

10 20 30 40 50 60 70

AAGTTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGT

*exon2-PSMB5 (1>307)* .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGT  
 RPMI-1-PSMB5-Ex2-750R.ab1 (23>258) .....← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGT  
 RPMI-1-PSMB5-Ex2-F.ab1 (254>560) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGT  
 RPMI-1-PSMB5-Ex2-R.ab1 (415>724) .....← AAGTTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGT

80 90 100 110 120 130 140

GAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGG

*exon2-PSMB5 (1>307)* .....→ GAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGG  
 RPMI-1-PSMB5-Ex2-750R.ab1 (23>258) .....← GAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGG  
 RPMI-1-PSMB5-Ex2-F.ab1 (254>560) .....→ GAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGG  
 RPMI-1-PSMB5-Ex2-R.ab1 (415>724) .....← GAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGG

150 160 170 180 190 200 210 220

AACGGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCC

*exon2-PSMB5 (1>307)* .....→ AACGGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCC  
 RPMI-1-PSMB5-Ex2-750R.ab1 (23>258) .....← AACGGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCC  
 RPMI-1-PSMB5-Ex2-F.ab1 (254>560) .....→ AACGGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCC  
 RPMI-1-PSMB5-Ex2-R.ab1 (415>724) .....← AACGGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCC

230 240 250 260 270 280 290

AAACTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGA

*exon2-PSMB5 (1>307)* .....→ AAACTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGA  
 RPMI-1-PSMB5-Ex2-750R.ab1 (23>258) .....← AAACTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGA  
 RPMI-1-PSMB5-Ex2-F.ab1 (254>560) .....→ AAACTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGA  
 RPMI-1-PSMB5-Ex2-R.ab1 (415>724) .....← AAACTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGA

300 310

TAAGAGAGGCCCTG

*exon2-PSMB5 (1>307)* .....→ TAAGAGAGGCCCTG  
 RPMI-1-PSMB5-Ex2-F.ab1 (254>560) .....→ TAAGAGAGGCCCTG  
 RPMI-1-PSMB5-Ex2-R.ab1 (415>724) .....← TAAGAGAGGCCCTG

10 20 30 40 50 60 70  
TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

exon2-PSMB5 (1>307) → TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
RPMI-2-PSMB5-Ex2-750R.ab1 (27>260) ← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
RPMI-2-PSMB5-Ex2-F.ab1 (256>562) → TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
RPMI-2-PSMB5-Ex2-R.ab1 (415>719) ← TTCCGCCATGGAGT**y**ATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140  
GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

exon2-PSMB5 (1>307) → GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
RPMI-2-PSMB5-Ex2-750R.ab1 (27>260) ← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
RPMI-2-PSMB5-Ex2-F.ab1 (256>562) → GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
RPMI-2-PSMB5-Ex2-R.ab1 (415>719) ← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

150 160 170 180 190 200 210 220  
GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

exon2-PSMB5 (1>307) → GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
RPMI-2-PSMB5-Ex2-750R.ab1 (27>260) ← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
RPMI-2-PSMB5-Ex2-F.ab1 (256>562) → GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
RPMI-2-PSMB5-Ex2-R.ab1 (415>719) ← GGCTGTTGGCT**y**GGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCT**y**CAAA

230 240 250 260 270 280 290  
CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

exon2-PSMB5 (1>307) → CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
RPMI-2-PSMB5-Ex2-750R.ab1 (27>260) ← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
RPMI-2-PSMB5-Ex2-F.ab1 (256>562) → CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
RPMI-2-PSMB5-Ex2-R.ab1 (415>719) ← CTGCTTGCCAAC**m**TGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300  
GAGAGGCCCTG

exon2-PSMB5 (1>307) → GAGAGGCCCTG  
RPMI-2-PSMB5-Ex2-F.ab1 (256>562) → GAGAGGCCCTG  
RPMI-2-PSMB5-Ex2-R.ab1 (415>719) ← GAGAGGCCCTG

CFE-R

10 20 30 40 50 60 70

TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

exon2-PSMB5 (1>307) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

RPMI-3-PSMB5-Ex2-750R.ab1 (22>258) ← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

RPMI-3-PSMB5-Ex2-F.ab1 (255>561) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

RPMI-3-PSMB5-Ex2-R.ab1 (417>680) .....← ..... CGGGTGCTTACATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140

GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

exon2-PSMB5 (1>307) .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

RPMI-3-PSMB5-Ex2-750R.ab1 (22>258) ← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

RPMI-3-PSMB5-Ex2-F.ab1 (255>561) .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

RPMI-3-PSMB5-Ex2-R.ab1 (417>680) .....← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

150 160 170 180 190 200 210 220

GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

exon2-PSMB5 (1>307) .....→ GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

RPMI-3-PSMB5-Ex2-750R.ab1 (22>258) ← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

RPMI-3-PSMB5-Ex2-F.ab1 (255>561) .....→ GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

RPMI-3-PSMB5-Ex2-R.ab1 (417>680) .....← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

230 240 250 260 270 280 290

CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

exon2-PSMB5 (1>307) .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

RPMI-3-PSMB5-Ex2-750R.ab1 (22>258) ← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

RPMI-3-PSMB5-Ex2-F.ab1 (255>561) .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

RPMI-3-PSMB5-Ex2-R.ab1 (417>680) .....← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300

GAGAGGCCCTG

exon2-PSMB5 (1>307) .....→ GAGAGGCCCTG

RPMI-3-PSMB5-Ex2-F.ab1 (255>561) .....→ GAGAGGCCCTG

RPMI-3-PSMB5-Ex2-R.ab1 (417>680) .....← GAGAGGCCCTG

10 20 30 40 50 60 70  
 TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

*exon2-PSMB5 (1>307)* .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
 RPMI-4-PSMB5-Ex2-750R.ab1 (22>257) ← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
 RPMI-4-PSMB5-Ex2-F.ab1 (255>561) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA  
 RPMI-4-PSMB5-Ex2-R.ab1 (419>672) .....← ..... CATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140  
 GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

*exon2-PSMB5 (1>307)* .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
 RPMI-4-PSMB5-Ex2-750R.ab1 (22>257) ← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
 RPMI-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC  
 RPMI-4-PSMB5-Ex2-R.ab1 (419>672) .....← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

150 160 170 180 190 200 210 220  
 GGCTGTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

*exon2-PSMB5 (1>307)* .....→ GGCTGTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
 RPMI-4-PSMB5-Ex2-750R.ab1 (22>257) ← GGCTGTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
 RPMI-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GGCTGTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA  
 RPMI-4-PSMB5-Ex2-R.ab1 (419>672) .....← GGCTGTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

230 240 250 260 270 280 290  
 CTGCTTGCCAACATGGTGTATCAGTACAAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

*exon2-PSMB5 (1>307)* .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
 RPMI-4-PSMB5-Ex2-750R.ab1 (22>257) ← CTGCTTGCCAACATGGTGTATCAGTACAAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
 RPMI-4-PSMB5-Ex2-F.ab1 (255>561) .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA  
 RPMI-4-PSMB5-Ex2-R.ab1 (419>672) .....← CTGCTTGCCAACATGGTGTATCAGTACAAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300  
 GAGAGGCCCTG

*exon2-PSMB5 (1>307)* .....→ GAGAGGCCCTG  
 RPMI-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GAGAGGCCCTG  
 RPMI-4-PSMB5-Ex2-R.ab1 (419>672) .....← GAGAGGCCCTG

10 20 30 40 50 60 70  
 TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

*exon2-PSMB5 (1>307)* .....  
 U266-1-PSMB5-Ex2-750R.ab1 (22>258) .....  
 U266-1-PSMB5-Ex2-F.ab1 (255>561) .....  
 U266-1-PSMB5-Ex2-R.ab1 (417>723) .....

80 90 100 110 120 130 140  
 GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGGCGACGGGATTGCAGCTTCTGGGAAC

*exon2-PSMB5 (1>307)* .....  
 U266-1-PSMB5-Ex2-750R.ab1 (22>258) .....  
 U266-1-PSMB5-Ex2-F.ab1 (255>561) .....  
 U266-1-PSMB5-Ex2-R.ab1 (417>723) .....

150 160 170 180 190 200 210 220  
 GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

*exon2-PSMB5 (1>307)* .....  
 U266-1-PSMB5-Ex2-750R.ab1 (22>258) .....  
 U266-1-PSMB5-Ex2-F.ab1 (255>561) .....  
 U266-1-PSMB5-Ex2-R.ab1 (417>723) .....

230 240 250 260 270 280 290  
 CTGCTTGCCAAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

*exon2-PSMB5 (1>307)* .....  
 U266-1-PSMB5-Ex2-750R.ab1 (22>258) .....  
 U266-1-PSMB5-Ex2-F.ab1 (255>561) .....  
 U266-1-PSMB5-Ex2-R.ab1 (417>723) .....

300  
 GAGAGGCCCTG

*exon2-PSMB5 (1>307)* .....  
 U266-1-PSMB5-Ex2-F.ab1 (255>561) .....  
 U266-1-PSMB5-Ex2-R.ab1 (417>723) .....

BTZ-R

10 20 30 40 50 60 70  
 TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

exon2-PSMB5 (1>307) .....  
 U266-2-PSMB5-Ex2-750R.ab1 (23>259) .....  
 U266-2-PSMB5-Ex2-F.ab1 (256>562) .....  
 U266-2-PSMB5-Ex2-R.ab1 (415>680) ..... AGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140  
 GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

exon2-PSMB5 (1>307) .....  
 U266-2-PSMB5-Ex2-750R.ab1 (23>259) .....  
 U266-2-PSMB5-Ex2-F.ab1 (256>562) .....  
 U266-2-PSMB5-Ex2-R.ab1 (415>680) ..... GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

150 160 170 180 190 200 210 220  
 GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

exon2-PSMB5 (1>307) .....  
 U266-2-PSMB5-Ex2-750R.ab1 (23>259) .....  
 U266-2-PSMB5-Ex2-F.ab1 (256>562) .....  
 U266-2-PSMB5-Ex2-R.ab1 (415>680) ..... GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

230 240 250 260 270 280 290  
 CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

exon2-PSMB5 (1>307) .....  
 U266-2-PSMB5-Ex2-750R.ab1 (23>259) .....  
 U266-2-PSMB5-Ex2-F.ab1 (256>562) .....  
 U266-2-PSMB5-Ex2-R.ab1 (415>680) ..... CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300  
 GAGAGGCCCTG

exon2-PSMB5 (1>307) .....  
 U266-2-PSMB5-Ex2-F.ab1 (256>562) .....  
 U266-2-PSMB5-Ex2-R.ab1 (415>680) .....  
 GAGAGGCCCTG

10 20 30 40 50 60 70

TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

U266-3-PSMB5-Ex2-750R.ab1 (22>258) ← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

U266-3-PSMB5-Ex2-F.ab1 (256>562) → TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGCTTACATTGCCTCCCAGACGGTGAA

U266-3-PSMB5-Ex2-R.ab1 (416>668) → ..... ATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140

GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

U266-3-PSMB5-Ex2-750R.ab1 (22>258) ← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

U266-3-PSMB5-Ex2-F.ab1 (256>562) → GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

U266-3-PSMB5-Ex2-R.ab1 (416>668) → GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAAC

150 160 170 180 190 200 210 220

GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-3-PSMB5-Ex2-750R.ab1 (22>258) ← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-3-PSMB5-Ex2-F.ab1 (256>562) → GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-3-PSMB5-Ex2-R.ab1 (416>668) → GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

230 240 250 260 270 280 290

CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-3-PSMB5-Ex2-750R.ab1 (22>258) ← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-3-PSMB5-Ex2-F.ab1 (256>562) → CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-3-PSMB5-Ex2-R.ab1 (416>668) → CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300

GAGAGGCCCTG

U266-3-PSMB5-Ex2-F.ab1 (256>562) → GAGAGGCCCTG

U266-3-PSMB5-Ex2-R.ab1 (416>668) → GAGAGGCCCTG

DXZ-R

10 20 30 40 50 60 70

TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGTACATTGCCTCCCAGACGGTGAA

exon2-PSMB5 (1>307) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGTACATTGCCTCCCAGACGGTGAA

U266-4-PSMB5-Ex2-750R.ab1 (23>259) .....← TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGTACATTGCCTCCCAGACGGTGAA

U266-4-PSMB5-Ex2-F.ab1 (255>561) .....→ TTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACAGCGGGTGTACATTGCCTCCCAGACGGTGAA

80 90 100 110 120 130 140

GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGCCGACGGGATTCGAGCTTCTGGGAAC

exon2-PSMB5 (1>307) .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGCCGACGGGATTCGAGCTTCTGGGAAC

U266-4-PSMB5-Ex2-750R.ab1 (23>259) .....← GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGCCGACGGGATTCGAGCTTCTGGGAAC

U266-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGGGCCGACGGGATTCGAGCTTCTGGGAAC

U266-4-PSMB5-Ex2-R.ab1 (414>608) .....← TGGCTGGGGCCGACGGGATTCGAGCTTCTGGGAAC

150 160 170 180 190 200 210 220

GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

exon2-PSMB5 (1>307) .....→ GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-4-PSMB5-Ex2-750R.ab1 (23>259) .....← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

U266-4-PSMB5-Ex2-R.ab1 (414>608) .....← GGCTGTTGGCTCGGCAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCCTCCAAA

230 240 250 260 270 280 290

CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

exon2-PSMB5 (1>307) .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-4-PSMB5-Ex2-750R.ab1 (23>259) .....← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-4-PSMB5-Ex2-F.ab1 (255>561) .....→ CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

U266-4-PSMB5-Ex2-R.ab1 (414>608) .....← CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAA

300

GAGAGGCCCTG

exon2-PSMB5 (1>307) .....→ GAGAGGCCCTG

U266-4-PSMB5-Ex2-F.ab1 (255>561) .....→ GAGAGGCCCTG

U266-4-PSMB5-Ex2-R.ab1 (414>608) .....← GAGAGGCCCTG