RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO$_2$ ppm	U_3O_8 ppm
Target A	RC-TGA-0009	TGA-RC-01301	0.0	1.0	1.0	511098.3	8117403.4	764.2	293.6	213.8	20.8	112.6	3.4	24.3	19.9	137.0	4.7	16.1	3.2	0.6	2.5	0.4	3.0	0.7	2.2	0.3	2.3	0.4	20.3	79.8	133.5	7.4	22.0	5.1
Target A	RC-TGA-0009	TGA-RC-01302	1.0	2.0	1.0	511098.3	8117403.4	764.2	325.4	239.5	20.2	122.7	3.8	24.0	20.9	159.1	4.6	15.6	2.6	0.6	2.4	0.5	3.3	0.7	2.2	0.4	2.7	0.4	23.4	85.9	142.5	7.9	24.9	5.6
Target A	RC-TGA-0009	TGA-RC-01303	2.0	3.0	1.0	511098.3	8117403.4	764.2	352.8	265.4	27.7	128.1	4.4	32.1	25.3	167.7	6.0	21.7	4.0	1.0	3.3	0.6	3.8	0.9	2.6	0.4	2.9	0.5	24.9	87.4	151.6	8.2	25.3	5.6
Target A	RC-TGA-0009	TGA-RC-01304	3.0	4.0	1.0	511098.3	8117403.4	764.2	351.4	264.0	25.7	125.8	3.9	29.6	27.0	169.5	5.9	19.8	3.4	0.7	2.6	0.5	3.4	0.8	2.4	0.4	2.8	0.5	24.3	87.4	154.5	8.2	25.7	6.0
Target A	RC-TGA-0009	TGA-RC-01305	4.0	5.0	1.0	511098.3	8117403.4	764.2	354.5	265.5	25.4	124.6	3.8	29.2	28.0	173.2	6.0	19.4	3.3	0.7	2.5	0.5	3.3	0.7	2.2	0.4	2.6	0.5	22.4	89.0	148.8	8.3	24.8	5.8
Target A	RC-TGA-0009	TGA-RC-01306	5.0	6.0	1.0	511098.3	8117403.4	764.2	373.0	281.0	29.2	129.6	3.9	33.0	32.3	178.1	6.9	22.3	3.8	0.7	2.7	0.5	3.4	0.8	2.4	0.4	2.7	0.5	23.5	92.0	141.0	7.2	24.0	6.0
Target A	RC-TGA-0009	TGA-RC-01308	6.0	7.0	1.0	511098.3	8117403.4	764.2	411.5	270.4	52.3	167.4	3.3	55.6	54.7	130.2	12.3	40.0	7.0	1.2	3.5	0.5	2.8	0.6	1.4	0.2	1.5	0.2	14.3	141.1	92.7	5.6	12.9	4.4
Target A	RC-TGA-0009	TGA-RC-01309	7.0	8.0	1.0	511098.3	8117403.4	764.2	447.7	268.2	59.5	206.1	3.6	63.1	59.1	115.2	13.3	46.2	7.8	1.6	4.2	0.5	3.1	0.5	1.4	0.2	1.2	0.2	13.7	179.5	73.2	4.5	6.7	3.4
Target A	RC-TGA-0009	TGA-RC-01310	8.0	9.0	1.0	511098.3	8117403.4	764.2	490.7	308.2	64.9	210.0	3.7	68.6	66.4	140.7	15.0	49.9	8.8	1.6	4.7	0.6	3.1	0.6	1.4	0.2	1.3	0.2	13.7	182.5	88.7	5.4	7.4	2.7
Target A	RC-TGA-0009	TGA-RC-01311	9.0	10.0	1.0	511098.3	8117403.4	764.2	469.4	285.3	61.9	210.4	3.7	65.6	59.0	129.6	14.4	47.5	8.5	1.6	4.7	0.6	3.1	0.5	1.5	0.2	1.4	0.2	12.6	184.1	69.0	4.8	5.4	2.4
Target A	RC-TGA-0009	TGA-RC-01312	10.0	11.0	1.0	511098.3	8117403.4	764.2	1,671.9	1,478.6	321.4	259.4	10.9	332.2	509.0	549.1	82.3	239.1	32.9	7.0	17.6	2.2	8.7	1.2	2.6	0.3	1.8	0.3	24.6	193.3	371.9	19.9	21.1	3.7
Target A	RC-TGA-0009	TGA-RC-01313	11.0	12.0	1.0	511098.3	8117403.4	764.2	3,165.9	2,963.4	765.2	342.2	25.5	790.7	1,056.7	921.3	186.7	578.5	80.5	18.2	41.7	4.8	20.7	2.5	4.6	0.5	2.7	0.3	43.6	202.5	436.3	22.1	25.0	3.5
Target A	RC-TGA-0009	TGA-RC-01315	12.0	13.0	1.0	511098.3	8117403.4	764.2	2,626.1	2,408.3	574.7	321.3	18.1	592.8	859.7	813.2	142.0	432.7	57.2	12.9	29.7	3.5	14.6	1.9	3.5	0.4	2.4	0.3	34.4	217.8	360.5	16.7	24.2	2.7
Target A	RC-TGA-0009	TGA-RC-01316	13.0	14.0	1.0	511098.3	8117403.4	764.2	604.1	394.0	102.0	246.9	5.2	107.2	104.8	138.2	22.9	79.1	12.2	2.6	6.7	0.8	4.4	0.7	1.8	0.3	1.8	0.2	17.5	210.1	82.3	5.5	7.2	2.2
Target A	RC-TGA-0009	TGA-RC-01317	14.0	15.0	1.0	511098.3	8117403.4	764.2	574.6	343.0	86.0	267.5	5.2	91.2	78.6	131.4	19.3	66.7	11.0	2.3	6.4	0.9	4.2	0.8	1.8	0.3	1.7	0.3	17.3	231.6	62.2	4.6	6.0	2.1
Target A	RC-TGA-0009	TGA-RC-01318	15.0	16.0	1.0	511098.3	8117403.4	764.2	522.2	264.5	62.9	286.6	4.3	67.3	56.2	107.9	14.0	49.0	8.6	1.8	4.9	0.7	3.6	0.6	1.5	0.2	1.3	0.2	14.1	257.7	48.4	3.5	3.2	1.7
Target A	RC-TGA-0009	TGA-RC-01319	16.0	17.0	1.0	511098.3	8117403.4	764.2	708.6	458.5	109.3	287.8	5.9	115.1	143.1	156.0	26.1	83.2	12.4	2.7	7.3	1.0	4.8	0.8	1.9	0.3	1.6	0.2	17.3	250.0	155.2	8.5	10.9	2.2
Target A	RC-TGA-0009	TGA-RC-01320	17.0	18.0	1.0	511098.3	8117403.4	764.2	3,533.1	3,270.8	830.9	404.0	24.5	855.4	1,360.4	857.4	215.1	615.9	80.4	18.1	42.8	4.6	19.9	2.4	4.9	0.5	2.7	0.3	45.5	262.3	592.2	30.5	34.7	2.6
Target A	RC-TGA-0009	TGA-RC-01322	18.0	19.0	1.0	511098.3	8117403.4	764.2	1,843.9	1,577.0	414.6	353.1	14.3	428.9	586.4	448.4	103.2	311.4	41.4	9.5	23.3	2.6	11.7	1.5	3.1	0.4	2.2	0.3	31.7	266.9	252.5	12.9	16.1	1.8
Target A	RC-TGA-0009	TGA-RC-01323	19.0	20.0	1.0	511098.3	8117403.4	764.2	935.9	704.3	185.4	285.3	8.5	193.9	231.6	213.1	44.8	140.6	20.5	4.7	11.8	1.4	7.1	1.0	2.6	0.3	1.8	0.3	22.6	231.6	108.6	6.1	7.4	1.5
Target A	RC-TGA-0009	TGA-RC-01324	20.0	21.0	1.0	511098.3	8117403.4	764.2	704.1	408.1	105.5	339.9	6.6	112.0	111.7	133.3	24.5	80.9	13.9	2.8	8.2	1.1	5.5	0.9	2.3	0.3	2.1	0.3	20.3	296.0	66.1	4.3	4.2	0.9
Target A	RC-TGA-0009	TGA-RC-01325	21.0	22.0	1.0	511098.3	8117403.4	764.2	536.5	257.4	65.4	320.3	5.7	71.2	44.7	96.1	13.8	51.7	10.0	2.4	6.4	0.9	4.8	0.8	2.2	0.4	2.1	0.3	20.8	279.2	43.8	3.4	2.7	0.8
Target A	RC-TGA-0009	TGA-RC-01326	22.0	23.0	1.0	511098.3	8117403.4	764.2	568.8	297.3	74.9	314.0	6.0	80.9	61.7	107.4	16.4	58.6	10.8	2.4	7.5	1.0	5.0	0.9	2.2	0.3	2.0	0.3	21.1	271.5	170.9	9.8	12.2	2.3
Target A	RC-TGA-0009	TGA-RC-01327	23.0	24.0	1.0	511098.3	8117403.4	764.2	506.1	245.4	54.6	296.2	5.2	59.8	37.1	110.3	11.1	43.5	7.9	1.9	5.9	0.8	4.4	0.7	1.8	0.3	1.7	0.3	17.8	260.7	65.2	4.3	4.1	1.5
Target A	RC-TGA-0009	TGA-RC-01328	24.0	25.0	1.0	511098.3	8117403.4	764.2	492.2	242.2	47.2	285.9	4.9	52.1	31.7	120.3	10.0	37.2	7.1	2.0	5.5	0.8	4.1	0.7	1.9	0.3	1.7	0.3	18.7	250.0	66.7	4.9	4.4	1.3
Target A	RC-TGA-0009	TGA-RC-01329	25.0	26.0	1.0	511098.3	8117403.4	764.2	609.6	359.6	42.2	282.5	4.6	46.7	21.9	256.7	8.7	33.5	6.4	1.8	5.1	0.8	3.8	0.7	1.9	0.3	1.6	0.2	16.4	250.0	45.1	3.7	4.3	1.1
Target A	RC-TGA-0009	TGA-RC-01330	26.0	27.0	1.0	511098.3	8117403.4	764.2	570.6	314.5	43.6	288.0	4.6	48.3	26.5	205.8	9.1	34.5	6.7	1.9	5.0	0.7	3.9	0.7	1.7	0.3	1.6	0.2	15.9	256.1	103.7	6.7	8.0	2.1
Target A	RC-TGA-0009	TGA-RC-01331	27.0	28.0	1.0	511098.3	8117403.4	764.2	1,798.3	1,565.2	488.1	351.1	19.6	507.7	496.1	410.3	112.5	375.6	52.8	14.5	35.2	3.9	15.7	2.2	3.9	0.4	2.4	0.3	39.5	233.1	97.7	6.1	9.4	4.3
Target A	RC-TGA-0009	TGA-RC-01332	28.0	29.0	1.0	511098.3	8117403.4	764.2	1,309.8	1,105.8	361.4	316.7	16.5	378.0	208.8	377.1	76.8	284.6	45.8	11.4	24.4	3.1	13.4	2.1	4.7	0.6	4.1	0.5	48.3	204.0	163.8	8.9	18.3	3.1
Target A	RC-TGA-0009	TGA-RC-01333	29.0	30.0	1.0	511098.3	8117403.4	764.2	1,319.1	1,124.3	418.1	365.4	24.2	442.4	131.9	342.7	79.9	338.3	60.9	15.8	35.7	4.5	19.7	3.2	7.0	0.9	5.2	0.7	78.0	194.8	90.6	5.5	8.1	1.7
Target A	RC-TGA-0009	TGA-RC-01335	30.0	31.0	1.0	511098.3	8117403.4	764.2	1,311.6	1,121.4	394.1	423.8	27.9	422.0	126.7	309.6	73.3	320.8	57.5	15.8	40.9	5.0	23.0	3.9	9.0	1.1	6.3	0.9	127.6	190.2	53.4	3.3	4.2	1.2
Target A	RC-TGA-0009	TGA-RC-01336	31.0	32.0	1.0	511098.3	8117403.4	764.2	4,050.3	3,901.5	1,701.1	997.9	118.7	1,819.8	634.5	479.1	319.0	1,382.2	237.7	66.1	171.2	21.2	97.4	15.8	35.6	4.3	24.0	3.3	410.2	148.8	98.4	6.5	7.6	1.8
Target A	RC-TGA-0009	TGA-RC-01337	32.0	33.0	1.0	511098.3	8117403.4	764.2	1,760.6	1,562.7	554.9	526.4	43.0	597.9	234.0	366.1	104.6	450.2	79.3	22.7	60.2	7.6	35.5	6.0	13.9	1.7	9.6	1.3	170.2	197.9	84.3	5.6	7.2	1.5
Target A	RC-TGA-0009	TGA-RC-01338	33.0	34.0	1.0	511098.3	8117403.4	764.2	1,162.6	1,006.1	272.5	385.4	26.9	299.4	132.5	331.7	51.5	221.0	40.5	11.9	35.3	4.6	22.3	4.2	9.8	1.3	7.2	1.1	131.4	156.4	149.5	9.5	12.2	2.3
Target A	RC-TGA-0009	TGA-RC-01339	34.0	35.0	1.0	511098.3	8117403.4	764.2	728.5	616.5	187.7	205.4	12.8	200.5	120.8	189.2	38.4	149.3	25.4	6.9	18.3	2.2	10.6	1.8	3.9	0.5	2.6	0.4	46.4	112.0	88.3	4.9	6.9	1.2
Target A	RC-TGA-0009	TGA-RC-01340	35.0	36.0	1.0	511098.3	8117403.4	764.2	328.1	226.9	61.8	134.0	4.5	66.2	35.4	88.0	12.3	49.5	9.0	2.4	6.5	0.8	3.7	0.6	1.4	0.2	0.9	0.1	16.1	101.2	34.9	2.2	3.3	0.6
Target A	RC-TGA-0009	TGA-RC-01341	36.0	37.0	1.0	511098.3	8117403.4	764.2	388.1	285.3	80.6	140.3	5.2	85.8	57.6	99.3	16.9	63.7	10.4	2.9	7.4	0.9	4.2	0.7	1.6	0.2	1.0	0.1	18.4	102.8	30.8	2.2	2.8	0.7
Target A	RC-TGA-0009	TGA-RC-01343	37.0	38.0	1.0	511098.3	8117403.4	764.2	325.6	224.3	59.9	132.0	4.2	64.1	38.8	86.4	12.3	47.6	8.4	2.3	6.3	0.8	3.4	0.6	1.3	0.2	0.9	0.1	15.0	101.2	33.5	1.8	2.9	0.7
Target A	RC-TGA-0009	TGA-RC-01344	38.0	39.0	1.0	511098.3	8117403.4	764.2	312.8	211.5	61.4	135.6	4.7	66.1	31.3	75.4	11.9	49.5	9.0	2.7	6.8	0.9	3.8	0.6	1.4	0.2	1.0	0.2	16.9	101.2	20.4	1.6	1.7	0.3
Target A	RC-TGA-0009	TGA-RC-01345	39.0	40.0	1.0	511098.3	8117403.4	764.2	361.6	261.9	74.3	131.4	4.4	78.6	43.5	102.2	14.7	59.6	10.2	2.5	6.3	0.8	3.6	0.6	1.5	0.1	0.8	0.1	15.4	99.7	34.2	2.4	4.9	0.7
Target A	RC-TGA-0009	TGA-RC-01346	40.0	41.0	1.0	511098.3	8117403.4	764.2	427.4	310.8	86.2	154.8	5.2	91.3	52.1	122.6	17.7	68.5	11.7	3.1	8.0	1.0	4.2	0.7	1.6	0.2	1.1	0.2	18.3	116.6	41.5	3.1	6.3	0.7
Target A	RC-TGA-0009	TGA-RC-01347	41.0	42.0	1.0	511098.3	8117403.4	764.2	512.0	403.1	106.1	156.5	6.5	112.6	74.5	161.5	22.7	83.4	13.5	3.7	9.4	1.2	5.3	0.9	2.1	0.3	1.4	0.2	23.1	108.9	77.0	4.4	8.6	1.2
Target A	RC-TGA-0009	TGA-RC-01348	42.0	43.0	1.0	511098.3	8117403.4	764.2	460.9	352.0	97.0	153.2	6.3	103.4	64.3	133.3	20.2	76.9	13.0	3.5	8.9	1.2	5.2	0.8	1.7	0.2	1.3	0.2	21.5	108.9	46.5	3.2	6.0	0.7
Target A	RC-TGA-0009	TGA-RC-01349	43.0	44.0	1.0	511098.3	8117403.4	764.2	367.7	263.4	73.0	139.4	4.7	77.7	41.8	103.4	15.0	58.0	10.2	2.7	7.2	0.9	3.8	0.7	1.5	0.1	1.0	0.1	17.0	104.3	29.6	2.3	4.4	0.6
Target A	RC-TGA-0009	TGA-RC-01350	44.0	45.0	1.0	511098.3	8117403.4	764.2	430.8	328.1	89.3	146.3	6.0	95.3	57.1	125.3	18.4	70.9	12.8	3.1	9.0	1.0	5.0	0.9	1.9	0.2	1.3	0.2	21.1	102.8	54.9	3.5	5.9	0.9
Target A	RC-TGA-0009	TGA-RC-01352	45.0	46.0	1.0	511098.3	8117403.4	764.2	360.1	261.9	50.3	160.0	7.0	57.3	48.1	93.8	11.3	39.1	7.8	1.5	6.8	1.1	5.8	1.2	3.9	0.5	3.4	0.5	37.1	98.2	30.6	2.2	23.6	7.0
Target A	RC-TGA-0009	TGA-RC-01353	46.0	47.0	1.0	511098.3	8117403.4	764.2	305.0	203.7	57.6	131.8	4.4	62.0	31.1	75.8	11.5	46.1	8.8	2.2	6.3	0.8	3.6	0.6	1.2	0.1	0.8	0.1	14.7	101.2	23.0	1.6	2.4	0.4
Target A	RC-TGA-0009	TGA-RC-01354	47.0	48.0	1.0	511098.3	8117403.4	764.2	472.8	382.3	95.3	137.6	6.4	101.7	72.5	154.8	19.8	75.6	12.6	3.5	9.0	1.2	5.2	0.9	2.1	0.2	1.3	0.2	23.6	90.5	78.8	3.8	7.2	1.5
Target A	RC-TGA-0009	TGA-RC-01355	48.0	49.0	1.0	511098.3	8117403.4	764.2	504.0	421.2	99.2	134.6	7.1	106.3	83.3	173.8	21.3	77.9	13.2	3.4	9.3	1.3	5.8	1.0	2.3	0.3	1.6	0.2	26.5	82.8	108.6	4.9	9.0	2.2
Target A	RC-TGA-0009	TGA-RC-01356	49.0	50.0	1.0	511098.3	8117403.4	764.2	295.9	196.2	54.9	130.1	4.4	59.3	29.4	73.0	10.9	44.0	8.5	2.2	5.9	0.8	3.5	0.6	1.3	0.1	0.8	0.1	15.0	99.7	26.5	1.7	2.2	0.6
Target A	RC-TGA-0009	TGA-RC-01358	50.0	51.0	1.0	511098.3	8117403.4	764.2	292.6	192.9	55.7	128.6	4.1	59.8	27.4	72.1	10.8	44.9	8.7	2.1	5.8	0.7	3.4	0.5	1.2	0.1	0.8	0.1	14.0	99.7	21.5	1.5	1.5	0.3
Target A	RC-TGA-0009	TGA-RC-01359	51.0	52.0	1.0	511098.3	8117403.4	764.2	316.8	214.0	58.3	134.1	4.5	62.8	33.5	81.9	11.7	46.7	8.9	2.3	6.2	0.8	3.7	0.6	1.3	0.1	0.9	0.1	15.2	102.8	35.2	1.8	2.2	0.6
Target A	RC-TGA-0009	TGA-RC-01360	52.0	53.0	1.0	511098.3	8117403.4	764.2	314.0	218.9	60.9	126.8	4.3	65.2	34.1	83.0	11.9	49.0	9.1	2.3	6.4	0.8	3.4	0.6	1.3	0.2	1.0	0.1	15.5	95.1	25.7	1.5	2.3	0.6
Target A	RC-TGA-0009	TGA-RC-01361	53.0	54.0	1.0	511098.3	8117403.4	764.2	318.6	228.1	64.0	122.3	4.5	68.5	33.1	89.6	12.7	51.2	9.7	2.4	6.3	0.8	3.7	0.6	1.5	0.2	1.0	0.1	15.2	90.5	26.5	2.0	3.2	0.6
Target A	RC-TGA-0009	TGA-RC-01362	54.0	55.0	1.0	511098.3	8117403.4	764.2	442.2	351.7	93.4	133.2	6.0	99.4	58.4	144.3	19.0	74.4	12.8	3.3	8.5	1.1	4.9	0.8	1.8	0.2	1.3	0.2	20.6	90.5	48.4	3.1	5.6	0.9
Target A	RC-TGA-0009	TGA-RC-01363	55.0	56.0	1.0	511098.3	8117403.4	764.2	331.5	225.7	64.4	135.9	4.2	68.6	33.3	88.2	12.9	51.6	9.6	2.4	6.1	0.7	3.5	0.5	1.3	0.1	0.8	0.1	14.5	105.8	22.8	2.0	3.4	0.4
Target A	RC-TGA-0009	TGA-RC-01364	56.0	57.0	1.0	511098.3	8117403.4	764.2	361.8	263.7	74.6	130.5	4.6	79.2	40.9	106.4	15.2	59.5	9.4	2.6	6.7	0.9	3.7	0.6	1.3	0.1	0.8	0.1	15.4	98.2	36.5	2.7	5.3	0.6
Target A	RC-TGA-0009	TGA-RC-01366	57.0	58.0	1.0	511098.3	8117403.4	764.2	318.0	265.9	62.5	90.7	5.0	67.5	53.0	102.7	13.0	49.5	9.1	2.3	6.3	0.9	4.1	0.7	1.8	0.2	1.4	0.2	20.6	52.1	230.3	4.5	3.0	1.3
Target A	RC-TGA-0009	TGA-RC-01367	58.0	59.0	1.0	511098.3	8117403.4	764.2	291.7	202.8	55.0	125.2	5.0	60.0	27.6	75.3	10.6	44.4	8.6	2.4	6.5	0.9	4.1	0.7	1.5	0.2	1.3	0.2	18.5	89.0	44.3	1.5	1.6	0.9
Target A	RC-TGA-0009	TGA-RC-01368	59.0	60.0	1.0	511098.3	8117403.4	764.2	739.8	676.9	173.1	158.8	13.0	186.0	127.8	256.7	36.0	137.1	23.3	6.0	17.0	2.3	10.7	1.8	4.5	0.5	3.0	0.4	49.7	62.9	178.1	8.7	11.0	2.7
Target A	RC-TGA-0009	TGA-RC-01369	60.0	61.0	1.0	511098.3	8117403.4	764.2	823.5	746.8	200.3	217.1	18.8	219.2	79.9	293.6	35.9	164.5	32.6	8.2	25.0	3.3	15.5	2.6	6.1	0.8	4.5	0.7	73.8	76.7	44.8	2.4	3.4	1.0
Target A	RC-TGA-0009	TGA-RC-01370	61.0	62.0	1.0	511098.3	8117403.4	764.2	592.5	502.0	129.2	164.5	10.0	139.2	77.3	202.1	25.5	103.7	19.4	4.9	13.9	1.8	8.2	1.3	3.3	0.4	2.2	0.3	37.7	90.5	35.9	2.2	3.1	0.8
Target A	RC-TGA-0009	TGA-RC-01371	62.0	63.0	1.0	511098.3	8117403.4	764.2	735.2	649.3	130.4	157.5	9.6	140.0	108.7	320.6	28.0	102.4	17.9	4.6	12.5	1.7	7.9	1.3	3.4	0.4	2.2	0.3	37.3	85.9	141.2	6.1	10.9	2.8
Target A	RC-TGA-0009	TGA-RC-01373	63.0	64.0	1.0	511098.3	8117403.4	764.2	544.6	477.1	95.0	121.4	7.2	102.2	70.6	244.5	19.9	75.1	13.1	3.5	9.3	1.3	5.9	1.0	2.4	0.3	1.8	0.3	28.2	67.5	90.7	4.6	8.6	1.9
Target A	RC-TGA-0009	TGA-RC-01374	64.0	65.0	1.0	511098.3	8117403.4	764.2	438.1	359.9	65.5	117.9	5.2	70.7	37.6	207.0	13.1	52.4	10.0	2.6	7.5	1.0	4.2	0.8	1.8	0.2	1.3	0.2	20.2	78.2	54.2	3.7	4.8	1.4
Target A	RC-TGA-0009	TGA-RC-01375	65.0	66.0	1.0	511098.3	8117403.4	764.2	339.1	259.4	54.6	111.4	4.4	59.0	27.7	137.0	10.5	44.1	8.6	2.2	6.0	0.8	3.7	0.6	1.4	0.2	1.0	0.1	15.6	79.8	36.3	2.3	2.7	0.8
Target A	RC-TGA-0009	TGA-RC-01376	66.0	67.0	1.0	511098.3	8117403.4	764.2	346.2	260.3	63.2	124.5	5.2	68.5	33.8	114.7	12.4	50.9	10.0	2.6	6.8	0.9	4.3	0.7	1.7	0.2	1.3	0.2	19.8	85.9	44.1	2.6	3.6	0.9
Target A	RC-TGA-0009	TGA-RC-01377	67.0	68.0	1.0	511098.3	8117403.4	764.2	363.5	273.0	58.1	125.4	4.7	62.9	29.8	140.7	11.3	46.8	9.5	2.3	6.7	0.8	3.9	0.7	1.4	0.2	1.3	0.2	17.5	90.5	42.5	2.8	3.1	1.1
Target A	RC-TGA-0009	TGA-RC-01378	68.0	69.0	1.0	511098.3	8117403.4	764.2	397.3	305.3	60.7	130.4	5.2	65.9	27.4	168.3	11.5	49.2	10.5	2.3	7.0	1.0	4.3	0.8	1.8	0.2	1.3	0.2	19.6

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO$_2$ ppm	U_3O_8 ppm
Target A	RC-TGA-0009	TGA-RC-01388	77.0	78.0	1.0	511098.3	8117403.4	764.2	313.4	226.0	60.5	124.6	5.3	65.8	28.0	90.9	11.4	49.1	9.5	2.6	7.4	0.8	4.5	0.7	1.7	0.2	1.0	0.1	18.2	87.4	32.6	2.7	2.9	0.9
Target A	RC-TGA-0009	TGA-RC-01389	78.0	79.0	1.0	511098.3	8117403.4	764.2	336.1	259.4	64.0	117.4	5.7	69.6	34.9	109.5	12.9	51.1	10.4	2.8	8.0	0.9	4.8	0.8	1.9	0.3	1.4	0.2	19.7	76.7	49.8	4.0	5.2	1.6
Target A	RC-TGA-0009	TGA-RC-01390	79.0	80.0	1.0	511098.3	8117403.4	764.2	323.0	241.7	60.4	119.2	5.2	65.6	32.0	102.2	12.0	48.4	9.2	2.7	7.3	0.9	4.4	0.7	1.7	0.2	1.2	0.2	18.7	81.3	45.6	3.8	4.5	1.2
Target A	RC-TGA-0015	TGA-RC-01391	0.0	1.0	1.0	511085.6	8116599.3	759.8	277.5	234.5	30.0	67.9	2.9	32.8	37.9	137.6	7.3	22.6	4.1	0.9	2.7	0.4	2.5	0.5	1.6	0.3	1.9	0.3	14.0	42.9	258.9	18.4	26.3	6.3
Target A	RC-TGA-0015	TGA-RC-01392	1.0	2.0	1.0	511085.6	8116599.3	759.8	296.3	250.3	31.7	72.1	3.1	34.8	39.4	148.6	7.5	24.1	4.4	0.9	2.9	0.4	2.7	0.5	1.6	0.3	1.9	0.3	14.5	46.0	238.2	17.1	27.5	6.6
Target A	RC-TGA-0015	TGA-RC-01394	2.0	3.0	1.0	511085.6	8116599.3	759.8	294.5	247.0	29.2	72.2	2.9	32.1	39.2	149.9	7.3	21.9	4.1	0.8	2.5	0.4	2.5	0.5	1.5	0.3	1.7	0.3	14.2	47.5	231.0	16.5	27.7	6.3
Target A	RC-TGA-0015	TGA-RC-01395	3.0	4.0	1.0	511085.6	8116599.3	759.8	334.7	270.3	37.3	89.5	3.2	40.5	44.8	158.5	8.9	28.3	4.7	1.1	3.3	0.4	2.8	0.5	1.6	0.3	1.8	0.3	13.0	64.4	193.8	13.9	28.3	7.8
Target A	RC-TGA-0015	TGA-RC-01396	4.0	5.0	1.0	511085.6	8116599.3	759.8	393.8	263.4	47.8	157.3	3.7	51.5	53.4	129.0	11.6	36.2	6.4	1.5	4.0	0.5	3.2	0.6	1.5	0.3	1.8	0.2	13.3	130.4	120.9	8.3	27.9	15.0
Target A	RC-TGA-0015	TGA-RC-01397	5.0	6.0	1.0	511085.6	8116599.3	759.8	164.3	135.2	27.9	43.2	1.9	29.8	32.3	57.4	6.5	21.5	3.6	0.7	2.1	0.2	1.6	0.3	0.9	0.1	0.9	0.1	7.1	29.1	53.9	4.0	9.2	3.3
Target A	RC-TGA-0015	TGA-RC-01398	6.0	7.0	1.0	511085.6	8116599.3	759.8	120.2	100.3	24.2	31.3	1.5	25.6	27.2	34.5	5.7	18.4	3.0	0.6	1.8	0.2	1.3	0.2	0.6	0.1	0.6	0.1	5.7	19.9	29.2	5.7	4.9	2.4
Target A	RC-TGA-0015	TGA-RC-01399	7.0	8.0	1.0	511085.6	8116599.3	759.8	208.5	180.9	42.6	48.8	2.7	45.3	48.7	62.9	9.9	32.8	5.5	1.1	3.5	0.4	2.3	0.4	1.2	0.2	1.1	0.2	10.9	27.6	61.5	4.2	9.8	3.4
Target A	RC-TGA-0015	TGA-RC-01401	8.0	9.0	1.0	511085.6	8116599.3	759.8	126.3	107.9	25.6	31.2	1.6	27.2	27.8	38.3	6.0	19.6	3.4	0.7	2.2	0.2	1.3	0.2	0.7	0.1	0.7	0.1	6.5	18.4	32.6	2.3	5.7	2.1
Target A	RC-TGA-0015	TGA-RC-01402	9.0	10.0	1.0	511085.6	8116599.3	759.8	94.7	79.3	20.3	27.1	1.6	22.0	19.0	25.4	4.7	15.6	2.8	0.7	2.1	0.3	1.4	0.3	0.7	0.1	0.5	0.1	5.7	15.3	11.9	0.7	3.2	1.6
Target A	RC-TGA-0015	TGA-RC-01403	10.0	11.0	1.0	511085.6	8116599.3	759.8	118.7	101.8	25.5	31.2	2.2	27.7	23.7	34.6	5.8	19.7	3.7	0.8	2.4	0.3	1.9	0.3	0.8	0.1	0.7	0.1	6.9	16.9	22.6	1.6	4.1	1.8
Target A	RC-TGA-0015	TGA-RC-01404	11.0	12.0	1.0	511085.6	8116599.3	759.8	167.2	148.8	37.3	38.5	2.9	40.2	37.3	49.5	8.6	28.7	4.6	1.2	3.7	0.4	2.5	0.4	1.0	0.1	1.0	0.2	9.7	18.4	16.8	1.2	3.7	1.8
Target A	RC-TGA-0015	TGA-RC-01405	12.0	13.0	1.0	511085.6	8116599.3	759.8	236.7	207.5	51.9	55.0	3.7	55.6	48.4	75.1	12.0	39.9	6.4	1.6	4.6	0.6	3.1	0.5	1.3	0.2	1.4	0.2	12.2	29.1	33.2	3.2	6.0	2.7
Target A	RC-TGA-0015	TGA-RC-01406	13.0	14.0	1.0	511085.6	8116599.3	759.8	334.5	294.7	83.4	77.6	5.6	89.0	73.7	88.9	19.3	64.0	10.9	2.6	7.3	0.9	4.7	0.8	2.1	0.3	1.8	0.3	17.0	39.9	23.7	1.6	5.6	3.0
Target A	RC-TGA-0015	TGA-RC-01407	14.0	15.0	1.0	511085.6	8116599.3	759.8	327.7	287.9	75.5	76.9	5.7	81.2	64.0	101.7	17.0	58.4	9.6	2.5	7.1	0.9	4.8	0.8	2.0	0.3	1.8	0.3	16.5	39.9	32.3	1.8	5.5	3.3
Target A	RC-TGA-0015	TGA-RC-01409	15.0	16.0	1.0	511085.6	8116599.3	759.8	293.5	255.2	70.6	71.3	5.0	75.6	62.3	80.3	16.1	54.5	9.1	2.1	6.0	0.8	4.2	0.7	1.9	0.3	1.7	0.2	15.0	38.3	23.6	1.5	5.4	2.8
Target A	RC-TGA-0015	TGA-RC-01410	16.0	17.0	1.0	511085.6	8116599.3	759.8	336.2	291.7	75.1	88.1	6.7	81.8	59.0	102.7	16.6	58.6	11.3	2.8	7.5	1.0	5.7	1.0	2.5	0.4	2.2	0.4	20.1	44.5	29.2	1.7	4.6	3.1
Target A	RC-TGA-0015	TGA-RC-01411	17.0	18.0	1.0	511085.6	8116599.3	759.8	367.4	319.8	78.9	124.8	10.0	88.9	52.2	98.0	15.9	63.0	13.5	3.4	10.9	1.4	8.6	1.5	4.0	0.6	3.5	0.5	42.9	47.5	28.8	1.6	3.7	2.8
Target A	RC-TGA-0015	TGA-RC-01412	18.0	19.0	1.0	511085.6	8116599.3	759.8	395.8	349.7	80.7	137.9	11.8	92.5	48.6	114.4	15.6	65.1	14.2	3.9	13.1	1.6	10.1	1.8	4.7	0.7	3.9	0.6	51.4	46.0	30.2	1.6	3.2	2.7
Target A	RC-TGA-0015	TGA-RC-01413	19.0	20.0	1.0	511085.6	8116599.3	759.8	256.8	209.2	45.8	110.3	7.6	53.5	26.2	65.2	8.9	37.0	9.3	2.6	8.6	1.2	6.5	1.2	3.6	0.5	2.8	0.4	35.3	47.5	38.2	1.5	1.6	2.2
Target A	RC-TGA-0015	TGA-RC-01414	20.0	21.0	1.0	511085.6	8116599.3	759.8	207.2	159.7	32.9	98.8	6.5	39.4	16.7	51.8	6.0	26.9	7.0	1.9	7.0	1.0	5.6	1.0	2.7	0.4	2.2	0.3	29.2	47.5	31.5	1.1	1.0	1.8
Target A	RC-TGA-0015	TGA-RC-01415	21.0	22.0	1.0	511085.6	8116599.3	759.8	198.5	146.4	31.6	93.0	5.3	36.9	17.4	49.9	5.9	25.7	6.7	1.7	5.7	0.8	4.6	0.8	2.4	0.3	2.0	0.3	22.4	52.1	23.8	1.0	1.2	1.8
Target A	RC-TGA-0015	TGA-RC-01417	22.0	23.0	1.0	511085.6	8116599.3	759.8	149.3	91.0	18.2	82.1	3.5	21.7	8.8	36.4	3.3	14.9	3.8	1.1	3.4	0.5	2.9	0.5	1.4	0.2	1.4	0.2	12.1	58.3	16.3	0.6	0.5	1.9
Target A	RC-TGA-0015	TGA-RC-01418	23.0	24.0	1.0	511085.6	8116599.3	759.8	297.4	240.7	55.2	157.8	12.0	67.2	20.9	52.5	9.1	46.1	11.1	3.3	12.4	2.0	10.0	1.9	5.2	0.7	4.2	0.6	60.7	56.8	36.0	1.2	1.0	2.1
Target A	RC-TGA-0015	TGA-RC-01419	24.0	25.0	1.0	511085.6	8116599.3	759.8	142.9	107.6	25.5	70.4	4.7	30.3	10.1	31.8	4.3	21.2	5.0	1.3	4.8	0.7	4.0	0.7	1.9	0.2	1.6	0.3	19.4	35.3	18.0	0.5	0.9	1.7
Target A	RC-TGA-0015	TGA-RC-01420	25.0	26.0	1.0	511085.6	8116599.3	759.8	167.4	122.9	27.1	83.6	5.0	32.1	11.6	39.7	4.7	22.4	5.3	1.5	5.2	0.8	4.2	0.8	2.2	0.3	1.8	0.3	22.1	44.5	24.0	0.7	0.9	1.8
Target A	RC-TGA-0015	TGA-RC-01421	26.0	27.0	1.0	511085.6	8116599.3	759.8	100.9	84.0	22.1	34.9	2.4	24.5	16.7	23.6	4.3	17.7	3.7	0.8	2.7	0.4	2.0	0.4	0.9	0.1	0.8	0.1	9.8	16.9	8.3	0.2	0.2	0.8
Target A	RC-TGA-0015	TGA-RC-01422	27.0	28.0	1.0	511085.6	8116599.3	759.8	186.9	165.4	38.5	47.2	3.4	41.9	39.5	56.1	7.9	30.6	5.6	1.4	4.1	0.6	2.9	0.5	1.1	0.1	0.9	0.1	14.0	21.5	20.5	0.6	0.8	1.0
Target A	RC-TGA-0015	TGA-RC-01423	28.0	29.0	1.0	511085.6	8116599.3	759.8	235.7	205.0	32.1	56.7	3.5	35.6	24.6	117.4	6.7	25.4	4.9	1.3	3.8	0.6	2.9	0.5	1.4	0.2	1.2	0.2	14.0	30.7	139.2	7.7	8.7	3.0
Target A	RC-TGA-0015	TGA-RC-01425	29.0	30.0	1.0	511085.6	8116599.3	759.8	1,114.1	1,089.5	213.8	93.5	10.0	223.8	226.9	554.0	50.5	163.3	25.9	6.2	14.9	2.0	8.0	1.3	2.8	0.3	1.6	0.2	31.6	24.5	426.3	21.5	27.3	5.6
Target A	RC-TGA-0015	TGA-RC-01426	30.0	31.0	1.0	511085.6	8116599.3	759.8	1,505.1	1,486.7	289.7	105.5	13.0	302.7	304.9	771.4	66.9	222.8	33.5	8.3	19.9	2.5	10.5	1.5	3.3	0.4	2.0	0.3	38.5	18.4	738.1	43.0	48.1	8.9
Target A	RC-TGA-0015	TGA-RC-01427	31.0	32.0	1.0	511085.6	8116599.3	759.8	4,870.2	4,862.5	1,016.0	298.0	44.3	1,060.3	1,132.9	2,303.3	236.8	779.2	120.0	28.6	69.3	8.8	35.5	5.2	10.9	1.1	5.8	0.7	124.6	7.7	814.0	51.5	70.2	9.7
Target A	RC-TGA-0015	TGA-RC-01428	32.0	33.0	1.0	511085.6	8116599.3	759.8	5,413.2	5,402.4	1,139.4	337.3	51.4	1,190.7	1,348.7	2,456.8	263.4	876.0	131.0	32.3	81.1	10.3	41.1	6.0	12.2	1.3	6.3	0.8	135.2	10.7	1,230.2	71.6	85.3	13.4
Target A	RC-TGA-0015	TGA-RC-01429	33.0	34.0	1.0	511085.6	8116599.3	759.8	3,849.1	3,836.8	818.9	286.7	41.5	860.4	1,001.6	1,646.1	187.9	631.0	95.9	24.8	63.5	8.1	33.4	5.1	10.9	1.1	5.6	0.7	121.3	12.3	783.9	43.7	48.9	8.5
Target A	RC-TGA-0015	TGA-RC-01430	34.0	35.0	1.0	511085.6	8116599.3	759.8	3,838.7	3,817.2	802.5	290.1	40.7	843.3	931.2	1,719.8	186.7	615.9	95.1	24.0	61.5	7.7	33.1	5.0	10.8	1.1	5.8	0.8	119.0	21.5	965.6	51.5	64.3	11.4
Target A	RC-TGA-0015	TGA-RC-01431	35.0	36.0	1.0	511085.6	8116599.3	759.8	1,698.5	1,677.0	338.9	138.7	17.6	356.5	435.1	745.6	78.8	260.1	40.1	10.7	26.9	3.4	14.2	2.2	4.7	0.5	2.7	0.4	51.7	21.5	527.9	20.8	23.9	5.2
Target A	RC-TGA-0015	TGA-RC-01432	36.0	37.0	1.0	511085.6	8116599.3	759.8	124.9	112.6	20.7	26.2	2.1	22.7	31.7	43.6	4.8	15.9	2.7	0.8	2.3	0.3	1.7	0.3	0.7	0.1	0.5	0.1	7.1	12.3	31.5	1.1	1.8	2.1
Target A	RC-TGA-0015	TGA-RC-01433	37.0	38.0	1.0	511085.6	8116599.3	759.8	1,771.1	1,758.9	352.4	129.0	18.1	370.5	449.2	798.5	81.8	270.6	42.1	10.8	28.5	3.4	14.6	2.2	4.4	0.4	2.4	0.3	49.7	12.3	610.8	31.6	29.9	5.4
Target A	RC-TGA-0015	TGA-RC-01434	38.0	39.0	1.0	511085.6	8116599.3	759.8	3,439.2	3,420.8	703.7	234.7	32.6	736.3	804.5	1,615.3	162.5	541.2	80.9	20.0	50.0	6.3	26.3	3.9	8.1	0.8	4.3	0.5	96.1	18.4	952.7	59.7	72.7	8.7
Target A	RC-TGA-0015	TGA-RC-01436	39.0	40.0	1.0	511085.6	8116599.3	759.8	3,032.3	3,015.4	610.9	212.1	29.4	640.3	731.8	1,406.5	142.0	468.9	71.0	18.0	45.5	5.8	23.6	3.5	7.7	0.7	3.8	0.4	86.1	16.9	908.4	50.2	56.6	9.1
Target A	RC-TGA-0015	TGA-RC-01437	40.0	41.0	1.0	511085.6	8116599.3	759.8	3,013.3	2,998.0	594.4	216.9	30.3	624.7	730.7	1,400.4	139.5	454.9	71.0	18.4	45.2	5.9	24.3	3.7	8.0	0.7	4.1	0.5	90.8	15.3	1,005.6	52.3	56.2	11.5
Target A	RC-TGA-0015	TGA-RC-01438	41.0	42.0	1.0	511085.6	8116599.3	759.8	1,392.5	1,380.2	253.5	116.2	15.9	269.4	340.1	651.1	59.3	194.2	31.5	8.5	21.2	3.0	13.0	2.0	4.1	0.4	2.2	0.3	49.3	12.3	497.8	19.7	16.3	5.2
Target A	RC-TGA-0015	TGA-RC-01439	42.0	43.0	1.0	511085.6	8116599.3	759.8	396.9	383.1	75.6	44.1	4.5	80.1	96.1	172.0	17.4	58.2	9.2	2.5	6.2	0.8	3.7	0.6	1.2	0.1	0.8	0.1	14.2	13.8	91.8	4.6	4.9	1.5
Target A	RC-TGA-0015	TGA-RC-01440	43.0	44.0	1.0	511085.6	8116599.3	759.8	506.6	492.8	86.4	54.3	6.3	92.7	136.0	218.7	20.2	66.1	11.2	3.1	8.3	1.1	5.2	0.8	1.7	0.2	1.0	0.1	19.0	13.8	263.9	9.3	8.4	2.9
Target A	RC-TGA-0015	TGA-RC-01441	44.0	45.0	1.0	511085.6	8116599.3	759.8	1,437.0	1,421.7	248.9	127.5	17.3	266.2	407.0	621.6	59.3	189.5	32.1	8.8	22.4	3.2	14.1	2.2	4.8	0.5	2.7	0.3	53.1	15.3	748.2	21.0	23.3	7.5
Target A	RC-TGA-0015	TGA-RC-01443	45.0	46.0	1.0	511085.6	8116599.3	759.8	215.1	201.3	36.3	32.6	2.8	39.1	52.5	88.4	8.4	27.9	5.3	1.3	3.8	0.5	2.3	0.4	0.7	0.1	0.5	0.0	9.0	13.8	56.6	1.8	2.0	1.0
Target A	RC-TGA-0015	TGA-RC-01444	46.0	47.0	1.0	511085.6	8116599.3	759.8	108.1	94.2	17.1	23.3	1.4	18.5	24.4	40.9	3.9	13.2	2.4	0.6	1.6	0.2	1.2	0.2	0.4	0.0	0.3	0.0	4.8	13.8	26.7	1.2	1.1	0.7
Target A	RC-TGA-0015	TGA-RC-01445	47.0	48.0	1.0	511085.6	8116599.3	759.8	123.6	111.3	20.5	23.0	1.8	22.2	29.4	47.9	4.8	15.6	2.8	0.8	2.1	0.3	1.5	0.2	0.4	0.1	0.3	0.0	5.0	12.3	28.0	1.1	1.3	0.8
Target A	RC-TGA-0015	TGA-RC-01446	48.0	49.0	1.0	511085.6	8116599.3	759.8	50.3	39.5	7.5	14.6	0.6	8.1	10.0	17.0	1.8	5.7	1.2	0.3	0.7	0.1	0.5	0.1	0.2	0.0	0.1	0.0	1.8	10.7	13.7	0.6	0.6	0.8
Target A	RC-TGA-0015	TGA-RC-01447	49.0	50.0	1.0	511085.6	8116599.3	759.8	62.9	52.2	9.7	15.4	0.7	10.4	13.0	23.3	2.3	7.5	1.4	0.4	1.0	0.1	0.5	0.1	0.2	0.0	0.2	0.0	2.0	10.7	15.2	0.7	0.8	0.7
Target A	RC-TGA-0015	TGA-RC-01448	50.0	51.0	1.0	511085.6	8116599.3	759.8	58.4	46.2	8.9	16.2	0.5	9.5	11.3	20.9	2.1	6.9	1.2	0.3	0.8	0.1	0.4	0.1	0.2	0.0	0.1	0.0	1.8	12.3	12.7	1.1	0.6	0.7
Target A	RC-TGA-0015	TGA-RC-01449	51.0	52.0	1.0	511085.6	8116599.3	759.8	55.3	41.5	7.7	17.3	0.5	8.1	9.1	20.1	1.8	5.8	1.0	0.3	0.7	0.1	0.4	0.1	0.2	0.0	0.1	0.0	1.7	13.8	17.5	0.7	0.7	1.1
Target A	RC-TGA-0015	TGA-RC-01451	52.0	53.0	1.0	511085.6	8116599.3	759.8	1,500.9	1,477.9	301.6	109.4	13.2	314.8	337.8	717.4	70.1	231.5	34.8	9.1	21.5	2.5	10.7	1.6	3.3	0.3	1.8	0.2	35.4	23.0	406.3	24.9	34.9	6.4
Target A	RC-TGA-0015	TGA-RC-01452	53.0	54.0	1.0	511085.6	8116599.3	759.8	127.6	112.3	22.7	29.2	1.6	24.3	29.2	43.2	5.0	17.7	3.3	0.8	2.1	0.3	1.3	0.2	0.5	0.1	0.5	0.0	8.0	15.3	32.0	1.6	1.8	2.0
Target A	RC-TGA-0015	TGA-RC-01453	54.0	55.0	1.0	511085.6	8116599.3	759.8	515.7	497.3	99.5	51.3	4.9	104.4	119.6	233.4	23.0	76.5	11.8	3.1	7.5	0.9	4.0	0.6	1.2	0.1	0.8	0.1	14.6	18.4	124.7	7.8	10.1	2.4
Target A	RC-TGA-0015	TGA-RC-01454	55.0	56.0	1.0	511085.6	8116599.3	759.8	61.0	42.6	8.8	22.9	0.6	9.4	10.0	18.2	1.8	7.0	1.2	0.3	0.7	0.1	0.5	0.1	0.1	0.0	0.2	0.0	2.4	18.4	9.8	0.5	0.7	1.1
Target A	RC-TGA-0015	TGA-RC-01455	56.0	57.0	1.0	511085.6	8116599.3	759.8	59.0	43.6	9.0	20.7	0.7	9.7	10.1	18.2	1.9	7.1	1.0	0.4	0.8	0.1	0.6	0.1	0.2	0.0	0.2	0.0	2.9	15.3	19.7	0.6	0.5	1.0
Target A	RC-TGA-0015	TGA-RC-01456	57.0	58.0	1.0	511085.6	8116599.3	759.8	44.8	31.0	7.1	17.9	0.4	7.5	6.1	12.8	1.5	5.6	1.0	0.3	0.7	0.1	0.4	0.1	0.1	0.0	0.1	0.0	2.3	13.8	8.8	0.4	0.3	1.2
Target A	RC-TGA-0015	TGA-RC-01457	58.0	59.0	1.0	511085.6	8116599.3	759.8	46.6	35.8	7.4	14.0	0.4	7.8	7.9	16.2	1.6	5.8	1.0	0.3	0.5	0.1	0.3	0.0	0.1	0.0	0.1	0.0	1.9	10.7	11.8	0.6	0.6	1.3
Target A	RC-TGA-0015	TGA-RC-01459	59.0	60.0	1.0	511085.6	8116599.3	759.8	57.4	48.2	9.5	13.9	0.6	10.1	11.7	20.9	2.0	7.5	1.4	0.3	0.7	0.1	0.5	0.1	0.2	0.0	0.1	0.0	2.7	9.2	21.5	0.9	0.7	1.2
Target A	RC-TGA-0015	TGA-RC-01460	60.0	61.0	1.0	511085.6	8116599.3	759.8	168.8	156.6	31.9	23.5	1.6	33.5	36.7	73.0	7.2	24.7	3.7	1.1	2.2	0.2	1.3	0.2	0.3	0.0	0.4	0.0	5.5	12.3	49.2	2.6	2.8	1.8
Target A	RC-TGA-0015	TGA-RC-01461	61.0	62.0	1.0	511085.6	8116599.3	759.8	77.6	66.8	13.0	15.8	0.6	13.6	16.1	31.0	3.1	9.9	1.7	0.5	0.9	0.1	0.5	0.1	0.2	0.0	0.2	0.0	2.7	10.7	18.0	1.0	1.1	1.4
Target A	RC-TGA-0015	TGA-RC-01462	62.0	63.0	1.0	511085.6	8116599.3	759.8	57.2	46.4	10.2	14.3	0.5	10.6	10.6	20.9	2.1	8.0	1.3	0.3	0.5	0.1	0.4	0.1	0.1	0.0	0.1	0.0	2.0	10.7	11.4	0.6	0.6	1.8
Target A	RC-TGA-0015	TGA-RC-01463	63.0	64.0	1.0	511085.6	8116599.3	759.8	38.7	29.5	5.7	11.5	0.3	6.0	7.7	13.0	1.3	4.4	0.7	0.2	0.4	0.0	0.3	0.0	0.0	0.0	0.1	0.0	1.3	9.2	6.4	0.4	0.4	1.5
Target A	RC-TGA-0015	TGA-RC-01464	64.0	65.0	1.0	511085.6	8116599.3	759.8	50.4	41.2	8.3	12.0	0.4	8.7	10.6	18.4	1.9	6.4	1.1	0.2	0.5	0.0	0.4	0.0	0.0	0.0	0.1	0.0	1.5	9.2	8.9	0.5	0.4	1.2
Target A	RC-TGA-0015	TGA-RC-01466	65.0	66.0	1.0	511085.6	8116599.3	759.8	67.1	56.4	11.9	14.3	0.4	12.3	14.7	24.7	2.8	9.1	1.6	0.3	0.7	0.1	0.4	0.0

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO$_2$ ppm	U_3O_8 ppm
Target A	RC-TGA-0015	TGA-RC-01476	74.0	75.0	1.0	511085.6	8116599.3	759.8	48.7	36.5	8.2	15.4	0.4	8.6	7.4	16.8	1.7	6.5	0.9	0.3	0.7	0.1	0.3	0.0	0.0	0.0	0.1	0.0	1.7	12.3	11.2	0.6	0.7	1.8
Target A	RC-TGA-0015	TGA-RC-01477	75.0	76.0	1.0	511085.6	8116599.3	759.8	26.3	15.5	3.6	12.6	0.2	3.8	3.3	6.3	0.8	2.8	0.6	0.2	0.2	0.0	0.2	0.0	0.0	0.0	0.1	0.0	1.1	10.7	4.2	0.2	0.3	2.1
Target A	RC-TGA-0015	TGA-RC-01478	76.0	77.0	1.0	511085.6	8116599.3	759.8	21.1	11.9	2.7	11.4	0.3	3.0	2.2	4.3	0.5	2.2	0.4	0.2	0.3	0.0	0.2	0.0	0.1	0.0	0.1	0.0	1.1	9.2	2.1	0.1	0.4	2.2
Target A	RC-TGA-0015	TGA-RC-01479	77.0	78.0	1.0	511085.6	8116599.3	759.8	29.4	12.5	2.8	19.6	0.3	3.1	2.2	4.4	0.5	2.2	0.4	0.1	0.4	0.1	0.3	0.0	0.2	0.0	0.2	0.0	1.4	16.9	2.4	0.1	0.4	2.0
Target A	RC-TGA-0015	TGA-RC-01480	78.0	79.0	1.0	511085.6	8116599.3	759.8	211.8	202.6	41.2	25.4	2.4	43.6	50.4	89.9	9.6	31.6	4.9	1.4	3.6	0.4	2.0	0.3	0.7	0.1	0.4	0.1	7.4	9.2	73.7	3.3	3.3	2.9
Target A	RC-TGA-0015	TGA-RC-01481	79.0	80.0	1.0	511085.6	8116599.3	759.8	130.8	121.6	24.7	17.6	1.2	25.9	30.3	55.3	6.0	18.8	3.0	0.8	1.9	0.2	0.9	0.2	0.3	0.0	0.2	0.0	3.7	9.2	34.3	1.8	2.3	2.1
Target A	RC-TGA-0015	TGA-RC-01482	80.0	81.0	1.0	511085.6	8116599.3	759.8	157.3	146.6	31.3	27.3	2.1	33.4	28.7	65.7	6.9	24.4	4.3	1.2	3.1	0.4	1.7	0.3	0.7	0.1	0.5	0.1	8.5	10.7	44.2	1.8	2.2	2.0
Target A	RC-TGA-0015	TGA-RC-01483	81.0	82.0	1.0	511085.6	8116599.3	759.8	57.0	41.7	10.7	22.2	0.9	11.7	6.8	15.8	2.2	8.5	1.5	0.4	1.2	0.2	0.8	0.1	0.3	0.0	0.2	0.0	3.6	15.3	6.9	0.2	0.5	1.6
Target A	RC-TGA-0015	TGA-RC-01484	82.0	83.0	1.0	511085.6	8116599.3	759.8	25.0	18.8	3.8	9.6	0.4	4.2	3.9	7.1	0.8	2.9	0.6	0.2	0.5	0.1	0.4	0.1	0.2	0.0	0.2	0.0	1.9	6.1	9.3	0.2	0.5	1.4
Target A	RC-TGA-0015	TGA-RC-01486	83.0	84.0	1.0	511085.6	8116599.3	759.8	13.9	9.3	1.9	6.4	0.2	2.1	1.9	3.4	0.4	1.5	0.3	0.1	0.3	0.0	0.1	0.0	0.1	0.0	0.1	0.0	1.0	4.6	2.8	0.1	0.3	1.4
Target A	RC-TGA-0015	TGA-RC-01487	84.0	85.0	1.0	511085.6	8116599.3	759.8	27.2	19.5	3.5	10.3	0.3	3.9	3.8	9.1	0.8	2.7	0.5	0.2	0.4	0.1	0.3	0.1	0.1	0.0	0.1	0.0	1.4	7.7	6.0	0.1	0.6	1.4
Target A	RC-TGA-0015	TGA-RC-01488	85.0	86.0	1.0	511085.6	8116599.3	759.8	43.0	27.7	5.7	18.9	0.5	6.2	4.7	12.8	1.3	4.4	0.9	0.3	0.7	0.1	0.4	0.1	0.2	0.0	0.1	0.0	1.7	15.3	7.1	0.4	0.6	1.3
Target A	RC-TGA-0015	TGA-RC-01489	86.0	87.0	1.0	511085.6	8116599.3	759.8	75.3	64.6	12.1	16.7	0.8	13.0	13.3	31.6	2.7	9.4	1.7	0.4	1.1	0.2	0.7	0.1	0.3	0.0	0.2	0.0	2.9	10.7	26.2	1.2	1.5	1.4
Target A	RC-TGA-0015	TGA-RC-01490	87.0	88.0	1.0	511085.6	8116599.3	759.8	14.7	5.5	1.1	10.4	0.2	1.2	1.1	2.0	0.3	0.8	0.2	0.0	0.2	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.6	9.2	1.5	0.5	0.2	0.8
Target A	RC-TGA-0015	TGA-RC-01491	88.0	89.0	1.0	511085.6	8116599.3	759.8	16.7	7.5	1.4	10.5	0.1	1.5	1.5	3.2	0.3	1.0	0.2	0.1	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.8	9.2	2.7	0.1	0.2	0.8
Target A	RC-TGA-0015	TGA-RC-01493	89.0	90.0	1.0	511085.6	8116599.3	759.8	1,208.3	1,197.6	220.0	98.2	13.2	233.2	312.0	550.3	53.8	166.2	27.8	7.7	20.3	2.4	10.8	1.6	3.6	0.3	1.8	0.2	38.7	10.7	353.3	14.9	16.0	5.7
Target A	RC-TGA-0015	TGA-RC-01494	90.0	91.0	1.0	511085.6	8116599.3	759.8	1,717.0	1,704.7	316.9	135.1	18.7	335.6	446.8	777.6	77.8	239.1	40.6	11.3	28.5	3.4	15.3	2.3	4.8	0.5	2.4	0.3	54.0	12.3	562.2	26.9	24.0	8.1
Target A	RC-TGA-0015	TGA-RC-01495	91.0	92.0	1.0	511085.6	8116599.3	759.8	2,092.6	2,081.8	394.5	154.7	22.1	416.6	536.0	958.2	97.0	297.4	49.3	13.4	33.8	4.1	18.1	2.7	5.6	0.5	2.7	0.3	62.9	10.7	670.9	32.5	32.3	9.6
Target A	RC-TGA-0015	TGA-RC-01496	92.0	93.0	1.0	511085.6	8116599.3	759.8	2,386.4	2,377.2	461.2	165.8	23.7	484.9	597.0	1,106.8	112.5	348.8	55.7	15.4	37.6	4.4	19.3	2.9	6.2	0.6	2.7	0.3	67.2	9.2	692.4	35.5	42.8	9.9
Target A	RC-TGA-0015	TGA-RC-01497	93.0	94.0	1.0	511085.6	8116599.3	759.8	1,937.2	1,921.8	380.1	140.9	19.1	399.2	466.8	904.1	93.2	286.9	45.3	12.0	29.9	3.5	15.6	2.3	5.0	0.5	2.4	0.3	54.1	15.3	486.4	27.5	39.0	6.8
Target A	RC-TGA-0015	TGA-RC-01498	94.0	95.0	1.0	511085.6	8116599.3	759.8	2,718.8	2,703.5	542.9	182.6	25.2	568.1	657.9	1,271.4	133.5	409.4	64.0	16.7	41.3	4.9	20.3	3.1	6.2	0.6	3.0	0.4	70.9	15.3	672.3	36.0	55.3	9.5
Target A	RC-TGA-0015	TGA-RC-01499	95.0	96.0	1.0	511085.6	8116599.3	759.8	2,494.6	2,477.7	499.3	174.2	24.6	523.9	615.7	1,147.3	121.4	377.9	58.0	15.6	38.4	4.6	20.0	3.0	6.1	0.6	3.0	0.4	65.8	16.9	670.9	40.5	50.0	9.3
Target A	RC-TGA-0015	TGA-RC-01501	96.0	97.0	1.0	511085.6	8116599.3	759.8	3,241.7	3,229.4	628.8	218.3	31.9	660.7	815.1	1,504.8	155.3	473.6	74.7	21.0	51.1	6.2	25.7	3.9	7.9	0.7	3.6	0.4	85.6	12.3	962.7	56.9	56.7	12.1
Target A	RC-TGA-0015	TGA-RC-01502	97.0	98.0	1.0	511085.6	8116599.3	759.8	2,210.0	2,196.1	410.6	167.2	23.8	434.4	567.6	1,013.4	101.5	309.1	51.1	14.1	36.2	4.3	19.5	2.9	6.2	0.6	2.9	0.4	66.3	13.8	735.3	38.6	32.3	9.2
Target A	RC-TGA-0015	TGA-RC-01503	98.0	99.0	1.0	511085.6	8116599.3	759.8	2,239.6	2,225.8	422.9	170.2	24.0	446.8	609.9	985.2	105.6	317.3	51.5	14.6	37.5	4.3	19.6	2.9	5.9	0.6	2.9	0.4	67.6	13.8	685.2	32.2	28.1	7.9
Target A	RC-TGA-0015	TGA-RC-01504	99.0	100.0	1.0	511085.6	8116599.3	759.8	182.3	168.5	31.2	31.4	2.6	33.9	40.3	75.2	7.8	23.4	4.1	1.3	3.5	0.4	2.2	0.4	0.9	0.1	0.5	0.1	8.3	13.8	37.8	1.8	2.9	1.5
Target A	RC-TGA-0015	TGA-RC-01505	100.0	101.0	1.0	511085.6	8116599.3	759.8	320.2	303.3	57.6	43.9	4.1	61.7	75.3	136.4	14.1	43.5	7.1	2.1	5.6	0.7	3.4	0.5	1.3	0.1	0.8	0.1	12.3	16.9	98.0	4.3	5.5	2.4
Target A	RC-TGA-0015	TGA-RC-01506	101.0	102.0	1.0	511085.6	8116599.3	759.8	78.3	66.0	12.4	21.7	1.3	13.7	14.5	27.9	2.9	9.6	1.8	0.5	1.5	0.2	1.0	0.2	0.5	0.1	0.4	0.1	4.8	12.3	16.4	0.7	1.3	1.2
Target A	RC-TGA-0015	TGA-RC-01508	102.0	103.0	1.0	511085.6	8116599.3	759.8	73.9	61.6	11.4	21.3	1.4	12.7	13.8	25.7	2.6	8.7	1.7	0.5	1.4	0.2	1.2	0.2	0.5	0.1	0.3	0.0	4.7	12.3	15.2	0.7	1.2	1.2
Target A	RC-TGA-0015	TGA-RC-01509	103.0	104.0	1.0	511085.6	8116599.3	759.8	88.5	70.1	13.4	29.8	1.7	15.2	14.4	28.9	3.0	10.4	2.0	0.6	1.8	0.2	1.5	0.3	0.6	0.1	0.5	0.1	5.7	18.4	13.6	0.6	2.2	1.4
Target A	RC-TGA-0015	TGA-RC-01510	104.0	105.0	1.0	511085.6	8116599.3	759.8	798.2	781.3	133.8	78.2	9.7	143.4	197.6	371.0	33.2	100.5	17.6	5.3	13.7	1.7	7.9	1.3	2.6	0.3	1.4	0.2	26.9	16.9	343.3	14.9	13.4	5.1
Target A	RC-TGA-0015	TGA-RC-01511	105.0	106.0	1.0	511085.6	8116599.3	759.8	2,713.9	2,700.1	476.6	202.7	31.1	507.7	743.6	1,228.4	118.5	358.1	62.6	18.3	44.7	5.6	25.5	3.8	7.3	0.8	3.6	0.4	79.0	13.8	1,054.3	48.6	38.1	13.6
Target A	RC-TGA-0016	TGA-RC-01872	15.0	16.0	1.0	512955.3	8116391.7	784.3	251.7	176.5	40.8	96.9	2.5	43.3	48.6	60.6	9.6	31.1	4.9	0.9	2.7	0.4	2.2	0.5	1.3	0.2	1.1	0.2	12.3	75.2	211.0	12.9	21.7	13.6
Target A	RC-TGA-0016	TGA-RC-01873	16.0	17.0	1.0	512955.3	8116391.7	784.3	235.4	138.7	35.8	113.5	2.0	37.8	37.8	44.4	8.3	27.5	4.0	0.9	2.4	0.3	1.7	0.4	1.0	0.1	0.9	0.1	9.1	96.6	206.0	12.9	20.9	14.4
Target A	RC-TGA-0016	TGA-RC-01874	17.0	18.0	1.0	512955.3	8116391.7	784.3	290.4	186.1	37.6	122.4	2.2	39.8	38.9	86.7	8.8	28.8	4.7	0.9	2.8	0.4	1.9	0.4	1.0	0.2	1.0	0.2	9.5	104.3	240.3	15.4	22.9	12.2
Target A	RC-TGA-0016	TGA-RC-01875	18.0	19.0	1.0	512955.3	8116391.7	784.3	553.7	409.6	37.9	163.4	2.4	40.2	36.6	310.8	8.7	29.2	5.1	0.9	3.0	0.4	2.0	0.4	1.1	0.2	1.1	0.1	10.2	144.2	313.3	19.8	28.1	10.8
Target A	RC-TGA-0016	TGA-RC-01876	19.0	20.0	1.0	512955.3	8116391.7	784.3	952.6	776.2	39.3	197.1	2.8	42.1	36.4	674.4	8.9	30.4	5.4	0.9	3.2	0.4	2.3	0.4	1.2	0.2	1.1	0.2	10.8	176.4	194.5	12.7	17.8	7.5
Target A	RC-TGA-0016	TGA-RC-01877	20.0	21.0	1.0	512955.3	8116391.7	784.3	1,021.5	816.0	40.8	229.2	3.1	43.8	37.2	708.8	9.2	31.6	5.5	1.2	3.4	0.5	2.6	0.5	1.3	0.2	1.3	0.2	12.6	205.5	191.0	12.7	16.2	5.6
Target A	RC-TGA-0016	TGA-RC-01878	21.0	22.0	1.0	512955.3	8116391.7	784.3	562.2	361.3	25.5	217.1	2.3	27.7	21.2	294.8	5.6	19.8	3.6	0.9	2.5	0.3	1.9	0.4	1.0	0.2	1.0	0.1	8.0	200.9	450.6	37.0	56.4	8.7
Target A	RC-TGA-0016	TGA-RC-01879	22.0	23.0	1.0	512955.3	8116391.7	784.3	944.3	735.7	17.1	218.2	1.6	18.7	10.8	695.3	3.8	13.3	2.9	0.6	1.7	0.3	1.3	0.2	0.6	0.1	0.7	0.1	4.1	208.6	286.1	21.9	35.4	6.0
Target A	RC-TGA-0016	TGA-RC-01880	23.0	24.0	1.0	512955.3	8116391.7	784.3	1,514.6	1,347.4	101.6	204.6	5.9	107.5	55.4	1,137.5	22.1	79.6	15.5	3.4	7.9	1.0	4.8	0.8	1.8	0.3	1.5	0.2	15.8	167.2	309.0	21.5	33.3	5.6
Target A	RC-TGA-0016	TGA-RC-01881	24.0	25.0	1.0	512955.3	8116391.7	784.3	3,293.3	3,155.2	847.7	530.0	60.4	908.1	527.8	1,259.1	177.0	670.7	128.7	29.8	83.8	10.4	49.9	8.3	19.0	2.4	14.1	1.5	172.7	138.0	187.4	10.3	14.2	3.2
Target A	RC-TGA-0016	TGA-RC-01882	25.0	26.0	1.0	512955.3	8116391.7	784.3	5,310.5	5,178.6	1,464.9	966.1	120.7	1,585.5	927.7	1,732.0	299.6	1,165.2	219.7	52.3	159.6	20.1	100.5	17.5	41.6	5.5	33.0	4.0	400.0	131.9	138.3	7.7	10.0	2.6
Target A	RC-TGA-0016	TGA-RC-01883	26.0	27.0	1.0	512955.3	8116391.7	784.3	542.9	424.8	112.6	169.2	7.5	120.1	66.4	178.1	23.4	89.1	16.7	3.8	9.8	1.3	6.2	1.1	2.6	0.4	2.3	0.3	23.4	118.1	159.5	8.7	11.7	2.1
Target A	RC-TGA-0016	TGA-RC-01885	27.0	28.0	1.0	512955.3	8116391.7	784.3	1,441.7	1,337.4	434.8	286.6	26.5	461.3	290.9	367.3	90.7	344.1	62.2	14.2	39.8	4.7	21.8	3.7	8.6	1.1	6.7	0.8	80.9	104.3	171.7	8.8	13.0	2.6
Target A	RC-TGA-0016	TGA-RC-01886	28.0	29.0	1.0	512955.3	8116391.7	784.3	3,149.0	3,035.4	1,099.4	656.0	77.3	1,176.7	796.3	434.9	221.1	878.3	162.3	37.8	114.6	13.6	63.7	10.9	25.4	3.4	20.0	2.4	250.8	113.5	135.6	7.6	9.2	2.6
Target A	RC-TGA-0016	TGA-RC-01887	29.0	30.0	1.0	512955.3	8116391.7	784.3	1,715.7	1,599.1	521.2	390.0	38.1	559.2	425.7	302.2	104.8	416.4	76.7	18.1	56.0	6.5	31.6	5.5	12.8	1.7	9.8	1.3	130.2	116.6	103.1	5.5	6.8	1.9
Target A	RC-TGA-0016	TGA-RC-01888	30.0	31.0	1.0	512955.3	8116391.7	784.3	1,246.7	1,144.0	292.2	442.3	36.5	328.7	259.2	209.4	59.0	233.3	43.6	11.6	42.5	5.6	30.9	6.5	17.6	2.3	14.2	2.0	206.4	102.8	85.8	4.9	6.2	2.0
Target A	RC-TGA-0016	TGA-RC-01889	31.0	32.0	1.0	512955.3	8116391.7	784.3	858.8	740.7	166.0	354.0	22.6	188.6	113.6	198.4	31.9	134.1	26.8	7.3	27.4	3.4	19.2	4.3	11.6	1.5	8.8	1.3	151.1	118.1	77.1	4.4	5.0	1.4
Target A	RC-TGA-0016	TGA-RC-01890	32.0	33.0	1.0	512955.3	8116391.7	784.3	703.6	597.7	136.0	263.2	15.0	151.0	86.3	197.2	26.8	109.2	20.9	5.6	19.3	2.3	12.6	2.7	7.3	0.9	4.9	0.8	101.0	105.8	55.1	2.8	3.2	1.4
Target A	RC-TGA-0016	TGA-RC-01891	33.0	34.0	1.0	512955.3	8116391.7	784.3	735.8	590.1	125.7	350.7	15.1	140.8	83.3	156.6	24.4	101.2	19.6	5.2	19.4	2.3	12.8	3.0	8.0	1.0	5.2	0.8	147.3	145.7	64.7	3.9	4.1	1.0
Target A	RC-TGA-0016	TGA-RC-01893	34.0	35.0	1.0	512955.3	8116391.7	784.3	537.5	434.7	105.2	171.6	7.6	112.8	78.7	167.7	21.6	83.6	14.3	3.8	10.8	1.3	6.3	1.3	2.9	0.3	1.9	0.2	40.0	102.8	81.4	4.6	7.2	1.4
Target A	RC-TGA-0016	TGA-RC-01894	35.0	36.0	1.0	512955.3	8116391.7	784.3	465.7	389.0	91.8	130.8	6.7	98.5	74.6	156.0	19.2	72.7	12.5	3.4	9.5	1.1	5.6	1.0	2.5	0.3	1.6	0.2	29.0	76.7	96.6	5.1	7.2	1.7
Target A	RC-TGA-0016	TGA-RC-01895	36.0	37.0	1.0	512955.3	8116391.7	784.3	482.0	403.8	97.8	131.4	6.8	104.7	74.6	165.2	20.5	77.3	13.0	3.3	9.4	1.1	5.7	1.1	2.4	0.3	1.8	0.3	27.8	78.2	92.1	5.0	7.5	1.9
Target A	RC-TGA-0016	TGA-RC-01896	37.0	38.0	1.0	512955.3	8116391.7	784.3	406.8	317.8	77.8	134.2	5.9	83.7	55.9	127.8	16.0	61.8	11.1	2.9	8.2	1.0	4.9	0.9	2.2	0.3	1.5	0.2	23.1	89.0	72.1	3.8	4.9	1.1
Target A	RC-TGA-0016	TGA-RC-01897	38.0	39.0	1.0	512955.3	8116391.7	784.3	416.5	330.6	79.7	130.2	5.5	85.2	59.8	135.7	17.0	62.8	11.0	2.9	8.1	1.0	4.5	0.9	2.1	0.3	1.4	0.2	23.0	85.9	77.8	4.2	5.0	1.2
Target A	RC-TGA-0016	TGA-RC-01898	39.0	40.0	1.0	512955.3	8116391.7	784.3	444.5	378.5	81.7	127.1	7.9	89.6	74.0	149.9	17.3	64.4	11.8	3.4	9.5	1.3	6.6	1.2	2.9	0.4	2.0	0.3	33.8	66.0	145.9	6.0	5.5	1.9
Target A	RC-TGA-0016	TGA-RC-01900	40.0	41.0	1.0	512955.3	8116391.7	784.3	509.1	426.2	104.3	133.5	7.0	111.3	78.3	179.4	22.0	82.4	13.5	3.6	9.1	1.2	5.7	0.9	2.2	0.3	1.6	0.2	25.9	82.8	92.6	5.1	7.6	1.4
Target A	RC-TGA-0016	TGA-RC-01901	41.0	42.0	1.0	512955.3	8116391.7	784.3	607.8	541.8	128.1	127.3	8.3	136.4	103.9	232.2	27.1	101.0	16.4	4.0	10.7	1.3	7.0	1.1	2.7	0.3	1.7	0.3	32.4	66.0	158.8	7.9	10.5	2.5
Target A	RC-TGA-0016	TGA-RC-01902	42.0	43.0	1.0	512955.3	8116391.7	784.3	588.7	516.6	123.8	131.9	8.2	132.1	100.0	217.4	25.7	98.1	15.5	4.0	10.5	1.5	6.8	1.1	2.5	0.3	1.7	0.2	31.4	72.1	134.0	6.7	9.7	2.3
Target A	RC-TGA-0016	TGA-RC-01903	43.0	44.0	1.0	512955.3	8116391.7	784.3	560.5	494.5	116.3	122.0	7.5	123.9	94.9	212.5	24.5	91.8	14.8	3.8	10.1	1.3	6.3	1.0	2.2	0.3	1.7	0.2	29.1	66.0	122.0	6.5	9.5	1.9
Target A	RC-TGA-0016	TGA-RC-01904	44.0	45.0	1.0	512955.3	8116391.7	784.3	563.3	494.2	117.5	122.4	7.6	125.1	94.3	213.7	25.4	92.2	15.3	3.6	9.1	1.2	6.4	1.0	2.4	0.3	1.5	0.2	27.8	69.0	132.2	6.7	10.5	1.9
Target A	RC-TGA-0016	TGA-RC-01905	45.0	46.0	1.0	512955.3	8116391.7	784.3	786.6	711.4	171.8	138.7	8.9	180.7	139.0	316.9	35.9	135.9	20.2	4.8	11.9	1.5	7.4	1.1	2.7	0.3	1.7	0.2	31.9	75.2	168.1	10.4	17.2	2.6
Target A	RC-TGA-0016	TGA-RC-01907	46.0	47.0	1.0	512955.3	8116391.7	784.3	801.8	706.7	167.0	151.0	8.4	175.4	144.8	319.4	37.0	130.1	19.6	5.1	11.6	1.4	7.0	1.0	2.4	0.3	1.5	0.2	25.5	95.1	147.3	9.4	16.2	2.3
Target A	RC-TGA-0016	TGA-RC-01908	47.0	48.0	1.0	512955.3	8116391.7	784.3	717.3	620.7	144.7	153.8	7.6	152.2	125.5	276.4	30.9	113.7	17.0	4.1	10.6	1.3	6.2	1.1	2.5	0.3	1.8	0.3	29.0	96.6	158.1	8.4	15.0	2.7
Target A	RC-TGA-0016	TGA-RC-01909	48.0	49.0	1.0	512955.3	8116391.7	784.3	870.8	809.5	205.4	133.9	10.3	215.6	149.5	357.5	42.7	162.7	24.6	5.8	15.1	1.9	8.4	1.3	3.0	0.3	1.8	0.3	34.8	61.4	143.1	8.8	19.5	2.6
Target A	RC-TGA-0016	TGA-RC-01910	49.0	50.0	1.0	512955.3	8116391.7	784.3	695.5	635.7	161.2	132.1	9.8	171.0	115.8	265.3	32.3	128.9	21.2	5.3	14.5	1.7	8.1	1.3	2.8	0.3	1.6	0.3	36.5	59.8	50.9	2.6	6.4	1.4
Target A	RC-TGA-0016	TGA-RC-01911	50.0	51.0	1.0	512955.3	8116391.7	784.3	564.9	466.7	113.2	144.6	6.9	120.1	89.5	202.7	23.6	89.6	14.9	3.5	9.0	1.1	5.7	0.9	1.9	0.2	1.3	0.2	22.6	98.2	105.9	6.1	10.8	2.0
Target A	RC-TGA-0016	TGA-RC-01912	51.0	52.0	1.0	512955.3	8116391.7	784.3	707.1	579.8	148.9	173.3	7.0	155.9	105.7	260.4	31.1	117.8	18.8	4.1	10.5	1.

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO$_2$ ppm	U_3O_8 ppm
Target A	RC-TGA-0016	TGA-RC-01923	60.0	61.0	1.0	512955.3	8116391.7	784.3	566.5	511.2	119.0	108.9	7.6	126.7	102.3	221.7	25.4	93.7	14.5	3.6	9.9	1.3	6.4	0.9	2.3	0.2	1.8	0.2	27.2	55.2	136.8	7.1	11.5	2.6
Target A	RC-TGA-0016	TGA-RC-01924	61.0	62.0	1.0	512955.3	8116391.7	784.3	606.2	551.0	124.7	115.9	8.2	132.9	111.1	238.9	26.8	97.9	15.7	4.2	10.8	1.3	6.9	1.2	2.6	0.3	1.8	0.2	31.4	55.2	160.2	7.9	12.9	2.9
Target A	RC-TGA-0016	TGA-RC-01925	62.0	63.0	1.0	512955.3	8116391.7	784.3	691.5	644.0	141.6	113.1	9.7	151.3	136.0	283.8	31.2	110.5	17.1	4.5	11.5	1.6	8.1	1.3	2.8	0.3	2.2	0.3	33.0	47.6	192.4	9.3	15.5	2.8
Target A	RC-TGA-0016	TGA-RC-01926	63.0	64.0	1.0	512955.3	8116391.7	784.3	510.4	450.6	101.8	110.9	7.1	109.0	90.7	194.7	21.9	79.9	12.4	3.5	9.1	1.2	5.9	1.0	2.2	0.2	1.6	0.2	26.2	59.8	144.5	6.6	11.3	2.8
Target A	RC-TGA-0016	TGA-RC-01927	64.0	65.0	1.0	512955.3	8116391.7	784.3	718.1	636.8	145.9	141.3	8.6	154.4	128.4	283.8	31.8	114.1	18.8	4.9	11.4	1.5	7.1	1.2	2.6	0.3	1.7	0.2	29.2	81.3	181.7	8.2	14.8	3.3
Target A	RC-TGA-0016	TGA-RC-01928	65.0	66.0	1.0	512955.3	8116391.7	784.3	725.5	668.7	148.8	124.2	8.9	157.7	142.5	292.4	32.6	116.2	17.6	4.5	11.9	1.6	7.3	1.3	2.8	0.4	2.0	0.3	35.4	56.8	196.7	7.8	18.0	3.3
Target A	RC-TGA-0016	TGA-RC-01929	66.0	67.0	1.0	512955.3	8116391.7	784.3	796.1	754.7	156.5	130.8	12.4	169.0	165.4	323.1	34.1	122.5	20.4	5.7	13.8	2.1	10.3	1.7	4.2	0.5	2.7	0.3	48.0	41.4	349.0	12.6	18.0	6.3
Target A	RC-TGA-0016	TGA-RC-01930	67.0	68.0	1.0	512955.3	8116391.7	784.3	446.7	383.8	93.9	112.0	6.8	100.7	69.7	158.5	19.0	74.9	12.7	3.3	8.7	1.2	5.7	0.9	2.2	0.2	1.5	0.2	25.4	62.9	104.6	4.5	7.1	2.9
Target A	RC-TGA-0016	TGA-RC-01931	68.0	69.0	1.0	512955.3	8116391.7	784.3	512.2	437.1	102.6	121.3	6.4	109.0	80.8	195.3	21.5	81.1	12.2	3.4	8.9	1.1	5.3	0.9	2.1	0.2	1.2	0.2	22.9	75.2	102.7	5.6	10.4	2.6
Target A	RC-TGA-0016	TGA-RC-01932	69.0	70.0	1.0	512955.3	8116391.7	784.3	758.3	683.1	160.1	132.9	8.5	168.6	139.0	307.1	35.3	124.8	19.2	5.0	12.2	1.5	7.0	1.0	2.2	0.2	1.5	0.2	26.9	75.2	157.4	9.0	15.7	3.4
Target A	RC-TGA-0016	TGA-RC-01933	70.0	71.0	1.0	512955.3	8116391.7	784.3	397.1	317.3	79.8	119.9	5.8	85.6	55.1	132.1	16.3	63.5	10.2	2.8	7.6	0.9	4.9	0.8	1.7	0.2	1.3	0.2	19.8	79.8	63.8	3.4	5.7	1.8
Target A	RC-TGA-0016	TGA-RC-01935	71.0	72.0	1.0	512955.3	8116391.7	784.3	441.7	366.5	90.6	120.6	6.2	96.7	65.9	152.3	19.5	71.0	12.2	3.2	9.3	1.1	5.1	0.9	2.0	0.2	1.4	0.2	22.1	75.2	84.7	4.8	6.4	1.7
Target A	RC-TGA-0016	TGA-RC-01936	72.0	73.0	1.0	512955.3	8116391.7	784.3	623.6	551.5	128.7	129.7	8.8	137.5	102.4	246.9	28.8	100.0	15.9	4.4	11.8	1.5	7.3	1.1	2.5	0.3	1.8	0.2	26.7	72.1	121.7	7.3	11.2	2.2
Target A	RC-TGA-0016	TGA-RC-01937	73.0	74.0	1.0	512955.3	8116391.7	784.3	456.5	384.4	90.8	122.5	6.9	97.7	65.3	165.8	19.3	71.5	12.0	3.4	9.3	1.1	5.7	0.9	2.3	0.3	1.7	0.2	25.4	72.1	81.7	4.4	8.3	2.1
Target A	RC-TGA-0016	TGA-RC-01938	74.0	75.0	1.0	512955.3	8116391.7	784.3	392.4	317.3	75.9	122.2	6.5	82.5	53.0	130.8	16.3	59.6	10.5	3.0	8.6	1.1	5.5	0.9	2.2	0.3	1.5	0.2	23.8	75.2	66.9	3.4	7.9	2.1
Target A	RC-TGA-0016	TGA-RC-01939	75.0	76.0	1.0	512955.3	8116391.7	784.3	513.7	438.6	106.5	129.8	7.6	114.0	79.8	184.3	23.1	83.4	13.5	3.7	10.3	1.3	6.3	1.0	2.4	0.3	2.0	0.3	27.1	75.2	101.0	5.5	10.5	2.5
Target A	RC-TGA-0016	TGA-RC-01940	76.0	77.0	1.0	512955.3	8116391.7	784.3	301.3	217.0	57.9	120.9	5.0	62.9	31.2	82.8	11.7	46.2	8.6	2.4	7.0	0.8	4.2	0.7	1.6	0.2	1.3	0.1	18.0	84.4	34.0	2.0	2.4	0.9
Target A	RC-TGA-0016	TGA-RC-01941	77.0	78.0	1.0	512955.3	8116391.7	784.3	356.7	273.8	71.1	123.3	6.1	77.2	43.6	108.5	14.5	56.6	10.2	2.8	7.8	1.0	5.1	0.7	1.7	0.3	1.4	0.2	19.6	82.8	51.9	2.9	3.4	1.1
Target A	RC-TGA-0016	TGA-RC-01943	78.0	79.0	1.0	512955.3	8116391.7	784.3	396.0	307.0	73.7	130.0	5.8	79.5	55.4	127.1	16.2	57.5	9.9	2.9	7.7	0.9	4.9	0.9	1.9	0.3	1.6	0.1	19.8	89.0	76.5	4.3	5.4	1.5
Target A	RC-TGA-0016	TGA-RC-01944	79.0	80.0	1.0	512955.3	8116391.7	784.3	398.4	327.9	78.9	109.8	5.6	84.6	60.4	138.2	17.5	61.5	11.1	2.9	7.6	1.0	4.7	0.8	1.8	0.2	1.2	0.2	19.1	70.6	80.0	4.5	5.6	1.2
Target A	RC-TGA-0016	TGA-RC-01945	80.0	81.0	1.0	512955.3	8116391.7	784.3	554.4	491.5	111.2	116.5	7.4	118.6	92.3	219.9	25.1	86.1	14.4	4.0	10.4	1.3	6.2	1.0	2.2	0.3	1.8	0.2	26.3	62.9	130.2	7.2	9.7	2.6
Target A	RC-TGA-0016	TGA-RC-01946	81.0	82.0	1.0	512955.3	8116391.7	784.3	674.7	610.3	143.2	125.5	8.5	151.7	117.9	270.3	32.6	110.6	17.9	4.6	12.9	1.5	7.1	1.2	2.5	0.3	1.7	0.2	29.2	64.4	146.6	8.7	12.5	2.8
Target A	RC-TGA-0016	TGA-RC-01947	82.0	83.0	1.0	512955.3	8116391.7	784.3	487.1	415.0	97.2	120.3	6.5	103.6	76.9	180.0	21.6	75.6	12.8	3.5	9.2	1.1	5.4	0.9	2.2	0.3	1.6	0.2	23.9	72.1	102.1	6.1	8.3	2.1
Target A	RC-TGA-0016	TGA-RC-01948	83.0	84.0	1.0	512955.3	8116391.7	784.3	395.7	329.7	79.1	109.5	6.0	85.1	56.5	139.4	16.9	62.3	11.1	2.9	8.5	1.0	5.0	0.8	1.8	0.2	1.5	0.2	21.7	66.0	77.4	4.2	5.0	1.4
Target A	RC-TGA-0016	TGA-RC-01950	84.0	85.0	1.0	512955.3	8116391.7	784.3	453.6	387.7	93.6	115.1	6.5	100.1	68.0	164.0	20.2	73.4	12.9	3.4	9.4	1.1	5.4	0.9	2.2	0.3	1.6	0.2	24.6	66.0	72.4	4.5	5.6	1.4
Target A	RC-TGA-0016	TGA-RC-01951	85.0	86.0	1.0	512955.3	8116391.7	784.3	418.6	354.2	83.4	109.4	6.1	89.6	62.7	151.7	17.8	65.7	11.3	3.2	8.5	1.1	5.1	0.8	1.9	0.3	1.4	0.2	22.6	64.4	83.8	4.5	5.9	1.6
Target A	RC-TGA-0016	TGA-RC-01952	86.0	87.0	1.0	512955.3	8116391.7	784.3	464.2	402.8	94.0	111.7	7.1	101.2	71.0	175.1	20.7	73.4	12.5	3.5	9.3	1.2	6.0	0.9	2.1	0.3	1.6	0.3	25.3	61.4	84.1	4.9	9.0	2.1
Target A	RC-TGA-0016	TGA-RC-01953	87.0	88.0	1.0	512955.3	8116391.7	784.3	496.5	433.6	105.5	117.7	7.6	113.1	77.9	181.2	22.5	82.9	14.3	3.8	10.6	1.3	6.3	1.0	2.2	0.3	1.8	0.3	27.2	62.9	72.7	4.3	6.1	1.4
Target A	RC-TGA-0016	TGA-RC-01954	88.0	89.0	1.0	512955.3	8116391.7	784.3	420.7	357.8	85.9	109.9	6.4	92.2	64.7	148.0	18.7	67.2	12.2	3.4	8.7	1.0	5.3	0.9	2.1	0.3	1.7	0.2	23.4	62.9	84.1	4.5	7.0	1.9
Target A	RC-TGA-0016	TGA-RC-01955	89.0	90.0	1.0	512955.3	8116391.7	784.3	431.4	365.4	89.4	110.7	6.1	95.5	65.6	153.6	18.9	70.6	12.1	3.2	8.6	1.1	5.1	0.9	1.9	0.3	1.5	0.2	22.1	66.0	77.4	4.5	7.5	1.7
Target A	RC-TGA-0016	TGA-RC-01957	90.0	91.0	1.0	512955.3	8116391.7	784.3	411.2	342.1	79.0	113.1	5.8	84.7	62.3	146.2	17.5	61.5	10.7	2.9	8.0	1.0	4.8	0.9	2.1	0.3	1.6	0.2	22.5	69.0	80.5	4.5	8.1	1.9
Target A	RC-TGA-0016	TGA-RC-01958	91.0	92.0	1.0	512955.3	8116391.7	784.3	384.2	318.3	77.3	111.1	6.6	84.0	55.4	129.6	16.7	60.7	10.9	3.1	8.5	1.0	5.6	0.8	2.1	0.2	1.5	0.2	22.2	66.0	82.7	4.2	5.3	1.5
Target A	RC-TGA-0016	TGA-RC-01959	92.0	93.0	1.0	512955.3	8116391.7	784.3	339.6	269.1	67.8	111.0	5.7	73.5	43.3	107.1	14.3	53.5	10.5	2.9	7.8	0.9	4.8	0.8	1.7	0.2	1.3	0.2	19.8	70.6	53.1	2.9	3.7	1.0
Target A	RC-TGA-0016	TGA-RC-01960	93.0	94.0	1.0	512955.3	8116391.7	784.3	446.3	378.8	83.6	113.7	6.2	89.8	65.6	172.0	18.4	65.2	11.5	3.1	8.1	1.0	5.2	0.9	2.1	0.3	1.6	0.3	23.6	67.5	90.7	4.6	8.8	2.2
Target A	RC-TGA-0016	TGA-RC-01961	94.0	95.0	1.0	512955.3	8116391.7	784.3	490.7	420.2	94.4	126.2	7.8	102.2	70.8	185.5	20.5	74.0	13.7	3.5	10.5	1.2	6.6	1.1	2.6	0.4	2.0	0.3	27.6	70.6	83.0	4.6	8.7	2.2
Target A	RC-TGA-0016	TGA-RC-01962	95.0	96.0	1.0	512955.3	8116391.7	784.3	431.8	362.8	83.7	115.3	6.6	90.3	63.1	158.5	18.4	65.3	11.1	3.1	8.4	1.1	5.5	0.9	2.1	0.3	1.6	0.2	23.1	69.0	78.7	4.4	7.9	2.0
Target A	RC-TGA-0016	TGA-RC-01963	96.0	97.0	1.0	512955.3	8116391.7	784.3	484.0	425.7	99.3	115.0	7.8	107.1	83.0	173.2	22.0	77.3	13.4	3.3	9.1	1.2	6.6	1.1	2.8	0.5	2.7	0.4	29.2	58.3	80.1	5.1	14.4	5.2
Target A	RC-TGA-0016	TGA-RC-01965	97.0	98.0	1.0	512955.3	8116391.7	784.3	482.1	428.4	100.5	110.8	7.7	108.1	89.1	168.9	22.5	77.9	12.8	3.2	9.1	1.1	6.6	1.1	3.0	0.5	3.0	0.4	29.3	53.7	83.1	5.5	16.2	6.2
Target A	RC-TGA-0016	TGA-RC-01966	98.0	99.0	1.0	512955.3	8116391.7	784.3	553.4	490.5	105.2	125.9	8.5	113.7	76.8	230.3	22.2	82.9	15.3	4.1	11.5	1.4	7.1	1.2	2.8	0.4	2.3	0.3	32.0	62.9	85.7	4.6	6.8	1.8
Target A	RC-TGA-0016	TGA-RC-01967	99.0	100.0	1.0	512955.3	8116391.7	784.3	739.2	670.2	132.9	150.6	11.3	144.2	90.1	346.4	27.8	105.1	19.3	5.0	14.7	1.9	9.4	1.6	3.6	0.5	3.0	0.4	41.5	69.0	72.8	4.3	7.7	1.7
Target A	RC-TGA-0016	TGA-RC-01968	100.0	101.0	1.0	512955.3	8116391.7	784.3	777.4	706.9	139.0	163.3	12.7	151.7	98.9	355.0	29.2	109.8	21.2	5.5	16.1	2.1	10.6	1.8	4.0	0.6	3.6	0.4	48.1	70.6	80.3	4.5	8.2	2.1
Target A	RC-TGA-0016	TGA-RC-01969	101.0	102.0	1.0	512955.3	8116391.7	784.3	597.9	527.4	101.0	142.2	9.3	110.3	64.9	275.2	20.7	80.3	14.8	4.0	11.8	1.6	7.7	1.3	3.4	0.4	2.6	0.4	38.4	70.6	57.1	3.4	6.2	1.4
Target A	RC-TGA-0016	TGA-RC-01970	102.0	103.0	1.0	512955.3	8116391.7	784.3	768.9	698.4	116.6	149.3	10.2	126.8	83.4	401.7	24.9	91.7	18.0	4.5	12.7	1.7	8.5	1.5	3.7	0.5	3.0	0.4	42.3	70.6	82.4	5.4	9.7	2.2
Target A	RC-TGA-0016	TGA-RC-01972	103.0	104.0	1.0	512955.3	8116391.7	784.3	556.8	483.2	85.4	134.5	8.1	93.5	58.6	265.3	18.1	67.3	12.9	3.5	10.0	1.4	6.7	1.2	2.9	0.4	2.3	0.3	32.3	73.6	67.9	4.4	8.0	1.9
Target A	RC-TGA-0016	TGA-RC-01973	104.0	105.0	1.0	512955.3	8116391.7	784.3	539.7	463.0	80.7	126.8	6.5	87.2	60.6	259.2	17.5	63.2	12.4	3.2	9.2	1.2	5.4	0.9	2.4	0.3	1.8	0.3	25.5	76.7	74.1	4.4	8.5	2.1
Target A	RC-TGA-0016	TGA-RC-01974	105.0	106.0	1.0	512955.3	8116391.7	784.3	770.5	701.5	119.3	148.2	10.3	129.6	94.8	390.6	26.7	92.6	17.6	4.7	13.7	1.7	8.6	1.5	3.7	0.5	3.1	0.4	41.3	69.0	98.3	6.0	12.8	3.2
Target A	RC-TGA-0016	TGA-RC-01975	106.0	107.0	1.0	512955.3	8116391.7	784.3	792.8	723.8	132.2	151.4	11.0	143.3	102.4	387.0	29.4	102.9	19.8	4.9	13.3	1.9	9.2	1.6	3.8	0.5	3.2	0.5	43.6	69.0	114.3	6.5	14.2	3.5
Target A	RC-TGA-0016	TGA-RC-01976	107.0	108.0	1.0	512955.3	8116391.7	784.3	817.5	747.0	131.1	153.7	11.3	142.4	104.3	409.1	29.4	101.7	19.4	4.8	14.0	1.9	9.5	1.6	3.9	0.6	3.1	0.5	43.4	70.6	115.4	6.5	14.1	3.5
Target A	RC-TGA-0016	TGA-RC-01977	108.0	109.0	1.0	512955.3	8116391.7	784.3	898.7	834.2	133.9	155.1	12.0	145.9	98.9	491.4	29.8	104.0	19.4	5.1	14.9	2.0	10.1	1.8	4.4	0.6	3.9	0.6	47.4	64.4	91.3	5.6	14.5	3.8
Target A	RC-TGA-0017	TGA-RC-01512	0.0	1.0	1.0	513277.0	8115962.8	777.7	247.2	210.4	22.8	74.0	3.7	26.5	29.2	118.4	5.5	17.3	2.9	0.6	2.7	0.5	3.3	0.8	2.4	0.4	2.9	0.5	23.1	36.8	132.8	7.8	25.7	6.6
Target A	RC-TGA-0017	TGA-RC-01513	1.0	2.0	1.0	513277.0	8115962.8	777.7	282.8	242.9	25.1	82.7	4.6	29.7	33.1	138.8	6.1	19.0	3.0	0.7	2.8	0.6	4.0	0.9	2.8	0.5	3.5	0.6	26.5	39.9	148.8	8.9	29.2	7.7
Target A	RC-TGA-0017	TGA-RC-01515	2.0	3.0	1.0	513277.0	8115962.8	777.7	332.4	291.0	36.5	91.0	5.4	41.9	37.9	162.2	8.4	28.1	4.9	1.1	4.1	0.8	4.6	1.0	3.1	0.5	3.8	0.6	30.0	41.4	129.2	7.9	25.4	7.1
Target A	RC-TGA-0017	TGA-RC-01516	3.0	4.0	1.0	513277.0	8115962.8	777.7	218.1	178.2	21.3	69.4	3.1	24.4	25.0	99.8	5.2	16.1	2.7	0.7	2.3	0.4	2.7	0.6	1.8	0.3	2.2	0.3	18.2	39.9	90.1	5.4	18.6	5.2
Target A	RC-TGA-0017	TGA-RC-01517	4.0	5.0	1.0	513277.0	8115962.8	777.7	394.6	305.7	65.0	123.7	4.5	69.4	65.8	131.4	14.9	50.0	8.7	1.4	4.4	0.7	3.7	0.8	2.1	0.4	2.7	0.4	18.3	89.0	48.5	2.4	28.0	12.6
Target A	RC-TGA-0017	TGA-RC-01518	5.0	6.0	1.0	513277.0	8115962.8	777.7	348.9	292.2	53.6	92.5	4.4	58.0	63.3	132.7	12.7	40.9	6.8	1.3	4.0	0.6	3.8	0.8	2.4	0.4	2.6	0.4	19.6	56.8	93.3	4.8	29.2	9.9
Target A	RC-TGA-0017	TGA-RC-01519	6.0	7.0	1.0	513277.0	8115962.8	777.7	385.6	348.8	52.6	80.3	4.9	57.5	78.0	168.9	12.9	39.7	5.9	1.4	4.2	0.7	4.2	0.9	2.9	0.5	3.5	0.5	24.8	36.8	176.7	8.9	28.1	10.4
Target A	RC-TGA-0017	TGA-RC-01520	7.0	8.0	1.0	513277.0	8115962.8	777.7	241.8	217.2	37.4	49.6	2.9	40.3	55.9	94.3	9.1	28.3	4.5	1.3	2.7	0.4	2.5	0.5	1.4	0.3	1.8	0.3	13.8	24.5	213.9	9.2	23.9	10.6
Target A	RC-TGA-0017	TGA-RC-01522	8.0	9.0	1.0	513277.0	8115962.8	777.7	211.9	190.4	36.9	42.9	2.5	39.4	53.5	74.2	8.8	28.1	4.5	1.5	2.9	0.4	2.1	0.4	1.2	0.2	1.4	0.2	11.2	21.5	254.6	10.1	26.2	8.2
Target A	RC-TGA-0017	TGA-RC-01523	9.0	10.0	1.0	513277.0	8115962.8	777.7	234.4	216.0	43.0	37.8	2.5	45.5	68.6	80.1	10.4	32.5	4.9	1.6	3.0	0.4	2.1	0.4	1.0	0.2	1.1	0.2	9.5	18.4	277.5	11.1	31.6	8.1
Target A	RC-TGA-0017	TGA-RC-01524	10.0	11.0	1.0	513277.0	8115962.8	777.7	278.5	260.1	54.4	38.7	2.7	57.1	85.2	94.2	13.1	41.3	6.1	1.7	3.8	0.5	2.3	0.4	1.0	0.1	1.0	0.1	9.4	18.4	286.1	11.4	31.2	7.1
Target A	RC-TGA-0017	TGA-RC-01525	11.0	12.0	1.0	513277.0	8115962.8	777.7	462.2	433.1	91.6	66.1	4.9	96.5	139.0	155.4	22.2	69.4	10.1	2.3	6.1	0.8	4.1	0.8	2.0	0.3	2.0	0.3	18.4	29.1	299.0	12.8	26.1	8.7
Target A	RC-TGA-0017	TGA-RC-01526	12.0	13.0	1.0	513277.0	8115962.8	777.7	564.1	545.7	108.5	58.2	5.5	113.9	166.5	219.3	27.4	81.1	11.6	3.0	7.2	0.9	4.5	0.8	1.9	0.3	2.0	0.3	18.9	18.4	268.2	11.5	26.9	4.7
Target A	RC-TGA-0017	TGA-RC-01527	13.0	14.0	1.0	513277.0	8115962.8	777.7	2,845.2	2,822.2	492.0	133.2	19.0	511.0	830.3	1,339.0	128.1	363.9	50.7	11.3	27.9	3.4	15.6	2.2	4.9	0.5	3.2	0.4	40.9	23.0	245.3	10.4	25.9	5.6
Target A	RC-TGA-0017	TGA-RC-01528	14.0	15.0	1.0	513277.0	8115962.8	777.7	1,639.5	1,622.6	318.1	94.3	12.2	330.2	451.5	742.0	80.1	238.0	33.6	7.4	18.9	2.2	10.0	1.5	3.3	0.5	2.3	0.3	31.2	16.9	233.9	11.2	27.7	6.1
Target A	RC-TGA-0017	TGA-RC-01529	15.0	16.0	1.0	513277.0	8115962.8	777.7	881.4	872.2	173.8	63.4	8.7	182.5	232.2	391.9	43.1	130.6	20.2	4.5	12.2	1.5	7.3	1.0	2.5	0.3	2.0	0.3	22.7	9.2	251.8	11.7	27.0	6.3
Target A	RC-TGA-0017	TGA-RC-01530	16.0	17.0	1.0	513277.0	8115962.8	777.7	920.8	902.4	163.7	69.8	8.0	171.7	238.1	431.2	41.8	121.9	18.1	4.3	11.4	1.3	6.6	1.0	2.2	0.3	1.9	0.3	22.1	18.4	276.8	13.6	28.6	6.6
Target A	RC-TGA-0017	TGA-RC-01531	17.0	18.0	1.0	513277.0	8115962.8	777.7	1,654.0	1,631.0	244.4	82.7	9.4	253.8	354.2	950.8	61.9	182.5	21.9	5.3	12.9	1.7	7.7	1.3	2.7	0.3	1.8	0.3	25.8	23.0	263.9	14.0	27.1	6.7
Target A	RC-TGA-0017	TGA-RC-01532	18.0	19.0	1.0	513277.0	8115962.8	777.7	929.9	913.0	162.9	63.8	6.9	169.8	225.2	461.9	39.9	123.1	16.1	3.8	9.7	1.2	5.7	0.9	2.3	0.3	1.7	0.3	21.1	16.9	264.6	12.6	27.1	6.5
Target A	RC-TGA-0017	TGA-RC-01533	19.0	20.0	1.0	513277.0	8115962.8	777.7	1,289.0	1,264.4	182.6	82.2	9.2	191.9	241.6	764.1	43.3	139.4	18.5	4.5	11.5	1.6	7.6	1.1	2.8	0.3	1.9	0.3	26.0	24.5	246.8	12.9	26.5	8.0
Target A	RC-TG

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0017	TGA-RC-01544	28.0	29.0	1.0	513277.0	8115962.8	777.7	827.7	815.5	196.4	97.7	12.7	209.1	194.1	315.7	44.2	152.2	23.8	6.6	14.9	2.1	10.5	1.7	4.3	0.6	3.4	0.5	40.9	12.3	169.5	8.7	24.1	5.2
Target A	RC-TGA-0017	TGA-RC-01545	29.0	30.0	1.0	513277.0	8115962.8	777.7	623.3	612.5	147.7	80.1	9.9	157.5	152.5	226.0	33.7	114.0	17.0	5.3	11.5	1.6	8.3	1.3	3.7	0.5	3.0	0.4	33.8	10.7	158.8	8.1	21.4	5.0
Target A	RC-TGA-0017	TGA-RC-01546	30.0	31.0	1.0	513277.0	8115962.8	777.7	597.9	587.2	142.9	79.2	10.1	153.0	136.6	222.3	31.7	111.3	16.8	5.4	11.3	1.6	8.5	1.3	3.5	0.5	2.7	0.4	33.5	10.7	165.2	8.5	18.5	4.1
Target A	RC-TGA-0017	TGA-RC-01547	31.0	32.0	1.0	513277.0	8115962.8	777.7	577.9	562.6	144.7	90.3	10.2	154.9	129.6	195.3	31.1	113.6	18.1	5.4	12.2	1.6	8.6	1.4	3.9	0.5	3.2	0.4	37.6	15.3	163.8	8.7	15.6	4.0
Target A	RC-TGA-0017	TGA-RC-01548	32.0	33.0	1.0	513277.0	8115962.8	777.7	800.8	783.9	230.3	145.5	18.2	248.5	150.1	243.8	46.6	183.7	31.0	8.9	20.9	3.0	15.2	2.5	6.3	0.8	5.2	0.7	65.3	16.9	120.3	6.2	9.9	2.5
Target A	RC-TGA-0017	TGA-RC-01549	33.0	34.0	1.0	513277.0	8115962.8	777.7	1,146.9	1,139.2	293.1	331.9	35.0	328.1	188.8	293.6	57.5	235.6	39.4	12.2	35.0	5.1	29.8	6.1	16.7	2.3	13.7	2.0	201.3	7.7	141.0	6.2	8.2	2.0
Target A	RC-TGA-0017	TGA-RC-01551	34.0	35.0	1.0	513277.0	8115962.8	777.7	1,639.6	1,627.3	382.3	522.9	55.9	438.1	221.1	458.2	72.0	310.3	55.2	16.1	53.5	8.1	47.7	9.5	26.6	3.5	21.3	2.9	321.3	12.3	145.9	6.8	9.6	2.5
Target A	RC-TGA-0017	TGA-RC-01552	35.0	36.0	1.0	513277.0	8115962.8	777.7	618.6	609.4	167.5	120.7	14.1	181.6	122.6	188.0	33.4	134.1	19.9	6.6	16.2	2.1	11.9	2.2	5.6	0.7	4.6	0.6	61.0	9.2	128.0	6.1	8.4	1.8
Target A	RC-TGA-0017	TGA-RC-01553	36.0	37.0	1.0	513277.0	8115962.8	777.7	820.8	811.6	196.0	213.5	24.0	220.0	134.9	248.1	38.5	157.5	28.3	8.3	23.6	3.5	20.5	3.8	10.7	1.5	8.8	1.2	122.4	9.2	143.8	6.7	8.9	2.2
Target A	RC-TGA-0017	TGA-RC-01554	37.0	38.0	1.0	513277.0	8115962.8	777.7	610.1	604.0	132.2	137.4	14.7	146.9	113.1	210.1	27.1	105.1	17.5	6.4	15.2	2.4	12.3	2.3	7.3	1.0	6.0	0.8	77.6	6.1	106.1	5.3	8.0	1.9
Target A	RC-TGA-0017	TGA-RC-01555	38.0	39.0	1.0	513277.0	8115962.8	777.7	575.5	569.4	114.4	155.3	15.9	130.3	105.6	186.1	23.5	90.9	14.2	5.5	14.6	2.4	13.5	2.8	7.8	1.1	6.8	1.0	93.7	6.1	127.0	6.5	8.4	1.8
Target A	RC-TGA-0017	TGA-RC-01556	39.0	40.0	1.0	513277.0	8115962.8	777.7	628.6	617.9	126.5	162.3	16.8	143.4	115.1	208.2	26.6	100.0	16.5	5.8	16.8	2.4	14.4	2.7	7.9	0.9	5.9	0.9	93.9	10.7	169.5	9.9	9.7	2.4
Target A	RC-TGA-0017	TGA-RC-01558	40.0	41.0	1.0	513277.0	8115962.8	777.7	707.4	673.7	157.9	150.0	14.3	172.2	129.6	250.6	32.5	125.4	19.3	6.7	16.5	2.2	12.1	2.1	5.6	0.8	4.5	0.6	65.3	33.7	163.1	8.4	11.3	2.6
Target A	RC-TGA-0017	TGA-RC-01559	41.0	42.0	1.0	513277.0	8115962.8	777.7	840.8	791.7	166.2	209.6	16.1	182.3	146.6	297.3	34.4	131.8	21.1	5.7	17.5	2.5	13.6	3.0	8.1	1.1	7.1	1.1	101.0	49.1	258.2	13.3	18.2	5.5
Target A	RC-TGA-0017	TGA-RC-01560	42.0	43.0	1.0	513277.0	8115962.8	777.7	583.2	572.4	115.4	142.8	12.9	128.3	107.9	202.1	24.2	91.2	15.0	4.9	13.6	1.8	11.1	2.2	6.2	0.8	4.6	0.8	86.0	10.7	149.5	8.1	9.9	2.4
Target A	RC-TGA-0017	TGA-RC-01561	43.0	44.0	1.0	513277.0	8115962.8	777.7	669.9	662.2	138.6	109.2	11.1	149.7	138.4	267.8	30.3	108.2	16.0	5.1	12.1	1.8	9.3	1.8	5.0	0.6	3.9	0.5	61.3	7.7	129.0	7.1	12.6	3.4
Target A	RC-TGA-0017	TGA-RC-01562	44.0	45.0	1.0	513277.0	8115962.8	777.7	637.3	629.6	133.0	98.8	10.3	143.3	132.5	256.7	28.9	104.2	16.1	5.0	11.1	1.5	8.8	1.6	4.2	0.6	3.6	0.4	54.4	7.7	134.0	7.3	11.8	3.0
Target A	RC-TGA-0017	TGA-RC-01563	45.0	46.0	1.0	513277.0	8115962.8	777.7	606.6	594.3	128.4	108.1	11.1	139.6	122.0	232.8	27.4	101.0	15.3	5.3	12.2	1.8	9.4	1.9	4.9	0.6	4.1	0.6	55.1	12.3	158.1	8.2	12.2	2.7
Target A	RC-TGA-0017	TGA-RC-01565	46.0	47.0	1.0	513277.0	8115962.8	777.7	697.8	687.1	136.6	109.1	11.0	147.6	131.9	302.2	30.7	105.9	18.0	4.8	12.5	1.7	9.3	1.7	4.9	0.6	4.0	0.6	58.2	10.7	191.7	9.6	14.2	3.2
Target A	RC-TGA-0017	TGA-RC-01566	47.0	48.0	1.0	513277.0	8115962.8	777.7	650.1	633.2	128.7	95.3	9.1	137.8	126.7	282.5	29.4	99.4	16.8	4.2	11.0	1.5	7.6	1.4	3.7	0.5	2.9	0.4	45.2	16.9	180.2	9.0	15.5	3.1
Target A	RC-TGA-0017	TGA-RC-01567	48.0	49.0	1.0	513277.0	8115962.8	777.7	783.9	754.7	153.1	115.3	10.8	163.8	170.6	326.8	34.7	118.4	18.1	4.4	11.9	1.7	9.1	1.7	4.2	0.6	3.5	0.5	48.8	29.1	232.5	11.0	20.7	4.6
Target A	RC-TGA-0017	TGA-RC-01568	49.0	50.0	1.0	513277.0	8115962.8	777.7	671.6	651.7	124.6	90.0	8.7	133.3	151.9	289.9	28.8	95.9	15.3	4.1	10.0	1.4	7.3	1.3	3.5	0.5	2.9	0.4	38.6	19.9	213.9	8.9	17.0	4.2
Target A	RC-TGA-0017	TGA-RC-01569	50.0	51.0	1.0	513277.0	8115962.8	777.7	548.6	531.7	102.1	76.7	7.3	109.4	126.1	231.6	23.7	78.4	12.1	4.4	8.7	1.2	6.0	1.2	3.0	0.4	2.5	0.4	32.0	16.9	184.5	8.7	11.5	3.0
Target A	RC-TGA-0017	TGA-RC-01570	51.0	52.0	1.0	513277.0	8115962.8	777.7	493.8	480.0	97.0	74.3	7.6	104.5	103.9	207.0	21.3	75.7	11.6	4.2	8.5	1.1	6.5	1.2	3.0	0.4	2.5	0.4	32.9	13.8	142.0	6.2	9.3	2.8
Target A	RC-TGA-0017	TGA-RC-01572	52.0	53.0	1.0	513277.0	8115962.8	777.7	563.7	546.9	113.3	86.4	8.6	121.9	114.5	235.9	25.5	87.8	13.7	4.6	10.1	1.5	7.1	1.3	3.5	0.5	2.5	0.4	38.1	16.9	142.6	6.8	12.2	3.1
Target A	RC-TGA-0017	TGA-RC-01573	53.0	54.0	1.0	513277.0	8115962.8	777.7	570.3	541.2	112.3	99.1	9.2	121.4	111.3	233.4	25.0	87.3	14.3	4.6	10.2	1.5	7.6	1.4	3.4	0.5	2.8	0.4	37.5	29.1	154.5	7.4	11.5	3.6
Target A	RC-TGA-0017	TGA-RC-01574	54.0	55.0	1.0	513277.0	8115962.8	777.7	408.1	398.9	83.0	74.5	8.2	91.2	77.3	161.5	18.1	64.9	11.8	2.6	8.8	1.3	6.9	1.3	3.5	0.5	2.5	0.4	37.5	9.2	79.0	5.3	10.5	2.9
Target A	RC-TGA-0017	TGA-RC-01575	55.0	56.0	1.0	513277.0	8115962.8	777.7	632.3	610.8	130.0	109.3	10.9	140.9	130.2	246.9	28.8	101.2	15.9	4.4	12.4	1.7	9.2	1.6	4.5	0.6	3.4	0.5	49.5	21.5	150.2	8.2	12.6	2.7
Target A	RC-TGA-0017	TGA-RC-01576	56.0	57.0	1.0	513277.0	8115962.8	777.7	550.0	534.7	109.3	85.3	9.2	118.6	116.0	226.0	24.9	84.5	13.4	3.8	10.0	1.5	7.7	1.3	3.4	0.5	2.9	0.4	38.5	15.3	144.5	7.1	11.3	3.1
Target A	RC-TGA-0017	TGA-RC-01577	57.0	58.0	1.0	513277.0	8115962.8	777.7	572.3	558.5	115.3	89.2	9.5	124.8	120.8	232.8	25.4	89.9	14.3	4.3	10.7	1.5	8.0	1.5	3.9	0.5	3.0	0.4	41.7	13.8	154.5	7.9	12.6	3.4
Target A	RC-TGA-0017	TGA-RC-01578	58.0	59.0	1.0	513277.0	8115962.8	777.7	759.8	727.6	154.0	113.8	10.5	164.5	154.8	318.2	34.4	119.6	19.1	5.4	12.3	1.7	8.8	1.6	3.9	0.5	2.9	0.5	43.9	32.2	222.4	10.9	16.8	3.9
Target A	RC-TGA-0017	TGA-RC-01579	59.0	60.0	1.0	513277.0	8115962.8	777.7	727.4	701.4	149.2	102.1	10.1	159.3	151.3	307.1	33.2	115.9	17.8	4.9	11.6	1.6	8.5	1.4	3.8	0.5	2.9	0.4	40.4	26.1	209.6	11.2	18.5	5.0
Target A	RC-TGA-0017	TGA-RC-01580	60.0	61.0	1.0	513277.0	8115962.8	777.7	573.0	559.2	116.2	87.7	9.4	125.7	116.7	237.7	25.6	90.6	14.6	4.2	10.2	1.5	8.0	1.5	3.7	0.5	2.9	0.4	41.1	13.8	170.2	10.0	14.3	4.0
Target A	RC-TGA-0017	TGA-RC-01581	61.0	62.0	1.0	513277.0	8115962.8	777.7	441.4	429.1	92.7	70.6	7.3	100.0	89.5	176.9	20.3	72.4	11.7	3.9	8.7	1.1	6.2	1.2	2.7	0.4	2.4	0.3	31.5	12.3	111.7	6.1	10.0	2.9
Target A	RC-TGA-0017	TGA-RC-01582	62.0	63.0	1.0	513277.0	8115962.8	777.7	549.5	534.1	110.7	93.7	9.3	120.0	108.0	222.3	24.4	86.3	14.7	4.3	10.6	1.4	7.9	1.5	3.8	0.6	3.1	0.5	44.7	15.3	132.5	7.0	9.9	2.7
Target A	RC-TGA-0017	TGA-RC-01583	63.0	64.0	1.0	513277.0	8115962.8	777.7	736.1	705.4	147.2	130.8	12.2	159.4	141.9	297.3	32.5	114.7	19.0	4.9	14.2	1.9	10.3	2.0	5.0	0.7	4.1	0.6	56.4	30.7	178.8	10.7	14.8	3.8
Target A	RC-TGA-0017	TGA-RC-01584	64.0	65.0	1.0	513277.0	8115962.8	777.7	791.7	748.7	171.1	133.0	11.4	182.6	145.4	320.6	37.0	134.1	21.5	5.9	15.3	1.9	9.6	1.6	4.0	0.5	3.2	0.4	47.8	43.0	238.2	12.2	15.1	3.3
Target A	RC-TGA-0017	TGA-RC-01586	65.0	66.0	1.0	513277.0	8115962.8	777.7	475.0	464.2	99.3	73.5	7.2	106.6	99.2	190.4	22.0	77.3	12.6	4.5	9.1	1.2	6.1	1.2	3.2	0.4	2.7	0.4	34.0	10.7	129.9	6.7	9.5	2.6
Target A	RC-TGA-0017	TGA-RC-01587	66.0	67.0	1.0	513277.0	8115962.8	777.7	613.2	585.6	131.5	101.9	9.2	140.7	115.3	248.1	28.0	103.5	16.4	5.3	12.2	1.6	7.7	1.4	3.5	0.5	2.7	0.4	39.1	27.6	179.5	9.4	12.3	3.2
Target A	RC-TGA-0017	TGA-RC-01588	67.0	68.0	1.0	513277.0	8115962.8	777.7	560.2	549.5	117.3	111.0	11.1	128.4	113.2	203.9	25.5	91.8	14.9	5.3	12.5	1.7	9.4	1.9	4.9	0.7	4.4	0.7	58.8	10.7	127.7	6.1	9.9	2.9
Target A	RC-TGA-0017	TGA-RC-01589	68.0	69.0	1.0	513277.0	8115962.8	777.7	496.2	480.9	103.2	92.3	9.1	112.3	100.9	186.7	22.6	80.6	13.2	4.8	10.3	1.4	7.7	1.4	3.8	0.5	3.4	0.5	43.2	15.3	120.2	5.9	10.6	3.0
Target A	RC-TGA-0017	TGA-RC-01590	69.0	70.0	1.0	513277.0	8115962.8	777.7	424.0	407.1	87.2	70.0	6.3	93.6	87.5	168.9	19.3	67.9	10.3	3.7	7.9	1.0	5.3	1.0	2.7	0.4	2.1	0.3	28.7	16.9	115.2	6.3	9.4	2.6
Target A	RC-TGA-0017	TGA-RC-01591	70.0	71.0	1.0	513277.0	8115962.8	777.7	572.8	554.4	117.1	90.3	8.7	125.8	116.0	234.6	26.2	90.9	14.8	4.7	10.4	1.3	7.4	1.4	3.3	0.5	2.9	0.4	39.6	18.4	157.4	7.7	12.2	3.3
Target A	RC-TGA-0017	TGA-RC-01593	71.0	72.0	1.0	513277.0	8115962.8	777.7	413.7	401.4	82.3	65.4	6.2	88.5	89.6	166.5	18.5	63.8	10.0	3.4	7.7	1.0	5.3	1.0	2.5	0.4	2.3	0.3	29.3	12.3	102.1	5.4	11.8	3.4
Target A	RC-TGA-0017	TGA-RC-01594	72.0	73.0	1.0	513277.0	8115962.8	777.7	382.1	372.9	76.7	60.6	5.9	82.6	84.1	151.7	17.3	59.4	9.1	3.3	7.2	0.9	5.0	0.9	2.7	0.4	2.3	0.3	28.5	9.2	91.4	4.4	13.8	4.1
Target A	RC-TGA-0017	TGA-RC-01595	73.0	74.0	1.0	513277.0	8115962.8	777.7	511.2	498.9	109.9	85.8	8.7	118.6	103.7	197.8	24.2	85.7	14.1	4.3	10.1	1.4	7.4	1.4	3.7	0.5	2.9	0.4	41.4	12.3	120.9	6.6	11.8	3.4
Target A	RC-TGA-0017	TGA-RC-01596	74.0	75.0	1.0	513277.0	8115962.8	777.7	471.2	460.5	101.6	79.9	8.1	109.7	97.9	178.7	22.3	79.3	13.0	4.2	9.6	1.3	6.8	1.3	3.4	0.5	2.9	0.5	38.9	10.7	116.4	6.5	11.3	3.2
Target A	RC-TGA-0017	TGA-RC-01597	75.0	76.0	1.0	513277.0	8115962.8	777.7	402.2	393.0	81.3	59.1	5.7	87.0	86.0	165.8	18.2	63.1	10.0	3.8	7.4	0.9	4.8	0.9	2.5	0.3	2.3	0.3	26.8	9.2	112.0	5.9	10.5	3.1
Target A	RC-TGA-0017	TGA-RC-01598	76.0	77.0	1.0	513277.0	8115962.8	777.7	411.2	403.6	81.9	57.0	5.8	87.8	92.2	170.1	18.6	63.3	9.9	3.7	7.3	1.0	4.9	0.9	2.5	0.4	2.1	0.3	26.3	7.7	108.1	5.5	11.0	3.2
Target A	RC-TGA-0017	TGA-RC-01599	77.0	78.0	1.0	513277.0	8115962.8	777.7	578.4	557.0	114.7	82.1	7.5	122.2	122.0	245.7	26.0	88.8	13.9	4.4	9.5	1.2	6.2	1.2	2.9	0.4	2.5	0.4	31.9	21.5	161.6	8.3	13.9	3.5
Target A	RC-TGA-0017	TGA-RC-01601	78.0	79.0	1.0	513277.0	8115962.8	777.7	599.2	574.6	117.5	87.6	7.8	125.3	123.1	256.7	27.2	90.3	14.2	4.2	9.6	1.3	6.5	1.3	3.2	0.4	2.4	0.4	33.8	24.5	163.8	9.3	12.2	3.2
Target A	RC-TGA-0017	TGA-RC-01602	79.0	80.0	1.0	513277.0	8115962.8	777.7	685.2	620.8	138.2	130.7	8.5	146.7	125.5	272.7	30.2	108.0	18.1	4.6	12.1	1.5	7.0	1.2	2.9	0.4	2.2	0.3	34.0	64.4	189.5	9.4	12.9	3.1
Target A	RC-TGA-0017	TGA-RC-01603	80.0	81.0	1.0	513277.0	8115962.8	777.7	627.9	588.1	127.4	105.5	8.5	135.9	123.1	255.5	27.7	99.7	16.4	4.4	12.0	1.4	7.1	1.2	2.9	0.4	2.0	0.3	33.9	39.9	205.3	8.9	10.6	2.9
Target A	RC-TGA-0017	TGA-RC-01604	81.0	82.0	1.0	513277.0	8115962.8	777.7	497.7	447.1	88.7	119.3	8.0	96.7	100.0	178.1	20.0	68.7	11.5	3.3	9.3	1.3	6.8	1.3	3.4	0.5	2.8	0.4	39.8	50.6	191.7	6.7	8.5	3.3
Target A	RC-TGA-0017	TGA-RC-01605	82.0	83.0	1.0	513277.0	8115962.8	777.7	701.7	655.7	142.6	136.6	10.7	153.3	132.5	271.5	31.1	111.5	18.6	5.2	14.0	1.8	9.0	1.7	4.4	0.6	3.5	0.6	50.0	46.0	134.3	7.2	10.2	2.5
Target A	RC-TGA-0017	TGA-RC-01606	83.0	84.0	1.0	513277.0	8115962.8	777.7	826.0	792.2	159.9	144.3	12.5	172.4	147.8	353.8	34.6	125.4	20.1	6.2	14.8	1.9	10.6	2.0	5.3	0.7	4.8	0.8	63.6	33.7	109.6	6.6	10.4	2.4
Target A	RC-TGA-0017	TGA-RC-01608	84.0	85.0	1.0	513277.0	8115962.8	777.7	635.9	619.0	141.5	100.5	10.5	152.0	140.2	235.9	31.7	109.9	17.8	5.7	12.6	1.6	8.9	1.6	4.0	0.6	3.5	0.5	44.7	16.9	106.3	6.0	11.1	2.6
Target A	RC-TGA-0017	TGA-RC-01609	85.0	86.0	1.0	513277.0	8115962.8	777.7	676.4	665.6	126.5	87.5	9.4	135.9	129.6	316.9	29.4	97.2	15.8	3.8	11.0	1.4	8.0	1.5	3.9	0.5	3.3	0.5	42.9	10.7	174.5	11.1	9.9	2.5
Target A	RC-TGA-0017	TGA-RC-01610	86.0	87.0	1.0	513277.0	8115962.8	777.7	777.8	767.1	131.8	87.9	9.5	141.3	138.4	404.1	30.5	101.4	15.6	4.0	11.3	1.5	8.0	1.5	4.0	0.6	3.2	0.4	42.7	10.7	168.8	10.1	9.9	2.9
Target A	RC-TGA-0017	TGA-RC-01611	87.0	88.0	1.0	513277.0	8115962.8	777.7	749.5	732.6	130.1	96.2	10.2	140.3	127.8	378.4	29.6	100.5	16.9	5.1	12.2	1.7	8.5	1.6	3.9	0.5	3.4	0.5	42.0	16.9	128.7	7.3	11.6	2.9
Target A	RC-TGA-0017	TGA-RC-01612	88.0	89.0	1.0	513277.0	8115962.8	777.7	615.3	599.9	127.3	89.3	9.5	136.8	121.4	261.7	28.9	98.4	15.7	4.0	11.3	1.5	7.9	1.4	3.7	0.5	2.9	0.4	40.3	15.3	148.1	10.3	10.7	2.6
Target A	RC-TGA-0017	TGA-RC-01613	89.0	90.0	1.0	513277.0	8115962.8	777.7	662.8	650.5	137.1	89.5	10.0	147.1	130.8	288.7	31.3	105.8	16.8	4.2	11.5	1.6	8.4	1.5	3.8	0.5	3.1	0.4	42.3	12.3	164.5	11.6	10.8	2.6
Target A	RC-TGA-0017	TGA-RC-01615	90.0	91.0	1.0	513277.0	8115962.8	777.7	721.3	709.0	144.4	103.6	11.5	155.8	144.8	309.6	32.4	112.0	19.0	5.5	13.4	1.8	9.7	1.7	4.4	0.7	4.0	0.6	49.7	12.3	125.6	7.1	12.7	3.1
Target A	RC-TGA-0017	TGA-RC-01616	91.0	92.0	1.0	513277.0	8115962.8	777.7	676.3	664.0	138.8	115.6	11.8	150.6	139.0	265.3	30.9	107.9	17.5	5.5	13.3	1.8	10.0	1.8	5.1	0.7	4.5	0.7	59.9	12.3	116.2	6.6	11.4	2.8
Target A	RC-TGA-0017	TGA-RC-01617	92.0	93.0	1.0	513277.0	8115962.8	777.7	599.1	586.8	133.2	97.5	10.4	143.6	124.9	227.3	30.3	102.9	16.2	4.9	12.2	1.6	8.9	1.5	4.2	0.6	3.4	0.5	47.5	12.3	137.3	6.8	13.7	3.4
Target A	RC-TGA-0017	TGA-RC-01618	93.0	94.0	1.0	513277.0	8115962.8	777.7	620.2	608.0	135.9	96.5	10.5	146.3	130.8	240.2	30.6	105.3	16.9	5.1	12.0	1.7	8.8	1.6	4.3	0.6	3.4	0.5	46.2	12.3	133.6	6.8	13.1	3.3
Target A	RC-TGA-0017	TGA-RC-01619	94.0	95.0	1.0	513277.0	8115962.8	777.7	622.3	610.0	134.7	97.1	10.4	145.1	129.0	245.1	30.3	104.4	16.4	5.2	11.9	1.6	8.8	1.6	4.1	0.6	3.5	0.5	47.0	12.3	133.0	6.6	13.4	3.2
Target A	RC-TGA-0017	TGA-RC-01620	95.0	96.0	1.0	513277.0	8115962.8	777.7	727.3	711.9	140.2	102.8	10.5	150.7	130.8	336.6	31.2	109.1	16.9	5.1	12.8	1.7	8.8	1.7	4.1	0.6	3.6	0.5	48.6	15.3	137.2	6.8	13.0	3.3
Target A	RC-TGA-0017	TGA-RC-01622	96.0	97.0	1.0	513277.0	8115962.8	777.7	663.3	651.1	142.3	103.5	10.6	152.9	134.9	265.3	32.1	110.1	17.4	5.5	12.8	1.7	8.9	1.7	4.2	0.6	3.8	0.6	51.4	12.3	128.2	6.7	12.3	3.0
Target A	RC-TGA-0017	TGA-

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO$_2$ ppm	U_3O_8 ppm
Target A	RC-TGA-0017	TGA-RC-01631	105.0	106.0	1.0	513277.0	8115962.8	777.7	752.1	738.3	131.3	97.7	10.4	141.8	126.7	380.8	29.8	101.5	15.6	5.3	11.9	1.7	8.8	1.6	4.2	0.6	3.5	0.5	46.0	13.8	126.0	6.3	13.7	3.5
Target A	RC-TGA-0017	TGA-RC-01632	106.0	107.0	1.0	513277.0	8115962.8	777.7	984.9	968.1	141.8	104.2	11.2	153.0	138.4	582.3	32.5	109.3	18.3	5.7	12.9	1.7	9.5	1.7	4.5	0.6	3.6	0.6	46.7	16.9	125.7	6.0	12.9	3.3
Target A	RC-TGA-0017	TGA-RC-01633	107.0	108.0	1.0	513277.0	8115962.8	777.7	1,071.8	1,054.9	156.4	122.8	12.8	169.2	145.4	627.7	35.6	120.7	19.5	5.9	14.7	2.0	10.9	1.9	5.6	0.7	4.6	0.7	58.9	16.9	133.8	6.6	14.3	3.8
Target A	RC-TGA-0017	TGA-RC-01634	108.0	109.0	1.0	513277.0	8115962.8	777.7	997.9	979.5	145.4	106.4	11.0	156.5	138.4	589.6	33.2	112.2	18.0	5.5	13.1	1.8	9.2	1.7	4.3	0.6	3.5	0.5	47.8	18.4	129.7	6.3	13.4	3.4
Target A	RC-TGA-0017	TGA-RC-01636	109.0	110.0	1.0	513277.0	8115962.8	777.7	902.9	886.0	137.9	111.7	11.3	149.2	132.5	503.6	31.4	106.5	17.1	5.5	12.9	1.7	9.6	1.7	4.8	0.7	4.1	0.6	53.3	16.9	126.7	6.1	13.3	3.3
Target A	RC-TGA-0017	TGA-RC-01637	110.0	111.0	1.0	513277.0	8115962.8	777.7	785.5	773.3	125.6	88.2	9.7	135.3	119.0	437.3	28.5	97.0	15.4	4.9	11.5	1.6	8.1	1.5	3.8	0.5	3.0	0.4	40.6	12.3	113.9	5.7	13.0	3.4
Target A	RC-TGA-0017	TGA-RC-01638	111.0	112.0	1.0	513277.0	8115962.8	777.7	676.9	664.6	119.9	83.1	8.9	128.8	119.6	340.3	27.4	92.5	14.0	4.9	10.4	1.4	7.5	1.3	3.4	0.5	2.8	0.4	38.1	12.3	114.2	5.5	12.9	3.3
Target A	RC-TGA-0017	TGA-RC-01639	112.0	113.0	1.0	513277.0	8115962.8	777.7	924.8	907.9	137.5	102.8	10.7	148.2	134.9	533.1	31.7	105.8	16.6	5.4	12.7	1.7	9.0	1.6	4.3	0.6	3.6	0.5	46.4	16.9	122.9	5.9	13.1	3.3
Target A	RC-TGA-0017	TGA-RC-01640	113.0	114.0	1.0	513277.0	8115962.8	777.7	710.1	696.3	122.3	86.3	9.3	131.6	124.3	362.4	28.0	94.3	14.8	5.0	11.2	1.5	7.8	1.4	3.7	0.5	2.8	0.4	38.1	13.8	110.1	5.4	12.6	3.2
Target A	RC-TGA-0017	TGA-RC-01641	114.0	115.0	1.0	513277.0	8115962.8	777.7	413.4	404.2	85.5	62.7	6.8	92.3	87.7	166.5	19.6	65.9	11.0	4.2	7.9	1.1	5.8	1.0	2.7	0.4	2.3	0.3	27.9	9.2	76.8	3.9	9.4	2.3
Target A	RC-TGA-0017	TGA-RC-01643	115.0	116.0	1.0	513277.0	8115962.8	777.7	1,168.3	1,157.5	151.5	107.7	11.5	163.0	146.0	744.4	33.7	117.8	18.7	6.2	13.2	1.8	9.7	1.7	4.9	0.6	3.9	0.5	54.5	10.7	115.0	5.4	12.0	3.2
Target A	RC-TGA-0017	TGA-RC-01644	116.0	117.0	1.0	513277.0	8115962.8	777.7	825.9	815.2	123.6	90.1	9.9	133.5	124.3	472.9	27.7	95.9	15.0	4.9	10.9	1.6	8.4	1.4	4.0	0.5	3.4	0.5	43.8	10.7	120.2	5.7	12.4	3.1
Target A	RC-TGA-0017	TGA-RC-01645	117.0	118.0	1.0	513277.0	8115962.8	777.7	907.3	896.6	136.7	93.7	10.5	147.2	138.4	522.1	30.6	106.1	16.5	5.3	11.3	1.7	8.8	1.6	3.7	0.5	3.2	0.5	46.4	10.7	132.9	6.6	13.3	3.3
Target A	RC-TGA-0017	TGA-RC-01646	118.0	119.0	1.0	513277.0	8115962.8	777.7	665.7	656.5	110.4	77.6	8.7	119.1	114.2	350.1	24.9	85.5	13.4	4.4	9.6	1.3	7.4	1.3	3.4	0.4	2.7	0.4	37.5	9.2	120.2	6.0	11.0	2.7
Target A	RC-TGA-0017	TGA-RC-01647	119.0	120.0	1.0	513277.0	8115962.8	777.7	582.4	571.6	106.0	77.1	8.6	114.6	111.2	276.4	23.9	82.1	11.7	3.9	8.9	1.3	7.3	1.3	3.5	0.4	2.5	0.4	37.0	10.7	125.3	6.2	11.8	2.8
Target A	RC-TGA-0018	TGA-RC-01648	0.0	1.0	1.0	513525.8	8115412.8	766.7	430.3	335.2	62.3	158.1	7.1	69.4	67.8	134.5	14.3	48.1	7.6	1.7	5.6	0.9	6.2	1.2	3.6	0.6	4.5	0.7	38.0	95.1	72.7	4.8	54.4	27.9
Target A	RC-TGA-0018	TGA-RC-01649	1.0	2.0	1.0	513525.8	8115412.8	766.7	387.0	313.4	54.9	134.0	6.4	61.3	62.6	129.0	12.8	42.1	6.5	1.4	4.7	0.8	5.6	1.1	3.8	0.6	4.6	0.7	37.1	73.6	72.2	4.9	52.7	21.9
Target A	RC-TGA-0018	TGA-RC-01651	2.0	3.0	1.0	513525.8	8115412.8	766.7	376.5	309.0	57.2	127.0	6.5	63.7	66.1	119.3	13.6	43.6	6.9	1.4	4.5	0.9	5.6	1.2	3.6	0.6	4.2	0.7	36.7	67.5	62.5	4.2	60.0	19.2
Target A	RC-TGA-0018	TGA-RC-01652	3.0	4.0	1.0	513525.8	8115412.8	766.7	361.2	293.7	48.3	140.7	6.7	55.0	54.9	111.4	11.4	37.0	5.8	1.1	4.7	0.9	5.8	1.3	4.6	0.7	6.4	1.0	46.6	67.5	80.8	6.6	63.8	18.9
Target A	RC-TGA-0018	TGA-RC-01653	4.0	5.0	1.0	513525.8	8115412.8	766.7	265.3	222.4	27.1	127.0	7.0	34.1	30.7	76.9	6.5	20.6	3.5	0.6	3.9	0.8	6.1	1.5	5.4	0.9	7.1	1.2	56.5	42.9	80.5	8.9	40.2	12.1
Target A	RC-TGA-0018	TGA-RC-01654	5.0	6.0	1.0	513525.8	8115412.8	766.7	274.4	237.6	31.1	129.4	7.7	38.8	35.1	74.6	7.3	23.8	4.2	0.7	4.1	0.9	6.8	1.6	6.0	1.1	7.9	1.3	62.2	36.8	81.8	9.6	37.3	14.3
Target A	RC-TGA-0018	TGA-RC-01655	6.0	7.0	1.0	513525.8	8115412.8	766.7	407.9	354.2	61.1	121.8	7.3	68.4	67.6	149.9	14.4	46.7	7.6	1.7	6.0	1.0	6.3	1.3	4.1	0.7	4.9	0.8	41.4	53.7	90.6	6.5	49.0	18.5
Target A	RC-TGA-0018	TGA-RC-01656	7.0	8.0	1.0	513525.8	8115412.8	766.7	296.5	247.4	43.5	103.5	5.4	49.0	54.8	89.1	10.4	33.1	5.6	0.9	4.4	0.7	4.7	1.0	3.3	0.6	3.9	0.6	34.3	49.1	233.9	12.9	28.8	35.0
Target A	RC-TGA-0018	TGA-RC-01657	8.0	9.0	1.0	513525.8	8115412.8	766.7	409.7	349.9	60.5	105.8	5.2	65.8	90.8	145.6	14.8	45.7	7.0	1.2	5.5	0.8	4.5	0.9	2.8	0.4	3.2	0.5	26.3	59.8	347.6	18.4	33.7	45.4
Target A	RC-TGA-0018	TGA-RC-01659	9.0	10.0	1.0	513525.8	8115412.8	766.7	496.8	420.1	70.5	123.6	5.6	76.1	127.2	167.7	18.4	52.1	7.7	1.3	5.6	0.8	4.8	0.9	2.7	0.5	3.0	0.5	27.0	76.7	369.1	18.4	35.7	39.4
Target A	RC-TGA-0018	TGA-RC-01660	10.0	11.0	1.0	513525.8	8115412.8	766.7	832.7	762.2	125.0	130.6	7.5	132.5	259.2	305.9	32.9	92.1	12.1	2.2	8.9	1.2	6.3	1.1	3.4	0.5	3.2	0.5	32.8	70.6	307.6	15.3	31.4	38.1
Target A	RC-TGA-0018	TGA-RC-01661	11.0	12.0	1.0	513525.8	8115412.8	766.7	498.5	406.5	67.2	130.5	4.8	72.0	133.7	160.3	17.8	49.5	6.8	1.1	5.1	0.7	4.0	0.7	2.3	0.4	2.5	0.4	21.2	92.0	367.6	18.3	36.8	38.7
Target A	RC-TGA-0018	TGA-RC-01662	12.0	13.0	1.0	513525.8	8115412.8	766.7	557.1	449.7	81.5	146.9	5.4	86.9	124.9	194.7	20.7	60.9	9.1	1.6	6.5	0.9	4.5	0.8	2.3	0.4	2.3	0.4	19.9	107.4	326.2	15.6	32.0	34.4
Target A	RC-TGA-0018	TGA-RC-01663	13.0	14.0	1.0	513525.8	8115412.8	766.7	849.9	756.3	150.8	176.4	11.0	161.8	204.1	301.0	36.9	114.0	17.6	3.1	12.7	1.7	9.3	1.6	4.3	0.7	4.2	0.6	44.6	93.6	267.5	12.6	29.7	26.4
Target A	RC-TGA-0018	TGA-RC-01664	14.0	15.0	1.0	513525.8	8115412.8	766.7	1,031.1	945.2	228.6	242.0	21.7	250.4	163.6	361.1	50.7	177.9	35.7	5.9	24.7	3.6	18.1	3.0	8.1	1.1	7.5	1.0	83.1	85.9	213.1	10.3	21.8	24.4
Target A	RC-TGA-0018	TGA-RC-01666	15.0	16.0	1.0	513525.8	8115412.8	766.7	3,922.5	3,842.7	989.5	823.1	96.8	1,086.4	538.3	1,412.7	215.1	774.5	158.9	25.1	109.5	15.7	81.1	13.8	37.0	5.6	37.7	5.0	412.7	79.8	198.1	10.1	20.9	24.2
Target A	RC-TGA-0018	TGA-RC-01667	16.0	17.0	1.0	513525.8	8115412.8	766.7	1,226.9	1,139.5	289.3	345.5	31.1	320.4	141.3	404.1	59.0	230.4	46.6	7.8	35.4	5.0	26.1	4.8	13.2	2.0	12.9	1.8	149.2	87.4	181.0	10.0	19.6	11.8
Target A	RC-TGA-0018	TGA-RC-01668	17.0	18.0	1.0	513525.8	8115412.8	766.7	6,745.9	6,678.5	624.6	5,125.8	472.0	1,096.6	197.0	603.1	104.4	520.2	195.4	46.4	314.7	58.8	413.2	90.5	279.0	43.1	289.2	43.9	3,479.5	67.5	164.5	8.8	17.5	6.7
Target A	RC-TGA-0018	TGA-RC-01669	18.0	19.0	1.0	513525.8	8115412.8	766.7	3,924.1	3,858.1	516.3	2,370.0	230.0	746.3	223.4	689.1	95.2	421.1	125.2	28.4	168.3	30.3	199.7	43.0	132.1	20.2	137.8	20.5	1,523.9	66.0	159.5	8.9	20.3	8.1
Target A	RC-TGA-0018	TGA-RC-01670	19.0	20.0	1.0	513525.8	8115412.8	766.7	787.4	732.2	159.7	214.8	19.3	179.1	151.3	237.7	34.9	124.8	23.9	4.6	19.5	3.0	16.4	3.0	8.8	1.3	9.0	1.3	92.7	55.2	190.3	13.4	22.4	9.3
Target A	RC-TGA-0018	TGA-RC-01671	20.0	21.0	1.0	513525.8	8115412.8	766.7	747.7	680.2	150.8	185.5	15.3	166.1	146.6	243.8	33.6	117.2	20.9	4.4	17.1	2.4	12.9	2.3	6.0	0.9	5.8	0.8	65.4	67.5	190.3	10.1	23.3	8.6
Target A	RC-TGA-0018	TGA-RC-01673	21.0	22.0	1.0	513525.8	8115412.8	766.7	680.0	617.1	129.8	179.5	14.1	143.9	109.4	243.2	29.1	100.7	18.0	3.9	14.5	2.1	12.0	2.2	6.5	0.9	6.6	0.9	66.9	62.9	157.4	9.5	23.9	8.3
Target A	RC-TGA-0018	TGA-RC-01674	22.0	23.0	1.0	513525.8	8115412.8	766.7	483.0	437.0	88.2	130.3	9.6	97.8	93.0	159.7	20.5	67.8	11.8	2.6	9.6	1.4	8.2	1.6	4.7	0.8	5.2	0.8	49.5	46.0	122.0	9.4	24.6	9.8
Target A	RC-TGA-0018	TGA-RC-01675	23.0	24.0	1.0	513525.8	8115412.8	766.7	312.2	290.8	47.4	126.0	9.7	57.1	46.9	84.6	11.0	36.4	7.3	1.2	6.7	1.3	8.4	1.9	6.2	1.1	7.9	1.2	68.7	21.5	97.0	8.8	28.1	8.1
Target A	RC-TGA-0018	TGA-RC-01676	24.0	25.0	1.0	513525.8	8115412.8	766.7	707.8	667.9	135.1	137.2	11.7	146.8	161.3	258.0	31.4	103.7	16.3	4.0	13.6	1.8	9.9	1.9	5.0	0.7	4.4	0.6	55.4	39.9	174.5	7.9	18.2	10.5
Target A	RC-TGA-0018	TGA-RC-01677	25.0	26.0	1.0	513525.8	8115412.8	766.7	713.0	642.4	129.8	181.9	13.3	143.1	143.7	240.8	30.0	99.8	16.8	3.9	14.4	2.1	11.2	2.0	5.6	0.8	5.3	0.8	65.3	70.6	139.8	7.4	19.1	8.9
Target A	RC-TGA-0018	TGA-RC-01678	26.0	27.0	1.0	513525.8	8115412.8	766.7	1,048.6	978.0	177.7	388.5	27.1	204.8	139.6	318.2	37.7	140.0	24.7	6.0	22.9	3.8	23.3	5.6	17.6	2.9	21.5	3.5	210.8	70.6	155.9	9.2	22.9	10.8
Target A	RC-TGA-0018	TGA-RC-01679	27.0	28.0	1.0	513525.8	8115412.8	766.7	482.0	440.6	83.8	163.7	12.4	96.2	67.9	154.2	17.5	66.3	12.5	2.4	10.4	1.8	10.6	2.3	7.4	1.1	8.7	1.3	76.2	41.4	113.0	9.4	26.7	9.1
Target A	RC-TGA-0018	TGA-RC-01680	28.0	29.0	1.0	513525.8	8115412.8	766.7	396.8	390.7	41.8	247.2	21.4	63.2	28.9	69.0	8.7	33.1	9.9	0.5	11.9	2.6	18.8	4.6	15.5	2.7	18.9	3.0	162.5	6.1	61.1	11.4	42.7	14.9
Target A	RC-TGA-0018	TGA-RC-01681	29.0	30.0	1.0	513525.8	8115412.8	766.7	421.8	415.7	47.7	244.7	22.3	69.9	34.7	83.8	10.4	37.3	10.9	0.5	12.0	2.7	19.6	4.4	15.0	2.5	18.4	2.8	160.6	6.1	65.1	11.0	44.0	12.2
Target A	RC-TGA-0018	TGA-RC-01682	30.0	31.0	1.0	513525.8	8115412.8	766.7	556.7	516.8	98.8	184.4	15.3	114.0	78.9	179.3	20.7	78.0	15.2	2.8	12.7	2.2	13.0	2.8	8.9	1.5	9.9	1.5	89.1	39.9	112.2	9.5	32.0	9.0
Target A	RC-TGA-0018	TGA-RC-01683	31.0	32.0	1.0	513525.8	8115412.8	766.7	574.3	502.2	112.6	163.1	10.8	123.4	98.5	185.5	24.3	88.3	14.7	3.6	11.0	1.6	9.2	1.7	4.8	0.7	4.7	0.7	53.0	72.1	149.5	8.9	20.1	6.0
Target A	RC-TGA-0018	TGA-RC-01685	32.0	33.0	1.0	513525.8	8115412.8	766.7	517.4	456.1	94.2	143.4	9.8	104.0	80.9	186.1	20.1	74.1	12.8	3.0	9.9	1.4	8.5	1.5	4.4	0.6	4.2	0.6	48.0	61.4	149.5	9.0	20.1	7.0
Target A	RC-TGA-0018	TGA-RC-01686	33.0	34.0	1.0	513525.8	8115412.8	766.7	523.4	488.1	95.6	147.5	11.5	107.1	84.0	183.0	20.6	75.0	13.3	2.7	10.7	1.7	9.8	2.1	6.5	1.0	7.2	1.1	69.3	35.3	142.8	10.1	25.9	7.4
Target A	RC-TGA-0018	TGA-RC-01687	34.0	35.0	1.0	513525.8	8115412.8	766.7	339.0	334.4	38.2	202.8	18.8	57.1	26.2	63.0	8.2	30.1	8.7	0.3	10.3	2.3	16.5	3.7	12.2	2.2	15.5	2.4	132.7	4.6	53.1	10.7	39.6	6.1
Target A	RC-TGA-0018	TGA-RC-01688	35.0	36.0	1.0	513525.8	8115412.8	766.7	444.8	411.1	70.1	164.5	12.8	82.9	61.1	138.2	15.5	54.6	11.0	1.8	9.4	1.7	11.1	2.5	7.6	1.2	9.3	1.3	84.7	33.7	118.6	11.1	30.3	6.6
Target A	RC-TGA-0018	TGA-RC-01689	36.0	37.0	1.0	513525.8	8115412.8	766.7	619.9	540.1	116.9	173.2	10.7	127.7	101.2	213.7	24.9	92.0	14.8	3.7	11.8	1.6	9.1	1.8	4.8	0.7	4.5	0.7	54.7	79.8	153.1	9.5	17.1	4.5
Target A	RC-TGA-0018	TGA-RC-01690	37.0	38.0	1.0	513525.8	8115412.8	766.7	533.4	433.7	95.8	168.8	8.2	104.0	87.3	168.3	20.2	75.6	13.2	3.3	9.6	1.3	6.9	1.3	3.4	0.5	3.1	0.4	39.4	99.7	125.7	6.5	13.1	3.8
Target A	RC-TGA-0018	TGA-RC-01691	38.0	39.0	1.0	513525.8	8115412.8	766.7	561.9	479.1	105.9	158.7	8.8	114.7	92.2	191.0	22.5	83.4	14.1	3.8	10.5	1.4	7.4	1.3	3.5	0.5	3.3	0.5	43.6	82.8	135.2	7.4	12.0	3.7
Target A	RC-TGA-0018	TGA-RC-01693	39.0	40.0	1.0	513525.8	8115412.8	766.7	465.7	356.8	82.0	168.8	6.8	88.8	63.9	139.4	16.9	65.1	11.5	2.9	8.3	1.1	5.7	1.1	2.9	0.4	2.5	0.4	34.7	108.9	94.7	5.3	8.2	2.6
Target A	RC-TGA-0018	TGA-RC-01694	40.0	41.0	1.0	513525.8	8115412.8	766.7	560.3	476.0	107.2	156.6	8.8	116.1	90.0	192.2	22.8	84.4	14.3	3.4	10.4	1.4	7.4	1.3	3.4	0.5	2.9	0.4	41.0	84.4	141.8	8.3	12.0	3.6
Target A	RC-TGA-0018	TGA-RC-01695	41.0	42.0	1.0	513525.8	8115412.8	766.7	524.7	438.8	98.2	151.1	8.0	106.2	83.0	179.3	20.6	77.6	13.0	3.4	9.8	1.3	6.7	1.2	3.3	0.5	2.7	0.4	35.9	85.9	127.9	7.1	11.1	3.3
Target A	RC-TGA-0018	TGA-RC-01696	42.0	43.0	1.0	513525.8	8115412.8	766.7	489.0	398.5	90.7	152.1	7.3	98.0	73.8	160.3	19.0	71.7	12.2	3.0	9.0	1.2	6.1	1.1	3.0	0.4	2.6	0.4	34.8	90.5	113.9	6.5	10.2	3.1
Target A	RC-TGA-0018	TGA-RC-01697	43.0	44.0	1.0	513525.8	8115412.8	766.7	513.5	427.6	96.5	149.9	7.9	104.4	80.3	173.8	20.6	75.9	12.9	3.3	9.1	1.2	6.7	1.2	3.1	0.4	2.7	0.4	35.9	85.9	125.3	7.3	10.6	3.5
Target A	RC-TGA-0018	TGA-RC-01698	44.0	45.0	1.0	513525.8	8115412.8	766.7	479.9	400.1	90.5	140.3	7.6	98.2	74.8	162.1	19.2	71.4	12.1	3.1	9.1	1.2	6.5	1.2	2.9	0.4	2.5	0.4	33.4	79.8	114.0	6.7	10.1	3.3
Target A	RC-TGA-0018	TGA-RC-01699	45.0	46.0	1.0	513525.8	8115412.8	766.7	485.4	394.9	89.9	151.1	7.4	97.4	73.1	159.7	18.7	71.3	11.7	2.8	9.0	1.2	6.2	1.1	2.8	0.4	2.4	0.4	34.2	90.5	111.4	6.7	9.9	3.0
Target A	RC-TGA-0018	TGA-RC-01701	46.0	47.0	1.0	513525.8	8115412.8	766.7	478.7	391.2	89.8	147.0	7.4	97.1	72.1	157.8	18.6	71.2	11.9	3.3	8.7	1.1	6.2	1.1	2.7	0.4	2.5	0.4	33.1	87.4	111.0	6.6	9.7	3.0
Target A	RC-TGA-0018	TGA-RC-01702	47.0	48.0	1.0	513525.8	8115412.8	766.7	481.8	400.5	89.8	141.2	7.2	97.0	75.6	162.8	19.0	70.8	12.3	2.9	8.7	1.2	6.0	1.1	2.8	0.4	2.5	0.4	33.9	81.3	119.4	7.1	10.1	3.2
Target A	RC-TGA-0018	TGA-RC-01703	48.0	49.0	1.0	513525.8	8115412.8	766.7	510.6	430.8	97.0	143.7	7.6	104.6	81.3	175.7	20.3	76.7	12.9	3.1	9.3	1.2	6.4	1.2	3.0	0.4	2.5	0.4	36.6	79.8	127.0	7.3	10.6	3.3
Target A	RC-TGA-0018	TGA-RC-01704	49.0	50.0	1.0	513525.8	8115412.8	766.7	472.7	385.3	86.2	150.7	7.7	93.9	69.5	154.2	18.2	68.0	12.1	2.9	8.9	1.2	6.5	1.2	3.1	0.4	2.8	0.5	35.8	87.4	109.4	6.2	10.9	2.9
Target A	RC-TGA-0018	TGA-RC-01705	50.0	51.0	1.0	513525.8	8115412.8	766.7	420.7	339.4	77.1	133.5	6.3	83.4	62.6	137.0	16.1	61.0	10.5	2.5	7.7	1.0	5.2	1.0	2.5	0.4	2.2	0.3	29.2	81.3	96.4	5.7	8.6	2.5
Target A	RC-TGA-0018	TGA-RC-01706	51.0	52.0	1.0	513525.8	8115412.8	766.7	405.3	344.0	76.4	110.9	6.0	82.4	66.7	141.3	16.7	59.7	10.1	2.6	7.2	1.0	5.0	1.0	2.4	0.3	2.0	0.3	27.7	61.4	106.0	6.0	8.5	1.7
Target A	RC-TGA-0018	TGA-RC-01708	52.0	53.0	1.0	513525.8	8115412.8	766.7	472.2	426.2	92.1	104.6	7.3	99.5	85.0	178.7	20.2	72.0	11.7	2.9	8.5	1.2	6.2	1.1	2.9	0.4	2.4	0.4	32.6	46.0	145.9	8.3	12.6	1.8
Target A	RC-TGA-0018	TGA-RC-01709	53.0	54.0	1.0	513525.8	8115412.8	766.7	450.5	398.4	88.3	108.2	7.0	95.3	77.5	165.2	19.1	69.2	11.3	2.9	8.3	1.2	5.9	1.1	2.7	0.4	2.5	0.4	30.9	52.1	126.3	7.1

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0018	TGA-RC-01719	62.0	63.0	1.0	513525.8	8115412.8	766.7	459.2	367.2	81.9	167.6	8.9	90.8	56.6	139.4	17.2	64.7	13.6	2.9	9.5	1.5	7.4	1.5	3.8	0.6	3.7	0.5	44.2	92.0	72.0	3.8	6.9	2.2
Target A	RC-TGA-0018	TGA-RC-01720	63.0	64.0	1.0	513525.8	8115412.8	766.7	506.2	434.1	94.4	155.9	9.8	104.3	73.9	167.7	20.8	73.6	14.3	3.3	10.6	1.6	8.2	1.5	4.1	0.7	4.2	0.6	48.9	72.1	103.6	5.5	10.5	3.6
Target A	RC-TGA-0018	TGA-RC-01722	64.0	65.0	1.0	513525.8	8115412.8	766.7	792.8	713.0	163.8	243.9	19.1	182.9	98.3	259.2	32.6	131.2	27.6	5.4	19.3	3.0	16.1	3.0	8.3	1.3	8.6	1.2	97.9	79.8	97.6	5.4	10.2	3.8
Target A	RC-TGA-0018	TGA-RC-01723	65.0	66.0	1.0	513525.8	8115412.8	766.7	791.2	726.8	162.8	227.1	18.8	181.7	105.8	269.0	34.0	128.9	26.4	5.5	19.4	2.9	16.0	3.2	8.3	1.3	8.5	1.2	96.5	64.4	110.0	6.0	11.2	4.0
Target A	RC-TGA-0018	TGA-RC-01724	66.0	67.0	1.0	513525.8	8115412.8	766.7	1,250.1	1,191.8	261.3	333.5	32.9	294.2	171.2	442.2	54.2	207.0	41.9	8.5	31.9	5.0	27.9	5.3	14.1	2.2	14.3	2.1	163.8	58.3	148.1	7.1	16.6	6.5
Target A	RC-TGA-0018	TGA-RC-01725	67.0	68.0	1.0	513525.8	8115412.8	766.7	1,037.8	1,013.3	219.8	212.7	22.6	242.3	168.9	402.9	47.7	172.0	33.5	6.8	23.6	3.6	19.0	3.5	9.8	1.5	9.7	1.4	109.3	24.5	178.1	7.9	22.4	5.9
Target A	RC-TGA-0018	TGA-RC-01726	68.0	69.0	1.0	513525.8	8115412.8	766.7	911.6	890.1	186.9	237.9	23.6	210.5	139.0	318.2	39.4	147.5	29.7	5.6	22.0	3.5	20.1	4.1	11.8	2.0	13.3	1.9	132.1	21.5	153.8	8.2	34.4	6.6
Target A	RC-TGA-0018	TGA-RC-01727	69.0	70.0	1.0	513525.8	8115412.8	766.7	415.6	409.5	48.1	244.3	21.5	69.6	32.7	78.9	10.4	37.7	11.7	0.6	11.6	2.7	18.8	4.3	14.0	2.6	18.8	2.9	161.9	6.1	59.5	9.4	37.1	9.9
Target A	RC-TGA-0018	TGA-RC-01728	70.0	71.0	1.0	513525.8	8115412.8	766.7	463.4	451.2	61.0	241.1	20.0	81.1	47.0	101.7	13.1	47.9	12.5	1.0	12.3	2.5	17.5	4.0	13.4	2.5	17.4	2.7	155.6	12.3	80.5	10.0	37.2	9.6
Target A	RC-TGA-0018	TGA-RC-01729	71.0	72.0	1.0	513525.8	8115412.8	766.7	486.2	481.6	48.6	308.3	26.3	75.0	34.7	82.1	10.7	37.9	12.5	0.3	13.8	3.2	23.2	5.3	18.2	3.4	23.8	3.6	208.9	4.6	59.7	10.3	59.4	15.4
Target A	RC-TGA-0018	TGA-RC-01730	72.0	73.0	1.0	513525.8	8115412.8	766.7	421.1	418.0	42.5	270.5	22.9	65.4	28.6	68.2	8.9	33.6	11.2	0.2	12.1	2.8	20.1	4.7	16.0	2.9	21.4	3.1	184.1	3.1	53.9	10.4	46.8	14.0
Target A	RC-TGA-0018	TGA-RC-01731	73.0	74.0	1.0	513525.8	8115412.8	766.7	434.1	429.5	47.2	259.3	22.2	69.4	35.3	80.5	10.0	37.2	11.8	0.5	11.6	2.8	19.5	4.5	14.9	2.8	19.8	3.1	175.2	4.6	64.8	11.4	40.2	16.1
Target A	RC-TGA-0018	TGA-RC-01732	74.0	75.0	1.0	513525.8	8115412.8	766.7	601.7	569.5	101.4	201.3	16.3	117.7	91.5	191.6	22.5	78.8	15.9	2.9	12.8	2.2	14.1	3.0	9.5	1.6	11.7	1.8	109.5	32.2	148.1	11.0	29.1	13.4
Target A	RC-TGA-0018	TGA-RC-01733	75.0	76.0	1.0	513525.8	8115412.8	766.7	408.5	403.9	43.4	256.0	22.2	65.6	28.7	69.8	9.2	34.2	10.6	0.2	11.9	2.7	19.5	4.4	15.3	2.7	20.0	3.2	171.4	4.6	61.9	10.5	43.6	25.1
Target A	RC-TGA-0018	TGA-RC-01735	76.0	77.0	1.0	513525.8	8115412.8	766.7	506.5	491.2	70.8	229.1	19.1	89.9	61.9	131.4	15.9	54.9	13.2	1.3	11.8	2.5	16.6	3.7	12.4	2.3	15.9	2.5	144.8	15.3	100.7	9.9	34.0	20.3
Target A	RC-TGA-0018	TGA-RC-01736	77.0	78.0	1.0	513525.8	8115412.8	766.7	583.4	557.4	98.3	207.3	17.2	115.5	83.9	178.7	21.7	76.6	15.2	2.4	12.7	2.3	14.9	3.2	10.4	1.8	12.6	2.0	119.0	26.1	141.9	10.5	28.9	13.9
Target A	RC-TGA-0018	TGA-RC-01737	78.0	79.0	1.0	513525.8	8115412.8	766.7	504.5	493.8	71.7	230.8	20.1	91.8	58.1	130.2	15.8	55.9	13.7	1.4	12.8	2.6	17.5	3.8	13.0	2.4	17.3	2.6	146.7	10.7	105.9	12.0	40.3	23.3
Target A	RC-TGA-0018	TGA-RC-01738	79.0	80.0	1.0	513525.8	8115412.8	766.7	333.4	327.3	38.5	189.4	17.1	55.6	29.4	67.8	8.4	30.1	8.3	0.5	9.4	2.1	15.0	3.4	11.2	2.0	15.0	2.3	122.3	6.1	66.4	10.5	29.5	20.1
Target A	RC-TGA-0018	TGA-RC-01739	80.0	81.0	1.0	513525.8	8115412.8	766.7	406.0	401.4	45.2	240.5	20.6	65.8	33.0	76.4	9.6	35.6	10.8	0.4	11.4	2.5	18.1	4.2	14.1	2.7	18.6	2.7	161.3	4.6	63.7	9.3	39.6	23.1
Target A	RC-TGA-0018	TGA-RC-01740	81.0	82.0	1.0	513525.8	8115412.8	766.7	541.8	518.8	89.0	201.3	16.7	105.7	75.1	162.1	19.6	69.4	14.3	2.1	12.2	2.2	14.5	3.1	10.4	1.9	12.6	1.9	117.3	23.0	137.0	10.5	31.2	16.2
Target A	RC-TGA-0018	TGA-RC-01741	82.0	83.0	1.0	513525.8	8115412.8	766.7	400.5	392.8	46.1	229.8	19.2	65.3	34.1	80.2	9.7	36.4	10.3	0.6	11.9	2.4	16.9	3.8	13.5	2.4	19.2	2.9	148.6	7.7	66.2	10.3	39.0	14.3
Target A	RC-TGA-0018	TGA-RC-01743	83.0	84.0	1.0	513525.8	8115412.8	766.7	394.8	391.7	39.1	253.0	21.5	60.6	26.3	66.2	8.3	30.8	10.2	0.2	12.9	2.6	18.9	4.5	15.0	2.8	22.1	3.2	167.6	3.1	54.5	10.5	42.3	14.7
Target A	RC-TGA-0018	TGA-RC-01744	84.0	85.0	1.0	513525.8	8115412.8	766.7	484.3	461.2	71.7	210.4	17.1	88.7	58.5	131.4	15.0	56.7	12.2	1.7	12.2	2.1	14.9	3.3	10.8	1.9	15.3	2.2	122.9	23.0	104.3	10.7	33.9	12.8
Target A	RC-TGA-0018	TGA-RC-01745	85.0	86.0	1.0	513525.8	8115412.8	766.7	548.7	491.9	108.9	114.2	7.0	116.0	100.3	211.3	23.3	85.6	14.0	3.6	9.8	1.2	5.9	1.0	2.7	0.4	2.4	0.3	30.2	56.8	163.1	8.9	13.3	5.7
Target A	RC-TGA-0018	TGA-RC-01746	86.0	87.0	1.0	513525.8	8115412.8	766.7	502.2	465.4	91.7	162.8	12.9	104.6	75.6	157.8	19.2	72.6	14.2	2.6	11.9	1.7	11.2	2.3	6.8	1.2	8.6	1.2	78.5	36.8	121.9	9.0	22.7	8.2
Target A	RC-TGA-0018	TGA-RC-01747	87.0	88.0	1.0	513525.8	8115412.8	766.7	554.2	512.8	100.6	160.1	12.3	112.9	88.7	190.4	21.6	79.1	14.4	3.1	12.1	1.8	10.5	2.2	6.4	1.0	7.8	1.1	72.6	41.4	147.3	10.4	21.7	7.6
Target A	RC-TGA-0018	TGA-RC-01748	88.0	89.0	1.0	513525.8	8115412.8	766.7	546.9	516.3	93.2	183.7	14.6	107.8	80.5	175.7	19.9	73.2	14.0	2.5	12.4	2.0	12.6	2.7	8.7	1.4	11.2	1.6	97.8	30.7	133.8	10.9	26.3	10.8
Target A	RC-TGA-0018	TGA-RC-01750	89.0	90.0	1.0	513525.8	8115412.8	766.7	622.7	590.5	105.8	197.7	15.1	120.9	97.0	206.4	22.8	83.0	15.8	2.8	14.0	2.2	12.9	2.9	9.1	1.6	11.4	1.8	106.8	32.2	148.8	11.6	28.4	8.7
Target A	RC-TGA-0018	TGA-RC-01751	90.0	91.0	1.0	513525.8	8115412.8	766.7	580.2	546.4	101.1	168.7	13.1	114.2	97.8	197.8	22.3	78.8	14.7	2.9	11.3	1.9	11.2	2.4	7.6	1.2	8.7	1.4	86.4	33.7	140.0	9.2	23.0	10.0
Target A	RC-TGA-0018	TGA-RC-01752	91.0	92.0	1.0	513525.8	8115412.8	766.7	393.4	390.3	38.3	250.1	21.2	59.5	28.1	66.3	8.1	30.2	10.6	0.2	11.4	2.6	18.7	4.4	16.0	2.8	20.0	3.3	167.6	3.1	55.6	10.3	42.0	24.8
Target A	RC-TGA-0018	TGA-RC-01753	92.0	93.0	1.0	513525.8	8115412.8	766.7	372.2	369.1	33.9	245.7	21.1	54.9	24.9	57.7	7.3	26.6	10.0	0.2	11.3	2.6	18.5	4.4	15.9	2.7	19.6	3.0	164.5	3.1	46.5	9.0	41.8	21.3
Target A	RC-TGA-0018	TGA-RC-01754	93.0	94.0	1.0	513525.8	8115412.8	766.7	377.7	374.6	35.6	240.2	21.0	56.5	27.9	63.9	7.7	27.9	10.1	0.2	11.5	2.5	18.4	4.2	15.0	2.7	19.5	3.1	160.0	3.1	54.1	9.8	39.1	23.7
Target A	RC-TGA-0018	TGA-RC-01755	94.0	95.0	1.0	513525.8	8115412.8	766.7	372.2	367.6	37.3	232.0	20.7	58.0	27.8	64.6	8.0	29.3	10.5	0.3	11.3	2.5	18.2	4.1	14.1	2.6	18.4	3.0	153.0	4.6	55.2	9.9	38.7	27.2
Target A	RC-TGA-0018	TGA-RC-01757	95.0	96.0	1.0	513525.8	8115412.8	766.7	361.2	358.1	34.2	229.7	18.8	53.0	26.9	61.2	7.3	26.9	9.3	0.2	10.5	2.3	16.4	3.9	14.5	2.5	18.3	2.9	154.9	3.1	51.2	9.9	37.7	20.9
Target A	RC-TGA-0018	TGA-RC-01758	96.0	97.0	1.0	513525.8	8115412.8	766.7	615.9	580.7	110.4	155.4	12.6	123.0	111.5	222.3	24.4	86.0	16.3	3.7	12.6	1.9	10.7	2.2	6.7	1.0	7.1	1.1	73.1	35.3	173.8	9.9	21.8	9.8
Target A	RC-TGA-0018	TGA-RC-01759	97.0	98.0	1.0	513525.8	8115412.8	766.7	337.9	334.8	32.5	216.6	19.2	51.7	23.7	55.8	7.0	25.5	9.3	0.2	10.3	2.4	16.8	3.9	13.8	2.4	18.0	2.7	142.9	3.1	46.6	9.9	37.7	17.1
Target A	RC-TGA-0018	TGA-RC-01760	98.0	99.0	1.0	513525.8	8115412.8	766.7	359.2	356.1	35.5	227.7	19.7	55.1	25.4	60.8	7.5	28.0	9.7	0.2	10.9	2.4	17.3	3.9	14.4	2.5	17.9	2.9	152.4	3.1	50.5	10.0	38.8	16.0
Target A	RC-TGA-0018	TGA-RC-01761	99.0	100.0	1.0	513525.8	8115412.8	766.7	607.8	578.7	104.2	175.0	14.3	118.5	104.0	209.4	23.3	80.9	15.1	3.0	12.6	2.0	12.3	2.6	8.4	1.4	9.8	1.5	92.3	29.1	177.4	11.6	27.8	13.1
Target A	RC-TGA-0018	TGA-RC-01762	100.0	101.0	1.0	513525.8	8115412.8	766.7	376.6	373.5	35.1	248.6	20.5	55.7	24.7	58.7	7.4	27.8	9.4	0.2	11.2	2.5	18.0	4.2	15.2	2.8	19.5	3.1	168.9	3.1	49.6	10.0	40.6	19.0
Target A	RC-TGA-0018	TGA-RC-01763	101.0	102.0	1.0	513525.8	8115412.8	766.7	384.8	381.8	36.3	247.8	20.5	56.8	27.3	63.6	7.7	28.6	9.8	0.2	11.6	2.6	18.0	4.3	15.1	2.7	19.5	3.1	167.6	3.1	51.4	10.1	41.8	19.3
Target A	RC-TGA-0018	TGA-RC-01765	102.0	103.0	1.0	513525.8	8115412.8	766.7	376.1	373.0	36.4	241.7	20.1	56.4	25.8	62.8	7.8	28.6	9.4	0.3	11.7	2.5	17.6	4.2	15.0	2.6	19.1	3.0	162.5	3.1	54.5	10.4	40.4	24.4
Target A	RC-TGA-0018	TGA-RC-01766	103.0	104.0	1.0	513525.8	8115412.8	766.7	384.0	381.0	37.0	246.0	21.0	58.0	26.9	64.1	7.9	29.2	10.0	0.2	11.8	2.6	18.4	4.2	15.1	2.7	19.2	3.0	165.7	3.1	57.1	11.4	42.9	23.9
Target A	RC-TGA-0018	TGA-RC-01767	104.0	105.0	1.0	513525.8	8115412.8	766.7	361.7	357.1	34.0	234.4	19.9	53.9	25.3	58.6	7.3	26.7	9.4	0.2	10.8	2.4	17.5	4.0	14.0	2.6	17.9	2.9	157.5	4.6	54.5	9.9	38.5	22.9
Target A	RC-TGA-0018	TGA-RC-01768	105.0	106.0	1.0	513525.8	8115412.8	766.7	401.3	395.2	41.8	243.6	19.7	61.4	32.5	72.8	8.9	32.9	10.6	0.5	11.1	2.5	17.2	4.0	14.6	2.6	18.8	2.9	163.2	6.1	59.5	10.7	38.0	28.1
Target A	RC-TGA-0018	TGA-RC-01769	106.0	107.0	1.0	513525.8	8115412.8	766.7	377.9	374.8	36.5	247.2	21.2	57.6	25.0	59.3	7.5	28.9	9.9	0.2	11.4	2.6	18.6	4.2	15.3	2.9	20.1	3.1	165.7	3.1	54.8	11.4	43.7	25.1
Target A	RC-TGA-0018	TGA-RC-01770	107.0	108.0	1.0	513525.8	8115412.8	766.7	374.6	360.8	47.8	189.0	15.7	63.6	40.3	87.7	10.0	37.8	9.7	1.0	10.4	2.0	13.7	3.1	10.9	1.9	13.5	2.1	116.6	13.8	74.8	9.6	31.7	20.2
Target A	RC-TGA-0018	TGA-RC-01772	108.0	109.0	1.0	513525.8	8115412.8	766.7	458.2	419.8	80.3	136.2	10.1	90.4	74.4	155.4	17.6	62.8	11.9	2.7	9.5	1.5	8.6	1.8	5.5	0.9	5.8	0.9	60.7	38.3	116.3	7.7	17.8	7.6
Target A	RC-TGA-0018	TGA-RC-01773	109.0	110.0	1.0	513525.8	8115412.8	766.7	433.4	424.2	52.1	242.4	21.1	73.2	36.5	89.9	10.8	41.3	12.5	1.1	13.3	2.7	18.4	4.2	14.6	2.5	17.5	2.7	156.2	9.2	64.2	11.7	34.5	20.0
Target A	RC-TGA-0018	TGA-RC-01774	110.0	111.0	1.0	513525.8	8115412.8	766.7	592.4	563.2	85.7	268.6	20.1	105.8	67.9	154.2	18.2	67.5	16.0	3.0	15.0	2.7	17.4	4.0	13.6	2.3	16.4	2.5	162.5	29.1	93.3	9.0	23.9	12.7
Target A	RC-TGA-0018	TGA-RC-01775	111.0	112.0	1.0	513525.8	8115412.8	766.7	504.0	479.4	78.6	192.5	16.0	94.6	69.0	149.9	16.9	61.7	14.0	2.3	11.9	2.2	13.8	3.0	9.9	1.6	11.8	1.9	109.5	24.5	111.6	9.9	25.6	15.0
Target A	RC-TGA-0018	TGA-RC-01776	112.0	113.0	1.0	513525.8	8115412.8	766.7	537.5	511.4	88.0	196.7	16.3	104.3	74.7	163.4	18.5	69.5	14.7	2.7	13.1	2.3	14.0	2.9	10.1	1.7	11.6	1.8	110.5	26.1	118.9	10.1	25.6	14.0
Target A	RC-TGA-0018	TGA-RC-01777	113.0	114.0	1.0	513525.8	8115412.8	766.7	492.3	478.5	67.5	236.1	20.3	87.8	52.3	122.6	14.0	53.5	13.7	1.6	14.1	2.8	17.5	3.9	13.7	2.3	17.1	2.5	146.7	13.8	82.8	11.0	31.4	19.6
Target A	RC-TGA-0018	TGA-RC-01778	114.0	115.0	1.0	513525.8	8115412.8	766.7	394.4	388.3	48.5	209.9	18.9	67.4	33.8	90.9	10.0	38.5	11.3	0.9	11.8	2.5	16.4	3.7	12.9	2.3	16.7	2.6	134.0	6.1	51.1	9.9	30.7	20.8
Target A	RC-TGA-0018	TGA-RC-01779	115.0	116.0	1.0	513525.8	8115412.8	766.7	421.4	415.3	52.7	225.3	19.8	72.6	36.5	95.1	10.8	41.9	11.8	1.0	12.4	2.6	17.3	3.9	13.9	2.4	17.6	2.7	145.4	6.1	55.6	11.2	33.2	19.9
Target A	RC-TGA-0018	TGA-RC-01780	116.0	117.0	1.0	513525.8	8115412.8	766.7	355.3	352.3	35.2	227.4	19.5	54.8	23.8	59.6	7.5	27.8	9.3	0.3	10.9	2.4	17.1	4.1	14.5	2.6	18.6	2.8	151.1	3.1	49.1	10.3	32.9	22.0
Target A	RC-TGA-0018	TGA-RC-01781	117.0	118.0	1.0	513525.8	8115412.8	766.7	324.8	321.7	31.1	211.7	18.2	49.3	21.1	52.2	6.5	24.6	8.6	0.2	10.2	2.2	16.0	3.7	12.8	2.4	16.9	2.7	141.6	3.1	48.1	11.0	32.8	23.7
Target A	RC-TGA-0018	TGA-RC-01782	118.0	119.0	1.0	513525.8	8115412.8	766.7	381.3	372.1	45.7	198.5	16.7	62.4	40.1	87.2	9.9	35.8	9.7	0.8	10.2	2.1	14.5	3.3	11.7	2.1	15.4	2.4	126.7	9.2	76.4	9.6	33.2	22.8
Target A	RC-TGA-0018	TGA-RC-01783	119.0	120.0	1.0	513525.8	8115412.8	766.7	357.2	352.6	36.5	223.6	18.9	55.4	25.7	62.2	7.6	28.9	9.3	0.5	10.4	2.4	16.5	3.9	14.2	2.5	18.6	2.8	147.3	4.6	54.4	9.5	35.2	23.8
Target A	RC-TGA-0019A	TGA-RC-01978	0.0	1.0	1.0	513535.8	8114987.6	757.6	125.0	98.9	8.0	68.2	4.1	12.1	7.7	39.3	1.9	6.1	1.7	0.3	2.0	0.4	3.7	0.9	3.0	0.5	3.6	0.6	27.2	26.1	72.8	6.1	24.2	4.8
Target A	RC-TGA-0019A	TGA-RC-01979	1.0	2.0	1.0	513535.8	8114987.6	757.6	131.1	105.1	7.4	66.8	3.7	11.1	7.2	48.4	1.7	5.7	1.4	0.3	1.7	0.4	3.3	0.9	3.0	0.5	3.4	0.6	26.7	26.1	74.8	6.2	24.9	5.1
Target A	RC-TGA-0019A	TGA-RC-01980	2.0	3.0	1.0	513535.8	8114987.6	757.6	140.1	114.0	7.5	69.2	4.1	11.6	7.6	54.1	1.9	5.6	1.8	0.3	1.8	0.5	3.7	0.9	3.1	0.5	4.0	0.6	27.7	26.1	79.5	6.5	26.1	5.4
Target A	RC-TGA-0019A	TGA-RC-01981	3.0	4.0	1.0	513535.8	8114987.6	757.6	148.1	120.5	8.7	73.1	4.6	13.3	8.0	56.6	2.0	6.8	1.7	0.3	2.0	0.5	4.1	1.0	3.0	0.6	4.0	0.6	29.3	27.6	78.4	6.6	25.4	5.5
Target A	RC-TGA-0019A	TGA-RC-01982	4.0	5.0	1.0	513535.8	8114987.6	757.6	157.6	131.5	11.4	70.6	4.6	16.0	11.0	62.5	2.6	8.8	2.1	0.4	2.2	0.5	4.1	1.0	3.0	0.5	3.8	0.6	28.3	26.1	79.4	6.5	26.4	6.1
Target A	RC-TGA-0019A	TGA-RC-01983	5.0	6.0	1.0	513535.8	8114987.6	757.6	213.6	187.5	26.4	74.5	5.1	31.5	27.3	81.7	6.1	20.3	3.7	0.7	3.2	0.6	4.5	1.1	3.2	0.5	4.1	0.7	30.0	26.1	80.7	6.5	26.3	7.4
Target A	RC-TGA-0019A	TGA-RC-01985	6.0	7.0	1.0	513535.8	8114987.6	757.6	206.3	178.7	23.9	74.7	4.8	28.6	25.3	79.1	5.7	18.2	3.4	0.6	3.0	0.6	4.2	1.0	3.1	0.5	3.9	0.6	29.5	27.6	82.5	7.1	26.2	7.2
Target A	RC-TGA-0019A	TGA-RC-01986	7.0	8.0	1.0	513535.8	8114987.6	757.6	275.3	249.2	46.3	83.2	6.1	52.4	50.2	88.8	10.7	35.6	6.8	1.1	4.7	0.8	5.3	1.1	3.7	0.6	4.3	0.7	34.9	26.1	79.8	6.7	23.1	5.4
Target A	RC-TGA-0019A	TGA-RC-01987	8.0	9.0	1.0	513535.8	8114987.6	757.6	298.7	274.1	53.9	88.3	7.2	61.0	56.5	92.4	12.6	41.3	7.7	1.3	5.6	1.0	6.2	1.4	4.0	0.6	5.0	0.7	37.8	24.5	71.5	6.6	19.3	4.2
Target A	RC-TGA-0019A	TGA-RC-01988	9.0	10.0	1.0	513535.8	8114987.6	757.6	259.3	234.7	42.1	82.8	6.3	48.4	44.3	84.0	9.8	32.3	6.0	1.1	4.8	0.8	5.5	1.2	3.8	0.6	4.6	0.7	35.2	24.5	74.5	6.2	21.8	5.2
Target A	RC-TGA-0019A	TGA-RC-01989	10.0	11.0	1.0	513535.8	8114987.6	757.6	316.9	290.8	58.0	94.1	7.5	65.5	60.4	96.1	13.2	44.8	8.3	1.4	5.9	1.0	6.6	1.5	4.5	0.7	5.0	0.8	40.8	26.1	74.2	6.5	19.6	4.3
Target A	RC-TGA-0019A	TGA-

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0019A	TGA-RC-02000	19.0	20.0	1.0	513535.8	8114987.6	757.6	479.2	462.4	95.9	144.5	14.2	110.1	63.8	157.2	20.0	75.9	17.8	1.8	11.2	1.9	12.3	2.6	8.0	1.4	10.8	1.6	76.1	16.9	88.7	13.9	31.4	4.7
Target A	RC-TGA-0019A	TGA-RC-02001	20.0	21.0	1.0	513535.8	8114987.6	757.6	501.5	492.3	96.2	194.4	21.4	117.7	54.7	136.4	18.7	77.6	19.9	2.0	15.0	2.7	18.8	3.9	11.7	2.1	14.8	1.8	112.4	9.2	66.1	12.3	26.4	5.4
Target A	RC-TGA-0019A	TGA-RC-02002	21.0	22.0	1.0	513535.8	8114987.6	757.6	1,337.7	1,287.1	308.6	323.3	37.3	346.0	166.5	481.5	60.2	248.4	57.8	8.2	39.5	5.6	31.8	5.8	14.8	2.3	16.6	2.0	146.0	50.6	136.6	8.7	22.4	10.9
Target A	RC-TGA-0019A	TGA-RC-02003	22.0	23.0	1.0	513535.8	8114987.6	757.6	1,288.9	1,232.2	283.6	356.9	42.5	326.0	126.7	461.9	53.8	229.8	60.0	9.2	45.3	6.5	36.0	6.4	16.8	2.6	17.4	2.0	158.1	56.8	141.3	7.9	12.9	10.0
Target A	RC-TGA-0019A	TGA-RC-02004	23.0	24.0	1.0	513535.8	8114987.6	757.6	1,918.2	1,853.8	464.0	441.4	57.8	521.8	234.6	683.0	90.7	373.3	95.3	14.1	69.0	9.0	48.8	8.0	19.3	2.8	18.5	2.2	185.4	64.4	155.9	8.5	15.1	9.5
Target A	RC-TGA-0019A	TGA-RC-02005	24.0	25.0	1.0	513535.8	8114987.6	757.6	2,352.2	2,292.4	321.0	1,376.6	156.8	477.8	143.7	416.4	57.4	263.6	94.5	17.7	120.5	20.2	136.6	27.5	76.2	11.9	81.9	10.5	814.0	59.8	155.2	8.5	12.3	6.5
Target A	RC-TGA-0019A	TGA-RC-02006	25.0	26.0	1.0	513535.8	8114987.6	757.6	6,451.5	6,387.1	552.5	5,025.5	561.6	1,114.2	148.4	503.6	84.8	467.7	221.5	50.1	390.7	69.3	492.4	103.8	288.2	44.3	296.1	38.8	3,187.5	64.4	173.1	8.4	19.1	5.5
Target A	RC-TGA-0019A	TGA-RC-02008	26.0	27.0	1.0	513535.8	8114987.6	757.6	1,636.8	1,577.0	258.0	845.5	90.9	348.9	131.9	342.7	48.1	210.0	58.6	11.9	76.4	12.1	78.9	16.3	46.0	6.8	46.6	5.8	485.1	59.8	160.9	9.4	22.0	5.7
Target A	RC-TGA-0019A	TGA-RC-02009	27.0	28.0	1.0	513535.8	8114987.6	757.6	1,316.5	1,282.8	147.5	867.2	79.5	227.0	73.8	188.0	26.2	121.3	40.1	8.3	64.8	9.8	69.7	15.9	44.6	6.5	43.3	5.6	565.1	33.7	129.6	9.6	20.4	5.3
Target A	RC-TGA-0019A	TGA-RC-02010	28.0	29.0	1.0	513535.8	8114987.6	757.6	1,084.4	1,029.1	171.6	432.8	29.0	200.5	149.5	304.6	36.3	135.3	25.9	6.5	28.7	3.8	25.1	5.7	15.7	2.4	14.5	2.0	273.0	55.2	208.9	11.2	19.5	5.0
Target A	RC-TGA-0019A	TGA-RC-02011	29.0	30.0	1.0	513535.8	8114987.6	757.6	562.2	499.3	103.2	160.1	11.6	114.8	92.0	191.0	22.4	80.8	15.9	3.4	11.8	1.7	9.9	2.0	5.1	0.7	5.2	0.7	56.9	62.9	140.5	8.4	16.2	4.7
Target A	RC-TGA-0019A	TGA-RC-02012	30.0	31.0	1.0	513535.8	8114987.6	757.6	519.8	479.9	85.5	194.5	17.1	102.6	71.9	152.9	18.3	67.2	15.0	2.6	13.7	2.1	15.0	3.0	8.7	1.4	10.6	1.3	96.1	39.9	127.0	11.0	22.3	6.0
Target A	RC-TGA-0019A	TGA-RC-02013	31.0	32.0	1.0	513535.8	8114987.6	757.6	457.5	410.0	76.3	170.7	14.8	91.0	62.6	135.1	16.4	59.8	12.9	2.0	11.1	1.8	12.9	2.8	8.0	1.4	10.0	1.3	71.8	47.6	107.3	10.6	21.2	5.2
Target A	RC-TGA-0019A	TGA-RC-02014	32.0	33.0	1.0	513535.8	8114987.6	757.6	606.6	545.3	118.1	146.3	10.5	128.6	106.4	219.3	25.7	92.4	16.5	4.0	12.5	1.6	8.9	1.7	4.2	0.6	4.1	0.5	47.0	61.4	176.7	9.4	22.8	3.9
Target A	RC-TGA-0019A	TGA-RC-02016	33.0	34.0	1.0	513535.8	8114987.6	757.6	646.9	576.3	124.9	152.2	10.0	134.9	115.8	236.5	27.6	97.4	17.6	4.2	13.0	1.6	8.4	1.6	3.9	0.6	3.6	0.5	44.3	70.6	170.9	8.8	21.6	4.8
Target A	RC-TGA-0019A	TGA-RC-02017	34.0	35.0	1.0	513535.8	8114987.6	757.6	560.2	500.4	90.9	200.6	15.2	106.1	80.7	173.2	19.5	71.4	14.8	3.1	13.4	2.1	13.1	2.7	7.5	1.2	9.3	1.2	87.2	59.8	134.3	9.6	25.5	8.7
Target A	RC-TGA-0019A	TGA-RC-02018	35.0	36.0	1.0	513535.8	8114987.6	757.6	479.6	456.6	68.2	216.3	20.7	88.9	55.7	125.9	15.2	53.1	13.5	1.5	13.3	2.5	18.2	4.0	11.7	2.1	15.3	2.0	122.8	23.0	110.7	10.7	28.0	7.2
Target A	RC-TGA-0019A	TGA-RC-02019	36.0	37.0	1.0	513535.8	8114987.6	757.6	435.5	424.7	52.9	239.8	25.0	77.9	37.4	92.9	11.1	41.8	12.5	0.9	14.9	2.9	22.2	4.8	14.4	2.5	19.2	2.5	144.8	10.7	94.4	11.4	32.5	8.7
Target A	RC-TGA-0019A	TGA-RC-02020	37.0	38.0	1.0	513535.8	8114987.6	757.6	366.8	359.2	37.0	238.0	24.6	61.6	22.1	57.7	7.5	29.5	12.1	0.3	14.0	2.9	21.7	4.9	15.2	2.7	19.6	2.5	146.7	7.7	63.2	10.4	33.0	7.9
Target A	RC-TGA-0019A	TGA-RC-02021	38.0	39.0	1.0	513535.8	8114987.6	757.6	436.0	413.0	56.1	221.5	21.5	77.5	43.9	101.6	11.8	44.2	13.0	1.2	13.5	2.5	18.9	4.0	13.0	2.4	16.9	2.3	123.7	23.0	92.4	10.9	29.4	8.0
Target A	RC-TGA-0019A	TGA-RC-02023	39.0	40.0	1.0	513535.8	8114987.6	757.6	406.6	398.9	41.6	263.2	27.7	69.3	25.2	64.1	8.4	33.1	12.5	0.5	14.8	3.1	24.6	5.3	16.5	2.9	20.8	2.7	164.5	7.7	74.0	11.2	33.5	8.5
Target A	RC-TGA-0019A	TGA-RC-02024	40.0	41.0	1.0	513535.8	8114987.6	757.6	462.1	443.7	65.0	215.4	21.0	86.1	53.4	115.0	13.7	51.3	13.3	1.3	13.0	2.8	18.3	4.1	13.0	2.4	17.0	2.5	122.7	18.4	123.0	11.8	33.1	11.3
Target A	RC-TGA-0019A	TGA-RC-02025	41.0	42.0	1.0	513535.8	8114987.6	757.6	402.6	394.9	41.3	262.3	26.5	67.8	24.3	62.2	8.3	33.0	12.6	0.4	14.8	3.4	23.1	5.1	16.3	2.9	22.3	3.2	163.2	7.7	69.4	11.7	34.1	11.3
Target A	RC-TGA-0019A	TGA-RC-02026	42.0	43.0	1.0	513535.8	8114987.6	757.6	402.3	394.7	42.4	261.5	26.4	68.7	23.3	63.0	8.2	34.2	12.1	0.5	15.1	3.4	23.0	5.2	16.6	3.0	22.0	3.2	161.9	7.7	73.7	12.2	34.3	10.3
Target A	RC-TGA-0019A	TGA-RC-02027	43.0	44.0	1.0	513535.8	8114987.6	757.6	530.6	512.2	71.8	270.7	27.0	98.8	52.4	120.6	14.8	57.0	15.0	1.6	16.4	3.6	23.4	5.3	17.4	3.1	21.6	3.2	156.8	18.4	130.6	12.7	34.4	8.7
Target A	RC-TGA-0019A	TGA-RC-02028	44.0	45.0	1.0	513535.8	8114987.6	757.6	444.6	430.8	56.6	243.9	25.3	82.0	38.4	92.7	11.7	44.9	13.1	1.0	14.8	3.3	22.0	5.0	15.8	2.8	20.2	2.9	142.2	13.8	108.0	12.9	33.6	10.2
Target A	RC-TGA-0019A	TGA-RC-02029	45.0	46.0	1.0	513535.8	8114987.6	757.6	477.8	464.0	59.9	264.6	25.5	85.3	41.3	97.7	12.3	47.6	14.5	1.1	15.5	3.2	22.3	5.0	16.1	3.0	20.8	3.1	160.6	13.8	104.4	11.5	31.7	10.3
Target A	RC-TGA-0019A	TGA-RC-02030	46.0	47.0	1.0	513535.8	8114987.6	757.6	412.3	404.7	40.0	275.1	26.6	66.6	23.7	61.3	8.0	32.0	12.2	0.2	15.1	3.4	23.2	5.3	17.7	3.2	22.8	3.3	173.3	7.7	69.2	10.7	35.5	8.2
Target A	RC-TGA-0019A	TGA-RC-02031	47.0	48.0	1.0	513535.8	8114987.6	757.6	484.4	450.6	77.2	192.0	17.1	94.3	65.1	137.0	16.9	60.3	13.1	2.1	12.0	2.3	14.9	3.0	9.2	1.5	11.1	1.6	100.7	33.7	111.7	8.7	23.4	5.5
Target A	RC-TGA-0019A	TGA-RC-02032	48.0	49.0	1.0	513535.8	8114987.6	757.6	403.7	385.3	50.9	215.7	21.0	71.9	38.5	87.2	11.0	39.9	11.4	0.9	11.9	2.7	18.4	3.7	12.8	2.2	15.5	2.3	127.0	18.4	83.3	10.6	27.9	10.7
Target A	RC-TGA-0019A	TGA-RC-02033	49.0	50.0	1.0	513535.8	8114987.6	757.6	455.1	442.8	54.6	251.7	26.2	80.8	41.8	93.5	12.0	42.7	13.6	0.7	14.3	3.3	22.9	5.0	16.0	2.9	20.2	3.0	151.1	12.3	113.2	13.3	35.2	12.1
Target A	RC-TGA-0019A	TGA-RC-02035	50.0	51.0	1.0	513535.8	8114987.6	757.6	397.6	388.4	42.1	249.9	24.6	66.7	27.1	66.6	9.0	33.1	11.9	0.3	13.4	3.0	21.6	4.6	15.4	2.6	19.8	3.0	156.8	9.2	75.2	12.2	33.2	13.3
Target A	RC-TGA-0019A	TGA-RC-02036	51.0	52.0	1.0	513535.8	8114987.6	757.6	645.3	585.4	129.1	125.0	8.3	137.4	119.6	255.5	29.2	99.8	16.1	4.0	11.3	1.4	6.9	1.2	2.9	0.4	2.1	0.3	34.7	59.8	176.0	8.9	14.6	3.7
Target A	RC-TGA-0019A	TGA-RC-02037	52.0	53.0	1.0	513535.8	8114987.6	757.6	539.5	499.6	97.3	163.7	14.6	111.9	86.4	177.5	21.7	75.6	14.6	2.7	11.8	1.9	12.7	2.4	7.4	1.3	8.5	1.2	73.9	39.9	139.3	10.3	20.8	5.3
Target A	RC-TGA-0019A	TGA-RC-02038	53.0	54.0	1.0	513535.8	8114987.6	757.6	430.2	410.2	57.7	223.5	21.9	79.6	42.8	92.9	12.6	45.1	13.3	1.1	13.2	2.8	19.1	4.1	13.3	2.4	16.9	2.5	128.3	19.9	137.9	11.6	28.6	9.9
Target A	RC-TGA-0019A	TGA-RC-02039	54.0	55.0	1.0	513535.8	8114987.6	757.6	497.8	448.7	93.3	146.6	10.6	104.0	78.5	165.8	20.5	72.8	13.6	3.0	10.4	1.5	9.1	1.8	5.4	0.9	6.1	1.0	58.3	49.1	138.2	6.7	23.3	5.0
Target A	RC-TGA-0019A	TGA-RC-02040	55.0	56.0	1.0	513535.8	8114987.6	757.6	399.4	371.8	58.6	175.8	14.9	73.5	51.0	103.8	12.8	45.8	10.2	1.9	10.5	1.9	13.0	2.8	9.0	1.4	10.5	1.7	95.5	27.6	88.7	5.4	20.5	6.2
Target A	RC-TGA-0019A	TGA-RC-02041	56.0	57.0	1.0	513535.8	8114987.6	757.6	390.4	379.7	42.2	239.3	24.4	66.6	29.1	69.2	9.1	33.1	10.6	0.6	12.5	3.0	21.5	4.6	15.5	2.7	18.3	2.7	147.3	10.7	59.8	10.5	25.0	6.9
Target A	RC-TGA-0019A	TGA-RC-02043	57.0	58.0	1.0	513535.8	8114987.6	757.6	595.4	541.7	113.1	149.6	11.8	124.9	104.1	213.1	25.4	87.7	15.5	3.8	11.7	1.7	10.0	1.8	5.0	0.9	5.3	0.9	54.9	53.7	157.4	8.5	17.5	4.6
Target A	RC-TGA-0019A	TGA-RC-02044	58.0	59.0	1.0	513535.8	8114987.6	757.6	553.3	513.5	98.3	174.0	14.7	112.9	87.1	179.4	21.5	76.8	14.6	3.0	12.5	2.0	12.6	2.6	7.9	1.3	8.5	1.3	82.5	39.9	136.8	9.0	16.9	5.4
Target A	RC-TGA-0019A	TGA-RC-02045	59.0	60.0	1.0	513535.8	8114987.6	757.6	432.5	415.6	54.5	230.8	22.7	77.2	41.4	93.1	11.8	42.7	12.7	1.0	13.0	2.8	20.0	4.3	13.6	2.4	17.1	2.6	137.2	16.9	100.1	11.4	30.8	14.9
Target A	RC-TGA-0019A	TGA-RC-02046	60.0	61.0	1.0	513535.8	8114987.6	757.6	388.9	381.2	37.5	258.0	24.3	61.8	23.7	58.5	8.0	29.5	11.3	0.3	13.1	3.0	21.4	4.7	15.4	2.7	19.8	3.0	167.0	7.7	67.9	11.2	32.7	15.9
Target A	RC-TGA-0019A	TGA-RC-02047	61.0	62.0	1.0	513535.8	8114987.6	757.6	378.6	370.9	40.6	237.7	24.1	64.7	25.9	62.5	8.6	32.1	11.8	0.3	13.3	3.0	21.1	4.5	14.8	2.7	19.0	2.8	148.6	7.7	86.4	13.2	34.3	17.1
Target A	RC-TGA-0019A	TGA-RC-02048	62.0	63.0	1.0	513535.8	8114987.6	757.6	463.6	440.6	68.8	207.7	21.6	90.4	54.9	118.9	14.9	53.9	13.3	1.6	13.6	2.8	18.8	4.1	13.2	2.2	15.5	2.4	110.6	23.0	134.5	15.8	27.3	13.1
Target A	RC-TGA-0019A	TGA-RC-02050	63.0	64.0	1.0	513535.8	8114987.6	757.6	532.6	498.9	91.0	194.9	17.4	108.3	74.0	157.2	19.6	71.4	15.5	2.5	13.4	2.4	15.0	3.0	9.5	1.6	10.6	1.7	101.6	33.7	129.5	10.5	21.8	10.0
Target A	RC-TGA-0019A	TGA-RC-02051	64.0	65.0	1.0	513535.8	8114987.6	757.6	456.8	430.7	73.2	186.8	17.0	90.2	58.3	125.3	15.8	57.4	13.2	2.2	11.8	2.3	14.7	3.1	9.8	1.7	11.6	1.8	102.0	26.1	103.6	8.7	19.6	10.1
Target A	RC-TGA-0019A	TGA-RC-02052	65.0	66.0	1.0	513535.8	8114987.6	757.6	486.9	470.0	71.1	212.9	20.5	91.6	60.4	128.4	15.8	55.3	14.2	1.8	13.3	2.6	17.9	3.8	12.0	2.1	14.5	2.2	126.0	16.9	120.7	11.5	28.4	11.5
Target A	RC-TGA-0019A	TGA-RC-02053	66.0	67.0	1.0	513535.8	8114987.6	757.6	357.3	345.0	39.4	218.1	21.8	61.2	26.7	62.7	8.4	31.0	10.4	0.5	11.8	2.7	19.1	4.0	13.4	2.4	16.2	2.5	133.3	12.3	79.1	11.1	30.0	18.3
Target A	RC-TGA-0019A	TGA-RC-02054	67.0	68.0	1.0	513535.8	8114987.6	757.6	451.3	432.9	59.8	235.7	23.4	83.2	42.6	98.9	12.8	47.0	14.4	1.0	14.2	3.0	20.4	4.4	14.1	2.4	17.3	2.6	137.8	18.4	99.1	12.1	32.0	17.6
Target A	RC-TGA-0019A	TGA-RC-02055	68.0	69.0	1.0	513535.8	8114987.6	757.6	570.5	542.9	97.6	192.9	18.3	115.8	86.4	177.5	21.4	76.2	16.1	3.0	14.1	2.6	15.7	3.2	10.2	1.7	11.7	1.7	101.5	27.6	138.2	9.6	23.2	10.2
Target A	RC-TGA-0019A	TGA-RC-02056	69.0	70.0	1.0	513535.8	8114987.6	757.6	446.8	431.5	59.8	228.3	22.9	82.7	45.0	101.0	13.0	46.8	12.8	1.2	13.5	3.0	19.9	4.4	14.4	2.5	16.5	2.4	135.2	15.3	91.6	12.6	32.5	20.2
Target A	RC-TGA-0019A	TGA-RC-02058	70.0	71.0	1.0	513535.8	8114987.6	757.6	647.8	606.3	121.8	179.4	15.5	137.3	107.7	221.1	27.1	94.7	17.8	4.0	14.6	2.3	13.1	2.6	7.8	1.3	8.9	1.3	81.9	41.4	207.4	14.8	28.8	11.1
Target A	RC-TGA-0019A	TGA-RC-02059	71.0	72.0	1.0	513535.8	8114987.6	757.6	608.5	556.4	122.4	159.5	13.1	135.5	98.2	211.9	25.4	97.0	16.5	3.6	12.5	1.9	11.2	1.9	5.9	0.9	5.9	0.9	62.6	52.2	148.8	9.2	20.8	6.3
Target A	RC-TGA-0019A	TGA-RC-02060	72.0	73.0	1.0	513535.8	8114987.6	757.6	632.2	592.4	117.5	218.5	20.5	138.0	85.7	192.2	23.7	93.8	18.2	3.5	16.1	2.8	17.7	3.3	10.6	1.7	10.6	1.6	110.7	39.9	135.3	9.0	20.9	10.3
Target A	RC-TGA-0019A	TGA-RC-02061	73.0	74.0	1.0	513535.8	8114987.6	757.6	675.9	617.6	119.7	256.6	19.5	139.2	86.0	195.3	23.7	96.0	18.3	4.3	17.5	2.9	16.6	3.6	10.1	1.5	9.7	1.4	130.8	58.3	120.7	6.8	11.4	4.0
Target A	RC-TGA-0019A	TGA-RC-02062	74.0	75.0	1.0	513535.8	8114987.6	757.6	755.5	703.4	137.2	284.5	24.4	161.6	95.5	218.0	26.5	110.7	20.3	4.6	20.2	3.4	21.0	4.3	12.8	1.8	11.8	1.9	150.5	52.2	135.2	8.2	15.1	5.9
Target A	RC-TGA-0019A	TGA-RC-02063	75.0	76.0	1.0	513535.8	8114987.6	757.6	480.0	464.6	58.2	277.7	27.4	85.6	38.5	90.7	12.2	46.0	15.0	1.1	15.7	3.4	24.0	5.1	16.9	2.9	20.7	3.1	169.5	15.3	94.3	11.7	32.2	20.2
Target A	RC-TGA-0019A	TGA-RC-02064	76.0	77.0	1.0	513535.8	8114987.6	757.6	436.6	425.9	49.9	260.1	26.4	76.4	34.5	79.4	10.6	39.3	12.8	0.5	14.0	3.3	23.2	5.0	16.4	3.0	21.9	3.3	158.7	10.7	77.1	10.9	33.5	23.1
Target A	RC-TGA-0019A	TGA-RC-02066	77.0	78.0	1.0	513535.8	8114987.6	757.6	457.7	442.3	58.8	246.3	24.8	83.6	42.2	97.0	12.9	46.0	13.3	0.9	14.1	3.1	21.8	4.5	14.8	2.7	19.5	3.0	146.7	15.3	96.6	11.7	32.4	22.3
Target A	RC-TGA-0019A	TGA-RC-02067	78.0	79.0	1.0	513535.8	8114987.6	757.6	406.4	392.6	43.7	253.7	25.1	68.8	28.2	68.7	9.1	34.5	12.2	0.5	14.1	3.2	21.9	4.8	15.8	2.8	20.6	3.2	153.0	13.8	76.5	11.0	31.2	26.5
Target A	RC-TGA-0019A	TGA-RC-02068	79.0	80.0	1.0	513535.8	8114987.6	757.6	429.1	423.0	43.2	283.0	29.0	72.2	25.0	64.3	9.1	34.2	13.6	0.2	15.4	3.6	25.4	5.5	17.9	3.3	23.6	3.6	178.4	6.1	64.9	10.5	34.3	20.7
Target A	RC-TGA-0019A	TGA-RC-02069	80.0	81.0	1.0	513535.8	8114987.6	757.6	763.2	680.4	159.6	161.5	9.5	169.2	126.1	297.3	35.4	124.2	18.7	4.5	12.0	1.6	8.0	1.4	3.7	0.5	3.5	0.5	43.1	82.8	181.0	10.7	19.1	4.7
Target A	RC-TGA-0019A	TGA-RC-02070	81.0	82.0	1.0	513535.8	8114987.6	757.6	450.0	436.2	56.3	255.0	25.4	81.7	35.9	89.1	12.0	44.3	13.7	0.7	14.9	3.3	22.2	4.9	15.0	2.7	20.2	3.2	154.3	13.8	82.4	11.4	34.0	21.5
Target A	RC-TGA-0019A	TGA-RC-02071	82.0	83.0	1.0	513535.8	8114987.6	757.6	491.0	477.2	67.8	251.7	24.6	92.4	47.7	110.6	13.9	53.9	13.3	1.1	14.2	3.0	21.7	4.5	15.0	2.6	18.1	2.8	154.9	13.8	83.5	9.9	30.3	16.7
Target A	RC-TGA-0019A	TGA-RC-02073	83.0	84.0	1.0	513535.8	8114987.6	757.6	359.2	353.1	38.6	232.5	23.9	62.5	21.1	56.1	7.7	30.9	10.9	0.2	12.8	3.0	20.9	4.6	14.3	2.4	18.1	2.9	147.3	6.1	68.2	11.1	29.4	20.6
Target A	RC-TGA-0019A	TGA-RC-02074	84.0	85.0	1.0	513535.8	8114987.6	757.6	370.2	364.0	35.1	251.3	25.2	60.2	19.5	52.8	7.2	27.9	11.5	0.1	13.1	3.0	22.2	4.8	15.6	2.6	18.9	3.0	161.9	6.1	64.4	11.6	30.5	15.0
Target A	RC-TGA-0019A	TGA-RC-02075	85.0	86.0	1.0	513535.8	8114987.6	757.6	354.6	348.5	36.4	232.7	24.2	60.6	20.2	55.0	7.3	29.2	10.2	0.2	12.3	2.9	21.4	4.6	14.2	2.5	18.7	2.7	147.3	6.1	65.8	12.5	29.8	16.5
Target A	RC-TGA-0019A	TGA-RC-02076	86.0	87.0	1.0	513535.8	8114987.6	757.6	373.8	369.2	35.7	256.2	24.5	60.2	19.6	51.5	7.0	28.7	10.9	0.1	13.1	3.1	21.5	4.8	15.6	2.8	20.0	3.0	167.6	4.6	61.5	10.6	30.4	25.7
Target A	RC-TGA-0019A	TGA-RC-02077	87.0	88.0	1.0	513535.8	8114987.6	757.6	346.0	341.4	33.9	234.7	23.7	57.6	18.2	49.6	6.6	27.3	9.6	0.1	12.2	2.9	20.8	4.5	14.6	2.5	18.1	2.7	151.8	4.6	62.7	10.9

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0019A	TGA-RC-02087	96.0	97.0	1.0	513535.8	8114987.6	757.6	380.3	374.2	38.3	252.9	25.3	63.7	21.8	55.2	8.0	30.3	12.2	0.2	13.9	3.2	22.2	5.1	16.4	3.0	21.0	3.3	158.7	6.1	64.4	10.7	32.4	35.1
Target A	RC-TGA-0019A	TGA-RC-02088	97.0	98.0	1.0	513535.8	8114987.6	757.6	362.6	358.0	35.7	244.7	25.0	60.7	19.6	51.4	7.6	28.1	11.3	0.1	12.7	3.1	21.9	4.9	16.2	2.8	20.9	3.2	154.3	4.6	62.9	10.3	31.6	23.5
Target A	RC-TGA-0019A	TGA-RC-02089	98.0	99.0	1.0	513535.8	8114987.6	757.6	435.0	422.7	55.2	243.9	24.8	80.0	37.3	85.5	11.7	43.5	13.1	0.9	13.7	3.1	21.8	4.7	15.2	2.8	20.4	3.1	146.0	12.3	94.1	10.7	29.7	29.1
Target A	RC-TGA-0019A	TGA-RC-02090	99.0	100.0	1.0	513535.8	8114987.6	757.6	396.1	383.8	47.7	227.9	22.5	70.2	32.6	75.8	10.6	37.1	12.0	0.7	12.6	2.8	19.7	4.4	14.2	2.5	18.7	2.9	137.2	12.3	84.5	10.9	26.9	19.4
Target A	RC-TGA-0019A	TGA-RC-02091	100.0	101.0	1.0	513535.8	8114987.6	757.6	508.8	499.6	51.7	334.7	33.3	85.0	28.5	78.9	10.7	41.1	15.0	1.0	18.8	4.1	29.2	6.3	21.2	3.6	26.1	3.8	211.4	9.2	68.4	10.3	30.3	15.9
Target A	RC-TGA-0019A	TGA-RC-02093	101.0	102.0	1.0	513535.8	8114987.6	757.6	406.8	400.6	40.5	272.6	28.6	69.1	21.8	58.7	8.4	32.2	13.1	0.3	14.9	3.5	25.0	5.4	17.7	3.2	23.2	3.6	169.5	6.1	62.9	10.5	31.4	19.9
Target A	RC-TGA-0019A	TGA-RC-02094	102.0	103.0	1.0	513535.8	8114987.6	757.6	361.9	355.8	36.5	243.9	25.2	61.7	19.5	50.0	7.6	28.9	12.1	0.1	13.4	3.3	21.9	5.0	16.2	2.8	21.2	3.2	150.5	6.1	58.9	10.4	32.4	13.0
Target A	RC-TGA-0019A	TGA-RC-02095	103.0	104.0	1.0	513535.8	8114987.6	757.6	443.5	429.7	59.4	235.0	23.7	83.0	40.6	94.5	12.9	46.4	14.1	1.0	14.5	3.1	20.6	4.5	14.4	2.5	18.9	2.8	139.1	13.8	87.7	10.1	29.8	10.9
Target A	RC-TGA-0019A	TGA-RC-02096	104.0	105.0	1.0	513535.8	8114987.6	757.6	578.4	553.9	87.6	247.8	22.8	110.3	73.4	153.6	19.8	67.8	16.1	2.1	14.3	2.8	19.9	4.4	14.1	2.4	17.7	2.7	142.9	24.5	140.2	11.7	27.8	13.7
Target A	RC-TGA-0019A	TGA-RC-02097	105.0	106.0	1.0	513535.8	8114987.6	757.6	693.2	656.3	127.0	174.4	15.5	142.5	122.6	251.8	29.5	97.5	17.3	3.5	13.0	2.2	13.3	2.8	8.3	1.4	9.9	1.5	81.8	36.8	203.1	11.6	25.1	9.9
Target A	RC-TGA-0019A	TGA-RC-02098	106.0	107.0	1.0	513535.8	8114987.6	757.6	382.3	376.2	40.0	248.5	25.9	65.9	23.9	58.4	8.5	31.5	11.5	0.3	12.8	3.2	22.7	5.0	16.5	3.1	21.2	3.4	154.3	6.1	71.4	11.0	30.0	23.7
Target A	RC-TGA-0019A	TGA-RC-02099	107.0	108.0	1.0	513535.8	8114987.6	757.6	379.7	372.0	38.6	250.8	24.8	63.4	22.6	55.8	8.1	30.6	11.8	0.2	13.5	3.2	21.6	4.8	16.0	3.0	22.0	3.4	155.6	7.7	61.2	9.5	30.2	15.6
Target A	RC-TGA-0019A	TGA-RC-02101	108.0	109.0	1.0	513535.8	8114987.6	757.6	371.9	365.8	36.4	250.8	25.5	61.8	20.4	52.6	7.8	28.6	11.8	0.1	13.3	3.2	22.3	4.9	16.4	2.9	21.5	3.3	156.8	6.1	62.2	10.5	32.7	21.3
Target A	RC-TGA-0019A	TGA-RC-02102	109.0	110.0	1.0	513535.8	8114987.6	757.6	352.7	348.1	35.8	233.7	24.9	60.7	20.2	51.7	7.8	28.0	11.3	0.1	12.2	3.1	21.8	4.8	15.8	2.8	20.7	3.1	144.8	4.6	49.2	10.0	29.1	18.7
Target A	RC-TGA-0019A	TGA-RC-02103	110.0	111.0	1.0	513535.8	8114987.6	757.6	414.3	411.2	43.4	267.7	27.8	71.3	25.2	64.5	9.5	33.9	13.5	0.1	14.9	3.5	24.3	5.4	17.7	3.3	24.0	3.7	167.6	3.1	36.3	10.4	32.3	12.0
Target A	RC-TGA-0019A	TGA-RC-02104	111.0	112.0	1.0	513535.8	8114987.6	757.6	379.6	375.0	39.2	251.4	26.0	65.1	21.1	55.2	8.2	30.9	12.7	0.1	13.7	3.4	22.6	5.1	16.8	2.9	21.5	3.4	157.5	4.6	63.7	12.2	33.0	24.4
Target A	RC-TGA-0019A	TGA-RC-02105	112.0	113.0	1.0	513535.8	8114987.6	757.6	383.0	375.3	40.9	240.4	24.6	65.5	27.1	63.5	8.9	32.0	11.1	0.4	11.8	3.0	21.6	4.7	16.1	2.9	21.1	3.2	147.9	7.7	58.2	9.5	31.5	41.0
Target A	RC-TGA-0019A	TGA-RC-02106	113.0	114.0	1.0	513535.8	8114987.6	757.6	376.7	372.1	45.7	223.7	21.6	67.3	27.2	68.2	9.5	36.2	11.9	0.5	12.2	2.8	18.8	4.4	14.4	2.6	19.1	2.9	141.6	4.6	32.3	7.9	32.0	9.4
Target A	RC-TGA-0019A	TGA-RC-02107	114.0	115.0	1.0	513535.8	8114987.6	757.6	441.9	435.8	43.8	295.7	30.2	74.0	24.3	64.4	9.3	34.5	13.8	0.2	15.2	3.8	26.4	6.0	19.6	3.5	26.0	4.1	184.8	6.1	52.5	14.4	32.0	25.9
Target A	RC-TGA-0019A	TGA-RC-02109	115.0	116.0	1.0	513535.8	8114987.6	757.6	361.7	355.6	34.6	244.4	26.1	60.6	18.7	53.4	6.8	27.8	10.7	0.1	13.4	3.1	23.0	5.0	16.5	3.3	23.2	3.4	147.3	6.1	50.8	9.5	29.9	23.6
Target A	RC-TGA-0019A	TGA-RC-02110	116.0	117.0	1.0	513535.8	8114987.6	757.6	357.8	353.2	36.1	233.6	24.8	60.8	19.9	56.9	7.3	28.8	11.3	0.1	13.2	3.0	21.8	4.6	15.1	3.0	22.2	3.3	142.9	4.6	50.8	10.6	30.6	19.0
Target A	RC-TGA-0019A	TGA-RC-02111	117.0	118.0	1.0	513535.8	8114987.6	757.6	353.9	349.3	36.7	234.1	24.1	60.8	19.7	51.6	7.3	29.4	11.8	0.1	13.9	2.9	21.2	4.4	14.9	2.8	20.5	3.0	146.0	4.6	56.4	12.1	32.3	16.0
Target A	RC-TGA-0019A	TGA-RC-02112	118.0	119.0	1.0	513535.8	8114987.6	757.6	344.0	339.4	32.9	234.8	24.3	57.2	17.1	49.0	6.4	26.5	10.2	0.1	12.9	2.9	21.5	4.5	15.3	3.0	21.4	3.4	145.4	4.6	53.9	11.4	28.3	14.6
Target A	RC-TGA-0019A	TGA-RC-02113	119.0	120.0	1.0	513535.8	8114987.6	757.6	358.4	352.3	34.8	242.8	25.8	60.6	18.1	52.1	7.0	27.8	10.7	0.1	13.5	3.1	22.8	4.8	16.1	3.2	23.1	3.4	146.7	6.1	60.7	11.8	29.5	16.6
Target A	RC-TGA-0020	TGA-RC-02114	0.0	1.0	1.0	513272.9	8115204.2	765.6	150.6	129.1	14.3	62.7	3.9	18.2	12.9	58.5	3.1	11.2	2.3	0.4	2.3	0.5	3.4	0.8	2.8	0.5	3.6	0.5	26.3	21.5	65.8	5.4	20.5	5.0
Target A	RC-TGA-0020	TGA-RC-02115	1.0	2.0	1.0	513272.9	8115204.2	765.6	165.5	139.4	12.6	73.8	4.6	17.2	11.5	65.2	2.7	9.9	2.4	0.4	2.5	0.5	4.1	1.0	3.1	0.6	4.4	0.7	30.5	26.1	81.1	6.0	23.9	5.6
Target A	RC-TGA-0020	TGA-RC-02117	2.0	3.0	1.0	513272.9	8115204.2	765.6	311.0	228.1	41.2	125.4	5.1	46.2	44.9	94.5	9.6	31.6	5.1	1.0	3.8	0.7	4.4	0.9	3.0	0.5	3.4	0.5	24.4	82.8	44.6	2.8	31.3	16.1
Target A	RC-TGA-0020	TGA-RC-02118	3.0	4.0	1.0	513272.9	8115204.2	765.6	367.4	276.9	55.0	132.7	5.4	60.5	56.6	116.3	12.6	42.5	6.8	1.3	4.4	0.7	4.7	0.9	2.7	0.5	3.4	0.5	23.1	90.5	43.5	2.7	34.9	15.5
Target A	RC-TGA-0020	TGA-RC-02119	4.0	5.0	1.0	513272.9	8115204.2	765.6	322.8	249.2	50.4	112.6	4.5	54.9	52.8	101.2	11.7	38.7	5.8	1.1	3.9	0.6	3.9	0.8	2.5	0.4	3.2	0.5	22.1	73.6	43.8	2.4	35.2	12.6
Target A	RC-TGA-0020	TGA-RC-02120	5.0	6.0	1.0	513272.9	8115204.2	765.6	249.7	205.3	33.2	97.9	5.2	38.4	35.3	79.5	7.5	25.7	4.0	0.7	3.3	0.6	4.6	1.0	3.5	0.7	4.5	0.7	33.8	44.5	58.7	4.9	26.1	10.1
Target A	RC-TGA-0020	TGA-RC-02121	6.0	7.0	1.0	513272.9	8115204.2	765.6	310.4	296.6	49.1	127.4	11.3	60.4	53.7	73.2	10.8	38.4	7.0	1.0	7.3	1.4	9.9	2.2	7.2	1.4	9.8	1.4	72.0	13.8	61.9	9.9	33.3	6.1
Target A	RC-TGA-0020	TGA-RC-02122	7.0	8.0	1.0	513272.9	8115204.2	765.6	294.2	280.4	45.5	135.8	12.5	58.0	41.9	63.6	10.1	35.5	7.4	0.6	7.5	1.4	11.0	2.5	8.2	1.6	11.1	1.6	76.4	13.8	65.2	11.2	35.7	6.8
Target A	RC-TGA-0020	TGA-RC-02124	8.0	9.0	1.0	513272.9	8115204.2	765.6	332.5	321.8	53.9	140.8	13.9	67.9	53.5	76.0	11.8	42.1	8.3	0.8	8.6	1.6	12.3	2.6	8.9	1.6	11.5	1.7	80.4	10.7	71.7	11.0	37.9	7.2
Target A	RC-TGA-0020	TGA-RC-02125	9.0	10.0	1.0	513272.9	8115204.2	765.6	326.5	306.6	49.3	145.4	11.9	61.1	54.3	70.8	11.3	38.0	6.7	1.0	7.1	1.5	10.4	2.4	7.9	1.5	10.6	1.6	81.4	19.9	70.5	10.3	31.9	7.4
Target A	RC-TGA-0020	TGA-RC-02126	10.0	11.0	1.0	513272.9	8115204.2	765.6	300.8	279.4	46.0	114.8	8.7	54.7	57.8	76.0	10.6	35.3	6.2	0.9	6.0	1.1	7.6	1.7	5.8	1.1	7.9	1.2	59.9	21.5	79.2	9.6	26.6	7.8
Target A	RC-TGA-0020	TGA-RC-02127	11.0	12.0	1.0	513272.9	8115204.2	765.6	503.0	475.4	80.7	88.8	7.4	88.1	112.2	211.9	18.8	61.8	9.4	1.7	7.4	1.1	6.3	1.2	3.6	0.6	4.3	0.6	34.4	27.6	127.2	12.5	27.2	8.1
Target A	RC-TGA-0020	TGA-RC-02128	12.0	13.0	1.0	513272.9	8115204.2	765.6	1,080.2	1,048.0	84.4	95.4	8.1	92.6	113.2	777.6	19.8	64.6	9.6	2.0	8.1	1.4	6.8	1.2	3.5	0.6	4.2	0.6	34.7	32.2	133.8	12.3	31.2	7.7
Target A	RC-TGA-0020	TGA-RC-02129	13.0	14.0	1.0	513272.9	8115204.2	765.6	1,012.5	948.0	173.2	145.9	12.3	185.4	210.5	463.1	39.6	133.6	19.7	4.3	15.0	2.1	10.1	1.6	4.1	0.7	4.2	0.6	38.7	64.4	266.8	16.7	33.2	13.7
Target A	RC-TGA-0020	TGA-RC-02130	14.0	15.0	1.0	513272.9	8115204.2	765.6	1,246.0	1,175.5	238.0	157.5	14.0	251.9	283.8	539.3	54.9	183.1	27.5	5.3	19.1	2.6	11.4	1.7	4.1	0.7	4.1	0.5	37.3	70.6	340.5	17.7	36.3	16.9
Target A	RC-TGA-0020	TGA-RC-02131	15.0	16.0	1.0	513272.9	8115204.2	765.6	2,313.2	2,231.9	476.1	198.7	22.8	498.9	580.5	1,002.4	113.3	362.8	55.4	10.6	31.7	4.1	18.7	2.4	5.0	0.7	3.9	0.5	39.9	81.3	364.8	17.5	31.0	17.9
Target A	RC-TGA-0020	TGA-RC-02132	16.0	17.0	1.0	513272.9	8115204.2	765.6	4,286.3	4,206.6	922.1	290.4	42.2	964.3	1,100.1	1,867.2	221.1	701.0	106.6	20.1	61.9	8.0	34.2	4.2	8.4	1.1	6.1	0.8	65.8	79.8	370.5	17.2	29.7	18.2
Target A	RC-TGA-0020	TGA-RC-02133	17.0	18.0	1.0	513272.9	8115204.2	765.6	4,736.5	4,656.7	1,073.6	328.5	49.4	1,123.0	1,219.7	1,990.0	250.1	823.5	124.7	23.6	73.0	9.2	40.2	4.9	9.9	1.3	6.6	0.9	79.2	79.8	340.5	15.6	28.0	18.1
Target A	RC-TGA-0020	TGA-RC-02135	18.0	19.0	1.0	513272.9	8115204.2	765.6	3,308.0	3,255.8	742.5	248.2	36.0	778.5	818.6	1,412.7	171.0	571.5	86.0	16.4	52.3	6.8	29.3	3.8	8.4	1.1	6.9	0.9	70.1	52.1	304.7	15.4	27.4	14.4
Target A	RC-TGA-0020	TGA-RC-02136	19.0	20.0	1.0	513272.9	8115204.2	765.6	2,012.5	1,975.7	484.1	248.6	31.4	515.5	423.4	794.8	105.0	379.1	61.7	11.4	39.0	5.2	26.3	4.1	10.3	1.6	9.7	1.3	102.9	36.8	206.7	15.3	28.4	10.1
Target A	RC-TGA-0020	TGA-RC-02137	20.0	21.0	1.0	513272.9	8115204.2	765.6	1,153.4	1,128.9	241.6	193.4	21.1	262.7	221.7	465.6	52.1	189.5	31.2	5.8	22.7	3.2	17.9	3.2	8.9	1.5	9.4	1.4	94.7	24.5	136.8	10.0	21.6	8.4
Target A	RC-TGA-0020	TGA-RC-02138	21.0	22.0	1.0	513272.9	8115204.2	765.6	278.8	275.7	46.2	110.6	12.3	58.5	31.0	82.1	9.6	36.6	8.9	1.1	8.2	1.6	10.7	2.1	6.7	1.2	8.9	1.2	65.8	3.1	38.1	5.5	20.8	4.1
Target A	RC-TGA-0020	TGA-RC-02139	22.0	23.0	1.0	513272.9	8115204.2	765.6	2,010.5	1,990.6	537.9	375.3	52.3	590.2	351.8	665.8	108.6	429.2	79.8	16.0	59.0	8.3	44.1	7.1	17.9	2.8	17.0	2.2	181.0	19.9	195.3	12.5	26.4	9.0
Target A	RC-TGA-0020	TGA-RC-02140	23.0	24.0	1.0	513272.9	8115204.2	765.6	1,020.5	1,006.7	291.6	231.9	29.0	320.6	191.8	262.9	58.4	233.3	42.3	8.1	32.2	4.6	24.4	4.1	11.2	1.7	11.0	1.5	119.2	13.8	128.2	9.8	23.9	6.1
Target A	RC-TGA-0020	TGA-RC-02141	24.0	25.0	1.0	513272.9	8115204.2	765.6	1,086.6	1,049.8	298.6	222.8	27.1	325.7	208.2	313.2	60.7	237.9	43.8	8.2	31.0	4.4	22.7	3.8	9.8	1.5	9.2	1.3	94.1	36.8	178.8	12.0	28.2	8.4
Target A	RC-TGA-0020	TGA-RC-02143	25.0	26.0	1.0	513272.9	8115204.2	765.6	737.6	700.8	175.8	206.3	21.4	197.2	144.3	184.3	37.0	138.8	27.0	4.5	20.1	3.2	18.2	3.4	9.7	1.4	9.6	1.3	98.0	36.8	189.5	12.8	31.3	10.0
Target A	RC-TGA-0020	TGA-RC-02144	26.0	27.0	1.0	513272.9	8115204.2	765.6	724.7	694.1	170.2	209.8	22.6	192.8	129.0	186.7	34.9	135.3	29.0	4.9	21.7	3.5	19.2	3.7	9.9	1.5	10.0	1.4	103.5	30.7	168.8	12.1	32.1	9.0
Target A	RC-TGA-0020	TGA-RC-02145	27.0	28.0	1.0	513272.9	8115204.2	765.6	998.9	954.4	244.0	209.6	24.0	268.1	185.3	321.8	50.4	193.6	38.2	7.5	27.8	4.0	20.1	3.5	8.8	1.2	7.6	1.0	83.6	44.5	249.6	14.2	27.1	10.6
Target A	RC-TGA-0020	TGA-RC-02146	28.0	29.0	1.0	513272.9	8115204.2	765.6	895.1	842.9	218.0	190.8	21.6	239.6	136.0	315.7	43.6	174.4	34.6	6.9	25.6	3.6	18.0	3.0	7.1	1.0	6.5	0.8	66.2	52.1	286.1	14.2	28.2	13.1
Target A	RC-TGA-0020	TGA-RC-02147	29.0	30.0	1.0	513272.9	8115204.2	765.6	692.7	635.9	169.1	189.3	19.6	188.8	93.2	211.9	33.2	135.9	29.1	5.2	21.8	3.2	16.4	2.8	7.2	1.1	6.8	0.9	67.1	56.8	175.2	10.5	26.4	10.5
Target A	RC-TGA-0020	TGA-RC-02148	30.0	31.0	1.0	513272.9	8115204.2	765.6	1,919.9	1,850.9	316.8	1,020.0	96.4	413.2	183.5	337.8	57.9	258.9	61.7	14.9	84.3	13.5	82.9	17.8	49.4	6.8	40.3	6.2	635.0	69.0	185.2	10.1	24.8	8.5
Target A	RC-TGA-0020	TGA-RC-02150	31.0	32.0	1.0	513272.9	8115204.2	765.6	3,499.1	3,414.8	358.6	2,390.5	195.3	553.9	188.2	481.5	62.3	296.3	80.2	22.6	151.6	25.4	169.9	40.6	117.8	16.6	100.9	16.4	1,644.5	84.4	166.7	8.8	18.1	6.1
Target A	RC-TGA-0020	TGA-RC-02151	32.0	33.0	1.0	513272.9	8115204.2	765.6	629.0	576.9	113.0	256.5	20.2	133.2	83.6	157.8	22.3	90.7	18.0	4.0	19.1	2.9	17.3	3.7	10.5	1.5	9.4	1.4	134.6	52.1	127.2	7.7	17.9	5.4
Target A	RC-TGA-0020	TGA-RC-02152	33.0	34.0	1.0	513272.9	8115204.2	765.6	380.2	372.6	58.7	162.4	15.5	74.2	46.4	101.8	12.6	46.1	10.8	1.1	11.0	2.1	13.4	2.9	8.8	1.4	9.6	1.4	103.0	7.7	53.8	6.5	25.6	4.7
Target A	RC-TGA-0020	TGA-RC-02153	34.0	35.0	1.0	513272.9	8115204.2	765.6	320.7	316.1	46.1	152.2	14.9	60.9	35.1	78.0	9.9	36.2	9.4	0.6	9.9	2.0	12.9	2.8	8.6	1.3	9.3	1.4	98.8	4.6	53.8	6.7	24.7	4.6
Target A	RC-TGA-0020	TGA-RC-02154	35.0	36.0	1.0	513272.9	8115204.2	765.6	380.9	376.3	45.6	219.5	18.3	63.9	33.1	72.7	9.4	36.2	10.0	0.5	11.4	2.3	16.0	3.7	11.9	2.0	14.9	2.3	149.8	4.6	42.9	8.9	26.3	5.7
Target A	RC-TGA-0020	TGA-RC-02155	36.0	37.0	1.0	513272.9	8115204.2	765.6	457.0	437.1	75.0	181.6	15.7	90.7	57.0	130.2	15.9	59.0	13.2	1.8	12.2	2.1	13.5	2.9	8.7	1.4	10.3	1.5	107.1	19.9	100.7	10.6	26.5	8.2
Target A	RC-TGA-0020	TGA-RC-02156	37.0	38.0	1.0	513272.9	8115204.2	765.6	294.4	291.4	40.8	154.4	15.1	55.9	27.6	63.0	8.5	32.3	8.7	0.3	9.0	1.9	13.2	2.9	9.2	1.6	11.0	1.8	100.3	3.1	55.2	8.9	27.5	6.6
Target A	RC-TGA-0020	TGA-RC-02158	38.0	39.0	1.0	513272.9	8115204.2	765.6	340.3	331.1	47.5	169.8	15.3	62.9	36.1	76.7	10.1	37.4	10.1	0.8	10.4	1.9	13.4	3.0	9.2	1.6	10.6	1.7	107.9	9.2	65.5	9.0	26.3	6.3
Target A	RC-TGA-0020	TGA-RC-02159	39.0	40.0	1.0	513272.9	8115204.2	765.6	415.7	401.9	54.7	223.5	19.4	74.1	40.6	86.0	11.2	43.5	11.0	1.1	12.3	2.4	17.0	3.8	11.5	1.9	13.6	2.0	144.1	13.8	77.7	8.4	26.7	8.6
Target A	RC-TGA-0020	TGA-RC-02160	40.0	41.0	1.0	513272.9	8115204.2	765.6	387.7	378.5	46.5	217.3	18.6	65.1	33.4	79.8	9.6	36.9	10.6	0.7	11.6	2.4	16.2	3.7	12.1	2.0	14.3	2.2	142.9	9.2	74.0	8.3	31.6	11.6
Target A	RC-TGA-0020	TGA-RC-02161	41.0	42.0	1.0	513272.9	8115204.2	765.6	330.9	327.8	36.0	204.1	17.8	53.8	24.0	57.2	7.3	28.7	9.5	0.3	10.2	2.2	15.6	3.6	11.9	2.0	14.5	2.2	138.4	3.1	57.4	7.8	34.0	10.7
Target A	RC-TGA-0020	TGA-RC-02162	42.0	43.0	1.0	513272.9	8115204.2	765.6	351.8	347.2	40.5	210.1	18.2	58.7	26.6	65.0	8.3	32.2	9.6	0.5	11.2	2.3	16.0	3.7	12.4	2.1	14.8	2.3	140.3	4.6	64.7	7.7	33.1	12.3
Target A	RC-TGA-0020	TGA-RC-02163	43.0	44.0	1.0	513272.9	8115204.2	765.6	356.8	353.7	49.1	186.3	17.3	66.4	32.5	77.9	10.1	39.0	11.1	0.5	10.7	2.2	15.1	3.3	10.7	1.7	12.6	1.8	124.7	3.1	53.6	7.8	38.0	9.7
Target A	RC-TGA-0020	TGA-RC-02165	44.0	45.0	1.0	513272.9	8115204.2	765.6	388.1	385.0	37.6	256.6	22.0	59.5	25.1	59.5	7.8	29.7	9.4	0.3	11.5	2.6	19.3	4.5	14.8	2.4

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0020	TGA-RC-02175	53.0	54.0	1.0	513272.9	8115204.2	765.6	366.7	362.1	39.6	220.1	19.9	59.5	29.7	67.7	8.4	31.3	9.5	0.5	10.6	2.4	17.5	4.0	13.4	2.3	16.3	2.5	146.0	4.6	63.7	8.7	34.4	11.0
Target A	RC-TGA-0020	TGA-RC-02176	54.0	55.0	1.0	513272.9	8115204.2	765.6	1,059.2	1,022.4	225.5	146.3	14.9	240.4	211.7	447.1	48.8	176.7	28.5	7.7	19.4	2.5	12.4	2.1	4.7	0.6	3.4	0.5	56.3	36.8	263.9	13.3	18.3	4.2
Target A	RC-TGA-0020	TGA-RC-02177	55.0	56.0	1.0	513272.9	8115204.2	765.6	1,060.1	1,023.3	220.5	151.6	14.5	235.0	212.9	447.1	47.8	172.6	27.9	7.5	19.8	2.5	12.1	2.1	5.1	0.6	3.9	0.5	60.8	36.8	261.1	12.9	18.5	3.8
Target A	RC-TGA-0020	TGA-RC-02178	56.0	57.0	1.0	513272.9	8115204.2	765.6	403.1	383.1	55.8	196.3	16.1	71.8	44.4	96.4	11.6	44.2	10.1	1.3	10.4	2.0	14.1	3.3	10.5	1.7	12.1	1.8	119.1	19.9	74.8	7.6	26.1	7.1
Target A	RC-TGA-0020	TGA-RC-02179	57.0	58.0	1.0	513272.9	8115204.2	765.6	439.7	421.2	60.8	212.6	17.9	78.7	48.1	107.1	13.6	47.2	11.1	1.3	10.7	2.2	15.7	3.6	11.3	2.0	13.8	2.1	131.4	18.4	93.1	7.8	32.1	15.4
Target A	RC-TGA-0020	TGA-RC-02180	58.0	59.0	1.0	513272.9	8115204.2	765.6	619.8	580.0	119.4	161.5	12.5	131.9	105.0	217.4	26.3	93.1	16.5	3.9	13.1	1.9	10.5	2.1	6.3	0.9	5.5	0.8	76.4	39.9	174.5	7.9	18.6	6.7
Target A	RC-TGA-0020	TGA-RC-02181	59.0	60.0	1.0	513272.9	8115204.2	765.6	500.9	470.3	75.4	213.5	17.1	92.5	59.7	140.0	16.7	58.7	12.3	1.9	12.1	2.2	14.9	3.3	10.0	1.7	10.8	1.8	124.1	30.7	111.4	9.0	29.7	12.1
Target A	RC-TGA-0020	TGA-RC-02182	60.0	61.0	1.0	513272.9	8115204.2	765.6	446.5	434.2	58.8	229.3	18.5	77.3	45.5	101.6	12.8	46.0	11.4	1.2	11.9	2.4	16.2	3.8	11.8	2.1	15.3	2.4	149.8	12.3	87.5	8.3	36.1	17.0
Target A	RC-TGA-0020	TGA-RC-02183	61.0	62.0	1.0	513272.9	8115204.2	765.6	514.9	495.0	76.2	226.5	18.4	94.6	62.4	136.4	17.0	59.3	13.5	1.8	12.9	2.4	16.0	3.4	11.5	1.9	13.7	2.1	141.0	19.9	109.7	8.3	39.0	18.3
Target A	RC-TGA-0020	TGA-RC-02185	62.0	63.0	1.0	513272.9	8115204.2	765.6	418.8	412.6	47.9	243.3	20.1	67.9	35.8	81.1	10.6	37.2	10.7	0.7	11.8	2.5	17.6	4.2	13.4	2.4	17.1	2.6	165.1	6.1	71.0	8.2	44.3	22.7
Target A	RC-TGA-0020	TGA-RC-02186	63.0	64.0	1.0	513272.9	8115204.2	765.6	397.8	388.6	47.9	224.4	18.8	66.7	34.6	80.7	10.6	37.3	10.2	0.8	10.7	2.3	16.5	3.8	12.6	2.2	15.3	2.4	148.6	9.2	71.1	8.5	37.2	18.2
Target A	RC-TGA-0020	TGA-RC-02187	64.0	65.0	1.0	513272.9	8115204.2	765.6	336.8	333.7	35.2	212.6	19.3	54.5	23.2	57.0	7.3	27.9	8.8	0.3	10.7	2.4	16.9	3.8	13.0	2.2	16.2	2.4	141.6	3.1	54.4	8.5	38.6	17.2
Target A	RC-TGA-0020	TGA-RC-02188	65.0	66.0	1.0	513272.9	8115204.2	765.6	492.5	469.5	82.1	178.9	14.5	96.5	69.2	149.3	18.5	63.6	13.2	2.0	11.1	2.0	12.5	2.8	8.6	1.5	10.5	1.6	103.4	23.0	116.3	8.7	26.4	10.8
Target A	RC-TGA-0020	TGA-RC-02189	66.0	67.0	1.0	513272.9	8115204.2	765.6	433.7	424.5	55.0	221.6	18.8	73.8	42.7	103.7	12.2	42.8	10.7	0.9	11.6	2.4	16.4	3.9	12.5	2.1	15.4	2.3	144.8	9.2	80.8	8.5	39.4	13.6
Target A	RC-TGA-0020	TGA-RC-02190	67.0	68.0	1.0	513272.9	8115204.2	765.6	463.9	445.5	72.0	193.5	15.9	87.9	58.2	128.4	15.6	56.3	11.9	1.7	11.3	2.1	13.8	3.0	9.3	1.5	11.4	1.7	119.1	18.4	101.9	8.1	29.0	7.4
Target A	RC-TGA-0020	TGA-RC-02191	68.0	69.0	1.0	513272.9	8115204.2	765.6	448.0	440.3	52.7	247.2	21.1	73.8	38.0	98.9	11.5	41.2	11.2	0.8	12.2	2.7	18.5	4.3	13.8	2.3	16.7	2.6	165.7	7.7	74.8	9.0	37.8	13.3
Target A	RC-TGA-0020	TGA-RC-02193	69.0	70.0	1.0	513272.9	8115204.2	765.6	378.8	369.6	46.6	201.3	17.2	63.8	34.4	87.0	10.5	36.0	9.6	0.6	9.7	2.1	15.0	3.5	11.3	2.0	14.2	2.1	131.4	9.2	68.4	8.9	31.1	10.4
Target A	RC-TGA-0020	TGA-RC-02194	70.0	71.0	1.0	513272.9	8115204.2	765.6	395.9	392.8	43.5	223.7	20.7	64.3	30.4	88.1	9.4	34.2	10.2	0.3	11.2	2.6	18.1	4.2	13.6	2.5	17.0	2.6	148.6	3.1	55.5	8.1	36.0	11.2
Target A	RC-TGA-0020	TGA-RC-02195	71.0	72.0	1.0	513272.9	8115204.2	765.6	387.0	382.4	40.0	233.2	21.4	61.4	27.8	76.4	8.7	31.4	9.6	0.4	11.8	2.7	18.7	4.3	14.0	2.4	17.0	2.5	154.9	4.6	58.8	8.3	37.4	12.3
Target A	RC-TGA-0020	TGA-RC-02196	72.0	73.0	1.0	513272.9	8115204.2	765.6	532.2	504.6	79.8	225.1	18.9	98.7	65.1	148.0	17.9	61.8	14.2	2.0	12.9	2.4	16.5	3.5	11.6	1.9	13.3	2.0	131.4	27.6	117.9	8.4	29.5	8.9
Target A	RC-TGA-0020	TGA-RC-02197	73.0	74.0	1.0	513272.9	8115204.2	765.6	529.0	493.7	91.1	186.0	15.1	106.2	74.4	163.4	19.9	71.2	14.1	2.7	12.7	2.1	13.0	2.8	8.3	1.3	9.2	1.4	97.1	35.3	128.5	7.1	22.9	5.6
Target A	RC-TGA-0020	TGA-RC-02198	74.0	75.0	1.0	513272.9	8115204.2	765.6	671.4	633.0	115.9	233.9	19.3	135.2	97.5	206.4	25.3	90.6	17.8	3.3	15.4	2.6	16.8	3.6	10.9	1.9	13.7	2.2	125.3	38.3	159.5	8.7	29.2	8.0
Target A	RC-TGA-0020	TGA-RC-02199	75.0	76.0	1.0	513272.9	8115204.2	765.6	432.3	423.1	49.1	254.1	21.5	70.5	31.8	86.0	10.2	38.8	11.4	0.7	12.2	2.7	18.8	4.2	14.7	2.7	20.6	3.3	165.1	9.2	60.1	7.2	20.7	8.1
Target A	RC-TGA-0020	TGA-RC-02200	76.0	77.0	1.0	513272.9	8115204.2	765.6	383.1	355.5	54.7	178.7	14.3	69.0	41.3	98.9	12.0	42.7	9.6	1.4	9.3	1.9	12.4	2.8	9.0	1.6	11.0	1.6	100.2	27.6	73.2	6.5	18.9	5.4
Target A	RC-TGA-0020	TGA-RC-02202	77.0	78.0	1.0	513272.9	8115204.2	765.6	443.9	422.5	66.1	194.3	17.2	83.3	50.7	121.1	14.7	51.3	11.8	1.5	11.1	2.2	15.0	3.2	10.0	1.7	10.8	1.6	115.7	21.5	100.1	7.6	24.7	7.0
Target A	RC-TGA-0020	TGA-RC-02203	78.0	79.0	1.0	513272.9	8115204.2	765.6	563.9	522.4	94.8	205.2	16.6	111.4	79.4	170.1	20.7	74.1	14.3	2.7	13.0	2.2	14.3	3.0	8.8	1.4	9.6	1.5	107.2	41.4	141.3	8.3	21.6	5.8
Target A	RC-TGA-0020	TGA-RC-02204	79.0	80.0	1.0	513272.9	8115204.2	765.6	362.8	356.6	36.8	223.7	20.1	56.9	25.6	67.4	7.8	29.0	9.2	0.4	10.6	2.4	17.7	3.9	13.2	2.3	16.1	2.4	148.6	6.1	57.1	9.3	31.5	7.9
Target A	RC-TGA-0020	TGA-RC-02205	80.0	81.0	1.0	513272.9	8115204.2	765.6	299.5	294.9	29.1	189.4	17.1	46.3	20.8	53.1	6.3	22.9	7.1	0.4	8.4	2.0	15.1	3.4	11.5	1.9	12.6	1.9	127.6	4.6	44.6	7.7	23.6	6.4
Target A	RC-TGA-0020	TGA-RC-02206	81.0	82.0	1.0	513272.9	8115204.2	765.6	407.5	384.5	63.6	166.4	13.7	77.3	52.3	114.5	14.0	49.6	10.7	1.7	9.4	1.8	11.9	2.6	8.3	1.3	9.2	1.3	95.9	23.0	103.0	7.6	20.6	5.2
Target A	RC-TGA-0020	TGA-RC-02208	82.0	83.0	1.0	513272.9	8115204.2	765.6	542.6	496.5	101.7	157.5	12.2	113.9	86.6	182.4	22.3	79.4	14.3	3.3	11.5	1.8	10.4	2.1	5.4	0.7	4.5	0.6	71.4	46.0	156.6	8.2	14.8	4.0
Target A	RC-TGA-0020	TGA-RC-02209	83.0	84.0	1.0	513272.9	8115204.2	765.6	458.2	413.7	85.2	138.4	10.4	95.6	71.4	150.5	18.5	66.7	12.7	2.7	9.9	1.5	9.0	1.7	4.7	0.7	4.1	0.6	59.1	44.5	136.6	6.5	14.3	4.6
Target A	RC-TGA-0020	TGA-RC-02210	84.0	85.0	1.0	513272.9	8115204.2	765.6	325.5	316.3	39.5	179.2	16.6	56.1	29.1	69.4	8.3	31.3	8.3	0.6	9.1	2.0	14.5	3.2	10.5	1.8	12.4	2.0	113.7	9.2	69.2	8.3	28.4	10.7
Target A	RC-TGA-0020	TGA-RC-02211	85.0	86.0	1.0	513272.9	8115204.2	765.6	305.9	301.3	34.1	177.1	17.2	51.3	24.3	61.9	7.5	26.6	8.5	0.3	9.5	2.3	15.0	3.3	11.3	1.9	13.7	2.1	113.1	4.6	57.9	8.2	31.9	15.2
Target A	RC-TGA-0020	TGA-RC-02212	86.0	87.0	1.0	513272.9	8115204.2	765.6	280.5	277.4	32.6	159.7	15.7	48.3	23.0	57.2	6.9	25.7	8.0	0.3	8.7	1.9	13.8	3.0	10.0	1.8	12.6	1.9	102.6	3.1	50.8	7.4	33.3	14.6
Target A	RC-TGA-0020	TGA-RC-02213	87.0	88.0	1.0	513272.9	8115204.2	765.6	348.0	343.4	35.6	214.9	19.8	55.4	25.2	63.3	7.8	27.9	9.1	0.3	10.9	2.3	17.4	3.9	13.3	2.3	16.8	2.6	140.3	4.6	58.5	8.8	37.9	13.4
Target A	RC-TGA-0020	TGA-RC-02214	88.0	89.0	1.0	513272.9	8115204.2	765.6	500.9	473.3	73.3	194.6	16.0	89.3	71.0	149.9	16.3	57.0	12.2	2.1	11.4	2.1	13.8	3.1	9.8	1.6	11.2	1.7	110.1	27.6	116.7	8.3	23.4	15.1
Target A	RC-TGA-0020	TGA-RC-02216	89.0	90.0	1.0	513272.9	8115204.2	765.6	396.2	379.3	48.0	191.5	16.3	64.3	39.2	108.1	10.4	37.7	9.4	1.1	10.0	2.1	14.2	3.3	10.2	1.8	13.0	2.0	117.0	16.9	73.1	7.4	30.0	18.7
Target A	RC-TGA-0020	TGA-RC-02217	90.0	91.0	1.0	513272.9	8115204.2	765.6	436.4	424.1	51.2	209.4	18.6	69.8	40.6	124.7	11.0	40.1	10.6	0.9	10.8	2.3	16.3	3.7	12.1	2.2	15.1	2.3	131.4	12.3	75.5	8.7	37.9	18.6
Target A	RC-TGA-0020	TGA-RC-02218	91.0	92.0	1.0	513272.9	8115204.2	765.6	505.6	490.3	59.5	221.3	19.4	78.9	48.7	164.6	13.2	46.3	11.5	1.2	11.8	2.5	16.9	3.7	12.5	2.2	15.1	2.2	137.8	15.3	77.0	7.7	34.6	16.6
Target A	RC-TGA-0020	TGA-RC-02219	92.0	93.0	1.0	513272.9	8115204.2	765.6	404.0	396.3	41.4	221.2	19.1	60.5	30.6	102.1	8.7	32.7	8.7	0.6	10.6	2.2	16.9	4.0	13.4	2.2	16.3	2.5	144.8	7.7	61.1	8.2	36.9	17.4
Target A	RC-TGA-0020	TGA-RC-02220	93.0	94.0	1.0	513272.9	8115204.2	765.6	502.5	458.0	57.3	133.4	9.6	66.9	54.4	248.1	13.0	44.3	9.2	1.6	7.5	1.4	8.3	1.8	5.4	0.9	6.1	1.0	55.1	44.5	47.3	4.8	30.2	12.1
Target A	RC-TGA-0020	TGA-RC-02221	94.0	95.0	1.0	513272.9	8115204.2	765.6	283.2	266.3	33.5	120.5	9.2	42.6	28.0	94.6	7.5	26.0	6.6	0.7	5.8	1.2	8.0	1.8	6.1	1.1	7.4	1.1	70.5	16.9	36.8	4.2	22.0	10.7
Target A	RC-TGA-0020	TGA-RC-02223	95.0	96.0	1.0	513272.9	8115204.2	765.6	352.5	334.1	37.9	115.0	8.9	46.7	32.0	160.3	8.4	29.5	7.3	0.8	6.7	1.3	7.6	1.8	5.5	1.0	6.8	1.0	64.1	18.4	36.6	3.9	23.7	8.3
Target A	RC-TGA-0020	TGA-RC-02224	96.0	97.0	1.0	513272.9	8115204.2	765.6	419.0	414.4	41.9	265.3	21.4	63.3	29.4	72.1	8.9	33.0	10.3	0.4	11.5	2.6	18.8	4.6	14.9	2.6	19.2	3.1	182.9	4.6	71.8	9.4	43.1	21.6
Target A	RC-TGA-0020	TGA-RC-02225	97.0	98.0	1.0	513272.9	8115204.2	765.6	363.3	360.3	34.7	240.0	20.6	55.3	22.0	57.0	7.3	27.4	9.6	0.1	11.4	2.5	18.1	4.2	14.1	2.4	16.6	2.5	165.1	3.1	60.5	8.8	42.0	21.4
Target A	RC-TGA-0020	TGA-RC-02226	98.0	99.0	1.0	513272.9	8115204.2	765.6	407.3	401.2	45.3	237.2	19.8	65.1	33.7	80.3	9.8	35.6	10.8	0.6	11.4	2.4	17.3	4.1	13.5	2.4	16.9	2.5	160.0	6.1	77.7	10.0	38.8	28.1
Target A	RC-TGA-0020	TGA-RC-02227	99.0	100.0	1.0	513272.9	8115204.2	765.6	439.6	431.9	53.8	234.4	19.9	73.7	42.0	97.5	11.7	42.1	11.8	1.0	12.1	2.5	17.4	4.1	13.2	2.3	16.1	2.5	155.6	7.7	90.7	9.9	38.5	20.3
Target A	RC-TGA-0020	TGA-RC-02228	100.0	101.0	1.0	513272.9	8115204.2	765.6	427.8	423.2	46.7	240.4	19.9	66.5	34.2	94.7	10.1	36.6	11.8	0.5	11.5	2.5	17.3	4.2	14.1	2.4	17.5	2.5	163.2	4.6	59.2	8.7	41.8	22.6
Target A	RC-TGA-0020	TGA-RC-02229	101.0	102.0	1.0	513272.9	8115204.2	765.6	354.4	340.6	37.4	77.4	6.7	44.2	31.0	202.1	8.3	29.2	6.5	0.9	5.1	1.0	5.8	1.2	3.8	0.7	4.8	0.7	39.7	13.8	27.5	2.7	16.2	7.1
Target A	RC-TGA-0020	TGA-RC-02230	102.0	103.0	1.0	513272.9	8115204.2	765.6	369.6	355.8	40.1	90.8	8.2	48.3	34.1	197.2	9.2	30.9	7.4	1.0	6.2	1.1	7.1	1.5	4.4	0.8	5.5	0.8	48.8	13.8	27.3	2.8	17.8	7.9
Target A	RC-TGA-0020	TGA-RC-02231	103.0	104.0	1.0	513272.9	8115204.2	765.6	281.5	269.2	39.3	61.3	5.5	44.8	34.4	140.0	8.9	30.4	6.5	1.1	4.8	0.8	4.6	1.0	2.8	0.5	3.3	0.5	29.6	12.3	26.0	2.2	13.0	4.9
Target A	RC-TGA-0020	TGA-RC-02232	104.0	105.0	1.0	513272.9	8115204.2	765.6	246.5	234.2	30.4	67.6	5.8	36.2	26.9	116.5	6.8	23.6	5.3	0.8	4.1	0.8	5.0	1.1	3.2	0.6	3.8	0.6	35.3	12.3	23.7	2.3	13.3	5.8
Target A	RC-TGA-0020	TGA-RC-02233	105.0	106.0	1.0	513272.9	8115204.2	765.6	628.6	593.3	117.2	148.8	12.1	129.3	110.6	235.2	26.3	90.9	16.8	3.1	12.0	1.8	10.3	2.1	6.0	0.9	6.6	1.0	69.6	35.3	143.8	8.9	22.5	9.3
Target A	RC-TGA-0020	TGA-RC-02235	106.0	107.0	1.0	513272.9	8115204.2	765.6	1,167.4	1,130.6	110.1	125.2	11.7	121.8	77.2	836.5	23.9	86.2	18.4	3.4	11.8	2.0	9.7	1.8	4.9	0.8	5.0	0.8	48.1	36.8	65.5	4.2	17.8	6.0
Target A	RC-TGA-0020	TGA-RC-02236	107.0	108.0	1.0	513272.9	8115204.2	765.6	852.8	805.3	121.8	125.8	10.3	132.1	103.1	484.0	26.7	95.1	18.2	3.8	11.6	1.8	8.5	1.5	3.9	0.6	3.5	0.5	42.4	47.5	132.0	7.2	17.7	5.2
Target A	RC-TGA-0020	TGA-RC-02237	108.0	109.0	1.0	513272.9	8115204.2	765.6	1,209.4	1,171.0	119.5	140.4	13.2	132.8	89.7	840.2	26.2	93.3	19.5	3.9	13.5	2.3	11.0	2.1	5.7	0.8	5.4	0.7	56.8	38.3	99.4	5.6	18.9	5.7
Target A	RC-TGA-0020	TGA-RC-02238	109.0	110.0	1.0	513272.9	8115204.2	765.6	526.1	498.5	74.2	83.8	7.2	81.4	60.4	296.0	16.6	57.6	11.7	2.4	7.9	1.2	6.0	1.1	2.9	0.4	3.2	0.4	30.7	27.6	68.8	3.8	14.1	4.3
Target A	RC-TGA-0020	TGA-RC-02239	110.0	111.0	1.0	513272.9	8115204.2	765.6	741.6	701.7	102.8	105.1	8.6	111.4	86.6	432.4	22.1	80.7	14.7	3.1	10.1	1.5	7.1	1.3	3.4	0.5	3.1	0.4	34.7	39.9	110.9	6.0	16.2	4.8
Target A	RC-TGA-0020	TGA-RC-02240	111.0	112.0	1.0	513272.9	8115204.2	765.6	633.4	578.2	119.2	117.9	8.1	127.3	105.9	273.9	25.9	93.3	16.5	3.7	10.4	1.4	6.7	1.2	2.9	0.4	2.4	0.4	33.3	55.2	152.3	7.3	14.1	3.6
Target A	RC-TGA-0020	TGA-RC-02241	112.0	113.0	1.0	513272.9	8115204.2	765.6	623.5	566.7	126.2	117.2	8.0	134.2	112.4	250.6	27.8	98.4	17.0	3.8	10.6	1.5	6.5	1.1	2.7	0.4	2.2	0.3	31.4	56.8	164.5	7.8	14.1	3.7
Target A	RC-TGA-0020	TGA-RC-02243	113.0	114.0	1.0	513272.9	8115204.2	765.6	485.5	462.5	69.1	219.6	17.3	86.4	55.9	127.8	15.2	53.9	13.1	1.4	11.3	2.2	15.1	3.6	11.8	1.9	14.0	2.0	133.3	23.0	94.3	8.9	30.4	14.0
Target A	RC-TGA-0020	TGA-RC-02244	114.0	115.0	1.0	513272.9	8115204.2	765.6	599.7	575.2	106.5	137.0	11.8	118.3	97.3	243.8	23.8	82.7	15.1	3.1	11.1	1.7	10.1	2.0	6.0	0.9	6.5	0.9	70.1	24.5	137.8	8.4	21.3	8.7
Target A	RC-TGA-0020	TGA-RC-02245	115.0	116.0	1.0	513272.9	8115204.2	765.6	413.2	405.5	47.1	209.0	17.7	64.9	35.7	110.9	10.2	37.0	10.5	0.7	10.3	2.2	15.6	3.7	12.2	2.1	15.3	2.3	137.1	7.7	62.7	7.8	34.0	17.0
Target A	RC-TGA-0020	TGA-RC-02246	116.0	117.0	1.0	513272.9	8115204.2	765.6	662.4	647.1	64.2	158.7	14.0	78.2	47.3	379.6	13.8	50.4	12.7	1.8	10.3	1.9	12.1	2.7	8.4	1.4	9.9	1.4	93.3	15.3	56.1	5.4	27.2	12.7
Target A	RC-TGA-0020	TGA-RC-02247	117.0	118.0	1.0	513272.9	8115204.2	765.6	776.9	760.0	77.0	194.5	17.6	94.6	54.2	436.1	16.7	60.3	15.1	2.2	13.5	2.5	15.1	3.3	10.3	1.7	11.7	1.8	115.4	16.9	54.5	5.5	27.7	12.6
Target A	RC-TGA-0020	TGA-RC-02248	118.0	119.0	1.0	513272.9	8115204.2	765.6	376.5	371.9	41.1	225.5	18.9	60.0	31.8	68.7	8.9	32.2	9.5	0.4	10.3	2.3	16.6	3.7	12.6	2.3	15.8	2.5	154.3	4.6	65.1	8.9	41.4	22.6
Target A	RC-TGA-0020	TGA-RC-02249	119.0	120.0	1.0	513272.9	8115204.2	765.6	351.6	348.6	34.5	225.1	18.3	52.8	25.4	58.5	7.4	27.1	8.1	0.2	9.6	2.3	16.0	3.7	12.9	2.2	15.7	2.5	156.8	3.1	58.4	8.7	39.4	21.5
Target A	RC-TGA-0020	TGA-RC-02251	0.0	1.0	1.0	513097.1	8115401.4	769.2	276.5	238.1	28.9	98.6	6.2	35.1	30.0	114.6	6.5	22.4	4.3	0.8	3.9	0.8	5.4	1.2	3.7	0.7	4.6	0.7	38.5	38.3	100.6	7.0	27.3	6.7
Target A	RC-TGA-0021	TGA-RC-02252	1.0	2.0	1.0	513097.1	8115401.4	769.2	408.8	369.0	56.9	116.6	7.9	64.8	63.1	164.0	13.2	43.7	8.2	1.3	6.2	1.1	6.8	1.5	4.5	0.7	5.4	0.8	48.5	39.9	110.7	7.7	29.7	8.4
Target A	RC-TGA-

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0021	TGA-RC-02262	10.0	11.0	1.0	513097.1	8115401.4	769.2	363.0	321.6	60.3	83.0	4.5	64.7	61.9	150.5	13.7	46.5	7.4	1.3	4.1	0.6	3.8	0.8	2.5	0.4	2.9	0.5	24.6	41.4	62.4	4.4	25.1	7.2
Target A	RC-TGA-0021	TGA-RC-02263	11.0	12.0	1.0	513097.1	8115401.4	769.2	343.1	280.2	41.8	105.3	4.3	46.1	43.9	146.8	9.6	32.2	5.3	0.9	3.4	0.6	3.7	0.8	2.6	0.5	3.2	0.5	26.0	62.9	76.4	5.1	28.8	8.1
Target A	RC-TGA-0021	TGA-RC-02265	12.0	13.0	1.0	513097.1	8115401.4	769.2	352.4	309.4	59.3	87.1	4.9	64.1	62.0	137.0	13.5	45.7	7.0	1.3	3.9	0.7	4.2	0.8	2.8	0.4	2.9	0.5	26.7	42.9	61.9	3.8	24.5	7.7
Target A	RC-TGA-0021	TGA-RC-02266	13.0	14.0	1.0	513097.1	8115401.4	769.2	278.0	236.6	44.6	86.2	4.9	49.6	46.3	95.1	10.2	34.4	5.8	1.1	3.6	0.6	4.3	0.9	2.7	0.5	2.9	0.5	27.7	41.4	62.1	4.0	21.0	5.8
Target A	RC-TGA-0021	TGA-RC-02267	14.0	15.0	1.0	513097.1	8115401.4	769.2	398.6	329.5	82.0	132.1	6.9	88.9	85.7	88.7	18.1	63.9	10.1	1.8	6.6	1.0	5.9	1.1	3.3	0.5	3.2	0.5	39.0	69.0	246.8	13.7	21.1	7.6
Target A	RC-TGA-0021	TGA-RC-02268	15.0	16.0	1.0	513097.1	8115401.4	769.2	921.7	841.9	182.6	151.3	9.7	192.4	256.8	308.3	42.6	140.0	22.6	4.4	14.6	1.7	8.0	1.2	3.3	0.4	2.8	0.4	34.7	79.8	310.4	17.1	20.9	10.9
Target A	RC-TGA-0021	TGA-RC-02269	16.0	17.0	1.0	513097.1	8115401.4	769.2	382.0	285.4	76.5	138.3	5.1	81.6	82.6	75.4	17.1	59.4	9.3	1.8	6.1	0.8	4.3	0.8	2.1	0.4	2.1	0.3	23.0	96.6	110.1	6.2	13.3	11.2
Target A	RC-TGA-0021	TGA-RC-02270	17.0	18.0	1.0	513097.1	8115401.4	769.2	427.9	314.4	77.8	157.8	5.6	83.4	83.6	98.9	17.6	60.2	9.8	1.8	6.1	0.9	4.7	0.8	2.3	0.3	2.4	0.3	24.5	113.5	130.0	7.9	16.0	8.7
Target A	RC-TGA-0021	TGA-RC-02272	18.0	19.0	1.0	513097.1	8115401.4	769.2	772.0	598.7	119.7	227.4	7.4	127.1	167.7	242.6	28.8	91.0	14.6	2.9	9.2	1.2	6.2	1.0	2.7	0.4	2.5	0.4	27.6	173.3	244.6	11.2	21.0	7.7
Target A	RC-TGA-0021	TGA-RC-02273	19.0	20.0	1.0	513097.1	8115401.4	769.2	1,567.7	1,382.1	271.8	250.2	10.6	282.3	401.1	614.2	67.7	204.1	30.4	6.0	16.1	2.0	8.6	1.1	2.6	0.4	2.1	0.3	25.4	185.6	430.6	16.0	21.6	7.6
Target A	RC-TGA-0021	TGA-RC-02274	20.0	21.0	1.0	513097.1	8115401.4	769.2	1,233.7	1,052.7	192.2	230.0	8.2	200.4	295.5	493.8	47.6	144.6	22.1	4.6	12.0	1.5	6.7	0.9	2.1	0.3	1.8	0.2	18.9	181.0	379.1	16.1	27.5	7.5
Target A	RC-TGA-0021	TGA-RC-02275	21.0	22.0	1.0	513097.1	8115401.4	769.2	651.1	508.4	92.7	208.7	8.9	101.6	75.6	259.2	19.3	73.4	14.8	3.3	10.3	1.4	7.4	1.3	3.5	0.5	2.9	0.4	34.9	142.6	155.2	7.0	12.0	4.7
Target A	RC-TGA-0021	TGA-RC-02276	22.0	23.0	1.0	513097.1	8115401.4	769.2	1,069.7	933.2	230.8	270.3	19.8	250.7	89.3	439.8	44.2	186.6	39.5	9.1	25.8	3.4	16.4	2.6	6.3	0.8	5.2	0.7	63.4	136.5	138.5	6.5	12.1	3.7
Target A	RC-TGA-0021	TGA-RC-02277	23.0	24.0	1.0	513097.1	8115401.4	769.2	2,586.2	2,508.0	678.6	394.6	48.0	726.6	536.0	878.3	144.4	534.2	98.8	21.9	64.5	8.3	39.7	6.1	14.7	1.9	11.6	1.5	146.0	78.2	219.6	10.9	19.2	5.8
Target A	RC-TGA-0021	TGA-RC-02278	24.0	25.0	1.0	513097.1	8115401.4	769.2	3,214.0	3,163.4	898.4	433.9	54.8	953.1	760.0	1,002.4	192.7	705.7	119.4	25.9	80.0	9.8	45.0	7.1	16.5	2.1	12.5	1.6	182.9	50.6	244.6	11.1	20.8	5.7
Target A	RC-TGA-0021	TGA-RC-02279	25.0	26.0	1.0	513097.1	8115401.4	769.2	2,999.6	2,956.7	770.9	557.5	66.3	837.3	666.2	902.9	166.7	604.2	102.2	24.2	80.2	10.9	55.4	9.8	24.9	3.3	19.9	2.7	283.2	42.9	311.8	13.3	23.9	7.0
Target A	RC-TGA-0021	TGA-RC-02280	26.0	27.0	1.0	513097.1	8115401.4	769.2	3,317.7	3,271.6	756.3	1,234.4	131.1	887.4	478.5	717.4	148.6	607.7	131.0	34.0	128.5	19.3	111.8	22.5	59.9	8.0	48.1	7.1	749.2	46.0	221.0	10.3	22.8	6.0
Target A	RC-TGA-0021	TGA-RC-02281	27.0	28.0	1.0	513097.1	8115401.4	769.2	2,587.2	2,556.5	540.3	1,106.3	120.1	660.4	315.5	525.8	100.5	439.7	99.4	27.2	113.8	17.6	102.5	21.1	57.5	7.8	49.3	7.1	671.8	30.7	266.1	12.2	25.1	6.6
Target A	RC-TGA-0021	TGA-RC-02282	28.0	29.0	1.0	513097.1	8115401.4	769.2	3,915.3	3,880.0	538.0	2,536.8	246.2	784.2	266.2	449.6	92.4	445.6	124.7	39.5	201.1	33.3	212.9	46.9	136.1	18.4	119.0	18.1	1,676.3	35.3	243.2	12.3	24.6	6.8
Target A	RC-TGA-0021	TGA-RC-02283	29.0	30.0	1.0	513097.1	8115401.4	769.2	1,814.5	1,780.8	346.1	823.9	78.3	424.5	225.8	356.2	62.7	283.4	62.5	16.7	76.4	10.8	67.5	14.5	39.6	5.9	36.3	5.6	516.8	33.7	246.0	12.5	24.2	7.0
Target A	RC-TGA-0021	TGA-RC-02285	30.0	31.0	1.0	513097.1	8115401.4	769.2	1,951.2	1,909.8	325.6	904.9	82.8	408.5	192.9	464.3	59.7	265.9	63.4	17.1	77.0	11.6	71.3	15.6	42.8	6.2	37.2	5.6	579.1	41.4	309.0	13.7	24.5	6.1
Target A	RC-TGA-0021	TGA-RC-02286	31.0	32.0	1.0	513097.1	8115401.4	769.2	2,655.8	2,606.7	399.3	1,453.7	129.5	528.8	177.7	536.8	69.2	330.1	88.2	25.1	117.6	17.7	111.8	25.0	68.3	9.9	58.9	9.2	961.3	49.1	300.4	13.7	23.6	6.5
Target A	RC-TGA-0021	TGA-RC-02287	32.0	33.0	1.0	513097.1	8115401.4	769.2	1,545.1	1,486.8	327.8	561.4	55.7	383.5	174.2	422.6	59.6	268.3	59.1	15.1	62.2	8.3	47.4	9.6	24.5	3.4	21.0	3.0	308.6	58.3	192.4	9.9	18.4	4.6
Target A	RC-TGA-0021	TGA-RC-02288	33.0	34.0	1.0	513097.1	8115401.4	769.2	1,201.0	1,162.7	241.7	387.1	35.3	277.0	203.5	330.4	47.5	194.2	38.3	9.5	39.6	5.2	30.1	6.3	16.2	2.4	13.8	2.1	223.5	38.3	233.2	11.8	23.1	5.7
Target A	RC-TGA-0021	TGA-RC-02289	34.0	35.0	1.0	513097.1	8115401.4	769.2	867.8	835.6	161.7	256.5	21.6	183.2	134.3	291.1	33.3	128.3	24.2	6.1	24.0	3.2	18.4	3.9	10.8	1.5	9.5	1.4	145.4	32.2	269.6	11.7	29.4	6.7
Target A	RC-TGA-0021	TGA-RC-02290	35.0	36.0	1.0	513097.1	8115401.4	769.2	765.6	724.1	139.7	155.2	11.7	151.4	141.9	309.6	30.7	109.1	19.2	4.4	13.7	1.9	9.8	1.9	5.1	0.7	4.6	0.7	71.0	41.4	254.6	11.7	23.0	5.8
Target A	RC-TGA-0021	TGA-RC-02291	36.0	37.0	1.0	513097.1	8115401.4	769.2	869.8	834.5	173.5	136.7	12.4	185.8	167.1	369.7	37.6	135.9	22.7	5.4	15.7	2.1	10.2	1.9	4.7	0.7	3.7	0.5	56.6	35.3	289.0	14.7	21.7	5.4
Target A	RC-TGA-0021	TGA-RC-02292	37.0	38.0	1.0	513097.1	8115401.4	769.2	814.0	778.7	165.2	134.1	12.2	177.4	156.0	336.6	35.8	129.5	22.0	4.9	15.3	1.9	10.2	1.8	4.6	0.7	3.9	0.5	55.0	35.3	254.6	12.0	20.5	5.0
Target A	RC-TGA-0021	TGA-RC-02294	38.0	39.0	1.0	513097.1	8115401.4	769.2	869.5	837.3	175.2	150.7	13.9	189.1	168.3	351.3	37.6	137.6	24.0	5.1	16.3	2.2	11.8	2.1	5.2	0.8	4.7	0.6	69.7	32.2	277.5	14.0	19.7	4.2
Target A	RC-TGA-0021	TGA-RC-02295	39.0	40.0	1.0	513097.1	8115401.4	769.2	826.7	757.7	171.9	154.6	10.7	182.5	149.5	328.0	36.0	135.9	22.7	5.2	15.2	1.8	8.9	1.5	3.7	0.5	3.3	0.5	45.0	69.0	228.9	11.7	18.7	4.2
Target A	RC-TGA-0021	TGA-RC-02296	40.0	41.0	1.0	513097.1	8115401.4	769.2	727.0	687.1	143.1	134.8	11.7	154.9	140.1	288.7	30.7	112.4	20.2	4.4	14.1	1.9	9.9	1.8	4.6	0.6	3.9	0.5	53.3	39.9	245.3	11.8	19.6	5.2
Target A	RC-TGA-0021	TGA-RC-02297	41.0	42.0	1.0	513097.1	8115401.4	769.2	793.3	750.4	161.8	129.7	10.7	172.5	151.3	329.2	34.7	127.1	21.3	5.0	14.1	1.8	8.9	1.6	4.0	0.6	3.3	0.5	47.1	42.9	284.0	12.6	20.3	5.0
Target A	RC-TGA-0021	TGA-RC-02298	42.0	43.0	1.0	513097.1	8115401.4	769.2	717.3	683.6	143.5	133.4	11.8	155.3	138.4	282.5	31.3	112.2	19.5	4.3	14.0	1.9	9.8	1.9	4.6	0.7	4.5	0.7	57.1	33.7	231.7	11.6	15.6	5.4
Target A	RC-TGA-0021	TGA-RC-02299	43.0	44.0	1.0	513097.1	8115401.4	769.2	732.8	697.5	145.7	126.1	11.0	156.7	139.6	302.2	31.5	114.2	19.2	4.1	13.5	1.8	9.2	1.7	4.3	0.6	3.7	0.5	51.3	35.3	238.2	12.3	17.5	4.3
Target A	RC-TGA-0021	TGA-RC-02301	44.0	45.0	1.0	513097.1	8115401.4	769.2	666.0	632.3	132.2	121.4	10.6	142.9	129.6	265.3	29.0	103.2	17.5	4.1	12.9	1.7	8.9	1.7	4.3	0.6	3.6	0.5	49.4	33.7	218.9	11.1	16.6	3.9
Target A	RC-TGA-0021	TGA-RC-02302	45.0	46.0	1.0	513097.1	8115401.4	769.2	599.7	567.5	118.5	115.7	9.7	128.1	115.4	234.0	25.5	93.0	16.2	3.9	11.8	1.6	8.1	1.6	4.1	0.6	3.5	0.6	47.9	32.2	206.7	9.8	19.6	5.3
Target A	RC-TGA-0021	TGA-RC-02303	46.0	47.0	1.0	513097.1	8115401.4	769.2	654.3	626.7	127.4	122.3	11.1	138.5	127.8	259.2	27.8	99.6	17.6	4.2	13.0	1.8	9.3	1.8	4.8	0.7	4.1	0.6	54.5	27.6	251.1	11.1	19.5	6.6
Target A	RC-TGA-0021	TGA-RC-02304	47.0	48.0	1.0	513097.1	8115401.4	769.2	804.2	779.7	159.2	146.0	14.1	173.4	154.2	323.1	34.4	124.8	21.7	5.0	16.9	2.2	11.9	2.3	5.9	0.8	5.3	0.7	70.4	24.5	277.5	13.7	18.9	4.7
Target A	RC-TGA-0021	TGA-RC-02305	48.0	49.0	1.0	513097.1	8115401.4	769.2	850.3	825.8	167.8	164.7	16.0	183.8	160.7	334.1	36.0	131.8	23.0	5.5	18.6	2.4	13.6	2.7	6.9	1.0	6.0	0.9	82.5	24.5	273.9	13.9	19.8	4.4
Target A	RC-TGA-0021	TGA-RC-02306	49.0	50.0	1.0	513097.1	8115401.4	769.2	727.4	695.2	143.1	157.4	14.7	157.8	131.4	275.2	30.8	112.3	20.4	4.9	16.3	2.2	12.5	2.4	5.9	0.9	5.4	0.8	73.9	32.2	220.3	11.1	19.7	5.0
Target A	RC-TGA-0021	TGA-RC-02307	50.0	51.0	1.0	513097.1	8115401.4	769.2	753.2	728.7	148.7	139.9	13.4	162.1	143.7	301.0	32.0	116.6	20.1	4.8	15.4	2.1	11.3	2.2	5.6	0.8	5.1	0.7	67.3	24.5	253.9	13.2	15.3	3.2
Target A	RC-TGA-0021	TGA-RC-02309	51.0	52.0	1.0	513097.1	8115401.4	769.2	684.7	660.2	136.7	128.5	12.4	149.1	132.5	267.8	29.8	106.8	19.2	4.2	14.2	1.9	10.5	1.9	5.1	0.7	4.8	0.7	59.9	24.5	229.6	11.7	15.5	3.8
Target A	RC-TGA-0021	TGA-RC-02310	52.0	53.0	1.0	513097.1	8115401.4	769.2	644.9	618.8	126.8	119.3	11.0	137.8	127.2	254.3	26.8	100.0	17.3	3.9	12.9	1.8	9.2	1.7	4.7	0.7	4.1	0.6	53.6	26.1	223.9	10.9	16.6	4.1
Target A	RC-TGA-0021	TGA-RC-02311	53.0	54.0	1.0	513097.1	8115401.4	769.2	506.8	473.1	97.4	98.9	7.7	105.0	98.4	198.4	21.2	76.2	13.8	3.3	9.3	1.2	6.5	1.2	3.2	0.4	3.0	0.4	36.6	33.7	181.7	8.1	22.0	6.6
Target A	RC-TGA-0021	TGA-RC-02312	54.0	55.0	1.0	513097.1	8115401.4	769.2	466.4	434.2	89.9	92.6	7.1	97.0	90.8	180.6	19.6	70.3	12.6	3.0	9.0	1.2	5.9	1.1	2.9	0.4	2.6	0.4	33.8	32.2	166.7	7.3	26.4	7.7
Target A	RC-TGA-0021	TGA-RC-02313	55.0	56.0	1.0	513097.1	8115401.4	769.2	438.2	404.4	84.1	87.0	6.4	90.6	84.8	170.7	18.2	65.9	11.5	2.8	8.1	1.0	5.4	1.0	2.7	0.4	2.4	0.4	29.0	33.7	160.2	7.1	24.2	7.1
Target A	RC-TGA-0021	TGA-RC-02314	56.0	57.0	1.0	513097.1	8115401.4	769.2	579.1	545.3	114.1	109.6	9.1	123.2	111.9	227.9	24.4	89.7	15.6	3.6	11.2	1.4	7.7	1.4	3.7	0.5	3.3	0.5	42.5	33.7	207.4	9.5	15.3	3.9
Target A	RC-TGA-0021	TGA-RC-02315	57.0	58.0	1.0	513097.1	8115401.4	769.2	793.1	763.9	155.8	142.0	13.4	169.3	149.5	324.3	34.0	121.9	21.5	4.8	15.6	2.1	11.4	2.2	5.6	0.8	4.9	0.6	65.0	29.1	273.2	14.7	15.7	3.2
Target A	RC-TGA-0021	TGA-RC-02317	58.0	59.0	1.0	513097.1	8115401.4	769.2	742.4	717.8	145.8	134.1	13.1	158.9	139.0	303.4	31.7	114.2	20.1	4.2	14.5	2.1	11.0	2.1	5.5	0.8	5.1	0.6	63.6	24.5	253.2	13.2	14.8	2.9
Target A	RC-TGA-0021	TGA-RC-02318	59.0	60.0	1.0	513097.1	8115401.4	769.2	677.7	659.3	129.9	129.3	12.8	142.7	126.7	273.9	28.6	101.2	17.9	3.7	13.6	1.9	10.9	2.1	5.8	0.8	5.4	0.8	65.8	18.4	224.6	12.3	15.1	3.3
Target A	RC-TGA-0021	TGA-RC-02319	60.0	61.0	1.0	513097.1	8115401.4	769.2	1,022.1	971.5	215.4	135.4	11.2	226.6	201.1	444.7	50.4	165.0	25.5	6.4	15.6	1.9	9.3	1.6	3.6	0.5	2.8	0.4	42.8	50.6	311.8	12.1	22.9	5.8
Target A	RC-TGA-0021	TGA-RC-02320	61.0	62.0	1.0	513097.1	8115401.4	769.2	444.4	398.4	90.6	100.0	7.0	97.5	76.8	164.6	20.2	70.3	12.4	3.1	8.8	1.1	5.9	1.0	2.5	0.3	2.1	0.3	28.8	46.0	150.9	7.2	15.2	4.8
Target A	RC-TGA-0021	TGA-RC-02321	62.0	63.0	1.0	513097.1	8115401.4	769.2	511.7	470.3	103.5	110.3	8.3	111.8	91.0	192.2	23.4	80.0	14.7	3.4	9.7	1.4	7.0	1.3	3.5	0.5	2.9	0.4	38.9	41.4	168.8	8.5	17.4	4.6
Target A	RC-TGA-0021	TGA-RC-02322	63.0	64.0	1.0	513097.1	8115401.4	769.2	639.4	582.7	131.0	127.6	8.9	139.9	117.9	245.7	30.0	101.0	17.3	4.1	11.6	1.5	7.4	1.3	3.2	0.4	2.9	0.4	38.0	56.8	191.7	8.5	22.0	5.3
Target A	RC-TGA-0021	TGA-RC-02323	64.0	65.0	1.0	513097.1	8115401.4	769.2	492.7	454.4	99.3	105.0	7.8	107.1	89.6	185.5	22.1	77.2	13.3	3.3	9.7	1.3	6.5	1.3	3.3	0.4	3.0	0.4	37.5	38.3	166.7	8.2	18.0	5.2
Target A	RC-TGA-0021	TGA-RC-02325	65.0	66.0	1.0	513097.1	8115401.4	769.2	677.2	623.5	144.7	125.5	9.3	154.0	122.0	265.3	32.5	112.2	19.7	4.8	12.4	1.6	7.7	1.4	3.3	0.4	2.5	0.4	37.3	53.7	206.0	9.8	16.2	4.0
Target A	RC-TGA-0021	TGA-RC-02326	66.0	67.0	1.0	513097.1	8115401.4	769.2	579.5	547.3	117.3	119.7	10.5	127.9	106.4	219.9	26.3	91.0	16.2	3.6	11.6	1.7	8.8	1.7	4.4	0.6	4.1	0.6	50.4	32.2	198.1	9.8	16.7	4.5
Target A	RC-TGA-0021	TGA-RC-02327	67.0	68.0	1.0	513097.1	8115401.4	769.2	352.6	274.4	64.8	136.1	7.4	72.2	42.0	99.1	13.2	51.6	10.6	2.4	7.9	1.2	6.2	1.1	2.9	0.4	2.7	0.4	32.8	78.2	55.1	2.9	5.2	1.5
Target A	RC-TGA-0021	TGA-RC-02328	68.0	69.0	1.0	513097.1	8115401.4	769.2	490.4	419.8	104.8	146.5	9.7	114.5	67.4	156.6	19.9	84.9	14.9	3.1	10.8	1.4	8.3	1.4	3.8	0.5	3.3	0.4	42.9	70.6	54.2	3.5	7.9	2.2
Target A	RC-TGA-0021	TGA-RC-02329	69.0	70.0	1.0	513097.1	8115401.4	769.2	370.6	289.3	73.0	135.2	6.7	79.8	46.2	105.4	14.1	58.9	10.8	2.7	7.7	1.0	5.7	1.1	2.7	0.3	2.0	0.3	30.2	81.3	62.8	3.3	4.8	1.4
Target A	RC-TGA-0021	TGA-RC-02330	70.0	71.0	1.0	513097.1	8115401.4	769.2	312.5	228.2	58.5	137.0	6.9	65.4	31.9	76.0	11.0	47.5	9.1	2.1	7.5	1.0	5.9	1.0	2.7	0.4	2.1	0.3	29.6	84.4	29.6	1.7	3.0	1.0
Target A	RC-TGA-0021	TGA-RC-02331	71.0	72.0	1.0	513097.1	8115401.4	769.2	293.7	213.9	54.0	126.7	5.7	59.8	32.5	72.2	10.2	43.9	8.2	2.0	6.7	0.9	4.8	0.8	2.0	0.3	1.7	0.3	27.3	79.8	33.6	1.7	3.9	1.6
Target A	RC-TGA-0021	TGA-RC-02332	72.0	73.0	1.0	513097.1	8115401.4	769.2	374.3	296.1	72.9	134.3	7.1	80.0	48.2	108.2	14.4	58.6	10.6	2.9	8.8	1.1	5.9	1.2	2.5	0.3	2.0	0.3	31.0	78.2	67.1	3.4	5.1	1.4
Target A	RC-TGA-0021	TGA-RC-02333	73.0	74.0	1.0	513097.1	8115401.4	769.2	264.4	183.1	48.8	127.9	5.6	54.4	22.0	58.0	8.7	40.1	7.7	2.2	7.0	1.0	4.6	0.9	2.3	0.3	1.9	0.3	26.2	81.3	24.9	1.5	1.9	0.8
Target A	RC-TGA-0021	TGA-RC-02335	74.0	75.0	1.0	513097.1	8115401.4	769.2	290.6	212.3	54.6	127.3	6.1	60.7	28.6	71.2	10.1	44.6	8.8	2.1	7.4	1.0	5.1	0.9	2.1	0.3	1.9	0.3	28.1	78.2	33.5	2.0	2.1	0.8
Target A	RC-TGA-0021	TGA-RC-02336	75.0	76.0	1.0	513097.1	8115401.4	769.2	282.9	206.2	51.6	128.4	6.5	58.1	27.3	66.8	9.4	42.2	8.7	2.1	7.5	1.1	5.4	1.0	2.4	0.3	2.0	0.3	29.6	76.7	30.8	1.8	2.3	0.8
Target A	RC-TGA-0021	TGA-RC-02337	76.0	77.0	1.0	513097.1	8115401.4	769.2	301.8	219.0	55.4	138.9	6.9	62.3	28.0	70.3	10.0	45.4	9.3	2.3	7.8	1.1	5.8	1.1	2.7	0.4	2.2	0.3	32.3	82.8	32.5	1.8	2.2	0.7
Target A	RC-TGA-0021	TGA-RC-02338	77.0	78.0	1.0	513097.1	8115401.4	769.2	291.7	221.2	55.6	129.9	7.0	62.6	28.4	69.0	9.9	45.7	8.8	2.1	7.8	1.0	6.0	1.0	2.8	0.4	2.3	0.4	35.6	70.6	33.3	1.8	2.2	0.8
Target A	RC-TGA-0021	TGA-RC-02339	78.0	79.0	1.0	513097.1	8115401.4	769.2	499.1	450.1	103.7	130.3	10.0	113.7	82.0	168.9	21.1	82.6	14.2	3.4	11.2	1.6	8.4	1.5	4.0	0.6	3.2	0.

RARE EARTHS AMERICAS

Complete Assay Results Associated with 11.11.2026 Release Titled: *Rare Earths Americas Expands Homer-A Mineralized Zone by More Than 60% and Identifies Strongest Heavy Rare Earth Enrichment to Date*

Target	Hole ID	Sample ID	From (m)	To (ppm)	Thickness (m)	Easting (m)	Northing (m)	Elevation (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La_2O_3 ppm	CeO_2 ppm	Pr_6O_{11} ppm	Nd_2O_3 ppm	Sm_2O_3 ppm	Eu_2O_3 ppm	Gd_2O_3 ppm	Tb_4O_7 ppm	Dy_2O_3 ppm	Ho_2O_3 ppm	Er_2O_3 ppm	Tm_2O_3 ppm	Yb_2O_3 ppm	Lu_2O_3 ppm	Y_2O_3 ppm	Sc_2O_3 ppm	Nb_2O_5 ppm	Ta_2O_5 ppm	ThO_2 ppm	U_3O_8 ppm
Target A	RC-TGA-0022	TGA-RC-02349	6.0	7.0	1.0	512904.0	8115599.8	772.0	297.3	246.7	23.7	98.0	4.5	28.3	24.3	148.0	5.3	18.4	3.3	0.7	2.7	0.5	4.0	1.0	3.1	0.5	4.0	0.6	30.2	50.6	111.9	7.6	28.3	6.6
Target A	RC-TGA-0022	TGA-RC-02350	7.0	8.0	1.0	512904.0	8115599.8	772.0	282.9	235.4	22.6	91.9	4.2	26.8	23.8	141.9	5.2	17.4	2.8	0.6	2.5	0.5	3.7	0.9	2.9	0.5	3.9	0.6	28.1	47.5	105.4	7.1	27.2	6.4
Target A	RC-TGA-0022	TGA-RC-02352	8.0	9.0	1.0	512904.0	8115599.8	772.0	710.4	543.2	55.4	208.0	4.5	59.9	62.4	378.3	13.2	42.2	6.3	1.1	4.0	0.6	3.9	0.8	2.5	0.4	3.1	0.5	23.9	167.2	58.8	3.7	34.6	11.7
Target A	RC-TGA-0022	TGA-RC-02353	9.0	10.0	1.0	512904.0	8115599.8	772.0	588.3	457.9	66.4	167.0	4.2	70.5	75.3	272.7	15.3	51.1	6.9	1.3	3.9	0.6	3.5	0.7	2.3	0.4	2.7	0.5	20.8	130.4	51.1	3.4	29.2	9.7
Target A	RC-TGA-0022	TGA-RC-02354	10.0	11.0	1.0	512904.0	8115599.8	772.0	396.5	327.5	55.7	124.0	5.5	61.2	64.6	145.6	12.8	42.9	6.6	1.0	4.0	0.7	4.7	1.0	3.5	0.6	4.3	0.6	34.4	69.0	73.4	5.9	29.1	8.8
Target A	RC-TGA-0022	TGA-RC-02355	11.0	12.0	1.0	512904.0	8115599.8	772.0	280.7	245.4	46.9	98.7	5.5	52.4	58.1	71.6	10.9	35.9	5.4	0.9	3.9	0.7	4.9	1.1	4.1	0.7	5.4	0.8	41.0	35.3	84.0	8.7	22.5	5.2
Target A	RC-TGA-0022	TGA-RC-02356	12.0	13.0	1.0	512904.0	8115599.8	772.0	289.5	234.3	51.9	98.7	4.2	56.1	61.0	72.0	12.1	39.9	5.9	1.1	3.4	0.5	3.6	0.8	2.6	0.5	3.4	0.5	27.0	55.2	236.0	18.6	34.4	8.3
Target A	RC-TGA-0022	TGA-RC-02358	13.0	14.0	1.0	512904.0	8115599.8	772.0	337.6	225.7	56.1	143.2	3.2	59.3	63.4	68.3	12.6	43.5	6.6	1.2	3.4	0.5	2.7	0.7	1.9	0.3	2.2	0.4	18.0	112.0	184.5	12.5	24.1	9.8
Target A	RC-TGA-0022	TGA-RC-02359	14.0	15.0	1.0	512904.0	8115599.8	772.0	369.0	218.6	59.4	176.9	3.1	62.5	59.9	66.0	13.0	46.4	6.7	1.3	4.0	0.5	2.6	0.5	1.4	0.2	1.4	0.2	14.5	150.3	306.1	23.1	40.7	11.8
Target A	RC-TGA-0022	TGA-RC-02360	15.0	16.0	1.0	512904.0	8115599.8	772.0	410.8	223.7	62.3	217.1	3.7	66.0	61.1	62.4	13.5	48.8	7.9	1.3	4.3	0.6	3.1	0.5	1.7	0.3	1.7	0.2	16.3	187.1	257.5	16.0	23.2	11.3
Target A	RC-TGA-0022	TGA-RC-02361	16.0	17.0	1.0	512904.0	8115599.8	772.0	374.8	212.3	57.5	190.8	3.6	61.1	55.0	64.5	12.7	44.8	7.1	1.4	4.5	0.6	3.0	0.5	1.5	0.2	1.7	0.2	14.5	162.6	278.9	13.6	14.6	9.1
Target A	RC-TGA-0022	TGA-RC-02362	17.0	18.0	1.0	512904.0	8115599.8	772.0	461.1	275.5	62.3	214.4	3.5	65.8	56.3	119.5	13.0	49.2	8.6	1.4	4.7	0.6	2.9	0.5	1.5	0.2	1.5	0.3	15.2	185.6	234.6	11.6	14.7	6.6
Target A	RC-TGA-0022	TGA-RC-02363	18.0	19.0	1.0	512904.0	8115599.8	772.0	554.0	351.5	63.6	231.6	3.7	67.3	84.1	167.1	14.8	48.8	7.7	1.5	4.5	0.6	3.1	0.6	1.5	0.2	1.6	0.2	15.2	202.5	238.2	14.9	22.8	7.1
Target A	RC-TGA-0022	TGA-RC-02364	19.0	20.0	1.0	512904.0	8115599.8	772.0	648.8	424.8	111.6	271.1	6.4	118.0	101.9	149.9	24.2	87.5	14.3	2.7	8.3	1.1	5.3	1.0	2.6	0.4	2.8	0.4	22.6	223.9	132.9	7.6	15.3	5.4
Target A	RC-TGA-0022	TGA-RC-02366	20.0	21.0	1.0	512904.0	8115599.8	772.0	559.3	333.9	61.6	268.5	5.5	67.1	59.9	160.3	13.5	48.1	9.0	1.7	5.7	0.8	4.7	1.0	2.5	0.5	3.0	0.3	22.9	225.5	158.1	6.8	10.9	5.6
Target A	RC-TGA-0022	TGA-RC-02367	21.0	22.0	1.0	512904.0	8115599.8	772.0	526.4	290.2	59.5	279.6	5.3	64.9	62.7	116.5	13.0	46.5	8.0	1.6	5.7	0.8	4.5	0.9	2.7	0.4	2.7	0.4	23.9	236.2	227.4	10.7	17.4	5.9
Target A	RC-TGA-0022	TGA-RC-02368	22.0	23.0	1.0	512904.0	8115599.8	772.0	692.9	384.6	25.6	331.3	2.8	28.4	16.7	315.7	5.3	20.3	3.7	0.8	2.8	0.4	2.4	0.5	1.4	0.2	1.3	0.2	13.0	308.3	229.6	9.0	12.0	5.8
Target A	RC-TGA-0022	TGA-RC-02369	23.0	24.0	1.0	512904.0	8115599.8	772.0	993.3	683.5	15.7	326.4	1.9	17.6	10.0	638.8	3.2	12.5	2.5	0.6	1.9	0.3	1.6	0.4	1.0	0.1	1.1	0.1	9.4	309.8	182.4	8.1	10.5	4.9
Target A	RC-TGA-0022	TGA-RC-02370	24.0	25.0	1.0	512904.0	8115599.8	772.0	1,274.7	995.5	48.5	301.4	3.6	52.1	30.3	886.9	10.5	38.0	7.6	1.6	4.2	0.5	3.1	0.5	1.1	0.2	1.2	0.2	9.8	279.2	130.5	5.7	7.9	3.9
Target A	RC-TGA-0022	TGA-RC-02371	25.0	26.0	1.0	512904.0	8115599.8	772.0	1,275.6	1,067.0	148.9	260.8	8.1	156.9	87.1	759.2	31.1	117.8	19.7	5.0	11.6	1.4	6.7	1.0	2.3	0.3	1.8	0.2	21.8	208.6	186.7	9.5	16.7	3.0
Target A	RC-TGA-0022	TGA-RC-02373	26.0	27.0	1.0	512904.0	8115599.8	772.0	2,078.7	1,909.9	303.3	275.2	16.8	320.2	180.0	1,277.5	63.1	240.3	42.6	9.7	24.6	3.1	13.8	2.1	4.4	0.6	3.4	0.4	44.4	168.7	194.5	9.5	16.8	2.5
Target A	RC-TGA-0022	TGA-RC-02374	27.0	28.0	1.0	512904.0	8115599.8	772.0	1,890.1	1,689.2	305.1	308.8	16.2	321.2	179.4	1,054.0	62.5	242.6	42.9	9.4	24.4	3.0	13.1	2.1	4.7	0.6	3.5	0.5	46.5	200.9	141.6	5.3	6.4	2.5
Target A	RC-TGA-0022	TGA-RC-02375	28.0	29.0	1.0	512904.0	8115599.8	772.0	744.5	597.2	139.2	205.3	8.6	147.8	91.9	288.7	28.6	110.6	19.4	4.5	11.9	1.5	7.1	1.1	2.7	0.4	2.7	0.4	25.8	147.2	225.3	9.9	14.2	4.1
Target A	RC-TGA-0022	TGA-RC-02376	29.0	30.0	1.0	512904.0	8115599.8	772.0	642.7	573.7	145.9	128.5	8.6	154.6	97.6	250.6	30.8	115.1	20.1	4.9	12.7	1.5	7.1	1.1	2.5	0.4	2.1	0.3	26.8	69.0	221.7	9.5	15.5	2.9
Target A	RC-TGA-0022	TGA-RC-02377	30.0	31.0	1.0	512904.0	8115599.8	772.0	894.4	823.8	250.9	188.0	17.0	267.9	182.4	238.3	51.5	199.5	34.8	8.9	23.5	2.9	14.1	2.2	5.0	0.7	3.9	0.5	55.7	70.6	156.6	7.0	9.7	2.4
Target A	RC-TGA-0022	TGA-RC-02378	31.0	32.0	1.0	512904.0	8115599.8	772.0	1,455.6	1,386.6	411.2	317.3	34.2	445.4	321.3	342.7	85.8	325.4	63.0	15.3	46.2	5.8	28.5	4.7	11.0	1.4	7.5	1.1	127.0	69.0	124.5	5.9	7.7	2.0
Target A	RC-TGA-0022	TGA-RC-02379	32.0	33.0	1.0	512904.0	8115599.8	772.0	1,719.6	1,667.4	419.5	435.6	44.2	463.6	435.1	367.3	88.2	331.3	62.2	15.9	53.0	7.0	37.2	6.9	17.5	2.3	13.6	2.1	227.9	52.1	208.9	10.1	13.7	2.9
Target A	RC-TGA-0022	TGA-RC-02380	33.0	34.0	1.0	512904.0	8115599.8	772.0	2,704.2	2,583.0	404.6	1,508.3	130.0	534.6	293.2	416.4	74.5	330.1	81.6	26.2	114.7	17.9	112.0	24.6	68.3	9.3	55.1	9.1	949.9	121.2	311.8	13.1	16.5	5.5
Target A	RC-TGA-0022	TGA-RC-02381	34.0	35.0	1.0	512904.0	8115599.8	772.0	1,008.2	845.6	171.3	397.1	24.5	195.8	138.4	273.9	34.8	136.5	27.5	7.3	26.6	3.7	20.8	4.2	11.4	1.6	9.3	1.6	147.9	162.6	238.2	9.9	13.4	4.0
Target A	RC-TGA-0022	TGA-RC-02382	35.0	36.0	1.0	512904.0	8115599.8	772.0	935.4	746.7	163.5	386.4	20.6	184.1	123.7	235.2	32.9	130.6	26.6	7.0	24.4	3.1	17.5	3.5	8.9	1.2	7.2	1.0	123.7	188.7	156.6	6.8	10.0	2.9
Target A	RC-TGA-0022	TGA-RC-02383	36.0	37.0	1.0	512904.0	8115599.8	772.0	582.5	438.4	102.3	226.2	10.1	112.3	84.0	154.2	21.4	80.8	15.9	3.9	12.3	1.6	8.5	1.5	3.6	0.5	2.6	0.4	47.2	144.2	109.3	4.8	6.8	2.5
Target A	RC-TGA-0022	TGA-RC-02385	37.0	38.0	1.0	512904.0	8115599.8	772.0	424.3	300.1	72.9	173.7	6.2	79.2	54.4	112.0	14.7	58.2	11.3	2.8	8.3	1.1	5.2	0.9	2.2	0.3	1.7	0.2	26.8	124.2	65.7	3.2	4.5	1.3
Target A	RC-TGA-0022	TGA-RC-02386	38.0	39.0	1.0	512904.0	8115599.8	772.0	374.0	259.0	59.7	164.2	5.9	65.6	45.5	94.8	12.3	47.5	9.7	2.4	7.1	0.9	5.0	0.9	2.2	0.3	1.9	0.3	28.2	115.0	64.1	2.6	3.2	1.2
Target A	RC-TGA-0022	TGA-RC-02387	39.0	40.0	1.0	512904.0	8115599.8	772.0	396.4	312.1	66.8	136.2	6.2	73.0	61.2	121.6	14.5	52.3	10.6	2.6	7.5	1.0	5.2	1.0	2.4	0.3	2.1	0.3	29.5	84.4	122.9	4.2	4.8	2.0
Target A	RC-TGA-0022	TGA-RC-02388	40.0	41.0	1.0	512904.0	8115599.8	772.0	466.2	372.6	83.8	142.5	6.5	90.3	75.5	152.3	17.7	66.1	12.0	3.1	8.4	1.1	5.3	0.9	2.1	0.3	1.5	0.2	25.9	93.6	127.3	5.9	7.6	1.9
Target A	RC-TGA-0022	TGA-RC-02389	41.0	42.0	1.0	512904.0	8115599.8	772.0	386.5	279.2	62.9	152.7	5.8	68.7	53.1	107.9	13.2	49.7	10.0	2.5	7.7	1.0	4.8	0.8	2.1	0.3	1.6	0.2	24.3	107.4	97.6	4.4	4.3	1.7
Target A	RC-TGA-0022	TGA-RC-02390	42.0	43.0	1.0	512904.0	8115599.8	772.0	433.6	340.0	75.0	146.1	7.0	82.0	68.8	132.1	15.8	59.3	11.5	3.0	8.7	1.1	5.9	1.0	2.3	0.3	1.6	0.2	28.3	93.6	122.3	4.6	5.6	2.1
Target A	RC-TGA-0022	TGA-RC-02391	43.0	44.0	1.0	512904.0	8115599.8	772.0	469.3	371.1	80.4	154.9	7.4	87.8	77.5	143.1	17.2	63.2	13.4	3.3	9.5	1.2	6.2	1.1	2.6	0.3	1.7	0.3	30.5	98.2	137.6	5.3	5.6	2.3
Target A	RC-TGA-0022	TGA-RC-02393	44.0	45.0	1.0	512904.0	8115599.8	772.0	411.6	313.4	70.0	147.3	6.2	76.3	62.4	120.9	14.6	55.4	11.0	2.9	8.4	1.1	5.2	1.0	2.3	0.3	1.6	0.2	26.3	98.2	112.7	4.6	4.9	1.8
Target A	RC-TGA-0022	TGA-RC-02394	45.0	46.0	1.0	512904.0	8115599.8	772.0	346.2	234.2	56.6	152.5	5.4	62.0	40.6	87.2	11.4	45.3	9.3	2.4	6.8	0.9	4.5	0.8	1.9	0.2	1.4	0.2	21.5	112.0	51.4	2.4	2.9	1.1
Target A	RC-TGA-0022	TGA-RC-02395	46.0	47.0	1.0	512904.0	8115599.8	772.0	351.0	239.0	58.2	151.3	5.3	63.4	42.1	89.9	11.6	46.5	9.5	2.3	7.1	0.9	4.4	0.8	1.8	0.2	1.4	0.2	20.2	112.0	55.5	2.9	3.2	1.0
Target A	RC-TGA-0022	TGA-RC-02396	47.0	48.0	1.0	512904.0	8115599.8	772.0	369.5	268.3	63.7	142.7	5.4	69.1	49.1	104.4	13.2	50.5	9.6	2.5	7.6	1.0	4.5	0.8	1.9	0.2	1.4	0.2	21.6	101.2	68.7	3.4	4.6	1.2
Target A	RC-TGA-0022	TGA-RC-02397	48.0	49.0	1.0	512904.0	8115599.8	772.0	376.1	270.3	64.7	149.0	5.8	70.5	47.9	104.2	13.3	51.4	10.3	2.7	8.0	1.0	4.8	0.8	1.9	0.3	1.5	0.2	22.0	105.8	63.1	3.1	4.1	1.4
Target A	RC-TGA-0022	TGA-RC-02398	49.0	50.0	1.0	512904.0	8115599.8	772.0	386.6	290.0	70.0	138.0	5.4	75.3	53.1	114.7	14.3	55.6	10.8	2.5	7.4	0.9	4.5	0.8	1.8	0.2	1.3	0.2	21.8	96.6	65.8	3.3	4.9	1.3
Target A	RC-TGA-0022	TGA-RC-02399	50.0	51.0	1.0	512904.0	8115599.8	772.0	258.0	169.1	40.8	125.5	4.8	45.5	26.6	57.6	7.8	33.0	7.5	1.8	6.0	0.8	4.0	0.7	1.7	0.2	1.3	0.2	19.8	89.0	38.5	1.3	1.4	0.9
Target A	RC-TGA-0022	TGA-RC-02400	51.0	52.0	1.0	512904.0	8115599.8	772.0	319.7	233.8	55.0	127.2	5.3	60.2	41.2	87.3	10.9	44.1	9.0	2.2	6.7	0.9	4.4	0.8	1.9	0.3	1.4	0.2	22.5	85.9	60.2	2.2	2.8	1.2
Target A	RC-TGA-0022	TGA-RC-02402	52.0	53.0	1.0	512904.0	8115599.8	772.0	415.1	343.0	76.8	124.4	6.8	83.7	67.4	134.5	16.3	60.5	11.9	3.0	8.8	1.2	5.6	1.0	2.3	0.3	1.7	0.2	28.1	72.1	104.3	4.2	5.9	1.9
Target A	RC-TGA-0022	TGA-RC-02403	53.0	54.0	1.0	512904.0	8115599.8	772.0	335.9	248.5	57.6	135.1	6.3	63.9	44.1	89.3	11.7	45.8	9.8	2.4	7.5	1.0	5.3	0.9	2.1	0.3	1.6	0.2	26.3	87.4	64.4	2.6	2.9	1.4
Target A	RC-TGA-0022	TGA-RC-02404	54.0	55.0	1.0	512904.0	8115599.8	772.0	397.4	308.4	74.4	138.8	6.2	80.7	52.9	119.9	14.9	59.5	11.4	2.7	8.0	1.1	5.2	0.9	2.1	0.3	1.8	0.3	27.4	89.0	94.4	3.3	4.9	1.5
Target A	RC-TGA-0022	TGA-RC-02405	55.0	56.0	1.0	512904.0	8115599.8	772.0	370.9	281.9	67.9	136.6	6.2	74.0	48.9	107.4	13.7	54.2	10.1	2.7	7.8	1.0	5.1	0.9	2.1	0.3	1.7	0.3	25.8	89.0	88.8	2.9	4.7	1.4
Target A	RC-TGA-0022	TGA-RC-02406	56.0	57.0	1.0	512904.0	8115599.8	772.0	347.7	254.2	60.6	135.2	5.5	66.1	40.3	102.0	12.0	48.5	9.7	2.4	6.8	0.9	4.6	0.8	1.9	0.2	1.4	0.3	22.2	93.6	61.2	2.4	3.1	1.0
Target A	RC-TGA-0022	TGA-RC-02408	57.0	58.0	1.0	512904.0	8115599.8	772.0	304.9	214.4	47.9	133.8	5.4	53.2	27.0	88.6	9.1	38.7	7.7	1.9	6.4	0.9	4.5	0.8	2.1	0.3	1.7	0.3	24.4	90.5	43.3	1.6	1.9	0.8
Target A	RC-TGA-0022	TGA-RC-02409	58.0	59.0	1.0	512904.0	8115599.8	772.0	364.4	296.9	59.8	122.1	6.9	66.7	50.2	122.7	12.1	47.7	9.6	2.5	7.8	1.1	5.8	1.1	2.7	0.4	2.1	0.3	30.9	67.5	115.4	3.3	2.9	1.7
Target A	RC-TGA-0022	TGA-RC-02410	59.0	60.0	1.0	512904.0	8115599.8	772.0	393.6	313.8	64.5	129.4	6.6	71.1	46.4	143.7	13.1	51.4	9.5	2.6	7.8	1.0	5.5	1.0	2.3	0.3	1.9	0.3	26.9	79.8	86.7	3.1	3.9	1.5
Target A	RC-TGA-0022	TGA-RC-02411	60.0	61.0	1.0	512904.0	8115599.8	772.0	446.9	357.9	86.1	135.7	6.4	92.5	58.5	154.2	17.8	68.4	12.4	2.9	8.4	1.0	5.3	0.9	2.1	0.3	1.5	0.2	24.1	89.0	79.2	4.0	6.8	1.4
Target A	RC-TGA-0022	TGA-RC-02412	61.0	62.0	1.0	512904.0	8115599.8	772.0	504.2	430.5	91.4	131.1	8.0	99.3	87.8	180.6	19.3	72.1	13.3	3.5	9.6	1.3	6.6	1.1	2.7	0.3	1.8	0.3	30.2	73.6	157.4	5.7	6.0	2.8
Target A	RC-TGA-0022	TGA-RC-02413	62.0	63.0	1.0	512904.0	8115599.8	772.0	365.0	262.2	59.3	144.8	5.6	64.9	42.7	109.1	11.7	47.6	9.1	2.3	6.5	0.9	4.6	0.8	1.9	0.3	1.5	0.2	22.9	102.8	66.4	2.6	3.3	1.1
Target A	RC-TGA-0022	TGA-RC-02414	63.0	64.0	1.0	512904.0	8115599.8	772.0	543.5	436.1	76.9	166.4	7.0	84.0	54.5	234.6	15.5	61.5	11.0	2.9	8.3	1.2	5.9	1.1	2.8	0.4	2.3	0.4	33.9	107.4	85.3	3.9	5.8	1.7
Target A	RC-TGA-0022	TGA-RC-02416	64.0	65.0	1.0	512904.0	8115599.8	772.0	449.8	348.6	74.9	155.5	6.8	81.7	53.9	154.8	15.3	59.6	10.7	2.9	8.4	1.1	5.7	1.1	2.5	0.4	2.0	0.3	30.0	101.2	78.8	3.8	5.2	1.5
Target A	RC-TGA-0022	TGA-RC-02417	65.0	66.0	1.0	512904.0	8115599.8	772.0	445.5	345.8	75.3	152.3	6.6	81.9	51.8	155.4	15.1	60.2	10.7	2.9	8.0	1.0	5.5	1.0	2.4	0.3	1.7	0.3	29.3	99.7	69.1	3.3	5.0	1.3
Target A	RC-TGA-0022	TGA-RC-02418	66.0	67.0	1.0	512904.0	8115599.8	772.0	597.8	488.9	73.5	173.6	7.8	81.3	52.2	287.4	14.7	58.8	11.0	2.9	8.6	1.2	6.6	1.2	3.1	0.4	2.4	0.4	38.0	108.9	78.0	3.7	4.7	1.5
Target A	RC-TGA-0022	TGA-RC-02419	67.0	68.0	1.0	512904.0	8115599.8	772.0	495.7	402.1	82.9	146.8	6.9	89.8	70.0	184.3	17.1	65.8	11.8	3.1	8.6	1.2	5.7	1.0	2.5	0.3	1.9	0.3	28.6	93.6	119.4	4.9	5.8	2.1
Target A	RC-TGA-0022	TGA-RC-02420	68.0	69.0	1.0	512904.0	8115599.8	772.0	462.1	365.5	76.5	145.2	6.3	82.8	59.5	170.1	16.0	60.5	10.8	2.9	8.2	1.1	5.2	0.9	2.2	0.3	1.7	0.2	25.8	96.6	96.6	4.0	5.4	1.7
Target A	RC-TGA-0022	TGA-RC-02421	69.0	70.0	1.0	512904.0	8115599.8	772.0	581.0	495.1	88.3	148.6	8.4	96.7	80.8	250.6	18.5	69.8	12.8	3.4	9.8	1.3	7.1	1.2	2.9	0.4	2.0	0.3	34.3	85.9	171.7	6.3	6.5	2.7
Target A	RC-TGA-0022	TGA-RC-02423	70.0	71.0	1.0	512904.0	8115599.8	772.0	639.7	535.4	81.3	156.7	6.8	88.1	61.0	329.2	16.3	65.0	11.5	2.9	8.2	1.1	5.7	1.0	2.4	0.3	1.9	0.3	28.6	104.3	92.7	4.3	6.2	1.8
Target A	RC-TGA-0022	TGA-RC-02424	71.0	72.0	1.0	512904.0	8115599.8	772.0	657.9	561.3	79.0	148.5	6.5	85.4	67.7	351.3	16.7	62.3	11.5	2.8	8.0	1.1	5.4	1.0	2.3	0.4	1.8	0.3	28.8	96.6	105.3	4.3	6.9	2.4
Target A	RC-TGA-0022	TGA-RC-02425	72.0	73.0	1.0	512904.0	8115599.8	772.0	717.3	582.3	79.5	186.3	6.2	85.7	60.9	379.6	16.6	63.0	11.0	3.0	8.3	1.1	5.1	1.0	2.4	0.3	1.9	0.3	28.1	135.0	103.0	5.0	6.5	1.9
Target A	RC-TGA-0022	TGA-RC-02426	73.0	74.0	1.0	512904.0	8115599.8	772.0	597.7	458.1	79.7	182.8	5.8	85.5	61.6	262.9	16.4	63.2	10.8	3.0	7.6	1.0	4.8	0.8	2.0	0.2	1.4	0.2	22.1	139.6	90.4	4.5	7.0	1.9
Target A	RC-TGA-0022	TGA-RC-02427	74.0	75.0	1.0	512904.0	8115599.8	772.0	887.8	771.2	88.5	186.1	8.3	96.8	77.4	523.3	18.5	70.0	12.5	3.3	9.7	1.4	6.9	1.3	3.2	0.5	2.7	0.4	40.1	116.6	134.5	6.1	7.7