<b>Reply to</b>	the	reviewers'	comments
-----------------	-----	------------	----------

Reviewer Number	Original comments of the reviewer	Reply by the author(s)	Changes done on the page number and line number
	ŀ	REVISION	
Main Reviewer	This case was not a candidate for combined PGT (PGT-A and PGT-M), why PGS was done for them?	Dear reviewer We are grateful immensely to the main reviewer for providing us with suggestions. We apologize for very late response as we need to re-run the PCR process to complete the figure after enzymatic digestion as your suggestion. Here are our responses point-to-point according to your comments: As the incidence of obtaining embryos with abnormal chromosome(s) (aneuploidy) following an IVF program is relatively high, the patient has been suggested to check the ploidy status of the embryo before performing PGT-M. This strategy would be more effective to attain a high probability of pregnancy rather than performing PGT-M only.	
	For what their abnormal embryo (17q11.2- 17q24.2, 39.50Mbp) was frozen, this deletion is normal variant?	The procedures of IVF – PGT-A/PGT-M in our clinic begin with trophectoderm biopsy. Well-trained embryologists will assess the quality and decide which blastocyst will be chosen for PGT-A/PGT-M. All biopsied embryos will be stored in liquid nitrogen until the clinicians and patients receive the	

	report of genetic analysis.	
	The deletion is not a normal variant. However, the termination of abnormal- frozen embryos is decided by the patient after having a round consultation with the expert geneticist in our clinics. The patient requested to keep the embryo up to now. Therefore, the abnormal embryo (17q11.2- 17q24.2, 39.50Mbp) remains to be kept up to now.	
Valuable work has been done for detecting SMN-1 and SMN-2 exon 7-8 deletion using PCR- restriction fragment length polymorph (RFLP) method, but you don't mentioned the size of expected bands resulting from enzym digestion?	Thank you very much for your reminder. We have added the data of expected band size before and after enzymatic digestion in the revised manuscript "The expected band for <i>SMN</i> Exon 7 and exon 8 after PCR was 187 bp and 186 bp. After enzyme digestion, the <i>SMN</i> exon 7 band in healthy embrio was expected to be cleaved into 2 bands, while exon 8 was into 3 bands, as shown in Figure 2. SMA positive and negative control samples were provided for comparison and quality control of the PCR and digestion process. Here, <i>SMN1</i> deletion was confirmed when the digestion only resulted in one band of <i>SMN</i> exon 7 and two bands of <i>SMN exon 8.</i> "	Page 3, Line 127-132
In addition, the image of PCR product before and after enzymatic digestion was not presented	The complete image of the PCR product has been provided, before and after the digestion, along with the expected size of the band and	Figure 2 Page 5, Line 147-160

	marker.	
Finally and most importantly please explain	Thank you very much for your comment.	Figure 2
how to control and verify the function of	In our deletion test analysis protocol, we	Page 5, Line 147-160
applied restriction	always use, already established positive and	
	negative control samples, as standards in	
	each analysis. Thus, the function of applied	
	restriction could be monitored and confirmed	
	by observing the band separation of positive	
	and negative control samples.	
	On the other hand, our protocol used Dra1	
	and HcoB1 as restriction enzymes which	
	digest the bands into two separated bands for	
	exon 7 and three separated bands for exon 8.	
	Thus, the malfunction of the restriction	
	enzyme could be found easily when there	
	was only single band present in the positive	
	and negative control samples, after the	
	digestion process.	
	We provided the band image of enzymatic	
	digestion in the manuscript and added	
	additional sentences in the method section.	



