



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. :	K5401
Concentration:	300 ng/ μ l
Storage condition:	-20°C
Mutation type:	--Med / -3.7 α

QC Results

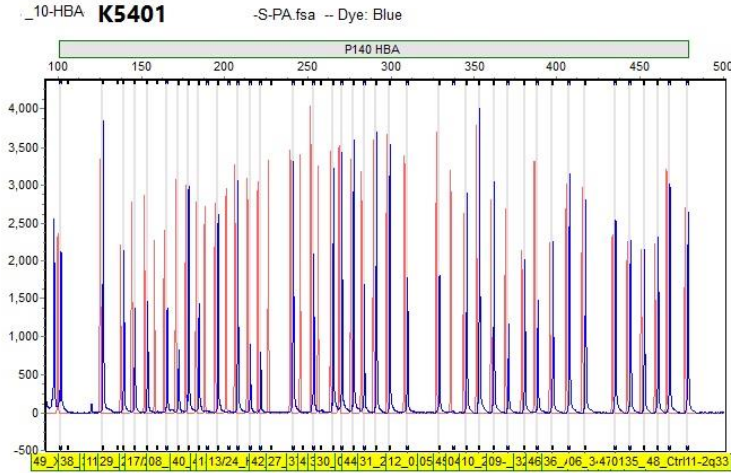
Test Items	Specifications	Results
Absorbance ratio	A260/A280>1.8 A260/A230>2.0	Passed
Electrophoresis	Average size larger than 50 kb	Passed
Sequencing	No other mutation in the gene	passed
Enzyme activity	<i>EcoRI</i> digestion	passed

Caution:

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

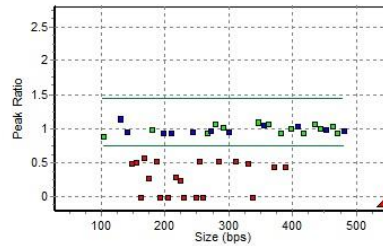
MLPA result :

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 - 09:44:48	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 - 11:44:01 -> 10/29/2015 - 12:30:20

Conclusion	Date	Initial
Authorization 1		
Authorization 2		



Probe Name	Bin Size	94-8-7_10-HBA-P140-C1
1 01-POLR3K gene	460.9	1.042
2 02_HS-40 (1)	178.5	0.996
3 03_HS-40 (2)	380.9	0.949
4 04_9.3kb up HBZ	362.4	1.082
5 05_3.5kb up HBZ	345.4	1.100
6 06_0.2kb up HBZ	435.4	1.085
7 07_HBZ/HBZP	291.2	1.030
8 08_HBA2P/HBA1P	184.7	0.519
9 09_3kupHBA2,e1	388.5	0.447
10 10_2.5 kupHBA2,	371.1	0.438
11 11_0.9kupHBA2,e	146.1	0.499
12 12_0.6kupHBA2,e1	329.1	0.492
13 13/24_HBA1+A2e1	221.7	0.236
14 14/25_HBA1+A2e1	215.5	0.291
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	0.266
18 18_C.S	136.0	-1
19 19_2.6kupHBA1,e1	190.0	0.000
20 20_2.1kupHBA1,e1	202.7	0.000
21 21_1.5kupHBA1,e1	258.0	0.000
22 22_0.9kupHBA1,e1	337.6	0.000
23 23_0.6kupHBA1,e1	228.1	0.000
24 26_HBA1 int2(a)	165.5	0.571
25 27_HBA1 int2(b)	253.5	0.519
26 29_0.2kb d HBA1	153.7	0.511
27 30_0.5kb d HBA1	284.0	0.530
28 31_2.3kb d HBA1	309.8	0.527
29 32_HBQ1,ex3	397.7	1.007
30 33_LUC7L gene	277.7	1.076
31 34_ITFG3 gene	444.2	1.009
32 35_RGS11 gene	467.9	0.940
33 36_AXIN1 gene	417.2	0.941
34 37_DECR2 gene	265.4	0.940
35 38_Ctr101-5q31	127.1	1.152
36 39_Ctr102-8p23	139.4	0.962
37 40_Ctr103-10q26	196.1	0.945
38 41_Ctr104-12p13	208.0	0.941
39 42_Ctr105-1q41	241.3	0.959
40 43_Ctr106-5q31	270.6	0.976
41 44_Ctr107-13q14	299.2	0.964
42 45_Ctr108-11q22	353.7	1.061
43 46_Ctr109-3q29	407.6	1.046
44 47_Ctr110-15q26	452.6	0.997
45 48_Ctr111-2q33	479.0	0.981
46 49_X_100	101.7	0.892
47 50_Y_105	106.1	-1

There was two deletions:
1) A deletion from prob 8(between HbA2P and HbA1P) to prob 31 (2.3kb down HbA1), compatible with Med deletion.
2) A deletion from prob 13 (exon 1 of HbA1) to prob 23 (0.6 kb up HbA1), compatible with 3.7 deletion.