SNP Biotechnology

IntRaFast-Q SMA NEWBORN SCREENING KIT
Cat. No: 200R-40-03

PRODUCT DESCRIPTION

Spinal muscular atrophy (SMA) is characterized by degeneration of the alpha motor neurons of the spinal cord anterior horn cells, leading to progressive proximal muscle weakness and atrophy. The carrier frequency of SMA from 1/20 to 1/60. IntRaFast-Q SMA Newborn Screening Kit detects the exon 7 & 8 deletion and C/T substitution at nucleotide 840 of exon 7 in the SMN1 gene to diagnose the carrier and homozygous types by Quantitative Real Time PCR (qPCR) from dried blood spots (DBS). The kit has % 100 sensitivity and % 100 specificity for the detection of above mentioned targets in homozygous and carrier types.

PRINCIPLE OF THE SYSTEM

Test uses 5′ Nuclease Assay. During the PCR reaction, the DNA polymerase cleaves the probe at the 5′ end and separates the reporter dye from the quencer dye only when the probe hybridizes perfectly to the target DNA. This cleavage results in the fluorescent signal which is monitored by Real-Time PCR detection system. An increase in the fluorescent signal (Ct) is proportional to the amount of the specific PCR product. The system is based on **"Intelligent Ratio (IR)"** between reference and target genes quantifications. **IR** values may vary according to Bio-Rad CFX96 Real Time PCR devices. Therefore IntRa-Q Software should be adjusted to the Bio-Rad CFX96 Real Time PCR device during system setup (see Validation of device and Data Analysis sections).

PRODUCT SPECIFICATION

Isolated DNA should be tested with IntRaFast-Q master mix including specific primer and probes for the exon 7 & 8 deletion and C/T substitution at nucleotide 840 of exon 7 in the SMN1 gene. The system provides all reagents as **"ready-to-use"** which has been specifically adapted for qPCR. The dyes of IntRaFast-Q master mix are FAM for SMN1 Exon 7 & C/T substitution at nucleotide 840, HEX for SMN1 Exon 8 and TEXAS RED for reference gene.

SYSTEM CONTENTS

Reagents	50 rxns	20 rxns
• IntRaFast-Q Master Mix	1150 µl	460 µl
• 10x Solution D	500 µl	200 µl
• Carrier Control DNA *	30 µl	15 µl
• Homozygous Deletion Control DNA *	30 µl	15 µl
• Wild-Type Control DNA *	30 µl	15 µl

* Control DNAs including plasmids were adjusted to DBS extracted DNA. Amplification plots of plasmid control DNA may appear slightly different from the sample DNA.

DNA EXTRACTION

The Kit provides high sensitivity with a limit of detection (LOD) level of 0.5 ng/µl.

DBS (Dry Blood Spot)

- The system is suitable for DBS samples from newborn (heel blood etc.).
- Prepare fresh **1x Solution D** by diluting the provided **10x Solution D** with PCR Grade water.
- A piece of DBS (punch-3 mm) is put into a 1.5 ml centrifuge tube.
- Add **100 µl of 1x Solution D** onto the punch. Lightly vortexed. Make sure that the punch is completely in the solution.
- Incubate for **5 minutes at room** temperature.
- **2 µl of DNA** is used from the supernatant part.

VALIDATION OF DEVICE;

- Leave the master mix and control DNAs at RT to melt.
- Mix the melted master mix gently by pipetting.
- For each control, pipette **23 µl master mix** into PCR tubes/strips.
- **2 µl** of different **Control DNAs** (carrier, homozygous deletion and wild type) and 5-10 **unknown DNAs** belonging to the isolation system to be studied are added to each tube to control the isolation system. Optical caps are closed. Run with the programme shown below.
- Control samples should identify expected genotypes for device validation. If they are not, please contact to manufacturer for validation of your device (tech@snp.com.tr).
- It is sufficient that the validation of each device should be made **only once for each lot.**
- After the device validation, continue with the standard test protocol.

STANDARD TEST PROTOCOL;

- Leave the master mix at RT to melt.
- Mix the melted master mix gently by pipetting.
- For each samples, pipette **23 µl master mix** into each PCR tubes/strips.
- Add **2 µl Sample DNA** into each tube and close the optical caps.
- Run with the programme shown below.

PCR PROGRAMME

96 °C	2 Sec.	**36 x Cycles**
60 °C	40 Sec.	

Select FAM, HEX and TEXAS RED as fluorescent dyes.

Real Time PCR time is **55 minutes for DBS** samples.

- To detect **Wild Type, carrier and homozygous deletion**; the system can be used only with **Bio-Rad CFX96** that is compatible with **Intra-Q Software.**
- To detect **only homozygous deletion;** all devices can be used.

DATA ANALYSIS

- You should use IntRa-Q Software that can calculate IR values for data analysis. Please check the manual of IntRa-Q Software.
- The results should be seen like **Figure 1.**
- You can also check the results by amplification plots **(Figures 2 to 4).**

File: D:\SMA Software Analysis\2019_BLOOD\Experiment_54 - Quantification Cq Results.xls

	1	2	3	4	5	6	7	8	9	10	11	12
A	A01 Wild Type 2.62	A02 Wild Type 2.88	A03 Wild Type 2.91	A04 Wild Type 3.13	A05 Wild Type 3.13	A06 Carrier 8.53	A07 Wild Type 3.08	A08 Wild Type 3.18	A09 Wild Type 2.67	A10 Wild Type 2.94	A11 Wild Type 3.13	A12 Wild Type 4.26
B	B03 Wild Type 2.61	B02 Wild Type 2.84	B01 Carrier 9.59	B04 Wild Type 3.44	B05 Wild Type 3.16	B06 Wild Type 3.33	B07 Wild Type 3.65	B08 Wild Type 3.07	B09 Wild Type 1.82	B10 Wild Type 2.70	B11 Wild Type 2.79	B12 Wild Type 3.87
C	C01 Wild Type 2.98	C02 Wild Type 3.26	C03 Wild Type 3.41	C04 Wild Type 2.83	C05 Wild Type 2.70	C06 Wild Type 3.17	C07 Wild Type 3.42	C08 Homozygous Deletion -1	C09 Wild Type 3.30	C10 Wild Type 3.27	C11 Wild Type 3.83	C12 Wild Type 3.91
D	D01 Wild Type 3.27	D02 Carrier 9.10	D03 Wild Type 2.03	D04 Wild Type 2.99	D05 Wild Type 3.08	D06 Wild Type 3.49	D07 Wild Type 3.87	D08 Wild Type 3.71	D09 Wild Type 3.77	D10 Wild Type 3.16	D11 Wild Type 3.37	D12 Wild Type 4.13
E	E01 Wild Type 2.84	E02 Wild Type 3.27	E03 Wild Type 3.21	E04 Wild Type 2.70	E05 Wild Type 3.08	E06 Wild Type 3.28	E07 Wild Type 3.38	E08 Carrier 10.08	E09 Wild Type 3.47	E10 Carrier 9.84	E11 Wild Type 3.14	E12 Wild Type 3.89
F	F01 Wild Type 3.44	F02 Wild Type 3.13	F03 Wild Type 3.06	F04 Carrier 9.04	F05 Wild Type 3.59	F06 Wild Type 3.21	F07 Wild Type 3.30	F08 Wild Type 3.76	F09 Wild Type 2.73	F10 Wild Type 2.77	F11 Wild Type 3.16	F12 Wild Type 3.42
G	G01 Wild Type 2.86	G02 Wild Type 3.36	G03 Wild Type 1.72	G04 Wild Type 3.04	G05 No DNA -2	G06 Homozygous Deletion -1	G07 Wild Type 3.47	G08 Wild Type 1.86	G09 Repeat 53.76	G10 Wild Type 2.94	G11 Wild Type 3.09	G12 Wild Type 3.36
H	H01 Homozygous Deletion -1	H02 Wild Type 2.85	H03 Wild Type 2.99	H04 Wild Type 2.47	H05 Wild Type 4.42	H06 Wild Type 3.51	H07 Wild Type 3.09	H08 Wild Type 2.73	H09 Wild Type 1.21	H10 Wild Type 2.68	H11 Wild Type 2.93	H12 Wild Type 2.91

Figure 1: Results by IntRa-Q Software

The IntRa-Q Software which is based on IR method calculates a ratio of "reference gene quantification / SMN1 gene Exon 7 and Exon 8 quantification. Both the quantifications of the reference gene and the SMN1 gene were detected by means of embedded slope value in the software, and the ratio of these quantification values determined the IR value. The software gives the results automatically based on these values [1].

To check the amplification plots of SMA carrier states and homozygous deletion, FAM (SMN1 Exon 7 - blue plot), HEX (SMN1 Exon 8 - green plot) and TEXAS RED (Reference gene - red plot) dyes should be analyzed together.

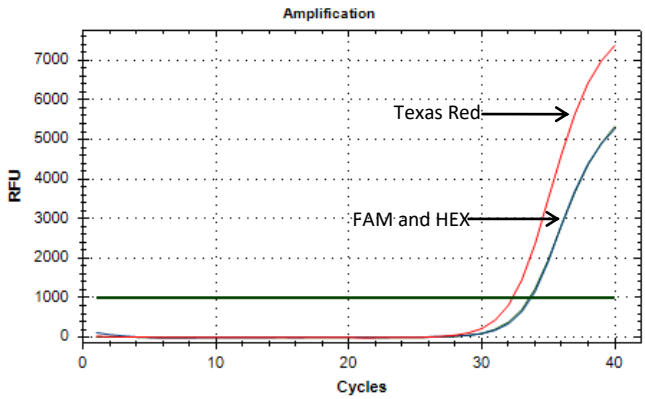

Figure 2: SMN1 Exon 7 and Exon 8 Wild-Type Sample

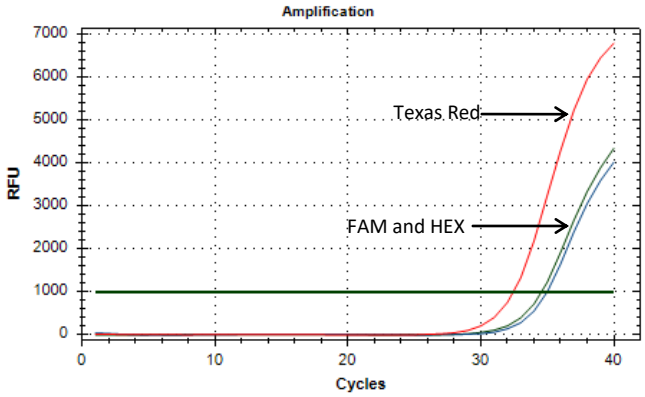

Figure 3: SMN1 Exon 7 and Exon 8 Carrier sample

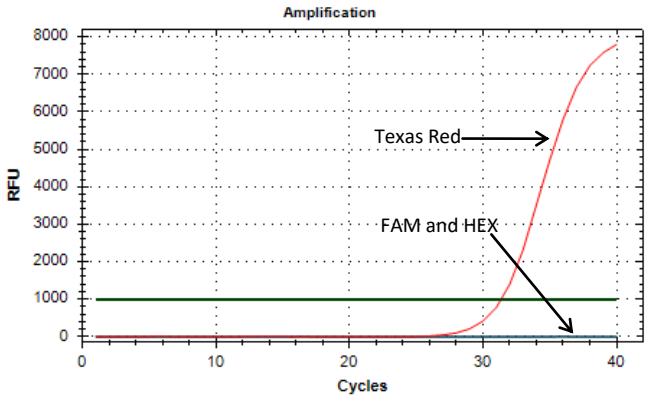

Figure 4: SMN1 Exon 7 and Exon 8 Homozygous Deletion

Important points to take into account;

- The results of homozygous deletion and carrier state should be checked from the data analysis screen as amplification plots.
- Some PCR failure problems; like air bubble formation, low quality DNA, etc. may cause unaccepted amplification plots as seen in Figure 5, 6, 7 and 8 it may not be evaluated properly by the software. Please check the amplification plots and re-test the sample if required.
- If the sample is SMN1 Exon 8 carrier and Exon 7 wild-type states, it should be re-tested. In case the results are same, it should be confirmed by DNA sequence analysis.
- If the sample is SMN1 Exon 7 carrier and Exon 8 wild-type states, it should be re-tested for confirmation.

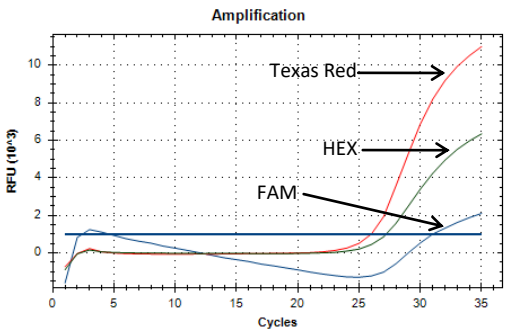

Figure 5: Unaccepted amplification plots

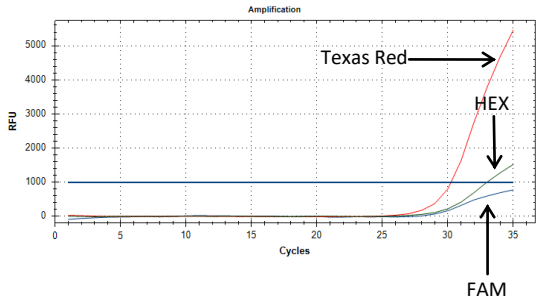

Figure 6: Unaccepted amplification plots

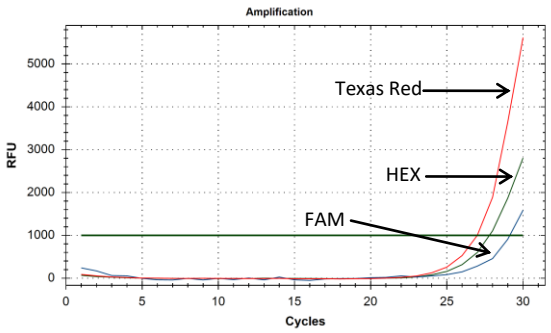

Figure 7: Unaccepted amplification plots

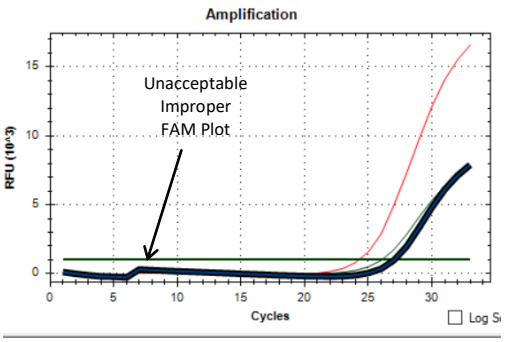

Figure 8: Unaccepted amplification plots

Inability in the IntRaFast-Q SMA Screening Analysis;

- The IntRaFast-Q SMA Newborn Screening Kit performs carrier state and homozygous deletion on Exon 7 and Exon 8 of SMN1 gene. Therefore, the kit does not detect other rare intragenic mutations (2-4%) that cause SMA disease.
- The IntRaFast-Q SMA Newborn Screening Kit detects the dosage of SMN1 gene. In a normal individual, 2 copies of the SMN1 gene are found (1 + 1). In rare cases (1-4%), there is no SMN1 gene in one chromosome but 2 SMN1 genes in the other chromosome (2 + 0). In this case, two copies of SMN1 are reported with the kit. However, the subject is the carrier state for SMA disease.

TROUBLE SHOOTING

If there is no amplification in the well,

- Absence of DNA
- Sample is containing DNA inhibitor(s)

Please contact us for your questions, tech@snp.com.tr

CAUTIONS

- All reagents should be stored at suitable conditions.
- Do not use the PCR master mixes forgotten at room temperature.
- Shelf-life of PCR master mix is 24 months. Please check the manufacturing date before use.
- Only use in vitro diagnostics and research.

STORAGE

- All reagents should be stored at – 20 °C and dark.
- All reagents can be used until the expiration date, mentioned on the box label.
- Repeated thawing and freezing (>5X) should be avoided, as this may reduce the sensitivity of the assay.

REFERENCES

1. B. Cavdarli,1F. N. Ozturk, S. G. Ergun, M. A. Ergun, O. Dogan and E. F. Percin. "Intelligent Ratio:A New Method for Carrier and Newborn Screening in Spinal Muscular Atrophy". Genetic Testing And Molecular Biomarkers, Volume 24, Number 9, 2020.
2. American College of Obstetricians and Gynecologists' Committee on Genetics in collaboration with committee members Britton Rink, Stephanie Romero, Joseph R. Biggio Jr, Devereux N. Saller Jr. and Rose Giardine.Committee Opinion. Number 691. March 2017.
3. Shin S1, Park SS, Hwang YS, Lee KW, Chung SG, Lee YJ, Park MH. Deletion of SMN and NAIP genes in Korean patients with spinal muscular atrophy. J Korean Med Sci. 2000;15:93-8.
4. Verhaart IEC, Robertson A, Wilson IJ, Aartsma-Rus A, Cameron S, Jones CC, Cook SF, Lochmüller H. Prevalence, incidence and carrier frequency of 5q-linked spinal muscular atrophy - a literature review. Orphanet J Rare Dis. 2017;12:124.

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