Table S2 Statistics of the alignment results of Reads on the reference genome sequence.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Statistics | All | UnMapped | Mapped | Mapped Rate | Unique  Mapped | Unique Mapped Rate | MultiMapped |
| OB *Fam20cf/f*-1 | 85613308 | 165889 | 85447419 | 0.998 | 79892877 | 0.933 | 5554542 |
| OB *Fam20cf/f*-2 | 131179680 | 206712 | 130972968 | 0.998 | 121672786 | 0.928 | 9300182 |
| OB *Fam20cf/f*-3 | 156972060 | 353390 | 156618670 | 0.998 | 147996816 | 0.943 | 8621854 |
| OB *Fam20cKO*-1 | 139044470 | 280528 | 138763942 | 0.998 | 128833616 | 0.927 | 9930326 |
| OB *Fam20cKO*-2 | 171135022 | 384854 | 170750168 | 0.998 | 158433157 | 0.926 | 12317011 |
| OB *Fam20cKO*-3 | 106671581 | 130273 | 106541308 | 0.999 | 94712010 | 0.888 | 11829298 |