



Complete Assay Results Associated with 9.23.2026 Release Titled: "Rare Earths Americas Reports Initial Drill Results at Homer-A: Widespread Near-Surface Rare Earth Mineralization with Heavy Rare Earth Enrichment"

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	Ce ₂ O ₃ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0001	TGA-RC-00001	0	1	1	Original	508635.6	8112521.2	716.9	316.0	240.8	42.4	35.5	4.4	46.8	44.9	113.1	9.5	32.9	4.8	1.1	3.7	0.6	3.7	0.8	2.2	0.3	2.5	0.4	20.1	75.2	41.9	2.4	37.1	13.0	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00002	1	2	1	Original	508635.6	8112521.2	716.9	419.5	373.5	72.9	45.2	5.6	78.5	88.8	158.5	17.4	55.8	8.1	1.6	5.7	0.8	4.8	0.9	2.6	0.4	3.5	0.5	24.6	46.0	51.2	2.8	33.5	12.0	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00004	2	3	1	Original	508635.6	8112521.2	716.9	363.9	328.6	70.3	44.6	5.5	75.8	82.9	122.5	16.3	54.0	8.3	1.7	6.2	0.8	4.6	0.9	2.6	0.4	2.7	0.3	24.4	35.3	40.1	2.3	24.0	15.4	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00005	3	4	1	Original	508635.6	8112521.2	716.9	263.0	232.3	47.0	35.3	4.3	51.3	60.2	84.3	10.8	36.2	5.6	1.1	4.1	0.7	3.6	0.8	2.3	0.3	2.4	0.4	19.6	30.7	38.3	2.2	24.1	11.5	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00006	4	5	1	Original	508635.6	8112521.2	716.9	180.6	142.3	25.1	28.4	3.1	28.2	27.4	58.0	5.8	19.4	3.3	0.7	2.7	0.5	2.6	0.6	1.9	0.3	2.4	0.4	16.4	38.3	43.2	2.4	13.1	8.3	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00007	5	6	1	Original	508635.6	8112521.2	716.9	131.4	106.9	16.6	26.3	2.8	19.4	20.9	41.0	3.8	12.8	2.0	0.5	2.2	0.4	2.4	0.6	1.7	0.4	2.3	0.4	15.5	24.5	42.3	2.3	13.0	5.2	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00008	6	7	1	Original	508635.6	8112521.2	716.9	432.4	406.4	52.6	40.5	5.6	58.2	49.6	256.7	11.6	41.1	6.8	1.4	5.8	0.9	4.7	0.9	2.4	0.3	2.5	0.4	21.2	26.1	33.9	2.0	18.8	6.1	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00009	7	8	1	Original	508635.6	8112521.2	716.9	286.5	261.9	55.4	41.8	5.4	60.8	44.3	113.0	11.9	43.5	7.4	1.6	6.1	0.9	4.5	0.9	2.3	0.3	2.6	0.4	22.1	24.5	32.9	1.8	15.7	6.0	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00010	8	9	1	Original	508635.6	8112521.2	716.9	115.2	86.1	15.0	25.1	2.5	17.5	18.1	25.9	3.3	11.7	2.0	0.4	2.1	0.3	2.2	0.6	1.8	0.4	2.3	0.4	14.7	29.1	45.3	2.6	10.5	5.2	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00012	9	10	1	Original	508635.6	8112521.2	716.9	322.1	300.6	75.7	49.5	7.5	83.2	52.7	112.3	16.1	59.6	10.4	2.2	8.2	1.2	6.3	1.1	2.6	0.4	2.6	0.4	24.6	21.5	26.5	1.5	10.6	4.5	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00013	10	11	1	Original	508635.6	8112521.2	716.9	408.4	393.0	120.7	69.0	10.5	131.2	80.1	106.4	25.1	95.5	16.9	3.5	12.1	1.8	8.8	1.5	3.9	0.6	3.3	0.5	33.0	15.3	25.4	1.5	6.5	3.4	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00014	11	12	1	Original	508635.6	8112521.2	716.9	580.2	568.0	186.5	141.0	22.3	208.9	125.5	86.4	37.8	148.7	28.5	6.6	25.0	3.7	18.6	3.2	7.9	1.1	6.9	0.9	67.2	12.3	22.0	1.2	5.9	2.7	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00015	12	13	1	Original	508635.6	8112521.2	716.9	323.0	306.1	82.6	81.6	11.1	93.7	60.2	69.3	16.7	65.9	12.5	2.8	11.7	1.6	9.4	1.8	5.0	0.7	4.7	0.6	43.3	16.9	23.5	1.5	9.2	2.1	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00016	13	14	1	Original	508635.6	8112521.2	716.9	426.5	405.0	102.9	89.1	12.7	115.5	89.4	108.3	21.7	81.2	15.3	3.3	13.8	2.0	10.7	2.0	5.2	0.7	4.2	0.7	46.5	21.5	25.1	1.3	13.1	2.2	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00018	14	15	1	Original	508635.6	8112521.2	716.9	488.8	465.8	106.6	109.8	16.8	153.4	96.4	101.7	27.8	108.8	21.3	4.5	18.4	2.7	14.1	2.5	6.3	0.9	5.2	0.6	54.7	23.0	25.1	1.6	11.2	2.2	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00019	15	16	1	Original	508635.6	8112521.2	716.9	538.7	517.3	104.9	229.6	26.8	131.7	72.8	91.4	20.9	84.0	18.6	4.2	21.0	3.6	23.2	5.1	14.8	2.1	14.4	2.0	139.1	21.5	23.6	1.5	10.9	2.5	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00020	16	17	1	Original	508635.6	8112521.2	716.9	352.3	330.8	76.6	113.8	13.9	90.4	59.2	69.6	15.2	61.4	11.5	2.6	12.5	1.9	12.0	2.5	6.7	1.0	6.5	0.9	67.3	21.5	26.8	1.7	13.5	2.3	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00021	17	18	1	Original	508635.6	8112521.2	716.9	318.4	298.4	64.2	103.3	12.1	76.3	45.3	76.2	12.5	51.7	9.5	2.4	11.0	1.7	10.4	2.2	5.9	0.8	5.5	0.8	62.5	19.9	26.4	1.5	14.1	2.4	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00022	18	19	1	Original	508635.6	8112521.2	716.9	341.1	319.6	65.2	105.0	12.8	78.0	48.4	90.8	13.1	52.1	10.2	2.4	12.0	1.9	10.9	2.3	6.1	0.8	5.6	0.8	62.2	21.5	24.0	1.5	15.2	2.6	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00023	19	20	1	Original	508635.6	8112521.2	716.9	310.0	291.6	55.8	96.5	11.2	67.0	43.4	86.7	11.4	44.4	9.2	2.1	10.2	1.6	9.6	2.0	5.7	0.8	5.6	0.8	62.2	23.36	23.36	1.5	15.0	2.7	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00024	20	21	1	Original	508635.6	8112521.2	716.9	275.1	256.7	49.8	71.3	8.2	58.0	39.9	88.8	10.3	39.4	7.0	1.7	7.6	1.2	7.0	1.5	4.0	0.6	3.5	0.6	43.6	18.4	25.5	1.3	13.6	2.7	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00025	21	22	1	Original	508635.6	8112521.2	716.9	220.5	205.2	39.6	51.4	5.7	45.3	34.0	73.8	8.9	30.7	6.3	1.4	5.2	0.8	4.9	0.9	2.8	0.4	2.6	0.3	32.1	15.3	20.0	1.2	12.8	2.4	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00027	22	23	1	Original	508635.6	8112521.2	716.9	162.5	148.7	28.0	39.2	4.3	32.4	24.7	52.2	6.4	21.6	4.5	1.0	3.9	0.6	3.8	0.7	2.4	0.3	2.1	0.3	24.1	13.8	18.7	1.3	9.6	2.1	HOM-RC-TGA-0001	GO26223336
Target A	RC-TGA-0001	TGA-RC-00028	23	24	1	Original	508635.6	8112521.2	716.9	195.7	172.7	33.4	37.4	4.2	37.6	30.3	66.7	7.4	26.0	5.0	0.9	3.6	0.5	3.6	0.8	2.2	0.4	2.4	0.4	22.6	23.0	27.3	1.7	12.1	3.9	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00029	24	25	1	Original	508635.6	8112521.2	716.9	197.0	175.5	34.2	34.5	4.0	38.2	31.0	71.1	7.4	26.8	4.7	0.9	3.6	0.6	3.4	0.7	1.8	0.3	2.2	0.4	20.6	21.5	25.5	1.5	12.0	3.7	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00030	25	26	1	Original	508635.6	8112521.2	716.9	172.7	158.9	32.4	35.2	4.0	36.4	27.9	58.8	6.9	25.4	4.6	0.9	3.5	0.6	3.4	0.7	2.0	0.3	2.2	0.4	21.2	13.8	19.2	1.1	9.6	2.4	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00031	26	27	1	Original	508635.6	8112521.2	716.9	169.0	156.7	31.1	34.4	3.9	35.0	27.7	58.6	6.6	24.5	4.9	0.9	3.5	0.6	3.3	0.7	2.0	0.3	2.1	0.3	20.7	12.3	15.7	1.0	7.0	1.8	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00032	27	28	1	Original	508635.6	8112521.2	716.9	130.8	120.0	24.0	26.4	3.2	27.2	21.0	45.2	5.1	18.9	3.5	0.7	2.7	0.5	2.7	0.5	1.4	0.3	1.8	0.3	15.5	10.7	14.2	1.0	5.7	1.3	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00033	28	29	1	Original	508635.6	8112521.2	716.9	193.0	177.7	34.3	41.0	4.6	38.9	29.0	68.3	7.1	27.2	5.1	1.0	3.8	0.6	3.9	0.8	2.4	0.4	2.4	0.4	25.3	15.3	20.5	1.2	7.3	1.7	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00034	29	30	1	Original	508635.6	8112521.2	716.9	210.8	198.6	39.5	32.3	3.4	42.9	36.8	85.3	8.9	30.6	4.7	0.9	4.0	0.6	2.9	0.6	1.9	0.3	2.1	0.3	18.7	12.3	20.1	1.2	6.4	1.6	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00036	30	31	1	Original	508635.6	8112521.2	716.9	200.6	186.8	36.3	35.9	4.0	40.3	33.4	76.0	8.2	28.1	5.1	1.1	3.9	0.6	3.4	0.7	2.1	0.3	2.2	0.3	21.3	13.8	19.8	1.2	7.6	1.5	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00037	31	32	1	Original	508635.6	8112521.2	716.9	177.7	165.4	32.8	36.5	4.2	37.0	28.4	62.8	6.8	26.0	5.0	1.0	3.6	0.6	3.6	0.7	2.1	0.3	2.0	0.3	22.2	12.3	20.9	1.1	8.1	1.5	HOM-RC-TGA-0002	GO26235696
Target A	RC-TGA-0001	TGA-RC-00038	32	33	1	Original	508635.6	8112521.2	716.9	191.0	177.2	37.1	46.0	5.0	42.1	29.8	58.5	7.7	29.4	5.8	1.1	4.5	0.7	4.3	0.9	2.7	0.4	2.8	0.4	28.2	13.8	25.0	1.3	10.6	1.8	HOM-RC-TGA-0002	GO26235696

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	Ce ₂ O ₃ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0002	TGA-RC-00080	6	7	1	Original	511479.5	8114424.7	745.2	442.5	421.0	117.4	56.1	7.9	125.3	99.3	130.8	25.1	92.3	17.3	3.5	10.8	1.3	6.6	1.1	2.6	0.4	2.6	0.4	26.9	21.5	25.7	1.6	13.2	3.1	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00081	7	8	1	Original	511479.5	8114424.7	745.2	356.7	338.3	98.8	50.3	6.9	105.3	80.3	94.5	21.8	77.0	14.3	3.1	9.5	1.2	5.8	1.0	2.5	0.4	2.1	0.3	24.5	18.4	19.1	1.1	8.5	2.2	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00082	8	9	1	Original	511479.5	8114424.7	745.2	354.0	340.2	96.9	42.1	5.9	102.9	86.6	100.6	22.3	74.7	14.0	3.0	9.0	1.0	4.9	0.8	2.0	0.3	1.7	0.2	19.3	13.8	14.5	1.0	7.3	2.0	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00084	9	10	1	Original	511479.5	8114424.7	745.2	184.0	174.8	48.6	21.7	3.1	51.7	44.7	53.4	11.2	37.4	6.4	1.6	4.5	0.6	2.6	0.4	0.9	0.1	0.9	0.1	10.0	9.2	7.6	0.5	4.0	1.6	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00085	10	11	1	Original	511479.5	8114424.7	745.2	171.5	146.8	38.2	34.1	4.3	42.5	32.5	36.1	8.2	30.0	6.1	1.3	4.7	0.7	3.6	0.8	2.0	0.3	1.9	0.3	18.5	24.5	25.3	1.5	6.2	3.2	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00086	11	12	1	Original	511479.5	8114424.7	745.2	142.7	127.4	29.6	24.5	3.2	32.8	27.1	41.6	6.5	23.1	4.5	1.0	3.7	0.5	2.7	0.5	1.4	0.2	1.5	0.2	12.8	15.3	23.3	1.3	5.9	3.2	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00087	12	13	1	Original	511479.5	8114424.7	745.2	190.5	169.1	38.9	31.0	4.0	42.8	34.1	59.0	8.5	30.3	6.1	1.2	4.3	0.6	3.3	0.6	1.8	0.3	1.9	0.3	16.5	21.5	35.6	2.1	8.8	2.8	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00088	13	14	1	Original	511479.5	8114424.7	745.2	363.6	337.5	70.7	43.1	5.8	76.5	74.7	138.8	16.7	54.0	10.1	1.9	6.7	1.0	4.8	0.9	2.3	0.4	2.4	0.4	22.4	26.1	44.1	2.4	8.7	3.7	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00089	14	15	1	Original	511479.5	8114424.7	745.2	220.8	197.8	38.3	37.0	4.1	42.4	40.0	77.3	8.9	29.4	5.3	1.2	4.1	0.7	3.5	0.7	2.2	0.4	2.5	0.4	21.3	23.0	43.8	2.4	7.5	3.7	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00090	15	16	1	Original	511479.5	8114424.7	745.2	281.4	259.9	57.1	39.7	4.9	62.0	53.1	101.2	12.7	44.4	8.7	1.7	5.6	0.8	4.1	0.8	2.3	0.4	2.3	0.4	21.2	21.5	38.9	2.2	10.9	3.8	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00092	16	17	1	Original	511479.5	8114424.7	745.2	272.0	255.1	56.3	37.1	5.0	61.3	51.3	102.3	12.4	43.9	8.1	1.6	5.9	0.8	4.1	0.7	2.0	0.3	2.0	0.4	19.3	16.9	28.3	1.7	10.7	3.8	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00093	17	18	1	Original	511479.5	8114424.7	745.2	369.9	349.9	77.9	46.4	6.6	84.5	70.7	143.1	17.0	60.9	11.8	2.4	8.7	1.1	5.4	0.9	2.2	0.4	2.0	0.3	22.9	19.9	25.0	1.6	12.3	4.3	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00094	18	19	1	Original	511479.5	8114424.7	745.2	222.1	203.7	43.7	35.8	4.7	48.4	38.5	79.1	9.7	33.9	6.6	1.3	5.1	0.7	4.0	0.8	1.9	0.3	2.0	0.3	19.3	18.4	25.0	1.5	10.3	3.4	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00095	19	20	1	Original	511479.5	8114424.7	745.2	277.0	258.6	57.4	38.9	5.0	62.4	50.8	103.7	12.7	44.7	7.9	1.6	5.9	0.9	4.2	0.8	2.0	0.3	2.1	0.3	20.8	18.4	26.6	1.6	14.6	3.5	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00096	20	21	1	Original	511479.5	8114424.7	745.2	334.9	313.4	70.5	43.8	6.2	76.6	58.5	129.6	15.3	55.2	11.1	2.1	7.1	1.0	5.1	0.9	2.3	0.4	2.4	0.3	22.1	21.5	25.8	1.6	19.9	3.3	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00097	21	22	1	Original	511479.5	8114424.7	745.2	330.9	311.0	72.2	47.0	6.5	78.6	58.5	122.5	15.3	56.8	10.9	2.2	7.7	1.1	5.4	0.9	2.6	0.4	2.2	0.3	24.1	19.9	26.0	1.5	14.6	3.1	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00098	22	23	1	Original	511479.5	8114424.7	745.2	273.8	258.5	56.7	45.5	6.0	62.8	47.7	100.1	12.3	44.4	8.4	1.7	6.5	1.0	5.1	1.0	2.4	0.4	2.4	0.4	24.6	15.3	25.3	1.6	10.0	2.7	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00100	23	24	1	Original	511479.5	8114424.7	745.2	191.6	180.9	36.9	32.7	4.4	41.3	33.9	71.7	8.3	28.7	5.6	1.1	4.2	0.7	3.7	0.7	1.9	0.3	1.8	0.3	18.0	10.7	18.0	1.2	8.1	1.9	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00101	24	25	1	Original	511479.5	8114424.7	745.2	181.6	169.4	34.6	27.6	3.6	38.2	34.6	67.4	7.8	26.8	5.1	1.1	3.8	0.6	3.0	0.6	1.7	0.3	1.6	0.3	14.7	12.3	17.5	1.1	8.0	1.5	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00102	25	26	1	Original	511479.5	8114424.7	745.2	205.4	188.6	36.2	36.5	4.4	40.6	35.8	74.9	7.9	28.2	5.2	1.0	4.0	0.7	3.8	0.7	2.1	0.3	2.4	0.4	21.1	16.9	22.8	1.3	9.9	2.1	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00103	26	27	1	Original	511479.5	8114424.7	745.2	238.0	219.6	40.5	45.2	5.4	45.9	44.2	84.3	9.2	31.3	5.5	1.2	4.6	0.8	4.6	1.0	2.7	0.5	2.8	0.5	26.5	18.4	25.5	1.5	11.1	1.9	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00104	27	28	1	Original	511479.5	8114424.7	745.2	267.7	249.3	42.2	64.0	7.3	49.5	37.6	99.0	9.2	33.0	6.5	1.4	5.5	1.0	6.3	1.3	4.0	0.6	3.8	0.6	39.5	18.4	24.7	1.5	10.9	1.8	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00105	28	29	1	Original	511479.5	8114424.7	745.2	238.4	221.5	40.8	60.6	7.2	48.0	37.4	76.2	8.8	32.0	6.5	1.4	5.9	1.0	6.2	1.3	3.5	0.5	3.3	0.5	37.0	16.9	24.7	1.5	11.2	1.7	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00106	29	30	1	Original	511479.5	8114424.7	745.2	215.6	198.7	34.3	64.3	7.0	41.4	32.8	61.8	7.6	26.7	5.5	1.2	5.3	1.0	6.0	1.3	3.7	0.5	3.5	0.6	41.1	16.9	25.4	1.6	10.0	1.5	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00108	30	31	1	Original	511479.5	8114424.7	745.2	208.5	190.1	33.8	54.7	6.0	39.8	33.5	63.3	7.7	26.1	4.9	1.1	4.8	0.9	5.1	1.1	3.1	0.5	3.1	0.5	34.5	18.4	25.3	1.5	10.6	1.4	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00109	31	32	1	Original	511479.5	8114424.7	745.2	204.1	187.3	33.7	50.1	5.7	39.4	32.4	66.3	7.6	26.0	4.8	1.1	4.6	0.8	4.9	1.0	2.9	0.5	2.8	0.4	31.1	16.9	23.5	1.3	10.6	1.3	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00110	32	33	1	Original	511479.5	8114424.7	745.2	261.5	244.6	45.8	57.8	6.8	52.6	41.4	92.7	10.3	35.6	6.9	1.5	6.0	1.0	5.8	1.1	3.2	0.5	3.1	0.5	35.2	16.9	26.6	1.6	12.7	1.5	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00111	33	34	1	Original	511479.5	8114424.7	745.2	251.8	251.0	47.0	62.7	7.6	54.6	40.1	93.2	10.3	36.7	8.0	1.6	6.5	1.1	6.5	1.2	3.6	0.5	3.1	0.5	38.0	0.8	23.7	1.5	11.3	1.4	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00112	34	35	1	Original	511479.5	8114424.7	745.2	339.7	316.7	63.3	72.4	9.2	72.5	48.9	121.1	13.6	49.7	11.0	2.2	8.9	1.4	7.9	1.4	4.0	0.6	3.6	0.5	41.9	23.0	23.4	1.5	12.5	1.5	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00113	35	36	1	Original	511479.5	8114424.7	745.2	190.4	179.7	35.5	51.5	6.0	41.4	29.3	57.9	7.8	27.6	5.5	1.2	5.1	0.9	5.1	1.0	3.0	0.4	2.8	0.5	31.5	10.7	20.9	1.2	9.2	1.3	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00114	36	37	1	Original	511479.5	8114424.7	745.2	151.2	140.5	25.3	48.0	5.1	30.3	23.8	39.3	5.4	19.8	4.1	0.8	4.2	0.7	4.3	1.0	2.8	0.4	2.6	0.5	30.7	10.7	21.7	1.2	7.7	1.4	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00116	37	38	1	Original	511479.5	8114424.7	745.2	177.4	166.7	28.3	57.3	6.3	34.6	27.9	48.3	6.2	22.2	4.8	1.0	4.7	0.8	5.5	1.2	3.4	0.5	3.1	0.5	36.7	10.7	24.0	1.3	8.4	1.6	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00117	38	39	1	Original	511479.5	8114424.7	745.2	123.7	116.0	17.8	31.7	3.8	21.6	17.1	46.4	3.8	14.0	2.9	0.6	3.1	0.6	3.2	0.7	2.2	0.3	2.0	0.3	18.8	7.7	14.8	0.9	6.3	1.2	HOM-RC-TGA-0003	GO26235697
Target A	RC-TGA-0002	TGA-RC-00118	39	40	1	Original	511479.5	8114424.7	745.2																												

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0002	TGA-RC-00159	75	76	1	Original	511479.5	8114424.7	745.2	105.2	91.4	15.1	27.0	2.7	17.7	13.0	33.9	3.2	11.9	2.4	0.4	2.0	0.3	2.4	0.6	1.7	0.3	2.1	0.3	16.9	13.8	31.3	2.1	6.8	1.4	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00160	76	77	1	Original	511479.5	8114424.7	745.2	99.4	84.1	13.9	27.1	2.8	16.8	13.8	26.8	3.1	10.8	2.4	0.3	1.9	0.4	2.5	0.6	1.8	0.3	2.2	0.4	16.8	15.3	33.3	2.2	8.3	1.4	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00161	77	78	1	Original	511479.5	8114424.7	745.2	108.1	91.3	15.1	28.8	2.9	18.0	13.8	31.3	3.2	11.9	2.2	0.4	2.0	0.4	2.6	0.6	1.9	0.3	2.3	0.4	18.0	16.9	36.9	2.6	8.9	1.7	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00162	78	79	1	Original	511479.5	8114424.7	745.2	142.2	123.8	18.1	35.5	3.7	21.8	17.6	49.9	3.9	14.2	2.7	0.5	2.5	0.5	3.2	0.8	2.4	0.4	2.9	0.4	21.8	18.4	40.2	2.7	10.1	1.9	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00163	79	80	1	Original	511479.5	8114424.7	745.2	148.6	136.4	27.3	30.8	3.2	30.4	25.5	49.9	5.7	21.6	3.4	0.6	3.2	0.4	2.7	0.8	2.0	0.3	2.2	0.3	18.3	12.3	29.0	1.8	8.4	1.3	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00164	80	81	1	Original	511479.5	8114424.7	745.2	188.3	176.0	33.5	37.5	4.4	37.9	25.8	74.1	7.1	26.4	5.1	0.9	3.8	0.6	3.7	0.8	2.4	0.4	2.6	0.4	22.0	12.3	29.0	2.0	8.6	1.2	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00165	81	82	1	Original	511479.5	8114424.7	745.2	187.1	174.8	36.3	34.2	4.1	40.4	33.0	65.8	7.9	28.5	5.5	1.0	3.8	0.6	3.4	0.7	2.0	0.3	2.2	0.4	19.7	12.3	26.6	1.7	9.9	1.2	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00167	82	83	1	Original	511479.5	8114424.7	745.2	155.3	144.5	25.5	27.2	3.4	28.9	20.9	67.6	5.6	19.8	3.5	0.7	2.7	0.5	2.9	0.6	1.8	0.3	1.8	0.3	15.5	10.7	23.7	1.6	7.2	1.3	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00168	83	84	1	Original	511479.5	8114424.7	745.2	143.1	132.3	23.8	26.2	3.2	27.0	17.6	61.3	5.1	18.8	3.4	0.7	2.5	0.5	2.7	0.6	1.7	0.3	2.0	0.3	15.0	10.7	26.2	1.7	7.0	1.2	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00169	84	85	1	Original	511479.5	8114424.7	745.2	199.7	187.5	39.6	37.2	4.7	44.3	27.8	76.8	8.6	31.0	6.0	1.2	4.2	0.7	4.0	0.8	2.2	0.4	2.7	0.4	20.8	12.3	32.8	2.1	8.9	1.4	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00170	85	86	1	Original	511479.5	8114424.7	745.2	144.2	131.9	27.6	31.5	3.7	31.4	22.0	46.6	5.9	21.7	4.1	0.8	3.2	0.5	3.2	0.7	1.8	0.3	2.2	0.4	18.4	12.3	29.5	2.3	9.6	1.4	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00171	86	87	1	Original	511479.5	8114424.7	745.2	229.1	213.8	42.7	49.1	5.6	48.3	31.1	84.1	8.9	33.7	6.2	1.4	5.2	0.9	4.7	1.0	2.8	0.5	3.0	0.5	29.2	15.3	32.9	2.1	9.7	1.5	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00172	87	88	1	Original	511479.5	8114424.7	745.2	258.1	242.8	53.4	44.6	5.0	58.5	47.9	90.3	11.8	41.6	6.6	1.5	5.5	0.8	4.2	0.9	2.7	0.4	2.5	0.4	25.7	15.3	38.2	2.3	10.5	1.7	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00173	88	89	1	Original	511479.5	8114424.7	745.2	217.9	205.6	42.5	33.2	4.0	46.4	36.8	87.5	9.3	33.1	5.6	1.0	4.1	0.6	3.3	0.7	1.8	0.3	2.0	0.3	19.0	12.3	30.3	2.0	8.8	1.5	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00175	89	90	1	Original	511479.5	8114424.7	745.2	138.2	127.5	26.9	28.9	3.2	30.2	22.8	45.1	6.1	20.9	3.8	0.7	3.2	0.5	2.8	0.5	1.8	0.3	1.8	0.3	17.0	10.7	31.3	2.1	7.9	1.6	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00176	90	91	1	Original	511479.5	8114424.7	745.2	170.7	159.9	25.8	31.6	3.4	29.2	21.8	77.0	5.6	20.2	3.7	0.7	3.0	0.5	2.9	0.6	1.9	0.4	2.2	0.3	19.0	10.7	31.9	2.2	8.1	1.5	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00177	91	92	1	Original	511479.5	8114424.7	745.2	123.5	117.4	23.4	23.5	2.7	26.0	19.4	47.9	5.2	18.2	3.2	0.6	2.6	0.4	2.3	0.5	1.5	0.2	1.6	0.2	13.7	6.1	18.4	1.3	5.1	1.1	HOM-RC-TGA-0004	GO26235699
Target A	RC-TGA-0002	TGA-RC-00178	92	93	1	Original	511479.5	8114424.7	745.2	154.1	144.9	25.2	30.3	3.4	28.7	20.4	65.0	5.6	19.6	4.0	0.7	3.0	0.5	3.0	0.6	1.8	0.3	2.1	0.4	17.9	9.2	28.5	2.0	8.2	1.7	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00179	93	94	1	Original	511479.5	8114424.7	745.2	149.7	137.4	26.4	33.4	3.7	30.1	22.3	51.6	5.9	20.5	3.8	0.7	3.3	0.5	3.2	0.7	2.1	0.4	2.7	0.4	19.6	12.3	35.3	2.3	10.0	1.9	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00180	94	95	1	Original	511479.5	8114424.7	745.2	112.8	100.5	19.4	28.8	3.0	22.5	17.5	32.1	4.3	15.2	2.8	0.6	2.6	0.4	2.6	0.5	1.7	0.3	2.0	0.3	17.7	12.3	33.2	2.2	10.3	1.5	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00181	95	96	1	Original	511479.5	8114424.7	745.2	113.6	99.8	18.9	29.3	3.1	22.0	17.5	31.2	4.0	14.8	3.0	0.5	2.6	0.4	2.7	0.5	1.8	0.3	1.9	0.3	18.2	13.8	33.2	2.2	9.4	1.4	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00182	96	97	1	Original	511479.5	8114424.7	745.2	105.2	93.0	17.4	26.4	3.0	20.4	15.7	31.1	3.8	13.6	2.4	0.5	2.4	0.4	2.6	0.5	1.5	0.3	1.9	0.3	16.1	12.3	34.3	2.3	9.5	1.6	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00183	97	98	1	Original	511479.5	8114424.7	745.2	171.5	162.3	34.8	33.5	3.9	38.8	30.1	59.5	7.9	26.9	4.4	0.9	3.7	0.6	3.3	0.6	2.0	0.3	2.2	0.3	19.6	9.2	40.1	2.6	11.2	2.1	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00184	98	99	1	Original	511479.5	8114424.7	745.2	766.7	754.4	98.3	56.0	7.7	106.0	80.0	507.3	22.3	76.1	12.7	2.4	8.6	1.2	6.4	1.1	3.0	0.5	3.2	0.5	29.2	12.3	41.9	2.7	11.5	2.7	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00186	99	100	1	Original	511479.5	8114424.7	745.2	449.1	436.8	79.1	58.9	8.0	87.1	72.2	215.6	17.8	61.4	11.0	2.2	8.6	1.2	6.8	1.2	3.5	0.6	3.7	0.5	30.6	12.3	41.1	2.7	9.7	2.2	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00187	100	101	1	Original	511479.5	8114424.7	745.2	337.6	325.3	58.9	66.4	7.6	66.5	57.7	134.8	12.7	46.2	7.8	1.7	7.6	1.1	6.5	1.3	3.6	0.5	3.5	0.5	40.0	12.3	41.1	2.7	9.2	1.7	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00188	101	102	1	Original	511479.5	8114424.7	745.2	286.5	275.8	49.5	71.5	7.7	57.1	49.3	98.3	10.9	38.6	7.3	1.5	7.5	1.1	6.6	1.3	3.6	0.5	3.3	0.5	45.6	10.7	33.0	2.1	8.0	1.2	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00189	102	103	1	Original	511479.5	8114424.7	745.2	228.5	217.8	41.6	49.3	5.4	47.0	38.4	82.5	8.9	32.7	6.0	1.3	5.7	0.8	4.6	0.9	2.4	0.4	2.3	0.4	30.5	10.7	29.9	1.8	7.1	1.0	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00190	103	104	1	Original	511479.5	8114424.7	745.2	216.4	207.2	37.0	42.0	4.9	41.9	33.9	88.8	8.0	28.9	5.5	1.1	5.0	0.7	4.2	0.8	2.3	0.3	2.1	0.3	25.1	9.2	26.6	1.7	6.5	1.0	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00191	104	105	1	Original	511479.5	8114424.7	745.2	158.1	150.4	31.3	31.4	3.5	34.8	29.7	53.8	6.9	24.4	4.3	0.9	3.8	0.5	3.0	0.6	1.6	0.3	1.7	0.2	18.8	7.7	24.5	1.5	5.8	1.3	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00192	105	106	1	Original	511479.5	8114424.7	745.2	140.4	132.7	27.1	28.1	3.4	30.5	24.4	49.4	5.9	21.2	3.7	0.8	3.3	0.5	2.9	0.5	1.6	0.2	1.6	0.2	16.5	7.7	21.6	1.3	5.4	0.8	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00194	106	107	1	Original	511479.5	8114424.7	745.2	154.2	145.0	28.7	26.8	3.2	31.9	24.4	60.9	6.4	22.3	4.2	0.8	3.4	0.5	2.7	0.5	1.5	0.2	1.4	0.2	15.5	9.2	24.4	1.5	6.2	0.9	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00195	107	108	1	Original	511479.5	8114424.7	745.2	185.2	176.0	38.7	39.8	4.9	43.6	35.9	55.6	8.5	30.2	6.0	1.2	4.9	0.7	4.2	0.7	2.1	0.3	2.0	0.3	23.4	9.2	23.1	1.5	5.8	0.8	HOM-RC-TGA-0005	GO26236452
Target A	RC-TGA-0002	TGA-RC-00196	108	109	1	Original	511479.5	8114424.7	745.2	143.7	137.6	31.1	3																								

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0003	TGA-RC-00237	24	25	1	Original	512289.7	8117006.2	791.1	1703.5	1349.2	189.5	62.4	9.2	198.6	339.0	739.5	48.3	141.1	18.9	4.4	12.1	1.6	7.6	1.2	3.0	0.4	2.7	0.4	29.0	354.3	171.7	12.0	21.4	4.9	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00238	25	26	1	Original	512289.7	8117006.2	791.1	1366.0	1060.84	241.6	75.0	11.4	253.1	336.6	738.0	59.1	182.6	25.5	5.8	15.7	2.0	9.4	1.5	3.5	0.4	2.9	0.4	33.3	305.2	126.0	9.2	11.8	2.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00239	26	27	1	Original	512289.7	8117006.2	791.1	955.9	620.0	131.3	56.4	8.1	139.4	158.3	258.0	30.2	101.1	15.9	3.8	10.5	1.3	6.7	1.1	3.0	0.4	2.4	0.3	26.8	335.9	136.6	11.0	17.0	3.5	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00240	27	28	1	Original	512289.7	8117006.2	791.1	1418.9	1142.8	281.2	59.2	10.0	291.1	350.7	423.8	71.8	209.4	27.9	6.6	15.4	1.8	8.1	1.1	2.6	0.3	1.8	0.3	21.1	276.1	287.5	17.0	19.6	4.4	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00241	28	29	1	Original	512289.7	8117006.2	791.1	953.0	626.3	39.8	19.1	3.4	43.2	37.2	524.5	8.9	30.9	5.7	1.4	3.5	0.5	2.8	0.4	1.2	0.2	1.2	0.2	7.7	326.7	89.3	7.2	9.1	1.8	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00242	29	30	1	Original	512289.7	8117006.2	791.1	1229.2	858.0	52.8	26.5	4.4	57.3	44.5	727.2	11.8	41.1	7.0	1.9	4.8	0.7	3.7	0.6	1.7	0.3	1.5	0.2	11.2	371.2	80.7	7.3	11.6	1.5	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00243	30	31	1	Original	512289.7	8117006.2	791.1	1217.2	887.4	50.9	39.7	6.1	115.7	93.8	631.4	25.7	83.9	12.9	3.2	7.9	1.0	5.1	0.8	2.0	0.3	1.8	0.2	17.4	329.8	140.1	11.7	18.8	2.3	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00245	31	32	1	Original	512289.7	8117006.2	791.1	1119.3	814.1	76.4	36.8	5.1	81.6	39.6	651.0	16.1	60.3	10.2	2.7	6.7	0.9	4.2	0.8	1.8	0.2	1.4	0.2	17.9	305.2	69.5	6.8	11.3	1.4	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00246	32	33	1	Original	512289.7	8117006.2	791.1	1145.0	827.5	72.2	36.1	5.2	77.4	43.4	665.8	15.2	57.0	10.0	2.5	6.5	0.9	4.3	0.7	1.8	0.3	1.6	0.2	17.4	317.5	91.7	8.4	13.3	1.7	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00247	33	34	1	Original	512289.7	8117006.2	791.1	955.9	679.8	85.2	33.9	5.1	90.3	69.9	480.3	18.7	66.5	10.5	2.7	6.8	0.9	4.2	0.7	1.7	0.2	1.3	0.2	15.2	276.1	148.8	10.0	15.3	2.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00248	34	35	1	Original	512289.7	8117006.2	791.1	1575.7	1440.8	366.5	118.0	19.1	385.6	231.6	680.5	76.0	290.4	44.2	12.1	31.5	3.7	15.4	2.3	4.3	0.4	1.9	0.3	46.1	135.0	123.6	5.6	9.5	2.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00249	35	36	1	Original	512289.7	8117006.2	791.1	2120.8	1979.6	513.2	204.9	32.3	545.5	307.3	889.4	102.6	410.6	64.9	18.0	51.1	5.9	26.4	4.1	7.5	0.7	3.6	0.4	87.1	141.1	112.7	5.3	9.1	2.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00250	36	37	1	Original	512289.7	8117006.2	791.1	1028.9	834.1	195.0	74.9	10.9	205.9	149.0	393.1	42.8	152.2	22.1	6.1	16.4	1.9	9.0	1.4	3.3	0.4	2.0	0.3	34.2	194.8	231.8	12.7	17.9	3.3	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00252	37	38	1	Original	512289.7	8117006.2	791.1	754.2	677.5	140.0	64.8	8.3	148.3	131.4	325.5	31.5	108.5	15.8	4.2	11.4	1.4	6.9	1.2	3.1	0.4	2.1	0.3	33.9	76.7	253.2	12.7	16.4	2.9	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00253	38	39	1	Original	512289.7	8117006.2	791.1	682.4	594.9	134.9	61.0	7.7	142.6	115.8	267.8	29.4	105.6	15.5	4.2	11.2	1.3	6.3	1.1	2.5	0.3	1.5	0.2	32.3	87.4	165.9	8.2	13.0	2.3	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00254	39	40	1	Original	512289.7	8117006.2	791.1	1413.2	1287.4	337.1	78.2	11.4	348.5	216.4	617.9	70.0	267.1	37.8	8.5	20.9	2.2	9.2	1.3	2.9	0.3	1.6	0.2	31.1	125.8	142.5	14.5	40.3	3.4	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00255	40	41	1	Original	512289.7	8117006.2	791.1	1979.1	1903.9	491.3	109.9	16.1	507.3	354.2	894.3	102.8	388.4	54.3	12.0	29.9	3.0	13.0	2.0	3.6	0.4	2.0	0.3	43.7	75.2	201.7	23.9	60.5	3.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00256	41	42	1	Original	512289.7	8117006.2	791.1	1034.2	893.1	234.7	60.4	8.7	243.4	148.4	422.6	48.7	186.1	27.0	6.1	15.7	1.7	7.0	1.1	2.1	0.2	1.4	0.1	25.1	141.1	100.4	10.4	28.1	1.5	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00257	42	43	1	Original	512289.7	8117006.2	791.1	633.3	461.5	128.0	35.6	5.1	133.1	78.2	205.1	25.7	102.3	14.5	3.4	8.8	1.0	4.1	0.6	1.2	0.1	0.8	0.1	15.4	171.8	56.7	5.5	13.9	0.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00258	43	44	1	Original	512289.7	8117006.2	791.1	1342.3	1198.2	323.8	67.6	9.7	333.6	192.9	579.8	67.2	256.6	34.0	7.7	18.2	1.9	7.8	1.2	2.1	0.2	1.4	0.2	26.9	144.2	125.3	15.1	44.6	1.8	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00259	44	45	1	Original	512289.7	8117006.2	791.1	682.8	524.8	144.6	44.8	6.3	150.9	86.9	230.3	28.8	115.8	18.1	4.2	10.5	1.2	5.1	0.8	1.7	0.2	1.0	0.1	19.9	158.0	68.2	6.2	19.2	1.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00261	45	46	1	Original	512289.7	8117006.2	791.1	900.3	762.3	202.0	57.4	7.9	209.9	123.7	355.0	41.6	160.4	24.1	5.3	13.9	1.6	6.4	1.1	2.3	0.2	1.5	0.2	25.0	138.0	99.3	9.2	26.7	1.7	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00262	46	47	1	Original	512289.7	8117006.2	791.1	722.6	555.5	150.3	43.7	6.2	156.5	93.9	249.4	30.7	119.6	18.2	3.9	10.2	1.1	5.1	0.8	1.8	0.2	1.1	0.2	19.3	167.2	73.0	7.2	26.2	1.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00263	47	48	1	Original	512289.7	8117006.2	791.1	1141.1	998.5	267.9	62.1	9.0	276.9	160.1	477.8	55.0	212.9	30.6	6.8	16.2	1.7	7.3	1.1	2.2	0.2	1.3	0.2	25.1	142.6	115.3	11.7	38.8	1.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00264	48	49	1	Original	512289.7	8117006.2	791.1	641.2	526.2	147.3	48.7	6.8	154.1	81.5	229.7	29.5	117.8	19.0	4.4	11.5	1.3	5.5	0.9	1.9	0.2	1.2	0.2	21.6	115.0	60.1	5.5	14.8	1.0	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00265	49	50	1	Original	512289.7	8117006.2	791.1	754.0	672.7	179.5	55.7	7.5	187.0	106.5	309.6	36.0	143.5	21.5	4.8	12.9	1.4	6.1	1.0	2.3	0.3	1.5	0.2	25.3	81.3	83.8	7.1	16.8	1.3	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00266	50	51	1	Original	512289.7	8117006.2	791.1	1331.2	1263.7	349.5	83.7	11.7	361.2	204.7	587.2	70.7	278.8	39.2	8.7	21.7	2.2	9.5	1.4	2.9	0.3	1.7	0.2	34.7	67.5	105.1	12.2	37.8	1.8	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00267	51	52	1	Original	512289.7	8117006.2	791.1	1172.9	1103.9	299.2	80.1	11.0	310.7	180.6	506.8	59.5	240.3	34.9	7.7	20.3	2.0	8.9	1.4	2.8	0.3	1.7	0.2	34.7	69.0	85.7	8.9	27.0	1.7	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00269	52	53	1	Original	512289.7	8117006.2	791.1	1099.4	1028.8	276.3	74.1	10.4	286.7	168.3	477.8	56.4	219.9	32.2	7.0	18.6	1.9	8.5	1.3	2.7	0.3	1.6	0.2	32.1	70.6	94.3	9.0	26.9	1.7	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00270	53	54	1	Original	512289.7	8117006.2	791.1	881.0	802.8	216.4	57.0	7.9	224.3	126.7	377.1	43.7	172.6	25.6	5.4	14.5	1.5	6.4	1.1	2.0	0.2	1.3	0.2	24.3	78.2	89.8	8.7	23.3	1.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00271	54	55	1	Original	512289.7	8117006.2	791.1	1538.3	1458.5	399.2	80.8	11.8	411.1	235.7	699.0	83.1	316.1	43.8	9.1	21.6	2.3	9.5	1.4	2.8	0.3	1.6	0.2	32.0	79.8	159.5	18.2	52.7	2.6	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00272	55	56	1	Original	512289.7	8117006.2	791.1	1169.5	1082.1	293.4	67.5	9.7	303.1	175.3	513.5	60.1	233.3	32.5	7.2	17.8	1.9	7.8	1.2	2.5	0.3	1.5	0.2	27.2	87.4	120.0	12.8	36.6	2.2	HOM-RC-TGA-0006	GO26243813
Target A	RC-TGA-0003	TGA-RC-00273	56	57	1	Original	512289.7	8117006.2	791.1	1087.1	988.9	267.9	62.9	8.9																							

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0004	TGA-RC-00315	15	16	1	Original	512301.0	8117404.8	790.4	996.7	818.8	121.2	32.8	4.9	126.1	239.3	414.0	30.1	91.1	11.6	2.7	7.2	0.9	4.0	0.6	1.5	0.2	1.3	0.2	14.1	177.9	164.5	10.6	14.6	6.6	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00317	16	17	1	Original	512301.0	8117404.8	790.4	1424.4	1240.3	169.5	38.1	5.8	175.3	354.2	663.3	43.5	126.0	15.2	3.3	8.9	1.0	4.8	0.7	1.8	0.2	1.4	0.2	15.7	184.1	169.5	11.2	16.3	5.3	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00318	17	18	1	Original	512301.0	8117404.8	790.4	1291.3	1093.4	153.5	36.4	5.3	158.8	289.7	599.5	39.5	114.0	14.4	3.1	8.0	1.0	4.3	0.7	1.8	0.2	1.4	0.2	15.7	197.9	158.1	10.3	13.2	4.9	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00319	18	19	1	Original	512301.0	8117404.8	790.4	1775.1	1591.0	254.8	49.3	7.5	262.3	422.2	842.7	64.0	190.7	22.0	4.8	12.4	1.4	6.1	0.9	2.0	0.3	1.7	0.2	19.6	184.1	181.0	10.9	15.7	5.0	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00320	19	20	1	Original	512301.0	8117404.8	790.4	2633.3	2457.3	277.3	54.7	8.6	285.9	378.8	1738.2	68.5	208.8	26.3	6.0	14.2	1.7	6.9	1.0	2.3	0.3	1.8	0.2	20.3	158.0	201.0	12.3	14.9	4.1	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00321	20	21	1	Original	512301.0	8117404.8	790.4	3360.4	3168.7	660.2	164.0	26.8	687.0	587.6	1676.8	150.4	509.7	80.1	18.8	42.2	5.1	21.7	2.9	6.8	0.8	4.5	0.6	60.8	191.7	178.1	9.9	14.0	4.4	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00322	21	22	1	Original	512301.0	8117404.8	790.4	3018.4	2858.9	866.6	297.6	46.3	912.9	521.9	1067.0	183.1	683.5	118.9	28.7	70.1	8.5	37.8	5.4	12.6	1.5	9.1	1.1	122.7	159.5	176.7	9.8	13.8	3.8	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00323	22	23	1	Original	512301.0	8117404.8	790.4	1032.5	931.2	287.0	85.8	14.1	301.1	230.5	291.1	61.9	225.1	36.9	8.5	20.7	2.5	11.6	1.8	4.3	0.6	3.6	0.5	31.7	101.2	225.3	7.0	8.9	3.5	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00325	23	24	1	Original	512301.0	8117404.8	790.4	2352.3	2198.9	838.2	302.3	47.4	885.7	399.9	545.4	154.7	683.5	113.1	28.8	70.0	9.0	38.4	5.8	13.3	1.8	9.8	1.3	124.1	153.4	169.5	10.4	15.5	3.5	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00326	24	25	1	Original	512301.0	8117404.8	790.4	3179.2	3042.7	1155.1	437.6	66.1	1221.3	574.7	721.1	211.5	943.7	154.2	41.3	101.9	12.4	53.7	8.2	17.9	2.3	12.8	1.6	185.4	136.5	173.8	10.5	15.2	3.5	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00327	25	26	1	Original	512301.0	8117404.8	790.4	4660.6	4525.6	1237.6	2060.4	230.4	1468.1	455.1	554.0	201.8	1035.8	218.6	71.8	252.4	37.1	193.4	38.8	100.8	13.3	71.5	11.4	1270.0	135.0	136.3	8.1	12.7	3.1	HOM-RC-TGA-0007	GO26243814
Target A	RC-TGA-0004	TGA-RC-00328	26	27	1	Original	512301.0	8117404.8	790.4	4277.1	4159.0	792.6	2460.5	236.5	1029.1	341.3	410.3	120.7	671.9	154.2	59.4	262.8	36.8	199.7	43.9	112.5	14.6	73.9	12.3	1644.6	118.1	221.7	10.7	18.1	4.3	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00329	27	28	1	Original	512301.0	8117404.8	790.4	1043.4	893.1	227.6	246.2	27.0	254.6	124.3	261.6	39.8	187.8	33.4	10.4	36.1	4.5	22.5	4.2	10.3	1.3	7.1	1.1	148.6	150.3	82.5	5.1	6.3	1.9	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00330	28	29	1	Original	512301.0	8117404.8	790.4	1042.6	923.0	226.6	147.5	17.8	244.4	150.7	368.5	42.3	184.3	29.7	8.7	24.6	3.0	14.8	2.5	6.0	0.7	3.7	0.7	82.7	119.6	171.7	9.9	13.7	2.7	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00331	29	30	1	Original	512301.0	8117404.8	790.4	645.8	513.9	128.1	92.9	10.9	391.0	81.6	193.5	24.0	104.0	17.9	5.1	15.3	1.9	9.0	1.6	3.9	0.5	2.8	0.4	52.2	131.9	79.5	4.4	5.1	1.5	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00332	30	31	1	Original	512301.0	8117404.8	790.4	772.2	640.3	163.8	107.3	13.0	176.9	108.1	238.9	31.4	132.4	22.1	6.1	17.9	2.2	10.9	2.0	4.8	0.6	2.9	0.5	59.4	131.9	82.8	4.9	6.4	1.7	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00333	31	32	1	Original	512301.0	8117404.8	790.4	1047.2	927.6	233.3	120.4	15.1	248.4	164.2	380.8	45.0	188.4	28.9	8.1	21.9	2.8	12.3	2.2	4.9	0.6	3.0	0.4	64.3	119.6	109.6	6.6	9.5	2.7	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00334	32	33	1	Original	512301.0	8117404.8	790.4	839.1	685.7	171.3	75.9	10.2	181.5	114.7	301.0	32.5	138.8	22.9	5.8	14.5	1.8	8.4	1.4	3.3	0.4	1.9	0.3	38.0	153.4	118.0	7.3	14.5	3.3	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00336	33	34	1	Original	512301.0	8117404.8	790.4	837.8	778.0	186.3	91.6	12.1	196.4	141.9	335.4	36.4	149.9	22.8	6.7	17.5	2.1	10.0	1.8	3.7	0.4	2.7	0.4	46.4	59.8	222.5	11.7	16.4	4.2	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00337	34	35	1	Original	512301.0	8117404.8	790.4	895.0	784.6	193.7	99.7	13.2	206.9	154.8	312.0	38.5	155.1	24.4	7.3	17.9	2.3	11.0	1.9	4.3	0.5	2.8	0.4	51.4	110.4	173.8	9.3	16.0	4.1	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00338	35	36	1	Original	512301.0	8117404.8	790.4	827.3	758.3	171.6	103.7	12.4	184.0	138.4	321.8	34.0	137.6	22.8	6.2	17.2	2.2	10.1	1.9	4.3	0.5	2.9	0.4	57.9	69.0	207.4	10.5	19.3	4.0	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00339	36	37	1	Original	512301.0	8117404.8	790.4	722.7	652.1	164.7	84.2	10.4	175.1	120.8	261.6	31.2	133.6	20.8	5.9	15.2	1.9	8.4	1.6	3.3	0.4	2.3	0.3	44.8	70.6	128.2	5.5	6.8	2.6	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00340	37	38	1	Original	512301.0	8117404.8	790.4	829.3	740.4	188.7	87.6	11.2	199.9	133.7	305.9	36.5	152.2	24.5	6.5	16.7	2.1	9.1	1.6	3.5	0.4	2.0	0.3	45.3	89.0	100.0	5.1	8.1	2.1	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00341	38	39	1	Original	512301.0	8117404.8	790.4	1154.6	1056.4	263.1	85.2	11.5	274.7	211.7	469.2	52.6	210.5	27.1	7.3	18.8	2.2	9.3	1.5	3.2	0.3	2.0	0.3	40.3	98.2	190.3	11.8	20.5	3.2	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00342	39	40	1	Original	512301.0	8117404.8	790.4	826.0	730.9	181.7	82.0	11.1	192.8	140.2	304.6	35.9	145.8	22.4	6.2	16.4	1.9	9.3	1.5	3.2	0.4	2.1	0.3	40.6	95.1	104.9	5.7	9.3	2.3	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00344	40	41	1	Original	512301.0	8117404.8	790.4	745.5	662.6	165.4	76.9	10.7	176.1	124.3	275.2	32.4	133.0	20.9	5.7	15.2	1.9	8.8	1.5	3.3	0.4	2.2	0.3	37.7	82.8	112.7	4.9	8.2	2.3	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00345	41	42	1	Original	512301.0	8117404.8	790.4	779.5	709.0	177.1	75.7	10.4	187.5	134.9	299.7	34.2	142.9	21.6	5.6	15.7	1.8	8.5	1.3	3.0	0.4	2.0	0.2	37.1	70.6	116.0	6.0	10.4	2.3	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00346	42	43	1	Original	512301.0	8117404.8	790.4	605.4	527.1	133.9	57.9	8.1	142.0	97.8	221.1	26.1	107.8	16.5	4.3	11.9	1.5	6.7	1.1	2.5	0.3	1.6	0.2	27.8	78.2	81.7	4.6	8.8	1.8	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00347	43	44	1	Original	512301.0	8117404.8	790.4	535.1	458.4	118.2	55.7	7.0	125.2	81.9	187.9	22.7	95.5	14.8	4.3	11.0	1.4	5.6	0.9	2.4	0.3	1.6	0.2	27.9	76.7	73.0	3.9	6.5	1.4	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00348	44	45	1	Original	512301.0	8117404.8	790.4	542.4	456.5	116.1	51.6	7.0	123.1	83.3	190.4	22.6	93.6	15.0	3.8	10.3	1.2	5.7	1.0	2.0	0.3	1.6	0.2	25.5	85.9	75.5	3.9	6.3	1.5	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00349	45	46	1	Original	512301.0	8117404.8	790.4	622.9	520.1	130.9	61.5	8.8	139.7	97.3	213.7	25.1	105.8	16.6	4.6	12.4	1.5	7.3	1.2	2.3	0.3	1.6	0.3	30.0	102.8	87.1	4.3	7.5	2.0	HOM-RC-TGA-0008	GO26243815
Target A	RC-TGA-0004	TGA-RC-00351	46	47	1	Original	512301.0	8117404.8	790.4	583.9	482.6	119.0	61.3	8.3	127.4	88.4	197.8	22.8	96.2	16.1	4.6	12.0	1.5	6.9	1.1	2.6	0.3	1.7	0.2	30.4	101.2	79.0	3.7	6.0			

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	Ce ₂ O ₃ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0005	TGA-RC-00393	24	25	1	Original	512090.5	8117995.7	777.9	1494.3	1357.8	498.8	148.9	23.6	52.2	347.2	297.3	104.5	394.3	65.6	16.0	35.0	4.2	19.4	2.9	6.3	0.8	5.0	0.6	58.7	136.5	222.5	11.7	15.2	3.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00395	25	26	1	Original	512090.5	8117995.7	777.9	745.1	568.7	154.3	53.1	8.3	162.6	113.5	227.9	33.6	120.7	19.9	4.9	11.0	1.4	6.9	1.1	2.8	0.4	2.8	0.4	21.5	176.4	94.1	5.9	5.5	2.2	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00396	26	27	1	Original	512090.5	8117995.7	777.9	1290.8	1140.5	437.0	128.6	20.2	457.2	281.5	235.9	91.7	345.3	57.5	13.8	30.9	3.7	16.5	2.5	5.5	0.7	4.4	0.6	50.0	150.3	200.3	10.4	13.9	3.0	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00397	27	28	1	Original	512090.5	8117995.7	777.9	782.3	625.8	195.8	79.3	12.0	207.7	100.6	221.7	37.7	158.1	28.4	6.9	17.5	2.2	9.8	1.5	3.6	0.5	2.8	0.5	34.0	156.4	90.0	5.4	5.4	2.3	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00398	28	29	1	Original	512090.5	8117995.7	777.9	4451.9	4336.9	1722.2	1028.4	142.2	1864.4	673.2	651.0	316.6	1405.6	262.1	71.4	201.1	24.6	117.6	18.7	41.7	5.4	31.8	4.1	511.8	115.0	180.3	9.8	11.5	3.3	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00399	29	30	1	Original	512090.5	8117995.7	777.9	6650.4	6552.2	2387.0	2175.4	257.5	2644.5	864.4	755.1	415.7	1971.3	369.9	106.8	328.5	41.8	215.8	38.6	91.5	11.8	66.6	9.3	1264.9	98.2	223.9	11.4	14.8	4.0	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00400	30	31	1	Original	512090.5	8117995.7	777.9	2601.0	2487.5	782.6	710.0	84.4	867.0	543.0	334.1	148.0	634.6	117.7	33.0	32.2	13.4	71.0	13.0	31.6	3.9	22.7	3.2	414.0	113.5	180.3	10.0	12.1	2.6	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00402	31	32	1	Original	512090.5	8117995.7	777.9	1268.1	1133.2	347.8	183.5	23.0	370.8	326.1	232.2	70.2	277.6	43.6	11.0	30.2	3.8	19.2	3.3	7.7	0.9	5.9	0.8	98.2	135.0	81.4	5.3	5.1	1.6	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00403	32	33	1	Original	512090.5	8117995.7	777.9	824.0	682.9	209.0	128.1	16.3	225.3	144.3	172.6	39.3	169.7	29.0	7.8	24.6	2.8	13.5	2.3	5.4	0.7	4.0	0.5	66.7	141.1	89.8	4.9	5.2	1.3	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00404	33	34	1	Original	512090.5	8117995.7	777.9	653.1	504.3	128.6	123.1	12.5	141.2	63.7	170.1	22.8	105.8	18.7	5.3	17.6	2.1	10.4	2.0	4.6	0.6	3.3	0.5	76.6	148.8	77.4	4.8	4.0	0.9	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00405	34	35	1	Original	512090.5	8117995.7	777.9	852.6	728.4	165.7	200.9	17.5	183.1	101.0	236.5	31.5	134.1	24.4	6.8	23.6	2.7	14.7	2.9	7.6	1.0	5.4	0.8	135.3	124.2	92.7	5.4	4.8	1.2	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00406	35	36	1	Original	512090.5	8117995.7	777.9	703.3	586.8	142.5	117.9	11.6	154.1	114.0	192.2	28.5	114.0	20.2	5.1	15.4	1.8	9.8	1.9	5.0	0.6	3.6	0.5	74.0	116.6	105.1	7.3	5.7	1.4	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00407	36	37	1	Original	512090.5	8117995.7	777.9	708.2	583.9	143.5	115.5	10.9	154.5	100.3	204.5	28.6	114.9	20.1	5.4	15.8	1.8	9.1	1.8	4.2	0.5	3.0	0.4	73.4	124.2	74.5	4.8	4.4	1.0	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00408	37	38	1	Original	512090.5	8117995.7	777.9	710.0	575.0	144.8	97.8	10.2	155.1	101.3	210.7	29.0	115.8	20.4	5.3	14.2	1.7	8.5	1.5	3.5	0.4	2.2	0.4	60.1	135.0	65.8	4.0	3.8	0.8	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00409	38	39	1	Original	512090.5	8117995.7	777.9	701.0	575.3	142.8	99.6	10.4	152.8	105.0	209.4	28.8	113.6	18.9	5.4	14.5	1.7	8.7	1.6	3.7	0.5	2.7	0.4	60.5	125.8	77.8	4.9	4.5	1.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00411	39	40	1	Original	512090.5	8117995.7	777.9	629.0	498.7	121.9	56.4	7.0	128.9	89.6	214.4	24.9	97.0	16.4	4.1	10.7	1.2	5.7	1.0	2.2	0.3	1.5	0.2	29.5	130.4	70.5	4.2	4.1	1.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00412	40	41	1	Original	512090.5	8117995.7	777.9	582.2	470.3	116.3	76.5	8.9	125.2	83.5	178.1	23.1	93.2	15.9	4.2	11.7	1.4	7.5	1.3	3.0	0.4	2.2	0.3	44.4	112.0	82.4	4.8	5.7	2.5	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00413	41	42	1	Original	512090.5	8117995.7	777.9	437.6	331.8	86.0	51.7	6.2	92.2	54.3	127.1	17.0	68.9	12.7	3.4	9.0	1.1	5.1	0.9	2.1	0.3	1.5	0.2	28.1	105.8	45.6	2.8	3.0	0.8	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00414	42	43	1	Original	512090.5	8117995.7	777.9	395.8	299.1	79.6	40.9	5.7	85.3	51.1	116.3	15.6	63.9	11.2	2.9	8.0	0.9	4.8	0.8	1.7	0.2	1.3	0.2	20.2	96.6	44.2	2.7	2.6	0.7	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00415	43	44	1	Original	512090.5	8117995.7	777.9	346.6	245.4	64.7	34.9	4.8	69.5	40.2	96.6	12.8	51.9	9.0	2.6	6.7	0.8	4.0	0.6	1.4	0.2	1.1	0.1	17.3	101.2	40.9	2.6	1.8	0.5	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00416	44	45	1	Original	512090.5	8117995.7	777.9	389.2	294.1	77.1	40.8	5.6	82.8	49.6	115.0	15.5	61.6	11.6	3.0	7.8	1.0	4.6	0.8	1.6	0.2	1.3	0.2	20.3	95.1	46.5	3.1	2.1	0.6	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00417	45	46	1	Original	512090.5	8117995.7	777.9	417.6	331.7	84.9	46.9	6.4	91.1	59.0	129.0	16.8	68.1	11.9	3.3	8.4	1.1	5.3	0.8	2.0	0.2	1.5	0.2	24.1	85.9	68.4	3.9	3.6	1.3	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00419	46	47	1	Original	512090.5	8117995.7	777.9	610.4	544.4	124.1	64.0	8.7	132.8	117.9	221.1	26.2	97.9	17.3	4.6	12.2	1.5	7.2	1.1	2.6	0.3	2.0	0.3	32.3	66.0	189.6	8.4	10.7	3.2	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00420	47	48	1	Original	512090.5	8117995.7	777.9	760.9	698.0	156.7	66.5	9.3	165.9	165.4	289.9	33.6	123.1	19.6	5.1	12.7	1.7	7.6	1.2	3.1	0.4	2.1	0.3	32.4	62.9	254.6	9.9	16.2	4.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00421	48	49	1	Original	512090.5	8117995.7	777.9	814.8	741.2	181.2	68.4	9.5	190.7	160.7	309.6	37.7	143.5	21.3	5.7	13.7	1.7	7.8	1.2	2.7	0.4	2.1	0.3	32.8	73.6	217.4	9.8	17.3	4.4	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00422	49	50	1	Original	512090.5	8117995.7	777.9	499.2	413.3	106.3	48.1	6.8	113.1	77.9	166.6	21.4	84.9	14.6	3.6	9.6	1.2	5.6	0.9	2.1	0.2	1.4	0.2	23.4	85.9	97.9	4.8	6.9	1.8	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00423	50	51	1	Original	512090.5	8117995.7	777.9	419.9	331.0	85.3	41.7	5.3	90.6	61.1	131.4	16.8	68.5	11.5	3.0	8.0	0.9	4.4	0.8	1.9	0.3	1.4	0.2	20.8	89.0	76.5	4.0	5.3	1.3	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00424	51	52	1	Original	512090.5	8117995.7	777.9	525.1	448.4	108.8	51.4	7.2	116.0	90.1	184.9	22.4	86.4	13.2	3.7	9.8	1.3	5.9	0.9	2.2	0.3	1.5	0.2	25.7	76.7	125.2	6.5	9.1	2.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00425	52	53	1	Original	512090.5	8117995.7	777.9	468.2	390.0	102.1	45.2	6.2	108.4	71.0	157.8	20.4	81.8	13.9	3.3	9.0	1.1	5.1	0.8	1.9	0.2	1.3	0.2	22.2	78.2	48.9	3.1	4.2	1.1	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00427	53	54	1	Original	512090.5	8117995.7	777.9	423.9	347.2	89.9	44.2	5.8	95.6	62.9	138.2	17.9	72.0	12.1	3.0	8.1	1.1	4.7	0.7	2.2	0.3	1.3	0.2	22.6	76.7	61.8	3.5	5.1	1.2	HOM-RC-TGA-0009	GO26243817
Target A	RC-TGA-0005	TGA-RC-00428	54	55	1	Original	512090.5	8117995.7	777.9	423.4	355.9	82.9	46.9	6.2	89.1	67.0	148.0	17.6	65.3	11.2	3.0	7.9	1.0	5.2	0.9	2.3	0.3	1.6	0.3	24.4	67.5	86.3	4.6	6.8	1.6	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0005	TGA-RC-00429	55	56	1	Original	512090.5	8117995.7	777.9	404.4	338.5	78.4	45.5	5.9	84.3	63.3	140.0	16.4	62.1	11.2	2.8	7.5	1.0	4.9	0.8	2.3	0.3	1.6	0.2	24.1	66.0	86.6	4.5	6.3	1.5	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0005	TGA-RC-00430	56	57	1	Original	512090.5	8117995.7	777.9	489.8	417.7	96.4	52.5	6.9	103.4	79.8	176.3																				

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	Ce ₂ O ₃ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0006	TGA-RC-00472	23	24	1	Original	511696.2	8117596.9	774.7	1252.2	968.4	312.7	164.4	22.6	335.3	166.0	277.6	65.4	247.3	47.8	12.9	30.8	4.0	18.6	3.0	7.0	0.9	4.8	0.7	81.9	283.8	163.8	7.4	9.5	2.6	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0006	TGA-RC-00473	24	25	1	Original	511696.2	8117596.9	774.7	1801.0	1555.6	597.4	318.5	44.4	641.8	348.3	201.5	123.9	473.6	89.9	23.9	62.5	7.7	36.7	5.8	13.6	1.6	8.7	1.2	156.8	245.4	148.8	6.8	8.3	2.6	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0006	TGA-RC-00474	25	26	1	Original	511696.2	8117596.9	774.7	2453.2	2157.2	761.1	622.1	73.1	834.1	499.6	162.1	149.8	611.2	112.3	32.8	98.8	12.1	60.9	10.5	26.1	2.9	16.1	2.4	359.4	296.0	92.6	4.6	5.7	1.5	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0006	TGA-RC-00475	26	27	1	Original	511696.2	8117596.9	774.7	1224.4	952.9	201.0	406.3	33.8	234.9	131.4	182.4	37.7	163.3	31.9	10.6	43.1	5.3	28.6	5.9	15.7	1.7	8.2	1.4	285.7	271.5	118.5	5.0	6.2	2.0	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0006	TGA-RC-00476	27	28	1	Original	511696.2	8117596.9	774.7	2052.7	1808.8	461.3	715.6	64.5	525.8	395.3	168.3	89.2	372.1	68.4	21.4	82.1	10.1	54.4	11.1	29.1	3.3	16.3	2.6	485.1	243.9	121.2	4.8	6.0	2.0	HOM-RC-TGA-0010	GO26243818
Target A	RC-TGA-0006	TGA-RC-00478	28	29	1	Original	511696.2	8117596.9	774.7	818.1	598.8	140.2	195.1	16.6	156.7	89.6	152.3	25.4	114.8	21.6	5.9	20.9	2.6	13.9	2.7	6.7	0.8	3.8	0.6	137.2	219.3	87.6	4.2	5.7	1.6	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00479	29	30	1	Original	511696.2	8117596.9	774.7	782.1	610.3	142.7	152.1	13.8	156.5	105.8	19.0	27.3	115.4	18.7	5.2	18.3	2.3	11.5	2.2	5.7	0.6	3.1	0.5	102.6	171.8	117.5	5.4	8.4	1.9	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00480	30	31	1	Original	511696.2	8117596.9	774.7	796.7	675.6	157.2	127.5	12.9	170.1	127.8	242.6	31.8	125.4	20.5	5.4	16.8	2.1	10.8	1.9	4.7	0.6	3.3	0.5	81.4	121.2	156.6	7.8	12.3	2.5	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00481	31	32	1	Original	511696.2	8117596.9	774.7	562.7	406.2	105.0	82.0	9.4	114.4	71.2	133.3	20.0	85.0	14.7	4.1	12.0	1.6	7.8	1.4	3.7	0.4	2.4	0.4	48.1	156.4	86.4	3.8	7.6	1.7	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00482	32	33	1	Original	511696.2	8117596.9	774.7	509.0	334.2	86.3	69.2	7.6	93.9	55.6	109.7	15.8	70.5	13.5	3.3	10.1	1.2	6.4	1.1	2.8	0.3	1.8	0.2	41.9	174.9	68.0	3.1	5.3	1.4	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00484	33	34	1	Original	511696.2	8117596.9	774.7	500.0	377.3	92.9	55.7	7.3	100.2	71.0	144.3	18.7	74.2	13.5	3.3	9.8	1.2	6.1	0.9	2.6	0.3	1.6	0.3	29.6	122.7	104.1	5.1	6.9	1.9	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00485	34	35	1	Original	511696.2	8117596.9	774.7	385.8	246.2	64.9	37.4	5.0	70.0	42.3	92.5	12.7	52.3	9.1	2.5	6.9	0.9	4.1	0.7	1.7	0.2	1.1	0.1	19.2	139.6	57.5	2.8	3.7	1.1	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00486	35	36	1	Original	511696.2	8117596.9	774.7	429.9	298.0	76.9	39.0	5.9	82.7	54.0	118.6	15.0	61.8	11.3	2.9	7.4	1.0	4.9	0.7	1.7	0.2	1.2	0.2	18.8	131.9	66.5	3.7	6.3	1.4	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00487	36	37	1	Original	511696.2	8117596.9	774.7	420.9	299.7	75.2	42.0	5.8	80.9	54.7	117.1	14.9	60.3	10.8	3.0	7.8	1.0	4.8	0.8	2.0	0.2	1.4	0.2	21.0	121.2	74.5	3.8	5.7	1.5	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00488	37	38	1	Original	511696.2	8117596.9	774.7	507.8	408.1	102.9	54.5	7.6	110.5	76.2	160.3	19.9	83.1	14.1	3.5	9.8	1.3	6.2	1.0	2.5	0.3	1.7	0.2	27.8	99.7	103.4	5.5	9.1	2.2	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00489	38	39	1	Original	511696.2	8117596.9	774.7	374.9	258.3	66.9	36.3	5.3	72.2	44.5	100.2	13.4	53.5	10.4	2.5	7.0	1.0	4.4	0.7	1.8	0.2	1.0	0.1	17.5	116.6	55.6	3.2	5.0	1.1	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00490	39	40	1	Original	511696.2	8117596.9	774.7	330.0	208.8	55.8	31.4	4.4	60.1	34.1	79.2	10.7	45.0	8.2	2.1	5.9	0.8	3.6	0.6	1.3	0.2	0.9	0.1	16.0	121.2	41.6	2.3	2.9	0.8	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00492	40	41	1	Original	511696.2	8117596.9	774.7	327.4	198.6	54.7	30.3	4.5	59.2	31.5	73.2	10.3	44.4	8.8	2.2	6.1	0.8	3.6	0.6	1.3	0.2	0.9	0.1	14.5	128.8	38.6	2.2	2.6	0.8	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00493	41	42	1	Original	511696.2	8117596.9	774.7	326.9	188.9	51.2	27.9	4.0	55.2	30.3	71.0	9.7	41.5	8.5	1.9	5.6	0.7	3.3	0.5	1.1	0.2	0.8	0.1	13.6	138.0	30.5	1.6	2.2	0.7	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00494	42	43	1	Original	511696.2	8117596.9	774.7	442.2	298.0	76.3	37.6	5.2	81.4	55.2	118.3	15.3	61.0	10.5	2.7	7.2	1.0	4.2	0.7	1.7	0.2	1.1	0.2	18.8	144.2	83.1	4.0	6.1	1.5	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00495	43	44	1	Original	511696.2	8117596.9	774.7	579.6	475.3	117.1	51.8	7.4	124.5	95.4	196.5	23.9	93.2	14.4	3.9	9.6	1.3	6.1	1.0	2.4	0.3	1.6	0.3	25.5	104.3	129.0	6.8	10.6	2.4	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00496	44	45	1	Original	511696.2	8117596.9	774.7	431.5	298.0	75.5	36.9	5.2	80.7	54.5	120.8	14.9	60.7	10.3	2.7	7.4	0.9	4.3	0.6	1.7	0.2	1.0	0.2	17.9	133.4	73.4	3.8	5.4	1.4	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00497	45	46	1	Original	511696.2	8117596.9	774.7	503.9	401.1	99.1	46.1	6.7	105.8	78.2	164.6	20.5	78.6	13.1	3.3	8.6	1.1	5.6	0.9	2.0	0.3	1.3	0.2	22.9	102.8	102.0	5.7	9.4	2.0	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00498	46	47	1	Original	511696.2	8117596.9	774.7	290.5	166.3	43.2	28.2	4.2	47.5	25.9	61.8	8.6	34.6	7.1	1.7	5.4	0.7	3.6	0.5	1.2	0.1	0.9	0.1	14.0	124.2	25.1	1.6	1.5	0.6	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00500	47	48	1	Original	511696.2	8117596.9	774.7	348.3	210.3	53.8	31.4	4.5	58.3	35.7	81.0	10.4	43.4	8.5	2.1	6.1	0.7	3.8	0.5	1.4	0.2	1.0	0.1	15.5	138.0	40.5	2.4	2.9	0.8	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00501	48	49	1	Original	511696.2	8117596.9	774.7	467.9	356.0	86.3	48.1	6.5	92.7	65.3	143.7	17.3	68.9	12.6	3.1	9.0	1.3	5.2	0.8	2.1	0.3	1.4	0.2	24.6	112.0	91.6	4.6	7.4	1.6	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00502	49	50	1	Original	511696.2	8117596.9	774.7	498.1	387.6	90.1	51.1	7.2	97.3	77.4	156.0	18.6	15.5	13.0	3.5	9.4	1.2	6.0	1.0	2.4	0.3	1.6	0.3	25.5	110.4	112.0	5.9	8.3	1.8	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00503	50	51	1	Original	511696.2	8117596.9	774.7	418.4	315.6	74.4	41.8	5.8	80.2	59.9	128.7	15.5	58.9	11.7	2.6	7.8	1.0	4.8	0.8	1.9	0.2	1.4	0.2	21.2	102.8	80.0	4.3	6.6	1.4	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00504	51	52	1	Original	511696.2	8117596.9	774.7	393.6	266.3	65.4	36.7	4.7	70.1	50.8	103.4	13.1	52.3	10.0	2.4	6.7	0.9	3.8	0.7	1.7	0.2	1.2	0.2	18.9	127.3	64.1	3.1	8.2	1.6	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00505	52	53	1	Original	511696.2	8117596.9	774.7	504.7	395.8	93.1	39.5	5.9	99.0	80.6	170.1	20.0	73.1	12.5	3.0	8.2	1.0	4.9	0.7	1.7	0.2	1.0	0.1	18.7	108.9	126.0	6.7	10.1	1.8	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00506	53	54	1	Original	511696.2	8117596.9	774.7	384.2	259.9	63.8	31.8	4.6	68.4	49.3	106.0	12.7	51.1	9.1	2.2	5.9	0.8	3.8	0.6	1.4	0.1	0.9	0.1	15.7	124.2	67.7	3.7	5.4	1.1	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00508	54	55	1	Original	511696.2	8117596.9	774.7	540.5	406.8	88.1	53.5	7.2	95.4	71.4	182.4	17.8	70.3	13.2	3.0	9.0	1.2	6.0	0.9	2.3	0.3	1.6	0.2	29.0	131.9	103.3	4.6	8.1	2.1	HOM-RC-TGA-0011	GO26246785
Target A	RC-TGA-0006	TGA-RC-00509	55	56	1	Original	511696.2	8117596.9	774.7	397.8	219.9	54.2	32.5	4.3	58.4	39.4	85.3	10.6	43.5	8.6	2.2	5.9	0.7	3.5	0.6	1.3	0.2	1.0	0.2								

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0007	TGA-RC-00551	22	23	1	Original	511499.8	8117803.2	767.3	1191.5	811.1	163.0	47.6	7.4	170.4	310.8	272.7	41.7	121.3	16.9	4.3	11.1	1.4	6.0	1.0	2.3	0.3	1.7	0.3	19.3	380.4	213.9	9.8	16.7	5.2	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00552	23	24	1	Original	511499.8	8117803.2	767.3	980.5	675.3	130.0	38.5	6.3	136.3	219.9	273.9	32.1	97.9	12.9	3.5	9.0	1.1	5.2	0.8	1.7	0.3	1.5	0.2	15.2	305.2	191.7	8.7	14.3	5.9	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00553	24	25	1	Original	511499.8	8117803.2	767.3	749.9	547.5	126.0	34.3	5.6	131.6	205.8	168.9	30.8	95.2	12.4	3.1	8.2	1.0	4.5	0.7	1.5	0.2	1.3	0.2	13.5	202.5	258.9	10.4	14.5	6.3	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00554	25	26	1	Original	511499.8	8117803.2	767.3	1859.0	1609.0	482.4	123.2	19.7	502.1	606.4	345.2	112.6	369.8	51.8	13.4	33.2	3.8	15.9	2.4	4.7	0.6	3.3	0.5	45.5	250.0	141.1	5.6	8.3	4.0	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00555	26	27	1	Original	511499.8	8117803.2	767.3	1632.5	1310.4	396.8	136.8	21.3	418.2	390.6	337.8	87.7	309.1	48.4	12.2	32.3	3.9	17.4	2.9	5.8	0.8	4.5	0.6	56.4	322.1	114.2	4.9	8.0	2.6	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00556	27	28	1	Original	511499.8	8117803.2	767.3	1190.7	905.4	267.6	113.8	16.9	284.6	235.7	253.0	58.2	209.4	35.1	9.2	24.7	3.1	13.9	2.4	5.5	0.7	4.3	0.6	49.4	285.3	119.5	4.4	6.6	2.7	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00557	28	29	1	Original	511499.8	8117803.2	767.3	997.9	660.5	195.9	104.4	14.5	210.4	153.6	179.3	41.3	154.6	26.7	7.5	19.9	2.6	11.9	2.1	4.7	0.7	3.7	0.6	51.2	337.4	115.9	5.3	8.5	2.3	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00559	29	30	1	Original	511499.8	8117803.2	767.3	913.9	690.0	181.5	133.5	16.7	198.2	111.2	236.5	36.9	144.6	27.4	7.2	21.7	2.9	13.8	2.7	6.1	0.8	4.7	0.7	72.9	223.9	129.3	5.4	9.4	3.3	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00560	30	31	1	Original	511499.8	8117803.2	767.3	681.0	515.4	99.3	95.5	11.5	110.9	62.2	243.2	19.9	79.4	15.2	4.3	13.7	1.9	9.7	2.0	4.8	0.7	4.0	0.6	53.8	165.7	106.9	3.8	5.8	2.9	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00561	31	32	1	Original	511499.8	8117803.2	767.3	788.3	642.6	148.3	165.5	16.4	164.6	120.8	186.1	30.5	117.8	21.9	6.7	21.7	2.7	13.7	2.9	6.5	0.9	4.5	0.7	105.3	145.7	100.6	4.4	7.1	2.4	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00562	32	33	1	Original	511499.8	8117803.2	767.3	455.8	337.7	80.1	62.9	7.5	87.6	63.0	119.8	16.3	63.8	11.9	3.5	10.2	1.3	6.2	1.2	2.6	0.4	2.1	0.3	35.2	118.1	75.8	2.9	3.7	1.7	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00563	33	34	1	Original	511499.8	8117803.2	767.3	558.1	463.1	105.5	62.4	8.0	113.6	87.0	193.5	22.8	82.7	14.6	4.2	11.8	1.4	6.6	1.2	2.8	0.4	1.9	0.3	31.9	95.1	129.6	5.7	8.9	2.5	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00564	34	35	1	Original	511499.8	8117803.2	767.3	339.8	206.4	51.0	34.8	4.7	55.7	33.3	79.5	10.4	40.6	7.8	2.3	6.7	0.9	3.9	0.7	1.7	0.2	1.1	0.2	17.4	133.4	45.8	1.8	2.4	1.0	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00565	35	36	1	Original	511499.8	8117803.2	767.3	329.8	191.7	46.9	31.4	4.2	51.1	31.1	75.3	9.6	37.3	7.0	2.2	6.0	0.7	3.4	0.6	1.4	0.2	0.9	0.2	15.7	138.0	42.9	2.0	2.8	0.9	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00567	36	37	1	Original	511499.8	8117803.2	767.3	345.2	187.2	45.9	33.3	4.5	50.4	29.9	71.0	9.3	36.6	7.1	2.3	6.4	0.9	3.6	0.7	1.4	0.2	1.0	0.1	16.6	158.0	38.1	1.7	3.8	1.0	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00568	37	38	1	Original	511499.8	8117803.2	767.3	359.6	200.1	48.0	36.1	4.8	52.7	32.3	76.4	9.8	38.1	7.4	2.4	6.7	0.9	3.9	0.7	1.5	0.2	1.1	0.1	18.5	159.5	47.4	2.0	6.2	0.8	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00569	38	39	1	Original	511499.8	8117803.2	767.3	388.3	227.3	53.4	38.2	4.9	58.3	39.5	88.0	11.1	42.3	8.2	2.6	7.0	1.0	4.0	0.8	1.6	0.2	1.3	0.2	19.6	161.0	57.2	2.6	5.6	1.1	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00570	39	40	1	Original	511499.8	8117803.2	767.3	386.1	241.9	58.3	34.1	4.7	63.1	42.1	98.6	12.3	46.1	8.7	2.4	6.5	0.8	3.9	0.7	1.5	0.2	1.1	0.2	16.9	144.2	57.7	2.7	7.3	1.1	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00571	40	41	1	Original	511499.8	8117803.2	767.3	370.1	229.0	56.2	36.2	4.7	60.9	40.5	88.2	11.4	44.8	7.9	2.3	6.5	0.8	3.9	0.7	1.6	0.2	1.2	0.2	18.9	141.1	50.9	2.3	5.5	0.9	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00572	41	42	1	Original	511499.8	8117803.2	767.3	389.5	225.4	55.6	38.3	5.3	60.9	35.8	87.0	11.4	44.2	8.7	2.5	6.8	0.9	4.4	0.8	1.8	0.3	1.5	0.2	19.3	164.1	49.2	2.4	7.3	1.0	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00573	42	43	1	Original	511499.8	8117803.2	767.3	412.2	238.9	58.3	38.0	5.2	63.4	39.8	94.1	12.1	46.2	8.7	2.5	6.7	0.9	4.3	0.8	1.7	0.3	1.4	0.2	19.4	173.3	50.5	2.3	9.0	1.1	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00575	43	44	1	Original	511499.8	8117803.2	767.3	396.9	228.2	55.4	36.0	4.9	60.3	37.9	90.4	11.3	44.1	8.5	2.4	6.6	0.9	4.0	0.7	1.7	0.2	1.2	0.2	18.2	168.7	48.6	2.4	5.9	0.9	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00576	44	45	1	Original	511499.8	8117803.2	767.3	556.8	392.6	92.2	46.2	6.6	98.7	73.0	168.9	20.3	71.9	12.5	3.3	8.6	1.1	5.5	0.9	2.2	0.3	1.3	0.2	22.9	164.1	100.3	5.7	10.4	1.8	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00577	45	46	1	Original	511499.8	8117803.2	767.3	410.5	251.0	59.6	36.3	5.0	64.7	44.0	102.1	12.4	47.2	9.0	2.5	6.4	0.8	4.2	0.7	1.9	0.2	1.2	0.2	18.3	159.5	67.0	3.2	6.1	1.2	HOM-RC-TGA-0012	GO26246788
Target A	RC-TGA-0007	TGA-RC-00578	46	47	1	Original	511499.8	8117803.2	767.3	457.0	283.6	67.8	41.1	5.4	73.2	49.8	115.3	14.6	53.2	9.6	2.7	7.1	0.9	4.5	0.7	1.7	0.2	1.4	0.2	21.6	173.3	69.0	3.4	10.5	1.4	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00579	47	48	1	Original	511499.8	8117803.2	767.3	481.7	308.3	71.5	48.3	6.1	77.6	55.5	122.8	15.2	56.3	10.2	2.9	7.3	1.0	5.1	0.9	2.4	0.3	1.8	0.3	26.3	173.3	86.3	3.8	13.9	1.6	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00580	48	49	1	Original	511499.8	8117803.2	767.3	457.6	308.7	70.0	53.9	6.2	76.2	56.2	118.8	15.0	54.9	10.0	2.8	7.7	1.0	5.3	0.9	2.4	0.3	2.1	0.3	31.1	148.8	79.8	2.8	14.1	2.2	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00581	49	50	1	Original	511499.8	8117803.2	767.3	534.3	443.8	100.0	58.7	7.3	107.3	84.7	187.9	21.5	78.5	12.5	3.6	9.6	1.2	6.1	1.0	2.6	0.4	2.0	0.3	32.0	90.5	107.9	4.3	10.7	2.1	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00582	50	51	1	Original	511499.8	8117803.2	767.3	421.5	254.3	61.9	39.7	5.1	67.0	44.3	99.7	12.7	49.1	8.7	2.5	6.8	0.8	4.3	0.8	1.7	0.2	1.3	0.2	21.1	167.2	56.2	2.4	7.6	1.2	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00583	51	52	1	Original	511499.8	8117803.2	767.3	373.0	235.0	57.5	35.2	4.5	62.0	40.7	93.6	12.0	45.5	8.0	2.3	6.3	0.8	3.7	0.6	1.6	0.2	1.2	0.2	18.3	138.0	58.2	2.7	7.0	1.0	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00585	52	53	1	Original	511499.8	8117803.2	767.3	485.2	357.9	86.4	40.8	5.5	92.0	65.9	153.5	18.7	67.8	11.2	3.0	7.8	0.9	4.6	0.8	1.7	0.2	1.2	0.2	20.4	127.3	91.0	5.0	9.4	1.6	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00586	53	54	1	Original	511499.8	8117803.2	767.3	465.6	335.2	79.7	42.4	5.5	85.2	62.4	140.0	17.4	62.3	10.7	3.0	7.7	0.9	4.6	0.8	1.8	0.2	1.4	0.2	21.8	130.4	78.0	4.2	7.7	1.4	HOM-RC-TGA-0013	GO26246790
Target A	RC-TGA-0007	TGA-RC-00587	54	55	1	Original	511499.8	8117803.2	767.3	443.1	334.2	77.7	44.9	6.0	83.7	62.6	138.2	16.9	60.8	10.8	3.0	7.8	1.0	5.0	0.9	1.9	0.3	1.5	0.2	23.5	108.9	87.7	4.3				

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	Ce ₂ O ₃ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS	
Target A	RC-TGA-0008	TGA-RC-00629	21	22	1	Original	511501.7	8117400.2	772.9	2338.7	1979.8	534.0	274.5	40.7	574.7	290.9	800.9	109.4	424.6	79.6	21.7	54.5	7.2	33.5	5.4	12.0	1.5	8.6	1.2	128.9	358.9	108.0	5.0	6.7	2.5	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00630	22	23	1	Original	511501.7	8117400.2	772.9	1935.7	1618.2	413.5	204.5	29.3	442.8	241.6	697.7	84.6	328.9	60.9	16.0	40.3	5.2	24.1	3.9	9.1	1.1	6.7	0.9	97.2	317.5	112.0	2.8	3.9	2.4	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00631	23	24	1	Original	511501.7	8117400.2	772.9	2387.0	2138.5	704.7	468.4	62.9	767.5	394.1	466.8	137.8	566.9	104.6	29.8	83.2	10.7	52.2	8.9	20.6	2.5	14.5	2.1	243.8	248.5	105.6	5.1	5.9	2.0	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00632	24	25	1	Original	511501.7	8117400.2	772.9	3570.5	3345.0	1331.6	831.9	118.0	1449.6	669.7	318.2	253.8	1077.8	193.7	56.5	157.3	20.5	97.6	16.4	37.5	4.4	26.2	4.0	411.5	225.5	110.0	5.9	7.0	1.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00633	25	26	1	Original	511501.7	8117400.2	772.9	3463.4	3254.8	1286.0	787.6	109.6	1395.5	629.8	362.4	250.1	1035.8	189.0	54.1	147.5	19.2	90.3	15.2	34.8	4.2	24.9	3.6	393.7	226.8	112.7	6.6	8.3	2.0	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00635	26	27	1	Original	511501.7	8117400.2	772.9	1750.5	1522.0	517.6	325.0	44.2	561.9	287.3	313.2	100.1	417.6	78.7	22.3	61.2	7.7	36.5	6.1	14.0	1.7	10.1	1.5	163.8	228.5	73.1	4.3	4.8	1.4	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00636	27	28	1	Original	511501.7	8117400.2	772.9	1970.0	1729.2	611.7	401.6	54.6	666.3	336.6	287.4	118.3	493.4	91.8	27.3	74.5	9.5	45.1	7.5	17.4	2.1	12.0	1.8	204.5	240.0	93.8	5.4	6.2	1.6	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00637	28	29	1	Original	511501.7	8117400.2	772.9	1863.2	1660.7	582.1	427.6	51.0	633.1	322.5	243.2	110.8	471.2	85.3	25.1	76.0	9.0	42.0	7.2	16.4	1.9	10.2	1.5	238.1	202.5	100.4	5.6	6.5	1.6	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00638	29	30	1	Original	511501.7	8117400.2	772.9	546.5	407.0	126.9	87.0	10.8	137.8	70.1	104.0	24.4	102.5	18.8	5.3	15.3	1.9	8.9	1.5	3.5	0.4	2.3	0.3	47.6	139.6	47.8	2.7	3.1	0.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00639	30	31	1	Original	511501.7	8117400.2	772.9	524.9	396.1	110.3	63.8	8.6	118.9	71.9	134.5	22.8	87.5	15.6	4.5	11.8	1.5	7.1	1.2	2.8	0.3	1.8	0.3	32.5	128.8	71.7	3.9	5.2	1.1	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00640	31	32	1	Original	511501.7	8117400.2	772.9	424.3	281.6	81.0	46.0	6.5	87.5	48.8	94.3	16.2	64.9	11.4	3.5	9.2	1.1	5.3	0.9	1.9	0.2	1.2	0.2	22.5	142.6	41.2	2.3	2.9	0.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00642	32	33	1	Original	511501.7	8117400.2	772.9	576.0	436.4	115.5	50.7	7.2	122.7	80.5	175.0	24.3	91.2	14.7	4.2	10.6	1.3	5.9	1.0	2.2	0.3	1.4	0.2	23.6	139.6	80.5	5.1	9.5	1.3	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00643	33	34	1	Original	511501.7	8117400.2	772.9	360.4	196.3	51.8	29.5	4.1	55.9	33.0	74.6	10.4	41.4	7.5	2.3	5.8	0.8	3.3	0.5	1.2	0.2	0.2	0.9	0.1	14.4	164.1	24.3	1.5	2.7	0.6	HOM-RC-TGA-0014	GO26256025
Target A	RC-TGA-0008	TGA-RC-00644	34	35	1	Original	511501.7	8117400.2	772.9	329.3	183.6	50.0	29.8	4.1	53.1	29.2	66.8	9.7	40.4	7.8	2.2	5.8	0.7	3.4	0.5	1.2	0.1	0.9	0.1	14.7	145.7	25.5	1.3	2.4	0.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00645	35	36	1	Original	511501.7	8117400.2	772.9	311.3	174.8	49.8	29.6	4.1	54.9	25.1	62.6	9.6	40.1	7.7	2.3	5.8	0.7	3.4	0.6	1.1	0.1	0.1	0.1	14.5	136.5	22.6	1.5	2.0	0.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00646	36	37	1	Original	511501.7	8117400.2	772.9	385.1	202.6	55.7	34.2	4.6	60.3	32.6	72.0	11.1	44.6	8.1	2.5	6.5	0.8	3.8	0.6	1.3	0.2	1.0	0.2	17.4	182.5	36.8	1.3	1.8	0.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00647	37	38	1	Original	511501.7	8117400.2	772.9	485.6	261.7	72.3	30.8	4.4	76.7	40.8	108.5	14.8	57.5	9.2	2.7	6.7	0.8	3.5	0.5	1.2	0.1	0.8	0.1	14.2	223.9	27.8	2.4	4.7	0.5	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00648	38	39	1	Original	511501.7	8117400.2	772.9	513.3	410.6	100.1	45.4	6.2	106.2	76.2	176.3	21.6	78.5	12.5	3.7	9.0	1.1	5.0	0.9	2.0	0.2	1.2	0.2	22.1	102.8	113.7	6.5	9.1	1.6	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00649	39	40	1	Original	511501.7	8117400.2	772.9	513.8	407.9	99.3	44.9	6.3	105.5	77.4	173.8	21.6	77.7	12.6	3.6	8.9	1.1	5.2	0.9	1.9	0.2	1.2	0.1	21.7	105.8	120.9	6.2	9.0	1.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00651	40	41	1	Original	511501.7	8117400.2	772.9	354.1	211.5	54.3	31.1	4.1	58.4	36.6	81.4	11.1	43.2	8.1	2.3	6.1	0.8	3.3	0.6	1.4	0.1	0.9	0.1	15.5	142.6	63.2	2.3	3.3	1.1	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00652	41	42	1	Original	511501.7	8117400.2	772.9	322.3	179.7	50.7	32.0	4.5	55.2	26.4	62.6	9.9	40.8	7.9	2.3	6.2	0.8	3.7	0.6	1.3	0.2	0.9	0.1	16.0	142.6	25.2	1.5	1.7	0.5	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00653	42	43	1	Original	511501.7	8117400.2	772.9	354.6	227.3	59.2	34.8	4.7	63.9	36.0	88.6	12.3	46.9	8.7	2.5	6.7	0.9	3.9	0.6	1.4	0.2	1.0	0.2	17.5	127.3	51.6	2.6	3.4	0.9	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00654	43	44	1	Original	511501.7	8117400.2	772.9	357.5	222.5	57.1	32.9	4.6	61.7	36.4	87.8	11.8	45.3	8.4	2.3	6.4	0.8	3.8	0.6	1.5	0.2	0.9	0.2	16.3	135.0	53.1	2.7	3.6	0.8	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00655	44	45	1	Original	511501.7	8117400.2	772.9	445.2	331.7	83.2	45.8	6.2	89.4	60.8	130.8	17.4	65.8	11.2	3.2	8.5	1.1	5.1	0.9	2.1	0.2	1.3	0.2	23.1	113.5	78.1	3.2	5.8	1.5	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00656	45	46	1	Original	511501.7	8117400.2	772.9	278.2	149.4	43.1	26.7	3.7	46.9	19.5	53.2	8.1	35.0	6.9	2.0	5.3	0.7	3.1	0.5	1.1	0.1	0.8	0.1	13.1	128.8	18.6	1.0	0.7	0.3	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00658	46	47	1	Original	511501.7	8117400.2	772.9	342.6	198.8	49.4	26.9	3.8	53.2	34.8	80.1	10.1	39.3	7.2	2.0	5.4	0.7	3.1	0.5	1.1	0.1	0.8	0.1	13.1	144.2	62.9	2.1	2.6	0.9	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00659	47	48	1	Original	511501.7	8117400.2	772.9	316.0	182.6	44.4	24.5	3.6	48.0	34.4	73.0	9.1	35.3	6.4	1.8	4.7	0.6	3.0	0.5	1.0	0.1	0.7	0.1	11.9	133.4	62.2	1.5	2.8	1.0	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00660	48	49	1	Original	511501.7	8117400.2	772.9	653.9	465.3	48.1	27.1	3.7	51.8	42.8	341.5	10.9	37.2	5.8	1.3	4.0	0.6	3.1	0.6	1.5	0.5	1.0	0.2	14.2	148.7	119.6	5.9	12.1	4.2	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00661	57	58	1	Original	511501.7	8117400.2	772.9	612.8	367.4	59.0	33.2	4.6	63.6	48.9	218.7	13.1	46.0	7.7	1.7	5.2	0.7	3.9	0.7	1.9	0.3	1.5	0.2	17.0	245.4	153.1	6.8	10.7	3.5	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00662	58	59	1	Original	511501.7	8117400.2	772.9	624.0	360.1	67.5	38.0	5.3	72.7	53.2	192.9	14.9	52.6	8.5	2.1	6.2	0.9	4.4	0.8	1.9	0.3	1.9	0.3	19.4	263.8	125.3	5.3	7.7	2.7	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00663	59	60	1	Original	511501.7	8117400.2	772.9	568.2	310.5	71.3	40.8	5.7	77.0	54.4	134.5	15.5	55.6	9.5	2.2	6.5	1.0	4.7	0.9	2.2	0.3	2.0	0.3	20.8	257.7	137.8	6.7	9.6	2.4	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00664	60	61	1	Original	511501.7	8117400.2	772.9	641.1	355.9	79.6	45.5	6.4	86.1	59.8	160.3	17.2	62.4	10.6	2.5	7.1	1.0	5.4	1.0	2.4	0.4	2.1	0.3	23.4	285.3	128.5	5.9	8.3	2.3	HOM-RC-TGA-0014	GO26256025	
Target A	RC-TGA-0008	TGA-RC-00666	61	62	1	Original	511501.7	8117400.2	772.9	700.0	364.1	82.1	48.9	6.9	89.0	60.8	160.9	17.8	64.3	11.4	2.6	7.8	1.1	5.8	1.													

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0010	TGA-RC-00707	8	9	1	Original	510099.2	8117604.5	761.2	1478.0	1419.8	517.3	380.6	49.4	566.7	287.3	156.0	106.7	410.6	78.5	16.7	58.3	8.2	41.2	7.8	19.6	2.8	16.5	2.4	207.0	58.3	19.9	1.1	3.7	1.8	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00709	9	10	1	Original	510099.2	8117604.5	761.2	1405.5	1338.0	480.6	341.4	47.9	528.5	292.0	148.0	98.0	382.6	76.0	15.9	56.7	7.9	39.9	7.4	18.1	2.5	15.5	2.1	175.3	67.5	140.8	7.0	12.5	3.4	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00710	10	11	1	Original	510099.2	8117604.5	761.2	2226.8	2144.0	774.8	552.8	75.7	850.5	442.2	253.0	158.9	615.9	121.2	25.4	90.4	12.7	63.0	11.5	28.2	3.9	23.7	3.1	290.8	82.8	195.3	9.8	15.5	3.7	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00711	11	12	1	Original	510099.2	8117604.5	761.2	2231.5	2159.4	763.0	529.2	72.6	835.7	487.9	260.4	156.5	606.6	118.9	24.9	88.2	12.4	60.3	11.1	26.4	3.6	22.4	3.1	276.9	81.2	142.5	6.7	12.7	3.0	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00712	12	13	1	Original	510099.2	8117604.5	761.2	2627.6	2558.5	894.2	614.9	84.5	978.8	573.5	339.0	188.5	705.7	136.8	29.2	106.8	14.3	70.2	12.9	31.3	4.4	25.8	3.6	316.2	69.0	150.2	7.1	13.5	3.2	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00713	13	14	1	Original	510099.2	8117604.5	761.2	2583.9	2521.0	865.4	628.2	82.4	947.9	621.6	277.6	181.9	683.5	128.1	27.1	99.6	13.7	68.7	12.7	31.8	4.4	27.2	3.8	339.1	62.9	107.7	5.0	10.1	2.5	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00714	14	15	1	Original	510099.2	8117604.5	761.2	2517.7	2457.9	855.6	557.0	76.5	932.1	635.7	283.8	184.9	670.7	125.8	26.5	95.2	13.1	63.4	11.6	28.6	3.9	24.5	3.2	287.0	59.8	174.5	6.7	11.6	2.7	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00716	15	16	1	Original	510099.2	8117604.5	761.2	3626.6	3562.2	1091.6	955.0	124.9	1216.5	755.3	593.3	228.4	863.2	167.0	38.1	145.8	20.7	104.2	19.6	48.7	6.7	39.9	5.5	525.8	64.4	198.1	8.1	12.9	3.9	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00717	16	17	1	Original	510099.2	8117604.5	761.2	6096.3	6016.5	1330.2	3270.6	346.9	1677.1	614.6	556.5	247.7	1082.5	244.7	65.8	321.6	50.8	296.1	66.1	175.0	24.7	146.9	21.9	2101.8	79.8	188.8	9.0	16.3	4.6	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00718	17	18	1	Original	510099.2	8117604.5	761.2	3851.0	3771.3	1041.5	1479.6	180.5	1222.1	572.4	497.5	198.2	843.4	180.3	44.4	191.3	28.5	152.1	30.0	77.1	11.0	65.8	9.5	869.9	79.8	190.3	9.3	16.2	4.0	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00719	18	19	1	Original	510099.2	8117604.5	761.2	2668.7	2602.8	713.0	629.1	87.6	800.6	484.4	663.3	142.6	570.4	112.9	26.4	101.0	14.5	73.1	13.6	32.6	4.4	27.0	3.7	332.7	66.0	172.4	8.1	17.5	4.4	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00720	19	20	1	Original	510099.2	8117604.5	761.2	1856.4	1790.5	509.9	405.7	57.3	567.2	341.3	452.0	102.8	407.1	81.5	18.8	69.3	9.7	47.6	8.8	21.3	2.9	17.2	2.4	207.6	66.0	181.0	8.2	16.5	4.4	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00721	20	21	1	Original	510099.2	8117604.5	761.2	2021.5	1954.0	430.1	427.2	58.5	488.6	254.5	771.4	84.8	345.3	70.9	17.0	65.0	9.7	48.8	9.2	22.9	3.2	19.5	2.8	229.2	67.5	192.4	9.3	17.8	4.1	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00723	21	22	1	Original	510099.2	8117604.5	761.2	1088.7	1028.8	288.2	357.3	45.0	333.2	183.6	152.3	56.1	232.1	47.5	11.9	48.4	7.0	38.0	7.5	19.4	2.7	16.2	2.3	203.8	59.8	46.9	2.4	5.9	2.4	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00724	22	23	1	Original	510099.2	8117604.5	761.2	1410.4	1378.2	301.8	557.7	63.2	364.9	251.0	216.2	60.3	241.5	51.5	12.5	59.7	9.2	53.9	11.6	31.1	4.4	26.0	3.9	345.4	32.2	43.5	2.2	10.2	2.3	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00725	23	24	1	Original	510099.2	8117604.5	761.2	1116.6	1067.6	259.8	270.9	35.2	295.0	233.4	264.1	53.9	205.9	39.4	9.2	38.0	5.6	29.6	5.9	15.0	2.1	13.0	1.9	150.5	49.1	105.4	5.3	13.4	3.1	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00726	24	25	1	Original	510099.2	8117604.5	761.2	1140.1	1081.8	283.0	290.7	37.5	320.4	232.2	232.8	56.7	226.3	43.1	10.1	42.5	6.0	31.4	6.1	15.6	2.2	14.1	1.9	160.7	58.3	124.6	6.2	13.5	3.0	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00727	25	26	1	Original	510099.2	8117604.5	761.2	3308.1	3240.6	707.8	1602.8	161.0	868.9	486.7	326.8	128.1	579.7	116.5	32.2	171.2	24.5	136.6	30.0	79.6	10.8	59.9	9.1	1049.0	67.5	100.7	5.1	9.5	2.4	HOM-RC-TGA-0015	GO26256027
Target A	RC-TGA-0010	TGA-RC-00728	26	27	1	Original	510099.2	8117604.5	761.2	1662.4	1602.6	321.6	755.4	69.2	390.0	281.5	194.1	58.0	263.6	50.0	13.8	79.3	9.8	59.3	12.9	35.0	4.4	24.1	3.6	513.1	59.8	105.4	5.4	9.8	2.3	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00729	27	28	1	Original	510099.2	8117604.5	761.2	827.1	761.1	150.5	207.3	21.5	127.0	131.4	249.4	29.7	120.7	22.7	5.8	24.6	3.1	18.5	3.9	10.5	1.4	8.2	1.2	130.2	66.0	160.2	7.8	14.7	3.5	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00730	28	29	1	Original	510099.2	8117604.5	761.2	630.4	596.7	120.2	149.1	17.6	137.8	103.4	205.8	24.9	95.3	18.2	3.5	18.2	2.5	15.0	3.0	8.3	1.1	6.6	0.9	89.8	33.7	103.1	5.1	17.7	2.8	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00731	29	30	1	Original	510099.2	8117604.5	761.2	850.7	793.9	154.2	151.6	16.7	171.0	164.2	303.4	33.5	120.7	20.5	5.0	18.8	2.6	14.2	2.7	7.3	1.0	5.5	0.9	93.6	56.8	171.7	7.9	15.4	3.6	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00732	30	31	1	Original	510099.2	8117604.5	761.2	1285.3	1217.8	265.7	267.4	31.3	298.9	221.1	421.3	55.8	217.1	40.5	10.0	35.6	4.8	26.5	4.9	13.0	1.7	10.5	1.6	158.7	67.5	168.8	7.6	15.2	4.4	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00733	31	32	1	Original	510099.2	8117604.5	761.2	639.1	610.0	127.4	187.8	19.6	146.9	101.5	172.6	26.1	101.2	20.8	4.7	19.6	2.8	16.8	3.4	9.0	1.3	8.4	1.3	120.5	29.1	42.1	2.2	10.1	1.8	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00734	32	33	1	Original	510099.2	8117604.5	761.2	737.6	700.8	132.2	254.1	24.0	156.2	109.2	184.9	26.7	105.4	20.5	5.2	21.6	3.3	20.7	4.4	13.5	2.0	12.0	2.0	169.5	36.8	98.9	5.5	10.7	2.6	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00736	33	34	1	Original	510099.2	8117604.5	761.2	808.8	781.2	159.9	298.0	29.6	188.6	112.1	184.3	31.3	127.7	27.8	6.8	27.3	4.1	25.5	5.2	15.2	2.3	13.8	2.3	195.6	27.6	30.6	1.8	6.5	2.1	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00737	34	35	1	Original	510099.2	8117604.5	761.2	537.2	503.5	105.4	142.2	16.2	121.6	85.0	154.2	21.4	84.0	16.6	4.1	16.1	2.3	13.9	2.6	7.5	1.1	6.4	0.9	87.2	33.7	76.7	4.6	6.7	2.1	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00738	35	36	1	Original	510099.2	8117604.5	761.2	679.9	655.3	135.2	172.7	19.5	154.7	106.4	219.9	27.8	107.4	21.2	4.0	19.5	2.9	16.6	3.2	9.3	1.3	8.3	1.2	106.3	24.5	65.1	3.2	12.6	2.2	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00739	36	37	1	Original	510099.2	8117604.5	761.2	553.2	540.9	115.3	126.3	15.5	130.9	90.2	190.4	24.1	91.2	18.7	2.3	16.1	2.3	13.3	2.6	7.0	1.0	6.4	1.0	74.2	12.3	49.1	2.3	13.8	1.9	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00740	37	38	1	Original	510099.2	8117604.5	761.2	1093.1	1080.9	222.2	276.8	33.8	256.0	171.8	373.4	46.0	176.1	36.9	4.7	32.8	4.9	28.9	5.6	15.8	2.3	14.7	2.3	164.5	12.3	87.8	5.1	26.7	4.3	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00741	38	39	1	Original	510099.2	8117604.5	761.2	532.8	523.6	112.2	123.8	15.5	127.7	87.7	182.4	23.3	88.9	17.4	2.5	15.2	2.3	13.2	2.5	6.9	1.0	6.3	1.0	73.0	9.2	47.6	2.8	12.7	2.0	HOM-RC-TGA-0016	GO26256028
Target A	RC-TGA-0010	TGA-RC-00743	39	40	1	Original	510099.2	8117604.5	761.2	521.1	510.3	110.5	116.6	15.1	125.6	87.0	178.7	22.7	87.8	17.5	2.4	15.1	2.3	12.9	2.5	6.7	1.0	6.2									

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0010	TGA-RC-00786	77	78	1	Original	510099.2	8117604.5	761.2	683.7	656.1	118.7	120.1	15.4	134.1	90.8	308.3	23.9	94.8	18.2	3.3	15.8	2.4	13.1	2.6	6.8	1.0	6.5	0.9	67.7	27.6	75.2	3.5	17.7	2.5	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00787	78	79	1	Original	510099.2	8117604.5	761.2	509.9	502.2	96.3	128.8	15.7	112.0	77.6	184.3	20.0	76.3	15.2	2.2	14.1	2.3	13.4	2.8	8.1	1.1	7.1	1.0	76.7	27.7	40.8	2.4	12.9	1.9	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00788	79	80	1	Original	510099.2	8117604.5	761.2	579.3	551.7	110.4	130.5	16.2	126.6	93.5	200.2	22.8	87.6	17.1	3.0	15.3	2.4	13.8	2.8	8.0	1.1	7.1	1.0	75.8	27.6	110.6	4.6	16.8	2.9	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00789	80	81	1	Original	510099.2	8117604.5	761.2	618.6	601.3	120.9	149.2	18.6	139.5	98.6	213.7	25.1	95.8	18.8	3.0	17.1	2.8	15.8	3.3	9.4	1.3	7.6	1.1	87.9	16.9	72.8	3.8	16.2	2.6	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00790	81	82	1	Original	510099.2	8117604.5	761.2	741.7	697.2	132.4	133.1	16.9	149.3	102.9	308.3	27.2	105.2	20.5	3.7	17.1	2.6	14.3	2.9	7.8	1.1	6.6	0.9	76.2	44.5	96.6	5.0	15.8	3.1	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00791	82	83	1	Original	510099.2	8117604.5	761.2	688.9	669.0	138.2	128.8	16.5	154.7	122.6	260.4	29.1	109.1	19.0	3.8	16.9	2.6	13.9	2.8	7.7	1.0	6.1	0.8	73.2	19.9	149.5	7.3	18.1	3.4	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00793	83	84	1	Original	510099.2	8117604.5	761.2	844.8	809.5	130.9	157.9	19.7	150.6	95.0	404.1	26.3	104.5	21.6	3.8	19.5	3.1	16.6	3.3	9.3	1.3	8.3	1.1	91.6	35.3	67.8	3.8	17.4	3.8	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00794	84	85	1	Original	510099.2	8117604.5	761.2	1080.9	1059.4	188.0	184.7	23.3	211.3	144.8	514.7	38.7	149.3	27.3	5.7	25.0	3.8	19.5	3.9	10.5	1.4	8.9	1.2	104.8	21.5	138.8	7.9	19.9	4.4	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00795	85	86	1	Original	510099.2	8117604.5	761.2	1065.1	1032.9	191.7	182.8	21.3	213.0	154.8	476.6	39.5	152.2	26.9	6.3	23.6	3.4	17.8	3.6	9.8	1.2	7.1	1.1	108.8	32.2	184.5	9.3	19.5	4.1	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00796	86	87	1	Original	510099.2	8117604.5	761.2	1745.7	1705.8	268.9	298.1	34.2	303.1	190.0	907.8	54.9	214.0	41.1	10.6	36.4	5.3	28.9	5.7	15.2	2.1	12.5	1.8	179.7	39.9	198.1	8.8	27.1	5.8	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00797	87	88	1	Original	510099.2	8117604.5	761.2	1840.4	1797.4	312.7	326.1	37.8	350.6	221.7	889.4	64.3	248.5	47.5	12.1	41.1	5.7	32.1	6.3	16.6	2.3	13.6	2.0	194.3	42.9	223.2	10.5	24.9	6.0	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00798	88	89	1	Original	510099.2	8117604.5	761.2	2171.1	2126.6	329.4	388.4	40.0	373.4	227.5	1128.9	66.9	262.5	52.1	13.2	46.5	6.8	37.2	7.6	20.0	2.8	16.6	2.5	235.6	44.5	214.6	9.6	28.4	6.9	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00799	89	90	1	Original	510099.2	8117604.5	761.2	918.6	887.9	151.3	169.7	20.2	171.5	113.2	429.9	31.2	120.1	23.8	5.0	20.6	3.1	17.2	3.4	9.1	1.4	7.8	1.2	101.0	30.7	103.7	5.0	17.1	4.3	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00801	90	91	1	Original	510099.2	8117604.5	761.2	1278.8	1254.3	201.6	286.5	32.5	234.0	134.3	598.2	40.6	161.0	33.7	6.9	31.7	4.8	27.7	5.7	15.4	2.2	13.6	2.0	176.5	24.5	90.6	3.9	19.2	5.1	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00802	91	92	1	Original	510099.2	8117604.5	761.2	1874.7	1831.7	290.5	363.1	39.6	330.1	197.6	934.8	58.4	232.1	45.7	11.3	42.1	6.0	33.6	6.9	17.7	2.5	14.2	2.2	226.7	42.9	186.7	8.4	20.5	5.5	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00803	92	93	1	Original	510099.2	8117604.5	761.2	1713.8	1677.0	263.6	289.4	31.6	295.2	209.4	874.6	53.7	210.0	40.0	10.5	34.7	5.0	26.6	5.5	14.0	2.0	11.6	1.8	177.8	36.8	258.9	9.8	19.7	6.1	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00804	93	94	1	Original	510099.2	8117604.5	761.2	1908.6	1871.8	290.2	336.6	38.0	328.2	203.5	997.5	58.6	231.5	44.1	11.1	40.0	5.8	32.2	6.4	16.5	2.4	13.8	2.1	206.4	36.8	201.0	9.4	21.3	5.5	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00805	94	95	1	Original	510099.2	8117604.5	761.2	1254.6	1208.6	231.1	332.2	34.1	265.2	167.1	442.2	47.4	183.7	35.9	9.4	35.8	5.2	28.9	6.1	16.5	2.2	12.7	1.9	213.4	46.0	172.4	8.1	15.4	4.0	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00806	95	96	1	Original	510099.2	8117604.5	761.2	697.5	651.5	133.7	144.1	15.8	149.5	103.2	250.6	27.8	105.9	19.9	4.6	16.7	2.5	13.3	2.7	7.3	1.0	5.9	0.9	89.2	46.0	132.2	6.2	12.1	2.8	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00808	96	97	1	Original	510099.2	8117604.5	761.2	1544.5	1504.7	252.9	367.9	38.9	281.9	166.0	676.8	50.5	202.4	41.1	9.9	39.4	5.9	33.1	7.0	18.5	2.5	15.0	2.3	234.3	39.9	116.9	5.7	17.5	3.7	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00809	97	98	1	Original	510099.2	8117604.5	761.2	1775.4	1737.1	274.7	416.6	44.8	319.5	171.8	827.9	53.7	221.0	46.0	10.7	45.2	6.7	38.1	8.0	21.7	3.0	17.7	2.7	262.9	38.3	83.5	4.2	20.5	4.3	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00810	98	99	1	Original	510099.2	8117604.5	761.2	1783.2	1743.3	299.0	480.6	50.4	349.4	187.1	726.0	58.7	240.3	50.7	12.0	49.9	7.4	43.0	9.1	24.6	3.4	19.5	3.0	308.6	39.9	99.0	4.9	19.1	3.9	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0010	TGA-RC-00811	99	100	1	Original	510099.2	8117604.5	761.2	1905.0	1862.1	302.1	470.5	49.7	351.8	184.1	855.0	59.5	242.6	50.4	11.9	51.9	7.6	42.1	8.9	24.5	3.3	20.0	3.0	297.2	42.9	78.1	3.8	20.4	4.4	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00812	0	1	1	Original	511301.2	8117197.3	769.9	309.0	232.3	19.1	35.5	3.7	22.9	19.0	156.0	4.4	14.7	2.7	0.6	2.4	0.5	3.2	0.8	2.2	0.4	2.8	0.5	22.1	76.7	137.8	7.9	24.0	5.6	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00813	1	2	1	Original	511301.2	8117197.3	769.9	323.5	245.3	19.4	39.4	4.1	23.4	20.5	163.4	4.5	14.8	2.7	0.5	2.4	0.5	3.6	0.8	2.7	0.5	3.0	0.5	24.9	78.2	139.8	7.6	25.7	6.2	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00815	2	3	1	Original	511301.2	8117197.3	769.9	1163.4	881.2	121.1	54.3	7.7	128.9	122.6	568.7	28.9	92.3	14.4	3.0	7.5	1.1	6.6	1.3	3.6	0.6	4.0	0.5	26.2	282.2	136.5	7.7	20.9	11.5	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00816	3	4	1	Original	511301.2	8117197.3	769.9	1187.5	860.128	120.1	55.1	8.0	128.1	122.0	550.3	28.2	91.9	13.3	3.0	7.4	1.2	6.8	1.3	3.6	0.6	3.7	0.6	27.1	326.7	136.5	7.6	20.2	11.8	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00817	4	5	1	Original	511301.2	8117197.3	769.9	1448.4	1187.7	118.6	47.4	6.9	125.5	124.3	884.4	28.4	90.2	12.9	2.6	6.8	1.0	5.9	1.1	3.0	0.5	3.2	0.5	22.7	260.7	126.9	7.2	18.6	11.4	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00818	5	6	1	Original	511301.2	8117197.3	769.9	1284.8	1053.2	113.6	41.9	6.2	119.8	128.4	756.7	27.7	86.0	12.5	2.4	6.1	1.0	5.2	1.0	2.6	0.5	3.0	0.4	19.8	231.6	122.3	6.7	19.2	11.0	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00819	6	7	1	Original	511301.2	8117197.3	769.9	597.5	411.9	82.4	37.0	5.1	87.6	88.6	194.7	19.3	63.1	9.2	1.9	5.4	0.8	4.4	0.8	2.3	0.4	2.3	0.3	18.4	185.6	153.8	7.9	16.2	8.7	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00820	7	8	1	Original	511301.2	8117197.3	769.9	564.2	380.1	70.2	34.9	4.8	75.0	67.0	199.0	15.5	54.7	9.1	1.9	5.1	0.7	4.1	0.8	2.2	0.3	2.2	0.3	17.4	184.1	165.9	5.6	5.5	6.2	HOM-RC-TGA-0017	GO26256030
Target A	RC-TGA-0011	TGA-RC-00822	8	9	1	Original	511301.2	8117197.3	769.9	814.7	658.3	140.4	43.7	6.2	146.6	217.0	242.0	33.0	107.4	15.2	3.3	8.5	1.0	5.2	0.9	2.2	0.3	1.9	0.3	20.1	156.4	189.6	6.0	5.3	4.9	HOM-RC-TGA-0017	GO26256030

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0011	TGA-RC-00865	46	47	1	Original	511301.2	8117197.3	769.9	630.9	561.8	135.6	58.3	8.3	144.0	105.7	243.8	28.8	106.8	18.4	4.8	12.0	1.5	6.9	1.1	2.3	0.3	1.3	0.2	27.9	69.0	172.4	8.9	11.1	2.3	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00866	47	48	1	Original	511301.2	8117197.3	769.9	355.7	289.7	66.8	47.2	5.9	72.7	55.5	110.4	13.8	53.0	9.9	2.8	7.5	1.0	5.0	0.8	2.0	0.2	1.6	0.2	26.0	66.0	120.2	3.9	4.9	1.8	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00867	48	49	1	Original	511301.2	8117197.3	769.9	585.6	527.3	131.5	56.7	8.0	139.4	98.1	223.6	27.6	103.9	17.6	4.6	11.6	1.4	6.5	1.0	2.3	0.3	1.3	0.2	27.4	58.3	144.5	6.8	10.7	2.0	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00868	49	50	1	Original	511301.2	8117197.3	769.9	857.4	805.2	214.7	62.7	8.9	223.6	137.2	364.8	45.6	169.1	25.7	6.1	15.2	1.7	7.2	1.1	2.3	0.3	1.3	0.2	27.3	52.1	158.8	12.0	25.4	2.3	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00869	50	51	1	Original	511301.2	8117197.3	769.9	1768.5	1716.3	464.8	113.4	16.7	481.4	301.4	782.5	98.5	366.3	54.3	12.6	29.7	3.2	13.4	2.0	3.9	0.4	2.1	0.3	45.8	52.1	313.3	25.2	58.8	4.4	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00870	51	52	1	Original	511301.2	8117197.3	769.9	1089.6	1025.1	265.0	81.4	11.6	276.6	180.0	466.8	56.8	208.2	31.9	7.8	19.2	2.1	9.4	1.4	3.0	0.3	1.5	0.2	36.4	64.4	226.0	15.3	28.9	3.2	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00872	52	53	1	Original	511301.2	8117197.3	769.9	356.1	270.2	63.6	39.7	5.3	68.9	51.3	106.1	13.4	50.3	9.5	2.5	7.0	0.9	4.4	0.7	1.7	0.2	1.1	0.1	21.0	85.9	107.9	3.9	6.6	1.5	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00873	53	54	1	Original	511301.2	8117197.3	769.9	516.0	422.5	107.3	46.5	6.5	113.8	72.0	181.8	22.4	84.9	14.8	3.7	9.2	1.1	5.3	0.8	1.9	0.2	1.2	0.2	22.9	93.6	106.1	6.3	11.5	1.7	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00874	54	55	1	Original	511301.2	8117197.3	769.9	499.9	386.4	99.2	42.4	5.9	105.0	65.1	166.4	20.9	78.3	13.3	3.5	8.9	1.1	4.8	0.8	1.7	0.2	1.1	0.1	20.2	113.5	90.8	5.7	8.8	1.5	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00875	55	56	1	Original	511301.2	8117197.3	769.9	457.1	329.8	83.4	41.9	5.5	88.8	59.8	133.9	17.3	66.0	10.8	3.0	7.9	0.9	4.5	0.7	1.7	0.2	1.3	0.2	21.3	127.3	106.4	3.4	12.5	1.6	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00876	56	57	1	Original	511301.2	8117197.3	769.9	646.6	516.2	129.3	54.2	7.1	136.3	90.8	225.4	27.1	102.2	16.6	4.3	11.1	1.3	5.8	1.0	2.1	0.3	1.4	0.2	26.7	130.4	137.1	7.3	17.9	2.4	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00877	57	58	1	Original	511301.2	8117197.3	769.9	357.1	239.0	59.4	32.7	4.6	64.0	43.3	95.2	12.5	46.9	8.4	2.3	6.1	0.8	3.8	0.6	1.5	0.2	0.9	0.1	16.5	118.1	77.1	3.3	6.5	1.0	HOM-RC-TGA-0018	GO26263402
Target A	RC-TGA-0011	TGA-RC-00878	58	59	1	Original	511301.2	8117197.3	769.9	395.2	260.2	66.5	32.0	4.6	71.1	45.2	107.0	13.5	53.1	9.5	2.5	6.5	0.8	3.8	0.6	1.3	0.1	0.8	0.1	15.5	135.0	63.5	3.8	5.8	1.0	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00879	59	60	1	Original	511301.2	8117197.3	769.9	432.6	282.3	72.6	38.4	5.3	77.9	47.9	113.6	14.5	58.1	9.8	2.7	7.3	1.0	4.4	0.7	1.6	0.2	1.1	0.2	19.3	150.3	48.9	2.7	9.1	1.2	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00880	60	61	1	Original	511301.2	8117197.3	769.9	411.0	254.6	62.1	37.5	4.6	66.7	44.5	108.1	12.6	49.5	8.7	2.3	6.1	0.8	3.8	0.7	1.9	0.2	1.6	0.3	19.7	156.4	37.1	1.8	5.1	1.7	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00881	61	62	1	Original	511301.2	8117197.3	769.9	542.0	379.4	97.0	44.7	6.2	103.2	66.7	157.8	19.6	77.3	13.1	3.5	8.8	1.1	5.1	0.8	1.9	0.2	1.2	0.1	22.0	162.6	44.3	2.9	6.9	0.9	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00882	62	63	1	Original	511301.2	8117197.3	769.9	473.9	340.5	82.7	41.7	5.6	88.3	61.6	143.1	17.0	65.7	11.4	3.0	7.9	1.0	4.6	0.8	1.8	0.2	1.4	0.2	20.8	133.4	63.2	3.3	4.8	0.7	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00883	63	64	1	Original	511301.2	8117197.3	769.9	390.9	251.4	62.4	33.5	4.7	67.1	45.5	101.5	12.5	49.9	8.5	2.4	6.2	0.8	3.9	0.6	1.3	0.2	1.1	0.1	16.8	139.6	53.6	2.6	3.6	0.9	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00885	64	65	1	Original	511301.2	8117197.3	769.9	456.6	321.7	78.5	40.5	5.6	84.1	60.6	130.8	16.1	62.4	11.1	2.9	7.7	1.0	4.6	0.8	1.7	0.2	0.1	0.1	20.4	135.0	70.1	4.2	4.4	1.1	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00886	65	66	1	Original	511301.2	8117197.3	769.9	286.6	151.6	40.8	23.8	3.2	44.0	23.1	57.9	7.9	32.9	6.1	1.7	4.6	0.6	2.6	0.4	1.0	0.1	0.7	0.1	11.9	135.0	25.5	1.7	1.5	0.5	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00887	66	67	1	Original	511301.2	8117197.3	769.9	380.0	246.6	55.4	46.0	5.7	61.1	44.7	92.3	11.2	44.2	8.2	2.3	6.3	0.9	4.8	0.9	2.3	0.3	1.8	0.3	26.2	133.4	71.7	2.8	3.6	1.2	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00888	67	68	1	Original	511301.2	8117197.3	769.9	716.3	598.2	142.3	55.7	8.1	150.4	115.6	266.6	30.5	111.9	18.0	4.5	11.1	1.4	6.7	1.1	2.4	0.3	1.4	0.2	26.7	118.1	134.3	8.8	13.5	2.0	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00889	68	69	1	Original	511301.2	8117197.3	769.9	612.1	486.4	122.8	47.5	6.6	129.4	86.2	214.4	26.3	96.5	15.5	3.9	9.3	1.2	5.5	0.8	1.8	0.2	1.3	0.2	23.2	125.8	82.1	6.0	11.1	1.3	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00890	69	70	1	Original	511301.2	8117197.3	769.9	612.7	526.8	130.5	58.0	7.4	138.0	94.6	227.9	26.9	103.6	15.7	4.2	10.3	1.3	6.2	1.0	2.7	0.3	2.0	0.3	29.8	85.9	110.7	7.0	11.9	1.7	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00891	70	71	1	Original	511301.2	8117197.3	769.9	731.7	656.6	156.3	76.8	9.8	166.1	120.2	283.8	32.6	123.6	19.5	5.2	13.5	1.7	8.1	1.4	3.4	0.5	2.6	0.4	40.0	75.2	167.4	9.6	14.4	2.6	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00893	71	72	1	Original	511301.2	8117197.3	769.9	694.7	619.6	137.9	60.0	8.6	146.5	131.4	272.7	30.3	107.5	17.6	4.7	12.2	1.6	7.1	1.2	2.5	0.3	1.4	0.2	29.0	75.2	193.1	12.0	12.9	2.9	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00894	72	73	1	Original	511301.2	8117197.3	769.9	276.9	224.7	51.2	32.8	4.0	55.2	43.2	90.4	10.7	40.5	7.2	2.0	5.6	0.7	3.3	0.6	1.5	0.2	1.1	0.2	17.7	52.1	75.7	3.2	4.4	1.1	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00895	73	74	1	Original	511301.2	8117197.3	769.9	316.8	201.7	50.9	31.1	4.3	55.2	33.7	78.1	10.0	40.9	7.9	2.1	5.6	0.8	3.6	0.6	1.6	0.2	1.0	0.1	15.6	115.0	50.4	2.1	3.6	0.8	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00896	74	75	1	Original	511301.2	8117197.3	769.9	328.2	207.0	52.2	28.9	4.0	56.2	36.2	82.2	10.5	41.8	7.5	2.0	5.2	0.7	3.3	0.5	1.2	0.1	0.9	0.1	14.9	121.2	50.4	2.1	2.8	0.7	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00897	75	76	1	Original	511301.2	8117197.3	769.9	432.8	313.2	78.8	39.6	5.5	84.3	55.1	129.0	16.0	62.8	10.7	2.8	7.6	0.9	4.6	0.8	1.7	0.2	1.2	0.2	19.7	119.6	67.5	3.3	4.7	1.1	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00898	76	77	1	Original	511301.2	8117197.3	769.9	1416.6	1335.3	342.6	80.1	11.4	354.0	242.8	633.8	73.1	269.5	36.1	8.8	20.1	2.3	9.1	1.4	2.7	0.3	1.6	0.2	33.5	81.3	226.7	18.1	39.4	3.3	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00899	77	78	1	Original	511301.2	8117197.3	769.9	1230.4	1138.4	300.5	68.4	9.9	310.4	197.6	539.3	63.7	236.8	32.6	7.7	18.1	1.9	8.0	1.2	2.3	0.3	1.3	0.2	27.6	92.0	150.9	14.8	33.2	2.3	HOM-RC-TGA-0019	GO26263423
Target A	RC-TGA-0011	TGA-RC-00901	78	79	1	Original	511301.2	8117197.3	769.9	971.3	868.5	231.7	58.4	8.4	240.1	146.6	405.4	48.0	183.7	26.4	6.1	15.0	1.6	6.8	1.0	2.2	0.2	1.2	0.2	24.1	102.8						

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0012	TGA-RC-00993	59	60	1	Original	511485.9	8116989.2	774.5	217.7	105.7	28.7	20.1	2.6	31.1	13.7	38.9	5.5	23.2	4.2	1.1	3.5	0.4	2.2	0.4	0.8	0.1	0.7	0.1	10.7	112.0	13.3	0.6	1.1	0.8	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00994	60	61	1	Original	511485.9	8116989.2	774.5	242.1	134.7	34.9	21.3	3.1	38.0	21.0	52.2	6.9	28.0	5.3	1.4	3.9	0.5	2.6	0.4	1.1	0.1	0.8	0.1	10.3	107.4	16.2	0.9	1.2	0.9	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00995	61	62	1	Original	511485.9	8116989.2	774.5	195.0	93.7	25.2	18.4	2.4	27.6	12.3	33.9	4.8	20.4	4.0	1.2	3.3	0.4	2.0	0.3	0.8	0.1	0.7	0.1	9.4	101.2	6.8	0.4	0.7	0.9	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00996	62	63	1	Original	511485.9	8116989.2	774.5	194.1	106.7	29.3	19.1	2.4	31.7	14.3	39.3	5.3	24.0	4.7	1.2	3.3	0.5	2.0	0.3	0.8	0.1	0.7	0.1	10.2	87.4	13.2	0.9	0.9	0.8	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00997	63	64	1	Original	511485.9	8116989.2	774.5	424.9	346.6	83.4	38.3	5.0	88.5	67.0	147.4	17.6	65.8	10.5	2.5	7.2	0.9	4.1	0.8	1.6	0.2	1.3	0.1	19.6	78.2	88.3	4.3	5.4	1.2	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00998	64	65	1	Original	511485.9	8116989.2	774.5	220.7	131.8	27.5	47.9	5.4	32.9	15.0	36.4	4.9	22.6	4.9	1.6	4.5	0.7	4.6	1.0	2.6	0.4	2.5	0.4	29.7	89.9	25.8	0.6	0.9	1.0	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-00999	65	66	1	Original	511485.9	8116989.2	774.5	180.4	85.3	21.9	18.0	2.3	24.2	11.0	30.3	4.2	17.7	4.0	0.9	3.1	0.4	1.9	0.4	0.8	0.1	0.6	0.1	9.7	95.1	7.8	0.4	0.7	1.1	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01001	66	67	1	Original	511485.9	8116989.2	774.5	308.0	203.7	49.6	24.6	3.5	53.1	38.1	85.1	10.1	39.4	6.2	1.7	5.0	0.6	2.9	0.5	1.0	0.1	0.8	0.1	11.9	104.3	35.9	1.8	2.4	1.0	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01002	67	68	1	Original	511485.9	8116989.2	774.5	196.6	96.9	25.3	19.1	2.5	27.8	12.8	35.3	5.1	20.3	4.4	1.0	3.3	0.4	2.0	0.4	0.9	0.1	0.7	0.1	10.2	99.7	9.1	0.4	0.7	1.0	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01003	68	69	1	Original	511485.9	8116989.2	774.5	163.9	104.1	24.5	16.9	2.6	27.0	19.7	39.1	4.9	19.6	3.9	0.9	3.1	0.4	2.1	0.3	0.8	0.1	0.6	0.1	8.4	59.8	23.7	0.6	0.7	1.1	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01004	69	70	1	Original	511485.9	8116989.2	774.5	192.6	97.5	27.5	17.7	2.6	30.0	12.7	35.7	5.2	22.3	3.9	1.2	3.2	0.4	2.1	0.4	0.8	0.1	0.7	0.1	8.6	95.1	7.5	0.4	0.7	0.7	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01005	70	71	1	Original	511485.9	8116989.2	774.5	157.0	86.4	22.9	17.6	2.4	25.3	11.5	31.0	4.4	18.5	3.5	1.0	3.4	0.4	2.0	0.3	0.9	0.1	0.5	0.1	8.8	70.6	7.7	0.4	0.8	0.9	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01006	71	72	1	Original	511485.9	8116989.2	774.5	161.3	89.2	23.3	16.8	2.3	25.6	12.3	32.8	4.8	18.5	3.9	1.0	3.1	0.4	1.9	0.3	0.8	0.1	0.7	0.1	8.5	72.1	10.4	0.5	0.7	0.7	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01008	72	73	1	Original	511485.9	8116989.2	774.5	177.4	126.8	30.9	17.5	2.5	33.4	22.4	51.6	6.6	24.3	4.3	1.1	3.4	0.4	2.0	0.4	0.7	0.1	0.5	0.1	8.8	50.6	30.3	1.6	2.2	1.2	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01009	73	74	1	Original	511485.9	8116989.2	774.5	134.3	80.6	19.4	18.8	2.6	22.0	11.8	27.5	3.8	15.6	3.0	1.1	2.5	0.4	2.2	0.4	0.9	0.1	0.9	0.1	10.2	53.7	12.0	0.5	0.9	0.7	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01010	74	75	1	Original	511485.9	8116989.2	774.5	243.7	157.8	31.2	62.9	7.3	38.5	17.0	41.3	5.8	25.4	5.4	1.9	6.0	1.0	6.3	1.3	3.6	0.5	2.8	0.5	39.1	85.9	25.0	0.7	0.7	1.1	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01011	75	76	1	Original	511485.9	8116989.2	774.5	182.1	90.1	24.8	18.6	2.8	27.5	11.3	31.3	4.7	20.1	4.1	1.1	3.1	0.4	2.3	0.4	0.9	0.1	0.7	0.1	9.5	92.0	6.1	0.2	0.6	0.8	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01012	76	77	1	Original	511485.9	8116989.2	774.5	342.0	265.3	60.6	39.8	5.0	65.5	49.5	106.6	12.6	47.9	8.8	2.4	6.2	0.8	4.1	0.7	2.2	0.2	1.3	0.2	21.6	76.7	92.8	4.0	3.5	1.1	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01013	77	78	1	Original	511485.9	8116989.2	774.5	300.4	202.3	48.9	29.1	3.8	52.7	35.2	82.5	10.1	38.8	6.5	1.7	5.0	0.6	3.1	0.5	1.3	0.2	0.9	0.1	15.5	98.2	53.4	2.2	2.7	1.0	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01015	78	79	1	Original	511485.9	8116989.2	774.5	225.1	94.7	25.0	17.9	2.3	27.3	12.7	32.5	4.9	20.1	4.0	1.1	3.2	0.4	1.9	0.3	0.8	0.1	0.6	0.1	9.5	130.4	9.3	0.4	0.8	0.4	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01016	79	80	1	Original	511485.9	8116989.2	774.5	282.7	135.4	34.4	23.5	2.9	37.3	21.0	51.2	7.1	27.3	5.3	1.4	4.0	0.6	2.4	0.4	1.0	0.1	0.7	0.1	12.8	147.2	18.2	0.9	1.3	0.5	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01017	80	81	1	Original	511485.9	8116989.2	774.5	339.6	230.7	35.9	114.9	12.0	47.8	24.2	48.4	7.0	28.9	7.4	2.8	9.5	1.7	10.3	2.3	6.8	0.9	5.5	0.8	74.4	108.9	49.5	1.1	0.7	1.5	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01018	81	82	1	Original	511485.9	8116989.2	774.5	286.5	140.8	35.4	36.6	4.2	39.6	17.1	45.9	6.6	28.8	5.7	1.7	4.7	0.7	3.5	0.7	1.9	0.2	1.4	0.2	21.7	145.7	15.6	0.6	0.8	0.6	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01019	82	83	1	Original	511485.9	8116989.2	774.5	319.6	175.4	46.1	31.0	4.2	50.2	25.9	66.6	9.0	37.1	6.8	1.9	5.5	0.7	3.5	0.6	1.4	0.2	0.9	0.1	16.3	144.2	15.7	1.0	1.4	0.5	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01020	83	84	1	Original	511485.9	8116989.2	774.5	506.4	489.5	35.6	315.2	32.0	67.6	55.6	73.0	7.1	28.5	10.1	4.9	19.1	4.0	28.0	6.5	19.8	2.9	17.6	2.2	210.2	16.9	213.9	4.3	1.1	4.7	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01022	84	85	1	Original	511485.9	8116989.2	774.5	464.1	433.8	28.3	311.4	31.7	60.0	34.4	50.1	5.4	22.9	9.3	4.7	17.6	4.0	27.7	6.5	19.8	2.9	16.9	2.2	209.5	30.7	128.6	2.7	0.5	3.3	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01023	85	86	1	Original	511485.9	8116989.2	774.5	237.1	137.4	36.4	36.0	4.5	40.9	16.9	41.9	7.3	29.0	6.3	1.7	5.0	0.8	3.8	0.7	1.7	0.2	1.3	0.2	20.6	99.7	12.4	0.5	0.8	0.6	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01024	86	87	1	Original	511485.9	8116989.2	774.5	251.0	137.5	37.4	25.5	3.3	40.7	19.4	49.5	7.1	30.2	5.8	1.5	4.4	0.6	2.7	0.5	1.1	0.1	0.7	0.1	13.7	113.5	11.4	0.5	1.3	0.7	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01025	87	88	1	Original	511485.9	8116989.2	774.5	275.5	146.7	38.0	29.1	3.6	41.6	18.9	54.0	7.4	30.6	6.6	1.6	4.5	0.6	3.0	0.6	1.4	0.2	1.1	0.1	16.0	128.8	16.0	0.7	1.1	0.5	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01026	88	89	1	Original	511485.9	8116989.2	774.5	264.9	165.2	41.3	23.6	3.2	44.6	25.9	68.2	8.8	32.5	6.2	1.6	4.3	0.6	2.7	0.5	0.9	0.1	0.7	0.1	12.1	99.7	24.8	1.6	2.0	0.6	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01027	89	90	1	Original	511485.9	8116989.2	774.5	241.1	155.2	39.0	24.1	2.9	41.9	24.4	62.2	7.6	31.4	5.4	1.6	4.2	0.5	2.4	0.4	1.1	0.2	0.8	0.1	13.0	85.9	26.3	1.5	1.6	0.8	HOM-RC-TGA-0021	GO26263407
Target A	RC-TGA-0012	TGA-RC-01028	90	91	1	Original	511485.9	8116989.2	774.5	330.8	271.0	37.4	111.4	12.6	50.0	43.0	71.2	7.7	29.6	7.9	3.0	9.9	1.7	10.9	2.3	6.6	0.9	5.8	0.8	69.6	59.8	131.2	2.2	1.0	3.5	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0012	TGA-RC-01029	91	92	1	Original	511485.9	8116989.2	774.5	200.0	103.4	27.7	20.0	2.8	30.5	13.4	37.8	5.3	22.4	4.5	1.3	3.5	0.4	2.3	0.4	1.0	0.1	0.6	0.1	10.3	96.6	9.7	0.5	0.8	0.6	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0012	TGA-RC-01030	92	93	1	Original	511485.9	8116989.2	774.5	138.6	80.3	21.0	18.0	2.																							

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0013	TGA-RC-01071	8	9	1	Original	511889.2	8116999.9	783.2	624.8	443.8	50.4	35.9	4.2	54.6	57.8	293.6	11.8	38.6	6.1	1.1	3.8	0.6	3.5	0.7	2.4	0.4	2.8	0.4	20.1	181.0	85.4	4.6	23.7	8.8	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01073	9	10	1	Original	511889.2	8116999.9	783.2	657.0	466.8	75.6	39.4	5.1	80.7	83.7	259.2	17.9	57.7	8.9	1.7	5.2	0.7	4.4	0.8	2.6	0.4	2.8	0.4	20.3	190.2	70.5	3.8	22.1	8.9	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01074	10	11	1	Original	511889.2	8116999.9	783.2	643.0	463.5	71.8	38.8	5.0	76.8	79.3	265.3	16.5	55.3	8.3	1.8	5.0	0.7	4.3	0.8	2.4	0.4	2.6	0.4	20.4	179.5	73.2	4.0	22.5	8.5	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01075	11	12	1	Original	511889.2	8116999.9	783.2	650.7	463.6	65.2	37.6	4.7	69.9	73.0	280.1	15.2	50.0	7.8	1.4	4.8	0.6	4.1	0.8	2.4	0.4	2.7	0.4	19.9	187.1	74.5	4.3	21.6	8.6	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01076	12	13	1	Original	511889.2	8116999.9	783.2	717.3	540.9	59.3	39.7	5.1	64.3	66.4	368.5	13.9	45.4	7.0	1.5	4.5	0.7	4.4	0.8	2.4	0.4	2.9	0.5	21.7	176.7	87.0	4.6	23.0	8.2	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01077	13	14	1	Original	511889.2	8116999.9	783.2	579.2	422.8	50.9	39.6	4.6	55.4	58.3	267.8	12.1	38.7	6.2	1.3	4.0	0.6	3.9	0.8	2.7	0.4	2.9	0.4	22.4	156.4	92.0	5.3	23.7	8.0	HOM-RC-TGA-0022	GO26267195
Target A	RC-TGA-0013	TGA-RC-01078	14	15	1	Original	511889.2	8116999.9	783.2	592.5	445.3	46.5	38.1	4.5	51.0	49.0	305.9	11.3	35.2	5.9	1.1	3.8	0.6	3.9	0.8	2.3	0.4	2.9	0.4	22.1	147.2	87.7	5.0	25.0	8.5	HOM-RC-TGA-0022	GO26263412
Target A	RC-TGA-0013	TGA-RC-01079	15	16	1	Original	511889.2	8116999.9	783.2	604.0	436.8	66.1	37.7	4.8	70.9	68.8	256.7	15.7	50.4	7.4	1.5	4.4	0.7	4.1	0.8	2.3	0.4	2.5	0.4	20.7	167.2	72.2	4.2	24.4	9.2	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01080	16	17	1	Original	511889.2	8116999.9	783.2	638.7	468.4	67.5	38.5	4.8	72.2	69.3	285.0	16.0	51.4	8.1	1.4	4.6	0.7	4.1	0.8	2.3	0.4	2.6	0.4	21.2	170.3	76.0	4.4	23.9	9.0	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01081	17	18	1	Original	511889.2	8116999.9	783.2	635.0	460.1	71.0	37.1	4.5	75.5	73.3	270.2	17.0	54.0	8.5	1.6	4.8	0.7	3.8	0.8	2.1	0.4	2.4	0.4	20.2	174.9	66.1	3.3	22.2	8.5	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01082	18	19	1	Original	511889.2	8116999.9	783.2	886.2	542.6	88.6	48.3	6.5	95.1	72.7	320.6	19.6	69.1	12.4	2.6	7.2	1.1	5.4	1.0	2.7	0.4	2.6	0.4	24.9	343.6	77.5	3.8	7.3	4.8	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01083	19	20	1	Original	511889.2	8116999.9	783.2	799.5	469.7	77.7	44.1	6.1	83.8	63.2	273.9	17.7	60.0	10.7	2.3	6.5	1.0	5.2	0.9	2.6	0.4	2.1	0.3	23.0	329.8	72.0	3.9	7.8	4.3	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01084	20	21	1	Original	511889.2	8116999.9	783.2	848.3	495.5	87.2	46.2	6.5	93.7	70.5	280.1	19.1	68.1	11.5	2.4	7.2	1.0	5.4	1.0	2.6	0.4	2.4	0.3	23.5	352.8	66.2	3.2	6.7	4.5	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01086	21	22	1	Original	511889.2	8116999.9	783.2	895.3	251.1	33.8	32.3	4.6	38.3	18.9	160.3	6.7	27.1	5.9	1.6	4.7	0.7	3.9	0.7	1.9	0.3	1.7	0.2	16.6	644.2	36.6	1.7	4.6	1.7	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01087	22	23	1	Original	511889.2	8116999.9	783.2	1410.5	870.6	250.2	160.6	20.9	281.1	139.6	283.8	50.1	200.0	36.4	9.5	28.0	3.4	17.5	2.9	7.1	0.9	5.1	0.8	85.5	539.9	32.3	1.5	3.4	1.4	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01088	23	24	1	Original	511889.2	8116999.9	783.2	1582.3	1119.1	336.6	241.9	32.1	368.7	173.0	314.5	67.2	269.5	53.1	13.8	39.5	5.2	26.9	4.5	11.1	1.5	8.6	1.3	129.5	463.2	35.5	1.2	2.7	1.1	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01089	24	25	1	Original	511889.2	8116999.9	783.2	1841.7	1412.2	479.5	314.8	43.6	523.0	224.6	315.7	95.7	383.8	77.7	20.3	54.7	7.5	36.0	5.9	14.6	2.1	12.0	1.6	160.0	429.5	31.8	1.1	2.1	0.8	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01090	25	26	1	Original	511889.2	8116999.9	783.2	688.5	430.9	125.4	98.2	12.5	138.0	62.9	124.7	24.8	100.7	19.7	5.5	15.7	2.1	10.4	1.8	4.8	0.7	3.6	0.5	53.1	257.7	20.0	0.9	1.2	0.6	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01091	26	27	1	Original	511889.2	8116999.9	783.2	801.3	440.8	107.7	92.4	12.0	119.7	54.3	168.9	21.7	86.0	17.6	4.8	14.3	2.0	10.1	1.8	4.4	0.6	3.7	0.5	50.2	360.4	35.0	1.2	1.6	0.8	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01093	27	28	1	Original	511889.2	8116999.9	783.2	983.8	629.5	183.3	146.4	19.1	202.5	91.5	178.7	36.4	147.0	26.9	7.8	23.7	3.2	16.0	2.7	7.1	1.0	5.5	0.9	78.5	354.3	42.1	1.3	1.8	1.0	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01094	28	29	1	Original	511889.2	8116999.9	783.2	852.5	263.5	58.9	54.5	7.3	66.2	31.7	108.8	11.6	47.4	9.6	2.6	7.9	1.2	6.1	1.1	2.9	0.4	2.4	0.3	29.6	589.0	47.4	1.6	2.1	1.0	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01095	29	30	1	Original	511889.2	8116999.9	783.2	829.4	392.3	95.9	62.0	8.5	104.4	50.1	169.5	19.3	76.5	14.8	3.9	10.2	1.4	7.1	1.2	2.9	0.4	2.4	0.3	32.1	437.1	66.4	3.1	2.9	1.0	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01096	30	31	1	Original	511889.2	8116999.9	783.2	809.9	374.3	77.1	53.0	7.3	84.4	39.5	192.2	15.4	61.7	12.4	3.3	8.8	1.2	6.1	1.1	2.7	0.4	2.4	0.4	26.7	435.6	59.2	2.8	2.7	0.9	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01097	31	32	1	Original	511889.2	8116999.9	783.2	776.0	285.2	55.4	43.1	5.9	61.3	28.4	149.2	11.0	44.4	9.1	2.3	7.0	1.0	5.0	0.8	2.2	0.3	1.9	0.3	22.2	490.8	44.9	2.2	2.4	0.9	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01098	32	33	1	Original	511889.2	8116999.9	783.2	667.6	235.1	33.3	31.0	4.3	37.6	17.8	147.4	6.6	26.7	5.6	1.5	4.5	0.7	3.6	0.6	1.7	0.2	1.5	0.2	16.3	432.5	27.4	1.6	1.9	0.7	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01099	33	34	1	Original	511889.2	8116999.9	783.2	807.7	389.0	90.1	64.0	9.1	99.3	41.6	178.1	17.6	72.6	15.1	4.1	10.9	1.6	7.6	1.3	3.0	0.4	2.6	0.4	32.3	418.7	28.5	1.5	2.0	0.7	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01101	34	35	1	Original	511889.2	8116999.9	783.2	1218.6	772.2	267.9	168.8	24.6	292.4	113.5	177.5	51.5	216.4	44.5	11.6	32.3	4.2	20.4	3.2	7.6	1.0	6.1	0.8	81.5	446.3	26.0	1.2	1.9	0.7	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01102	35	36	1	Original	511889.2	8116999.9	783.2	834.0	533.4	113.1	152.7	18.3	189.6	86.3	95.2	32.5	138.8	27.8	8.0	23.7	3.2	15.1	2.7	6.6	0.8	4.9	0.8	86.9	300.6	24.3	1.2	2.0	0.6	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01103	36	37	1	Original	511889.2	8116999.9	783.2	493.5	248.1	73.3	63.1	7.8	81.1	34.4	65.4	13.8	59.5	11.9	3.4	9.4	1.3	6.5	1.1	2.6	0.3	1.7	0.3	36.6	245.4	11.3	0.6	1.1	0.3	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01104	37	38	1	Original	511889.2	8116999.9	783.2	434.8	198.6	56.6	45.7	6.1	62.7	26.5	60.3	11.0	45.6	9.5	2.6	7.6	1.0	5.1	0.8	2.0	0.3	1.5	0.2	24.6	236.2	12.1	0.6	1.3	0.3	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01105	38	39	1	Original	511889.2	8116999.9	783.2	432.6	199.5	58.6	45.6	5.7	64.3	26.5	59.2	11.0	47.6	9.6	2.8	7.9	1.0	4.7	0.8	1.9	0.3	1.4	0.2	24.5	233.1	12.5	0.6	1.3	0.4	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01106	39	40	1	Original	511889.2	8116999.9	783.2	608.1	347.3	108.0	88.6	11.2	119.2	52.9	80.1	20.5	87.5	17.7	4.9	14.7	1.9	9.3	1.6	3.8	0.5	2.7	0.4	48.8	260.2	20.2	1.0	1.7	0.5	HOM-RC-TGA-0023	GO26263412
Target A	RC-TGA-0013	TGA-RC-01108	40	41	1	Original	511889.2	8116999.9	783.2	403.7	190.5	52.6	38.0	5.2	57.8	26.9	64.7	10.2	42.5	8.3	2.3	6.8	0.9	4.3	0.7	1.7	0.2	1.3	0.2	19.6	213.2	17.1	0.7	1.2			

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0013	TGA-RC-01149	77	78	1	Original	511889.2	8116999.9	783.2	401.8	309.8	69.7	34.4	4.5	74.1	64.4	132.7	14.6	55.1	8.6	2.4	6.9	0.8	3.7	0.7	1.4	0.2	0.9	0.2	17.3	92.0	97.6	3.8	4.6	1.2	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01150	78	79	1	Original	511889.2	8116999.9	783.2	347.2	206.1	52.0	27.0	3.9	55.9	35.7	84.5	10.5	41.5	6.9	1.8	5.4	0.6	3.2	0.5	1.1	0.2	0.8	0.1	13.2	141.1	40.8	2.1	3.3	0.6	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01152	79	80	1	Original	511889.2	8116999.9	783.2	414.5	287.2	71.0	34.4	4.5	75.5	51.0	121.7	14.5	56.5	9.1	2.5	6.9	0.8	3.7	0.6	1.3	0.2	1.0	0.2	17.3	127.3	70.5	4.0	6.3	1.0	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01153	80	81	1	Original	511889.2	8116999.9	783.2	450.8	318.9	79.0	31.0	4.1	83.1	60.5	138.2	16.5	62.5	10.2	2.6	6.7	0.8	3.3	0.6	1.2	0.1	0.8	0.1	14.7	131.9	61.8	3.8	7.1	1.0	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01154	81	82	1	Original	511889.2	8116999.9	783.2	438.6	306.6	79.0	29.6	4.1	81.1	58.8	134.5	15.8	58.2	9.7	2.5	6.2	0.6	3.4	0.5	1.2	0.1	0.9	0.2	14.0	131.9	70.8	3.8	6.0	0.7	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01155	82	83	1	Original	511889.2	8116999.9	783.2	433.5	312.4	74.7	30.3	4.1	78.9	61.0	137.0	16.1	58.7	9.4	2.6	6.5	0.7	3.4	0.5	1.2	0.1	1.0	0.1	14.1	121.2	69.1	3.4	6.2	0.8	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01156	83	84	1	Original	511889.2	8116999.9	783.2	450.9	329.7	79.0	31.4	4.2	83.2	65.0	145.0	16.8	62.2	9.4	2.8	6.5	0.8	3.4	0.5	1.2	0.2	0.8	0.1	15.0	121.2	76.7	4.2	6.6	1.0	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01158	84	85	1	Original	511889.2	8116999.9	783.2	496.4	373.7	91.6	32.3	4.4	96.0	71.9	166.4	19.5	72.1	11.4	2.6	7.0	0.8	3.6	0.6	1.3	0.2	0.8	0.1	15.2	122.7	79.3	4.9	8.4	1.1	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01159	85	86	1	Original	511889.2	8116999.9	783.2	380.3	260.7	63.6	29.2	4.0	67.6	49.4	110.2	12.8	50.7	8.4	2.2	6.1	0.7	3.3	0.5	1.2	0.1	0.9	0.1	14.1	119.6	55.1	2.4	4.3	0.9	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01160	86	87	1	Original	511889.2	8116999.9	783.2	384.3	252.4	60.8	28.3	3.8	64.5	47.7	107.1	13.2	47.6	8.4	2.2	6.0	0.7	3.1	0.5	1.3	0.1	0.9	0.1	13.5	131.9	49.9	2.3	4.8	0.7	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01161	87	88	1	Original	511889.2	8116999.9	783.2	376.1	255.0	60.6	29.1	3.9	64.5	48.6	108.7	12.7	47.9	7.9	2.1	5.8	0.6	3.3	0.5	1.1	0.1	0.8	0.1	14.6	121.2	54.8	2.7	4.8	0.8	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01162	88	89	1	Original	511889.2	8116999.9	783.2	446.3	329.7	78.0	34.2	4.7	82.7	64.0	144.3	16.4	61.6	9.0	2.6	7.2	0.8	3.9	0.6	1.4	0.2	0.8	0.1	16.8	116.6	79.8	4.0	8.0	1.1	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01163	89	90	1	Original	511889.2	8116999.9	783.2	486.6	374.7	87.3	36.7	5.2	92.5	76.2	163.4	18.9	68.5	11.0	3.3	7.4	0.9	4.3	0.6	1.5	0.2	1.0	0.1	17.5	112.0	104.1	5.5	7.5	1.4	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01164	90	91	1	Original	511889.2	8116999.9	783.2	404.5	275.7	65.9	32.6	4.7	70.6	52.9	116.2	13.8	52.1	8.1	2.5	6.6	0.8	3.9	0.6	1.4	0.1	0.9	0.1	15.6	128.8	59.8	3.1	5.3	1.0	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01166	91	92	1	Original	511889.2	8116999.9	783.2	361.8	229.9	55.3	30.8	4.0	59.4	43.6	93.0	11.4	44.0	7.1	2.0	6.0	0.8	3.3	0.5	1.1	0.2	0.9	0.1	15.7	131.9	49.4	2.1	3.6	0.7	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01167	92	93	1	Original	511889.2	8116999.9	783.2	365.9	241.7	57.2	30.7	4.4	61.6	47.0	98.6	11.8	45.4	8.0	2.3	5.9	0.7	3.7	0.5	1.3	0.1	1.1	0.1	15.0	124.2	57.4	2.6	4.2	0.8	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01168	93	94	1	Original	511889.2	8116999.9	783.2	355.0	224.7	54.6	28.7	3.9	58.4	41.4	93.2	11.0	43.5	6.7	1.9	5.8	0.7	3.2	0.5	1.2	0.2	0.9	0.1	14.2	130.4	54.4	2.6	4.1	0.8	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01169	94	95	1	Original	511889.2	8116999.9	783.2	363.0	223.4	56.6	29.2	3.9	60.4	38.9	90.4	11.6	45.0	8.3	2.1	5.2	0.7	3.2	0.5	1.1	0.1	0.9	0.1	15.1	139.6	43.5	2.2	4.3	0.7	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01170	95	96	1	Original	511889.2	8116999.9	783.2	397.8	256.7	62.3	31.6	4.1	66.4	47.4	106.9	13.1	49.2	8.5	2.4	6.1	0.8	3.3	0.6	1.3	0.1	0.9	0.1	16.0	141.1	59.8	2.9	5.1	0.9	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01171	96	97	1	Original	511889.2	8116999.9	783.2	400.9	278.2	67.4	30.1	4.0	71.4	52.0	120.1	14.4	53.0	8.7	2.3	6.0	0.7	3.2	0.5	1.3	0.1	0.8	0.1	15.0	122.7	58.1	3.3	6.1	1.1	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01173	97	98	1	Original	511889.2	8116999.9	783.2	381.0	253.7	59.4	32.7	4.4	63.8	48.4	104.4	12.5	46.9	8.8	2.4	5.9	0.8	3.7	0.6	1.4	0.2	0.9	0.1	16.6	127.3	67.0	2.9	4.2	1.2	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01174	98	99	1	Original	511889.2	8116999.9	783.2	352.5	228.3	51.6	33.4	4.5	56.0	45.6	89.7	10.6	40.9	8.1	2.2	5.8	0.8	3.7	0.6	1.4	0.2	1.0	0.1	17.7	124.2	81.0	3.1	5.8	1.1	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01175	99	100	1	Original	511889.2	8116999.9	783.2	404.5	274.1	63.8	55.4	7.3	71.1	44.0	101.2	12.7	51.1	9.7	2.6	7.3	1.2	6.1	1.1	2.6	0.3	2.0	0.3	32.0	130.4	49.9	1.8	10.3	0.7	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01176	100	101	1	Original	511889.2	8116999.9	783.2	272.4	145.1	34.7	27.1	3.3	38.0	24.2	53.6	6.9	27.8	5.6	1.6	4.3	0.6	2.8	0.5	1.2	0.1	0.9	0.1	15.0	127.3	38.1	1.2	2.6	0.6	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0013	TGA-RC-01177	101	102	1	Original	511889.2	8116999.9	783.2	320.6	199.4	47.2	32.5	4.1	51.3	35.7	77.3	9.5	37.7	6.8	1.8	5.3	0.7	3.4	0.6	1.4	0.2	1.2	0.2	17.8	121.2	50.9	2.2	2.9	0.8	HOM-RC-TGA-0024	GO26267196
Target A	RC-TGA-0014	TGA-RC-01178	0	1	1	Original	510901.5	8116802.1	758.3	306.2	231.1	24.8	32.2	3.5	28.3	25.2	146.5	5.4	19.5	3.3	0.8	2.9	0.5	3.0	0.7	2.0	0.3	2.2	0.4	19.4	75.2	198.9	10.9	23.3	6.1	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01179	1	2	1	Original	510901.5	8116802.1	758.3	297.1	225.0	21.2	29.2	3.2	24.4	24.2	147.4	4.7	16.4	3.0	0.7	2.4	0.4	2.8	0.7	1.9	0.3	2.0	0.4	17.7	72.1	198.1	10.7	24.5	6.2	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01180	2	3	1	Original	510901.5	8116802.1	758.3	373.9	283.4	42.7	37.5	4.4	47.1	40.1	157.2	9.2	33.5	5.9	1.6	4.1	0.6	3.8	0.7	2.0	0.3	2.1	0.3	22.0	90.5	164.5	8.3	20.0	5.0	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01181	3	4	1	Original	510901.5	8116802.1	758.3	324.6	252.5	26.4	34.1	3.7	30.1	28.9	159.7	6.2	20.3	3.4	0.8	2.6	0.5	3.2	0.7	2.3	0.4	2.6	0.4	20.6	72.1	189.6	10.5	25.8	6.8	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01182	4	5	1	Original	510901.5	8116802.1	758.3	354.3	268.4	39.3	32.1	3.6	42.9	46.1	145.6	9.2	30.1	5.4	1.0	3.2	0.5	3.1	0.7	2.0	0.3	2.0	0.3	19.0	85.9	160.2	8.3	23.3	6.8	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01183	5	6	1	Original	510901.5	8116802.1	758.3	998.3	940.0	245.3	31.5	4.4	249.7	509.0	136.4	73.2	172.1	17.9	3.0	6.0	0.8	3.6	0.7	1.7	0.2	1.8	0.2	13.5	58.3	32.5	2.1	6.1	2.7	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01185	6	7	1	Original	510901.5	8116802.1	758.3	1496.4	1440.1	410.5	43.5	6.5	417.0	760.0	195.9	118.9	291.6	30.2	4.9	9.1	1.2	5.3	0.8	2.0	0.3	2.0	0.2	17.5	56.8	31.2	1.7	6.5	2.7	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01186	7	8	1	Original	510901.5	8116802.1	758.3	1748.5	1694.8	473.5	52.8	8.1	481.7	821.0	310.8	132.9	340.6	36.6	6.2	12.3	1.6	6.6	1.0	2.7	0.3	2.5	0.3	19.4	53.7	30.8	1.7	5.9	2.8	HOM-RC-TGA-0025	GO26267198
Target A	RC-TGA-0014	TGA-RC-01187	8	9																																	

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₃ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0014	TGA-RC-01228	53	54	1	Original	510901.5	8116802.1	758.3	213.2	190.2	37.3	20.4	3.0	40.2	47.6	80.3	8.7	28.6	4.6	1.4	3.9	0.5	2.5	0.4	0.9	0.1	0.6	0.1	9.9	23.0	77.1	3.5	3.3	1.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01229	54	55	1	Original	510901.5	8116802.1	758.3	150.4	135.0	23.5	15.9	2.2	25.7	32.4	59.6	5.6	18.0	3.7	1.0	2.8	0.4	1.8	0.4	0.9	0.1	0.6	0.1	7.9	15.3	83.4	2.7	2.4	1.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01230	55	56	1	Original	510901.5	8116802.1	758.3	96.6	79.8	15.8	12.9	2.0	17.8	18.5	30.1	3.4	12.4	2.4	0.7	2.1	0.3	1.7	0.3	0.7	0.1	0.5	0.1	6.3	16.9	30.9	0.7	1.5	0.6	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01231	56	57	1	Original	510901.5	8116802.1	758.3	91.1	75.8	13.9	11.8	1.8	15.6	18.2	29.8	3.3	10.6	2.1	0.7	1.9	0.3	1.5	0.3	0.7	0.1	0.4	0.1	5.8	15.3	29.0	0.9	1.4	0.6	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01232	57	58	1	Original	510901.5	8116802.1	758.3	117.2	97.3	19.7	13.4	2.0	21.7	22.8	38.4	4.3	15.4	3.0	0.8	2.4	0.3	1.7	0.3	0.7	0.1	0.5	0.1	6.6	19.9	35.8	1.1	1.7	0.7	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01233	58	59	1	Original	510901.5	8116802.1	758.3	428.5	414.3	74.4	38.1	5.7	80.1	105.2	186.7	17.9	56.5	10.3	2.9	7.3	1.0	4.7	0.8	1.6	0.2	1.0	0.1	18.5	13.8	299.0	12.5	9.6	2.7	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01234	59	60	1	Original	510901.5	8116802.1	758.3	454.1	440.7	77.1	42.7	6.4	83.5	111.1	199.0	18.8	58.3	10.5	2.9	8.2	1.1	5.2	0.9	1.8	0.2	1.1	0.1	21.1	13.8	327.6	13.1	9.8	2.8	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01236	60	61	1	Original	510901.5	8116802.1	758.3	356.2	340.9	60.5	33.9	5.0	65.5	86.3	151.7	14.4	46.1	8.4	2.4	6.2	0.9	4.1	0.7	1.5	0.2	1.0	0.1	16.9	15.3	257.5	10.1	7.7	2.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01237	61	62	1	Original	510901.5	8116802.1	758.3	284.5	269.1	48.5	26.9	4.2	52.7	68.8	118.3	11.5	37.0	6.6	1.8	4.9	0.7	3.6	0.6	1.3	0.1	0.8	0.1	13.0	15.3	198.9	7.4	6.0	1.9	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01238	62	63	1	Original	510901.5	8116802.1	758.3	288.7	273.4	47.4	26.9	4.0	51.4	71.8	121.1	11.5	35.8	6.3	2.0	4.9	0.7	3.3	0.5	1.2	0.1	0.8	0.1	13.2	15.3	208.9	7.7	5.7	1.9	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01239	63	64	1	Original	510901.5	8116802.1	758.3	1949.9	1940.7	324.5	174.3	25.6	350.1	581.7	815.7	79.5	245.0	44.5	12.7	34.1	4.5	21.1	3.4	7.6	0.8	4.5	0.6	84.8	9.2	948.5	33.2	23.2	7.9	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01240	64	65	1	Original	510901.5	8116802.1	758.3	2500.6	2489.8	425.4	215.2	31.7	457.2	736.5	1056.4	108.2	317.3	56.2	16.5	45.4	5.3	26.4	4.0	8.8	1.0	5.2	0.6	102.0	10.7	981.4	41.8	36.6	10.0	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01241	65	66	1	Original	510901.5	8116802.1	758.3	2630.7	2620.0	453.7	214.7	31.8	485.4	770.6	1119.1	115.4	338.3	61.9	17.4	48.5	5.5	26.3	4.1	8.8	0.9	4.2	0.6	98.3	10.7	1084.4	44.3	29.5	12.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01243	66	67	1	Original	510901.5	8116802.1	758.3	2421.8	2409.6	417.7	199.2	29.6	447.2	692.0	1045.4	106.2	311.4	55.3	16.2	42.6	5.0	24.6	3.7	8.3	0.9	4.5	0.5	93.0	12.3	935.6	39.3	26.6	10.6	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01244	67	68	1	Original	510901.5	8116802.1	758.3	2384.8	2369.5	402.6	187.1	28.5	431.0	645.1	1081.0	101.6	300.9	53.8	15.2	42.1	4.8	23.6	3.4	7.8	0.8	3.7	0.5	85.2	15.3	1187.4	50.2	31.1	11.7	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01245	68	69	1	Original	510901.5	8116802.1	758.3	2095.0	2082.7	352.6	174.3	26.1	378.7	586.4	921.3	90.1	262.5	48.1	14.1	37.0	4.5	21.6	3.3	7.4	0.8	3.6	0.5	81.5	12.3	872.7	38.5	23.0	9.0	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01246	69	70	1	Original	510901.5	8116802.1	758.3	2407.2	2396.5	414.8	198.4	29.9	444.7	652.1	1076.1	104.5	310.3	55.1	15.9	42.2	5.1	24.8	3.7	8.2	0.9	4.1	0.4	93.2	10.7	1055.8	49.2	33.5	10.2	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01247	70	71	1	Original	510901.5	8116802.1	758.3	1336.6	1327.4	225.2	110.3	16.7	241.9	415.2	546.6	57.3	168.0	30.0	9.3	24.3	2.9	13.7	2.0	4.8	0.4	2.6	0.3	49.9	9.2	648.1	23.8	14.5	5.8	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01248	71	72	1	Original	510901.5	8116802.1	758.3	2160.8	2148.5	375.7	183.5	27.1	402.7	621.6	917.6	95.7	280.0	50.2	14.4	40.6	4.6	22.4	3.4	7.7	0.9	4.2	0.5	84.7	12.3	672.4	28.3	21.1	7.6	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01249	72	73	1	Original	510901.5	8116802.1	758.3	1806.0	1795.3	298.0	183.4	27.3	325.4	529.0	741.9	74.1	224.0	42.9	13.3	36.4	4.6	22.8	3.6	8.4	0.9	4.5	0.5	88.5	10.7	642.3	24.8	26.2	7.2	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01251	73	74	1	Original	510901.5	8116802.1	758.3	1680.0	1672.3	256.8	215.2	34.6	291.3	480.9	679.3	64.9	191.9	40.2	13.4	39.3	5.5	29.0	4.8	10.5	1.2	5.4	0.6	105.4	7.7	884.1	28.3	19.5	10.0	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01252	74	75	1	Original	510901.5	8116802.1	758.3	1629.3	1620.1	250.8	200.9	32.6	283.3	455.1	674.4	63.6	187.2	39.0	12.4	37.5	5.0	27.5	4.4	9.6	1.0	4.9	0.6	98.0	9.2	825.5	25.8	17.1	10.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01253	75	76	1	Original	510901.5	8116802.1	758.3	175.2	161.4	29.2	22.8	3.4	32.6	41.8	62.8	6.7	22.5	4.9	1.4	4.0	0.5	2.8	0.4	1.2	0.1	0.7	0.1	11.4	13.8	82.1	2.7	2.3	1.4	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01254	76	77	1	Original	510901.5	8116802.1	758.3	98.9	91.3	15.0	11.6	1.6	16.6	23.9	38.6	3.7	11.3	2.2	0.7	2.2	0.2	1.4	0.2	0.5	0.0	0.3	0.0	6.0	7.7	60.1	2.3	1.5	1.4	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01255	77	78	1	Original	510901.5	8116802.1	758.3	124.4	116.7	18.7	13.2	2.0	20.8	30.1	51.8	4.6	14.1	2.8	0.8	2.3	0.3	1.7	0.3	0.6	0.1	0.4	0.1	6.6	7.7	82.8	3.1	2.1	1.8	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01256	78	79	1	Original	510901.5	8116802.1	758.3	82.7	68.9	10.7	7.2	1.3	12.1	16.7	32.9	2.7	8.0	1.4	0.5	1.2	0.2	1.1	0.2	0.4	0.0	0.3	0.0	3.3	13.8	50.9	2.1	1.8	1.0	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01257	79	80	1	Original	510901.5	8116802.1	758.3	130.8	118.5	18.7	12.6	1.8	20.4	29.1	55.5	4.7	14.0	2.6	0.8	2.4	0.3	1.5	0.3	0.6	0.1	0.3	0.1	6.3	12.3	89.3	3.8	2.9	1.3	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01259	80	81	1	Original	510901.5	8116802.1	758.3	1524.8	1512.5	250.8	121.3	19.1	269.8	416.4	691.6	63.0	187.8	32.5	10.1	26.6	3.2	15.8	2.4	5.2	0.5	2.6	0.4	54.4	12.3	759.6	33.6	21.6	8.7	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01260	81	82	1	Original	510901.5	8116802.1	758.3	1472.5	1460.3	239.2	142.2	21.1	260.3	408.2	637.5	60.2	179.1	33.2	10.1	28.2	3.4	17.7	2.7	6.6	0.7	3.4	0.4	69.0	12.3	678.1	28.8	18.3	7.1	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01261	82	83	1	Original	510901.5	8116802.1	758.3	1032.3	1021.5	154.3	95.5	14.3	168.5	286.2	463.1	38.9	115.4	22.4	7.0	19.0	2.4	11.9	1.8	4.1	0.5	2.2	0.3	46.5	10.7	563.7	19.9	11.0	5.6	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01262	83	84	1	Original	510901.5	8116802.1	758.3	2311.6	2302.4	352.4	216.9	33.2	385.7	620.4	1061.3	91.1	261.3	51.4	16.0	44.7	5.7	27.5	4.1	9.3	1.0	5.0	0.6	102.9	9.2	1452.0	49.3	24.8	13.2	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01263	84	85	1	Original	510901.5	8116802.1	758.3	993.6	981.3	149.5	91.0	14.2	163.7	279.1	439.8	38.4	111.0	21.9	6.7	18.6	2.4	11.9	1.8	4.2	0.4	2.2	0.3	42.7	12.3	403.4	14.8	14.1	5.0	HOM-RC-TGA-0026	GO26267199
Target A	RC-TGA-0014	TGA-RC-01264	85	86	1	Original	510901.5	8116802.1	758.3	522.1	509.8	80.6	52.2	7.8	88.4	141.9	224.2	20.4	60.2	10.9																	

TARGET	HOLE ID	SAMPLE ID	FROM (m)	TO (m)	INTERVAL (m)	TYPE	EASTING (m)	NORTHING (m)	ELEVATION (m)	TREO+Sc ppm	TREO ppm	NdPr ppm	HREO ppm	DyTb ppm	MREO ppm	La ₂ O ₃ ppm	CeO ₂ ppm	Pr ₂ O ₃ ppm	Nd ₂ O ₃ ppm	Sm ₂ O ₃ ppm	Eu ₂ O ₃ ppm	Gd ₂ O ₃ ppm	Tb ₂ O ₃ ppm	Dy ₂ O ₃ ppm	Ho ₂ O ₃ ppm	Er ₂ O ₃ ppm	Tm ₂ O ₃ ppm	Yb ₂ O ₃ ppm	Lu ₂ O ₃ ppm	Y ₂ O ₃ ppm	Sc ₂ O ₃ ppm	Nb ₂ O ₅ ppm	Te ₂ O ₅ ppm	ThO ₂ ppm	U ₃ O ₈ ppm	BATCH	Workorder ALS
Target A	RC-TGA-0009	TGA-RC-01306	5	6	1	Original	511098.3	8117403.4	764.2	373.0	281.0	29.2	37.6	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	141.1	7.2	24.0	6.0	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01308	6	7	1	Original	511098.3	8117403.4	764.2	411.5	270.4	52.3	26.3	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	14.4	141.1	92.7	5.6	12.9	4.4	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01309	7	8	1	Original	511098.3	8117403.4	764.2	447.7	268.2	59.5	26.6	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01310	8	9	1	Original	511098.3	8117403.4	764.2	490.7	308.2	64.9	27.5	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01311	9	10	1	Original	511098.3	8117403.4	764.2	469.4	285.3	61.9	26.3	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01312	10	11	1	Original	511098.3	8117403.4	764.2	1671.9	1478.6	321.4	66.2	10.9	332.3	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	372.0	19.9	21.1	3.7	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01313	11	12	1	Original	511098.3	8117403.4	764.2	3166.0	2963.6	765.3	139.8	25.5	790.8	1056.7	921.3	186.7	578.6	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01315	12	13	1	Original	511098.3	8117403.4	764.2	2626.2	2408.4	574.7	103.5	18.1	592.9	859.7	813.2	142.0	432.8	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01316	13	14	1	Original	511098.3	8117403.4	764.2	604.1	394.0	102.0	36.8	5.2	107.2	104.9	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01317	14	15	1	Original	511098.3	8117403.4	764.2	574.6	343.0	86.1	35.9	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01318	15	16	1	Original	511098.3	8117403.4	764.2	522.2	264.5	62.9	28.9	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01319	16	17	1	Original	511098.3	8117403.4	764.2	708.6	458.6	109.3	37.8	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01320	17	18	1	Original	511098.3	8117403.4	764.2	3533.3	3271.0	831.0	141.7	24.5	855.5	1360.5	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	592.3	30.5	34.7	2.6	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01322	18	19	1	Original	511098.3	8117403.4	764.2	1844.0	1577.1	414.6	86.3	14.3	429.0	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01323	19	20	1	Original	511098.3	8117403.4	764.2	935.9	704.3	185.4	53.7	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01324	20	21	1	Original	511098.3	8117403.4	764.2	704.1	408.1	105.5	43.8	6.6	112.0	111.7	133.3	24.5	81.0	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01325	21	22	1	Original	511098.3	8117403.4	764.2	536.5	257.4	65.5	41.2	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	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01326	22	23	1	Original	511098.3	8117403.4	764.2	568.8	297.3	74.9	42.6	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	171.0	9.8	12.2	2.3	HOM-RC-TGA-0027	GO26267200
Target A	RC-TGA-0009	TGA-RC-01327	23	24	1	Original	511098.3	8117403.4	764.2	506.2	245.4	54.6	35.5	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	HOM-RC-TGA-0027	GO26267200

Technical Notes:

- *Data Status:* This table presents the received analytical results for reverse circulation drill holes RC-TGA-0001 through RC-TGA-0014 (comprising laboratory batches HOM-RC-TGA-0001 to HOM-RC-TGA-0027). Please note that analytical results for drill holes RC-TGA-0009 and RC-TGA-0012 are currently partial, and assays corresponding to batch HOM-RC-TGA-0020 remain pending from the laboratory.
- *Oxide Calculations:* All elemental assays have been converted to their respective stoichiometric oxide values. For the purposes of this data table, the reported aggregate columns are calculated as follows:
 - *TREO (ppm):* Sum of the oxides of La, Ce, Pr, Nd, Sm, Eu, Gd, Tb, Dy, Ho, Er, Tm, Yb, Lu, and Y.
 - *TREO+Sc (ppm):* Sum of TREO plus Scandium (Sc) oxide.
 - *HREO (ppm):* Sum of the heavy and medium-heavy rare earth oxides of Eu, Gd, Tb, Dy, Ho, Er, Tm, Yb, Lu, and Y.
 - *NdPr (ppm):* Sum of Neodymium (Nd) and Praseodymium (Pr) oxides.
 - *DyTb (ppm):* Sum of Dysprosium (Dy) and Terbium (Tb) oxides.
 - *MREO (ppm):* Magnetic Rare Earth Oxides, calculated as the sum of Nd, Pr, Dy, and Tb oxides.