



Human genomic control DNA

Mutation in α -globin gene (α -thalassemia)

CERTIFICATE OF ANALYSIS

Product Information

Product name :	Mutant Control DNA for α -Thalassemia
Cat. No. :	K5413
Concentration:	300 ng/ μ l
Storage condition :	-20°C
Mutation type:	α -Triplex-anti3.7 (Probe 12 to 22)

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

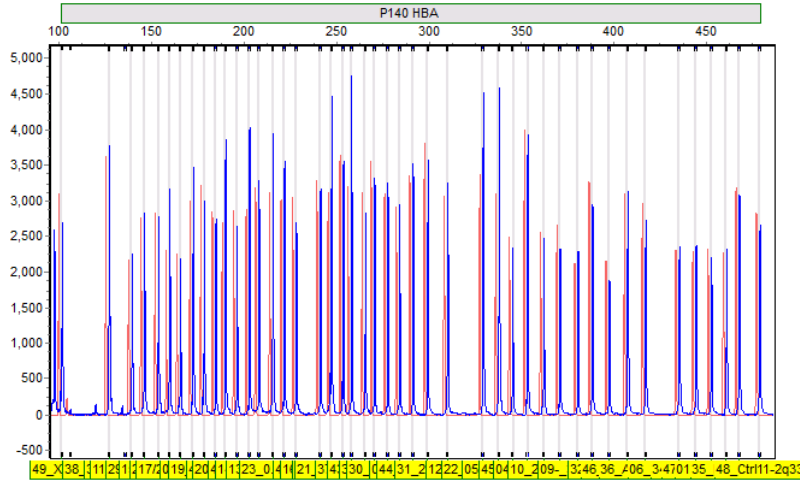
Caution:

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

MLPA result :

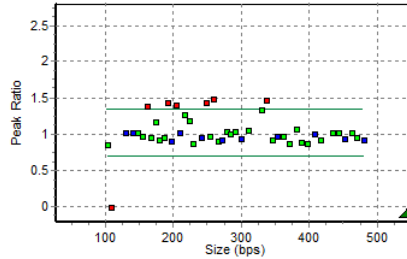
MLPA Analysis Report - SoftGenetics	
Software: GeneMarker V1.95	Analysis Type: MLPA
Project: Untitled	Compare Type: MLPA Ratio
Technician:	Normalization By: Population Normalization
Report Time: 01/09/2016 - 08:44:01	Quantification By: Peak Height
Panel: 0	Classification: Loss < 0.70 <= Equivalent <= 1.35 < Gain
Control: Synthetic Control Sample	Report Value Type: Peak Ratio
Synthetic Used: 94-10-17_21-P140-C1-H-NOF-NL.fsa /// 94-10-17_29-P140-C1-12777PP-NL.fsa /// 94-10-17_38-P140-C1-K-FAT-NL.fsa	

94-10-17_ **K5413** .Dye: Blue



Machine: 3130XL-52038
Run Time: 01/07/2016 - 11:27:27 -> 01/07/2016 - 12:13:55

Conclusion	Date	Initial
Authorization 1		
Authorization 2		



	Probe Name	Bin Size	94-10-17_26-P140-C1-K
1	01-POLR3K gene	461.0	1.025
2	02_HS-40 (1)	178.5	0.929
3	03_HS-40 (2)	380.8	1.074
4	04_9.3kb up HBZ	362.4	0.972
5	05_3.5kb up HBZ	345.5	0.937
6	06_0.2kb up HBZ	435.4	1.024
7	07_HBZ/HBZP	291.2	1.048
8	08_HBA2P/HBA1P	184.7	0.962
9	09_3kupHBA2,e1	388.6	0.901
10	10_2.5 kupHBA2,	371.2	0.878
11	11_0.9kupHBA2,e	146.2	1.025
12	12_0.6kupHBA2e1	329.0	1.341
13	13/24_HBA1+A2e1	221.8	1.178
14	14/25_HBA1+A2e1	215.6	1.258
15	15_HBA2 int2(1)	159.8	1.383
16	16_HBA2 int2(2)	247.2	1.435
17	17/28_HBA1+2ex3	172.6	1.159
18	18_C_S	136.0	-1
19	19_2.6kupHBA1e1	190.0	1.428
20	20_2.1kupHBA1e1	202.9	1.396
21	21_1.5kupHBA1e1	257.9	1.487
22	22_0.9kupHBA1e1	337.6	1.473
23	23_0.6kupHBA1e1	228.1	0.882
24	26_HBA1 int2(a)	165.6	0.968
25	27_HBA1 int2(b)	253.6	0.978
26	29_0.2kb d HBA1	153.8	0.983
27	30_0.5kb d HBA1	283.9	1.014
28	31_2.3kb d HBA1	309.8	1.060
29	32_HBO1.ex3	397.7	0.878
30	33_LUC7L gene	277.6	1.049
31	34_ITFG3 gene	444.5	1.038
32	35_RGS11 gene	467.9	0.967
33	36_AXIN1 gene	417.4	0.921
34	37_DECR2 gene	265.5	0.907
35	38_Ctrl01-5q31	127.2	1.036
36	39_Ctrl02-8p23	139.5	1.035
37	40_Ctrl03-10q26	196.2	0.920
38	41_Ctrl04-12p13	208.0	1.035
39	42_Ctrl05-1q41	241.2	0.960
40	43_Ctrl06-5q31	270.4	0.933
41	44_Ctrl07-13q14	299.2	0.939
42	45_Ctrl08-11q22	353.7	0.984
43	46_Ctrl09-3q29	407.7	1.012
44	47_Ctrl10-15q26	452.8	0.950
45	48_Ctrl11-2q33	478.9	0.937
46	49_X_100	101.9	0.868
47	50_Y_105	106.3	0.000

There was a Triplication from prob 12(0.6 kb up HBA2,exon1) to prob 22(0.9kb up HBA1,exon1).
(compatible with anti 3.7 deletion).