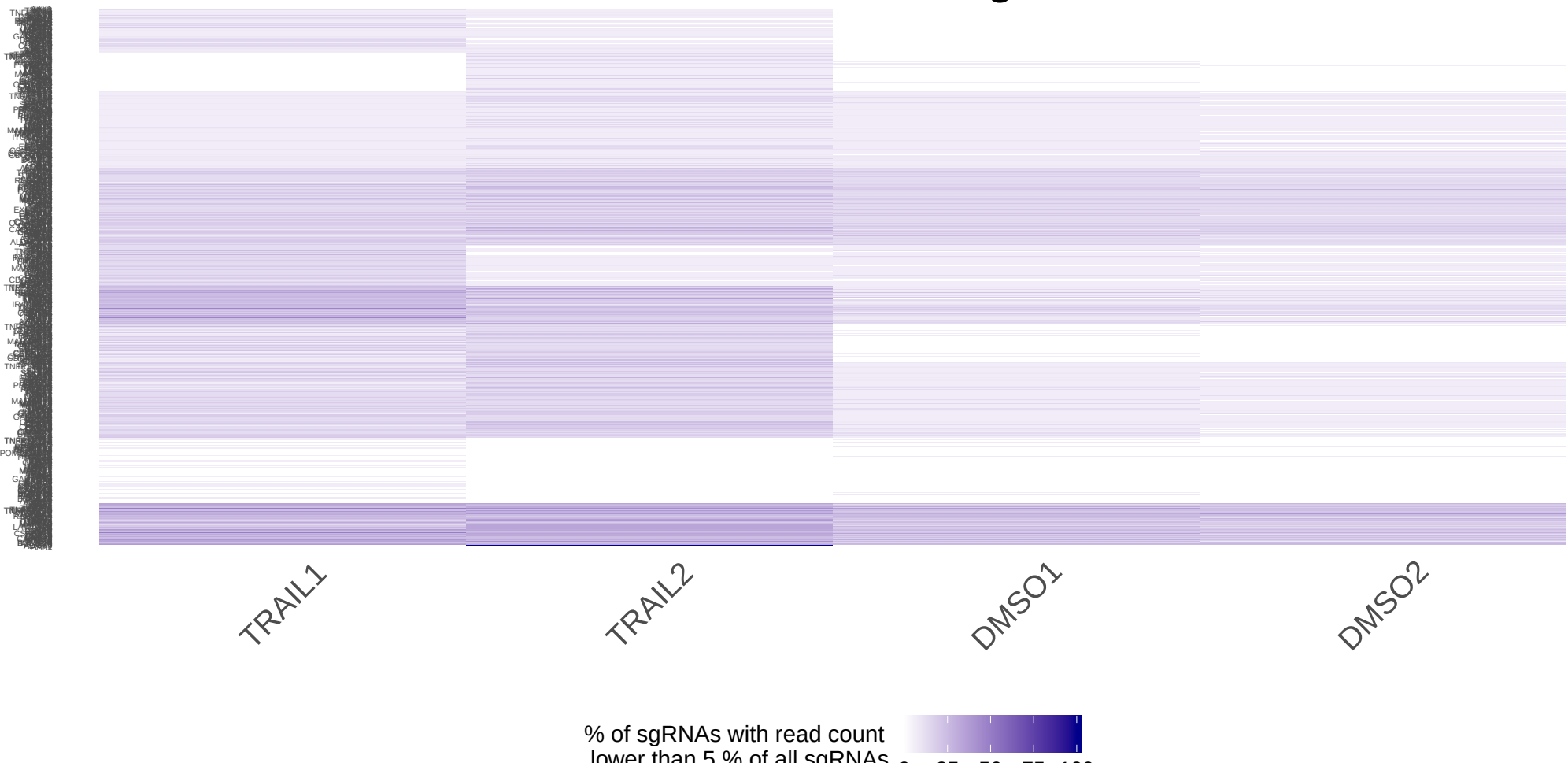% of sgRNAs with read count lower than 5 % of all sgRNAs