

<b>Procedures for computational screening</b>	<b>Number of remaining clones</b>
Defined as "Non-protein-coding TU"	15,815
No homologies to other known protein sequences (BLASTX)	12,382
Could be aligned to mouse genome sequence ( ident. > 90% , leng. > 90%)	11,652
CDS prediction could not be made by GENSCAN ( 10kb around mapped region )	4,280

表1. 新規候補配列のスクリーニングプロセス