

Dataset S2: Alignments of tumor-isolated Mps1^{WT} and Mps1^{DK} to annotated murine Mps1

Tumor 63, p53^{ε/ε}; MMTV-Cre⁺ aligned to murine Mps1

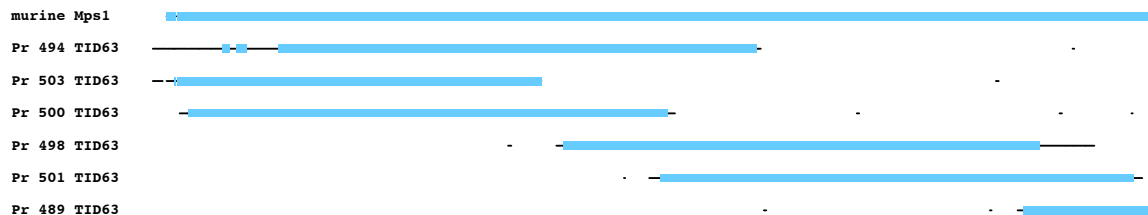
Alignment: Assembled DNA alignment against reference molecule
Parameters: Method: FastScan - Max Qual

Reference molecule: murine Mps1, Region 1 to 2493
Number of sequences to align: 7
Total length of aligned sequences with gaps: 2549 bps
Settings: Similarity significance value cutoff: >= 100%

Summary of Percent Matches:

Ref: murine Mps1	1 to 2493	(2493 bps)	--
2: Pr 494 TID63	1 to 1529	(1529 bps)	61%
3: Pr 503 TID63	1 to 968	(968 bps)	44%
4: Pr 500 TID63	1 to 1256	(1256 bps)	51%
5: Pr 498 TID63	1 to 1360	(1360 bps)	90%
6: Pr 501 TID63	1 to 1257	(1257 bps)	93%
7: Pr 489 TID63	1 to 367	(367 bps)	36%

■ Areas of significant similarity (in windows 20 bases in length)



Tumor 18, Mps1^{ε/ε} p53^{ε/ε}; Lck-Cre⁺ aligned to murine Mps1

Alignment: Assembled DNA alignment against reference molecule
Parameters: Method: FastScan - Max Qual

Reference molecule: murine Mps1, Region 1 to 2493
Number of sequences to align: 7
Total length of aligned sequences with gaps: 2620 bps
Settings: Similarity significance value cutoff: >= 100%

Summary of Percent Matches:

Ref: murine Mps1	1 to 2493	(2493 bps)	--
2: Pr 494 TID18	1 to 1266	(1266 bps)	49%
3: Pr 503 TID18	1 to 627	(627 bps)	30%
4: Pr 500 TID18	1 to 1352	(1352 bps)	61%
5: Pr 501 TID18	1 to 1352	(1352 bps)	57%
6: Pr 498 TID18	1 to 1326	(1326 bps)	62%
7: Pr 489 TID18	1 to 366	(366 bps)	90%

■ Areas of significant similarity (in windows 20 bases in length)

