

### S3 Figure

#### Sequence alignment of LEAP TA clones

L1.3  
2-7 ATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAT TATAAGCTGCAATAAACAAAGTTAACAA C (A)<sub>156</sub>  
2-9 .....C..... (A)<sub>136</sub>  
2-21 ..... (A)<sub>133</sub>  
2-23 ..... (A)<sub>108</sub>  
2-15 ..... (A)<sub>101</sub>  
2-5 ..... (A)<sub>98</sub>  
2-3 .....G..... (A)<sub>94</sub>  
2-10 ..... (A)<sub>93</sub>  
2-8 ..... (A)<sub>91</sub>  
2-2 ..... (A)<sub>82</sub>  
2-4 ..... (A)<sub>81</sub>  
2-6 ..NN..... (A)<sub>72</sub>  
2-13 ..... (A)<sub>70</sub>  
2-20 ..... (A)<sub>69</sub>  
2-11 ..... (A)<sub>65</sub>  
2-22 ..... (A)<sub>59</sub>  
2-16 ..... (A)<sub>59</sub>  
2-1 ..... (A)<sub>44</sub>  
2-14 .....G.....G..... (A)<sub>12</sub>  
n = 19

L1.3-Y282A  
4-13 ATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAT TATAAGCTGCAATAAACAAAGTTAACAA C (A)<sub>111</sub>  
4-5 ..... (A)<sub>110</sub>  
4-1 ..... (A)<sub>100</sub>  
4-24 ..... (A)<sub>89</sub>  
4-9 .....A.....T..... AAC (A)<sub>86</sub>  
4-20 ..... (A)<sub>80</sub>  
4-12 ..... (A)<sub>80</sub>  
4-19 .....C..... (A)<sub>69</sub>  
4-25 ..... (A)<sub>60</sub>  
4-16 ..... (A)<sub>58</sub>  
4-4 ..... (A)<sub>58</sub>  
4-10 .....G..... (A)<sub>57</sub>  
4-14 .....A.....C..... (A)<sub>57</sub>  
4-15 ..... (A)<sub>50</sub>  
4-11 ..... AAC (A)<sub>46</sub>  
n = 15