

**Whole-genome resequencing reveals domestication and signatures of selection in Ujimqin, Sunit, and
Wu Ranke Mongolian sheep breeds**

Hanning *Wang*^{1a}, Liang *Zhong*^{2a}, Yanbing *Dong*¹, Lingbo *Meng*¹, Cheng *Ji*¹, Hui *Luo*¹, Mengrong *Fu*¹, Zhi
Qi^{1*}, and Lan *Mi*^{1*}

***Corresponding Author: Lan Mi**

E-mail: lanmi_90@126.com

Zhi Qi

E-mail: qizhi@imu.edu.cn

¹ State Key Laboratory of Reproductive Regulation and Breeding of Grassland Livestock, School of Life Sciences, Inner Mongolia University, Hohhot 020020, China

² Hebei Provincial Key Laboratory of Basic Medicine for Diabetes, The Shijiazhuang Second Hospital, Shijiazhuang 050051, China

^a These authors contributed equally to this work.

Table S4 KEGG between UJMQ and WRK

	<u>P-value</u>	<u>Term</u>	<u>Symbols</u>
<u>1</u>	<u>0.004522</u>	<u>Long-term potentiation</u>	<u>ITPR2;GRIN2B</u>
<u>2</u>	<u>0.005766</u>	<u>Phosphatidylinositol signaling system</u>	<u>ITPR2;DGKB</u>
<u>3</u>	<u>0.028939</u>	<u>Calcium signaling pathway</u>	<u>ITPR2;PDE1A</u>
<u>4</u>	<u>0.029241</u>	<u>Alzheimer's disease</u>	<u>ITPR2;GRIN2B</u>
<u>5</u>	<u>0.060525</u>	<u>Neuroactive ligand-receptor interaction</u>	<u>GRIN2B;GRID1</u>
<u>6</u>	<u>0.074186</u>	<u>Glycerolipid metabolism</u>	<u>DGKB</u>
<u>7</u>	<u>0.079904</u>	<u>Amyotrophic lateral sclerosis (ALS)</u>	<u>GRIN2B</u>
<u>8</u>	<u>0.094061</u>	<u>p53 signaling pathway</u>	<u>CHEK2</u>
<u>9</u>	<u>0.102462</u>	<u>Melanoma</u>	<u>MITF</u>
<u>10</u>	<u>0.103856</u>	<u>Gastric acid secretion</u>	<u>ITPR2</u>
<u>11</u>	<u>0.105247</u>	<u>Long-term depression</u>	<u>ITPR2</u>
<u>12</u>	<u>0.112176</u>	<u>Salivary secretion</u>	<u>ITPR2</u>
<u>13</u>	<u>0.117685</u>	<u>Glycerophospholipid metabolism</u>	<u>DGKB</u>
<u>14</u>	<u>0.129969</u>	<u>Gap junction</u>	<u>ITPR2</u>
<u>15</u>	<u>0.136727</u>	<u>Melanogenesis</u>	<u>MITF</u>
<u>16</u>	<u>0.139417</u>	<u>Pancreatic secretion</u>	<u>ITPR2</u>
<u>17</u>	<u>0.139417</u>	<u>GnRH signaling pathway</u>	<u>ITPR2</u>
<u>18</u>	<u>0.163296</u>	<u>Vascular smooth muscle contraction</u>	<u>ITPR2</u>
<u>19</u>	<u>0.169824</u>	<u>Oocyte meiosis</u>	<u>ITPR2</u>
<u>20</u>	<u>0.172422</u>	<u>Axon guidance</u>	<u>PLXNA2</u>
<u>21</u>	<u>0.175013</u>	<u>Osteoclast differentiation</u>	<u>MITF</u>
<u>22</u>	<u>0.18146</u>	<u>Cell cycle</u>	<u>CHEK2</u>
<u>23</u>	<u>0.220437</u>	<u>Purine metabolism</u>	<u>PDE1A</u>
<u>24</u>	<u>0.253031</u>	<u>Systemic lupus erythematosus</u>	<u>GRIN2B</u>
<u>25</u>	<u>0.262453</u>	<u>Huntington's disease</u>	<u>GRIN2B</u>
<u>26</u>	<u>0.339436</u>	<u>MAPK signaling pathway</u>	<u>RAPGEF2</u>
<u>27</u>	<u>0.388689</u>	<u>Pathways in cancer</u>	<u>MITF</u>
<u>28</u>	<u>0.845593</u>	<u>Metabolic pathways</u>	<u>DGKB</u>