



# Human genomic control DNA

Mutation in  $\alpha$ - globin gene ( $\alpha$ - thalassemia)

## CERTIFICATE OF ANALYSIS

### Product Information

Product name :	Mutant Control DNA for $\alpha$ - Thalassemia
Cat. No. :	K5405
Concentration:	300 ng/ $\mu$ l
Storage condition:	-20°C
Mutation type:	-- <sup>med</sup> / $\alpha\alpha$

### QC Results

Test Items	Specifications	Results
Absorbance ratio	A260/A280>1.8 A260/A230>2.0	Passed
Electrophoresis	Average size larger than 50 kb	Passed
Sequencing	No other mutation in the gene	passed
Enzyme activity	<i>EcoRI</i> digestion	passed

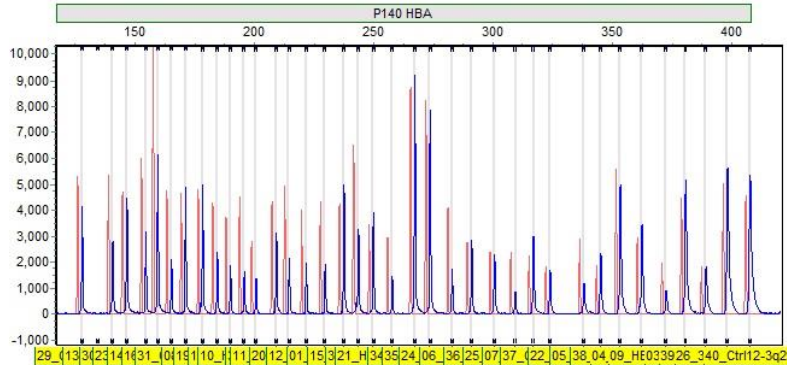
### Caution:

This product is pure human genomic DNA, and must be kept away from PCR products to avoid contamination

# MLPA result :

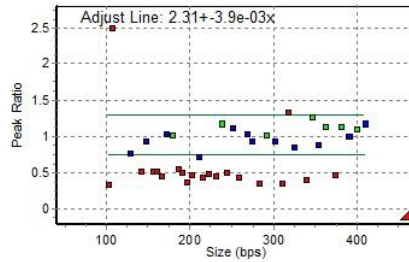
MLPA Analysis Report - SoftGenetics	
Software: GeneMarker V1.95	Analysis Type: MLPA
Project: 931010-P140-B4.PROJECT.SGF	Compare Type: MLPA Ratio
Technician:	Normalization By: Population Normalization (Adjusted)
Report Time: 01/03/2015 - 10:44:45	Quantification By: Peak Height
Panel: 00	Classification: Loss < 0.75 <= Equivalent <= 1.30 < Gain
Control: Synthetic Control Sample	Report Value Type: Peak Ratio
Synthetic Used: 93-10-10_61-HBA-P140B4-Z-SHA-NL_2014-12-31.fsa // 93-10-10_68-HBA-P140B4-H-NOF-NL_2014-12-31.fsa // 93-10-10_70-HBA-P140B4-R085M-P.C. 2014-12-31.fsa	

93-10-10\_69-HBA-P140B4| **K5405** .fsa -- Dye: Blue



Machine: 3130XL-52038  
Run Time: 12/31/2014 - 12:06:24 -> 12/31/2014 - 12:52:54

Conclusion	Date	Initial
Authorization 1		
Authorization 2		



Probe Name	Bin Size	93-10-10_69-HBA-P140
1 01_16p13 POLR3K	237.7	1.177
2 02_HS-40 (1)	178.6	1.035
3 03_HS-40 (2)	381.0	1.156
4 04_9.3kb up HBZ	362.6	1.150
5 05_3.5kb up HBZ	345.6	1.264
6 06_HBZ/HBZP(1)	291.1	1.037
7 07_HBZ/HBZP(2)	317.4	1.335
8 08_HBA2P/HBA1P	184.7	0.565
9 09_HBA1P/HBA2(1)	372.9	0.473
10 10_HBA1P/HBA2(2)	201.0	0.482
11 11_HBA1P/HBA2(3)	214.8	0.439
12 12_HBA1P/HBA2(4)	229.7	0.454
13 13_HBA1+2 ex1	141.1	0.520
14 14_HBA2 int2(1)	159.8	0.525
15 15_HBA2 int2(2)	243.6	0.502
16 16_HBA1+2 ex3	165.5	0.450
17 17_CS	135.0	-1
18 18_End HBA2 ex3	196.0	0.367
19 19_HBA2/HBA1(1)	190.2	0.503
20 20_HBA2/HBA1(2)	221.9	0.492
21 21_HBA2/HBA1(3)	257.8	0.442
22 22_HBA2/HBA1(4)	338.5	0.407
23 23_0.2kb d HBA1	154.9	0.529
24 24_0.5kb d HBA1	283.0	0.363
25 25_2.4kb d HBA1	309.7	0.353
26 26_3.7kb d HBA1	398.5	1.113
27 27_X_100	101.9	0.344
28 28_Y_105	106.3	528.550
29 29_Ctrl01-5q31	128.2	0.779
30 30_Ctrl02-9q22	147.0	0.945
31 31_Ctrl03-15q11	171.5	1.050
32 32_Ctrl04-17q21	209.5	0.719
33 33_Ctrl05-1p21	250.1	1.134
34 34_Ctrl06-5p15	267.4	1.052
35 35_Ctrl07-5q22	273.8	0.954
36 36_Ctrl08-11p13	300.6	0.948
37 37_Ctrl09-16p13	324.3	0.859
38 38_Ctrl10-11q22	353.7	0.889
39 39_Ctrl11-5q22	389.4	1.007
40 40_Ctrl12-3q29	407.9	1.181

**There was a hetero deletion from prob 8 (between HBA2P and HBA1P) to prob 25 (2.4 kb down of HBA1), (compatible with MED deletion).**