



SDI FINAL EVALUATION FORM 1.1

PART 1:

Journal Name:	Journal of Advances in Medical and Pharmaceutical Sciences
Manuscript Number:	Ms_JAMPS_34294
Title of the Manuscript:	CORRELATION BETWEEN GENE PROMOTER POLYMORPHISM AND ANDROGEN RECEPTOR GENE EXPRESSION WITH HYPOSPADIA INCIDENCE
	THE CORRELATION OF PROMOTER POLYMORPHISM AND EXPRESSION OF ANDROGEN RECEPTOR GENE WITH HYPOSPADIA INCIDENCE
Type of Article:	Original Research Article

PART 2:

FINAL EVALUATOR'S comments on revised paper (if any)	Authors' response to final evaluator's comments
- The article's title implies that a correlation analysis was performed; however, I do not see any correlation analysis in this document. If a correlation analysis was indeed performed, please explain with detail in the Methodology, indicating the type of correlation (Pearson, Spearman) including the correlation coefficient and significance values, as well as a figure showing the result. Table 5 does not show any correlation analysis, it shows gene expression values, which should be presented in a figure. - When I asked for the whole promoter sequence, the idea was to show how much (in %) of the promoter was analysed for polymorphisms, I did not ask for multiple alignment. - Table 2 does not show the reference gene, it shows qPCR primers for the AR. The authors did not answer my question regarding qPCR analysis, I asked them to indicate the reference gene(s) used for qPCR analysis, and the methods used to calculate gene expression (standard curve, comparative CT...). This information should be explained in the Methodology section. In addition, I asked them to include a figure showing gene expression results, I did not asked for the standard curve. - Please refer to tables and figures in the text. - The document needs English edition; there are several grammatical and spelling mistakes, as well as typos.	- We analyzed the statistic result with chi square test and Mann-Whitney test - The promoter that was analyzed was 67.3% (688) bp from 1.022 bp (100%) - We used Real time PCR for absolute qPCR analysis so we didn't need reference genes because we only used standard curve. - We could see the standard curve at picture 6 - Ok, I will fix it