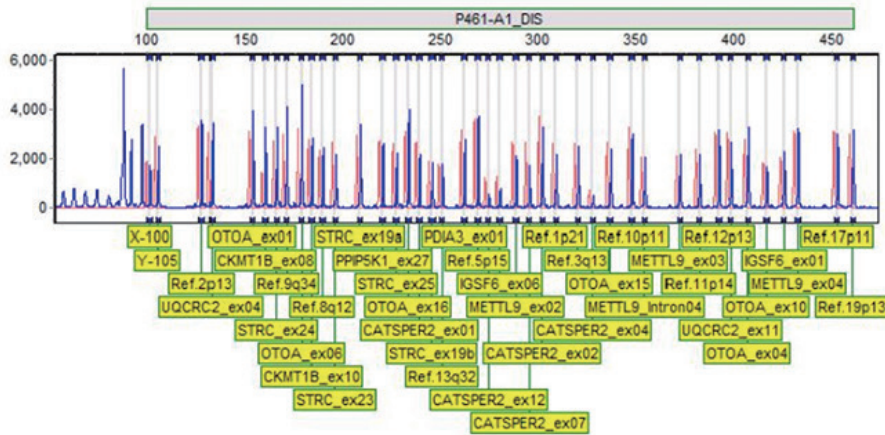


Clinical and Experimental Otorhinolaryngology

<b>MLPA Analysis Report -</b>	
Software: GeneMarker V1.91	Analysis Type: MLPA
Project: Untitled	Compare Type: MLPA Ratio
Technician:	Normalization By: Internal Control Probe Normalization
Report Time: 07/04/2018 - 09:22:05	Quantification By: Peak Height
Panel: P461-A1_DIS	Classification: Loss < 0.70 <= Equivalent <= 1.30 < Gain
Control: Synthetic Control Sample	Report Value Type: Peak Ratio
Synthetic Used: SB254-502.fsa /// SB268-527.fsa	

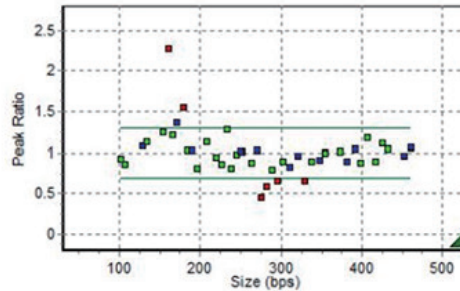
SB237-461.fsa



Probe Name	Bin Size	SB237-461
1 CATSPER2_ex01	239.2	0.806
2 CATSPER2_ex02	302.4	0.888
3 CATSPER2_ex04	328.3	0.653
4 CATSPER2_ex07	295.6	0.653
5 CATSPER2_ex12	274.7	0.449
6 CKMT1B_ex08	160.1	2.275
7 CKMT1B_ex10	184.0	1.032
8 IGSF6_ex01	425.8	1.116
9 IGSF6_ex06	280.6	0.596
10 METTL9_intron04	355.0	0.998
11 METTL9_ex02	288.8	0.791
12 METTL9_ex03	372.4	1.012
13 METTL9_ex04	432.9	1.046
14 OTOA_ex01	153.7	1.258
15 OTOA_ex04	407.3	1.182
16 OTOA_ex06	178.7	1.549
17 OTOA_ex10	416.8	0.858
18 OTOA_ex15	337.3	0.897
19 OTOA_ex16	233.7	1.287
20 PDIA3_ex01	282.4	0.873
21 PPIPSK1_ex27	220.3	0.951
22 Ref.10p11	348.5	0.915
23 Ref.11p14	382.3	0.893
24 Ref.12p13	392.3	1.040
25 Ref.13q32	251.0	1.005
26 Ref.17p11	453.1	0.964
27 Ref.19p13	461.2	1.056
28 Ref.1p21	309.4	0.833
29 Ref.2p13	128.0	1.073
30 Ref.3q13	320.7	0.957
31 Ref.5p15	269.3	1.032
32 Ref.8q12	189.6	1.029
33 Ref.9q34	171.1	1.363
34 STRC_ex19a	208.8	1.140
35 STRC_ex19b	245.8	0.972
36 STRC_ex23	196.2	0.808
37 STRC_ex24	166.1	1.216
38 STRC_ex25	227.4	0.864
39 UQCRC2_ex04	133.1	1.125
40 UQCRC2_ex11	398.5	0.884
41 X-100	101.4	0.928
42 Y-105	105.9	0.885

Sample Name: SB237-461  
 Machine: Macrogen3730XL19-20143-018  
 Run Time: 06/06/2018 - 03:23:50 -> 06/06/2018 - 04:07:19  
 Statistics # Probes Mean StdDev  
 Control/Sample 12/30 1.01/1.00 0.13/0.33

Conclusion		
	Date	Initial
Authorization 1		
Authorization 2		



Supplementary Fig. 2. Multiplex ligation dependent probe amplification (MLPA) screening to identify *STRC* variants and large deletion in the *STRC* gene.