



Human genomic control DNA

Mutation in α -globin gene (*α -thalassemia*)

CERTIFICATE OF ANALYSIS

Product Information

Product name :	Mutant Control DNA for <i>α-Thalassemia</i>
Cat. No. :	K5408
Concentration:	300 ng/ μ l
Storage condition :	-20°C
Mutation type:	-4.2 α / α α

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>Eco</i> RI digestion	passed

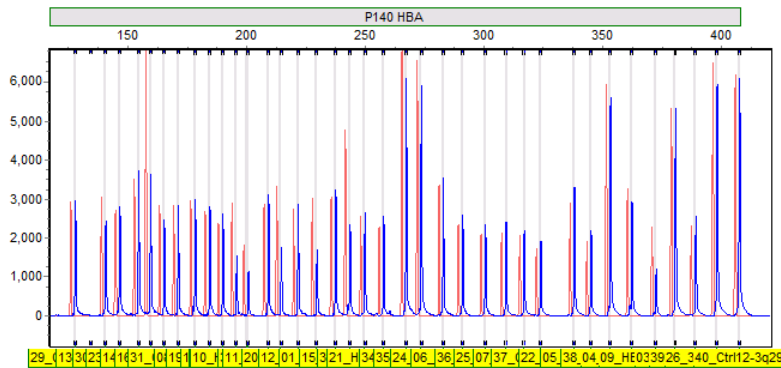
Caution:

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

MLPA result :

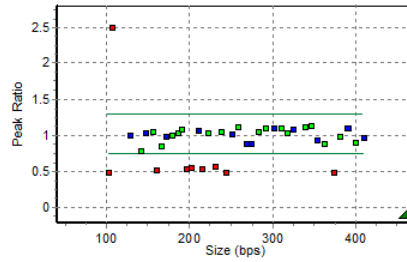
MLPA Analysis Report - SoftGenetics	
Software: GeneMarker V1.95	Analysis Type: MLPA
Project: 931010-P140-B4-PROJECT.SGF	Compare Type: MLPA Ratio
Technician:	Normalization By: Population Normalization
Report Time: 01/03/2015 - 10:44:45	Quantification By: Peak Height
Panel: 00	Classification: Loss < 0.75 <= 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-P140B4-8085M-P.C 2014-12-31.fsa	

_71-HBA-P140B4 k5408 -PA_2014-12-31.fsa -- Dye: Blue



Sample Name: 71-075PO-S-PA
 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_71-HBA-P140
1	01_16p13 POLR3K	237.7	1.070
2	02_HS-40 (1)	178.6	1.012
3	03_HS-40 (2)	381.0	0.998
4	04_9.3kb up HBZ	362.6	0.891
5	05_3.5kb up HBZ	345.6	1.141
6	06_HBZ/HBZP(1)	291.1	1.108
7	07_HBZ/HBZP(2)	317.4	1.046
8	08_HBA2P/HBA1P	184.7	1.044
9	09_HBA1P/HBA2(1)	372.9	0.484
10	10_HBA1P/HBA2(2)	201.0	0.564
11	11_HBA1P/HBA2(3)	214.8	0.539
12	12_HBA1P/HBA2(4)	229.7	0.568
13	13_HBA1+2 ex1	141.1	0.795
14	14_HBA2 int2(1)	159.8	0.528
15	15_HBA2 int2(2)	243.6	0.494
16	16_HBA1+2 ex3	165.5	0.860
17	17_CS	135.0	-1
18	18_End HBA2 ex3	196.0	0.539
19	19_HBA2/HBA1(1)	190.2	1.103
20	20_HBA2/HBA1(2)	221.9	1.040
21	21_HBA2/HBA1(3)	257.8	1.127
22	22_HBA2/HBA1(4)	338.5	1.136
23	23_0.2kb d HBA1	154.9	1.064
24	24_0.5kb d HBA1	283.0	1.056
25	25_2.4kb d HBA1	309.7	1.114
26	26_3.7kb d HBA1	398.5	0.915
27	27_X_100	101.9	0.498
28	28_Y_105	106.3	1000
29	29_Ctrl01-5q31	126.2	1.014
30	30_Ctrl02-9q22	147.0	1.041
31	31_Ctrl03-15q11	171.5	1.004
32	32_Ctrl04-17q21	209.5	1.085
33	33_Ctrl05-1p21	250.1	1.031
34	34_Ctrl06-5p15	267.4	0.888
35	35_Ctrl07-5q22	273.8	0.902
36	36_Ctrl08-11p13	300.6	1.110
37	37_Ctrl09-16p13	324.3	1.095
38	38_Ctrl10-11q22	353.7	0.940
39	39_Ctrl11-5q22	389.4	1.113
40	40_Ctrl12-3q29	407.9	0.986

There was a hetero deletion from prob 9 (between HBA1P and HBA2) to prob 18 (end of HBA2, exon3), compatible with 4.2 kb del. Z.Sharifi