



Human genomic control DNA

Mutation in α - globin gene (α - thalassemia)

CERTIFICATE OF ANALYSIS

Product Information

Product name :	Mutant Control DNA for α - <i>Thalassemia</i>
Cat. No. :	K5404
Concentration:	300 ng/ μ l
Storage condition :	-20°C
Mutation type:	--20.5 / -3.7 α

QC Results

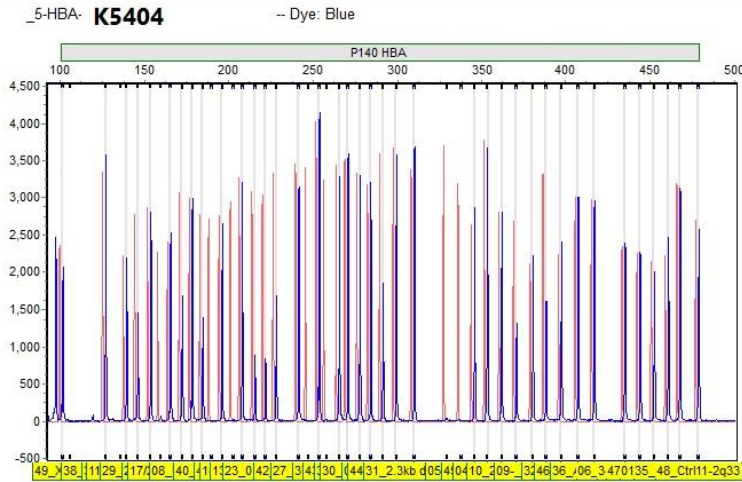
Test Items	Specifications	Results
Absorbance ratio	A260/A280>1.8 A260/A230>2.0	Passed
Electrophoresis	Average size larger than 50 kb	Passed
Sequencing	No other mutation in the gene	passed
Enzyme activity	<i>EcoRI</i> digestion	passed

Caution:

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

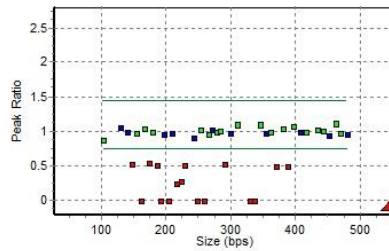
MLPA result :

MLPA Analysis Report - SoftGenetics	
Software: GeneMarker V1.95	Analysis Type: MLPA
Project: 940807-P140-C1-PROJECT.SGF	Compare Type: MLPA Ratio
Technician:	Normalization By: Population Normalization
Report Time: 11/01/2015 - 09:44:49	Quantification By: Peak Height
Panel: 00	Classification: Loss < 0.75 <= Equivalent <= 1.45 < Gain
Control: Synthetic Control Sample	Report Value Type: Peak Ratio
Synthetic Used: 94-8-7_16-HBA-P140-C1-12777PP-NL.fsa /// 94-8-7_1-HBA-P140-C1-Z-SHA-NL.fsa /// 94-8-7_6-HBA-P140-C1-H-NO-F-NL.fsa	



Machine: 3130XL-52038
Run Time: 10/29/2015 - 10:49:11 -> 10/29/2015 - 11:44:00

Conclusion	Date	Initial
Authorization 1		
Authorization 2		



Probe Name	Bin Size	94-8-7_5-HBA-P140-C1-
1 01-POLR3K gene	460.9	1.112
2 02_HS-40 (1)	178.5	0.996
3 03_HS-40 (2)	380.9	1.040
4 04_9.3kb up HBZ	362.4	1.000
5 05_3.5kb up HBZ	345.4	1.093
6 06_0.2kb up HBZ	435.4	1.024
7 07_HBZ/HBZP	291.2	0.519
8 08_HBA2PHBA1P	184.7	0.503
9 09_3kupHBA2.e1	388.5	0.485
10 10_2.5 kupHBA2	371.1	0.491
11 11_0.9kupHBA2.e	146.1	0.522
12 12_0.6kupHBA2e1	329.1	0.000
13 13/24_HBA1+A2e1	221.7	0.271
14 14/25_HBA1+A2e1	215.5	0.245
15 15_HBA2 int2(1)	159.7	0.000
16 16_HBA2 int2(2)	247.2	0.000
17 17/28_HBA1+2ex3	172.5	0.548
18 18_C.S	136.0	-1
19 19_2.6kupHBA1e1	190.0	0.000
20 20_2.1kupHBA1e1	202.7	0.000
21 21_1.5kupHBA1e1	258.0	0.000
22 22_0.9kupHBA1e1	337.6	0.000
23 23_0.6kupHBA1e1	228.1	0.509
24 26_HBA1 int2(a)	165.5	1.050
25 27_HBA1 int2(b)	253.5	1.031
26 29_0.2kb d HBA1	153.7	0.981
27 30_0.5kb d HBA1	284.0	1.007
28 31_2.3kb d HBA1	309.8	1.089
29 32_HBQ1.ex3	397.7	1.075
30 33_LUC7L gene	277.7	0.993
31 34_ITFG3 gene	444.2	1.009
32 35_RGS11 gene	467.9	0.978
33 36_AXIN1 gene	417.2	0.996
34 37_DECR2 gene	265.4	0.957
35 38_Ctr101-5q31	127.1	1.072
36 39_Ctr102-8p23	139.4	0.991
37 40_Ctr103-10q26	196.1	0.961
38 41_Ctr104-12p13	208.0	0.986
39 42_Ctr105-14q41	241.3	0.914
40 43_Ctr106-5q31	270.6	1.023
41 44_Ctr107-13q14	299.2	0.976
42 45_Ctr108-11q22	353.7	0.972
43 46_Ctr109-3q29	407.6	1.001
44 47_Ctr110-15q26	452.6	0.941
45 48_Ctr111-2q33	479.0	0.955
46 49_X_100	101.7	0.876
47 50_Y_105	106.1	-1

There was two deletion:
1) A deletion from prob 7 (between HbZ and HbZP) to prob 23 (0.6 kb up HbA1), compatible with 20.5 kb deletion.
2) A deletion from prob 13(exon 1 of HbA2) to prob 22 (0.9kb up HbA1), compatible with 3.7 kb deletion.