

Additional file1: Primer sequences for the pyrosequencing assays

Genomic locations ^a	Gene	Primer sequences ^b	Biotin labeled primer
chr12:121824850	CCDC62	F: 5' ATTGGGGGTTTTTAAGTGGTTTAG 3'	Forward
chr12:121824853	CCDC62	R: 5' AACAACTTTATTAACCTCTTCATTCTCTA 3' S: 5' ATTCTTTCAAACCTTCCA 3'	
chr11:122214681	CRTAM	F: 5' ATGTTTAAATTATGTATTTGAGGGATGTT 3' R: 5' AAAACCCACAAAAACACACACT 3' S: 5' ATGTATTTGAGGGATGTTA 3'	Reverse
chr7:96488107	DLX5	F: 5' GGAATTGATTGAGTTGGTTGTATTTG 3' R: 5' CTCAACCACCACCCTCATA 3' S: 5' TATTTGTGTATTAGGATGTAGAGT 3'	Reverse
chr17:30783625	FLJ10260	F: 5' TGGTTATTTGGTGTGTATATAATGTAAA 3' R: 5' ATAACCTCACCTCAACCTCCCATTA 3' S: 5' AGATTAGTTTGAATGGTTGTA 3'	Reverse
chr5:115326619	FLJ90650	F: 5' GTAGTTTGGGAAGAGGTTATGT 3'	Reverse
chr5:115326640	FLJ90650	R: 5' ATCTTCCCCTCCCTCAA 3'	
chr5:115326626	FLJ90650	S: 5' TTTGGAAGAGGTTATGTA 3'	
chr5:115326614	FLJ90650		
chr11:22646220	GAS2	F: 5' AGAGTTTGGAGTAAAGAAGTATAGG 3' R: 5' AAAAAACACCCATTTAACATCC 3' S: 5' TGTGAATTTTAGGGGAT 3'	Reverse
chr7:50816700	GRB10	F: 5' ATTGTTTTTTTAAAGTTTGAAAGGTAG 3'	Reverse
chr7:50816682	GRB10	R: 5' CAAAAAATCCAAACAACACC 3'	
chr7:50816674	GRB10	S: 5' TTTTTTTTAAAGTTTGAAAGGTAG 3'	
chr7:50816802	GRB10	F: 5' TTTTGTAGGGTGTGGG 3' R: 5' CCCTCACTAACTAAAAAAACTTTAC 3' S: 5' GTATATAGGTGGTTATG 3'	Reverse
chr17:70368047	GRIN2C	F: 5' GGGGTTAGGGATTGAATTAAGA 3'	Reverse
chr17:70368057	GRIN2C	R: 5' CCCTAATACCCACCCCATTC 3' S: 5' GGTTAGGGATTGAATTAAGATA 3'	
chr11:1975300	H19	F: 5' AAGAAGGGGGAGTTAGGTATTTA 3' R: 5' AAACCTCCTTCTTTCAAAAACTAA 3' S: 5' GTGGTAGTTGGTTGGA 3'	Reverse
chr5:53787676	HSPB3	F: 5' GGGTGAAGTTTTTTGAGATAAAAT 3' R: 5' AAAACAAATCCCACTTTCAAATC 3' S: 5' GTGTTATTTATTTTGGT 3'	Reverse
chr1:157245543	IFI16	F: 5' TGTGAGTAGAGGATTAAATAGATTT 3'	Reverse
chr1:157245550	IFI16	R: 5' ACTATCCTCTTAACCATAACTAAATTACT 3' S: 5' TTAGTGTATTTTATAGGAT 3'	
chr5:131908379	IL5	F: 5' GGTTTGAATATATATGATGGAGGTGTATGT 3' R: 5' TATATCTACCTCCCACTACCTCTACT 3' S: 5' ATGTTGTAGTTTAGAAGTTTGAT 3'	Reverse
chr1:234113562	LYST	F: 5' AGTTAAAAGGTTATTGGGATGGT 3' R: 5' AACTTAATTTACCAAATCCCCATATAA 3' S: 5' ATTGGGATGGTTTTTTAGA 3'	Reverse
chr7:129913072	MEST	F: 5' TTGGTTTTTGTGAGTATGTGATG 3'	Reverse
chr7:129913081	MEST	R: 5' ATAAAAACCAAAAAATAACATTTTAATAA 3' S: 5' AAATTAGGGGAAGGG 3'	
chr7:129913254	MEST	F: 5' GAAATTAGGGGAAGGGTTGAAA 3'	Reverse
chr7:129913259	MEST	R: 5' CCTTCTCCCTACCAAAC 3' S: 5' TATTTATATTTTTTGTAAATAGGTGG 3'	
chr15:21483466	NDN	F: 5' GGGTTTAGAGGAGGG 3'	Reverse
chr15:21483463	NDN	R: 5' CAAAAACCTACCTTACCAA 3' S: 5' AGATTTTTATTTGTTTGTATATG 3'	
chr5:140777470	PCDHGB7	F: 5' GGTAATTTGGTGTGTTGGGTAAG 3'	Reverse

chr5:140777464	<i>PCDHGB7</i>	R: 5' ATCCCTCAACCTCTAACCTA 3' S: 5' GTTGGGTAAGGTTTG 3'	
chr5:140777418	<i>PCDHGB7</i>	F: 5' GGTGTGTTGGGTAAGGTTTG 3' R: 5' CCCTCAACCTCTAACCTAAAAT 3' S: 5' CAACCTCTAACCTAAAATTCCCT 3'	Forward
chr14:23633270	<i>PCK2</i>	F: 5' AAGAGTGGATTTAGTTTTTAATGG 3' R: 5' AAACCTAATAAACTAACACTAACTT 3' S: 5' AGGGAGTTGGTTTGT 3'	Reverse
chr14:23633275	<i>PCK2</i>		
chr10:48448112	<i>PTPN20B</i>	F: 5' GTTTGGGAGAGGGGATT 3' R: 5' CCCCACCACCTTTCCTCA 3' S: 5' CAAAACACTAAAACCCAT 3'	Forward
chr10:48448103	<i>PTPN20B</i>		
chr10:48448106	<i>PTPN20B</i>		
chr10:48448108	<i>PTPN20B</i>		
chr10:48448115	<i>PTPN20B</i>		
chr15:22644337	<i>SNRPN</i>	F: 5' TGAGGTTGGAGGATTTAGGTTGTG 3' R: 5' ATATTTCCCTACACATCACTCT 3' S: 5' GATTTAGGTTGTGAGGTA 3'	Reverse
chr15:22644327	<i>SNRPN</i>		
chr15:22620469	<i>SNRPN</i>	F: 5' TGGTTGAAAAGGAGAGGGTTAGA 3' R: 5' ATTAATTCCTTATACACCTCCACAA 3' S: 5' AGGTTTAAAGAAGTTATGATAG 3'	Reverse
chr17:33179448	<i>TCF2</i>	F: 5' ATTTAATTTTGGATTTGTTAAGTTAGTGT 3' R: 5' CCCTTCCTAAATAATCAATTTCTCTT 3' S: 5' ATTTGTAAAGTTAGTGTTTGTGTA 3'	Reverse
chr17:33179450	<i>TCF2</i>		
chr18:27424926	<i>TTR</i>	F: 5' GTTTTGGTTTTTTAAAGTGTGGGATTA 3' R: 5' CAACTATCAACCTTATTCCTACATACCC 3' S: 5' TTTTTTAAAGTGTGGGATTAT 3'	Reverse

- Corresponds to genome build 36.1
- F forward ; R reverse ; S sequencing