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Summary

- The DAYBREAK study investigated response to setmelanotide melanocortin-4 receptor (MC4R) agonist therapy in patients with genetic variants in the MC4R pathway linked to obesity and hyperphagia
- Stage 1 found that 6 genes or gene families responded to setmelanotide MC4R agonist therapy, with the most consistent responses seen in individuals with variants in PHIP and SEMA3 genes

Introduction

- The hypothalamic MC4R pathway is a key regulator of energy balance and food intake¹⁻⁴
- Impairment in MC4R pathway signaling resulting from rare variants in genes within this pathway can cause hyperphagia (a pathologic, insatiable hunger accompanied by abnormal food-seeking behaviors) and early-onset, severe obesity4-7
- The MC4R agonist setmelanotide has been shown to reduce weight and hunger in patients with certain MC4R pathway diseases caused by variants in genes central to this pathway, namely proopiomelanocortin and leptin receptor deficiency, and Bardet-Biedl syndrome8-10
- DAYBREAK (NCT04963231) was a 2-stage Phase 2 study designed to evaluate the efficacy of setmelanotide in individuals carrying a variant in ≥1 gene with strong or very strong relevance to the MC4R pathway

Objective

The objective of the DAYBREAK trial was to determine the efficacy of setmelanotide for achieving weight loss in children and adults with obesity related to variants in genes identified by Rhythm's ClinGen-based framework¹¹ as having strong or very strong relevance to the MC4R pathway, in order to identify which populations may be most likely to benefit from setmelanotide therapy

Methods

- DAYBREAK is a 2-stage, double-blind, placebo-controlled trial conducted at 37 sites across 8 countries
- Individuals aged 6 to 65 years with body mass index (BMI) ≥40 kg/m² (aged ≥18 years) or ≥97th percentile (aged ≥6 to <18 years) and hyperphagia who carried variants classified as variants of uncertain significance (VUS), likely pathogenic, or pathogenic according to the American College of Medical Genetics (ACMG) criteria in ≥1 of the 31 genes (Figure 1, Table)
- Individuals with ≥5% BMI reduction from baseline (ie, responders) at the end of the 16-week, open-label, run-in period (Stage 1) were eligible to enter a 24-week, double-blind, randomized, placebo-controlled period (Stage 2)

The primary endpoint of Stage 1 was the proportion of responders per gene cohort at the end of the Stage (Figure 2)

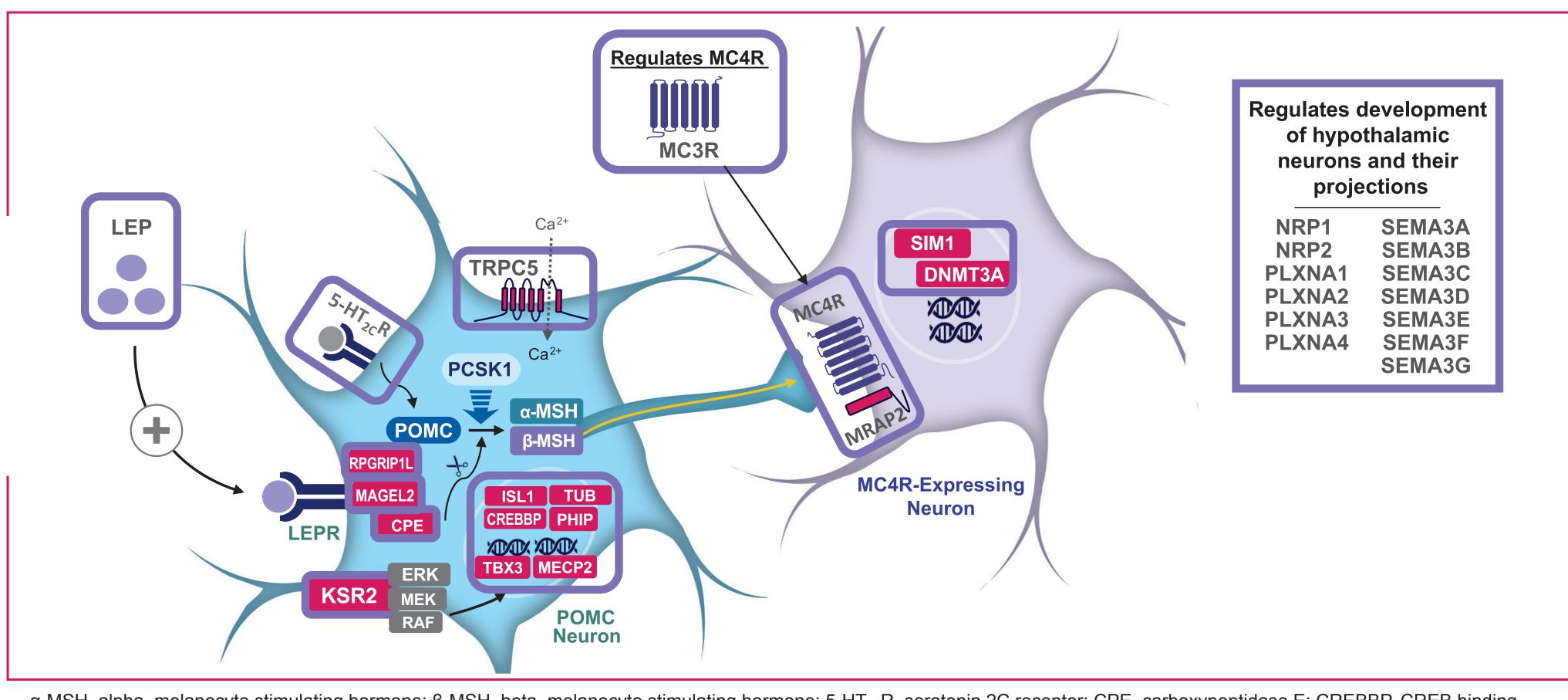
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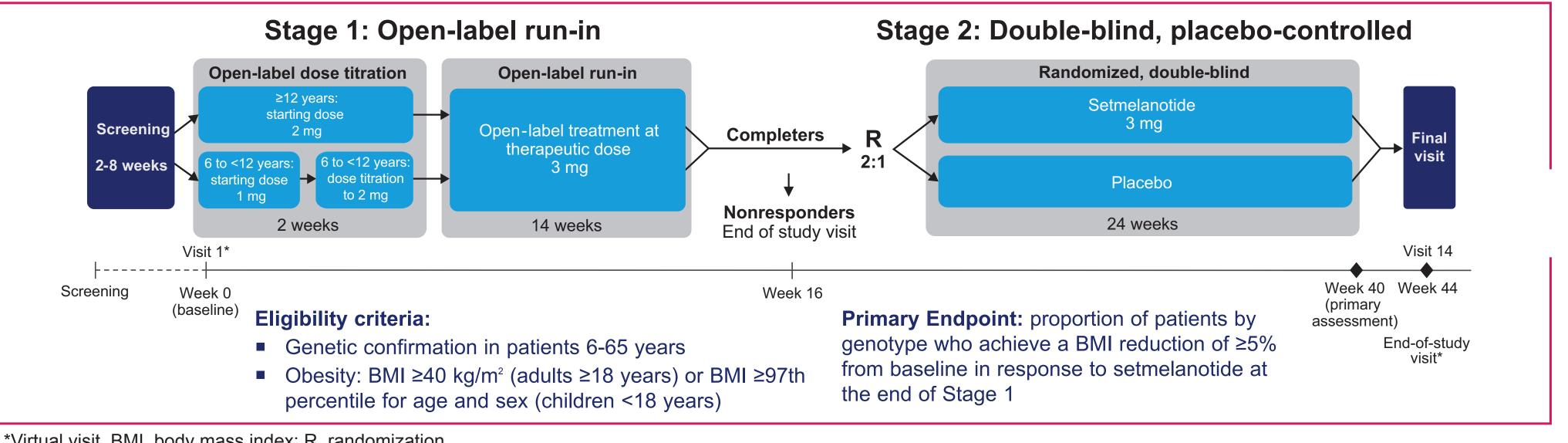
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Figure 1. Genes under study in the DAYBREAK Trial. 12



EPR, leptin receptor; MAGEL2, melanoma antigen gene family member L2; MC3R, melanocortin-3 receptor; MC4R, melanocortin-4 receptor; MECP2, methyl-CpG binding protein i like; SEMA, semaphorin; SIM1, single-minded homolog 1; TBX3, T-Box transcription factor 3; TRPC5, transient receptor potential cation channel subfamily C member 5; TUB, TUB bipartite

Figure 2. DAYBREAK study design.



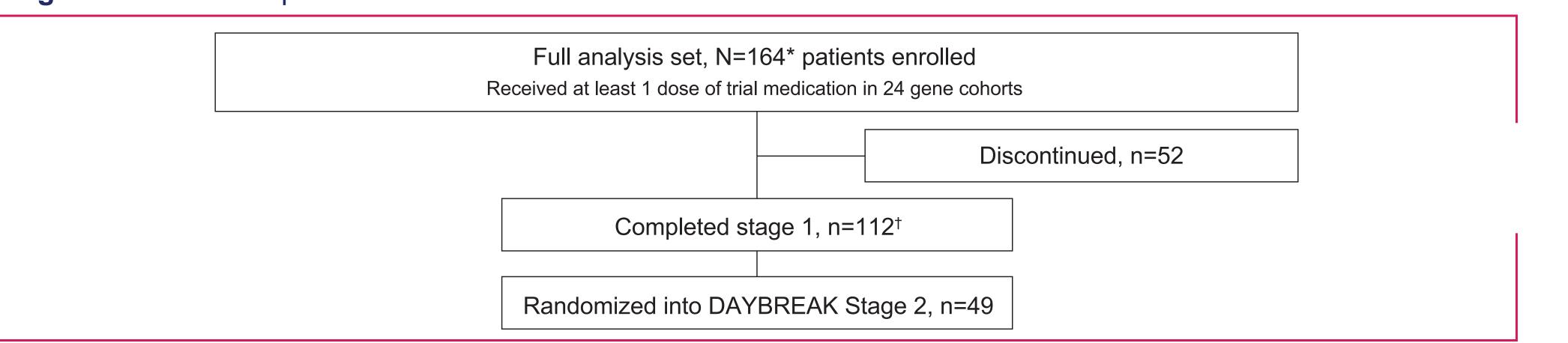
*Virtual visit. BMI, body mass index; R, randomization

Table. Baseline Demographics

Total (N=164) **Parameter** Age, mean (SD) Male, n (%) Female, n (%) BMI at baseline, mean (SD; range; n), kg/m² (age ≥18 years) 48.5 (8.1; 40-74.4; 109) BMI Z score at baseline, mean (SD; n) (age <18 years)

Figure 3. Patient disposition.

BMI, body mass index; SD, standard deviation.



*165 patients consented and enrolled and 1 discontinued before 1 dose. †Includes 12 discontinued patients who withdrew prior to week 16 but had their end-of-study visit within 2 weeks of week 16: their data are included in completer analysis.

Results

Patient disposition and baseline characteristics

- 164 individuals were enrolled (Figure 3); 100 patients who completed Stage 1 and 12 patients who discontinued treatment within a prespecified 2 weeks before the end of Stage 1 were included in the completer analysis (Figure 3)
- Patients were divided into 15 gene cohorts. Of 7 cohorts with ≥5 patients, 6 (SEMA3[A-G], PLXNA[1-4], PHIP, TBX3, MAGEL2, and SIM1) showed potential setmelanotide efficacy (KSR2 did not) and are discussed further below

Efficacy outcomes

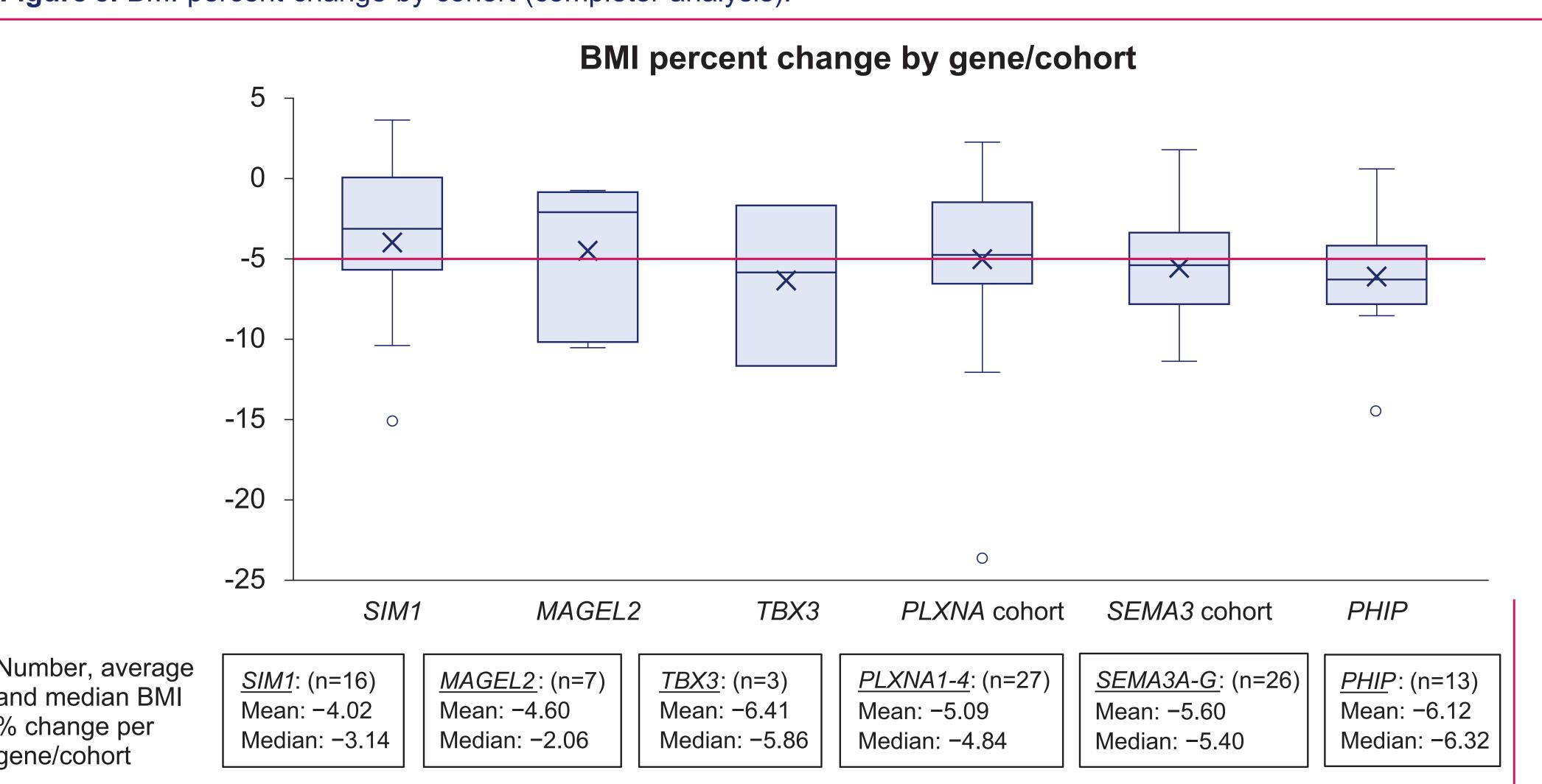
- Response rate was highest in the PHIP cohort (56.3% of the full cohort and 69.2% of completers; Figures 4 and 5)
- ≥1 patient per cohort achieved ≥10% BMI reduction (Figure 6)

Figure 4. Proportion of responders per cohort.

PLXNA	SEMA3	PHIP	TBX3	MAGEL2	SIM1	
30% (12 of 40)	35.6% (16 of 45)	56.3% (9 of 16)	40% (2 of 5)	30% (3 of 10)	25% (5 of 20)	
Patients with ≥5% reduction in BMI at 16 weeks						

BMI, body mass index.

Figure 5. BMI percent change by cohort (completer analysis).



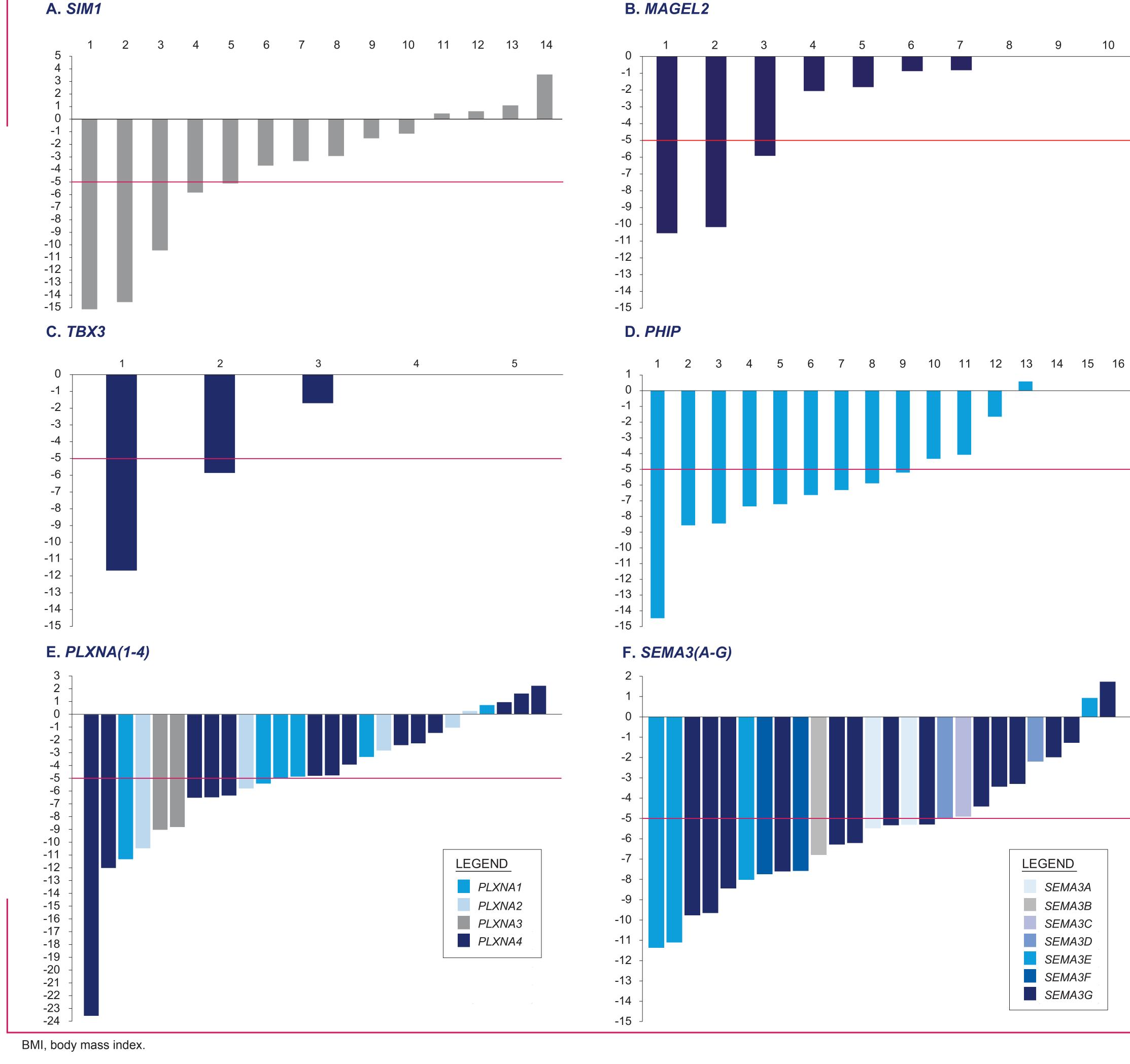
BMI, body mass index.

Ad hoc genetic analysis

- As ~80% of VUS are reclassified to benign or likely benign, VUS inclusion may have contributed to response variability
- An ad hoc analysis showed an increased response rate with updated versus starting ACMG variant classification
- For example, in the SEMA3G cohort, 5 variants were reclassified from VUS or likely pathogenic to likely benign. Excluding these variants from the analysis of those who completed Stage 1 would result in a shift in response rate from 8/14 or 57% to 7/9

- Setmelanotide was well tolerated with no new safety concerns
- The most common adverse events (incidence >20%) were skin hyperpigmentation, injection site reactions, nausea, melanocytic nevus, headache, and vomiting

Figure 6. Individual percent BMI change from baseline to 16 weeks within cohorts.



- Overall, 49 responders across 6 gene cohorts were randomized into Stage 2

Conclusions

- DAYBREAK Stage 1 identified 6 additional genes or gene families within the MC4R pathway that respond to setmelanotide MC4R agonist therapy
- There was variable response within cohorts, with at least 1 individual displaying >10% BMI reduction within each of these 6 cohorts Within-group differences in response may be partially reflective of genetic burden as well as nongenetic factors
- An ad hoc analysis showed an increased response rate with updated versus initial ACMG variant classification
- Response was associated with predicted variant pathogenicity, allowing for further refinement of patient selection
- Stage 2 of the trial will enable further elucidation of Stage 1 results by demonstrating the response to randomized withdrawal of therapy