primer sequences for RT-qPCR shown in Figure 1</b>		
<b>Genes</b>	<b>Forward primer (5' to 3')</b>	<b>Reverse primer (5' to 3')</b>
<i>ANLN</i>	agaaatttgtctgcaatctcaatct	ttccaggaaaggcttaattcc
<i>BRCA2</i>	agcttactccggcctcaaaa	ttcctccaatgcttggttaataa
<i>CASC5</i>	tacagaaacccccgacagagc	tcttctggagtaggtggtgtgtt
<i>DEPDC1</i>	ctatggagagtcaggggtgtgc	gaaaagatgtggtaacttcattcca
<i>DIAPH3</i>	gggaaaaggacttcagtatcaaaa	tgagatctgtcggcttctctta
<i>DLG7</i>	catgtgaagaagactttgtttttga	ggtaatccaggacactgagca
<i>DTL</i>	atgctcttcaattcgggtgct	gggtattgtgaagaccatccat
<i>FANCI</i>	caccacacttacagcccttg	attcctccggagctctgac
<i>FOXMI</i>	actttaagcacattgccaagc	cgtgcagggaaagggtgt
<i>GRHL2</i>	gaaagtccagtttcaccagagg	ggcactaaggccactagtctttt
<i>TERT</i>	gccttcaagagccacgctc	ccacgaactgtcgcagt
<i>LCE3D</i>	ctcctctgcacctggacaa	cacttgggtgagggacactt
<i>LCE3E</i>	acgcatgccttcccatatac	gagctcagatccccacag
<i>PBK</i>	ccactggatgaaaatatgactgtg	tccacagcttctttgggttt
<i>TOP2A</i>	caacatgcccaattgagtgaaa	acttgggctttaaacttcacc
<i>INK4A</i>	gtggacctggctgaggag	ctttcaatcggggatgtctg
<i>GRHL1</i>	gccagatcaaggctcttctgtg	tgctttgctttcgttcttca
<i>GRHL3</i>	caagaaatgcaagcgagga	gaattttgccgtccagctc
<i>HELLS</i>	ggatggctgaattcaaaagatt	caagatccctttccgtttgt
<i>SPRR2A</i>	aaccctggtacctgagca	cttgcactgctgctgttgat
<i>IVL</i>	gaaagcagaaaaccagagc	tagctgctgatccctttgtg
<i>GAPDH</i>	agccacatcgctcagacac	gccaataacgaccaaatcc

<b>Supplement Table S2. Primer sequences for ChIP analyses (shown in Figure 2) for GRHL2 binding to promoters.</b>		
<b>Genes</b>	<b>Forward sequence (5' to 3')</b>	<b>Reverse sequence (5' to 3')</b>
<i>ANLN</i> (-230 to -89): R1	gggggtggagccaggaacc	tgcgctcgggtcacgtggc
<i>ANLN</i> (-103 to 57): R2	acgtgaccgagcgcaggg	ggcgggggaactctcca
<i>NCAPG2</i> (-396 to -245):R1	tctcttctctctccttctctct cct	acagctggggaacctatgc
<i>NCAPG2</i> (-260 to -111):R2	tgggttccccagctgtggc	cccgcctccagatcatgcc
<i>PBK</i> (-258 to -101): R1	ttggagagagcttcagccttc agc	tctcccaggactcccgggtgc
<i>PBK</i> (-101 to 57): R2	agggaggaggaacggcgaat	ccctgcagctgcctctagca
<i>ADFP</i> (-237 to -96): R1	ggctcccagacaggctcctctc	agcccagtggtcaccctcgg
<i>ADFP</i> (-106 to 33): R2	acactcgggcttgggacagg	gaagacgactccggctgcca
<i>Ki67</i> (-256 to -107): R1	cgttttcgtttgaaattgggcg	gaccgggtggcctacagg
<i>Ki67</i> (-114 to 45): R2	accgggtccccgctcagagg	agtccgcccagaggagagc
<i>GRHL1</i> (-278 to -113): R1	agcgtccctctcctgtcag	gattggtcggcgagaagagc
<i>GRHL1</i> (-116 to 92): R2	aatcaggaggcgcgaccgg	acagtacaccgatccggg
<i>GRHL3</i> (-278 to -111): R1	gtccctgtacttttctcttag ttat	agctgttaactcttagcccc
<i>GRHL3</i> (-110 to 43): R2	gcacctgttgaggatatacctc	tgcttgacacagacattctc

<i>CCNB1</i> (-241 to -91): R1	gcagaggcagaccacgtgag	tgttcgtggcactcactccc
<i>CCNB1</i> (-96 to 53): R2	cgaacaggccaataaggagg	cagcggggagaagcagaaca
<i>TRIP13</i> (-260 to -110): R1	cttcttggtgcttcttgccat	ccagcgagctcggcaacct
	gg	
<i>TRIP13</i> (-128 to 56): R2	aggttgccgagctcgetgg	ccacctcacgcccagcgtc
<i>CCNA2</i> (-297 to -150): R1	ttccctaaaggcttagagtc	agggagaaacaaactggctg
	ag	
<i>CCNA2</i> (-181 to -3): R2	tttctccctcctgccccgc	gagcggcggtgttcttgc
<i>TPX2</i> (-249 to -98): R1	caaatagtttggagcagagca	cagcaataccggaagtcaga
	c	
<i>TPX2</i> (-105 to 45): R2	tattgctgcggtctgtaggg	cagatctgacaacgaagcgc
<i>BUB1</i> (-291 to -92): R1	aaaccaattccctacgcccg	tgctcggaggtaagtcca
<i>BUB1</i> (-84 to 92): R2	cggtgattggccaaccttc	gaaggacattttccggggtg
<i>RRM2</i> (-250 to -99): R1	ggaaccgggaggtcccgg	tccgacccttcccattggc
<i>RRM2</i> (-100 to 56): R2	gaggcatggcacagccaatg	cagcgaagcagagcgagcag
<i>CDC20</i> (-218 to -23): R1	cagtactagtcctctggcgc	ttaaactctccgctccgag
<i>CDC20</i> (-17 to 188): R2	gtaagccaggcgtgttaaagc	tggaggaaaggaggcgacg
	c	
<i>CRCT1</i> (-295 to -101): R1	cctcccaggtacaaacagtg	gtgctcagctgacactcaca
<i>CRCT1</i> (-103 to 69): R2	cacgtctggtgggaaatggg	cccagaccctgctaggagac
<i>NUF2</i> (-307 to -140): R1	acttctccttgtcaccctg	actgcaggaagtgggagcac
<i>NUF2</i> (-142 to 9): R2	agtccgaggttccgactcgac	ccccattccgccaagcccac
	gc	
<i>DTL</i> (-206 to -57): R1	tcaagccctgttacgcatgc	gcgctcagagtcatttccc
<i>DTL</i> (-45 to 134): R2	gtcgctcggaagccaatcag	cggaggaaaagcctcagctg
<i>EXO1</i> (-305 to -153): R1	cacagtgagttaggggctcg	gaggtgacgcgcaggtcgc
	g	
<i>EXO1</i> (-152 to 7): R2	cgaccctcctctcgggatc	ccctccgttactgaactgc
<i>SPRR2A</i> (-249 to -99): R1	agtccctctttgccataagt	ccagatgcaaatttatccat
<i>SPRR2A</i> (-98 to 70): R2	cttaagaaattactggatcag	aacgagggaactcaaggaag
	c	
<i>CEP55</i> (-243 to -81): R1	cagaattagctggcgggcc	aagaaggaggagcagcgcgc
<i>CEP55</i> (-94 to 60): R2	tgctcctccttcttgccgg	ccttggggccagctagcagc
<i>HELLS</i> (-246 to -97): R1	ttctccacgatcggccacct	at ttggcgcagcttgccggtt
<i>HELLS</i> (-110 to 42): R2	aagctgcgccaaatctcgcg	ctcctcacaaccgctgccgg
<i>C13orf3</i> (-251 to -102): R1	tccagagaagcggggagccc	gacgggtgcgcttacgccac
<i>C13orf3</i> (-110 to 46): R2	cgtctcgcggggtctcctgg	ccaggcgtacgcagacccca
<i>DIAPH3</i> (-259 to -110): R1	aaagaaatccaggccgatga	cactgcaggacatgattggc
<i>DIAPH3</i> (-96 to 64): R2	gtgcctcagcgtgtcattga	aacaggttttactcccgggg
<i>DLG7</i> (-233 to -79): R1	cactcccgccttcacctga	tgcgattggtttgctccgtg
<i>DLG7</i> (-80 to 79): R2	caagcctcgttgagtggag	agaacactcggctctggacg
<i>ARHGAP11A</i> (-281 to -131): R1	cgggaaataagttgtctttat	gcaaaccagcaaacatgaa
	at tt	
<i>ARHGAP11A</i> (-125 to 25): R2	ttgcccgttacacccttgc	acaccgcagtttcagccca
<i>PCNA</i> (-250 to -65): R1	ggaccgatctccacatatgc	ttgcggggaagactttaggg

<i>PCNA</i> (-65 to 126): R2	tggacagcgtggtgacgtc	aggcgggaaggaggaaagt
<i>LCE3D</i> (-260 to -114): R1	ttgaaacaaggaagaaggag	aaggcacacgcccgaagacta
<i>LCE3D</i> (-112 to 31): R2	g	
<i>LCE3D</i> (-112 to 31): R2	ccttgttgacacctcccctg	gtgcagaggaggcaggagaa
<i>KIF11</i> (-277 to -89): R1	tatttctctctctgcagctgag	tatcctcactggagccccgc
	gga	
<i>KIF11</i> (-90 to 129): R2	tactgcatcccatggtgcctt	ggcctggaggaccgacgcac
	gc	
<i>CCNB2</i> (-266 to -111): R1	aaattcgtagatgaggccttg	acgtttgattgtcacaacag
		c
<i>CCNB2</i> (-108 to 96): R2	cgtgtctaagaaaattcagcc	gggaggacactagcgtacga
	a	
<i>KIF23</i> (-292 to -92): R1	aaccctcagtttcgtcatgcg	acctccgcggaagtgacttc
<i>KIF23</i> (-100 to 50): R2	gaggctctgcctctcccctgc	gacgttaggaccggcagcaa
<i>KIAA0101</i> (-300 to -150): R1	gaaacttagcaccactagtc	aaccaattgccaatgccag
	ggg	
<i>KIAA0101</i> (-96 to 55): R2	aattggttcagggggaacgg	ccgcaccatgttcaacaag
		aag
<i>CCNB1</i> (-241 to -91): R1	gcagaggcagaccacgtgag	tgttcgtggcactcactccc
<i>CCNB1</i> (-96 to 53): R2	cgaacaggccaataaggaggg	cagcggggagaagcagaaca
<i>FANCI</i> (-288 to -114): R1	cggggccaccaattgtgagt	ccagctcacagtcggagggg
<i>FANCI</i> (-131 to 32): R2	cctccgactgtgagctggga	aaaagcccgtcaacccaac
<i>PRC1</i> (-250 to -111): R1	gaggagtcccttgaggctgcc	gcaatcgggggtgggactc
<i>PRC1</i> (-115 to 48): R2	attgcgcaccgcgacttca	cccgcaaacaccggcgatg
	aattcctcctctctcggggct	taaaatccaaacccgcccgc
<i>PLK1</i> (-272 to -96): R1	g	
<i>PLK1</i> (-101 to 44): R2	atthtaaatccccgcggcca	tgcagcactcatgctcccga
	atatctcatttccaggcattg	accaacactgccccctcgc
<i>SHCBP1</i> (-251 to -98): R1	ctgg	
<i>SHCBP1</i> (-106 to 38): R2	agtgttggtgggggctgga	ccgtcagcgaccctcag
<i>TOP2A</i> (-250 to -101): R1	attccctgtcaatctctccg	gaaccaatcgtagcttgcc
<i>TOP2A</i> (-103 to 49): R2	ttcttctggacggagacggtg	taaacaggcaggaccccacg
<i>NCAPG</i> (-263 to -92): R1	aaggccactccgctcagctc	aagagagcgggaagcagtg
<i>NCAPG</i> (-91 to 89): R2	ctcccaaagcgcttacggca	ggaaccctgccgggacgagt
<i>HIST1H2BM</i> (-254 to -107): R1	gagctttgcctccctgctta	aaacgtaagccaatcgcaca
<i>HIST1H2BM</i> (-98 to 62): R2	tttagaccaataggactcgag	acaaccttagggctgthttcg
	tatg	
<i>HIST1H1B</i> (-233 to -84): R1	ctttcatcaattgcacaagat	cccaaattgtgthttgtagt
	tc	cc
<i>HIST1H1B</i> (-97 to 78): R2	aaacacaatttgggagtgcca	ggtggcaagaaactgctaga

Note: R1 and R2 represent Region 1 and Region 2 of promoters as denoted in Figure 2.

**Supplement Figure S1 – Specificity of the GRHL2 antibody for in situ staining.** NHEK/LXSN and NHEK/GRHL2, as well as HaCaT cells infected with LV-EGFP or LV-GRHL2i, were cultured in chamber slides and stained in situ for GRHL2 by immunoperoxidase (IPS) staining, according to the methods described elsewhere (Kang et al., 2000). We included IgG as negative control. Bar represents 50  $\mu$ m.

Supplement Figure S1

