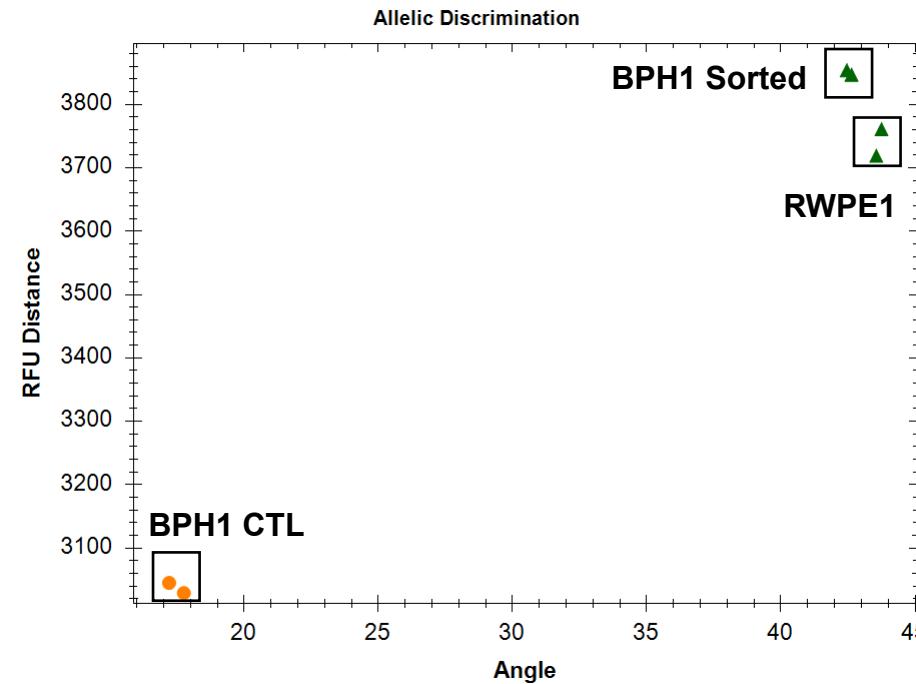
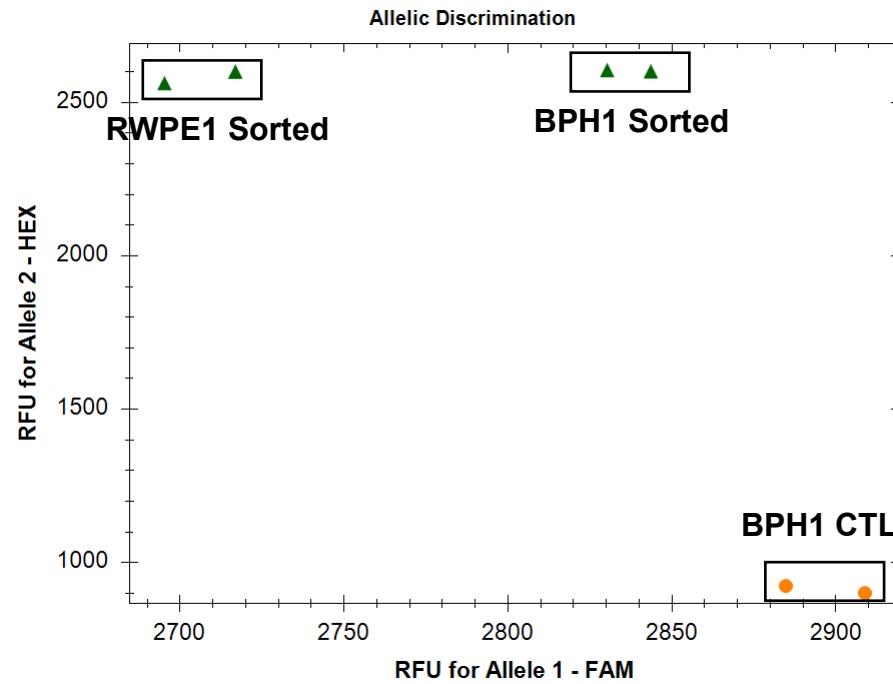


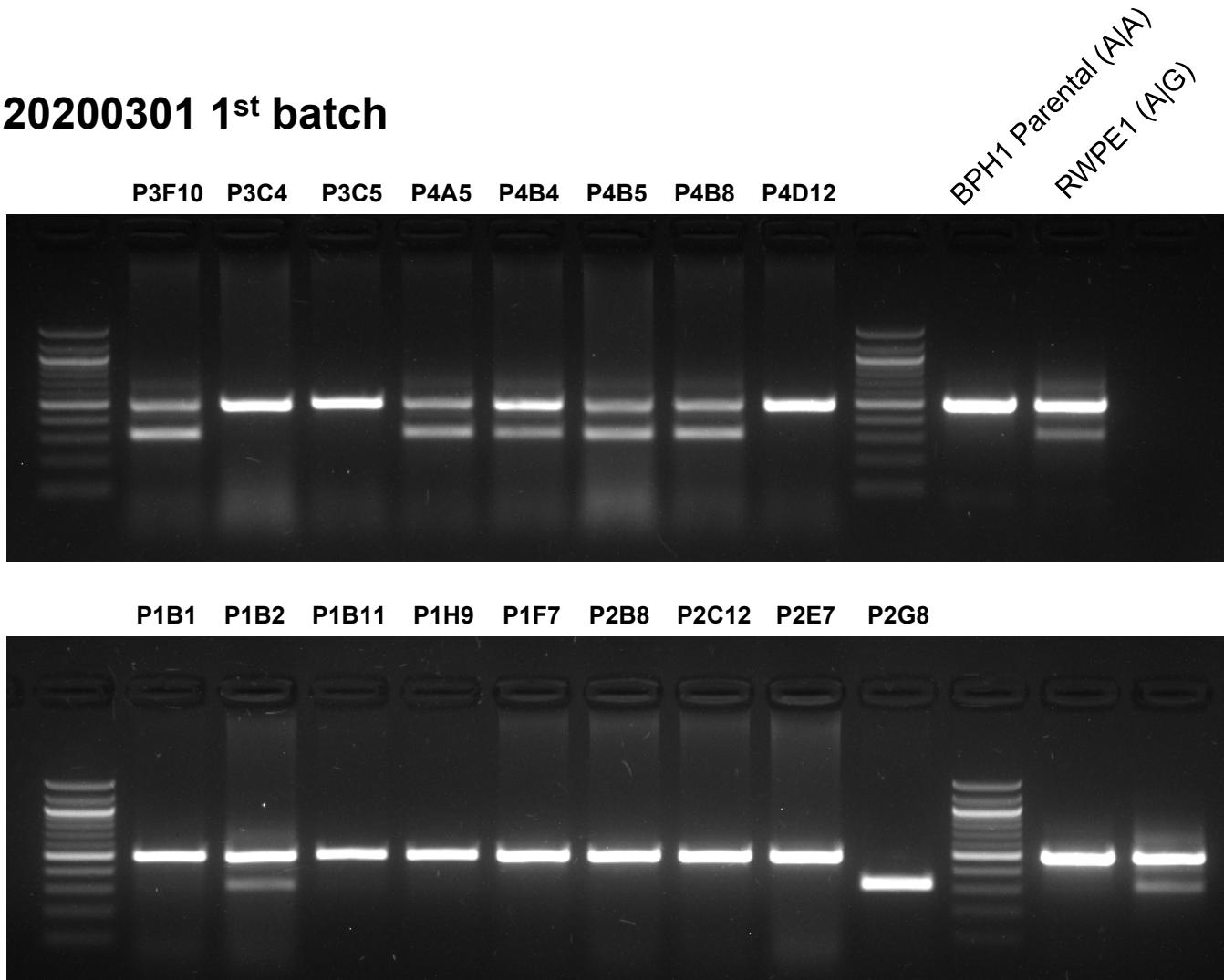
BPH1 cells rs60464856 A2G edited population genotyping (rhAmp PCR)



	FAM-A			HEX-G		
	CTL	SORTED	RWPE1	CTL	SORTED	RWPE1
Rep1	26.39	27.28	28.02	35.47	28.54	28.61
Rep2	26.33	27.16	27.73	35.59	28.45	28.52
Average	26.36	27.22	27.875	35.53	28.495	28.565
G/A	0.001736	0.413225	0.619854			
G allele% normalized to RWPE1	0.14%	33.3%	50%			

BPH1

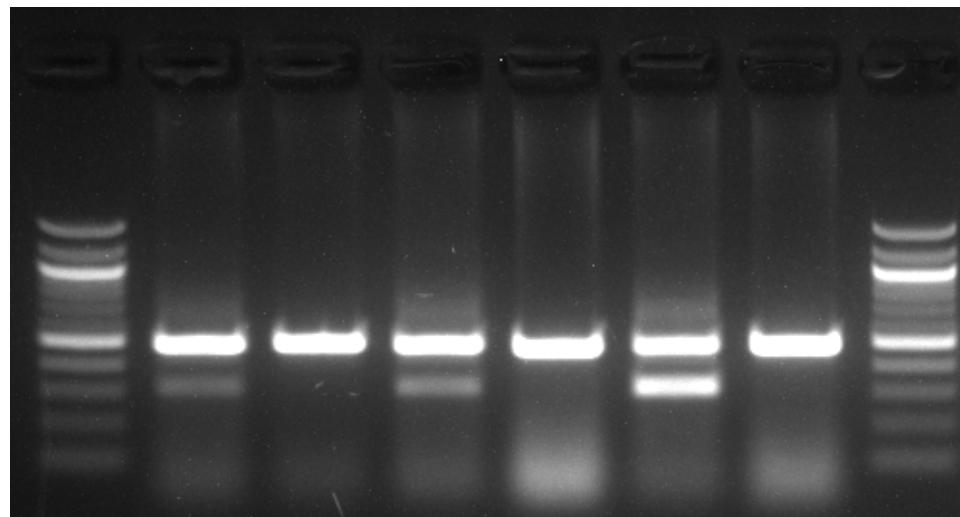
20200301 1st batch



BPH1

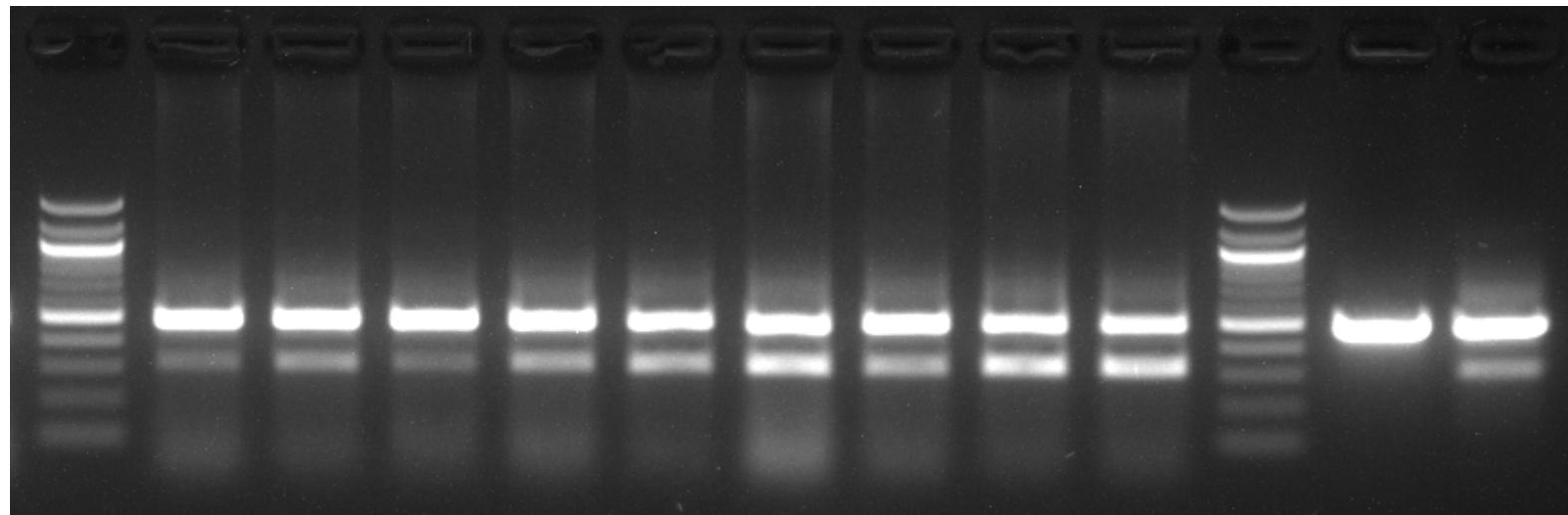
20200305 2nd batch

P3C3 P3C11 P3D5 P3D9 P3G10 P3H7



P4B3 P4C2 P4E11 P4F3 P4F10 P4F12 P4G5 P4G7 P4H11

BPH1 Parental (A/A)
RWPE1 (A/G)

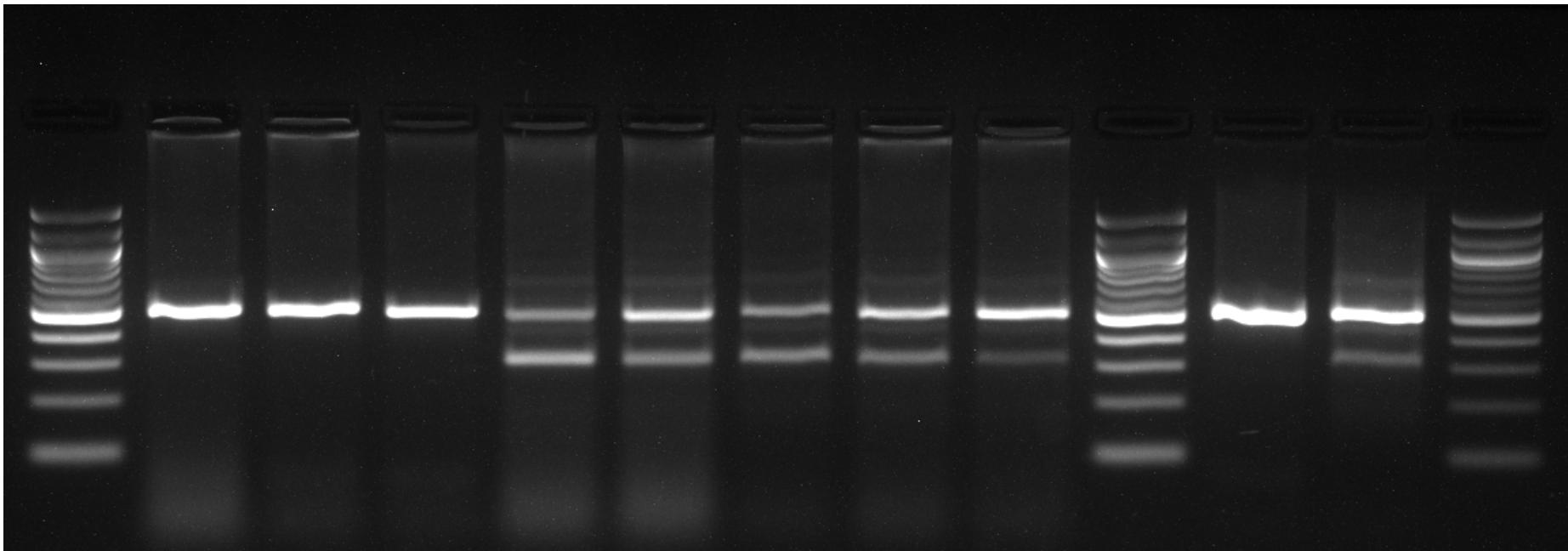


BPH1

20200318 3rd batch

P2B6 P3A6 P3D10 P3F8 P4A12 P4D1 P4E3 P4H6

BPH1 Parental (A/A)
RWPE1 (A/G)

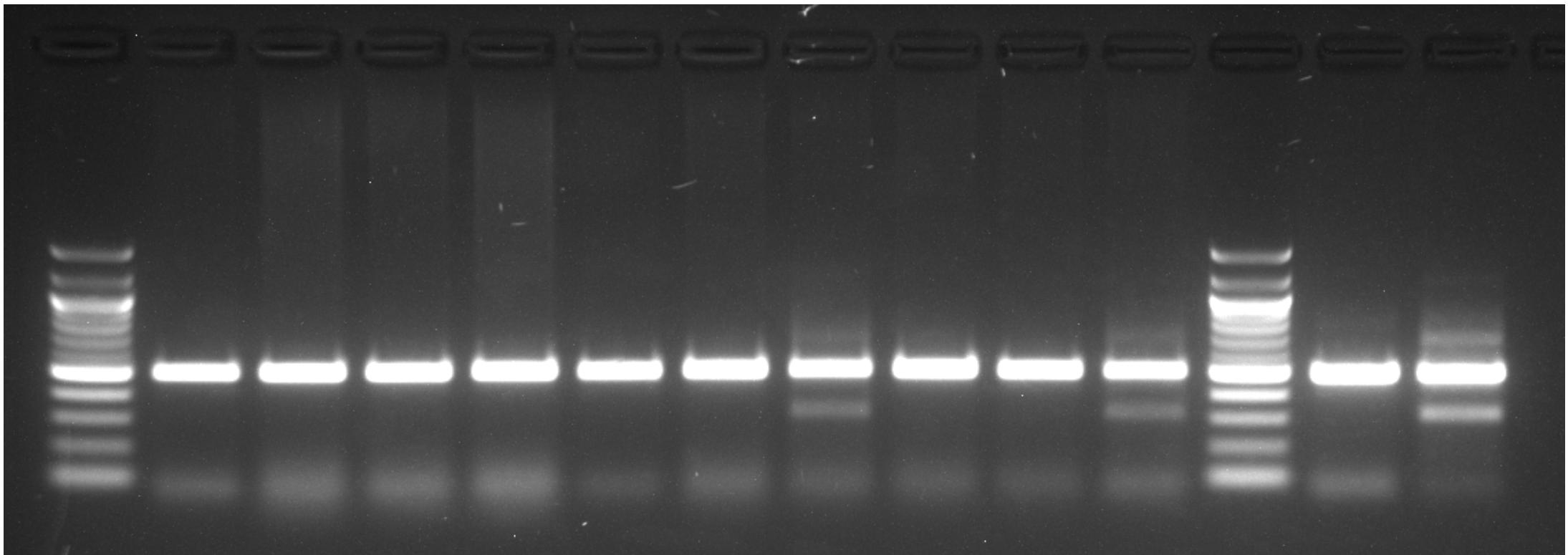


BPH1

20200401 4rd batch

P2A7 P3H11 P4F4 P4G3 P5D11 P5G10 P6B2 P6C7 P6E3 P6H3

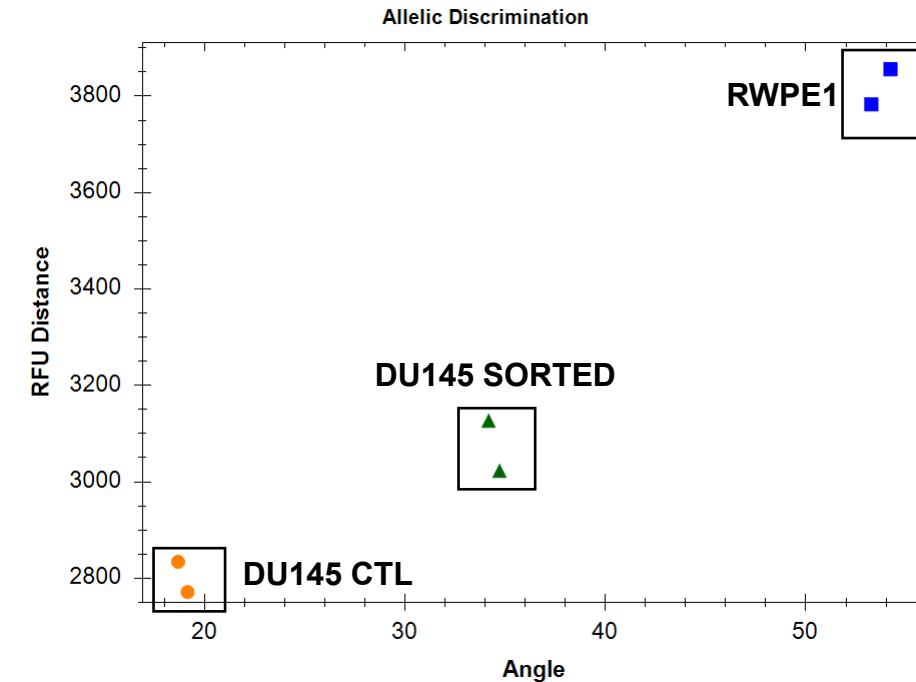
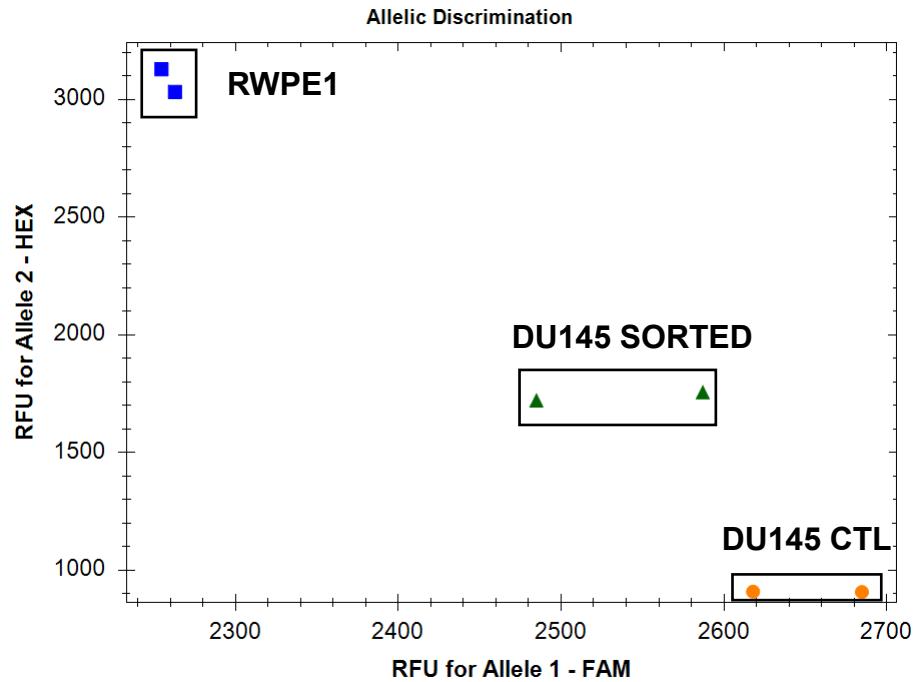
BPH1 Parental (A/A)
RWPE1 (A/G)



BPH1 rs60464856 A2G base editing Summary

Genotype	Clone count
A A A	24
A A G	12
A G G	13
G G G	1 (this clone died after genotyping)

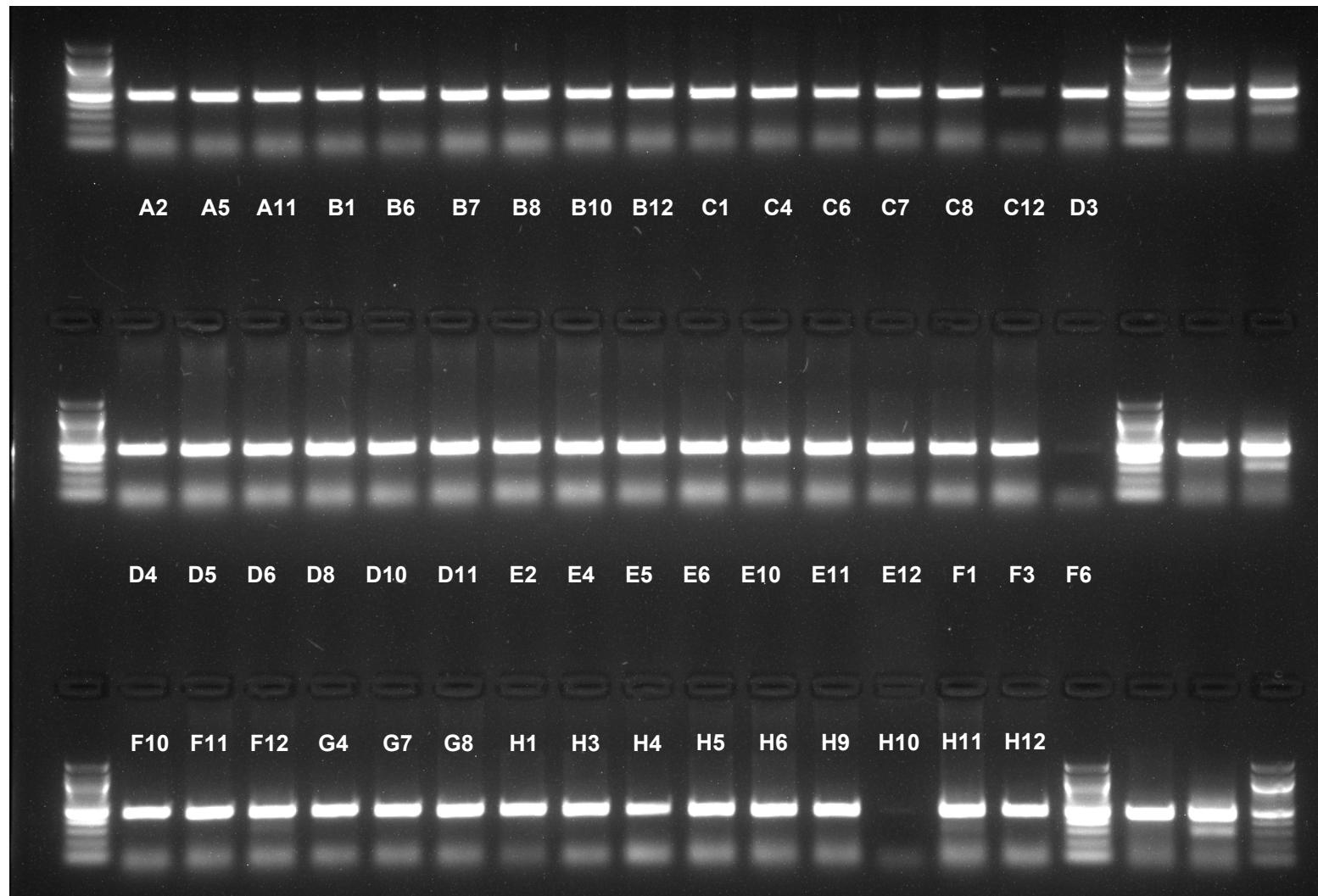
DU145 cells rs60464856 A2G edited population genotyping (rhAmp PCR)



	FAM-A			HEX-G		
	CTL	SORTED	RWPE1	CTL	SORTED	RWPE1
Rep1	28.52	29.47	29.45	33.78	32.16	28.28
Rep2	28.49	29.49	29.37	33.7	32.19	28.29
Average	29.49	29.48	29.41	33.74	32.175	28.285
G/A %	0.052556	0.154427	2.181015			
G allele% normalized to RWPE1	1.20%	3.54%	50%			

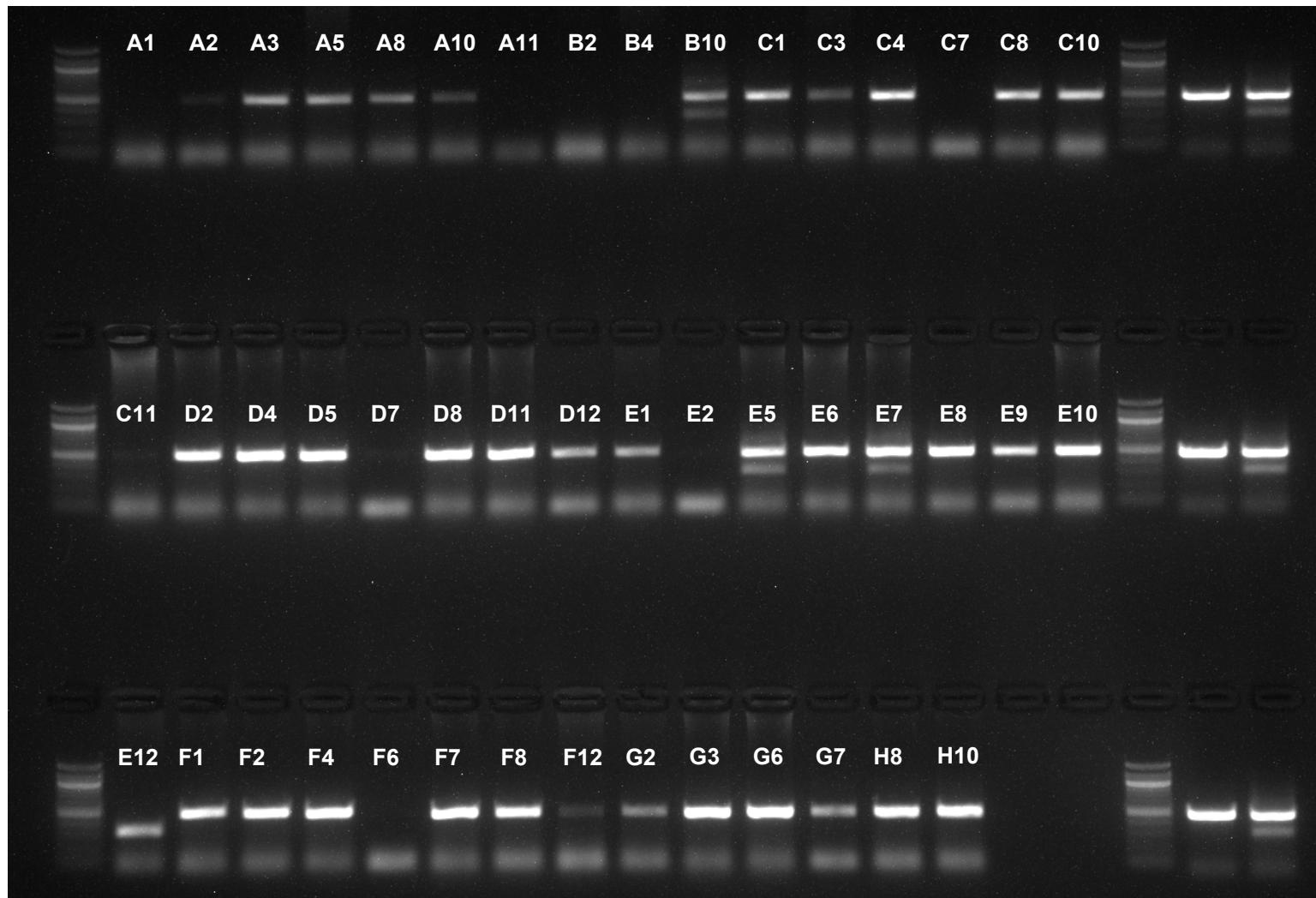
DU145

20200504 P1



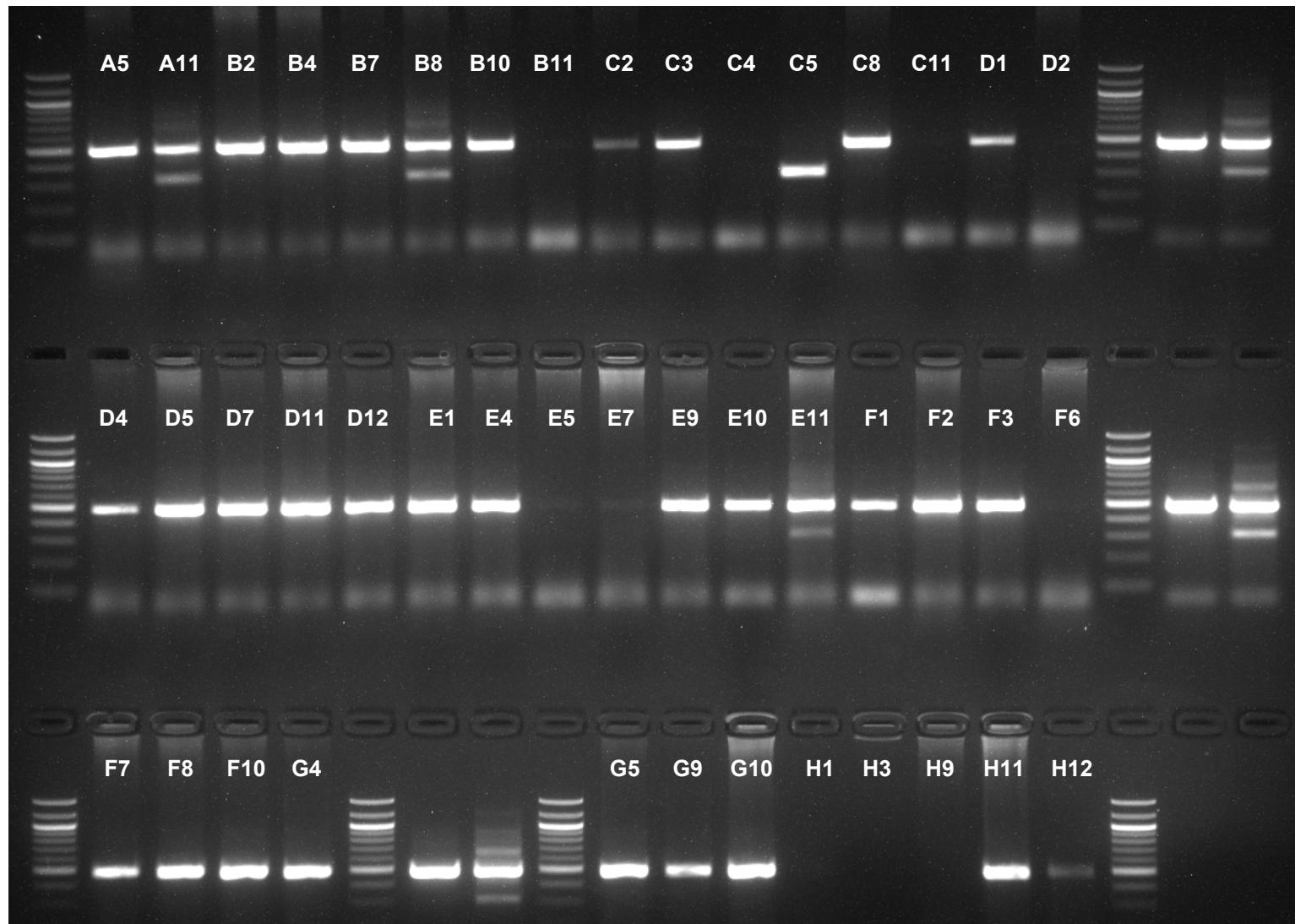
DU145

20200512 Plate2



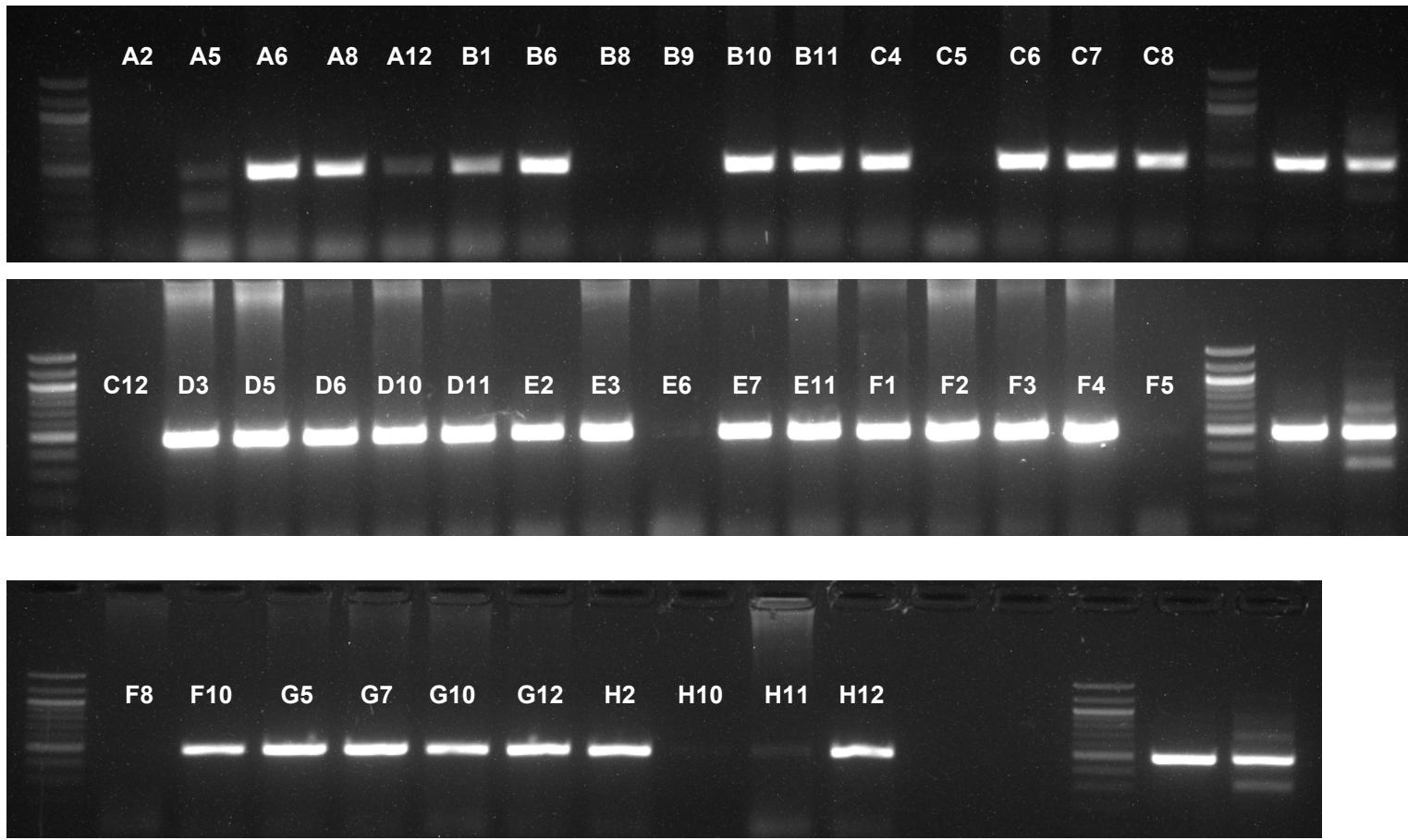
DU145

20200512 Plate3



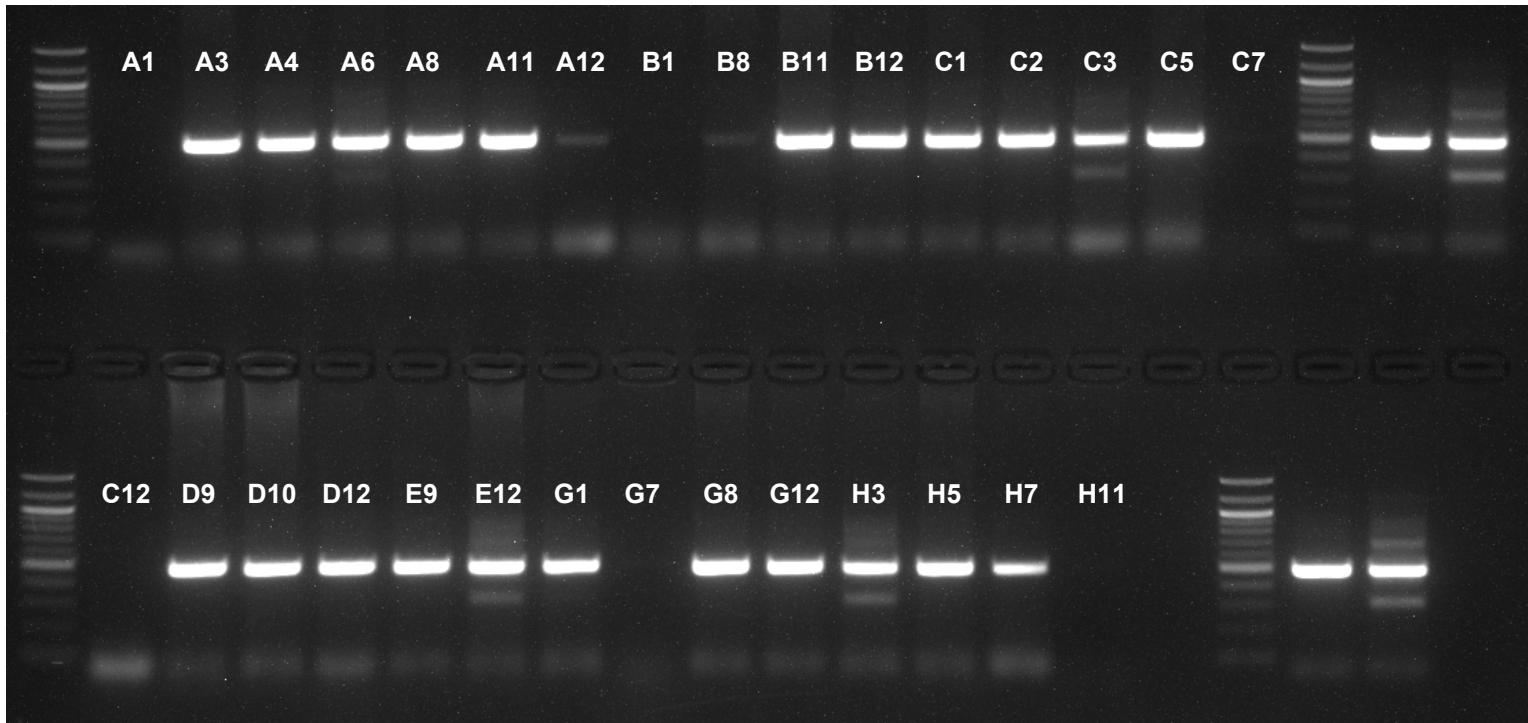
DU145

20200512 Plate4



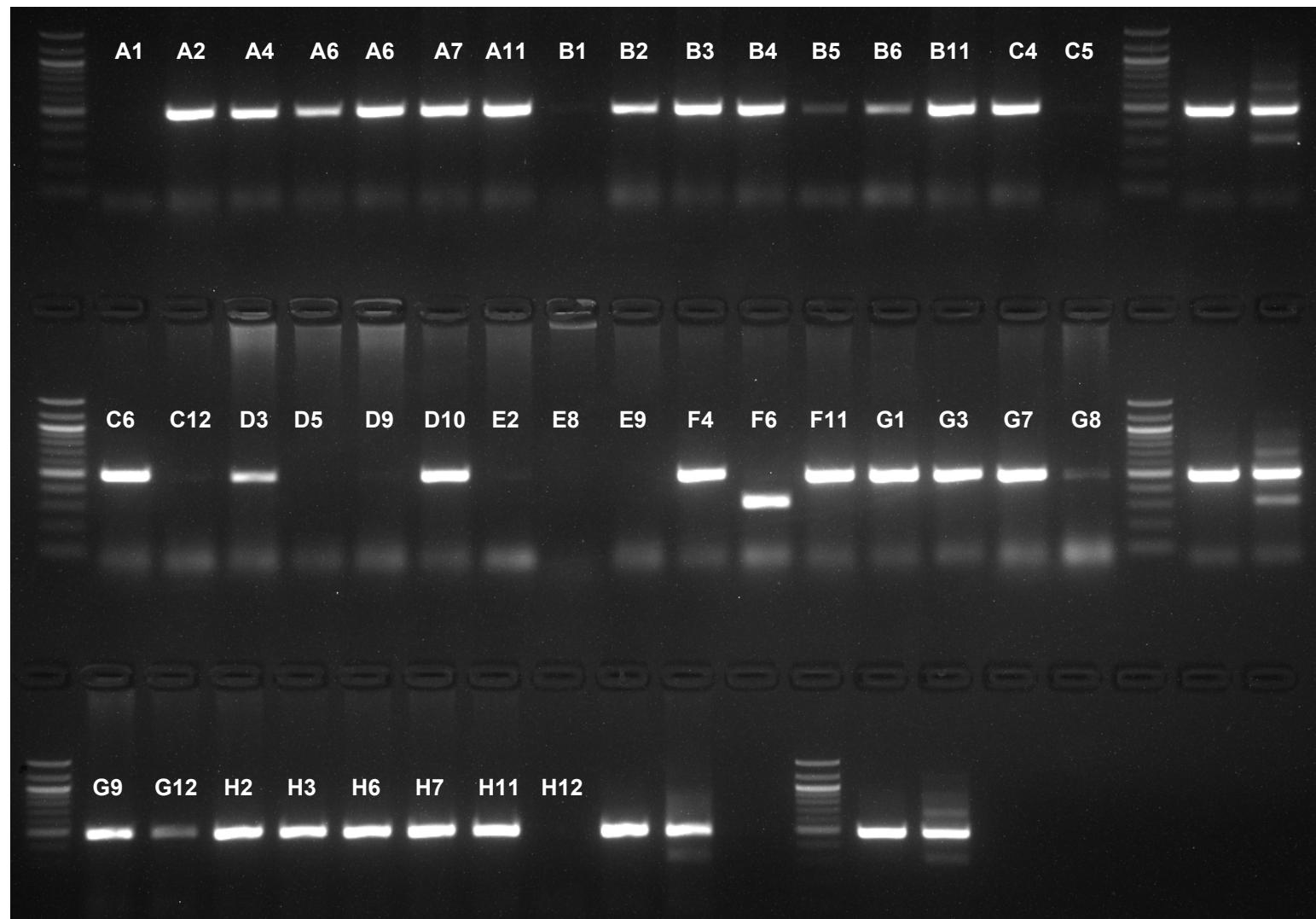
DU145

20200512 Plate5



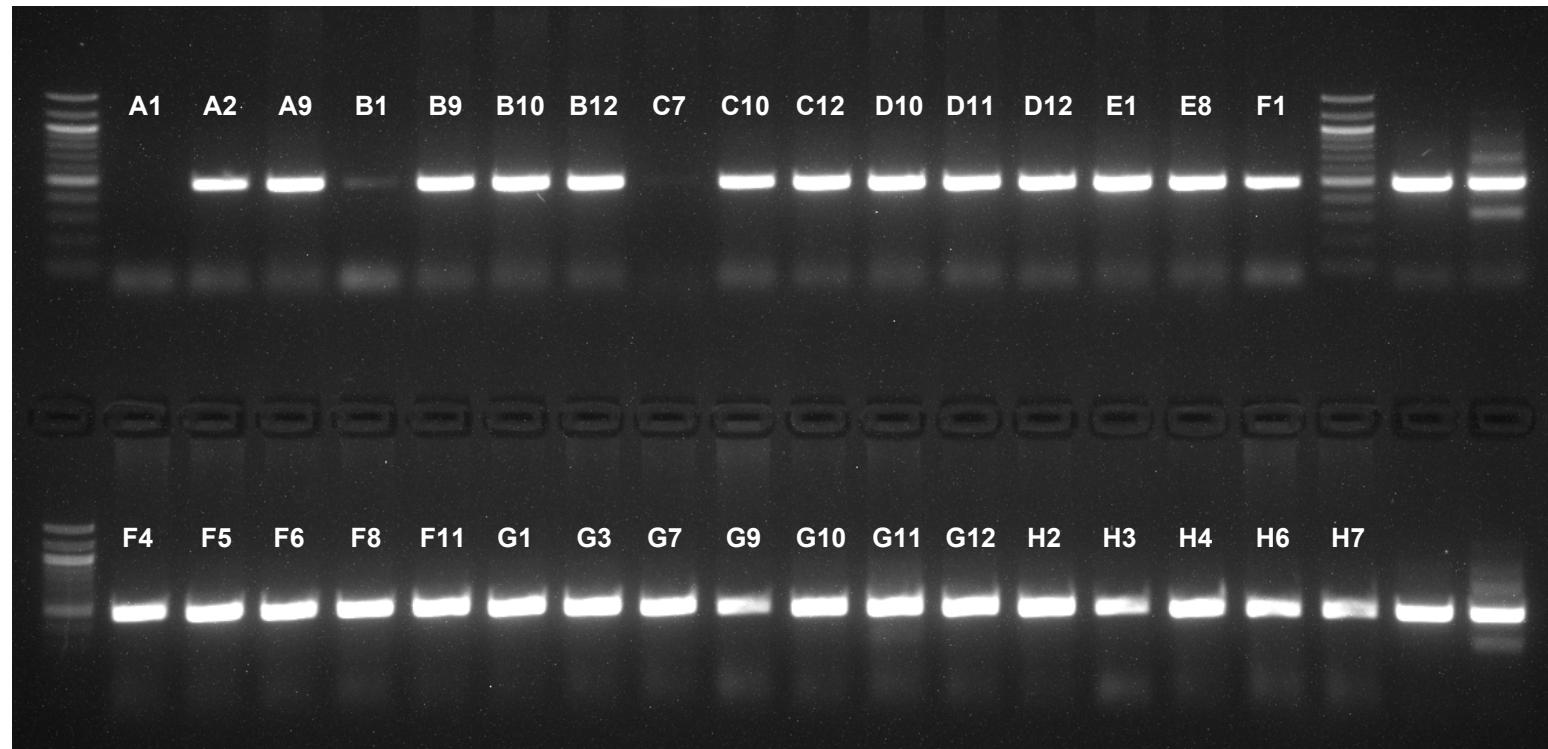
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200512 Plate6



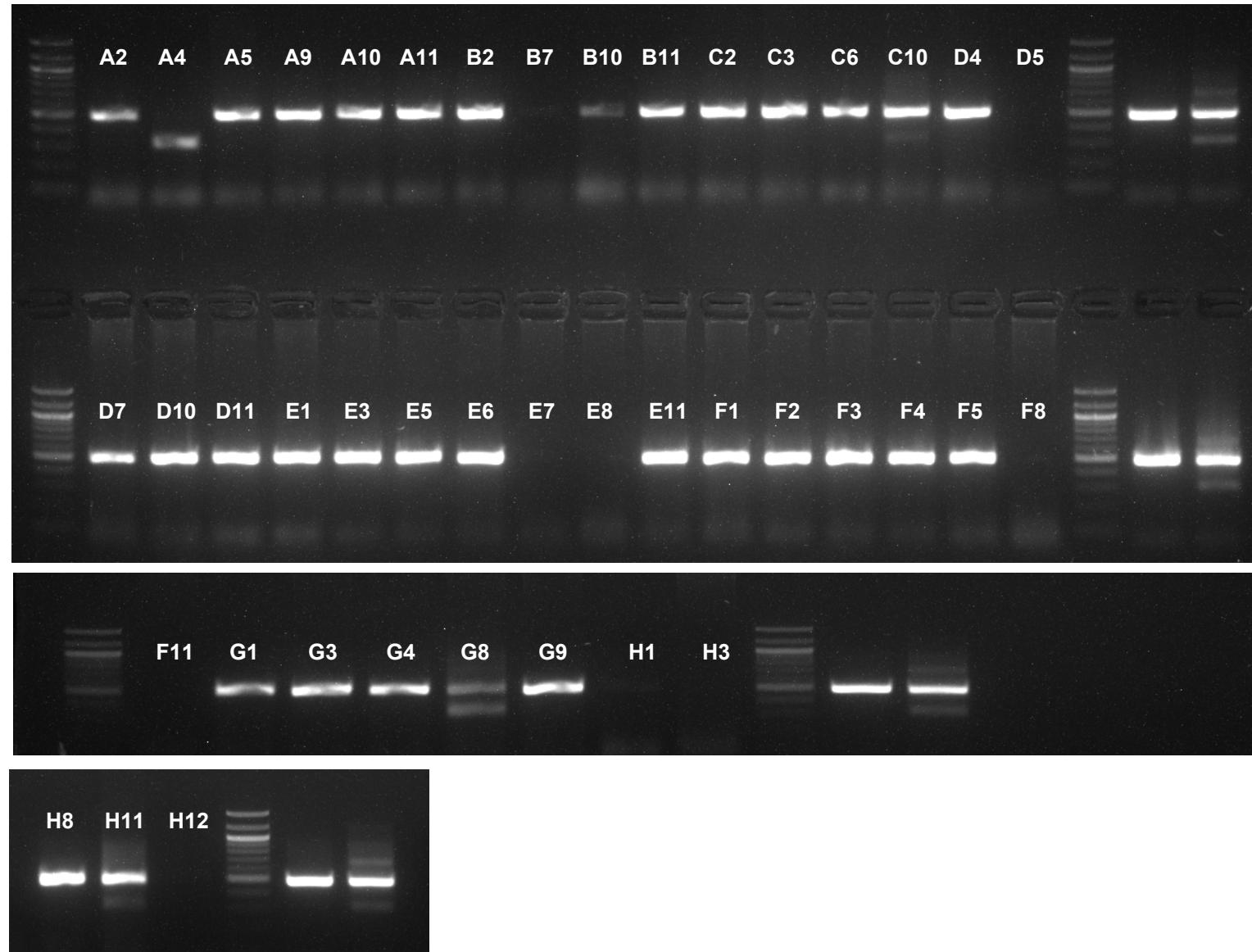
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200512 Plate7



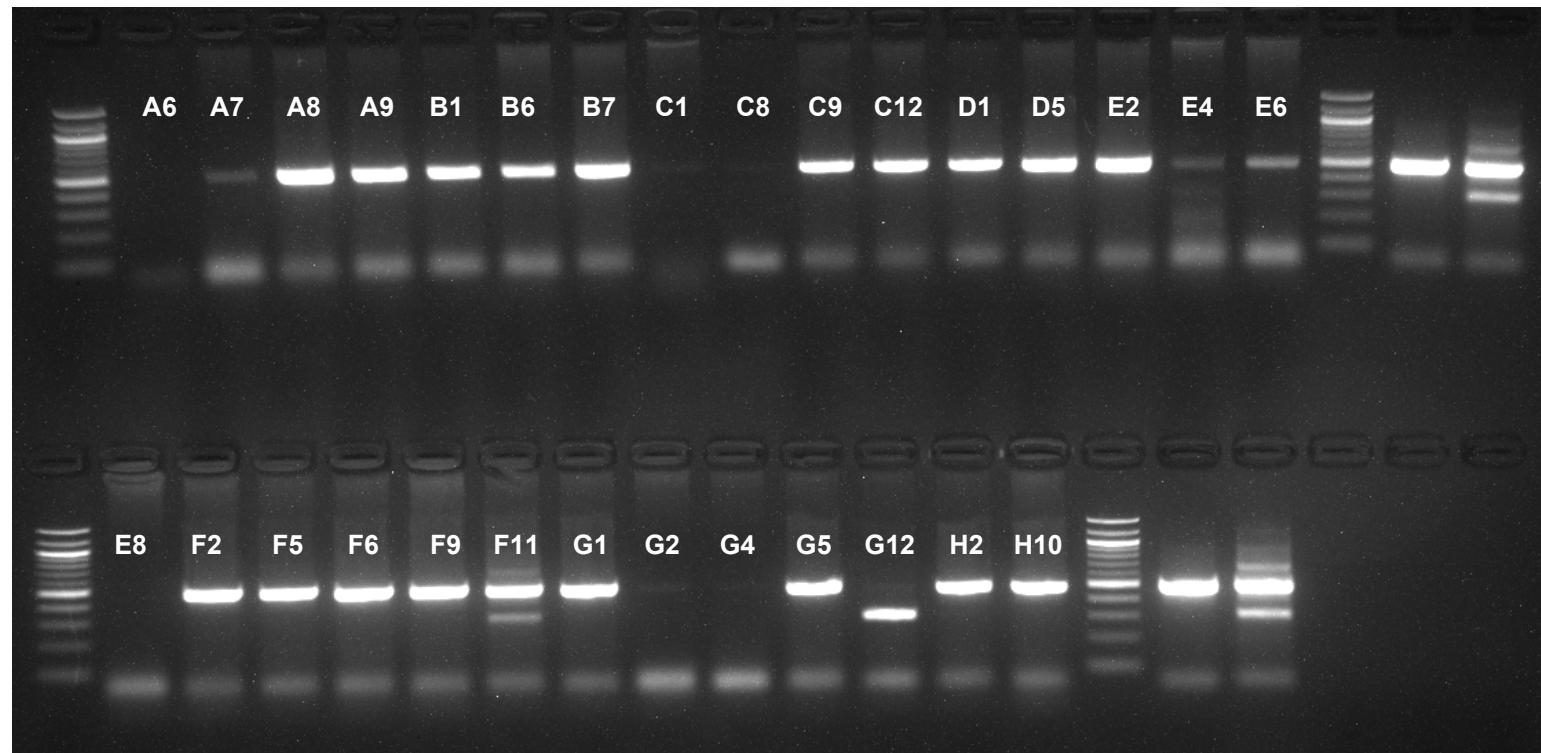
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200512 Plate8



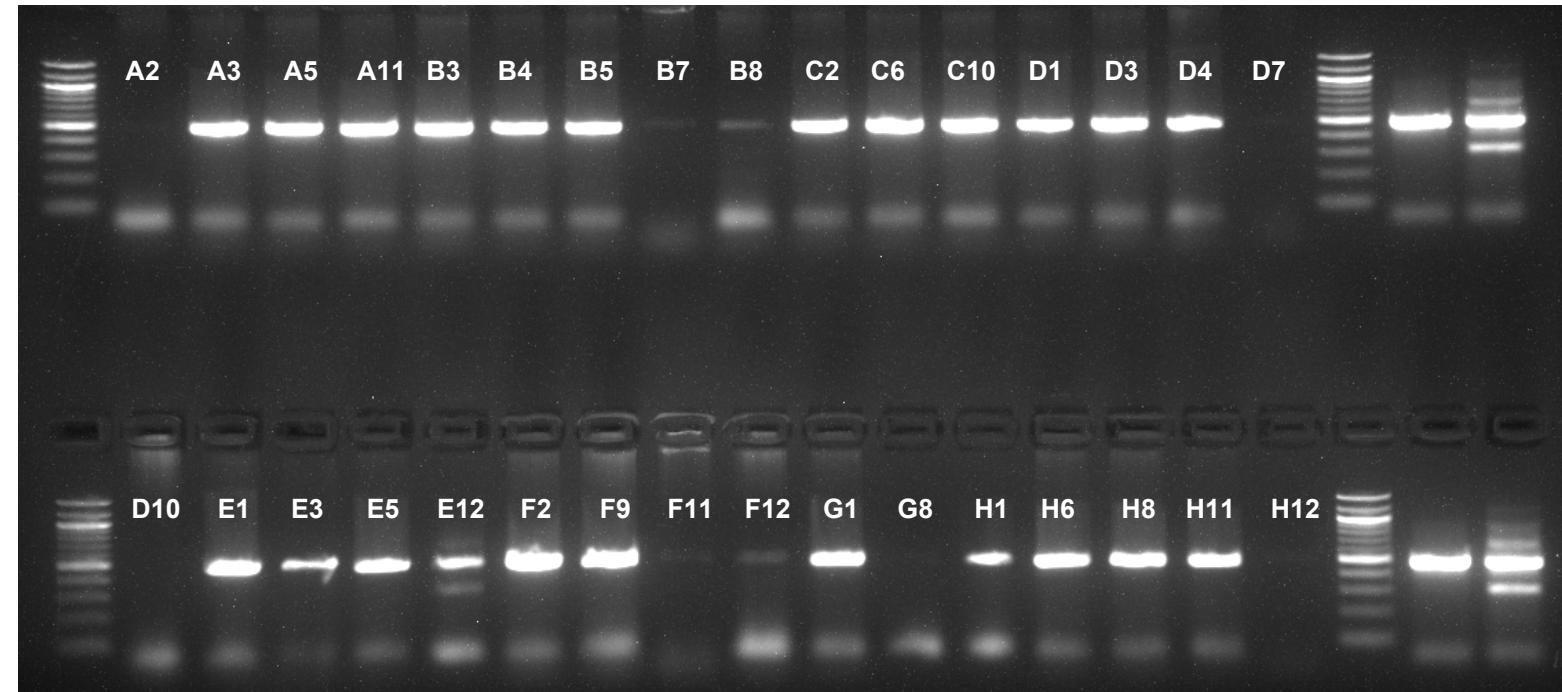
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200512 Plate9



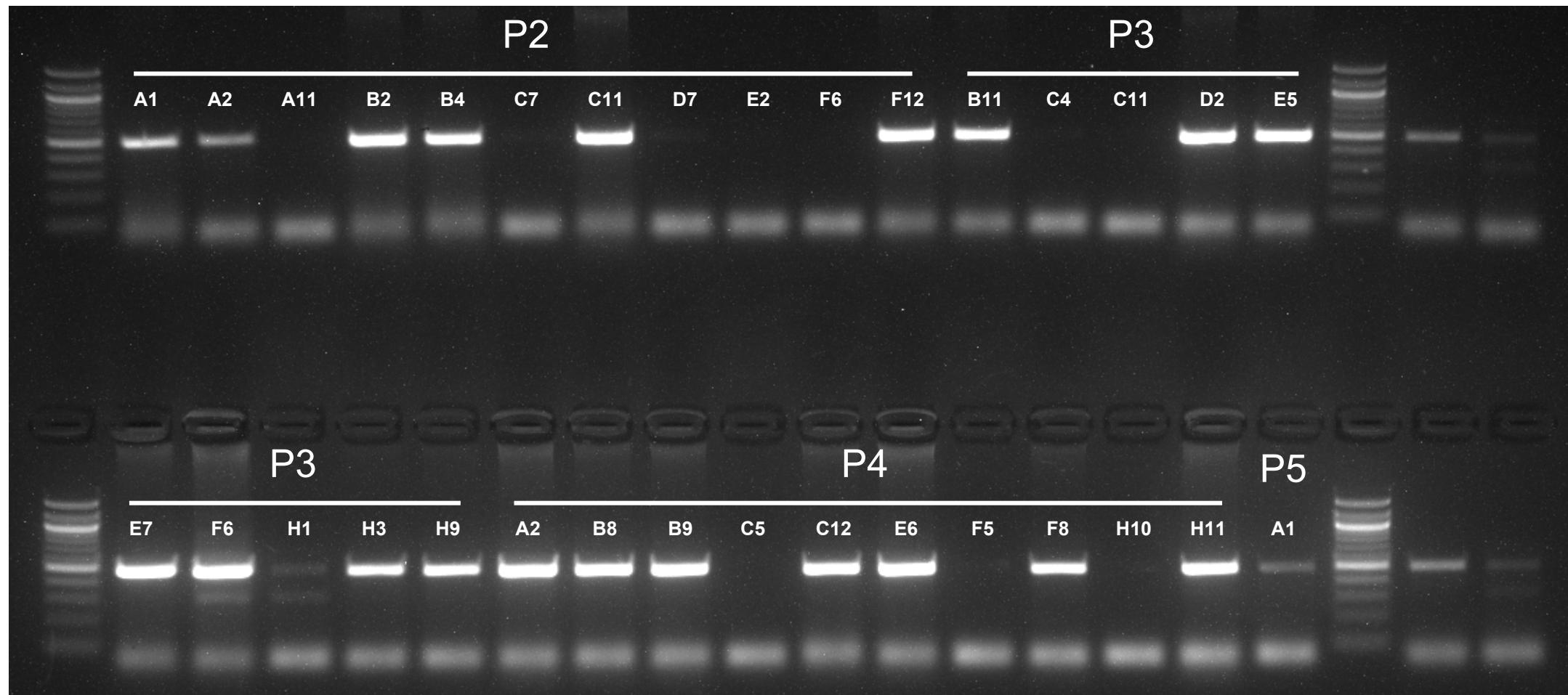
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200512 Plate10



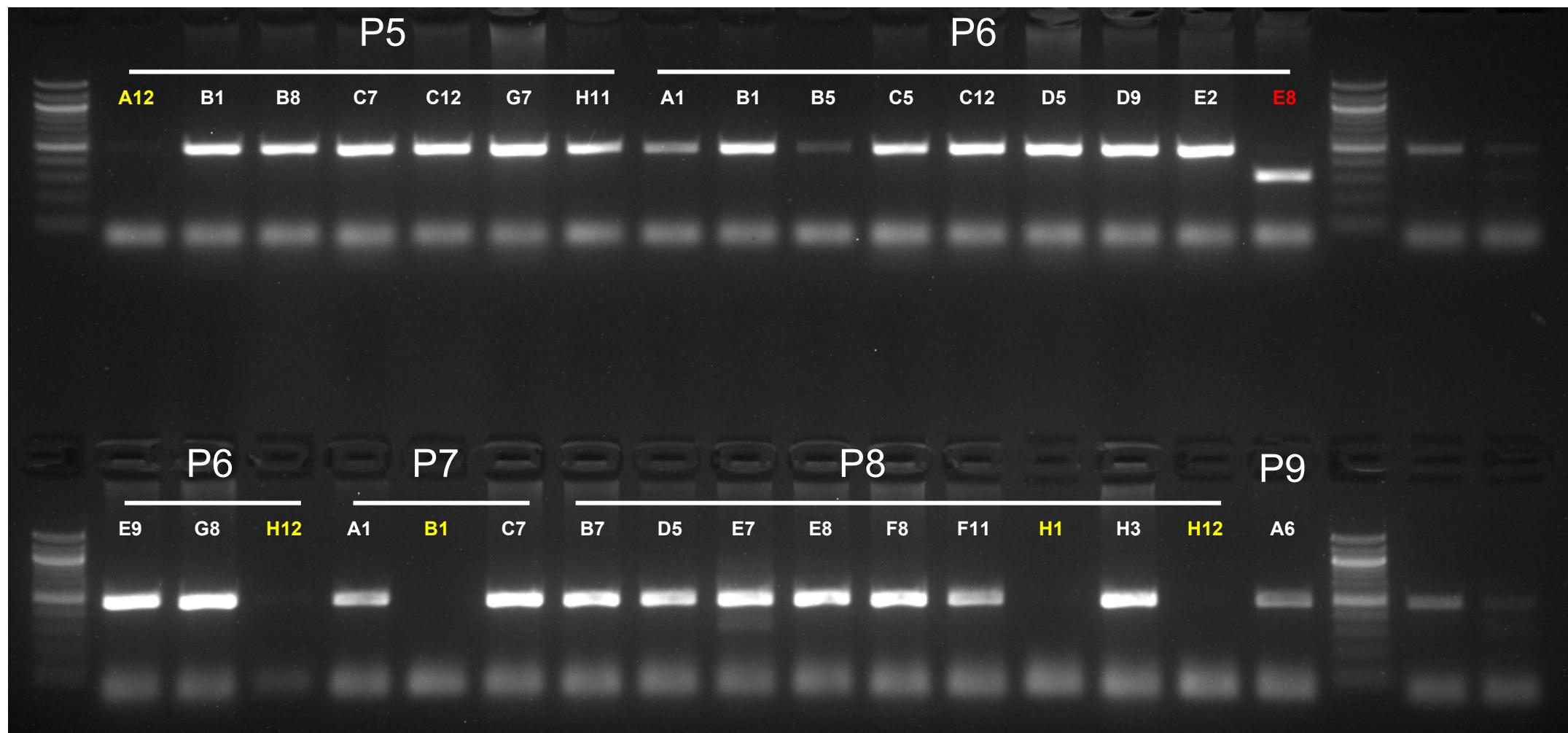
DU145

DU145 cells rs60464856 A2G edited single clone genotyping 20200513 Edge Repeat1



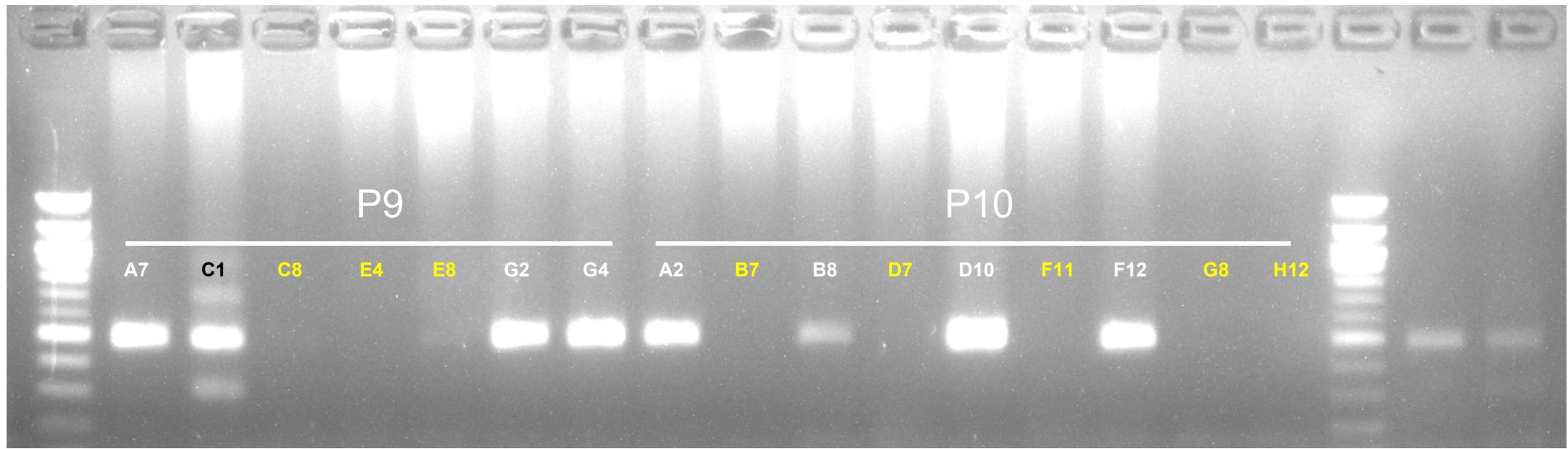
DU145

20200513 Edge Repeat2



DU145

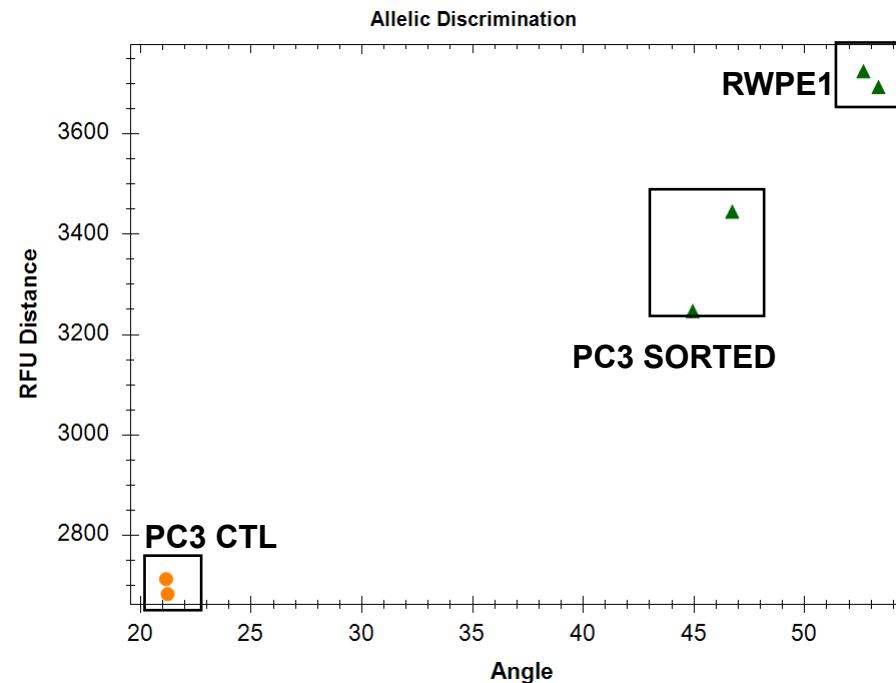
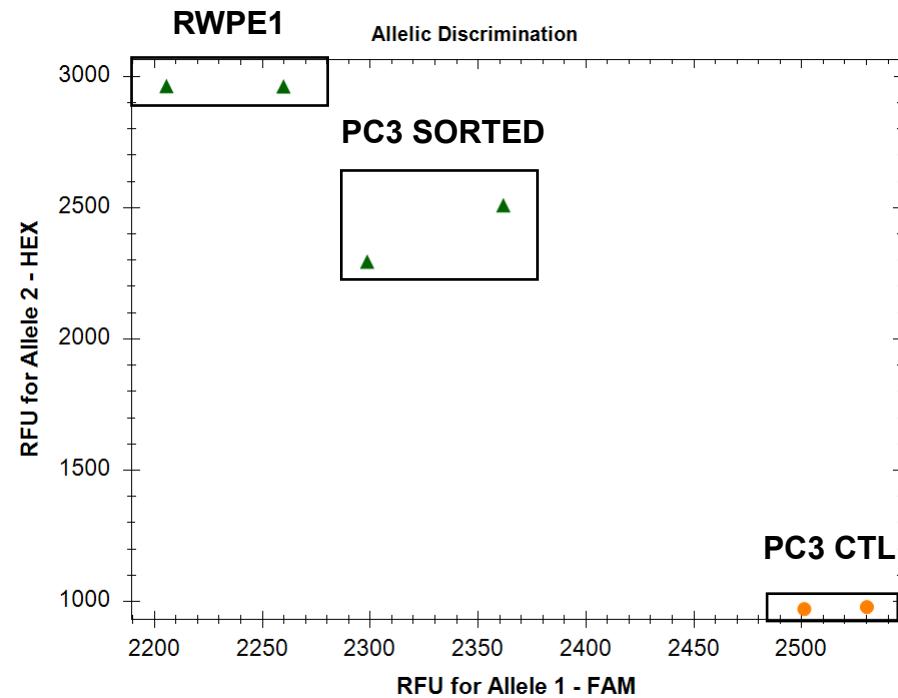
20200513 Edge Repeat3



DU145 rs60464856 A2G base editing Summary

Genotype	Clone count
A A	52
A G	21
G G	6

PC3 cells rs60464856 A2G edited population genotyping (rhAmp PCR)



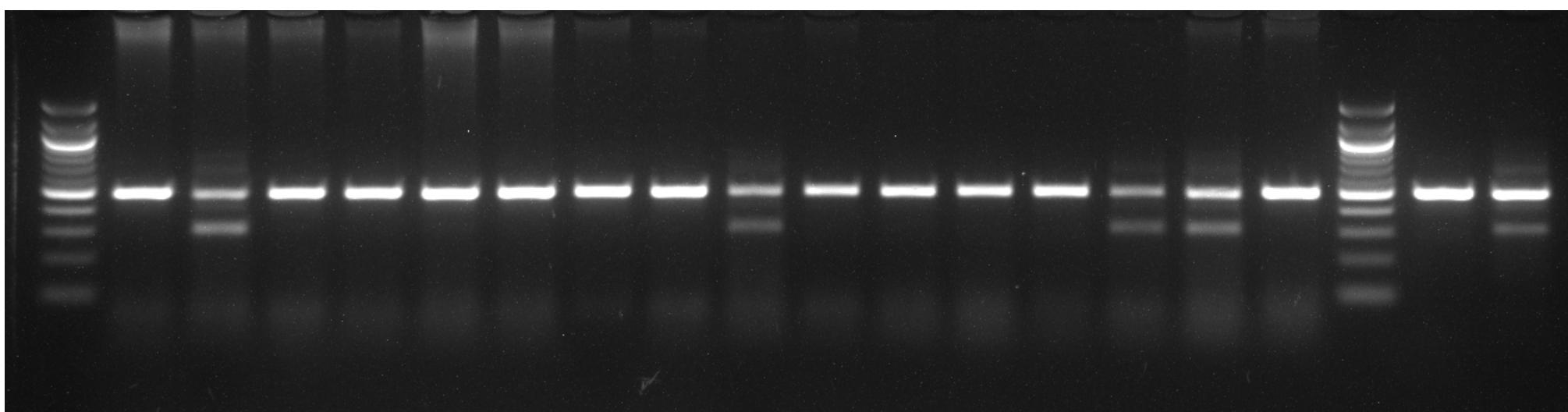
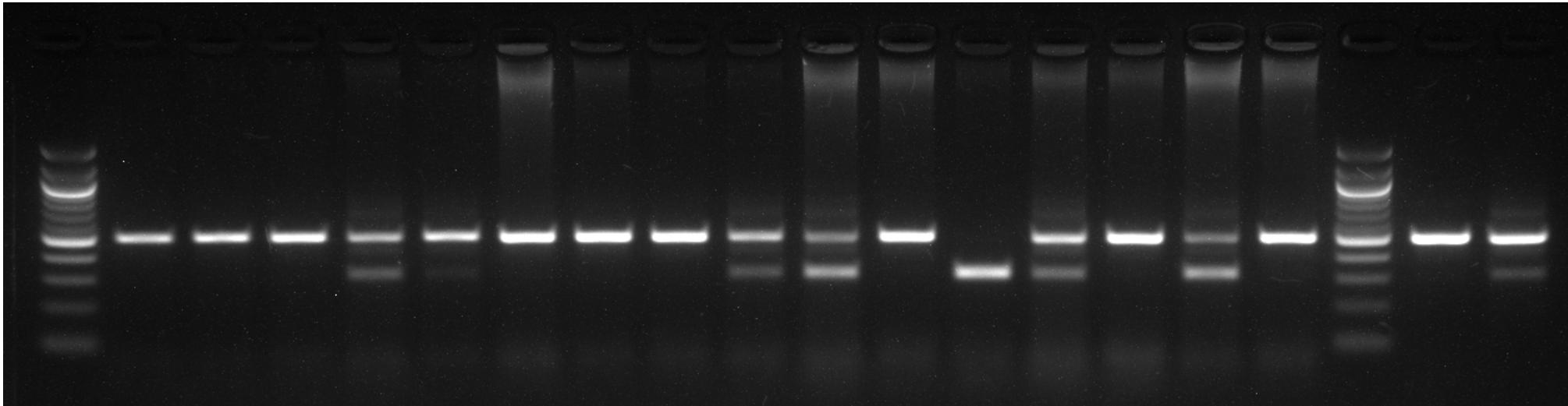
	FAM-A			HEX-G		
	CTL	SORTED	RWPE1	CTL	SORTED	RWPE1
Rep1	26.78	27.92	27.98	30.2	28.13	25.78
Rep2	26.75	27.81	27.89	30.23	27.76	25.88
Average	26.765	27.865	27.935	30.215	27.945	25.83
G/A %	0.092	0.946	4.302			
G allele% normalized to RWPE1	1.0%	11.0%	50%			

PC3

20200405 1st batch

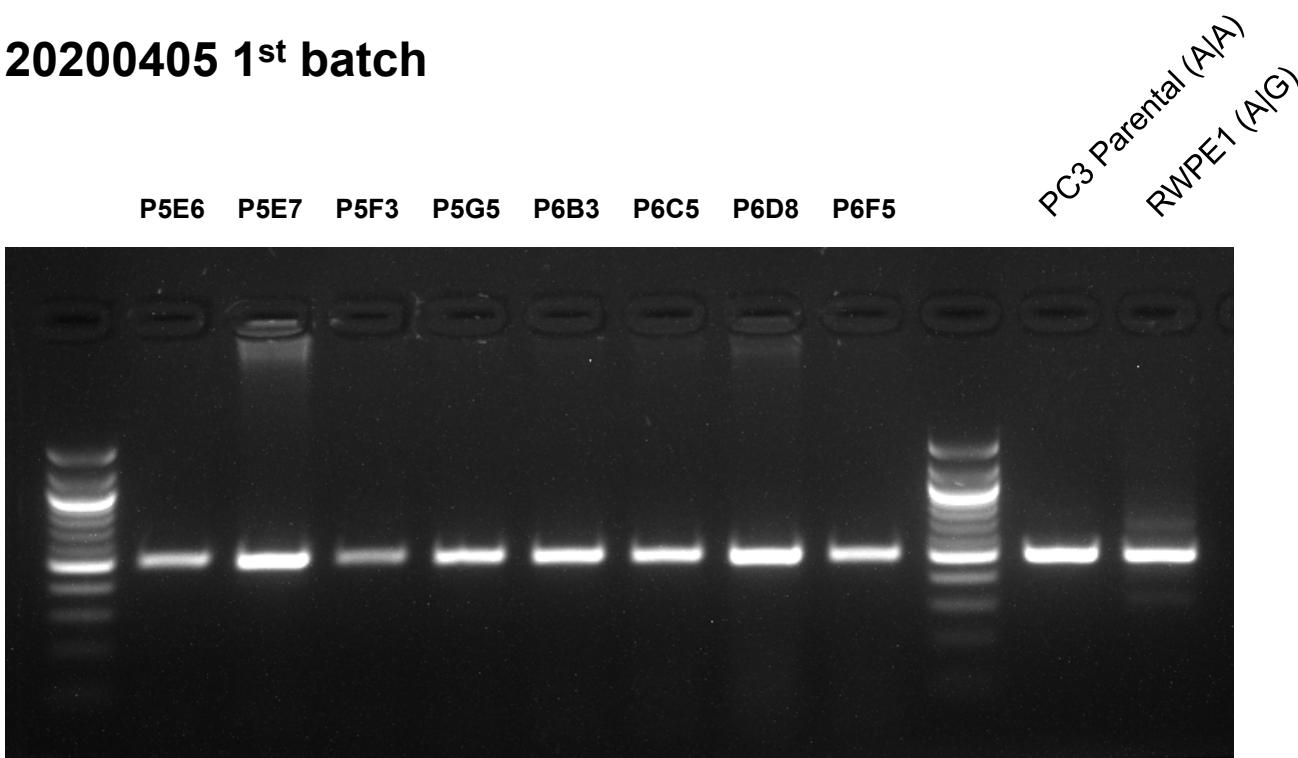
P1B3 P1C6 P1D9 P1F2 P1F4 P1F11 P2B4 P2B7 P2B8 P2B10 P2D8 P2E9 P2E11 P2F7 P3B2 P3B4

PC3 Parental (A/A)
RWPE1 (A/G)



PC3

20200405 1st batch

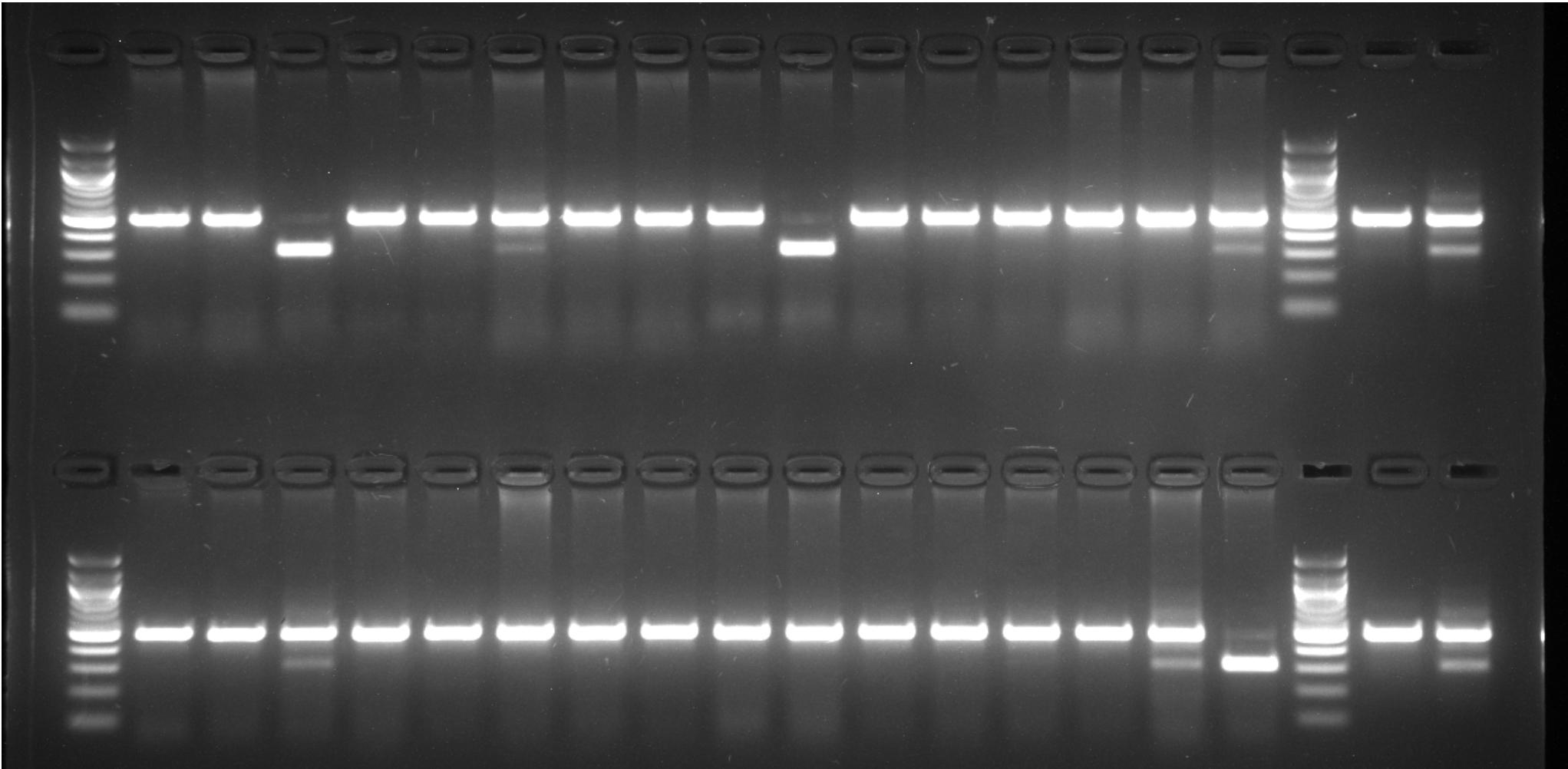


PC3

20200409 2nd batch

PC3 Parental (A/A)
RWPE1 (A/G)

P1D4 P1E11 P1G5 P1G7 P1H3 P2A6 P2C7 P2D1 P2E5 P2H2 P3B3 P3E9 P3F1 P3G7 P4A10 P4B10



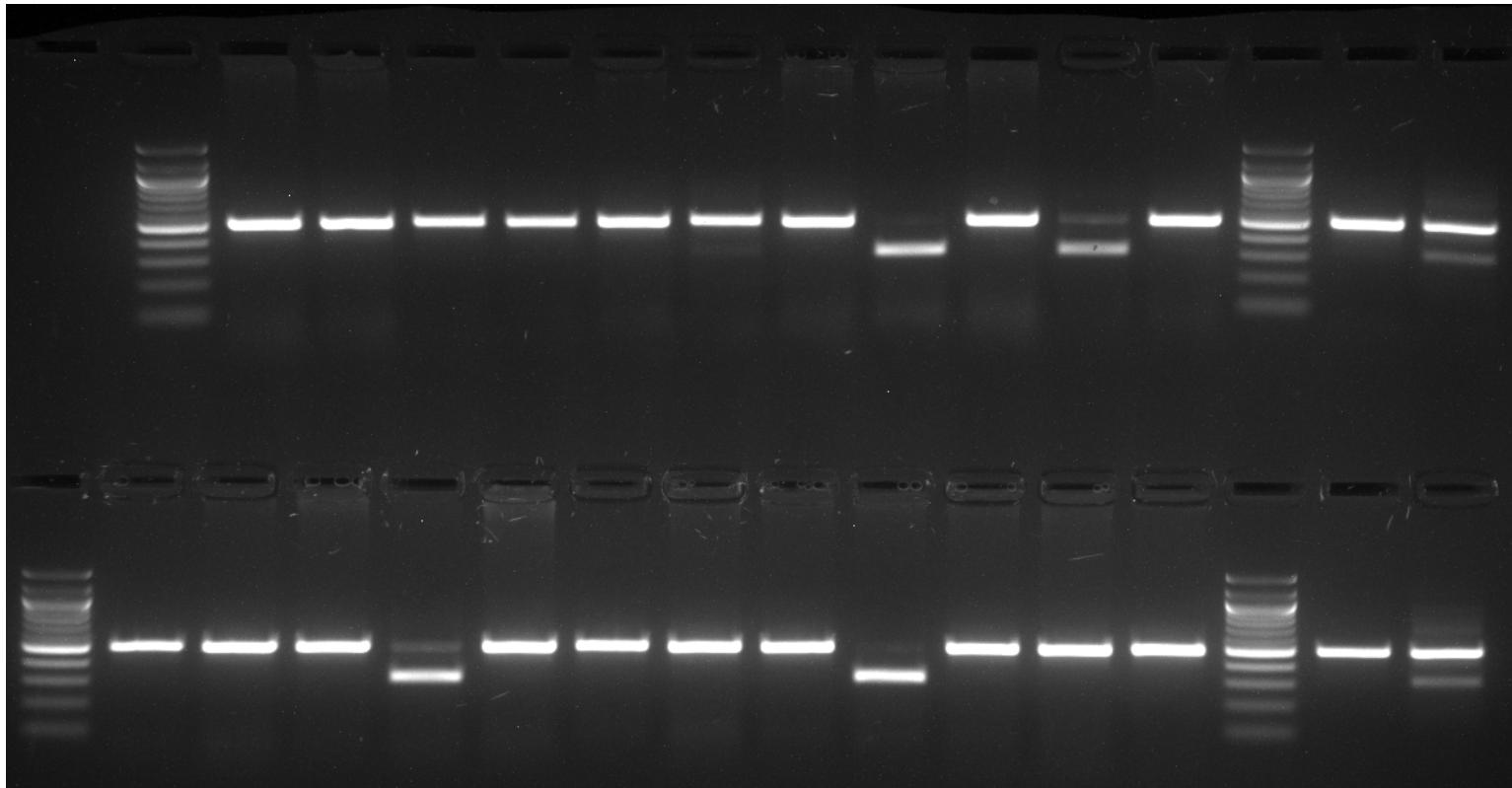
P4C2 P4C11 P4D12 P4E8 P4E11 P5B9 P5C8 P5D10 P5F2 P5G3 P5G4 P5H2 P6A8 P6B8 P6E7 P6G8

PC3

20200415 3rd batch

P1A2 P1A4 P1C9 P1C11 P1E2 P1F10 P2D9 P2D12 P2E2 P2F2 P2H3

PC3 Parental (A/A)
RWPE1 (A/G)

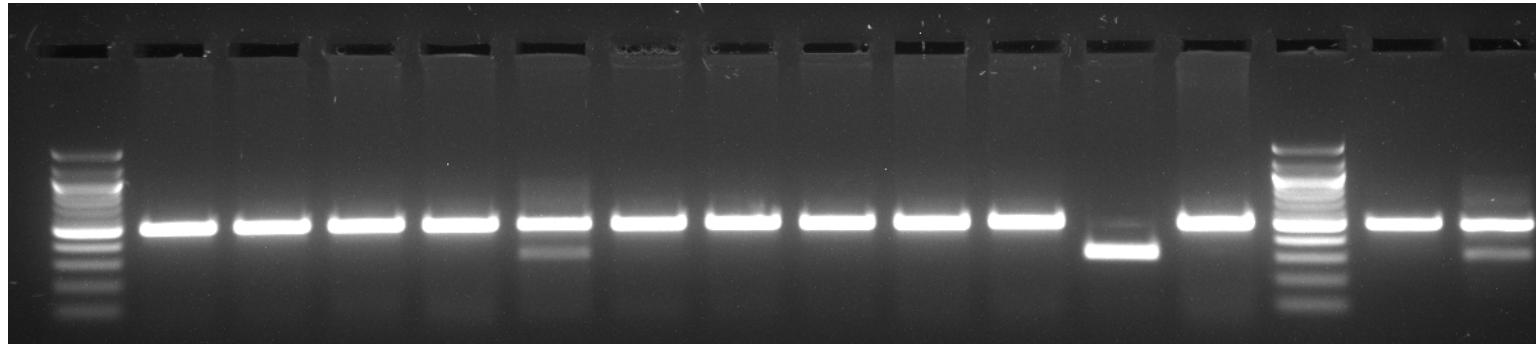


P3A4 P3B5 P3C2 P3C12 P3D6 P3D8 P3F11 P3G10 P3H2 P3H3 P4B1 P4B8

PC3

20200415 3rd batch

P4B9 P4C9 P4D3 P4F11 P4G4 P5B11 P5C1 P5E10 P5G1 P5H3 P6D7 P6F1



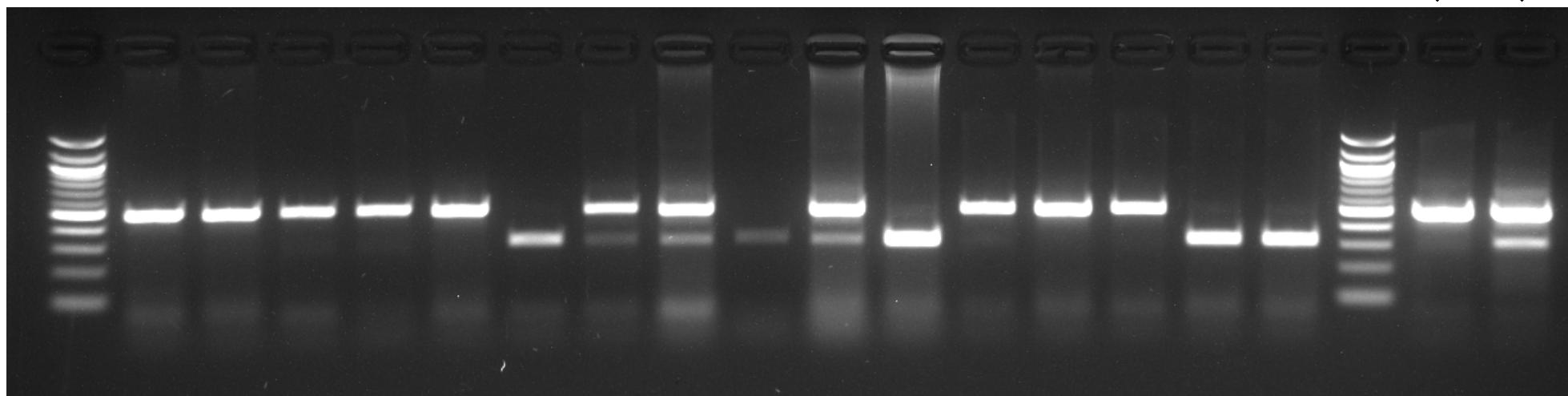
PC3 Parental (A/A)
RWPE1 (A/G)

PC3 rs60464856 base editing Summary

Genotype	Clone count
A G	15
G G	11

20200427 4th batch

P1G4 P1G9 P2C5 P2C9 P2E8 P2G4 P3B7 P3E10 P3E12 P4E1 P4F8 P5B8 P5E8 P5E11 P6B11 P6H10



PC3 Parental (A/A)
RWPE1 (A/G)