**Reply to Reviewers**

Thank you for your useful comments.

Description of responses/corrections to reviewer comments are in italics.

**Reviewer #1:**  
  
1. KIR2DL2 and KIR2DL3, as well as KIR3DL1 and KIR3DS1, segregate as alleles of the same locus. Accordingly, the sentence reporting KIR gene number (lines 19-20) should be revised.

*This sentence now reads “The KIR loci that are currently known are KIR2DL1, KIR2DL2/KIR2DL3, KIR2DL4, KIR2DL5A, KIR2DL5B, KIR2DS1-5, KIR3DL1/KIR3DS1, KIR3DL2-3 and two pseudogenes, KIR2DP1 and KIR3DP1.”*

2. Introduction fails to report knowledge about some KIR/KIR ligand pairs (lines 35-36). In particular, it has been demonstrated that HLA Cl-I molecules are also recognized by KIR2DL4, KIR2DS2 and KIR3DS1 (Rajagopalan 1999 J. Exp. Med., Liu 2014 Proc. Natl. Acad. Sci. USA, David, 2013 J. Immunol., Burian 2016 PLoS One, Carlomagno 2017 Front. Immunol.)

*Introduction has been modified and appropriate references added to relay this information; “HLA Class I molecules have been identified as the ligands for certain inhibitory receptors (KIR2DL1, KIR2DL2, KIR2DL3, KIR3DL1), activating receptors (KIR2DS1, KIR2DS2, KIR2DS4, KIR2DS5 and KIR3DS1) receptors and for KIR2DL4 which is a unique KIR that contains long cytoplasmic tails like other inhibitory KIR receptors but also has a positively charged residue near the extracellular domain which is a common feature of other activating KIR receptors. The combination of variants within the KIR genes and the HLA genes influence receptor-ligand interaction shaping potential NK cell responsiveness at the individual level7,8.”*

3. Pseudogenes are not mentioned in the introduction section but are both target in the protocol. A sentence about KIR2DP1 and KIR3DP1 could be added in the introduction.

*The pseudogenes are now included in the introduction; “The KIR loci that are currently known are KIR2DL1, KIR2DL2/KIR2DL3, KIR2DL4, KIR2DL5A, KIR2DL5B, KIR2DS1-5, KIR3DL1/KIR3DS1, KIR3DL2-3 and two pseudogenes, KIR2DP1 and KIR3DP1.”*  
  
4. Ramping temperature (i.e. °C/sec) can be included in the description of cycling conditions.

*Non-applicable – temperature ramping was not used in the qPCR cycling program.*  
5. The Y-axis labels in Figures 1B and 2B are difficult to read. Please increase the font size.

*The font size has been increased.*  
  
6. Last step of flowchart should be identified with the number 6.

*Corrected.*  
  
7. Reference at line 38 is indicated using author name and publication year, please use the corresponding reference list number. *Corrected*  
  
8. The authors should carefully revise the references according to journal style  
-Last page number is not always correctly indicated (i.e. ref. 1, 4, 6, 9, 13).

*Our citations are consistent with the journals. Please note that PLoS Genetics references do not contain page numbers.*  
-In my opinion reference 13 supports sentence at lines 37-38. A study reporting relevance of donor B content analysis in allogenic hematopoietic stem cell transplantation could be added (i.e. Cooley, 2010 Blood).

*This reference has now been used to support this sentence.*  
-Title and page numbers of reference 16 are missing.

*This reference has been replaced by three more relevant publications:*

*Vilches et al. 2007, Ashouri et al. 2009 and Martin et al. 2008.*  
-References 23 and 24 are identical.

*Duplicate reference has been removed.*  
  
**Reviewer #2:**  
  
9. Compliance with the MIQE guidelines (1) should be checked.

*After careful review, we believe the manuscript is fully compliant with MIQE guidelines in relation to qPCR of genomic DNA.*