

Table of Content of the RNA-seq Quality check:
Appendix Figure S1 (p. 1-2)

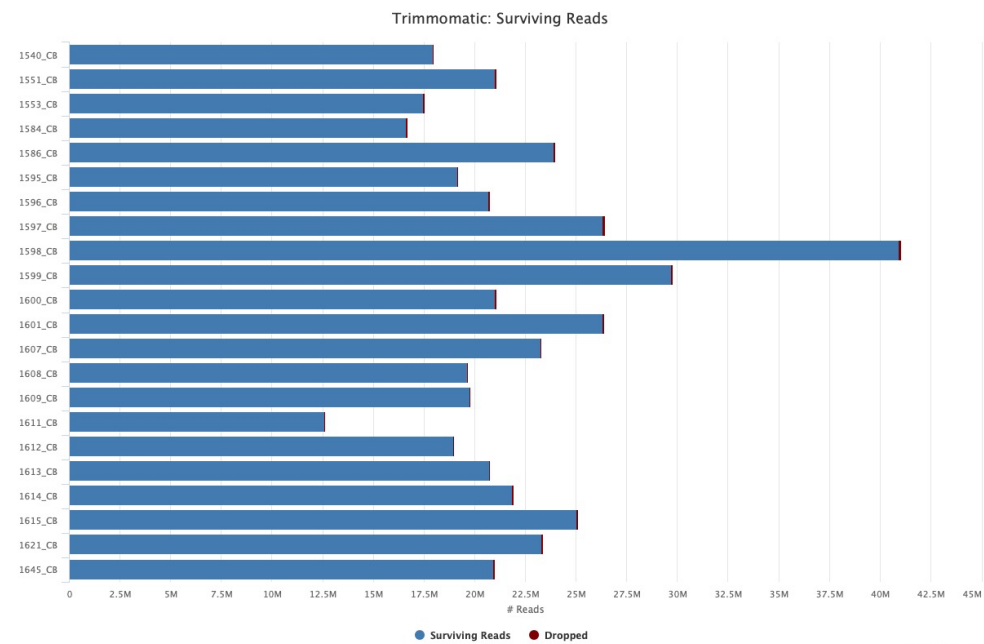
Appendix Figure S1

- A) Table reporting sample IDs, genotypes and transplantation conditions of the sequenced samples.
B) Number of retained reads after Trimmomatic adapter trimming.
C) Unique versus duplicated number of reads
D) STAR alignment scores: number of uniquely mapped reads, mapped to many loci or unmapped.
E) Number of reads assigned to genes by HTSeq.

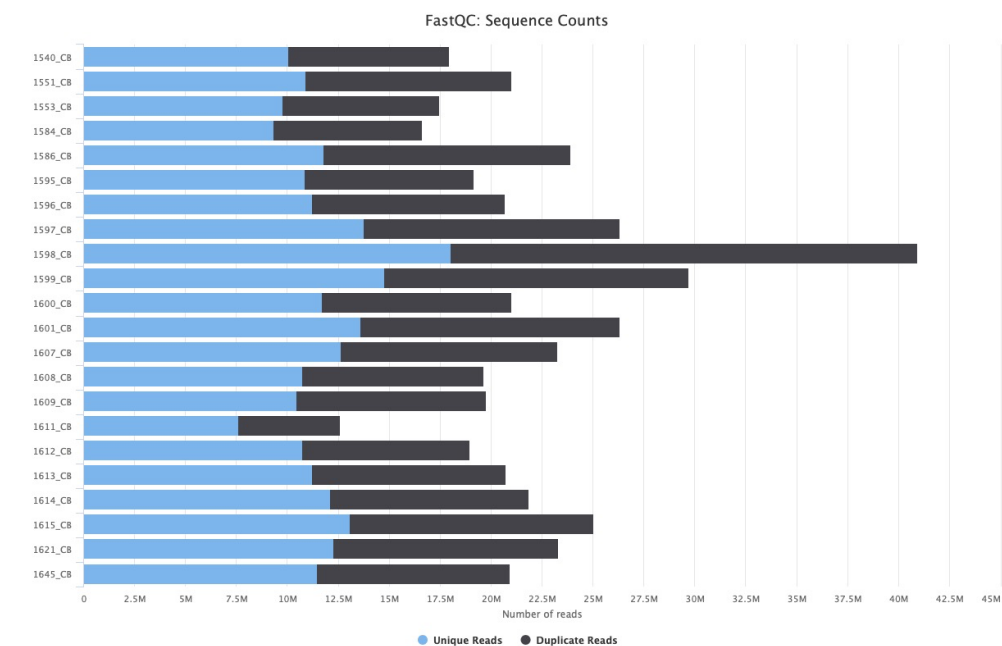
A

sampleID	1540	1551	1553	1584	1586	1595	1596	1597	1598	1599	1601	1607	1608	1609	1611	1612	1613	1614	1615	1621	1645
genotype	KO	WT	WT	KO	WT	WT	WT	WT	WT	KO	KO	KO	KO	KO	KO	WT	WT	WT	WT	KO	KO
condition	PBS	PBS	PBS	NPC	PBS	PBS	PBS	NPC	NPC	NPC	PBS	NPC	NPC	NPC	PBS	PBS	PBS	NPC	NPC	NPC	PBS

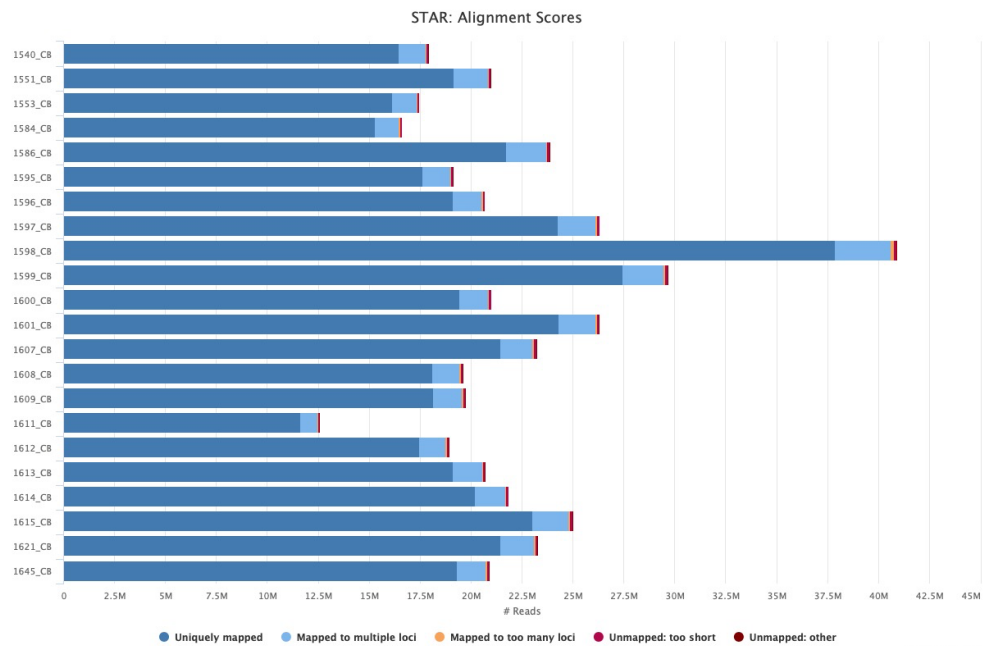
B



C



D



E

