

**Molecular Pharmacology (MOLPHARM-AR-2023-000671)**

**Supplemental Material**

**A Point Mutation at C151 of Keap1 of Mice Abrogates Nrf2 Signaling, Cytoprotection  
*In Vitro* and Hepatoprotection *In Vivo* by Bardoxolone Methyl (CDDO-Me)**

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**Supplemental Table 1: Primers Used**

<i>Nqo1</i>	Forward	5' – GGCATCCTGCGTTTCTGTG – 3'
	Reverse	5' – GGTTTCCAGACGTTTCTTCCAT – 3'
<i>Gstm1</i>	Forward	5' – AACTGGGATACTGGAACGTCC – 3'
	Reverse	5' – AGTCAGGGTTGTAACAGAGCAT – 3'
<i>Gpx2</i>	Forward	5' – ATTGCCAAGTCGTTCTACGA – 3'
	Reverse	5' – GTAGGACAGAAACGGATGGA – 3'
<i>Srxn1</i>	Forward	5' – AGGGGCTTCTGCAAACCTA – 3'
	Reverse	5' – TGGCATAGCTACCTCACTGCT – 3'
<i>Cbr3</i>	Forward	5' – CGGGCATCGCCTTTAGAATG – 3'
	Reverse	5' – GCTTGAATGTCGAAGGGTGTT – 3'
<i>Beta-actin</i>	Forward	5' – GAACCCTAAGGCCAACCGTG – 3'
	Reverse	5' – CAGAGGCATACAGGGACAGC – 3'

## Supplemental Methods

*Alignment Parameters used:*

*STARref mm10 downloaded from:*

*[https://support.illumina.com/sequencing/sequencing\\_software/igenome.html](https://support.illumina.com/sequencing/sequencing_software/igenome.html)*

*gtfFile annotations downloaded from:*

*[https://www.gencodegenes.org/mouse/release\\_M23.html](https://www.gencodegenes.org/mouse/release_M23.html)*

STAR \

```
--genomeDir $STARref \  
--readFilesIn ${R1} ${R2} \  
--readFilesCommand zcat \  
--runThreadN 4 \  
--sjdbGTFfile $gtfFile \  
--outFilterMultimapNmax 20 \  
--alignIntronMax 500000 \  
--alignMatesGapMax 1000000 \  
--sjdbScore 2 \  
--alignSJDBoverhangMin 1 \  
--outFilterMatchNminOverLread 0.33 \  
--outFilterScoreMinOverLread 0.33 \  
--sjdbOverhang 100 \  
--twopassMode Basic \  
--outSAMstrandField intronMotif \  
--outSAMattributes NH HI NM MD AS XS \  
--outSAMtype BAM SortedByCoordinate \  
--outSAMunmapped Within \  
--outSAMheaderHD @HD VN:1.4 \  
--quantMode TranscriptomeSAM GeneCounts
```